

## SUPPLEMENTARY DATA

### Patients

The subject designation corresponds to the following pedigree status in a published pedigree (1): D1 = III-9, D2 = IV-11, D3 = III-5, P1 = IV-8, P2 = IV-12.

### Sample preparation for tissue samples for kinase activity and proteolytic degradation assays

Pancreatic tissue was homogenized using a Dounce homogenizer and ice-cold lysis buffer: 10 mM K<sub>2</sub>HPO<sub>4</sub> pH 7.5, 1 mM EDTA, 10 mM MgCl<sub>2</sub>, 50 mM β-glycerophosphate, 5 mM EGTA, 0.5% Nonidet P-40, 0.1% Brij 35, 0.1% deoxycholic acid, 1mM sodium orthovanadate, 1mM phenylmethylsulfonyl fluoride and protease inhibitors (Complete protease inhibitor tablet, Roche). Following homogenization, the lysate was centrifuged at 10,000 rpm for 10 min at -4 °C and the supernatant was snap frozen with liquid nitrogen and stored at -80 °C. Kinase activities were determined on lysate that had only been frozen once following harvesting since freeze-thaw cycles decrease kinase activities. Protein concentration was determined by the modified Bradford assay (Pierce).

### Proteomic analysis of pancreatic fluid

The purified peptides following digestion were labeled with TMT. Each tube of 0.8 mg for each TMT label was dissolved in 40 μL of anhydrous acetonitrile, of which 5 μL of each was used to label peptides from 40 μg of pancreatic fluid protein. The labeling reaction was quenched by the addition of 10 μl of 5% hydroxylamine and the individual samples combined and desalted with C18 solid-phase extraction (Sep-Pak, Waters, Milford, MA).

The combined sample was fractionated by strong cation exchange chromatography (SCX), similar to that described previously (2). Briefly, a 2.1 x 200 mm polySULFOETHYL A HPLC column (particle size, 5 μm; pore size, 200 Å; PolyLC, Columbia, MD) was used to separate the sample that was resuspended in 300 μL SCX buffer A (7 mM KH<sub>2</sub>PO<sub>4</sub>, 30% ACN, pH 2.6). A two-buffer (SCX A and B) gradient from 0 to 50% SCX buffer B (7 mM KH<sub>2</sub>PO<sub>4</sub>, 350 mM KCl, pH 2.6, 30% ACN) in 47 min was used at a flow rate of 0.2 ml/min, followed by 50 to 100% SCX buffer A to buffer B in 4.5 min using an Agilent 1100 quaternary pump with a degasser and a photodiode array detector (PDA) (Thermo Scientific, San Jose, CA). Fractions were collected every 90 s into a 96-well plate, and dried with a speed-vac. The dried peptide fractions were then resuspended with 1% FA, and combined into 14 fractions based on the intensity from the SCX chromatographic UV trace and then desalted by C18 SPE, and dried using a speed-vac.

Dried peptides were resuspended in 15 μL 4% formic acid, 5% ACN, and 2 μL was loaded onto a microcapillary column (100 μm I.D, 20 cm, packed with Magic C18AQ resin: 5 μm, 100 Å, Michrom Bioresources, Auburn, CA) with Famos autosampler (LC Packings, Sunnyvale, CA) and an Agilent 1100 binary HPLC pump (Agilent Technologies, Santa Clara, CA). Reverse phase chromatography was used for peptide separation with a 150 minute gradient of 9 to 32% ACN in 0.125% FA at a flow rate of around 300 nL/min. An LTQ Orbitrap Velos (Thermo Fischer Scientific) was used, with XCalibur 2.0.7 acquisition software. Data acquisition was performed in data-dependent mode with a survey scan in the range of 300-1500 m/z with a 30,000 resolution. The top 10 most intense ions were selected for fragmentation in the LTQ with a precursor isolation width window of 2 m/z. The AGC target was set at 3x10<sup>6</sup> for the survey scan and ions were selected for MS<sub>2</sub> and their intensity was greater than 500 accounts. Ions with unassigned or 1+ charge states were excluded. Selected ions were excluded from further analysis for 30 s. Maximum ion accumulation times were 1000 ms and 250 ms for survey and MS/MS scans respectively. An MS<sub>3</sub> method developed by the lab was used to overcome the problem of interfering peaks in the analysis of TMT data. The instrument parameters used were the same as those described (3). Briefly, after each MS<sub>2</sub> analysis, the most intense fragment ion in an m/z range between 110-160% of the precursor m/z was selected for HCD-MS<sub>3</sub>. The fragment ion isolation width was set to

## SUPPLEMENTARY DATA

4 m/z, the MS3 AGC was 20 x 10<sup>4</sup> and the maximum ion time set to 250 ms. The normalized collision energy was set to 35% and 60% at an activation time of 20 ms and 50 ms for MS2 and MS3 scans, respectively.

