

Table Legends:

Supplementary Table 1. Differentially expressed transcripts between insulin treated (T) and insulin deprived (D) type 1 diabetic patients. P values were calculated using paired *t*-tests, and not adjusted for multiple comparison errors. Annotations for each transcript were provided by Affymetrix NetAffx Analysis Center.

Supplementary Table 2. Differentially expressed mitochondrial genes between insulin treated (T) and insulin deprived (D) type 1 diabetic patients. This EXCEL file has multiple data sheets. The data sheet "MITO GENE" lists the 68 mitochondrial genes, which were grouped into 11 functional groups in 11 data sheets. P values were calculated using paired *t*-tests, and not adjusted for multiple comparison errors. Annotations for each transcript were provided by Affymetrix NetAffx Analysis Center. OXPHOS- oxidative phosphorylation; TCA - tricarboxylic acid cycle.

Supplementary Table 3. Differentially expressed pathways by Ingenuity Pathway Analysis (IPA). This EXCEL file has two data sheets that listed the significantly up- and down-regulated pathways in insulin-deprived vs. insulin-treated patients, respectively. P values associated with each pathway were calculated by IPA. Genes were represented by HUGO symbols.

Supplementary Table 1

probe set	T1	T2	T3	T4	T5	T6	T7	T8
214046_at	71.6231	78.4793	69.0236	71.6228	71.3996	61.9447	66.1693	61.9322
240081_at	145.816	133.058	155.18	126.734	137.149	130.863	157.818	127.17
227644_at	132.603	132.984	144.789	127.445	134.055	115.207	141.926	126.212
233926_at	13.1944	14.7052	12.8407	17.9612	20.5816	21.2891	17.7716	19.2921
203900_at	113.539	110.389	116.157	123.636	109.456	120.694	136.221	141.172
240005_at	104.18	99.029	102.556	103.292	113.72	101.343	100.952	109.203
219674_s	213.709	245.661	224.924	216.232	197.479	178.472	161.245	183.982
208163_s	189.431	165.864	191.09	180.08	206.643	194.894	197.991	191.252
223999_at	108.548	94.3448	109.847	103.064	109.493	102.445	105.859	103.434
226729_at	136.196	142.109	154.438	145.668	163.991	149.435	164.251	151.957
237355_at	172.322	181.409	188.252	152.167	202.369	186.77	165.47	190.295
203176_s	184.774	237.473	194.103	220.764	195.596	210.557	193.794	238.674
213678_at	183.204	178.73	169.345	160.303	196.975	185.61	174.562	191.96
211592_s	180.121	170.147	207.013	153.487	198.602	184.428	197.474	170.539
202400_s	339.141	282.199	316.555	306.394	356.159	355.371	385.543	423.047
216557_x	116.31	107.042	107.678	96.4333	109.235	99.0346	104.39	93.1137
1554470_s	682.528	580.964	820.094	637.99	700.131	704.517	703.26	805.511
238797_at	94.219	72.2882	77.7071	84.195	90.8287	69.2672	77.1329	70.1294
243473_at	107.266	109.32	114.531	126.583	115.511	110.386	117.067	122.993
1555048_e	159.902	133.231	121.046	132.756	134.261	145.691	158.837	137.249
233268_s	1003.26	1282.11	1109.68	1124.67	1116.56	1120.3	1001.71	1174.74
1554235_e	29.5742	31.4312	41.7629	35.6667	36.04	39.7772	22.5037	31.2674
202857_at	663.362	697.742	582.362	607.92	635.548	604.674	634.915	633.469
1565849_e	353.531	291.661	330.808	334.725	323.914	356.149	388.458	344.145
223264_at	205.853	220.687	204.361	191.505	253.519	208.138	178.321	208.99
233371_at	144.99	136.397	149.226	119.371	150.932	148.048	145.22	142.039
202100_at	416.339	409.15	384.676	396.879	434.582	372.416	370.454	378.108
236867_at	216.737	218.711	226.034	192.639	226.701	219.258	233.487	211.691
240275_at	65.2385	65.4184	65.9767	65.3642	64.1741	76.9124	82.7221	78.761
230334_at	327.983	351.205	337.283	314.302	345.883	344.147	378.167	338.77
211905_s	103.344	87.9378	114.443	95.3616	100.32	86.6301	110.164	95.541
213050_at	372.547	348.876	353.071	384.72	407.605	396.811	496.582	371.784
228109_at	177.077	193.433	182.413	187.926	200.21	185.349	188.82	199.327
212360_at	183.143	181.801	190.196	215.774	207.712	190.516	200.376	221.106
215118_s	73.6616	80.4126	74.5545	65.9221	74.8326	53.4132	71.0354	62.2409
226278_at	234.075	273.808	226.121	197.1	234.384	206.124	221.32	229.6
227485_at	187.693	167.471	208.372	192.408	184.401	172.93	185.523	160.703
235222_x	230.725	237.321	246.859	245.533	243.524	238.347	243.16	237.361
213747_at	114.864	125.786	128.314	125.953	134.59	127.58	109.901	115.544
217555_at	356.851	381.665	367.227	319.28	375.9	358.343	300.781	354.538
1564160_e	34.4118	34.3093	21.5988	24.9987	29.5506	26.9158	24.3544	19.554
200974_at	1032.56	1115.84	1418.62	1325.59	1354.31	1457.09	1814.18	1350.77
212492_s	469.624	466.635	347.025	384.849	321.497	396.326	366.166	413.467
1566163_e	46.8407	44.0604	58.4003	42.7284	51.5333	40.909	42.4723	48.9468
1558722_e	86.5705	86.1568	97.5994	79.958	78.3789	113.749	84.4636	98.2049
217160_at	137.392	127.893	140.377	123.948	148.165	130.997	139.882	122.102
229193_at	95.6922	92.8051	83.5504	99.9889	106.076	92.43	102.536	99.0617
229765_at	63.1642	63.8632	49.6402	66.492	53.9389	47.0332	48.5757	50.8151
239897_at	281.403	261.542	301.286	290.505	253.371	264.076	340.579	309.84
1569341_e	76.8763	72.9679	78.4443	69.6564	72.6625	60.0157	68.4685	72.4005

228042_at	176.663	180.008	189.997	185.444	196.101	168.504	192.516	171.99
227606_s	110.376	97.4865	98.4015	92.9249	91.7825	113.233	114.683	92.7002
228340_at	115.852	107.663	125.753	111.877	117.617	99.786	117.615	100.288
224800_at	370.016	460.503	443.917	471.474	372.481	383.603	423.203	404.898
204260_at	92.9704	94.2702	107.284	97.6237	86.7177	96.2585	103.676	98.0154
222046_at	141.15	129.241	141.709	132.616	136.105	140.686	148.395	131.878
213867_x	3313.17	2897.28	3813.93	3880.54	4092.03	3294.86	4227.83	4716.53
227738_s	239.766	223.705	265.238	221.509	254.092	211.067	237.708	198.88
204728_s	35.8022	33.3791	27.6562	51.6139	42.8451	33.7239	33.0653	31.9961
213252_at	265.438	267.214	251.472	250.065	284.117	267.749	279.563	263.607
1559534_a	41.3217	44.9197	49.5092	44.519	40.614	32.8282	45.4931	33.5663
208443_x	56.0264	51.3488	61.3446	51.5051	57.9798	50.9163	59.6133	48.9198
236996_at	127.809	101.732	117.456	114.738	123.89	116.894	127.264	109.394
205956_x	300.231	252.94	274.167	277.028	264.695	323.696	409.503	335.219
1559936_a	129.808	115.435	136.496	112.324	123.598	104.734	105.316	108.921
237941_at	182.359	168.372	168.918	127.99	187.221	163.951	149.963	164.732
35671_at	748.887	732.048	793.666	764.347	907.6	910.472	1064.11	1010.76
230823_at	164.229	161.835	190.848	165.58	185.381	187.964	211.314	202.819
200801_x	3310.76	2842.31	3877.5	3891.52	4181.88	3316.81	4149.73	4691.63
227581_at	317.764	298.8	324.305	324.412	329.798	324.585	404.672	327.501
1557239_a	19.9656	20.9451	27.0169	23.1325	29.2567	19.868	22.9707	23.776
214858_at	80.3552	88.2488	86.512	79.5999	86.4318	84.6765	84.4436	76.9056
1558747_a	162.552	155.496	129.538	143.726	125.577	152.159	150.261	161.747
214409_at	54.15	56.8152	43.5476	55.1458	53.5537	46.753	58.8559	59.2569
230076_at	91.1782	83.8503	93.4151	87.7773	70.7695	79.1026	83.3633	83.5322
233289_at	46.6145	42.1749	46.8371	42.9368	45.0531	44.6453	38.9733	40.4024
213746_s	274.878	248.567	288.487	259.673	327.323	414	384.833	428.876
239898_x	393.892	355.29	362.383	397.462	358.396	377.772	434.607	389.861
227481_at	109.632	108.334	123.731	97.8815	104.453	110.861	115.545	108.786
217464_at	173.164	213.252	191.902	211.587	189.127	152.767	131.258	138.054
215505_s	146.014	147.017	150.59	159.37	146.578	143.914	198.492	186.044
212871_at	228.999	242.465	239.726	226.724	225.57	197.818	197.644	217.575
231008_at	109.426	105.418	112.771	101.955	110.287	102.502	120.926	99.9273
217182_at	175.412	163.189	173.4	141.352	176.794	162.055	155.751	159.834
1554577_a	530.31	450.407	519.367	533.346	491.614	379.741	437.396	390.333
237889_s	167.424	169.055	151.945	166.536	161.318	151.853	163.041	167.023
1570128_a	284.289	255.247	252.343	282.614	290.276	301.609	323.055	288.545
1557472_a	22.9502	20.9548	28.7857	18.6322	31.5425	18.5873	16.5081	23.1867
215418_at	146.942	153.283	137.898	156.652	166.62	136.427	137.791	134.825
223001_at	392.533	469.567	462.239	511.263	361.882	399.807	397.428	464.908
217150_s	264.03	269.26	235.121	249.637	273.373	271.72	266.716	299.431
223159_s	130.094	134.322	103.721	139.854	140.065	134.895	150.256	134.042
1558748_a	90.1661	104.558	80.535	86.6448	81.002	68.2254	76.5224	71.8129
235204_at	51.2018	52.3039	52.0759	37.1201	49.2144	48.3395	44.422	47.0356
239402_at	103.082	77.0117	89.5466	83.7368	78.4198	79.9127	93.4205	86.3832
241806_at	111.215	107.54	86.1918	95.8154	103.701	88.0306	96.0976	100.401
224594_x	3368.51	2916.4	3848.79	3876.89	4106.43	3337.75	4113.93	4551.17
242129_at	356.322	374.347	357.184	404.332	367.079	489.454	559.755	464.756
1567334_a	119.939	110.065	114.534	134.14	126.213	125.632	149.445	142.29
201772_at	291.31	408.675	467.833	546.931	327.383	463.261	412.697	590.303
203610_s	187.021	183.662	189.826	214.349	202.159	195.572	226.522	198.709
243030_at	158.61	135.59	180.315	137.536	162.937	144.546	152.454	142.086

214644_at	157.013	151.122	152.002	131.13	162.905	151.998	147.052	140.982
209196_at	216.983	176.952	206.329	204.033	211.021	191.332	190.442	197.114
201021_s	771.817	1014.21	931.256	1068.24	777.806	1037.91	791.157	892.422
241765_at	32.9635	34.3258	44.1116	34.0626	31.8393	23.0001	30.9691	20.7606
204140_at	265.367	234.415	234.976	249.374	258.294	238.414	237.535	258.835
204530_s	64.4555	68.9548	83.5519	66.2074	70.2812	59.6435	61.0225	54.4571
1563978_e	85.7361	91.0021	94.0758	91.2541	97.0442	92.7542	96.2874	92.7433
238925_at	127.988	115.175	142.859	123.259	122.271	122.001	157.23	134.326
239971_at	48.5606	42.1766	39.5288	39.3117	45.9811	46.8346	47.4388	40.1134
220544_at	125.367	113.309	135.716	121.595	129.327	115.492	131.122	123.766
1562747_e	80.2745	64.4711	69.1653	68.0333	66.777	81.8039	74.2713	73.3714
201261_x	247.556	261.725	275.39	255.073	272.824	278.695	305.7	354.138
236243_at	199.169	186.782	220.235	173.536	218.079	176.438	176.484	159.22
1555636_e	77.0948	80.4829	86.7438	80.8506	86.6567	62.8017	61.4066	65.5082
242347_at	58.6784	46.2481	41.1512	55.4297	47.5561	42.2967	38.8112	50.2719
233295_at	46.9357	30.342	34.961	36.2721	42.8512	37.9946	41.542	35.4659
1560285_e	116.696	103.782	142.052	111.597	124.207	110.006	143.178	112.891
230838_s	69.0202	81.998	84.7885	78.9582	82.127	92.6628	98.5843	74.8491
203005_at	461.995	438.805	454.828	428.444	442.661	422.235	473.435	385.194
208847_s	1108.59	937.767	826.466	877.74	895.431	954.741	800.786	988.612
235701_at	228.608	221.433	201.523	215.234	226.06	193.438	233.225	201.24
230876_at	90.5443	73.274	73.5448	65.2934	74.2621	68.9706	66.8975	65.932
204264_at	369.843	525.631	333.512	361.073	269.403	321.676	289.511	322.355
215104_at	155.534	160.216	162.204	138.793	146.051	146.982	159.364	143.761
229201_at	53.4614	65.9666	61.1256	74.8506	62.7995	63.7265	70.1788	59.69
210802_s	169.188	170.158	172.736	164.644	201.947	211.697	208.713	211.652
1562368_e	111.82	102.316	117.56	96.2551	115.309	94.2326	122.669	94.0612
238568_s	123.722	107.865	144.923	125.084	112.719	115.419	125.577	104.089
236823_at	81.5001	74.9799	77.1173	85.6623	71.8105	78.1733	82.2485	86.3395
1566767_e	193.873	184.272	228.109	184.74	193.17	221.582	294.081	224.393
204096_s	185.899	212.701	202.796	194.987	199.019	200.064	201.094	195.468
206819_at	84.1403	97.4718	94.7187	98.6713	93.4942	119.244	117.518	103.133
241635_at	99.992	89.837	99.3301	90.3518	101.831	84.1891	88.0212	71.6324
222381_at	135.312	137.694	155.295	109.037	139.293	118.726	132.166	124.136
241943_at	205.012	169.246	197.174	215.032	198.262	199.362	230.309	193.937
209830_s	158.454	173.105	189.456	154.272	178.219	179.919	173.068	190.031
220838_at	238.709	228.67	265.619	203.787	258.06	222.047	257.259	240.442
213290_at	306.041	296.6	255.31	249.795	295.135	293.834	262.218	287.373
221907_at	316.254	306.463	309.815	293.006	321.45	311.046	313.696	293.791
219981_x	171.24	184.791	169.654	184.759	156.49	138.726	158.862	146.241
1553518_e	169.643	165.147	159.202	169.269	185.682	153.983	173.479	148.96
1557012_e	19.5679	17.7262	24.0258	20.7616	17.3715	12.3279	15.6697	9.6287
215399_s	311.813	291.714	310.251	314.115	332.053	362.623	328.305	348.721
212418_at	314.625	363.73	358.937	326.798	371.673	340.017	267.504	315.239
215602_at	84.2539	75.6783	79.0841	79.5704	75.4227	88.1234	86.4184	86.1714
1562038_e	33.655	34.2652	31.8555	30.1896	39.1192	39.3074	30.8879	34.0214
226376_at	222.309	225.045	252.27	211.224	228.858	233.658	235.553	230.356
235579_at	328.03	351.222	347.76	296.676	348.884	340.742	308.771	347.292
235829_at	146.986	124.683	145.117	105.397	121.953	95.5107	128.493	114.63
204836_at	119.102	141.406	120.799	109.413	116.15	115.43	133.83	122.978
209710_at	270.841	233.393	257.894	212.542	242.775	266.904	263.238	253.285
219577_s	195.681	155.299	218.711	177.188	188.789	170.702	194.833	164.053

225258_at	119.259	120.729	114.123	128.52	129.406	115.579	127.412	116.888
210263_at	146.051	121.969	160.979	145.715	154.905	130.607	155.633	122.425
240829_at	22.6745	23.7243	24.391	12.6683	24.1985	15.5341	12.3811	19.152
203207_s_	177.407	215.78	192.181	165.201	176.388	175.054	161.658	212.448
244286_at	120.139	144.872	123.903	151.739	119.169	117.576	121.371	119.336
230136_at	202.66	144.925	179.114	193.386	189.621	154.229	193.632	168.409
243713_at	79.4224	65.8347	77.6408	83.1849	62.9954	93.5055	88.3503	76.2128
212163_at	291.542	345.001	230.66	403.053	222.686	202.028	186.573	243.266
231161_x_	337.052	310.85	343.894	298.753	376.68	338.731	360.418	322.936
1566557_a	50.2115	46.317	50.5024	55.1779	48.2971	44.3882	44.302	47.9268
214395_x_	352.98	441.845	398.186	414.132	297.94	273.718	297.53	327.826
211778_s_	177.34	169.15	150.463	165.311	164.786	183.712	199.053	185.54
204657_s_	216.719	199.621	209.604	189.772	202.664	198.096	215.948	213.271
242175_at	20.1873	18.427	21.1821	21.1271	17.1605	12.857	25.7657	16.236
221401_at	96.8067	99.4653	115.532	94.3692	103.676	98.2931	100.873	107.467
240138_at	84.6187	70.519	67.4261	69.3831	78.4373	72.5698	78.285	64.9609
241831_at	194.766	203.338	209.519	182.936	208.905	208.11	207.778	209.266
221207_s_	264.873	278.229	265.377	292.393	223.514	237.493	217.406	290.512
233981_at	188.697	178.27	167.211	157.218	201.717	186.367	196.857	200.495
231244_at	153.005	148.799	137.574	147.226	146.078	147.419	153.607	142.929
222441_x_	356.263	317.574	342.627	389.961	297.951	362.622	336.78	440.975
244308_at	28.9136	20.1586	26.4508	29.0195	25.5954	25.6625	19.4126	23.8709
210328_at	141.151	134.882	123.878	120.825	118.767	113.946	119.858	117.341
209818_s_	373.335	360.658	373.028	359.696	431.727	349.053	398.899	397.07
1552731_a	477.874	465.251	583.642	539.435	519.949	536.831	548.206	614.18
43934_at	331.179	305.191	329.023	358.21	325.456	346.157	388.411	369.139
239423_at	51.5602	56.9295	51.2361	54.1488	52.3346	54.5979	53.2873	50.5902
243906_at	171.383	166.037	193.121	154.527	191.103	157.829	164.035	157.388
1569257_a	31.4962	22.2895	20.6283	21.4304	26.1839	23.7611	20.4748	25.5541
202523_s_	270.183	254.428	287.182	257.317	266.234	284.015	277.934	257.358
241843_at	96.5876	103.834	93.4317	90.8849	102.324	97.7346	99.8988	102.999
201408_at	2614.25	2940.95	3316.61	2251.68	2240.91	2635.35	2286.62	2758.68
218972_at	163.354	191.092	147.589	172.897	150.744	148.457	144.828	162.675
213736_at	835.674	814.122	839.347	675.115	603.134	599.902	718.929	675.549
241102_at	235.364	200.597	220.379	225.552	218.162	210.48	229.044	188.342
235506_at	98.2333	94.3502	99.7497	94.033	107.627	88.9482	119.634	87.2676
238191_at	1240.59	1362.22	1286.13	1075.1	971.558	967.104	1029.68	951.507
241165_at	118.149	99.4793	130.328	93.3225	115.88	98.1591	125.516	99.866
213815_x_	211.949	194.781	205.528	218.96	203.669	209.679	227.086	211.938
1560995_s	98.3956	100.676	86.5231	86.0479	99.3312	95.7567	104.338	89.2098
236325_at	84.1699	74.5729	93.7913	92.1521	85.5049	69.336	58.6695	74.4263
205848_at	88.4602	125.405	134.156	102.749	94.3545	97.1692	97.4141	83.4704
221865_at	113.907	117.229	103.039	106.606	98.2827	103.85	116.805	110.053
240616_at	217.629	196.148	226.842	175.302	198.875	215.572	224.098	203.255
201651_s_	635.492	712.842	459.89	593.015	610.243	578.569	594.797	506.124
237808_at	39.3257	35.3608	40.8228	36.1922	41.1627	41.0718	31.9635	34.6089
235674_at	302.024	344.619	326.488	308.937	309.921	291.529	266.608	282.046
229271_x_	17.5659	16.0498	20.6556	16.4331	24.3942	18.1583	20.1594	15.5377
235616_at	237.942	182.378	230.853	202.261	210.31	210.562	231.171	188.65
239886_at	115.132	124.232	125.557	121.414	124.958	106.853	129.936	120.556
222643_s_	128.283	120.202	142.98	130.613	139.725	129.658	170.592	147.842
204606_at	316.051	285.288	322.899	267.615	309.989	313.761	301.552	295.999

1552975_x	39.3023	32.8757	49.5282	40.1034	51.2432	35.7767	38.2173	31.4618
208779_x_	555.46	489.725	461.347	495.912	475.65	514.813	537.623	486.078
200859_x_	345.618	327.092	385.555	316.352	412.732	497.833	487.486	489.765
204045_at	753.864	903.848	951.689	1160.56	884.504	665.591	763.173	894.37
239496_at	138.179	135.765	141.787	111.907	127.576	128.593	131.59	134.906
230514_s_	124.987	122.443	150.827	128.292	102.572	121.304	127.973	104.177
231889_at	68.696	63.2481	77.4897	67.0292	67.3072	65.0797	70.4609	72.8601
217026_at	46.2796	43.6313	45.189	41.297	44.0137	37.6688	33.5791	37.5773
203599_s_	497.933	598.819	591.282	475.452	481.29	443.69	468.487	541.867
1562250_a	19.2223	9.73875	14.2925	11.5404	8.54951	8.44762	13.9105	9.32626
208696_at	1442.97	1506.44	1500.97	1588.65	1282.02	1270.07	1210.66	1541.49
208738_x_	3461.27	3820.8	3539.41	3658.8	3664.67	3113.92	3241.22	3471.2
204721_s_	59.5357	55.2554	56.5647	57.0112	82.7512	61.3199	49.57	48.8912
200795_at	3324.96	3547.65	3193.77	3165.06	3131.85	2868.1	2812.08	2910.83
225205_at	229.619	217.988	212.171	222.664	250.52	200.124	210.86	203.729
230779_at	196.568	250.611	266.76	260.742	201.691	223.138	233.069	273.795
243118_at	147.957	146.037	151.829	124.497	156.891	150.244	132.598	146.929
244622_at	179.38	181.725	174.726	145.383	177.558	163.037	164.794	166.068
213716_s_	172.559	166.924	183.019	162.596	182.234	170.621	180.191	184.275
222070_at	216.325	204.395	211.932	199.372	207.007	201.384	213.469	210.504
203607_at	119.063	131.498	114.184	123.986	90.9065	88.2917	115.012	105.196
225150_s_	112.479	108.496	118.857	105.546	109.454	89.8225	103.349	107.896
238169_at	71.9019	76.6683	91.744	69.2326	69.2707	76.9154	78.3546	69.7769
1560817_a	234.621	238.609	241.021	202.943	280.562	273.125	295.202	295.081
203415_at	316.707	346.013	303.665	340.262	295.992	320.36	373.704	384.489
205998_x_	440.976	409.43	421.325	454.338	418.592	372.103	427.462	396.728
204256_at	37.2525	32.061	43.2595	38.8453	42.9467	38.2268	31.2337	32.986
232988_at	250.323	210.96	243.684	173.41	231.506	206.584	216.508	206.676
209320_at	208.462	200.956	204.877	180.117	205.729	181.258	196.442	185.526
243814_at	85.4924	85.385	77.2554	84.7254	71.4471	63.6259	58.2177	62.3753
242248_at	42.1755	41.9835	34.1298	32.6877	41.1863	40.3152	34.643	46.8592
231997_at	123.812	132.163	133.265	139.564	125.288	143.441	159.732	133.87
1555429_a	149.003	148.884	154.883	161.767	134.742	167.162	171.782	161.558
1562249_e	11.5782	14.0257	13.2784	8.77013	16.6404	12.9659	9.05472	8.46612
1568868_e	62.9956	59.431	54.7429	51.2859	50.3053	35.9996	53.6259	43.2853
235593_at	93.4662	80.0712	86.3507	103.031	90.4353	76.7679	78.5794	78.603
204243_at	266.553	326.575	271.505	298.408	269.795	276.314	242.569	243.69
1562491_a	40.868	44.0079	36.5317	40.6143	31.5178	38.3963	45.846	30.7121
213730_x_	419.733	427.146	444.082	389.569	450.956	444.474	493.641	465.014
241931_at	169.717	155.698	155.495	147.206	164.296	159.72	153.786	138.461
1559617_a	64.5166	48.0576	58.9407	58.4483	58.9907	59.0857	53.8419	50.2432
229866_at	150.423	175.191	155.117	180.362	163.923	203.467	197.7	199.796
1554393_a	156.551	182.265	164.972	184.913	165.496	179.854	204.607	184.516
204910_s_	145.792	146.789	146.749	175.768	139.395	164.39	153.448	159.104
210375_at	25.015	31.2201	29.8398	27.7776	22.3128	30.8282	27.396	27.7972
225548_at	234.86	213.937	221.186	211.885	311.457	275.468	265.254	264.591
1561557_e	406.054	382.73	443.871	422.714	422.365	405.999	409.687	392.529
1553547_e	61.3631	60.9532	64.8898	62.3104	71.566	54.5233	63.7929	59.6442
237109_at	214.802	195.021	237.744	203.307	229.652	214.488	226.406	222.308
236332_at	191.161	174.627	178.998	195.451	175.689	177.325	198.631	175.292
35846_at	592.299	535.306	598.002	627.067	607.152	608.875	707.115	652.987
1567704_a	100.826	77.9432	88.4599	96.8915	90.4885	96.1408	98.882	96.5278

244465_at	98.9233	94.573	118.514	118.977	108.189	115.228	117.554	100.592
228955_at	149.535	158.617	154.558	155.551	164.11	157.206	144.464	161.185
241633_x	256.683	241.214	277.429	219.701	270.158	253.206	260.245	246.629
236067_at	174.185	196.975	190.36	175.609	187.351	165.601	192.387	163.9
211091_s	64.3315	47.8332	68.8021	56.9101	66.307	54.4117	64.8774	66.8635
1555235_s	97.7121	104.621	103.261	112.262	107.303	103.686	92.7725	92.8724
234434_at	86.8895	73.4032	102.199	73.2318	83.9158	59.7337	86.9013	64.8004
228183_s	1381.15	1332.59	1444.8	1146.32	1122.78	1223.74	1436.5	1109.55
243174_at	17.2504	16.7835	9.23313	21.5863	21.4957	17.2953	26.4312	24.4939
200044_at	456.462	471.013	480.228	483.568	506.809	480.247	419.278	491.248
216276_s	51.7949	69.8798	70.011	55.0785	72.7525	60.2951	60.8342	60.057
32625_at	444.374	449.451	448.881	465.49	463.452	524.609	536.866	517.119
234110_at	87.6301	112.566	92.5971	86.2877	95.9791	85.2401	69.2978	67.1253
227659_at	130.665	132.785	122.153	133.249	139.125	119.642	110.673	109.615
240314_at	127.216	126.558	131.197	134.945	115.122	124.858	149.326	132.699
1566823_e	288.046	304.317	285.085	341.823	292.476	339.722	407.159	325.83
201792_at	150.746	136.309	151.489	154.233	143.546	166.692	173.362	160.622
220620_at	88.5173	90.457	88.8758	81.3971	93.7746	93.722	90.4004	83.657
208737_at	1680.24	1923.65	1792.15	1963.05	1687.27	1672.35	1902.5	1778.5
205675_at	55.6391	71.2043	51.4654	56.2375	49.2315	56.7259	68.441	51.2457
225280_x	264.434	260.828	266.082	237.016	258.478	256.353	265.634	256.8
210172_at	69.9849	82.8789	61.8745	76.2419	58.3987	68.3148	67.8169	83.3037
222758_s	129.732	125.455	140.573	117.751	139.96	124.353	130.321	127.175
213919_at	220.714	225.722	272.838	225.273	255.822	243.863	266.75	226.242
65635_at	2324.87	1871.77	2121.35	2168.43	2600.22	2504.28	3032.33	2722.3
241435_at	212.206	198.356	224.575	179.295	224.881	196.572	226.079	187.97
212210_at	136.692	123.805	148.018	149.881	149.916	141.707	156.271	155.144
225555_x	232.609	237.08	234.859	210.397	235.474	207.755	206.79	205.418
236062_at	45.6689	47.894	48.1557	46.2548	39.8681	39.3996	50.615	51.1756
227597_at	88.5596	85.9952	88.7911	84.9124	71.2263	80.2682	86.3419	92.5302
1555718_x	71.1244	53.1279	74.6775	57.2362	62.9113	55.4114	81.6137	57.426
1553792_e	12.4938	9.44642	12.8535	18.3889	15.7868	19.4251	9.76521	18.5684
1555634_e	74.1765	68.0132	84.4313	76.2591	80.5719	67.1457	82.1352	74.3725
228743_at	256.51	246.47	241.083	224.024	161.219	228.591	299.152	240.796
1570350_e	103.31	89.7041	89.9343	103.937	112.116	103.606	130.279	107.763
242454_at	402.801	314.198	331.867	307.384	326.429	285.6	318.164	267.758
243652_at	96.0384	93.3786	125.948	86.9478	120.995	82.6802	79.274	91.6712
205302_at	93.6733	98.7309	94.8422	110.06	95.0691	87.3444	114.885	122.018
214021_x	35.0006	34.228	27.196	36.5259	24.9908	33.9742	32.6487	42.9617
1557807_e	171.197	183.852	156.704	154.515	150.195	144.795	162.634	133.616
233130_at	187.72	187.313	188.454	178.867	185.114	182.57	211.541	171.073
211709_s	156.365	171.131	152.925	129.785	167.707	156.855	127.727	141.153
211478_s	51.5716	42.1563	53.146	53.7322	51.5456	53.9519	56.5953	52.1858
1562316_e	49.8167	42.5825	50.1566	41.4353	44.2921	44.8343	56.6542	43.7626
237272_at	86.7196	58.596	77.2841	83.5273	78.2672	85.1353	86.1803	90.593
230057_at	227.885	239.557	234.83	211.176	249.936	255.94	247.502	233.693
236916_at	143.406	160.582	146.947	148.181	152.589	138.842	144.146	140.775
214073_at	134.039	125.776	130.912	138.76	133.598	145.208	152.344	132.434
222726_s	354.534	375.346	386.509	404.928	305.567	319.263	337.506	416.666
1555289_e	220.013	193.581	197.499	207.531	224.556	212.375	233.535	230.193
239949_at	146.459	166.229	144.154	199.383	159.241	164.179	196.918	178.018
240941_at	113.624	77.4315	119.885	90.7825	110.245	77.3484	96.6757	73.6398

1557067_s	90.1416	86.5046	84.6762	86.1075	86.1056	92.9138	92.4607	116.082
224659_at	603.401	533.749	589.095	485.896	567.609	651.519	773.404	612.735
238917_s_	198.511	173.93	185.754	208.401	196.214	179.116	218.262	177.355
214638_s_	92.7237	99.6769	102.438	123.417	108.251	115.594	131.36	148.101
1553750_a	53.7369	52.02	45.4493	41.1273	56.6912	47.5313	41.855	46.5791
234924_s_	321.979	305.879	312.317	311.592	360.917	342.885	350.977	335.707
1560322_a	153.877	127.985	134.012	155.767	135.207	165.789	175.194	157.342
211736_at	42.8581	28.2115	46.6872	41.8455	42.3466	38.1881	47.2647	46.6549
216036_x_	1422.76	1272.78	1254.6	1227.86	1337.6	1337.04	1645.53	1457.72
213632_at	201.877	190.765	184.317	175.051	174.442	186.909	204.448	200.878
234770_at	239.222	206.924	202.02	237.588	240.99	200.78	225.477	212.871
218045_x_	257.334	234.269	268.836	219.345	262.665	243.012	230.679	258.125
234038_at	46.7713	38.3457	46.1726	37.4677	41.7286	42.6334	42.2819	42.9701
231369_at	59.1696	60.8211	62.8015	57.7719	62.4981	58.1981	52.0913	62.0778
208417_at	255.607	236.823	229.297	249.718	267.954	231.334	288.687	285.067
1563728_a	85.0945	81.4226	76.0517	94.5884	74.8588	75.735	74.1838	77.0369
222145_at	92.4502	93.7078	95.8731	94.9708	84.0787	95.0135	99.1134	102.755
1559956_a	7.87092	5.19645	9.60401	11.4377	13.9121	5.74988	6.5308	6.03243
218985_at	436.388	348.501	356.061	351.043	425.68	398.592	453.289	408.496
203055_s_	597.159	558.472	649.499	475.528	519.27	601.551	665.049	531.308
231191_at	269.479	256.06	325.587	332.265	358.005	312.17	372.425	306.548
230125_at	174.842	180.031	202.626	165.108	204.11	192.981	179.109	178.678
224616_at	1423.66	1332.66	1308.5	1157.56	1039.69	891.852	840.985	1052.64
221679_s_	146.072	162.232	171.162	134.901	156.791	153.119	148.857	160.354
204451_at	271.23	323.432	292.665	303.024	309.376	297.903	290.763	274.06
1553123_a	66.1952	70.7411	83.8991	60.4248	72.7997	62.312	63.2502	56.6393
229437_at	59.13	57.7602	56.6495	46.3864	49.7787	37.4589	51.4347	42.928
1553243_a	194.243	196.263	205.785	211.447	250.564	208.846	205.324	228.009
200825_s_	335.167	306.633	323.191	309.749	299.484	289.383	283.554	335.607
243459_x_	237.724	205.6	301.039	238.572	228.11	215.255	250.529	212.276
217670_at	52.7655	50.2023	55.4915	41.8146	56.0493	57.1151	52.5618	51.4858
1561451_a	44.8125	48.7821	39.7145	44.7145	49.6974	37.6843	34.5396	43.8277
1563947_a	343.685	382.871	301.48	309.12	360.421	277.702	258.496	261.036
217802_s_	3162.45	3565.34	3194.88	3453.2	3223.35	2342.19	2760.47	2925.36
208913_at	415.555	492.441	429.161	454.63	437.435	347.615	416.577	387.298
224232_s_	130.921	115.928	132.172	128.394	124.866	124.885	128.269	142.937
215564_at	80.9063	102.37	72.4315	64.7783	81.5516	66.0884	57.9176	61.8061
1557353_a	238.963	238.461	232.943	242.706	244.456	265.772	291.205	246.67
209640_at	68.403	57.489	74.1602	56.602	50.3798	57.6029	72.3779	63.3412
222502_s_	129.177	135.783	156.479	141.641	158.161	272.387	247.395	270.636
221996_s_	179.242	148.474	148.686	152.094	140.931	160.648	193.35	149.4
230241_at	97.7633	92.6373	94.6397	81.8532	87.2587	89.1615	80.0386	81.9897
202740_at	621.53	535.311	580.245	523.867	611.648	639.878	739.334	686.129
211978_x_	1811.93	2089.29	1561.22	2691.03	2068.39	1776.77	1822.86	2131.96
239815_at	186.351	173.823	194.986	173.139	192.084	183.428	191.005	186.112
235694_at	132.896	132.692	121.953	107.26	127.242	115.078	144.842	123.873
223984_s_	61.1701	62.5562	63.1756	63.8303	48.9403	63.9985	66.1994	68.2742
202210_x_	795.126	678.613	754.722	736.742	923.119	860.304	978.718	942.581
207122_x_	314.899	273.379	318.479	307.642	285.472	284.463	334.562	323.055
228565_at	141.212	125.505	138.48	114.039	131.258	122.424	121.538	122.488
201853_s_	326.122	319.123	322.054	325.136	324.292	342.512	381.755	348.447
1560615_a	249.424	204.669	195.553	205.025	196.071	201.718	210.183	206.407

225789_at	601.944	548.753	572.861	560.966	694.051	630.073	836.156	697.373
1560776_e	68.2378	81.3745	71.0907	66.3072	75.1461	57.7578	65.9129	54.3882
211711_s	80.3741	64.5738	82.8656	93.7359	57.0163	72.9221	67.4982	66.7406
221299_at	148.23	135.184	132.181	147.611	149.781	145.849	160.943	155.416
228815_s	145.098	135.722	157.43	122.2	164.904	135.004	129.647	140.058
212926_at	231.34	276.187	213.103	303.103	215.703	212.31	220.3	213.536
218693_at	267.184	219.098	294.72	278.674	265.361	260.863	294.798	263.241
216464_x	96.705	93.677	124.625	103.672	101.874	112.211	112.526	102.454
203318_s	720.563	815.181	728.153	756.711	820.962	577.275	575.999	635.171
217641_at	181.473	168.969	181.889	140.692	182.581	175.738	171.663	169.221
209940_at	211.188	169.995	197.324	175.977	190.642	178.777	187.663	181.247
235842_at	122.247	111.69	129.39	120.826	114.741	108.508	122.47	115.098
1555578_e	210.937	216.555	182.378	183.823	188.072	158.612	152.445	171.096
243735_at	87.6807	97.4975	87.8483	91.4021	95.7055	110.79	88.5957	104.227
232202_at	70.3743	84.3034	81.657	73.5062	82.5608	64.2319	74.1055	68.5514
241426_at	107.678	125.463	111.517	104.202	121.229	105.814	105.333	99.7505
235902_at	146.411	156.976	167.001	126.188	157.368	149.007	134.673	139.018
1555913_e	135.099	159.497	114.632	141.939	127.175	120.647	116.51	139.808
215265_at	177.844	161	171.779	151.196	156.732	165.884	172.658	178.923
226373_at	282.254	248.692	259.105	243.109	244.765	244.631	259.048	248.839
1558394_s	138.165	123.923	136.236	130.157	115.349	136.443	176.528	135.999
1565641_e	89.8686	104.3	109.342	87.2972	95.3993	83.8518	93.6809	90.3058
229857_s	55.0318	106.035	135.639	165.797	50.9727	73.4518	128.299	116.999
208177_at	182.06	175.99	193.425	154.106	188.948	175.557	186.392	178.184
242488_at	89.457	87.289	81.4706	83.5865	74.5532	90.0982	97.2854	93.3255
218360_at	220.68	214.012	207.411	244.648	196.605	203.121	211.836	216.538
209396_s	50.9207	39.393	47.9865	44.7852	43.0203	28.1563	42.5439	36.3813
206953_s	231.232	215.174	242.167	235.642	234.714	266.231	275.551	288.673
226210_s	137.788	130.654	168.771	117.768	141.704	115.032	128.248	122.39
223626_x	477.477	549.102	460.934	469.371	467.748	408.431	404.148	449.256
1562648_e	29.5007	37.4079	34.0332	35.441	36.9634	39.607	29.3473	35.1885
217685_at	91.5532	73.3881	99.3554	83.9775	85.6905	68.4654	86.1092	71.3502
206961_s	168.636	162.005	204.033	169.327	188.816	168.655	213.775	172.858
1007_s_at	925.321	833.426	851.446	943.532	930.563	1007.71	1070.07	1021.07
200632_s	782.285	775.009	752.145	771.344	767.527	906.552	995.924	881.011
238053_at	241.788	201.856	199.992	206.858	196.082	207.661	222.575	197.686
208582_s	45.6316	52.2388	54.8743	45.3573	54.3091	52.9274	57.4899	52.7731
220536_at	212.832	192.9	237.035	192.745	226.201	191.163	236.313	186.046
218550_s	1337.01	1470.26	1595.37	1438.29	1706.69	1321.18	1524.04	1753.49
220416_at	43.8457	53.7405	46.4574	51.1885	38.6131	39.9159	44.1763	47.975
230190_at	88.4697	83.9037	93.9654	90.112	86.607	92.0879	94.907	97.0145
226238_at	528.597	536.483	504.808	477.054	356.517	382.211	408.708	407.432
236461_at	193.467	169.103	164.932	143.255	186.575	168.33	170.323	185.143
1569289_e	122.105	126.049	110.727	128.879	146.807	140.413	107.484	123.109
240255_at	236.625	202.942	206.047	201.688	218.035	204.971	224.323	222.532
241674_s	15.8768	15.0056	22.585	11.5158	25.4735	13.3046	15.7576	10.0486
1557585_e	190.473	142.502	174.617	180.457	196.507	180.407	215.378	200.652
221992_at	340.261	305.056	324.994	316.825	349.903	311.678	391.925	349.512
216284_at	130.657	104.913	142.956	116.767	115.348	117.469	135.017	115.966
222061_at	104.88	118.649	102.106	119.979	92.9308	98.7977	97.6154	100.846
227590_at	241.744	207.232	221.58	242.287	243.347	228.041	252.673	240.259
242864_at	151.405	156.086	151.711	128.195	140.803	127.621	131.161	129.675

1559780_e	79.0168	114.691	103.273	124.308	108.991	122.839	162.919	144.99
1569348_e	183.044	192.839	182.642	161.849	200.149	165.619	166.255	199.88
243557_at	21.1787	32.0486	31.6059	28.8739	24.8005	25.8868	27.468	23.0544
233465_at	61.5117	47.0798	64.0777	42.4278	55.7769	53.1164	40.1314	46.3084
206197_at	64.3879	70.9976	71.0138	83.9151	69.906	70.5811	64.1351	62.0171
243135_x_	127.98	102.357	148.842	111.108	125.678	98.2212	128.807	98.8363
205717_x_	470.495	467.587	489.088	518.209	563.872	543.733	566.813	620.916
218193_s_	137.669	130.143	133.719	148.477	128.12	152.271	173.58	179.658
209280_at	313.612	310.56	337.858	288.994	350.362	350.718	378.604	343.366
221198_at	137.769	118.37	158.439	112.852	155	124.277	121.239	129.679
234103_at	130.09	140.822	129.396	142.162	147.606	130.07	141.067	124.641
212661_x_	1960.47	2318.02	1723.51	2981.06	2240.75	1943.2	1971.24	2349.38
201058_s_	256.329	211.642	294.126	204.278	268.579	333.106	311.688	252.232
215385_at	130.42	115.88	112.684	135.079	111.74	98.7146	113.152	102.717
31826_at	293.705	299.091	288.12	278.702	267.738	256.41	273.794	295.868
1555042_e	111.952	100.284	105.086	110.121	95.9953	102.432	124.651	119.014
235209_at	240.688	214.467	202.693	243.021	292.558	234.541	213.333	216.14
205570_at	201.943	205.232	226.767	235.517	193.001	230.647	224.357	194.111
221264_s_	205.763	223.804	196.601	193.356	204.108	180.186	173.762	175.628
1564338_e	101.02	95.6078	85.9424	100.267	81.3675	82.6009	103.719	88.8047
1554469_e	171.888	146.219	199.446	156.741	188.803	208.699	201.693	219.734
1556831_e	228.363	220.57	184.216	230.571	210	227.017	267.193	254.761
1570355_e	65.0375	52.365	84.1958	60.23	74.4475	56.5452	67.325	58.4153
1552625_e	165.75	152.335	149.768	156.351	171.266	145.694	159.179	145.122
215212_at	56.2031	59.0018	83.9825	80.7102	61.2169	49.7384	61.9563	50.8619
236708_at	105.214	81.5496	109.87	82.9798	108.643	81.7099	103.85	93.8711
1569661_e	7.31325	18.7746	14.8168	15.4768	11.1433	20.0316	20.2733	13.1354
1555853_e	82.1113	74.7498	83.6382	91.5619	86.5042	83.0102	95.3795	85.1558
205694_at	148.395	123.701	177.894	88.3471	106.569	213.54	150.21	180.217
238178_at	36.1178	35.7027	33.4879	42.257	37.9436	45.4093	36.7905	45.7415
203076_s_	464.565	455.313	503.376	517.587	488.389	484.361	603.176	560.618
1566463_e	62.3065	56.1109	55.3394	47.9323	54.1147	43.307	50.9941	44.8784
210886_x_	834.168	468.907	559.368	442.004	594.176	706.173	1028.62	539.59
220593_s_	91.4974	87.089	103.586	87.3585	87.3391	71.6654	91.6277	80.1749
221712_s_	304.404	312.532	279.162	308.681	339.748	320.054	316.4	343.464
214378_at	158.85	211.394	156.13	154.243	181.401	168.565	140.361	148.505
202225_at	450.743	515.973	462.487	552.422	357.419	458.743	343.406	457.827
228575_at	175.244	173.951	171.383	148.355	198.811	154.51	158.832	174.031
240510_at	61.1559	55.4363	48.2216	72.1131	63.0708	61.965	69.7388	67.1735
223915_at	106.968	94.4845	127.876	108.544	92.6302	83.5792	119.005	91.5164
1568777_e	47.9359	62.3937	44.9145	51.891	45.8219	58.267	55.5136	46.7349
201496_x_	170.648	139.715	224.045	185.094	200.902	165.293	226.055	176.277
200785_s_	317.13	357.941	367.131	355.721	427.961	347.632	369.395	371.265
219357_at	156.54	186.886	170.493	189.231	175.181	174.694	159.201	185.211
222623_s_	638.13	567.594	569.373	566.399	534.749	524.754	614.688	546.028
210688_s_	130.782	125.372	130.491	122.22	152.995	141.047	141.063	139.602
221046_s_	1285.46	1325	1313.31	1190.49	1005.53	1098.37	786.417	1070.05
238861_at	138.994	180.319	168.63	174.033	179.876	160.016	152.276	134.096
218309_at	272.04	250.254	315.24	260.19	222.823	223.614	294.395	242.178
1560705_e	206.426	199.621	166.689	197.972	211.873	172.813	141.958	144.858
210185_at	188.069	180.215	187.669	177.693	217.442	208.172	225.669	210.612
1560024_e	357.944	289.944	305.254	279.895	350.911	323.693	374.772	285.545

224888_at	331.877	337.006	340.448	303.099	330.355	302.515	299.235	301.349
216527_at	61.391	51.0908	54.8152	56.9794	66.1924	58.9124	59.7519	61.1619
1570163_a	64.0829	68.3163	59.071	72.4202	58.0452	67.8695	61.1712	73.0632
230981_at	218.33	179.225	212.857	212.565	193.612	205.294	280.104	239.307
230549_at	224.949	211.989	293.022	245.08	249.011	206.871	256.645	247.19
228926_s_	89.7541	100.52	95.6197	100.589	81.0531	106.192	87.32	95.5076
230265_at	283.71	336.1	335.327	295.678	294.475	260.214	286.904	309.968
57715_at	284.72	310.667	304.214	332.166	316.748	313.149	351.021	333.192
228319_at	265.997	235.298	276.988	202.233	258.929	244.14	270.604	256.683
236659_x_	133.037	122.741	136.165	133.673	131.142	132.056	129.188	122.416
1563521_a	172.96	166.033	148.593	163.633	165.569	126.053	124.752	118.074
243799_x_	37.9915	25.253	40.7291	24.2577	28.6666	23.1223	25.1642	15.5621
209157_at	713.72	781.591	931.549	862.388	817.23	815.415	840.738	964.856
220451_s_	234.618	240.399	273.163	228.02	267.092	253.088	274.221	211.551
211658_at	1873.16	1641.25	1606.16	1392.83	1562.12	1309.87	1171.5	1360.45
218051_s_	207.861	181.758	186.331	162.528	156.043	187.585	247.858	203.228
223651_x_	51.8263	67.8081	54.6831	64.8247	49.2159	54.3868	51.7875	60.1981
235466_s_	114.114	100.126	100.024	110.1	106.626	96.3961	97.2021	108.542
207517_at	149.399	135.947	166.803	126.491	163.61	135.716	159.038	148.054
210879_s_	322.248	301.506	307.419	288.996	339.866	303.911	314.951	291.193
227171_at	288.451	271.139	262.976	304.1	270.102	248.387	268.714	288.091
218590_at	264.5	271.503	242.459	256.562	232.172	234.554	223.231	248.279
232604_at	183.935	181.22	168.58	172.539	198.033	185.074	194.12	188.904
231581_at	29.4897	33.6973	20.3695	28.3138	23.3934	22.7341	21.4035	24.105
1566511_a	28.5023	30.7691	26.5515	29.7995	39.6024	35.5791	32.5707	26.68
206078_at	387.01	406.712	558.744	273.804	404.045	372.799	388.333	375.236
201830_s_	238.639	226.349	260.364	240.138	254.135	291.184	252.421	284.319
1570039_a	53.3717	54.7338	59.2606	53.5904	48.5987	50.588	60.1532	46.9718
225917_at	649.241	856.448	741.122	856.767	658.914	538.981	532.409	664.571
1556768_a	168.307	148.576	129.289	168.611	138.257	143.007	165.805	143.568
208837_at	149.637	149.208	155.674	153.871	134.886	125.25	161.502	178.245
217850_at	481.633	589.735	535.391	556.197	444.407	408.198	339.197	503.383
221240_s_	242.944	225.195	225.757	223.404	211.551	203.949	213.17	224.206
242327_x_	278.939	247.383	275.461	270.592	286.431	239.508	244.798	247.639
208727_s_	353.883	711.761	388.449	450.311	761.311	469.44	567.85	522.771
227852_at	545.858	529.393	461.289	385.271	363.684	437.883	399.69	493.955
201293_x_	1745.17	2035.95	1531.78	2710.45	1943.47	1658.65	1734.7	1999.09
203613_s_	4021.3	3783.81	3726.04	3646.5	3296.13	3207.82	3264.81	3277.47
232264_at	96.5822	71.5935	92.3181	84.6658	92.0069	94.3253	89.5249	77.7
1557642_a	40.403	50.0017	35.0102	50.3916	37.2529	35.1063	41.4307	52.013
240634_x_	63.6018	63.3193	64.9193	56.3447	68.2975	56.0665	60.4505	55.4052
1556242_a	109.302	109.075	109.178	102.719	100.767	97.4971	105.089	100.098
209153_s_	224.131	218.447	242.087	198.895	239.654	239.683	203.981	223.273
205323_s_	266.759	264.056	251.808	291.493	251.483	270.566	264.717	305.534
202806_at	281.717	271.287	275.884	290.165	315.02	317.927	349.876	317.83
223254_s_	108.347	108.582	88.9048	105.659	94.7348	106.701	96.3574	108.642
205896_at	181.683	176.338	181.101	164.444	192.972	176.668	208.521	212.979
223695_s_	102.064	82.7602	103.164	87.7839	96.4062	80.4687	99.6435	79.1422
238256_at	163.893	169.228	163.073	167.728	158.097	159.609	153.88	144.661
238727_at	68.2755	80.5564	68.84	97.3981	75.4696	71.7841	85.3018	80.1183
244367_at	42.2109	42.3797	34.1784	35.0814	43.6392	47.5862	42.8556	49.4457
238252_at	23.675	18.5682	18.3119	26.1748	27.1319	27.8436	27.4845	24.4647

244094_at	55.3868	54.5748	52.8461	57.3416	53.0908	32.6193	57.8595	33.1317
214752_x	305.998	285.85	332.629	292.536	340.323	416.97	418.165	417.715
216823_at	81.9204	81.6795	74.3867	86.5254	70.9319	61.7085	66.233	63.5976
203550_s	761.357	652.418	731.771	655.612	767.304	708.76	769.641	753.203
239371_at	125.144	121.633	120.239	100.17	117.1	116.798	122.74	103.955
205919_at	197.144	171.9	187.104	167.326	195.83	175.141	167.179	141.887
1560174_a	80.8692	85.9338	65.4903	80.5182	93.1138	87.2685	69.4645	75.4716
1558301_a	40.7985	44.5768	38.9686	49.2664	38.9646	36.1	41.9355	39.1843
235972_at	133.281	117.75	185.119	146.785	156.461	129.797	181.41	140.703
212223_at	416.331	445.913	448.284	424.444	514.243	515.712	489.833	487.561
241358_at	237.824	234.388	227.541	206.897	222.834	234.518	250.604	249.006
209912_s	131.523	123.991	134.51	127.735	151.436	135.164	131.745	133.379
1553959_a	384.421	398.019	445.607	496.073	409.284	407.442	533.969	479.917
213811_x	299.517	326.829	317.589	322.047	410.227	370.974	425.677	371.927
233695_s	85.5154	80.5227	84.8342	91.6062	83.2573	81.5447	89.9673	75.4889
214724_at	639.654	709.095	634.398	666.54	460.404	563.434	646.54	627.862
241472_at	85.4676	83.1838	108.533	80.4329	94.6068	78.5662	109.365	78.2946
240959_at	30.4178	18.6476	23.0692	29.6785	30.6113	24.3207	25.3817	23.0858
220689_at	124.421	112.926	109.707	116.635	132.984	139.097	116.278	127.086
235388_at	77.6234	90.0629	83.0496	96.7752	79.4517	95.8348	89.9144	92.3161
206662_at	1198.34	2290	1731.75	2132.22	1741.53	1168.39	1117.21	1449.54
240630_at	222.743	209.528	204.66	194.321	220.343	221.912	242.103	237.979
54037_at	77.8412	84.8658	86.7624	84.627	87.9804	64.8957	80.1193	81.9979
214779_s	429.795	353.08	351.186	409.828	355.192	349.927	433.012	442.875
204875_s	56.2342	46.982	70.3585	52.2944	65.1117	58.3569	42.0684	59.8407
201163_s	2236.08	2880.29	3221.12	3268.26	2108.4	2579.92	2643.26	2100.38
1568943_a	77.6716	77.1619	75.0889	81.7138	76.1575	99.3976	85.153	81.3715
221939_at	564.499	621.738	598.854	603.774	572.297	491.634	519.538	573.036
235863_at	320.277	286	363.78	300.41	351.694	279.053	327.017	349.598
227317_at	171.94	183.595	175.701	156.521	120.564	129.815	127.626	127.576
242240_at	146.214	150.894	190.94	150.052	159.759	125.975	168.219	125.445
233416_at	114.644	96.1268	124.633	102.386	114.837	110.451	134.999	105.084
220336_s	39.6477	31.8506	32.5481	39.5229	29.2497	41.6624	35.2477	39.0909
211378_x	1561.31	1906.09	1404.63	2456.33	1660.6	1441.93	1502.46	1738.3
200745_s	419.13	445.331	384.437	497.484	430.197	440.611	429.96	460.694
207505_at	160.651	139.229	117.903	135.843	147.365	127.25	110.141	106.196
204788_s	162.655	151.851	138.884	147.316	151.854	137.485	150.635	156.929
204250_s	113.921	116.238	137.584	125.018	117.245	118.277	122.559	119.653
242629_at	78.05	86.8598	99.1419	89.43	94.6203	74.5576	80.8959	61.673
227025_at	191.578	259.423	211.578	260.029	199.291	181.061	157.022	174.803
219516_at	169.637	161.486	182.871	163.916	168.254	155.791	185.978	172.794
230034_x	189.234	177	162.129	153.965	151.537	167.949	143.867	140.43
243845_at	138.2	128.352	141.105	109.726	143.942	129.176	131.536	127.04
228061_at	301.069	339.837	320.847	285.174	314.04	333.535	304.235	308.876
206781_at	173.353	150.128	205.657	146.275	144.4	142.962	203.78	153.067
239936_at	26.5045	35.5245	28.3321	32.7041	30.3346	32.4507	31.3922	32.9405
212991_at	228.438	212.632	235.942	189.206	228.205	209.314	226.057	196.213
214087_s	14960.9	15751.7	15746	14849.8	15049.2	15022.2	15654.1	14924.5
203087_s	104.006	97.7567	71.8664	106.18	96.6432	107.842	98.0603	110.278
209098_s	52.5356	63.5682	82.6907	66.0364	52.8846	77.8197	84.2417	87.5244
231731_at	12.5716	9.4645	19.2106	22.6296	16.2173	14.265	19.9966	11.9874
217398_x	18972.5	18010.8	19298	19050.8	18929.4	18536.9	18704.3	18727.2

211387_x_	88.0681	86.5124	81.0224	84.4938	93.048	92.9902	83.2884	97.551
210015_s_	140.971	127.43	131.804	149.55	144.161	134.064	132.636	141.051
1559680_e	141.863	140.048	134.188	119.334	135.662	157.769	141.69	124.413
238732_at	18.7265	19.0462	24.8231	20.3512	16.3402	24.972	24.8715	19.1884
1569053_e	28.2744	38.3244	34.8283	32.1604	40.8135	44.6706	38.549	34.9513
227390_at	290.345	300.336	288.86	239.331	312.794	292.276	283.547	276.111
217666_at	69.8644	59.4634	59.2828	72.0798	64.031	77.1775	78.3956	71.6783
232857_at	328.48	385.414	316.381	319.516	208.488	294.177	242.064	332.594
239940_at	180.918	172.773	173.241	146.479	186.861	185.508	170.403	157.314
243708_at	286.481	310.178	304.102	256.969	316.686	299.509	296.095	293.328
1555358_e	96.3655	95.3676	97.9813	93.2982	116.757	100.866	99.9782	120.711
218538_s_	396.187	314.772	398.15	327.337	336.345	314.238	326.209	370.847
206583_at	105.222	135.469	106.501	110.293	100.604	85.3224	86.9957	85.7007
206061_s_	421.258	468.371	456.777	590.622	468.634	413.2	520.979	499.826
202173_s_	948.738	1148.61	1314.66	1176.45	896.031	1050.17	1002.77	1350.04
226205_at	165.457	139.568	166.427	167.831	144.724	135.87	193.284	149.193
207478_at	108.726	89.1467	78.6505	105.187	95.1765	92.8539	87.2725	83.7639
203808_at	103.605	103.454	131.273	115.739	92.2847	103.512	110.183	107.169
220554_at	205.42	189.264	224.327	198.462	213.39	214.973	230.743	188.371
1554850_e	127.069	120.404	124.983	139.082	132.125	134.809	162.362	147.767
222756_s_	137.055	134.845	153.948	125.527	157.908	134.124	148.541	134.363
242067_at	49.3289	44.3484	55.3251	49.8185	46.5525	47.4488	52.048	44.2205
1555571_e	67.0213	64.0677	60.1679	62.2407	54.523	61.5252	41.5971	52.8515
218522_s_	521.634	438.74	589.377	722.598	365.811	501.031	649.995	459.302
238190_at	326.978	259.488	303.937	356.083	306.034	242.369	388.936	307.583
238598_s_	61.8585	58.7447	77.1335	69.0349	66.6766	51.334	51.596	67.3849
1562671_s	39.1936	31.2355	38.9665	42.0358	36.1614	34.7166	32.0331	38.4983
211079_s_	167.575	172.46	177.053	127.003	181.279	171.488	188.118	168.657
230790_x_	243.846	272.383	295.384	314.281	249.025	210.118	245.029	237.955
221987_s_	249.117	263.862	273.94	285.212	275.966	279.507	252.124	301.387
219723_x_	378.411	359.768	388.365	370.879	362.038	423.558	406.979	439.836
235881_at	63.3724	61.7201	56.267	57.6818	53.3431	56.1362	60.0748	54.3459
1554962_e	297.153	268.685	253.928	273.826	244.266	265.376	293.945	276.327
227995_at	327.225	304.726	290.08	342.611	281.775	291.558	330.184	331.928
1558381_e	115.418	111.763	126.066	145.866	103.173	107.189	170.454	127.799
214328_s_	6289.87	5812.81	5337.26	5954.72	5442.11	5145.68	5057.9	6013.27
229981_at	111.929	97.2657	122.892	99.8376	112.432	97.3334	118.254	77.3025
239273_s_	98.1702	80.0001	105.664	92.9616	93.5376	91.1803	104.663	96.7863
238844_s_	137.205	196.22	178.571	175.053	138.224	145.232	115.103	134.613
1566633_e	223.747	208.707	197.712	220.482	234.246	197.246	207.28	205.95
1552327_e	112.607	134.298	95.1991	143.91	104.61	87.0591	112.5	108.822
218907_s_	219.877	206.518	207.672	221.61	236.442	198.216	200.981	190.408
1554702_e	75.5455	67.1589	70.2673	67.2177	71.9638	79.4761	81.2147	74.548
214316_x_	376.292	360.646	432.247	308.596	372.332	374.757	421.438	364.384
242929_at	59.1134	68.1853	67.9869	44.7624	65.2123	65.1311	55.8699	57.7864
230752_at	68.5741	67.9565	69.5309	72.5755	73.0016	58.5539	59.8453	55.4392
220102_at	112.439	112.89	120.763	99.8376	139.652	113.175	104.909	107.358
206976_s_	476.456	608.716	521.428	568.219	398.183	398.94	350.828	538.325
211765_x_	1730.82	2001.61	1513.2	2664.83	1949.26	1576.15	1759.73	1994.65
1559054_e	37.7289	32.5076	33.5324	31.2848	30.3111	26.0014	26.9114	21.2825
221737_at	405.426	324.162	344.484	298.106	474.102	372.297	483.931	438.057
242577_at	47.5699	36.0532	44.6356	29.5453	35.7156	35.5969	31.5743	29.3313

235217_at	78.2697	73.0785	74.3947	72.8228	75.198	79.7131	61.6796	72.3634
212412_at	275.882	219.044	286.25	283.714	238.025	227.502	223.898	287.161
241004_at	151.524	158.167	146.348	132.408	139.865	159.725	152.459	151.683
221304_at	44.6202	51.6234	48.0633	67.6478	48.916	68.5144	52.4536	58.1857
237438_at	233.638	217.838	242.161	235.566	229.787	240.408	282.529	242.618
217356_s	4127.82	3051.4	3848.68	4315.9	4292.95	4048.52	4158.69	4110.04
207131_x	442.833	324.202	368.854	358.504	289.448	318.292	376.011	287.194
211775_x	25.1506	15.1597	25.5076	14.2844	20.1862	9.08736	21.2442	16.8279
232626_at	93.0187	78.2761	109.255	78.7223	94.7836	83.353	90.3833	79.1045
1561300_a	52.098	59.1744	49.8306	53.8353	50.0741	54.6377	65.7683	57.5176
160020_at	242.94	224.53	221.892	220.329	221.164	222.705	254.437	240.532
200848_at	681.552	802.852	655.625	882.874	639.701	662.699	669.064	813.379
210146_x	101.414	80.9991	110.475	98.165	93.3912	76.0003	82.5282	68.753
1560918_a	51.9429	70.457	55.3057	53.7312	41.6552	48.776	50.779	46.3541
202334_s	1514.04	1962.59	2103.82	1915.02	1527.64	1520.54	1447.31	1733.98
1561561_x	297.408	272.55	284.338	288.227	282.911	292.835	362.005	334.355
237496_at	35.9347	37.3598	28.9059	34.7495	36.6658	33.1935	32.455	35.5159
1556678_a	12.9153	19.7671	16.4948	20.4531	16.3912	14.8709	19.5244	19.7483
204518_s	280.283	402.64	488.087	377.878	420.004	508.169	447.43	530.208
234861_at	28.4945	18.2673	26.575	14.2311	24.9369	23.2595	25.398	18.2959
227170_at	255.857	241.77	273.993	216.136	260.392	259.156	266.088	255.608
202884_s	66.7185	73.4189	77.5437	81.7478	76.9072	79.7349	71.4141	82.3112
222692_s	335.615	347.027	320.547	305.114	366.991	347.302	349.385	380.039
223527_s	132.186	136.127	133.031	146.799	117.806	121.17	139.056	134.732
1567853_a	35.3356	35.4418	37.5283	30.7886	36.062	41.3749	31.2626	42.0324
1569830_a	58.3725	45.0932	69.0531	61.2416	62.6513	35.2938	60.3159	39.827
1569461_a	152.071	140.567	178.915	139.105	174.167	145.208	165.28	151.526
205371_s	169.98	193.075	146.461	153.707	116.607	208.601	171.741	170.439
231732_at	175.517	187.447	199.804	150.665	203.76	179.023	169.785	188.405
229691_at	167.072	171.092	186.444	160.645	196.655	179.742	199.313	165.936
219431_at	408.692	514.686	365.304	492.793	284.982	369.221	386.569	419.659
1566113_a	122.722	115.931	119.288	123.737	134.363	146.35	154.727	128.225
1553365_a	16.3445	19.1905	17.4308	13.8636	15.7148	19.3284	16.7499	21.1816
235096_at	213.224	236.245	232.855	228.551	220.177	205.681	181.941	225.624
240120_at	54.2605	62.1409	59.0866	75.0795	56.9148	66.2271	53.1268	53.953
1562380_a	75.2551	64.6845	72.1542	97.7262	63.422	78.0466	108.851	73.9381
1563070_a	78.404	71.6653	86.4446	101.981	79.3797	93.9437	84.791	88.4608
236235_at	51.5959	76.3969	64.3294	77.6165	65.338	59.2252	61.7511	49.4391
215615_x	51.7092	57.4189	43.9273	43.0651	45.4654	36.5773	45.8482	37.8865
1559237_a	228.034	225.172	227.416	259.736	225.394	237.835	254.384	251.873
242787_at	51.9957	55.0635	53.5884	47.0997	50.2993	55.8756	49.9848	51.2729
238498_at	46.7073	42.0915	56.4079	45.2905	51.2772	46.3442	61.3	59.2486
214353_at	89.6151	78.2849	97.4791	95.1957	76.3607	80.2817	91.9339	65.8977
1558375_a	267.243	226.073	213.317	224.63	188.175	156.285	244.628	179.526
218011_at	2064.34	2292.29	1998.1	2080.04	1774.67	1594.92	1524.84	1825.01
223546_x	209.963	235.647	217.349	228.158	234.81	213.659	233.659	246.902
240943_at	387.862	334.071	347.177	330.567	311.576	279.693	303.807	268.42
214800_x	3015.58	3580.66	3431.19	3567.57	3012.25	2888.24	3143.43	3009.56
242161_at	27.4556	24.7051	29.5209	23.221	37.6372	29.4906	25.9752	18.7949
224546_at	136.711	205.559	122.311	178.702	147.468	134.794	121.658	104.631
224498_x	144.879	153.796	138.556	140.068	146.548	156.799	139.637	145.396
1570098_a	184.021	171.942	163.493	169.254	173.013	143.742	151.865	149.541

209207_s_	206.473	236.352	218.505	240.665	212.69	234.615	239.296	235.416
226736_at	1541.5	634.002	1510.89	579.446	517.853	710.979	578.557	793.321
218305_at	257.194	208.262	222.987	259.864	257.301	259.938	260.677	263.18
1568977_e	143.155	129.959	141.864	135.221	137.413	141.662	159.27	156.073
1555829_e	61.8147	59.8568	44.9912	49.8275	60.3241	67.4853	49.0499	52.0996
242224_at	37.0366	38.3657	44.5367	44.6627	44.1302	44.8978	38.5974	50.2544
242841_at	134.904	137.132	143.844	127.345	133.629	121.963	138.012	144.814
209276_s_	594.651	1277.04	998.883	1166.76	964.986	518.965	561.072	743.961
217288_at	139.623	130.39	134.824	101.704	143.625	131.682	106.769	122.407
1557341_x	401.121	388.621	298.576	423.74	313.623	362.322	366.554	398.889
227854_at	239.32	269.775	212.107	241.846	188.26	223.647	205.61	229.492
209975_at	201.749	207.698	177.183	200.154	211.688	198.846	188.717	180.466
235317_at	352.959	373.246	414.34	368.656	360.237	395.17	459.694	407.431
221818_at	393.799	352.266	370.275	389.65	414.957	383.595	471.887	446.381
201976_s_	252.74	304.888	250.046	261.937	254.151	231.032	256.329	252.79
1554793_e	11.8811	17.6001	18.9712	18.3075	11.8133	8.5889	26.7199	14.1389
214992_s_	258.984	272.286	306.216	338.652	272.999	279.522	308.619	312.935
220363_s_	307.326	331.25	314.347	331.886	330.016	361.062	411.475	373.843
233406_at	32.1614	52.0268	33.2067	37.0398	42.7525	44.6784	32.0139	30.776
217264_s_	320.254	335.66	379.871	287.051	359.406	322.478	307.975	328.646
221082_s_	235.284	192.876	231.51	195.374	225.129	224.951	258.104	253.542
1554719_e	109.799	97.4644	115.817	102.55	112.547	98.4367	98.7204	98.2292
217280_x_	202.155	150.811	193.396	179.851	184.098	167.14	205.468	196.175
204840_s_	106.321	118.02	99.7475	99.2472	65.0572	98.7314	97.7258	107.997
219655_at	241.429	254.299	210.149	225.68	196.568	210.863	187.208	203.895
214373_at	348.671	347.004	349.926	316.122	394.786	430.573	572.715	389.211
225124_at	84.0337	71.4376	77.4176	68.3914	84.6052	114.663	106.507	120.434
210679_x_	215.488	195.533	207.023	195.287	157.152	164.478	229.716	196.04
243374_x_	227.533	222.353	241.332	198.655	240.554	229.736	218.16	226.108
214518_at	127.631	125.366	117.9	108.554	137.091	130.491	126.677	117.806
233734_s_	216.686	180.697	257.791	205.579	225.892	178.307	260.552	185.303
1559029_e	180.506	208.445	196.113	209.731	223.197	177.877	183.407	168.195
225476_at	339.124	337.097	301.932	322.477	314.647	333.331	303.078	289.716
217039_x_	593.439	563.274	551.478	601.034	580.632	599.839	732.477	641.407
204512_at	64.5842	69.5881	68.3757	58.1211	59.2449	41.8949	52.8784	46.7365
241365_at	238.297	289.092	284.988	268.296	249.921	230.154	203.184	224.017
1555734_x	40.8918	41.7712	50.28	38.1598	43.7325	55.4896	40.6015	33.0153
236570_at	176.985	135.38	211.708	165.908	179.306	140.408	196.253	136.98
235874_at	28.8604	32.799	33.4897	24.9169	29.9447	31.7102	17.8224	25.8467
242214_at	258.975	269.624	255.179	227.224	223.409	251.116	216.621	244.264
215725_at	172.216	166.59	180.753	171.788	197.443	194.154	181.432	189.145
243432_at	204.651	198.887	201.427	193.619	214.336	220.554	229.345	210.536
209114_at	415.974	378.28	399.06	519.991	472.863	521.539	418.678	436.835
244617_at	134.068	126.541	146.641	122.335	147.893	122.475	137.273	132.626
207180_s_	311.822	240.872	276.075	247.946	290.34	275.731	258.141	299.768
223882_at	80.5137	70.4893	87.015	80.168	75.7204	77.4958	71.4446	71.1432
237562_at	161.699	171.994	164.984	138.674	163.898	173.075	162.13	164.648
238018_at	53.0308	50.237	81.2411	72.6508	77.1521	51.5646	55.5702	49.1162
203197_s_	960.568	1082.93	1033.23	1039.23	1130.7	962.536	1019.57	1066.4
208747_s_	773.057	726.808	844.052	749.924	964.687	802.064	951.323	712.073
1555801_s	106.446	122.608	124.097	68.9701	88.1331	145.215	139.847	151.435
238295_at	124.703	113.627	123.391	113.703	140.524	103.685	121.103	92.6157

221139_s_	54.2814	61.3853	72.9722	64.5154	51.942	64.2689	60.3194	66.8791
1565662_e	239.412	237.504	250.12	248.709	252.476	227.365	242.135	236.983
230837_at	37.2124	34.0892	31.1169	38.0218	26.6717	42.7279	35.5098	53.1153
219948_x_	21.6243	17.9806	22.931	17.4509	19.4519	24.3356	21.6218	31.3204
242737_at	54.8341	50.6252	52.0177	41.1069	50.6588	44.8429	46.6147	40.6221
1569961_e	107.161	136.542	121.728	152.189	111.142	127.778	151.904	134.738
230441_at	117.603	95.9857	136.375	109.916	136.086	101.487	119.639	100.351
205508_at	3100.44	3696.05	3317.66	3066.16	3399	2943.26	3022.91	3231.43
204897_at	223.219	262.997	186.218	168.914	189.037	181.713	146.042	194.029
209835_x_	140.371	149.713	148.404	179.295	167.338	157.508	170.357	161.08
1558607_e	82.6383	65.9311	76.84	65.7781	72.1005	60.79	65.756	62.4017
215993_at	125.037	118.211	131.783	88.8287	122.855	136.687	116.532	124.859
216847_at	86.3043	85.2008	95.817	87.7442	80.2418	80.8083	97.0683	78.3163
243510_at	180.001	149.662	188.005	191.574	153.287	145.044	160.835	138.494
211376_s_	312.505	320.763	331.617	405.09	372.319	316.609	421.195	392.618
231738_at	86.368	82.7489	102.196	88.6486	108.834	74.7016	78.5806	61.9097
235041_at	426.433	368.512	446.577	451.909	456.202	507.173	541.135	525.969
225023_at	134.254	167.766	165.096	175.563	151.558	152.505	164.618	182.659
233891_at	114.583	109.296	149.659	139.804	127.23	108.913	123.761	109.708
1560033_e	57.8297	59.1562	52.0387	61.3518	53.4745	47.8169	49.2083	49.8856
216155_at	72.5107	80.4425	78.6138	63.5705	77.4135	70.2346	72.1728	84.1073
229558_at	380.403	414.354	423.525	365.906	418.537	394.52	419.569	419.922
202812_at	306.388	337.954	371.146	334.895	401.105	436.83	429.167	456.844
1557038_s	227.952	220.868	170.58	174.726	211.483	203.728	192.179	177.002
230648_at	333.952	318.832	356.083	374.298	389.168	418.833	499.766	424.777
240860_at	79.3322	85.3454	81.3754	89.0041	94.1334	104.339	115.215	108.161
1569274_e	156.875	132.639	149.001	146.487	151.067	143.557	162.288	173.427
228603_at	117.475	146.416	133.324	155.583	127.733	108.296	101.891	119.759
1557810_e	32.8784	36.3793	43.5627	34.443	45.391	38.3975	43.005	40.9697
202224_at	476.207	439.838	350.432	427.281	393.408	401.419	379.23	421.448
1568871_e	27.8485	26.4491	24.0966	24.505	29.58	40.6821	29.8892	27.2182
235332_at	229.416	211.959	225.147	191.046	230.938	223.758	216.518	213.19
203597_s_	588.568	741.722	638.382	482.579	601.252	432.85	412.146	525.301
220566_at	222.41	202.541	215.295	222.828	204.22	208.591	239.76	218.414
34868_at	288.616	255.903	282.946	273.573	270.03	249.764	272.845	271.439
214184_at	91.8256	90.0426	85.6115	110.655	95.0746	98.6327	91.0517	96.2632
240031_at	155.749	127.352	161.713	154.362	155.549	146.588	179.003	154.843
216111_x_	210.219	206.003	206.426	216.111	205.664	243.978	223.989	234.935
200850_s_	1407.36	1337.42	1185.22	1371.51	1347.07	1005.32	1035.55	1148.82
220143_x_	256.142	271.38	256.117	253.12	280.737	257.616	277.085	265.347
230683_at	102.264	118.166	113.06	100.574	101.119	105.047	91.5365	102.117
200627_at	2399.88	2808.38	2642.27	2783.87	2483.45	2659.52	2602.41	3238.58
212727_at	192.659	172.55	175.957	192.951	182.646	172.865	182.413	174.231
201325_s_	292.293	315.348	340.929	292.056	336.486	296.466	299.443	304.809
232208_at	215.618	231.536	227.038	204.915	250.734	253.14	192.208	245.457
212354_at	182.511	195.556	185.725	204.243	182.981	192.126	251.917	209.052
218864_at	439.933	488.855	436.859	455.336	486.855	558.068	495.647	506.337
226144_at	184.458	167.845	195.354	176.502	164.714	177.374	176.787	185.026
219817_at	272.312	282.661	256.529	246.418	241.391	226.666	241.244	220.253
36865_at	303.57	263.768	313.367	304.285	299.407	288.042	314.874	345.966
235653_s_	204.617	284.643	205.178	220.439	179.824	187.191	167.285	163.874
1554131_e	12.451	9.55012	9.91163	6.90744	7.64312	14.4085	12.261	13.7195

235666_at	181.791	188.66	193.055	183.72	208.179	188.696	167.209	225.491
212789_at	247.35	258.035	243.049	267.763	275.687	241.758	295.05	231.274
212854_x	956.272	741.917	922.78	998.763	940.245	812.263	1125.11	946.181
1555051_e	230.567	234.542	235.323	249.128	260.111	243.198	324.964	270.389
230671_at	1385.52	1165.05	1796.43	1005.93	1430.13	856.345	1193.11	914.791
239562_at	102.6	116.121	88.0065	104.68	92.3053	80.1912	92.7891	91.7883
237566_at	48.1526	54.1161	62.4792	58.4693	52.0721	32.4598	52.9487	39.6063
236657_at	170.313	160.139	165.978	206.921	192.34	178.025	211.536	236.358
234973_at	182.026	186.718	215.133	170.299	212.447	192.483	214.65	193.397
239670_at	207.365	179.608	204.528	169.509	196.394	184.451	205.373	201.59
1556682_s	53.9715	48.3667	70.4068	45.7242	68.194	35.7739	44.1092	43.3328
210896_s	321.842	330.074	341.237	309.414	396.97	334.363	302.988	337.987
243223_at	89.8335	89.9063	89.1786	101.181	75.5346	83.5937	92.2568	92.2025
230473_s	82.4775	76.2853	92.1408	81.5588	82.2438	93.8417	107.054	85.285
227096_at	333.818	269.606	345.933	308.274	359.297	369.885	494.219	412.661
203333_at	622.045	596.331	621.111	722.737	688.713	562.059	521.682	566.935
214592_s	83.6806	75.9149	102.451	75.5089	74.1802	70.5579	107.502	76.8245
220921_at	117.1	96.5988	103.223	92.0375	89.1013	104.836	97.3337	93.2594
201768_s	587.517	539.72	641.331	640.882	714.35	700.924	733.74	713.801
1552736_e	230.241	200.384	231.433	237.137	209.825	242.141	251.89	221.899
230513_at	385.78	347.066	369.263	393.392	419.628	390.424	443.661	429.813
241247_at	96.469	95.8715	113.753	95.2561	103.204	84.5122	103.294	85.8434
1553923_e	51.2036	52.6596	62.0506	69.8298	64.2973	54.4898	58.9612	55.1231
204060_s	96.2491	93.5676	96.8416	118.252	99.3732	101.773	108.317	102.138
208299_at	205.956	219.326	209.925	172.599	211.313	194.795	198.597	200.908
202499_s	172.739	148.53	179.003	141.274	129.308	123.006	131.507	140.209
240644_at	280.913	265.189	267.95	253.739	245.121	251.157	289.664	268.318
205538_at	150.403	127.746	138.409	142.567	122.189	144.998	142.096	125.396
228567_at	400.68	421.031	427.565	385.9	460.366	415.51	394.144	428.291
234544_at	40.3474	45.6072	45.9542	34.5974	47.2402	35.7748	34.8386	36.8335
1560695_e	60.8243	55.4873	61.1873	47.9546	66.6101	58.2669	47.5418	51.1298
230731_x	343.015	311.212	327.023	310.377	360.22	339.473	345.161	310.628
1570395_e	54.7647	50.4461	58.4082	50.7378	40.8903	59.9133	69.9786	56.0245
230929_s	229.366	196.963	231.985	177.202	238.977	208.967	244.063	210.561
216358_at	77.6474	78.3024	109.562	87.2498	92.9777	76.4429	89.576	81.7002
210647_x	283.425	279.11	278.189	277.862	313.215	309.212	329.212	305.567
1554796_e	153.249	148.952	137.95	146.513	168.311	151.133	160.654	135.151
240689_at	73.4234	60.9505	81.9316	73.7882	68.6383	71.8677	83.3464	86.8956
1558959_e	234.125	183.348	179.632	198.945	209.735	202.712	222.141	235.884
207916_at	103.662	84.6972	126.348	84.5366	111.846	88.6956	93.1608	95.9206
224297_s	195.844	177.244	259.9	194.546	218.748	164.581	217.148	168.972
202746_at	496.436	722.004	689.971	729.803	516.374	574.794	609.03	573.193
205606_at	414.979	406.97	427.584	389.995	517.911	415.216	489.466	443.747
210969_at	42.5505	36.0212	45.8887	37.5145	36.1249	39.1475	36.6003	36.5526
229493_at	438.793	460.828	451.677	489.983	505.417	471.96	506.812	441.706
210882_s	47.6174	50.4168	40.4771	42.6021	39.8657	46.0748	45.9559	50.2673
225625_at	237.736	239.981	266.221	276.76	226.453	228.535	278.038	233.023
216716_at	148.004	135.095	162.019	121.446	152.949	119.563	131.424	119.367
223767_at	157.746	162.529	143.254	157.89	151.89	165.424	175.833	159.477
214523_at	209.682	205.602	223.413	189.542	225.158	211.824	201.82	216.822
204112_s	110.563	116.257	101.728	128.747	96.2761	100.868	102.67	106.734
220242_x	76.8785	67.2049	88.683	70.7961	78.8526	77.8872	79.3593	74.4793

207618_s_	630.776	564.288	536.382	725.928	540.654	469.065	565.434	534.67
223868_s_	71.6695	73.5962	82.4541	71.2772	65.4341	82.6712	74.4048	67.8673
243067_at	96.8827	91.7812	91.3351	88.5217	106.76	112.676	111.903	100.702
202989_at	22.2458	14.8727	16.7992	16.9843	19.5696	22.5481	16.8855	21.6972
202349_at	502.543	438.606	517.475	499	659.453	478.944	653.56	485.728
203203_s_	510.421	604.663	612.583	668.787	447.5	412.795	452.286	557.86
243062_at	121.047	88.3891	127.382	102.101	108.021	92.5228	127.082	95.4228
204777_s_	136.778	127.214	140.118	120.004	130.11	133.703	132.486	129.144
203911_at	601.208	547.499	579.921	569.301	584.243	600.707	616.611	564.451
1561345_a	107.728	87.1241	88.7922	102.268	92.2633	92.5415	105.652	101.135
227808_at	201.269	300.511	304.279	281.722	185.265	268.244	238.821	307.606
211584_s_	90.5125	109.176	96.2492	112.73	99.9387	120.566	108.849	117.104
1560081_a	182.245	171.064	147.879	226.803	164.995	392.119	270.828	284.464
1566129_a	71.0815	68.7908	68.5033	65.1388	58.5927	68.8719	65.1826	53.9555
211672_s_	150.55	184.837	162.913	171.104	179.238	207.665	196.02	202.44
221680_s_	229.939	240.589	226.07	204.553	242.329	230.038	243.682	220.358
1561855_x	31.5974	22.3122	33.8222	31.2586	36.7964	27.0149	31.8434	21.4989
211776_s_	261.568	272.62	268.938	267.735	288.786	279.278	256.044	265.788
240462_at	137.424	131.759	139.297	118.687	156.01	138.66	127.806	130.307
225468_at	549.042	524.995	517.592	599.59	560.486	450.401	542.39	567.115
203345_s_	391.091	421.654	386.94	467.848	384.551	359.279	381.253	425.318
1555902_a	360.101	266.688	383.503	338.925	363.171	276.916	358.411	303.703
231437_at	107.366	101.089	112.382	93.0096	96.4253	86.9047	113.779	104.769
222608_s_	11.4066	7.27464	10.0413	7.93732	10.9459	9.64473	10.0609	3.31127
238652_at	287.536	247.652	261.8	249.273	339.53	300.07	329.478	291.262
209445_x_	755.952	745.322	630.076	418.2	558.639	541.701	639.24	620.38
43511_s_a	269.908	273.147	260.718	271.484	251.944	266.075	294.76	283.529
213700_s_	271.59	261.534	272.52	227.155	300.796	297.555	269.543	297.735
237625_s_	58.724	52.8101	64.7883	56.825	67.5632	47.4058	62.0994	54.8849
202277_at	290.015	362.036	290.605	393.981	266.746	273.742	259.794	279.956
235430_at	129.46	111.804	132.677	101.91	120.023	118.329	121.561	120.755
222191_s_	197.314	184.423	223.49	176.079	204.503	172.487	209.479	198.766
234867_at	175.206	185.217	176.365	175.015	175.143	161.045	195.81	167.687
225605_at	378.418	393.82	400.102	310.534	419.755	360.919	371.299	380.996
220401_at	84.7277	75.5501	70.5593	72.2631	98.6746	79.4338	76.6413	69.887
210973_s_	210.223	216.968	208.02	241.537	243.095	270.178	262.556	294.893
231330_at	166.235	168.701	159.926	176.966	165.337	172.199	186.13	175.017
206592_s_	1601.85	1688.71	1507.87	1490.52	1511.37	1042.88	966.712	1177.89
1556365_a	215.134	189.456	172.152	154.841	135.634	152.862	180.426	168.499
236471_at	122.9	116.925	117.136	102.622	122.06	132.101	123.007	110.533
232087_at	104.865	109.424	114.967	122.612	111.908	111.868	87.7063	100.292
203242_s_	88.4096	83.8385	101.259	103.944	109.07	114.718	95.9693	115.473
214237_x_	211.951	206.45	245.831	252.992	227.271	211.075	231.772	221.915
207149_at	47.322	36.2854	37.0019	40.5899	40.9388	45.215	40.1967	45.2069
244647_at	157.451	171.585	174.248	171.236	155.454	152.658	191.064	158.096
238405_at	159.582	127.422	197.84	153.91	125.54	126.102	146.791	116.602
212544_at	843.013	941.666	880.275	904.604	755.212	634.4	679.489	750.636
1558236_a	76.4588	84.7437	76.1243	82.1146	74.1033	69.2598	73.5064	64.3685
211716_x_	340.372	324.249	347.17	355.971	402.21	450.09	500.001	520.177
208261_x_	25.179	25.6011	25.6591	34.6656	40.2009	24.5682	29.4431	26.6371
244021_at	164.868	109.038	188.204	132.75	168.982	125.198	173.08	130.443
241009_at	193.499	190.755	166.012	168.865	199.654	181.807	175.014	162.583

207169_x_	523.014	436.636	407.975	475.258	473.531	478.09	473.789	397.381
203983_at	680.581	793.368	947.233	996.753	753.179	700.246	729.343	763.395
209929_s_	693.687	630.075	666.671	654.595	678.716	685.471	774.773	648.231
236834_at	83.1909	108.394	95.8058	123.932	84.5558	88.9006	89.094	79.7468
213734_at	835.644	865.821	952.473	967.83	609.711	569.595	641.192	800.559
240370_at	38.2762	38.0403	37.0708	45.539	41.3185	39.5318	45.9137	44.5084
213265_at	164.39	166.029	190.833	145.636	194.3	180.319	166.45	175.194
238882_at	143.279	130.558	139.206	125.992	130.058	145.315	126.984	129.625
206153_at	70.3319	75.8302	65.4913	74.7426	84.7973	138.431	131.002	140.678
200000_s_	2091.35	2264.55	2285.63	2385.13	2248.21	2503.15	2806.23	2729.54
226647_at	243.056	225.858	228.314	227.211	236.025	217.047	256.581	220.043
233403_x_	89.8626	85.6211	80.0978	80.1731	71.9774	79.015	82.3401	91.6887
232164_s_	49.0922	51.0461	52.4487	58.3704	64.042	60.0448	56.2283	51.8963
221078_s_	112.167	92.385	101.442	105.358	111.036	111.045	117.198	125.124
201561_s_	553.94	649.866	574.61	566.934	594.628	569.792	603.18	604.019
229409_s_	110.68	98.6874	104.217	87.5335	90.4143	90.0522	112.814	94.274
243404_at	143.598	148.646	138.601	123.765	153.26	134.112	168.522	155.873
226906_s_	113.775	102.431	126.651	105.831	130.397	86.1991	104.803	90.8734
216119_s_	227.797	232.663	206.577	214.377	238.948	195.131	200.992	202.504
1553952_e	876.459	536.879	664.252	542.371	623.79	711.499	952.156	642.835
201148_s_	610.878	577.13	568.544	575.908	631.407	866.037	744.09	823.917
237753_at	135.452	114.548	163.908	118.264	132.676	122.37	156.854	130.451
230684_at	146.173	140.763	155.098	123.561	142.948	146.284	132.944	128.73
223188_at	623.028	491.045	558.597	529.947	554.931	562.279	632.78	558.91
226389_s_	739.416	750.436	777.259	898.001	903.215	805.969	878.266	908.208
211891_s_	69.294	78.0092	84.8168	82.0479	97.4511	70.813	83.0215	76.5668
214702_at	41.1843	35.8012	37.6733	37.6296	38.6573	51.4612	37.1179	34.6393
243022_at	272.347	238.293	315.491	273.958	275.404	224.29	286.149	234.822
1568695_s	127.583	109.523	133.109	141.663	114.343	100.451	121.132	119.654
1564413_e	387.365	328.612	345.661	404.744	430.553	429.699	513.645	399.693
215852_x_	147.711	127.32	136.004	137.693	112.462	115.052	128.987	118.315
238445_x_	263.272	282.998	285.179	199.124	292.771	285.744	257.502	274.31
1569484_s	22.0608	25.552	17.1478	23.4068	13.0845	19.6853	12.8911	15.8799
227901_at	158.18	161.586	172.704	142.442	166.756	156.212	121.379	129.852
228859_at	67.6219	59.7554	57.4722	54.1841	62.9711	59.648	55.7105	48.2063
211040_x_	301.752	316.745	312.18	321.222	351.036	301.813	331.213	291.093
237110_at	193.206	170.401	205.489	162.171	207.347	179.597	209.138	190.337
217764_s_	358.21	321.47	337.993	333.186	343.095	255.181	278.261	336.444
200996_at	479.596	470.437	541.223	541.584	462.197	463.249	462.797	506.008
1563496_e	73.382	61.8064	51.0073	54.2656	61.0668	56.2099	70.875	58.6971
240560_at	166.961	153.858	156.996	133.554	158.216	136.483	153.033	131.257
1570210_x	90.4743	81.4245	81.5077	83.3939	75.0248	89.7165	84.0719	74.338
232573_at	221.597	209.469	205.616	229.726	202.098	234.644	280.286	240.887
203175_at	571.712	449.447	561.706	498.858	568.516	607.664	656.98	645.719
1552721_e	47.9992	48.4189	48.6788	44.3339	46.5379	65.4675	51.5449	54.8387
227022_at	148.022	151.576	178.197	192.633	167.146	137.692	158.485	136.434
228049_x_	614.504	942.145	536.066	584.992	599.911	532.313	409.941	561.598
208270_s_	232.584	266.316	301.928	312.863	307.38	269.329	319.923	336.712
230510_at	120.791	106.115	121.477	117.119	119.785	99.9953	115.09	109.95
229701_at	190.367	213.669	209.002	165.022	199.627	199.159	169.612	192.112
234433_at	57.3112	59.4687	50.6341	51.003	60.0137	62.5748	59.2609	50.6967
231909_x_	26.2069	19.302	25.74	25.3478	31.2105	16.7023	35.0971	24.9842

1554846_e	93.8475	90.1996	95.2547	85.4561	87.3571	85.8501	94.5928	87.8697
50314_i_at	221.004	193.098	234.643	223.913	232.06	233.458	280.79	269.508
241049_at	74.732	82.7434	81.3809	75.9963	69.0054	83.0438	86.8174	80.0954
244611_at	182.948	145.449	147.61	165.016	167.131	142.836	168.798	134.381
236847_at	148.717	134.94	138.097	131.083	126.148	111.823	114.933	126.279
241671_x	207.805	189.817	228.888	168.459	220.344	183.23	210.834	193.164
224307_x	181.654	157.299	183.602	153.177	174.99	165.844	182.369	157.352
1569597_e	312.574	280.19	284.709	270.544	323.756	268.615	242.097	253.439
209489_at	812.029	835.361	818.724	1053.29	1133.21	830.245	963.766	894.564
243275_at	43.8467	31.4484	64.5376	43.3805	52.8689	29.6764	52.1452	40.0869
1559078_e	89.309	103.328	101.041	89.5638	91.0729	77.3176	88.9688	84.5945
239481_at	212.049	223.946	215.541	227.381	190.19	158.127	191.289	158.693
205662_at	130.314	116.917	140.533	125.207	130.427	106.961	128.582	115.644
212938_at	223.836	196.433	275.885	192.664	234.525	220.323	233.943	213.282
228475_at	128.359	132.717	138.443	120.852	130.365	136.5	153.171	135.665
1562942_e	120.086	135.872	111.387	172.88	129.63	113.33	140.57	127.878
223314_at	365.585	328.199	348.934	372.498	365.064	355.46	418.377	336.747
205906_at	258.756	247.406	244.486	217.556	234.821	254.544	276.417	248.655
240303_at	96.1096	95.8998	114.146	88.2251	105.078	113.062	104.414	116.954
1555301_e	64.0827	48.8958	62.7748	52.4768	55.105	49.719	48.4042	45.9016
229206_at	72.8915	75.4509	77.2363	70.1354	59.1162	65.2205	61.5628	75.4594
1562903_e	97.0655	90.9569	144.091	102.66	83.3333	116.49	169.885	139.854
200983_x	2290.58	2187.01	2081.01	2066.54	2816.09	2619.56	2863.17	3488.3
201247_at	423.667	415.694	440.589	423.318	480.714	486.911	545.93	514.222
207836_s	139.643	110.751	118.186	133.706	109.731	119.419	111.854	131.76
227162_at	206.112	254.083	210.471	158.003	184.379	198.502	159.841	174.868
203886_s	372.519	441.028	459.015	523.762	448.757	349.44	378.915	587.57
1564387_e	105.915	84.0549	77.7815	79.0755	100.764	96.135	101.396	75.0661
227393_at	243.553	219.069	246.765	210.635	252.318	230.559	253.974	239.436
208361_s	294.365	305.699	289.157	273.604	296.683	297.539	300.527	291.51
208730_x	467.635	323.239	567.106	453.463	432.463	404.281	618.122	432.203
201311_s	210.128	222.377	258.64	229.084	240.419	291.167	285.06	336.423
216836_s	507.656	460.279	457.438	448.411	474.682	513.944	786.824	559.039
203388_at	489.487	467.826	518.167	493.961	581.839	592.328	720.368	597.547
244657_at	114.387	92.795	122.95	115.924	111.001	118.176	130.735	117.134
232840_at	61.9743	67.5431	82.3848	92.4332	76.1274	83.4166	92.9799	84.1727
225963_at	115.008	107.478	111.999	116.317	121.841	115.733	131.268	115.262
1565587_e	282.092	205.013	224.051	234.656	234.54	255.009	342.5	245.703
217456_x	1179.29	1185.02	1040.48	1044.4	1463.88	1645.33	1235.2	1330.18
204234_s	157.747	192.771	175.591	205.047	174.626	167.135	164.286	164.11
213995_at	637.637	660.946	815.429	708.339	631.18	602.151	693.042	671.106
209289_at	1565.77	1620.9	1759.83	1509.53	1209.14	1460.62	1274.73	1646.5
219815_at	283.496	261.069	239.25	232.564	273.964	251.438	238.804	237.773
233530_at	90.5604	90.8859	84.0112	111.176	93.4288	94.3831	106.593	98.1703
232497_at	91.3538	92.3529	104.171	92.5257	81.4629	73.6732	77.625	68.4353
208131_s	252.69	257.224	288.803	287.167	240.876	277.57	275.954	295.061
215551_at	67.243	50.4715	56.9052	48.8757	54.6293	60.1647	67.6525	69.2465
202962_at	167.616	149.941	166.645	218.416	187.338	155.61	162.425	155.31
227447_at	657.964	795.889	698.159	800.216	644.679	494.283	509.005	489.338
238814_at	169.854	177.149	168.495	137.793	160.839	150.929	173.691	184.377
213844_at	272.409	357.52	289.779	309.066	241.016	252.875	253.378	332.48
241826_x	57.6127	60.1563	71.3253	53.5299	68.2018	40.9284	60.7777	55.9377

212604_at	663.395	661.243	593.485	615.666	515.795	538.094	515.536	595.795
200696_s	1799.8	1446.52	2053.69	2119.58	2750.04	2482.73	2624.98	3025.45
212363_x	8815.96	8344.09	9057.25	9061.06	8831.08	9189.08	9508.11	9845.21
203071_at	196.262	183.406	213.913	155.76	191.177	185.986	186.483	179.583
1565898_e	34.6807	35.931	33.9745	36.1791	34.0494	34.2158	35.3111	31.9567
244723_at	44.4485	48.6548	62.7988	48.0474	74.4534	52.3571	50.515	51.4367
50277_at	1025.33	1024.54	913.306	1002.5	1097.5	892.278	913.707	1008.36
233977_at	223.045	176.43	189.655	201.491	208.284	222.151	246.358	215.265
1555298_e	38.1145	40.626	40.7947	40.8877	39.3096	40.17	34.3578	38.82
202274_at	237.467	258.054	231.36	212.424	261.027	277.118	241.597	259.951
242081_at	225.202	248.142	253.598	185.626	258.564	245.2	222.576	221.398
1570330_e	184.9	176.634	190.624	195.504	197.363	179.899	212.684	184.165
227145_at	306.792	313.349	282.899	414.389	311.166	272.989	319.039	328.497
1569850_e	39.5887	36.439	45.8498	47.0974	50.085	46.0533	46.2553	50.3416
237511_at	175.072	144.722	176.461	147.854	147.884	137.863	176.573	137.262
221155_x	133.755	132.157	123.409	105.128	123.987	124.36	112.318	117.551
219612_s	46.2646	45.0559	53.7833	37.2737	48.0152	50.8285	43.2338	37.0236
233004_x	72.1946	68.617	80.7038	82.7163	69.9296	52.1012	71.107	71.925
223295_s	212.312	235.815	192.533	248.766	213.77	207.645	206.915	230.782
213092_x	174.214	253.748	190.624	211.025	146.754	132.619	116.602	154.129
238618_at	251.417	211.062	224.981	230.838	222.39	248.478	248.174	239.827
1554476_x	36.4292	27.0456	35.2959	24.3908	31.7578	38.9634	39.1056	28.5157
233563_s	280.027	243.024	271.846	266.134	268.84	295.257	358.347	328.057
211989_at	485.267	591.582	505.153	632.88	528.639	461.62	415.267	551.889
230566_at	698.44	607.566	660.026	655.699	923.577	807.226	1000.49	838.415
239962_at	44.1795	48.9007	73.3767	38.5986	52.0685	43.0469	47.7048	37.5905
216328_at	115.244	84.5784	132.11	101.802	116.746	106.468	116.013	112.199
204003_s	193.959	202.875	193.573	220.936	163.428	158.625	177.563	164.679
1558725_e	27.2026	21.9247	16.2899	22.9581	19.7794	23.8761	29.3695	27.5192
1569677_e	37.0729	41.463	43.5626	42.7227	39.7969	49.684	43.7915	49.2719
221087_s	380.413	363.684	375.102	359.542	392.219	395.187	440.598	381.887
236402_at	122.69	125.782	117.504	106.642	124.575	117.087	96.5545	102.01
201011_at	738.807	706.689	779.328	789.32	942.861	1036.83	838.387	959.659
214408_s	129.276	130.043	127.425	104.815	121.367	114.983	110.85	118.159
240900_at	148.375	149.754	165.419	141.809	156.209	147.182	162.436	136.875
216873_s	384.454	387.751	387.063	418.48	412.494	387.935	416.831	408.735
240302_at	165.062	147.648	151.504	141.879	147.032	155.929	165.295	157.822
229436_x	478.727	534.529	498.96	453.365	444.957	347.563	349.869	375.794
1556842_e	33.1677	29.8169	44.4397	36.9334	35.2125	27.1136	32.8955	35.9916
203859_s	296.444	252.436	344.035	326.854	276.237	282.256	365.782	290.442
241515_at	90.3439	86.7408	87.5375	79.8005	76.3376	71.9799	80.2253	75.7191
228296_at	164.341	164.845	148.893	186.719	167.238	175.862	166.81	170.84
206388_at	223.388	224.025	217.692	185.982	246.537	216.461	210.579	215.704
208851_s	544.831	572.869	588.01	549.632	659.532	671.496	754.062	682.363
205096_at	151.799	139.274	174.287	144.481	156.916	132.943	171.8	143.958
238583_at	578.051	518.471	626.449	627.365	658.724	785.431	980.171	958.511
235124_at	407.351	450.013	389.454	413.1	376.731	336.788	345.281	326.434
1559030_e	60.2434	63.2767	54.8816	63.4987	60.2072	60.9101	61.3168	65.0437
229002_at	295.934	295.503	330.698	256.507	352.53	311.928	261.817	296.828
1558014_s	96.8133	99.6928	128.034	109.655	109.663	140.487	131.152	151.81
224596_at	221.412	222.41	214.312	203.936	176.365	200.514	221.079	201.876
234762_x	894.742	1005.75	975.536	931.344	908.122	780.537	879.814	942.888