### **Database searches and data filtering and quantitation**

Following mass spectrometric acquisition, the RAW files were converted into the mzXML format and individual precursors selected for MS2 fragmentation were checked for erroneous monoisotopic m/z and the mass measurements refined (4). The MS/MS spectra were searched against the human ipi database (version 3.6) using the Sequest algorithm (version 28) (5). A decoy database search approach was employed, where each protein sequence was listed in both the forward and reversed direction, to enable the estimation of the peptide and protein identification false discovery rates (FDR). The search parameters were as follows: 50 ppm precursor ion tolerance; 1.0 Da product mass tolerance; variable modifications: oxidation of methionine (+15.9949); fixed modifications: carbamidomethylation of cysteine (+57.0214), Six-plex TMT tags on lysine residues and peptide N termini (+ 229.162932 Da). Two different types of searches were performed. Firstly, LysC specificity was required and secondly, 'no enzyme specificity' was required. On account of the large numbers of proteolytic enzymes known to be present in pancreatic fluid, it is likely that during the clinical sampling of pancreatic fluid degradation by enzymes had occurred in addition to the desired Lys-C digestion, hence the reason to search with 'no enzyme' specified'.

The data was filtered to a false discovery rate of less than 1% based on the target-decoy database approach (6). Filtering using linear discriminant analysis was performed to generate a classifier to distinguish between correct and incorrect identifications based on the following parameters: XCorr, ΔCn, peptide ion mass accuracy, charge state and peptide length, as described (4).

Further filtering of the list to include only 'pancreas specific' proteins was based on analyses of nine different mouse tissues (4) (<https://gygi.med.harvard.edu/phosphomouse/index.php>).

To test the hypothesis that secretin-stimulated duodenal secretory proteins truly reflected pancreatic disease, an investigator (F.M.) blinded to the samples, performed unsupervised clustering analysis based on protein abundance (i.e. algorithmic classification procedure to group samples based on protein expression similarities and blinded to a knowledge of sample disease status).

Peptide quantification using TMT reporter ion intensity was performed using in-house software, as described previously (3). Briefly, a 0.06 m/z window around the theoretical m/z value of each reporter ion (126, 127, 128, 129, 130 and 131) was scanned for ions, and the intensity of the signal nearest to the theoretical m/z value was recorded. The intensities of the reporter ion intensities were denormalised by multiplying them with the ion accumulation time for each MS3 spectrum and. Adjustment based on the overlap of isotopic envelopes for the reporter ions was performed.

**Immunoblotting.** Secretions from the pancreas (15 microgram applied to each well; concentration estimated by BCA assay; Pierce) was applied directly to and separated by SDS-PAGE, electrophoretically transferred to a nitrocellulose membrane and stained with anti-keratin 18 antibody (4548S ;1:2000; Cell Signaling Technology), anti-SKP1 antibody (2156S; 1:500; Cell Signaling Technology), anti-PKM2 antibody (4053S; 1:1000; Cell Signaling Technology), anti-LMNA (4777S;1:1000; Cell Signaling Technology), anti-GSN (AB2969; 1:2000; Millipore) or anti-amylase (3796S;1:500; Cell Signaling Technology). Staining was developed using a chemoilluminescence method (Pierce ECL Western blotting substrate; Pierce).

### **Kinase activity assay**

The procedures were similar to that described (7) but with a few changes to the method as described below. A set of 60 synthetic peptide substrates, each at 5 μM, were incubated with 10 μg lysate and

## SUPPLEMENTARY DATA

kinase reaction buffer containing Tris-Cl (25 mM, pH 7.5), ATP (5 mM), MgCl<sub>2</sub> (7.5 mM), EGTA (0.2 mM),  $\beta$ -glycerophosphate (7.5 mM), Na<sub>3</sub>VO<sub>4</sub> (0.1 mM) and DTT (0.1 mM). After incubation for 45 minutes at room temperature, the reaction was quenched with 100  $\mu$ L of 1% trifluoroacetic acid (TFA). A known amount (5 pmol) of internal standard phosphorylated stable-isotope labeled peptides were spiked into the quenched reaction. The solution was desalted using Sep-Pak C18 50 mg cartridges (Waters) and dried using vacuum centrifugation. Different to the previous method (7), enrichment for phosphoproteins using immobilized metal affinity chromatography (IMAC) was not performed. The desalted sample were resuspended in 100  $\mu$ L of 5% formic acid of which 2  $\mu$ L was then subjected to analysis by reverse phase liquid chromatography- mass spectrometry. Technical duplicates were performed for each lysate.

### Kinase abbreviation

Category	Kinase
AA	PKA
CC	PKC
DD	Acidic
MM	MAPK
PP	Proline directed
RR	RSK
KK	AKT
XX	pY_group_1
YY	pY_group_2
ZZ	pY_group_3
QQ	DNA damage
GG	GSK3
CH	CHEK
OO	Other S/T kinase
WW	Y other
BB	Basic
AM	AMPK

### Proteolytic degradation assay

A set of 45 synthetic peptide substrates, each at 1  $\mu$ M, were incubated with 10  $\mu$ g pancreatic fluid and reaction buffer containing Tris-Cl (25 mM, pH 7.5), MgCl<sub>2</sub> (7.5 mM), EGTA (0.2 mM),  $\beta$ -glycerophosphate (7.5 mM), Na<sub>3</sub>VO<sub>4</sub> (0.1 mM) and DTT (0.1 mM). The reaction was incubated at

## SUPPLEMENTARY DATA

room temperature for 0, 15, 60 min, after which the reaction was quenched with 100  $\mu$ L of 1% trifluoroacetic acid (TFA). Twenty five pmol of internal standard stable-isotope labeled substrate peptides was spiked into the quenched reaction. The solution was desalted using Sep-Pak C18 50 mg cartridges (Waters) and dried using vacuum centrifugation. The desalted sample was then resuspended in 100  $\mu$ L of 5% formic acid of which 2  $\mu$ L was then subjected to analysis by mass spectrometry. Technical duplicates were performed for each sample at each time point.

The peptides from the kinase activity and proteolytic degradation assays were analysed by LC-MS on a high resolution Exactive Orbitrap mass spectrometer (Thermo). The experimental details are outlined in the Suppl. information. Briefly, a 45 minute gradient was used to separate the peptides from 10-37% solvent B (0.125% formic acid in acetonitrile) at a flow rate of 300 mL/min. LC-MS data was collected from 350-1500 m/z and the extracted ion chromatograms of the light and heavy peptides were used to quantitate the absolute kinase activity and the extent of peptide degradation respectively. Data analysis was performed using Pinpoint (Thermo).

### **Mass spectrometry and data analysis for kinase and proteolytic degradation assays**

The peptides from the kinase activity and proteolytic degradation assay, dissolved in 5% formic acid, were analysed by LC-MS on a high resolution Exactive Orbitrap mass spectrometer (Thermo) equipped with a Nanospray II electrospray ionisation source (Thermo) coupled to a Thermo binary pump and a Famos autosampler (LC Packings). Peptides were separated on a hand-pulled fused silica microcapillary with an internal diameter of 175  $\mu$ m, 15 cm long, packed with a C18 reversed-phase resin (Magic C18AQ, particle size 5  $\mu$ m, pore size 200 Å, Michrom Bioresources, Auburn, CA). The needle tip had an internal diameter of approximately 5  $\mu$ m. Once loaded, the peptides were separated across a 45 minute linear gradient of 10-37% solvent B (0.125 % FA in ACN) at a flow rate of 300 nl/min provided across a flow splitter by the HPLC pumps. Buffer A comprised 0.125% FA and 3% ACN in water. Data was collected from 350-1500 m/z full MS with a resolution setting of 60,000.

Analysis was performed using the commercial software package Pinpoint (Thermo). The amount of substrate phosphorylation was determined by comparing the area of the light phosphorylated substrate peptide with that of the heavy phosphorylated internal standard peptide. The phosphorylated substrate peptides are chemically identical to the heavy internal standard and therefore should have the same chromatographic characteristics and ionisation efficiency. In the case of the proteolytic degradation assay, the amount of peptide degradation was determined by comparing the area of the light substrate (degraded during the reaction) with that of the heavy substrate internal standard peptide that was added following quenching of the reaction. Extracted ion chromatograms were generated from the MS scan with  $\pm$  10 ppm mass accuracy around the monoisotopic peak of the most abundant charge state. The extracted ion chromatograms were integrated using Pinpoint. Whilst Pinpoint generates the area of the extracted ion chromatograms semi-automatically, each chromatogram required manual inspection to ensure that the correct boundaries had been selected. Where this was not the case, the peak boundaries were manually altered. It was required that heavy and light peptides co-eluted perfectly for accurate quantitation. Measurements were excluded where the peak height was less than 10000 or where the peak area was less than 1% of the internal standard (50 fmol). Since a known amount of internal standard was added to the reaction (5 pmol for the kinase assay, 25 pmol for the proteolytic degradation assay) prior to purification, the absolute amount of product formed could be determined. The product formed/kinase activity is presented with units of fmol/ $\mu$ g/min. The ratio of the light to heavy peptide area was divided by the amount of lysate (10  $\mu$ g) and the time of the reaction (45 min for the kinase activity assay). For the proteolytic digestion assay, the degradation is normalized to the light peptide/heavy peptide ratio for the zero time point.