243927_x_	65.5154	79.8892	72.4649	90.7678	68.7907	64.2648	70.3762	62.4271
202709_at	347.532	331.276	357.731	265.157	314.799	328.948	376.883	340.236
1553575_e	529.252	674.336	646.798	621.01	442.069	328.471	461.087	423.993
211740_at	661.271	530.692	521.546	575.841	591.254	606.487	700.507	645.729
210293_s_	111.863	138.638	99.2311	174.607	89.6717	83.6569	146.754	128.684
221212_x_	57.434	63.4334	74.6581	61.557	63.4952	40.5721	62.3809	53.5701
242324_x_	368.74	390.685	355.958	327.745	422.808	353.959	360.369	401.302
231198_at	90.5681	79.408	96.3545	85.8297	82.0312	89.3631	98.668	81.583
241346_at	320.243	330.077	341.409	261.574	329.706	320.064	303.741	298.334
1569796_s	165.689	167.526	175.379	213.533	173.32	139.078	163.278	154.728
228948_at	134.627	123.131	125.79	135.651	133.501	136.939	159.954	163.945
215189_at	249.87	230.02	237.328	235.068	258.7	239.081	268.264	237.318
237732_at	89.3478	89.0146	97.3233	93.3842	89.7953	87.9343	86.6178	90.3319
215063_x_	744.255	772.021	828.168	784.267	666.59	498.251	678.713	593.764
235331_x_	53.9466	55.3074	61.979	55.2103	53.6095	82.8626	68.65	63.8147
242150_at	134.347	124.614	134.736	110.532	146.02	130.946	114.62	131.178
1316_at	249.3	240.997	223.379	246.617	259.896	253.293	281.881	270.772
228812_at	67.2922	80.8788	76.1022	80.7049	62.7597	56.1427	59.5795	71.3469
238155_at	61.0058	77.455	55.1536	71.2125	65.755	61.9336	67.7546	56.7208
203400_s_	53.052	57.1906	64.6705	57.386	56.7132	56.9321	60.2623	52.3821
214997_at	182.906	206.435	182.183	201.447	204.485	182.851	211.049	171.147
237982_at	121.02	96.2605	103.21	102.231	132.359	103.552	119.354	114.857
232350_x_	190.112	183.362	240.921	186.051	208.101	174.702	195.635	191.589
227386_s_	130.911	145.625	130.04	133.515	129.499	114.967	99.8872	127.194
211684_s_	1067.7	1246.14	1146.98	1128.88	1004.31	1013.48	966.496	1121.59
227250_at	326.959	683.43	690.041	552.248	657.604	714.088	776.642	945.153
216384_x_	692.138	624.514	709.527	766.828	803.757	802.247	999.371	888.529
221498_at	482.588	436.961	526.201	461.343	522.606	499.471	508.332	485.215
218509_at	393.676	385.319	413.179	368.452	401.865	431.107	449.612	411.436
243695_at	186.3	163.56	193.563	161.008	168.897	121.234	190.58	137.209
241745_at	49.1471	59.1307	90.5433	79.0288	43.8911	77.0407	77.4162	70.1335
238612_at	92.6801	86.1003	110.116	89.7461	90.0246	87.9907	87.2701	86.5582
235415_at	164.414	156.678	162.437	177.267	152.574	142.029	157.927	174.669
219158_s_	350.612	422.674	320.27	394.211	289.733	283.177	223.988	311.61
215310_at	184.535	203.117	194.005	192.07	205.918	173.524	147.187	159.695
209100_at	1316.74	1190.5	1288.46	1082.24	1310.91	1218.19	1285.77	1405.39
230893_at	485.064	674.437	509.253	633.808	438.027	424.089	409.418	476.107
208191_x_	400.711	385.615	367.157	350.046	431.237	396.392	409.603	366.351
238205_at	80.6223	71.385	72.0621	96.7067	73.0184	77.4961	86.5804	86.2351
1562190_e	89.5332	79.898	112.614	79.2573	84.5034	73.6959	85.0737	72.0551
204368_at	324.058	289.164	311.861	318.797	322.735	323.979	401.124	332.037
220765_s_	308.069	293.203	337.675	320.913	331.637	363.577	365.849	381.86
216739_at	117.411	118.584	110.223	118.933	103.227	115.693	125.419	109.506
214902_x_	419.12	415.748	441.177	473.799	422.564	306.555	391.15	416.226
243827_at	109.337	108.778	121.838	98.5933	135.387	119.13	121.89	116.2
205396_at	183.555	186.335	191.613	163.223	212.006	231.994	275.924	273.874
208114_s_	219.612	227.218	183.102	232.991	229.327	211.403	216.158	218.16
228023_x_	168.361	189.079	178.066	165.783	187.777	173.431	152.615	159.526
222129_at	158.634	155.558	165.289	161.829	153.281	150.985	160.042	156.639
232794_at	73.7312	84.9333	72.4498	76.3008	68.1366	64.4469	57.9346	63.6052
227513_s_	117.536	136.103	120.385	138.437	130.138	129.784	108.775	121.825
208735_s_	520.531	473.769	465.009	562.834	545.929	608.58	549.292	616.635

202796_at	411.236	350.307	366.736	406.917	438.716	360.177	400.491	384.35
232614_at	132.293	133.336	148.644	130.524	128.31	108.05	126.441	121.735
1561433_e	84.3276	79.417	92.6557	91.1009	92.1539	58.7651	71.3383	66.3696
220539_at	288.62	193.946	325.708	272.715	332.906	241.832	243.694	286.343
226834_at	68.0656	59.5039	67.2753	86.19	78.4918	72.8287	89.15	67.0402
224895_at	773.558	844.431	921.256	1018.73	937.062	904.97	1033.94	1238.61
205442_at	402.014	316.457	330.055	216.641	290.77	167.284	238.248	254.09
1556520_e	341.661	297.133	300.405	292.765	342.692	355.07	419.452	334.104
213503_x	957.794	1002.53	1265.09	1436.77	1424.5	938.266	936.47	1082.75
235406_x	170.481	205.772	230.461	205.227	189.745	146.616	172.376	158.915
232942_at	134.282	147.223	171.602	145.7	167.567	138.372	156.115	131.607
205651_x	35.936	26.9938	32.4538	28.97	33.8352	25.705	31.3821	35.8176
1563621_e	223.349	229.832	187.893	170.988	175.637	160.426	181.368	150.846
1566885_e	134.611	148.65	122.244	145.395	148.533	153.242	167.98	132.504
236892_s	77.6882	82.1772	95.6201	75.1141	78.654	77.2404	97.3081	92.5367
201671_x	860.285	747.869	904.488	984.504	810.109	694.135	800.714	746.792
209807_s	242.379	256.963	243.551	320.08	314.072	223.042	211.141	280.688
200011_s	197.078	205.127	189.133	216.885	216.773	198.96	199.063	201.521
204288_s	221.046	213.023	199.709	220.89	229.676	228.571	191.146	189.467
211385_x	297.579	247.282	297.656	283.295	261.843	274.942	306.379	304.836
212684_at	153.37	171.176	147.156	155.126	145.254	157.838	160.031	174.715
1559753_e	339.085	297.974	287.992	295.804	337.269	323.243	354.563	319.954
243126_x	37.7321	27.884	30.0639	26.7234	31.3768	20.929	30.8351	32.8974
240530_at	254.719	326.751	347.312	277.894	225.422	295.055	323.294	289.617
1554294_s	68.0796	53.4673	67.3926	57.3145	66.0296	64.0848	62.2716	64.9353
1559372_e	108.166	86.2546	103.91	102.44	102.134	109.15	106.732	116.19
1553113_s	78.1803	99.538	110.119	115.364	90.7635	75.5683	78.8569	99.7461
1566288_e	80.6727	65.3581	79.3327	85.4232	80.015	79.1342	89.3108	90.672
219751_at	180.254	258.485	209.01	245.919	222.698	182.173	152.783	193.776
235253_at	323.987	360.007	359.398	330.64	285.271	256.177	269.149	293.518
234502_at	117.053	108.265	125.689	109.587	140.167	128.125	127.873	114.069
224182_x	274.154	238.303	277.818	244.095	269.289	258.106	300.413	288.347
220254_at	112.108	116.994	125.898	123.079	132.005	150.857	162.23	185.432
218551_at	523.116	478.928	464.382	497.432	484.843	451.504	539.698	505.426
224284_x	751.346	854.58	821.883	810.954	757.039	643.836	600.549	653.777
243623_at	138.721	117.786	150.131	147.92	142.538	115.027	164.822	179.705
214924_s	473.946	491.026	524.208	496.124	606.011	595.295	693.005	609.2
208792_s	196.709	148.296	218.103	204.086	205.093	176.397	205.931	174.631
202896_s	348.178	337.413	330.89	296.421	330.065	343.852	349.721	335.787
215248_at	101.531	109.214	96.5361	89.7774	106.776	105.538	109.551	99.8659
243501_at	196.447	210.462	210.274	204.725	175.75	154.638	155.317	148.804
222812_s	132.328	106.461	152.348	135.934	127.661	108.459	130.926	127.972
240210_at	174.894	159.342	152.793	132.854	143.339	141.701	163.125	145.366
209129_at	137.331	124.31	144.188	122.883	143.662	124.711	140.047	115.989
240189_at	185.538	179.965	193.368	183.476	189.481	204.886	219.392	191.326
215693_x	403.439	459.05	413.835	416.295	399.37	389.323	387.808	370.368
217524_x	91.7666	115.581	98.99	89.8285	85.5422	91.7926	110.438	90.9007
209593_s	362.182	365.963	406.914	432.23	463.406	536.49	660.138	548.341
231496_at	127.414	158.744	144.733	176.178	136.092	124.789	167.195	163.146
242571_at	31.462	36.0692	23.7864	38.2181	29.9538	45.8272	39.9884	32.6471
1556284_e	79.977	100.772	91.7252	79.0825	52.189	61.1394	40.9974	66.5843
223617_x	480.466	386.792	454.812	467.968	370.484	531.601	591.304	553.828

214051_at	269.704	261.924	244.569	217.918	227.028	252.411	295.346	222.893
216293_at	212.879	176.079	243.411	209.543	205.245	162.721	227.188	189.03
1563118_e	158.698	134.387	148.295	137.122	153.844	151.566	155.091	151.026
1568986_x	1949.22	1814.72	1805.6	1886.19	2484.32	2398.5	2736.7	2386.6
201022_s	1248.69	1692.8	1349.4	1680.14	1084.03	1064.86	940.167	1046.66
223349_s	221.676	195.711	183.118	189.077	194.323	235.912	222.364	205.837
217772_s	1966.91	1496.18	1522.63	1084.35	1612.38	1537.22	1121.69	1603.11
209639_s	176.893	171.106	168.268	158.823	184.141	153.685	142.013	151.682
201566_x	147.134	101.177	99.6444	109.251	79.5666	94.8054	76.257	117.285
220874_at	133.485	241.801	140.573	170.764	153.973	150.315	174.322	157.551
223781_x	113.529	113.269	155.605	113.659	122.143	102.921	119.178	100.739
207081_s	447.942	499.083	489.025	515.728	499.063	583.994	680.826	721.818
243800_at	82.0432	66.2789	61.988	70.3901	79.6149	106.759	59.919	80.5318
212555_at	211.086	217.255	245.231	244.173	257.515	250.433	279.262	265.336
241181_x	235.054	176.394	272.839	227.391	212.795	184.283	275.133	194.637
1557883_e	35.4364	63.5912	30.8284	56.0634	32.4913	51.9951	29.5051	48.7685
235781_at	155.931	140.925	134.705	159.176	142.701	129.133	150.071	137.734
209473_at	320.681	285.871	290.414	284.602	341.286	303.855	313.989	273.578
219104_at	551.521	493.995	588.434	538.698	544.068	579.174	638.575	528.971
1557954_e	206.201	235.756	192.257	232.303	207.509	234.657	254.277	236.832
219013_at	513.566	510.6	461.782	474.596	466.015	419.456	456.134	456.985
237076_at	85.2404	73.2063	78.076	117.024	79.9255	86.8774	101.574	93.2968
215890_at	148.774	133.832	152.477	138.254	152.899	151.227	154.919	151.106
203652_at	290.616	281.919	279.939	283.454	290.622	284.938	290.091	270.988
203828_s	1927.13	763.335	1240.82	3144.02	2157.55	814.65	715.277	1888.09
212336_at	81.1704	90.8361	96.0739	94.8615	107.354	95.3128	103.619	95.1851
243488_at	83.0436	84.3402	85.0393	81.321	82.5043	84.9307	92.7163	89.6451
1570103_e	14.1455	22.2262	15.0664	14.6067	13.5521	11.5469	10.8575	9.91439
221995_s	266.722	309.987	214.563	274.41	216.74	189.383	185.73	201.763
237950_s	162.292	149.352	158.447	121.782	156.628	141.997	139.577	145.978
219608_s	91.8878	83.1198	109.258	114.436	101.36	106.449	113.534	111.527
228280_at	94.049	116.018	111.641	142.011	109.692	90.2317	124.558	110.585
221545_x	402.381	350.922	373.042	335.239	426.974	410.447	546.061	488.008
1553960_e	349.101	385.487	343.848	318.714	341.364	278.25	322.911	311.565
1560439_e	976.897	1083.42	987.752	1128.4	1055.96	947.153	1201.88	997.951
202348_s	280.166	262.761	268.144	279.435	289.31	277.128	331.202	312.145
243717_at	122.584	114.675	139.067	133.364	133.099	112.914	140.08	120.087
231341_at	115.193	109.53	83.1641	88.1024	109.66	78.0813	85.5048	78.3868
218255_s	335.906	343.646	371.195	314.8	376.816	351.555	399.884	373.3
242999_at	101.988	93.4014	102.96	91.3812	89.5342	96.6954	92.3152	93.0551
1565554_e	106.712	95.678	122.884	100.947	119.326	99.6252	114.589	93.1567
219909_at	155.336	141.892	151.171	113.299	149.153	145.925	150.625	142.317
200675_at	2414.26	2384.05	2098.88	2518.49	2437.18	2029.18	1868.56	2177.42
1558693_s	107.999	96.8761	102.81	102.573	106.685	98.3541	99.6999	102.885
1569392_e	219.869	208.764	201.158	222.257	239.347	212.655	219.275	180.765
211594_s	663.911	707.011	612.45	629.192	651.511	749.323	724.182	873.383
1560369_e	50.8153	53.2097	47.7464	58.3232	69.0103	64.594	43.7496	36.7638
243059_at	61.1463	59.346	61.6951	62.1554	63.012	53.4698	71.7061	49.7051
222035_s	458.33	422.449	452.932	405.579	333.165	361.161	311.279	429.616
226740_x	757.595	781.92	751.705	924.367	805.726	694.243	720.44	712.874
1565621_e	120.929	123.928	130.831	134.346	109.23	112.828	128.074	103.21
205262_at	213.507	169.636	197.115	198.187	192.982	188.711	236.572	235.344

221794_at	201.241	179.469	197.894	160.85	195.879	192.697	199.328	188.13
1554119_e	24.4119	57.7377	76.7113	60.36	62.274	50.0325	53.5975	52.5661
217582_at	46.7187	56.6593	56.5103	57.4148	35.0694	48.2328	46.7679	51.3349
217648_at	126.918	158.205	131.937	163.024	118.241	170.932	151.51	144.831
225537_at	290.871	334.26	343.877	375.022	276.683	248.117	240.786	275.688
216519_s	214.924	336.178	210.502	169.445	184.001	173.775	173.798	154.659
1561657_e	35.986	30.5421	36.2824	33.2393	38.6408	28.0139	32.6045	29.189
212800_at	75.495	74.8512	64.9196	79.4461	65.6596	74.9193	72.8223	73.2582
243258_at	761.506	726.572	914.976	800.028	1068.46	1401.78	1748.9	1347.24
230628_at	73.5132	53.8989	81.7193	77.6417	67.5223	49.8902	69.2757	47.7104
205560_at	114.901	85.4498	134.194	114.528	112.808	105.571	115.185	87.5416
212895_s	405.112	399.852	402.659	331.167	376.771	436.043	519.129	447.223
218007_s	1573.65	1778.45	1649.5	2280.07	1489.67	1457.55	1468.93	1575.07
210427_x	1015.91	1053.78	1382.2	1509.53	1409.5	987.299	964.159	1131.39
214755_at	90.3179	72.5848	103.568	87.9983	101.847	80.839	98.5853	95.1551
221382_at	473.731	454.947	505.254	484.383	471.575	509.643	547.669	448.435
1562981_e	239.283	218.527	217.768	232.513	229.182	204.546	253.494	250.462
202291_s	384.389	397.348	572.566	879.435	534.193	590.042	447.184	611.823
239902_at	75.7539	77.8988	53.3952	80.058	68.7879	54.4149	57.9467	62.9059
1566833_x	69.7397	58.9339	73.0653	64.6571	63.8973	50.6753	61.9139	52.199
242160_at	452.798	424.733	434.707	432.91	522.461	502.471	584.894	431.095
244320_at	95.4931	101.747	107.863	105.258	98.2791	87.5322	114.807	104.96
200625_s	247.499	285.9	265.495	313.443	249.072	248.448	246.501	287.254
223829_at	93.8628	96.1667	96.9303	92.1732	100.996	79.9323	89.3682	70.1958
237240_at	116.7	109.192	130.89	118.916	129.658	116.06	156.79	135.869
224363_at	75.6665	59.8662	53.9179	58.2267	75.2945	64.6497	65.6789	56.228
240916_x	164.234	130.626	176.565	140.857	144.712	131.122	146.951	137.384
220833_at	168.927	157.047	172.517	177.452	172.212	157.954	170.733	172.219
202090_s	7912.23	7393.77	7233.19	6548.46	6780.37	6655.94	6752.11	6289.26
217143_s	169.935	169.195	165.997	158.481	143.183	156.929	173.297	128.405
212154_at	148.826	160.409	185.384	244.755	185.874	193.359	198.02	256.959
212432_at	716.852	576.046	512.285	531.352	574.697	552.975	492.772	617.109
221215_s	299.62	259.161	280.425	269.734	320.934	313.973	372.366	314.494
211630_s	176.496	139.156	185.942	158.516	152.161	155.016	183.208	162.468
1559232_e	83.3412	69.4149	78.8173	71.6568	82.1817	81.14	87.0185	75.8006
228275_at	413.898	401.865	471.006	245.626	344.641	267.744	321.665	332.827
221715_at	407.513	457.481	440.712	425.197	409.445	430.233	385.957	404.856
233873_x	495.91	483.139	489.158	485.545	434.931	366.965	441.969	415.444
244366_at	306.111	251.139	263.949	262.646	288.163	296.421	329.439	288.933
212653_s	415.333	453.325	434.644	515.412	434.992	400.535	424.639	395.812
236723_at	76.2399	91.4588	81.1857	84.7351	76.3132	86.1181	87.0406	93.4025
243232_at	107.553	132.104	138.934	102.567	123.569	124.542	96.8128	125.927
227677_at	210.091	202.985	199.368	220.273	189.391	215.687	256.54	213.666
220475_at	237.798	236.337	247.594	236.67	231.107	222.29	251.173	215.763
219933_at	940.432	898.732	763.55	684.497	595.93	605.626	483.388	742.253
239831_at	198.749	191.467	220.567	197.955	207.606	191.318	238.377	221.207
221681_s	65.2392	43.2374	69.8889	63.8951	47.6911	42.0083	60.8682	47.199
240093_x	22.316	20.3541	18.2626	18.4304	19.8009	13.5345	14.513	14.5782
219083_at	531.233	501.5	542.637	544.638	679.407	931.156	1030.46	949.545
217965_s	236.259	231.605	232.863	238.376	228.191	194.786	207.24	205.381
1560977_e	52.2346	56.217	47.7276	44.8105	45.8252	50.4355	38.2648	47.6578
239593_at	129.321	116.758	166.898	139.205	116.147	113.641	132.497	105.94

244340_x_	56.1322	59.3848	56.4567	56.9642	38.5829	35.8293	24.7497	54.8311
221697_at	263.899	264.641	310.436	300.67	262.336	251.868	275.318	274.681
1561222_e	7.99084	7.26556	7.1489	7.46678	12.43	6.44578	6.49174	10.1285
1553186_x	183.534	283.991	161.009	194.061	202.189	179.533	193.614	212.705
1560204_e	61.907	61.8	60.4037	62.0357	54.2915	42.9448	61.1831	53.9159
200020_at	1313.4	1549.64	1165.86	1151.01	1448.13	1228.35	940.908	1256.01
222481_at	181.64	167.053	159.259	175.52	178.483	147.156	155.84	162.953
212676_at	289.561	326.266	339.535	304.858	331.16	335.106	328.422	352.769
1569935_e	347.98	399.828	361.29	435.451	397.226	372.446	376.61	359.368
214011_s_	857.595	780.908	788.02	742.386	777.78	797.585	857.249	858.296
211506_s_	93.7689	83.8115	130.901	89.1553	103.918	78.1476	108.068	88.8718
207844_at	239.579	220.32	229.786	206.175	220.155	214.244	260.274	237.817
244092_at	135.91	132.485	135.434	133.843	127.545	122.067	150.81	128.366
224792_at	176.43	206.162	193.736	170.309	214.791	188.992	189.221	191.66
1566924_e	106.633	107.216	134.185	119.602	130.086	115.893	135.507	132.415
200908_s_	573.949	759.293	714.665	769.712	614.228	407.236	406.361	473.519
238165_at	290.065	336.992	314.949	329.622	301.987	236.46	197.48	221.035
234702_x_	25.1861	18.8661	24.7561	19.4106	28.2114	29.1478	24.2763	37.3015
236300_at	290.296	271.45	311.991	279.915	232.404	249.291	321.171	255.987
230502_s_	271.534	297.865	274.964	291.096	290.78	262.952	318.458	320.915
208933_s_	98.5386	109.216	113.347	108.615	90.8494	98.5333	103.565	92.1231
44790_s_a	33.6388	37.3646	36.3168	47.4722	35.7492	34.6826	33.8993	29.35
209013_x_	364.472	348.339	396.794	376.509	393.541	430.853	464.375	432.791
210701_at	134.613	121.75	133.274	153.352	131.241	101.748	136.52	119.519
212916_at	226.367	220.127	210.174	207.388	260.403	256.12	243.548	234.619
1556063_s	185.516	171.783	167.169	199.718	202.525	184.419	199.036	192.23
222987_s_	356.255	337.439	304.32	246.741	234.093	223.307	266.87	286.458
212882_at	348.8	287.074	302.998	321.209	328.479	300.792	422.939	354.192
1559712_e	240.62	216.418	207.805	233.669	220.952	248.689	246.022	217.539
238589_s_	161.951	128.354	167.665	138.523	159.061	134.079	146.19	144.65
207363_at	105.279	80.6436	128.418	102.366	121.652	74.7936	88.0587	72.8998
210507_s_	153.004	146.28	175.27	125.649	163.399	146.329	158.995	165.197
223350_x_	841.551	882.087	863.914	799.641	835.327	1010.56	1134.32	1028.82
233292_s_	133.316	122.307	144.338	141.52	153.401	203.511	192.942	205.969
1556598_e	54.7985	63.3574	48.7666	37.907	45.3568	60.141	58.5672	67.2724
200714_x_	973.874	828.296	921.155	885.681	986.674	1028.68	1136.31	1022.31
201301_s_	317.499	260.675	314.897	260.148	316.043	329.915	228.602	324.365
203863_at	8163.38	9237.47	8556.88	7132.55	8265.97	9518.93	9636.64	9298.85
220190_s_	47.127	56.9633	67.8232	48.0946	71.92	56.877	59.1	55.9228
236970_s_	61.3542	56.1101	68.8138	57.1865	74.2155	68.2414	70.5724	55.2374
234189_at	164.508	152.076	160.468	121.713	170.002	157.475	164.986	146.622
1560717_e	22.7009	29.6503	30.0687	19.1438	25.7759	21.9834	17.0097	24.432
224465_s_	296.808	294.271	295.405	291.602	333.927	269.444	264.858	268.833
203254_s_	336.895	271.576	301.603	276.779	388.746	509.345	492.193	669.897
237122_at	86.74	81.6167	78.914	91.9346	87.5249	96.5564	94.2296	86.5791
221269_s_	338.501	351.596	402.429	319.543	390.216	424.164	390.138	446.639
209875_s_	53.5932	70.7569	76.5403	68.8087	65.326	67.1949	70.7187	57.9104
230932_at	196.182	203.432	197.792	169.528	170.54	179.012	171.792	182.672
223700_at	47.206	39.0279	34.055	48.956	29.2307	32.3066	40.2901	34.3942
207018_s_	20.5702	18.6561	12.7569	15.8704	8.83544	20.879	17.5002	10.8912
1552553_e	91.8834	75.9121	76.5561	100.64	82.2303	93.3351	82.5239	87.9264
228553_at	99.8441	102.801	110.954	109.099	118.711	102.378	116.016	98.7611

212626_x_	860.449	1035.45	866.83	1097.87	964.211	956.762	956.56	1209.2
234344_at	98.1777	116.846	114.113	153.487	98.4865	66.3461	78.612	89.4348
229265_at	469.725	429.332	404.313	534.688	370.517	434.73	455.067	558.031
228069_at	38.5723	33.4939	30.8468	42.0762	38.6252	32.6831	38.249	29.6053
230319_at	191.503	180.706	173.119	160.624	180.604	147.25	152.552	136.103
219997_s_	238.638	214.012	227.75	202.98	227.814	207.926	235.954	250.372
237210_at	104.942	126.265	119.483	105.473	119.086	109.749	98.6915	105.532
217252_at	158.221	166.18	166.672	143.607	156.905	149.153	155.802	140.061
238020_at	305.749	428.791	428.649	511.641	327.101	327.592	354.466	320.207
240405_at	163.962	166.185	160.171	174.193	149.18	184.081	222.645	175.822
208120_x_	737.433	857.324	826.437	817.272	772.036	713.66	642.829	730.172
242837_at	89.2654	85.2271	82.8228	82.7117	87.4372	100.437	92.7359	94.6589
1557128_e	149.021	142.124	114.446	109.4	109.597	120.76	155.041	128.546
218988_at	341.837	337.286	333.877	349.306	249.693	234.381	252.107	299.16
1564475_s	87.5506	81.255	87.8851	85.1994	90.855	75.2328	82.3895	80.9806
239468_at	22.1222	24.9559	23.4277	21.2382	24.6376	26.0624	23.654	21.034
202392_s_	365.198	376.77	359.007	286.217	373.329	321.522	365.114	341.776
225297_at	196.394	221.593	181.395	223.986	176.194	151.683	127.701	173.324
219707_at	1128.62	865.478	998.079	859.184	1065.7	1153.83	1476.8	1171.02
206017_at	134.614	120.363	133.306	107.376	129.073	129.283	130.735	133.871
1570447_e	269.106	227.253	252.061	318.266	234.025	254.193	305.328	261.701
1567213_e	198.571	229.166	213.496	234.653	228.278	192.705	179.928	171.254
240107_at	48.1806	52.1068	59.5601	41.2391	55.6703	65.1914	54.5448	54.1716
233601_at	252.891	242.778	232.516	245.412	285.969	277.468	286.954	294.916
234308_at	239.222	224.865	235.514	239.976	253.069	263.603	294.469	251.778
1558661_e	64.3785	73.1354	67.4387	58.3301	72.1501	80.8641	75.2185	73.5357
233472_at	180.681	191.31	166.326	176.373	210.025	166.59	138.126	148.286
220078_at	187.794	169.834	181.168	164.585	178.139	180.324	164.041	161.829
1567214_e	193.376	262.237	239.925	264.977	210.248	131.209	134.296	151.662
208094_s_	307.685	360.473	347.84	309.311	330.764	331.383	288.646	324.606
225488_at	216.218	191.335	221.65	197.949	226.981	197.478	253.444	223.287
220625_s_	52.8216	37.6146	52.6239	52.5479	42.2588	34.7601	40.9085	49.4784
222343_at	145.715	148.848	160.762	135.704	169.755	171.313	152.171	155.312
238144_s_	145.921	135.538	159.176	125.362	147.922	133.422	148.421	134.433
1556452_e	83.8065	75.1656	75.6299	92.3846	80.3024	87.1808	107.424	107.199
231146_at	140.298	126.39	149.549	122.18	149.149	145.702	133.753	127.906
226464_at	275.763	259.631	269.888	304.164	237.852	302.59	274.897	268.578
203280_at	421.193	358.996	424.106	337.862	410.372	458.286	474.664	469.099
230874_at	32.0789	32.8096	36.3554	29.7896	39.217	30.1745	25.7826	24.1808
227669_at	538.793	572.862	718.217	519.694	447.563	507.451	452.541	571.116
1559006_e	46.8563	66.4267	65.9077	69.5747	63.3022	51.8331	39.6773	55.4493
220206_at	81.2375	85.8766	85.3198	88.508	91.2303	77.7952	79.7341	74.0706
230528_s_	170.951	173.821	158.939	175.597	169.162	172.342	164.335	173.531
208488_s_	155.423	150.372	166.184	157.963	156.514	144.409	164.049	162.941
214149_s_	118.096	156.994	122.051	134.639	113.794	89.4618	89.9116	122.662
200769_s_	232.512	189.962	213.07	236.028	271.351	504.032	504.728	686.614
235327_x_	398.419	471.552	461.171	495.458	395.614	332.091	442.239	441.595
205971_s_	211.439	207.233	210.237	204.28	219.749	215.157	200.265	188.464
224886_at	520.376	429.374	479.862	391.081	485.126	543.995	613.222	496.706
233318_at	28.3852	29.4044	33.3901	29.2213	26.3329	15.4395	39.1931	12.8178
1566749_e	10.5288	9.82963	14.5602	7.27937	7.60752	6.70337	12.3094	4.06271
208178_x_	377.847	337.783	346.313	371.277	376.846	429.111	458.256	439.555

241406_at	95.2514	91.1081	108.464	86.8042	119.043	92.8788	114.601	100.432
216243_s	159.297	171.172	169.664	183.832	174.873	174.778	199.926	194.5
226836_at	244.826	232.523	221.539	221.767	225.964	217.318	275.292	236.568
1559595_e	82.8493	79.6454	72.8532	83.0687	85.3418	91.6593	87.6026	81.7022
243841_at	82.3736	108.078	78.8289	67.8932	96.1574	93.6842	74.5388	83.8253
233809_at	315.205	427.981	303.433	373.725	280.836	246.488	224.287	279.421
235449_at	57.9783	58.2262	60.9333	71.6995	57.6717	63.0384	65.0119	58.1683
236453_at	150.448	133.292	165.225	195.014	141.821	131.549	144.991	113.742
222898_s	165.258	156.78	185.043	152.364	167.422	160.784	191.847	181.911
230402_at	203.597	197.929	228.155	168.466	212.164	190.136	211.429	197.027
238040_at	160.171	199.684	166.214	167.628	170.136	173.428	167.561	162.25
1565661_x	215.306	187.194	175	178.656	172.709	205.721	209.166	206.61
218492_s	326.445	267.945	295.931	292.102	287.111	262.56	328.212	311.821
242990_at	104.011	104.595	112.609	82.5028	121.196	115.041	90.3987	97.2346
1552993_e	49.4103	46.8067	43.9271	52.8727	34.1453	45.2464	39.3148	43.0959
202365_at	210.07	231.379	204.897	247.086	180.638	214.79	211.042	228.74
1556679_e	193.346	191.351	203.613	188.678	188.966	147.238	195.024	159.159
233419_at	79.5639	62.0393	87.2294	58.413	74.0939	54.4147	70.8361	61.3606
232088_x	98.3529	82.5257	96.428	110.566	84.7111	75.8186	83.419	63.852
214837_at	37.7708	42.2756	43.238	48.7001	39.0588	40.7713	42.4431	48.3832
1566694_e	18.7228	15.5836	13.1238	18.225	14.9169	20.2649	16.3215	20.6478
211066_x	510.268	525.828	559.125	631.306	644.319	573.012	615.169	633.572
1561754_e	85.7399	94.3759	83.751	84.6286	79.6782	81.3546	73.4785	70.3766
239190_at	84.5364	83.1588	83.6072	88.0361	81.4844	85.5899	75.9858	77.664
231233_at	154.312	132.015	158.082	140.721	134.585	139.668	133.226	147.186
218582_at	358.297	341.331	326.901	362.097	340.172	360.844	306.953	412.267
203724_s	120.638	128.321	124.743	174.454	116.334	102.493	108.537	128.625
203846_at	390.574	536.298	428.908	588.353	398.469	432.902	529.257	535.104
1557248_e	243.106	204.162	219.344	263.372	230.124	224.822	291.384	258.53
238677_at	95.1777	81.6821	79.4471	78.6927	82.2373	103.02	87.3595	101.025
226733_at	170.698	179.19	130.857	129.172	181.099	160.811	189.811	152.177
229420_at	854.978	1053.12	875.307	844.396	647.371	460.765	547.66	538.422
1564822_e	209.242	215.102	207.833	215.1	232.787	229.034	202.765	172.178
230808_at	241.45	242.359	228.431	185.22	248.176	228.433	213.563	231.891
234275_at	248.064	230.998	238.379	210.033	271.105	279.346	263.514	245.201
241771_at	156.756	184.028	165.828	165.038	173.445	152.703	177.282	156.071
217750_s	516.612	487.289	463.01	491.404	604.407	559.929	594.55	636.133
237521_x	54.8433	57.5963	66.2524	53.5319	65.8524	53.8241	58.7339	58.3462
1556425_e	98.1167	77.4183	83.6601	91.9589	89.7564	89.7421	115.281	94.6173
208109_s	45.1254	42.176	47.1462	42.9587	45.637	46.6877	38.5044	35.1257
225134_at	296.339	292.297	319.344	282.566	307.339	323.925	323.391	338.964
1560047_s	105.332	123.047	149.616	133.866	137.266	94.1913	235.798	83.4917
232896_at	67.309	69.9825	104.856	60.9597	71.2054	64.6591	76.6268	69.6533
240702_at	31.2426	28.2365	44.4562	29.5432	32.641	39.1405	36.6918	32.3013
234394_at	100.344	91.814	105.902	87.6808	84.1237	88.4197	74.0831	81.8692
230475_at	197.687	190.801	178.81	213.015	219.839	193.595	256.312	226.024
1570486_e	72.1344	82.3338	76.8077	68.4465	71.4711	63.4604	70.2873	70.1118
230946_at	226.061	249.764	251.311	212.223	250.841	238.908	231.749	243.438
213612_x	780.383	788.499	805.405	938.639	779.438	677.823	711.434	666.278
225730_s	155.639	147.42	149.101	154.834	171.797	181.383	157.215	183.435
208859_s	343.289	456.999	310.598	454.7	315.94	413.776	296.965	420.853
232681_at	69.3375	127.121	92.3063	118.627	78.8702	74.0929	81.8058	81.5486

227861_at	306.09	360.299	359.493	346.577	333.985	289.968	270.356	277.399
239478_x	94.6468	79.0843	117.514	98.776	99.3234	76.1113	87.188	81.4103
1560864_e	41.9057	38.8563	51.6277	40.2223	49.196	50.4382	46.4882	45.7888
1552564_e	105.645	81.4468	103.945	85.7484	109.562	92.6342	107.527	98.3244
200002_at	9922.87	10568.5	9840.19	10589.2	9866.16	9153.56	9086.76	9285.33
217419_x	209.547	201.138	201.416	189.395	194.834	217.391	228.067	218.155
221426_s	232.96	230.647	233.204	194.991	247.046	219.463	204.96	215.186
235722_at	288.652	296.161	255.988	299.269	248.356	321.17	238.057	307.804
226880_at	1767.04	2490.48	2770.66	2720.25	1941.68	2076.9	2288.73	2322.72
204771_s	345.211	437.162	366.371	418.781	327.421	246.598	262.231	294.889
234881_at	339.1	355.251	341.483	307.869	369.983	354.286	331.177	335.631
1566576_e	73.9672	80.1213	80.6083	70.1191	67.0741	61.5573	62.8877	66.3909
241998_at	95.9536	88.1408	91.3118	80.9704	88.1386	59.2898	77.2481	76.8843
204943_at	364.649	339.037	346.126	381.203	419.165	376.663	533.354	389.052
232220_at	140.17	120.393	141.309	113.924	126	117.152	125.316	122.786
214140_at	171.707	175.594	177.286	167.384	180.117	143.016	139.777	149.516
1559256_e	53.4952	50.703	51.1502	60.0266	52.006	54.4615	54.2116	54.4825
223959_at	108.128	98.9248	112.553	110.646	122.826	124.554	130.674	100.837
1556204_e	25.8315	25.1363	27.8452	20.9173	26.5171	16.6489	34.3136	20.1926
229140_at	794.871	640.177	622.021	593.241	716.776	587.902	658.064	646.596
223337_at	498.954	455.891	474.454	436.046	395.678	423.603	427.962	475.203
240016_at	78.5728	80.3918	90.5275	82.1751	88.6482	68.3139	77.8239	73.5354
235628_x	130.265	136.744	146.624	133.219	120.589	119.227	140.161	131.772
214135_at	278.873	254.307	271.302	312.28	259.745	281.972	316.161	251.637
225110_at	1311	1540.82	1186.09	1311.89	1043.97	1069.5	1001.06	1116.64
239282_at	18.2819	25.3073	20.1337	25.8253	24.1527	25.9213	25.7658	17.3912
214320_x	313.552	276.031	308.856	293.566	304.744	299.072	356.406	310
215945_s	206.043	221.45	214.495	190.911	233.86	195.555	203.264	207.397
222078_at	114.219	86.916	134.138	104.515	109.743	100.022	109.279	93.4116
225748_at	699.274	677.144	733.605	800.016	876.357	824.745	1000.82	857.698
217009_at	243.667	253.616	252.262	229.311	256.909	241.109	234.791	238.379
210435_at	103.623	93.7015	122.32	105.76	110.647	97.3523	106.876	105.825
43977_at	763.299	995.973	770.69	821.083	694.936	682.951	781.695	841.068
214942_at	39.587	43.0385	39.8378	33.0479	36.2908	39.5732	51.0532	30.8362
202915_s	575.492	469.945	506.722	486.26	684.455	591.051	725.874	648.487
232519_at	184.999	166.811	204.395	154.486	177.318	174.236	205.089	194.116
1562736_e	88.2711	106.718	101.651	92.6983	85.6143	115.135	124.071	80.0537
205024_s	258.431	262.666	264.095	285.533	295.217	310.573	340.111	296.195
215679_at	147.324	145.119	148.519	130.549	163.302	152.273	196.767	170.154
1553411_s	60.7707	65.0467	60.5217	55.634	72.7601	58.545	56.4339	58.086
202427_s	2037.05	2113.62	2343.65	1924.21	1956.9	2024.86	1896.37	2331.54
213635_s	128.163	142.093	124.165	136.647	123.374	133.453	134.115	152.033
209700_x	1519.91	1966.71	1645.38	2134.45	1661.76	2069.4	2222.96	1912.73
244129_at	46.0209	44.4368	45.8992	43.0281	47.928	43.3007	40.8498	43.8537
1559239_s	243.995	213.711	229.43	169.52	194.537	222.023	237.3	215.233
239335_at	127.518	116.742	151.625	135.756	112.091	114.121	142.256	130.054
218302_at	226.956	219.92	242.846	258.937	266.018	290.787	368.209	341.797
210556_at	102.715	77.7225	109.27	100.506	96.489	91.1749	85.5589	78.4652
218103_at	530.436	492.727	506.399	552.932	597.912	546.05	670.192	623.069
228920_at	159.813	174.278	138.271	166.952	163.309	160.518	158.879	153.944
1557801_x	307.204	276.313	267.571	339.254	270.734	306.084	360.426	346.878
221597_s	321.105	296.773	281.778	291.584	278.592	277.233	297.889	295.36

244832_at	125.337	106.146	134.114	137.71	185.055	128.495	96.5494	98.4617
229202_at	99.5436	126.246	106.699	119.029	90.9236	89.0283	96.3589	73.3432
211437_at	99.8164	79.0429	103.838	76.2988	106.838	89.1586	95.289	93.6895
221068_at	304.688	308.768	347.963	289.904	335.157	310.635	280.778	334.232
231539_at	64.4526	56.1103	72.3364	59.7742	64.9964	43.9026	58.8823	47.4728
224196_x	525.273	558.362	524.096	482.398	536.142	518.854	552.144	517.308
209848_s	236.887	242.838	249.222	251.104	233.531	255.711	259.372	287.647
206264_at	254.587	255.838	247.024	283.454	259.142	270.837	318.656	298.936
235052_at	39.5131	40.0592	48.2026	36.2998	40.5602	34.0351	38.0026	34.1949
223551_at	38.0298	32.1757	36.3025	34.3363	30.4993	38.8065	28.876	28.6204
208777_s	1187.76	1111.36	1105.08	1267.09	1145.03	962.799	952.204	1210.95
233775_x	646.826	794.77	800.204	783.341	825.774	613.001	687.861	717.166
202747_s	833.777	951.657	921.634	935.428	1043.67	921.637	882.459	860.707
216479_at	585.449	612.44	577.084	599.094	539.393	376.184	464.858	475.837
236019_at	100.413	105.559	102.116	111.571	125.024	125.064	133.852	129.134
1555456_e	70.6208	74.9928	64.3555	64.1403	56.1789	59.0306	68.163	60.085
205830_at	40.1915	38.2518	37.3911	32.6682	46.3362	53.4943	43.5508	38.0892
210776_x	413.161	418.746	417.035	399.936	467.406	431.662	488.491	459.881
239960_x	389.844	512.819	440.161	443.679	329.241	391.483	318.8	381.134
223909_s	344.66	310.47	361.54	357.405	313.775	428.815	524.738	424.991
233214_at	128.921	122.488	143.176	115.979	132.142	144.67	150.972	141.256
233341_s	251.734	226.143	244.383	260.147	225.472	236.387	302.196	259.112
221303_at	107.595	104.648	101.172	98.4363	89.2647	101.905	111.021	106.452
236840_at	94.1879	88.2047	69.797	93.4906	87.0594	83.8149	117.78	80.8077
223021_x	383.367	443.042	471.191	470.413	371.099	422.081	377.187	462.827
227061_at	149.371	167.014	176.033	214.28	166.643	169.817	150.997	135.705
232530_at	61.3443	63.518	47.5981	52.5834	51.0748	57.0433	75.2196	65.8569
225095_at	133.044	143.068	146.004	140.532	163.785	163.493	143.811	140.806
214869_x	639.908	720.247	695.726	523.903	683.6	681.078	799.744	861.085
243692_at	358.939	301.559	333.86	359.67	395.318	448.64	575.706	447.786
221791_s	6131.04	6225.87	5452.58	6189.84	5619.13	5563.6	5339.1	5460.43
217188_s	191.763	184.361	194.733	214.227	202.607	238.977	246.372	255.155
242225_at	82.3178	78.5643	97.6748	79.9837	75.5373	68.022	83.2375	61.5602
203468_at	178.431	150.197	168.734	135.756	141.396	141.426	165.326	166.321
222961_at	303.062	282.596	269.051	222.337	318.071	288.012	339.204	289.351
1563502_e	52.8954	41.3892	50.1433	50.3271	52.616	42.5911	57.7602	52.5151
1559691_e	50.9548	59.9202	61.2337	63.685	52.7729	48.645	59.6378	44.5882
211935_at	377.332	401.711	339.461	468.814	376.203	359.933	292.101	367.137
1559614_e	61.5103	50.3603	77.3006	63.7907	57.4941	55.1674	53.4275	70.2449
228311_at	214.26	202.432	232.587	175.282	206.717	218.505	223.435	197.397
209118_s	446.898	441.533	610.283	822.621	488.595	444.737	473.88	708.686
218398_at	625.977	504.514	621.413	497.794	522.827	517.811	487.681	528.272
238532_at	500.552	735.197	661.462	620.712	568.75	488.096	478.157	504.545
202803_s	152.221	184.25	193.899	163.343	173.996	148.552	183.966	186.573
209066_x	9030.27	8885.33	8837.82	8232.48	8421.9	8090.66	7579.91	7820.91
202575_at	285.809	317.068	331.205	299.917	356.883	339.163	351.96	342.335
234675_x	1100.95	2205.21	1169.04	1437.47	1622.12	1168.33	1517.36	1384.63
234097_s	1.46379	2.71842	0.13365	0.096127	0.996243	1.53868	3.70874	4.94224
46256_at	1772.44	1661	1513.4	1509.27	1827.98	1779.56	2046.64	2094.77
209834_at	205.224	209.127	194.989	238.864	237.6	200.989	204.065	226.524
237980_at	40.9082	39.3155	40.9235	50.3472	29.9644	35.1482	36.9728	44.104
1563715_e	112.751	107.827	101.017	112.827	100.216	92.0164	112.648	95.244

206065_s_	156.582	132.881	173.587	166.091	127.121	185.351	182.659	136.077
224551_s_	158.798	154.464	202.568	133.746	169.089	155.84	160.48	147.566
243867_at	145.797	123.51	131.203	147.049	165.136	136.007	133.64	115.389
243642_x_	299.578	330.438	301.101	320.08	333.989	317.053	351.126	328.571
204336_s_	309.195	317.1	316.218	280.462	340.762	311.656	344.306	317.161
200971_s_	274.88	279.457	255.221	320.631	280.13	264.946	240.291	260.175
221268_s_	167.263	173.312	160.596	165.717	168.393	172.836	181.274	182.63
222877_at	56.5519	66.3409	50.9377	66.8669	50.3803	57.3196	59.8507	52.7097
201929_s_	152.256	151.348	149.697	161.595	171.242	162.358	154.73	175.303
205172_x_	1118.55	707.859	914.785	866.968	974.038	889.319	877.211	1080.16
237513_at	86.7488	63.1941	77.5917	72.689	86.8106	73.2812	88.7391	79.2061
210036_s_	190.304	172.146	175.214	189.179	196.136	194.503	229.883	223.648
241642_x_	134.039	191.478	135.931	167.033	152.238	129.19	150.004	136.708
207252_at	242.773	241.26	231.529	236.199	226.737	245.11	248.781	225.851
213441_x_	1027.68	920.207	894.521	928.834	1056.51	1025.61	1147.16	1088.27
227450_at	162.156	147.063	143.879	150.248	174.472	156.464	160.457	147.873
212556_at	316.842	318.817	271.234	273.077	276.36	260.259	274.416	296.239
202943_s_	288.207	259.358	245.887	268.284	262.345	277.449	317.797	300.144
1562462_e	192.313	179.982	209.105	215.17	186.357	209.569	261.51	235.838
208104_s_	312.388	296.044	293.192	268.736	316.123	303.788	350.806	343.243
213099_at	403.382	409.704	409.665	452.33	382.282	369.982	441.048	438
227477_at	244.228	265.137	222.822	239.332	249.084	244.817	238.76	254.214
1553207_e	190.292	222.356	224.409	167.503	179.565	182.848	200.774	147.315
234403_at	267.796	259.069	272.24	251.224	282.247	290.653	317.69	288.214
1562572_e	197.36	196.976	171.658	192.422	204.665	160.52	143.545	145.147
226951_at	315.214	474.384	373.975	393.556	321.357	359.079	287.038	341.785
1555015_e	192.44	219.135	167.837	212.071	229.4	163.516	182.732	180.464
204150_at	220.692	211.395	246.196	294.859	247.463	212.739	266.067	249.614
1557881_e	32.5884	26.8138	26.6789	29.1249	20.7703	28.4164	36.2817	29.3556
240665_at	84.5981	107.002	82.8693	109.825	87.6397	108.959	94.4827	95.4697
240060_at	295.72	277.679	291.646	301.1	300.622	305.645	340.948	349.648
207495_at	123.952	107.583	151.693	117.661	111.368	120.779	136.963	126.924
236203_at	65.9062	33.8449	62.7999	36.8408	43.8097	45.3096	49.668	35.5349
242778_at	100.137	82.5321	113.669	87.1316	99.8536	91.2052	106.298	95.1684
207438_s_	775.861	746.428	699.41	666.043	605.541	663.454	811.795	708.795
203167_at	495.017	416.464	418.105	372.152	399.452	449.746	459.128	435.702
237077_at	64.3395	69.4	60.9208	82.8566	57.483	71.7928	71.8862	66.7766
203729_at	240.385	229.893	245.484	219.391	254.534	276.981	282.542	300.07
1566217_e	101.901	89.0347	114.205	89.8888	117.134	95.7342	80.6131	90.6126
1564178_e	85.5882	84.3909	77.0483	90.0714	93.3611	107.785	90.7978	85.566
203138_at	1150.53	1222.53	1227.45	1261.44	947.795	919.637	790.239	1124.02
211233_x_	212.829	201.153	215.708	213.679	231.789	237.823	247.546	243.435
223409_at	173.733	151.427	211.054	168.688	178.733	154.412	184.158	156.56
204400_at	86.9213	86.6102	89.239	87.0943	80.7489	61.4137	110.339	99.9702
212813_at	347.829	356.997	350.484	356.88	399.072	354.763	393.3	367.941
222043_at	56.7325	52.3677	61.7575	77.7753	64.3298	59.7485	42.3503	54.4214
221541_at	688.692	699.372	714.184	690.513	852.98	901.544	1065.06	904.74
211171_s_	140.779	137.144	136.792	152.425	149.23	142.202	168.308	139.217
227600_at	326.853	390.947	349.539	277.299	292.467	329.965	269.866	354.55
1569777_e	62.8589	73.3553	74.7036	88.191	74.9858	66.4594	74.0135	62.0946
1556188_e	226.165	229.431	205.722	232.564	229.829	237.038	257.794	250.749
217092_x_	6914.17	7087.17	6945.82	7214.43	6826.65	6201.52	5915.32	6286.14

241240_at	238.627	197.064	215.331	210.538	234.882	230.504	300.913	263.382
206649_s_	359.795	339.465	366.376	350.843	396.569	379.1	383.561	406.636
1554737_e	98.4034	96.0162	116.657	111.107	112.287	90.2397	97.4999	80.2895
1570250_e	32.724	18.7923	29.9604	24.0162	32.7879	15.5001	27.3213	28.0647
206257_at	338.811	331.531	337.661	315.104	356.639	347.357	339.752	351.447
244116_at	53.2063	112.062	95.0351	114.862	88.5715	61.6266	50.6049	46.3028
224560_at	605.123	681.32	686.258	1020.51	718.957	796.961	654.661	727.401
214732_at	108.436	117.57	98.2585	100.966	108.538	159.277	132.416	137.227
1554522_e	14.0027	9.73921	17.1751	12.1469	10.9958	9.63851	14.9784	13.3274
239754_at	157.512	133.634	144.542	117.24	146.41	127.386	154.589	129.459
226949_at	271.044	224.677	239.517	224.645	246.721	235.909	259.127	260.508
243375_at	73.3227	84.03	83.7331	84.7756	76.3464	84.9717	94.6775	88.9247
212039_x_	2631.85	2689.6	2632.89	2877.58	3731.41	3486.92	2498.93	3144.39
208791_at	236.969	185.986	281.994	276.343	290.817	304.323	284.68	259.952
1553645_e	57.0583	67.1683	58.9908	47.3573	61.3346	54.8518	46.5283	55.8195
1562878_e	88.042	91.2369	89.177	87.8655	84.3718	94.5853	94.6561	90.8317
224725_at	132.426	130.6	125.863	132.925	138.655	126.581	124.928	136.13
1563244_e	113.993	96.8039	100.269	112.487	128.207	122.925	104.59	106.258
201590_x_	1262.73	1442.44	1731.99	1749.59	2153.84	1353.29	1066.64	1296.25
216421_at	218.084	221.335	228.358	193.324	191.613	177.777	193.154	196.95
243876_at	94.5661	76.9762	96.0109	70.1632	81.4379	78.3197	96.5195	72.7022
226334_s_	119.397	124.157	118.269	123.51	103.922	93.7239	95.9218	121.772
230564_at	148.022	127.826	151.287	153.436	134.728	144.327	155.038	131.323
222798_at	284.93	430.607	338.248	353.332	250.945	258.222	274.065	248.475
205247_at	256.052	267.789	247.552	234.462	254.337	282.784	297.048	270.26
229395_at	242.057	215.188	233.452	247.54	223.14	230.29	238.44	260.687
239918_at	108.347	98.981	113.504	96.9709	90.7149	107.465	114.14	111.227
239419_at	252.73	258.451	250.311	201	266.992	251.324	277.595	255.382
1561280_e	53.4317	52.0534	40.7081	42.055	59.1322	62.6154	61.122	45.8083
230840_at	188.273	174.461	200.336	165.814	175.143	165.511	179.103	180.675
235669_at	116.203	110.493	120.378	107.726	122.922	139.986	134.052	119.901
208790_s_	278.344	278.283	312.616	315.371	285.394	319.567	370.992	371.571
212765_at	343.78	292.352	320.055	360.943	296.11	270.937	291.038	298.956
227208_at	551.57	616.613	605.156	509.385	658.842	613.058	551.602	593.587
202437_s_	75.7502	65.3704	71.4371	131.805	92.1646	82.6692	77.5854	70.5936
212565_at	252.438	242.261	246.824	233.912	223.67	252.473	269.111	221.39
206023_at	86.0576	81.0679	90.6486	92.9791	77.3012	84.8939	87.8341	85.6206
209620_s_	615.243	555.851	651.097	499.385	554.532	487.761	489.33	466.094
226811_at	849.189	1323.98	1145.74	926.891	1285.31	913.601	883.378	1178.6
220676_at	86.0262	80.4397	99.0692	77.0268	83.5795	77.0682	79.4006	79.9114
201482_at	535.529	442.211	443.623	475.29	506.453	472.378	555.505	524.915
203956_at	340.223	411.23	321.486	366.479	321.742	318.366	253.561	298.807
211685_s_	173.843	217.94	204.78	222.718	212.123	208.821	184.614	199.624
1556507_e	2227.78	1816.42	2280.89	2190.59	2606.68	2260.87	2754.52	2197.18
225449_at	264.839	222.874	250.984	241.326	253.055	266.29	319.639	287.558
1565265_e	129.489	112.971	121.848	170.201	130.785	104.668	142.845	153.366
242089_at	69.0954	65.5593	67.4725	65.7763	63.6995	61.316	67.2088	47.7438
202261_at	647.091	571.975	587.82	640.484	742.404	605.162	596.667	647.707
223475_at	27.2287	44.7291	36.7709	42.4931	37.4764	40.5929	41.1173	36.2791
221595_at	86.493	94.7164	83.3562	97.8969	74.0227	83.5193	94.8519	85.4936
226014_at	167.044	204.989	192.37	193.721	168.68	146.827	148.277	136.074
242539_at	44.3892	54.7954	48.5462	40.8688	40.6969	39.2611	51.854	43.9162

203219_s_	336.013	291.043	300.489	327.942	269.144	299.297	373.239	320.426
1557861_e	68.3915	60.156	65.0982	55.2281	65.8219	51.539	58.6614	52.7601
228530_at	68.6032	73.5235	63.4076	76.4117	56.565	57.7967	60.0019	58.0955
200881_s_	683.889	794.828	505.537	716.892	377.072	520.809	509.608	656.192
212349_at	363.443	368.34	394.23	337.022	391.739	368.086	365.046	362.382
1566969_e	23.4489	18.7097	22.5702	22.506	31.2133	24.8927	24.5612	21.0113
233193_x_	116.734	101.497	105.749	93.6555	119.224	119.505	122.453	103.849
241293_x_	225.941	183.208	267.364	214.344	233.396	174.759	257.503	193.128
232876_at	164.231	161.417	150.639	136.759	166.217	177.338	173.318	166.417
214512_s_	794.334	770.094	785.909	900.86	812.184	795.769	721.918	945.239
226351_at	232.663	252.888	238.439	256.07	274.555	259.15	286.46	264.726
205767_at	18.4837	22.6033	18.0466	24.1141	20.6084	28.5513	19.4344	21.1554
235309_at	1237.8	1894	1613.91	1756.88	1130.9	1300.96	913.534	1056.06
236700_at	42.4385	46.8218	41.2652	47.712	25.6505	37.2594	35.04	28.0414
220860_at	65.8762	57.2496	62.7347	71.732	64.2129	57.0001	65.1582	57.0612
215194_at	231.843	227.617	222.747	197.406	226.235	223.902	232.678	239.215
220696_at	119.075	97.0437	140.181	107.564	109.151	101.48	123.996	100.617
216218_s_	301.342	405.757	388.459	403.49	343.392	425.508	355.827	530.952
203159_at	311.203	266.755	280.609	269.33	312.08	275.255	265.716	256.923
205277_at	254.781	224.789	200.285	225.066	210.195	194.079	196.904	210.519
244010_at	56.8909	49.4159	63.1874	53.2141	57.0308	40.6468	72.3737	34.2337
217775_s_	228.741	231.262	253.698	273.946	225.058	220.304	246.096	246.286
241978_at	227.154	246.907	240.341	243.608	203.813	235.347	241.523	245.485
228369_at	91.7054	85.1986	83.8349	93.0197	100.007	88.5576	88.6165	102.68
223802_s_	625.943	635.069	626.571	678.136	592.784	656.626	665.223	744.853
223057_s_	101.3	96.4661	103.166	106.222	111.563	124.246	125.36	108.092
231135_at	178.693	161.994	186.748	157.153	177.327	161.758	175.958	176.241
223043_at	2971.47	2619.01	2834.97	2726.5	3297.95	2709.2	2890.64	3229.72
213771_at	536.037	458.119	461.595	491.769	558.097	559.077	556.15	617.361
229593_at	208.379	188.953	202.061	176.573	194.537	220.845	219.376	207.568
242866_x_	211.546	185.662	239.182	207.718	208.634	185.914	237.987	192.609
240230_s_	89.303	78.3464	91.8776	77.8408	76.3627	73.7466	79.809	63.995
240239_at	149.985	174.503	149.563	178.682	127.267	138.342	143.985	175.984
211172_x_	303.518	305.493	316.722	301.691	281.892	277.496	309.816	318.018
1553401_e	48.5782	44.503	65.5844	60.4186	72.6887	42.5067	58.2388	45.809
206313_at	215.211	195.848	181.985	196.996	212.712	194.029	250.551	228.77
229697_at	208.666	185.245	191.43	203.188	175.85	197.152	221.125	202.592
206826_at	34.501	37.0288	47.3765	42.1626	41.1351	36.8654	33.4497	29.851
225779_at	295.511	262.165	309.453	259.079	267.52	249.826	291.853	284.258
208659_at	448.55	437.442	435.94	477.119	493.4	451.925	483.112	449.077
205664_at	121.215	118.245	150.471	114.671	115.897	136.546	104.001	130.181
215919_s_	95.5551	83.9557	87.3804	74.2839	91.6066	93.304	54.8962	65.6746
214453_s_	122.949	114.261	111.167	98.313	129.98	119.383	112.651	112.008
238650_x_	515.428	491.967	447.233	482.255	500.023	486.043	564.63	500.329
210367_s_	153.697	136.375	162.529	153.894	153.149	148.189	183.57	163.413
244200_at	175.232	165.042	166.041	191.64	173.566	148.888	189.98	177.235
215456_at	86.4079	82.1126	80.5706	93.081	105.084	82.7101	81.0735	88.3309
228864_at	65.3156	77.506	72.95	89.6777	75.6274	65.9171	71.1642	82.7002
1555171_e	70.6492	44.2822	75.2221	49.9404	48.1448	59.3759	58.0778	55.1445
219901_at	122.656	134.179	115.523	119.336	120.296	111.03	138.115	118.328
214159_at	44.7356	37.2973	37.4886	33.3967	42.4497	27.2583	33.3759	34.2816
1555335_e	82.1383	82.8843	87.0321	83.2946	87.9606	73.3966	87.6529	70.9944

241031_at	58.1104	62.8339	55.1091	56.2975	64.798	56.8114	42.9146	47.8723
231403_at	110.121	91.0302	114.987	120.484	119.473	86.9923	122.098	110.301
1554341_e	210.986	216.498	208.478	233.469	203.1	216.848	209.008	227.387
243078_at	245.245	251.09	245.533	227.055	236.856	235.676	214.477	265.545
212291_at	291.315	331.63	339.496	395.798	318.022	286.057	381.769	406.828
200998_s	293.902	264.213	270.028	312.669	300.815	268.497	334.37	303.984
206432_at	118.343	95.8203	101.472	134.139	99.7169	109.392	100.717	95.5428
241419_at	153.825	141.132	140.448	137.775	147.648	151.766	193.893	157.897
1567359_e	58.5912	65.2675	57.8	62.5399	66.0041	49.3672	53.3875	63.5236
220764_at	142.269	137.188	121.644	172.708	152.075	163.383	157.171	188.562
239605_x	76.4991	74.0152	86.4916	86.2119	79.5063	65.8262	96.0112	89.9891
240918_at	308.899	310.278	318.661	263.793	349.637	309.884	316.26	310.487
1561611_e	340.6	302.281	310.225	356.112	308.471	280.556	359.409	278.158
235727_at	188.291	222.107	191.262	247.448	190.1	245.188	259.823	238.175
242132_x	78.3934	68.7504	96.8312	73.3355	81.6235	90.5311	104.466	90.9725
204973_at	220.009	211.022	230.867	193.582	209.643	205.696	234.671	200.746
222881_at	129.906	129.614	147.874	113.37	151.912	140.729	136.214	144.126
202951_at	304.744	290.745	299.451	299.201	282.055	292.461	260.694	335.619
242836_at	31.567	28.9663	25.8452	17.7142	35.6329	31.8516	23.6664	26.7905
235115_at	38.6514	30.9754	26.5612	33.9764	37.3732	24.2044	37.5542	32.8192
213631_x	149.597	187.475	169.596	177.611	166.696	134.452	153.884	160.481
235165_at	30.9906	29.1263	33.0324	29.8662	29.4641	19.6976	8.79806	19.937
236320_at	226.344	211.32	200.537	228.416	244.665	230.966	227.418	227.384
1557480_e	1909.34	1175.22	1365.23	1804.22	1526.85	1007.67	1514.96	1363.29
217481_x	204.435	205.414	254.26	220.89	188.728	207.817	290.796	222.024
1565765_x	541.057	642.253	573.333	636.943	484.594	428.61	513.362	489.348
1558813_e	43.2958	34.8446	32.3421	35.0637	39.5974	55.3195	46.322	41.9883
1562349_e	63.9015	62.1851	52.0386	57.8078	73.4342	49.8378	55.0813	50.0227
206551_x	249.372	257.41	273.961	273.487	232.3	235.84	232.319	232.403
1556117_e	90.2129	88.9262	92.0043	89.3704	103.41	101.023	107.351	98.8877
239108_at	69.2417	67.7053	72.8057	71.8191	70.9066	70.7518	72.4995	64.9974
1569881_e	65.7394	49.0901	60.0007	57.8906	61.1578	71.2718	59.1777	57.0079
201441_at	8653.76	8190.03	7759.34	6100.96	7333.98	7806.96	7226.15	7201.75
215198_s	101.451	89.75	124.376	88.0967	109.15	89.433	94.1362	90.8365
1556434_e	134.054	124.384	110.69	142.64	117.654	146.05	142.635	136.313
243048_at	106.074	92.4274	100.948	86.8311	97.2422	99.916	90.2458	89.3325
234231_at	122.881	114.263	129.959	114.919	115.317	104.947	119.889	116.198
237747_at	173.657	159.879	169.921	169.816	197.471	187.961	185.153	189.353
218159_at	384.02	394.919	353.873	416.17	377.157	371.661	439.383	444.387
210260_s	47.5501	62.9249	61.4692	68.3635	47.4277	48.9299	58.4782	46.1622
204628_s	258.177	257.737	259.364	224.522	271.266	257.561	272.535	250.658
216033_s	126.755	136.851	125.163	132.044	117.675	158.964	136.752	163.298
241440_at	108.369	120.663	97.4045	126.507	116.999	189.344	178.952	193.485
219813_at	33.6099	37.739	37.2357	35.1977	38.2164	44.4765	48.1011	54.0042
224726_at	221.762	229.603	222.258	272.942	218.81	181.518	242.811	223.054
1557754_e	63.7263	55.2959	56.5656	63.0962	67.5109	69.7943	63.1768	65.339
241615_x	136.661	148.862	135.786	137.173	124.824	134.845	167.682	140.227
226623_at	283.576	297.487	255.318	298.81	278.589	235.272	227.289	240.737
223292_s	326.849	329.09	332.161	298.211	265.292	210.093	192.712	218.048
210347_s	327.447	298.554	321.196	418.071	367.321	426.191	382.474	441.835
230968_at	215.664	214.467	179.837	203.95	199.758	164.579	182.927	182.158
237883_at	118.869	99.2413	129.726	117.472	130.488	144.558	149.285	134.34

221048_x_	117.376	116.548	143.049	126.696	127.64	128.414	149.918	128.52
244730_x_	565.534	713.884	572.131	619.602	609.964	398.052	401.915	425.31
240300_at	126.985	120.676	134.743	123.424	147.797	120.147	135.548	127.929
217618_x_	361.242	398.296	366.134	397.157	254.927	222.519	303.243	265.91
201970_s_	232.749	225.352	223.137	248.086	243.072	239.577	237.561	253.442
208967_s_	1794.72	1503.87	1450.45	1112.79	1455.46	1299.44	1144.6	1331.91
222671_s_	188.162	155.327	170.874	167.376	178.72	164.636	185.375	183.394
221667_s_	4393.27	3952.59	4033.89	6280.01	5181.13	4913.05	3828.28	4503.45
215997_s_	111.55	120.766	159.547	122.399	153.017	87.6825	103.375	101.757
210021_s_	58.0018	68.5627	60.3737	63.3183	50.351	51.7749	59.8864	62.262
242521_at	117.389	149.75	125.598	135.527	93.7255	96.4765	123.786	105.026
1552657_e	176.727	158.783	167.094	185.052	196.356	200.792	230.565	211.547
201562_s_	206.496	210.253	196.105	206.16	229.338	215.513	236.781	253.062
230437_s_	117.619	109.181	118.31	116.05	120.067	132.475	121.183	130.324
236059_at	88.5727	83.0124	85.8937	84.5851	108.646	78.8583	77.7565	75.89
225673_at	233.613	243.933	273.342	252.734	248.128	239.872	245.934	326.468
228640_at	25.7767	31.8638	29.7481	28.3641	29.5507	36.7028	23.8191	27.4297
232380_at	101.996	95.2876	81.4234	76.1222	113.184	83.7204	70.1474	80.1068
203750_s_	246.018	188.465	279.05	209.878	214.026	180.275	262.939	188.845
223341_s_	264.398	355.317	372.858	351.651	250.74	345.358	324.879	396.68
36829_at	3404.28	2759.19	2861.87	2951.44	3143.09	3803.39	4091.79	3909.95
225676_s_	353.859	418.783	398.444	440.258	299.065	284.19	249.566	420.491
238719_at	297.295	361.715	346.81	391.664	311.479	245.625	281.245	310.467
202995_s_	114.374	122.5	124.062	193.328	155.327	205.756	168.214	204.75
221236_s_	176.622	172.494	157.214	164.374	169.2	168.371	171.039	156.774
1555561_e	23.8633	27.3241	29.0572	28.321	28.6327	28.9107	24.748	22.1344
224744_at	650.446	543.548	664.037	733.324	737.275	833.556	987.902	951.502
239311_at	157.285	138.346	176.781	122.7	160.011	146.878	160.689	155.879
1555385_e	205.549	164.172	210.637	177.002	182.315	204.8	214.134	213.887
201726_at	744.443	871.058	796.09	793.549	733.918	750.773	655.851	916.402
228353_x_	48.8007	36.0375	51.0913	46.5855	29.9696	41.6614	56.5099	49.9557
1569472_s	46.7545	58.1025	49.4973	57.5579	43.2314	85.5944	85.3408	91.5165
209418_s_	342.907	340.171	323.727	354.42	317.542	294.538	301.41	317.345
206374_at	159.68	133.736	154.973	151.092	162.331	165.261	202.186	177.09
214314_s_	1548	1666.72	1464.62	1587.34	1243.12	1085.76	974.583	1264.82
1566454_e	154.533	141.102	127.749	128.457	116.558	137.515	193.625	140.065
236158_at	165.482	134.199	136.942	159.826	135.59	156.437	178.88	161.246
1557301_e	43.3387	45.4805	47.8538	42.0695	45.9403	47.4381	36.9774	37.2506
227624_at	253.998	252.812	262.138	275.814	243.137	232.57	229.194	251.606
228263_at	344.452	337.837	322.829	298.956	346.962	368.244	372.134	376.306
201944_at	543.679	487.03	482.884	579.3	518.764	486.565	404.258	468.991
244531_at	86.2737	72.6119	92.9155	64.1514	67.84	66.8557	70.448	72.4016
200916_at	381.874	348.163	386.446	375.467	373.351	393.726	463.162	467.991
201915_at	180.455	154.49	146	160.224	157.131	140.824	150.79	170.556
1559276_e	87.368	89.2016	87.6339	97.2883	86.9963	71.3576	92.6139	83.4081
243173_at	105.004	98.2013	112.118	85.4736	97.4541	104.688	104.311	94.4536
225604_s_	151.563	173.434	163.192	147.569	172.812	158.648	175.057	192.558
1558428_e	51.9833	63.2681	65.5788	50.8336	65.7976	56.6285	43.7612	44.8493
212147_at	366.165	360.741	391.524	335.807	383.524	376.737	406.025	409.903
230388_s_	361.746	842.015	1325.23	1161.44	320.373	562.62	1104.03	1080.13
204743_at	167.846	159.802	171.72	184.083	177.986	179.788	185.95	176.292
1567687_e	45.0444	30.8766	59.7823	38.1063	49.9118	29.1674	40.4566	35.7947

214660_at	32.6843	47.0983	27.7398	41.0138	23.0631	39.4591	42.8876	37.3302
1558782_e	220.203	215.033	240.792	269.78	242.344	254.841	287.304	246.854
228133_s	88.177	74.9677	105.593	87.3466	82.0234	93.2609	96.337	83.4711
209651_at	217.814	192.044	225.787	209.051	230.837	246.056	210.341	237.84
207939_x	928.591	893.907	888.141	928.932	995.503	934.512	1014.81	1234.18
224529_s	327.987	310.855	307.004	362.236	252.232	322.652	395.907	371.3
208307_at	226.333	211.79	220.046	226.553	225.324	239.398	294.9	262.591
211044_at	133.44	135.947	115.883	141.615	126.522	100.506	85.9791	102.525
225929_s	365.642	384.714	362.026	363.142	439.879	356.458	378.014	389.947
1560209_e	16.7189	17.6642	8.33831	13.1566	19.677	8.56239	5.25666	6.63933
1569802_e	131.17	123.505	111.095	112.816	126.152	120.834	73.1903	88.2495
1560386_e	155.047	144.042	130.738	173.386	141.937	156.312	171.802	162.747
221607_x	1553.73	1770.58	1984.14	1984.7	2363.68	2299.13	1876.31	2483.01
220631_at	434.388	464.391	441.472	408.577	504.442	485.918	408.875	429.722
201881_s	420.622	481.193	416.53	479.308	429.348	477.008	467.764	572.123
227541_at	87.5479	103.737	99.5955	116.004	82.0807	86.1158	73.2449	77.9662
234547_at	133.133	130.341	115.905	124.184	155.914	127.339	137.588	119.709
241470_x	56.1898	85.0553	79.6107	79.5762	47.5193	67.5676	89.0086	91.968
206996_x	2363.01	2292.63	2436.67	2536.44	2957.92	2505.06	2958.6	2710.51
209079_x	490.803	493.854	516.808	547.539	615.025	567.601	568.656	623.959
216963_s	109.606	93.273	100.149	107.757	102.376	91.5255	115.639	100.638
1569025_s	48.4405	57.1985	55.4455	69.4125	54.2991	72.1537	57.974	61.6671
218706_s	57.174	67.2865	68.7648	69.0518	72.2753	71.2533	76.6969	69.481
219501_at	106.788	104.675	104.103	136.937	94.6996	102.867	108.471	111
204010_s	248.548	301.945	238.71	243.542	167.177	116.672	118.085	141.11
1569225_e	121.685	114.693	100.756	125.957	144.219	96.5394	84.4644	94.2486
221187_s	442.338	458.737	484.789	378.494	528.302	473.586	430.099	421.61
1569929_e	50.6576	46.7293	45.851	45.2673	36.1562	37.0781	39.9983	39.3364
206735_at	380.702	258.705	306.545	213.596	318.791	293.46	341.59	238.815
233431_x	114.708	96.3531	108.627	97.1844	100.165	87.6551	112.769	88.2121
228487_s	238.173	394.849	533.065	389.62	155.859	229.729	350.552	176.567
219505_at	218.095	222.336	211.842	216.465	207.781	224.373	249.159	265.642
231701_s	233.797	252.406	211.007	243.662	187.946	241.16	265.042	232.545
242314_at	201.616	194.895	204.394	167.948	204.679	206.39	198.815	193.918
212545_s	229.781	181.684	206.195	191.778	220.283	198.056	203.21	209.762
204892_x	5224.93	5261.48	5389.69	6850.06	6079.14	6158.81	4427.23	7079.94
206029_at	115.269	106.48	125.031	108.693	133.897	98.3848	126.143	127.135
210264_at	207.75	172.873	191.187	193.851	190.259	180.567	213.179	189.581
208597_at	146.025	128.334	128.707	137.268	134.154	151.641	158.391	134.134
1553805_e	439.995	259.732	337.076	250.78	330.015	338.963	470.271	320.501
230380_at	63.8258	55.8768	55.4622	57.3278	63.9419	53.6564	57.9508	48.3684
213881_x	3813.81	4237.99	3888.33	4124.77	3755.54	3323.41	3317.99	3547.38
229365_at	294.461	272.338	261.043	247.065	296.521	239.229	251.757	251.307
212696_s	635.789	654.227	638.155	689.099	713.242	613.08	702.637	708.655
227967_at	186.135	208.306	173.363	176.705	140.901	120.809	136.448	158.28
241608_at	55.6113	61.39	45.1826	60.6811	46.1968	59.617	48.9837	45.1637
210753_s	404.267	448.241	440.054	389.005	449.888	393.522	367.78	432.487
201523_x	623.27	612.157	688.182	634.956	638.234	738.244	746.348	802.673
1566279_e	88.3128	95.0144	75.7181	69.6156	83.38	74.2861	57.5626	60.3588
49485_at	240.559	253.16	237.467	241.682	233.316	213.277	236.047	242.515
215162_at	70.0459	66.9285	67.6928	87.0165	78.401	77.5732	83.0924	70.2961
241467_at	428.329	427.988	452.847	406.766	446.76	453.951	485.417	428.792

216280_s	65.3932	62.156	71.8104	63.2768	57.0726	61.2773	61.0747	62.31
220252_x	344.113	408.396	396.281	420.188	341.608	307.952	427.326	446.602
228337_at	186.157	176.543	180.67	188.688	165.213	167.827	213.922	209.254
229447_x	646.387	637.782	646.334	882.981	653.486	612.314	655.655	684.07
210767_at	113.836	88.6982	133.285	99.6792	115.767	89.1847	112.729	101.697
239857_at	114.216	118.396	107.985	111.55	117.465	77.2106	96.4196	88.8837
234293_x	199.071	163.851	233.313	163.935	194.157	164.898	213.844	166.651
1568012_e	58.8862	62.8616	48.272	50.5889	49.5703	62.363	69.3513	61.7354
210937_s	84.0558	89.1306	138.556	105.06	102.609	81.7324	116.383	74.1122
1562275_e	63.4611	73.5005	76.2548	97.0348	70.6736	75.9608	66.7531	82.2031
205006_s	154.728	173.749	133.535	154.011	133.154	120.337	133.928	123.198
1560002_e	109.151	140.928	111.735	107.316	94.1031	84.0325	99.2765	87.0748
226896_at	1005.54	1126.13	991.719	938.242	707.322	712.943	680.21	870.003
239617_at	177.013	193.499	208.282	227.761	200.675	188.276	244.96	189.643
217006_x	188.458	161.155	219.152	160.529	183.329	155.382	175.276	170.891
239258_at	32.2004	23.0182	36.6279	25.2256	25.0879	25.0771	22.56	22.5909
215946_x	181.88	184.112	176.448	192.909	184.474	181.126	188.761	181.498
1559469_s	340.945	288.174	276.656	267.514	313.684	283.238	374.995	259.857
220115_s	140.735	125.57	118.492	156.67	133.17	125.824	127.232	148.191
224758_at	131.881	148.031	162.083	146.993	105.883	88.6928	91.2486	103.861
209376_x	1276.1	1217.45	1312.03	1299.25	1404.43	1643.9	1812.79	1705.05
225096_at	936.05	915.197	779.532	837.257	801.068	698.492	793.059	791.144
213974_at	147.774	158.59	149.446	140.549	144.373	142.618	160.507	156.894
219995_s	18.2015	13.9702	19.7491	13.6912	15.1737	15.7112	12.4148	23.0676
244441_at	75.9614	72.2821	67.9984	87.0585	69.6812	66.5216	63.6056	57.5308
219137_s	702.497	720.979	809.101	855.089	576.559	569.475	601.099	682.977
204520_x	309.042	283.753	274.431	335.601	290.924	297.656	270.301	314.051
200605_s	1771.57	2105.49	2295.12	2747.61	2180.99	2065.35	2121.6	2629.58
1555898_e	78.862	77.8227	73.9124	64.0559	77.6999	68.6134	63.4747	73.9774
232733_s	206.17	212.14	213.565	190.192	207.814	214.543	207.82	206.469
207765_s	265.251	226.927	239.439	200.067	245.854	262.565	263.06	272.998
202159_at	323.57	324.268	312.4	315.083	283.761	249.218	248.752	310.743
222216_s	527.058	523.368	493.148	462.537	457.078	441.038	497.449	529.786
209036_s	8423.52	7200.13	7344.16	6780.07	7304.52	7894.2	7413.77	7842.14
1554744_e	64.2748	75.077	52.5148	49.3716	87.6761	57.8871	63.7919	62.3305
221783_at	470.22	453.572	417.699	431.493	571.412	448.99	452.526	438.151
223221_at	436.726	403.842	383.175	418.48	418.765	406.507	333.613	370.735
206105_at	90.7091	93.105	112.816	101.647	85.6079	86.4926	89.2026	90.4954
225320_at	901.004	1038.5	1039.66	1028.7	1025.07	1217.28	1310.15	1456.34
237302_at	7.25471	8.54711	8.54906	9.76545	10.4528	7.31839	12.8926	13.977
78047_s_a	1676.62	1610.01	1718.44	1903.96	1936.42	1868.31	2166.15	1867.06
202886_s	65.0962	56.9288	68.7603	68.2135	74.3709	70.5926	71.2913	77.7669
1559343_e	209.644	294.787	210.346	277.353	157.016	127.925	125.79	154.529
1557580_e	16.7684	14.5393	12.2099	14.6282	9.75754	15.7604	8.32297	17.8556
235705_at	111.962	122.76	122.252	101.03	127.04	130.618	116.397	93.9382
241072_s	79.3056	78.9612	62.5904	100.708	73.4085	60.4291	92.9997	63.1426
208166_at	35.7175	37.8718	43.021	43.3392	45.407	42.0445	50.3208	49.2585
1553202_e	61.4257	49.2476	58.138	44.1615	48.8096	45.5371	52.5174	38.6642
224504_s	185.459	182.15	178.446	207.867	185.684	181.548	208.304	192.859
201217_x	2682.76	2724.56	2698.27	2872.61	3539.27	3593.95	2464.73	3018.15
1558643_s	94.1609	92.7574	108.398	113.854	104.814	104.95	105.009	87.6509
204407_at	42.9883	50.0615	60.8451	49.681	58.3325	57.1313	62.1283	47.8276

1560187_e	39.565	46.36	37.3326	35.7629	38.6872	31.6909	30.2901	35.9684
1570335_e	60.5784	62.8701	48.2628	65.3717	62.5353	58.9141	55.7742	54.3027
227378_x	617.204	581.243	585.24	565.935	613.371	654.578	704.239	719.046
203871_at	266.536	240.117	261.946	224.486	263.526	271.882	239.751	250.339
221877_at	648.126	615.895	571.831	629.872	562.773	534.884	606.034	588.998
228304_at	121.365	155.341	168.334	182.539	155.154	154.749	122.968	135.171
204562_at	122.157	124.797	111.35	135.935	109.467	116.252	115.405	112.928
216361_s	57.492	60.1097	45.4675	69.1203	51.2692	99.2914	81.6076	101.797
229277_at	163.41	170.406	151.492	131.183	144.64	154.705	125.65	141.531
231368_at	151.598	150.752	152.449	140.667	151.635	145.275	133.869	136.584
217577_at	87.7102	79.5498	69.4708	65.7726	95.2902	86.5258	80.2957	70.1917
1566267_e	63.2578	60.2274	87.3034	64.9488	62.8357	52.0009	57.9187	54.3846
236016_at	143.294	175.167	168.35	319.561	200.168	112.818	166.553	139.744
244259_s	123.121	119.65	176.767	151.439	168.206	115.784	126.192	99.9003
215987_at	86.7758	91.2833	96.9024	68.5232	84.1752	63.5622	73.6309	69.1004
226435_at	86.089	71.7214	78.5326	84.8104	82.135	67.3493	70.3826	54.8795
1555737_e	160.87	151.728	133.966	152.919	149.362	176.494	182.027	173.235
1553470_e	57.7864	51.7768	51.7316	50.0058	44.1135	59.3573	57.3719	45.5128
223345_at	196.892	189.363	212.967	193.575	205.321	209.108	229.674	207.796
238871_at	136.424	136.27	149.351	106.258	159.728	139.029	126.978	138.129
1555807_e	114.86	106.436	119.884	117.862	129.89	129.206	128.762	106.394
215504_x	1386.89	1409.77	1515.71	1532.07	1360.46	1148.7	1508.51	1248.73
201720_s	301.541	249.542	269.811	275.465	341.174	317.335	323.925	343.629
1561789_e	5.21507	8.17752	13.697	8.21401	1.75937	17.6402	9.89266	16.7674
230305_at	184.188	230.723	211.718	239.939	206.159	157.764	178.494	169.653
1569730_e	140.348	148.835	139.074	154.847	137.398	132.912	152.097	133.523
214647_s	59.4254	45.4732	70.6463	55.5207	49.1485	58.7899	56.0382	74.1111
209883_at	309.004	363.632	245.225	260.655	328.09	275.443	332.716	379.224
205673_s	61.6322	59.7498	62.4985	62.3174	52.4994	62.2139	59.1449	48.7229
219878_s	186.972	171.142	197.441	202.483	240.974	289.404	267.509	271.88
206679_at	327.371	327.212	348.054	309.356	349.032	363.772	422.938	340.894
226242_at	181.063	188.756	187.37	207.091	187.712	160.84	174.882	175.656
224359_s	143.267	129.852	162.527	160.028	112.53	139.731	145.217	124.066
214044_at	77.2457	97.4402	102.174	86.1618	77.6761	75.4185	64.76	58.2623
238860_at	146.63	154.467	120.054	140.033	135.738	124.479	109.678	101.505
217346_at	102.765	130.826	107.73	147.291	77.3883	95.2243	109.42	103.953
201864_at	651.21	660.298	700.294	712.563	911.823	731.912	805.258	733.936
227442_at	263.333	234.112	224.498	234.009	201.824	158.162	162.761	186.876
203858_s	1115.6	932.181	1059.94	769.237	1013.7	947.624	943.016	1096.83
222087_at	236.788	245.593	267.569	278.763	258.213	253.146	306.945	261.69
217461_x	122.22	166.959	160.271	202.517	127.56	128.464	153.958	146.823
1556933_e	65.0717	67.0821	60.1833	54.9234	63.8833	55.866	56.6546	55.047
1562330_s	131.437	115.035	127.948	147.856	119.63	142.955	166.864	135.472
241029_at	68.9171	64.0272	66.716	62.4623	62.5665	46.638	57.2192	62.2845
227012_at	226.179	210.808	276.943	213.089	157.856	245.67	217.796	304.554
218599_at	209.122	178.075	213.593	205.804	175.638	198.684	214.014	210.234
1558459_s	241.073	241.708	251.303	267.442	259.776	219.958	304.142	240.227
200742_s	425.527	463.31	479.492	505.365	466.056	571.826	556.233	562.326
201156_s	398.398	358.219	349.828	395.408	363.865	317.265	383.52	398.07
237553_at	164.609	146.694	166.243	144.017	158.091	154.506	145.548	143.735
1562166_e	143.339	120.735	119.898	138.205	128.331	137.289	139.823	131.392
221781_s	148.518	161.059	140.298	140.751	134.845	147.629	132.4	160.648

211074_at	1307.7	1465.73	1647.54	1715.45	1287.6	1062.45	1474.21	1261.79
238008_at	145.229	135.635	137.694	156.277	147.056	133.771	169.414	145.666
237873_s	70.8489	66.2428	66.1939	68.4724	74.9876	56.4929	72.8009	52.8284
240338_at	150.593	143.837	136.958	129.309	162.971	143.761	176.113	147.506
203560_at	68.2085	97.2815	84.4641	97.3342	68.1976	77.5366	77.6	74.6593
204688_at	196.772	235.105	218.822	222.733	211.017	223.394	232.439	232.792
235313_at	9807.56	8997.67	9736.94	9142.73	10473.8	11885.9	12061	9868.15
238235_at	203.736	195.069	202.811	206.524	213.231	201.633	234.346	192.264
217815_at	478.995	471.26	419.79	496.719	485.433	447.467	441.973	473.94
228075_x	355.164	395.616	334.706	389.234	356.364	291.493	307.627	294.297
204044_at	187.894	170.142	180.678	160.962	192.354	187.211	190.5	195.379
225930_at	681.129	701.714	690.917	694.516	693.528	636.86	590.536	658.951
222333_at	479.024	431.891	486.499	470.713	478.185	502.236	545.263	511.733
205594_at	156.25	189.246	157.5	178.669	191.009	185.259	198.973	150.476
244398_x	74.6974	73.4185	83.5591	55.8583	86.2995	43.1413	52.8124	54.159
230267_at	76.1671	65.5677	79.5825	79.3834	86.8502	68.017	74.5382	58.4986
1568616_e	157.203	150.091	149.768	171.779	129.649	137.236	172.407	162.982
201928_at	519.591	668.414	627.555	595.259	470.308	475.689	489.658	513.013
223601_at	453.238	419.129	420.123	457.092	458.858	481.094	613.098	544.419
1570352_e	35.4843	30.0474	32.3192	35.9181	29.0536	24.6555	31.3904	37.9021
238468_at	893.005	691.596	827.633	862.581	928.155	943.547	973.982	1013.44
222247_at	109.597	106.902	115.212	108.761	109.287	106.108	109.819	113.124
223372_at	164.946	133.672	164.439	118.23	140.657	139.668	153.032	141.552
222341_x	56.2019	58.5087	53.1104	42.8953	47.0435	37.3096	17.5936	58.5277
211570_s	412.666	423.784	369.579	429.299	379.869	332.685	326.605	393.585
1554922_e	39.0968	34.9103	30.936	31.1036	37.0091	26.0178	14.1325	22.7353
1552283_s	134.845	145.368	144.028	120.348	120.88	105.927	136.089	144.277
1561564_e	24.5068	19.8767	26.1136	20.9533	30.7443	3.9731	11.4922	11.5555
224639_at	320.534	414.1	383.468	423.42	321.626	297.493	357.974	343.201
208739_x	942.282	1006.82	985.163	1080.08	987.51	1176.08	1161.98	1407.07
215715_at	178.827	141.405	138.701	152.791	180.04	179.884	189.232	149.822
229459_at	95.4073	103.875	114.086	89.1306	101.77	105.48	96.77	101.169
206875_s	435.732	419.941	429.005	542.493	432.975	375.627	397.864	429.527
223429_x	303.582	352.285	279.394	363.97	279.044	289.1	273.299	326.883
1562091_e	67.0917	54.4922	69.0061	76.3074	84.5759	89.8475	90.2931	64.3094
243081_at	103.319	108.31	119.015	108.996	97.7298	78.2322	102.72	84.0236
226814_at	388.481	343.424	408.606	389.423	510.147	488.223	637.729	524.279
209478_at	489.627	499.087	516.275	534.617	522.296	488.041	501.374	486.363
208789_at	1196.23	1177.38	1286.14	1284.11	1412.22	1056.77	1310.48	1237.09
241199_x	169.946	199.919	217.452	153.51	230.203	191.59	159.638	200.815
229479_at	70.2978	68.9122	90.9379	77.5586	89.7936	83.2042	88.7831	74.5865
208626_s	589.802	525.138	559.007	606.091	578.694	614.678	625.436	600.326
234382_x	39.2067	32.1046	47.2367	37.0527	39.3754	35.7005	33.463	43.4824
1566760_e	181.966	165.227	146.783	182.901	183.517	171.352	171.607	147.775
1565150_e	73.3742	77.1016	63.1329	89.5126	90.6909	63.9352	84.3462	71.0139
225617_at	120.654	136.367	124.21	140.854	153.854	164.952	185.013	164.1
215384_s	213.541	214.824	238.864	232.528	251.757	194.825	212.697	186.339
229160_at	438.3	577.128	699.785	567.06	378.818	322.277	469.299	431.63
207163_s	486.783	398.237	418.943	353.671	494.597	488.865	606.657	610.44
228654_at	30.2136	37.1027	34.5718	48.1608	42.0891	32.7778	30.9587	28.4312
206284_x	1313.97	813.21	1093.6	1013.28	1199.03	1089.77	1088.51	1324.32
203696_s	188.73	194.005	164.962	210.682	165.356	171.303	191.177	198.132

230952_at	223.707	234.404	228.721	196.929	225.975	240.61	237.012	261.682
241432_at	85.2383	94.9957	95.8598	104.456	103.283	66.9966	57.9449	66.3085
213067_at	75.7481	70.4118	86.5777	83.1271	81.7409	71.528	74.407	71.1183
1569073_x	119.59	108.918	150.334	136.826	129.636	114.683	125.254	102.797
242300_at	193.55	239.084	175.846	193.551	159.334	161.611	138.488	172.711
213034_at	507.535	665.175	576.865	677.536	559.424	389.382	435.574	533.374
204690_at	818.576	751.658	697.74	688.455	617.292	495.452	480.33	545.455
242501_at	39.0237	38.8245	38.4625	43.9885	37.4704	38.8073	48.3359	44.2487
206927_s	289.744	298.213	302.642	314.842	299.736	333.037	328.026	362.049
200601_at	249.043	254.232	283.949	263.69	280.406	365.219	342.869	376.08
205392_s	530.227	495.824	483.252	437.924	640.227	627.75	657.12	531.572
228823_at	409.404	411.481	442.538	353.166	433.834	432.727	468.645	427.768
238518_x	129.937	119.446	153.669	133.906	139.266	125.328	148.825	123.059
1561403_a	173.912	172.934	173.63	165.699	161.52	181.198	195.159	186.603
37170_at	70.5708	73.7748	69.2987	72.3795	71.8662	71.5213	68.5458	70.6626
33322_i_at	253.781	266.486	262.574	305.07	255.133	206.304	228.989	230.267
209448_at	340.464	254.371	281.909	319.719	280.036	221.571	207.186	274.613
228273_at	51.8093	72.2016	62.1827	64.526	56.0735	52.1356	56.26	65.5806
244788_at	142.086	148.443	147.528	129.78	156.543	141.763	133.197	135.235
1564758_a	37.5534	43.5712	37.7522	43.1642	50.8178	59.4365	41.8087	42.269
206492_at	280.596	210.65	221.546	209.249	283.154	220.956	234.794	192.704
206159_at	246.587	212.778	276.347	254.142	253.636	270.73	288.187	244.615
44617_at	285.229	266.209	278.665	279.461	271.866	295.832	324.227	310.359
1557050_a	41.5993	39.1196	37.0591	40.8295	32.8904	36.7054	49.1272	50.094
211535_s	389.74	404.204	420.125	429.141	468.615	384.993	399.767	413.464
241972_at	136.782	139.018	131.916	161.372	133.807	149.423	185.173	161.647
224765_at	867.067	928.226	1041.17	1443.86	1280.27	1078.54	1215.21	943.706
206239_s	95.2613	78.5749	100.41	96.2498	84.3239	106.8	112.83	98.553
206766_at	164.978	170.125	173.5	164.355	171.529	177.083	196.988	182.631
213521_at	156.515	169.794	167.903	171.59	174.613	190.99	212.954	185.305
213953_at	76.4514	71.6122	77.2053	54.6551	70.4871	68.6929	64.8677	58.4375
229793_at	223.045	261.22	229.998	259.841	236.156	245.276	263.148	250.126
215015_at	119.04	98.3533	113.536	145.035	125.156	126.021	143.286	154.047
1569334_a	47.6639	33.5799	55.3433	36.643	47.1437	32.9339	54.5477	28.9832
215566_x	512.513	493.587	536.143	471.245	503.699	433.264	506.802	476.582
229650_s	228.763	257.124	243.16	210.498	245.826	219.436	193.67	239.736
39729_at	4900.04	4434.33	4136.65	3729.16	3706.39	3235.49	2887.31	3445.97
219606_at	56.6291	61.3017	75.3322	57.7686	68.7978	48.1852	59.8121	57.9473
214428_x	478.964	435.571	438.874	474.037	480.064	490.283	546.324	486.271
241992_at	121.51	151.438	140.73	132.59	133.077	137.247	129.499	127.783
213540_at	714.382	625.304	662.96	647.432	594.824	575.485	635.13	604.187
207231_at	169.157	243.78	197.387	202.464	199.73	188.56	169.126	194.996
214823_at	190.434	204.593	201.524	181.696	288.579	213.644	225.111	191.764
49051_g_a	228.236	142.095	194.366	245.302	193.153	172.721	234.466	213.673
217299_s	87.9081	161.428	89.6895	92.8718	87.2548	75.6831	83.8526	93.1634
231276_at	338.402	319.408	355.478	238.819	342.629	325.653	303.022	301.066
209550_at	519.73	472.554	391.16	492.359	382.669	303.366	269.365	332.421
210150_s	143.041	160.108	139.925	141.511	149.426	133.117	142.737	160.595
225288_at	143.194	168.983	148.288	180.234	171.045	159.265	168.008	168.281
202425_x	1144.53	1599.23	1297.01	1891.2	1152.65	1193.79	1360.08	1651.71
225355_at	533.81	501.258	533.278	413.89	543.783	580.044	458.981	488.505
216771_at	146.742	126.64	125.928	141.105	121.974	129.286	149.603	131.642