SUPPLEMENTARY DATA

**Supplementary Table 1.** Clinical, imaging and cytokine characteristics for CEL mutation carriers and controls.

Status	Control	Control (N2)	Control	Control	Control	Control	Control (N1)	Control (N3)	CEL carrier	CEL carrier
<b>Sex</b>	F	F	M	F	F	F	M	M	M	M
<b>Age (yrs)</b>	32	38	40	50	53	64	63	25	9	14
EGF	442.88	110.76	20.13	39.72	110.37	63.48	143.63	128.28	101.22	32.19
EOTAXIN	0	1.55	1.07	0	0	1.58	1.79	7.26	1.18	0.53
FGF-2	0	2.5	0	0	0	8.66	2.50	16.71	2.5	0
Flt-3 ligand	1.03	0	0	0	0	3.85	2.49	7.86	1.77	3.18
fractalkine	0	0	0	0	0	0	<1.28	<1.28	0	0
G-CSF	1.11	0	0	0	0	0	<0.42	0.59	0	1.11
GM-CSF	0	0.72	0.96	0	0	0.82	0.74	1.49	2.17	0.74
GRO	2.46	7.32	5.91	0	2.46	9.73	4.32	11.29	2.46	11.05
IFN-a2	0	0	0	0	0	0	<1.05	<1.05	0	0
IFN-G	0	0	0	0	0	1.68	<1.38	2.92	0	0
IL-1a	2.08	0.56	20.53	2.32	0.68	16.15	510.68	79.36	35.79	5.48
IL-1b	0	0	0	0	0	0.76	8.71	1.97	1.14	3.67
IL-1ra	0.79	1.77	7.37	1.91	0	3.51	67.50	10.07	6.38	13.15
IL-2	0	0	0.45	0	0	0.45	<0.45	2.06	0	0
IL-3	4	16.28	4.94	11.56	0	8.52	6.26	12.45	0	0
IL-4	0	0	0	0	0	0	<0.84	<0.84	0	0
IL-5	0	0	0	0	0	0	0.18	<0.16	0	0.2
IL-6	0	0	0	0	0	0.52	1.20	5.19	0	4.75
IL-7	0	0	0	0	0	0	<0.62	<0.62	0	3.56
IL-8	0.31	0	1.52	0.22	0.14	2.13	2.64	4.40	1.95	4.53
IL-9	0	0	0	0	0	0	<1.12	<1.12	0	0
IL-10	0	0	0	0.8	0	0.39	6.40	2.25	0	9.45
IL-12(P40)	0	0.9	0	1.04	0	3.21	5.02	10.94	6.13	7.25
IL-12(P70)	0	0	1.28	0	0	0	<1.23	3.93	0	0
IL-13	0	0	0	0	0	0	2.81	2.02	0	3.47
IL-15	0	0	1.99	0	1.85	2.84	2.70	5.41	0	1.65
IL-17A	0	0	0	0	0	0	<0.36	0.90	0	0
IP-10	0	0	0	0	0	0	<0.41	7.08	0	0
MCP-1	16.4	1.07	1.07	0	0	1.07	<0.38	1.40	104.43	23.22
MCP-3	3.64	3.64	4.49	0	0	8.15	4.49	12.96	0	7.49
MDC	3.25	2.32	7.74	0	0	10.24	<1.98	14.83	0	13.36
MIP-1a	0	1.73	7.1	0	0	15.78	14.93	22.33	0	18.64
MIP-1b	0	0	0	0	0	0	<0.41	4.40	0	0
PDGF-AA	75.46	69.6	64.7	73.02	135.13	118.56	149.74	73.18	58.35	109.98

SUPPLEMENTARY DATA

PDGF-AB/BB	0	0	0	0	0	0	19.27	10.71	0	0
RANTES	17.26	0	0	0	0	0	<1.51	<1.51	1.77	7.38
sCD-40L	1.56	0.99	0.99	0.51	0.99	1.88	0.51	1.41	1.26	2.21
sIL-2Ra	0	1.9	0	0	0	2.12	<0.7	3.44	0	0
TGF-a	1.4	0	0	0.63	0.7	0	<0.82	1.28	0	0
TNF-a	0	0	0	0	0	0	<0.42	<0.42	0	0
TNF-b	0	0	0	0	0	0	<0.6	<0.6	0	1.41
VEGF	5.55	0	5.55	0	0	12.51	<0.88	16.84	2.02	12.51
Status	CEL carrier (P2)	CEL carrier (P1)	CEL carrier (D2)	CEL carrier	CEL carrier	CEL carrier	CEL carrier (D4)	CEL carrier (D1)	CEL carrier (D3)	CEL carrier (C1)
Sex	M	M	F	F	M	M	F	M	M	F
Age (yrs)	37	40	43	45	56	57	57	65	69	78
EGF	NA	44.74	80.68	23.95	5.5	13.84	125.19	1.76	6.85	19.4
EOTAXIN	NA	1.07	0.92	0.1	68.8	0.41	0.57	3.24	40.57	0.71
FGF-2	NA	3.9	19.62	0	14.3	7.57	10.2	3.9	12.57	13.45
Flt-3 ligand	NA	0	6.26	0	6.81	3.18	1.77	1.03	5.69	1.77
fractalkine	NA	0	0	0	26.05	0	0	0	487	0
G-CSF	NA	0	0.59	0	26.4	3.86	0	0	0	1.95
GM-CSF	NA	0.35	1.73	0.19	1.33	0.77	0.77	1.54	2.98	1.58
GRO	NA	7.32	116.7	45.11	97.31	15.2	109.7	2.46	88.81	161.02
IFN-a2	NA	0	7.32	0	2.1	0	0	0	0	3.9
IFN-G	NA	0	0	0	0	0	0	0	1.45	6.45
IL-1a	NA	33.67	273.25	109.59	14.57	37.1	594.34	10.72	6.5	2.16
IL-1b	NA	2.39	2.82	1.5	0.67	0	1.24	0	0.76	0
IL-1ra	NA	16.26	22.85	186.32	69.2	150.09	41.18	7.71	43.41	15.74
IL-2	NA	0.5	0.54	0	0.74	0.74	0.54	0.45	1.22	0.74
IL-3	NA	0	0	0	0	0	0	5.64	0	0
IL-4	NA	0	2.1	0	3.3	0	0	0	0	0
IL-5	NA	0	0.28	0	0	0	0	0	0	0
IL-6	NA	0	5.19	0	0	0	0	0	0	15.46
IL-7	NA	0	1.36	0	6.23	0	0	0	0	0
IL-8	NA	7.67	21.1	16.76	4.28	3.08	373.59	1.16	4.4	167.74
IL-9	NA	0	0	0	0	0	0	0	0	0
IL-10	NA	0.2	1.53	0.86	0.5	0.39	0	0	0.2	0
IL-12(P40)	NA	2.16	18.45	0	4.29	1.83	1.5	7.8	5.02	0
IL-12(P70)	NA	0	1.44	0	0	0	0	0	0	0
IL-13	NA	0	2.33	0	11.32	0	0	0	0	0
IL-15	NA	1.85	5.96	0	3.14	3.28	0	4.49	3.21	0

SUPPLEMENTARY DATA

IL-17A	NA	0	0	0	0	0	0	0.39	1.47	0
IP-10	NA	0	50.3	0	333.95	23.96	13.9	3.89	165.19	1.12
MCP-1	NA	0	119.07	10.28	225.49	48.74	34.65	5.89	441.82	61.38
MCP-3	NA	6.79	14.62	3.64	6.79	7.49	5.3	3.64	11.14	6.43
MDC	NA	4.18	24.01	5.09	16.26	28.57	6.87	3.25	21.56	3.25
MIP-1a	NA	4.31	22.97	0	18.39	0	0	10.42	26.41	3.6
MIP-1b	NA	0	14.68	0	19.84	0	0	0	39.28	9.49
PDGF-AA	NA	55.77	202.14	53.72	61.89	61.12	51.57	370.6	74.34	23.48
PDGF-AB/BB	NA	0	0	0	0	0	0	0	0	0
RANTES	NA	0	31.26	35.13	202.69	106.27	10.65	0	69.44	4.71
sCD-40L	NA	1.88	2.92	0.73	4.47	2.21	0.99	0.73	4.07	2.56
sIL-2Ra	NA	0	0.74	0	10.45	2.01	0	0	4.35	1.2
TGF-a	NA	0	12.11	0	8.63	0	8.27	0	3.16	4.96
TNF-a	NA	0	0	0	0.45	0	0	0	0	0
TNF-b	NA	0	0.73	0	0	0	0	0	0	0
VEGF	NA	0	50.92	0	176.64	6.68	0	0	21.28	32.91

SUPPLEMENTARY DATA

**Supplementary Table 2.** Protein expression values for proteins identified in the pancreatic proteome by proteomics analysis. Log<sub>2</sub> ratio, Log<sub>2</sub> of the ratio of mass spectrometry abundance for the sum of the three healthy controls divided by the sum of the three diabetic mutation carriers. Log<sub>2</sub> total, Log<sub>2</sub> of the total mass spectrometry abundance for a protein as the sum of the abundances of three healthy controls and the three diabetic mutation carriers.