208781_x_	2546.34	2608.07	2645.49	2286.7	2409.14	2588.19	2419.58	3068.5
1558573_e	124.149	113.298	111.011	117.527	111.068	107.013	110.44	104.425
237065_s_	132.367	114.274	131.955	138.373	152.968	138.851	132.756	121.213
209291_at	82.4131	70.5618	70.4128	116.684	71.9826	72.0319	75.1663	70.8263
230605_at	320.647	313.505	404.662	325.396	355.611	369.792	426.615	435.732
214953_s_	670.357	599.462	570.317	748.224	592.011	582.573	596.565	615.184
1563591_e	73.0498	61.3231	47.5686	64.0749	100.938	55.4243	46.5146	43.489
202766_s_	368.196	363.629	566.552	664.934	497.102	370.384	340.355	392.769
236855_at	212.908	172.18	180.573	215.742	220.057	209.483	239.693	231.143
226031_at	772.986	819.823	761.639	733.208	676.888	807.548	914.148	818.643
225884_s_	219.973	230.293	207.051	244.056	196.841	189.528	196.09	222.097
235508_at	139.612	116.614	149.656	121.972	132.046	112.147	147.332	117.644
238360_s_	215.17	191.134	206.989	165.436	193.441	193.363	206.138	194.124
216788_at	51.8785	50.8138	56.3082	61.3296	38.247	35.9003	44.2285	34.6745
207447_s_	74.7586	64.8595	62.3351	61.126	80.3817	52.4428	33.9239	46.4828
1561328_e	23.9056	27.0352	22.1561	21.9799	27.6323	23.0976	19.2953	20.1388
218393_s_	292.72	276.534	280.768	254.297	284.332	315.516	315.066	304.937
239191_at	141.254	140.041	172.453	151.579	145.57	130.779	158.177	133.076
241925_x_	91.8408	111.57	104.814	126.327	108.334	126.959	128.477	108.226
234466_at	574.732	327.792	504.04	462.195	490.64	371.342	553.75	441.155
1554039_e	347.215	326.736	341.412	345.35	400.149	338.009	363.138	338.197
205876_at	113.932	134.826	124.575	125.732	110.852	147.61	125.003	153.035
225531_at	253.213	255.476	215.946	211.07	227.731	228.641	227.535	225.317
1560617_e	158.326	142.926	147.681	161.131	159.909	138.256	171.13	154.898
226136_at	95.4976	85.9617	86.1761	91.3779	96.8345	72.8712	103.118	98.318
209193_at	255.516	250.905	240.445	269.429	266.927	218.659	226.711	237.205
234954_at	2846.35	2530.81	3189.69	3124.64	3228.34	2930.4	3580.35	3115.3
40837_at	729.378	779.923	725.536	631.536	861.162	867.992	837.877	947.557
205050_s_	269.665	251.513	288.891	215.302	297.596	273.294	260.748	239.486
231188_at	165.101	188.988	171.544	151.449	172.295	164.118	176.936	162.223
214728_x_	364.234	499.802	473.931	591.822	510.259	439.58	499.088	508.148
225799_at	190.347	185.33	170.819	200.653	193.642	173.803	167.083	191.693
208284_x_	484.576	311.454	379.609	348.329	305.098	290.049	381.636	278.96
210218_s_	110.091	98.8799	121.975	105.701	111.316	108.48	104.485	95.1741
216094_at	53.1537	50.9951	52.79	58.1282	49.3347	53.2594	26.6914	49.3416
200960_x_	792.031	897.574	749.389	926.564	834.519	729.543	674.876	766.004
202240_at	307.868	301.23	277.344	291.217	305.705	245.489	234.99	259.43
240830_at	125.03	99.4157	136.535	133.198	119.625	121.623	145.004	112.604
1558345_e	208.301	221.771	211.733	233.609	246.439	205.054	254.76	194.125
215326_at	120.386	114.995	121.576	103.286	127.53	118.258	130.872	127.798
208866_at	220.226	215.964	224.7	258.7	209.132	194.311	217.057	232.897
226705_at	432.417	421.075	458.347	421.905	505.706	485.831	417.408	468.644
209480_at	132.41	110.124	116.05	87.7882	130.05	111.217	111.949	104.209
201424_s_	1616.18	1690.28	1876.72	1518.22	1309.75	1194.82	1136.7	1347.92
201670_s_	234.214	240.465	218.703	258.678	228.615	290.375	285.498	346.264
89948_at	445.063	417.652	431.733	463.233	446.574	501.49	590.633	532.975
231876_at	130.13	136.97	139.741	121.661	124.065	141.179	131.868	139.028
205166_at	199.074	185.349	196.864	204.687	223.597	202.963	238	197.566
215464_s_	188.794	158.414	183.304	186.301	203.538	233.937	262.992	231.208
213453_x_	19301.3	17541.3	19200.2	18919.5	19435.3	18369.9	18540.5	18627.5
244682_at	103.489	94.3108	98.8703	79.0158	90.8029	83.6378	98.3516	87.4644
1561100_e	311.839	267.474	291.28	304.527	313.594	330.207	366.462	327.572

230393_at	243.826	241.919	272.327	253.374	198.467	164.149	180.124	165.693
233451_at	301.414	272.117	310.318	306.875	322.387	335.338	418.77	342.65
231523_at	59.5374	50.537	55.4025	46.3656	42.0036	52.7485	44.86	45.9757
236813_at	254.721	238.438	262.746	207.133	240.492	235.3	252.709	234.891
214193_s_	71.8879	106.354	67.9268	77.4093	58.2535	67.4576	56.3817	66.4514
232229_at	137.445	161.461	173.321	200.962	168.455	181.703	192.323	193.89
217525_at	168.568	162.568	173.669	195.812	158.394	178.264	196.447	180.659
232928_at	86.5518	95.0198	101.148	80.3384	88.6189	86.9365	93.4625	91.1573
206706_at	97.7727	117.077	134.753	125.894	125.018	118.962	118.089	128.443
203844_at	76.5048	84.6874	100.938	72.0132	107.507	66.0163	67.8054	65.0009
231851_at	221.814	223.721	218.204	263.446	157.253	214.646	213.604	242.77
1557540_a	386.631	370.926	378.153	464.551	377.888	393.641	477.338	439.476
1557065_a	160.712	135.971	138.688	152.068	167.632	152.854	158.339	170.086
238906_s_	84.1057	87.5497	91.2259	91.3072	94.7635	92.1849	86.3368	84.238
225591_at	1137.84	891.71	961.933	1021.17	1227.67	1222.16	1396.59	1392.65
1562049_a	18.2891	84.8782	31.9678	20.8024	22.4431	29.4145	22.6444	26.6844
224174_at	383.68	316.774	361.834	373.626	342.766	420.373	472.044	451.453
223691_at	283.76	240.242	263.948	246.052	238.78	242.53	307.176	239.758
229659_s_	320.403	339.601	349.79	303.043	333.288	324.984	240.503	262.916
235255_at	138.49	135.804	157.184	122.186	145.147	129.155	133.025	137.785
238723_at	33.4681	39.4048	31.3747	30.0035	21.1164	34.9544	27.604	34.5669
225948_at	935.737	896.867	891.967	661.861	790.57	1136.99	1179.94	1159.26
216883_x_	165.827	169.325	188.333	160.681	176.787	166.389	176.558	181.13
53076_at	313.164	269.363	295.249	273.201	283.541	263.564	307.234	287.473
209685_s_	89.719	85.1942	90.9573	82.1581	108.914	88.8447	107.284	87.3203
231032_at	348.127	382.188	474.655	310.678	349.715	447.961	423.26	412.623
206004_at	226.537	214.378	209.747	232.238	192.947	183.324	238.402	228.086
1566979_a	83.0363	83.9066	82.9787	85.5786	84.4969	90.0611	95.4067	89.5491
204983_s_	199.074	188.036	184.774	225.118	188.356	212.2	264.905	278.777
233041_x_	203.083	209.789	227.434	206.808	217.012	187.082	218.094	197.255
1562283_a	64.1776	54.7656	62.6447	53.1999	58.3253	53.9103	44.2086	47.2925
232490_s_	126.127	134.276	142.444	156.312	145.14	149.431	179.797	184.804
202208_s_	327.553	318.841	316.639	280.999	315.399	305.068	326.608	318.749
230113_at	175.325	166.776	188.453	157.089	164.32	164.229	164.548	161.999
244323_at	106.712	82.7758	99.9114	109.682	95.5349	85.1716	102.515	90.5413
208771_s_	1041.99	1157.74	1080.93	1029.29	986.254	769.037	809.873	863.156
1555558_a	40.802	32.7218	49.0022	39.9237	35.534	28.7036	40.9141	34.9295
1554844_a	44.7045	18.9453	32.5383	30.1476	25.2477	33.0408	25.7162	27.4957
240489_at	129.17	132.168	124.07	146.467	151.01	128.331	156.699	116.718
228024_at	253.12	367.192	342.164	376.469	248.996	251.769	238.888	280.041
211234_x_	232.671	220.873	229.43	220.257	240.248	261.555	282.494	261.724
232927_at	84.5137	91.5606	129.828	91.5356	124.362	79.7826	81.5168	70.5109
206134_at	81.6377	83.9931	83.6349	80.7894	69.1279	86.9082	92.0929	83.2145
235859_at	143.273	133.638	143.27	121.797	149.057	132.171	126.618	144.327
209832_s_	136.354	120.708	130.132	110.274	121.74	131.352	145.782	117.981
216751_at	194.298	201.976	193.871	173.407	221.265	202.316	175.271	216.092
218435_at	1180.99	1409.79	1321.68	1125.59	965.229	829.016	773.77	941.684
223259_at	587.121	558.268	565.406	535.958	627.09	543.752	645.221	634.328
239070_at	138.837	134.643	162.34	148.707	163.909	145.217	164.441	156.343
228032_s_	337.482	348.474	385.279	251.786	237.128	227.388	241.359	239.449
223008_s_	1281.42	1596.41	1542.35	1236.76	1549.12	1214.31	1297.84	1398.22
219113_x_	398.815	382.327	387.992	337.909	389.52	369.33	331.559	352.3

240958_at	161.88	126.043	154.703	144.643	149.064	144.661	157.111	124.504
1557513_e	64.5159	51.7382	78.2547	48.5268	66.0493	51.5384	48.534	39.1414
229525_at	295.554	356.599	276.77	360.977	248.498	232.149	232.849	226.764
236202_at	92.1554	105.513	102.942	109.41	94.1701	96.8264	104.578	81.2235
200755_s	720.882	664.233	809.232	649.49	897.091	773.807	920.252	775.307
1558622_e	167.162	178.083	165.534	179.744	194.631	200.709	214.415	195.632
237725_x	122.994	133.667	100.125	122.995	90.9116	77.7809	81.088	95.3861
215836_s	414.218	446.762	432.301	477.902	482.514	469.48	514.562	531.803
243702_at	229.743	234.375	238.784	187.858	235.081	242.173	206.061	233.168
1560557_e	53.0078	47.6965	49.1562	51.3748	58.8307	55.2162	56.025	50.4576
238504_at	426.691	376.779	354.349	364.298	265.184	282.306	292.559	259.415
233703_x	6.09701	7.21643	7.44346	2.5361	11.5901	11.7321	11.7694	9.86343
1552368_e	100.907	85.4149	88.8863	94.057	104.704	100.336	94.943	88.5334
230379_x	200.371	248.79	176.096	171.562	123.864	133.209	110.71	99.0388
1566301_e	74.8593	66.3019	82.0994	70.4893	68.0316	67.605	74.7036	79.0522
54970_at	643.811	638.192	679.213	729.219	770.764	694.329	748.394	730.297
227271_at	610.336	555.651	642.221	526.845	738.713	686.367	800.925	683.481
240818_at	243.439	258.429	264.42	224.005	273.214	224.134	224.046	235.323
238824_at	77.262	97.7009	90.1921	81.7766	87.0902	70.6323	84.0492	63.339
1565242_e	60.934	63.6597	55.1809	56.9128	49.5401	53.8528	66.4271	52.5037
218642_s	645.803	686.575	625.528	698.828	618.83	543.694	515.28	478.045
225615_at	470.324	362.027	389.027	398.819	545.409	450.737	463.285	428.324
229998_x	394.183	376.02	439.843	359.99	420.556	367.359	445.166	409.18
1558082_e	56.275	51.64	65.9677	55.3111	51.9278	52.7444	50.6723	46.4221
221402_at	307.53	266.003	284.512	337.653	268.966	297.54	323.08	322.638
242940_x	19.9294	21.0706	26.9749	18.0944	21.1583	15.0336	18.7965	10.5796
206178_at	285.52	242.995	273.654	249.549	268.573	249.374	276.644	238.207
228977_at	690.915	613.605	1084.51	474.944	830.032	762.4	858.769	784.249
244673_at	80.165	73.5389	75.3037	70.5958	82.3285	78.1141	78.8246	68.0606
1553239_e	283.24	274.023	294.273	317.278	280.676	337.767	379.676	346.453
213214_x	1418.26	1673.68	1906.07	1886.64	2104.22	2016.23	1695.66	2215.78
216699_s	295.14	290.897	314.675	294.217	314.206	329.113	377.028	333.445
232106_s	238.456	219.961	228.707	227.287	260.413	250.257	300.935	250.985
230418_s	91.4223	104.006	100.638	112.069	103.071	80.9077	100.705	105.028
201026_at	311.74	410.537	334.44	442.13	313.459	286.315	321.632	344.144
212581_x	21070.1	19751.8	21127.3	20638.2	20950.6	20090.5	20223.9	20425
210318_at	206.189	210.337	210.782	189.259	199.606	181.121	209.963	195.889
233355_at	117.105	120.328	115.212	111.36	131.408	96.0828	119.5	100.772
212700_x	296.425	251.16	270.457	283.393	273.318	282.773	333.007	296.455
205132_at	1710.72	1402.94	1607.23	2693.73	1549.28	2170.8	2243.06	2470.52
228326_at	231.421	231.696	251.7	232.553	246.85	276.045	328.883	289.166
233127_at	86.7071	76.6655	56.7856	63.2225	112.062	64.3081	34.3866	43.4482
206364_at	54.4856	62.6011	58.2187	58.8396	58.2438	66.9009	54.1928	54.9096
207687_at	276.472	257.323	260.38	244.38	267.945	275.809	270.125	265.46
243311_at	67.8664	56.5029	46.0897	59.6062	44.1503	57.4091	46.563	55.4932
225925_s	249.875	289.55	226.192	276.763	245.41	197.484	182.187	192.132
213309_at	873.665	1140.08	1083.73	1007.24	897.85	855.665	848.494	1132.72
1554286_e	135.674	142.396	147.246	145.868	128.944	160.541	166.17	150.322
232436_at	97.7675	108.39	86.3428	105.009	95.7509	86.4824	95.8859	101.297
209907_s	166.564	168.936	159.367	158.852	166.798	160.954	165.966	171.98
209423_s	182.452	173.651	189.2	176.059	183.283	205.299	220.043	233.196
202987_at	125.897	136.251	141.729	139.562	129.785	125.857	165.521	157.79

235857_at	214.105	197.778	225.314	258.964	218.048	193.315	256.304	211.145
55616_at	531.564	486.68	568.239	573.549	639.198	586.913	704.466	637.589
214143_x	7788.26	9225.33	7997.15	8835.08	7787.79	7033.81	6533.5	7291.01
223789_s	122.793	118.539	136.353	142.346	134.849	149.382	153.129	146.296
1562051_a	39.9366	33.0052	37.816	36.3243	40.85	36.9931	38.1568	36.4059
201638_s	101.56	95.5273	101.656	117.633	100.038	108.904	124.2	132.583
208699_x	152.487	155.934	156.644	126.964	145.364	168.544	147.406	171.627
1552698_a	646.586	433.464	550.501	593.312	527.758	434.086	377.424	338.026
211536_x	248.591	258.25	301.542	292.148	318.675	275.719	317.486	309.809
202683_s	362.046	376.15	374.998	367.312	361.085	378.897	362.44	343.494
238716_at	120.908	128.681	130.05	124.829	152.991	109.729	108.552	123.226
227201_at	219.321	199.667	213.737	175.294	205.413	209.689	190.743	170.11
208782_at	500.439	635.149	725.261	873.092	719.498	637.99	615.687	681.626
210257_x	135.053	118.55	151.955	138.471	139.511	140.217	134.432	138.347
222462_s	621.517	581.91	669.656	605.546	700.995	669.445	772.482	662.099
203572_s	542.25	579.504	560.689	475.413	525.004	543.561	541.499	566.742
228173_at	141.095	146.978	138.916	136.094	159.521	145.998	150.005	154.096
201843_s	51.8204	54.7364	51.5267	73.4465	64.0972	51.4131	27.3398	47.2294
204490_s	134.93	141.883	149.982	168.663	155.596	159.202	165.027	156.582
210115_at	142.544	114.047	138.998	156.743	120.014	121.037	147.721	136.05
219090_at	1134.25	1012.33	1025.53	1345.27	1334.35	1249.63	1507.36	1778.82
210749_x	652.258	548.844	481.262	545.833	571.052	573.771	594.588	498.351
215858_at	291.399	253.585	264.389	271.901	269.416	283.55	298.101	239.351
211076_x	183.283	169.767	204.37	212.31	162.206	164.504	213.131	171.6
201279_s	171.732	177.66	210.45	217.671	216.892	218.625	199.192	210.59
210519_s	430.028	320.66	412.838	560.146	880.41	343.93	380.417	405.905
203153_at	810.673	953.129	853.262	599.264	404.989	674.274	795.914	802.04
225483_at	367.608	329.383	338.874	365.073	376.401	413.341	461.081	450.7
230078_at	184.443	217.998	183.339	222.925	187.737	155.521	180.519	186.031
203417_at	269.755	231.892	258.005	308.922	241.843	273.866	311.582	289.082
232371_at	58.5978	52.2593	63.2479	43.3982	58.4226	44.6491	55.2818	44.9315
223457_at	218.369	197.012	177.964	219.243	192.449	189.956	225.129	249.086
241076_at	221.946	202.59	211.115	195.258	237.222	230.713	208.882	205.936
218481_at	541.605	542.607	518.235	498.432	515.492	550.604	628.593	606.259
214761_at	1174.57	1279.3	1045.34	1151.62	966.199	893.466	795.913	982.316
242518_at	55.1187	64.4903	57.6051	42.6697	66.121	52.6904	87.3564	52.3205
218094_s	3507.49	3008.07	3181.39	2814.41	3287.03	3163.45	3840.68	3670.27
44146_at	717.133	643.646	666.901	649.279	694.12	642.732	769.332	688.224
237798_at	64.1351	72.0532	60.6038	47.3153	36.853	41.8748	49.9923	39.7479
231013_at	141.028	145.732	144.042	129.225	165.538	120.2	170.099	145.121
1554163_a	142.344	121.551	126.16	143.722	116.377	136.713	160.589	157.364
204726_at	691.568	933.606	805.236	1001.88	751.304	601.56	530.907	555.455
218395_at	268.056	319.05	268.717	316.065	198.274	204.191	173.179	212.376
241373_at	293.857	293.371	277.971	252.757	277.089	292.169	335.994	298.249
218844_at	269.43	309.993	270.629	222.077	290.109	304.597	310.756	295.46
204057_at	259.832	236.059	245.987	214.338	243.713	221.367	237.519	208.931
214484_s	169.522	162.771	154.918	175.534	178.161	176.902	179.923	199.785
203156_at	742.856	673.636	714.269	821.658	658.238	601.216	819.069	715.513
1569904_x	111.834	104.188	141.619	108.809	117.067	101.753	103.509	74.3805
1557632_e	70.2193	55.2166	76.7294	60.4012	63.7615	48.3671	63.4707	60.6885
201426_s	1294.39	1243.1	1607.35	1929.07	1821.01	2237.13	1843.81	2123.77
1555131_e	344.781	281.443	322.263	342.169	288.38	290.184	346.899	295.815

225242_s_	165.772	184.652	167.384	216.934	181.278	185.393	182.453	167.07
220376_at	74.5694	54.7729	71.4855	63.4881	58.3915	50.2199	58.6983	54.2457
1566002_e	123.423	108.786	166.342	142.523	126.489	96.9831	129.293	88.6516
214705_at	35.5548	48.6187	47.9708	46.2724	37.136	37.4584	37.1046	40.699
236798_at	723.419	656.994	848.042	465.296	504.576	422.726	551.852	509.941
229633_at	126.956	129.626	147.043	97.8107	147.095	135.432	139.817	133.796
222600_s_	476.041	400.662	376.469	382.061	300.674	274.466	307.706	302.126
216954_x_	2206.87	1793.52	1823.66	1542.64	1276.1	1231.33	1302.3	1252.99
204032_at	507.565	616.427	561.293	451.754	601.108	403.264	431.708	443.401
218256_s_	339.918	404.062	415.103	417.321	338.512	325.576	336.29	398.695
228867_at	350.311	347.554	402.014	378.357	277.485	297.245	277.817	306.336
218113_at	218.946	216.768	221.671	213.803	242.48	232.751	249.24	213.282
242002_at	103.248	146.033	117.165	99.4351	127.534	104.693	85.9143	76.3136
221627_at	206.344	198.033	211.528	213.076	204.99	204.417	221.639	207.538
220018_at	91.2494	135.809	98.7591	133.774	93.2407	141.483	120.897	133.152
241639_at	212.71	203.943	179.803	190.248	227.091	220.377	209.049	193.856
1555127_e	117.838	110.441	119.775	100.016	119.618	111.722	130.783	106.947
241637_at	184.665	159.578	191.41	176.047	199.303	162.647	190.413	183.049
219696_at	445.839	476.104	519.54	346.851	348.768	370.657	399.332	402.665
45297_at	427.988	393.033	417.396	361.77	419.414	466.481	473.16	479.399
207024_at	413.819	321.05	384.007	385.233	361.039	420.218	434.386	439.047
236134_at	328.248	327.355	328.263	363.927	392.329	382.578	411.672	367.499
229835_s_	209.685	233.274	205.765	192.724	204.865	213.382	203.877	177.123
222631_at	251.883	241.301	265.382	311.958	343.803	285.553	341.567	280.238
244347_at	106.745	81.4783	97.9308	70.7085	87.1444	95.0987	91.6192	75.0484
206012_at	217.157	194.353	191.076	198.314	181.374	188.291	233.168	196.802
200660_at	228.011	234.28	262.195	276.092	249.605	322.793	271.652	378.39
229456_s_	312.913	307.187	320.967	313.395	312.061	337.42	355.277	343.762
207549_x_	861.534	1041.24	805.157	912.058	921.148	907.378	1026.5	949.534
232810_at	177.554	181.143	158.966	171.385	180.197	158.466	136.665	144.841
1560648_s	159.303	242.646	177.147	269.621	185.969	158.768	141.666	171.515
1559190_s	143.812	150.78	135.996	117.426	87.2796	96.4067	99.1837	91.1279
1557452_e	63.6158	55.8356	54.816	61.378	63.422	77.5112	67.8009	65.1772
225250_at	90.2747	76.6125	94.6008	96.6699	85.1135	84.8421	83.9006	77.0047
236772_s_	297.741	493.306	282.361	354.655	204.225	252.87	303.265	289.758
213316_at	173.452	134.962	207.612	153.877	151.638	126.324	149.124	109.157
231640_at	427.25	463.506	462.451	444.266	307.672	280.226	253.759	307.323
240703_s_	29.6007	49.2108	36.4951	42.4375	39.9832	216.469	142.124	182.509
1564207_e	1274.25	984.421	1410.5	1436.5	1860.18	2153.93	2552.83	2137.53
230657_at	91.9325	74.1852	71.8287	97.5738	87.1813	112.506	117.166	74.3027
224358_s_	57.9077	65.0048	52.2554	66.9043	64.9216	50.1348	44.8988	47.3357
222663_at	168.128	176.927	175.993	207.059	145.021	124.797	123.642	142.987
236841_at	113.062	110.788	104.217	104.145	113.059	99.8129	85.9328	96.6902
1553178_e	365.188	316.569	345.207	348.555	348.755	397.164	500.904	446.21
1555932_e	15.3062	19.5913	17.462	22.6016	19.2061	18.2856	8.14933	14.9052
203103_s_	588.18	589.938	575.36	694.322	631.049	539.064	533.328	576.776
212256_at	108.285	137.051	131.768	135.009	132.131	135.923	132.485	138.735
238912_x_	191.368	226.121	189.594	204.171	164.903	147.059	153.322	154.548
210966_x_	1628.96	1557.08	1547.76	1567.6	1636.76	1326.19	1571.14	1443.65
1554770_x	6.82369	19.2758	10.9994	14.3257	21.8588	12.3809	14.1095	19.2147
214359_s_	3094.2	2854.92	2935.11	3114.53	3309.36	4114.27	3897.81	4665.29
1553426_e	180.226	149.984	164.759	169.892	169.559	162.273	189.689	186.278

1552414_e	262.221	241.682	227.009	282.16	243.644	227.045	301.233	282.058
215272_at	77.3779	69.2709	77.4009	56.0078	63.8604	65.9714	61.2435	63.6286
1569885_e	118.305	126.005	85.4538	132.574	99.6346	85.9688	109.462	97.6941
205908_s	74.6378	67.1742	58.7148	82.1684	77.4456	74.7996	80.4915	73.3736
200600_at	471.111	425.236	520.25	478.639	471.256	519.726	490.329	473.753
216475_at	442.135	440.451	432.108	407.548	456.838	463.466	502.857	459.49
222012_at	241.981	229.56	237.962	185.757	230.03	240.44	241.554	242.438
233080_s	421.759	471.094	418.716	520.031	440.35	378.13	349.714	404.485
206527_at	283.979	279.357	289.977	272.997	290.612	378.739	441.531	421.353
1561785_e	72.2859	82.6014	69.2723	73.2665	83.1835	73.6484	68.8369	73.8434
200703_at	611.678	850.361	757.067	1283.25	487.032	663.001	523.167	735.721
217368_at	408.689	412.967	365.301	382.573	371.569	396.955	458.529	363.556
208920_at	209.98	260.456	224.028	280.293	208.687	190.431	185.528	195.385
233365_at	89.528	85.2498	64.3081	85.8059	94.2337	80.278	82.1742	74.8636
215854_at	145.228	136.163	155.91	136.484	135.502	119.68	141.624	122.99
229151_at	114.039	90.0109	116.343	85.0466	81.8869	59.5827	75.8037	70.7247
218231_at	364.271	343.95	321.762	355.673	348.905	356.477	301.667	359.854
212848_s	1966.5	1615.57	1925.87	1156.18	1416.15	1325.34	1661.62	1586.24
1569139_s	93.0763	93.2519	102.951	75.0179	95.5354	102.967	96.3963	87.5534
228966_at	92.1215	91.146	89.7335	113.498	78.4238	69.2826	93.1079	119.163
228113_at	97.0087	88.2788	90.5865	99.4542	68.8537	76.7928	83.2998	80.1814
208420_x	628.923	649.777	628.495	662.291	671.945	660.295	720.648	735.012
240099_at	232.787	214.152	241.347	204.573	241.952	225.701	183.263	212.629
216484_x	2004.16	2038.51	2020.59	2024.98	2482.52	1899.2	2245.54	2285.5
238003_at	230.776	218.281	226.487	246.182	203.559	214.159	262.852	219.926
218770_s	191.87	169.644	199.819	206.804	219.006	201.843	242.807	234.485
224229_s	82.1189	93.1345	80.6634	76.4569	80.6359	75.5105	72.0877	69.9273
228232_s	76.8534	83.756	93.6815	75.1599	74.792	85.7427	92.191	84.0479
221205_at	77.3223	91.283	79.6755	98.5931	70.0326	92.4218	97.6228	99.1973
229824_at	41.572	34.4686	41.4113	44.16	33.4579	27.8654	35.8743	38.0439
222874_s	110.979	102.912	115.133	106.222	119.229	123.817	123.383	127.152
241755_at	47.1891	34.3231	41.6379	37.5564	46.7592	55.4798	49.1278	60.8726
217361_at	74.9134	71.0589	69.0911	89.1886	68.3651	68.6313	80.5731	79.8008
234316_x	252.167	259.118	242.692	236.321	280.854	270.124	270.754	263.496
201917_s	403.771	365.362	417.982	447.75	422.253	458.851	443.106	476.687
205058_at	215.183	193.458	205.603	232.161	195.105	208.285	227.407	231.845
1553158_e	202.597	200.491	146.26	177.624	185.896	141.583	104.838	116.239
218061_at	427.283	445.1	393.485	367.265	390.176	396.067	363.989	431.516
221529_s	304.938	308.17	317.309	300.139	299.069	335.364	322.436	329.386
205559_s	71.9933	75.69	70.5058	59.5683	58.9989	69.2146	77.1214	60.5574
200735_x	4805.93	4975.01	4644.71	4577.42	5040.54	4770.92	4844.61	5809.34
216444_at	104.199	103.975	96.7178	111.254	105.862	111.814	111.539	115.346
218201_at	5480.94	5325.42	4913.53	4966.02	4551.61	4639.39	4566.35	4591.58
223089_at	346.129	609.292	576.338	581.461	327.238	421.992	389.091	441.114
220155_s	456.77	404.159	406.474	438.559	483.372	395.251	440.698	440.003
233316_at	48.1159	56.4066	39.2024	47.6732	44.8567	47.4114	64.7768	54.6538
238512_at	47.4104	38.7877	41.4352	48.7258	43.2204	47.065	40.1494	42.6328
239837_at	181.117	197.157	197.855	147.143	187.835	185.166	174.308	170.663
40255_at	512.3	459.728	486.083	564.4	537.834	588.326	692.024	647.987
1555433_e	62.7525	57.3789	49.1563	53.796	52.4944	58.5755	44.8515	57.4937
1570117_e	60.3905	54.9507	87.7071	71.8848	69.2989	51.5117	71.4695	43.4544
217497_at	113.341	96.4494	107.438	86.2197	112.791	100.015	105.382	102.705

243877_at	87.3523	77.0709	72.215	95.1983	70.9378	75.2776	95.7645	79.3773
227090_at	346.11	329.218	348.144	338.221	349.777	351.962	389.167	376.869
223463_at	84.9695	114.966	97.9374	167.664	68.4597	124.051	81.6258	120.051
226163_at	333.177	297.676	353.458	304.937	345.792	387.842	464.981	363.986
240374_at	146.039	142.477	169.539	146.578	156.724	144.881	163.83	153.357
221067_s_	424.428	377.032	475.197	491.633	446.085	563.391	659.002	554.016
219923_at	257.102	271.614	266.197	265.112	269.929	257.185	271.936	264.794
222640_at	526.92	490.033	502.356	481.794	443.671	427.306	461.676	460.479
212042_x_	9034.75	9504.34	9342.28	9624.46	8651.64	8644.02	8128.42	8460.71
1564208_x	1028.02	906.081	1279.93	1274.75	1609.34	1905.86	2249.66	1892.1
1565027_a	285.42	269.043	251.933	263.587	318.726	262.543	210.04	206.655
59631_at	383.964	390.656	393.176	424.828	398.594	341.212	369.397	392.561
216038_x_	211.705	189.496	185.345	197.435	215.488	188.386	167.088	193.566
211073_x_	2708.76	2685.57	2649.82	2891.23	3568.91	3584.79	2341.69	3042.21
213934_s_	166.17	198.223	165.277	187.085	127.781	107.528	115.036	111.377
221037_s_	7.22457	4.85648	8.68041	10.262	12.5051	17.9953	8.48802	12.1558
201810_s_	569.39	602.328	475.034	584.473	655.375	463.464	467.957	397.535

T9	D1	D2	D3	D4	D5	D6	D7	D8
84.158	63.2272	68.8293	59.4883	55.5952	64.299	50.1802	56.3753	54.7037
120.972	177.961	175.576	168.671	148.053	161.766	168.442	184.578	160.616
120.888	151.732	149.919	160.89	145.589	149.246	140.457	158.314	135.882
18.2414	6.78274	13.0161	9.98732	12.4026	17.4585	14.9473	12.917	14.3561
124.991	124.272	115.365	131.634	144.26	120.509	142.577	151.856	162.241
108.195	88.8986	85.8776	89.4618	92.8252	108.01	98.5188	92.5796	98.7088
153.097	182.383	220.635	204.091	172.526	182.773	167.377	143.663	163.362
181.937	212.594	183.071	211.284	190.394	230.066	219.891	207.948	207.825
102.714	130.789	119.767	121.255	104.875	128.989	122.852	122.118	113.748
152.699	171.353	149.206	190.831	196.727	178.472	178.055	187.729	182.058
181.545	205.695	184.444	210.3	177.579	219.698	207.119	189.067	206.005
211.544	176.498	207.26	183.659	184.076	181.867	168.874	160.779	200.018
181.169	209.732	186.121	190.833	180.625	220.943	205.711	181.818	199.193
153.942	215.63	194.782	221.145	193.173	230.612	209.027	208.408	192.533
369.97	357.058	312.467	347.297	356.168	388.34	407.885	401.841	443.964
101.68	123.448	112.38	112.184	108.53	115.38	109.392	117.639	98.8692
684.147	739.355	649.526	882.07	772.52	814.698	811.956	791.39	795.589
76.5733	100.544	76.973	85.7478	87.4602	92.8167	74.6572	84.4135	83.4109
100.377	137.14	133.084	124.5	146.525	127.686	142.473	140.45	125.276
139.39	133.451	127.161	103.409	95.015	85.7906	122.571	146.374	114.29
1175.41	906.709	1199.75	983.236	1005.5	1084.22	1010.26	884.294	1164.12
38.286	21.9274	19.4992	29.1152	31.1369	29.3412	27.3634	23.0717	23.0415
636.026	780.862	736.454	653.166	675.616	661.874	644.524	725.27	663.965
411.464	322.616	281.271	314.371	321.822	301.223	298.399	361.737	321.914
219.631	234.849	233.752	235.607	235.025	249.417	228.678	211.977	245.802
137.061	151.847	144.776	152.741	133.272	164.458	158.648	147.58	147.203
355.242	532.869	484.16	453.712	499.98	468.471	403.326	431.365	381.496
212.68	249.547	238.498	243.818	232.641	247.335	257.243	239.678	226.997
85.9703	56.4865	59.8789	52.6107	65.1558	49.5451	72.1774	70.4376	66.5701
331.39	366.034	391.697	360.929	390.208	367.47	361.014	410.23	374.912
93.4886	125.852	120.667	137.266	99.8545	123.174	117.441	123.727	101.677
387.299	436.76	392.319	386.411	422.804	421.902	482.15	516.783	390.449
200.601	188.655	219.418	195.281	223.716	210.56	198.277	210.558	201.361
202.892	200.295	208.407	205.735	230.47	216.497	221.108	221.477	235.739
66.2808	84.2853	90.9663	85.0744	76.9059	85.6308	82.9384	79.5719	82.2206
194.423	203.246	242.335	194.397	178.317	230.48	175.508	213.262	203.943
171.667	220.04	225.648	222.903	211.52	220.687	212.986	208.783	179.703
239.159	240.263	236.971	268.845	259.41	261.185	271.618	258.05	270.191
103.577	130.037	139.647	135.423	132.321	139.069	128.579	118.175	128.713
336.398	358.579	396.774	397.446	353.666	417.257	364.543	337.911	369.351
32.6098	26.7717	30.6572	22.7121	20.7248	21.1861	19.9943	19.6507	16.7957
1239.42	1495.54	1563.01	1647.68	1363.57	1451.1	1617.35	1984.52	1676.97
394.663	421.945	425.431	242.473	289.761	306.68	322.975	356.973	373.08
41.7429	58.0971	53.4434	60.6576	48.1205	64.164	54.0715	45.9659	59.7995
116.77	74.3823	72.8077	82.0966	59.328	81.7991	90.3054	67.5218	93.6552
129.731	171.401	140.793	165.927	137.879	159.233	131.932	163.218	144.658
105.792	88.9058	83.3448	83.8982	92.8695	94.1652	91.8835	93.0298	91.6788
77.3549	50.2151	61.2368	44.2972	44.8579	44.0339	43.8889	38.4314	42.6375
229.803	302.568	330.761	329.194	339.404	285.536	353.74	360.091	321.727
61.6558	87.8861	88.5797	92.7577	74.1342	85.8408	74.6916	84.5409	69.9667

190.16	221.993	224.901	228.278	247.015	210.507	197.17	226.522	206.051
107.918	100.096	85.5348	93.7976	91.8833	80.1523	88.7763	107.513	82.8692
109.672	128.001	117.989	139.441	120.654	122.536	130.314	125.843	124.767
383.945	399.745	503.194	452.255	469.741	393.676	399.492	445.034	448.451
91.0678	128.325	120.923	109.474	123.819	103.192	122.969	112.01	113.379
126.35	155.111	144.404	155.562	139.601	161.654	149.103	148.089	145.51
3826.71	3762.68	4728.55	4420.94	5817.21	4387.53	4674.17	5324.85	5438.25
218.888	288.424	290.949	277.093	251.14	283.075	272.878	256.555	247.947
47.1256	47.2059	36.8811	35.3043	56.8606	43.7137	44.0779	46.6275	36.7732
280.923	311.08	292.179	269.29	291.526	312.873	307.785	287.859	281.874
36.3999	21.2313	31.4909	23.1576	32.7852	28.2031	28.8135	20.2911	35.5513
49.1003	56.3357	60.6255	67.3089	55.2246	59.5212	57.8158	64.4964	56.2726
114.806	109.188	83.3364	96.9531	102.5	106.944	94.3098	101.562	101.588
316.949	325.487	279.184	308.472	309.004	290.968	337.306	411.637	336.711
86.4759	167.561	137.441	141.327	133.028	135.486	122.575	142.602	111.819
162.34	191.233	191.628	177.974	162.104	210.06	169.477	155.096	174.014
983.29	854.429	773.555	919.804	970.283	997.651	1110.45	1141.84	1079.23
179.082	166.423	181.179	222.988	215.542	201.103	233.621	256.932	212.761
3791.89	3703.75	4876.34	4311.07	5970.16	4471.95	4627.8	5312.98	5761.16
350.689	381.769	348.69	345.628	369.02	351.243	391.001	425.285	392.078
23.6684	29.013	25.6714	32.466	24.6473	31.336	30.9022	26.5263	27.3994
78.8773	89.304	99.9394	85.6478	82.7252	101.115	87.6248	91.9416	90.0562
160.14	125.386	128.716	130.319	131.125	100.428	148.596	134.542	142.179
59.4869	45.0283	41.2192	40.0858	38.998	39.7934	43.6247	58.6109	47.371
79.1184	95.0894	94.9139	100.999	92.3345	101.859	106.927	97.1095	103.656
53.874	34.1109	33.0712	42.3896	37.1928	32.8633	37.2756	37.5611	39.0439
360.097	313.877	332.049	338.654	392.338	367.27	423.063	406.544	506.965
382.617	463.536	419.333	426.084	439.978	367.08	455.407	523.087	411.569
107.315	127.493	116.068	143.641	105.944	111.381	126.757	128.935	129.541
154.776	152.903	196.818	171.936	184.403	160.107	130.244	136.875	132.397
178.058	168.401	159.311	184.956	205.421	164.29	171.253	212.141	207.241
212.258	177.88	189.877	207.554	195.892	190.107	193.407	177.46	211.793
96.3546	128.102	109.3	116.894	113.129	128.406	122.229	129.06	118.049
157.707	191.701	185.756	176.151	154.773	198.77	173.908	160.751	164.181
407.496	559.417	497.974	509.833	577.357	571.94	424.454	483.491	475.231
170.891	164.772	169.743	133.572	133.272	152.003	128.824	149.219	142.014
310.072	304.032	279.825	288.044	317.58	297.88	296.793	344.735	304.119
14.2759	32.3721	23.655	35.5869	19.0834	46.2054	23.9987	22.5126	25.9297
170.394	125.832	138.811	130.149	108.965	126.357	96.361	123.588	134.484
422.459	393.922	510.641	539.583	664.072	401.802	472.013	561.353	549.25
300.464	259.961	222.372	224.435	247.793	232.321	231.064	244.598	274.33
134.767	170.821	148.544	150.193	157.039	145.2	143.543	175.247	146.83
76.884	73.6833	85.8907	64.3233	64.6743	73.4905	64.6867	75.431	64.3912
51.0815	74.2995	57.0121	59.4944	57.8982	73.7746	55.7052	57.9138	61.2868
71.9452	102.923	92.8577	101.401	95.8857	102.429	84.8015	98.3443	97.961
107.894	108.001	91.5474	77.4867	69.6452	100.337	78.7511	81.2243	68.256
3771.91	3619.33	4728.12	4384.74	5850.96	4272.12	4553.28	5185.21	5430.01
474.423	457.219	433.586	439.026	447.337	403.617	596.401	594.875	483.751
136.188	147.593	144.053	124.573	171.997	147.328	142.023	184.697	151.264
369.396	302.964	586.27	469.783	665.38	381.322	614.648	548.899	642.086
204.892	207.576	231.936	205.318	249.849	217.234	214.216	258.632	214.538
138.308	201.992	179.872	181.437	174.544	208.2	166.468	167.166	156.27

137.058	186.473	159.148	167.783	145.651	173.458	162.109	145.91	147.709
191.921	228.929	208.004	214.962	235.526	216.081	218.618	206.949	236.125
957.636	940.705	1220.83	1020.14	1171.84	977.548	1110.79	920.15	1361.48
18.3366	51.619	43.5239	43.3865	40.2883	43.3167	30.6314	38.2699	35.4471
223.764	360.362	277.772	278.5	268.267	295.135	274.047	297.796	262.527
57.3254	89.9509	84.6178	87.7087	72.7754	90.0923	59.4777	71.3094	83.3477
87.6489	110.475	98.1384	110.349	104.984	104.988	110.183	101.541	102.786
122.786	153.883	151.441	156.214	152.651	137.393	158.838	153.702	147.183
42.3065	52.8508	47.6965	50.2304	51.1066	53.9862	49.6898	71.3085	46.4817
126.544	144.575	137.731	145.117	136.867	140.684	144.185	144.63	136.788
79.5885	90.9512	70.1611	66.8923	76.3557	78.953	82.5461	87.7399	81.6183
265.706	309.704	400.86	319.139	356.826	340.816	365.796	393.409	358.167
182.764	232.97	218.641	240.961	195.927	257.208	198.954	189.084	196.857
60.7494	97.4669	87.768	89.4765	83.9354	91.9966	69.7431	65.0658	77.7055
44.1287	43.5038	33.9744	45.9062	37.9845	39.1484	26.5307	36.0114	32.2372
41.6536	40.0428	24.2207	33.3678	29.6752	27.6845	30.993	40.561	25.5888
99.9086	164.097	124.797	167.413	124.454	159.23	149.405	138.83	142.388
91.9014	103.146	101.229	95.3674	89.1462	93.751	100.85	121.244	102.129
424.98	506.618	457.43	489.287	453.276	441.052	443.509	486.079	423.463
955.471	1150	1036.35	1096.49	1036.34	1025.58	1025.67	1035.02	1033.92
244.973	224.568	216.402	171.528	180.925	203.256	173.24	224.751	198.124
67.4403	85.7286	66.425	61.444	54.2807	69.2086	57.1125	62.6311	62.0995
337.442	323.27	373.908	272.317	283.714	276.386	232.457	237.332	280.742
152.184	168.262	163.571	164.819	147.684	161.534	161.327	170.854	148.463
56.1316	72.9239	70.703	63.2065	76.5738	75.2906	69.4854	80.6625	66.6292
200.037	189.434	174.785	183.829	200.459	211.341	215.65	214.806	233.002
98.0593	121.259	115.063	121.854	116.286	129.477	117.111	130.196	106.576
105.643	155.997	158.045	163.329	136.26	139.621	145.265	147.586	113.547
77.8392	87.1201	77.1024	80.7575	86.8775	77.5305	92.5123	87.4186	93.4467
201.667	268.913	243.266	275.693	244.219	227.473	275.211	389.016	197.889
187.57	193.318	233.058	239.892	223.951	192.364	211.582	217.398	217.51
106.146	91.6207	85.8372	83.1456	84.9382	77.6614	98.973	84.3033	76.7737
77.7581	117.334	105.519	104.181	97.7541	109.079	81.0513	95.6761	87.2621
124.072	175.545	136.461	170.213	141.031	173.157	148.319	133.105	159.583
201.016	256.94	199.163	216.787	222.528	200.285	224.157	247.957	206.943
177.133	190.943	184.464	201.664	192.471	207.119	198.403	176.879	188.533
214.019	296.54	248.645	299.076	253.431	295.215	276.577	243.228	263.928
281.501	305.943	346.775	277.093	315.84	295.515	322.127	312.982	318.427
270.056	328.039	310.14	334.693	304.801	324.815	312.261	320.391	306.63
166.813	152.514	173.138	136.598	157.87	156.257	130.23	136.779	146.231
159.462	158.881	168.278	149.686	144.479	147.674	133.724	157.961	135.079
8.86224	25.5106	23.9276	23.2643	24.0445	19.2898	18.6442	16.7167	14.1862
373.3	389.13	361.976	359.989	466.726	358.977	378.754	411.966	408.309
311.544	320.719	381.499	367.599	369.025	393.299	355.464	275.173	323.444
78.7693	104.305	84.5487	79.6366	89.7574	86.7278	90.2996	98.1597	88.3046
40.7331	30.9189	27.2896	27.6164	33.4926	32.5962	28.752	25.3963	26.9052
225.906	247.865	243.062	244.092	256.145	262.086	254.043	249.521	250.217
363.865	329.614	336.728	328.255	291.332	343.315	332.211	283.322	335.947
107.483	112.478	91.6517	104.775	87.5214	108.823	102.347	105.199	97.8294
112.658	107.211	122.236	96.2654	108.19	109.218	110.071	103.898	92.7873
268.445	304.095	281.028	271.474	261.281	277.999	271.287	308.383	267.049
165.934	233	194.406	222.997	205.349	250.895	204.797	207.744	201.612

126.236	151.449	186.183	126.911	167.917	125.341	128.373	155.518	148.165
125.812	180.582	160.557	167.198	159.776	169.932	155.552	163.289	154.117
17.2645	28.6459	23.5008	24.4345	22.8221	27.0106	20.5393	21.1297	25.9218
178.221	169.227	187.458	157.405	142.874	160.188	161.904	155.201	194.091
118.914	142.476	168.349	136.889	180.637	128.982	134.547	152.019	129.692
186.754	178.048	152.832	157.466	160.114	170.408	140.218	162.458	164.145
87.8191	59.2299	62.109	53.2815	63.1591	55.3057	68.9121	85.5195	73.5964
236.32	279.016	490.618	307.845	479.373	253.517	285.446	274.406	331.051
320.623	422.073	340.475	395.807	341.148	421.579	369.113	351.684	350.748
51.5172	66.3001	61.7624	48.4118	56.2243	65.7668	59.6475	60.0705	54.5475
282.391	233.542	378.882	276.312	256.746	288.707	260.883	244.28	312.871
182.299	193.105	162.131	178.242	186.181	178.168	212.477	213.686	192.488
196.073	235.855	198.004	218.952	227.557	227.068	216.824	226.131	216.67
15.3478	28.6341	22.0417	23.3226	27.3761	18.1689	21.8404	27.0988	17.2149
103.349	125.922	118.525	123.568	109.983	124.066	133.643	101.197	108.945
77.267	88.1442	59.5675	53.9402	59.3273	60.9113	56.0695	77.8529	56.1578
206.087	220.684	228.195	208.699	199.443	249.897	221.18	204.276	232.304
255.451	198.21	233.118	210.33	260.31	242.646	198.197	205.581	245.263
209.004	171.345	158.725	169.276	156.534	193.77	174.103	180.125	170.35
137.472	137.5	146.302	138.744	144.9	135.269	127.903	146.408	124.777
386.109	383.261	351.795	400.445	437.597	332.72	379.17	415.387	471.968
18.6393	29.7808	31.9044	34.7502	35.1901	26.8705	28.7616	26.7284	24.9857
111.849	121.953	124.204	120.936	102.52	117.032	108.106	102.898	117.481
394.021	485.659	402.472	420.214	462.466	425.655	415.119	461.008	477.434
526.138	578.332	510.155	702.065	557.809	513.39	656.19	665.117	638.174
367.775	361.734	358.637	355.673	420.288	333.98	392.719	399.925	408.233
60.5691	52.5417	49.263	41.9922	48.8543	41.3497	43.5728	51.9907	46.6625
166.006	209.219	179.933	201.538	164.533	201.62	190.722	173.167	181.486
23.8386	27.1509	29.8316	29.2002	29.9746	33.3113	27.6322	25.3133	30.798
289.95	302.586	294.512	290.383	267.5	291.811	300.745	287.849	269.846
110.519	94.7641	92.2537	94.3895	87.1954	91.3843	87.3283	94.8712	89.3021
2158.47	2227.1	2420.12	2355.09	1711.37	2121.21	2184.6	2430.22	2367.47
150.164	144.08	186.237	116.359	130.497	136.613	128.66	147.206	139.117
653.133	596.961	692.314	568.833	439.425	648.072	559.067	564.222	628.51
205.36	273.084	240.996	243.964	225.803	223.076	240.721	273.014	222.896
94.1131	123.937	104.643	115.235	94.9359	107.309	104.676	124.216	105.884
861.885	1064.49	1068	974.738	671.432	1049.72	672.948	813.289	956.498
102.679	163.406	137.279	144.299	128.021	140.255	138.755	132.669	121.621
217.945	228.798	196.279	212.519	248.542	209.156	224.454	240.64	228.538
139.745	93.3495	78.9672	76.8551	80.4955	76.3504	91.1838	99.7352	70.1814
54.74	117.641	101.949	115.562	90.0757	116.548	87.7494	84.8439	76.5778
96.1314	73.8594	97.4894	83.919	71.8235	96.4785	88.935	70.0402	79.4985
115.821	94.0226	103.947	105.335	90.4058	88.488	98.7464	115.056	103.794
198.828	250.862	215.065	245.524	217.957	249.728	239.034	225.842	229.888
549.187	620.723	883.972	617.497	742.164	639.836	644.856	639.35	646.182
39.259	34.9951	38.0489	31.2247	33.3586	34.2335	34.027	28.7049	31.52
318.164	271.21	273.622	263.223	266.685	319.506	287.828	223.979	266.295
21.7342	16.0158	15.0402	14.0036	15.5429	18.5228	15.3139	16.2186	13.9477
214.027	265.672	222.735	230.072	251.327	249.098	240.373	250.792	239.278
111.91	144.523	133.895	135.068	135.089	138.379	138.942	138.777	122.697
133.304	150.567	147.225	157.677	143.192	142.467	166.835	192.102	151.487
297.068	359.128	295.237	352.229	315.169	376.161	312.615	304.53	317.1

26.1089	65.1714	60.0611	46.3175	51.4413	58.4498	42.9803	45.377	45.0907
467.144	539.991	553.374	501.251	591.964	477.674	548.029	634.604	547.545
447.734	387.787	402.617	445.166	505.24	482.586	517.696	496.149	577.574
710.524	617.103	851.496	854.283	1101.24	847.179	657.405	716.653	882.043
134.905	158.205	134.899	148.649	124.458	151.035	156.447	137.786	135.976
98.8187	138.868	145.751	152.226	140.319	131.761	136.675	130.432	113.51
62.5464	71.877	68.3286	83.5819	77.3049	72.9181	76.7095	87.8493	71.6952
37.6333	61.0884	48.1911	48.6848	48.2656	48.6091	43.6983	52.8578	37.9131
490	458.837	521.935	512.464	345.265	474.372	463.383	394.412	483.782
11.5155	20.3642	15.4365	12.8082	12.4258	13.7466	17.656	22.3176	15.227
1377.89	1690.36	1566.57	1489.27	1797.29	1430.89	1386.35	1451.18	1585.68
3198.56	3670.2	4087.89	3519.46	3760.56	3928.97	3465.05	4063.39	3753.42
66.9657	49.9495	56.0422	53.6174	41.6271	60.827	47.248	46.9059	44.1172
2665.77	3364.78	4257.08	3168.34	3721.55	3466.24	3250.71	3502.76	2950.48
201.304	264.17	248.269	235.96	244.418	232.351	214.084	229.975	235.116
225.487	153.116	249.082	193.209	278.615	175.055	178.448	175.475	218.731
148.75	154.287	155.427	164.174	131.692	169.075	148.676	130.328	153.641
166.529	183.603	181.153	184.16	173.544	193.277	184.7	173.403	170.319
181.896	191.034	181.171	190.019	185.156	210.863	208.051	186.361	190.269
205.187	234.822	238.386	224.784	213.926	217.34	228.123	235.774	204.181
95.0657	117.034	148.42	133.82	135.002	117.797	108.874	135.977	99.5214
103.432	123.255	138.136	125.425	115.247	119.605	103.018	102.899	118.996
74.514	83.8888	80.5175	90.4641	80.0266	76.4177	81.5875	89.4036	72.9956
284.598	333.798	267.779	278.799	287.879	296.145	310.032	343.589	294.256
328.682	296.799	378.194	384.518	429.583	320.219	384.416	409.9	411.27
408.455	423.911	413.049	393.483	431.389	400.479	361.921	384.688	389.723
32.6926	42.1036	38.1503	44.3473	45.4035	47.1654	44.3832	36.1009	29.6531
216.191	285.134	238.029	239.038	200.66	273.006	237.098	217.62	229.207
201.881	207.769	218.6	204.604	200.499	212.474	212.219	214.794	196.271
66.5	77.8688	62.1462	59.5683	62.3083	72.4048	57.1124	53.7169	52.7908
32.4595	35.0765	36.757	35.3541	28.1808	34.4269	33.4472	29.6021	37.1862
139.035	140.844	136.874	133.007	167.59	131.716	181.522	186.709	175.263
170.49	134.858	126.102	134.714	156.058	136.225	168.743	158.848	140.801
13.6087	18.7018	14.4449	17.0359	12.2247	21.4012	16.2181	12.4478	12.3136
51.1915	47.0378	46.5887	47.8748	40.2066	43.0448	35.1368	39.9829	44.8512
91.0073	108.542	94.1936	80.0788	116.086	104.879	77.9666	92.3287	92.1079
255.906	240.795	327.789	251.035	247.535	263.613	228.486	208.871	234.198
32.3571	36.3575	38.4639	25.0107	31.606	29.8853	32.9721	35.7209	33.5492
452.046	450.601	470.583	473.14	463.345	519.369	480.565	473.797	483.489
158.388	148.851	140.07	142.622	129.635	137.669	143.083	147.638	147.684
49.6556	75.32	63.1575	64.5512	60.4012	72.1045	61.7607	62.5929	62.4168
199.037	203.192	231.101	183.392	189.537	191.588	227.834	234.418	196.447
177.397	182.234	197.543	172.94	193.172	169.879	193.024	219.759	180.306
152.419	130.593	130.292	141.295	143.447	123.388	135.085	160.066	131.215
26.3493	29.4659	30.1113	27.6929	35.0783	29.6175	36.8444	37.6302	33.4904
252.69	351.375	246.131	303.19	291.15	324.282	273.83	279.323	308.13
418.035	498.829	425.776	495.296	510.074	404.177	503.979	483.842	453.232
60.6758	74.5458	62.7125	66.4144	83.1667	84.263	67.4158	71.8717	57.8227
206.463	276.503	236.476	246.768	227.184	271.405	237.883	238.993	225.474
174.275	184.529	163.098	176.434	184.284	168.331	176.004	199.95	159.327
685.262	735.009	638.323	647.2	729.854	614.689	712.334	881.838	752.511
84.1756	108.35	90.1338	106.876	109.851	97.1062	93.6205	105.852	101.078

102.506	139.173	143.417	143.221	126.82	123.88	130.191	139.986	107.355
161.482	184.56	161.251	178.605	160.821	165.535	166.517	179.84	184.8
256.182	304.889	265.769	304.17	246.373	325.597	276.553	264.631	263.036
181.761	204.31	224.016	211.585	200.868	206.576	199.358	172.562	189.507
54.607	70.7732	70.0451	75.4793	64.1159	72.8381	68.968	64.6596	73.4373
103.622	99.5698	97.7799	96.8392	105.273	99.2154	95.9075	93.576	87.7287
66.2185	108.303	103.837	93.786	94.9905	96.0716	96.1302	103.022	80.2489
1239.56	1151.69	1274.62	1193.96	1115.03	1133.6	904.397	1160.64	1069.56
26.5778	24.3107	23.8471	28.6183	31.1726	22.8285	28.0142	29.551	28.7671
438.828	490.477	553.846	508.994	561.146	486.541	478.189	497.548	571.265
60.799	48.3249	62.1738	58.2638	57.5208	64.0491	57.311	54.1592	58.6782
529.919	551.876	538.266	510.234	560.004	537.179	557.363	550.198	540.407
89.0967	86.3451	72.7252	71.399	44.5719	75.6081	59.873	64.8574	65.3228
120.795	117.523	116.112	112.462	121.404	110.096	109.618	112.89	102.184
134.81	131.72	160.234	139.906	154.988	132.894	145.797	166.354	141.429
358.377	346.543	396.156	329.165	389.203	298.81	415.181	450.264	381.267
158.108	166.243	216.733	171.894	212.333	166.702	179.518	178.338	198.494
91.8889	89.9943	83.4256	87.5302	75.791	87.6049	82.8489	87.9625	74.2845
1619.14	1368.7	1731.49	1401.41	1544.71	1687.23	1527.84	1527.3	1860.86
52.8703	54.2701	64.5388	42.6713	46.3759	31.9862	40.8251	39.8626	41.5732
254.186	281.039	308.589	262.795	301.276	290.584	281.047	288.88	286.287
77.4779	64.0765	77.8189	52.8828	65.3735	61.6384	60.3784	67.2988	67.1906
130.372	140.267	137.373	144.034	130.668	148.11	150.107	136.151	130.53
223.635	287.317	240.896	291.652	246.379	280.29	274.288	259.899	262.855
2863.07	2770.31	2067.55	2493.44	2506.22	2464.83	3114.09	3521.58	3082.56
191.651	240.033	218.16	217.476	201.501	251.873	223.344	222.735	204.512
148.438	165.515	143.746	179.11	149.318	166.05	177.354	168.791	159.2
211.226	215.92	208.44	211.022	196.406	243.207	204.766	179.128	198.668
38.2774	59.7525	55.8559	63.4238	44.0395	47.621	59.3999	51.7093	63.6734
91.7311	90.5425	106.4	90.2765	103.144	77.0678	95.4117	102.827	97.7061
46.0328	81.9205	71.8741	75.8212	77.924	77.5513	78.7603	74.1734	76.35
16.6405	12.4689	6.68725	10.29	15.4327	10.9951	14.3574	10.8104	11.3287
71.639	104.438	109.269	103.903	83.1508	103.729	88.5592	91.284	92.1016
253.268	241.768	219.81	219.276	180.473	161.877	205.244	244.493	247.437
101.803	116.639	110.414	109.391	112.622	116.086	112.757	128.669	133.312
300.688	304.17	322.232	233.938	240.247	283.692	271.254	286.42	252.77
73.2893	151.426	107.205	134.812	110.405	142.455	111.296	93.1156	94.7379
82.0763	102.199	122.891	97.2049	121.326	114.499	114.362	139.172	113.934
30.125	22.6655	34.1621	22.8045	35.7754	25.1388	23.9025	23.9434	30.2177
141.695	150.179	160.277	135.483	130.95	130.446	149.284	164.17	123.357
178.274	197.309	185.96	201.283	193.201	205.927	185.209	217.519	175.251
145.159	169.9	174.96	171.109	159.701	162.182	165.469	136.53	160.385
49.8648	58.3211	62.5037	59.1943	64.3903	50.731	62.2681	57.7324	71.3803
44.1195	55.3751	46.7282	59.7275	54.7505	53.6644	63.0075	51.5961	62.1801
70.9448	108.861	78.9598	94.8873	81.2344	86.7811	101.001	106.716	87.5013
240.358	222.528	211.85	228.679	202.409	195.937	223.156	218.173	231.021
147.662	137.063	136.29	140.587	137.342	148.742	139.669	126.709	129.886
138.02	156.237	147.755	130.187	166.822	137.468	165.731	167.701	147.449
314.334	353.995	440.086	374.132	454.706	327.545	368.038	414.046	454.367
227.163	220.178	189.143	164.223	193.595	189.537	197.794	227.585	211.748
189.546	176.068	182.07	159.013	258.253	160.056	185.633	214.267	204.193
78.5775	167.685	132.919	128.713	96.7533	122.298	117.604	121.299	122.373

103.344	98.4684	100.935	108.23	126.054	93.7428	107.387	106.861	124.882
647.283	685.229	567.351	602.842	600.447	529.102	706.647	866.883	691.463
193.585	241.423	208.092	229.667	212.364	184.842	194.706	248.565	219.576
102.656	117.034	144.97	141.359	149.865	108.359	134.629	164.834	144.225
47.9475	47.6944	52.4362	43.9535	39.8086	52.8575	40.3909	36.9655	46.4497
342.044	390.543	324.181	345.116	354.79	403.838	337.995	348.14	358.475
169.195	135.93	128.334	134.173	151.609	129.595	141.838	160.071	138.622
41.8334	45.6494	38.0637	48.8319	44.3775	47.497	52.9807	55.9177	55.3292
1499.34	1496.72	1439.9	1399.12	1390.9	1281.27	1707.38	1907.23	1539.67
183.729	222.964	186.259	197.749	190.419	178.586	195.427	216.897	201.573
217.893	252.562	218.015	229.696	262.905	252.435	222.829	237.452	227.487
266.808	271.537	254.909	282.835	257.04	286.882	276.315	226.918	264.239
43.9673	47.0448	40.8859	46.8975	46.2297	48.7553	48.772	58.5207	49.7996
61.8707	56.4505	65.9306	64.2762	60.436	66.3457	63.1867	55.1512	68.8914
263.203	299.528	260.021	261.707	278.572	260.008	289.396	324.575	295.923
78.6948	71.091	75.0777	70.7386	74.328	64.415	61.8491	83.4214	57.5672
89.0688	106.688	94.4955	101.344	105.618	103.471	112.289	99.3343	102.359
8.0721	14.8436	19.9703	13.3378	10.271	18.4818	12.692	17.8481	19.245
418.295	420.409	332.009	348.484	363.093	367.352	349.321	420.067	380.005
613.127	731.632	617.392	712.329	469.871	536.562	704.825	792.077	626.154
343.472	382.048	307.025	351.117	363.472	333.957	357.016	460.949	390.224
192.255	217.602	199.177	237.82	180.084	208.478	197.894	192.762	203.022
919.972	1367.88	1487.78	1422.58	1276.58	1160.8	1024.37	1000.6	1073.64
157.606	165.388	156.52	190.61	147.094	169.87	163.364	155.103	171.023
281.659	287.815	355.418	330.067	310.726	375.366	300.361	292.38	300.674
62.2066	90.6748	81.7627	83.787	66.3087	83.303	65.3775	78.0644	70.8701
49.2636	45.9369	41.691	39.6585	43.3291	42.5139	43.5602	40.3613	31.4535
194.698	244.766	211.559	235.008	227.336	250.999	220.255	253.488	225.077
316.192	366.951	324.466	330.495	380.445	325.055	351.541	372.466	340.401
208.825	289.901	297.283	295.981	280.831	290.651	319.213	317.92	271.953
51.8971	54.8439	46.1902	46.6281	39.3169	43.072	46.9224	38.7549	45.6216
44.2821	41.149	41.5036	39.8062	42.2027	44.0952	37.5319	28.9969	34.7601
227.137	343.805	337.152	240.711	236.044	287.508	203.466	228.348	199.548
2508.73	2735.22	3253.17	2746.35	2451.68	3012.72	2362.29	2380.1	2584.29
327.202	355.137	383.685	352.064	354.983	400.277	365.806	323.444	366.197
133.06	142.234	139.484	143.837	135.371	138.587	143.625	154.7	146.093
84.4607	79.564	85.2622	53.1805	55.9222	68.6736	59.7743	59.2579	53.6227
278.983	230.692	178.127	216.366	238.279	220.568	268.085	265.442	219.385
63.5524	71.6632	73.4111	80.4455	78.0946	59.6514	65.5946	73.5119	68.8091
265.903	143.383	170.107	190.391	189.624	166.587	301.677	238.904	304.646
160.06	152.803	159.447	136.44	142.93	137.335	138.001	170.929	132.638
87.2599	101.321	88.0607	105.48	95.541	104.698	101.857	79.9359	99.2416
639.649	755.003	520.187	604.385	666.755	656.146	719.363	857.85	691.045
1922.42	1907.52	2843.21	2076.08	4405.25	2343.56	1917.16	2370.3	2783.13
181.565	211.017	189.62	216.606	196.866	207.798	208.058	180.736	196.577
138.965	153.036	145.655	153.453	120.884	144.528	147.954	138.272	130.229
59.9586	58.2263	66.5895	65.4791	73.6392	57.2185	77.5004	72.5411	90.7381
909.393	1031.5	751.266	862.491	904.186	906.764	1072.43	1127.07	947.836
315.683	320.864	306.021	325.648	343.328	321.046	353.296	371.961	344.883
123.663	159.087	132.713	149.346	118.779	152.668	127.964	129.388	133.344
329.109	352.048	372.196	340.082	351.536	326.468	360.403	437.486	346.134
225.817	222.966	203.833	185.392	165.162	174.979	189.297	192.723	213.845

710.682	804.84	606.761	697.267	766.447	754.735	766.932	898.198	776.092
52.5248	112.475	84.0612	89.2164	76.3824	78.8695	75.9053	83.0434	61.1171
72.5117	121.522	106.424	92.4318	107.883	61.7482	92.8777	101.202	73.3325
150.777	173.052	133.529	153.135	160.845	154.636	168.11	173.208	164.393
127.323	178.655	144.675	175.032	135.306	185.753	159.267	119.852	143.856
195.038	217.043	272.598	214.025	234.752	184.427	154.433	185.912	176.439
233.599	280.636	243.588	277.569	335.174	295.836	332.954	310.027	297.642
97.7215	145.184	124.358	129.086	116.521	115.594	119.329	128.662	118.347
602.478	720.53	788.124	637.135	708.687	699.726	502.928	521.343	610.107
169.664	189.61	174.871	195.866	172.971	210.601	173.466	173.786	179.633
184.163	210.664	198.023	209.568	212.717	189.527	224.801	208.723	214.042
109.738	141.02	131.897	148.569	123.019	131.336	133.725	121.041	122.167
174.763	165.813	173.75	171.807	152.287	156.024	112.152	165.59	157.79
101.412	86.2317	75.7476	80.3521	88.9155	75.0034	87.8386	84.9071	98.2764
67.9384	69.7473	70.7405	68.1882	67.684	73.4509	61.8756	67.8071	69.6778
104.793	123.41	116.605	120.748	113.36	149.934	111.309	125.55	116.744
161.567	179.279	161.256	181.417	141.62	167.876	152.476	143.709	165.999
143.814	110.349	143.489	116.837	125.383	118.919	109.988	119.343	130.495
161.853	172.619	169.729	201.687	175.416	192.513	197.171	172.439	209.019
273.026	286.013	251.781	275.45	248.791	266.765	269.18	277.403	268.036
125.924	169.92	164.528	134.583	171.493	124.02	155.088	185.852	150.899
79.0275	109.692	112.023	103.806	95.9584	113.836	104.491	104.485	95.0073
114.214	49.6156	92.9725	97.8017	96.2578	49.3201	48.2414	88.4781	115.683
173.983	193.655	194.021	210.497	184.749	212.368	184.587	170.145	197.714
82.3335	78.8835	85.4274	77.7316	76.1193	57.3667	83.6703	94.2079	68.335
212.053	246.312	239.526	233.353	276.296	200.117	211.987	250.627	241.992
28.2665	61.5407	61.1834	49.6397	76.3699	55.9582	38.8658	45.2031	34.4328
264.039	313.766	259.372	286.267	270.844	298.342	268.344	322.088	299.544
120.171	202.914	156.587	168.729	136.078	180.672	152.069	144.553	155.498
432.292	526.28	579.945	480.002	540.917	478.296	424.02	404.291	483.511
29.7237	28.4705	24.8843	33.7725	20.8414	27.0818	27.316	26.0599	25.7326
65.6682	115.101	111.554	105.494	88.2521	95.6179	89.005	88.3419	87.2253
181.419	250.234	206.21	209.742	198.87	227.855	213.7	236.895	203.934
1007.76	1120.36	1069.25	964.227	1179.85	949.373	1063.26	1272.5	1112.34
1010.82	837.833	874.214	809.068	891.608	753.421	961.777	1103.82	969.393
202.112	204.965	198.335	185.041	202.578	148.185	199.258	209.142	187.669
54.0979	60.6991	56.6954	65.9904	52.8837	60.584	63.9093	59.8235	53.4425
194.16	250.855	242.496	228.614	216.423	244.952	232.774	231.571	224.576
1724.98	1086.54	1137.56	1458.89	1407.18	1618.71	1363.62	1433.48	1670.51
41.5323	44.563	56.3391	50.7333	54.1144	41.574	45.7215	54.7024	48.5235
92.0335	97.6154	93.4472	106.785	112.723	90.5969	100.136	93.3931	105.15
348.779	408.18	481.594	399.84	385.901	423.324	308.602	295.807	339.835
180.789	182.925	144.553	152.205	158.396	172	153.405	156.275	165.942
126.418	116.074	110.111	114.048	111.181	123.587	117.002	114.33	95.7469
216.005	245.179	207.953	244.497	233.573	243.69	232.224	223.44	225.5
10.997	25.7179	31.9856	25.8453	23.0409	23.4561	18.8248	17.3016	20.3329
195.652	220.208	157.785	215.66	210.075	267.548	240.9	226.195	211.165
329.518	465.27	384.426	377.574	412.037	420.377	412.939	404.542	402.83
113.505	145.061	137.923	148.624	129.359	140.424	145.416	141.802	139.743
104.613	90.5838	122.727	102.771	103.284	82.9333	86.9342	94.2082	90.7531
258.559	271.357	238.595	226.497	284.993	261.062	273.146	265.717	273.614
124.386	129.932	142.722	144.966	122.014	138.414	119.544	110.763	129.049

130.591	125.153	126.79	147.014	146.153	131.478	182.52	188.508	129.693
165.135	169.216	176.491	178.535	148.293	180.545	161.543	160.693	173.234
27.495	21.7399	24.0062	26.0345	24.1379	21.6784	22.012	26.6702	23.1459
51.1661	71.885	57.6938	66.7327	49.5797	64.3514	62.323	56.344	59.5346
64.6435	84.2114	81.3291	72.9186	85.4826	68.8676	73.3199	75.7986	70.3983
104.247	166.079	146.78	151.497	127.887	157.041	147.857	137.849	129.444
566.652	571.163	541.353	526.69	730.631	557.849	582.47	691.848	743.656
156.181	141.964	148.192	156.667	185.807	129.676	188.062	171.8	198.547
352.885	366.063	330.02	357.97	340.046	361.868	375.746	359.311	397.354
137.025	176.027	144.758	162.517	150.586	166.499	173.349	126.47	156.651
158.688	130.127	117.715	131.958	121.282	131.733	125.031	114.31	122.106
2239.07	2165.68	3055.97	2267.07	4859.29	2605.75	2093.67	2535.23	3049.98
229.333	259.038	331.606	304.159	420.188	428.839	337.425	331.633	395.702
107.838	110.48	112.549	106.817	104.833	82.3046	75.2289	117.313	96.9734
277.7	232.31	274.162	251.937	270.776	257.143	228.911	284.732	269.211
89.7402	125.239	116.608	111.313	125.083	107.153	118.152	122.845	113.422
221.697	227.107	195.885	185.722	189.896	199.142	154.952	191.443	200.089
212.316	251.446	260.55	223.415	246.149	217.183	267.761	245.121	245.619
178.413	181.652	184.017	169.471	177.025	179.458	162.214	175.044	172.609
96.0091	74.1812	86.3318	82.8699	80.9589	71.5368	73.4691	84.5207	92.636
202.08	161.241	161.245	147.495	138.575	158.535	198.409	169.84	197.094
243.337	269.802	260.467	250.426	291.03	234.022	307.086	306.937	265.218
58.0673	96.0395	84.4277	79.6532	73.6505	85.4466	73.0573	74.8949	77.8806
188.118	199.828	197.011	175.469	182.553	192.48	180.061	186.409	171.11
51.4959	92.5474	88.524	92.5264	80.06	65.6018	77.2295	107.002	73.7746
91.5113	128.435	103.241	121.325	101.699	129.765	114.686	91.7293	110.21
10.0231	18.6805	22.3072	17.4982	20.0137	17.6714	17.277	25.5277	15.2789
76.8492	100.932	105.145	97.4084	92.6348	92.7937	98.7284	94.6982	88.2421
159.792	118.572	118.586	94.1646	44.7281	128.954	59.9955	91.2931	70.8878
38.3858	29.7958	29.9379	25.8969	21.4505	28.4634	30.0715	40.7749	33.1289
489.241	506.482	495.321	572.36	585.419	497.509	585.495	648.161	577.41
53.6204	66.9002	54.5312	56.7924	59.8849	60.827	50.5981	58.5577	53.3936
819.452	629.195	436.208	422.431	433.134	548.695	569.107	815.428	580.323
80.4471	97.9691	106.62	105.667	93.8667	98.5443	97.3994	86.7662	95.7588
308.135	354.581	380.514	334.231	422.606	323.353	323.345	346.889	373.051
170.304	166.088	174.29	131.034	137.986	123.762	121.834	148.543	101.147
347.582	453.436	642.102	553.612	566.138	468.861	424.438	467.282	514.004
163.325	183.245	191.582	175.998	171.3	188.935	179.929	173.676	190.159
68.151	72.9322	67.5799	63.568	72.2152	65.7664	66.0323	77.3243	64.6848
98.7454	129.989	135.577	129.023	116.851	109.736	118.505	128.868	112.628
46.3292	47.1524	42.5601	34.0073	40.5264	38.399	39.3665	41.1478	43.8929
165.872	245.546	249.746	251.113	180.722	251.502	251.323	255.377	235.279
402.529	441.821	416.751	408.179	490.988	406.159	394.093	446.363	428.335
156.853	128.88	156.089	170.159	184.766	159.999	146.476	141.39	179.196
568.209	550.038	529.677	520.396	463.744	545.558	485.532	559.305	568.442
130.322	150.613	142.539	154.58	142.106	152.617	140.446	137.761	154.625
1056.66	963.27	1034.86	1104.24	754.752	1094.61	765.749	683.298	1130.43
162.251	150.628	140.948	120.469	111.196	149.964	138.501	118.287	142.01
231.777	268.426	322.718	372.27	310.072	279.561	297.422	345.963	229.001
193.174	185.917	176.197	139.645	136.828	146.198	118.969	128.941	149.421
219.898	223.48	186.126	214.268	223.447	221.223	242.211	227.684	264.36
339.396	361.215	294.341	267.645	282.503	305.237	279.948	331.672	265.038

308.284	326.983	352.017	345.919	320.057	339.258	319.223	311.56	298.35
49.9737	51.9709	48.6167	48.5035	48.4954	53.6879	52.1414	49.6062	55.2097
62.6237	53.3974	62.8202	54.986	62.7067	59.5787	57.3606	61.7475	56.3371
251.244	187.119	186.226	187.923	185.983	169.621	73.6789	217.185	209.049
242.135	283.842	269.997	312.737	299.319	289.288	250.323	342.873	239.988
91.839	89.1015	88.3308	80.3966	86.2681	86.6633	82.7626	80.8191	77.5955
263.53	261.443	328.48	283.526	264.453	283.324	268.527	251.676	298.778
336.881	308.213	340.183	330.257	356.025	330.007	333.592	351.615	343.58
232.314	278.789	256.907	291.898	246.591	307.006	286.27	262.719	270.021
121.685	153.109	145.79	140.471	159.736	139.872	127.841	140.751	133.869
151.115	129.49	145.792	117.315	114.754	120.085	104.629	132.357	128.673
14.0347	39.1706	42.8986	39.9927	30.4429	30.7634	32.8553	33.6043	29.9791
846.916	818.923	831.189	1005.58	964.358	895.009	954.413	783.396	1052.5
249.423	317.196	309.885	277.34	249.558	277.004	265.937	308.596	271.599
1373.45	1624.67	1305.76	1451.47	1323.13	1473.24	995.568	1134.28	1371.38
178.587	246.795	241.456	210.239	204.874	167.052	220.017	258.42	184.983
59.734	37.8977	45.7723	50.3969	54.2271	48.799	47.3648	54.6666	54.0138
98.7033	118.981	107.445	103.39	113.537	121.795	107.032	111.518	109.511
158.784	193.926	159.371	192.895	155.145	182.262	172.104	158.614	178.014
294.843	339.796	371.067	335.729	358.548	358.098	319.18	312.488	344.206
259.678	296.6	312.995	297.316	379.935	290.212	282.692	311.436	311.786
237.772	238.787	259.72	248.723	251.515	214.195	194.027	213.542	232.29
184.228	184.78	174.283	161.269	160.774	187.843	159.963	197.347	163.667
20.2369	25.901	28.4563	17.2891	20.8152	21.2066	15.4707	22.3419	19.0887
34.7993	39.3649	28.3285	31.9088	29.8643	41.6139	39.2595	38.9402	33.1248
407.624	338.439	342.998	393.976	221.787	438.038	339.241	318.731	346.972
253.454	259.323	263.302	251.011	276.537	237.906	333.161	281.205	343.578
53.3908	51.2796	49.5418	50.5127	45.6543	47.0448	41.3172	42.7028	31.2178
608.377	518.41	836.662	608.101	673.439	636.615	521.421	542.817	572.161
155.087	130.593	141.695	137.441	153.721	122.524	128.279	157.697	130.511
149.877	157.933	194.072	177.134	211.12	152.711	180.162	188.362	182.921
421.157	467.972	659.455	561.112	658.062	450.631	459.674	424.935	551.925
229.635	209.075	212.459	209.046	205.842	211.627	213.981	201.889	201.334
254.336	347.877	279.69	298.256	273.789	308.174	271.519	283.488	260.37
453.769	469.238	943.792	463.959	552.818	854.811	548.76	604.99	508.857
388.59	452.986	480.621	421.879	338.012	365.376	391.494	354.712	390.101
1857.73	1862.19	2801.84	1964.25	4384.94	2268.2	1809.78	2203.39	2638.04
3420.38	3831.98	3402.43	3329.27	3095.39	3249.35	2981.36	3179.11	3347.9
89.9486	108.619	96.5819	105.414	89.1185	105.592	92.5105	89.5422	101.139
42.7017	49.21	57.9561	47.4246	51.5088	46.139	49.5341	58.7016	46.494
53.1401	53.1764	46.3005	58.4933	54.8742	65.0057	51.9568	57.5403	54.8155
93.9802	113.57	114.231	111.449	113.857	104.881	116.152	117.524	103.825
210.818	242.436	243.687	231.546	254.475	267.937	242.461	251.998	229.051
278.419	278.713	293.755	285.161	324.739	264.127	284.973	328.338	306.345
344.317	351.952	296.555	316.102	358.314	321.328	364.264	347.183	354.166
103.071	85.9607	106.022	94.5592	88.6485	84.8016	91.3693	85.6584	96.5622
199.57	230.585	196.765	194.41	211.556	205.581	201.789	249.11	200.948
80.2203	121.557	110.782	110.374	95.1564	118.131	111.716	96.3763	114.407
149.293	148.535	169.934	154.41	139.619	147.241	139.959	129.326	146.298
81.6702	93.3659	83.1227	75.569	106.861	74.9584	90.8559	111.757	90.547
38.2886	41.2547	36.5975	33.3841	35.1841	40.4537	42.8843	41.9374	39.3934
25.6399	37.5331	20.6409	29.2484	31.6183	28.1561	28.3343	27.1837	30.5285

38.7532	44.6291	36.6175	41.0227	34.1016	37.2593	40.4249	33.192	30.5411
405.616	298.406	354.908	395.124	428.264	396.447	438.465	406.745	523.24
71.2193	58.2992	72.0838	52.7384	58.9227	53.6012	65.0377	68.2019	62.2029
755.285	886.968	691.534	780.745	734.392	764.857	787.532	897.503	750.709
108.566	121.357	102.484	108.303	91.8418	113.019	93.1979	92.2369	97.5916
159.901	182.558	162.661	155.415	156.164	178.023	134.938	144.009	139.166
72.0286	81.5149	66.3864	71.4762	65.4922	66.4843	59.0656	59.8115	55.0465
30.2401	58.3417	49.1892	51.6956	52.9272	41.4502	46.5229	65.6499	41.2958
137.399	176.551	155.688	193.767	163.364	184.162	186.747	192.157	175.465
458.22	468.404	466.053	486.181	439.766	508.204	526.587	484.956	537.245
247.172	245.671	240.959	234.406	236.724	255.927	246.289	271.188	245.58
142.819	138.215	140.131	141.253	139.379	146.664	140.447	144.073	150.469
462.332	467.944	416.154	533.181	623.897	388.684	572.221	632.735	584.138
359.245	387.981	355.798	370.683	374.394	389.043	432.41	421.808	419.43
80.713	106.168	83.299	106.971	95.3404	95.599	79.8334	90.6145	83.7444
675.158	577.335	617.816	528.16	584.485	559.243	496.114	529.34	508.754
87.2533	123.939	129.903	108.114	84.1832	111.195	111.453	116.106	120.06
21.9205	40.2907	23.1683	31.1246	25.7214	31.863	28.1688	32.2405	28.3453
138.142	111.147	101.239	116.179	94.0993	114.625	107.303	123.469	93.1749
86.5241	71.3304	73.2539	89.5113	87.4486	80.3596	84.7186	76.6461	82.6321
1502.17	1385.4	2641.78	1561.27	2705.95	1821.34	1915.46	1954.74	1736.21
247.171	207.931	198.48	183.7	203.966	208.366	210.153	237.299	199.284
79.718	89.9566	107.495	104.342	106.398	85.8512	90.0063	95.0062	80.6149
397.208	432.228	424.944	443.52	465.065	368.859	413.426	485.852	451.555
62.4794	67.2643	67.6279	67.9623	69.5471	74.0743	56.0895	59.4925	72.2106
2361.63	2654.15	4497.53	2867.27	4560.38	2286.89	3067.1	3222.84	2841.01
82.2188	71.9926	59.0574	74.9095	70.2212	58.2459	74.6903	87.1142	69.2891
545.961	505.835	633.63	544.559	539.356	495.915	484.313	496.63	578.02
317.479	390.742	306.574	359.668	372.931	360.368	350.849	330.512	412.498
115.178	116.762	134.903	124.177	93.1681	142.2	111.685	115.883	105.908
134.712	201.001	199.992	187.41	176.356	181.667	187.862	177.14	169.313
111.285	147.754	126.233	151.316	117.192	134.577	151.562	126.746	141.25
41.1061	35.946	31.1383	34.1673	31.901	26.1086	26.1568	30.6073	27.8363
1647.47	1701.66	2606.88	1794.92	3968.95	2002.56	1568.65	1893.26	2266.38
465.401	452.361	574.15	374.663	595.655	466.995	455.243	526.845	518.903
133.409	151.826	124.836	111.55	114.381	128.927	101.803	104.774	111.162
153.387	151.882	157.557	163.575	180.023	167.227	156.638	165.952	168.039
117.259	119.595	145.841	158.123	140.893	124.665	139.308	123.034	118.595
73.2173	123.688	111.469	102.778	85.8885	104.841	94.5045	101.792	86.5131
200.728	160.613	212.866	177.129	194.782	185.16	135.555	157.032	189.976
155.166	214.305	192.722	183.571	185.532	211.066	202.492	183.67	175.818
133.951	159.3	150.391	150.903	129.563	147.97	136.603	127.765	141.834
121.918	177.096	141.952	142.203	134.973	170.947	146.516	125.061	148.486
298.167	340.836	355.717	321.254	306.975	309.538	342.841	309.773	328.951
143.284	195.418	184.518	219.744	173.078	209.409	210.049	197.808	192.239
27.583	36.7176	30.9334	41.9563	38.3987	37.1076	36.6442	33.3335	36.6429
216.518	226.253	187.068	210.643	172.852	203.287	186.948	192.611	198.402
15125.7	14905.2	15980.2	15430.1	14654.5	14844.5	14269.1	15197.2	14321.8
111.659	113.531	121.601	95.077	128.359	112.825	100.461	111.734	110.746
78.5673	76.7606	79.697	92.9371	77.2562	85.6585	83.0423	92.6471	76.8176
17.5501	20.9644	17.6822	17.1455	23.5565	15.3895	22.2338	28.2977	15.6332
18656.9	19124.1	18420.8	19285	18986.1	19107.1	18867	19416.3	19168.6

95.0157	71.8037	79.0704	70.5601	68.5461	69.9965	71.4102	96.9575	84.6736
149.024	147.36	124.097	118.847	132.465	135.101	115.773	121.007	135.384
170.889	135.851	100.701	118.112	110.813	113.13	153.246	143.536	119.17
27.7037	32.0203	33.9441	23.3195	30.6656	21.9855	28.3441	28.031	19.592
26.789	34.8451	35.8633	45.4251	43.8497	41.9397	48.5203	43.6491	38.7235
282.796	311.64	311.148	296.458	274.82	317.019	315.363	280.567	277.302
80.4959	56.2894	49.4603	66.2957	61.1753	60.6506	57.6919	59.133	70.9941
250.229	207.012	326.179	264.459	204.729	224.173	228.327	258.625	243.931
178.709	213.325	178.327	183.712	170.748	203.207	180.121	172.422	168.296
304.092	361.614	325.959	318.541	302.98	344.93	357.076	321.819	285.872
116.313	98.5646	90.545	87.9223	80.3189	108.413	104.469	79.1779	94.7943
368.052	339.083	242.199	296.062	232.604	299.949	279.62	291.779	422.449
98.1819	90.6821	115.117	82.7518	81.1559	85.1237	64.0721	73.8044	94.1093
469.826	531.801	574.583	450.264	676.998	545.143	447.27	601.996	493.764
1068.79	834.317	1085.13	1247.69	907.581	915.712	985.87	941.996	991.979
145.566	194.527	194.871	201.706	178.506	173.385	215.88	212.152	199.556
90.6313	102.72	88.6955	77.8527	83.4405	79.6846	86.845	84.0651	77.0146
109.901	124.165	136.581	128.399	137.326	120.064	125.92	115.141	108.5
200.189	274.298	248.668	255.026	210.037	239.668	238.682	248.9	223.439
147.696	135.663	129.386	125.672	151.344	139.002	158.125	164.998	150.905
131.008	169.707	142.697	157.46	143.734	154.438	144.671	158.706	149.552
43.0928	41.0267	40.9002	46.2939	37.8276	45.5437	44.5172	49.1328	33.5059
54.5912	56.967	55.1265	36.1682	44.7059	57.3418	48.7774	44.3112	40.6997
542.682	541.549	627.806	727.035	759.574	389.48	643.861	914.566	610.881
273.905	367.049	339.154	392.001	421.477	303.98	328.743	529.798	333.973
60.001	60.8188	60.6115	55.338	57.797	55.331	50.7216	45.293	60.3952
42.6001	39.7742	31.8189	33.3594	36.8003	29.8492	32.9715	30.1615	37.2966
199.604	194.005	198.389	193.717	172.163	200.601	183.595	188.276	179.859
214.145	210.826	279.212	217.855	227.323	227.121	220.796	207.349	201.128
300.923	260.09	289.749	284.54	338.061	285.007	289.686	262.421	350.385
433.014	332.281	339.677	370.174	345.052	361.793	290.681	314.609	412.339
61.2903	77.8336	65.7961	61.0723	65.7313	64.0974	57.4603	64.6921	50.5432
277.779	264.622	265.125	256.988	257.912	235.796	264.304	286.037	250.096
307.803	309.888	305.573	265.202	289.325	273.381	242.901	333.434	319.89
125.096	121.458	151.529	146.754	148.36	117.598	140.603	177.914	137.943
5200.23	6338.93	6330.63	6051.12	6242.87	6087.86	5478.26	5715.41	5636.86
90.162	143.675	122.89	125.014	115.735	119.548	122.792	119.578	119.33
93.9574	100.817	97.3146	115.615	108.639	102.849	125.601	106.539	112.171
138.028	107	125.974	113.309	121.563	126.24	141.275	107.654	135.488
202.072	267.582	226.85	215.765	249.817	236.322	217.709	253.557	218.108
117.387	87.8048	130.883	87.0465	119.313	80.0674	96.1703	109.708	91.7458
202.584	245.978	239.397	215.688	223.27	227.385	223.237	231.596	207.94
74.0022	68.2328	61.3186	61.5355	65.1003	70.8305	82.6507	76.7512	64.1501
366.123	491.054	434.801	464.739	389.698	501.339	453.378	393.914	399.26
57.1376	74.0433	74.2625	68.3514	53.3359	76.0102	71.815	54.249	56.4666
61.1516	61.9938	58.8105	55.1345	49.8327	63.6081	57.231	51.448	55.6823
95.1233	105.908	99.7828	111.356	91.694	114.052	109.757	89.9501	96.2521
363.651	478.912	700.472	528.757	621.428	499.603	510.691	441.233	514.087
1877.48	1797.59	2765.07	1967.03	4329.44	2185.32	1784.11	2171.29	2639.57
26.7618	39.1167	39.1453	33.825	42.6371	32.9345	32.0405	27.451	36.367
379.75	639.527	411.011	485.111	406.55	478.612	503.742	577.888	416.232
42.6565	39.8772	24.4408	38.4251	22.2018	41.3303	29.4518	26.7337	28.773

69.8501	89.1014	85.5594	85.0756	67.9775	84.4191	78.7375	82.4958	84.5624
281.983	379.041	338.047	274.391	326.761	328.502	299.19	348.937	332.716
156.843	175.716	152.872	158.596	161.254	171.573	163.042	183.562	147.519
60.2348	57.0766	69.5274	62.117	86.6922	59.1492	68.1323	73.4833	73.3209
249.149	216.953	226.626	221.588	221.794	214.696	241.395	265.334	238.213
5001.82	4504.27	3691.07	4291.15	5092.74	4271.73	4277.03	4677.23	5912.94
365.255	354.389	323.535	288.43	300.388	284.788	280.535	365.662	292.056
16.8621	24.5368	22.269	26.3756	27.8357	23.8156	23.5547	24.05	21.0862
77.3713	120.862	112.575	111.331	89.4441	96.3753	102.736	90.8363	104.294
49.4441	62.5321	58.4493	62.9095	67.699	50.473	64.8753	76.1161	52.967
241.933	243.241	244.427	242.168	271.944	221.128	247.066	274.104	261.957
797.698	581.875	936.045	1047.29	1022.15	685.865	876.292	1172.16	1046.93
72.8579	131.548	122.451	116.834	102.025	106.119	92.449	85.8405	78.227
61.0602	49.032	70.9317	45.3931	46.0661	43.2954	39.9254	48.3109	44.1482
1437.53	1331.27	1852.93	1605.46	1410.91	1554.57	1377.57	1427.64	1392.26
316.016	318.661	288.741	321.732	362.781	300.309	381.867	364.75	366.699
38.9958	37.7158	31.9036	26.3726	25.5213	25.3414	29.4047	33.7981	27.9626
17.6966	12.8417	14.3276	12.8981	15.1953	16.4582	12.5413	21.0198	14.5155
481.447	266.5	463.626	626.165	647.874	442.133	553.904	497.824	623.616
23.9461	32.8642	29.5381	24.1995	29.4368	28.9367	28.2357	32.8948	20.4457
271.783	299.375	250.925	274.576	243.806	284.421	276.878	269.776	272.503
75.3473	81.7519	81.5012	80.0613	86.7586	92.2158	82.957	79.4864	81.3122
312.327	378.628	353.484	350.404	346.91	403.712	359.27	356.265	366
128.986	140.824	143.499	137.06	151.636	126.733	129.191	157.23	140.508
30.286	30.1916	27.0319	21.9084	25.9797	32.032	32.4951	30.874	23.4607
49.1387	94.9333	91.0215	88.2316	62.437	83.3074	75.4516	66.8215	54.4526
148.199	186.828	152.831	181.982	154.096	175.359	170.54	177.686	167.214
183.135	145.146	159.067	100.552	110.093	115.854	160.716	136.084	177.953
182.865	220.579	197.738	189.348	182.169	249.069	198.59	175.405	209.901
174.807	212.444	197.664	211.187	200.514	200.583	176.869	186.471	199.393
389.269	300.699	451.228	371.38	454.019	318.661	307.131	350.344	364.412
147.802	172.926	135.231	140.497	154.466	137.037	157.858	170.609	140.951
13.8361	20.1701	26.3508	23.5073	22.3273	38.5828	27.1745	19.0968	18.0612
195.966	215.902	224.834	251.067	242.451	251.03	221.02	191.936	235.275
54.2379	62.6726	67.5911	65.127	73.5993	73.1385	64.515	67.9931	57.7892
86.8274	96.3936	70.9187	100.398	101.263	63.7297	102.411	150.024	100.017
84.5669	89.8043	101.56	89.9465	96.7079	82.4532	104.866	104.896	101.468
55.3544	43.0833	70.2289	48.987	53.9624	54.8772	46.9156	40.2671	58.2912
40.7103	58.1552	59.6346	56.0727	46.5467	41.868	51.3492	58.8571	42.9977
235.016	275.581	261.357	255.422	289.846	268.386	274.085	297.281	240.45
54.6941	48.1326	50.2704	40.6375	48.4264	44.4839	51.1485	48.7761	51.1729
67.5615	60.5946	57.6059	64.8313	63.403	55.2008	68.6735	79.9799	65.1775
71.9653	109.965	99.598	105.796	98.6559	100.188	102.305	80.7136	86.2293
193.634	313.221	278.903	236.081	221.152	238.903	224.01	284.77	205.792
1615.58	1642.67	1910.73	1633.6	1638.29	1775.25	1507.32	1430.77	1768.27
217.413	282.198	294.663	257.86	285.354	265.607	240.514	244.066	237.473
326.813	351.014	317.072	289.769	260.475	239.99	308.561	270.888	269.248
3083.75	2897.71	3403.5	3169.78	3406.87	3012.67	2886.45	2743.62	3038.93
33.0717	40.6226	33.0944	29.065	23.7183	42.6569	29.5092	33.2236	24.8197
125.21	105.968	157.376	133.314	134.738	110.275	82.675	106.723	94.4031
156.614	151.311	142.06	138.854	128.653	144.575	137.328	123.737	121.206
162.332	149.981	149.489	120.61	144.685	130.449	131.008	166.681	155.503

241.618	251.273	246.544	225.728	275.125	252.981	242.691	245.349	245.153
733.518	1363.99	539.64	1274.8	514.121	543.482	642.808	574.514	765.677
255.056	276.805	248.784	259.134	337.288	248.841	269.653	274.718	304.34
144.502	170.158	162.094	167.183	167.116	142.368	148.617	177.933	156.189
55.2114	54.7596	41.782	37.5389	41.3737	48.6267	36.1104	53.1236	32.0922
45.2155	49.349	55.7522	51.6619	52.1295	47.7096	51.2664	51.8239	52.8473
137.627	147.506	146.734	162.712	144.877	134.07	158.68	149.891	151.721
773.795	674.16	1565.91	813.958	1751.97	1155.02	987.657	883.079	948.586
132.095	125.804	115.9	122.544	103.924	134.476	101.007	105.66	100.586
328.643	308.396	423.934	331.195	326.593	259.776	294.486	314.685	305.2
191.225	185.009	215.368	175.511	171.581	208.326	203.556	204.839	182.949
229.539	197.786	179.247	159.98	151.624	172.408	173.612	208.551	165.85
393.821	396.22	403.466	410.839	411.755	381.382	484.281	462.477	447.535
406.103	422.22	371.189	420.398	427.78	409.313	472.636	494.2	473.048
269.462	255.617	295.176	296.863	314.355	272.208	257.322	283.76	257.768
13.9961	11.9495	8.2606	16.9846	11.1914	8.51249	7.171	12.1081	13.067
285.795	269.034	293.457	361.827	348.078	287.788	328.996	347.285	314.893
358.105	360.744	372.841	323.209	455.419	329.866	427.303	489.216	389.631
46.762	35.3351	32.1127	28.8816	23.6024	35.2361	24.9821	27.4812	32.3657
315.562	377.439	369.549	346.855	333.012	400.634	355.307	334.252	339.424
225.065	259.161	194.947	263.135	265.303	259.279	279.873	275.692	249.231
91.4652	126.167	120.767	119.093	108.616	114.678	103.527	107.159	100.974
183.477	207.289	190.85	203.4	211.831	183.64	215.127	238.197	242.256
86.9674	84.854	112.821	68.061	87.8282	67.0816	82.7258	81.4254	98.2626
200.182	210.37	216.001	185.931	186.566	208.084	167.907	178.746	181.84
398.384	498.296	402.923	350.554	362.697	405.648	543.126	571.558	426
112.821	85.7265	77.8673	111.809	121.262	84.2252	135.939	115.958	134.638
195.613	137.326	169.148	185.462	198.862	143.454	145.383	161.048	195.257
234.518	271.044	244.237	242.612	245.275	253.992	244.946	264.609	220.935
126.607	122.936	104.63	113.803	115.503	125.956	107.532	109.363	113.796
198.788	315.287	271.42	274.891	233.162	275.856	266.337	246.877	279.238
191.686	181.904	180.657	184.692	187.508	181.317	160.657	193.65	146.062
334.163	349.396	275.957	277.983	275.606	294.336	257.105	302.098	287.593
665.059	686.376	642.496	643.218	797.147	556.209	792.525	981.059	697.697
52.4921	73.52	78.0998	76.4377	50.4644	59.9402	67.5489	69.0058	73.5285
204.21	265.903	263.175	241.16	194.47	229.966	158.6	170.378	182.572
35.1743	55.0395	48.2514	55.5567	42.7623	57.231	46.461	47.74	44.0407
149.298	280.949	229.661	247.784	177.365	214.498	221.013	207.879	207.168
22.6408	33.8467	31.943	36.9726	29.7196	37.9927	29.4748	31.6098	32.1759
248.979	207.484	248.686	196.555	205.134	237.204	210.219	219.253	233.274
178.455	219.361	167.81	203.257	197.571	204.333	203.376	227.846	194.136
211.862	242.211	212.834	200.041	216.563	235.109	247.444	240.1	215.225
555.946	420.176	414.765	507.645	795.233	453.457	617.156	503.192	644.871
127.844	155.705	144.77	147.684	135.165	154.11	152.337	139.13	133.521
281.98	347.249	288.654	278.537	386.369	351.404	313.048	297.064	313.684
69.8495	106.265	73.2215	88.5889	84.795	93.4418	84.7557	87.108	68.4894
172.171	186.71	162.786	172.749	150.902	213.789	187.008	173.903	174.845
58.4208	108.55	79.5965	91.02	78.76	87.4483	59.0064	77.1576	63.4729
1044.17	1212.26	1123.06	1067.07	1130.47	1147.69	1061.33	1165.94	1073.87
997.857	1418.45	1116.58	882.852	1349.85	1056.95	914.117	1218.44	1002.06
104.193	82.4146	79.0174	78.1753	70.2309	112.623	131.02	74.4572	99.9189
108.329	141.235	136.59	145.909	122.705	150.422	124.665	126.687	137.118