Gene	D1	D3	D2	N2	N3	N1
CLEC3B	1.0E+06	5.5E+06	3.1E+06	5.0E+01	5.0E+01	5.0E+01
ATP5A1	1.1E+06	2.9E+06	4.4E+06	5.0E+01	5.0E+01	5.0E+01
KRT18	1.5E+06	1.2E+06	3.0E+06	5.0E+01	5.0E+01	5.0E+01
CAPZA1	7.4E+05	1.4E+06	2.8E+06	5.0E+01	5.0E+01	5.0E+01
LOC100133511	7.3E+05	1.3E+06	2.4E+06	5.0E+01	5.0E+01	5.0E+01
FETUB	1.2E+05	1.7E+06	2.5E+06	5.0E+01	5.0E+01	5.0E+01
HSPD1	5.0E+01	7.5E+05	3.5E+06	5.0E+01	5.0E+01	5.0E+01
GPR126	1.5E+05	2.5E+06	5.8E+05	5.0E+01	5.0E+01	5.0E+01
TPM1	7.7E+04	5.7E+05	1.5E+06	2.0E+01	5.0E+01	5.0E+01
SUCLG2	2.7E+05	9.6E+05	1.9E+06	5.0E+01	1.1E+02	5.0E+01
TTBK2	8.8E+04	2.8E+05	1.9E+06	5.0E+01	5.0E+01	5.0E+01
SERPINA10	5.0E+01	1.4E+06	7.0E+05	5.0E+01	5.0E+01	5.0E+01
ATP1A2	5.0E+01	4.1E+05	2.6E+06	5.0E+01	1.5E+02	5.0E+01
LUM	5.0E+01	1.2E+06	6.2E+05	5.0E+01	5.0E+01	5.0E+01
BCAS1	6.9E+04	6.9E+05	1.1E+06	5.0E+01	5.0E+01	5.0E+01
HPGD	5.0E+01	4.0E+05	1.4E+06	5.0E+01	5.0E+01	5.0E+01
ATP6V1E1	4.2E+05	4.9E+05	8.8E+05	5.0E+01	5.0E+01	5.0E+01
AKR1D1	2.6E+05	1.1E+06	3.5E+05	5.0E+01	5.0E+01	5.0E+01
MUPCDH	5.0E+01	4.4E+05	1.2E+06	5.0E+01	5.0E+01	5.0E+01
EFNA1	5.0E+01	1.1E+06	5.3E+05	5.0E+01	5.0E+01	5.0E+01
CYB5A	5.5E+05	4.3E+05	6.2E+05	5.0E+01	5.0E+01	5.0E+01
CRNN	3.3E+05	6.1E+05	6.3E+05	5.0E+01	5.0E+01	5.0E+01
TRAP1	7.2E+04	5.6E+05	8.3E+05	5.0E+01	5.0E+01	5.0E+01
IGLC1;IGLV1-44;IGLV1-40;IGLV3-21;IGLV2-11;IGLV2-14;IGL@;IGLC2;IGLC3	4.2E+06	7.2E+05	5.0E+01	4.5E+02	5.0E+01	5.0E+01
APOL1	5.0E+01	1.2E+06	9.0E+04	5.0E+01	5.0E+01	5.0E+01
HIBADH	2.9E+05	3.2E+05	7.0E+05	5.0E+01	5.0E+01	5.0E+01
COL1A1	2.0E+05	7.7E+05	2.7E+05	5.0E+01	5.0E+01	5.0E+01
IPI00386135	1.7E+06	5.0E+01	4.1E+03	1.3E+02	5.0E+01	5.0E+01
AK3	2.6E+05	3.6E+05	5.1E+05	5.0E+01	5.0E+01	5.0E+01
ARHGDI1	2.3E+05	2.9E+05	5.8E+05	5.0E+01	5.0E+01	5.0E+01
ATP5B	1.0E+06	1.4E+06	1.4E+06	5.0E+01	4.4E+02	5.0E+01
EPS8	1.1E+05	4.0E+05	5.5E+05	5.0E+01	5.0E+01	5.0E+01
COPZ1	1.9E+05	1.9E+05	6.8E+05	5.0E+01	5.0E+01	5.0E+01
PSME1	1.8E+05	4.6E+05	4.1E+05	5.0E+01	5.0E+01	5.0E+01
PTGR1	1.1E+05	4.0E+05	5.1E+05	5.0E+01	5.0E+01	5.0E+01