70.095	64.5745	66.4363	68.1297	72.2174	63.4519	71.5757	84.6317	70.4448
239.137	277.471	280.8	276.945	296.449	247.959	291.699	309.758	253.819
42.2198	30.3734	26.0285	18.6019	31.2149	18.9718	29.1531	31.5798	15.5844
18.0402	28.4257	21.1229	26.0814	32.4619	25.4644	32.9187	34.6073	25.2649
49.055	62.7635	50.7945	57.4538	45.4137	57.6147	61.2723	49.4252	52.3993
132.591	142.834	145.527	148.636	160.807	142.439	146.387	182.461	137.596
115.683	174.204	146.533	132.726	126.704	181.379	129.989	124.34	143.73
2893.99	2886.61	3323.3	2888.96	2621.03	3225.19	2859.34	2900.61	3295.06
200.139	182.112	211.541	158.898	150.149	191.645	167.998	152.634	170.977
167.01	166.134	248.581	158.608	258.694	155.058	186.861	217.605	215.287
58.7791	100.178	83.6278	82.4794	71.302	88.4707	68.1128	72.6618	68.5392
127.87	99.6538	109.79	125.173	93.9585	122.008	113.136	96.4157	105.424
70.6784	101.448	91.4471	94.6313	89.1886	90.3395	93.141	94.477	88.4291
135.38	199.672	204.155	199.335	193.893	161.858	181.145	185.33	170.171
421.435	430.312	388.282	377.048	525.228	405.009	452.037	438.769	452.573
78.6774	137.548	112.334	113.062	88.6664	109.252	95.2864	100.988	95.8344
593.479	472.036	461.44	577.742	642.187	456.62	574.47	639.026	612.035
173.891	150.241	192.524	193.349	193.116	163.56	175.774	167.713	198.03
108.789	185.148	147.931	147.811	139.28	150.373	135.751	156.16	140.455
54.5767	42.005	48.118	56.4147	59.7635	49.6575	43.832	43.9272	44.3427
82.0993	65.0779	61.1856	70.1652	64.3018	76.7462	66.952	68.291	67.6528
401.424	483.921	442.788	411.087	417.035	464.566	425.07	447.135	412.75
446.699	353.802	359.014	462.903	471.021	406.421	473.499	429.959	528.833
215.849	233.159	179.789	170.796	163.352	165.958	163.85	195.714	151.562
491.837	379.128	392.955	406.487	467.231	348.971	509.928	667.531	509.247
105.388	101.359	98.8367	104.44	120.529	113.284	118.919	121.101	119.752
154.357	191.086	157.539	196.713	171.027	174.114	172.764	189.299	153.007
104.137	95.9492	122.658	113.804	123.203	115.869	105.729	102.547	122.04
38.3349	35.8561	36.3251	35.5951	32.3995	31.8944	32.5252	38.2118	24.8035
380.955	471.401	492.814	432.965	440.33	400.715	389.807	437.512	461.284
22.1323	22.7344	25.7499	23.3146	21.7771	20.999	22.8858	18.2944	19.011
214.163	243.624	210.751	234.84	210.077	281.241	235.071	214.865	229.012
402.201	555.174	712.836	574.683	365.056	624.832	375.304	338.704	453.154
212.297	236.342	219.273	217.189	228.536	213.09	226.725	278.14	221.865
283.794	296.803	272.102	295.999	300.519	268.197	249.444	275.773	315.015
97.374	90.4697	91.5145	85.0137	98.256	89.5907	88.4596	90.2606	88.635
142.185	189.994	178.926	177.873	171.072	148.476	193.013	186.245	173.422
236.903	226.697	222.173	243.843	273.299	242.442	240.916	240.85	252.001
1130.09	1297.98	1492.84	1463.65	1574.5	1263.33	1220.64	1371.57	1595.34
257.592	296.804	307.225	303.911	323.652	286.433	288.276	273.441	262.986
91.3251	130.19	112.006	118.961	105.164	123.025	106.562	108.845	108.908
2690.4	2748.84	3126.97	2864.8	3299.87	2886.12	2795.06	3060.92	2883.09
180.869	206.233	199.225	190.807	196.801	184.034	198.658	209.231	192.412
322.757	325.948	388.226	333.413	372.458	332.228	351.736	315.39	352.485
230.321	276.658	230.918	246.61	221.364	298.438	252.141	204.725	251.568
205.349	205.063	262.819	222.259	251.759	194.347	232.736	264.608	215.268
536.315	463.81	501.45	513.485	520.127	472.443	541.656	540.237	568.168
165.52	190.099	203.795	198.169	193.953	179.847	186.642	184.621	183.865
216.453	236.076	268.155	236.275	214.549	198.756	199.643	246.428	205.275
301.529	342.422	300.688	337.812	382.807	341.4	337.384	349.55	360.294
203.566	187.684	226.865	169.475	170.727	187.177	147.427	181.489	147.025
11.9446	11.4065	4.707	4.56489	9.18876	7.24644	11.3229	9.19665	5.2569

161.6	240.468	237.842	224.123	184.483	237.618	197.226	235.698	202.973
240.635	318.291	263.804	261.25	292.847	269.206	265.58	315.451	250.788
1090.76	1059.88	910.399	1039.55	1108.5	915.997	1145.82	1354.74	1283.37
238.971	343.463	265.81	282.696	331.605	275.841	292.15	372.591	245.01
1154.97	1141.43	657.026	1361.17	723.63	1022.68	1081.26	812.039	984.998
83.5066	68.1229	115.605	81.5571	73.1631	72.4472	84.8932	73.6419	86.7675
33.9861	80.4064	72.0356	66.3587	59.4178	50.3979	47.9328	68.9696	43.2871
178.086	164.301	139.444	146.989	169.856	187.891	184.366	154.052	174.982
195.247	248.901	195.389	219.166	209.154	229.529	218.584	218.487	205.918
196.156	208.386	194.901	205.354	194.089	203.106	219.215	206.452	210.829
47.1393	72.3441	66.0941	71.224	55.5027	75.8417	50.3142	49.5611	67.9701
323.203	363.44	354.339	353.646	333.649	383.423	355.613	338.602	334.456
88.3333	90.4748	96.0743	100.08	105.955	91.1122	107.278	102.417	85.7676
82.5369	112.653	112.576	104.149	96.8807	95.5695	100.881	110.73	75.2366
385.869	453.221	343.182	362.749	425.807	367.493	465.746	505.348	441.713
608.311	656.777	608.87	719.478	969.767	740.211	560.285	601.562	724.549
77.708	102.185	115.028	109.066	97.5332	92.2377	120.735	95.3284	95.2911
94.925	119.851	90.3822	78.0783	83.5829	86.7856	82.2681	88.4268	76.7227
728.12	668.049	617.118	659.325	723.481	689	704.797	795.233	747.078
260.075	190.803	223.958	173.415	201.015	184.181	209.797	212.692	213.542
416.404	465.613	387.127	470.032	430.561	428.022	462.221	585.239	415.519
77.9756	140.664	135.52	113.103	104.984	105.49	106.112	121.049	94.6495
54.4706	64.7535	64.4001	79.2172	60.2072	71.826	64.1477	66.322	72.9772
114.837	132.278	109.66	112.025	117.594	110.509	127.425	128.061	109.196
193.679	242.569	204.256	211.598	198.414	230.607	221.413	207.745	213.325
110.81	202.856	178.153	191.48	169.016	177.493	160.028	174.322	117.716
260.913	299.723	280.186	277.053	281.106	266.839	280.558	306.229	258.21
137.054	130.107	134.888	120.266	113.79	130.65	126.698	122.047	116.625
403.087	403.351	399.161	410.648	372.122	429.637	420.151	384.004	383.38
37.8532	48.8641	49.035	45.8057	43.2422	59.0838	51.9698	39.6889	33.6537
53.2714	50.9325	47.0123	47.2633	49.1608	56.894	46.6604	41.8601	55.0828
338.426	358.072	297.221	302.992	287.885	298.244	287.72	339.476	291.205
57.4244	65.349	61.0154	55.7334	49.657	48.9213	61.1919	79.3942	63.036
213.283	247.725	228.824	235.8	215.735	269.365	281.66	227.797	231.163
73.8357	114.492	114.84	101.59	97.2587	112.079	99.0004	96.0639	88.7321
289.549	383.047	319.741	313.126	349.569	341.425	309.236	356.993	290.412
149.727	154.792	119.436	135.549	142.83	136.048	127.732	157.737	122.805
83.2468	86.2234	82.2228	76.8118	97.6071	71.0755	93.782	94.888	92.979
199.015	205.453	194.582	159.585	170.538	208.383	202.503	187.124	199.619
94.9637	141.577	122	120.231	105.172	133.212	99.4942	120.854	98.9024
190.865	272.076	248.379	262.936	219.096	261.307	243.8	221.404	235.067
582.39	471.081	841.28	636.439	754.101	590.81	686.887	732.731	675.579
432.902	640.777	410.541	481.52	452.965	606.626	475.788	505.797	466.566
31.3915	52.4649	38.7743	44.6118	45.8933	44.1322	42.6772	38.3481	41.6063
538.479	494.518	466.822	519.028	504.093	500.507	531.837	606.461	504.967
40.7539	53.1759	46.3226	48.001	51.9384	52.272	53.5046	54.0435	49.2838
240.566	256.552	253.067	275.207	287.003	224.11	269.683	301.542	245.768
141.558	159.912	159.587	169.823	122.549	165.537	142.396	128.138	136.223
182.386	152.377	166.026	138.281	154.141	138.392	146.557	177.273	148.735
199.368	256.54	212.458	224.769	232.767	240.848	235.216	228.211	206.534
106.424	110.409	185.446	108.454	178.296	107.592	128.374	125.84	133.443
61.9687	88.3476	83.0808	91.3068	81.7934	81.7386	72.3185	79.7623	92.8794

617.796	700.117	743.278	732.218	709.846	510.474	655.985	784.172	718.794
70.9846	92.5513	77.1939	88.0087	77.1062	85.4767	78.1473	86.0146	73.4145
101.658	99.6763	83.8565	82.4977	87.7088	99.8892	99.9772	105.117	77.3674
22.9633	23.3462	23.7869	18.3158	18.4158	21.2851	22.4473	22.4924	26.2013
540.311	694.251	514.857	605.796	570.602	615.668	567.203	743.61	593.804
499.796	394.713	563.662	512.176	449.92	422.686	442.833	403.6	546.164
99.149	147.056	130.151	127.546	114.799	130.961	149.695	121.302	130.949
145.532	122.48	116.172	138.021	127.28	109.808	123.825	126.213	127.263
624.203	593.757	530.933	532.139	527.35	522.429	585.901	636.137	536.526
92.5913	91.6642	103.087	100.505	111.621	102.398	111.983	116.478	115.115
210.679	156.664	193.626	275.581	243.507	190.05	245.507	250.575	257.955
131.402	102.589	104.417	91.4225	100.461	77.0447	105.354	101.601	96.542
322.266	132.044	168.886	169.076	203.497	114.108	225.516	129.034	242.214
62.4544	67.7864	63.5648	55.1377	56.4825	49.6388	48.8406	60.3864	57.1922
187.603	176.141	199.353	180.454	226.686	163.855	219.026	210.273	213.842
226.804	244.592	227.215	237.841	226.492	251.056	238.08	268.343	229.924
25.7028	42.3594	40.3297	40.4873	33.2472	35.3306	34.823	30.9286	34.2697
281.131	319.273	259.021	292.182	282.447	330.204	280.119	278.289	333.05
130.803	128.804	123.249	136.757	105.76	135.944	111.108	105.96	113.53
549.34	594.737	556.343	513.416	612.003	553.343	478.678	673.684	648.514
365.265	391.976	435.744	355.922	382.374	353.394	325.407	356.594	398.473
315.246	438.962	315.228	434.057	335.255	380.07	376.05	459.654	357.733
86.4401	119.585	108.662	116.719	105.305	126.846	124.617	116.287	117.998
6.12385	10.7458	20.1709	9.8016	26.4173	10.2181	12.3252	16.2687	16.2529
313.976	375.887	320.141	338.777	301.596	309.134	336.825	377.742	307.515
577.702	647.033	625.194	650.624	418.695	577.799	468.495	544.557	533.334
256.531	311.076	304.969	287.105	355.634	267.532	299.928	340.633	271.228
279.706	280.717	276.174	289.214	300.888	326.758	307.899	269.254	312.314
49.8766	68.1683	66.5968	70.0252	59.2778	75.8491	68.9759	61.6786	67.2913
245.39	280.035	473.801	325.107	411.51	288.705	281.403	314.443	332.73
119.724	123.154	135.948	153.939	120.422	135.353	134.052	117.725	136.165
181.12	217.807	203.419	229.763	200.859	235.241	211.324	188.955	206.094
167.781	247.806	208.781	210.113	171.857	194.507	182.619	232.262	179.853
381.379	415.639	381.723	413.065	386.624	411.388	402.161	398.74	406.769
71.4261	104.777	89.119	87.6623	91.2252	92.1898	78.3799	81.9269	72.134
281.398	229.243	233.9	242.476	313.848	232.859	288.432	289.093	308.998
177.079	178.231	210.311	162.947	203.264	159.257	221.603	220.405	199.299
1036.69	1597.4	1712.64	1571.06	1632.74	1576.17	1273.36	1178.66	1240.2
156.085	214.249	173.167	135.003	125.363	134.621	142.846	186.153	124.101
129.978	107.948	118.087	114.7	90.6026	111.31	107.981	108.762	107.751
107.153	93.2466	102.504	96.5287	93.0983	107.767	89.7999	97.7305	82.441
112.177	108.942	129.799	100.215	126.215	115.123	124.848	133.906	128.583
201.317	282.496	260.818	263.829	250.42	267.119	247.249	256.515	233.854
37.3809	50.5268	40.8317	48.5667	41.5298	47.5889	45.5153	41.3629	44.4946
210.717	138.264	130.807	154.801	147.523	134.153	155.656	162.039	175.524
114.734	195.111	194.261	184.279	163.18	186.154	165.544	157.886	142.362
738.572	577.417	845.675	765.42	721.444	721.141	600.679	564.811	804.673
62.8785	75.8762	79.6819	62.1813	71.5652	59.4855	71.0602	58.8756	62.7502
456.391	345.746	373.893	443.678	566.583	376.564	500.868	589.712	604.624
25.5254	37.9429	39.3998	24.935	42.7026	35.5637	34.6324	42.4598	27.8162
137.705	238.786	198.448	197.023	152.229	239.929	210.38	192.741	189.618
181.769	172.37	156.886	155.32	165.59	180.76	165.62	158.869	171.72

425.905	547.764	573.396	457.869	561.212	468.189	438.326	569.578	521.175
710.509	561.147	712.195	694.219	735.856	687.603	667.35	530.255	866.362
684.288	594.595	613.587	627.211	631.199	600.267	624.001	727.167	691.747
87.3929	75.5543	93.3693	84.0861	90.0635	66.0667	76.5721	83.9326	89.5382
599.358	610.017	844.567	650.307	503.606	592.789	597.892	553.03	695.862
33.3863	46.2974	32.1265	29.2692	36.7057	31.1297	33.5212	39.4965	26.8598
178.72	188.91	188.269	181.909	162.023	207.364	180.345	184.443	184.439
149.291	158.883	162.167	143.491	152.128	137.817	145.174	144.395	154.515
114.492	76.5566	66.0801	61.1804	62.556	74.0362	76.5989	85.6872	73.9307
2630.28	2263.33	2395.78	2739.18	2548.15	2198.42	2802.16	3163.37	2751.19
252.991	267.446	243.136	240.008	254.855	237.171	247.893	264.573	257.432
73.2344	83.4368	97.1781	98.892	92.0058	77.537	104.98	88.1077	92.5797
56.6507	43.8754	50.5348	50.7419	52.0159	46.9338	56.2604	56.9154	44.8436
108.02	129.645	110.267	107.621	118.583	118.865	132.41	116.742	115.86
572.471	561.119	643.956	633.565	618.131	591.733	605.678	611.8	619.081
105.477	111.65	103.128	145.103	97.0159	104.446	122.409	122.098	117.103
147.547	169.246	152.736	141.477	165.234	174.588	155.388	194.378	168.436
114.704	163.652	132.492	142.22	122.533	141.548	122.032	114.513	123.852
210.345	223.239	204.002	222.873	189.278	206.649	177.856	161.37	189.724
729.124	809.158	597.961	525.779	516.067	477.933	645.192	863.98	627.514
865.612	703.323	659.311	667.951	670.309	605.833	872.325	907.695	885.554
129.156	197.577	148.646	170.937	154.103	168.353	189.535	150.267	175.917
143.658	128.528	112.214	131.251	125.328	148.189	122.136	113.056	119.87
589.166	653.999	517.807	585.575	540.641	541.991	562.55	699.224	604.636
768.838	805.273	809.418	796.224	1050.36	883.082	823.185	988.066	907.415
78.2559	103.942	86.7199	90.9096	83.8903	98.3841	90.2825	83.7049	91.6594
37.5945	36.624	30.7624	27.9068	31.7696	39.8874	28.5538	29.4229	23.8863
260.635	288.025	236.055	389.204	305.998	343.401	319.422	315.663	295.546
124.036	160.044	149.676	155.011	147.539	136.332	136.498	179.668	138.615
440.012	538.102	373.373	428.709	458.354	440.161	446.958	498.497	452.417
120.959	138.024	126.596	124.274	140.148	109.059	113.503	108.187	113.393
274.894	300.838	321.319	274.781	256.806	342.417	279.666	272.765	272.536
16.0329	14.1219	20.4716	13.8973	18.2184	11.1676	11.4929	16.8792	8.49573
133.603	181.034	160.802	179.354	153.871	181.801	143.878	142.781	156.134
68.705	58.8225	52.2042	54.7767	47.1623	59.373	54.8504	53.8696	53.8614
312.814	440.134	348.615	329.098	333.691	352.122	347.614	401.884	319.538
186.458	224.128	186.664	214.074	173.908	242.401	205.654	185.627	213.169
265.261	387.958	354.63	326.094	367.383	360.166	324.094	295.645	347.177
480.21	641.619	537.853	552.365	575.127	499.18	507.461	503.623	571.523
57.3748	67.0686	50.3147	40.1123	49.8305	55.8388	64.8767	65.0853	45.5109
126.091	180.802	168.006	169.429	147.786	188.604	158.684	131.627	148.53
83.5439	85.4136	77.8973	82.2436	80.6897	74.74	80.9241	76.3526	74.4863
238.558	257.735	273.902	260.084	247.641	203.368	282.949	325.61	250.393
632.208	725.998	534.851	619.908	640.308	596.693	583.761	727.151	700.534
51.169	40.96	47.3435	40.668	39.7209	41.9776	43.4768	54.1618	42.8807
155.307	132.824	127.235	128.566	127.485	137.99	117.141	130.705	165.119
412.931	429.337	800.523	566.625	456.338	595.641	375.261	397.403	545.733
293.216	344.876	351.938	390.547	426.772	363.189	333.401	322.94	312.548
94.1331	140.583	123.314	123.394	112.428	133.043	117.351	109.876	120.971
173.927	207.407	221.577	193.481	191.396	208.663	212.051	183.279	201.157
57.5929	65.5695	46.4123	41.7463	48.6515	49.3882	37.5392	49.2418	39.4611
24.1233	17.6022	22.0947	17.8354	17.5045	28.388	14.7118	13.6486	20.7057

82.2669	102.751	110.206	95.1826	97.9419	83.1324	94.9038	120.054	91.5908
260.045	262.817	253.626	242.137	304.522	229.784	285.798	304.882	294.169
86.1601	84.1415	89.8633	76.8085	87.4252	79.8605	84.963	114.204	83.0755
149.956	158.17	140.37	127.595	137.177	119.442	134.741	158.915	142.732
123.489	122.512	142.397	116.269	125.353	117.778	107.506	107.702	116.536
178.364	237.37	213.964	224.738	194.135	241.508	226.926	194.282	221.979
170.477	162.062	158.646	163.187	145.097	168.609	157.771	160.955	161.214
259.969	299.804	269.451	241.187	202.019	250.206	205.789	245.402	208.47
903.026	1143.31	844.212	859.657	1151.02	1158.53	1026.54	1032.45	974.099
44.5244	73.0265	52.9887	66.5758	52.7634	57.4945	57.4293	51.1447	67.9637
96.9116	78.3704	91.6175	76.0748	75.7103	82.4004	80.7645	93.5215	81.794
197.015	179.264	216.713	183.505	173.502	192.102	148.965	169.631	170.718
119.407	137.881	131.665	141.585	128.821	144.148	154.357	137.75	146.443
236.941	309.281	248.875	272.567	229.698	314.341	267.292	249.65	252.132
136.919	155.631	138.354	142.89	143.298	149.366	141.612	155.172	140.479
119.684	138.885	149.581	161.265	180.303	118.453	138.307	161.019	154.436
395.201	444.562	371.904	371.598	393.539	351.087	384.587	447.921	413.158
247.155	318.716	269.127	270.499	259.329	303.164	267.596	280.871	238.318
102.43	112.487	111.327	112.956	119.325	120.963	113.419	111.724	114.668
43.7164	60.9434	69.7823	59.3253	60.0495	67.4422	55.2076	53.4514	56.0696
72.6167	61.4005	60.8772	72.0783	64.1394	58.7113	63.0972	54.4003	58.9135
117.621	59.1063	95.7479	89.5866	73.5873	87.0301	128.562	136.608	92.6979
3116.03	2811.18	2713.85	2404.04	3029.11	2855.53	2900.95	2853.06	3518.74
527.319	550.037	427.095	523.638	520.274	502.78	545.32	554.594	533.379
140.022	161.427	127.753	180.08	170.336	143.621	144.477	152.602	133.507
183.935	189.969	242.266	170.145	134.574	200.147	147.942	140.819	164.352
527.504	396.684	612.54	594.518	688.26	381.787	558.947	622.757	806.4
107.43	99.2774	81.0869	72.9461	79.9423	71.3255	73.4204	102.271	66.2499
221.079	272.185	243.858	243.833	240.573	265.525	276.232	256.586	233.996
275.809	380.355	359.945	329.94	343.459	281.894	325.395	345.242	300.582
427.66	606.909	551.072	637.649	559.536	634.035	685.654	568.444	624.289
239.741	269.154	310.073	265.763	307.448	309.139	301.107	342.757	293.838
543.246	482.843	458.511	584.088	577.328	502.234	685.866	880.714	570.171
642.619	694.969	544.716	544.818	516.062	648.999	691.859	725.738	607.852
127.943	105.013	104.224	92.508	104.348	91.0604	119.867	103.929	108.871
88.1303	84.1722	83.0499	83.9773	101.292	82.4219	91.7852	117.128	115.641
112.958	136.72	138.336	136.688	133.636	106.943	137.039	135.061	123.073
264.932	237.719	214.56	213.952	233.784	190.988	239.759	273.402	237.922
1682.89	1452.84	1464.4	1296.27	1971.95	1517.9	1454.96	1837.29	1657.78
172.952	127.294	169.911	158.206	152.481	165.819	136.272	154.809	168.466
676.807	592.127	561.111	649.786	599.156	582.016	625.041	562.32	732.869
1385.37	1434.49	1506.64	1525.27	1279.71	1296.36	1316.68	1361.14	1483.26
252.721	292.907	259.069	255.954	243.109	282.351	246.254	252.289	239.1
89.2263	95.0468	75.2876	85.078	98.6399	84.8697	85.1302	99.3868	77.0891
75.3625	104.905	105.347	104.102	90.1452	105.043	88.0912	82.1116	84.563
293.253	278.756	324.881	273.417	358.112	262.566	299.523	364.999	312.241
60.1464	61.3724	75.2747	54.6578	68.6796	63.9812	72.8686	82.5682	95.9037
170.308	190.471	205.719	186.792	259.494	186.968	165.501	171.436	212.635
459.351	507.039	670.951	518.419	597.117	614.619	428.644	423.68	577.099
180.671	188.017	165.187	185.206	177.51	197.254	175.631	189.885	182.97
293.13	272.783	313.938	213.322	225.414	249.466	207.059	268.576	298.198
59.8739	72.1941	68.225	72.9065	66.4224	67.2182	57.3855	62.1691	66.6643

545.526	523.298	493.432	545.787	456.071	535.031	472.193	507.155	581.173
3229.17	2119.91	1916.5	2980.29	3608.07	2205.51	3558.24	3112.02	4368.6
9523.79	8633.5	8176.58	9118.06	8937.54	8977.42	8754.95	9190.58	9272.95
186.284	228.112	209.971	230.346	176.33	222.262	190.31	194.143	170.311
35.2353	29.5788	34.9343	20.5904	27.9091	36.5355	30.2205	35.2424	27.4368
58.671	70.4272	62.4635	58.9643	61.9135	75.2472	56.1696	54.3516	58.6155
920.178	1033.66	995.282	1039.31	1070.15	1109.68	985.581	1001.17	1043.09
219.674	236.843	204.015	211.648	218.872	229.7	218.255	260.002	206.549
44.4261	37.2882	33.6002	37.0685	35.9083	38.3628	41.8792	31.2044	36.3796
224.346	296.218	250.858	267.306	260.768	278.331	261.695	261.498	291.342
229.009	238.103	247.559	253.786	220.209	278.366	258.096	216.944	240.587
197.677	238.702	213.267	217.847	197.925	194.047	227.008	237.781	198.035
316.935	318.966	419.377	294.21	435.093	323.97	274.024	364.831	383.302
46.0902	65.2851	40.4609	49.3106	51.7815	50.3279	48.3657	60.9323	53.4216
145.894	207.267	202.696	191.438	166.219	179.348	185.129	172.433	160.807
116.672	150.72	136.084	141.81	118.056	136.186	120.04	118.846	112.438
44.5896	41.0997	36.347	36.7077	30.7697	47.422	43.9125	41.6921	40.9293
74.8214	51.4957	67.4067	80.4406	73.668	62.4567	56.8253	61.945	63.9683
201.847	247.568	309.559	255.119	326.803	214.852	214.688	247.208	245.625
149.267	120.851	195.119	139.463	123.877	136.657	135.633	111.528	162.931
293.158	242.416	212.568	204.128	227.576	197.612	211.661	245.132	234.109
36.0341	38.8747	39.114	42.1045	34.3666	37.8674	42.2564	37.1636	42.0242
314.274	281.391	334.491	318.823	363.765	279.233	341.615	410.634	325.496
456.996	535.823	736.503	545.536	740.622	591.392	475.973	471.218	543.525
903.521	978.438	673.547	760.598	789.118	872.376	913.021	1116.49	919.127
51.2721	74.2707	58.4997	63.231	54.549	65.3503	58.9271	56.4111	51.4317
106.591	150.373	116.565	118.778	118.625	139.358	132.244	132.272	131.005
178.696	196.762	230.003	218.243	225.081	187.47	178.659	184.508	186.466
19.8785	24.5812	23.9864	28.6497	32.3957	30.4325	23.2819	31.3097	33.2873
41.554	41.5269	39.1247	38.5517	36.5377	37.327	40.043	33.6567	37.6094
387.273	491.974	438.651	412.059	441.687	409.294	391.574	456.645	380.869
120.546	114.899	117.946	99.4562	95.8986	98.3902	89.2819	99.3389	107.361
998.312	1032.23	752.488	837.023	1198.54	1041.71	1005.03	942.058	1119.62
112.336	134.033	131.538	136.324	120.652	138.426	126.27	103.252	120.476
152.089	158.517	178.213	181.701	144.499	155.883	174.157	168.065	155.204
425.914	485.094	446.009	411.691	436.862	425.162	471.903	490.781	438.872
146.093	176.313	165.494	157.901	154.542	170.293	170.73	158.069	156.201
347.575	385.235	475.509	415.124	408.949	447.198	358.574	309.276	372.761
30.2656	41.4365	45.0418	44.3695	35.9847	43.7454	37.0896	35.0885	35.725
284.108	370.68	339.697	349.819	338.786	335.289	369.889	378.47	340.343
80.6578	96.1008	85.9863	103.312	83.211	87.928	88.6817	76.501	86.0903
186.132	200.64	213.567	162.002	259.51	185.83	176.239	183.473	196.294
213.07	227.61	228.518	250.174	218.327	243.446	234.063	214.444	221.34
721.775	749.029	687.763	636.544	799.511	609.17	776.845	916.26	695.584
142.471	185.749	163.654	178.411	164.441	184.516	174.041	161.612	168.519
863.473	748.13	549.167	703.971	766.1	683.489	962.162	1041.98	890.595
368.058	350.928	378.816	379.99	363.48	354.17	262.619	286.446	362.768
58.3212	62.5027	55.0752	49.6344	59.3769	61.8223	58.61	56.8959	60.4395
290.897	377.948	305.821	328.429	296.959	390.042	296.723	287.483	313.917
118.731	86.0071	86.5245	106.716	111.733	88.2926	134.315	123.889	148.123
199.966	222.909	290.986	221.596	227.839	214.123	245.738	239.539	200.774
983.231	720.654	859.591	890.838	959.575	778.797	723.694	684.635	1038.76

81.1154	57.5062	63.0338	57.8799	58.3016	63.8808	53.0033	62.1716	75.1163
361.28	392.409	385.282	385.497	430.831	338.624	365.186	417.277	400.636
387.197	391.382	685.686	528.255	433.917	450.066	380.526	334.637	361.379
720.149	778.627	635.152	709.377	793.783	762.708	709.393	1000.97	625.69
80.2678	179.559	188.86	184.72	214.583	99.7624	97.3841	201.705	104.859
51.811	71.985	79.6208	74.4667	60.5565	73.4998	71.22	60.797	66.1036
393.329	445.248	415.547	372.54	395.57	445.752	353.985	396.367	384.621
80.7472	97.4554	111.448	106.805	91.0058	98.6156	100.127	84.5184	103.851
306.338	335.941	341.431	354.471	288.067	356.756	336.243	286.553	324.487
161.088	201.149	179.743	180.999	210.42	184.492	154.104	219.23	172.713
147.36	145.526	141.359	169.402	169.917	149.446	145.829	170.774	151.497
245.503	287.575	245.001	245.443	245.345	281.638	242.133	276.465	257.53
74.0986	130.312	99.8527	98.0477	110.209	102.803	114.487	104.739	77.7412
625.609	582.152	781.02	728.781	680.614	600.952	527.675	548.877	622.291
54.9196	41.4561	55.3932	53.7544	46.8357	34.1955	49.8658	45.2143	64.0195
122.065	149.672	119.268	142.659	122.798	151.483	150.764	117.49	132.427
263.248	304.608	264.406	254.09	255.754	269.726	269.912	282.42	274.569
60.0243	46.5986	75.2681	58.5746	66.5169	62.656	57.2865	61.4357	53.45
63.018	68.7389	79.9596	72.091	76.847	66.2313	62.0644	79.8042	62.2276
52.8493	67.0394	59.555	70.5628	57.2672	70.0109	51.2828	76.0419	64.8047
156.443	203.505	229.408	217.334	205.598	203.431	219.613	258.266	185.109
109.454	113.935	99.5127	102.852	98.3812	111.088	83.0897	118.521	93.624
184.912	239.299	236.005	233.984	213.583	240.705	237.412	191.617	226.563
112.741	120.614	126.565	116.434	112.824	118.785	111.945	107.641	104.378
1083.14	1060.72	1377.74	1176.01	1266.98	1117.07	1045.96	1151.53	1289.08
548.6	278.14	626.145	608.044	480.467	700.795	483.651	556.039	556.087
921.254	781.969	842.908	812.301	965.781	724.05	970.813	1197.7	1022.46
513.98	526.79	494.774	535.852	548.099	509.574	484.327	540.509	561.495
429.366	456.604	383.663	451.5	444.078	441.056	440.552	441.822	448.647
138.318	159.844	133.3	127.3	113.017	145.699	149.228	102.674	137.995
63.0669	47.3235	63.0356	57.7779	70.8058	44.0237	61.6141	57.1541	58.313
89.1802	116.866	120.366	111.713	109.315	119.453	94.3197	104.703	83.3672
174.346	119.617	114.859	144.428	158.117	145.725	156.668	143.774	173.102
254.141	276.543	349.879	271.851	253.875	265.456	243.215	264.499	289.264
167.311	184.256	209.083	170.208	146.34	163.289	152.315	140.91	148.802
1309.41	1404.8	1225.75	1445.46	1286.24	1330.63	1368.22	1406.99	1480.97
419.283	450.201	617.005	439.559	429.855	443.498	369.314	406.386	407.631
373.479	468.696	402.772	390.792	372.595	419.164	414.23	465.127	360.543
90.119	83.0098	77.2425	86.4087	99.1069	86.217	85.2899	104.865	97.9869
80.0988	138.562	116.601	115.471	88.1594	106.833	91.1537	79.4084	91.977
343.603	352.345	342.722	348.321	337.686	321.024	363.523	427.751	319.684
329.493	359.693	339.959	348.649	347.723	346.042	379.81	366.307	371.548
108.497	123.438	138.846	116.083	138.228	113.812	117.036	130.023	130.07
352.088	334.87	432.943	454.467	415.224	333.859	295.81	350.541	392.511
122.91	147.18	122.224	132.175	113.48	149.773	121.526	119.935	111.411
245.91	222.362	169.085	209.534	213.917	223.401	294.342	293.383	278.723
216.644	265.485	256.442	214.036	233.573	209.141	252.69	272.865	246.999
190.738	182.699	211.08	201.186	201.007	195.746	172.496	200.419	226.424
150.573	180.149	157.171	165.15	198.636	192.749	171.853	176.536	176.887
76.8493	66.7891	74.9627	56.9967	57.2967	51.4918	55.5286	66.5613	66.1248
114.379	131.266	139.239	105.322	100.987	105.599	101.943	101.044	101.598
620.038	454.197	522.713	377.587	549.469	557.901	489.727	407.677	563.73

372.324	431.434	454.752	501.054	492.468	407.165	423.649	430.172	448.624
120.056	144.039	163.059	150.356	139.889	132.023	139.856	147.733	117.396
66.9029	99.6053	90.8531	97.3484	81.1149	91.9211	82.8855	89.8473	77.2373
171.852	210.231	143.672	300.973	225.424	274.159	278.028	229.735	222.452
81.3363	98.4352	94.6797	74.4543	94.6339	87.2871	78.9966	98.4898	83.4205
1260.48	924.409	919.904	873.564	1397	1251.81	1146.24	1352.04	1307.04
136.457	350.188	224.228	273.512	141.139	246.373	176.04	215.401	127.852
317.626	391.38	319.877	312.138	316.642	335.095	355.35	431.926	336.391
1081.9	1068.35	1825.14	1302.4	2451.34	1334.72	1423.36	1321.63	1536.32
162.681	141.802	152.07	195.446	156.91	164.768	146.759	162.526	177.347
151.137	203.801	184.034	186.173	164.788	185.138	172.897	170.178	170.864
34.9847	35.7722	35.7869	37.2259	36.9041	35.6633	44.4046	27.8248	44.1238
142.985	195.25	226.407	154.758	144.246	159.686	151.779	176.187	155.258
141.582	184.899	164.601	155.082	149.811	147.17	158.353	175.799	144.185
93.5069	94.8908	94.2829	108.513	83.2404	97.2249	92.2297	93.7288	89.1554
665.105	781.785	651.183	738.191	851.768	754.906	720.445	771.22	775.642
223.147	195.403	230.376	259.45	262.384	229.039	231.667	213.958	220.198
213.753	220.361	240.244	178.173	263.807	211.27	207.419	233.49	259.211
179.94	265.673	253.551	239.25	226.767	268.419	204.685	181.829	234.5
315.392	308.367	286.336	298.073	313.523	269.277	332.471	356.62	332.452
164.106	141.097	158.24	138.704	155.962	145.401	146.16	157.584	177.625
310.482	382.498	276.63	342.574	343.588	339.407	341.252	354.234	353.708
28.0266	22.6403	27.7779	22.2725	24.131	20.823	26.4503	26.2506	24.2826
262.692	204.606	360.725	253.358	266.437	242.91	236.169	230.979	238.07
59.6538	74.1544	80.8673	75.8199	59.5994	74.797	68.9929	65.5472	70.568
106.099	98.3252	87.2062	93.2543	101.993	90.1065	72.7098	100.859	97.881
67.0691	72.6224	96.4753	93.6853	84.9666	65.9684	80.2355	68.2102	78.8634
72.009	83.8248	93.4176	81.9914	117.071	81.2829	94.7201	112.455	86.2221
184.983	175.154	210.558	191.017	224.479	183.69	147.089	149.441	202.818
267.867	299.479	279.191	315.694	250.232	272.816	237.371	244.749	297.279
128.085	135.037	113.641	130.421	133.063	135.031	133.083	127.076	123.405
241.961	303.965	245.054	323.379	288.94	289.85	289.896	319.443	255.81
136.771	159.16	130.597	145.106	171.59	153.52	165.777	180.578	159.966
463.321	533.37	495.163	543.376	528.805	531.814	534.817	551.106	486.942
616.092	764.505	838.736	699.987	701.773	742.819	630.03	556.787	640.215
132.572	146.939	146.411	158.471	183.055	150.16	167.496	180.353	186.726
607.243	695.82	567.605	569.975	631.746	614.407	676.548	717.601	632.58
199.461	213.865	223.502	203.807	222.761	230.656	216.988	232.641	283.037
443.809	324.831	319.788	310.08	314.115	315.575	307.648	307.305	314.105
103.839	107.901	121.738	110.434	104.744	99.0926	113.361	108.657	103.713
150.306	172.903	152.126	159.118	119.255	159.13	139.827	132.425	158.66
126.439	181.311	163.164	153.514	131.728	160.769	141.16	145.23	144.657
152.136	167.401	169.509	174.195	153.584	167.754	161.289	154.424	159.414
133.453	158.825	157.634	149.185	148.085	151.289	131.695	128.32	150.839
189.551	212.611	191.22	203.056	195.202	195.396	201.826	212.865	208.464
383.097	470.644	497.911	429.403	452.745	476.619	370.278	405.656	364.075
100.521	63.1394	100.453	97.1316	81.5142	83.4737	77.6164	82.0503	99.3498
571.845	409.986	423.274	502.118	589.622	384.007	655.959	726.443	676.149
134.749	164.589	186.203	174.306	198.553	154.305	175.701	186.464	149.324
30.5503	30.1638	33.0436	25.0536	28.5197	23.2964	30.2522	35.8576	21.7028
59.7644	71.3646	87.1053	56.3222	48.7322	50.0071	50.7507	52.4577	54.7079
535.58	474.195	475.045	522.137	540.761	416.847	603.828	659.018	563.253

242.659	241.994	251.191	237.582	217.63	217.737	222.886	271.436	230.992
188.225	297.295	257.487	245.976	250.903	222.908	238.534	284.142	203.374
146.353	197.007	156.367	160.925	152.957	156.035	152.153	188.309	155.718
2601.61	2828.05	2091.35	2179.01	2351.29	2336.47	2592.23	3175.25	2514.55
1029.72	1220.18	2066.96	1406.22	1539.23	1286.22	1237.45	1214.59	1608.41
220.339	235.863	224.307	191.763	238.863	189.091	242.145	275.159	227.385
1575.24	2227.86	1409.8	1418.89	1400.48	1695.58	1808.61	1455.38	1980.65
173.732	161.29	161.095	154.519	142.687	172.541	132.812	143.042	146.131
132.364	140.111	139.203	118.819	105.824	94.8899	90.4928	132.576	161.802
142.267	107.34	156.008	134.75	127.752	121.225	139.737	148.167	165.52
94.5704	164.439	165.687	149.716	115.174	142.552	137.543	130.768	141.604
652.54	416.047	532.9	507.859	411.812	445.233	559.232	517.319	599.769
84.1542	77.6472	58.7623	59.0954	57.1564	54.1376	72.0144	71.1789	65.6921
256.963	268.56	243.087	278.485	271.896	273.906	262.566	312.969	273.609
199.882	299.706	284.831	283.018	250.073	255.141	296.606	267.975	276.298
32.2824	22.0268	46.2664	29.7197	43.5839	42.4034	41.4424	23.6129	23.1008
155.749	140.024	137.938	132.504	134.968	117.298	132.348	155.684	122.8
340.721	377.557	312.337	305.524	314.372	330.134	299.945	353.763	360.986
562.315	772.305	576.851	616.485	611.605	623.049	603.955	836.549	538.258
216.355	263.084	279.147	241.763	262.521	207.258	234.066	307.034	230.73
446.639	552.451	499.494	514.065	505.42	446.835	501.948	454.085	544.885
97.9662	133.735	92.3461	127.138	121.22	101.003	99.2347	157.462	87.7356
154.714	159.73	148.451	162.787	146.603	168.793	160.924	154.937	152.168
291.003	281.211	293.341	304.242	317.414	309.571	296.587	287.465	322.643
2373.91	1841.27	1383.22	1531.5	5381.57	1732.04	1996.52	2442.44	3746.42
101.245	105.834	109.359	116.376	123.544	93.4873	105.319	118.892	105.895
87.7317	89.5773	88.6486	92.6447	92.5327	87.6354	100.621	89.8055	91.936
11.3656	21.8271	35.4076	16.6418	13.0724	12.0537	14.6929	20.7089	13.3219
201.51	210.942	267.775	163.104	172.093	181.359	198.265	182.261	213.516
143.826	182.112	148.217	184.034	137.596	186.333	142.52	137.595	145.652
115.462	140.434	142.329	132.454	123.331	127.588	133.086	123.668	115.042
104.897	106.628	138.866	118.356	158.04	101.69	112.91	149.532	111.315
464.678	472.336	370.437	477.305	461.52	446.99	493.023	544.443	507.003
302.189	360.262	300.641	187.706	225.836	306.364	295.805	253.653	244.928
1079.32	1231.26	1201.34	1110.38	1170.23	948.525	1242.07	1588.36	1158.12
295.093	294.781	286.97	289.279	308.545	289.505	303.311	366.921	303.608
120.448	159.019	146.098	151.847	127.687	141.365	151.842	143.886	139.858
87.1942	93.111	86.7461	78.8226	74.2981	91.362	60.9346	69.1352	82.9509
372.448	398.699	369.881	380.119	391.284	371.132	409.723	385.733	386.537
96.018	103.681	96.4477	110.116	104.465	117.808	103.561	112.767	106.347
93.5207	150.421	110.322	117.755	105.91	142.329	123.413	122.158	111.088
141.188	183.458	171.098	159.427	136.019	167.603	146.594	140.411	154.016
2143.16	2466.18	2937.56	2251.51	2918.62	2208.23	2286.61	2807.6	2611.2
100.724	103.189	121.096	105.148	128.003	105.833	114.352	111.707	123.978
211.049	254.837	255.104	187.397	240.637	230.585	216.306	259.549	218.94
792.308	688.523	646.764	788.273	755.81	756.14	805.197	845.915	898.925
55.0884	53.6059	41.8157	43.6297	36.2985	46.6707	42.1233	38.9716	41.2654
59.134	80.6399	66.7035	68.4985	60.7019	70.3426	74.1006	64.9289	63.8775
353.317	432.443	492.053	488.715	454.047	326.907	425.262	350.327	448.972
808.816	738.68	943.459	860.91	1090.72	744.647	911.405	872.524	965.757
108.666	144.525	149.443	149.866	127.369	131.057	131.739	130.729	106.95
206.598	253.372	202.147	239.893	225.907	218.271	219.745	252.649	211.1

196.587	220.622	189.118	205.779	205.044	213.766	211.814	208.873	175.234
48.5692	82.8446	74.11	74.989	57.9704	81.895	80.4131	66.584	55.6329
59.9942	65.7468	70.4199	55.7774	69.1821	60.8643	67.449	66.5168	59.2066
133.666	111.904	128.686	109.472	149.733	120.867	130.452	154.743	105.974
277.261	218.508	295.618	272.572	323.141	254.43	258.429	226.115	304.029
158.373	174.402	210.571	161.193	152.698	195.102	144.99	153.023	129.106
30.5366	41.2359	29.4839	31.0487	28.6701	30.9829	20.9237	25.4343	20.501
67.9656	77.5015	80.0823	79.6507	89.6017	69.5816	77.3055	80.1632	69.1474
1408.81	994.717	951.229	1088	1166.98	1068.26	1587.98	1783.08	1309.16
58.6637	85.9597	80.4642	80.4913	73.71	78.4265	86.1496	84.2402	90.1863
96.5902	161.68	163.391	143.006	114.889	131.503	119.237	133.089	130.594
433.776	492.652	405.989	449.548	352.312	393.898	513.679	533.912	441.736
1575.53	1445.82	2032.78	1751.05	3011.83	1744.48	1701.04	1624.61	1997.8
1189.39	1161.63	1970.69	1410.96	2793.69	1418.57	1493.05	1348.47	1641.66
82.8987	140.153	110.081	114.985	90.5794	104.393	111.344	99.6609	103.693
481.58	555.497	500.263	496.093	542.288	466.913	516.57	587.218	463.496
207.397	257.634	227.243	245.002	263.392	213.31	240.885	292.216	251.027
668.087	582.503	1207.12	658.414	1421.19	553.284	743.428	617.529	1015.21
57.8906	59.1747	53.1823	56.0005	58.1375	56.0913	44.3868	64.1754	53.932
62.6519	78.6046	71.5328	70.9426	65.2626	94.8101	65.4963	73.4287	60.4644
495.87	689.326	465.711	518.756	523.39	548.47	497.194	630.478	516.272
103.236	117.919	120.758	102.191	118.956	97.7331	105.6	117.329	118.999
258.545	200.245	418.254	307.547	426.238	254.865	277.691	301.504	386.567
81.4773	126.378	116.329	98.3234	90.6586	100.533	95.0553	108.084	82.651
128.367	112.317	118.288	143.872	165.767	139.123	162.386	165.835	154.206
51.7634	92.834	62.7682	59.7126	62.1896	85.3903	58.5145	71.3699	58.6059
114.936	180.051	161.074	178.922	151.943	168.541	168.847	139.507	142.76
184.698	169.275	167.878	158.453	178.211	155.245	141.011	154.329	155
6965.35	7370.89	7072.65	6489.85	5714.56	7048.76	6294.73	6289.08	6421.48
155.523	151.35	185.412	123.284	143.248	137.279	135.834	152.611	127.245
193.771	172.781	233.66	190.837	378.195	176.384	231.337	232.87	297.46
574.764	750.853	570.511	537.078	584.85	626.374	523.247	536.338	632.788
332.708	320.9	294.174	300.503	312.143	315.172	349.107	348.235	365.369
165.387	181.35	153.885	198.724	197.647	187.784	200.361	168.831	210.027
89.6324	75.9469	68.2917	70.0566	74.0979	69.7492	70.3626	88.5785	74.6805
339.087	318.21	320.733	423.969	196.818	310.976	297.249	285.415	361.976
443.791	492.492	506.149	424.813	521.142	500.819	461.782	427.84	433.619
407.948	367.541	472.591	477.438	446.671	401.25	348.287	354.09	424.801
275.603	318.675	270.099	272.799	289.715	275.207	303.783	357.879	287.46
405.845	466.965	484.293	446.548	493.563	439.429	446.56	469.044	479.584
87.8118	64.3349	84.6408	78.2088	81.9876	67.7688	72.4712	88.0581	96.0833
136.355	117.656	124.821	145.853	120.757	137.188	120.736	111.081	129.812
213.355	245.946	228.914	202.26	265.721	212.455	241.596	287.947	187.18
236.718	251.877	244.727	268.379	223.638	273.878	246.943	255.87	224.325
593.991	943.398	933.865	858.178	810.079	763.61	636.239	675.795	688.043
207.804	237.257	221.631	232.203	236.639	240.159	242.158	235.635	230.613
42.1896	79.3586	72.7341	74.6121	59.0834	68.0365	69.2613	60.9967	66.938
17.93	24.7224	18.0475	18.7973	22.4604	19.5121	17.3945	19.6415	23.8658
958.069	691.963	639.953	650.291	780.431	702.229	986.259	1107.1	881.264
214.526	254.769	281.04	226.008	266.681	233.717	214.485	237.284	228.939
46.5371	42.04	38.3859	38.3308	41.7622	51.452	43.2039	41.4664	33.2375
115.059	197.981	198.408	158.46	144.932	176.406	148.75	168.47	151.941

24.8473	30.1756	46.1777	51.8605	46.9482	26.0908	31.7321	28.2137	24.3891
280.686	306.901	300.952	343.857	326.955	270.49	278.877	367.601	332.745
8.92587	3.87739	7.74491	4.27643	9.01938	4.91139	4.65722	4.24873	7.0641
185.413	141.512	170.568	197.436	179.724	147.185	137.018	146.859	166.065
56.5701	63.9541	49.6281	56.1614	54.7978	45.3156	49.9113	50.1437	47.0063
1218.77	1574.02	1763.89	1177.65	1379.75	1590.16	1144.63	1082.02	1550.55
162.797	192.523	184.231	171.089	181.074	172.397	165.855	170.828	183.014
334.716	311.859	357.472	356.063	364.145	359.887	341.369	330.792	356.545
382.385	449.287	472.381	395.673	466.786	382.085	404.701	479.368	394.547
827.008	950.504	924.838	852.779	967.447	731.27	914.788	932.156	895.672
81.5501	125.522	114.844	115.258	108.278	120.727	117.598	107.621	104.244
222.925	263.499	251.812	250.175	244.065	246.522	261.754	263.742	227.233
126.545	123.977	119.198	115.012	125.447	116.446	135.358	151.294	104.587
174.257	214.124	201.812	207.762	218.609	203.317	211.699	185.344	237.06
123.157	146.267	161.285	138.313	155.082	133.432	141.845	146.684	136.521
426.211	480.892	732.8	527.192	529.019	535.446	440.271	398.704	473.039
253.73	273.833	222.253	271.996	243.891	247.157	173.076	189.798	220.059
22.813	27.3083	20.805	19.1129	14.5182	19.3198	14.6612	21.1567	26.163
273.881	210.475	235.026	196.017	242.295	230.086	298.796	211.945	239.572
288.736	332.368	298.991	335.239	379.213	317.056	329.404	388.065	300.492
99.0622	103.473	132.598	104.55	124.605	103.572	99.7744	118.91	97.4058
31.6548	34.1878	45.5505	42.4743	65.7514	39.8972	37.9025	32.8672	40.2433
477.023	402.569	400.475	409.761	427.658	370.352	447.938	490.777	506.714
114.135	102.614	139.016	100.593	112.492	114.715	109.696	125.094	96.916
240.754	282.102	241.41	232.391	231.187	271.864	231.552	254.818	250.669
193.839	232.225	178.317	186.501	237.204	207.328	207.943	231.661	209.006
337.491	367.245	357.648	430.554	418.834	208.872	492.407	313.57	428.324
383.038	351.523	341.365	348.486	389.078	316.931	401.611	445.993	388.154
239.703	258.682	185.138	196.341	199.969	181.831	215.628	237.04	223.046
130.644	162.821	151.493	166.927	146.465	172.71	164.738	154.444	143.1
77.692	158.61	150.219	129.439	102.522	126.607	111.107	115.271	105.387
142.357	178.588	156.113	192.352	178.853	189.748	171.847	151.61	167.423
978.626	811.209	934.799	747.211	758.369	880.456	852.39	970.516	790.056
200.267	144.06	151.367	150.376	178.595	149.47	195.722	221.966	223.176
52.9605	37.4509	44.8995	50.8579	43.1492	37.2798	45.6931	44.7723	58.7475
1182.46	1046.85	995.646	914.42	1170.46	967.988	1171.46	1425.12	1149.55
315.331	465.084	360.832	326.738	351.005	319.522	297.97	346.92	363.027
8699.52	8223.26	8802.42	8783.38	6023.52	8309.31	8497.91	8542.5	7954.15
71.0989	87.079	79.0564	86.3065	57.5247	88.401	62.69	61.6009	76.5378
64.0653	93.0639	57.284	78.0526	66.5268	85.7747	60.8746	82.6442	65.7613
144.2	198.556	156.948	177.407	167.473	190.758	177.31	154.758	152.298
15.4119	28.0109	30.9963	29.3985	25.2443	24.2224	26.7698	18.6375	27.4123
289.281	349.193	281.673	349.352	347.253	320.628	281.652	309.109	327.659
513.799	332.516	301.114	506.286	632.012	454.494	588.497	612.806	669.051
100.082	75.4758	75.6476	83.7073	83.4965	90.666	86.6163	92.6201	78.0919
414.617	379.19	480.401	415.882	520.895	385.656	451.94	427.005	519.966
64.5226	103.097	104.1	78.9484	90.3668	68.5557	82.0876	76.1814	63.6167
182.014	193.166	218.594	190.593	202.328	195.439	193.32	199.207	190.183
35.2056	34.5396	40.1472	30.1158	38.9046	30.4497	34.0215	31.992	30.721
21.8733	21.7757	21.9609	19.2284	22.1163	26.6358	17.0121	33.4321	12.5956
88.2491	75.7351	69.6232	79.3052	86.1052	78.9642	62.844	68.6988	90.4082
108.475	109.419	87.7094	98.1312	84.5975	105.321	84.783	87.7535	92.1308

1041.38	893.956	1040.51	1096.16	1343.91	1066.14	1020.27	1201.9	1206.39
73.1492	77.9205	106.502	79.4287	87.5599	85.5202	64.3587	75.5437	86.2216
500.29	357.879	529.133	488.617	676.784	399.56	565.953	519.613	723.305
39.0611	39.2133	30.6117	25.4719	40.5023	28.7917	27.04	33.4067	33.1825
133.277	166.654	189.738	135.416	107.649	154.333	126.503	136.765	107.703
224.813	245.32	214.306	284.232	264.963	236.417	239.534	281.228	258.71
106.396	95.9528	103.974	103.278	99.8015	114.398	98.2323	93.7477	107.478
142.225	169.396	166.251	159.547	150.667	168.019	160.57	163.98	163.295
336.952	289.825	282.778	315.094	326.193	270.505	284.485	322.316	339.348
202.896	194.091	181.601	166.661	221.173	161.695	205.643	254.867	183.682
665.402	757.118	856.964	732.671	697.238	759.318	653.069	643.999	684.615
98.5109	84.2241	76.5977	73.5815	90.7927	70.6502	89.6383	85.2759	86.8966
116.291	125.003	125.751	83.9999	93.6689	130.706	116.998	115.089	93.7171
248.764	261.567	269.924	274.113	291.692	245.132	242.166	238.051	318.097
82.757	104.281	99.7145	94.4597	82.3652	93.1269	90.3415	98.8138	88.9947
20.5377	28.9763	26.3685	30.7789	21.9346	25.2127	28.5605	22.5461	27.2355
322.312	392.675	373.53	364.548	350.883	393.993	378.041	344.653	369.566
190.815	162.52	205.483	151.531	167.02	146.1	127.254	150.891	177.927
1318.74	1204.09	965.667	1058.87	1060.6	1017.13	1321.19	1759.27	1237.69
131.646	129.05	113.704	121.926	111.526	124.386	123.757	123.73	108.93
268.237	258.987	296.389	284.932	341.624	248.81	310.336	338.595	283.69
180.093	196.028	218.564	173.327	182.181	176.426	167.948	184.479	176.351
46.7301	49.9406	48.2989	51.523	44.3065	36.5678	51.9876	46.5203	34.0315
274.883	364.046	240.178	319.228	304.965	356.634	295.511	305.765	280.362
279.547	276.747	259.299	249.321	274.529	245.153	285.627	295.547	266.304
72.24	70.9579	70.5133	50.2709	53.3402	61.5264	76.0532	73.9581	59.8884
164.079	170.506	140.725	138.327	158.003	139.593	124.128	144.338	152.727
168.023	216.292	163.498	207.461	193.185	188.51	186.661	161.57	162.544
144.433	127.498	239.355	210.588	222.789	162.795	126.093	116.872	177.855
339.087	355.818	363.707	348.528	333.206	381.826	341.531	290.843	337.112
205.796	282.871	213.991	239.687	216.735	268.214	267.039	245.013	225.124
45.9114	59.3834	70.197	53.572	59.3655	59.2283	56.7781	67.4141	39.1132
160.884	195.725	174.429	172.982	169.705	188.416	166.732	174.07	157.388
133.125	164.079	147.217	171.151	136.46	155.958	161.544	156.694	162.877
90.295	79.0934	61.3171	79.8226	94.3044	73.5123	76.5215	94.282	77.4303
127.268	155.764	142.434	150.038	142.774	156.218	143.595	128.687	146.419
274.711	276.258	305.7	312.513	292.454	247.476	304.811	340.954	307.834
351.502	482.71	417.17	486.354	458.902	436.601	464.201	561.84	409.729
31.1941	42.8824	42.1202	41.3898	35.1395	40.4422	34.0056	31.2201	23.7989
489.638	430.397	483.64	518.163	434.763	503.155	437.142	413.485	523.03
60.7589	39.9237	47.5859	56.1557	60.6195	50.9857	40.3263	41.8592	64.7992
84.9683	86.4022	81.2764	67.917	73.5039	80.7369	72.1406	67.2817	63.6552
154.875	182.142	197.351	179.997	180.988	172.863	195.854	206.128	172.143
139.795	203.031	197.073	184.051	168.856	177.797	175.689	173.447	150.533
112.346	90.1791	166.781	93.9014	104.686	111.455	90.9072	87.4762	98.4578
529.538	318.35	207.182	355.222	332.678	270.721	498.992	575.04	662.902
409.581	327.164	492.513	427.954	408.346	348.507	376.27	358.785	401.549
199.878	213.994	193.657	188.328	190.974	214.377	194.702	200.312	186.179
560.407	556.973	452.229	503.585	484.16	518.783	586.199	596.318	615.663
21.1672	35.3429	42.8261	40.3354	37.6974	21.9525	29.035	36.8266	26.2777
6.56829	11.9418	10.9687	12.5755	11.5334	15.3837	13.8561	13.2732	11.7478
488.668	384.643	409.097	410.885	416.574	356.698	445.747	473.827	482.341

97.7996	119.294	120.022	108.289	106.311	114.029	108.435	113.548	116.375
177.205	205.212	190.069	182.245	223.411	177.212	208.254	245.449	181.471
234.401	289.077	264.234	279.177	243.457	208.327	252.641	262.219	245.497
72.9	85.8937	84.6583	81.0809	88.4328	85.5522	99.6504	109.079	80.1684
94.4318	79.6712	74.2285	74.8143	68.3635	85.1545	66.5262	75.6897	79.6095
237.233	253.848	347.83	244.468	301.831	253.063	239.793	257.819	292.248
64.8653	66.5297	57.3623	66.9404	73.2323	62.6479	79.3424	61.6372	66.1857
117.146	176.153	183.426	162.642	182.416	158.943	166.698	166.668	151.493
157.395	177.863	178.641	193.542	174.792	212.073	200.264	173.286	181.579
184.714	241.742	196.626	237.138	189.74	229.819	237.23	210.767	229.142
176.282	141.066	174.313	158.503	162.069	184.235	149.856	132.027	151.172
190.723	198.007	181.105	161.129	181.661	165.203	188.623	200.965	184.444
282.27	308.095	303.734	335.339	304.398	302.038	310.791	357.039	325.933
109.501	139.04	106.61	116.529	106.949	138.029	114.368	94.2233	113.638
47.175	39.9992	39.7367	39.7721	42.6618	28.7021	41.4557	42.2474	47.4068
219.395	193.991	260.766	213.674	281.397	201.02	249.287	274.854	236.448
171.791	221.112	209.257	203.015	211.428	192.978	203.932	227.549	177.813
59.6671	101.459	101.676	89.8067	70.8988	84.1579	77.3953	81.3124	83.8017
78.0032	97.4839	68.9952	75.9363	84.1597	75.6948	52.253	85.3195	70.9165
40.8801	39.5757	37.6462	38.599	39.2934	35.4169	43.1311	40.8106	45.0463
14.1061	20.0728	18.561	17.4455	17.9707	23.4865	21.5579	22.2774	24.3602
636.945	594.572	654.076	558.947	817.784	574.153	670.509	734.5	841.366
83.4367	93.7842	73.075	68.0568	69.5314	80.1554	65.4988	70.3003	67.66
79.9957	89.1835	94.8275	87.5005	85.4298	93.1363	83.1589	86.9986	78.1973
151.477	169.752	151.07	155.641	150.372	131.618	162.384	163.123	175.464
367.8	353.599	382.922	381.718	452.123	358.28	376.829	343.424	427.01
108.685	102.744	133.138	151.678	215	132.238	133.02	118.694	138.916
452.709	369.284	530.144	479.799	765.278	552.221	464.527	563.033	611.742
279.585	257.763	254.329	244.681	302.589	247.586	279.225	346.587	241.668
104.577	77.637	78.0992	79.284	81.7441	75.7796	76.6993	82.7311	97.3424
131.228	169.726	173.17	115.447	116.52	157.262	133.745	104.461	145.002
544.276	563.301	1045.05	549.161	611.029	686.309	459.807	462.571	530.784
209.692	224.793	202.396	178.918	190.342	184.96	162.655	196.308	163.941
226.541	246.494	248.398	248.358	228.725	270.349	253.047	221.328	217.154
240.657	283.18	238.825	251.074	232.431	278.269	272.54	256.635	260.805
195.181	133.945	155.113	162.375	160.586	137.172	158.187	167.762	160.524
587.758	623.131	530.153	564.256	702.07	639.161	624.256	650.314	606.487
70.7439	95.3748	69.5227	71.4051	53.9371	76.8155	57.5848	70.8527	74.8061
81.2416	104.777	98.5739	89.6321	89.857	99.9746	101.424	111.886	99.8713
35.8496	71.931	57.0199	49.6938	44.2224	55.8926	41.7068	60.1742	39.4004
337.619	330.237	325.127	334.521	341.19	304.16	374.382	355.742	350.469
291.571	128.865	171.274	138.164	134.462	494.72	313.2	395.563	266.27
79.9398	93.1278	106.331	100.582	86.6021	83.797	91.3674	92.0725	71.5287
31.2246	43.4654	43.511	45.3053	33.4835	42.7848	37.1829	37.8572	44.3253
86.7959	118.078	102.524	109.396	87.7583	103.802	89.2445	101.936	101.374
215.101	296.276	194.238	231.726	240.03	238.058	239.58	253.113	228.824
69.5793	72.7154	87.3178	74.1689	81.909	85.7196	76.2985	67.6825	77.109
245.836	250.777	240.73	264.831	245.043	264.466	246.382	241.595	244.318
801.461	733.925	1001.26	892.426	1073.77	720.639	901.361	851.286	1003.04
170.759	149.789	142.809	157.285	146.618	134.906	152.66	144.289	162.222
378.603	271.377	460.88	348.283	383.053	268.15	319.195	304.122	346.891
76.4852	39.7598	137.668	72.9209	76.416	72.1098	63.9312	62.4881	76.9639

318.602	262.272	300.689	288.816	260.362	315.514	239.963	231.944	340.405
86.2154	134.68	96.3951	120.767	93.9621	115.217	100.935	102.613	128.532
34.9444	50.7132	44.5972	47.0126	48.2619	60.1461	49.0696	46.8603	51.1622
100.173	127.341	101.721	108.382	106.539	124.277	123.053	103.388	106.375
9604.96	9212.9	9945.84	9297.97	9892.16	9496.28	8261.94	9099.3	9527.04
212.526	220.365	217.742	225.397	259.957	219.748	239.213	223.337	230.997
204.979	256.659	244.592	220.074	232.37	254.058	225.671	230.766	213.359
252.137	283.308	219.521	282.482	235.029	208.515	261.153	241.205	285.963
1693.68	1771.27	2557.98	2109.28	1913.1	1927.49	2083	1683.98	1833.32
288.371	276.731	361.226	313.255	281.286	303.333	237.885	283.119	288.65
367.022	346.768	347.122	353.154	328.996	386.347	343.59	360.93	357.132
73.4535	86.0248	85.0253	81.5438	76.9256	77.9033	66.5615	63.3069	67.8942
67.9557	111.685	112.137	86.2147	84.8185	92.069	86.2897	83.2233	87.0883
410.066	545.357	370.141	450.803	431.221	417.475	433.205	578.587	408.268
123.389	145.35	147.17	152.462	119.644	136.331	139.873	122.69	137.54
154.731	160.495	175.311	137.973	153.089	146.138	130.021	153.607	132.1
62.4151	66.3294	54.3179	57.1688	55.5534	52.9883	59.5466	72.3635	58.686
114.093	157.566	120.57	122.027	123.378	110.145	125.544	167.797	112.297
20.3268	43.8906	46.2184	31.2818	20.8643	26.2978	31.331	30.1438	36.6353
582.668	813.405	613.935	637.624	646.064	742.165	683.009	655.655	706.131
464.273	473.272	437.666	461.901	417.308	409.984	401.982	437.275	448.884
86.4732	85.4404	104.756	97.4832	96.029	98.9273	83.3354	80.8665	80.6041
133.987	153.351	157.689	152.851	139.423	137.722	149.577	149.047	139.576
314.276	319.096	289.442	299.279	323.741	283.254	273.652	363.407	276.022
1019.81	1150	1357.37	1012.27	1000.43	1056.21	1050.08	890.04	1050.24
17.8322	18.0645	18.4977	17.9389	17.3575	20.8391	20.1902	22.2286	22.092
331.019	296.135	276.66	301.423	292.137	279.782	207.15	333.982	296.247
206.081	222.923	218.528	220.902	211.712	248.63	218.924	211.895	198.685
101.135	140.363	141.688	125.252	113.333	135.176	121.651	117.203	124.534
873.569	1169.18	687.925	874.834	843.481	902.722	1034.05	1328.39	917.154
264.921	284.647	250.306	257.626	262.71	268.6	247.261	251.489	290.477
100.895	130.339	129.322	150.415	125.881	113.076	118.508	105.002	128.09
756.375	803.172	972.835	895.493	834.005	666.302	781.891	885.409	866.822
32.8052	40.921	41.8694	34.0604	23.7283	37.6911	33.4169	37.4553	31.0771
589.108	808.834	470.706	601.882	512.905	647.143	721.509	835.023	661.152
181.069	210.402	182.189	225.511	177.148	225.126	199.857	198.264	199.292
112.811	96.6362	94.7373	78.7367	73.2145	86.3431	78.6948	103.336	85.6366
303.839	340.243	306.844	272.996	311.322	282.915	316.615	373.704	322.208
162.813	169.844	177.844	185.086	166.166	210.511	195.909	183.508	164.389
68.8606	53.7361	56.9801	63.2292	60.3446	49.5944	47.9553	54.2293	42.8185
2089.44	2063.04	1976.96	1783.03	1761.81	2124.51	1870.36	1677.13	2042.12
161.175	125.05	144.987	102.052	128.69	110.344	138.108	124.021	143.615
2409.39	1285.83	1601.17	971.93	1790.31	1769.82	1780.07	1955.42	2136.91
40.7576	53.9956	66.0371	46.3533	43.1629	61.9762	47.2519	47.7507	40.474
244.867	224.497	185.824	181.371	180.144	209.311	209.07	220.757	176.625
118.937	147.787	132.531	151.302	135.181	149.332	148.506	142.237	146.462
254.856	285.144	259.022	272.695	310.229	310.968	321.97	338.475	341.976
68.5779	121.895	108.509	103.029	98.6957	115.091	99.4028	81.9166	99.1238
559.661	719.12	548.35	574.702	744.999	594.98	629.822	700.25	645.769
178.918	184.527	182.006	155.166	169.842	162.995	164.01	178.085	175.435
337.659	320.604	314.059	299.304	374.787	289.138	313.602	412.542	359.43
296.893	318.426	335.572	296.077	328.193	268.665	304.521	342.84	316.645

153.196	237.766	176.355	320.501	197.685	261.839	95.2575	169.021	135.701
101.633	90.8209	109.778	85.7499	71.5146	85.7773	77.8338	81.1651	87.1103
87.8115	112.768	100.766	99.1938	91.901	107.601	93.2272	93.7268	101.491
311.395	368.485	347.999	347.068	330.735	395.541	343.744	278.015	325.342
51.3616	76.7495	74.1791	75.2912	59.7915	69.8315	69.7556	61.5531	84.0753
527.73	636.934	535.874	535.945	579.859	575.025	547.357	571.916	545.902
256.111	256.101	268.994	282.846	289.011	266.893	278.045	289.519	263.15
270.861	282.134	305.372	316.91	309.538	269.753	301.518	363.259	274.048
38.7727	48.8708	55.3123	47.8254	41.0523	37.3499	41.8939	38.9993	38.4005
38.0469	36.6983	42.388	39.359	38.192	40.3732	41.9912	39.5143	37.8854
1006.73	1315.34	1237.04	1107.29	1640.4	1146.1	1172.52	1076.18	1285
687.014	605.014	784.39	742.449	763.62	754.463	669.72	574.547	666.904
922.604	1193.3	992.77	990.734	1063.11	1057.21	898.617	1026.13	892.76
519.854	422.988	489.22	556.64	516.154	419.072	427.607	440.085	500.891
135.738	155.902	133.989	131.605	141.35	149.464	122.654	158.586	128.839
64.4539	67.0694	64.0202	53.0777	55.3434	57.3307	64.3296	64.9124	50.2658
36.3014	38.4352	32.7074	32.9949	34.563	27.6591	40.3638	37.0322	33.5096
450.967	431.195	448.761	467.413	474.396	477.809	477.02	473.403	461.955
372.434	400.784	421.387	394.539	254.116	343.941	253.888	336.086	345.004
443.242	273.19	316.105	327.912	388.19	302.621	392.557	406.519	376.656
130.211	122.557	123.98	112.973	105.257	129.599	125.56	129.432	131.697
229.297	276.832	244.738	276.537	247.638	222.287	262.002	328.943	257.749
122.752	85.8694	90.392	96.6506	94.8273	82.9465	76.744	116.23	109.726
81.9743	99.6593	62.8639	71.0438	73.5388	81.646	76.2494	91.2544	75.9901
420.526	347.204	424.746	410.106	432.983	362.531	449.848	359.485	457.001
168.855	157.819	368.686	222.895	466.183	180.061	191.485	160.626	287.867
66.1789	85.0912	59.0708	55.1324	60.1567	61.6547	69.0513	100.029	76.6636
140.429	166.374	183.258	160.522	191.226	142.957	162.553	161.362	166.523
636.488	717.282	634.635	428.893	470.291	675.037	647.485	537.175	459.798
441.208	588.528	355.318	405.902	454.017	462.672	470.76	585.337	465.555
4762.05	5921.03	5856.82	4852.63	5160.12	5739.48	5047.71	5128.83	5061.32
248.195	191.663	203.651	218.458	252.246	217.887	249.3	260.879	259.693
74.7067	110.421	116.883	87.7078	80.5474	86.706	85.9007	106.19	80.1382
152.999	174.752	170.748	175.552	175.145	168.291	172.781	163.956	173.854
286.676	318.38	270.646	241.686	205.908	281.688	271.726	292.473	214.791
47.2025	54.9754	56.1457	52.9641	50.2796	61.3413	51.0587	63.6611	53.3697
45.4602	64.7537	62.1729	68.0286	62.7456	50.7779	59.4718	59.6024	49.2253
350.598	417.43	520.103	301.848	508.237	402.907	358.869	400.457	385.052
53.7024	80.9244	66.3167	77.8767	63.8654	83.2716	76.676	70.8189	62.4655
214.989	229.321	209.018	259.888	223.373	236.582	223.703	210.995	214.519
577.245	417.793	1045.61	724.602	1063.65	435.852	718.78	801.285	1022.88
503.548	475.744	411.402	514.458	447.381	557.216	464.765	425.236	557.571
459.061	510.575	551.203	456.459	374.655	503.324	379.713	468.757	451.453
161.976	178.039	273.923	200.29	282.972	188.181	191.869	205.782	187.719
8170.2	8605.53	8433.47	8300.57	7154.37	8452.77	7420.02	7412.27	8072.02
349.826	339.602	425.631	339.638	356.471	354.281	356.822	364.192	375.243
1161.63	866.603	1469.67	1405.97	1169.78	1236.49	1160.26	1152.75	1198
0.400951	2.6716	5.25986	2.97498	1.74342	4.91043	2.67243	0.367171	9.09789
1869.62	2020.02	1672.76	1770.96	2018.68	1861.37	2000.42	2453.46	1981.74
205.456	255.5	217.522	200.979	335.422	221.372	212.315	266.543	254.901
35.5192	48.6859	48.2093	51.279	51.5943	35.3294	47.2987	67.1267	46.1504
104.219	144.835	119.878	115.812	104.69	109.324	117.737	134.856	100.904

129.713	181.655	175.393	205.154	198.263	150.738	166.856	187.173	135.239
151.394	195.749	178.872	216.48	167.18	213.917	168.027	140.431	160.695
139.016	215.454	108.63	141.585	172.09	202.953	129.933	155.174	147.216
331.258	299.865	312.829	291.439	341.653	300.503	277.007	310.471	306.909
305.229	358.467	318.237	335.976	337.168	353.211	350.147	346.59	320.328
245.517	286.921	404.101	292.336	349.727	268.152	268.886	283.231	304.574
171.012	186.601	186.821	157.999	200.37	157.521	185.059	233.874	202.335
57.8092	60.6498	86.9106	59.4556	82.8554	52.2842	63.2035	71.5509	48.6134
175.679	174.087	184.559	149.665	207.288	163.84	157.271	197.425	201.064
983.805	1145.53	664.779	991.229	1276.4	1022.14	1037.75	972.941	1259.73
83.295	100.564	77.6014	77.2658	87.5543	85.4476	90.894	110.95	77.9147
194.642	220.495	197.696	229.952	219.196	201.435	225.979	216.906	226.369
120.786	112.677	170.539	148.202	138.461	106.229	122.036	132.354	143.097
244.311	272.256	258.567	223.162	235.749	240.577	266.871	276.941	233.723
1084.89	1117.78	925.219	1007.5	1085.57	1020	1051.57	1200.24	1119.5
158.337	184.124	150.187	162.703	180.721	207.035	155.295	168.803	141.829
253.177	244.296	308.439	280.127	283.171	244.52	237.925	241.27	260.474
294.939	306.955	266.065	271.022	306.545	265.883	285.423	376.825	310.877
231.386	220.111	197.384	258.344	233.284	190.573	246.141	295.745	228.739
314.882	361.014	305.593	352.966	340.565	384.563	354.097	314.867	342.741
424.441	448.057	432.324	430.22	508.526	423.09	501.541	482.796	530.628
233.639	269.19	251.728	262.044	245.91	242.99	252.035	266.72	273.071
166.117	189.216	240.333	178.898	158.697	165.276	162.467	163.993	131.506
281.968	303.008	281.724	272.2	277.984	280.998	307.06	322.042	284.376
163.616	161.326	162.8	156.654	135.844	170.569	119.313	148.657	155.8
353.467	246.358	367.836	371.631	272.881	354.638	244.301	277.138	313.876
185.628	176.448	187.358	171.545	181.046	177.487	155.858	187.484	130.986
251.51	248.395	276.647	266.348	358.109	248.577	265.933	310.751	263.017
37.0844	36.9116	31.2994	28.6644	32.495	35.3833	32.8608	47.2384	29.307
101.117	112.375	121.492	113.292	116.076	99.5444	98.9799	108.512	103.121
334.943	268.153	278.67	305.549	287.946	263.447	298.054	338.522	318.554
113.335	161.411	136.117	148.854	130.435	153.988	144.919	133.001	132.868
41.6558	49.9626	31.0886	40.5322	39.0515	38.7467	38.9296	42.6895	31.4936
95.9803	114.072	112.031	105.093	102.881	108.007	124.103	108.676	106.16
707.407	665.965	728.788	664.853	591.986	664.866	570.263	734.099	575.319
466.273	462.35	384.676	388.242	379.439	407.201	426.691	424.813	445.879
68.6373	68.7108	78.9197	71.9189	83.2509	66.4041	66.5519	77.1309	71.5002
300.225	264.701	335.183	269.247	390.42	233.399	332.148	319.54	363.43
98.789	116.735	130.996	115.123	109.382	136.019	93.9527	114.076	95.9644
100.994	79.0074	83.7322	77.6825	76.0482	68.9017	100.208	86.7799	88.94
810.086	1098.48	1215.38	1043.39	1133.19	964.331	845.008	801.151	925.207
230.817	276.466	253.545	254.355	237.957	233.197	261.123	265.153	227.967
156.77	278.78	196.234	202.499	187.952	210.16	194.116	225.945	172.144
88.9616	115.58	128.005	95.9094	100.988	95.5961	97.1726	105.379	97.7574
353.156	439.83	429.873	359.483	380.492	394.183	390.247	420.59	379.822
59.4188	68.9661	70.9612	63.5444	73.2957	85.736	62.2312	78.5051	71.4467
899.643	1053.82	749.011	767.996	875.375	791.816	1196.32	1241.03	903.322
145.794	156.661	156.973	153.467	159.406	136.316	167.56	204.109	148.694
346.003	269.38	305.559	337.176	234.063	318.671	302.206	259.431	355.306
73.9384	81.9996	98.2039	76.1324	85.4003	79.2599	73.0984	97.667	68.0165
216.72	272.485	230.748	252.887	278.249	274.03	238.945	272.205	244.857
6435.01	6943.02	7206.74	7064.26	7178.71	7059.96	6355.15	6476.35	6968.45

254.816	288.21	198.73	277.282	257.72	252.42	273.48	314.988	257.833
403.951	413.157	365.827	369.678	427.069	405.483	393.295	407.365	427.134
95.0723	112.563	129.527	108.111	122.142	107.219	116.474	115.611	104.057
28.7994	44.9409	31.5391	34.8053	24.3106	40.9115	33.6939	28.8271	39.9086
338.34	378.544	338.42	373.186	371.583	369.367	338.492	349.229	343.267
74.7129	56.4996	68.032	45.5037	60.386	64.2078	45.2577	48.6089	51.1705
850.577	630.499	1131.56	894.859	1368.78	621.46	906.869	949.966	1351.47
145.27	96.7094	110.451	94.9814	101.839	108.598	114.738	118.329	115.242
8.50351	13.7278	11.9597	13.8417	14.0527	18.0403	13.9648	17.9455	18.2824
141.18	172.4	130.566	158.358	150.277	169.355	168.414	150.688	154.051
270.25	305.735	247.594	247.295	256.798	281.049	254.18	269.741	285.011
100.314	106.16	84.1596	109.018	95.1771	91.7652	89.905	126.365	89.8996
3051.14	3748.23	3260.01	2854.38	4348.39	3537.47	3144.21	4231.84	3670.95
302.523	274.146	307.461	248.976	305.896	321.379	325.152	351.913	445.494
48.0631	52.0732	56.9149	38.7981	44.354	46.5014	47.1884	46.8621	42.2972
94.1896	96.0148	87.2172	80.5886	82.4598	82.3466	86.714	86.4845	80.3478
129.6	158.736	144.58	122.029	135.698	145.342	146.745	116.437	170.659
111.529	122.484	85.435	85.9804	86.8131	89.6726	101.356	102.467	97.6911
1355.48	1729.08	2248.4	1716.89	2890.64	1727.55	1573.59	1410.93	1914.35
182.788	175.483	196.823	204.114	186.834	198.972	179.492	163.46	177.913
78.4084	95.0121	85.1004	112.842	95.7631	102.98	92.643	96.955	87.8092
106.07	129.063	156.032	126.9	151.88	96.5263	120.402	121.328	121.154
148.752	175.169	145.595	168.233	162.651	140.461	153.393	185.014	157.677
296.57	239.669	323.88	240.618	218.189	240.191	250.5	262.948	264.749
285.465	262.48	302.531	281.906	275.957	242.857	304.241	350.413	274.368
242.853	274.736	277.768	266.183	271.543	227.767	261.695	316.639	245.267
109.992	112.604	112.23	127.531	102.281	102.501	116.634	112.53	111.512
260.739	291.572	267.156	247.62	263.002	302.008	302.917	273.672	272.366
67.6868	59.6136	54.3093	33.0213	34.5036	42.8396	38.8181	54.4532	36.9928
156.541	192.021	192.08	190.384	187.327	193.702	190.115	175.421	183.51
129.435	130.228	127.992	131.03	115.632	123.292	134.781	134.753	127.527
385.562	277.137	383.633	282.09	345.563	284.931	373.598	441.501	436.843
274.102	365.936	391.51	393.292	355.277	383.698	341.988	302.604	317.112
575.03	672.808	530.711	481.585	421.955	511.397	475.632	491.695	459.659
82.7103	82.6516	116.566	80.0616	197.368	99.806	89.0558	111.58	73.9588
235.571	258.434	281.006	273.895	323.789	246.158	269.581	265.229	254.772
95.8455	76.9876	83.9104	78.3938	85.1972	84.8279	78.7216	80.4759	74.5917
491.135	537.627	573.463	591.981	440.202	514.278	437.217	394.797	473.914
804.57	966.073	1246.36	816.276	636.899	1382.17	820.772	697.087	824.319
75.6237	102.411	93.8485	93.2401	83.3384	102.972	81.8544	82.8363	80.6456
526.629	621.57	502.213	520.606	536.751	477.011	559.575	740.238	512.945
332.402	342.876	550.391	355.013	380.81	325.356	325.909	312.001	365.532
209.878	217.563	266.095	226.408	241.311	198.061	185.862	222.45	259.596
2550.96	2815.4	2150.09	2289.09	2235.24	2373.77	2926.5	3082.61	2808.48
288.802	281.257	294.034	290.994	292.588	270.313	325.305	348.745	302.972
120.697	141.255	145.46	155.517	179.337	122.193	153.702	243.947	163.541
57.7753	70.176	79.8349	67.7569	59.3518	68.011	75.9172	87.2959	74.0769
672.602	702.688	633.022	569.161	809.762	767.685	709.26	643.777	799.676
35.4635	33.025	50.6399	34.6266	43.335	41.3639	40.7805	42.9552	41.5547
78.5683	68.185	98.0555	79.0234	88.6765	67.9144	72.8412	76.2787	79.4553
152.876	143.73	177.255	145.753	139.885	170.871	138.341	127.225	152.295
47.5871	44.0708	43.8651	39.7185	38.3024	37.5233	45.0512	44.0666	40.6214

350.556	340.342	318.693	370.61	389.998	341.551	317.239	345.554	383.981
59.2963	71.9559	77.3624	62.8035	59.4694	82.843	65.9421	56.2523	67.5202
58.354	55.5396	67.2512	58.7823	57.6329	55.445	55.842	62.5679	58.9038
405.085	748.834	1026.45	822.491	697.517	494.94	539.895	631.361	569.728
363.029	373.449	393.824	382.772	381.28	417.365	401.107	348.149	376.616
19.4102	25.5075	19.6192	18.6094	16.3806	21.1901	24.3268	22.1263	16.8608
128.274	110.004	95.6974	92.5321	94.4386	96.4476	98.2777	123.688	103.69
204.94	313.472	251.673	293.126	221.229	315.397	293.816	237.802	292.171
178.977	139.535	144.955	154.623	144.404	172.506	150.788	161.249	140.049
777.768	811.355	808.27	832.26	999.067	862.163	805.754	684.657	1006.76
275.344	281.839	272.275	255.141	320.962	264.798	302.58	330.325	287.206
24.7205	17.9518	16.0513	14.5721	20.1559	23.5271	18.5228	19.3111	10.426
852.15	885.119	1291.83	1302.87	1124.61	1233.27	772.582	885.7	1062.11
28.6159	40.4476	52.5974	45.0586	43.7367	37.5351	48.4587	36.6292	32.7371
63.0361	64.6956	50.559	52.6228	58.55	63.8728	57.9178	63.9378	57.6466
223.057	210.687	184.99	214.769	188.278	244.26	212.446	184.66	198.182
111.987	174.836	107.456	156.17	141.551	157.297	159.785	109.833	154.176
400.218	271.497	330.111	362.996	445.013	326.148	311.725	331.214	381.727
275.932	359.758	280.275	264.191	334.542	301.85	294.738	298.405	283.936
216.935	260.376	249.852	242.599	235.459	206.992	200.641	229.935	231.065
43.8275	72.2623	93.1677	74.7515	66.6887	57.353	65.7272	68.6171	44.6726
223.512	240.511	282.37	260.316	297.4	209.269	265.132	300.054	279.386
243.622	256.195	251.497	261.266	266.189	212.956	268.536	300.195	230.911
83.6727	103.072	112.403	116.469	122.45	88.9936	107.421	111.712	93.7767
703.667	488.944	605.975	669.596	645.048	486.541	657.972	647.849	687.923
114.783	107.5	99.6503	116.442	133.834	112.311	133.344	137.584	107.411
157.022	203.478	169.431	197.653	188.648	199.499	180.041	177.661	156.803
3203.15	3338.52	2457.55	3027.62	3199.69	3308.57	2814.04	2994.3	3489.7
579.396	575.211	449.565	511.312	564.182	531.312	564.854	633.496	659.311
193.865	210.785	182.67	187.552	176.019	177.692	195.489	225.128	184.997
216.154	257.782	226.967	247.927	234.69	247.696	252.774	234.694	240.782
77.0381	96.445	86.2901	86.3674	75.5383	85.286	88.6647	90.243	89.6932
147.921	133.116	144.73	122.565	141.203	116.765	137.298	169.004	149.466
310.896	315.863	319.985	314.389	327.542	301.271	315.65	321.073	331.508
48.8088	75.2803	75.9168	74.6854	61.0612	77.2196	69.8918	50.4598	87.3106
222.847	243.593	207.751	225.01	239.78	220.727	243.879	260.61	217.21
193.701	195.447	188.543	182.138	183.518	171.998	198.325	225.463	182.881
33.5663	54.5314	48.6413	39.4258	36.1027	55.3675	42.4153	48.9046	43.4284
257.088	340.348	334.881	316.347	301.83	302.373	327.292	330.66	262.736
446.759	487.916	655.739	506.574	681.511	456.907	459.004	530.745	529.411
108.609	102.575	104.213	99.9346	100.327	123.308	101.021	112.911	116.976
88.9654	85.9724	73.2284	74.8425	60.5089	81.8716	58.5801	61.7565	58.5024
109.543	136.008	134.476	118.984	112.962	116.851	120.791	122.183	123.945
468.606	607.034	467.428	513.482	516.307	536.603	497.819	579.569	494.786
141.916	198.707	167.309	172.315	165.965	161.161	195.504	188.473	167.867
182.609	191.711	193.43	167.805	220.911	177.696	194.748	217.645	193.036
94.3967	115.135	77.8552	93.0051	107.027	99.6424	93.2109	103.096	85.2824
74.9877	62.7315	95.1185	88.4997	99.2881	64.7133	88.733	81.6484	94.6314
42.9543	74.5258	62.5329	69.362	53.1409	71.2724	66.4301	57.1095	61.811
128.257	116.695	122.295	95.4626	98.3399	111.85	105.331	147.646	91.3218
37.2127	49.9569	30.0342	43.7619	45.0121	43.9431	38.1071	38.416	37.8778
67.7565	99.9121	87.6093	91.6532	71.6687	101.024	82.1709	101.457	76.9359

65.8401	53.4291	52.2642	47.7686	45.6912	51.2681	43.8794	52.1048	51.2231
89.1614	160.617	144.405	139.083	110.062	133.347	131.147	113.487	142.665
240.993	198.003	196.316	169.732	211.169	212.52	184.716	229.244	203.741
243.271	218.728	253.233	232.304	219.463	219.171	224.528	222.192	217.353
339.939	341.438	390.802	384.69	396.148	341.524	393.238	423.913	383.706
299.822	293.765	348.821	285.961	426.825	264.214	358.235	379.847	343.258
104.77	99.4609	100.746	87.6058	84.9913	89.0678	91.9136	90.8831	93.9103
160.013	155.276	139.064	163.088	161.149	145.918	182.941	199.405	180.721
55.1679	56.9514	54.1194	50.0721	56.0951	59.1295	43.1542	59.6391	32.207
161.052	134.83	141.387	139.826	134.843	107.294	157.61	133.354	155.135
73.557	85.139	86.889	93.0517	112.862	71.0339	101.164	130.048	91.6554
297.637	373.933	329.892	310.075	309.776	357.108	313.489	337.919	313.637
316.692	338.01	287.156	300.008	296.514	287.894	282.323	348.323	280.687
214.037	190.001	218.139	191.191	236.733	191.858	187.165	174.118	201.388
80.7949	92.1221	91.3187	101.98	91.8619	101.666	101.036	93.7953	95.0337
195.485	233.986	197.265	247.008	199.018	255.703	244.324	233.636	222.674
147.457	139.758	130.847	129.786	114.602	145.571	125.549	117.799	115.264
300.496	265.868	348.405	339.772	426.164	312.983	339.809	284.552	385.043
38.3808	20.4459	23.41	24.8699	20.477	29.4096	17.9078	23.2253	27.9104
39.2149	36.493	24.9879	27.1707	31.8137	24.1736	28.5539	26.6195	29.0892
135.664	164.115	187.524	198.034	202.642	155.282	150.913	173.523	158.007
18.3747	22.0859	19.8004	23.745	18.8389	22.1039	18.0555	14.9937	20.7757
210.816	294.328	223.133	234.353	236.094	271.05	229.485	260.487	215.436
1279.66	1947.29	1468.87	1482.87	2199.92	1180.28	1623.97	1801.31	1822.6
236.93	140.24	206.997	201.71	238.046	190.808	181.082	199.292	211.096
517.568	449.183	659.085	395.97	373.265	484.439	440.182	385.454	507.264
47.7951	39.3607	38.7096	22.1824	31.6604	37.7053	43.5981	42.1958	24.4503
52.887	62.1084	54.55	47.7701	44.9672	51.7132	45.709	48.2831	49.317
237.186	231.256	297.687	237.834	243.484	207.792	186.239	168.294	231.517
113.438	104.156	103.684	95.1297	93.4532	96.5633	100.48	117.673	102.288
66.8699	68.5497	58.7914	54.9665	59.7694	74.0837	54.2578	62.602	62.2297
68.3854	58.6169	52.6863	58.6453	47.5501	53.3733	55.7097	64.4402	49.2005
7002.8	8110.23	7313.09	6753.97	4993.71	7775.93	6188.58	6978.44	6787.11
92.3596	119.391	107.257	111.138	102.546	112.445	109.432	98.8447	103.573
137.391	147.453	145.625	157.705	152.468	137.601	156.646	163.528	136.797
98.8481	105.823	94.918	107.544	97.451	114.319	94.7931	99.012	103.219
105.519	147.423	135.279	139.987	110.021	134.309	131.338	111.348	121.069
175.548	242.57	192.171	188.353	200.182	202.804	180.644	227.572	178.847
407.557	400.88	407.464	440.065	534.357	380.934	493.434	446.292	480.717
49.7174	46.216	86.1236	64.3097	63.0731	67.9651	55.3506	57.6844	65.5697
244.112	260.909	232.755	253.559	216.358	252.799	231.688	254.516	231.951
150.041	139.941	172.633	142.769	188.799	126.565	158.125	165.681	151.523
168.093	92.0235	107.232	113.214	132.316	90.727	166.44	155.782	148.746
39.0016	45.0101	47.7611	40.0841	39.4239	47.4519	47.4291	49.9069	46.4766
197.972	238.701	316.622	230.096	305.005	223.214	229.708	264.607	251.384
56.9167	56.5893	48.1213	54.5864	61.8312	42.126	56.5208	61.8126	47.0329
145.536	132.117	152.624	156.71	146.07	121.379	149.475	170.926	147.904
269.498	340.444	337.304	284.379	317.83	273.865	243.171	313.846	277.919
221.405	257.518	281.466	263.692	201.203	279.554	220.483	201.991	211.847
440.43	375.11	393.011	423.025	594.569	380.585	424.181	446.353	513.963
157.438	225.142	245.257	186.636	204.417	190.946	186.663	202.538	181.084
136.835	174.367	130.927	135.421	129.037	141.366	150.944	180.049	130.892

134.756	143.407	142.449	145.733	137.006	141.094	147.296	128.821	154.625
455.244	452.662	651.117	469.071	453.116	589.939	418.024	350.636	469.533
123.161	159.081	137.223	133.393	135.867	138.569	146.633	188.869	133.413
276.107	244.878	332.016	306.927	256.808	288.162	226.143	238.052	271.743
228.611	267.253	308.87	242	347.43	235.891	238.941	259.418	274.439
1446.8	1928.04	1478.59	1298.87	1378.22	1642.14	1495.85	1394.2	1424.33
165.876	195.272	167.534	187.847	214.379	178.985	193.53	188.308	200.999
5599.02	4565.16	4690.46	4623.84	7230.05	4899.85	5379.25	5577.43	6793.44
93.4696	172.066	171.857	153.213	114.108	164.347	122.43	120.418	144.715
59.3344	50.0613	57.3669	57.5285	58.4705	48.3618	52.5441	59.5983	55.5518
99.9721	86.609	139.617	94.7409	128.549	84.8254	93.9786	110.452	108.415
218.702	216.105	193.242	183.711	204.347	181.568	236.908	247.055	227.581
234.652	252.8	227.022	234.454	243.631	233.556	251.095	253.315	234.927
125.363	140.794	113.12	126.76	137.741	117.47	128.962	128.386	132.95
93.019	131.933	103.125	111.179	89.3468	116.71	83.4044	86.1185	79.7497
261.72	197.451	333.785	302.656	409.473	246.615	323.244	313.379	398.621
27.156	23.8394	41.2597	33.1015	30.8017	32.6018	33.3762	29.8066	32.3803
88.3582	109.674	74.1328	72.3534	68.6947	94.9655	42.9854	59.9991	77.088
233.566	294.689	292.266	290.935	254.754	296.476	288.889	248.424	272.433
368.324	233.94	343.271	312.153	268.377	285.217	357.328	246.649	374.871
4007.83	3618.7	3153.01	3289.25	3606.51	3454.19	4021.81	4411.11	3956.5
333.569	338.647	412.567	425.494	482.107	345.758	344.86	338.405	410.493
268.365	201.96	290.416	283.336	256.922	254.456	274.413	256.103	345.863
275.478	133.726	178.148	166.341	316.938	136.653	217.336	238.408	393.857
160.116	147.7	164.173	157.087	155.424	156.589	158.251	167.93	143.338
23.227	31.4226	35.2571	29.6397	27.278	31.7575	24.362	32.8213	28.9961
928.321	695.192	556.893	767.952	818.734	664.534	1066.9	1117.26	1123.39
150.412	179.404	173.13	168.754	139.172	170.539	157.691	155.3	159.764
190.708	231.934	176.812	225.216	211.145	223.3	208.347	244.696	200.577
700.616	786.303	865.046	826.025	937.237	872.398	726.38	797.68	894.745
46.2344	37.3332	39.0096	44.084	44.7313	30.5908	39.6941	45.2818	40.4882
70.262	43.3641	48.9157	49.0376	46.3699	31.7144	86.16	62.8504	72.7379
292.298	325.2	364.626	325.13	374.395	333.356	339.833	322.123	320.089
173.425	173.411	181.481	204.354	171.471	141.902	183.084	208.113	196.784
1046.06	1204.46	1539.51	1254.27	1101.71	1042.94	1001.35	1068.3	1167.83
166.858	130.988	115.097	129.825	127.676	126.812	134.136	166.371	125.894
157.734	161.32	160.557	161.115	184.994	144.12	194.483	229.954	159.704
41.7407	41.5922	36.4563	42.5322	34.062	40.8864	42.9006	40.0441	39.9677
243.689	251.055	293.614	281.415	300.289	235.017	287.279	271.113	291.73
343.117	371.085	356.082	372.327	368.076	370.786	365.81	374.316	359.303
476.677	575.972	698.107	574.722	770.938	540.754	443.849	444.183	567.298
74.0816	105.132	87.6688	84.0097	74.7972	86.3209	85.8274	81.704	79.9358
412.901	370.191	472.73	444.164	534.99	377.147	438.015	510.885	488.098
162.346	162.059	154.394	144.776	152.516	139.709	136.788	159.298	158.352
82.2531	83.3341	87.2658	70.3244	77.6811	81.8186	76.0746	86.9353	69.4204
91.8075	105.544	113.025	114.821	102.119	112.106	110.666	97.4112	94.6298
183.215	172.144	169.927	179.454	179.462	205.541	197.189	179.8	181.457
59.5096	56.3199	52.024	38.7414	45.3026	49.9732	46.6135	40.9044	35.3427
426.392	389.69	346.581	409.709	375.189	404.72	385.585	428.527	429.25
1037.66	265.349	703.049	1223.34	1054.45	318.336	258.589	883.123	1154.73
172.368	230.918	180.502	166.837	214.339	160.958	202.429	242.111	185.996
35.4086	59.1562	56.2192	53.3861	42.3491	50.7414	46.1362	48.8636	50.7552

48.3992	36.3893	61.2271	32.8485	55.5885	46.9699	58.7759	41.6318	40.6483
275.013	233.642	244.584	262.337	324.889	212.295	280.086	318.069	308.253
90.7687	91.4694	115.751	99.8945	101.566	99.3148	112.986	95.3473	112.634
246.326	194.828	406.603	236.636	386.262	222.557	277.681	308.277	353.313
1004.18	886.074	855.461	923.698	1231.51	1048.82	1127.85	1249.68	1374.18
360.9	292.692	303.05	286.902	254.492	268.87	343.638	349.765	310.182
231.208	241.329	228.971	249.041	260.086	234.771	259.573	336.224	240.732
109.678	110.871	101.881	110.341	96.4152	109.434	83.7742	106.368	85.1624
364.707	369.274	419.128	367.959	422.838	409.128	388.933	416.926	403.433
10.93	18.74	21.4129	14.8377	16.4505	16.9076	9.24095	20.1834	8.16186
97.5168	96.2147	114.071	97.5821	84.1838	90.8612	72.8716	72.7801	75.6018
157.186	171.988	207.838	147.887	214.994	132.646	188.373	194.538	173.768
1899.39	1590.59	2491.36	1721.23	3211.77	2426.24	2465.77	2619.92	2884.43
457.938	461.212	417.371	400.871	375.404	437.023	319.753	372.652	386.343
504.131	496.39	522.104	483.875	623.012	512.245	483.683	493.093	567.507
80.4256	73.3712	85.8866	77.8958	83.4973	93.0784	69.3839	67.532	79.8319
129.54	183.089	150.088	153.168	177.82	137.242	132.637	150.132	132.323
40.7021	52.016	50.8485	50.8298	65.1189	59.2149	54.5018	48.8504	54.262
3000.95	2875.87	2329.47	2727.16	2895.29	2448.68	3115.52	3815.19	3408.92
614.949	599.89	584.867	542.557	744.686	550.969	591.188	694.106	784.056
93.9333	102.545	105.619	101.012	125.271	108.237	112.229	134.897	101.05
61.4801	62.4339	60.4869	63.8096	74.3492	70.638	68.0825	68.6981	63.9519
72.2696	73.0153	58.293	76.6683	83.8137	89.9524	86.9396	64.7747	90.2785
109.44	102.25	115.576	112.148	147.428	118.962	113.023	107.211	121.465
124.699	152.879	264.174	164.752	124.184	163.445	119.794	115.266	149.603
118.813	125.528	96.8311	78.5175	96.4912	92.9133	68.9609	90.0769	94.0058
454.776	514.547	455.458	500.72	429.017	567.019	466.367	424.292	428.988
40.6085	58.2194	56.5494	43.2596	44.8785	56.085	50.3658	44.0391	40.9386
338.197	367.29	267.388	244.053	192.324	256.682	263.684	319.879	265.995
102.467	133.451	120.992	123.681	93.3629	110.255	119.624	105.54	117.985
211.579	162.758	249.461	311.92	222.1	195.767	193.774	148.907	261.76
261.374	255.104	272.688	242.623	307.941	219.543	228.513	302.856	262.762
215.652	231.459	271.912	235.298	330.356	213.281	255.35	305.795	219.558
212.401	217.894	221.558	204.403	177.466	238.068	213.257	196.821	191.943
187.95	235.297	202.775	216.62	216.953	221.122	231.125	208.481	199.271
7036.26	5566.5	7967.41	5876.35	9788.26	6528.83	6871.95	8054.51	8967.25
93.6586	159.892	183.074	202.74	114.48	107.94	143.636	181.665	116.815
192.051	209.985	196.939	191.69	227.996	189.957	213.664	235.416	213.956
168.955	148.556	121.897	130.524	113.346	123.316	141.748	155.738	132.775
402.577	361.078	271.656	257.666	272.479	302.624	283.419	348.749	342.695
63.2638	55.8988	54.6952	44.8413	47.5715	50.7099	51.6659	57.5188	52.7558
3514.24	3983.72	4501.13	3799.4	4135.82	3941.71	3566.84	4236.72	3912.28
236.505	320.674	251.668	299.111	263.623	300.544	259.056	255.566	274.864
666.008	825.842	713.268	721.178	734.944	725.201	709.851	745.535	712.836
150.311	147.635	147.749	154.172	131.217	122.376	130.71	151.44	141.59
38.7794	43.2689	45.1138	38.5539	40.6765	59.0255	37.0937	34.5121	37.2747
422.787	383.913	416.412	361.256	371.859	406.849	406.304	395.546	364.515
800.427	682.239	654.442	672.616	887.011	806.947	763.777	813.009	850.607
75.0812	79.1829	75.6714	59.8825	60.4014	65.5408	53.8409	68.2045	53.0613
217.665	255.388	254.904	256.891	263.994	254.86	236.865	248.316	222.887
79.3179	91.5207	75.5013	78.9036	87.7591	80.2152	87.8419	78.3332	72.0859
486.024	488.792	438.255	444.285	420.293	440.065	487.466	489.628	449.437

65.6735	68.6078	68.562	73.5637	64.6689	80.2608	66.4486	70.1152	67.3754
383.329	293.894	373.422	396.254	446.701	330.752	304.717	343.656	408.124
179.207	263.629	180.917	226.43	235.394	251.336	184.459	252.835	170.851
733.904	663.053	840.734	725.605	935.741	570.677	852.552	861.671	850.306
82.3803	157.263	132.662	129.41	103.735	121.211	128.563	108.203	125.047
97.1688	95.8486	111.191	87.8298	92.4206	107.516	85.08	90.9333	92.3877
183.245	263.07	222.499	234.842	186.571	236.612	224.377	198.646	242.78
58.801	58.1918	65.0119	49.9086	47.9424	45.7762	56.5059	64.8632	53.486
82.5311	148.518	151.475	136.304	111.847	150.611	121.495	100.921	132.714
68.0089	92.3995	63.9387	83.4101	95.7658	85.5373	89.2858	100.707	86.5744
114.767	125.064	142.194	138.857	111.423	139.695	112.941	102.366	118.877
76.2403	94.8196	109.234	86.1034	89.723	89.7957	79.1465	92.5799	81.5759
727.242	775.001	917.158	809.485	705.563	794.441	631.594	679.904	810.155
213.006	211.203	242.367	220.869	282.978	184.2	224.224	236.259	288.839
154.312	232.211	195.688	207.449	171.941	222.969	200.255	181.387	181.073
23.2695	44.055	35.1367	30.3783	29.6844	34.1189	25.6321	30.2062	29.9099
191.826	201.086	188.249	210.74	231.872	178.42	215.546	199.074	195.832
351.563	350.473	323.62	258.607	212.373	276.336	245.168	294.931	240.54
140.036	131.895	109.365	108.965	106.444	132.374	89.5822	127.704	110.417
101.039	80.7393	103.976	123.785	110.794	96.5163	88.3043	87.0032	108.796
1719.15	1543.77	1517.07	1491.33	1474.16	1294.44	1877.94	2247.38	1604.32
763.103	1078.15	999.731	902.162	919.998	873.788	796.562	888.152	740.041
149.813	150.932	183.963	153.871	168.767	137.404	172.029	194.492	151.523
12.9557	17.0115	6.85495	6.35355	10.909	21.0364	9.23177	4.38016	21.9411
74.4678	70.9212	63.429	67.714	75.4577	55.9656	62.2959	58.5103	65.759
666.513	522.628	589.658	700.799	521.57	552.277	564.35	564.323	708.482
261.241	312.767	317.474	314.174	343.044	297.425	290.438	285.826	310.47
2317.36	1904.48	2468.5	2442.15	5115.37	2305.82	3055.04	2465.7	3758.49
69.6313	62.7206	59.4109	57.5528	56.2138	76.9042	66.0591	54.348	65.859
211.303	222.075	215.696	239.86	196.061	235.512	217.314	232.004	196.635
250.066	267.928	253.887	262.418	272.033	254.358	276.055	265.06	266.108
271.03	315.266	307.706	336.859	406.956	342.477	319.16	308.359	342.375
480.166	537.544	511.567	510.035	533.591	484.294	484.532	532.426	506.933
7732.8	8016.78	6442.73	7155.09	6493.46	7289.91	7337.52	7477.08	7557.83
71.651	58.8847	41.565	50.9872	59.39	57.2834	47.8032	53.7899	58.2917
464.598	646.403	438.658	536.837	467.239	581.206	489.399	490.837	423.892
454.204	500.553	414.941	428.946	575.107	423.334	424.215	393.087	561.313
69.1794	108.847	116.546	100.137	117.695	91.7452	99.0381	135.937	89.6313
1212.22	870.591	977.322	899.44	1031.45	1154.16	963.58	1046.77	1065.18
4.28764	4.08737	3.71661	4.86541	9.90133	13.8886	4.64939	5.9819	10.1821
2023	2043.42	1766.94	1908.3	2111.25	1690.79	2055.4	2600.74	2198.86
73.0139	83.2297	68.3779	68.7562	66.7289	77.1085	76.0833	80.2203	82.0774
123.24	137.938	267.072	139.466	129.502	134.812	121.978	119.613	149.612
19.6954	11.0852	11.3365	13.1971	13.3753	11.1085	11.3769	8.95994	8.81012
121.641	115.866	103.615	102.224	99.9636	103.163	106.09	110.421	99.9475
74.9	85.8809	91.6051	85.2873	91.5581	72.4787	77.1271	109.564	75.7472
37.8385	54.3703	36.6783	43.9206	44.818	48.29	48.1275	52.2459	53.277
40.5227	59.9471	60.5521	55.7355	49.3461	59.2115	49.0832	52.2782	60.5952
191.227	204.759	223.954	193.519	216.788	195.575	186.188	206.028	194.486
3038.97	3796.76	3323.44	2914.43	4574.46	3632.31	2999.7	4066.86	3646.07
110.993	113.295	99.0131	117.023	115.128	116.671	123.11	121.993	103.733
55.6148	66.9793	69.715	58.0295	61.3864	53.745	72.9112	63.2821	72.8223

36.3068	42.1272	35.5164	35.0338	29.6831	32.3306	30.6609	30.2499	34.4551
55.1049	55.1306	49.3125	49.3636	52.3652	49.0641	51.7077	58.795	47.4966
658.93	636.669	553.984	683.7	697.735	674.147	665.408	703.114	740.045
255.814	263.098	254.115	276.277	284.754	271.22	273.905	240.759	300.683
577.379	492.23	554.94	542.692	601.602	554.886	566.503	517.702	585.142
169.551	139.166	126.654	113.456	144.276	124.46	124.431	129.562	138.14
115.663	107.393	114.433	119.754	124.922	92.4227	112.824	116.523	108.635
95.7329	59.4807	61.1834	51.939	53.9508	44.3868	69.3568	73.6407	75.1982
148.215	147.601	124.216	136.88	129.623	154.802	136.023	117.32	125.171
153.248	160.167	152.532	153.067	138.522	175.978	150.159	141.891	152.824
89.6246	92.4549	70.2177	60.3191	54.4218	75.126	55.4154	71.3883	78.0942
59.7951	85.488	85.3343	80.7937	71.6092	85.5661	62.7351	58.6739	71.1791
115.222	105.528	130.985	121.253	154.365	130.328	97.3878	116.142	160.303
114.111	211.908	206.715	166.765	145.451	188.17	148.332	175.994	154.273
59.2019	109.584	107.202	99.5633	68.6338	93.6823	73.1947	84.0762	58.6924
73.7935	102.257	96.3727	74.5652	81.6791	80.5886	77.9546	84.6714	77.3887
185.101	171.661	167.593	153.757	173.055	197.325	195.893	199.175	186.59
47.7373	61.3162	55.6196	49.816	48.7458	51.4907	62.921	58.397	60.3908
206.098	229.735	216.259	208.724	220.25	211.694	230.27	240.319	208.369
117.187	150.803	136.52	155.73	143.258	165.904	147.242	135.129	138.22
112.03	135.702	125.932	117.27	123.636	127.786	133.713	136.051	120.347
1545.29	1146.85	1510.84	1374.33	1416.15	1226.81	1085.5	1156.84	1338.76
321.14	321.665	306.621	296.431	380.303	294.164	368.319	343.652	390.257
5.003	5.6942	7.21522	3.53335	3.34944	1.21078	7.53219	10.47	8.98509
166.43	154.005	155.858	162.903	176.462	185.963	183.027	164.228	174.532
149.307	136.595	178.006	155.699	149.989	138.947	152.323	172.491	146.899
58.7428	89.6536	60.4756	78.0551	68.6651	78.4965	59.6879	74.9929	54.6388
282.184	294.405	302.717	220.54	260.454	343.946	252.059	290.432	238.803
51.7535	62.2817	58.4837	55.051	58.3072	54.751	47.1562	49.4819	43.6035
244.559	200.74	177.193	231.308	261.922	220.367	288.749	284.286	321.441
364.47	388.081	377.37	361.711	330.901	368.738	402.687	389.746	384.085
172.044	157.757	162.331	161.432	150.887	154.523	155.018	165.029	188.002
137.595	162.78	184.577	174.609	161.073	162.596	160.416	177.209	136.504
71.068	71.2809	84.8408	58.8796	54.0317	73.5878	50.9877	54.9609	69.644
111.624	124.537	125.34	111.01	108.342	123.539	107.175	93.624	112.851
99.8357	89.2164	159.993	102.604	194.558	94.4625	104.817	139.744	120.308
893.705	905.889	706.063	818.05	791.3	787.63	873.119	999.212	1032.06
191.932	183.149	176.423	173.08	187.885	177.413	140.901	180.646	200.001
936.988	978.081	778.931	1133.58	737.17	987.392	868.654	895.107	986.565
267.563	311.948	272.343	288.85	349.009	266.911	275.349	444.266	267.773
144.946	121.511	146.965	135.299	169.851	139.072	128.402	119.408	144.207
61.6742	67.3284	52.9961	48.4801	43.39	62.8835	45.9601	62.3411	43.2934
140.866	134.281	165.306	171.662	175.883	121.471	157.736	182.893	143.186
49.4284	45.9321	50.3801	66.8645	65.1122	49.0074	44.8969	48.7713	63.9094
268.106	209.714	233.448	165.811	142.964	195.257	200.74	181.64	251.236
204.984	216.772	202.345	216.391	235.493	189.868	216.585	217.514	221.504
227.91	286.874	287.527	300.209	263.789	243.25	293.547	354.03	229.776
617.311	569.871	575.632	533.047	547.706	445.082	573.577	756.816	651.298
398.12	367.472	431.701	389.357	507.965	336.517	322.253	496.886	474.098
145.397	177.29	185.921	168.529	150.541	149.455	157.417	169.832	155.263
149.827	141.107	128.609	109.49	130.637	118.162	117.218	138.358	128.313
171.166	150.204	181.193	164.393	163.463	155.025	162.839	144.949	175.014

1170.78	1147.39	1715.45	1273.34	1145.23	1094.99	1063.72	1265.78	1037.6
149.459	173.824	151.315	146.005	178.034	144.233	152.449	177.971	137.053
69.6473	63.4937	52.5488	71.5783	67.2666	66.2631	54.9269	55.3192	53.8954
130.604	176.854	159.739	178.393	150.172	182.531	168.282	148.772	143.445
88.0796	71.4976	102.807	87.0348	104.479	67.6969	91.4002	88.4862	80.383
237.732	209.974	300.504	246.956	261.471	202.67	226.249	245.568	253.699
11541.2	9756.98	8171.72	9223.83	8080.98	8751.52	11962.7	8163.5	10253.5
207.739	209.86	205.311	206.694	199.551	216.185	233.56	236.294	219.687
459.058	471.835	520.701	481.883	575.357	482.852	421.217	451.878	520.655
288.534	328.286	394.286	292.288	365.177	316.824	242.367	314.07	268.398
180.833	210.541	195.817	187.592	185.293	195.232	199.925	176.8	192.739
639.984	727.042	638.91	616.557	630.344	696.706	531.586	577.581	587.545
518.575	584.373	471.727	497.44	502.563	530.76	527.525	574.361	516.765
182.083	182.325	187.754	135.448	131.315	137.523	128.831	164.639	158.107
58.52	58.6682	59.1319	63.2315	66.9431	65.9519	34.9273	41.2301	57.2307
65.5829	94.2921	82.0932	91.3883	71.3892	100.149	80.3562	82.7439	72.9296
159.093	167.112	172.801	184.063	194.443	142.425	205.968	219.953	162.25
385.904	616.492	791.143	667.111	607.024	569.924	518.865	719.086	415.763
535.469	514.399	495.211	503.261	558.675	443.863	642.008	745.034	513.715
41.3346	42.0574	36.1292	37.3666	36.9856	35.0937	29.5746	33.2622	32.8581
1005.3	1183.21	726.649	1018.26	979.143	1006.11	1040.85	1353.76	901.173
92.9102	126.612	106.626	122.642	110.805	105.998	124.863	135.442	113.971
130.595	159.505	149.329	169.115	128.696	167.243	150.658	143.422	151.436
24.6627	34.3853	58.3365	42.4905	41.9558	19.4856	20.5623	19.6974	15.2581
328.17	422.271	430.374	429.225	466.793	419.633	327.535	444.742	371.815
25.4125	34.0914	27.8158	20.8997	21.1007	24.0644	13.1835	17.4389	22.9135
115.926	118.192	133.685	127.878	118.554	111.282	90.5246	149.528	108.73
9.32781	30.4546	35.0888	27.2997	16.8774	29.445	19.4867	17.5303	27.5211
298.944	369.235	473.334	361.926	436.396	318.274	346.428	389.846	345.163
1193.49	915.437	1111.43	1149.55	1543.28	1026.78	1133.95	1293.25	1496.92
177.608	226.855	173.791	145.269	168.954	176.843	169.414	221.902	184.743
91.6931	103.959	105.863	105.37	98.0622	110.803	106.67	111.692	105.76
406.495	459.018	459.26	454.167	535.824	483.927	452.893	384.009	485.331
310.094	276.106	376.457	336.508	432.389	294.078	308.931	302.743	354.814
80.7355	109.299	77.4551	82.1684	71.9384	87.7388	88.261	109.847	83.1451
105.415	110.376	149.49	119.869	141.85	96.0066	120.572	131.768	122.435
514.115	596.613	422.468	515.226	481.784	494.215	591.984	667.025	475.247
516.012	386.531	511.857	481.739	477.986	487.066	455.289	486.198	517.011
1254.13	1187.79	1416.94	1315.45	1573.18	1205.61	1400.11	1496.85	1573.72
196.525	256.043	201.14	195.067	186.447	287.258	219.13	171.173	216.266
70.4649	100.205	96.1254	93.8736	90.1432	88.3235	84.3577	83.4801	82.6248
703.221	675.52	713.032	660.528	780.431	536.39	683.829	714.751	838.451
29.7691	49.084	44.5327	44.8067	44.5	44.6174	35.0891	39.9483	44.1212
174.369	156.266	154.834	152.345	163.56	142.448	140.307	165.098	146.977
93.3961	100.481	83.8922	72.1933	94.0317	92.6649	75.9834	99.9561	87.126
175.891	145.938	154.116	139.859	172.307	150.899	177.309	198.731	165.166
182.909	352.587	256.651	245.422	202.361	284.701	217.992	275.093	244.788
342.011	269.229	289.149	501.437	363.764	471.814	406.156	343.615	374.502
664.939	436.685	403.953	503.544	581.762	660.812	625.849	758.798	665.721
33.4856	36.7611	59.1652	43.541	64.5511	40.4929	31.0858	31.6898	35.1526
1206.82	1364.76	748.526	1150.71	1504.23	1260.48	1293.97	1144.68	1479.03
183.301	165.93	168.627	173.856	201.357	164.944	166.536	185.704	189.908

207.629	292.381	211.781	280.958	261.017	243.892	261.043	284.109	236.889
60.7901	83.0663	91.1424	76.5455	52.4394	70.8543	43.793	67.3181	53.8532
72.757	77.0939	96.2287	90.3924	85.7173	87.5382	77.9479	87.5355	80.9694
108.678	160.023	160.011	169.402	120.191	163.705	153.705	132.757	152.441
205.254	141.199	187.81	166.985	178.307	151.311	147.697	148.334	181.663
440.954	385.157	576.948	555.218	565.371	575.556	414.092	414.108	460.192
521.465	673.611	697.88	636.125	571.056	635.878	450.972	454.683	586.405
43.8046	42.2915	49.1568	49.6082	46.7087	44.8721	48.4751	53.6701	37.1776
339.702	372.111	325.295	325.659	359.526	402.816	362.395	407.44	335.266
320.651	246.344	334.689	319.91	432.406	300.312	355.354	373.583	398.503
575.811	771.505	565.31	510.482	597.36	655.802	587.925	655.645	621.597
428.099	556.406	404.271	447.484	445.135	490.861	438.75	477.206	453.739
137.688	173.829	162.103	147.234	143.563	151.758	147.317	152.253	138.592
175.059	201.143	181.251	191.316	205.029	154.338	198.33	207.667	197.669
78.253	89.6323	82.7842	77.5154	77.1466	82.2528	77.0081	75.9906	86.3771
229.389	288.789	316.619	259.396	400.708	228.052	266.836	313.445	275.2
248.683	344.915	371.498	264.167	422.216	298.977	295.391	304.441	285.351
61.4711	54.6349	56.5868	56.1018	66.3079	43.0291	52.7695	56.5655	54.2482
148.461	188.006	146.578	155.78	133.777	166.771	155.024	149.059	149.849
38.7994	48.0485	41.4296	47.6216	57.801	57.192	52.799	49.2187	43.1592
239.323	273.883	224.545	190.407	177.634	217.443	190.442	198.392	204.492
255.889	256.411	222.335	231.349	211.624	228.427	258.102	267.939	238.772
291.328	294.891	268.441	286.188	304.431	282.856	314.178	315.427	316.884
37.5338	46.2046	42.398	38.0382	57.4408	38.6929	49.7236	60.0197	40.9739
414.193	400.657	484.545	446.558	496.627	406.675	456.475	446.484	494.166
155.893	116.649	147.788	128.093	141.664	103.982	162.603	169.391	137.709
1283.19	1004.92	1436.46	1004.33	1742.58	1091.04	1124.71	1341.31	1467.81
89.1392	110.605	101.883	90.6655	126.207	85.7548	110.559	145.312	95.0623
181.2	189.277	173.732	184.077	188.35	176.984	186.659	214.91	180.25
200.987	173.796	197.473	192.656	226.185	155.24	201.751	233.268	208.422
72.9908	76.6416	71.2008	79.2645	58.8477	69.5753	75.8444	68.079	75.2057
242.832	221.326	244.837	191.73	232.705	180.876	224.358	285.14	245.893
119.852	125.172	137.293	158.251	162.289	124.979	134.799	156.597	145.146
41.0636	57.4163	43.5813	65.0737	42.9875	66.6079	58.7644	42.324	58.1455
477.28	549.606	487.613	536.617	501.77	538.017	491.108	528.408	490.136
216.695	232.558	255.889	231.3	236.94	258.434	227.583	209.071	254.594
3276.49	4008.55	3733.98	3615.25	3375.9	3854.07	2828.06	2806.49	3362.61
51.8625	69.079	79.8219	67.0649	70.2421	70.6368	63.965	68.9523	55.6006
521.01	510.364	449.238	411.471	391.12	413.257	485.717	512.365	443.217
139.026	127.297	129.667	116.198	123.863	126.062	140.52	117.054	124.704
612.61	730.154	674.025	648.262	875.707	621.015	712.198	685.658	672.276
203.137	156.755	159.639	183.707	169.435	188.177	144.766	154.361	205.965
183.951	247.254	206.011	211.968	222.498	309.416	200.467	225.894	203.329
204.757	197.46	178.641	249.824	251.981	203.579	218.908	259.954	262.065
77.6304	70.4749	173.419	88.9837	76.2583	72.3538	65.784	66.6326	74.174
310.072	330.435	309.267	365.178	313.051	376.987	355.915	297.92	338.944
366.454	468.79	473.385	578.004	635.233	329.728	599.485	382.986	548.95
126.694	135.646	213.693	167.989	253.951	159.011	163.561	146.817	164.699
159.251	171.905	192.455	169.017	208.542	145.769	190.363	219.961	173.745
1204.35	935.461	1686.7	1130.15	1497.4	1201.05	1066.61	1297.87	1414.63
474.864	588.679	773.995	561.612	697.318	551.641	567.624	539.467	480.737
127.837	123.176	150.98	105.473	133.752	103.352	116.872	131.143	119.042

2746.14	2808.49	2580.86	2601.76	2651.84	2825.1	2635.08	2957.29	2933.63
109.093	109.659	90.2008	104.657	101.352	115.703	100.944	96.3162	106.086
132.359	139.422	121.713	112.139	115.216	136.373	121.796	133.68	107.243
89.6184	79.3834	157.956	76.9658	208.88	72.6272	81.2852	112.292	129.902
412.065	306.744	285.059	370.93	341.864	355.501	371.69	403.708	371.337
621.733	661.131	908.341	569.186	871.303	553.639	779.947	682.964	835.081
78.7159	76.3163	50.089	46.6922	38.4423	71.7504	38.5387	42.1982	47.8675
487.682	341.594	1312.84	714.541	1340.68	333.758	805.648	571.375	921.396
266.304	245.18	183.855	244.275	233.658	229.115	246.085	260.244	308.158
857.786	944.661	843.63	1056.37	726.816	731.234	914.459	1085.95	860.098
210.658	178.527	224.752	188.176	197.175	208.157	171.549	200.184	194.739
124.3	147.37	170.53	159.913	149.125	146.566	158.817	146.874	151.814
192.052	223.106	203.896	217.982	183.769	222.858	211.599	186.748	209.832
49.0618	44.1309	49.8841	45.3451	42.993	33.6352	33.7262	43.3622	38.9096
59.01	73.5675	44.4932	45.1856	42.927	51.762	30.4993	34.6755	35.3952
33.5898	21.8629	23.9912	12.663	15.1101	27.083	22.5117	22.7002	16.7129
274.531	326.044	287.127	281.31	283.867	313.682	312.247	343.411	284.467
152.323	137.876	111.368	135.116	127.535	131.689	145.469	140.362	140.894
98.7108	100.112	103.025	98.2089	91.9347	104.461	84.1062	97.8799	106.56
440.716	711.772	357.414	516.092	512.521	494.848	513.875	595.906	530.337
341.108	427.735	369.765	361.401	372.659	372.143	348.176	409.975	340.228
136.483	85.4003	148.895	118.908	118.145	110.813	121.746	119.742	135.187
243.306	242.661	234.904	223.008	208.457	209.518	195.036	224.512	204.153
141.56	186.771	161.104	176.759	166.029	181.742	159.259	169.194	141.652
91.367	122.154	86.6172	98.7143	107.203	91.9466	94.3791	99.2471	109.99
208.979	269.154	268.856	295.017	306.243	233.256	237.542	262.577	244.734
3364.75	2878.92	2621.66	3406.33	3119.05	3187.84	3777.39	3930.89	3447.45
828.251	710.408	636.548	818.91	617.181	766.174	678.278	655.044	803.316
256.637	307.296	264.372	278.647	247.574	314.525	275.271	265.06	270.481
168.729	185.512	199.956	167.371	168.271	172.162	183.764	182.762	156.914
491.108	479.33	504.488	527.055	694.05	477.292	495.446	554.956	627.757
160.636	199.852	244.289	189.982	321.53	196.69	197.028	213.67	182.518
361.109	380.141	349.767	267.23	313.984	275.58	279.35	315.108	286.844
93.3582	138.243	142.28	121.784	113.804	116.743	110.257	120.928	116.798
64.4503	55.3142	38.6521	33.0097	39.2912	45.7435	30.3975	39.9515	39.6943
802.915	777.934	978.588	849.321	1076.88	936.861	618.93	823.809	920.258
282.638	294.334	270.891	261.933	278.954	286.344	215.864	252.717	221.305
121.263	136.188	122.946	134.674	145.907	129.125	136.2	177.768	141.603
245.811	215.357	245.363	201.606	190.026	193.241	194.764	223.286	171.097
119.097	157.29	125.483	139.362	110.698	159.822	128.697	136.834	126.129
217.427	231.071	287.772	240.962	351.791	220.882	258.015	257.353	252.197
453.738	562.079	462.742	438.081	454.937	535.13	505.815	443.926	457.307
110.911	115.647	94.6056	104.364	91.5628	129.698	101.538	79.5223	99.3512
1166.87	1434.56	1486.24	1440.46	1139.15	1389.38	1252.82	1106.47	1209.09
347.473	217.106	392.694	272.984	469.731	210.881	344.241	387.16	409.649
534.475	555.987	483.028	490.241	522.191	442.778	557.294	572.715	548.969
130.807	118.531	156.427	145.863	149.791	132.229	145.066	140.119	155.471
226.104	216.939	192.501	214.8	220.014	223.113	226.03	301.461	216.289
198.702	255.721	210.67	202.226	217.153	201.392	258.804	250.135	219.715
18602.8	18869.1	17882.9	19109.8	19105.6	19533.3	19264.2	19394.7	19429.3
80.7374	125.772	93.5728	116.152	87.2457	119.831	106.787	84.4144	105.562
347.428	368.088	295.678	291.053	313.346	332.676	355.942	411.934	356.022

194.95	183.042	153.091	175.031	161.743	186.547	179.812	125.913	213.414
405.728	289.735	289.358	346.084	379.921	280.384	422.19	482.751	475.248
47.009	38.0318	46.3396	43.2454	44.2481	27.3503	39.304	44.0144	46.2831
234.801	286.061	241.574	246.964	218.563	272.072	253.09	278.718	235.594
67.0183	61.8176	79.1766	70.6135	63.9415	60.342	52.37	60.6957	54.7263
142.276	176.607	215.692	200.44	236.186	198.344	177.377	190.89	173.449
187.711	177.949	214.226	182.275	203.354	169.683	185.595	230.255	200.358
88.5159	104.067	88.251	108.814	91.833	102.522	100.127	85.5962	95.956
121.446	132.692	138.445	139.356	151.273	118.537	134.489	149.407	129.35
77.9304	120.527	120.87	98.9956	91.1719	104.142	82.2772	79.1841	82.932
206.816	167.315	195.385	222.056	183.208	153.889	161.175	215.784	236.317
439.548	417.253	413.96	416.757	522.38	380.211	474.685	515.852	509.198
163.917	152.385	131.533	120.782	169.01	140.644	147.537	150.975	138.95
92.3657	91.5821	90.5742	79.6409	83.8132	68.9886	80.9231	81.7808	73.4665
1332.7	1452.41	929.435	1184.21	1314.22	1301.3	1452.14	1603.64	1354.09
11.182	13.9719	43.5569	14.3737	17.3737	5.957	28.6233	15.2914	24.4532
470.066	378.067	299.749	344.115	350.116	322.82	443.878	425.099	449.07
240.982	339.747	358.534	265.546	308.208	249.95	251.984	393.038	212.989
264.355	285.187	272.8	300.68	274.159	273.539	202.102	217.957	247.095
155.381	133.737	122.789	132.155	128.28	140.722	130.362	127.491	132.843
26.261	40.9776	34.767	30.9176	35.9372	39.9718	45.1681	30.4427	39.4413
1146.68	884.993	839.998	791.017	667.394	846.78	552.01	928.28	980.895
197.314	206.009	184.877	169.389	190.126	173.983	200.464	211.836	184.343
290.281	306.18	300.375	299.413	299.691	306.13	309.979	317.975	292.348
98.6736	94.5751	90.8676	75.9443	77.8851	85.3694	77.7085	91.9026	77.0853
450.492	344.434	273.758	353.06	328.355	409.537	394.417	335.773	363.961
215.3	200.034	185.343	206.191	202.585	173.343	212.189	230.563	184.996
90.993	87.1726	78.8727	84.8184	85.7384	90.6464	97.9655	102.594	93.1209
257.955	170.73	189.489	269.185	317.435	195.126	247.744	307.421	309.12
188.027	247.284	216.845	224.037	212.076	246.47	212.248	216.478	215.683
46.2572	65.4156	83.6608	65.393	63.3414	67.3697	56.4243	68.1799	51.8614
181.054	146.627	170.556	149.463	208.157	137.823	179.485	184.648	195.675
311.927	311.559	343.804	326.676	313.642	337.09	343.916	318.06	322.801
158.647	184.84	197.75	172.865	185.734	177.32	193.203	173.67	183.611
86.8117	117.535	94.2225	96.2877	106.382	106.472	122.144	112.178	119.396
774.213	1108.5	1231.08	1026.79	1012.19	995.471	922.184	946.586	890.208
31.1412	55.2392	53.3503	54.5579	35.7629	49.0451	45.7065	36.8211	45.9954
25.6392	19.0546	26.8457	28.68	23.9201	18.5144	19.3993	16.0569	20.2827
127.864	131.041	136.591	124.889	112.006	116.414	112.822	144.145	112.239
213.286	217.529	311.395	238.593	246.232	266.728	214.884	247.295	239.774
259.706	270.525	271.444	259.105	275.646	238.053	287.427	304.91	250.914
87.9601	153.543	155.363	116.798	102.893	139.712	90.759	111.039	110.004
74.736	101.069	104.663	88.8121	82.6271	76.7114	98.2818	120.402	75.0303
138.442	136.948	130.172	132.872	124.619	138.379	127.13	120.025	127.058
121.157	131.823	122.713	146.135	130.672	126.856	140.696	143.019	121.287
187.985	221.781	202.954	188.881	221.441	253.802	206.349	197.852	200.784
612.42	997.975	1217.51	1063.29	894.527	1040.95	735.306	797.505	802.565
628.295	697.979	605.911	636.118	697.139	634.7	646.681	657.648	675.762
166.293	188.564	179.459	177.727	162.963	177.122	178.658	191.586	159.857
237.768	252.845	285.981	264.355	206.204	295.217	183.839	221.666	235.655
1251.72	1297.87	1511.5	1271.71	1171.25	1543.6	1052.87	1050.09	1288.25
370.659	421.805	413.533	373.651	361.386	449.8	365.504	323.902	375.202

145.707	208.5	172.747	157.467	146.537	167.84	142.086	180.494	157.762
44.9521	101.106	78.3365	71.9266	57.6077	83.0772	46.7789	56.8769	63.5322
221.007	268.28	357.108	227.358	257.327	220.927	205.265	229.244	246.844
97.8386	97.9816	95.2522	101.549	81.4133	82.8299	86.6825	99.0529	85.0261
808.616	1053.58	703.857	788.028	762.182	846.797	908.863	1046.88	879.874
195.882	203.59	205.115	182.642	212.438	175.082	202.293	251.241	196.446
89.1614	84.0779	126.93	104.069	88.6124	85.7594	66.8942	84.8505	77.3601
551.784	470.025	513.2	440.861	677.738	450.156	523.969	587.918	655.831
231.884	267.416	224.976	249.539	221.443	299.872	229.661	218.369	244.417
47.6426	58.1683	61.327	52.2565	49.5292	64.1491	50.6069	59.6731	55.1269
315.234	340.525	327.949	276.536	260.899	258.371	230.709	261.075	298.92
8.77838	4.97458	8.49349	3.80783	5.14163	3.31693	10.8612	8.27071	3.74016
100.521	95.8407	75.2496	69.8689	84.6374	72.9962	75.0091	107.632	90.859
109.545	142.884	196.801	146.551	110.683	129.781	98.6962	100.771	107.747
64.2063	93.4883	81.9557	81.9877	74.3296	77.0585	79.8322	71.6478	80.4074
765.342	752.659	672.978	752.574	903.193	763.07	811.068	806.606	795.295
755.344	962.298	605.513	688.93	584.906	739.005	779.415	894.708	765.58
236.753	284.012	247.815	262.794	236.984	280.346	240.055	238.907	239.337
72.9044	95.6556	94.984	89.0231	105.042	99.1824	85.8164	83.4668	91.6313
61.6409	52.4836	50.155	56.3648	47.4637	54.046	49.8526	57.1347	53.4765
599.35	565.355	529.263	551.487	472.493	510.902	465.761	435.698	633.619
447.928	662.179	382.434	432.168	445.115	628.398	417.056	484.439	472.545
394.031	458.369	409.205	468.138	430.019	437.843	463.1	442.19	389.859
41.8289	78.7639	70.2657	68.7674	48.3632	66.9082	50.192	58.5515	51.5339
323.019	325.223	307.291	340.452	367.756	308.27	353.26	335.677	334.038
14.7373	31.5304	25.6799	23.2557	19.34	24.7288	15.4603	21.3826	21.6218
253.407	287.785	250.798	235.42	213.084	225.255	228.17	284.478	236.07
699.45	720.673	501.915	466.443	293.498	952.248	757.146	435.671	549.666
68.6515	83.625	78.0318	87.8769	91.1228	83.7326	94.3308	67.0204	93.3118
365.974	322.703	310.588	315.533	354.122	330.98	399.237	404.082	357.582
1694.39	1531.52	2338.98	1536.95	3032.93	2169.71	2253.91	2417.84	2507.26
328.606	317.406	301.44	367.91	356.102	344.915	337.527	360.838	327.86
265.213	274.116	262.274	267.365	228.382	238.127	284.429	316.013	266.362
112.929	106.896	120.125	113.462	145.923	99.7146	107.261	109.874	117.966
322.552	262.322	420.076	283.77	289.337	279.038	303.659	295.232	342.526
20378.3	20830.8	19934.1	21072.2	20629.6	21207.4	20930.8	20967.5	21135.5
188.495	216.793	242.755	211.639	204.593	216.563	205.151	199.375	198.546
97.5537	119.862	145.198	122.017	119	144.212	117.84	102.961	114.584
306.598	416.534	276.562	327.705	326.868	351.833	312.124	328.587	297.656
2115.57	1929.31	3125.46	1947.32	6470.18	1454.73	2740.05	2831.01	3876.72
268.566	286.88	253.687	250.917	343.333	279.449	327.243	337.828	270.636
59.4582	76.9776	47.4522	42.8234	41.093	60.1301	22.785	42.5665	44.7146
49.1881	55.808	54.0137	60.585	55.0522	49.3809	66.0012	54.5627	44.3188
294.139	341.011	265.909	280.267	262.607	288.99	280.008	318.567	267.841
52.1915	51.4617	38.6113	47.6485	50.8749	45.7568	51.3296	45.6803	52.0168
193.856	241.515	254.26	182.716	183.474	208.28	178.784	183.875	186.421
946.162	769.716	838.431	982.289	1036.72	988.107	774.686	800.445	969.372
164.228	162.539	170.82	150.988	156.06	134.925	169.637	192.893	147.97
99.1064	108.904	118	99.2417	107.505	98.5341	108.714	107.906	96.1002
153.598	234.281	198.84	164.574	181.855	181.79	155.792	189.122	159.328
205.863	205.4	193.814	213.191	221.422	212.483	239.251	232.163	195.363
132.07	170.576	144.6	163.637	153.226	146.33	159.209	181.503	147.074

220.484	221.388	232.844	260.695	248.969	200.931	263.653	323.205	226.869
645.995	841.149	495.41	639.617	691.07	662.976	687.588	824.956	680.4
7177.28	6964.77	8703.16	7394.38	7846.1	7568.42	6798.83	6679.02	7310.56
145.57	140.927	143.014	168.482	148.752	115.851	188.913	195.107	155.103
31.9906	38.7804	40.0502	40.4311	47.8986	48.6017	38.0827	38.7761	34.5163
123.37	88.7119	88.9396	97.765	96.7281	99.4925	123.571	109.947	108.97
165.52	158.277	159.871	155.516	156.724	173.679	165.161	188.024	178.629
506.551	511.902	448.51	691.132	972.456	568.746	517.968	523.059	573.693
319.888	287.706	279.022	291.092	344.478	301.633	354.326	327.844	368.369
378.618	334.505	352.357	296.078	329.642	329.054	317.141	374.811	371.831
117.663	166.824	125.155	152.962	127.74	156.292	121.263	124.853	122.164
201.212	195.888	183.93	162.328	161.894	175.792	166.257	192.428	178.524
871.451	548.308	2316.21	903.588	2033.02	652.517	1058.76	980.838	1458.44
142.806	126.992	134.681	126.314	135.402	126.207	110.549	108.578	139.59
718.509	738.325	684.887	656.615	695.05	623.375	772.378	892.219	690.566
571.302	598.084	586.621	533.559	565.137	554.924	552.617	584.413	570.446
163.105	143.638	143.531	141.979	128.08	154.492	136.65	151.218	138.634
63.0357	49.1019	90.7681	48.2883	97.7967	63.7352	51.8143	47.0265	69.2485
161.509	188.176	216.633	149.294	200.472	152.4	166.496	198.127	156.513
131.817	146.04	143.677	155.242	155.306	130.756	147.888	179.111	140.861
1505.07	1252.07	1200.96	1418.46	1612.12	1233.12	1591.72	2268.14	1760.78
534.499	619.434	659.527	550.469	637.345	551.48	560.67	705.127	610.048
292.925	286.765	283.245	293.353	276.814	278.503	283.643	314.923	268.014
178.973	201.752	228.023	214.306	196.399	180.784	201.675	234.849	182.559
237.907	252.523	263.333	209.572	332.983	219.851	209.771	266.147	236.872
407.628	394.893	363.774	558.158	682.52	1196.49	413.675	477.689	445.579
669.905	637.822	705.443	769.172	476.519	605.758	542.339	646.416	578.432
409.97	381.17	368.028	395.099	440.074	354.243	440.532	508.574	455.105
170.383	158.059	209.617	178.672	180.186	169.027	153.193	179.815	185.899
283.206	261.383	269.794	280.38	335.309	231.999	341.655	347.409	319.002
48.2144	64.9731	61.1514	58.7491	54.7994	74.7345	53.8542	52.8562	63.8874
208.477	208.116	197.566	205.526	270.079	208.591	221.411	238.283	260.426
203.561	278.022	205.396	213.358	193.796	282.43	233.019	229.848	211.173
587.805	614.774	516.086	582.796	628.607	519.861	616.141	715.486	595.456
835.008	743.748	903.585	979.041	781.936	980.199	779.695	870.112	865.34
60.4095	127.734	99.4003	86.1082	60.3814	70.3837	58.1462	115.09	41.5947
3210.05	3068.34	2971.82	3478.58	2588.04	3185.27	2942.09	3406.91	3190.26
720.227	803.738	742.067	690.535	787.3	684.073	765.614	802.218	734.245
45.869	44.8771	54.6118	44.1728	37.5932	49.5364	36.7742	47.4431	35.0031
123.231	194.247	172.404	155.983	145.874	152.993	158.489	180.487	144.981
139.255	135.049	175.888	142.235	181.159	113.948	193.165	181.223	161.175
574.858	571.147	889.446	747.932	681.007	557.398	484.384	501.872	648.021
207.782	178.803	301.033	215.598	194.548	205.06	178.075	180.28	217.459
305.497	330.779	308.576	271.543	330.951	277.849	310.709	367.263	309.286
305.132	327.968	301.19	282.727	246.388	346.148	299.246	316.037	296.22
206.591	282.838	258.904	248.708	221.013	258.872	246.625	219.828	249.55
164.634	179.412	176.261	165.746	225.838	159.049	187.694	214.17	208.971
464.73	731.133	759.161	606.455	980.433	842.242	737.857	813.157	884.795
92.84	159.093	138.007	136.379	105.172	140.523	100.311	110.103	116.322
68.0649	88.4448	73.2837	70.1223	65.7507	92.9754	74.393	71.0073	68.459
2662.53	1434.16	2896.31	2263.89	3820.43	1830.48	2333.45	2751.71	3509.51
295.941	281.967	296.991	295.433	324.497	278.294	292.402	325.599	285.936

193.43	153.119	357.65	206.556	411.468	170.205	210.433	195.818	301.164
62.382	82.9869	75.1003	67.8724	64.0266	72.26	62.078	66.5511	72.28
100.332	151.744	161.621	157.285	137.03	131.031	143.335	150.47	110.564
45.3634	33.7761	31.0501	35.776	42.569	39.0231	42.7537	27.5718	32.0323
454.849	531.409	517.087	646.042	296.406	525.683	484.512	407.443	558.072
127.647	138.42	134.092	152.207	119.203	157.496	140.923	129.771	134.412
309.77	352.06	375.524	341.312	358.544	329.953	202.335	284.66	289.034
1405.97	1627.05	1544.65	1390.36	1089.02	1368.78	1131.71	904.9	1506.41
412.153	510.913	490.725	491.102	388.621	515.037	391.831	423.825	360.535
349.663	275.204	382.078	335.142	293.543	343.141	280.37	347.909	387.11
308.769	287.903	313.797	351.533	282.879	247.99	303.762	222.519	363.668
241.543	284.18	250.36	230.341	233	234.862	244.127	269.568	215.705
109.579	111.126	133.133	77.0356	64.3211	92.1039	64.7199	89.0972	75.3776
260.343	200.227	196.37	191.395	197.677	184.034	214.145	216.802	179.371
115.621	81.1848	136.877	89.7891	109.344	75.6188	109.156	112.282	137.548
228.716	235.311	189.922	162.194	165.312	193.769	182.673	204.566	193.825
125.776	112.377	108.138	103.257	100.778	105.473	106.442	117.143	115.645
175.237	272.97	189.171	217.155	191.017	258.481	190.137	189.536	189.371
404.272	333.363	393.818	380.306	269.072	436.607	367.409	340.809	394.513
442.108	432.05	446.937	426.694	514.268	440.09	506.998	489.524	468.393
430.259	408.592	391.015	373.328	511.281	370.223	481.822	513.641	508.34
403.181	389.249	371.805	383.05	392.819	349.389	413.833	489.678	374.259
199.438	213.656	286.363	212.372	214.902	214.032	205.501	211.659	225.787
322.159	349.755	292.087	299.512	378.626	300.667	346.223	364.371	354.616
96.0475	166.355	80.2113	133.815	74.532	95.0519	99.929	136.949	86.2988
189.341	223.508	211.03	188.121	213.827	180.375	219.209	285.405	196.602
299.137	254.89	448.277	297.634	693.099	268.566	346.442	396.085	464.825
325.288	339.149	334.136	326.457	351.821	324.817	343.797	361.79	327.133
1008.3	1203.42	1250.37	970.475	908.995	1019.88	1164.77	1152.88	933.683
147.709	171.11	163.48	155.724	146.501	166.839	137.8	141.061	131.558
176.051	107.85	239.984	176.082	181.748	155.71	116.808	152.766	181.411
102.106	57.2666	74.1856	83.5218	58.3706	80.5232	77.3124	79.1228	133.346
57.3647	60.6246	67.9339	62.5854	64.7959	67.4567	82.1824	80.9888	60.1954
81.5943	104.1	93.471	106.522	90.8327	96.6997	105.933	82.2892	109.142
299.751	310.356	410.902	242.142	250.443	188.362	270.172	281.364	288.675
110.73	197.821	205.459	177.317	165.291	191.769	170.133	167.765	141.679
225.856	357.603	412.077	286.947	230.683	336.029	282.057	244.965	289.34
156.56	35.6129	50.1938	35.9744	47.5752	39.4867	137.703	79.7948	118.387
2557.04	1386.86	1312.64	1867.35	2209.22	1524.18	2218.6	2819.95	2789.21
94.8774	97.9556	111.188	98.5267	83.1692	80.228	157.486	135.739	104.043
53.237	54.3731	61.5887	41.7896	46.0625	57.2698	46.0914	50.3122	44.3814
120.741	129.023	124.431	130.679	123.518	118.059	125.199	144.185	135.039
88.6827	92.0283	104.628	109.177	91.6346	119.296	79.2616	73.3448	88.7338
426.375	411.762	345.696	414.431	435.263	338.259	489.922	496.404	428.877
20.0587	23.7072	21.7627	18.3378	22.9265	24.414	18.8709	22.2133	15.7997
557.752	616.393	614.555	593.914	708.667	630.446	561.005	544.585	647.667
131.186	115.117	148.159	164.318	181.801	133.066	132.546	135.952	176.774
148.853	124.676	230.065	129.416	149.645	147.496	150.174	141.695	160.449
1501.77	1709.46	1669.13	1576.53	1577.82	1551.5	1580.13	1787.96	1668.52
12.6064	10.2745	19.7083	21.7894	14.3774	19.6529	13.5508	20.3858	20.816
4141.97	3778.77	3440.28	3681.76	4621.96	3369.77	4237.22	4466.72	4226.05
171.477	239.645	210.056	205.543	183.075	166.62	195.809	202.934	194.077

264.189	284.462	261.444	301.168	343.316	248.471	256.945	352.347	277.207
72.5752	60.4692	70.0929	57.5553	56.0553	63.1233	65.5686	56.7944	60.223
96.2886	148.37	126.646	130.083	171.959	105.8	101.895	130.473	107.039
76.8112	102.145	72.7103	72.9286	80.4258	73.4818	88.0125	114.186	72.3563
533.261	401.339	697.371	608.412	981.227	500.689	621.101	542.746	703.1
494.752	541.134	461.491	451.279	463.31	506.084	532.184	506.227	439.623
229.017	217.916	210.542	227.021	207.143	230.303	219.33	211.137	210.114
382.081	384.666	429.873	376.494	380.984	373.975	350.806	328.044	432.094
410.735	245.678	296.495	313.091	272.062	222.563	365.653	280.53	340.416
80.1169	72.2293	69.5367	65.499	63.4436	64.252	70.4408	72.915	53.2243
471.54	506.793	1091.05	1147.48	1218.59	631.35	572.204	845.36	908.419
448.243	265.911	383.798	331.281	384.009	304.145	309.81	298.112	427.942
181.04	174.204	224.509	203.454	227.926	164.628	179.428	191.716	219.099
98.07	79.3689	78.1131	81.1189	64.2869	64.1559	59.4345	74.7898	68.3535
144.153	156.424	154.499	158.476	156.003	150.79	142.701	134.901	134.401
62.4601	95.8188	66.4314	98.7331	63.8516	74.7685	74.7501	69.8278	59.8999
366.415	413.551	349.563	359.278	418.158	328.257	339.179	386.536	419.913
1551.08	1576.24	1464.5	1481.48	1116.44	1603.59	1337.84	1155.02	1526.46
92.2221	84.9242	84.5915	91.5851	88.7975	91.2092	93.8277	77.9553	84.0362
82.1924	61.1461	91.2844	38.7815	106.609	74.4158	82.494	81.0297	76.9486
85.4754	98.5565	104.921	95.391	99.8186	83.0552	102.721	85.7326	83.0518
723.332	683.221	636.365	618.367	781.813	710.756	755.386	728.103	802.398
221.576	269.761	230.162	216.384	222.92	297.409	226.779	216.597	235.923
2165.82	2494.14	1943.18	2098.42	2369.69	2326.5	2380.49	2639.04	2386.27
220.255	249.257	253.622	235.362	254.288	218.733	241.765	272.977	206.511
225.771	201.759	198.538	217.767	222.425	211.786	244.606	253.454	232.847
90.2598	71.6991	80.3958	79.0029	68.3244	79.3575	76.2152	72.0012	73.1527
79.9056	84.7096	86.5017	89.1656	73.0085	75.8405	96.0458	96.4638	90.8795
83.2467	84.7604	111.422	81.9323	94.9809	94.2853	100.59	120.566	87.9913
35.2901	38.3363	38.6709	46.9049	43.8254	43.9104	38.3495	42.6951	36.1823
130.77	121.225	97.6952	114.428	130.043	116.057	149.533	139.334	146.084
60.1012	42.4201	40.7147	32.732	34.0217	50.3363	35.1759	43.533	46.3321
80.6656	90.6588	91.7551	84.5758	100.539	66.2479	89.0085	72.6308	80.6538
270.971	310.944	257.689	258.451	278.75	282.305	281.844	291.993	263.127
521.677	430.435	370.122	399.913	378.63	334.578	457.12	408.805	450.642
211.066	240.619	216.842	237.282	256.048	214.659	234.987	250.066	210.374
125.395	156.145	161.157	129.091	146.19	145.875	89.9234	103.337	114.947
398.279	398.296	452.353	581.907	490.391	431.205	402.631	474.114	449.132
330.072	342.771	381.751	298.801	423.372	301.338	360.348	371.178	368.132
62.9404	66.4221	126.919	74.6648	81.1449	72.7446	78.4516	76.8772	89.7411
4927.79	5120.72	4820.07	5518.58	5621.21	5141.92	4937.65	5589	5443.55
130.011	110.426	122.971	122.228	157.636	122.038	113.825	154.555	122.342
3897.83	5228.54	5019.22	4351.37	4096.63	4476.2	4586.19	4187.7	4466.94
337.402	261.882	501.962	396.026	299.477	291.637	381.362	402.924	424.434
445.402	463.628	411.977	454.298	518.314	447.84	462.49	454.487	497.517
45.4351	57.5742	58.0379	48.9262	52.3863	48.7571	51.8792	61.9891	53.6504
37.6473	57.5303	48.12	47.2765	41.2748	46.4278	48.0595	41.2744	51.5374
168.854	189.597	203.375	193.034	184.386	205.977	185.722	172.146	177.547
650.361	596.344	532.944	585.541	738.419	515.511	680.346	711.402	728.95
51.5079	50.5026	49.2288	43.7175	52.5583	58.3161	49.6255	45.5893	42.6317
55.6499	88.0603	89.586	82.2758	75.4712	70.3703	80.0126	82.1721	57.3187
115.824	123.483	117.198	107.984	109.343	121.476	117.232	99.323	106.61

86.3623	93.4187	88.6352	73.6945	92.8167	89.3434	96.6708	132.52	77.3081
369.785	348.541	370.411	362.526	362.698	357.281	400.821	378.8	407.535
143.116	70.7913	166.755	100.906	193.678	89.2171	126.885	118.858	160.957
386.705	439.546	302.192	368.78	346.104	348.041	428.814	479.34	383.977
146.312	169.181	179.199	170.699	161.751	173.681	170.703	153.444	162.003
561.546	473.029	432.444	566.646	511.077	406.399	625.672	742.393	611.316
292.748	316.946	288.289	268.599	324.492	262.584	292.672	304.203	308.734
438.67	584.961	499.687	502.32	483.43	439.91	525.397	518.206	477.732
8901.32	8448.17	9285.43	8973.4	9464.23	8443.73	7883.51	8087.61	8899.46
2332.77	1264.42	1172.66	1690.02	1883.47	1349.89	1942.6	2467.38	2332.33
261.486	280.587	249.343	233.381	251.714	224.756	208.066	234.045	191.787
349.099	356.295	387.655	401.686	404.133	358.677	331.029	332.525	410.077
188.079	237.168	233.839	209.937	265.945	212.561	169.202	178.663	206.883
3063.36	3881.29	3285.65	2917.83	4500.45	3543.1	3008.89	4058.36	3578.58
117.434	141.701	163.742	143.491	120.962	109.21	97.6385	119.621	117.026
7.35219	9.16765	5.99777	7.29801	6.61246	7.5862	4.92676	3.68404	2.87522
537.457	758.388	617.932	608.095	734.598	612.464	441.715	492.214	586.291

D9	Average-T	Average-D	T-test	Deprived/T	Probe_set	Gene_Sym	AC_numbe	gene_full_r
66.0487	70.70584	59.86077	2.87E-05	0.846617	214046_at	---	AA017721	MRNA; cDI
134.92	137.1956	164.5092	3.85E-05	1.199086	240081_at	MYO5C	AA004803	Myosin VC
125.371	130.6788	146.3778	4.16E-05	1.120134	227644_at	RIMS4	AL049000	regulating s
14.8327	17.3197	12.96671	4.88E-05	0.748668	233926_at	---	AF131853	Clone 2501
135.84	121.8061	136.506	6.12E-05	1.120683	203900_at	KIAA0467	NM_02454	KIAA0467
100.495	104.7189	95.04171	7.98E-05	0.907589	240005_at	---	AI146467	Transcriber
135.582	197.2001	174.7102	0.000133	0.885954	219674_s	PRO2900	NM_01863	hypothetica
185.526	188.798	205.3999	0.000135	1.087935	208163_s	OSBPL7	NM_01773	oxysterol bi
119.374	104.4165	120.4186	0.000158	1.153252	223999_at	PPIL2	AF320072	Peptidylpro
178.95	151.1938	179.2646	0.000169	1.185661	226729_at	USP37	BF789968	ubiquitin sp
191.225	180.0666	199.0147	0.000214	1.105228	237355_at	---	AW448981	Transcriber
181.254	209.6977	182.6983	0.000222	0.871246	203176_s	TFAM	BE552470	transcriptio
213.199	180.2064	198.6861	0.000302	1.102547	213678_at	C6orf137	F09448	chromosom
159.031	179.5281	202.7046	0.000316	1.129096	211592_s	CACNA1C	L29536	calcium cha
380.017	348.2643	377.2263	0.000343	1.083161	202400_s	SRF	AI188786	serum resp
103.383	103.8796	111.245	0.000386	1.070903	216557_x	IGHA1 /// I	U92706	immunoglo
774.795	702.1269	781.3221	0.000485	1.112793	1554470_s	BTBD15	BC030580	BTB (POZ)
87.8858	79.14898	85.9899	0.000495	1.086431	238797_at	TRIM11	BF059582	tripartite mc
113.035	113.7816	132.241	0.0005	1.162236	243473_at	KIAA0999	BF111990	KIAA0999 p
119.997	140.2626	116.451	0.000523	0.830236	1555048_a	C21orf29	BC021197	chromosom
1139.95	1123.16	1042.004	0.000534	0.927743	233268_s	CHURC1	AF113700	churchill do
24.2338	34.03437	25.41448	0.000576	0.74673	1554235_a	CTNNA3	BC022004	catenin (ca
668.947	632.8909	690.0753	0.000609	1.090354	202857_at	TMEM4	NM_01425	transmemb
372.86	348.3172	321.8014	0.000628	0.923875	1565849_a	C19orf37	BG720339	Chromosom
244.389	210.1117	235.4996	0.000685	1.12083	223264_at	MESDC1	BC001373	mesoderm
154.25	141.476	150.5306	0.000704	1.064001	233371_at	ABCC13	AP001660	ATP-bindin
431.794	390.8718	454.1303	0.000732	1.16184	202100_at	RALB	BG169673	v-ral simian
219.636	217.5487	239.4881	0.000744	1.100848	236867_at	TRPV1	AW119132	Transient re
66.7946	72.28197	62.18408	0.000826	0.860299	240275_at	ARMC3	AI936559	armadillo re
342.004	341.0144	373.8331	0.000863	1.096238	230334_at	---	AA398901	---
101.091	98.58112	116.7499	0.000883	1.184303	211905_s	ITGB4	AF011375	integrin, be
422.394	391.0328	430.2191	0.000914	1.100212	213050_at	COBL	AA594937	cordon-ble
217.898	190.5729	207.3027	0.000977	1.087787	228109_at	RASGRF2	AI912976	Ras protein
200.471	199.2796	215.5777	0.000978	1.081785	212360_at	AMPD2	AI916249	adenosine
69.7093	69.15041	81.92254	0.000983	1.184701	215118_s	IGHG1	AW519168	Immunoglo
190.792	224.1061	203.5867	0.001018	0.908439	226278_at	DKFZp313	AI150224	hypothetica
174.463	181.2409	208.5259	0.001044	1.150545	227485_at	DDX26B	AI828015	DEAD/H (A
253.813	240.221	257.8162	0.001137	1.073246	235222_x	BIRC4	AW675725	baculoviral
123.89	120.6788	130.6504	0.001144	1.08263	213747_at	---	AA047234	---
368.783	350.1092	373.8122	0.001153	1.067702	217555_at	SMC1L1	AI042030	SMC1 struc
24.6682	27.58924	22.57342	0.001195	0.818196	1564160_a	FLJ16686	AK094684	FLJ16686 p
1458.14	1345.376	1584.209	0.00124	1.177522	200974_at	ACTA2	NM_00161	actin, alpha
345.705	395.5836	342.7803	0.001285	0.866518	212492_s	JMJD2B	AW237172	jumonji don
42.4385	46.40379	54.08422	0.001287	1.165513	1566163_a	MEIS2	AL832482	Meis1, mye
95.9512	93.53901	79.76081	0.001309	0.852701	1558722_a	ZNF252	BC019922	zinc finger j
135.904	133.3874	150.105	0.001337	1.125331	217160_at	TSPY1	M94893	testis speci
99.8689	97.54803	91.07161	0.001353	0.933608	229193_at	CROP	AA005430	Cisplatin re
68.7528	57.87527	48.70572	0.001411	0.841564	229765_at	ZNF207	AW511239	Zinc finger
272.013	281.3783	321.6704	0.001441	1.143195	239897_at	BCLAF1	AW152620	BCL2-asso
66.442	70.34977	80.53774	0.001455	1.144819	1569341_a	POLH	BM468397	Polymerase

180.047	183.487	215.8316	0.001473	1.176277	228042_at	ADPRH	N54957	ADP-ribosy
97.3578	102.1673	91.99781	0.001485	0.900462	227606_s	STAMBPL	AI638611	STAM bind
117.34	111.7914	125.2094	0.001488	1.120027	228340_at	TLE3	BE967118	transducin-
416.454	412.6711	436.4491	0.00149	1.05762	224800_at	WDFY1	AK022888	WD repeat
95.8023	96.43152	114.4326	0.001504	1.186672	204260_at	CHGB	NM_00181	chromograi
132.357	136.4589	147.9323	0.001512	1.08408	222046_at	ARS2	AI523895	ARS2 prote
4255.54	3784.764	4756.636	0.001531	1.256785	213867_x	ACTB	AA809056	actin, beta
221.127	230.0948	265.4653	0.00154	1.153722	227738_s	ARMC5	BG151528	armadillo re
50.0993	37.46749	44.1715	0.00157	1.178929	204728_s	WDHD1	NM_00708	WD repeat
279.177	267.7942	292.627	0.001584	1.092731	213252_at	SH3PXD2/	AI739005	SH3 and P
16.7284	41.01901	26.47249	0.001668	0.645371	1559534_a	---	BC040901	Homo sapi
50.9855	54.08382	58.7318	0.001689	1.08594	208443_x	SHOX2	NM_00688	short statur
121.701	117.1092	102.0091	0.001712	0.87106	236996_at	---	AA724992	---
327.601	306.0476	325.1522	0.001734	1.062424	205956_x	PSMC3IP	NM_01329	PSMC3 inte
101.254	113.6787	132.5659	0.001816	1.166146	1559936_a	CCNF	BF343599	Cyclin F
183.052	163.9829	179.4042	0.001818	1.094042	237941_at	RPL22	AV720804	Ribosomal
987.71	879.4644	981.6613	0.00183	1.116204	35671_at	GTF3C1	U02619	general tra
196.749	183.228	209.6998	0.001847	1.144475	230823_at	---	AA401247	---
4354.35	3783.781	4821.062	0.001861	1.274139	200801_x	ACTB	NM_00110	actin, beta
344.693	333.614	372.1563	0.00187	1.11553	227581_at	DKFZP434	BE616972	DKFZP434
26.4448	23.39999	28.26738	0.001882	1.208008	1557239_a	BBX	BU689085	Bobby sox
91.5267	82.89452	91.09786	0.001899	1.098961	214858_at	GPC1	AF070536	Glypican 1
128.478	149.0218	129.9743	0.001912	0.872183	1558747_a	SMCHD1	AA336502	structural r
53.2236	54.17389	45.32832	0.001927	0.836719	214409_at	RFPL3S	AL021937	ret finger p
91.495	83.56743	98.26481	0.001938	1.175874	230076_at	---	BF063164	---
50.6272	44.61238	38.23729	0.001961	0.8571	233289_at	C1orf26	AU155234	Chromosor
409.533	331.8593	387.8103	0.001998	1.168599	213746_s	FLNA	AW051856	filamin A, a
380.105	383.5867	431.7977	0.002033	1.125685	239898_x	ZNF286 ///	AI498484	zinc finger j
103.327	109.6154	121.4541	0.002089	1.108002	227481_at	CNKSR3	BG165333	CNKSR far
143.29	172.8763	156.5526	0.002114	0.905575	217464_at	RPS2	L48784	ribosomal p
173.77	161.7863	182.976	0.002122	1.130973	215505_s	STRN3	AF243424	striatin, cal
202.338	220.9754	194.0342	0.002161	0.87808	212871_at	MAPKAPK	NM_00366	mitogen-ac
96.1719	106.6185	117.9268	0.002166	1.106062	231008_at	UNC5CL	AI733001	Unc-5 hom
162.309	162.8327	174.2556	0.002167	1.070151	217182_at	MUC5AC	Z34282	mucin 5AC
426.097	460.0011	502.866	0.002187	1.093184	1554577_a	PSMD10	AY057056	proteasome
145.921	163.2318	146.5933	0.002206	0.898069	237889_s	LOC55313	AV649033	Hypothetic
324.342	287.5611	306.3722	0.002224	1.065416	1570128_a	DDX19A	BC025771	DEAD (Asp
24.673	21.71371	28.22409	0.002261	1.299828	1557472_a	FLJ30838	AK055400	hypothetica
140.526	148.9813	125.0081	0.002286	0.839086	215418_at	PARVA	AK022316	parvin, alph
480.429	431.3429	508.1183	0.002349	1.177992	223001_at	DC2	AF201937	DC2 proteir
277.099	269.9724	245.997	0.002366	0.911193	217150_s	NF2	S73854	neurofibron
150.754	133.5573	154.2412	0.002369	1.154869	223159_s	NEK6	BC000101	NIMA (neve
71.6336	81.81673	70.91162	0.002377	0.866713	1558748_a	NAPE-PLD	AL832759	N-acyl-pho
50.4164	48.0883	60.86678	0.002383	1.265729	235204_at	COX15	BF878343	COX15 hor
79.3423	84.82872	95.10506	0.002451	1.121142	239402_at	---	AW117206	Transcribec
94.5444	99.65404	85.53257	0.002477	0.858295	241806_at	FLJ10292	AA701443	Mago-nash
4275.79	3765.753	4699.951	0.002517	1.248077	224594_x	ACTB	AK025873	actin, beta
472.05	427.5169	480.8736	0.002549	1.124806	242129_at	---	BF510861	---
131.294	128.7162	149.4247	0.002553	1.160884	1567334_a	---	AJ431618	MRNA adja
477.43	430.8654	520.9758	0.002554	1.209138	201772_at	AZIN1	NM_01587	antizyme in
199.939	200.3013	222.1376	0.002559	1.109017	203610_s	TRIM38	AI363270	tripartite mc
143.375	150.2647	175.4804	0.002579	1.167809	243030_at	MAP3K1	AA211369	Mitogen-ac

149.82	147.918	159.7846	0.00261	1.080224	214644_at HIST1H2A	BF061074 histone 1, H
193.509	198.4586	217.6337	0.002612	1.09662	209196_at WDR46	BC000388 WD repeat
1073.16	915.8282	1088.516	0.002652	1.188559	201021_s_ DSTN	BF697964 destrin (act
20.4362	30.04102	38.54656	0.002683	1.283131	241765_at CPM	AI469884 carboxypep
236.887	244.5527	283.477	0.002698	1.159165	204140_at TPST1	NM_00359 tyrosylprote
71.1946	65.09992	78.94161	0.002726	1.212622	204530_s_ TOX	NM_01472 thymus high
85.6049	92.06068	103.2277	0.00274	1.121301	1563978_a LOC33945	AK094642 Hypothetica
130.758	129.7661	149.1181	0.002754	1.14913	238925_at ---	AW958415 CDNA clon
49.1914	43.58357	52.50466	0.002773	1.204689	239971_at C16orf45	AI298297 Chromosom
119.927	124.6931	138.9449	0.002774	1.114295	220544_at TSKS	NM_02173 testis-speci
88.7082	73.08403	80.4362	0.002808	1.100599	1562747_a ---	BC041469 Homo sapi
260.024	279.6452	344.9712	0.002809	1.233603	201261_x_ BGN	BC002416 biglycan
169.235	188.0786	211.093	0.002824	1.122366	236243_at ZCCHC6	AW070776 Zinc finger,
73.9607	73.5883	81.90206	0.002825	1.112977	1555636_a CD300LG	AF427619 CD300 mol
33.5468	47.17467	36.53816	0.002853	0.774529	242347_at TMEM4	AI821954 Transmembr
39.3393	38.66868	32.3859	0.00287	0.837523	233295_at LOC64535	AF253316 Similar to n
104.811	118.2575	141.7139	0.002963	1.19835	1560285_a ---	BC038556 Homo sapi
89.23	83.87661	99.56584	0.002971	1.187051	230838_s_ ---	AW771492 ---
428.397	436.953	458.7901	0.002976	1.049976	203005_at LTBR	NM_00234 lymphotoxin
990.019	927.2893	1047.71	0.00298	1.129863	208847_s_ ADH5	M29872 alcohol dehyd
225.96	218.4149	202.0838	0.003	0.925229	235701_at R3HDM2	AW592510 R3H domain
69.4177	71.79544	65.37197	0.003048	0.910531	230876_at LOC16983	AI827906 hypothetica
302.193	347.8273	286.9243	0.003055	0.824905	204264_at CPT2	NM_00009 carnitine pa
151.438	151.6766	159.7724	0.003059	1.053376	215104_at NRIP2	AL136557 nuclear rec
62.6213	63.1034	70.89958	0.003094	1.123546	229201_at ---	AW044658 Full-length
217.124	190.0858	204.4922	0.003108	1.075789	210802_s_ HSA9761	BC002841 dimethylad
94.4477	105.8091	116.9189	0.003119	1.104998	1562368_a CARD11	AL833692 Caspase re
101.232	118.3379	140.098	0.003164	1.183881	238568_s_ C18orf8	BE742377 Chromosom
81.0614	79.51896	84.86967	0.003164	1.067288	236823_at ---	BF055317 ---
230.176	213.9874	261.3173	0.003178	1.221181	1566767_a ---	BC043172 ---
221.034	197.7331	216.6786	0.003221	1.095813	204096_s_ ELL	AL136771 elongation f
91.0884	101.6153	86.03794	0.003226	0.846703	206819_at DKFZP434	NM_01454 POM121-like
85.1172	89.21586	98.1082	0.00327	1.099672	241635_at EVI1	BE049061 Ecotropic v
133.975	130.6368	152.3766	0.003279	1.166414	222381_at PDCD6	AI907083 Programme
215.583	201.0389	221.1492	0.003283	1.100032	241943_at CCDC58	AA776829 coiled-coil c
196.412	174.8508	192.9876	0.00336	1.103727	209830_s_ SLC9A3R2	AF035771 solute carri
230.626	236.5124	267.474	0.003372	1.130909	220838_at FLJ20433	NM_01782 hypothetica
308.847	280.8674	311.5054	0.003378	1.109083	213290_at COL6A2	AL531750 collagen, ty
287.583	303.953	314.3726	0.003396	1.03428	221907_at C14orf172	AI679213 chromosom
138.498	164.1751	147.5683	0.003442	0.898847	219981_x_ ZNF587	NM_01796 Zinc finger
148.745	164.9808	149.3897	0.003486	0.905497	1553518_a DEFT1P	AF355799 defensin, th
11.1564	16.21573	19.63781	0.003493	1.211035	1557012_a ---	BC040670 CDNA clon
378.906	330.3217	390.5259	0.003501	1.182259	215399_s_ OS9	AI683900 amplified in
350.708	330.0074	348.5478	0.003513	1.056182	212418_at ELF1	M82882 E74-like fac
86.4085	81.4991	89.79421	0.003575	1.101782	215602_at FGD2	AK024456 FYVE, Rho
34.233	34.8927	29.68891	0.003637	0.850863	1562038_a LIPC	AK091917 Lipase, hep
237.389	229.4643	249.38	0.003642	1.086792	226376_at ZC3H5	AI885018 zinc finger (
338.419	337.0269	324.3492	0.003644	0.962384	235579_at ---	AA679858 ---
99.9672	121.1392	101.1769	0.003647	0.835212	235829_at LOC64323	AW003893 Hypothetica
106.299	121.3073	106.2417	0.003662	0.875806	204836_at GLDC	NM_00017 glycine dehyd
265.494	252.1463	278.6767	0.003706	1.105218	209710_at GATA2	AL563460 GATA bind
160.625	181.2433	209.0472	0.003708	1.153406	219577_s_ ABCA7	NM_01911 ATP-bindin

146.058	122.0169	148.435	0.003795	1.216512	225258_at	FBLIM1	AL133035	filamin bind
123.696	140.4551	159.411	0.003831	1.13496	210263_at	KCNF1	AF029780	potassium v
21.1053	19.10981	23.90111	0.003841	1.250725	240829_at	PEX3	BF439431	Peroxisom
182.759	183.8153	167.9008	0.003876	0.913421	203207_s	MTFR1	BF214329	mitochondr
109.847	126.3354	142.6042	0.003893	1.128774	244286_at	FNBP1	AI017983	Formin binc
145.613	179.1922	159.0336	0.003986	0.887503	230136_at	LOC40009	AI573252	hypothetica
80.3074	79.44066	66.82451	0.003989	0.841188	243713_at	SLC1A1	AI734054	Solute carri
241.599	262.3477	326.9857	0.004007	1.246383	212163_at	KIDINS220	AB033076	kinase D-in
331.088	334.4374	369.3017	0.004128	1.104247	231161_x	---	BF064181	---
55.6819	48.73779	58.71253	0.004138	1.204661	1566557_a	FLJ90757	AK096609	hypothetica
187.796	342.9498	271.1132	0.004164	0.790533	214395_x	EEF1D	AI335509	Eukaryotic
191.866	175.2949	189.816	0.004172	1.082838	211778_s	OVOL2	BC006148	ovo-like 2 (
214.988	204.6409	220.2277	0.00419	1.076166	204657_s	SHB	NM_00302	Src homolo
19.7738	18.69894	22.83014	0.004196	1.220932	242175_at	RNF169	AI732181	Ring finger
114.353	102.2035	117.8002	0.004196	1.152605	221401_at	CACNG5	NM_01440	calcium ch
69.1877	73.71854	64.57316	0.004206	0.875942	240138_at	---	BF433815	Transcriber
232.595	203.4117	221.9192	0.004208	1.090986	241831_at	ZNF614	AV718349	Zinc finger
229.882	258.3609	224.8374	0.004212	0.870246	221207_s	NBEA	NM_01567	neurobeact
194.895	187.3151	174.347	0.004229	0.930768	233981_at	---	AK021739	CDNA FLJ
123.077	146.0121	136.0978	0.004273	0.932099	231244_at	CASD1	AI767570	CAS1 dom
370.501	358.9847	393.6493	0.004275	1.096563	222441_x	C20orf45	BF032213	chromosom
30.2683	24.19147	29.91556	0.004299	1.236616	244308_at	---	BF514096	---
94.184	122.4997	112.146	0.004324	0.91548	210328_at	GNMT	AF101477	glycine N-n
386.277	381.943	437.3671	0.004327	1.145111	209818_s	HABP4	AF241831	hyaluronan
572.148	534.6118	599.2644	0.004366	1.120934	1552731_a	ABRA	NM_13916	actin-bindin
359.583	346.7268	376.7524	0.004374	1.086597	43934_at	GPR137	AA479495	G protein-c
58.0491	53.91708	48.25289	0.004404	0.894946	239423_at	---	AW043836	---
166.213	169.0477	185.3812	0.00443	1.096621	243906_at	PCYT1A	AI248622	Phosphate
35.661	23.96188	29.87479	0.004435	1.246763	1569257_a	FMNL1	BC042925	formin-like
292.5	271.6223	288.6369	0.00445	1.06264	202523_s	SPOCK2	AI952009	sparc/ostec
106.872	99.80151	93.15118	0.004468	0.933364	241843_at	SNORA28	AA215701	small nucle
1835.91	2578.169	2183.677	0.004469	0.846987	201408_at	PPP1CB	W67887	protein pho
142.023	159.0889	141.1991	0.004473	0.887549	218972_at	TTC17	NM_01825	tetratricope
459.757	712.7672	573.0179	0.004485	0.803934	213736_at	COX5B	AI557312	Cytochrom
202.65	214.8089	238.4671	0.004533	1.110136	241102_at	PBX1	AA705396	Pre-B-cell l
103.531	98.21734	109.3741	0.004576	1.113593	235506_at	NOSTRIN	AI076788	Nitric oxide
666.749	1082.864	881.9849	0.004602	0.814493	238191_at	---	AW771908	Transcriber
91.0485	109.2643	133.0393	0.004615	1.217591	241165_at	DCAMKL1	AA012953	Doublecorti
218.874	211.2817	223.0889	0.004621	1.055884	213815_x	C19orf29	AI913329	chromosom
104.143	100.0026	85.69568	0.004671	0.856935	1560995_s	FUT4	AF086444	Fucosyltrar
56.0651	76.37366	94.11243	0.00472	1.232263	236325_at	KIAA1377	BF057799	KIAA1377
68.2435	102.1455	81.143	0.004724	0.794386	205848_at	GAS2	NM_00525	growth arre
99.8883	109.5103	99.96479	0.004727	0.912835	221865_at	C9orf91	BF969986	chromosom
192.365	206.2832	229.585	0.004863	1.11296	240616_at	---	AV699953	Transcriber
588.781	582.2399	669.2623	0.004909	1.149461	201651_s	PACSIN2	NM_00722	protein kin
31.3118	37.75193	33.04717	0.004922	0.875377	237808_at	ST7OT2	AI421301	ST7 overlaj
261.612	305.5929	270.44	0.004928	0.884968	235674_at	KIAA0922	AW575183	KIAA0922
20.7348	18.96536	16.14892	0.004934	0.851496	229271_x	---	BG028597	---
203.482	212.0171	239.2032	0.004939	1.128226	235616_at	---	AI694059	---
114.799	120.0609	133.5743	0.004953	1.112555	239886_at	RNF130	N72610	Ring finger
133.677	138.1332	153.9143	0.005052	1.114246	222643_s	BBS1	BF116243	Bardet-Biec
351.789	301.1358	331.5509	0.005134	1.101001	204606_at	CCL21	NM_00298	chemokine

38.8097	38.29083	50.41098	0.005135	1.316529	1552975_x---	NM_01413---
526.319	498.1947	546.7501	0.005149	1.097463	208779_x_DDR1	L20817 discoidin dc
495.465	412.2408	478.92	0.005153	1.161748	200859_x_FLNA	NM_00145 filamin A, a
686.043	854.2359	801.4939	0.005156	0.938258	204045_at TCEAL1	NM_00478 transcriptio
155.642	131.6898	144.7886	0.005277	1.099467	239496_at RSU1	AW515913 Ras suppre
101.284	120.1549	132.314	0.00528	1.101196	230514_s_LYZL1 /// L	BF979319 lysozyme-li
66.42	68.30192	75.18717	0.0053	1.100806	231889_at ZUBR1	AB037728 zinc finger,
44.664	40.76323	48.21913	0.005343	1.182907	217026_at CFTR	M96936 cystic fibros
439.181	509.8689	454.8479	0.005368	0.892088	203599_s_WBP4	NM_00718 WW domai
17.2998	11.83815	16.36463	0.00537	1.382364	1562250_a C9orf164	AF289567 Chromosor
1411.09	1413.462	1534.298	0.005405	1.085489	208696_at CCT5	AF275798 chaperonin
3542.82	3463.317	3754.64	0.00544	1.084117	208738_x_SUMO2 ///	AK024823 SMT3 supp
52.2015	59.76278	50.28176	0.005467	0.841356	204721_s_DNAJC6	NM_01478 DnaJ (Hsp4
3358.69	3068.897	3448.959	0.005474	1.123843	200795_at SPARCL1	NM_00468 SPARC-like
221.362	216.5532	236.1894	0.005497	1.090676	225205_at KIF3B	AI819734 kinesin fam
187.18	236.8734	200.9901	0.005537	0.848513	230779_at TNRC6B	BF594371 trinucleotid
159.26	145.0813	151.84	0.005559	1.046585	243118_at C6orf182	AW592456 chromosorr
177.319	168.8	180.1642	0.005662	1.067324	244622_at BRWD1	AW183692 Bromodom.
180.938	176.035	191.5402	0.005663	1.08808	213716_s_SECTM1	BF939675 secreted ar
208.595	207.7306	222.8812	0.005679	1.072934	222070_at DND1	AW090043 dead end h
109.031	109.2448	122.8307	0.005699	1.124362	203607_at INPP5F	NM_01493 inositol poly
106.766	106.5924	117.0386	0.0057	1.098001	225150_s_RTKN	BC004558 rhotekin
75.6842	75.37538	81.22062	0.005705	1.077548	238169_at ---	AI307778 Transcribec
300.512	260.6402	301.421	0.005706	1.156464	1560817_a---	BM146472 CDNA FLJ:
365.854	334.4304	375.6392	0.005744	1.123221	203415_at PDCD6	NM_01323 programme
356.942	416.601	395.065	0.005761	0.948305	205998_x_CYP3A4	NM_01746 cytochrome
37.6693	36.61157	40.55296	0.005762	1.107654	204256_at ELOVL6	NM_02409 ELOVL6 farr
219.426	217.3158	237.6909	0.005764	1.093758	232988_at KIAA0182	AK025308 KIAA0182
212.677	196.1387	208.8786	0.005778	1.064953	209320_at ADCY3	AF033861 adenylate c
61.7439	72.78047	62.18449	0.005791	0.854412	243814_at PRKCBP1	AW135141 Protein kinz
34.0758	38.4933	33.78962	0.005836	0.877805	242248_at PHKB	AW873632 phosphoryl
146.882	136.6856	155.6008	0.005959	1.138385	231997_at LRRC35	R69910 leucine rich
139.389	157.8079	143.9709	0.006018	0.912317	1555429_a---	BC007806 ---
11.7911	12.04314	15.17546	0.006022	1.260091	1562249_a LOC28596	AL833583 hypothetica
49.2778	51.42922	43.77793	0.006065	0.851227	1568868_a FLJ16008	BC039307 FLJ16008 p
96.1888	86.47911	95.81904	0.006075	1.108002	235593_at ZFHX1B	AL546529 zinc finger l
244.906	272.3683	249.692	0.006114	0.916744	204243_at RLF	NM_01242 rearranged
28.2037	37.87236	32.41881	0.006123	0.856002	1562491_a LOC64237	BC036345 hypothetica
477.611	442.9623	476.9444	0.006128	1.076716	213730_x_TCF3	BE962186 transcriptio
150.836	155.863	143.1209	0.00613	0.918248	241931_at XG	AI168338 Xg blood gr
46.5492	55.75337	63.206	0.00613	1.133671	1559617_a NEU4	D55640 Sialidase 4
199.638	180.5573	206.3497	0.006168	1.142848	229866_at ---	AI826125 Transcribec
184.241	177.8412	188.122	0.006171	1.057809	1554393_a ADC	AY050636 arginine de
146.868	153.7616	138.0277	0.006229	0.897673	204910_s_TRIM3	AI419307 tripartite mc
33.8144	27.61511	32.63837	0.006235	1.181902	210375_at PTGER3	X83858 prostaglan
299.752	250.1476	297.4626	0.006281	1.189148	225548_at SHRM	AB040914 shroom
404.385	411.5538	464.3989	0.006282	1.128404	1561557_a LIPA	BC040833 Lipase A, ly
70.7363	62.19097	70.99432	0.006295	1.141554	1553547_a---	NM_01860 ---
210.523	216.6879	241.2454	0.006316	1.113331	237109_at TOM1L2	AA399639 target of my
168.981	182.3832	175.6598	0.006325	0.963136	236332_at DHRS7	AI823497 Dehydroge
642.035	623.785	705.977	0.006362	1.131763	35846_at THRA	M24899 thyroid horr
86.1067	92.25948	99.88602	0.006368	1.082664	1567704_a TFE3	AY034077 Transcriptic

100.316	108.3396	128.2621	0.00637	1.18389	244465_at	LOC28303	AA399576	Hypothetica
172.024	156.3009	172.6614	0.006413	1.104673	228955_at	---	AL041761	Transcribec
247.091	253.4941	277.5677	0.006467	1.094967	241633_x	NFIX	AI054381	Nuclear fac
194.305	180.9032	200.343	0.006486	1.10746	236067_at	MBNL2	AA453791	Muscleblinc
57.1671	60.54928	68.60929	0.006493	1.133115	211091_s	NF2	AF122828	neurofibron
101.207	102.0124	97.45517	0.006498	0.955326	1555235_s	IQCF3	BC021188	IQ motif coi
69.083	77.47702	93.94136	0.006536	1.212506	234434_at	---	AL117506	MRNA; cDI
1085.55	1270.777	1121.005	0.006539	0.882142	228183_s	RPAIN	BF342428	RPA intera
27.3039	20.12747	27.15704	0.006547	1.349253	243174_at	---	AI733637	Transcribec
503.253	469.7423	516.8066	0.00657	1.100192	200044_at	SFRS9	NM_00376	splicing fac
49.8342	62.38911	56.70167	0.006571	0.908839	216276_s	ADAM3A	X89657	ADAM met;
507.631	486.6846	539.2398	0.006588	1.107986	32625_at	NPR1	X15357	natriuretic p
77.8699	87.31332	68.73027	0.006602	0.787168	234110_at	LOC28307	AK023065	Hypothetica
119.02	124.3002	113.4788	0.006618	0.912941	227659_at	PLEKHA3	BE550332	pleckstrin h
128.509	130.7479	144.6479	0.006643	1.106311	240314_at	NCOR1	AI018235	Nuclear rec
329.227	326.9817	370.6462	0.006655	1.133538	1566823_a	---	AK057226	CDNA FLJ;
173.669	155.0119	184.8804	0.006678	1.192686	201792_at	AEBP1	NM_00112	AE binding
89.6119	89.18779	84.33931	0.006699	0.945637	220620_at	C1orf42	NM_01906	chromosom
1448.49	1779.872	1566.448	0.006713	0.88009	208737_at	ATP6V1G1	BC003564	ATPase, H-
53.9527	57.00674	46.22843	0.006748	0.810929	205675_at	---	AI623321	---
252.75	257.7568	283.6941	0.006775	1.100627	225280_x	ARSD	N51673	arylsulfatas
66.7849	71.81024	64.82698	0.006808	0.902754	210172_at	SF1	D26121	splicing fac
130.551	129.5213	138.6434	0.00681	1.070429	222758_s	TMEM132	W74594	transmemb
235.352	240.0954	264.3253	0.006812	1.100918	213919_at	DNAJC4	AW024467	DnaJ (Hsp-
2829.01	2467.624	2761.066	0.006848	1.118916	65635_at	FLJ21865	AL044097	endo-beta-l
203.143	204.6206	220.3086	0.006848	1.076669	241435_at	ETS1	AA702930	V-ets erythi
148.293	145.5413	161.9308	0.006859	1.11261	212210_at	INTS1	BF513430	integrator c
193.579	220.1787	205.6818	0.006899	0.934159	225555_x	LOC64355	AI991669	Similar to A
41.0079	45.25657	54.05369	0.00691	1.194383	236062_at	UBE2E1	AI742722	Ubiquitin-cc
92.6387	85.59511	95.1127	0.006953	1.111193	227597_at	MGC42174	AI935717	hypothetica
54.2711	62.17347	74.29399	0.006978	1.194947	1555718_x	CNOT1	M15530	CCR4-NOT
13.7656	14.81874	11.79289	0.007008	0.79581	1553792_a	KIAA1109	NM_03220	KIAA1109
61.2726	75.41604	93.07858	0.007023	1.234201	1555634_a	LILRA5	AF499919	leukocyte ir
220.641	239.0126	215.6688	0.007044	0.902332	228743_at	TXNL5	AW338089	Thioredoxir
102.997	104.7169	115.8763	0.007093	1.106567	1570350_a	RUNX1	BC032403	runt-relatec
260.697	317.2099	272.8244	0.007114	0.860075	242454_at	AMBP	BF433866	Alpha-1-mii
77.5333	94.46917	113.6651	0.007186	1.203198	243652_at	EYA2	H49285	Eyes abser
97.2516	99.85547	113.6488	0.007201	1.138133	205302_at	IGFBP1	NM_00059	insulin-like
23.7116	33.07232	26.92461	0.007217	0.814113	214021_x	ITGB5	AI335208	Integrin, be
136.198	155.467	142.2604	0.00722	0.915052	1557807_a	---	BG197397	Full length
182.817	185.6584	193.8307	0.007266	1.044018	233130_at	THRB	AU147515	Thyroid hor
156.415	149.8674	161.8501	0.007267	1.079955	211709_s	CLEC11A	BC005810	C-type lecti
55.5833	51.63883	60.23383	0.007284	1.166445	211478_s	DPP4	M74777	dipeptidyl-p
49.7181	46.40598	55.19417	0.007286	1.189376	1562316_a	---	AL833225	---
76.6774	79.69418	91.40214	0.007302	1.146911	237272_at	---	AL042437	CDNA clon
224.873	237.8752	217.6251	0.007307	0.914871	230057_at	LOC28517	AI609832	hypothetica
144.085	147.0144	137.8192	0.007315	0.937454	236916_at	---	AU151944	Transcribec
133.433	136.7879	150.3092	0.007368	1.098849	214073_at	CTTN	BG475299	cortactin
339.339	357.1837	391.806	0.007376	1.096931	222726_s	EXOC5	BF696912	exocyst cor
178.794	216.2718	196.9552	0.007377	0.910684	1555289_a	LZTR2	BC009106	leucine zip
190.445	171.5697	192.222	0.007402	1.120373	239949_at	FLJ10916	AA425220	hypothetica
73.6189	93.13438	120.3626	0.007412	1.292354	240941_at	ITSN2	BF222862	Intersectin :

100.126	93.14844	107.4096	0.007487	1.153101	1557067_s	LUC7L	AI744735	LUC7-like (
709.739	607.1879	662.1892	0.007493	1.090584	224659_at	SEPN1	AL020996	selenoprote
203.354	192.3476	215.8432	0.007503	1.122152	238917_s_	MGC24036	AI732405	hypothetica
106.172	113.802	134.6052	0.007506	1.182802	214638_s_	CCNT2	AV681875	cyclin T2
44.1969	48.10418	44.97258	0.007525	0.9349	1553750_a	FAM76B	NM_14466	family with
367.28	331.5886	358.9287	0.007552	1.082452	234924_s_	ZNF687	AK023105	zinc finger
160.341	152.7076	142.2792	0.007577	0.93171	1560322_a	RBMS3	AL831860	RNA bindin
40.3706	41.76556	47.66863	0.007585	1.141338	211736_at	SP2	BC005914	Sp2 transcr
1585.12	1383.914	1527.479	0.007593	1.103738	216036_x_	WDTC1	AK001734	WD and tet
198.781	189.1573	198.7394	0.007599	1.050657	213632_at	DHODH	M94065	dihydroorot
205.302	220.4183	234.2981	0.007618	1.06297	234770_at	---	X81445	---
268.463	249.0081	265.4598	0.007664	1.066069	218045_x_	PTMS	NM_00282	parathymos
47.4709	42.48207	48.26404	0.007675	1.136104	234038_at	C16orf52	AK021824	Chromosom
69.6421	59.70001	63.36782	0.007691	1.061437	231369_at	ZNF333	BG149482	Zinc finger
262.442	256.41	281.3524	0.007716	1.097276	208417_at	FGF6	NM_02099	fibroblast g
62.8925	79.74072	69.04228	0.007721	0.865835	1563728_a	C9orf14	AF418573	chromosom
105.107	94.11459	103.4118	0.007779	1.098786	222145_at	---	AK027225	CDNA: FLJ
7.53586	8.267377	14.91394	0.007838	1.803951	1559956_a	SYT7	BF109699	synaptotag
391.319	399.5939	374.6732	0.007872	0.937635	218985_at	SLC2A8	NM_01458	solute carri
600.949	578.9959	643.5323	0.007923	1.111463	203055_s_	ARHGEF1	NM_00470	Rho guanin
366.016	319.5568	367.9804	0.007997	1.151534	231191_at	ANKMY1	AA932692	Ankyrin rep
189.321	185.5267	202.9067	0.008018	1.093679	230125_at	GUSB	AA767279	Glucuronid
937.16	1107.502	1194.599	0.00805	1.078643	224616_at	DYNC1LI2	BG110975	dynein, cyt
158.246	154.566	164.1353	0.008061	1.061911	221679_s_	ABHD6	AF225418	abhydrolas
304.613	293.7902	317.4911	0.008065	1.080673	204451_at	FZD1	NM_00350	frizzled hon
62.3096	66.49644	75.82864	0.008135	1.140341	1553123_a	WDR62	NM_17363	WD repeat
45.291	50.08778	41.53282	0.008153	0.829201	229437_at	BIC	BG231961	BIC transcr
227.296	210.5754	232.8649	0.008242	1.10585	1553243_a	ITIH5	NM_03281	inter-alpha
327.802	310.9956	346.6247	0.008286	1.114565	200825_s_	HYOU1	NM_00638	hypoxia up-
179.555	233.1033	282.5876	0.008351	1.212284	243459_x_	---	AW300077	---
50.8564	52.15367	45.80071	0.008357	0.878188	217670_at	TSPAN4	AW149827	Tetraspanir
43.7493	43.11719	39.31054	0.008514	0.911714	1561451_a	---	BC034301	CDNA FLJ:
258.946	302.4387	259.5031	0.008516	0.858035	1563947_a	RAB6IP2	AK097177	RAB6 inter:
2501.43	3015.108	2669.694	0.008528	0.885439	217802_s_	NUCKS1	NM_02273	nuclear cas
329.145	411.9904	358.9709	0.008542	0.871309	208913_at	GGA2	AA868560	golgi assoc
125.712	129.048	141.0714	0.008546	1.09317	224232_s_	PX19	AF112203	px19-like pi
82.8443	74.70117	66.45574	0.008558	0.889621	215564_at	AREG	AV652031	Amphiregul
255.387	253.351	232.4812	0.008606	0.917625	1557353_a	---	BM985423	CDNA FLJ:
64.1668	62.65649	70.59424	0.008623	1.126687	209640_at	PML /// LO	M79462	promyelocy
266.248	197.5069	219.063	0.008674	1.109141	222502_s_	UFM1	BC005193	ubiquitin-fo
142.362	159.2094	145.8761	0.008709	0.916253	221996_s_	CLTB	AW170546	Clathrin, lig
96.12	88.06688	96.91724	0.008748	1.100496	230241_at	IFRG15	BF196874	Interferon r
696.259	619.7323	685.2214	0.008757	1.105673	202740_at	ACY1	NM_00066	aminoacyla
2262.02	1986.208	2545.359	0.008818	1.281517	211978_x_	PPIA	AI708767	peptidylpro
181.222	184.7214	198.7222	0.008826	1.075794	239815_at	NCOA5	R16784	Nuclear rec
142.406	127.2001	141.8241	0.008834	1.114968	235694_at	TCFL5	N49233	Transcriptic
71.0416	62.01147	70.33042	0.008879	1.134152	223984_s_	NUPL1	BC001104	nucleoporir
925.726	842.1464	947.6966	0.008929	1.125335	202210_x_	GSK3A	NM_01988	glycogen sy
306.535	306.4038	332.6202	0.008935	1.085562	207122_x_	SULT1A2	NM_00105	sulfotransfe
117.944	126.7341	135.6926	0.008948	1.070687	228565_at	KIAA1804	AI809005	mixed linea
340.018	335.3944	358.4857	0.008983	1.068848	201853_s_	CDC25B	NM_02187	cell division
196.43	210.5408	193.8474	0.008988	0.920712	1560615_a	RP11-529I	AW626574	Deleted in :

644.377	650.3177	746.1832	0.009008	1.147413	225789_at	CENTG3	BE876194	centaurin, c
61.7077	65.86	80.30867	0.009025	1.219385	1560776_a	CDRT4	AU121725	CMT1A dup
69.8853	73.13759	91.92294	0.009034	1.25685	211711_s_	PTEN	BC005821	phosphatas
148.233	147.3302	158.7934	0.009035	1.077806	221299_at	GPR173	NM_01896	G protein-c
143.19	139.7096	153.954	0.009054	1.101958	228815_s_	ABP1	AI359215	Amiloride b
189.756	231.18	203.265	0.009062	0.87925	212926_at	SMC5L1	AW183677	SMC5 struc
266.428	264.1709	293.3171	0.009137	1.110331	218693_at	TSPAN15	NM_01233	tetraspanin
98.6278	105.0517	121.7454	0.009163	1.158909	216464_x_	GPR44	AF118265	G protein-c
610.313	692.4992	644.3214	0.009164	0.930429	203318_s_	ZNF148	NM_02196	zinc finger j
191.892	171.3211	184.744	0.009191	1.078349	217641_at	GPR135	AA634446	G protein-c
186.696	186.3307	206.0846	0.009246	1.106015	209940_at	PARP3	AF083068	poly (ADP-i
107.744	117.1898	128.9464	0.009246	1.100322	235842_at	---	AA521154	Transcribec
170.262	182.0757	158.3861	0.009255	0.869892	1555578_a	PTPRM	BC029442	protein tyro
96.5949	96.12876	85.98526	0.009296	0.89448	243735_at	---	N58363	CDNA FLJ:
64.327	74.13654	68.16649	0.009298	0.919472	232202_at	FAM83B	AK024927	Family with
115.285	109.5311	121.4383	0.009299	1.108711	241426_at	KIAA1712	AA629743	KIAA1712
159.506	148.6899	161.4598	0.009305	1.085883	235902_at	LOC64517	AI090764	Similar to N
115.602	133.2357	121.1561	0.009313	0.909337	1555913_a	GON4L	AK098734	gon-4-like (
166.664	166.4299	184.1397	0.009319	1.10641	215265_at	EMX1	BF515060	empty spiræ
267.048	255.941	267.8297	0.009322	1.046451	226373_at	SFXN5	AW166098	sideroflexin
127.044	135.4138	153.7141	0.009378	1.135144	1558394_s	KRT7	BC042076	keratin 7
82.2529	92.56368	102.3946	0.009424	1.106207	1565641_a	C16orf45	BE503823	Chromosor
62.6615	105.1599	77.89241	0.009504	0.740704	229857_s_	LOC64424	AW117584	Hypothetica
202.457	178.7383	194.4659	0.009504	1.087992	208177_at	SLC34A1	NM_00305	solute carri
78.9703	86.59988	77.85689	0.009507	0.899042	242488_at	---	R55784	CDNA FLJ:
196.841	214.1004	233.0057	0.009518	1.088301	218360_at	RAB22A	NM_02067	RAB22A, m
47.7917	40.16152	52.3317	0.009529	1.303031	209396_s_	CHI3L1	M80927	chitinase 3-
248.272	250.3803	285.2043	0.009571	1.139084	206953_s_	LPHN2	NM_01230	latrophilin 2
110.769	131.3918	156.4299	0.009621	1.190561	226210_s_	MEG3	AI291123	maternally i
435.618	457.6399	483.6533	0.009637	1.056843	223626_x_	FAM14A	AF208232	family with
31.2248	34.13474	27.26487	0.009651	0.798742	1562648_a	KIAA1212	BC035848	KIAA1212
67.6748	80.61752	94.25178	0.009723	1.169123	217685_at	SLC16A3	AA853175	Solute carri
162.8	181.0582	212.2489	0.009763	1.172269	206961_s_	TRFP	NM_00427	Trf (TATA b
937.472	954.5442	1074.292	0.00977	1.125451	1007_s_at	DDR1	U48705	discoidin dc
977.519	849.1797	908.7392	0.009814	1.070138	200632_s_	NDRG1	NM_00609	N-myc dow
188.24	208.5122	191.4903	0.009832	0.918365	238053_at	DHRX	AI934204	dehydroger
51.8323	52.18882	58.42891	0.009865	1.119568	208582_s_	DUX5 /// D	NM_01214	double horr
205.871	207.7106	230.9036	0.009878	1.11166	220536_at	C14orf115	NM_01822	chromosor
1555.47	1541.257	1414.662	0.009917	0.917863	218550_s_	LRR20	NM_01820	leucine rich
54.5569	45.27163	50.09201	0.009933	1.106477	220416_at	ATP8B4	NM_02483	ATPase, Cl
91.8068	91.01119	99.0726	0.009944	1.088576	230190_at	NDFIP2	AW301706	Nedd4 fam
324.094	438.9543	374.1308	0.009959	0.852323	226238_at	MCEE	AI934339	methylmalc
164.524	173.5463	161.1361	0.009994	0.92849	236461_at	ABHD1	AI554273	abhydrolas
106.887	125.7768	112.1074	0.010048	0.891321	1569289_a	BIVM	BC039587	Basic, imm
223.099	214.7964	231.0172	0.010052	1.075517	240255_at	---	AW054766	Transcribec
13.8083	15.61828	22.25704	0.010063	1.425064	241674_s_	---	AI820854	Transcribec
185.602	186.2939	215.0153	0.010069	1.154173	1557585_a	ATP6V1H	AW468382	ATPase, H-
276.28	335.5191	395.1417	0.010095	1.177702	221992_at	LOC28397	AI925734	hypothetica
102.35	121.3998	136.7447	0.01014	1.1264	216284_at	---	AK024123	CDNA FLJ:
83.1601	104.4908	95.26163	0.01015	0.911675	222061_at	CD58	AA700015	CD58 mole
241.035	237.3024	259.5573	0.010172	1.093783	227590_at	LOC15038	BE501980	similar to R
123.937	137.8937	129.0379	0.010182	0.935778	242864_at	ZNF554	AI924872	zinc finger j