SUPPLEMENTARY DATA

DSC2	1.7E+05	2.3E+05	1.0E+06	5.0E+01	1.3E+02	5.0E+01
SIRPA	1.2E+05	8.2E+05	6.2E+02	5.0E+01	5.0E+01	5.0E+01
ARPC5	1.6E+05	3.8E+05	3.7E+05	5.0E+01	5.0E+01	5.0E+01
NUCB2	2.2E+05	1.5E+05	4.8E+05	5.0E+01	5.0E+01	5.0E+01
PBLD	5.0E+01	2.3E+05	6.2E+05	5.0E+01	5.0E+01	5.0E+01
SULT1A3;SULT1A4	5.0E+01	2.6E+05	5.7E+05	5.0E+01	5.0E+01	5.0E+01
APOF	5.0E+01	5.7E+05	2.4E+05	5.0E+01	5.0E+01	5.0E+01
HEPH	1.8E+05	1.3E+05	3.7E+05	5.0E+01	5.0E+01	5.0E+01
HSPA9	3.8E+05	2.7E+05	1.9E+03	5.0E+01	5.0E+01	5.0E+01
DDX3X	9.9E+04	1.1E+05	4.2E+05	5.0E+01	5.0E+01	5.0E+01
RPL17;LOC100133931	5.0E+01	1.6E+05	4.6E+05	5.0E+01	5.0E+01	5.0E+01
DGAT1	1.3E+05	2.3E+05	2.5E+05	5.0E+01	5.0E+01	5.0E+01
COPB1	5.0E+01	1.9E+05	4.1E+05	5.0E+01	5.0E+01	5.0E+01
PGLYRP2	6.4E+04	3.4E+05	1.9E+05	5.0E+01	5.0E+01	5.0E+01
ARPC2	5.0E+01	1.9E+05	3.6E+05	5.0E+01	5.0E+01	5.0E+01
DBI	1.8E+05	2.1E+05	1.4E+05	5.0E+01	5.0E+01	5.0E+01
IGHG1;IGHG2;IGHV4-31;IGH@	5.2E+05	5.0E+01	6.6E+04	5.0E+01	7.4E+01	5.0E+01
MYH14	2.9E+05	2.3E+05	6.4E+05	5.0E+01	2.7E+02	5.0E+01
IGLV10-54	1.6E+05	3.1E+05	8.1E+02	5.0E+01	5.0E+01	5.0E+01
DCI	2.4E+05	2.2E+05	3.3E+05	5.0E+01	1.7E+02	5.0E+01
MYL1	9.6E+04	1.7E+05	1.7E+05	5.0E+01	5.0E+01	5.0E+01
KIAA1967	5.0E+01	1.5E+05	2.7E+05	5.0E+01	5.0E+01	5.0E+01
IPI00384394	4.2E+05	5.0E+01	2.1E+03	5.0E+01	5.0E+01	5.0E+01
SLC16A1	5.0E+01	1.1E+05	3.1E+05	5.0E+01	5.0E+01	5.0E+01
UGT2B28	4.3E+05	5.0E+01	1.2E+05	5.0E+01	1.4E+02	5.0E+01
ARPC4;TTL3	5.0E+01	1.0E+05	2.4E+05	5.0E+01	5.0E+01	5.0E+01
RPLP2	7.9E+05	2.2E+06	6.4E+06	4.1E+03	5.0E+01	5.0E+01
SKP1	7.0E+04	1.3E+05	7.4E+04	5.0E+01	5.0E+01	5.0E+01
RPLP0	3.7E+05	1.2E+06	1.9E+06	2.1E+03	5.0E+01	5.0E+01
PSMD2	5.0E+01	1.2E+05	1.2E+05	5.0E+01	5.0E+01	5.0E+01
ACAA1	5.0E+01	8.4E+04	2.8E+05	5.0E+01	1.9E+02	5.0E+01
PHB	5.5E+05	6.8E+05	1.2E+06	5.0E+01	5.0E+01	1.9E+03
IPI00017870	1.7E+06	1.8E+06	5.0E+06	7.1E+03	5.0E+01	5.0E+01
LIPF	1.8E+05	5.0E+01	2.9E+05	5.0E+01	3.4E+02	5.0E+01
RAB14	1.3E+05	5.0E+01	2.8E+05	5.0E+01	3.3E+02	5.0E+01
HNRNPK	1.2E+05	5.0E+01	1.8E+05	5.0E+01	2.1E+02	5.0E+01
RPN1	1.2E+05	5.0E+01	2.0E+05	5.0E+01	2.4E+02	5.0E+01
MARCKSL1	5.0E+01	5.6E+04	8.1E+04	5.0E+01	5.0E+01	5.0E+01
DDAH1	9.9E+04	5.0E+01	1.9E+05	5.0E+01	2.2E+02	5.0E+01
SPTAN1	8.9E+04	5.0E+01	9.4E+04	5.0E+01	1.1E+02	5.0E+01
SPRR2C;SPRR2G	1.3E+05	5.0E+01	6.3E+02	5.0E+01	5.0E+01	5.0E+01
RPLP1	5.0E+01	5.0E+01	2.8E+06	5.0E+01	3.3E+03	5.0E+01