139.907	121.291	146.3573	0.01022	1.206663	1559780_a	DDAH1	BC036577	Dimethylar
170.844	179.7124	168.8216	0.010249	0.939398	1569348_a	---	BC017420	Homo sapi
24.9015	26.93464	23.81406	0.010273	0.884142	243557_at	MAP3K7IP	AA769450	Mitogen-ac
43.2208	51.28847	59.07389	0.010292	1.151797	233465_at	SPRED1	AA026390	Sprouty-rel
75.7274	69.06636	76.45039	0.010295	1.106912	206197_at	NME5	NM_00355	non-metast
90.8076	116.2307	139.4713	0.010325	1.199952	243135_x	---	R26456	MRNA; cDI
564.206	534.1517	612.2073	0.010359	1.14613	205717_x	#####	NM_00258	protocadhe
162.874	148.8687	164.8432	0.010368	1.107306	218193_s	GOLT1B	NM_01607	golgi transp
374.709	336.3288	362.5652	0.010373	1.078008	209280_at	MRC2	U58856	mannose re
128.62	132.7389	153.9419	0.010394	1.159735	221198_at	SCT	NM_02192	secretin
133.691	138.2824	125.3281	0.01041	0.90632	234103_at	KCNT2	AU145191	Potassium
2407.16	2191.856	2782.2	0.010425	1.269335	212661_x	PPIA	BE731738	peptidylpro
362.195	262.3681	352.3094	0.010445	1.342806	201058_s	MYL9	NM_00609	myosin, lig
98.2807	114.2472	100.5311	0.010445	0.879944	215385_at	FTO	AK022473	Fatso
260.873	281.2364	258.895	0.010476	0.92056	31826_at	KIAA0674	AB014574	KIAA0674
97.8712	106.5862	115.2985	0.010485	1.08174	1555042_a	TRPV5	BC034740	transient re
216.132	231.0153	195.5964	0.010488	0.846682	235209_at	RPESP	AW662373	RPE-sponc
203.512	213.7657	240.084	0.010543	1.123118	205570_at	PIP5K2A	NM_00502	phosphatid
183.338	192.4023	176.092	0.010551	0.915228	221264_s	TARDBP	NM_03121	TAR DNA b
93.0162	92.81538	82.16896	0.010552	0.885295	1564338_a	MKL1	AK097769	Megakaryo
180.406	188.367	168.0933	0.010569	0.892371	1554469_a	BTBD15	BC030580	BTB (POZ)
211.921	229.5587	266.3232	0.010594	1.160153	1556831_a	DYNC1H1	AI986267	Dynein, cyt
57.034	64.06984	78.00937	0.010596	1.217568	1570355_a	DPY19L1	BI461155	dpy-19-like
158.323	159.287	182.5827	0.010621	1.14625	1552625_a	TRNT1	AB063105	tRNA nucle
48.6817	61.68522	80.66082	0.010653	1.30762	215212_at	PIK3CA	AU147166	Phosphoinc
91.8515	95.46652	110.3269	0.010702	1.15566	236708_at	CAPZB	BE675714	Capping pr
14.0969	14.55424	18.70572	0.01072	1.285242	1569661_a	NPAS3	BC035075	Neuronal P
86.8519	84.3289	95.2705	0.010742	1.129749	1555853_a	---	BI524781	---
92.2896	149.8517	91.0523	0.010756	0.607616	205694_at	TYRP1	NM_00055	tyrosinase-
37.9647	39.0929	30.83161	0.010771	0.788675	238178_at	---	BF110268	---
465.317	507.4029	548.1638	0.010784	1.080332	203076_s	SMAD2	U65019	SMAD, moi
52.5642	52.06708	57.11659	0.01079	1.096981	1566463_a	---	AL833708	MRNA; cDI
659.111	665.8287	565.9591	0.01081	0.850007	210886_x	TP53AP1	AB007457	TP53 activ
89.5361	86.7539	96.90307	0.010814	1.116988	220593_s	CCDC40	NM_01795	coiled-coil c
346.163	314.7311	356.0814	0.010831	1.131383	221712_s	WDR74	BC006351	WD repeat
152.124	165.5281	139.6453	0.010925	0.843635	214378_at	TFPI	BF109662	tissue facto
427.834	438.5113	501.9674	0.010942	1.144708	202225_at	---	AW612311	CDNA FLJ:
170.244	168.7158	180.5631	0.010957	1.070221	228575_at	FNDC6	AL578102	fibronectin
85.219	63.00289	70.59134	0.010967	1.120446	240510_at	NBN	H66741	Nibrin
92.7786	102.5943	119.3284	0.010977	1.163109	223915_at	BCOR	AF317392	BCL6 co-re
51.0079	51.08908	42.0067	0.011006	0.822225	1568777_a	EML5	BM677635	echinoderr
147.29	183.7668	229.7664	0.011017	1.250315	201496_x	MYH11	S67238	myosin, he
396.886	368.5228	425.5083	0.011033	1.154632	200785_s	LRP1	NM_00233	low density
160.186	172.6989	158.5712	0.01104	0.918195	219357_at	GTPBP1	NM_01402	GTP bindin
502.271	569.9916	524.9959	0.011059	0.921059	222623_s	ZNF639	BF001614	zinc finger j
164.275	134.8771	148.8402	0.011064	1.103525	210688_s	CPT1A	BC000185	carnitine pa
830.697	1125.699	929.1007	0.011077	0.825355	221046_s	GTPBP8	NM_01417	GTP-bindin
139.592	161.1657	134.6217	0.011105	0.8353	238861_at	---	AI692322	MRNA; clor
228.205	256.9457	294.8487	0.011111	1.147514	218309_at	CAMK2N1	NM_01858	calcium/cal
195.609	181.7093	153.0806	0.011119	0.842447	1560705_a	SLC25A28	AW627717	Solute carri
217.951	201.7154	224.5278	0.011133	1.113092	210185_at	CACNB1	AB054985	calcium ch
306.524	323.0393	299.347	0.011196	0.926658	1560024_a	---	BC035383	CDNA clon

321.13	317.1298	326.0552	0.01124	1.028144	224888_at SELI	AB051511	selenoprote
56.747	57.80763	51.6643	0.011284	0.893728	216527_at HCG18	AL049252	HLA compl
59.4979	65.1848	58.71468	0.011301	0.900742	1570163_a---	BC014585	Homo sapi
190.431	221.3931	178.5795	0.011317	0.806617	230981_at CATSPER:	AI219834	cation char
221.849	241.8769	278.9129	0.011332	1.153119	230549_at ELK4	BF433322	ELK4, ETS
87.0656	94.26606	84.33368	0.011356	0.894635	228926_s_ SMARCA2	N25952	SWI/SNF r
250.992	296.2118	276.7999	0.011361	0.934466	230265_at SEL1L	BE671138	Sel-1 suppl
324.131	320.3064	335.2892	0.011416	1.046776	57715_at FAM26B	W72694	family with
234.758	249.2429	270.551	0.011441	1.085491	228319_at FAM84A	AI540230	Family with
121.832	129.1226	140.3634	0.011448	1.087056	236659_x_ ZNF277	AI479440	Zinc finger
131.847	148.5313	124.9936	0.0115	0.84153	1563521_a MOBKL2B	AK074231	MOB1, Mps
16.5312	26.0868	32.91534	0.011566	1.261762	243799_x_---	T40942	---
849.723	841.6003	906.1212	0.011611	1.076665	209157_at DNAJA2	AF011793	DnaJ (Hsp
251.303	247.9528	280.9353	0.011613	1.13302	220451_s_ BIRC7	NM_02216	baculoviral
1346.44	1476.754	1336.215	0.011619	0.904832	211658_at PRDX2	L19185	peroxiredo
197.849	190.1977	214.6317	0.011632	1.128466	218051_s_ NT5DC2	NM_02290	5'-nucleotid
40.676	57.16272	48.20158	0.011669	0.843234	223651_x_ CDC23	BC005258	CDC23 (ce
96.5181	103.5371	109.9697	0.011682	1.062129	235466_s_ LOC64405	AI677948	hypothetica
140.179	149.3158	170.2789	0.011687	1.140394	207517_at LAMC2	NM_01889	laminin, gai
295.176	307.2148	337.1431	0.011704	1.097418	210879_s_ RAB11FIP1	AF334812	RAB11 fam
238.36	273.5153	302.3702	0.011711	1.105496	227171_at---	AI189673	---
229.149	245.6702	231.3276	0.011712	0.941618	218590_at PEO1	NM_02183	progressive
170.174	184.0703	173.3444	0.011713	0.941729	232604_at ZNF541	AL136846	zinc finger j
21.8108	24.86036	21.37559	0.01172	0.859826	231581_at LOC40068	AW977428	Hypothetica
41.1402	31.65043	35.94946	0.011757	1.135828	1566511_a FBXO9	AK095315	F-box prote
305.203	397.1452	338.3761	0.011774	0.852021	206078_at KALRN	NM_00706	kalirin, Rho
299.548	255.667	282.8412	0.011794	1.106288	201830_s_ NET1	NM_00586	neuroepithe
56.5559	53.40656	46.20299	0.011796	0.865118	1570039_a MGC3990	BC029803	hypothetica
551.786	678.5367	606.8236	0.011804	0.894312	225917_at---	AA766897	CDNA FLJ:
142.22	151.1674	138.2979	0.011814	0.914866	1556768_a---	AK093148	CDNA FLJ:
139.787	150.9056	176.0224	0.011832	1.166441	208837_at TMED3	BC000027	transmemb
427.269	475.4776	517.8928	0.01185	1.089206	217850_at GNL3	NM_01436	guanine nu
210.333	222.2012	208.3984	0.011861	0.937882	221240_s_ B3GNT4	NM_03076	UDP-GlcN/
243.369	260.5652	285.1702	0.01189	1.094429	242327_x_ ESPN	AI198829	Espin
446.946	519.9494	599.3523	0.011892	1.152713	208727_s_ CDC42	BC002711	cell division
415.861	445.0681	401.2269	0.011913	0.901495	227852_at RP9	BF438270	retinitis pig
2006.95	1912.999	2437.731	0.011925	1.274298	201293_x_ PPIA	NM_02113	peptidylpro
3310.01	3516.029	3302.978	0.01193	0.939406	203613_s_ NDUFB6	NM_00249	NADH dehy
93.5738	87.62948	98.0101	0.01196	1.11846	232264_at EDD1	AK022204	E3 ubiquitir
45.9344	42.70123	50.32251	0.011978	1.178479	1557642_a IQCA	AK090907	IQ motif coi
49.2077	60.17166	54.59671	0.012	0.907349	240634_x_ LOC65339	BE348555	similar to P
92.38	103.0784	109.7632	0.012004	1.064852	1556242_a GSDMDC1	BC040715	Gasdermin
258.437	222.3299	246.892	0.012011	1.110476	209153_s_ TCF3	M31523	transcriptio
276.321	271.6483	293.608	0.012011	1.080839	205323_s_ MTF1	NM_00595	metal-regul
334.671	307.1137	338.2817	0.012029	1.101487	202806_at DBN1	NM_00439	drebrin 1
102.236	102.3332	92.86866	0.012031	0.907512	223254_s_ KIAA1333	AA887053	KIAA1333
202.864	188.2529	210.4009	0.012043	1.11765	205896_at SLC22A4	NM_00305	solute carri
75.6896	90.18367	106.021	0.012164	1.175612	223695_s_ ARSD	BC003660	arylsulfatas
148.077	158.8291	147.0443	0.012185	0.925802	238256_at---	AI939596	Transcribec
81.7837	78.82378	89.86896	0.012185	1.140125	238727_at LOC44093	AA031832	Hypothetica
31.5357	41.74063	38.06943	0.012191	0.912047	244367_at LMO2	AI140519	LIM domair
34.7269	24.36606	29.77447	0.012228	1.221965	238252_at ATE1	AI040743	Arginyltrans

35.6574	48.40042	37.04951	0.012243	0.765479	244094_at	C9orf93	AA406237	Chromosom
444.475	357.3113	409.5638	0.012254	1.146238	214752_x_	FLNA	AI625550	filamin A, a
56.1053	73.13359	60.79923	0.012256	0.831345	216823_at	LOC43999	AL356115	similar to ril
757.322	728.3723	783.5069	0.012261	1.075696	203550_s_	C1orf2	NM_00658	chromosom
111.865	115.1494	103.544	0.012266	0.899214	239371_at	FOXK2	BF874134	Forkhead b
168.388	173.7124	157.9247	0.01228	0.909115	205919_at	HBE1	NM_00533	hemoglobir
68.4282	78.9065	65.96731	0.012305	0.836019	1560174_a	SPAG16	AK095036	sperm assc
30.5471	40.00387	48.6244	0.012313	1.215493	1558301_a	EFCAB5	AI200825	EF-hand ca
118.601	147.6339	171.8336	0.012326	1.163917	235972_at	TMEM131	AW771265	transmemb
511.762	466.7268	492.1287	0.012331	1.054426	212223_at	IDS	AI926544	iduronate 2
251.75	234.5316	247.6104	0.012346	1.055766	241358_at	WFIKKN2	AI833106	WAP, follis
142.224	134.7002	142.5394	0.01235	1.058198	209912_s_	KIAA0415	AI373854	KIAA0415 p
435.904	446.3404	517.2064	0.012352	1.158771	1553959_a	B3GALT6	N95564	UDP-Gal:bi
379.89	356.0036	392.3819	0.012384	1.102185	213811_x_	TCF3	AW062341	transcriptio
95.8691	83.71663	93.04876	0.012396	1.111473	233695_s_	CECR2	AB051527	cat eye syn
576.84	624.7872	553.1208	0.012434	0.885295	214724_at	DIXDC1	AF070621	DIX domair
86.6543	89.52258	110.1786	0.012449	1.230735	241472_at	DMXL1	N74444	Dmx-like 1
25.2143	25.23701	29.57077	0.012452	1.171722	240959_at	---	AA181233	Transcribec
112.877	124.1418	108.2348	0.012511	0.871864	220689_at	---	NM_01805	---
76.4391	87.95024	80.25997	0.012519	0.912561	235388_at	CHD9	BG538482	chromodon
1717.1	1592.35	1937.694	0.012589	1.216877	206662_at	GLRX	NM_00206	glutaredoxi
216.939	222.3067	207.3464	0.01265	0.932705	240630_at	RARA	AI820647	Retinoic ac
77.0724	80.97863	92.9714	0.012666	1.148098	54037_at	HPS4	AL041451	Hermansky
384.633	391.3448	430.0091	0.012687	1.098799	214779_s_	RUTBC3	R51077	RUN and T
63.3255	57.08069	66.39933	0.012712	1.163254	204875_s_	GMDS	NM_00150	GDP-mann
2931.85	2599.927	3214.336	0.01275	1.236318	201163_s_	IGFBP7	NM_00155	insulin-like
81.3567	81.77051	71.87521	0.0128	0.878987	1568943_a	INPP5D	BC027960	inositol poly
506.123	565.7034	531.5979	0.012827	0.939711	221939_at	YIPF2	AL529396	Yip1 domai
328.364	321.7009	356.9451	0.012851	1.109556	235863_at	JSRP1	AI805145	junctional s
101.456	145.3907	116.238	0.012876	0.799487	227317_at	LMCD1	AA045042	LIM and cy:
122.957	150.2456	178.1887	0.012897	1.185983	242240_at	PTK2	AI805700	PTK2 prote
99.1658	112.7162	132.8662	0.012907	1.178768	233416_at	---	AU144915	CDNA FLJ:
24.0375	36.65846	29.76657	0.012913	0.811997	220336_s_	GP6	AB043821	glycoproteii
1724.02	1702.124	2169.698	0.012945	1.2747	211378_x_	PPIA	BC001224	peptidylpro
466.743	441.4717	492.3953	0.012954	1.11535	200745_s_	GNB1	AF070603	guanine nu
132.883	130.8874	120.238	0.012963	0.918637	207505_at	PRKG2	NM_00625	protein kin
159.234	150.1107	163.3474	0.012972	1.08818	204788_s_	PPOX	NM_00030	protoporph
120.128	120.8616	132.2424	0.013045	1.094165	204250_s_	CEP164	AI655714	centrosoma
73.4052	82.04953	98.31992	0.013045	1.1983	242629_at	---	BF056092	---
183.479	203.9459	177.3991	0.013049	0.869834	227025_at	PPHLN1	BG284497	periphilin 1
160.751	168.4326	189.9919	0.01305	1.128	219516_at	TRPV4	NM_02162	transient re
140.758	157.7847	142.7874	0.013052	0.904951	230034_x_	MRPL41	BF590212	Mitochondr
123.136	130.1106	145.5967	0.013068	1.119023	243845_at	PREI3	AI762164	Preimplant:
315.924	311.7533	325.7566	0.013085	1.044918	228061_at	LOC90693	BF062262	LOC90693
135.508	162.5451	190.8634	0.013089	1.174218	206781_at	DNAJC4	NM_00552	DnaJ (Hsp
35.3417	30.86291	36.34177	0.013096	1.177522	239936_at	DLEU2	AA126428	deleted in l
224.918	215.8361	200.3313	0.013101	0.928164	212991_at	FBXO9	AL137520	F-box prote
14636.1	15231.57	14915.41	0.013118	0.979243	214087_s_	MYBPC1	BF593509	myosin bin
115.138	100.4768	112.1636	0.013122	1.116312	203087_s_	KIF2	NM_00452	kinesin hea
100.473	71.76318	85.03216	0.013153	1.1849	209098_s_	JAG1	U61276	jagged 1 (A
22.9741	15.98808	20.43077	0.01316	1.277875	231731_at	OTX2	NM_02172	orthodentic
18820.5	18765.2	19021.72	0.013249	1.01367	217398_x_	GAPDH	AK026525	glyceraldeh

86.1406	89.11	77.6843	0.01326	0.87178	211387_x_RNGTT	AB012143 RNA guany
146.356	138.9657	130.71	0.013264	0.940592	210015_s_MAP2	U89330 microtubule
138.422	140.6507	125.8868	0.013296	0.895032	1559680_a_TTL	BG115434 tubulin tyro:
31.9148	21.78031	27.75743	0.013309	1.274428	238732_at COL24A1	AI631241 collagen, ty
44.8165	35.48454	41.95914	0.013388	1.182463	1569053_a AP3M2	BG110196 Adaptor-rel
318.556	285.1551	300.3192	0.013394	1.053178	227390_at MEG3	H89790 maternally i
68.0324	70.2743	61.0803	0.013403	0.86917	217666_at ---	AW974481 CDNA clon
234.887	297.4826	243.5913	0.013409	0.818842	232857_at POLR3H	AL023553 polymerase
216.029	172.4673	187.3541	0.013413	1.086317	239940_at ADK	BE674244 Adenosine
303.948	296.3822	324.7488	0.013421	1.095709	243708_at TMEM132	AI678145 transmemb
94.6454	104.182	93.2056	0.013436	0.894642	1555358_a ENTPD4	BC034477 ectonucleo:
322.17	350.2374	302.8794	0.013482	0.864783	218538_s_MRS2L	NM_02066 MRS2-like,
104.763	101.5877	87.95326	0.013499	0.865786	206583_at ZNF673	NM_01777 zinc finger j
460.019	478.8326	531.3153	0.013499	1.109606	206061_s_DICER1	NM_03062 Dicer1, Dcr
930.858	1106.251	982.3481	0.013535	0.887997	202173_s_ZNF161	NM_00714 zinc finger j
120.03	156.4356	187.8459	0.013558	1.200788	226205_at ANKRD13	AW512315 ankyrin rep
85.1789	92.3787	85.05521	0.013567	0.920723	207478_at ---	NM_01854 ---
109.152	108.569	122.8053	0.013607	1.131127	203808_at ---	M95936 ---
177.64	207.2377	235.1509	0.013621	1.134692	220554_at SLC22A7	NM_00667 solute carri
148.656	137.3663	144.8612	0.013665	1.054561	1554850_a LOC90113	BC009862 hypothetica
134.665	139.7021	150.6256	0.013696	1.078191	222756_s_ARRB1	BC003636 arrestin, be
46.1935	48.02039	42.77128	0.013724	0.89069	242067_at LOC64614	T84046 Similar to tc
50.9479	57.62062	48.3384	0.013734	0.838908	1555571_a IMMP2L	BC008497 IMP2 inner
501.474	532.3522	635.1362	0.013747	1.193075	218522_s_BPY2IP1	NM_01817 BPY2 inter:
242.478	307.257	362.0726	0.01379	1.178403	238190_at TUFM	AI143752 Tu translati
48.7371	62.64046	55.0048	0.013803	0.878103	238598_s_RNF32	BE962709 Ring finger
38.8531	37.27121	34.54274	0.013829	0.926794	1562671_s---	AK093301 CDNA FLJ:
190.661	172.5819	189.0296	0.013857	1.095304	211079_s_DYRK1A	Z25423 dual-specifi
183.088	253.574	219.4109	0.01387	0.865274	230790_x---	AI589978 ---
300.131	275.782	295.5633	0.013915	1.071728	221987_s_TSR1	AI803633 TSR1, 20S
400.943	395.872	351.9499	0.013928	0.88905	219723_x_AGPAT3	NM_02013 1-acylglyce
78.4485	58.24796	65.07498	0.013939	1.117206	235881_at FMNL2	AW293988 formin-like :
257.894	272.365	259.8638	0.01394	0.954101	1554962_a FGFR4	AF359241 fibroblast g
253.275	311.9878	288.0966	0.013971	0.923423	227995_at ---	AI051950 MRNA; cDI
123.116	125.8693	140.5861	0.013976	1.116921	1558381_a GAPDHS	AA322821 Glyceraldel
6181.78	5583.761	6007.08	0.013976	1.075812	214328_s_HSP90AA1	R01140 heat shock
86.5132	103.0454	119.4528	0.014024	1.159225	229981_at SNX5	AA131508 sorting nex
91.0908	95.21339	106.7374	0.014025	1.121033	239273_s_MMP28	AI927208 matrix meta:
121.635	150.9166	122.2376	0.014039	0.809968	238844_s_NPHP1	BF216535 nephronopl
188.737	210.8269	230.4941	0.014056	1.093286	1566633_a---	BC018655 CDNA clon
84.1655	112.9325	98.54492	0.014067	0.8726	1552327_a ARMCX4	NM_15258 armadillo re
206.95	209.3676	224.6046	0.014119	1.072776	218907_s_LRRC61	NM_02394 leucine rich
71.3702	73.48824	69.10443	0.01412	0.940347	1554702_a VGCNL1	BC028390 voltage gat
352.292	375.2017	431.1639	0.014145	1.149152	214316_x---	AI378706 Transcribec
70.21	60.1317	66.5271	0.014158	1.106357	242929_at RHOH	AW275093 Ras homok
62.1178	65.18096	57.31763	0.014164	0.879362	230752_at CBX5	AI638063 Chromobox
102.903	111.7941	102.4061	0.014169	0.916024	220102_at FOXL2	NM_02306 forkhead bc
394.796	469.4162	521.1088	0.014232	1.110121	206976_s_HSPH1	NM_00664 heat shock
2020.33	1896.414	2406.639	0.014236	1.269047	211765_x_PPIA	BC005982 peptidylpro
30.456	29.59132	34.8859	0.014252	1.178923	1559054_a PPP1R7	BC027905 Protein phc
373.15	391.1461	476.8692	0.014253	1.219159	221737_at GNA12	AK024696 guanine nu
31.0085	36.96429	31.36024	0.014271	0.848393	242577_at LOC64239	BF109197 hypothetica

72.6947	73.0411	81.18038	0.014272	1.111434	235217_at ---	AW148862 CDNA clon
238.667	258.1621	318.4724	0.014315	1.233614	212412_at PDLIM5	AV715767 PDZ and LI
172.645	149.8913	165.1977	0.014322	1.102116	241004_at GAB2	BF510198 GRB2-assc
48.7093	55.58436	66.46758	0.014339	1.195796	221304_at UGT1A10	NM_01907 UDP glucur
222.928	241.5216	229.9474	0.014344	0.952078	237438_at ---	BF433065 Transcribed
5180.02	4106.202	4655.353	0.014369	1.133737	217356_s_PGK1	S81916 phosphogly
285.556	347.8437	308.371	0.014378	0.886522	207131_x_GGT1	NM_01343 gamma-glu
20.1584	18.25667	23.74244	0.014414	1.30048	211775_x_MGC13053	BC006134 hypothetica
79.1183	87.14087	100.8413	0.014454	1.157222	232626_at TAS2R14	AK024205 Taste rece
66.9514	54.7089	62.55252	0.014463	1.14337	1561300_a---	BC041998 CDNA clon
239.993	232.2736	249.5587	0.014463	1.074417	160020_at MMP14	Z48481 matrix meta
909.76	733.9382	919.8186	0.014481	1.253264	200848_at AHCYL1	AA479488 S-adenosyl
74.9826	87.17597	101.164	0.01449	1.160458	210146_x_LILRB2	AF004231 leukocyte ir
54.4714	53.34014	49.0638	0.014543	0.919829	1560918_a---	AF086316 Full length
1365.74	1684.719	1479.817	0.014554	0.878376	202334_s_UBE2B	AI768723 ubiquitin-cc
313.901	303.405	335.4934	0.014561	1.105761	1561561_x---	BC026219 CDNA clon
34.5105	34.86399	30.28118	0.014604	0.868552	237496_at PAPSS2	AI821404 3'-phospho
13.4594	17.54019	14.80632	0.014614	0.844137	1556678_aLOC28437	AF086256 Hypothetic
581.274	437.3496	522.5462	0.014651	1.194802	204518_s_PPIC	NM_00094 peptidylpro
25.8136	22.60048	28.04057	0.014662	1.240707	234861_at LOC93463	AL122100 hypothetica
267.786	255.6426	271.1162	0.01469	1.060529	227170_at ---	BF338409 MRNA; cDI
74.8779	76.12707	82.3247	0.014715	1.081412	202884_s_PPP2R1B	NM_00271 protein pho
328.731	340.483	360.3782	0.014752	1.058432	222692_s_FNDC3B	BF444916 fibronectin
122.544	132.2103	138.8028	0.014774	1.049863	223527_s_CDADC1	AL138875 cytidine anc
33.035	35.56802	28.55649	0.01478	0.80287	1567853_aZNF28	X52355 zinc finger j
38.9032	53.44301	72.83997	0.014796	1.362947	1569830_aPTPRC	BC031525 Protein tyrc
142.784	155.0042	167.7022	0.014834	1.08192	1569461_aKCNT1	BC035730 potassium c
192.611	168.194	144.2307	0.014857	0.857526	205371_s_DBT	M27093 dihydrolipo
188.778	181.919	201.2863	0.01487	1.106461	231732_at SMPD3	NM_01866 sphingomy
201.699	177.9673	198.536	0.014886	1.115576	229691_at ---	BF221887 Full-length
327.414	403.4639	360.5876	0.014893	0.893729	219431_at ARHGAP11	NM_02460 Rho GTPas
138.802	132.5717	149.8197	0.014906	1.130103	1566113_aTMCC1	AA176313 Transmeml
32.4909	17.07113	25.30686	0.01491	1.482436	1553365_aDEPDC4	NM_15231 DEP domai
217.019	215.5849	227.8371	0.014972	1.056832	235096_at LEO1	AA074729 Leo1, Paf1,
60.0376	59.44746	65.82927	0.015001	1.107352	240120_at SORBS2	H72914 Sorbin and
80.7647	80.10057	96.2133	0.015022	1.201156	1562380_a---	BC041838 CDNA clon
92.4594	85.51522	96.01792	0.015041	1.122817	1563070_a---	BC038579 CDNA clon
52.9966	62.3385	52.17881	0.015093	0.837024	236235_at ITCH	AA868238 Itchy homo
42.9218	44.73424	50.93367	0.015104	1.138583	215615_x_RERE	AU148274 Arginine-glu
212.948	238.3178	263.9284	0.015115	1.107464	1559237_a---	BC039687 Homo sapi
47.4927	52.20822	47.83789	0.015121	0.91629	242787_at ---	AI924134 Transcribed
56.1043	52.9143	63.50787	0.015123	1.200202	238498_at ---	AA583038 MRNA full l
75.181	83.00157	95.40353	0.015124	1.149418	214353_at ---	AW241864 Transcribed
166.796	210.3901	241.0698	0.015126	1.145823	1558375_aLRRC38	BG472587 leucine rich
1651.23	1863.31	1662.014	0.015139	0.891969	218011_at UBL5	NM_02429 Ubiquitin-lik
205.881	226.3956	257.0684	0.015142	1.135484	223546_x_LUC7L	AY005111 LUC7-like (
266.623	321.1096	285.96	0.015207	0.890537	240943_at PSMF1	AA678195 Proteasom
2716.14	3192.47	3030.63	0.015253	0.949306	214800_x_BTF3	R83000 basic trans
35.1897	27.76358	32.43327	0.015324	1.168195	242161_at STK17A	AI458049 Serine/thre
133.078	141.8938	117.6167	0.015372	0.828907	224546_at ---	AF257098 ---
143.746	146.9214	136.83	0.015419	0.931314	224498_x_AXIN2	BC006295 axin 2 (con
135.749	163.2448	142.6839	0.015422	0.874049	1570098_aLOC64349	BC013917 Hypothetic

239.4	229.5144	247.1382	0.015459	1.076787	209207_s_SEC22B	BC001364	SEC22 ves
617.175	844.4518	759.5786	0.015465	0.899493	226736_at CHURC1	BE568660	churchill do
260.409	249.3843	275.5524	0.015481	1.104931	218305_at IPO4	NM_02465	importin 4
135.517	143.2354	158.575	0.015485	1.107093	1568977_a RNASET2	BC019871	ribonucleas
55.6469	55.62894	44.56156	0.015488	0.80105	1555829_a FAM62B	BC001224	family with
38.8766	43.07744	50.15738	0.015495	1.164354	242224_at GPATC2	R40111	G patch do
132.734	135.4744	147.6583	0.015519	1.089935	242841_at ---	N68415	Full length
888.087	844.457	1074.27	0.01553	1.272143	209276_s_GLRX	AF162769	glutaredoxi
133.245	127.0132	115.9051	0.01561	0.912544	217288_at FLJ13236	AL049983	Hypothetic
233.654	364.6766	310.8799	0.015645	0.852481	1557341_x ---	AL523099	---
182.363	222.3647	192.1669	0.01568	0.864197	227854_at FANCL	BE620258	Fanconi an
203.701	199.56	179.1954	0.015688	0.897953	209975_at CYP2E1	AF182276	cytochrome
394.104	391.7282	421.3399	0.015714	1.075592	235317_at LOC28445	AW975045	hypothetica
401.483	403.2126	432.4741	0.015762	1.072571	221818_at INTS5	BF446693	integrator c
285.74	259.2639	279.8677	0.015767	1.07947	201976_s_MYO10	NM_01233	myosin X
9.17315	15.77967	10.93532	0.015779	0.693	1554793_a UBE3C	BC014029	ubiquitin pr
280.453	292.8898	314.6457	0.015833	1.07428	214992_s_DNASE2	AD000092	deoxyribon
355.793	346.59	389.3358	0.015876	1.123332	220363_s_ELMO2	NM_02208	engulfment
34.5317	39.04639	30.50318	0.015901	0.781204	233406_at KIAA0256	AK022100	KIAA0256 (
338.568	328.5448	355.0044	0.01592	1.080536	217264_s_SCNN1A	U81961	sodium cha
225.516	226.8706	252.4597	0.015923	1.112792	221082_s_NDRG3	NM_02247	NDRG fam
92.4578	102.781	110.3821	0.015941	1.073954	1554719_a NDUFA10	BC031332	NADH dehy
171.377	184.7301	207.1074	0.015953	1.121135	217280_x_GABRA5 //	AF061785	gamma-am
92.0909	97.75717	86.12783	0.016009	0.881039	204840_s_EEA1	AI916242	early endos
208.916	214.4748	193.8179	0.01601	0.903686	219655_at C7orf10	NM_02472	chromosom
449.933	394.1547	445.6372	0.016026	1.130615	214373_at ---	AI582773	CDNA clon
128.274	93.36783	110.6332	0.016059	1.184918	225124_at PPP1R9B	BF508705	protein pho
165.711	195.1478	166.8501	0.016063	0.854994	210679_x ---	BC002629	---
237.009	226.5499	247.1843	0.016067	1.091081	243374_x ---	AW452674	Transcriber
117.865	124.2359	114.5982	0.016108	0.922424	214518_at PDHA2	NM_00539	pyruvate de
178.222	212.1772	260.1433	0.016175	1.226066	233734_s_OSBPL5	AW271225	oxysterol bi
181.3	193.2397	177.5274	0.016185	0.91869	1559029_a ---	BI560014	CDNA clon
273.342	319.5072	288.1573	0.016254	0.901881	225476_at BAT4	H10318	HLA-B assc
625.631	614.2932	713.5953	0.016285	1.161653	217039_x_IGHG1	AB016195	Immunoglo
65.3042	57.10177	68.2055	0.016311	1.194455	204512_at HIVEP1	NM_00211	human imr
198.785	243.5732	211.6677	0.016317	0.86901	241365_at ---	AA002140	CDNA FLJ
44.92	42.124	49.1114	0.016318	1.165877	1555734_x AP1S3	AF393369	adaptor-rel
116.258	165.8029	211.3972	0.016324	1.274991	236570_at ZNF366	BE552137	zinc finger j
26.9817	27.55898	32.30187	0.016456	1.1721	235874_at PRSS35	AL574912	protease, s
220.553	243.9323	219.818	0.016468	0.901143	242214_at RPS27A ///	AU152194	ribosomal p
179.815	181.3307	199.7228	0.016474	1.101429	215725_at DGCR11	L77561	DiGeorge s
204.832	209.4686	223.8177	0.016484	1.068502	243432_at LOC64289	BF114921	hypothetica
618.949	457.6851	552.8271	0.016496	1.207877	209114_at TSPAN1	AF133425	tetraspanin
131.012	133.0773	143.7149	0.016521	1.079935	244617_at GPR26	R46128	G protein-c
283.009	275.8528	317.6687	0.016546	1.151588	207180_s_HTATIP2	NM_00641	HIV-1 Tat ir
79.0548	75.98217	85.08001	0.016559	1.119737	223882_at C5orf21	AL136630	chromosom
196.213	163.697	179.8783	0.016568	1.098849	237562_at KIAA0240	BF478143	KIAA0240
57.4101	60.99818	78.04687	0.016582	1.279495	238018_at LOC28501	BF449053	hypothetica
1073.09	1037.704	1117.198	0.016585	1.076606	203197_s_C1orf123	AW157077	chromosom
878.846	835.7606	1093.127	0.016669	1.307943	208747_s_C1S	M18767	complemer
66.9359	116.7716	88.31036	0.01669	0.756266	1555801_s_ZNF533	BC038422	zinc finger j
96.1888	115.7423	131.28	0.016704	1.134244	238295_at C17orf42	N22706	Chromosom

75.4827	62.96208	70.77163	0.016762	1.124036	221139_s_CSAD	NM_01598	cysteine su
214.907	241.5379	272.2008	0.016765	1.126949	1565662_a MUC6	BF476613	Mucin 6, oli
41.815	37.85387	27.03587	0.016779	0.714217	230837_at ---	N67108	---
23.6105	21.63963	27.77308	0.016813	1.283436	219948_x_ UGT2A3	NM_02474	UDP glucur
46.0871	47.81971	53.69157	0.016872	1.122792	242737_at RAD51L1	AW293315	RAD51-like
117.883	130.6414	147.1744	0.016873	1.126552	1569961_a---	BC033124	Homo sapi
102.64	114.7917	140.2494	0.016877	1.221773	230441_at KIAA1909	AI890356	KIAA1909 p
2942.8	3185.656	2993.656	0.016879	0.93973	205508_at SCN1B	NM_00103	sodium cha
193.626	194.7009	175.5089	0.016894	0.901428	204897_at PTGER4	AA897516	prostaglanc
165.861	160.1196	196.9654	0.016899	1.230115	209835_x_ CD44	BC004372	CD44 mole
50.1814	67.89053	76.17257	0.016926	1.121991	1558607_a PAPPA	BQ024803	pregnancy-
126.438	121.407	110.2219	0.017003	0.907871	215993_at ODZ2	AF070543	Odz, odd C
74.8362	84.6866	90.88198	0.017029	1.073157	216847_at KIAA1660	AB051447	KIAA1660 p
124.044	160.2536	179.9559	0.017069	1.122945	243510_at ---	AI273692	---
365.613	366.0168	426.0968	0.017072	1.164145	211376_s_ C10orf86	BC005212	chromosorr
74.5843	84.74053	103.0617	0.017073	1.216203	231738_at PCDHB7	NM_01894	protocadhe
533.765	479.7099	552.1468	0.01708	1.151001	235041_at GOSR2	AW005457	golgi SNAP
156.936	163.1011	176.8048	0.017104	1.084019	225023_at GOPC	BE547542	golgi assoc
104.287	121.3048	145.244	0.01711	1.197348	233891_at ---	AF007192	---
41.7339	53.92649	47.75494	0.017128	0.885556	1560033_a MCCC2	AK090834	Methylcrotc
78.8694	75.685	68.80466	0.017143	0.909092	216155_at NAV1	AK024543	Neuron nav
439.025	404.24	438.153	0.017152	1.083893	229558_at MGC16824	AI927643	Esophagea
450.671	391.2253	437.347	0.017187	1.11789	202812_at GAA	NM_00015	glucosidase
189.558	199.3741	179.3042	0.017194	0.899336	1557038_s---	AK097488	Clone IMA
478.049	400.8384	462.1697	0.017268	1.153007	230648_at LOC28366	AI377398	hypothetica
88.1461	95.81039	109.5963	0.01727	1.143888	240860_at ---	AI417160	---
149.452	152.1887	172.7779	0.017271	1.135287	1569274_a LOC28355	BC033249	Hypothetica
101.254	123.846	111.4504	0.017279	0.899911	228603_at LOC44090	AA977481	Hypothetica
30.9301	39.26239	33.1712	0.01728	0.844859	1557810_a CCT5	BM352108	Chaperonir
435.863	407.802	440.299	0.017282	1.079688	202224_at CRK	BF304695	v-crk sarco
23.0308	28.04456	21.97744	0.017321	0.783662	1568871_a---	BC032557	---
233.606	217.3483	232.5652	0.017336	1.070012	235332_at FAM22A	AW501360	family with
419.886	536.1112	491.0699	0.017336	0.915985	203597_s_ WBP4	AI734228	WW domai
212.01	216.2618	228.13	0.017358	1.054879	220566_at PIK3R5	NM_01430	phosphoinc
308.077	272.1011	286.881	0.017361	1.054318	34868_at SMG5	AB029012	Smg-5 horr
91.7204	95.1701	90.43558	0.017372	0.950252	214184_at NPFF	AW195837	neuropepti
140.346	153.0382	173.263	0.017378	1.132155	240031_at ---	AA994467	---
227.3	220.4698	241.0579	0.017389	1.093383	216111_x_ PMS2L3	U38979	postmeiotic
1305.14	1218.707	1398.332	0.017473	1.14739	200850_s_ AHCYL1	NM_00662	S-adenosyl
262.961	263.904	289.521	0.017531	1.097069	220143_x_ LUC7L	NM_01803	LUC7-like (
111.48	102.801	113.9046	0.017543	1.108011	230683_at ---	W56760	CDNA: FLJ
2948.82	2700.973	2957.166	0.017607	1.094852	200627_at PTGES3	BC003005	prostaglanc
168.788	180.7934	194.021	0.017622	1.073164	212727_at DLG3	AB033058	discs, large
325.078	311.1763	344.1069	0.017684	1.105826	201325_s_ EMP1	NM_00142	epithelial m
259.084	227.8852	249.0562	0.017711	1.092902	232208_at ISLR2	AW007241	immunoglo
187.752	201.0511	226.2901	0.01772	1.125535	212354_at SULF1	BE500977	sulfatase 1
589.842	489.3561	523.4687	0.017787	1.069709	218864_at TNS1	AF116610	tensin 1
170.803	177.0644	187.9771	0.017805	1.061631	226144_at REXO1	AB032964	REX1, RN/
230.993	244.8808	226.2389	0.017809	0.923874	219817_at C12orf47	NM_01653	chromosorr
263.285	303.8676	335.0713	0.017838	1.102689	36865_at ANGEL1	AB018302	angel homc
181.865	201.8463	177.7482	0.017839	0.880612	235653_s_ THAP6	BF685315	THAP dom.
8.0919	10.97743	7.886882	0.017839	0.718463	1554131_a KIAA1128	BC030528	KIAA1128

196.674	188.7112	217.4561	0.017957	1.152322	235666_at ---	AA903473 ---
252.227	255.6223	276.6049	0.017997	1.082084	212789_at hCAP-D3	AI796581 KIAA0056 ;
1001.97	948.2546	1091.136	0.018013	1.150679	212854_x_ NBPf10	AB051480 neuroblastc
243.395	254.1326	294.729	0.018054	1.159745	1555051_a C10orf53	BC028127 chromosom
955.632	1211.364	971.0961	0.018089	0.801655	230671_at LOC38925	BF056222 Similar to L
74.856	94.66533	81.22821	0.018096	0.858057	239562_at MTHFD2L	AW272411 methylenet
40.9965	48.25447	58.86693	0.018138	1.219927	237566_at ---	BF060696 Transcribec
166.903	188.8551	165.4204	0.018143	0.875912	236657_at ---	AW014647 Full length
202.118	195.8222	216.3607	0.018173	1.104883	234973_at SLC38A5	BG325630 solute carri
206.181	193.886	205.3903	0.018208	1.059336	239670_at ---	BG231979 ---
38.3833	50.77982	60.80392	0.018212	1.197403	1556682_s AUTS2	AF086391 Autism sus
336.515	333.1198	350.4092	0.01826	1.051902	210896_s ASPH	AF306765 aspartate b
99.7341	89.11337	97.65478	0.018296	1.095849	243223_at ---	AA453526 Transcribec
95.8955	87.04709	100.5079	0.018335	1.154639	230473_s HMGB4	BF057167 high-mobili
370.013	364.3958	415.0302	0.018341	1.138955	227096_at JOSD2	AI218850 Josephin d
636.068	612.2138	690.8408	0.018364	1.128431	203333_at KIFAP3	NM_01497 kinesin-ass
81.0589	82.70311	100.9404	0.018429	1.220515	214592_s SNAPC5	BE259395 small nucle
95.2427	98.71274	89.03781	0.01846	0.901989	220921_at SPANXB1	NM_01345 SPANX fan
740.866	666.7094	704.9941	0.01847	1.057423	201768_s ENTH	BC004467 enthoprotin
145.065	231.6694	194.9409	0.018491	0.841461	1552736_a NETO1	NM_13896 neuropilin (
410.289	399.4923	450.5137	0.018541	1.127715	230513_at BAT3	AW104426 HLA-B assc
79.5715	95.13098	111.2381	0.018541	1.169315	241247_at ---	BF740043 ---
55.1925	58.12062	66.56038	0.018551	1.145211	1553923_a MGC34821	NM_17358 hypothetica
105.148	103.4832	116.8773	0.018556	1.129433	204060_s PRKX /// P	NM_00504 protein kin
212.403	200.7887	215.8144	0.018563	1.074834	208299_at CACNA1I	NM_02109 calcium ch
107.73	141.8207	164.3104	0.018566	1.158579	202499_s SLC2A3	NM_00693 solute carri
254.707	264.7738	278.2901	0.018591	1.051049	240644_at ---	BF433665 Transcribec
123.745	136.762	124.3129	0.01861	0.908972	205538_at CORO2A	NM_00338 coronin, ac
395.549	415.1749	399.7781	0.018617	0.962915	228567_at ---	BG109230 CDNA FLJ:
40.876	39.89406	45.80213	0.018631	1.148094	234544_at ARHGEF1:	AL080067 Rho guanin
52.6111	55.80817	49.7197	0.018717	0.890904	1560695_a QTRTD1	AL832215 Queuine tR
320.412	331.7261	309.2474	0.018737	0.932237	230731_x_ ---	AI453548 ---
59.6879	55.39866	60.4429	0.018746	1.091054	1570395_a FAM66C	BC034777 family with
229.572	216.8186	240.849	0.018764	1.110832	230929_s_ ---	AW167553 ---
77.0174	85.2549	100.1193	0.018769	1.174352	216358_at ---	AL137010 ---
307.989	296.149	330.1709	0.01878	1.114881	210647_x_ PLA2G6	AF102988 phospholip:
142.619	150.1822	137.7276	0.018862	0.91707	1554796_a DPP6	BC035912 dipeptidyl-p
81.8589	76.00983	86.38317	0.018871	1.136474	240689_at LOC28367	AI989520 hypothetica
187.679	207.2819	190.6073	0.0189	0.919556	1558959_a ---	AK095236 CDNA FLJ:
89.9072	98.20339	114.5944	0.018914	1.166909	207916_at RBM	NM_00540 similar to R
163.265	198.6498	236.37	0.018929	1.189883	224297_s_ SPTBN4	AY004227 spectrin, be
713.934	610.4439	678.0936	0.018942	1.11082	202746_at ITM2A	AL021786 integral me
478.676	437.6411	502.1396	0.018954	1.147377	205606_at LRP6	NM_00233 low density
29.7604	37.97686	42.02983	0.018978	1.106722	210969_at PKN2	AF118089 protein kin
523.149	478.4061	516.8202	0.018984	1.080296	229493_at HOXD9	BF315468 Homeobox
42.235	44.89233	50.08631	0.019012	1.115699	210882_s TRO	U04811 trophinin
235.504	247.4792	260.9373	0.019026	1.054381	225625_at ALKBH2	AI865555 alkB, alkyla
138.508	136.825	146.9637	0.019026	1.0741	216716_at ABO	U15197 ABO blood
164.216	161.8254	153.9998	0.019067	0.951641	223767_at GPR84	AF237762 G protein-c
210.721	209.2479	227.5627	0.01908	1.087527	214523_at CEBPE	NM_00180 CCAAT/enl
102.028	107.8075	131.098	0.019094	1.216038	204112_s_ HNMT	NM_00689 histamine N
75.7926	75.12329	83.00222	0.0191	1.10488	220242_x_ ZNF701	NM_01826 zinc finger j

581.19	576.1103	681.786	0.019103	1.18343	207618_s_BCS1L	NM_00432 BCS1-like (
74.4049	73.37322	81.36868	0.019138	1.10897	223868_s_WWOX	AF227528 WW domai
99.5647	100.2466	92.85053	0.019153	0.926221	243067_at ---	BG290999 Transcribec
23.8256	19.39619	22.23516	0.019194	1.146367	202989_at RGS1	NM_00292 regulator of
503.361	530.6244	601.0169	0.019205	1.13266	202349_at TOR1A	NM_00011 torsin famil
372.563	529.6323	456.4797	0.019212	0.86188	203203_s_KRR1	NM_00704 KRR1, sma
97.493	106.7907	127.7724	0.019238	1.196475	243062_at FLCN	AV694665 Folliculin
131.248	132.7877	124.7011	0.019263	0.939102	204777_s_MAL	NM_00237 mal, T-cell
609.844	587.5716	563.8907	0.019272	0.959697	203911_at RAP1GAP	NM_00288 RAP1 GTP
107.354	96.67727	106.6895	0.019296	1.103563	1561345_a---	BC038426 CDNA clon
183.413	255.3773	221.8753	0.019316	0.868814	227808_at DNAJC15	AI091398 DnaJ (Hsp4
110.198	109.6142	98.84769	0.019322	0.901779	211584_s_NPAT	U58852 nuclear pro
155.346	240.2959	171.0801	0.019338	0.711956	1560081_a LOC90408	AL702091 hypothetica
62.3572	64.73017	57.93184	0.019338	0.894974	1566129_a LIMS1	AK098109 LIM and se
218.019	182.4856	200.8499	0.019345	1.100634	211672_s_ARPC4	AF019888 actin relate
235.397	229.3736	239.8822	0.019355	1.045815	221680_s_ETV7	AF147782 ets variant
27.8876	29.09409	35.51812	0.019384	1.220802	1561855_x---	AY034469 Clone BGL
295.261	271.3209	296.6496	0.019411	1.093353	211776_s_EPB41L3	BC006141 erythrocyte
143.889	134.5281	122.7779	0.019421	0.912656	240462_at CLYBL	AI419840 Citrate lyas
644.671	540.1057	586.1543	0.019422	1.085259	225468_at FLJ36874	AI761804 FLJ36874 p
343.803	398.1332	371.5208	0.019437	0.933157	203345_s_MTF2	AI566096 metal respc
277.326	329.6293	374.9261	0.019472	1.137417	1555902_a ARMCX5	BC022066 armadillo re
82.4887	100.2405	113.1675	0.019478	1.12896	231437_at SLC35D2	AA693722 Solute carri
23.911	8.52739	16.23461	0.019483	1.903819	222608_s_ANLN	AK023208 anillin, actir
304.49	291.1752	330.2341	0.019523	1.134142	238652_at AOF2	AW419203 Amine oxid
537.383	609.6902	555.9016	0.019539	0.911777	209445_x_FLJ10803	AI765280 hypothetica
246.619	269.7884	298.3027	0.019572	1.105691	43511_s_a---	AI201594 MRNA; cDI
300.452	275.3482	295.9633	0.019573	1.074869	213700_s_PKM2	AA554945 Pyruvate ki
45.7499	57.2197	64.84588	0.019575	1.133279	237625_s_---	BG548679 Immunoglo
264.552	295.8072	330.254	0.01959	1.11645	202277_at SPTLC1	AL568804 serine palrr
119.276	119.5826	130.6704	0.019601	1.092722	235430_at C14orf43	AA158537 chromosom
206.071	194.1846	211.0592	0.019606	1.0869	222191_s_B4GALT7	AK022566 xylosylprote
159.532	175.4743	198.5922	0.019648	1.131745	234867_at ---	AE000661 T cell recep
414.37	377.4691	403.3866	0.019661	1.068661	225605_at TP53I13	AL540867 tumor prote
84.9691	77.68478	86.93147	0.019664	1.119028	220401_at FLJ21369	NM_02480 hypothetica
287.613	247.652	269.6069	0.019673	1.088652	210973_s_FGFR1	M63889 fibroblast g
170.387	171.9544	191.7449	0.019692	1.115091	231330_at ---	AW450689---
1020.8	1336.055	1422.559	0.019739	1.064746	206592_s_AP3D1	NM_00393 adaptor-rel:
138.879	169.4543	152.7091	0.01975	0.901182	1556365_a RP3-398D	BC031936 Hypothetica:
132.884	119.6958	111.114	0.01978	0.928303	236471_at NFE2L3	AI949827 nuclear fac
104.019	107.8661	96.34833	0.019788	0.893221	232087_at CXorf23	AW628045 chromosom
106.3	102.762	119.3257	0.019852	1.161184	203242_s_PDLIM5	BG054550 PDZ and LI
185.247	223.3971	249.7274	0.019873	1.117863	214237_x_PAWR	AI760470 PRKC, apo
45.0862	41.12639	45.05588	0.019878	1.095547	207149_at CDH12	L33477 cadherin 12
153.684	171.3899	150.2723	0.019911	0.876786	244647_at ---	AA233885 Transcribec
115.114	140.947	167.099	0.019934	1.185545	238405_at GAB2	AI792896 GRB2-assc
706.633	791.9852	700.877	0.019962	0.884962	212544_at ZNHIT3	AI131008 zinc finger,
62.7082	73.72866	67.13159	0.020011	0.910522	1558236_a---	BC014318 ---
483.97	410.7368	476.182	0.020042	1.159336	211716_x_ARHGDI	BC005851 Rho GDP c
30.1322	28.60883	35.06496	0.020053	1.225669	208261_x_IFNA10	NM_00217 interferon, :
94.5717	147.8076	190.414	0.020104	1.288256	244021_at KIAA0256	AI467800 KIAA0256 g
181.748	179.9953	167.6537	0.020125	0.931433	241009_at FOXN4	AI243313 forkhead bc

465.341	454.6199	511.4278	0.020191	1.124957	207169_x_DDR1	NM_00195 discoidin dc
622.546	786.0674	675.2814	0.020211	0.859063	203983_at TSNAX	NM_00599 translin-ass
652.554	679.6119	640.2587	0.020222	0.942095	209929_s_IKBKG	AF091453 inhibitor of
80.5621	93.44587	82.19388	0.020224	0.879588	236834_at SCFD2	AI025103 sec1 family
423.263	760.2426	607.9259	0.020243	0.799647	213734_at WSB2	BG260658 WD repeat
29.695	40.39833	33.90011	0.020244	0.839146	240370_at PKD2	AI432451 Polycystic l
180.673	173.5412	184.2639	0.02028	1.061787	213265_at PGA5 /// L	AI570199 pepsinoger
139.547	135.5898	148.6797	0.020281	1.09654	238882_at LOC38764	BF000697 Hypothetica
91.6632	99.53292	74.25437	0.020281	0.746028	206153_at CYP4F11	NM_02118 cytochrome
2597.91	2438.23	2606.61	0.020283	1.069058	200000_s_PRPF8	NM_00644 PRP8 pre-r
237.533	234.1251	250.0052	0.020289	1.067827	226647_at TMEM25	AL562445 transmemb
81.707	81.55669	90.71379	0.020292	1.112279	233403_x_TM6SF2	AK026307 transmemb
52.4677	55.5355	50.50988	0.020292	0.909506	232164_s_EPPK1	AL137725 epiplakin 1
117.832	109.3083	118.6472	0.020295	1.085436	221078_s_KIAA1212	NM_01808 KIAA1212
629.837	587.7156	612.7667	0.020312	1.042625	201561_s_CLSTN1	NM_01494 calsyntenin
100.75	99.34993	113.7448	0.020315	1.14489	229409_s_C10orf22	AW195553 Chromosor
133.481	145.9916	161.6627	0.020346	1.107343	243404_at ---	AA553477 ---
92.185	108.4072	128.3363	0.020352	1.183836	226906_s_ARHGAP9	AL548053 Rho GTPas
205.355	214.3704	197.8162	0.020365	0.922777	216119_s_C20orf28	AL109804 chromosor
667.23	697.7072	636.7571	0.020451	0.912642	1553952_a_ZDHHC19	NM_14463 zinc finger,
840.996	695.947	757.033	0.020488	1.087774	201148_s_TIMP3	AW338933 TIMP meta
107.883	133.7421	162.5798	0.02051	1.215621	237753_at ---	AW504569 Transcribec
146.516	140.0177	127.4542	0.020521	0.910272	230684_at DKFZP686	T65158 hypothetica
600.977	566.7426	589.7111	0.020539	1.040527	223188_at FLJ12886	AL136606 hypothetica
917.978	825.512	886.7779	0.020548	1.074216	226389_s_RAPGEF1	AU158380 Rap guanin
86.1754	80.03069	90.62979	0.020583	1.132438	211891_s_ARHGEF4	AB042199 Rho guanin
39.4684	39.08429	32.03129	0.020617	0.819544	214702_at FN1	AJ276395 fibronectin
231.565	264.5988	302.7643	0.020636	1.144239	243022_at ---	BF509158 ---
96.6061	121.2771	144.4432	0.020637	1.191018	1568695_s_INTS6	AW665713 integrator c
462.564	408.8871	455.4594	0.020645	1.1139	1564413_a_FLJ36116	AK093435 hypothetica
105.697	127.167	119.8757	0.020688	0.942663	215852_x_KIAA0889	AK022023 KIAA0889 p
317.699	268.4216	293.203	0.020742	1.092323	238445_x_MGAT5B	AI609043 mannosyl (;
16.0361	18.41568	14.53119	0.020774	0.789066	1569484_s_MDN1	AL603301 MDN1, mid
149.343	149.1904	160.9998	0.020776	1.079156	227901_at LOC64898	AI056871 hypothetica
58.982	59.36383	54.87801	0.020801	0.924435	228859_at LOC91431	BF056790 prematurely
329.811	315.5409	355.8341	0.020812	1.127696	211040_x_GTSE1	BC006325 G-2 and S-
207.334	189.3493	205.8843	0.020814	1.087325	237110_at ---	BF445178 Transcribec
265.887	314.3446	336.5593	0.020814	1.07067	217764_s_RAB31	AF183421 RAB31, me
455.976	489.7001	538.303	0.020841	1.09925	200996_at ACTR3	NM_00572 ARP3 actin
51.2634	60.52054	54.43347	0.020847	0.899421	1563496_a_LOC20246	AL713649 hypothetica
163.839	146.2721	161.923	0.02085	1.106998	240560_at ---	BE855599 ---
70.2829	82.61061	78.11446	0.020858	0.945574	1570210_x_SAPS2	BC022346 SAPS dom.
212.905	229.209	257.1763	0.020872	1.122017	232573_at FBXO32	AL389956 F-box prote
606.03	576.9789	637.2482	0.020872	1.104457	203175_at RHOG	NM_00166 ras homolo
47.1273	50.99876	44.2574	0.020882	0.867813	1552721_a_FGF1	NM_03313 fibroblast g
137.197	158.388	133.8069	0.020882	0.844804	227022_at GNPDA2	AI817388 glucosamin
349.154	577.1557	501.7794	0.021006	0.869401	228049_x ---	AA523172 Transcribec
267.569	293.3612	345.9756	0.021071	1.17935	208270_s_RNPEP	NM_02021 arginyl amii
104.852	111.6062	120.6458	0.021089	1.080996	230510_at HSPB9	BF439726 heat shock
201.043	190.2774	202.2282	0.021098	1.062807	229701_at ---	AW205929 ---
53.433	56.50622	47.9381	0.021143	0.848369	234433_at ---	AL117577 MRNA; cDI
18.8199	25.41268	19.03453	0.021155	0.749017	231909_x_ODF2L	AB033055 outer dense

87.422	89.18828	98.13161	0.021155	1.100275	1554846_a	FLJ25770	BC035224	hypothetica
242.35	238.7243	268.8983	0.021173	1.126397	50314_i_at	C20orf27	AI761506	chromosom
95.0329	79.99719	88.37493	0.021183	1.104725	241049_at	GRM7	AA018686	glutamate r
144.267	156.0139	140.3788	0.021216	0.899784	244611_at	THRAP1	H38035	Thyroid hor
115.456	128.3899	119.0566	0.021227	0.927305	236847_at	C19orf18	AI650509	chromosom
186.409	197.8783	215.7012	0.021232	1.09007	241671_x_	FLJ22536	H14782	hypothetica
167.951	169.6404	160.6102	0.021266	0.946768	224307_x_	MAGI3	AF213259	membrane
281.794	277.3214	244.9024	0.021273	0.8831	1569597_a	PITPNC1	BC015861	Phosphatid
940.084	916.0239	1014.434	0.02128	1.107431	209489_at	CUGBP1	N25915	CUG triplet
39.8596	44.72389	57.69402	0.021288	1.290005	243275_at	BMPR1A	BE644666	Bone morp
80.4736	91.34524	82.303	0.021302	0.90101	1559078_a	BCL11A	BM193618	B-cell CLL/
156.13	197.1368	176.7256	0.02131	0.896462	239481_at	RP1-32F7.	AI864183	hypothetica
122.087	123.7769	138.3041	0.021311	1.117366	205662_at	EPPB9	NM_01568	B9 protein
205.411	225.3147	261.0274	0.02138	1.158502	212938_at	COL6A1	M20776	collagen, ty
134.513	134.7768	144.5906	0.021411	1.072815	228475_at	---	AC007785	Transcribec
119.021	130.1463	146.8078	0.021436	1.128021	1562942_a	---	BC035345	Homo sapi
385.076	365.1183	395.9369	0.021448	1.084407	223314_at	TSPAN14	BF025955	tetraspanin
250.193	247.7551	273.0903	0.021472	1.102259	205906_at	FOXJ1	NM_00145	forkhead bc
111.48	104.0354	114.261	0.021475	1.09829	240303_at	LOC64676	BG484769	Hypothetica
53.3928	52.34181	59.51823	0.021494	1.137107	1555301_a	DIP2A	BC033718	DIP2 disco
77.4001	69.96552	63.44642	0.02153	0.906824	229206_at	---	BE551650	CDNA FLJ
92.7725	117.9952	95.07762	0.021531	0.805775	1562903_a	FLJ10661	BC035792	similar to C
3189.8	2614.254	2919.584	0.021551	1.116794	200983_x_	CD59	BF983379	CD59 mole
510.726	473.1516	518.6492	0.021564	1.096159	201247_at	---	BE513151	---
114.435	123.8969	147.582	0.021567	1.191168	207836_s_	RBPMS	NM_00686	RNA bindin
176.364	192.2438	174.0642	0.021575	0.905435	227162_at	ZBTB26	BF214688	zinc finger ;
459.815	454.2789	569.0787	0.021597	1.252708	203886_s_	FBLN2	NM_00199	fibulin 2
87.2355	91.95756	81.52833	0.021617	0.886587	1564387_a	DOPEY1	AK094766	dopey fami
231.014	235.2653	251.5336	0.021617	1.069148	227393_at	TMEM16J	AW084755	transmemb
260.438	291.6548	325.25	0.021622	1.115188	208361_s_	POLR3D	NM_00172	polymerase
333.993	458.4636	577.9534	0.021632	1.260631	208730_x_	RAB2	AA535244	RAB2, men
272.027	257.0043	296.8118	0.021694	1.15489	201311_s_	SH3BGRL	AL515318	SH3 domai
591.798	527.9466	592.617	0.021706	1.122494	216836_s_	ERBB2	X03363	v-erb-b2 er
669.793	567.1269	627.2007	0.021707	1.105927	203388_at	ARRB2	NM_00431	arrestin, be
98.7197	116.7828	103.1711	0.021786	0.883445	244657_at	GBA3	AW341707	Glucosidas
78.0639	81.01803	93.05904	0.021792	1.148621	232840_at	FNDC3B	AK025004	Fibronectin
119.165	116.4293	129.629	0.021798	1.113371	225963_at	KLHDC5	AW293538	kelch doma
230.636	254.2773	230.3024	0.021805	0.905714	1565587_a	---	BC033401	CDNA clon
1857.06	1311.852	1612.272	0.021815	1.229004	217456_x_	HLA-E	M31183	major histo
180.416	174.9183	157.0749	0.02185	0.89799	204234_s_	ZNF195	AI476267	zinc finger j
549.893	677.4041	606.0354	0.021852	0.894644	213995_at	ATP5S	AW195882	ATP synthe
1192.98	1492.488	1377.392	0.021854	0.922883	209289_at	NFIB	AI700518	nuclear fac
261.971	252.3421	259.2227	0.021866	1.027267	219815_at	GAL3ST4	NM_02463	galactose-3
88.1307	95.38167	87.62876	0.021866	0.918717	233530_at	FKBP1A	W26305	FK506 binc
72.4432	84.10692	92.97236	0.021937	1.105407	232497_at	ZNF3	AF217988	zinc finger j
292.239	274.2887	307.4149	0.02197	1.120771	208131_s_	PTGIS	NM_00096	prostaglanc
60.2901	59.48164	70.62181	0.021988	1.187287	215551_at	ESR1	AI073549	estrogen re
159.468	170.401	193.1649	0.022019	1.13359	202962_at	KIF13B	NM_01525	kinesin fam
438.153	616.5427	530.6357	0.02202	0.860663	227447_at	SKIV2L2	AA525163	superkiller
185.398	167.0887	183.0064	0.022029	1.095265	238814_at	---	AW772411	---
253.429	289.0726	255.7983	0.022042	0.884893	213844_at	HOXA5	NM_01910	homeobox
56.8506	58.70486	65.55952	0.022047	1.116765	241826_x_	---	AI758317	Transcribec

526.581	582.7261	515.6357	0.022048	0.884868	212604_at MRPS31	AI937794 mitochondr
3236	2392.44	3011.682	0.022061	1.258833	200696_s_ GSN	NM_00017 gelsolin (an
9010.94	9130.626	8896.947	0.022067	0.974407	212363_x_ ACTG1	AU145192 actin, gamr
183.553	186.5393	200.5931	0.022074	1.075339	203071_at SEMA3B	NM_00463 sema doma
29.1157	34.61484	30.17372	0.022082	0.871699	1565898_a METT5D1	AI687680 Methyltrans
67.9939	54.59808	62.90514	0.022107	1.152149	244723_at ACSM2	BF510430 Acyl-CoA s
941.9	977.5221	1024.425	0.022114	1.047981	50277_at GGA1	AW001443 golgi assoc
222.13	211.3726	223.1127	0.022132	1.055542	233977_at KIAA1772	AB051559 KIAA1772
32.9782	39.72293	36.07438	0.022156	0.90815	1555298_a MGC26733	BC026091 hypothetica
239.824	244.816	267.5378	0.022183	1.092812	202274_at ACTG2	NM_00161 actin, gamr
240.99	232.1461	243.8489	0.022185	1.050411	242081_at CENTB1	AI808637 Centaurin,
186.457	191.05	212.341	0.022233	1.111442	1570330_a ---	BC013641 Homo sapi
332.449	318.4506	349.5802	0.022259	1.097754	227145_at LOXL4	AW190565 lysyl oxidas
56.7188	45.31114	52.95604	0.022358	1.16872	1569850_a LOC64656	BC031321 hypothetica
126.666	154.3983	176.8892	0.022409	1.145668	237511_at DEADC1	AA702788 Deaminase
127.176	121.0374	129.0396	0.02245	1.066113	221155_x_ ---	NM_01860 PRO1496
37.2534	45.11869	39.57038	0.022541	0.877029	219612_s_ FGG	NM_00050 fibrinogen c
56.2338	71.56843	63.82668	0.022558	0.891827	233004_x_ NFIA	AU146087 Nuclear fac
180.951	216.7094	249.1526	0.022579	1.149708	223295_s_ LUC7L	BE049621 LUC7-like (
124.121	169.8869	138.9089	0.022599	0.817655	213092_x_ DNAJC9	AW241779 DnaJ (Hsp
239.901	241.1472	223.9003	0.022607	0.92848	238618_at NF2	BE313317 neurofibron
33.0053	33.05979	38.53074	0.022624	1.165487	1554476_x LOC38855	BC033230 hypothetica
306.176	291.7562	329.0693	0.022626	1.127891	233563_s_ CPSF3L	AK023356 cleavage ai
435.684	514.3659	564.0307	0.022635	1.096555	211989_at SMARCE1	NM_00307 SWI/SNF re
878.365	788.3289	877.8978	0.02266	1.113619	230566_at FLJ35801	AI806805 hypothetica
49.9455	48.52648	59.17957	0.022674	1.219531	239962_at EPS15L1	AA972452 Epidermal c
96.3201	110.1946	126.1711	0.022683	1.144985	216328_at SIGLEC8	AF287892 sialic acid b
164.459	183.8149	196.8501	0.022713	1.070915	204003_s_ NUPL2	NM_00734 nucleoporin
24.4817	23.19978	28.04512	0.022762	1.208853	1558725_a ---	BU579943 ---
40.8413	43.21328	38.3576	0.022789	0.887635	1569677_a C8orf45	BC034576 chromosom
399.932	386.2117	424.7428	0.022856	1.099767	221087_s_ APOL3	NM_01434 apolipoprot
113.867	114.8212	104.0488	0.022865	0.906181	236402_at ---	AW184034 CDNA FLJ
1033.37	865.577	995.7854	0.02289	1.15043	201011_at RPN1	NM_00295 ribophorin I
125.133	118.806	126.2338	0.022893	1.06252	214408_s_ RFPL3S ///	AL021937 ret finger pr
145.733	151.1276	162.4413	0.022916	1.074862	240900_at MGC11257	BF508795 hypothetica
386.807	403.2952	443.6868	0.022924	1.100154	216873_s_ ATP8B2	AL137537 ATPase, Cl
149.905	153.1404	162.1609	0.022949	1.058903	240302_at ---	AW450681 Transcribed
337.53	425.7043	390.0173	0.022991	0.91617	229436_x_ BRCC3	AI672084 BRCA1/BR
34.3668	33.98183	39.20531	0.022992	1.153714	1556842_a LOC28608	AI033510 hypothetica
250.655	302.066	341.5142	0.022993	1.130595	203859_s_ PALM	NM_00257 paralemmir
82.4783	81.03804	87.80993	0.023	1.083564	241515_at DHRS3	AA007535 Dehydroge
171.957	170.1867	194.3902	0.02303	1.142218	228296_at YPEL1	AW450686 yippee-like
223.513	217.0487	229.0483	0.023052	1.055286	206388_at PDE3A	U36798 phosphodie
718.111	638.2856	732.0908	0.023085	1.146964	208851_s_ THY1	AL161958 Thy-1 cell s
132.451	150.881	168.1549	0.023104	1.114487	205096_at POM121	NM_01483 POM121 m
910.884	732.9607	806.2753	0.023113	1.100025	238583_at MSRB3	BG023974 methionine
363.584	379.2456	344.7557	0.023132	0.909057	235124_at LOC64521	BE502930 hypothetica
55.5613	60.85549	57.76869	0.023135	0.949277	1559030_a ---	BI560014 CDNA clon
345.892	299.1824	327.0238	0.023148	1.093058	229002_at FAM69B	AI095583 family with
123.398	120.6709	112.1109	0.02316	0.929063	1558014_s MLSTD2	BG261090 male sterilit
200.205	206.8744	229.301	0.023163	1.108407	224596_at SLC44A1	AI634866 solute carri
787.967	922.4404	827.1679	0.023174	0.896717	234762_x_ NLN	AK026655 Neurolysin

63.0168	72.84572	61.54559	0.023194	0.844876	243927_x_KIAA1429	AI636247	KIAA1429
335.354	335.9824	383.4551	0.023204	1.141295	202709_at FMOD	NM_00202	fibromoduli
244.728	501.5792	423.3973	0.023223	0.844129	1553575_a---	NM_17371	---
598.558	617.0529	734.9176	0.023317	1.191012	211740_at ICA1	BC005922	islet cell au
79.3991	117.0415	150.0924	0.023333	1.282386	210293_s_SEC23B	BC005032	Sec23 hom
57.901	58.76798	68.46116	0.023336	1.16494	221212_x_PB1	NM_01831	polybromo
413.432	374.9883	402.5624	0.023383	1.073533	242324_x_CCBE1	AA740403	collagen an
98.4702	87.17253	99.14404	0.02339	1.137331	231198_at CDK6	AW665776	Cyclin-depe
307.195	312.3873	325.6827	0.02342	1.04256	241346_at ARHGAP3	AW974499	Rho GTPas
163.654	168.1799	185.1671	0.023425	1.101006	1569796_s ATRNL1	BC035157	attractin-lik
217.192	140.0998	162.3269	0.02348	1.158652	228948_at EPHA4	T15545	EPH recept
234.485	244.5724	257.2906	0.023502	1.052001	215189_at KRTHB6 //	X99142	keratin, hai
85.6105	88.64976	102.6447	0.023516	1.157868	237732_at ---	AI432195	---
518.635	687.9598	621.2219	0.023541	0.902992	215063_x_LRRC40	AL390149	leucine rich
58.109	61.14441	49.8715	0.02355	0.815635	235331_x_PCGF5	AI341142	polycomb g
126.775	127.6731	134.8151	0.023597	1.05594	242150_at ---	AI304876	Transcribec
263.149	254.3759	270.9593	0.023604	1.065193	1316_at THRA	X55005	thyroid horr
57.0409	68.31458	59.8697	0.023612	0.876382	228812_at ---	AI652899	Transcribec
61.9555	64.44543	69.99106	0.023619	1.086051	238155_at ---	AI638235	Transcribec
56.7398	56.82646	63.7005	0.023654	1.120966	203400_s_TF	NM_00106	transferrin
142.22	188.7718	207.1649	0.023723	1.097436	214997_at GOLGA1	AW675473	Golgi autoa
100.205	111.3664	102.3565	0.023727	0.919097	237982_at ---	AI023219	CDNA clon
170.882	195.0428	221.1167	0.023732	1.133683	232350_x_GPR161	AI754926	G protein-c
115.959	124.931	115.0161	0.023753	0.920637	227386_s_TTMB	N63821	TTMB prote
1015.99	1086.524	1166.787	0.023801	1.073871	211684_s_DYNC112	AF250307	dynein, cyto
502.9	654.9739	532.4742	0.023843	0.81297	227250_at KREMEN1	BF221745	kringle cont
841.102	800.9072	906.5649	0.023875	1.131922	216384_x_LOC64328	AF257099	similar to p
538.306	492.9663	526.6362	0.023907	1.068301	221498_at SNX27	BF939727	sorting nex
426.929	409.3347	437.2057	0.023917	1.068089	218509_at LPPR2	NM_02273	lipid phospl
106.645	162.2966	130.6336	0.023923	0.804907	243695_at ---	AA435933	Transcribec
55.0002	67.71092	57.22754	0.023931	0.845174	241745_at ---	BF671564	Full-length
82.3785	91.07403	104.7202	0.023931	1.149835	238612_at ---	AW298070	Transcribec
150.261	162.4823	145.1723	0.02397	0.893465	235415_at ---	BE781857	---
226.518	316.7129	271.2333	0.024001	0.856401	219158_s_NARG1	NM_02508	NMDA rece
161.235	180.818	164.0487	0.024013	0.907258	215310_at APC	AF038181	Adenomac
1211.15	1267.512	1351.134	0.024036	1.065974	209100_at IFRD2	BC001327	interferon-r
394.193	496.6096	439.738	0.024068	0.88548	230893_at DNAJA5	AI223870	DnaJ homc
399.127	386.7323	410.3384	0.024074	1.06104	208191_x_PSG4	NM_00278	pregnancy
81.5932	81.58057	89.07999	0.024075	1.091927	238205_at WDR40B	AW572906	WD repeat
78.241	84.08104	100.7118	0.024088	1.197795	1562190_a---	BG717200	CDNA clon
339.825	329.7064	350.3201	0.024109	1.062521	204368_at SLCO2A1	NM_00563	solute carri
340.459	336.9196	355.5767	0.024123	1.055376	220765_s_LIMS2	NM_01798	LIM and se
100.597	114.1659	123.1259	0.024157	1.078482	216739_at ---	AK024527	CDNA: FLJ
309.767	404.2697	368.888	0.024182	0.91248	214902_x_LPP	AL080232	LIM domair
143.815	117.1181	129.0577	0.024188	1.101944	243827_at ---	AL038125	Transcribec
262.19	218.2704	240.7708	0.024276	1.103085	205396_at SMAD3	BF971416	SMAD, mol
214.153	217.1794	240.5982	0.024286	1.107831	208114_s_ISG20L2	NM_03098	interferon s
178.289	173.9307	196.594	0.024323	1.130301	228023_x_AMY2B	AV699389	amylase, al
137.173	156.9811	172.9227	0.024366	1.101551	222129_at C2orf17	AK026155	Chromosor
68.1195	70.93197	62.65236	0.024368	0.883274	232794_at LOC64401	AL137383	Hypothetic
99.303	124.1513	109.589	0.024368	0.882705	227513_s_LRRFIP1	AW027170	Leucine ricl
494.032	551.4019	490.7814	0.024388	0.890061	208735_s_CTDSP2	AF022231	CTD (carbc

356.592	387.9171	438.4344	0.024396	1.130227	202796_at SYNPO	NM_00728 synaptopoc
122.318	127.7099	139.6299	0.024402	1.093337	232614_at BCL2	AU146963 B-cell CLL/
76.8509	78.11456	87.5182	0.024409	1.120383	1561433_a LOC28510	BC036597 hypothetica
172.146	261.9573	228.5356	0.024416	0.872415	220539_at C10orf92	NM_01760 chromosom
71.4822	74.43131	86.87548	0.024429	1.16719	226834_at ---	BG112263 Transcribec
1162.71	992.5597	1148.302	0.024437	1.15691	224895_at YAP1	AA557632 Yes-associ
176.676	261.3351	214.601	0.024453	0.821172	205442_at MFAP3L	NM_02164 microfibrilla
355.432	333.4342	350.4701	0.02448	1.051092	1556520_a ---	BC029602 CDNA clon
1055.29	1125.119	1479.839	0.024502	1.315273	213503_x_ ANXA2	BE908217 annexin A2
152.018	182.4749	161.0718	0.024537	0.882707	235406_x_ ---	BF512190 CDNA clon
123.342	149.2894	173.4683	0.024575	1.16196	232942_at C10orf33	AU147503 Chromosor
41.3003	31.78647	37.66732	0.02459	1.185011	205651_x_ RAPGEF4	NM_00702 Rap guanin
145.06	180.3693	167.6257	0.024592	0.929347	1563621_a KIAA1706	AL713724 KIAA1706 j
150.347	143.8601	158.9163	0.024692	1.104659	1566885_a C17orf84	AK026247 chromosom
91.3279	85.53841	93.84376	0.024716	1.097095	236892_s_ ---	BF590528 ---
622.469	801.5557	740.8454	0.024728	0.92426	201671_x_ USP14	BC003556 ubiquitin sp
183.692	257.2292	225.1297	0.024737	0.87521	209807_s_ NFIX	U18759 nuclear fac
220.278	204.2548	226.0281	0.02476	1.106599	200011_s_ ARF3	NM_00165 ADP-ribosy
214.612	208.1631	232.1429	0.024774	1.115197	204288_s_ SORBS2	NM_02106 sorbin and
296.765	287.6893	310.4316	0.02479	1.079051	211385_x_ SULT1A2	U28169 sulfotransfe
157.186	158.7524	153.1066	0.024792	0.964436	212684_at ZNF3	AI752257 zinc finger j
343.669	318.4851	341.9511	0.024795	1.07368	1559753_a GPR133	AI024349 G protein-c
21.84	29.60759	24.05202	0.024868	0.81236	243126_x_ CHM	AW452782 Choroidere
190.4	289.1951	247.0727	0.024875	0.854346	240530_at SLC25A16	BF222808 Solute carri
59.3113	62.58101	69.96193	0.024902	1.117942	1554294_s TTBK2	BC041876 tau tubulin
103.78	104.564	94.01278	0.024922	0.899094	1559372_a ---	BC039533 Homo sapi
70.9162	90.57836	79.10481	0.024934	0.87333	1553113_s CDK8	BF700678 Cyclin-depe
78.5816	80.21419	92.17406	0.025057	1.149099	1566288_a OR2M4	X89666 olfactory re
184.493	203.3423	185.4154	0.02506	0.911839	219751_at SETD6	NM_02486 SET domai
278.617	305.1127	275.0476	0.02506	0.901462	235253_at RAD1	AI742925 RAD1 hom
145.439	122.1014	130.6884	0.025067	1.070327	234502_at ---	AL049254 MRNA; cDI
272.199	265.8318	287.6151	0.025075	1.081944	224182_x_ SEMA6B	AF293363 sema doma
156	138.3749	158.0327	0.025127	1.142062	220254_at LRP12	NM_01343 low density
479.579	489.85	520.5524	0.025167	1.062677	218551_at RP5-1077E	NM_02193 invasion inf
547.798	723.3396	680.2944	0.025188	0.940491	224284_x_ FKSG49	AF338193 FKSG49
122.967	143.2469	160.2864	0.025201	1.118952	243623_at SLC1A7	N39099 solute carri
593.938	566.2287	633.3578	0.02521	1.118555	214924_s_ TRAK1	AK000754 trafficking p
206.558	192.0786	225.9794	0.025229	1.176495	208792_s_ CLU	M25915 clusterin
344.331	346.2373	317.5309	0.025232	0.91709	202896_s_ SIRPA	NM_00464 signal-regu
114.138	102.5143	109.3087	0.025238	1.066278	215248_at GRB10	AU145003 growth fact
157.042	178.5248	150.054	0.02526	0.840522	243501_at ---	BF002823 ---
117.95	127.6142	148.8314	0.025267	1.166261	222812_s_ RHOF	AF239923 ras homolo
159.277	151.7278	162.983	0.025277	1.07418	240210_at ATAD3C	AW024933 ATPase far
137.98	131.8416	145.9836	0.025283	1.107265	209129_at TRIP6	AF000974 thyroid horr
198.75	192.9981	202.1544	0.025294	1.047443	240189_at ACOXL	BF064226 Acyl-Coenz
412.229	402.5094	431.0622	0.025302	1.070937	215693_x_ DDX27	AL512707 DEAD (Asp
90.2765	97.26229	86.11166	0.025311	0.885355	217524_x_ ---	AA018923 Transcribec
573.371	483.0566	548.9921	0.025314	1.136497	209593_s_ TOR1B	AF317129 torsin famil
120.73	148.1156	167.7972	0.025341	1.13288	231496_at FCAMR	AW028140 Fc receptor
32.3722	34.27806	28.91799	0.025344	0.84363	242571_at REPS2	AW962020 RALBP1 as
46.425	70.24791	57.54141	0.025344	0.819119	1556284_a PPA2	AF086012 Pyrophospl
490.015	485.8706	527.2332	0.025352	1.085131	223617_x_ ATAD3B	BC002542 ATPase far

237.465	248.2724	236.5459	0.025362	0.952767	214051_at MGC3990	BF677486	hypothetica
152.186	201.5912	239.2006	0.025383	1.186562	216293_at CLTA	X81636	Clathrin, lig
140.819	148.4869	162.2544	0.025404	1.092719	1563118_a---	AK024576	CDNA: FLJ
2532.71	2229.273	2511.212	0.02543	1.126471	1568986_x PIGT	AF305815	Phosphatid
1305.53	1237.385	1431.643	0.025446	1.156991	201022_s_ DSTN	NM_00687	destrin (act
217.173	207.5952	226.861	0.025451	1.092805	223349_s_ BOK	BE614255	BCL2-relate
1633.46	1502.19	1670.079	0.025471	1.111763	217772_s_ MTCH2	NM_01434	mitochondr
184.874	164.4826	155.4434	0.025477	0.945045	209639_s_ RGS12	AF030111	regulator of
162.953	106.3872	127.4079	0.025486	1.197587	201566_x_ ID2 /// ID2E	D13891	inhibitor of
137.043	162.7834	137.5047	0.025517	0.844709	220874_at ---	NM_01857	---
84.8593	115.0682	136.9269	0.02554	1.189964	223781_x_ ADH4	M15943	alcohol deh
558.846	565.5577	505.4463	0.025543	0.893713	207081_s_ PIK4CA	NM_00265	phosphatid
65.0604	76.85323	64.52719	0.02555	0.839616	243800_at NR1H4	AI051958	nuclear rec
230.615	247.4727	268.4103	0.025577	1.084606	212555_at PRKAR1B	AI814660	protein kin
173.456	219.8231	265.2338	0.025582	1.206578	241181_x_ ---	AI732986	Transcribec
25.9375	42.32909	33.12153	0.025734	0.782477	1557883_a---	AI806183	CDNA FLJ:
131.827	145.125	133.9323	0.025735	0.922876	235781_at CACNA1B	AA448208	calcium cha
351.643	306.1108	334.029	0.025747	1.091203	209473_at ---	AV717590	---
533.781	558.4168	634.7598	0.025749	1.136713	219104_at RNF141	NM_01642	ring finger p
212.304	224.0163	248.6563	0.025756	1.109992	1557954_a CXorf15	BM757251	chromosom
526	467.3081	505.0203	0.025771	1.080701	219013_at GALNT11	NM_02208	UDP-N-ace
90.4491	90.35407	112.2582	0.025815	1.242425	237076_at ---	AI634534	---
146.937	148.6891	155.7033	0.025837	1.047174	215890_at GM2A	X61094	GM2 gangl
302.167	284.8411	301.6268	0.025837	1.05893	203652_at MAP3K11	NM_00241	mitogen-ac
2644.65	1669.42	2522.181	0.025849	1.510813	203828_s_ IL32	NM_00422	interleukin :
97.9265	96.1842	108.5148	0.025862	1.128197	212336_at EPB41L1	AA912711	erythrocyte
86.0114	85.69691	91.04584	0.025863	1.062417	243488_at ---	BF223653	Transcribec
16.3171	13.69792	18.22704	0.025881	1.330643	1570103_a---	BC017995	Homo sapi
175.784	228.9787	196.1221	0.025885	0.856508	221995_s_ ---	BF195165	---
156.987	146.6532	157.894	0.025888	1.076649	237950_s_ ---	AV649666	---
98.5871	105.226	126.2799	0.025912	1.200083	219608_s_ FBXO38	NM_02486	F-box prote
103.721	111.5203	122.3398	0.025933	1.097018	228280_at MGC14285	AI188445	similar to R
442.154	421.9724	468.3568	0.025935	1.109923	221545_x_ THRAP5	AF106934	thyroid horr
307.466	328.1588	275.8512	0.025993	0.840603	1553960_a C20orf161	CA447177	chromosom
1072.83	1050.97	1191.457	0.02604	1.133674	1560439_a LOC64519	AW304683	similar to le
287.188	288.376	303.3453	0.026074	1.051909	202348_s_ TOR1A	BC000674	torsin famil
114.808	126.2576	141.8233	0.02608	1.123286	243717_at EPHA10	AI681862	EPH recepti
98.4988	92.7574	81.76214	0.026105	0.881462	231341_at SLC35D3	BE670584	solute carri
404.49	359.95	388.622	0.026107	1.079656	218255_s_ FBS1	NM_02245	fibrosin 1
88.695	95.26094	104.8764	0.026112	1.100938	242999_at ARHGEF7	AI990366	Rho guanin
89.0773	105.1598	119.1637	0.026132	1.133167	1565554_a LOC12784	BC015457	hypothetica
142.611	143.434	155.693	0.026143	1.085468	219909_at MMP28	NM_02430	matrix met
2300.99	2230.131	2532.056	0.026153	1.135384	200675_at CD81	NM_00435	CD81 mole
100.803	102.0673	112.6788	0.026168	1.103965	1558693_s C1orf85	AW090182	chromosom
231.963	212.7932	232.8131	0.0262	1.094081	1569392_a LOC64834	BC034484	hypothetica
809.723	711.4746	777.2522	0.02622	1.092453	211594_s_ MRPL9	AB049636	mitochondr
48.3747	53.25563	43.6395	0.026228	0.819434	1560369_a ANKH	AL833238	Ankylosis, p
64.7829	60.1522	68.28626	0.026356	1.135225	243059_at LOC28390	AI680624	hypothetica
366.725	391.9809	420.6057	0.02641	1.073026	222035_s_ PAPOLA	AI984479	poly(A) pol
771.356	773.0762	877.7176	0.026412	1.135357	226740_x_ NBPF14 ///	BF740216	neuroblast
104.138	119.1158	130.6462	0.026418	1.0968	1565621_a---	AW117431	---
198.561	204.2947	224.6272	0.026442	1.099526	205262_at KCNH2	NM_00023	potassium v

204.541	190.2306	203.8657	0.026479	1.071677	221794_at DOCK6	AI198543	dedicator o
65.2267	54.02891	71.07397	0.026491	1.31548	1554119_a C16orf57	BC010099	chromosom
45.1954	50.96692	62.26203	0.026528	1.221617	217582_at ---	AA018777	---
140.705	144.3627	128.0596	0.026564	0.887068	217648_at RWDD3	AW295367	RWD doma
223.352	295.8406	264.0216	0.026624	0.892445	225537_at TRAPPC6	AA936745	trafficking p
144.126	197.295	162.8012	0.026645	0.825166	216519_s_ PROSC	AK021923	proline synt
30.0405	32.78162	28.70233	0.026692	0.875562	1561657_a NCAM1	AF086073	Neural cell
70.2545	72.14854	77.03204	0.026704	1.067687	212800_at STX6	AI740832	syntaxin 6
1379.69	1130.919	1258.788	0.026705	1.113067	243258_at KIAA0664	AW291521	KIAA0664
56.9441	64.42616	79.6191	0.026706	1.23582	230628_at EP400	AI809582	E1A binding
88.1991	107.4187	131.732	0.026716	1.226341	205560_at PCSK5	NM_00620	proprotein c
438.015	416.8591	446.8601	0.026717	1.071969	212895_s_ ABR	AL527773	active BCR
1565.68	1649.824	1875.01	0.02672	1.136491	218007_s_ RPS27L	NM_01592	ribosomal p
1104.98	1182.573	1593.744	0.02679	1.347692	210427_x_ ANXA2	BC001388	annexin A2
86.2614	90.42157	106.7945	0.026831	1.181074	214755_at UAP1L1	AK022632	UDP-N-acti
496.474	486.3574	513.868	0.026864	1.056564	221382_at ---	NM_01234	---
212.001	228.1302	244.7456	0.026868	1.072833	1562981_a HBB	AY034472	Hemoglobin
576.411	565.0074	819.4543	0.026876	1.450343	202291_s_ MGP	NM_00090	matrix Gla p
57.1228	65.45021	55.80037	0.026888	0.852562	239902_at ---	AI766224	---
60.692	61.97038	71.24823	0.026897	1.149714	1566833_x TOP1P2	M55630	topoisomer
489.322	475.771	542.1021	0.026947	1.139418	242160_at STX17	AI733506	Syntaxin 17
102.964	102.1306	111.3832	0.026965	1.090596	244320_at NHLRC2	BE046449	NHL repeat
287.274	266.9063	317.7983	0.026972	1.190674	200625_s_ CAP1	NM_00636	CAP, aden
80.3644	89.0114	99.81963	0.026998	1.121425	223829_at TKTL2	AL136779	transketola
128.902	126.938	143.4107	0.027019	1.129769	237240_at PSMD6	AW590101	Proteasom
66.0728	62.36576	68.60642	0.02702	1.100066	224363_at FLJ34870	AF251048	FLJ34870 p
116.234	143.043	156.431	0.027052	1.093594	240916_x_ ---	AI793205	---
158.665	170.4177	159.7852	0.027078	0.937609	220833_at ---	NM_01624	---
6829.14	6947.853	6614.571	0.027089	0.952031	202090_s_ UQCR	NM_00683	ubiquinol-c
130.23	157.8828	142.9437	0.027097	0.905378	217143_s_ TRA@ /// T	X06557	T cell rece
201.747	196.373	235.0301	0.027142	1.196856	212154_at SDC2	AI380298	syndecan 2
654.304	572.0947	601.8159	0.027162	1.051952	212432_at GRPEL1	AL542571	GrpE-like 1
350.03	307.0461	328.4037	0.027177	1.069558	221215_s_ RIPK4	NM_02063	receptor-int
161.885	164.2611	184.4993	0.027208	1.123208	211630_s_ GSS	L42531	glutathione
73.4038	79.88927	73.90752	0.027233	0.925125	1559232_a SLC33A1	BC029450	Solute carri
260.104	348.7066	308.3833	0.027239	0.884363	228275_at ---	AI200555	CDNA FLJ:
408.164	422.7983	464.0911	0.027267	1.097665	221715_at MYST3	Z25437	MYST histc
380.164	446.7788	408.0926	0.027277	0.913411	233873_x_ PAPD1	AL122121	PAP assoc
295.316	284.7116	296.7703	0.027277	1.042354	244366_at ---	AA758547	---
411.387	431.1708	459.7081	0.027282	1.066186	212653_s_ EHBP1	AB020710	EH domain
85.5573	84.92286	79.9012	0.027339	0.940868	236723_at HNRPU	AW196279	Heterogene
153.411	120.9293	129.035	0.027351	1.067028	243232_at LOC55424	AW139588	Hypothetic
222.481	213.484	232.7222	0.027381	1.090116	227677_at JAK3	BF512748	Janus kina
249.222	235.05	248.7621	0.027382	1.058337	220475_at SLC28A3	NM_02212	solute carri
645.497	700.9332	772.7449	0.027396	1.102452	219933_at GLRX2	NM_01606	glutaredoxi
186.338	208.3389	229.1814	0.027412	1.100042	239831_at TMEM106	R19392	Transmeml
38.2004	53.57964	65.46901	0.02743	1.221901	221681_s_ DSPP	AF094508	dentin sialo
23.4842	17.74663	20.88063	0.02744	1.176597	240093_x_ FLJ20366	H09269	Hypothetic
963.991	740.9606	822.609	0.027487	1.110193	219083_at SHQ1	NM_01813	SHQ1 hom
201.964	221.0252	238.3208	0.027496	1.078252	217965_s_ SAP30BP	NM_01326	SAP30 binc
37.9929	47.74557	40.87462	0.027496	0.856093	1560977_a ZD77D08	W74646	hypothetica
86.6051	126.1629	159.1059	0.027513	1.261115	239593_at LOC15500	AI769774	hypothetica

27.7072	45.30869	34.81054	0.027541	0.768297	244340_x_---	AW975183---
242.149	276.0594	307.8363	0.027547	1.115109	221697_at	MAP1LC3(AF276659 microtubule
7.38094	8.254886	5.908943	0.027557	0.715812	1561222_a	LOC28343 BC037211 hypothetica
180.541	199.561	162.9898	0.027653	0.816742	1553186_x	RASEF NM_15257 RAS and E
46.9379	57.22798	51.53958	0.027681	0.900601	1560204_a	NT5DC4 BC041437 5'-nucleotid
1149.94	1252.453	1379.179	0.027692	1.101182	200020_at	TARDBP NM_00737 TAR DNA b
154.16	165.6334	175.019	0.027719	1.056665	222481_at	FXC1 W67995 fracture cal
326.931	326.9326	345.007	0.027732	1.055285	212676_at	---
354.5	381.3982	422.1476	0.027734	1.106842	1569935_a	ZNF664 BC033539 Zinc finger
796.225	809.6474	885.0754	0.027735	1.093162	214011_s	HSPC111 BE314601 hypothetica
85.2216	95.35469	111.0348	0.027762	1.16444	211506_s	IL8 AF043337 interleukin i
210.733	227.9194	246.615	0.027775	1.082027	207844_at	IL13 NM_00218 interleukin
112.251	132.5561	122.6189	0.02779	0.925034	244092_at	ZRANB3 AI670931 zinc finger,
210.9	189.5064	210.0697	0.027804	1.108509	224792_at	TNKS1BP1 AL566438 tankyrase 1
113.973	122.7438	141.4891	0.027861	1.152719	1566924_a	---
281.559	571.686	488.7691	0.027862	0.854961	200908_s	RPLP2 BC005354 ribosomal p
280.306	275.8133	235.8188	0.027863	0.854994	238165_at	PDZRN3 AW665629 PDZ domai
21.2804	25.5521	20.48061	0.027882	0.801524	234702_x	CFTR S64699 Cystic fibro
167.4	276.2651	225.7347	0.027884	0.817094	236300_at	---
268.463	290.8111	327.699	0.027893	1.126845	230502_s	LOC14983 BE501966 Hypothetica
105.335	101.5388	110.0248	0.027949	1.083573	208933_s	---
31.2322	35.56981	41.12293	0.027959	1.156119	44790_s_a	C13orf18 AI129310 chromosom
472.28	409.4108	436.5027	0.02796	1.066173	209013_x	TRIO AF091395 triple functi
91.0634	127.3502	110.2444	0.027983	0.865679	210701_at	CFDP1 D85939 craniofacial
274.945	233.2778	252.3264	0.028003	1.081657	212916_at	PHF8 AW249934 PHD finger
171.422	188.4706	206.8452	0.028011	1.097494	1556063_s	LOC28301 AW182934 hypothetica
351.561	288.1082	374.335	0.028072	1.299286	222987_s	TMEM9 NM_01645 transmemb
370.589	338.8357	372.6367	0.02809	1.099756	212882_at	KLHL18 AB018338 kelch-like 1
181.495	230.1574	208.7967	0.028102	0.907191	1559712_a	LOC15482 BC042556 hypothetica
136.689	145.6797	155.4874	0.028114	1.067324	238589_s	ATXN2 AW601184 Ataxin 2
68.0597	94.64474	118.5802	0.028115	1.252898	207363_at	RS1 NM_00033 retinoschisi
139.81	152.9422	169.5938	0.028137	1.108875	210507_s	AVIL BC004134 advillin
806.806	930.5384	839.0902	0.028162	0.901725	223350_x	LIN7C N63709 lin-7 homol
207.038	166.3968	180.1967	0.028182	1.082934	233292_s	ANKHD1 // AK024189 ankyrin rep
54.5181	54.34749	46.37426	0.028239	0.853292	1556598_a	FLJ32997 / AI698023 hypothetica
1128.53	996.16	1107.78	0.028248	1.112051	200714_x	OS9 NM_00681 amplified in
327.775	296.3861	350.9859	0.028266	1.184218	201301_s	ANXA4 BC000182 annexin A4
8517.65	8723.354	8183.789	0.02829	0.938147	203863_at	---
56.8177	59.43631	72.89044	0.028302	1.226362	220190_s	ALF /// SAL NM_00687 TFIIA-alpha
69.5995	63.9774	73.28684	0.028307	1.145511	236970_s	BCAP29 BF433093 B-cell recep
145.106	153.5611	168.9571	0.028324	1.10026	234189_at	---
26.4038	22.90851	26.34398	0.028326	1.149965	1560717_a	---
287.265	289.381	317.0871	0.028342	1.095743	224465_s	WIBG BC006135 within bgcn
582.303	417.8703	519.8977	0.028354	1.24416	203254_s	TLN1 NM_00628 talin 1
89.1062	89.35303	83.93641	0.028376	0.93938	237122_at	---
428.68	386.427	445.5128	0.02839	1.152903	221269_s	SH3BGR1 NM_03128 SH3 domai
63.8427	66.15241	81.19959	0.028452	1.227462	209875_s	SPP1 M83248 secreted pf
182.88	183.6627	196.19	0.028461	1.068208	230932_at	---
26.8904	37.85246	33.08687	0.028462	0.874101	223700_at	MND1 AY028916 meiotic nuc
28.5455	16.42586	22.58916	0.028484	1.375219	207018_s	RAB27B NM_00416 RAB27B, nr
83.1437	86.58404	77.20307	0.028497	0.891655	1552553_a	CARD12 NM_02120 caspase re
115.122	107.4488	96.10749	0.02851	0.894449	228553_at	ENAH AI692870 Enabled ho

1015.48	998.7458	1098.302	0.028517	1.099681	212626_x_HNRPC	AA664258	heterogene
60.8737	98.73914	80.43656	0.028555	0.814637	234344_at RAP2C	AF093744	RAP2C, me
553.407	461.8548	534.9168	0.028557	1.158193	229265_at ---	AA927480	---
33.063	35.91254	32.36479	0.028569	0.901211	228069_at FAM54A	AL138828	family with
152.937	161.7487	141.9664	0.028591	0.877698	230319_at ---	AI222435	CDNA FLJ:
214.991	225.5843	248.8557	0.0286	1.10316	219997_s_COPS7B	NM_02273	COP9 cons
111.203	110.6242	103.1184	0.028609	0.93215	237210_at NFRKB	AI304853	nuclear fac
145.146	153.2029	160.7634	0.028649	1.04935	217252_at OSIL	U46752	oxidative st
345.879	371.2387	308.4914	0.028658	0.830979	238020_at PSMC2	BG166796	Proteasom
182.62	177.6817	194.6703	0.028662	1.095613	240405_at WDR42A	AA707411	WD repeat
598.637	751.3961	709.2921	0.028678	0.943966	208120_x_FKSG49	NM_03122	FKSG49 ///
99.2587	90.42299	84.10174	0.028694	0.930093	242837_at SFRS4	AI435248	Splicing fac
110.248	127.2473	110.5757	0.028701	0.868982	1557128_a FAM111B	AA960844	family with
219.541	294.0457	262.2537	0.028702	0.891881	218988_at SLC35E3	NM_01865	solute carri
75.7946	83.78944	91.98799	0.028709	1.097847	1564475_s LOC28571	AK055144	hypothetica
35.0076	23.07441	27.4023	0.028793	1.187562	239468_at MKX	AW023227	mohawk hc
364.081	345.6939	370.2189	0.028816	1.070944	202392_s_PISD	NM_01433	phosphatid
170.255	182.565	162.109	0.028861	0.887952	225297_at CCDC5	AV715391	coiled-coil c
1275.87	1115.272	1211.153	0.028903	1.085971	219707_at CPNE7	NM_01442	copine VII
129.993	127.8074	120.778	0.028906	0.945	206017_at KIAA0319	NM_01480	KIAA0319
249.959	265.5744	290.3691	0.028942	1.093362	1570447_a FLJ44054	BC034570	hypothetica
169.833	203.1271	182.793	0.028954	0.899895	1567213_a PNN	U59479	pinin, desm
46.0727	53.04387	45.4721	0.029001	0.857255	240107_at ---	AI002006	Transcribec
278.725	265.9763	305.046	0.029022	1.146892	233601_at LOC64621	AF143882	hypothetica
271.744	253.5603	269.3634	0.029044	1.062325	234308_at TUBGCP6	AK000636	tubulin, gar
64.3217	70.81012	64.53668	0.029051	0.911405	1558661_a ---	BC040612	Homo sapi
161.996	171.3107	147.8159	0.02907	0.862853	233472_at TCP11L1	AK021448	t-complex 1
184.198	172.8597	184.8799	0.029084	1.069537	220078_at USP48	NM_01839	ubiquitin sp
134.55	192.4848	168.7106	0.029125	0.876488	1567214_a PNN	U59479	pinin, desm
343.36	326.6439	343.9923	0.029139	1.053111	208094_s_MGC10471	NM_03081	hypothetica
202.639	214.9042	240.1459	0.029171	1.117455	225488_at DERL1	AI967978	Der1-like d
51.8706	45.43613	57.4358	0.029177	1.2641	220625_s_ELF5	AF115403	E74-like fac
151.749	155.6071	172.3551	0.029193	1.10763	222343_at BCL2L11	AA629050	BCL2-like 1
115.464	140.3689	152.3827	0.029205	1.085587	238144_s_FLJ27365	BF514993	FLJ27365 p
83.7411	88.82087	80.00274	0.029237	0.90072	1556452_a LOC28376	BC039350	hypothetica
132.103	135.7994	144.2258	0.029267	1.06205	231146_at FAM24B	AI300541	family with
287.672	274.2304	297.2969	0.02929	1.084113	226464_at C3orf58	BE348597	chromosom
396.267	411.7867	457.086	0.029365	1.110007	203280_at SAFB2	NM_01464	scaffold att:
27.2076	31.28694	35.35626	0.029376	1.130064	230874_at ---	AI241896	CDNA FLJ:
498.357	535.3194	471.348	0.029405	0.880499	227669_at BRP44	AI654636	Brain prote
51.3303	57.75402	50.39839	0.029455	0.872639	1559006_a ---	BC007784	CDNA clon
90.5994	83.19338	75.94592	0.029467	0.912884	220206_at ZMYM1	NM_02477	zinc finger,
147.639	168.1726	181.6783	0.029482	1.080309	230528_s_MGC2752	AI651726	hypothetica
133.602	155.2944	173.7866	0.029493	1.119078	208488_s_CR1	NM_00065	complemer
96.2289	117.7728	104.4525	0.029514	0.886898	214149_s_ATP6V0E	AI252582	ATPase, H-
712.971	374.2039	437.1176	0.029534	1.168127	200769_s_MAT2A	NM_00591	methionine
346.172	427.5244	387.4733	0.029568	0.906319	235327_x_UBXD4	BG111015	UBX domai
200.319	206.3002	198.0936	0.029597	0.96022	205971_s_CTRB1 ///	(NM_00190	chymotryps
552.012	502.2388	540.658	0.02962	1.076496	224886_at LOC33912	AL577395	hypothetica
20.749	26.15017	32.33807	0.029626	1.236629	233318_at ---	BC003386	---
6.91431	8.827699	12.02161	0.029642	1.361806	1566749_a ---	AK024520	CDNA: FLJ
489.056	402.8507	429.8742	0.029654	1.067081	208178_x_TRIO	NM_00711	triple functi

98.6455	100.7091	111.6609	0.029674	1.108747	241406_at	FAM83H	AW207504	family with
170.449	178.3608	198.1969	0.029682	1.111213	216243_s_	IL1RN	BE563442	interleukin
265.342	234.4664	256.6634	0.029699	1.09467	226836_at	SFT2D1	AA044813	SFT2 doma
76.0077	81.95806	87.83593	0.029739	1.071718	1559595_a_	---	AK055062	CDNA FLJ:
74.8274	86.64569	75.43164	0.02974	0.870576	243841_at	SYNE2	BE673396	spectrin re
176.514	298.7343	263.046	0.02974	0.880535	233809_at	HYPK	AK022435	Huntingtin i
69.4708	61.95477	67.03874	0.029744	1.08206	235449_at	LRSAM1	BG029705	leucine rich
113.276	143.692	162.4128	0.029771	1.130284	236453_at	LOC64347	AW243154	hypothetica
180.415	168.756	185.8283	0.02981	1.101166	222898_s_	DLL3	BE350882	delta-like 3
175.122	199.2908	216.3696	0.029813	1.085698	230402_at	DUSP15	AL160175	dual specifi
173.534	171.4838	158.5306	0.029819	0.924464	238040_at	POGZ	AW966903	Pogo transp
199.925	193.4539	184.5624	0.029824	0.954038	1565661_x	FUT6	BC040472	Fucosyltrar
277.299	294.933	313.8518	0.029826	1.064146	218492_s_	THAP7	NM_03057	THAP dom:
108.205	104.121	115.2879	0.029843	1.107249	242990_at	PPFIA1	AL038704	Protein tyrc
39.9535	44.66602	40.21503	0.029847	0.90035	1552993_a_	DYDC1	NM_13881	DPY30 don
220.893	216.4486	236.9256	0.029855	1.094604	202365_at	MGC5139	BC004815	hypothetica
156.681	182.1296	200.4183	0.029859	1.100416	1556679_a_	YPEL2	AF085961	Yippee-like
42.4152	67.51311	81.43589	0.029904	1.206223	233419_at	---	AK021913	CDNA FLJ:
70.307	85.96406	75.67399	0.029913	0.880298	232088_x_	---	AL137569	CDNA clon
32.6846	42.61344	39.13376	0.029925	0.918343	214837_at	ALB	M12523	albumin
11.9297	16.87916	19.74019	0.029929	1.169501	1566694_a_	---	AK024600	CDNA: FLJ
622.07	592.1716	674.2197	0.029946	1.138555	211066_x_	#####	BC006439	protocadhe
73.1167	81.86889	73.46429	0.02995	0.897341	1561754_a_	---	AF086134	Full length
86.9547	82.2287	87.26523	0.029951	1.06125	239190_at	VRK3	AI802331	vaccinia rel
143.502	143.4747	155.8807	0.029995	1.086468	231233_at	---	AI382195	---
352.924	352.9624	380.981	0.030002	1.079381	218582_at	5-Mar	NM_01782	membrane-
120.697	123.6478	138.4583	0.030005	1.11978	203724_s_	RUFY3	NM_01496	RUN and F
486.361	476.9527	535.821	0.03002	1.123426	203846_at	TRIM32	BC003154	tripartite mc
262.148	246.0477	270.7307	0.030049	1.100318	1557248_a_	ZNF587	BM512320	Zinc finger
89.2484	90.3576	82.06279	0.030079	0.9082	238677_at	WDR36	AA235202	WD repeat
110.596	158.3381	136.2143	0.030144	0.860275	226733_at	PFKFB2	AA587884	6-phosphof
362.098	707.3661	585.5678	0.030195	0.827814	229420_at	---	AI557425	CDNA FLJ:
197.85	210.4148	189.1292	0.030202	0.89884	1564822_a_	---	AL137609	MRNA; cDI
239.82	227.3404	241.5192	0.030207	1.062368	230808_at	FNTA	AA833870	farnesyltrar
275.974	247.4774	261.0814	0.030207	1.054971	234275_at	ESR1	AL050116	Estrogen re
158.759	169.5924	154.9359	0.030222	0.913578	241771_at	---	AA889573	---
569.681	549.0102	612.1677	0.030259	1.115039	217750_s_	UBE2Z	NM_02307	ubiquitin-cc
68.7896	59.96938	71.00982	0.030269	1.184101	237521_x_	---	R55749	Transcribec
84.324	91.31027	97.81332	0.030276	1.071219	1556425_a_	LOC28421	BF509747	hypothetica
40.493	42.13452	51.17046	0.030297	1.214454	208109_s_	C15orf5	NM_03094	chromosom
312.644	313.5316	336.4969	0.030359	1.073247	225134_at	SPRYD3	AF131774	SPRY dom
307.243	150.4643	261.0846	0.030381	1.735192	1560047_s_	LOC43996	AA127813	hypothetica
67.69	73.91018	88.12206	0.030396	1.192286	232896_at	ERBB2IP	AK026757	ErbB2 inter
29.7442	33.94197	39.73996	0.030413	1.170821	240702_at	HERC1	AW591969	hect (homo
79.1723	89.0036	99.2539	0.030424	1.115167	234394_at	ZNF124	AB046850	zinc finger j
226.256	210.1316	238.6779	0.030426	1.13585	230475_at	LOC38813	AI368415	similar to R
73.9896	71.62581	77.43448	0.030447	1.081097	1570486_a_	SOX6	BC029429	SRY (sex d
250.003	238.9034	249.7939	0.03053	1.045585	230946_at	FMN2	BG149866	Formin 2
811.008	772.1511	887.635	0.030574	1.149561	213612_x_	NBPF15 ///	AI800419	neuroblastc
169.409	163.5092	151.1097	0.030589	0.924166	225730_s_	THUMPD3	AI921788	THUMP do
226.673	376.8581	325.4027	0.030591	0.863462	208859_s_	ATRX /// L	AI650257	alpha thala:
74.0191	88.9105	75.14187	0.030596	0.845141	232681_at	---	AI252087	CDNA: FLJ

286.301	318.0854	280.6962	0.030597	0.882455	227861_at MGC33214	AI650251	hypothetica
76.4233	91.14106	107.7249	0.030634	1.181958	239478_x_---	AI761411	Full-length
47.8262	44.38529	49.51659	0.030661	1.115608	1560864_a LRRC7	AF147403	Leucine ricl
89.3445	98.33398	110.0467	0.030697	1.119112	1552564_a NUDT9P1	NM_15320	nudix (nucl
9827.79	9768.614	9395.691	0.030706	0.961824	200002_at RPL35	NM_00720	ribosomal p
209.161	208.0521	227.3241	0.030714	1.092631	217419_x_ AGRN	AK021586	agrln
242.764	220.3818	235.5903	0.030718	1.06901	221426_s_ OR3A3	NM_01237	olfactory re
222.437	278.6216	248.8459	0.030722	0.893132	235722_at SYNJ2BP	AI671431	Synaptojan
1510.32	2230.238	1932.193	0.030743	0.866362	226880_at NUCKS1	AL035851	nuclear cas
267.089	331.8928	290.286	0.030749	0.874638	204771_s_ TTF1	AI632304	transcriptio
384.445	344.6447	356.4982	0.030752	1.034394	234881_at ---	L33988	---
70.266	70.6866	75.05016	0.030796	1.061731	1566576_a DPYSL5	AL831879	Dihydropyri
67.561	80.65479	90.12072	0.030798	1.117364	241998_at LOC38907	AL535414	similar to R
393.214	395.4794	447.5857	0.030798	1.131755	204943_at ADAM12	NM_02164	ADAM met:
115.917	125.6043	135.2197	0.030811	1.076553	232220_at ---	AJ243672	---
145.003	162.1253	148.193	0.030814	0.914064	214140_at SLC25A16	AI827990	solute carri
67.1363	54.77241	60.45447	0.030849	1.103739	1559256_a MAG11	AI637778	membrane
128.569	113.6929	129.7659	0.030892	1.141372	223959_at C14orf168	BC005343	chromosom
24.6099	24.19214	32.36366	0.030897	1.337775	1556204_a LOC40072	AK096401	Similar to Z
627.083	649.1462	680.5634	0.030906	1.048398	229140_at ZNF579	AI689676	zinc finger j
448.687	450.2293	437.4399	0.030908	0.971593	223337_at SDCCAG1	AF039693	serological
75.1811	80.71798	89.18033	0.030942	1.104839	240016_at SENP6	AW273732	SUMO1/se
118.202	132.5098	144.1598	0.030981	1.087918	235628_x_---	BG025030	---
291.62	282.2837	302.1681	0.030992	1.070441	214135_at CLDN18	BE551219	claudin 18
1100.16	1177.864	1074.089	0.030999	0.911895	225110_at OGFOD1	AK024314	2-oxoglutar
12.6719	22.29016	18.8756	0.031048	0.846813	239282_at CCDC41	AI651679	Coiled-coil
281.986	310.3607	285.0558	0.031121	0.918466	214320_x_ CYP2A6	T67741	cytochrome
210.86	208.784	218.1177	0.031121	1.044705	215945_s_ TRIM2	BC005016	tripartite mc
92.5394	105.931	123.5266	0.031155	1.166105	222078_at ---	BF110802	Transcribed
869.031	815.9142	958.5297	0.031159	1.174792	225748_at LTV1	AI458051	LTV1 homc
259.782	246.1072	263.6553	0.031177	1.071303	217009_at PGK2	AL121974	phosphogly
82.3796	105.2222	120.3347	0.031205	1.143625	210435_at NBR2	BC000924	neighbor of
857.104	789.7856	840.337	0.031211	1.064007	43977_at FLJ20422	AI660497	hypothetica
22.3713	38.4522	33.6212	0.031219	0.874363	214942_at RBM34	D38491	RNA bindin
660.872	586.3771	657.7807	0.031219	1.121771	202915_s_ FAM20B	BF115776	family with
168.664	182.5021	198.4948	0.031256	1.08763	232519_at NSFL1C	AK023585	NSFL1 (p9'
92.5986	100.7804	87.77042	0.03127	0.870908	1562736_a LHX9	AJ277914	LIM homeo
306.784	290.74	314.8479	0.031308	1.082919	205024_s_ RAD51	NM_00287	RAD51 hor
152.435	157.4244	178.4102	0.031332	1.133307	215679_at ---	AL109706	MRNA full l
60.1504	61.85097	54.33754	0.031339	0.878524	1553411_s SALL3	NM_17199	sal-like 3 (L
1829.46	2079.738	1903.158	0.031364	0.915095	202427_s_ BRP44	NM_01541	brain protei
130.881	137.2464	127.5276	0.031373	0.929187	213635_s_ SAFB	AI761858	Scaffold att
1446.72	1949.188	1637.576	0.031383	0.840132	209700_x_ PDE4DIP	AB042555	phosphodie
65.4809	44.00831	52.49807	0.031392	1.192913	244129_at ---	AI806973	Transcribed
178.704	218.9573	196.2559	0.031397	0.89632	1559239_s ACAT1	AW750026	Acetyl-Coe
116.105	127.6778	141.0492	0.031401	1.104728	239335_at ZNF710	BF514761	zinc finger j
255.306	274.4807	299.5317	0.031445	1.091267	218302_at PSENEN //	NM_01846	presenilin e
82.3655	90.05327	101.1143	0.031499	1.122827	210556_at NFATC3	U85430	nuclear fac
529.431	564.3753	631.9359	0.031506	1.119709	218103_at FTSJ3	NM_01764	FtsJ homol
170.748	161.6536	171.4238	0.031508	1.060439	228920_at ZFP260	BE328273	zinc finger j
309.553	312.4581	332.5577	0.031527	1.064327	1557801_x C11orf31	AF085883	chromosom
289.168	293.023	311.123	0.031543	1.06177	221597_s_ HSPC171	BC003080	HSPC171 p

112.661	129.4516	189.6429	0.031608	1.464972	244832_at	EDNRA	AI088707	Endothelin
87.7817	100.3116	86.3924	0.031635	0.86124	229202_at	---	AI768826	Transcribec
98.2539	92.4203	99.88097	0.031652	1.080725	211437_at	MAP3K4	AF130093	Mitogen-ac
309.943	313.7244	338.5413	0.031674	1.079104	221068_at	ANKRD25	NM_01761	ankyrin rep
50.091	57.6988	69.03531	0.031674	1.196477	231539_at	FLJ42117	AW204126	FLJ42117 Ꞥ
543.111	526.923	563.547	0.031726	1.069505	224196_x	DPH5	AF161492	DPH5 hom
245.787	252.4914	271.1496	0.031742	1.073896	209848_s	SILV	U01874	silver homc
263.598	273.2594	298.4589	0.031749	1.092218	206264_at	GPLD1	L11702	glycosylphc
43.0802	38.84891	43.64273	0.031791	1.123397	235052_at	FLJ38451	AV758821	FLJ38451 Ꞥ
32.9395	33.96593	38.81566	0.031828	1.142782	223551_at	PKIB	AF225513	protein kin
959.712	1105.445	1215.509	0.031832	1.099566	208777_s	PSMD11	AF001212	proteasome
627.624	728.4397	687.6368	0.031834	0.943986	233775_x	---	AK023304	CDNA FLJ
1037.23	919.2859	1016.873	0.031872	1.106156	202747_s	ITM2A	NM_00486	integral me
381.296	527.7992	461.5503	0.031876	0.874481	216479_at	RPL21 /// L	AL356414	ribosomal Ꞥ
117.886	118.719	137.8083	0.03189	1.160794	236019_at	RAB12	AI076335	RAB12, me
60.9561	64.66898	59.70059	0.031892	0.923172	1555456_a	A2BP1	AF204269	Ataxin 2-bir
37.5837	40.69717	34.98321	0.031895	0.859598	205830_at	CLGN	NM_00436	calmegin
454.874	438.5872	462.9807	0.031901	1.055618	210776_x	TCF3	M31222	transcriptio
230.077	397.7328	331.0913	0.031945	0.832447	239960_x	LOC90624	AW303539	Hypothetica
383.388	389.9596	351.9042	0.032005	0.902412	223909_s	HDAC8	AF212246	histone dea
137.111	134.4239	124.2407	0.03201	0.924245	233214_at	KLHL23	AK021962	Kelch-like 2
241.321	248.319	262.0052	0.032044	1.055115	233341_s	POLR1B	AK025574	polymerase
94.8245	104.8051	94.24559	0.032068	0.899246	221303_at	PCDHB1	NM_01334	protocadhe
76.0864	88.5685	78.70357	0.032074	0.888618	236840_at	C12orf56	AI522132	chromosom
369.795	424.637	401.5221	0.032077	0.945566	223021_x	C6orf55	BF241590	chromosom
196.59	166.5239	248.0236	0.032101	1.489417	227061_at	---	AI088063	CDNA FLJ
58.284	60.04637	69.4593	0.032122	1.156761	232530_at	LOC65222	AA132961	hypothetica
149.646	146.108	164.9357	0.032126	1.128861	225095_at	SPTLC2	W81119	Serine paln
490.052	693.531	562.2942	0.032162	0.81077	214869_x	GAPVD1	AK021533	GTPase ac
430.199	406.9651	468.6987	0.032182	1.151693	243692_at	GATA4	AW181962	GATA bind
5009	5638.182	5308.549	0.032196	0.941536	221791_s	CCDC72	BG167522	coiled-coil c
235.57	219.5989	232.1497	0.032208	1.057153	217188_s	C14orf1	AC007182	chromosom
70.2014	77.95603	91.63283	0.032216	1.175442	242225_at	MON2	AI569482	MON2 hom
150.429	155.6207	169.5009	0.03223	1.089193	203468_at	CDK10	NM_00367	cyclin-depe
291.124	288.7067	265.3802	0.03223	0.919204	222961_at	---	AF116607	---
45.0444	49.71554	54.31556	0.032261	1.092527	1563502_a	ZDHHC2	AL833080	Zinc finger,
61.7022	54.09976	59.83116	0.032265	1.105941	1559691_a	NDUFS1	BC032767	NADH dehy
439.031	370.3656	414.8816	0.032372	1.120195	211935_at	ARL6IP	D31885	ADP-ribosy
53.9936	60.33313	70.68987	0.032416	1.171659	1559614_a	FLJ38773	AK096092	hypothetica
216.888	209.5116	224.9208	0.032449	1.073548	228311_at	BCL6B	AI827455	B-cell CLL/
507.298	557.1642	748.6389	0.032464	1.343659	209118_s	TUBA3	AF141347	tubulin, alp
484.55	534.4263	482.0359	0.032493	0.901969	218398_at	MRPS30	NM_01664	mitochondr
514.909	557.3924	467.8942	0.032502	0.839434	238532_at	DPF3	AI125562	D4, zinc an
163.721	172.0862	208.0551	0.032521	1.209017	202803_s	ITGB2	NM_00021	integrin, be
8096.39	8341.053	7994.157	0.032525	0.958411	209066_x	UQCRB	M26700	ubiquinol-c
344.892	330.4629	361.8636	0.032526	1.09502	202575_at	CRABP2	NM_00187	cellular reti
1026.37	1418.527	1187.321	0.032532	0.83701	234675_x	---	AK027219	CDNA: FLJ
4.07836	1.777649	3.752905	0.032542	2.111162	234097_s	C6orf12	AF032109	chromosom
1882.01	1786.076	1962.38	0.032544	1.098711	46256_at	SPSB3	AA522670	splA/ryanoc
225.47	213.6487	243.336	0.03257	1.138954	209834_at	CHST3	AB017915	carbohydra
31.8599	39.24478	47.50373	0.032611	1.210447	237980_at	LOC33886	AI201082	hypothetica
97.2797	104.3073	116.1462	0.032621	1.1135	1563715_a	---	AL713632	MRNA; cDI

139.222	154.4513	171.077	0.032642	1.107643	206065_s_DPYS	NM_00138 dihydropyri
149.24	159.3272	176.7323	0.032743	1.109241	224551_s_SPTBN4	AY004226 spectrin, be
155.733	137.4163	158.752	0.032759	1.155263	243867_at ZNF518	AW292846 Zinc finger
317.115	323.6882	306.4212	0.032772	0.946655	243642_x_---	R43103 ---
299.443	315.7877	335.5074	0.032836	1.062446	204336_s_RGS19	NM_00587 regulator of
264.517	269.0276	302.4939	0.032864	1.124397	200971_s_SERP1	NM_01444 stress-assc
178.724	171.4481	187.7004	0.032887	1.094794	221268_s_SGPP1	NM_03079 sphingosine
55.9271	57.64077	64.60561	0.032899	1.120832	222877_at NRP2	AK024680 Neuropilin ;
178.563	161.5787	179.3069	0.0329	1.109719	201929_s_PKP4	NM_00362 plakophilin
1041.86	934.7439	1045.818	0.032961	1.118828	205172_x_CLTB	NM_00709 clathrin, lig
79.9093	79.06173	87.56679	0.033	1.107575	237513_at TRY1	AI807285 trypsin X3
192.337	196.1839	214.485	0.033056	1.093285	210036_s_KCNH2	AB044806 potassium
107.617	146.3786	131.2458	0.033078	0.896619	241642_x_TLK1	AI791189 tousel-like
240.896	238.0612	249.8602	0.033134	1.049563	207252_at INE1	NM_00366 inactivation
1104.79	1019.298	1070.241	0.03318	1.049979	213441_x_SPDEF	AI745526 SAM pointe
159.713	155.661	167.8233	0.033181	1.078133	227450_at C12orf46	AI051248 chromosom
243.175	282.269	260.3774	0.033187	0.922444	212556_at SCRIB	AI469403 scribbled h
284.581	279.3789	297.1307	0.033199	1.06354	202943_s_NAGA	M38083 N-acetylgl
215.481	213.47	231.7558	0.03321	1.08566	1562462_aDNAH10	AL046829 dynein, axc
326.839	311.0224	342.5828	0.033221	1.101473	208104_s_TSC22D4	NM_03093 TSC22 don
369.024	414.5371	458.4673	0.033281	1.105974	213099_at ANGEL1	AB018302 angel homc
271.105	243.5592	259.4214	0.03331	1.065127	227477_at ZMYND19	AL565563 zinc finger,
147.904	186.7977	170.9211	0.033389	0.915007	1553207_aARL10	NM_17366 ADP-ribosy
288.666	279.0112	290.8953	0.033466	1.042594	234403_at OR111	AC004794 olfactory re
173.847	175.101	153.8678	0.033467	0.878737	1562572_a---	BC016627 Homo sapi
338.991	357.7617	309.7389	0.033482	0.865769	226951_at ---	AI741415 ---
190.653	192.5803	173.2072	0.033486	0.899402	1555015_aZNF398	BC043295 zinc finger j
215.471	244.5039	272.5831	0.033491	1.114842	204150_at STAB1	NM_01513 stabilin 1
34.052	29.67938	34.24577	0.033617	1.153857	1557881_aC10orf44	BC033403 chromosom
98.2412	96.88472	107.9593	0.033639	1.114307	240665_at CUGBP2	R40515 CUG triplet
304.887	310.8834	295.9758	0.03368	0.952047	240060_at DGKQ	AW025020 Diacylglyce
108.95	123.362	138.9492	0.033701	1.126354	207495_at RAB28	NM_00424 RAB28, me
42.6853	46.1522	39.4644	0.033789	0.855092	236203_at HLA-DRB1	AI377755 Major histo
94.7679	96.88613	108.4212	0.033798	1.119058	242778_at LPXN	AA250935 leupaxin
715.953	709.4149	656.8991	0.033815	0.925973	207438_s_RNUT1	NM_00570 RNA, U tra
446.471	434.671	418.418	0.033825	0.962609	203167_at TIMP2	NM_00325 TIMP meta
69.3407	68.23253	72.63646	0.033832	1.064543	237077_at ACPP	AI821895 Acid phosp
293.102	261.0561	311.2411	0.033843	1.192238	203729_at EMP3	NM_00142 epithelial m
91.5984	97.54582	111.5385	0.033907	1.143447	1566217_aA2BP1	AK054922 Ataxin 2-bir
87.0762	90.62252	83.1529	0.033927	0.917574	1564178_aLOC28303	AK093142 hypothetica
795.603	1050.414	980.1933	0.033936	0.933149	203138_at HAT1	NM_00364 histone ace
226.033	226.0866	248.4218	0.033943	1.098791	211233_x_ESR1	M12674 estrogen re
139.887	170.615	200.8574	0.03395	1.177255	223409_at ---	N49941 ---
86.8376	87.92202	102.5806	0.03396	1.166722	204400_at EFS	NM_00586 embryonal
345.268	364.4913	393.3098	0.033986	1.079065	212813_at JAM3	AA149644 junctional a
56.4982	58.76687	70.13162	0.033987	1.193387	222043_at CLU	AI982754 clusterin
930.522	824.0809	945.468	0.034025	1.1473	221541_at CRISPLD2	AL136861 cysteine-ric
141.832	145.7657	158.3353	0.034091	1.086232	211171_s_PDE10A	AB026816 phosphodie
296.668	326.3877	297.6067	0.0341	0.91182	227600_at ---	AW272333 Full-length
72.5078	72.28894	81.36509	0.034106	1.125554	1569777_aZPLD1	BC031261 zona pelluc
209.181	231.7791	252.6208	0.034125	1.08992	1556188_a---	AF052118 Clone 2382
6468.97	6647.359	6857.957	0.034129	1.031681	217092_x_RPL7 /// LC	AL031589 ribosomal p

237.929	238.4508	262.0658	0.034175	1.099035	241240_at ATF6	AI821787 Activating t
387.147	376.2551	399.5728	0.034176	1.061973	206649_s_ TFE3	NM_00652 transcrip
94.1789	99.73022	112.2092	0.034178	1.125127	1554737_a FBN2	AF193046 fibrillin 2 (c
20.6553	26.4407	33.28803	0.034181	1.258969	1570250_a RP11-35N	BC029380 plasticity re
364.557	339.6269	358.5161	0.034187	1.055618	206257_at CCDC9	NM_01560 coiled-coil c
74.7808	77.44268	57.16078	0.034215	0.738104	244116_at ---	AI194016 Transcribec
763.888	749.0853	957.7057	0.03422	1.2785	224560_at TIMP2	BF107565 TIMP meta
138.776	123.1065	111.0738	0.034222	0.902257	214732_at SP1	AU121035 Sp1 transcr
11.7883	12.27861	14.8448	0.034223	1.208996	1554522_a CNM2	BC021222 cyclin M2
131.588	139.1058	153.9663	0.034241	1.106829	239754_at ---	BE671886 ---
240.039	248.0442	265.2713	0.034256	1.069452	226949_at GOLGA3	N25563 golgi autoa
91.6644	85.6773	98.23488	0.03427	1.146568	243375_at GRIK1	AI742685 Glutamate
3386.13	2971.634	3575.734	0.03428	1.203289	212039_x_ RPL3	BG339228 ribosomal p
332.075	269.2874	323.6102	0.03429	1.201728	208791_at CLU	M25915 clusterin
56.3067	55.24133	47.92178	0.03429	0.867499	1553645_a FLJ39502	NM_17364 hypothetica
90.8181	90.55066	85.88793	0.034293	0.948507	1562878_a ---	AK098632 CDNA FLJ:
144.785	130.8564	142.779	0.034304	1.091112	224725_at MIB1	AB037744 mindbomb
113.445	110.7847	98.37158	0.034313	0.887953	1563244_a ---	BC038193 CDNA clon
1681.87	1490.25	1877.033	0.034328	1.259543	201590_x_ ANXA2	NM_00403 annexin A2
187.585	200.3759	185.6307	0.034332	0.926412	216421_at ---	AL121886 ---
66.6747	82.78934	92.86439	0.034334	1.121695	243876_at FNBP1	AA806845 Formin binc
100.966	111.8603	124.9168	0.034365	1.116722	226334_s_ AHSA2	AW117717 AHA1, activ
127.044	143.8599	157.2486	0.03438	1.093067	230564_at SIPA1L3	AA744809 Signal-indu
283.514	303.9327	258.2509	0.034411	0.849698	222798_at PTER	BF112019 phosphotrie
276.877	266.1943	285.7367	0.034419	1.073414	205247_at NOTCH4	AI743713 Notch hom
230.681	237.0719	263.5866	0.034425	1.111842	229395_at ---	BF939292 ---
105.313	105.7046	111.4596	0.034429	1.054443	239918_at ---	AI139114 CDNA FLJ:
251.892	252.7249	274.6894	0.034456	1.086911	239419_at PTPRA	AA652313 Protein tyrc
62.2186	53.84588	46.30779	0.034464	0.860006	1561280_a LOC28457	AK090497 hypothetica
177.149	176.2063	186.8566	0.034478	1.060442	230840_at LOC38858	BE504634 hypothetica
131.488	122.344	128.5248	0.034521	1.05052	235669_at HNRPAB	BF000693 Heterogene
415.925	324.1889	360.1357	0.034552	1.110882	208790_s_ PTRF	AF312393 polymerase
243.356	305.3637	343.8637	0.034567	1.126079	212765_at CAMSAP1	AB029001 calmodulin
573.225	586.0937	513.1852	0.034691	0.875603	227208_at CCDC84	BF446390 coiled-coil c
81.7576	83.34287	103.645	0.034696	1.243598	202437_s_ CYP1B1	NM_00010 cytochrome
227.462	241.9611	266.7029	0.034714	1.102255	212565_at STK38L	BE302191 serine/threc
73.3633	86.9165	79.60771	0.034727	0.91591	206023_at NMU	NM_00668 neuromedir
516.659	534.492	497.7931	0.03473	0.931339	209620_s_ ABCB7	AB005289 ATP-bindin
608.743	1034.584	888.7443	0.034741	0.859035	226811_at FAM46C	AL046017 family with
78.499	82.01614	88.84948	0.03475	1.083317	220676_at ADAMTS8	NM_00703 ADAM met:
516.754	498.0592	554.1848	0.034786	1.112689	201482_at QSCN6	NM_00282 quiescin Q
346.709	329.3662	367.1774	0.034805	1.1148	203956_at MORC2	NM_01494 MORC fam
228.519	203.8157	227.3183	0.034805	1.115313	211685_s_ NCALD	AF251061 neurocalcin
2609.77	2320.654	2587.883	0.034809	1.115152	1556507_a ---	BC038725 CDNA clon
245.18	266.1519	294.5987	0.034834	1.106882	225449_at RDH13	AI871379 retinol dehy
129.675	131.8744	159.403	0.034851	1.208748	1565265_a BDNF	AJ011602 Brain-deriv
63.5653	62.84966	71.77621	0.034875	1.14203	242089_at ---	AW293350 CDNA FLJ:
625.003	634.6569	695.5593	0.034877	1.095961	202261_at VPS72	NM_00599 vacuolar pr
35.8378	38.01678	40.45762	0.03495	1.064204	223475_at CRISPLD1	AF142573 cysteine-ric
84.5692	86.54648	79.44436	0.034957	0.917939	221595_at ---	AL527334 ---
145.308	167.8731	148.9626	0.034972	0.887352	226014_at EIF3S5	BF115977 Eukaryotic
35.4565	45.76832	40.96398	0.034979	0.895029	242539_at MGC4217	AW665509 Hypothetic:

343.165	318.6832	350.1259	0.034992	1.098664	203219_s_ APRT	NM_00048 adenine ph
57.8341	59.66139	66.88699	0.034999	1.12111	1557861_a ---	BC041958 CDNA clon
46.0152	63.6399	57.55332	0.035	0.904359	228530_at RP11-11C!	AA648525 Similar to R
656.956	574.4347	687.5747	0.035017	1.196959	200881_s_ DNAJA1	NM_00153 DnaJ (Hsp4
395.287	368.1463	385.5388	0.035057	1.047243	212349_at POFUT1	AL045513 protein O-ft
15.6683	23.14706	20.03211	0.035095	0.865428	1566969_a FARP1	AF339798 FERM, Rhc
125.968	112.3267	104.527	0.035118	0.930563	233193_x_ INTS4	AK000455 integrator c
164.209	217.1759	264.7661	0.035137	1.219132	241293_x_ SPTLC2	H68862 Serine paln
157.868	163.9237	151.7752	0.035165	0.92589	232876_at MAPK14	AK025534 Mitogen-ac
786.303	811.5639	844.0654	0.035223	1.040048	214512_s_ SUB1	NM_00671 SUB1 homi
248.199	260.0328	284.8139	0.035227	1.0953	226351_at NSUN4	AK021577 NOL1/NOP
22.564	21.96863	18.12023	0.035232	0.824823	205767_at EREG	NM_00143 epiregulin
934.509	1306.244	1054.733	0.035245	0.807455	235309_at ---	AA126311 CDNA clon
37.3953	36.98274	41.62174	0.035279	1.125437	236700_at LOC65335	AI377875 similar to ei
52.8883	62.67344	58.07674	0.035284	0.926656	220860_at PURG	NM_01335 purine-rich
220.773	224.9667	206.5606	0.035302	0.918183	215194_at PRKCA	AF035594 protein kin
86.9392	112.3439	138.6715	0.035322	1.234348	220696_at PRO0478	NM_01412 PRO0478 p
363.612	394.9939	347.1159	0.035331	0.878788	216218_s_ PLCL2	AK023546 phospholip
292.052	279.3114	301.083	0.035348	1.077947	203159_at GLS	NM_01490 glutaminas
206.653	214.8392	229.2858	0.035382	1.067244	205277_at PRDM2	NM_01223 PR domain
41.1122	52.31342	64.92803	0.035383	1.241135	244010_at ABP1	AI057455 Amiloride b
211.807	238.767	260.6939	0.035412	1.091834	217775_s_ RDH11	NM_01602 retinol dehy
243.076	236.4222	254.5357	0.035424	1.076615	241978_at AKR1A1	AA551756 Aldo-keto r
85.7222	90.81027	104.6688	0.035432	1.15261	228369_at TNRC5	AI262560 trinucleotidi
607.217	658.7636	610.785	0.035485	0.927169	223802_s_ RBBP6	AF063596 retinoblastc
113.02	110.1331	117.8996	0.035485	1.070519	223057_s_ XPO5	BC000129 exportin 5
174.093	170.3216	183.0341	0.035491	1.074639	231135_at LOC15117	AI917513 hypothetica
3292.19	2942.512	3102.464	0.03553	1.054359	223043_at TMEM85	AF151018 transmemb
597.441	535.289	565.1871	0.035545	1.055854	213771_at IRF2BP1	AI401612 interferon r
188.041	201.3508	192.0414	0.03557	0.953766	229593_at H2AFY	BE503981 H2A histon
180.509	209.4896	235.9801	0.035578	1.126453	242866_x_ POU2F2	BF509229 POU doma
79.8132	78.70213	86.48232	0.035588	1.098856	240230_s_ LOC64282	AW000942 hypothetica
129.848	154.0258	138.2217	0.035609	0.897393	240239_at ZNF566	N63953 zinc finger j
295.136	302.838	315.8241	0.035615	1.042881	211172_x_ AKAP7	AF161075 A kinase (F
46.8843	54.12624	68.74553	0.035619	1.270096	1553401_a MRGPRX1	NM_14719 MAS-relate
213.355	210.9943	230.2128	0.035662	1.091085	206313_at HLA-DOA	NM_00211 major histo
176.57	197.661	189.4314	0.035672	0.958365	229697_at HIRIP3	AI392830 HIRA intera
40.0345	37.32627	45.42794	0.03576	1.21705	206826_at PMP2	NM_00267 peripheral r
234.474	275.1948	305.6601	0.035763	1.110705	225779_at SLC27A4	AK000722 solute carri
466.826	458.1471	530.5148	0.035767	1.157957	208659_at CLIC1	AF034607 chloride inti
97.441	122.204	106.523	0.03577	0.871681	205664_at KIN	NM_01231 KIN, antige
91.9621	81.73577	71.91388	0.035801	0.879834	215919_s_ MRPS11	BC000200 mitochondr
116.199	114.4728	122.4888	0.035814	1.070025	214453_s_ IFI44	NM_00641 interferon-ii
512.898	495.1682	525.1029	0.03588	1.060454	238650_x_ C14orf150	AI419825 chromosom
130.176	155.1924	171.9419	0.03588	1.107927	210367_s_ PTGES	AF010316 prostaglan
161.468	174.4703	190.9389	0.035891	1.094392	244200_at YPEL2	AW902013 Yippee-like
110.95	88.19637	98.356	0.035894	1.115193	215456_at ---	AF070625 Clone 2473
79.3157	75.09399	83.85329	0.035913	1.116644	228864_at ZNF653	AA775830 zinc finger j
64.3159	55.9768	64.50006	0.035944	1.152264	1555171_a ST3GAL3	AF425865 ST3 beta-g
130.7	123.08	113.2935	0.035944	0.920486	219901_at FGD6	NM_01835 FYVE, Rho
42.0147	36.38849	41.01376	0.035959	1.127108	214159_at PLCE1	AW771015 Phospholip
73.9284	80.34559	87.37328	0.036045	1.087468	1555335_a ITGA9	BC030198 integrin, alp

50.6739	56.73192	49.81138	0.036061	0.878013	241031_at NLF1	BE218239 Nuclear loc
83.0069	107.1831	128.6467	0.036081	1.200251	231403_at ---	N21108 ---
183.944	218.5297	198.8206	0.036106	0.90981	1554341_a HEL308	BC011863 DNA helica
234.243	240.5276	226.8017	0.036114	0.942934	243078_at ---	AW006258 ---
333.997	343.4282	376.6062	0.036118	1.096608	212291_at HIPK1	AI393355 homeodom
312.81	294.2556	334.8596	0.036129	1.137989	200998_s_ CKAP4	AW029619 cytoskeleto
103.288	106.657	93.54076	0.036176	0.877024	206432_at HAS2	NM_00532 hyaluronan
158.325	153.8219	165.0986	0.036204	1.07331	241419_at ARHGAP1	AA709154 Rho GTPas
44.4361	59.0721	50.64488	0.036221	0.85734	1567359_a BDNF	AJ011597 Brain-deriv
133.176	155.1169	137.495	0.036251	0.886396	220764_at PPP4R2	NM_01985 protein pho
73.7027	80.90084	93.94952	0.036268	1.161292	239605_x_ TGFBR1	AI743727 Transformir
313.328	309.504	328.7952	0.036269	1.062329	240918_at ---	AI015324 Transcribec
278.726	316.9449	299.9601	0.03628	0.946411	1561611_a ---	AF086374 Full length
165.728	221.8257	195.1468	0.036331	0.87973	235727_at BTBD5	AI219490 BTB (POZ)
79.2931	85.07761	94.23409	0.036332	1.107625	242132_x_ ---	AI419966 ---
207.838	211.3023	226.828	0.036336	1.073476	204973_at GJB1	NM_00016 gap junctioi
119.806	137.9113	126.5536	0.036341	0.917644	222881_at HPSE	AF155510 heparanase
300.771	296.1629	333.7074	0.036354	1.12677	202951_at STK38	BE048506 serine/threc
25.7295	28.93499	23.70949	0.036367	0.819405	242836_at ATP1B3	AI800470 ATPase, N:
27.9133	33.48114	28.53498	0.036407	0.85227	235115_at PDE8B	AV722254 phosphodie
145.78	159.4951	170.6467	0.036422	1.069918	213631_x_ HP	BE789211 Haptoglobir
15.2989	24.36522	19.52199	0.036465	0.801224	235165_at PARD6B	AW151704 par-6 partiti
221.64	223.0962	242.8896	0.036567	1.088721	236320_at CCDC17	AA010540 coiled-coil c
1509.15	1438.493	1670.696	0.036625	1.16142	1557480_a DYSFIP1	AI972007 dysferlin int
192.419	225.6993	195.7433	0.036651	0.867275	217481_x_ FLJ45455	AL110201 FLJ45455 p
350.948	536.3409	449.5322	0.036654	0.838146	1565765_x FLJ14834	AL832478 Hypothetica
47.5525	41.84094	36.37946	0.03669	0.86947	1558813_a TMED5	BI561660 transmemb
56.7158	57.46622	51.23709	0.036719	0.891604	1562349_a ---	AK098253 ---
180.605	247.142	220.5231	0.036751	0.892293	206551_x_ KLHL24	NM_01764 kelch-like 2
128.368	98.2915	104.6439	0.036753	1.064628	1556117_a ADA	AK090842 Adenosine
71.0975	69.733	62.92752	0.036758	0.902407	239108_at MLSTD1	H16791 Male sterilit
57.856	61.08016	55.34203	0.036767	0.906056	1569881_a DRP2	BC036095 dystrophin
7324.89	7475.081	6913.994	0.036796	0.924939	201441_at COX6B1	NM_00186 cytochrome
94.8128	97.73211	106.6044	0.036808	1.090782	215198_s_ CALD1	AU147402 caldesmon
121.732	132.4234	146.6172	0.036812	1.107185	1556434_a COBRA1	BQ777552 Cofactor of
99.2266	95.76279	101.8117	0.036843	1.063166	243048_at CECR7	AA521486 cat eye syn
109.172	115.988	126.6607	0.036854	1.092015	234231_at LOC19735	AF098666 hypothetica
185.716	178.751	199.8732	0.036855	1.118166	237747_at ---	W80594 ---
393.639	398.7919	441.9758	0.036863	1.108287	218159_at C20orf116	NM_02393 chromosom
67.1914	54.55812	63.7204	0.036871	1.167936	210260_s_ TNFAIP8	BC005352 tumor necr
259.198	255.1036	243.7481	0.036874	0.955487	204628_s_ ITGB3	NM_00021 integrin, be
156.489	138.6159	155.8361	0.036884	1.12423	216033_s_ FYN	S74774 FYN oncog
159.058	144.4241	129.5043	0.036896	0.896695	241440_at FLJ30375	BF108881 hypothetica
48.4577	40.84246	45.77793	0.036914	1.120842	219813_at LATS1	NM_00469 LATS, large
177.747	223.4144	248.5649	0.036915	1.112573	224726_at MIB1	W80418 mindbomb
61.5377	62.38019	54.46202	0.036971	0.873066	1557754_a LOC40106	BC028186 hypothetica
155.513	141.2884	148.0798	0.036976	1.048067	241615_x_ CD55	AI270858 CD55 mole
245.585	265.1751	292.7048	0.036984	1.103817	226623_at PHYHIPL	AI829726 phytanoyl-C
158.619	265.9846	230.7081	0.037021	0.867374	223292_s_ MRPS15	AF265439 mitochondr
381.532	380.391	436.9254	0.037063	1.148622	210347_s_ BCL11A	AF080216 B-cell CLL/
172.594	188.9753	199.4752	0.037102	1.055562	230968_at ---	AW953794 Full-length
133.427	128.9794	145.1589	0.037123	1.125443	237883_at ---	AI027100 Transcribec

145.514	130.3241	142.8828	0.037156	1.096365	221048_x_C17orf80	NM_01794	chromosom
412.274	529.0707	474.0413	0.037171	0.895989	244730_x_ZNF435	BF671528	Zinc finger
130.05	128.9344	144.7887	0.037193	1.122963	240300_at TK2	AL038860	Thymidine
249.342	316.1706	268.2301	0.037198	0.848372	217618_x_HUS1	AW007988	HUS1 chec
233.702	236.843	267.5493	0.037204	1.129648	201970_s_NASP	NM_00248	nuclear aut
1512.62	1393.338	1505.873	0.037225	1.080767	208967_s_AK2	U39945	adenylate k
157.222	173.3044	187.1196	0.037234	1.079716	222671_s_JMJD4	AA582199	jumonji don
5351.5	4742.743	5456.776	0.037236	1.150553	221667_s_HSPB8	AF133207	heat shock
87.7126	117.0626	138.9852	0.037256	1.187273	215997_s_CUL4B	AV694732	cullin 4B
61.514	59.31836	55.66636	0.037282	0.938434	210021_s_UNG2	BC004877	uracil-DNA
104.037	116.3611	105.6915	0.037283	0.908306	242521_at ---	BF512556	Homo sapi
204.197	193.9576	210.5238	0.037339	1.085412	1552657_a TXNDC2 //	NM_03224	thioredoxin
226.474	220.9289	239.6971	0.037384	1.084951	201562_s_SORD	NM_00310	sorbitol def
134.836	121.1747	129.0021	0.037439	1.064596	230437_s_PRKCB1	AA724722	Protein kin
86.2017	86.24819	98.6409	0.037439	1.143687	236059_at C11orf61	AW168168	Chromosor
250.993	258.416	308.4686	0.037498	1.19369	225673_at MYADM	BE908995	myeloid-as:
32.6732	28.93456	32.20449	0.03752	1.113011	228640_at ---	BE644809	CDNA clon
86.487	87.81622	76.26443	0.037528	0.868455	232380_at FLJ10986	AK022237	hypothetica
179.858	222.5624	268.7471	0.037547	1.207513	203750_s_RARA	NM_00096	retinoic aci
295.715	336.6894	301.9468	0.037581	0.896811	223341_s_SCOC	AF330205	short coilec
3610.26	3436.981	3680.149	0.037595	1.07075	36829_at PER1	AF022991	period hom
360.955	355.3583	384.3651	0.03762	1.081627	225676_s_WDSOF1	BE409290	WD repeats
239.639	312.7406	267.012	0.037654	0.853781	238719_at ---	BF060712	Transcribec
274.548	173.7543	228.4394	0.037667	1.314727	202995_s_FBLN1	NM_00648	fibulin 1
168.7	166.2449	157.688	0.037685	0.948528	221236_s_STMN4	NM_03079	stathmin-lik
28.5881	26.24649	30.0136	0.037718	1.143528	1555561_a UGCGL2	BC032302	UDP-gluco:
923.068	781.1012	859.3248	0.03772	1.100145	224744_at IMPAD1	AW628838	inositol mor
164.198	152.109	163.1058	0.03774	1.072295	239311_at DHX57	AI367034	DEAH (Asp
182.655	195.9116	211.6313	0.03775	1.080239	1555385_a B4GALNT1	BC029828	beta-1,4-N-
781.731	773.6333	831.9494	0.037831	1.07538	201726_at ELAVL1	BC003376	ELAV (emb
45.3719	45.20511	40.73166	0.037862	0.901041	228353_x_STS-1	AA233308	Cbl-interact
76.6269	65.31748	57.53077	0.037874	0.880787	1569472_s TTC3	BC026260	tetratricope
310.829	320.4842	335.0646	0.037884	1.045495	209418_s_THOC5	BC003615	THO compl
178.88	164.4193	182.1644	0.0379	1.107926	206374_at DUSP8	NM_00442	dual specifi
1121.65	1320.114	1166.891	0.037912	0.883932	214314_s_EIF5B	BE138647	eukaryotic 1
129.896	145.1624	131.855	0.037935	0.908327	1566454_a AATK	AK090481	Apoptosis-2
145.925	154.0373	171.3524	0.037952	1.112409	236158_at LOC14797	R42281	Hypothetica
38.216	43.12107	39.62861	0.037959	0.919008	1557301_a ---	AL043897	CDNA FLJ:
225.37	249.4398	270.7647	0.037966	1.085491	227624_at FLJ20032	AB046766	hypothetica
369.038	345.6486	367.4248	0.037979	1.063001	228263_at GRASP	AI190755	GRP1 (gen
471.517	494.2387	565.26	0.037992	1.143698	201944_at HEXB	NM_00052	hexosamini
64.8394	74.17549	83.35947	0.038025	1.123814	244531_at NNT	BE501279	Nicotinamic
405.457	400.3423	449.0752	0.038031	1.121728	200916_at TAGLN2	NM_00356	transgelin 2
147.612	158.0907	150.6116	0.038033	0.952691	201915_at SEC63	AI806665	SEC63-like
83.2795	86.45787	79.57042	0.038091	0.920338	1559276_a ---	AK056805	CDNA FLJ:
104.981	99.27901	106.1448	0.038101	1.069156	243173_at CABP7	AI989906	calcium bin
184.597	168.672	183.2857	0.038101	1.08664	225604_s_C9orf19	AA284532	chromosom
63.9199	55.80111	47.6824	0.038105	0.854506	1558428_a ALS2CR11	AL833429	amyotrophi
415.244	384.0909	398.2772	0.038137	1.036935	212147_at SMG5	AB029012	Smg-5 horr
403.905	866.1382	696.0968	0.038149	0.803679	230388_s_LOC64424	AI797017	hypothetica
185.071	175.0928	196.5734	0.038161	1.122682	204743_at TAGLN3	NM_01325	transgelin 3
33.2193	40.50541	48.9807	0.038187	1.209238	1567687_a CECR9	AF307449	cat eye syn

41.1774	37.74171	46.13963	0.038197	1.22251	214660_at PELO	X68742	Pelota hom
273.611	250.2404	273.0851	0.0382	1.091291	1558782_a LOC64413	BG390627	hypothetica
89.1238	89.10504	102.0096	0.038217	1.144825	228133_s_ MYH11	BF732767	myosin, he
262.334	224.0107	294.2768	0.03824	1.313673	209651_at TGFB1I1	BC001830	transformin
1035.85	980.3062	1081.458	0.038253	1.103184	207939_x_ RNPS1	NM_00671	RNA bindin
281.656	334.5637	299.0274	0.038272	0.893783	224529_s_ NT5C1A	AY028778	5'-nucleotid
229.53	237.5714	253.3619	0.038286	1.066466	208307_at RBMY1A1	NM_00505	RNA bindin
107.573	116.8995	101.3133	0.038291	0.866671	211044_at TRIM14	BC006333	tripartite mc
408.806	378.281	400.7139	0.038325	1.059302	225929_s_ C17orf27	AA233374	chromosom
19.0026	11.8826	16.10417	0.038333	1.355273	1560209_a ---	BC033530	CDNA clon
120.474	109.3921	91.6267	0.038333	0.837599	1569802_a ---	BC026124	CDNA clon
141.925	154.7997	174.8841	0.038347	1.129745	1560386_a XPO1	BC041658	Exportin 1 (
2179.97	2023.852	2399.031	0.038361	1.185379	221607_x_ ACTG1	BC001920	actin, gamr
464.642	448.4137	403.919	0.038366	0.900773	220631_at OSGEPL1	NM_02235	O-sialoglyc
468.421	472.003	516.7033	0.038367	1.094703	201881_s_ ARIH1	NM_00574	ariadne hor
77.6124	89.63529	78.67661	0.038395	0.877741	227541_at WDR20	AA811466	WD repeat
132.196	130.4059	149.855	0.03842	1.149143	234547_at EYA3	AF083121	Eyes abser
52.3729	70.79973	54.22391	0.038426	0.765877	241470_x_ ---	R97781	Transcribec
3182.67	2640.199	2977.641	0.038459	1.127809	206996_x_ CACNB1	NM_00072	calcium chz
590.875	559.9104	631.466	0.03848	1.127798	209079_x_ #####	AF152318	protocadhe
96.6216	101.6552	109.7202	0.038517	1.079337	216963_s_ GAP43	AF279774	growth assi
58.3903	59.78567	65.64893	0.038555	1.098071	1569025_s FAM13A1	BC041029	family with
90.5811	69.36147	79.36851	0.038562	1.144274	218706_s_ GRAMD3	AW575493	GRAM dom
107.072	108.7756	116.1261	0.038573	1.067575	219501_at RP11-3011	NM_01799	proliferator
98.2177	188.9431	150.2572	0.038579	0.795251	204010_s_ KRAS	NM_00498	v-Ki-ras2 K
116.721	111.2639	95.56063	0.038604	0.858864	1569225_a SCML4	BC021582	sex comb c
499.969	452.5257	476.2641	0.03861	1.052458	221187_s_ FLJ22688	NM_02512	hypothetica
41.5526	42.40919	48.432	0.038611	1.142017	1569929_a MECP2	AF361491	Methyl CpC
279.498	298.9334	272.977	0.038693	0.91317	206735_at CHRNA4	NM_00074	cholinergic
96.5621	100.9045	113.4948	0.038696	1.124774	233431_x_ PHC3	AU148142	Polyhomeo
147.356	297.777	210.4226	0.038702	0.706645	228487_s_ ---	BF591556	Transcribec
240.148	230.7852	259.1309	0.038745	1.122823	219505_at CECR1	NM_01742	cat eye syn
230.783	231.4686	254.8658	0.038781	1.101082	231701_s_ SHMT1	AV648432	Serine hyd
217.431	198.3396	208.7601	0.038876	1.052539	242314_at TNRC6C	AI337097	Trinucleotic
195.913	203.1888	214.173	0.038892	1.054059	212545_s_ ZHX3	AW292783	zinc fingers
5658.16	5945.282	7253.247	0.038899	1.22	204892_x_ EEF1A1	NM_00140	eukaryotic 1
102.763	114.9657	145.8894	0.038919	1.268982	206029_at ANKRD1	NM_01439	ankyrin rep
178.305	192.3664	206.4342	0.038925	1.07313	210264_at GPR35	AF089087	G protein-c
159.118	143.0677	136.3353	0.03893	0.952943	208597_at CNTF	NM_00061	ciliary neu
319.258	349.99	306.6249	0.038934	0.876096	1553805_a C3orf49	NM_13880	chromosom
61.0155	57.74154	52.96363	0.038958	0.917253	230380_at THAP2	AW235671	THAP dom
3590.05	3724.829	3963.074	0.038968	1.063961	213881_x_ SUMO2	AI971724	SMT3 supp
249.608	261.1362	274.9682	0.038985	1.052969	229365_at PPP1R3F	BF475372	protein pho
622.459	668.988	723.4571	0.039023	1.08142	212696_s_ RNF4	BF968633	ring finger p
141.534	161.2509	140.9359	0.039072	0.874016	227967_at TUBGCP5	N47680	tubulin, gar
42.1112	51.28951	41.95892	0.039076	0.81808	241608_at SNTB2	AW296081	Syntrophin,
387.765	416.4479	388.2688	0.039078	0.932335	210753_s_ EPHB1	AF037334	EPH recept
792.26	698.2768	769.212	0.03908	1.101586	201523_x_ UBE2N	BE262760	ubiquitin-cc
81.4344	75.48107	66.35779	0.039082	0.879132	1566279_a ---	AV659648	---
223.813	235.0764	246.4353	0.039116	1.04832	49485_at PRDM4	W22625	PR domain
84.8179	75.59603	81.88653	0.039127	1.083212	215162_at GARNL1	AB020691	GTPase ac
528.816	446.3193	465.2263	0.039146	1.042362	241467_at OSBPL5	AW204093	Oxysterol b

63.7404	63.33828	69.26031	0.039147	1.093498	216280_s_ DICER1	AK001827 Dicer1, Dcr
329.224	386.1994	358.5271	0.039173	0.928347	220252_x_ CXorf21	NM_02515 chromosom
187.383	185.2757	217.026	0.03919	1.171368	228337_at MST101	BE552097 MSTP101
702.4	683.657	778.0821	0.039212	1.138118	229447_x_ NBPF11 ///	N32025 neuroblastc
83.675	104.1396	121.0854	0.039249	1.162722	210767_at NF2	BC003112 neurofibron
92.8472	103.255	95.11713	0.039268	0.921187	239857_at ---	BF940997 Transcribec
153.951	186.9961	218.1498	0.039272	1.166601	234293_x_ HRES1	X16660 HTLV-1 rel:
46.583	58.04774	54.25211	0.039273	0.934612	1568012_a RSN	AF045652 Restin (Ree
68.1859	97.13001	124.6745	0.03934	1.283584	210937_s_ IPF1	U35632 insulin pron
77.3791	74.8723	86.11086	0.039341	1.150103	1562275_a ADAMTS9	AL832835 ADAM met:
113.151	137.9341	122.7298	0.039366	0.889771	205006_s_ NMT2	NM_00480 N-myristoyl
89.212	101.0952	90.24333	0.039382	0.892657	1560002_a FAM27A	BI917658 Family with
750.367	862.1501	763.7409	0.03939	0.885856	226896_at CHCHD1	AI992290 coiled-coil-l
218.173	204.7906	234.3458	0.039435	1.144319	239617_at GHRL	AI056187 Ghrelin/obe
142.853	174.276	192.8696	0.039439	1.10669	217006_x_ ---	U52428 ---
22.3044	26.18417	31.26954	0.039496	1.194216	239258_at RHOQ	BE551407 Ras homok
178.42	184.7816	199.9154	0.039504	1.081902	215946_x_ CTA-246H:	AL022324 similar to oi
286.158	306.2918	276.4673	0.039536	0.902627	1559469_s SIPA1L2	BC006013 signal-induc
149.548	135.1022	118.4771	0.039545	0.876944	220115_s_ CDH10	NM_00672 cadherin 10
109.124	119.968	101.0042	0.03956	0.841926	224758_at LOC64184	BG393032 hypothetica
1716.48	1487.794	1640.766	0.039603	1.102817	209376_x_ SFRS2IP	AW084759 splicing fac
681.171	812.7669	875.5283	0.039608	1.077219	225096_at C17orf79	AJ272196 chromosom
155.581	150.0627	163.1736	0.039616	1.087369	213974_at ADAMTSL:	AB033059 ADAMTSL-li
7.15055	16.10389	11.65211	0.039621	0.723559	219995_s_ FLJ13841	NM_02470 hypothetica
67.3303	70.56749	65.26478	0.039636	0.924856	244441_at USP31	AI128170 Ubiquitin sp
634.879	687.1432	595.4407	0.039655	0.866545	219137_s_ C2orf33	NM_02019 chromosom
304.575	293	308.4659	0.039673	1.052785	204520_x_ BRD1	NM_01457 bromodom:
2337.46	2248.297	2872.557	0.039674	1.277659	200605_s_ PRKAR1A	NM_00273 protein kin
80.6746	72.00552	64.41589	0.039675	0.894597	1555898_a LOC15075	BQ003366 Hypothetica
212.121	207.7796	218.5864	0.039752	1.052011	232733_s_ COL20A1	BF344604 collagen, ty
280.602	247.3586	266.4943	0.039788	1.07736	207765_s_ KIAA1539	NM_02518 KIAA1539
254.727	293.2028	325.9872	0.03979	1.111815	202159_at FARSLA	NM_00446 phenylalani
529.4	490.1809	514.4802	0.039813	1.049572	222216_s_ MRPL17	AK026857 mitochondr
7932.06	7548.368	7300.273	0.039872	0.967133	209036_s_ MDH2	BC001917 malate deh
54.9736	64.95276	53.66319	0.039877	0.826188	1554744_a COP1	BC033638 caspase-1
535.762	460.9623	512.2481	0.039881	1.111258	221783_at WIZ	W67467 widely-inter
430.209	402.8941	461.3006	0.039882	1.144967	223221_at SCO1	AF183424 SCO cytocl
81.0605	91.02833	104.5152	0.039899	1.148162	206105_at AFF2	NM_00202 AF4/FMR2
1053.35	1136.547	1006.871	0.039911	0.885904	225320_at CCDC109/	AA579630 coiled-coil c
3.48882	9.227196	6.751281	0.039912	0.731672	237302_at ---	BF445031 Transcribec
1961.2	1863.33	2037.433	0.039916	1.093437	78047_s_a ---	AW001777 ---
71.5739	69.55938	74.90623	0.039917	1.076868	202886_s_ PPP2R1B	M65254 protein pho
121.712	186.7367	146.8561	0.039917	0.786434	1559343_a SNRPN	AF400500 Small nucle
12.4427	14.39308	11.29914	0.039934	0.78504	1557580_a CABIN1	BC027347 Calcineurin
117.539	116.4042	106.5366	0.039944	0.915229	235705_at TRIO	BF676361 Triple funct
73.679	76.27168	84.76971	0.039956	1.111418	241072_s_ ---	AV648433 ---
47.3822	42.75764	47.67887	0.039972	1.115096	208166_at MMP16	NM_02256 matrix met:
65.7092	48.78042	56.93979	0.040036	1.167267	1553202_a STOX1	NM_15270 storkhead t
191.476	190.3938	201.4192	0.040038	1.057909	224504_s_ BUD13	BC006350 BUD13 hor
3194.05	2959.252	3572.009	0.040049	1.207065	201217_x_ RPL3	NM_00096 ribosomal p
94.9193	102.5097	111.6539	0.040054	1.089204	1558643_s EDIL3	AA297258 EGF-like re
53.6849	53.8456	63.6173	0.040062	1.181476	204407_at TTF2	AF080255 transcriptio

32.4623	36.88488	33.61326	0.040065	0.911302	1560187_a	LOC64714	BC042094	hypothetica
58.9903	58.19047	52.46951	0.040066	0.901686	1570335_a	ELP4	BC020904	Elongation
715.64	633.3096	674.4936	0.040112	1.06503	227378_x	MGC13114	BF339831	hypothetica
273.149	252.7108	270.8844	0.040138	1.071915	203871_at	SENP3	NM_01567	SUMO1/se
516.863	592.8658	548.0622	0.040141	0.924429	221877_at	---	BF508835	CDNA FLJ:
150.8	151.6858	132.3272	0.040153	0.872377	228304_at	---	BE674118	Transcribec
108.463	118.2171	111.7077	0.04016	0.944937	204562_at	IRF4	NM_00246	interferon r
79.6716	73.54307	63.20089	0.040165	0.859372	216361_s	MYST3	AJ251844	MYST histc
145.205	147.9147	135.2046	0.040177	0.914071	229277_at	---	T96352	Beta-1 adre
153.809	146.2308	153.2166	0.040177	1.047772	231368_at	FAM44C	AI016643	family with
81.2716	80.49238	70.96767	0.040185	0.881669	217577_at	XPO1	AW576871	Exportin 1 (
52.8022	62.51916	72.68684	0.040195	1.162633	1566267_a	LTBP1	AF075098	Latent trans
126.82	171.2086	127.0124	0.040233	0.741858	236016_at	---	AI702962	CDNA FLJ:
94.3588	132.7967	165.7741	0.04024	1.24833	244259_s	---	AI184127	CDNA FLJ:
68.2558	77.01726	84.76494	0.040258	1.100597	215987_at	RAPGEF2	AV654984	Rap guanin
75.667	74.41037	83.46048	0.040268	1.121624	226435_at	PAPLN	AU145309	papilin, pro
159.179	162.8558	178.2476	0.040274	1.094512	1555737_a	KLK4	AF259971	kallikrein 4
53.9284	51.71038	55.84728	0.040322	1.080001	1553470_a	DNAHL1	NM_17362	dynein, axc
196.549	205.6438	218.0188	0.04034	1.060177	223345_at	HDAC8	AF230097	histone dea
119.59	134.3727	143.5996	0.040454	1.068666	238871_at	MLLT4	AI086124	myeloid/lym
110.749	118.3693	125.6873	0.040472	1.061823	1555807_a	MOG	U18840	myelin oligo
1190.99	1406.237	1271.897	0.040473	0.904468	215504_x	ANKRD10	AF131777	Ankyrin rep
340.032	304.8402	337.9382	0.040475	1.108575	201720_s	LAPTM5	AI589086	lysosomal a
4.91631	9.596248	5.878509	0.040542	0.612584	1561789_a	DKFZP779	BG200397	PRO0845
153.116	193.8964	167.7882	0.040569	0.86535	230305_at	---	AW000995	Transcribec
148.053	143.149	153.2224	0.040575	1.07037	1569730_a	FLJ40243	BC034600	hypothetica
74.1499	58.65512	70.97949	0.040587	1.210116	214647_s	HFE	BG402460	hemochron
242.663	308.4637	271.7799	0.04063	0.881076	209883_at	GLT25D2	AF288389	glycosyltrar
51.0079	57.83694	53.34712	0.040659	0.922371	205673_s	ASB9	NM_02408	ankyrin rep
268.418	230.2627	250.4916	0.040667	1.087851	219878_s	KLF13	NM_01599	Kruppel-like
361.906	350.3443	373.9139	0.040688	1.067275	206679_at	APBA1	NM_00116	amyloid bei
181.889	181.7127	164.0964	0.040749	0.903055	226242_at	C1orf131	BF515750	chromosorr
112.867	139.4237	159.1812	0.040772	1.141709	224359_s	HOOK3	AF241830	hook homo
69.0334	78.91184	65.24964	0.040808	0.826868	214044_at	---	BE968750	---
123.613	127.1342	114.4479	0.04081	0.900213	238860_at	C6orf130	AA398043	chromosorr
105.781	108.2704	123.4982	0.040822	1.140646	217346_at	PPIA /// LO	AL021395	peptidylpro
865.869	755.6666	864.3547	0.040822	1.143831	201864_at	GDI1	NM_00149	GDP disso
191.032	206.3897	178.9478	0.040826	0.867038	227442_at	COX18	BG283902	COX18 cyti
930.767	979.4573	921.8052	0.04087	0.941139	203858_s	COX10	NM_00130	COX10 hor
247.799	264.03	302.6942	0.040873	1.146439	222087_at	PVT1	AW451806	Pvt1 oncog
131.494	150.4131	137.3566	0.040905	0.913195	217461_x	BTF3	M90355	basic transi
60.3076	60.04284	54.10892	0.04097	0.901172	1556933_a	SPIN	AF085888	Spindlin
126.796	136.4514	153.246	0.040981	1.123081	1562330_s	CSMD1	AB067477	CUB and S
42.6358	60.0288	53.05663	0.040991	0.883853	241029_at	---	AI820633	Transcribec
199.678	235.6668	197.832	0.041041	0.839456	227012_at	MCFP	AI823986	mitochondr
189.984	201.1276	211.8284	0.041046	1.053204	218599_at	REC8L1	NM_00513	REC8-like
233.463	250.3932	276.9406	0.041051	1.106023	1558459_s	LOC40132	BC041636	Hypothetica
575.987	516.3829	581.0018	0.041076	1.125138	200742_s	TPP1	BG231932	tripeptidyl p
433.737	373.6326	417.7762	0.041079	1.118147	201156_s	RAB5C	AF141304	RAB5C, me
155.295	152.0933	163.2826	0.04108	1.073568	237553_at	---	AI569399	Transcribec
140.079	134.3154	127.997	0.041105	0.952958	1562166_a	---	AF085977	Full length
148.069	148.5904	160.5721	0.041114	1.080636	221781_s	DNAJC10	BG168666	DnaJ (Hsp

997.219	1377.028	1193.413	0.041135	0.866659	211074_at FOLR1	AF000381	folate recep
149.136	146.689	156.6689	0.041171	1.068034	238008_at MGC3530E	AW612149	hypothetica
49.6595	66.50168	59.43906	0.041172	0.893798	237873_s_ TMEM117	AV659201	Transmeml
166.977	146.8502	163.9072	0.041192	1.116152	240338_at LRAP	AI807341	Leukocyte-
82.2581	81.4846	86.22698	0.041196	1.0582	203560_at GGH	NM_00387	gamma-glu
232.539	223.4229	242.1811	0.04121	1.083958	204688_at SGCE	NM_00391	sarcoglycar
8417.39	10390.55	9198.013	0.041224	0.885229	235313_at NRAP	AA195854	nebulin-rel
221.355	206.3726	216.4997	0.041316	1.049072	238235_at ---	AA013222	---
515.242	463.8483	493.5133	0.04133	1.063954	217815_at SUPT16H	NM_00719	suppressor
312.582	334.7817	314.9198	0.041348	0.940672	228075_x_ TFB1M	AI341648	transcriptio
215.113	182.8837	195.4502	0.041397	1.068713	204044_at QPRT	NM_01429	quinolinate
631.857	665.3483	626.4587	0.041509	0.94155	225930_at NKIRAS1	AI970120	NFKB inhib
487.989	491.5688	521.5003	0.041514	1.06089	222333_at ALS2CL	AV661533	ALS2 C-ter
154.585	176.6072	153.3919	0.04152	0.868548	205594_at ZNF652	NM_01489	zinc finger
56.3979	64.71839	55.96807	0.041536	0.864794	244398_x_ ZNF684	BE328243	zinc finger
54.9663	72.68751	81.14531	0.041763	1.116358	230267_at ---	AI673025	Transcribec
136.101	154.4676	176.124	0.041765	1.140201	1568616_a---	AI192615	---
488.943	527.2657	599.3723	0.041773	1.136756	201928_at PKP4	AA194254	plakophilin
493.396	486.9467	545.5069	0.041801	1.12026	223601_at OLFM2	AF131839	olfactomed
42.1611	33.1228	36.16539	0.041844	1.091858	1570352_a ATM	BG623786	ataxia telar
1012.15	904.3599	1024.589	0.041845	1.132944	238468_at TNRC6B	AA214704	trinucleotidi
97.4547	107.9689	116.046	0.041873	1.074809	222247_at DXS542	S58722	putative X-l
151.6	142.9768	152.3338	0.041895	1.065444	223372_at DNAJC4	BF116164	DnaJ (Hsp-
28.0356	43.98371	31.13412	0.041916	0.707856	222341_x_ CCDC14	AW973235	Coiled-coil
430.447	377.3602	415.8706	0.041925	1.102052	211570_s_ RAPSN	BC004196	receptor-as
30.3708	29.03932	23.54208	0.041956	0.810697	1554922_a ZNF678	BC042500	zinc finger
112.567	129.7431	118.9934	0.041962	0.917146	1552283_s ZDHHC11	NM_02478	zinc finger,
10.6596	17.61592	23.81813	0.042044	1.35208	1561564_a TMCC1	BC030741	Transmeml
317.922	351.1956	373.1693	0.042073	1.062568	224639_at UNQ1887	AI928466	signal pepti
1346.57	1104.497	1224.13	0.042091	1.108314	208739_x_ SUMO2	L76416	SMT3 supp
172.622	165.3678	182.2659	0.042096	1.102185	215715_at SLC6A2	BC000563	solute carri
112.185	99.93122	106.7071	0.042104	1.067806	229459_at FAM19A5	AV723914	family with
392.522	429.9621	456.3279	0.042132	1.061321	206875_s_ SLK	NM_01472	STE20-like
305.215	308.6279	331.9157	0.042138	1.075456	223429_x_ KIAA1160	BC004122	KIAA1160
78.0104	75.18431	87.54036	0.042151	1.164343	1562091_a---	BC041963	CDNA clon
83.3107	100.8623	119.5197	0.042158	1.184979	243081_at ---	AA824282	CDNA clon
523.887	467.1586	529.8277	0.042197	1.13415	226814_at ADAMTS9	AI431730	ADAM met:
467.658	505.9658	474.5928	0.042203	0.937994	209478_at ---	U95006	---
1372.42	1246.061	1393.563	0.042205	1.118375	208789_at PTRF	BC004295	polymerase
215.393	191.0664	216.4352	0.042222	1.132775	241199_x_ DPPA4	AV756594	developme
84.6304	79.3932	89.30708	0.042241	1.124871	229479_at LOC64632	AI739132	Hypothetica
594.143	600.2659	688.5639	0.042247	1.147098	208626_s_ VAT1	BC001913	vesicle ami
28.8756	37.4879	41.73056	0.042281	1.113174	234382_x_ ---	X55777	---
181.729	169.4997	155.9516	0.04229	0.92007	1566760_a FLJ34208	AK094122	hypothetica
80.4999	78.5004	87.42539	0.042322	1.113694	1565150_a---	AL110290	EST from c
162.892	151.7661	163.0241	0.042323	1.07418	225617_at ODF2	AL138382	outer dense
191.739	214.2538	252.3704	0.042328	1.177904	215384_s_ MAP1A	AF095910	microtubule
268.241	469.5898	365.323	0.042366	0.777962	229160_at MUM1L1	AI967987	melanoma
608.012	502.5702	582.7929	0.042368	1.159625	207163_s_ AKT1	NM_00516	v-akt murin
34.7624	35.31014	41.91132	0.042375	1.186948	228654_at RP11-93B	AU145277	hypothetica
1328.55	1126.946	1252.771	0.042382	1.111651	206284_x_ CLTB	NM_00183	clathrin, ligl
174.855	185.2942	176.8574	0.042397	0.954468	203696_s_ RFC2	NM_00291	replication l

232.872	228.5188	256.1047	0.042425	1.120716	230952_at ---	AW299630 ---
60.1849	81.76366	66.57746	0.042431	0.814267	241432_at SLIT2	AA778610 Slit homolo
67.4201	76.37954	83.42704	0.042455	1.092269	213067_at MYH10	AI382123 myosin, he
85.2123	121.8573	144.1608	0.042468	1.183029	1569073_x SMARCA4	BC033232 SWI/SNF re
164.781	182.1588	163.1208	0.042483	0.895487	242300_at ---	BF432276 Ubiquitin B
438.003	531.7577	487.1828	0.042485	0.916174	213034_at KIAA0999	AB023216 KIAA0999 p
486.244	624.047	576.9838	0.042488	0.924584	204690_at STX8	NM_00485 syntaxin 8
43.4483	41.44068	46.15649	0.042526	1.113797	242501_at RPL5	AA778773 Ribosomal
310.945	318.6657	355.717	0.042552	1.11627	206927_s_GUCY1A2	NM_00085 guanylate c
364.66	304.0154	347.3068	0.042561	1.142398	200601_at ACTN4	U48734 actinin, alp
638.661	553.3008	622.6986	0.042567	1.125425	205392_s_CCL14 /// C	NM_00416 chemokine
458.137	423.0736	463.5543	0.042589	1.095683	228823_at POLR2J2	AW615396 DNA direct
129.74	134.5693	149.5988	0.042606	1.111686	238518_x_GLYCTK	AI239772 CG9886-lik
163.024	176.1904	188.863	0.04263	1.071925	1561403_a SOHLH1	BC031861 spermatoge
64.5044	71.87474	79.24572	0.042702	1.102553	37170_at BMP2K	AB015331 BMP2 indu
207.865	248.6659	284.1011	0.042722	1.142501	33322_i_at SFN	X57348 stratifin
231.54	269.8391	313.1662	0.042744	1.160566	209448_at HTATIP2	BC002439 HIV-1 Tat ir
47.0906	60.24893	54.14826	0.042767	0.898742	228273_at ---	BG165011 Transcribec
143.978	142.5596	154.3136	0.042782	1.08245	244788_at ---	AI038503 Homo sapi
46.5948	43.90804	49.31827	0.042782	1.123217	1564758_a LOC64365	AK056971 hypothetica
231.549	232.5524	212.0874	0.042811	0.911998	206492_at FHIT	NM_00201 fragile histi
245.588	255.879	240.0608	0.042815	0.938181	206159_at GDF10	NM_00496 growth diffe
291.439	289.2418	297.1928	0.042831	1.027489	44617_at OGFOD2	AI431902 2-oxoglutar
45.8389	40.55092	46.59229	0.042837	1.148982	1557050_a ---	CA448125 ---
426.456	413.8047	450.9603	0.042882	1.08979	211535_s_FGFR1	M60485 fibroblast g
140.703	150.559	138.7313	0.042883	0.921442	241972_at LOC40158	AA507555 hypothetica
1608.22	1120.138	1313.487	0.042885	1.172612	224765_at LOC33928	AA001203 hypothetica
103.662	95.79357	107.7456	0.042911	1.124769	206239_s_SPINK1	NM_00312 serine pept
171.379	175.821	185.0687	0.042965	1.052597	206766_at ITGA10	AF112345 integrin, alp
194.111	181.1834	198.1002	0.042967	1.093368	213521_at PTPN18	AW575379 Protein tyrc
81.0107	68.37778	72.85219	0.042972	1.065437	213953_at KRT20	AI732381 keratin 20
224.621	245.738	227.9429	0.042983	0.927585	229793_at RP11-564C	AI656964 N-acylsphir
126.005	127.1474	141.1701	0.043002	1.110287	215015_at CCDC64	AA319460 coiled-coil c
37.8726	41.98913	52.53036	0.043011	1.251046	1569334_a STRA6	BC015881 stimulated l
459.667	490.1239	509.2158	0.043021	1.038953	215566_x_LYPLA2	AK024724 lysophosph
227.618	228.3231	237.1097	0.04305	1.038483	229650_s_C19orf42	BG538931 chromosom
3474.83	3750.203	3451.082	0.043093	0.920239	39729_at PRDX2	L19185 peroxiredox
56.1151	59.73739	66.83086	0.043129	1.118744	219606_at PHF20L1	NM_01601 PHD finger
460.175	483.4887	452.9916	0.043136	0.936923	214428_x_C4A /// C4E	K02403 complemer
133.998	134.7667	126.5959	0.043141	0.939371	241992_at FLJ11259	AA724995 Hypothetic
607.228	630.2571	691.8359	0.043204	1.097704	213540_at HSD17B8	AL031228 hydroxyste
202.895	196.4819	173.9667	0.043205	0.885408	207231_at DZIP3	NM_01464 zinc finger l
210.056	209.0329	226.3214	0.043216	1.082707	214823_at ZNF204	AF033199 zinc finger p
206.522	203.1966	225.4371	0.043237	1.109453	49051_g_a DTX3	N92708 deltex 3 ho
81.0805	94.38686	85.46231	0.043246	0.905447	217299_s_NBN	AK001017 nibrin
348.685	314.9499	337.3758	0.043254	1.071205	231276_at PDE3B	BF591245 Phosphodie
401.538	392.2309	490.8999	0.043256	1.251558	209550_at NDN	U35139 necdin horr
152.749	144.1282	173.124	0.043263	1.20118	210150_s_LAMA5	BC003355 laminin, alp
156.535	162.9499	180.9213	0.043271	1.110288	225288_at ---	AI949136 Full-length
1178.35	1388.283	1267.58	0.043316	0.913056	202425_x_PPP3CA	NM_00094 protein pho
583.942	503.157	593.8906	0.04332	1.180329	225355_at DKFZP761	AK026748 hypothetica
114.187	133.4174	121.9974	0.043328	0.914404	216771_at ---	AK025194 CDNA: FLJ

3014.15	2590.906	2778.689	0.043347	1.072478	208781_x_SNX3	AF062483	sorting nex
112.666	112.0027	104.176	0.043361	0.930121	1558573_a_C1GALT1C	AF456465	C1GALT1-s
123.579	132.7907	123.4623	0.043364	0.929752	237065_s_---	BF444997	---
82.7645	79.96636	111.3396	0.043369	1.39233	209291_at ID4	AW157094	inhibitor of
386.648	373.7806	354.8312	0.043401	0.949304	230605_at KCNAB1	BF433830	Potassium
617.031	621.8251	719.847	0.043401	1.157636	214953_s_APP	X06989	amyloid bet
72.2254	63.45536	53.79111	0.043426	0.8477	1563591_a---	AL832222	MRNA; cDI
407.548	450.1781	749.9311	0.043451	1.665854	202766_s_FBN1	NM_00013	fibrillin 1
231.402	216.4537	242.4413	0.043465	1.120061	236855_at C10orf85	R43204	chromosom
791.628	795.8521	883.8718	0.043486	1.110598	226031_at FLJ20097	AA523733	hypothetica
209.289	212.9541	196.9498	0.04353	0.924846	225884_s_ZNF336	AL046381	zinc finger j
102.143	129.0359	148.128	0.043538	1.14796	235508_at PML	AW291023	promyelocy
195.236	195.3163	206.114	0.043559	1.055283	238360_s_---	AI885665	CDNA clon
43.0613	46.93802	41.67196	0.04359	0.887808	216788_at---	AK025564	CDNA: FLJ
75.4445	59.48004	48.21664	0.043592	0.810636	207447_s_MGAT4C	NM_01324	mannosyl (;
21.5429	24.31451	20.46421	0.043666	0.841646	1561328_a---	BC039338	CDNA clon
306.117	288.7446	304.2524	0.043688	1.053708	218393_s_SMU1	NM_01822	smu-1 sup
132.979	147.2502	133.6987	0.04383	0.907969	239191_at DHRS7B	AW071789	Dehydroge
93.7367	111.6954	97.78049	0.043847	0.875421	241925_x_---	BF207870	Transcribec
388.288	462.9291	513.4503	0.043866	1.109134	234466_at---	AL390137	---
359.032	349.0349	373.4571	0.043867	1.069971	1554039_a_C14orf159	BC009182	chromosom
114.398	130.2276	119.2483	0.043869	0.915691	205876_at LIFR	NM_00231	leukemia in
248.486	232.0261	221.1928	0.043888	0.95331	225531_at CABLES1	AK025627	Cdk5 and A
141.208	152.8686	164.8576	0.043893	1.078427	1560617_a---	BG720400	CDNA clon
92.4317	91.28022	100.2981	0.043897	1.098793	226136_at---	N32834	---
233.495	241.6418	261.2082	0.043935	1.080973	209193_at PIM1	M24779	pim-1 onco
3503.44	3101.181	3319.219	0.043944	1.070308	234954_at---	AL035604	---
827.914	801.0236	723.7526	0.043954	0.903535	40837_at TLE2	M99436	transducin-
252.539	261.4591	275.085	0.043967	1.052115	205050_s_MAPK8IP2	NM_01232	mitogen-ac
175.172	169.0426	176.876	0.043982	1.04634	231188_at ZSCAN2	AW206602	zinc finger ;
449.837	486.4413	534.4679	0.04399	1.09873	214728_x_SMARCA4	AK026573	SWI/SNF re
172.084	181.5562	213.0714	0.043994	1.173584	225799_at MGC4677	BF209337	hypothetica
319.003	348.98	309.6674	0.044025	0.88735	208284_x_GGT1	NM_01342	gamma-glu
84.5637	105.4956	118.3779	0.044025	1.122112	210218_s_SP100	U36501	SP100 nuc
53.2559	50.90493	41.7011	0.044065	0.819196	216094_at WASL	AK025323	Wiskott-Ald
828.586	797.0461	867.9074	0.044117	1.088905	200960_x_CLTA	NM_00709	clathrin, ligl
292.298	278.4346	263.8489	0.044125	0.947615	202240_at PLK1	NM_00503	polo-like kir
102.733	123.8109	136.3493	0.04415	1.101271	240830_at SCARNA1	AI300126	small Cajal
210.566	224.6226	205.034	0.04415	0.912793	1558345_a_LOC43991	BI715235	hypothetica
108.106	120.422	132.4912	0.044167	1.100224	215326_at PAK4	AB032968	p21(CDKN
177.292	221.1571	253.0372	0.044174	1.144151	208866_at CSNK1A1	BF510713	casein kina
520.537	451.6746	486.7282	0.044184	1.077608	226705_at FGFR1	BE467261	fibroblast g
115.042	112.7454	103.4812	0.044186	0.917831	209480_at HLA-DQB1	M16276	major histo
1114.59	1428.607	1285.862	0.044188	0.900081	201424_s_CUL4A	NM_00358	cullin 4A
323.145	272.2539	336.399	0.044206	1.235608	201670_s_MARCKS	M68956	myristoylat
512.325	484.8698	520.6142	0.04421	1.07372	89948_at C20orf67	AI743331	chromosom
133.257	132.8277	141.8616	0.044246	1.068012	231876_at TRIM56	AL512757	tripartite mc
212.951	208.2449	224.8998	0.044259	1.079977	205166_at CAPN5	NM_00405	calpain 5
227.072	205.2433	226.9876	0.044268	1.105944	215464_s_TAX1BP3	AK001327	Tax1 (hum;
19328.6	18726.48	19101.94	0.044282	1.02005	213453_x_GAPDH	BF689355	glyceraldeh
79.029	90.74222	102.0407	0.044299	1.124511	244682_at CAMSAP1	H11471	calmodulin
317.416	317.8203	338.0172	0.044311	1.063548	1561100_a---	BC039348	CDNA clon

171.515	212.7588	172.2342	0.044332	0.809528	230393_at	CUL5	BF448201	cullin 5
429.62	335.0663	377.2546	0.044401	1.12591	233451_at	C20orf54	AL118502	chromosom
52.6798	49.38214	42.3885	0.044402	0.858377	231523_at	FGF14	BE221273	fibroblast g
241.355	240.1368	252.6657	0.044438	1.052174	236813_at	C10orf83	N21659	chromosom
62.1331	71.01561	62.86848	0.044496	0.885277	214193_s_	C1orf107	AI770084	chromosom
155.036	172.4262	191.5579	0.044527	1.110956	232229_at	SETX	AK024331	senataxin
172.612	178.0102	192.923	0.044527	1.083775	217525_at	OLFML1	AW305097	olfactomed
98.531	90.19434	97.29969	0.044531	1.078778	232928_at	FARP1	AK025341	FERM, Rhc
111.472	120.8283	133.8912	0.044572	1.108111	206706_at	NTF3	NM_00252	neurotrophi
67.2629	79.8226	94.15141	0.044575	1.179508	203844_at	VHL	NM_00055	von Hippel-
205.722	218.0304	193.4279	0.044575	0.88716	231851_at	RAVER2	AL359613	ribonucleo
378.622	414.2391	447.6576	0.044589	1.080674	1557540_a_---		BQ006233	CDNA FLJ:
146.824	155.5852	144.2933	0.04459	0.927423	1557065_a	YLPM1	AA927802	YLP motif c
85.6084	89.34193	81.81976	0.04461	0.915805	238906_s_	RHOJ	BE218803	ras homolo
1163	1176.047	1306.049	0.044623	1.110542	225591_at	FBXO25	AA749085	F-box prote
10.5188	29.81177	19.34666	0.044638	0.64896	1562049_a	SCTR	BC040633	Secretin re
438.883	399.1796	383.533	0.044681	0.960803	224174_at	TTY11	AF332240	testis-speci
254.712	255.9142	292.7453	0.044706	1.14392	223691_at	RGS22	AY009106	regulator of
321.792	304.3203	266.1457	0.04471	0.874558	229659_s_	---	BE501712	Transcribec
136.876	139.3508	131.695	0.044722	0.945061	235255_at	ATP6V0A2	BG106215	ATPase, H-
28.8616	30.97264	36.2761	0.044798	1.17123	238723_at	ATXN3	AW083849	Ataxin 3
951.662	977.7636	827.0032	0.044863	0.845811	225948_at	C14orf153	BF197057	chromosom
205.311	175.816	191.8153	0.044866	1.091	216883_x_	PDE6D	AJ001626	phosphodie
281.886	287.0078	301.553	0.044871	1.050679	53076_at	B4GALT7	AI040029	xylosylprote
97.6286	93.22947	85.44072	0.044882	0.916456	209685_s_	PRKCB1	M13975	protein kina
352.602	399.9666	350.6552	0.044883	0.876711	231032_at	LOC28607	BE503158	hypothetica
197.803	215.6621	199.2274	0.044911	0.923794	206004_at	TGM3	NM_00324	transglutar
93.4772	87.33411	90.48957	0.044917	1.036131	1566979_a	KIAA0317	AF085823	KIAA0317
270.013	222.1328	252.9181	0.044957	1.13859	204983_s_	GPC4	AF064826	glypican 4
183.944	206.0649	219.4517	0.044984	1.064964	233041_x_	BTBD9	AK025009	BTB (POZ)
41.536	53.86463	62.57579	0.044997	1.161723	1562283_a	MAPK1	AL833111	Mitogen-ac
171.953	155.4872	171.5986	0.045032	1.103618	232490_s_	PRUNE	U67085	prune hom
337.105	313.5314	328.2948	0.045033	1.047087	202208_s_	ARL4C	BC001051	ADP-ribosy
150.333	166.8207	179.9251	0.045039	1.078554	230113_at	---	AW665447	MRNA; cDI
85.005	95.5173	106.6247	0.045043	1.116287	244323_at	BHLHB5	AI968349	basic helix-
962.545	945.8314	1010.617	0.04506	1.068496	208771_s_	LTA4H	J02959	leukotriene
26.9814	37.07468	44.82887	0.045075	1.209151	1555558_a	USP25	AF419247	Ubiquitin s
25.3202	29.27503	22.00821	0.045086	0.751774	1554844_a	EYA3	BC041667	eyes absen
118.19	134.7219	123.1486	0.045127	0.914095	240489_at	---	AA034014	Transcribec
225.844	285.7694	245.3638	0.045135	0.858607	228024_at	VPS37A	AW028100	Vacuolar pi
239.972	245.4398	266.444	0.045188	1.085578	211234_x_	ESR1	AF258449	estrogen re
73.6625	93.50781	117.0859	0.045209	1.252151	232927_at	TMTC2	AU147356	Transmeml
72.4355	81.79273	91.11469	0.045212	1.11397	206134_at	ADAMDEC	NM_01447	ADAM-like,
144.793	136.9548	131.3329	0.04524	0.958951	235859_at	ABP1	BE551763	Amiloride b
130.708	126.1644	132.6566	0.045308	1.051458	209832_s_	CDT1	AF321125	chromatin I
229.552	196.2757	213.7107	0.045312	1.088829	216751_at	CDRT4	AK024879	CMT1A dup
685.86	1017.797	915.0542	0.045328	0.899054	218435_at	DNAJC15	NM_01323	DnaJ (Hsp
557.318	591.7154	645.4729	0.045354	1.09085	223259_at	ORMDL3	BC000638	ORM1-like
135.865	153.4144	172.4223	0.045358	1.123899	239070_at	ITFG2	AI434790	Integrin alp
201.256	278.457	238.5576	0.045415	0.856712	228032_s_	---	AW071458	CDNA FLJ:
1337.44	1374.239	1280.509	0.045433	0.931795	223008_s_	C9orf5	AF153415	chromosom
402.244	368.9346	387.4474	0.045446	1.050179	219113_x_	DHRS10	NM_01624	dehydroger

131.152	145.3684	162.7317	0.045505	1.119443	240958_at	UNC5C	R02580	Unc-5 hom
42.1185	54.80564	66.81783	0.045505	1.219178	1557513_a	---	W95281	---
188.897	272.3519	244.5833	0.045544	0.898042	229525_at	---	AW118132	---
77.991	98.29522	89.75317	0.045549	0.913098	236202_at	---	AW467480	Transcribec
830.867	779.8789	868.992	0.045557	1.114265	200755_s	CALU	BF939365	calumenin
201.65	187.9769	203.3886	0.04557	1.081987	1558622_a	ZNF548	AK057494	zinc finger j
85.8021	101.5677	89.37284	0.045611	0.879934	237725_x	SMC5L1	BE502701	SMC5 struc
522.176	480.1473	537.986	0.045644	1.12046	215836_s	#####	AK026188	protocadhe
254.301	226.5697	245.5549	0.045645	1.083794	243702_at	---	AA722627	Full length
60.3285	52.15638	56.79617	0.045645	1.088959	1560557_a	---	BC039046	CDNA clon
336.293	326.3128	287.9197	0.045681	0.882343	238504_at	C6orf57	AA521023	chromosom
2.74565	8.55849	5.705798	0.045788	0.666683	233703_x	FLJ42117	AK024236	FLJ42117 p
89.9895	95.36696	84.67582	0.045801	0.887895	1552368_a	CTCFL	NM_08061	CCCTC-bir
126.282	152.5762	128.9107	0.045808	0.844894	230379_x	PRO1853	BF439153	hypothetica
62.7403	71.92762	78.16083	0.045826	1.086659	1566301_a	PPP1R11	AV755778	Protein phc
677.873	711.0623	770.5907	0.045877	1.083717	54970_at	DKFZp761	AA868332	hypothetica
739.678	666.6537	751.1148	0.045896	1.126694	227271_at	FGF11	AU151265	fibroblast g
255.948	242.6403	254.022	0.045916	1.046908	240818_at	---	AA770459	---
68.0185	80.54963	90.31334	0.045921	1.121214	238824_at	---	BF844863	CDNA FLJ:
57.2451	57.85022	53.13578	0.04597	0.918506	1565242_a	TNXB	U52700	Tenascin X
523.256	601.3259	520.8704	0.045999	0.866203	218642_s	CHCHD7	NM_02430	coiled-coil-l
470.434	439.5422	488.3076	0.046002	1.110946	225615_at	LOC12691	AK024480	hypothetica
385.091	400.7031	431.5349	0.04602	1.076944	229998_x	C1orf78	AI304355	Chromosom
47.7176	52.53214	60.11816	0.046041	1.144407	1558082_a	C9orf93	AK094506	chromosom
278.115	303.4379	327.7869	0.046042	1.080244	221402_at	OR1F1	NM_01236	olfactory re
17.8811	18.48607	22.32007	0.046102	1.207399	242940_x	DLX6	AA040332	distal-less l
231.421	259.7692	243.609	0.046123	0.93779	206178_at	PLA2G5	NM_00092	phospholip:
490.891	755.4304	574.239	0.04614	0.760148	228977_at	IL17D	AI669535	Interleukin
75.847	75.06474	83.87768	0.046148	1.117404	244673_at	---	AW271558	Transcribec
314.702	319.9289	345.5032	0.046155	1.079938	1553239_a	FLJ30707	NM_14501	hypothetica
1937.71	1845.659	2191.868	0.046174	1.18758	213214_x	ACTG1	AW190090	actin, gamr
343.477	319.703	339.7194	0.04618	1.062609	216699_s	KLK1	L10038	kallikrein 1,
262.267	249.1349	266.5928	0.046207	1.070074	232106_s	FLJ14640	AK001375	Hypothetica:
95.7915	101.1973	113.0015	0.046214	1.116645	230418_s	GALNTL1	AI097463	UDP-N-ace
236.584	342.9943	301.3938	0.04624	0.878714	201026_at	EIF5B	AB018284	eukaryotic i
20668.2	20517.3	20819.57	0.046249	1.014732	212581_x	GAPDH	BE561479	glyceraldeh
190.003	199.0712	209.4909	0.046261	1.052341	210318_at	RBP3	J03912	retinol bind
108.446	112.1468	121.5689	0.046288	1.084015	233355_at	LOC28473	AL157500	hypothetica
277.651	288.1762	323.9467	0.046303	1.124127	212700_x	PLEKHM1	AJ002220	pleckstrin h
2184.65	1995.983	2951.048	0.046332	1.478493	205132_at	ACTC	NM_00515	actin, alpha
278.638	261.8756	292.0679	0.046335	1.115293	228326_at	WDR27	AI016894	WD repeat
67.5324	66.3382	49.56387	0.04637	0.747139	233127_at	ZNF331	AK022474	Zinc finger
43.646	57.50891	53.70761	0.046396	0.933901	206364_at	KIF14	NM_01487	kinesin fam
278.666	268.0037	287.0962	0.046424	1.07124	207687_at	INHBC	NM_00553	inhibin, bet:
50.943	53.98581	48.2581	0.046456	0.893903	243311_at	RP5-1103C	BE044548	defensin, b
208.123	228.161	203.0498	0.046466	0.889941	225925_s	USP48	AA044730	ubiquitin sp
839.318	976.1784	888.7871	0.046476	0.910476	213309_at	PLCL2	AL117515	phospholip:
153.427	149.0432	159.9177	0.046478	1.072962	1554286_a	FLJ25758	BC033035	hypothetica
94.3271	97.33688	104.3591	0.046494	1.072144	232436_at	ZNF274	AI057616	zinc finger j
171.311	163.6683	181.877	0.0465	1.111253	209907_s	ITSN2	AF182198	intersectin :
220.618	196.5607	214.8561	0.046512	1.093078	209423_s	PHF20	AY027523	PHD finger
119.183	139.3847	153.9264	0.046522	1.104328	202987_at	TRAF3IP2	AW296296	TRAF3 inte

233.659	221.7174	245.8014	0.046554	1.108625	235857_at	KCTD11	AI859242	potassium c
583.375	597.1326	678.5046	0.04656	1.136271	55616_at	PERLD1	AI703342	per1-like dc
7393.65	7741.023	7406.543	0.046589	0.956791	214143_x_	RPL24 /// S	AI560573	ribosomal p
139.209	138.8063	155.0398	0.04662	1.11695	223789_s_	GTPBP2	AF116627	GTP bindin
36.0534	36.83094	40.3545	0.04663	1.095668	1562051_a	LOC28475	AK092805	hypothetica
109.067	111.719	102.5769	0.04664	0.918169	201638_s_	CPSF1	BE676642	cleavage ai
167.243	154.4989	167.0138	0.046655	1.081003	208699_x_	TKT	BF696840	transketola
611.831	489.7453	602.1441	0.046697	1.229505	1552698_a	MGC16703	NM_14504	alpha tubul
320.969	293.5676	319.4932	0.04672	1.088312	211536_x_	MAP3K7	AB009358	mitogen-ac
365.344	367.2267	341.1959	0.046791	0.929115	202683_s_	RNMT	NM_00379	RNA (guan
126.955	124.0699	136.0231	0.046798	1.096343	238716_at	---	AL527331	Homo sapi
212.617	198.354	181.0731	0.046804	0.912879	227201_at	LOC64383	AI679230	hypothetica
664.401	695.577	1179.565	0.046807	1.695807	208782_at	FSTL1	BC000055	follistatin-lik
126.107	137.7047	126.0467	0.046825	0.915341	210257_x_	CUL4B	AF212995	cullin 4B
735.309	666.9066	720.9693	0.046834	1.081065	222462_s_	BACE1	AI653425	beta-site AI
599.199	545.1071	571.6667	0.046866	1.048724	203572_s_	TAF6	NM_00564	TAF6 RNA
150.09	148.4231	143.1458	0.046873	0.964444	228173_at	GNAS	AA810695	GNAS com
68.445	53.84947	65.13606	0.046875	1.209595	201843_s_	EFEMP1	NM_00410	EGF-contai
162.43	154.8193	176.7268	0.046931	1.141503	204490_s_	CD44	M24915	CD44 mole
118.191	134.3301	146.3413	0.047012	1.089416	210115_at	RPL39L	L05096	ribosomal p
1454.81	1321.401	1532.464	0.047014	1.159727	219090_at	SLC24A3	NM_02068	solute carri
542.174	555.6064	604.0304	0.047033	1.087155	210749_x_	DDR1	L11315	discoidin dc
284.597	273.8463	285.5397	0.047039	1.0427	215858_at	---	AK022363	CDNA FLJ'
173.406	184.4604	201.5281	0.047058	1.092528	211076_x_	ATN1	Z22814	Atrophin 1 /
216.787	206.7466	245.3154	0.047076	1.186552	201279_s_	DAB2	BC003064	disabled hc
366.916	460.218	544.4104	0.04709	1.18294	210519_s_	NQO1	BC000906	NAD(P)H d
657.072	729.2722	624.3303	0.047217	0.856101	203153_at	IFIT1	NM_00154	interferon-ir
397.098	390.2701	415.547	0.047242	1.064768	225483_at	VPS26B	AI971602	vacuolar pr
170.14	187.6551	176.0676	0.047259	0.938251	230078_at	RAPGEF6	AI640834	Rap guanin
270.098	274.2392	295.2254	0.047287	1.076525	203417_at	MFAP2	NM_01745	microfibrilla
44.483	52.1114	58.83203	0.047339	1.128967	232371_at	7-Mar	AU155401	Membrane-
203.313	208.6317	223.7012	0.047351	1.07223	223457_at	COPG2	AB047847	coatomer p
216.314	213.0248	229.2618	0.047387	1.076221	241076_at	SH3BGR1	AA001939	SH3 domai
579.188	554.4036	596.4883	0.047405	1.07591	218481_at	EXOSC5	NM_02015	exosome c
866.292	1013.748	863.3276	0.047411	0.851619	214761_at	ZNF423	AW149417	zinc finger j
56.8945	59.86462	79.52589	0.047419	1.328429	242518_at	---	AA748423	CDNA FLJ'
3120.35	3298.093	3105.74	0.047448	0.941677	218094_s_	DBNDD2	NM_01847	dysbindin (
650.425	687.9549	740.0239	0.047458	1.075687	44146_at	GMEB2	AA045183	glucocortic
39.6527	50.93827	43.29604	0.047474	0.849971	237798_at	MSRA	AI074612	Methionine
123.04	142.6907	158.722	0.047477	1.11235	231013_at	---	W80446	---
134.585	138.2306	157.603	0.047557	1.140146	1554163_a	TWIST2	BC033168	twist homol
544.499	716.2638	625.0784	0.047568	0.872693	204726_at	CDH13	NM_00125	cadherin 13
180.22	240.8544	205.6751	0.047582	0.853939	218395_at	ACTR6	NM_02249	ARP6 actin
303.283	291.8838	312.2488	0.047619	1.069771	241373_at	IMPDH2	AW015588	IMP (inosin
340.142	286.4648	306.2296	0.047622	1.068995	218844_at	FLJ20920	NM_02514	hypothetica
207.865	230.4819	243.8003	0.047658	1.057785	204057_at	IRF8	AI073984	interferon r
178.008	173.5722	188.3499	0.04767	1.085138	214484_s_	OPRS1	AF226604	opioid rece
553.906	690.1317	767.6821	0.04769	1.112371	203156_at	AKAP11	NM_01624	A kinase (F
95.3256	106.2222	122.3595	0.047691	1.151921	1569904_x	PALLD	BC015161	Palladin, cy
57.732	62.99102	73.57424	0.047698	1.168012	1557632_a	---	BU681135	---
1964.14	1862.462	2533.787	0.047715	1.36045	201426_s_	VIM	AI922599	vimentin
274.865	311.9861	295.1093	0.047715	0.945905	1555131_a	PER3	BC026102	period hom

206.375	182.7073	245.8653	0.047732	1.345679	225242_s_ CCDC80	AW303375 coiled-coil c
53.7521	60.91703	68.54527	0.04774	1.125223	220376_at LRRC19	NM_02290 leucine rich
97.399	120.3136	137.831	0.047748	1.145598	1566002_a ANKRD11	AK096064 Ankyrin rep
41.5981	41.79757	36.23891	0.047764	0.86701	214705_at INADL	AJ001306 InaD-like (E
420.603	570.855	487.473	0.047778	0.853935	236798_at ---	AW268719 CDNA FLJ:
139.753	131.6914	138.4752	0.04778	1.051513	229633_at INTS10	AA115512 Integrator c
296.145	347.775	314.3963	0.04779	0.904022	222600_s_ UBE1L2	AB014773 ubiquitin-ac
1326.02	1537.264	1320.989	0.047792	0.859311	216954_x_ ATP5O	S77356 ATP synthe
464.831	492.0748	448.6022	0.047794	0.911655	204032_at BCAR3	NM_00356 breast canc
356.72	369.46	333.4686	0.047814	0.902584	218256_s_ NUP54	NM_01742 nucleoporin
264.324	327.3209	293.1528	0.047827	0.895613	228867_at TATDN3	BE541548 TatD DNas
241.512	227.8316	244.8506	0.047841	1.0747	218113_at TMEM2	NM_01339 transmemb
115.456	107.7683	91.37448	0.04785	0.847879	242002_at TCBA1	N62814 T-cell lymph
192.705	214.212	196.9696	0.047928	0.919508	221627_at TRIM10	AF220123 tripartite mc
121.391	118.2206	108.1323	0.047929	0.914666	220018_at CBLL1	NM_02481 Cas-Br-M (
209.087	207.3103	192.9621	0.047951	0.930789	241639_at LOC64547	BE049158 Hypothetica
97.8758	115.8796	107.4588	0.047977	0.927331	1555127_a MOCS1	BC036839 molybdenu
153.129	180.261	205.663	0.047984	1.140918	241637_at LOC64547	BE049158 Hypothetica
315.582	412.6698	359.0532	0.04803	0.870074	219696_at FLJ20054	NM_01904 hypothetica
494.048	431.1943	468.778	0.048039	1.087162	45297_at EHD2	AI417917 EH-domain
397.607	398.7842	439.5388	0.048069	1.102197	207024_at CHRND	NM_00075 cholinergic
400.431	367.228	396.057	0.04808	1.078504	236134_at WDR68	AA769995 WD repeat
203.129	204.4592	220.8223	0.048099	1.080031	229835_s_ ---	AA004210 Transcribec
290.417	293.7604	330.6971	0.048142	1.125737	222631_at PI4K2B	AI862887 phosphatid
90.0878	89.0912	107.0255	0.048152	1.201303	244347_at C10orf61	BE825318 Chromosor
197.077	198.8751	212.7949	0.048155	1.069993	206012_at LEFTY2	NM_00324 left-right de
297.478	280.2394	385.2551	0.048179	1.374735	200660_at S100A11	NM_00562 S100 calci
331.777	325.3633	337.8752	0.048187	1.038455	229456_s_ DDAH1	AI885718 Dimethylar
871.225	936.9832	1052.855	0.048196	1.123665	207549_x_ CD46	NM_00238 CD46 mole
159.308	161.8807	152.5979	0.048216	0.942657	232810_at AIG1	AK001347 androgen-ir
140.364	186.9651	161.4137	0.0483	0.863336	1560648_s TSPYL1	AI625538 TSPY-like
96.2421	113.7909	82.21012	0.048321	0.722467	1559190_s RDH13	AL833150 MRNA; cDI
62.293	62.99127	67.6729	0.048327	1.074322	1557452_a SSBP2	AF088024 Single-strar
73.63	85.62368	95.84662	0.04834	1.119394	225250_at STIM2	N48266 stromal inte
240.092	308.6591	275.8342	0.048353	0.893653	236772_s_ ---	AA554330 Transcribec
104.784	146.3196	169.1131	0.048361	1.155779	213316_at KIAA1462	AL050154 KIAA1462
164.277	352.4788	289.3309	0.048395	0.820846	231640_at LOC14436	AV654063 Hypothetica
91.0511	99.4877	70.6421	0.048418	0.710059	240703_s_ HERC1	AW591969 hect (homo
2605.47	1818.576	2081.498	0.048422	1.144576	1564207_a FLJ35390	BC014556 hypothetica
96.1792	91.28373	107.1683	0.048456	1.174013	230657_at CLOCK	AI423466 Clock homc
50.7921	55.84446	50.29564	0.048493	0.900638	224358_s_ MS4A7	AF237916 membrane-
125.339	153.9217	128.3858	0.048507	0.834098	222663_at R1OK2	AK001697 RIO kinase
88.4286	101.8211	94.05919	0.048526	0.923769	236841_at FLJ25222	BE464132 CXYorf1-re
431.848	388.3252	421.3847	0.048533	1.085133	1553178_a SSTR3	NM_00105 somatostat
20.6708	17.28511	20.96699	0.048555	1.213008	1555932_a TSGA10	AK094208 Testis spec
538.467	587.3077	606.1888	0.04856	1.032149	203103_s_ PRPF19	NM_01450 PRP19/PS
128.17	131.397	146.2114	0.04857	1.112746	212256_at GALNT10	BE906572 UDP-N-ace
141.176	175.5488	152.7547	0.048577	0.870155	238912_x_ C9orf85	AA824363 chromosorr
1488.86	1531.212	1623.323	0.048615	1.060156	210966_x_ LARP1	BC001460 La ribonucl
20.1038	14.62165	17.85099	0.048642	1.22086	1554770_x FLJ32130	BC040642 hypothetica
4197.67	3569.718	4002.244	0.048683	1.121166	214359_s_ HSP90AB1	AI218219 heat shock
146.023	171.5708	193.7536	0.048687	1.129292	1553426_a FLJ37543	NM_17366 hypothetica

235.265	259.0268	284.5139	0.048705	1.098396	1552414_a	WFDC9	NM_14719	WAP four-c
64.184	67.48184	61.56289	0.048728	0.912288	215272_at	---	R59977	---
73.7823	105.7095	121.783	0.04874	1.152053	1569885_a	---	BC036229	CDNA clon
81.4663	73.95741	84.19029	0.048765	1.138362	205908_s	OMD	NM_00501	osteomodu
539.992	487.0623	621.7752	0.048825	1.276582	200600_at	MSN	NM_00244	moesin
477.758	455.5161	486.5656	0.048849	1.068163	216475_at	---	AL133269	---
225.714	230.971	217.6911	0.048853	0.942504	222012_at	LOC90379	AA535066	Hypothetic
395.671	420.7067	383.623	0.048861	0.911854	233080_s	PRPF40A	AF155096	PRP40 pre
285.13	341.0311	291.2909	0.048876	0.854148	206527_at	ABAT	NM_00066	4-aminobut
82.4808	75.22836	68.22461	0.048897	0.9069	1561785_a	MUC4	AK074437	Mucin 4, ce
894.808	709.2019	868.4504	0.048897	1.224546	200703_at	DYNLL1	NM_00374	dynein, ligh
416.78	400.9313	346.8653	0.048907	0.865149	217368_at	---	X69909	---
176.237	215.092	195.689	0.048907	0.909792	208920_at	SRI	AV752215	sorcin
92.2832	83.83459	73.54497	0.048929	0.877263	233365_at	PRKG1	AU147809	Protein kin
132.823	137.526	146.7798	0.048951	1.067287	215854_at	FBXO22	AU146050	F-box prote
64.9177	83.98862	74.33321	0.048978	0.885039	229151_at	SLC14A1	BE673587	Solute carri
368.88	346.5527	375.9239	0.048992	1.084753	218231_at	NAGK	NM_01756	N-acetylglu
1331.48	1578.283	1399.228	0.049021	0.88655	212848_s	C9orf3	BG036668	chromosom
79.9792	93.21903	86.32288	0.049047	0.926022	1569139_s	FAM53A	BC042071	family with
70.3979	92.0743	75.90078	0.049104	0.824343	228966_at	PANK2	BE674076	Pantothena
82.5319	85.54792	92.8644	0.049104	1.085525	228113_at	RAB37	R62453	RAB37, me
708.944	675.6353	713.9281	0.049173	1.056677	208420_x	SUPT6H	NM_00317	suppressor
224.708	219.7756	237.8492	0.049199	1.082237	240099_at	ARSG	AA573201	Arylsulfatas
2227.91	2129.647	2318.404	0.049218	1.088633	216484_x	---	L24521	Full-length
214.757	226.9419	238.5858	0.049222	1.051308	238003_at	FLJ25530	AI885128	hepatocyte
221.529	210.2277	222.7457	0.049223	1.059545	218770_s	TMEM39B	NM_01805	transmemb
77.3524	80.08832	75.27791	0.049229	0.939936	224229_s	AKT3	AL117525	v-akt murin
90.5483	82.90333	87.01814	0.049252	1.049634	228232_s	VSIG2	NM_01431	V-set and ir
97.8083	87.71057	97.1485	0.049273	1.107603	221205_at	---	NM_01804	---
38.0514	36.90483	40.76958	0.049353	1.104722	229824_at	---	AL133706	CDNA FLJ
129.843	117.733	127.138	0.04936	1.079884	222874_s	CLN8	AF123757	ceroid-lipof
49.9911	48.11634	41.69521	0.049364	0.86655	241755_at	UQCRC2	AI961429	Ubiquinol-c
80.4762	75.80977	84.06066	0.049412	1.108837	217361_at	---	X73110	---
269.689	260.7219	277.1991	0.049466	1.063198	234316_x	KLK12	AF135025	kallikrein 12
409.007	439.7154	404.3613	0.049491	0.919598	201917_s	SLC25A36	AI694452	solute carri
194.848	213.3459	228.4139	0.049509	1.070627	205058_at	SLC26A1	M74715	solute carri
160.044	155.6581	134.0788	0.049525	0.861367	1553158_a	C3orf34	AY099509	chromosom
421.943	401.4622	455.7747	0.04953	1.135287	218061_at	MEA1	NM_01462	male-enhar
312.304	316.3203	351.1106	0.049535	1.109984	221529_s	PLVAP	AF326591	plasmalemi
63.6136	67.3989	81.17543	0.049541	1.204403	205559_s	PCSK5	NM_00620	proprotein c
5522.61	4932.919	5301.701	0.049542	1.074759	200735_x	NACA	NM_00559	nascent-po
109.249	110.0798	126.1411	0.049569	1.145907	216444_at	SMURF2	AK024138	SMAD spec
4202.92	4770.297	4512.857	0.049599	0.946033	218201_at	NDUFB2	NM_00454	NADH dehy
372.269	447.7841	370.2192	0.049604	0.826781	223089_at	VEZT	AI805297	vezatin, adl
455.842	434.5209	462.9326	0.049606	1.065386	220155_s	BRD9	NM_02392	bromodom
45.509	49.83688	53.18993	0.049663	1.067281	233316_at	MKLN1	AK023427	Muskelin 1,
44.1588	43.00822	47.2955	0.049667	1.099685	238512_at	ST7L	BF961733	Suppressio
199.736	178.8998	190.1689	0.049669	1.062991	239837_at	ADAM11	T15748	ADAM met:
569.452	571.0048	628.7677	0.049674	1.10116	40255_at	DDX28	AC004531	DEAD (Asp
49.9146	54.22297	49.12049	0.049674	0.905898	1555433_a	SLC39A14	BC015770	solute carri
48.1358	62.92417	74.82253	0.049684	1.189091	1570117_a	---	BC037877	CDNA clon
111.312	104.4628	112.6623	0.049715	1.078492	217497_at	ECGF1	AW613387	endothelial

86.7428	82.17289	92.35002	0.049723	1.12385	243877_at C1orf25	BF514803 Chromosom
359.025	355.4726	371.9598	0.04973	1.046381	227090_at PHF21A	AA194264 PHD finger
135.024	111.4267	129.2302	0.049755	1.159777	223463_at RAB23	AF161486 RAB23, me
378.842	359.8393	386.1818	0.049758	1.073206	226163_at ZBTB9	AW291499 zinc finger ;
138.326	152.193	164.3319	0.049776	1.07976	240374_at ---	BF448248 ---
520.367	505.8144	543.2603	0.049788	1.074031	221067_s_ C12orf39	NM_03057 chromosom
262.794	268.513	292.1459	0.049818	1.088014	219923_at TRIM45	NM_02518 tripartite mc
445.964	470.3228	497.5119	0.049862	1.057809	222640_at DNMT3A	N26002 DNA (cytos
8365.4	8921.327	8650.104	0.049879	0.969598	212042_x_ RPL7 /// LC	BG389744 ribosomal p
2254.67	1608.723	1817.493	0.049884	1.129774	1564208_x FLJ35390	BC014556 hypothetica
224.711	258.8259	233.1544	0.049901	0.900816	1565027_a OFCC1	AF548114 orofacial ck
323.333	382.6097	367.2678	0.049924	0.959902	59631_at TXNRD3	AI247566 thioredoxin
199.558	192.9542	212.6396	0.049971	1.102021	216038_x_ DAXX	BE965715 death-asso
3113.03	2948.482	3543.02	0.049972	1.201642	211073_x_ RPL3	BC006483 ribosomal p
122.189	143.9901	126.1756	0.049992	0.87628	213934_s_ ZNF19 /// Z	AL567808 zinc finger j
7.22143	9.946652	6.152171	0.049993	0.618517	221037_s_ SLC25A31	NM_03129 solute carri
543.551	528.1126	599.472	0.049998	1.135122	201810_s_ SH3BP5	AL562152 SH3-domai

name

NA DKFZp686F1844 (from clone DKFZp686F1844)

synaptic membrane exocytosis 4

16 mRNA sequence

id locus

al protein PRO2900

inding protein-like 7

yl isomerase (cyclophilin)-like 2

pecific peptidase 37

id locus

n factor A, mitochondrial

ne 6 open reading frame 137

annel, voltage-dependent, L type, alpha 1C subunit

onse factor (c-fos serum response element-binding transcription factor)

bulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglob

domain containing 15

otif-containing 11

protein

ne 21 open reading frame 29

main containing 1

dherin-associated protein), alpha 3

rane protein 4

ne 19 open reading frame 37

development candidate 1

g cassette, sub-family C (CFTR/MRP), member 13

1 leukemia viral oncogene homolog B (ras related; GTP binding protein)

ceptor potential cation channel, subfamily V, member 1

repeat containing 3

ita 4

u homolog (mouse)

1-specific guanine nucleotide-releasing factor 2

monophosphate deaminase 2 (isoform L)

bulin heavy constant gamma 1 (G1m marker)

al protein DKFZp313A2432

sp-Glu-Ala-Asp/His) box polypeptide 26B

IAP repeat-containing 4

ctural maintenance of chromosomes 1-like 1 (yeast)

protein

α 2, smooth muscle, aorta

main containing 2B

loid ecotropic viral integration site 1 homolog 2 (mouse)

protein 252

ific protein, Y-linked 1

istance-associated overexpressed protein

protein 207

ciated transcription factor 1

e (DNA directed), eta

arginine hydrolase
protein-like 1
like enhancer of split 3 (E(sp1) homolog, Drosophila)
and FYVE domain containing 1
nin B (secretogranin 1)
in

repeat containing 5
and HMG-box DNA binding protein 1
X domains 2A
ens, clone IMAGE:5743779, mRNA
re homeobox 2

eracting protein

protein L22
nscription factor IIIc, polypeptide 1, alpha 220kDa

B0335 protein
homolog (Drosophila)

maintenance of chromosomes flexible hinge domain containing 1
rotein-like 3 antisense

ne 1 open reading frame 26
lpha (actin binding protein 280)
protein 286 /// similar to zinc finger protein 286
nily member 3
rotein S2
modulin binding protein 3
:tivated protein kinase-activated protein kinase 5
olog C (C. elegans)-like
, oligomeric mucus/gel-forming
e (prosome, macropain) 26S subunit, non-ATPase, 10
al LOC553137
>-Glu-Ala-As) box polypeptide 19A
al gene supported by AL832565
ra
n
nin 2 (bilateral acoustic neuroma)
er in mitosis gene a)-related kinase 6
sphatidylethanolamine-hydrolyzing phospholipase C
molog, cytochrome c oxidase assembly protein (yeast)
d locus
ii homolog

acent to 3' end of integrated HPV16 (INT421)
hibitor 1
otif-containing 38
:tivated protein kinase kinase kinase 1

-2ak
domain 46
in depolymerizing factor)
tidase M
in sulfotransferase 1
h mobility group box protein TOX
al protein LOC339457
e IMAGE:5263917
ne 16 open reading frame 45
ific kinase substrate
ens, clone IMAGE:5219794, mRNA

, CCHC domain containing 6
lecule-like family member g
brane protein 4
uclear receptor co-repressor 1
ens, clone IMAGE:3446976, mRNA

n beta receptor (TNFR superfamily, member 3)
ydrogenase 5 (class III), chi polypeptide
in containing 2
al protein LOC169834
almitoyltransferase II
eceptor interacting protein 2
cDNA clone CS0DF014YC15 of Fetal brain of Homo sapiens (human)
enosine transferase
cruitment domain family, member 11
ne 18 open reading frame 8

factor RNA polymerase II
ke protein
iral integration site 1
ed cell death 6
domain containing 58
er family 9 (sodium/hydrogen exchanger), member 3 regulator 2
al protein FLJ20433
/pe VI, alpha 2
ne 14 open reading frame 172
protein 587
eta 1 pseudogene
e IMAGE:4816709
osteosarcoma
ctor 1 (ets domain transcription factor)
GEF and PH domain containing 2
atic
CCCH-type containing 5

al protein LOC643234
ydrogenase (decarboxylating)
ing protein 2
g cassette, sub-family A (ABC1), member 7

ling LIM protein 1
voltage-gated channel, subfamily F, member 1
al biogenesis factor 3
ial fission regulator 1
ding protein 1
al gene supported by BC024195
ier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
iteracting substance of 220 kDa

al protein LOC440465
translation elongation factor 1 delta (guanine nucleotide exchange protein)
Drosophila) /// ovo-like 2 (Drosophila)
ogy 2 domain containing adaptor protein B
protein 169
annel, voltage-dependent, gamma subunit 5
d locus
protein 614
hin
11677 fis, clone HEMBA1004778
ain containing 1
ne 20 open reading frame 45

nethyltransferase
binding protein 4
g Rho activating protein
coupled receptor 137

cytidyltransferase 1, choline, alpha
1
nnectin, cwcv and kazal-like domains proteoglycan (testican) 2
olar RNA, H/ACA box 28
sphatase 1, catalytic subunit, beta isoform
ptide repeat domain 17
e c oxidase subunit Vb
eukemia transcription factor 1
synthase trafficker
d locus
in and CaM kinase-like 1
ne 19 open reading frame 29
sferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)

st-specific 2
ne 9 open reading frame 91
d locus, moderately similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens]
ase C and casein kinase substrate in neurons 2
pping transcript 2 (antisense non-coding RNA)

protein 130
dl syndrome 1
(C-C motif) ligand 21

omain receptor family, member 1
lpha (actin binding protein 280)
n elongation factor A (SII)-like 1
essor protein 1
ike 1 /// lysozyme-like 2
UBR1 type 1
is transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)
n binding protein 4 (formin binding protein 21)
ne 9 open reading frame 164
i containing TCP1, subunit 5 (epsilon)
ressor of mif two 3 homolog 2 (S. cerevisiae) /// similar to SMT3 suppressor of mif two 3 homolog 2 /// s
40) homolog, subfamily C, member 6
e 1 (mast9, hevin)
ily member 3B
e repeat containing 6B
ne 6 open reading frame 182
ain and WD repeat domain containing 1
nd transmembrane 1
omolog 1 (zebrafish)
yphosphate-5-phosphatase F

d locus
20814 fis, clone ADSE01064
ad cell death 6
P450, family 3, subfamily A, polypeptide 4
ily member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)

yclase 3
ase C binding protein 1
ase kinase, beta
i repeat containing 35

al protein LOC285965
protein
homeobox 1b
L-myc fusion
al protein LOC642372
n factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
roup

d locus
carboxylase
otif-containing 3
din E receptor 3 (subtype EP3)

ysosomal acid, cholesterol esterase (Wolman disease)

yb1-like 2 (chicken)
nase/reductase (SDR family) member 7
none receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)
on factor binding to IGHM enhancer 3

al protein LOC283033
d locus, weakly similar to NP_990560.1 very low density lipoprotein (VLDL)/vitellogenin receptor [Gallus
tor I/X (CCAAT-binding transcription factor)
d-like 2 (Drosophila)
nin 2 (bilateral acoustic neuroma)
ntaining F3
NA DKFZp434F0535 (from clone DKFZp434F0535)
cting protein
d locus
:tor, arginine/serine-rich 9 /// splicing factor, arginine/serine-rich 9
allopeptidase domain 3a (cyrtestin 1)
eptide receptor A/guanylate cyclase A (atriatriuretic peptide receptor A)
al protein LOC283075
omology domain containing, family A (phosphoinositide binding specific) member 3
eptor co-repressor 1
32664 fis, clone TEST11000088
protein 1
ne 1 open reading frame 42
+ transporting, lysosomal 13kDa, V1 subunit G1

se D
:tor 1
rane protein 132A
40) homolog, subfamily C, member 4
N-acetylglucosaminidase
roblastosis virus E26 oncogene homolog 1 (avian)
:omplex subunit 1
urora kinase A-interacting protein (AURKA-interacting protein)
onjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
al protein MGC42174
Γ transcription complex, subunit 1

mmunoglobulin-like receptor, subfamily A (with TM domain), member 5
γ-like 5
l transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
roglobulin/bikunin precursor
nt homolog 2 (Drosophila)
growth factor binding protein 1
:ta 5
insert cDNA clone ZB77E08
rmone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)
in domain family 11, member A /// C-type lectin domain family 11, member A
eptidase 4 (CD26, adenosine deaminase complexing protein 2)

ie IMAGE:5296164
al protein LOC285178
d locus

mplex component 5
per transcription regulator 2
al protein FLJ10916
2

(S. cerevisiae)
ain N, 1
al protein MGC24039

sequence similarity 76, member B
protein 687
ig motif, single stranded interacting protein
ription factor /// Sp2 transcription factor
tratricopeptide repeats 1
late dehydrogenase

sin
ne 16 open reading frame 52
protein 333
rowth factor 6
ne 9 open reading frame 14
J23572 fis, clone LNG12403
min VII
er family 2, (facilitated glucose transporter) member 8
re nucleotide exchange factor (GEF) 1
heat and MYND domain containing 1
ase, beta
oplasmic 1, light intermediate chain 2
e domain containing 6
nolog 1 (Drosophila)
domain 62
ipt
(globulin) inhibitor H5
-regulated 1

n 4
35945 fis, clone TESTI2011915
acting protein 2
sein kinase and cyclin-dependent kinase substrate 1
iated, gamma adaptin ear containing, ARF binding protein 2
rotein
lin (schwannoma-derived growth factor)
38904 fis, clone NT2NE2001524
ytic leukemia /// similar to promyelocytic leukemia protein isoform 1
ld modifier 1
jht polypeptide (Lcb)
esponsive gene 15
ase 1
lyl isomerase A (cyclophilin A)
eceptor coactivator 5
on factor-like 5 (basic helix-loop-helix)
r like 1
ynthase kinase 3 alpha
erase family, cytosolic, 1A, phenol-preferring, member 2
age kinase 4
r cycle 25B
a mouse model of primary ciliary dyskinesia

gamma 3
plicated region transcript 4
se and tensin homolog (mutated in multiple advanced cancers 1) /// phosphatase and tensin homolog (nr
coupled receptor 173
inding protein 1 (amine oxidase (copper-containing))
ctural maintenance of chromosomes 5-like 1 (yeast)
1 15
coupled receptor 44
protein 148 (pHZ-52)
coupled receptor 135
ribose) polymerase family, member 3
d locus
sine phosphatase, receptor type, M
38461 fis, clone FEBRA2020977
1 sequence similarity 83, member B

neuronal acetylcholine receptor protein, beta-4 subunit precursor (Neuronal acetylcholine receptor non-a
(C.elegans)
acles homolog 1 (Drosophila)
1 5

ne 16 open reading frame 45
al protein LOC644246
er family 34 (sodium phosphate), member 1
38396 fis, clone FEBRA2007957
nember RAS oncogene family
-like 1 (cartilage glycoprotein-39)
2
expressed 3
sequence similarity 14, member A

ier family 16 (monocarboxylic acid transporters), member 3
inding protein-related factor)-proximal homolog (Drosophila)
omain receptor family, member 1
nstream regulated gene 1
nase/reductase (SDR family) X-linked
neobox, 5 /// double homeobox, 3 /// double homeobox, 1
ne 14 open reading frame 115
1 repeat containing 20
lass I, type 8B, member 4
ily interacting protein 2
nyl CoA epimerase
e domain containing 1
unoglobin-like variable motif containing
d locus
d locus
+ transporting, lysosomal 50/57kDa, V1 subunit H
al protein LOC283970
14061 fis, clone HEMBB1000749
:cule
:IKEN cDNA 2210021J22
protein 554

arginine dimethylaminohydrolase 1
ens, clone IMAGE:4685786, mRNA
activated protein kinase kinase kinase 7 interacting protein 2
ated, EVH1 domain containing 1
tatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
NA DKFZp761E1721 (from clone DKFZp761E1721)
erin gamma subfamily C, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily A
ort 1 homolog B (S. cerevisiae)
eceptor, C type 2

channel, subfamily T, member 2
lyl isomerase A (cyclophilin A)
ht polypeptide 9, regulatory

receptor potential cation channel, subfamily V, member 5
lin
ylinositol-4-phosphate 5-kinase, type II, alpha
inding protein /// TAR DNA binding protein
blastic leukemia (translocation) 1
domain containing 15
oplasmic 1, heavy chain 1
1 (C. elegans)
otidyl transferase, CCA-adding, 1
ositide-3-kinase, catalytic, alpha polypeptide
otein (actin filament) muscle Z-line, beta
AS domain protein 3

related protein 1

thers against DPP homolog 2 (Drosophila)
NA DKFZp667M159 (from clone DKFZp667M159)
ated protein 1
domain containing 40
domain 74 /// WD repeat domain 74
r pathway inhibitor (lipoprotein-associated coagulation inhibitor)
38130 fis, clone D6OST2000464
type III domain containing 6

pressor
n microtubule associated protein like 5
avy polypeptide 11, smooth muscle
lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)
ig protein 1
protein 639
almitoyltransferase 1A (liver)
ig protein 8 (putative)
ne CD 43T7
lmodulin-dependent protein kinase II inhibitor 1
ier family 25, member 28
annel, voltage-dependent, beta 1 subunit
e IMAGE:4825318

ain I
ex group 18
ens, clone IMAGE:4047715, mRNA
anel, sperm associated 3
i-domain protein (SRF accessory protein 1)
elated, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
ressor of lin-12-like (C. elegans)
sequence similarity 26, member B
i sequence similarity 84, member A
protein 277
s One Binder kinase activator-like 2B (yeast)

40) homolog, subfamily A, member 2
IAP repeat-containing 7 (livin)
xin 2 /// peroxiredoxin 2
lase domain containing 2
ill division cycle 23, yeast, homolog)
al protein LOC644053
mma 2
ily interacting protein 5 (class I)

external ophthalmoplegia 1
protein 541
al gene supported by AK097381; BC040866
ain 9
GEF kinase
elial cell transforming gene 1
al protein MGC39900
43113 fis, clone CTONG2028208
35829 fis, clone TESTI2006460
rane emp24 protein transport domain containing 3
icleotide binding protein-like 3 (nucleolar)
Ac:betaGal beta-1,3-N-acetylglucosaminyltransferase 4 /// UDP-GlcNAc:betaGal beta-1,3-N-acetylgluco:

cycle 42 (GTP binding protein, 25kDa)
mentosa 9 (autosomal dominant)
lyl isomerase A (cyclophilin A)
ydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
protein ligase, HECT domain containing, 1
ntaining with AAA domain
'DZ domain containing 1
domain containing 1
n factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
latory transcription factor 1

er family 22 (organic cation transporter), member 4
se D
d locus
al gene supported by BC008048
only 2 (rhombotin-like 1)
sferase 1

ne 9 open reading frame 93
lpha (actin binding protein 280)
osomal protein S3a
ne 1 open reading frame 2
ox K2
γ, epsilon 1 /// hemoglobin, epsilon 1
ociated antigen 16
alcium binding domain 5
rane protein 131
?-sulfatase (Hunter syndrome)
tatin/kazal, immunoglobulin, kunitz and netrin domain containing 2
protein
etaGal beta 1,3-galactosyltransferase polypeptide 6
n factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
ndrome chromosome region, candidate 2
γ containing 1

d locus

nain helicase DNA binding protein 9
n (thioltransferase)
:id receptor, alpha
/-Pudlak syndrome 4
BC1 domain containing 3
iose 4,6-dehydratase
growth factor binding protein 7
yphosphate-5-phosphatase, 145kDa
in family, member 2
;arcoplasmic reticulum protein 1
steine-rich domains 1
;in tyrosine kinase 2
30762 fis, clone FEBRA2000575
n VI (platelet)
lyl isomerase A (cyclophilin A)
icleotide binding protein (G protein), beta polypeptide 1
ase, cGMP-dependent, type II
yrinogen oxidase
al protein 164kDa

:ceptor potential cation channel, subfamily V, member 4
ial ribosomal protein L41
ation protein 3
protein
40) homolog, subfamily C, member 4
ymphocytic leukemia, 2
;in 9
ding protein C, slow type
ivy chain member 2
lagille syndrome)
le homolog 2 (Drosophila)
yde-3-phosphate dehydrogenase

lyltransferase and 5'-phosphatase
ε-associated protein 2
sine ligase
ype XXIV, alpha 1
lated protein complex 3, mu 2 subunit
expressed 3
ie IMAGE:4797099
ε (RNA) III (DNA directed) polypeptide H (22.9kD)
kinase
rane protein 132E
side triphosphate diphosphohydrolase 4
magnesium homeostasis factor (*S. cerevisiae*)
protein 673
-1 homolog (*Drosophila*)
protein 161
eat domain 13 family, member D

er family 22 (organic anion transporter), member 7
al protein BC009862
ta 1
ousled-like kinase 2
mitochondrial membrane peptidase-like (*S. cerevisiae*)
acting protein 1
ion elongation factor, mitochondrial
protein 32
35982 fis, clone TESTI2013604
icity tyrosine-(Y)-phosphorylation regulated kinase 1A /// dual-specificity tyrosine-(Y)-phosphorylation re

rRNA accumulation, homolog (*S. cerevisiae*)
rol-3-phosphate O-acyltransferase 3
2
rowth factor receptor 4
NA DKFZp564O0862 (from clone DKFZp564O0862)
hyde-3-phosphate dehydrogenase, spermatogenic
protein 90kDa alpha (cytosolic), class A member 1
in 5
allopeptidase 28
hthisis 1 (juvenile)
ie IMAGE:3950788
εpeat containing, X-linked 4
repeat containing 61
ed channel like 1
d locus
og gene family, member H
x homolog 5 (HP1 alpha homolog, *Drosophila*)
ox L2
105kDa/110kDa protein 1
lyl isomerase A (cyclophilin A) /// peptidylprolyl isomerase A (cyclophilin A)
sphatase 1, regulatory subunit 7
cleotide binding protein (G protein) alpha 12
al protein LOC642398

ie IMAGE:5302680
IM domain 5
ociated binding protein 2
ronosyltransferase 1 family, polypeptide A10
d locus
/cerate kinase 1
rtamyltransferase 1
al MGC13053 /// hypothetical MGC13053
ptor, type 2, member 14
ie IMAGE:5310903
allopeptidase 14 (membrane-inserted)
lhomocysteine hydrolase-like 1
mmunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2
insert cDNA clone ZD52G03
onjugating enzyme E2B (RAD6 homolog)
ie IMAGE:4420497
adenosine 5'-phosphosulfate synthase 2
al protein LOC284371
lyl isomerase C (cyclophilin C)
al protein LOC93463
NA DKFZp686B2320 (from clone DKFZp686B2320)
sphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
type III domain containing 3B
d dCMP deaminase domain containing 1
protein 28
sine phosphatase, receptor type, C
channel, subfamily T, member 1
amide branched chain transacylase E2
elin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
cDNA clone CS0DH005Y118 of T cells (Jurkat cell line) of Homo sapiens (human)
se activating protein 10
brane and coiled-coil domain family 1
in containing 4
/RNA polymerase II complex component, homolog (*S. cerevisiae*)
SH3 domain containing 2
ie IMAGE:5268742
ie IMAGE:5396656
log E3 ubiquitin protein ligase (mouse)
utamic acid dipeptide (RE) repeats
ens, clone IMAGE:5248198, mRNA
d locus
length insert cDNA clone EUROIMAGE 1090207
d locus
1 repeat containing 38
e 5
(*S. cerevisiae*)
e (prosome, macropain) inhibitor subunit 1 (PI31)
ription factor 3
online kinase 17a (apoptosis-inducing)

ductin, axil) /// axin 2 (conductin, axil)
al protein LOC643496

icle trafficking protein homolog B (*S. cerevisiae*)
main containing 1

se T2
sequence similarity 62 (C2 domain containing) member B
main containing 2
insert cDNA clone YS02G11
n (thioltransferase)
al protein FLJ13236

emia, complementation group L
P450, family 2, subfamily E, polypeptide 1
al protein LOC284454
omplex subunit 5

rotein ligase E3C
uclease II, lysosomal
and cell motility 2
gene product
annel, nonvoltage-gated 1 alpha
ily member 3
ydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
inobutyric acid (GABA) A receptor, alpha 5 /// similar to Gamma-aminobutyric-acid receptor alpha-5 sub
some antigen 1, 162kD
ne 7 open reading frame 10
ie IMAGE:3613219
sphatase 1, regulatory subunit 9B, spinophilin

d locus
hydrogenase (lipoamide) alpha 2
inding protein-like 5
ie IMAGE:5295909
ociated transcript 4
bulin heavy constant gamma 1 (G1m marker)
nunodeficiency virus type I enhancer binding protein 1
42259 fis, clone TKIDN2011289
ated protein complex 1, sigma 3 subunit
protein 366
erine, 35
rotein S27a /// similar to ubiquitin and ribosomal protein S27a precursor
syndrome critical region gene 11
al protein LOC642891 /// hypothetical protein LOC649158
1
coupled receptor 26
nteractive protein 2, 30kDa
ne 5 open reading frame 21

al protein LOC285016
ne 1 open reading frame 123
nt component 1, s subcomponent
protein 533
ne 17 open reading frame 42

lfinic acid decarboxylase
igomeric mucus/gel-forming

ronosyltransferase 2 family, polypeptide A3
› 1 (*S. cerevisiae*)
ens, clone IMAGE:2960615, mRNA
protein
annel, voltage-gated, type I, beta
din E receptor 4 (subtype EP4)
›cule (Indian blood group)
-associated plasma protein A, pappalysin 1
›z/ten-m homolog 2 (*Drosophila*)
protein

ne 10 open reading frame 86
›rin beta 7
› receptor complex member 2
›iated PDZ and coiled-coil motif containing

›noyl-Coenzyme A carboxylase 2 (beta)
›igator 1
›l cancer associated protein
e, alpha; acid (Pompe disease, glycogen storage disease type II)
GE:110862, mRNA sequence
›l protein LOC283663

›l protein LOC283551
›l LOC440900
› containing TCP1, subunit 5 (epsilon)
›ma virus CT10 oncogene homolog (avian)

› sequence similarity 22, member A /// family with sequence similarity 22, member B /// family with sequer
›n binding protein 4 (formin binding protein 21)
›sitide-3-kinase, regulatory subunit 5, p101
›olog, nonsense mediated mRNA decay factor (*C. elegans*)
›de FF-amide peptide precursor

› segregation increased 2-like 3
›homocysteine hydrolase-like 1
› (*S. cerevisiae*)
›J20892 fis, clone ADKA03430
›din E synthase 3 (cytosolic)
› homolog 3 (neuroendocrine-dlg, *Drosophila*)
›embrane protein 1
›bulin superfamily containing leucine-rich repeat 2

› A exonuclease 1 homolog (*S. cerevisiae*)
›ne 12 open reading frame 47
›olog 1 (*Drosophila*)
›ain containing 6

protein
omega breakpoint family, member 10
the 10 open reading frame 53
leucine-rich repeat-containing protein 14
tetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
d locus
insert cDNA YI37C01
er family 38, member 5

ceptibility candidate 2
eta-hydroxylase
d locus
ty group box 4
omain containing 2
ociated protein 3
ar RNA activating complex, polypeptide 5, 19kDa
nily, member B1 /// SPANX family, member B2
i
NRP) and tollid (TLL)-like 1
ociated transcript 3

al protein MGC34821
ase, X-linked /// protein kinase, Y-linked
annel, voltage-dependent, alpha 1I subunit
er family 2 (facilitated glucose transporter), member 3
d locus
tin binding protein, 2A
38388 fis, clone FEBRA2004485
ie nucleotide exchange factor (GEF) 12
NA-ribosyltransferase domain containing 1

sequence similarity 66, member C

ase A2, group VI (cytosolic, calcium-independent)
eptidase 6
al LOC283677
37917 fis, clone CTONG1000137
NA binding motif protein, Y chromosome, family 2 member B
eta, non-erythrocytic 4
mbrane protein 2A
lipoprotein receptor-related protein 6
ase N2
D9

ation repair homolog 2 (E. coli)
group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyl
coupled receptor 84
hancer binding protein (C/EBP), epsilon
N-methyltransferase
protein 701

(yeast)
n containing oxidoreductase
d locus
f G-protein signalling 1
y 1, member A (torsin A)
all subunit (SSU) processome component, homolog (yeast)

differentiation protein
'ase activating protein
ie IMAGE:4824668
40) homolog, subfamily C, member 15
tein, ataxia-telangiectasia locus
al protein LOC90408
nescent cell antigen-like domains 1
d protein 2/3 complex, subunit 4, 20kDa /// actin related protein 2/3 complex, subunit 4, 20kDa
gene 7 (TEL2 oncogene)
.1 mRNA sequence
: membrane protein band 4.1-like 3 /// erythrocyte membrane protein band 4.1-like 3
:e beta like
protein
onse element binding transcription factor 2
epeat containing, X-linked 5
ier family 35, member D2
r binding protein (scraps homolog, Drosophila)
lase (flavin containing) domain 2
al protein FLJ10803
NA DKFZp762M127 (from clone DKFZp762M127)
inase, muscle
bulin light chain variable region complementarity determining region (CDR3) mRNA
itoyltransferase, long chain base subunit 1
ne 14 open reading frame 43
ein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
ctor V alpha gene segment V-alpha-w27, clone IGRa05
ain p53 inducible protein 13
al protein FLJ21369
rowth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)

ated protein complex 3, delta 1 subunit
al protein FLJ33708
tor (erythroid-derived 2)-like 3
ne X open reading frame 23
IM domain 5
ptosis, WT1, regulator
2, type 2 (N-cadherin 2)
d locus
ociated binding protein 2
HIT type 3

dissociation inhibitor (GDI) alpha /// Rho GDP dissociation inhibitor (GDI) alpha
alpha 10
gene product
ox N4

omain receptor family, member 1
ociated factor X
kappa light polypeptide gene enhancer in B-cells, kinase gamma
r domain containing 2
and SOCS box-containing 2
kidney disease 2 (autosomal dominant)
γ 5, group I (pepsinogen A) /// similar to Pepsin A precursor /// similar to Pepsin A precursor
al gene supported by BC014163
ε P450, family 4, subfamily F, polypeptide 11
mRNA processing factor 8 homolog (S. cerevisiae) /// PRP8 pre-mRNA processing factor 8 homolog (S.
rane protein 25
rane 6 superfamily member 2

ι 1
ne 10 open reading frame 22

se activating protein 9
ne 20 open reading frame 28
DHHC-type containing 19
llopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)
d locus
al protein
al protein FLJ12886
ne nucleotide exchange factor (GEF) 1
ne nucleotide exchange factor (GEF) 4
1

omplex subunit 6
al locus LOC388666
protein
alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B
lasin homolog (yeast)
al protein LOC648987
y terminated mRNA decay factor-like
phase expressed 1 /// G-2 and S-phase expressed 1
d locus
ember RAS oncogene family
r-related protein 3 homolog (yeast)
al protein LOC202460

ain family, member 2
εin 32
g gene family, member G (rho G)
rowth factor 1 (acidic)
ie-6-phosphate deaminase 2
d locus
nopeptidase (aminopeptidase B)
protein, alpha-crystallin-related, B9

NA DKFZp434C108 (from clone DKFZp434C108)
e fiber of sperm tails 2-like

al protein FLJ25770
ne 20 open reading frame 27
receptor, metabotropic 7
rmone receptor associated protein 1
ne 19 open reading frame 18
al locus LOC401237
associated guanylate kinase, WW and PDZ domain containing 3
tylinositol transfer protein, cytoplasmic 1
: repeat, RNA binding protein 1
hogenetic protein receptor, type IA
lymphoma 11A (zinc finger protein)
al protein FLJ37659

rpe VI, alpha 1
d locus, strongly similar to XP_371182.1 PREDICTED: similar to BC282485_1 [Homo sapiens]
ens, clone IMAGE:5180681, mRNA
i 14
ox J1
al protein LOC646769
-interacting protein 2 homolog A (Drosophila)
13350 fis, clone OVARC1002143
:G7889-PA
:cule, complement regulatory protein

ig protein with multiple splicing
and BTB domain containing 26

ly member 1
rane protein 16J
e (RNA) III (DNA directed) polypeptide D, 44kDa
nber RAS oncogene family
in binding glutamic acid-rich protein like
ythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
:ta 2
:e, beta, acid 3 (cytosolic)
i type III domain containing 3B
ain containing 5
ie IMAGE:4828283
compatibility complex, class I, E
protein 195
ase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)
tor I/B
3-O-sulfotransferase 4
Jing protein 1A, 12kDa
protein 3
din I2 (prostacyclin) synthase /// prostaglandin I2 (prostacyclin) synthase
eceptor 1
iily member 13B
viralicidic activity 2-like 2 (S. cerevisiae)

A5
d locus

ial ribosomal protein S31
nyloidosis, Finnish type)
na 1
ain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B
sferase 5 domain containing 1
ynthetase medium-chain family member 2
iated, gamma adaptin ear containing, ARF binding protein 1

al protein MGC26733
na 2, smooth muscle, enteric
beta 1
ens, clone IMAGE:4151631, mRNA
se-like 4
al protein LOC646562 /// hypothetical protein LOC652572
domain containing 1

gamma chain
ctor I/A
(*S. cerevisiae*)
40) homolog, subfamily C, member 9
nin 2 (bilateral acoustic neuroma)
al gene supported by BC033230
nd polyadenylation specific factor 3-like
elated, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
al protein FLJ35801
growth factor receptor pathway substrate 15-like 1
inding Ig-like lectin 8
like 2

ne 8 open reading frame 45
tein L, 3
42263 fis, clone TKIDN2014570
|
rotein-like 3 antisense /// ret finger protein-like 1 antisense
al protein MGC11257
lass I, type 8B, member 2
d locus
!CA2-containing complex, subunit 3
al protein LOC286087
|
nase/reductase (SDR family) member 3
1 (*Drosophila*)
esterase 3A, cGMP-inhibited
surface antigen
embrane glycoprotein (rat)
sulfoxide reductase B3
al protein LOC645212
ie IMAGE:5295909
sequence similarity 69, member B
ty domain containing 2
er family 44, member 1
(metallopeptidase M3 family)

n

islet cell autoantigen 1, 69kDa /// islet cell autoantigen 1, 69kDa

Yolag B (S. cerevisiae)

1

EGF calcium binding domains 1

kinase 6

transforming protein 30

1

tor A4

hair, basic, 6 (monilethrix) /// similar to keratin, hair, basic, 6

repeat containing 40

group ring finger 5

locus

erbB receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)

locus

locus, weakly similar to NP_787073.2 hypothetical protein MGC35023 [Homo sapiens]

antigen, golgin subfamily a, 1

see IMAGE:4827146

coupled receptor 161

1

cytoplasmic 1, intermediate chain 2 /// dynein, cytoplasmic 1, intermediate chain 2

containing transmembrane protein 1 /// hypothetical protein LOC644512

prothymosin, alpha (gene sequence 28)

in family member 27

late phosphatase-related protein type 2

locus

cDNA clone CS0DI029YI16 of Placenta Cot 25-normalized of Homo sapiens (human)

locus

receptor regulated 1

colitis polyposis coli

related developmental regulator 2

glycology subfamily A member 5

specific beta-1-glycoprotein 4

domain 40B

see IMAGE:4821793

organic anion transporter family, member 2A1

nascent cell antigen-like domains 2

J20874 fis, clone ADKA02818

containing preferred translocation partner in lipoma

locus

orthologous against DPP homolog 3 (Drosophila)

interferon stimulated exonuclease gene 20kDa-like 2 /// interferon stimulated exonuclease gene 20kDa-like 2

alpha 2B (pancreatic)

frame 2 open reading frame 17

protein LOC644009

repeat (in FLII) interacting protein 1

3'-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2

lin
lymphoma 2
al protein LOC285103
ne 10 open reading frame 92
d locus, strongly similar to NP_079045.1 adipocyte-specific adhesion molecule; CAR-like membrane pro
ated protein 1, 65kDa
r-associated protein 3-like
e IMAGE:5296510
?
e IMAGE:4814828
ne 10 open reading frame 33
e nucleotide exchange factor (GEF) 4
protein
ne 17 open reading frame 84

pecific peptidase 14 (tRNA-guanine transglycosylase)
tor I/X (CCAAT-binding transcription factor)
lation factor 3 /// ADP-ribosylation factor 3
SH3 domain containing 2
rase family, cytosolic, 1A, phenol-preferring, member 2
protein 3
coupled receptor 133
mia (Rab escort protein 1)
ier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16
kinase 2
ens, clone IMAGE:5743964, mRNA
endent kinase 8
ceptor, family 2, subfamily M, member 4
in containing 6
olog (*S. pombe*)
NA DKFZp564D043 (from clone DKFZp564D043)
ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B
lipoprotein-related protein 12
hibitory protein 45

er family 1 (glutamate transporter), member 7
rotein, kinesin binding 1

latory protein alpha
or receptor-bound protein 10

g gene family, member F (in filopodia)
nily, AAA domain containing 3C
none receptor interactor 6
zyme A oxidase-like
>Glu-Ala-Asp) box polypeptide 27
d locus
y 1, member B (torsin B)
r, IgA, IgM, high affinity
ssociated Eps domain containing 2
hatase (inorganic) 2
nily, AAA domain containing 3B

al protein MGC39900
jht polypeptide (Lca)
J20923 fis, clone ADSE00893
tylinositol glycan, class T
in depolymerizing factor)
ed ovarian killer
ial carrier homolog 2 (C. elegans)
f G-protein signalling 12
DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant neg:

ydrogenase 4 (class II), pi polypeptide
ylinositol 4-kinase, catalytic, alpha polypeptide
eptor subfamily 1, group H, member 4
ase, cAMP-dependent, regulatory, type I, beta /// similar to cAMP-dependent protein kinase type I-beta r
d locus, weakly similar to NP_079012.2 gasdermin domain containing 1; 1810036L03Rik [Homo sapiens
30446 fis, clone BRACE2009255
annel, voltage-dependent, L type, alpha 1B subunit

protein 141
ne X open reading frame 15
tyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)

ioside activator
tivated protein kinase kinase kinase 11
32 /// interleukin 32
: membrane protein band 4.1-like 1
d locus
ens, clone IMAGE:4250593, mRNA

ain 38
:IKEN cDNA 1200014N16 gene
mone receptor associated protein 5
ne 20 open reading frame 161
ucine rich repeat neuronal 6C
y 1, member A (torsin A)
tor A10
er family 35, member D3

ne nucleotide exchange factor (GEF) 7
al protein LOC127841
allopeptidase 28
:cule
ne 1 open reading frame 85
al protein LOC648342
ial ribosomal protein L9 /// mitochondrial ribosomal protein L9
progressive homolog (mouse)
al protein LOC283904 /// hypothetical gene supported by AK091834
ymerase alpha
oma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 1 /// KIAA1245 /// neurc

voltage-gated channel, subfamily H (eag-related), member 2

if cytokinesis 6
ne 16 open reading frame 57

ain containing 3
rotein particle complex 6B
thetase co-transcribed homolog (bacterial)
adhesion molecule 1

g protein p400
convertase subtilisin/kexin type 5
!-related gene
rotein S27-like
!
eylglucosamine pyrophosphorylase 1-like 1

n, beta
protein

ase (DNA) I pseudogene 2
7
t containing 2
ylate cyclase-associated protein 1 (yeast)
se-like 2
e (prosome, macropain) 26S subunit, non-ATPase, 6
protein /// FLJ34870 protein

ytochrome c reductase, 6.4kDa subunit
tor alpha locus /// T cell receptor delta locus
2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
, mitochondrial (E. coli)
teracting serine-threonine kinase 4
synthetase /// glutathione synthetase
ier family 33 (acetyl-CoA transporter), member 1
32438 fis, clone SKMUS2001402
one acetyltransferase (monocytic leukemia) 3 /// MYST histone acetyltransferase (monocytic leukemia) 3
iated domain containing 1

i binding protein 1
eous nuclear ribonucleoprotein U (scaffold attachment factor A)
al LOC554248
se 3 (a protein tyrosine kinase, leukocyte)
er family 28 (sodium-coupled nucleoside transporter), member 3
n 2
brane protein 106C
hosphoprotein
al protein FLJ20366
riolog (S. cerevisiae)
ding protein
al protein ZD77D08
al protein LOC155006

α-associated protein 1 light chain 3 gamma /// microtubule-associated protein 1 light chain 3 gamma
al protein LOC283432
F-hand domain containing
ase domain containing 4
inding protein /// TAR DNA binding protein
llus 1 homolog (rat)
23 mRNA sequence
protein 664
al protein HSPC111
8
13
RAN-binding domain containing 3
1 binding protein 1, 182kDa
J20971 fis, clone ADSU01565
rotein, large, P2
in containing RING finger 3
sis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)
37884 fis, clone BRSTN2012451
al protein LOC149832

ne 13 open reading frame 18
onal domain (PTPRF interacting)
l development protein 1
rotein 8
al protein LOC283012
rane protein 9
8 (Drosophila)
al protein LOC154822

is (X-linked, juvenile) 1

og C (C. elegans)
eat and KH domain containing 1 /// MASK-4E-BP3 alternate reading frame gene
al LOC389105 /// hypothetical protein LOC651410
osteosarcoma
l

α/beta-like factor /// stoned B/TFIIA-alpha/beta-like factor
ptor-associated protein 29
J22799 fis, clone KAIA2625
ens, clone IMAGE:5164889, mRNA
l homolog (Drosophila) /// within bgcn homolog (Drosophila)

d locus
in binding glutamic acid-rich protein like 3 /// SH3 domain binding glutamic acid-rich protein like 3
osphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)
d locus
lear divisions 1 homolog (S. cerevisiae)
nember RAS oncogene family
cruitment domain family, member 12
molog (Drosophila)

ous nuclear ribonucleoprotein C (C1/C2)
ember of RAS oncogene family

sequence similarity 54, member A
36413 fis, clone THYMU2010816
stitutive photomorphogenic homolog subunit 7B (Arabidopsis)
tor related to kappaB binding protein
tress induced like
e (prosome, macropain) 26S subunit, ATPase, 2
domain 42A
' FKSG49
ctor, arginine/serine-rich 4
sequence similarity 111, member B
er family 35, member E3
al LOC285711
meobox
ylserine decarboxylase
domain containing 5 (spindle associated)

al protein LOC643364
osome associated protein
d locus
al protein LOC646215
nma complex associated protein 6
ens, clone IMAGE:5539086, mRNA
11 (mouse) like 1
pecific peptidase 48
osome associated protein
al protein MGC10471 /// hypothetical protein MGC10471
omain family, member 1
ctor 5 (ets domain transcription factor)
11 (apoptosis facilitator)
protein
al protein LOC283761
sequence similarity 24, member B
ne 3 open reading frame 58
achment factor B2
36579 fis, clone TRACH2012647
in 44
e IMAGE:4304686
MYM-type 1
al protein MGC2752
rt component (3b/4b) receptor 1 (Knops blood group)
+ transporting, lysosomal 9kDa, V0 subunit e
adenosyltransferase II, alpha
in containing 4
sinogen B1 /// chymotrypsinogen B2 /// similar to Chymotrypsinogen B precursor
al LOC339123

J20867 fis, clone ADKA02259
onal domain (PTPRF interacting)

sequence similarity 83, member H
1 receptor antagonist
ain containing 1
30500 fis, clone BRAWH2000471
eat containing, nuclear envelope 2
interacting protein K
1 repeat and sterile alpha motif containing 1
al protein LOC643473 /// hypothetical protein LOC643519
(Drosophila)
icity phosphatase 15
ossible element with ZNF domain
nsferase 6 (alpha (1,3) fucosyltransferase)
ain containing 7
sine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
nain containing 1
al protein MGC5139
: 2 (Drosophila)
11851 fis, clone HEMBA1006744
e IMAGE:4829494

J20947 fis, clone ADSE01841
rin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily B
insert cDNA clone ZA88B06
lated kinase 3

-associated ring finger (C3HC4) 5
YVE domain containing 3
otif-containing 32
protein 587
domain 36
fructo-2-kinase/fructose-2,6-biphosphatase 2
37566 fis, clone BRCOC2002085
NA DKFZp434J2111 (from clone DKFZp434J2111)
nsferase, CAAX box, alpha
eceptor 1

onjugating enzyme E2Z (putative)
d locus
al protein LOC284219
ne 15 open reading frame 5 /// chromosome 15 open reading frame 5
ain containing 3
al LOC439962
acting protein
ologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1
protein 124 (HZF-16)
IKEN cDNA 6030419C18 gene
etermining region Y)-box 6

oma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma br
main containing 3
ssemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) /// similar to transcription
J23242 fis, clone COL01514

al protein MGC33214
cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)
h repeat containing 7
eoside diphosphate linked moiety X)-type motif 9 pseudogene 1
rotein L35 /// ribosomal protein L35

ceptor, family 3, subfamily A, member 3 /// olfactory receptor, family 3, subfamily A, member 3
in 2 binding protein
sein kinase and cyclin-dependent kinase substrate 1
n termination factor, RNA polymerase I

imidinase-like 5
IKEN cDNA D630023F18
allopeptidase domain 12 (meltrin alpha)

er family 25 (mitochondrial carrier; Graves disease autoantigen), member 16
associated guanylate kinase, WW and PDZ domain containing 1
ne 14 open reading frame 168
inc finger protein 418
protein 579
ly defined colon cancer antigen 10
ntrin specific peptidase 6

rate and iron-dependent oxygenase domain containing 1
domain containing 41
P450, family 2, subfamily A, polypeptide 6
otif-containing 2
d locus, strongly similar to NP_065948.1 hyperpolarization activated cyclic nucleotide-gated potassium c
log (*S. cerevisiae*)
cerate kinase 2
f BRCA1 gene 2
al protein FLJ20422
ig motif protein 34
sequence similarity 20, member B
7) cofactor (p47)
obox 9
nolog (RecA homolog, *E. coli*) (*S. cerevisiae*)
length insert cDNA clone EUROIMAGE 362430
Drosophila)
in 44
achment factor B
esterase 4D interacting protein (myomegalin)
d locus
nzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)
protein 710
nhancer 2 homolog (*C. elegans*) /// protein F25965
tor of activated T-cells, cytoplasmic, calcineurin-dependent 3
og 3 (*E. coli*)
protein 260
ne 11 open reading frame 31
protein

receptor type A
d locus
activated protein kinase kinase kinase 4
heat domain 25
protein
olog (*S. cerevisiae*)
olog (mouse)
phosphatidylinositol specific phospholipase D1
protein
ase (cAMP-dependent, catalytic) inhibitor beta
e (prosome, macropain) 26S subunit, non-ATPase, 11
13242 fis, clone OVARC1000578
membrane protein 2A
rotein L21 /// similar to 60S ribosomal protein L21 /// similar to ribosomal protein L21 isoform 1 /// ribosc
ember RAS oncogene family
nding protein 1

n factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
al protein LOC90624
acetylase 8
23 (*Drosophila*)
e (RNA) I polypeptide B, 128kDa
rin beta 1
ne 12 open reading frame 56
ne 6 open reading frame 55
44429 fis, clone UTERU2015653
al protein LOC652226
nitoyltransferase, long chain base subunit 2
activating protein and VPS9 domains 1
ing protein 4
domain containing 72
ne 14 open reading frame 1
olog (*S. cerevisiae*)
ndent kinase (CDC2-like) 10

, DHHC-type containing 2
ydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
lation factor-like 6 interacting protein
al protein FLJ38773
lymphoma 6, member B (zinc finger protein)
ha 3
ial ribosomal protein S30
id double PHD fingers, family 3
ita 2 (complement component 3 receptor 3 and 4 subunit)
ytochrome c reductase binding protein
noic acid binding protein 2
J23566 fis, clone LNG10880
ne 6 open reading frame 12
dine receptor domain and SOCS box containing 3
ite (chondroitin 6) sulfotransferase 3
al protein LOC338864
NA DKFZp761B0221 (from clone DKFZp761B0221)

midinase

eta, non-erythrocytic 4 /// spectrin, beta, non-erythrocytic 4
protein 518

f G-protein signalling 19

ociated endoplasmic reticulum protein 1

e-1-phosphate phosphatase 1 /// sphingosine-1-phosphate phosphatase 1

2

4

ht polypeptide (Lcb)

voltage-gated channel, subfamily H (eag-related), member 2

kinase 1

escape 1

ed domain containing ets transcription factor

ne 12 open reading frame 46

omolog (Drosophila)

lactosaminidase, alpha-

onemal, heavy polypeptide 10

nain family, member 4 /// TSC22 domain family, member 4

olog 1 (Drosophila)

MYND-type containing 19

lation factor-like 10

ceptor, family 1, subfamily I, member 1

ens, clone IMAGE:4456091, mRNA

protein 398

ne 10 open reading frame 44

: repeat, RNA binding protein 2

rol kinase, theta 110kDa

ember RAS oncogene family

compatibility complex, class II, DR beta 1

nsporter 1

llopeptidase inhibitor 2

hatase, prostate

embrane protein 3

nding protein 1

al protein LOC283033

tyltransferase 1

ceptor 1

Fyn-associated substrate

adhesion molecule 3

h secretory protein LCCL domain containing 2

esterase 10A

cDNA clone CS0DK012YA15 of HeLa cells Cot 25-normalized of Homo sapiens (human)

ida-like domain containing 1

22 mRNA sequence

rotein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S r

transcription factor 6
transcription factor binding to IGHM enhancer 3
(congenital contractural arachnodactyly)
isolated gene 3
domain containing 9
d locus
allopeptidase inhibitor 2
transcription factor

antigen, golgin subfamily a, 3
receptor, ionotropic, kainate 1
protein L3

protein FLJ39502
25766 fis, clone TST06382
homolog 1 (Drosophila)
see IMAGE:3881027
!

binding protein 1
catalyzer of heat shock 90kDa protein ATPase homolog 2 (yeast)
induced proliferation-associated 1 like 3
esterase related
protein 4 (Drosophila)

25946 fis, clone JTH14258
inosine phosphatase, receptor type, A
protein LOC284576
protein gene supported by BC035379; BC042129
leucine nuclear ribonucleoprotein A/B
protein 1 and transcript release factor
down-regulated spectrin-associated protein 1-like 1
domain containing 84
protein P450, family 1, subfamily B, polypeptide 1
protein kinase 38 like
n U
drug cassette, sub-family B (MDR/TAP), member 7
sequence similarity 46, member C
allopeptidase with thrombospondin type 1 motif, 8
6
family CW-type zinc finger 2
gamma delta /// neurocalcin delta
see IMAGE:5267328
hydrogenase 13 (all-trans/9-cis)
induced neurotrophic factor
30383 fis, clone BRACE2008102
protein sorting 72 (S. cerevisiae)
secretory protein LCCL domain containing 1

translation initiation factor 3, subunit 5 epsilon, 47kDa
protein MGC42174

ribose 5-phosphoribosyltransferase
Gene ID: 5302109
RIKEN cDNA 2410129H14
40) homolog, subfamily A, member 1
Nucleoside diphosphate-uridylyltransferase 1
GTPase (ARHGAP) and pleckstrin domain protein 1 (chondrocyte-derived)
Complex subunit 4
Nucleoside diphosphate-uridylyltransferase, long chain base subunit 2
Activated protein kinase 14
Homolog (S. cerevisiae)
p21/Sun domain family, member 4

Gene ID: 4140029
Eukaryotic translation initiation factor 3, subunit 8
Element binding protein G
Casein kinase II, alpha
Protein
Casein kinase II-like 2
e
i) containing 2, with ZNF domain
Binding protein 1 (amine oxidase (copper-containing))
Hydrogenase 11 (all-trans/9-cis/11-cis)
Aldehyde reductase family 1, member A1 (aldehyde reductase)
e repeat containing 5
Gamma binding protein 6

Protein LOC151174
Ornithine decarboxylase protein 85
Regulatory factor 2 binding protein 1
e family, member Y
in, class 2, transcription factor 2
Protein LOC642826
Protein 566
pRKA) anchor protein 7
pGPR, member X1
Compatibility complex, class II, DO alpha
Acting protein 3
Myelin protein 2
er family 27 (fatty acid transporter), member 4
Intracellular channel 1
Genetic determinant of recA protein homolog (mouse)
Ribosomal protein S11
Induced protein 44
ne 14 open reading frame 150
Din E synthase
i) 2 (Drosophila)
34 mRNA sequence
Protein 653
Galactose 4-epimerase alpha-2,3-sialyltransferase 3
GTPase and PH domain containing 6
Casein kinase II, epsilon 1
pha 9

alized factor 1

use HEL308

rain interacting protein kinase 1

n-associated protein 4

synthase 2

se activating protein 1

ed neurotrophic factor

sphatase 4, regulatory subunit 2

ng growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)

d locus, strongly similar to NP_775751.1 hypothetical protein LOC126295 [Homo sapiens]

insert cDNA clone ZD67H01

domain containing 5

n protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)

e

onine kinase 38

a+/K+ transporting, beta 3 polypeptide

esterase 8B

n

ioning defective 6 homolog beta (C. elegans)

domain containing 17

teracting protein 1 (toonin)

protein

al protein FLJ14834

rane emp24 protein transport domain containing 5

4 (Drosophila)

deaminase

ty domain containing 1

related protein 2

c oxidase subunit Vib polypeptide 1 (ubiquitous)

1

BRCA1

ndrome chromosome region, candidate 7

al protein LOC197350

ne 20 open reading frame 116

osis factor, alpha-induced protein 8

ta 3 (platelet glycoprotein IIIa, antigen CD61)

gene related to SRC, FGR, YES

al gene supported by AK054937

e tumor suppressor, homolog 1 (Drosophila)

homolog 1 (Drosophila)

al gene supported by BC028186

ucle, decay accelerating factor for complement (Cromer blood group)

CoA 2-hydroxylase interacting protein-like

ial ribosomal protein S15

lymphoma 11A (zinc finger protein)

cDNA clone CS0DF032YA11 of Fetal brain of Homo sapiens (human)

d locus

ne 17 open reading frame 80
protein 435
kinase 2, mitochondrial
:kpoint homolog (S. pombe)
:oantigenic sperm protein (histone-binding)
kinase 2
nain containing 4
22kDa protein 8

glycosylase 2
ens, Similar to neuronal thread protein, clone IMAGE:4106635, mRNA
domain containing 2 (spermatzoa) /// similar to thioredoxin domain-containing 2
hydrogenase
ase C, beta 1
ne 11 open reading frame 61
sociated differentiation marker
ie IMAGE:4800096
al protein FLJ10986
d receptor, alpha
l-coil protein
olog 1 (Drosophila)
s and SOF1 domain containing
d locus

ce 4 /// stathmin-like 4
se ceramide glucosyltransferase-like 2
nophosphatase domain containing 1
>-Glu-Ala-Asp/His) box polypeptide 57
-acetyl-galactosaminyl transferase 1
ryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
ting protein Sts-1
ptide repeat domain 3
lex 5
icity phosphatase 8
translation initiation factor 5B
associated tyrosine kinase
al LOC147975
33905 fis, clone CTONG2008405
al protein FLJ20032
eral receptor for phosphoinositides 1)-associated scaffold protein
idase B (beta polypeptide)
de nucleotide transhydrogenase
2
(S. cerevisiae)
32243 fis, clone PROST1000039
iding protein 7
ne 9 open reading frame 19
ic lateral sclerosis 2 (juvenile) chromosome region, candidate 11
olog, nonsense mediated mRNA decay factor (C. elegans)
al protein LOC644246 /// hypothetical protein LOC649063
3
idrome chromosome region, candidate 9

olog (Drosophila)
al protein LOC644137
avy polypeptide 11, smooth muscle
ig growth factor beta 1 induced transcript 1
ig protein S1, serine-rich domain
lase, cytosolic IA /// 5'-nucleotidase, cytosolic IA
ig motif protein, Y-linked, family 1, member A1 /// RNA binding motif protein, Y-linked, family 1, member
otif-containing 14 /// tripartite motif-containing 14
ne 17 open reading frame 27
ie IMAGE:4820928
ie IMAGE:4828523
(CRM1 homolog, yeast)
na 1
:oprotein endopeptidase-like 1
molog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)
domain 20
nt homolog 3 (Drosophila)
d locus, moderately similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens]
annel, voltage-dependent, beta 1 subunit
rin gamma subfamily C, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily A
ociated protein 43
sequence similarity 13, member A1
nain containing 3
n-inducing protein 38
irsten rat sarcoma viral oncogene homolog
n midleg-like 4 (Drosophila)
al protein FLJ22688
3 binding protein 2 (Rett syndrome)
receptor, nicotinic, alpha 4
tic like 3 (Drosophila)
d locus, strongly similar to NP_002946.3 ras responsive element binding protein 1; RAS-responsive eler
idrome chromosome region, candidate 1
roxymethyltransferase 1 (soluble)
de repeat containing 6C
s and homeoboxes 3
translation elongation factor 1 alpha 1
eat domain 1 (cardiac muscle)
:oupled receptor 35
otrophic factor
ne 3 open reading frame 49
ain containing, apoptosis associated protein 2
ressor of mif two 3 homolog 2 (S. cerevisiae)
sphatase 1, regulatory (inhibitor) subunit 3F
protein 4
nma complex associated protein 5
, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)
tor B1
njugating enzyme E2N (UBC13 homolog, yeast)

i containing 4
:ivating Rap/RanGAP domain-like 1
inding protein-like 5

-1 homolog (Drosophila)
ne X open reading frame 21

oma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 9
nin 2 (bilateral acoustic neuroma)
d locus
ated endogenous sequence
ed-Steinberg cell-expressed intermediate filament-associated protein)
noter factor 1, homeodomain transcription factor
allopeptidase with thrombospondin type 1 motif, 9
ltransferase 2
i sequence similarity 27, member A
helix-coiled-coil-helix domain containing 1
estatin preprohormone

og gene family, member Q
mega protein
ced proliferation-associated 1 like 2
J, type 2 (T2-cadherin)
al protein LOC641845 /// hypothetical protein LOC647087
tor, arginine/serine-rich 2, interacting protein
ne 17 open reading frame 79
ike 3
al protein LOC79755
pecific peptidase 31
ne 2 open reading frame 33
ain containing 1
ase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
al protein LOC150759
pe XX, alpha 1

ine-tRNA synthetase-like, alpha subunit
ial ribosomal protein L17
ydrogenase 2, NAD (mitochondrial)
dominant-negative inhibitor pseudo-ICE
rspaced zinc finger motifs
hrome oxidase deficient homolog 1 (yeast)
family, member 2
domain containing 109A
d locus, weakly similar to XP_496435.1 PREDICTED: similar to FLJ46489 protein [Homo sapiens]

osphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
ear ribonucleoprotein polypeptide N
i binding protein 1
ional domain (PTPRF interacting)

allopeptidase 16 (membrane-inserted)
cox 1
nolog (yeast) /// BUD13 homolog (yeast)
rotein L3
peats and discoidin I-like domains 3
n termination factor, RNA polymerase II

al protein LOC647149
protein 4 homolog (S. cerevisiae)
al protein MGC13114
ntrin/SMT3 specific peptidase 3
38849 fis, clone MESAN2008936
d locus
egulatory factor 4
one acetyltransferase (monocytic leukemia) 3
energic receptor mRNA, 3' UTR
sequence similarity 44, member C
(CRM1 homolog, yeast)
sforming growth factor beta binding protein 1
38419 fis, clone FEBRA2009846
11179 fis, clone PLACE1007450
re nucleotide exchange factor (GEF) 2
teoglycan-like sulfated glycoprotein
(prostase, enamel matrix, prostate)
nemal, heavy like 1
acetylase 8
mphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4
odendrocyte glycoprotein
eat domain 10
associated multispinning membrane protein 5

d locus
al protein FLJ40243
natosis
nsferase 25 domain containing 2
eat and SOCS box-containing 9
e factor 13
ta (A4) precursor protein-binding, family A, member 1 (X11)
ne 1 open reading frame 131
log 3 (Drosophila) /// hook homolog 3 (Drosophila)

ne 6 open reading frame 130
lyl isomerase A (cyclophilin A) /// similar to peptidylprolyl isomerase A isoform 1 /// similar to peptidylprol
ciation inhibitor 1
ochrome c oxidase assembly homolog (S. cerevisiae)
nalog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)
jene homolog, MYC activator (mouse)
ription factor 3

ushi multiple domains 1
d locus
ial carrier family protein
1 (yeast)
al LOC401320
eptidase I
ember RAS oncogene family
d locus
insert cDNA clone YT87C03
40) homolog, subfamily C, member 10

ctor 1 (adult) /// folate receptor 1 (adult)
al protein MGC35308
brane protein 117
derived arginine aminopeptidase
itamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
n, epsilon
ated anchoring protein

· of Ty 16 homolog (S. cerevisiae)
n factor B1, mitochondrial
phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))
itor interacting Ras-like 1
rminal like
protein 652
protein 684
d locus, weakly similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens]

4
in 2
ngiectasia mutated (includes complementation groups A, C and D)
e repeat containing 6B
linked retinopathy protein
40) homolog, subfamily C, member 4
domain containing 14
sassociated protein of the synapse, 43kD
protein 678
DHHC-type containing 11
brane and coiled-coil domain family 1
ide peptidase 3
ressor of mif two 3 homolog 2 (S. cerevisiae)
er family 6 (neurotransmitter transporter, noradrenalin), member 2
sequence similarity 19 (chemokine (C-C motif)-like), member A5
kinase (yeast)
protein
ie IMAGE:5302310
ie IMAGE:5296106
allopeptidase with thrombospondin type 1 motif, 9

è I and transcript release factor
ntal pluripotency associated 4
al protein LOC646324
ine transport protein 1 homolog (T californica)

al gene supported by AK091527
olone 76558, 5' end
e fiber of sperm tails 2
è-associated protein 1A
associated antigen (mutated) 1-like 1
ie thymoma viral oncogene homolog 1
al protein LOC139886
ht polypeptide (Lcb)
factor C (activator 1) 2, 40kDa

g 2 (Drosophila)
avy polypeptide 10, non-muscle
elated, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
(UBB) mRNA, 3' UTR and genetic suppressor element
protein

protein L5
cyclase 1, soluble, alpha 2
ha 4
(C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15
ed RNA polymerase II polypeptide J-related gene
e
nesis and oogenesis specific basic helix-loop-helix 1
cible kinase

nteractive protein 2, 30kDa
d locus
ens, clone IMAGE:4344826, mRNA
al protein LOC643659 /// hypothetical protein LOC649255
dine triad gene
erentiation factor 10
rate and iron-dependent oxygenase domain containing 2

rowth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
al LOC401588
al protein LOC339287
idase inhibitor, Kazal type 1
aha 10
sine phosphatase, non-receptor type 18 (brain-derived)

rgosine amidohydrolase (non-lysosomal ceramidase) 2B
domain containing 64
by retinoic acid gene 6 homolog (mouse)
olipase II
ne 19 open reading frame 42
xin 2
protein 20-like 1
nt component 4A (Rodgers blood group) /// complement component 4B (Chido blood group)
al protein FLJ11259
roid (17-beta) dehydrogenase 8
DAZ interacting protein 3
protein 204
molog (Drosophila)

esterase 3B, cGMP-inhibited
rolog (mouse)
aha 5
cDNA clone CS0DI001YP15 of Placenta Cot 25-normalized of Homo sapiens (human)
sphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
al protein DKFZP761M1511
J21541 fis, clone COL06166

in 3
specific chaperone 1

DNA binding 4, dominant negative helix-loop-helix protein
voltage-gated channel, shaker-related subfamily, beta member 1
ta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)
NA DKFZp686K0736 (from clone DKFZp686K0736)

ne 10 open reading frame 85
al protein LOC55610, isoform b
protein 336
/tic leukemia
ie IMAGE:5259979
J21911 fis, clone HEP03855
alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)
ie IMAGE:5268518
ressor of mec-8 and unc-52 homolog (C. elegans)
nase/reductase (SDR family) member 7B
d locus

ne 14 open reading frame 159
hibitory factor receptor alpha
\bl enzyme substrate 1
ie IMAGE:4824791

gene /// pim-1 oncogene

-like enhancer of split 2 (E(sp1) homolog, Drosophila)
:tivated protein kinase 8 interacting protein 2
and SCAN domain containing 2
elated, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
al protein MGC4677 /// hypothetical LOC541471
itamytransferase 1
lear antigen
Irish syndrome-like
ht polypeptide (Lca)
nase 1 (Drosophila)
body-specific RNA 17
al gene supported by NM_194304
1A)-activated kinase 4
se 1, alpha 1
rowth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
compatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 1

ed alanine-rich protein kinase C substrate
ne 20 open reading frame 67
otif-containing 56

an T-cell leukemia virus type I) binding protein 3
yde-3-phosphate dehydrogenase
regulated spectrin-associated protein 1
ie IMAGE:5269545

ne 20 open reading frame 54
rowth factor 14
ne 10 open reading frame 83
ne 1 open reading frame 107

in-like 1
GEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
in 3
-Lindau tumor suppressor
rotein, PTB-binding 2
31833 fis, clone NT2RP6000130
containing 1
g gene family, member J
in 25
ceptor
ific transcript, Y-linked 11
f G-protein signalling 22
d locus
+ transporting, lysosomal V0 subunit a2

ne 14 open reading frame 153
sterase 6D, cGMP-specific, rod, delta
ein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
ase C, beta 1
al protein LOC286071
ninase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)

domain containing 9
:tivated protein kinase 1
olog (Drosophila)
/lation factor-like 4C
NA DKFZp779M2422 (from clone DKFZp779M2422)
-loop-helix domain containing, class B, 5
A4 hydrolase
pecific peptidase 25
rt homolog 3 (Drosophila)
d locus
rotein sorting 37 homolog A (S. cerevisiae)
ceptor 1
brane and tetratricopeptide repeat containing 2
, decysin 1
inding protein 1 (amine oxidase (copper-containing))
icensing and DNA replication factor 1
plicated region transcript 4
40) homolog, subfamily C, member 15
3 (S. cerevisiae)
ha FG-GAP repeat containing 2
36663 fis, clone UTERU2002826
ne 9 open reading frame 5
nase/reductase (SDR family) member 10

olog C (C. elegans)

d locus

protein 548

ctural maintenance of chromosomes 5-like 1 (yeast)

irin gamma subfamily C, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily A

insert cDNA clone YZ94H06

ie IMAGE:4823654

ne 6 open reading frame 57

protein

rding factor (zinc finger protein)-like

al protein PRO1853

osphatase 1, regulatory (inhibitor) subunit 11

al protein DKFZp76112123

rowth factor 11

30581 fis, clone BRAWH2007069

IB

helix-coiled-coil-helix domain containing 7

al protein LOC126917

ne 1 open reading frame 78

ne 9 open reading frame 93

ceptor, family 1, subfamily F, member 1

homeobox 6

ase A2, group V

17D

d locus

al protein FLJ30707

na 1

, renal/pancreas/salivary

al protein FLJ14640

ethyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1 /// similar to UDP-N-ac

translation initiation factor 5B

ryde-3-phosphate dehydrogenase

ing protein 3, interstitial

al protein LOC284739

omology domain containing, family M (with RUN domain) member 1 /// similar to pleckstrin homology dc

a, cardiac muscle

domain 27

protein 331

ily member 14

a C

eta 32 (UNQ827) (DEFB32)

pecific peptidase 48

ase C-like 2

al locus FLJ25758

protein 274

2

protein 20

reacting protein 2

channel tetramerisation domain containing 11
omain containing 1
rotein L24 /// solute carrier family 36 (proton/amino acid symporter), member 2
ig protein 2
al protein LOC284757
nd polyadenylation specific factor 1, 160kDa
se (Wernicke-Korsakoff syndrome)
in-like
:tivated protein kinase kinase kinase 7
ine-7-) methyltransferase
ens, clone IMAGE:5396854, mRNA
al protein LOC643837
e 1

PP-cleaving enzyme 1
polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa
plex locus
ining fibulin-like extracellular matrix protein 1
:cule (Indian blood group)
rotein L39-like
er family 24 (sodium/potassium/calcium exchanger), member 3
omain receptor family, member 1
12301 fis, clone MAMMA1001858
/// Atrophin 1
omolog 2, mitogen-responsive phosphoprotein (Drosophila)
lehydrogenase, quinone 1
nduced protein with tetratricopeptide repeats 1 /// interferon-induced protein with tetratricopeptide repeat
rotein sorting 26 homolog B (S. cerevisiae)
e nucleotide exchange factor (GEF) 6
r-associated protein 2
-associated ring finger (C3HC4) 7
rotein complex, subunit gamma 2
in binding glutamic acid-rich protein like 2
omponent 5
protein 423
43403 fis, clone OCBBF2016612
dystrobrevin binding protein 1) domain containing 2
oid modulatory element binding protein 2
sulfoxide reductase A

log 2 (Drosophila)
3, H-cadherin (heart)
i-related protein 6 homolog (yeast)
ie monophosphate) dehydrogenase 2
al protein FLJ20920
egulatory factor 8 /// interferon regulatory factor 8
ptor, sigma 1
RKA) anchor protein 11
/toskeletal associated protein

olog 3 (Drosophila)

domain containing 80
repeat containing 19
heat domain 11
(Drosophila)
32438 fis, clone SKMUS2001402
complex subunit 10
activating enzyme E1-like 2
ase, H⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
er anti-estrogen resistance 3
γ 54kDa
e domain containing 3
rane protein 2
homa breakpoint associated target 1
otif-containing 10
murine) ecotropic retroviral transforming sequence-like 1
al protein LOC645478
m cofactor synthesis 1
al protein LOC645478
al protein FLJ20054
containing 2
receptor, nicotinic, delta
domain 68
d locus
ylinositol 4-kinase type 2 beta
ne 10 open reading frame 61
termination factor 2
um binding protein A11 (calgizzarin)
guanine dimethylaminohydrolase 1
:cule, complement regulatory protein
nduced 1
1
NA DKFZp313H0740 (from clone DKFZp313H0740) /// Retinol dehydrogenase 13 (all-trans/9-cis)
nded DNA binding protein 2
raction molecule 2
d locus

al protein LOC144363
ologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1
al protein FLJ35390
olog (mouse)
-spanning 4-domains, subfamily A, member 7 /// membrane-spanning 4-domains, subfamily A, member
: 2 (yeast)
lated protein
in receptor 3
ific, 10
O4 pre-mRNA processing factor 19 homolog (*S. cerevisiae*)
tyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
ne 9 open reading frame 85
eoprotein domain family, member 1
al protein FLJ32130
protein 90kDa alpha (cytosolic), class B member 1
al protein FLJ37543

disulfide core domain 9

IMAGE:5284861
lin

protein BC002926
-mRNA processing factor 40 homolog A (yeast)
tyrate aminotransferase
cell surface associated
light chain, LC8-type 1

ase, cGMP-dependent, type I
chain 22
protein family 14 (urea transporter), member 1 (Kidd blood group)
icosamine kinase /// N-acetylglucosamine kinase
gene 9 open reading frame 3
sequence similarity 53, member A
tyrosine kinase 2 (Hallervorden-Spatz syndrome)
member RAS oncogene family
homolog of Ty 6 homolog (*S. cerevisiae*)
class G
cDNA clone CS0DM011YA01 of Fetal liver of *Homo sapiens* (human)
cell adhesion molecule
transmembrane protein 39B
thymoma viral oncogene homolog 3 (protein kinase B, gamma)
immunoglobulin domain containing 2

45325 fis, clone BRHIP3006717
muscinosis, neuronal 8 (epilepsy, progressive with mental retardation)
cytochrome c reductase core protein II

2
protein family 25, member 36
protein family 26 (sulfate transporter), member 1
gene 3 open reading frame 34
mucosal antigen 1
lysosomal vesicle associated protein
convertase subtilisin/kexin type 5
polypeptide-associated complex alpha polypeptide
catalytic E3 ubiquitin protein ligase 2
hydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
hemidesmosomes junctional transmembrane protein
domain containing 9
intracellular mediator containing kelch motifs
inhibitor of tumorigenicity 7 like
allopeptidase domain 11
D-Glu-Ala-Asp box polypeptide 28
protein family 39 (zinc transporter), member 14
IMAGE:5273799
cell growth factor 1 (platelet-derived)

ne 1 open reading frame 25
protein 21A
member RAS oncogene family
and BTB domain containing 9

ne 12 open reading frame 39
otif-containing 45
sine-5-)-methyltransferase 3 alpha
rotein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7
al protein FLJ35390
eft 1 candidate 1
eductase 3
ciated protein 6
rotein L3 /// ribosomal protein L3
protein 19 /// zinc finger protein 23 (KOX 16)
er family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31 /// solute carrier family :
in binding protein 5 (BTK-associated)

ulin heavy constant gamma 3 (G3m marker) /// similar to Ig heavy chain V-III region VH26 precursor ///

similar to SMT3 suppressor of mif two 3 homolog 2 /// similar to SMT3 suppressor of mif two 3 homolog 2

gallus;

mutated in multiple advanced cancers 1)

alpha-2 chain) (N-alpha 2)

, 8 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 5 /// protocadherin g:

saminyltransferase 4

gulated kinase 1A

unit precursor (GABA(A) receptor)

nce similarity 22, member C /// similar to nuclear protein in testis

ltransferase)

cerevisiae)

stein [Homo sapiens]

ative helix-loop-helix protein

egulatory subunit
s]

oblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 15 /// neuroblasto

i, 4 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily A, 8 /// protocadherin gar

reakpoint family, member 16

ial regulator ATRX isoform 1

channel 3; potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3 [Homo sapie

mal protein L21 pseudogene /// similar to 60S ribosomal protein L21 /// similar to ribosomal protein L21

ribosomal protein L7 /// 60S ribosomal protein L7-like /// similar to 60S ribosomal protein L7 /// similar to

F /// RNA binding motif protein, Y-linked, family 1, member B /// RNA binding motif protein, Y-linked, fan

., 8 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 5 /// protocadherin ga

ment binding protein-1; DNA-binding protein [Homo sapiens]

lyl isomerase A isoform 1 /// similar to peptidylprolyl isomerase A isoform 1 /// similar to peptidylprolyl isc

, 8 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 5 /// protocadherin g:

:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1

omain containing, family M (with RUN domain) member 1; adapter protein 162

ts 1

25 (mitochondrial carrier; adenine nucleotide translocator), member 31

myosin-reactive immunoglobulin heavy chain variable region /// anti-RhD monoclonal T125 gamma1 he:

2 /// similar to SMT3 suppressor of mif two 3 homolog 2 /// similar to SMT3 suppressor of mif two 3 homc

amma subfamily C, 4 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily B, 6 ///

oma breakpoint family, member 9 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma bre

mma subfamily A, 8 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 12 //

ans

isoform 1 /// similar to 60S ribosomal protein L21 /// similar to 60S ribosomal protein L21 /// similar to rib

60S ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7

nily 1, member D /// RNA binding motif protein, Y-linked, family 1, member E /// RNA binding motif protei

amma subfamily C, 4 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily B, 6 ///

omerase A-like /// similar to peptidylprolyl isomerase A isoform 1 /// peptidylprolyl isomerase A-like /// sim

amma subfamily C, 4 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily B, 6 ///

avy chain

olog 2 /// similar to SMT3 suppressor of mif two 3 homolog 2 /// similar to SMT3 suppressor of mif two 3

' protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma :

akpoint family, member 12 /// neuroblastoma breakpoint family, member 16

// protocadherin gamma subfamily C, 5 /// protocadherin gamma subfamily C, 5 /// protocadherin gamma

ribosomal protein L21 isoform 1 /// similar to 60S ribosomal protein L21 /// similar to ribosomal protein L21

in, Y-linked, family 1, member J

' protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma :

ilar to peptidylprolyl isomerase A isoform 1 /// similar to peptidylprolyl isomerase A isoform 1 /// similar to

' protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma :

homolog 2

subfamily B, 2 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily A, 11 /// proto

a subfamily C, 4 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily B, 7 /// protc

isoform 1 /// similar to ribosomal protein L21 isoform 1

subfamily B, 2 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily A, 11 /// proto

o peptidylprolyl isomerase A isoform 1 /// similar to peptidylprolyl isomerase A isoform 1 /// similar to pep

subfamily B, 2 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily A, 11 /// proto

ocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subf

ocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfa

ocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subf

ctidylprolyl isomerase A isoform

ocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subf

family A, 7 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 5 /// protocadh

amily B, 6 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 5 /// protocadhe

family A, 7 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 5 /// protocadh

family A, 7 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 5 /// protocadh

erin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily /

ocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B

erin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily /

erin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily /

A, 2 /// protocadherin gamma subfamily A, 1

, 2 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 1 /// protocadherin gar

A, 2 /// protocadherin gamma subfamily A, 1

A, 2 /// protocadherin gamma subfamily A, 1

subfamily B, 1 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily A, 11 /// protc

subfamily E

Supplementary Table 2

Probe Set ID	Mean-Depr	Mean-Treat	T-test	Deprived/T	Log2(D/T)	(-1)Log10(p)	Gene_Sym	AC_number
209066_x_at	7994.157	8341.053	0.033	0.958	-0.061	1.488	UQCRB	M26700
241755_at	41.695	48.116	0.049	0.867	-0.207	1.307	UQCRC2	AI961429
213995_at	606.035	677.404	0.022	0.895	-0.161	1.661	ATP5S	AW195882
216954_x_at	1320.989	1537.264	0.048	0.859	-0.219	1.321	ATP5O	S77356
201441_at	6913.994	7475.081	0.037	0.925	-0.113	1.434	COX6B1	NM_00186
1556284_at	57.541	70.248	0.025	0.819	-0.288	1.596	PPA2	AF086012
203858_s_at	921.805	979.457	0.041	0.941	-0.088	1.389	COX10	NM_00130

Gene_Full_Name	Gene Onto	Gene Onto	Gene Ontology	Molecular Function
ubiquinol-cytochrome c r	6118	elec	5739 // mitr	8121 // ubiquinol-cytochrome-c reductase activity // inferre
Ubiquinol-cytochrome c	6118	elec	5739 // mitr	4222 // metalloendopeptidase activity // inferred from elec
ATP synthase, H+ transp	6811	ion	5739 // mitr	15078 // hydrogen ion transporter activity // inferred from :
ATP synthase, H+ transp	6811	ion	5624 // mei	5215 // transporter activity // non-traceable author statem
cytochrome c oxidase su	6118	elec	5739 // mitr	4129 // cytochrome-c oxidase activity // non-traceable aut
Inorganic pyrophosphata	6796	phc	5737 // cytc	287 // magnesium ion binding // inferred from electronic al
COX10 homolog, cytoch	6783	hen	5739 // mitr	8495 // protoheme IX farnesyltransferase activity // inferre

ded from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation
:tronic annotation /// 8121 // ubiquinol-cytochrome-c reductase activity // inferred from electronic annotation
sequence or structural similarity /// 15078 // hydrogen ion transporter activity // non-traceable author state
ent /// 16787 // hydrolase activity // inferred from electronic annotation /// 46872 // metal ion binding // infe
:hor statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 4129 // cytochr
nnotation /// 4427 // inorganic diphosphatase activity // inferred from electronic annotation /// 16787 // hyc
:ded from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4659

on /// 16491 // oxidoreductase activity // inferred from electronic annotation
ement /// 15078 // hydrogen ion transporter activity // inferred from electronic annotation
ferred from electronic annotation /// 46933 // hydrogen-transporting ATP synthase activity, rotational mech
ome-c oxidase activity // inferred from electronic annotation
drolase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from elector
) // prenyltransferase activity // inferred from electronic annotation /// 4311 // farnesyltranstransferase acti

mechanism // inferred from electronic annotation /// 46961 // hydrogen-transporting ATPase activity, rotational

mechanism // inferred from electronic annotation

activity // traceable author statement

il mechanism // inferred from electronic annotation /// 15078 // hydrogen ion transporter activity // inferrec

activity // inferred from electronic an

Supplementary Table 3

Pathway_Down_in_Deprived

	Significance	Genes
Oxidative Phosphorylation	0.00776	COX6B1,UQCR,PPA2,ATP6V1G1
Arachidonic Acid Metabolism	0.03981	CYP2A6,CYP4F11,CYP3A4,CYP3A5
Stilbene, Coumarine and Lignin Biosynthesis	0.04898	PRDX2,GBA3
Valine, Leucine and Isoleucine Degradation	0.05623	ACAT1,MCCC2,ABAT,DBT,MCEE
Cyanoamino Acid Metabolism	0.07244	GBA3,GGT1
Linoleic Acid Metabolism	0.08128	CYP2A6,CYP4F11,CYP3A4,CYP3A5
Fatty Acid Metabolism	0.09550	ACAT1,CYP2A6,CYP4F11,CYP3A5
Selenoamino Acid Metabolism	0.14655	PAPSS2,GGT1
Butanoate Metabolism	0.16672	PDHA2,ACAT1,ABAT
Tryptophan Metabolism	0.16672	ACAT1,CYP2A6,CYP4F11,CYP3A5
FGF Signaling	0.19143	FGF14,FGF1,MAPK14,FGFR4
Metabolism of Xenobiotics by Cytochrome P450	0.19143	CYP2A6,CYP4F11,CYP3A4,CYP3A5
Toll-like Receptor Signaling	0.23014	MAPK14,IKBKG,MAP3K7IP2
Propanoate Metabolism	0.28774	ACAT1,ABAT,MCEE
Synthesis and Degradation of Ketone Bodies	0.28907	ACAT1
Eicosanoid Signaling	0.30903	PTGER4,GGT1
Taurine and Hypotaurine Metabolism	0.32659	GGT1
Fatty Acid Biosynthesis	0.33884	MCCC2
Methane Metabolism	0.36224	PRDX2
Pentose and Glucuronate Interconversions	0.37325	HPSE
Starch and Sucrose Metabolism	0.38726	HPSE,GBA3
Glycerolipid Metabolism	0.38994	DGKQ,AGPAT3,LIPC
Valine, Leucine and Isoleucine Biosynthesis	0.39537	PDHA2
Sulfur Metabolism	0.40644	PAPSS2
IL-10 Signaling	0.41783	MAPK14,IKBKG,SP1
IL-4 Signaling	0.47206	IRF4,INPP5D
Pantothenate and CoA Biosynthesis	0.50350	PANK2
Fc Epsilon RI Signaling	0.52240	INPP5D,PRKCB1,MAPK14
Complement and Coagulation Cascades	0.52845	FGG,TFPI
Glycine, Serine and Threonine Metabolism	0.53333	GLDC,GNMT
Inositol Phosphate Metabolism	0.53580	INPP5D,PLCL2,PIK4CA
Sterol Biosynthesis	0.54702	COX10
Parkinson's Signaling	0.56234	MAPK14
Pyruvate Metabolism	0.57016	PDHA2,ACAT1
Aminosugars Metabolism	0.57810	GNPDA2
Alanine and Aspartate Metabolism	0.58614	ABAT
Citrate Cycle	0.61376	CLYBL
Glycosaminoglycan Degradation	0.62087	HPSE
Nicotinate and Nicotinamide Metabolism	0.62087	NT5C1A
Actin Cytoskeleton Signaling	--	FGF14,FGF1,APC,PPP1CB,ITGB
Amyloid Processing	--	MAPK14
Amyotrophic Lateral Sclerosis Signaling	--	CACNA1B
Antigen Presentation Pathway	--	HLA-DRB1
Apoptosis Signaling	--	IKBKG,GAS2
Axonal Guidance Signaling	--	PRKCB1,SLIT2,KALRN,WASL,EF
B Cell Receptor Signaling	--	INPP5D,PRKCB1,MAPK14,IKBKG
Calcium Signaling	--	CHRNA4,CABIN1,CACNA1B,HD/
Cardiac β -adrenergic Signaling	--	PPP1CB
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	--	PLK1
Chemokine Signaling	--	PRKCB1,MAPK14

Death Receptor Signaling	--	IKBK
ERK/MAPK Signaling	--	PRKCB1,PPP1CB,MAPKAPK5
Ephrin Receptor Signaling	--	FGF1,KALRN,WASL,EPHB1
G-Protein Coupled Receptor Signaling	--	PRKCB1,IKBK,RAP1GAP (inclu
GABA Receptor Signaling	--	ABAT
GM-CSF Signaling	--	PRKCB1
Glutamate Metabolism	--	ABAT
Glutamate Receptor Signaling	--	SLC1A1
Glutathione Metabolism	--	GGT1
Glycerophospholipid Metabolism	--	DGKQ,AGPAT3
Glycolysis/Gluconeogenesis	--	PDHA2
Huntington's Disease Signaling	--	PRKCB1,CACNA1B,SP1,HDAC8
IL-6 Signaling	--	MAPK14,IKBK
Insulin Receptor Signaling	--	INPP5D,PPP1CB
Integrin Signaling	--	PARVA,ITGB5,TSPAN4 (includes
Leukocyte Extravasation Signaling	--	PRKCB1,CTNNA3,MAPK14,RAP'
Lysine Degradation	--	ACAT1
NF-κB Signaling	--	PRKCB1,TRA@,IKBK
Natural Killer Cell Signaling	--	INPP5D,PRKCB1
Neuregulin Signaling	--	PRKCB1,EREG
Nitric Oxide Signaling in the Cardiovascular System	--	PRKG2
PDGF Signaling	--	PRKCB1
PI3K/AKT Signaling	--	INPP5D,IKBK,LIMS1
PPAR Signaling	--	IKBK
PTEN Signaling	--	INPP5D,MAGI-3,IKBK
Phenylalanine Metabolism	--	PRDX2
Phospholipid Degradation	--	DGKQ
Protein Ubiquitination Pathway	--	CDC23 (includes EG:8697),USP4.
Purine Metabolism	--	FHIT,PSMC2,ATP6V1G1,ENTPD.
Pyrimidine Metabolism	--	TXNRD3,ENTPD4,NT5C1A,POLF
SAPK/JNK Signaling	--	TRA@
Synaptic Long Term Depression	--	PRKCB1,PRKG2
Synaptic Long Term Potentiation	--	PRKCB1,PPP1CB
T Cell Receptor Signaling	--	TRA@
TGF-β Signaling	--	NODAL
VEGF Signaling	--	PRKCB1,ACTN2
Wnt/β-catenin Signaling	--	KREMEN1,APC
Xenobiotic Metabolism Signaling	--	PRKCB1,MAPK14,CYP3A4
cAMP-mediated Signaling	--	PDE8B,RAP1GAP (includes EG:5
p38 MAPK Signaling	--	MAPK14,MAPKAPK5
β-alanine Metabolism	--	ABAT

1,ATP6V0A2,COX10,COX5B,UQCRC2,ATP5O,ATP6V0E
2E1

≡

2E1
A4,CYP2E1,CPT2

A4,CYP2E1

2E1

5,WASL,FGFR4,ACTN2

HB1
3
AC8

des EG:5909)

EG:7106),RHOJ,BCAR3,LIMS1,ACTN2
1GAP (includes EG:5909),ACTN2

8,PSMC2
4,PDE8B,PAPSS2,NT5C1A,ATP6V0E,POLR3H
R3H

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