SUPPLEMENTARY DATA

ALPI	7.0E+04	5.0E+01	2.3E+05	5.0E+01	2.7E+02	5.0E+01
AK2	2.0E+06	2.1E+06	1.9E+06	5.0E+01	5.0E+01	7.6E+03
ALDH3A2	6.4E+04	5.0E+01	1.2E+05	5.0E+01	1.4E+02	5.0E+01
IGLV3-25	5.0E+01	5.0E+01	5.7E+05	5.0E+01	6.7E+02	5.0E+01
SFN	5.0E+01	5.0E+01	5.5E+05	5.0E+01	6.5E+02	5.0E+01
ICAM1	5.0E+01	1.0E+05	5.0E+01	5.0E+01	5.0E+01	5.0E+01
ELANE	5.0E+01	5.0E+01	3.0E+05	5.0E+01	3.5E+02	5.0E+01
EPB41L3	8.0E+05	1.4E+06	2.4E+06	5.0E+01	5.0E+01	6.9E+03
LOC723972;ANP32A	5.0E+01	9.6E+04	5.0E+01	5.0E+01	5.0E+01	5.0E+01
TXNDC17	5.0E+01	5.0E+01	2.6E+05	5.0E+01	3.0E+02	5.0E+01
PGA3;PGA4;PGA5	5.0E+01	5.0E+01	2.5E+05	5.0E+01	3.0E+02	5.0E+01
ITIH2	3.1E+06	1.5E+07	2.0E+07	3.4E+03	7.3E+02	5.7E+04
GPD1	5.0E+01	5.0E+01	1.7E+05	5.0E+01	2.0E+02	5.0E+01
UBE2V1;TMEM189-UBE2V1	5.0E+01	5.0E+01	1.6E+05	5.0E+01	1.8E+02	5.0E+01
SERPINF1	1.4E+06	4.0E+06	3.8E+06	5.0E+01	5.0E+01	1.7E+04
GSTT1	5.0E+01	7.9E+04	5.0E+01	5.0E+01	5.0E+01	5.0E+01
MEP1B	5.0E+01	5.0E+01	1.0E+05	5.0E+01	1.2E+02	5.0E+01
CHGA	5.0E+01	7.0E+04	5.0E+01	5.0E+01	5.0E+01	5.0E+01
RANP1;RAN	5.0E+01	6.6E+04	5.0E+01	5.0E+01	5.0E+01	5.0E+01
YWHAH	5.0E+01	5.0E+01	8.3E+04	5.0E+01	9.8E+01	5.0E+01
YWHAQ	5.0E+01	5.0E+01	7.2E+04	5.0E+01	8.5E+01	5.0E+01
HIST2H2BE	3.6E+05	8.5E+04	1.7E+06	4.8E+03	4.9E+02	5.0E+01
C9	1.3E+06	1.2E+07	5.7E+06	1.2E+04	5.0E+01	4.6E+04
HSP90AA1	1.1E+06	1.7E+06	2.2E+06	5.0E+01	5.0E+01	2.0E+04
APOC1	3.9E+05	4.6E+06	2.6E+06	5.0E+01	5.0E+01	3.0E+04
AGR2	8.5E+05	7.5E+05	1.1E+06	1.1E+04	5.0E+01	5.0E+01
AHSG	1.1E+07	2.6E+07	2.0E+07	1.0E+04	1.0E+05	1.2E+05
EIF5A2	2.3E+05	2.7E+06	5.2E+06	5.0E+01	5.0E+01	3.4E+04
FBP1	9.0E+05	1.9E+06	2.1E+06	5.0E+01	5.0E+01	2.5E+04
YWHAZ	6.8E+05	4.1E+05	5.7E+05	6.6E+01	6.6E+02	8.3E+03
PKM2	4.5E+05	2.3E+06	2.4E+06	5.0E+01	2.9E+04	5.0E+01
HIST1H2AB;HIST1H2AE;HIST1H2AL;HIST1H2AG;HIST1H2AJ;HIST1H2AK;HIST1H2AI;HIST1H2AM	1.8E+05	4.4E+05	5.2E+06	5.0E+01	5.0E+01	3.5E+04
HIST1H4J;HIST1H4E;HIST1H4H;HIST1H4K;HIST2H4A;HIST1H4D;HIST1H4F;HIST2H4B;HIST1H4C;HIST1H4B;HIST1H4I;HIST1H4L;HIST1H4A;HIST4H4	4.5E+06	2.3E+06	9.7E+06	5.8E+02	2.4E+03	1.1E+05
AFM	1.7E+06	5.3E+06	3.7E+06	5.0E+01	5.0E+01	7.8E+04
IDH1	1.5E+06	2.3E+06	2.2E+06	5.0E+01	5.0E+01	4.5E+04
ETFB	1.1E+06	1.8E+06	2.3E+06	4.1E+03	5.0E+01	4.2E+04

SUPPLEMENTARY DATA

PFN1	3.4E+06	3.1E+06	7.4E+06	5.0E+01	5.0E+01	1.3E+05
MYL6;MYL6B	5.0E+01	2.9E+05	1.1E+06	1.3E+04	5.0E+01	5.0E+01
CFL1	3.2E+05	2.1E+06	3.4E+06	5.0E+01	2.2E+02	5.5E+04
FABP2	4.4E+05	5.0E+01	7.3E+04	5.0E+01	9.0E+01	4.7E+03
APOA1	1.1E+05	7.6E+07	5.1E+07	5.2E+05	3.5E+05	4.0E+05
KRT19	6.0E+05	1.0E+06	3.2E+06	1.4E+04	1.3E+02	4.1E+04
CMAS	2.1E+05	2.1E+05	8.9E+05	5.0E+01	5.0E+01	1.7E+04
MYH14	3.8E+05	6.7E+05	4.0E+06	5.0E+01	9.2E+02	6.6E+04
PURA	9.4E+04	5.0E+01	1.6E+06	5.0E+01	1.9E+03	2.1E+04
HGFAC	6.5E+04	3.0E+06	1.0E+06	5.0E+01	5.6E+04	5.0E+01
ACSL5	2.5E+05	6.5E+05	7.1E+05	5.0E+01	2.6E+02	2.2E+04
IPI00398129	2.2E+05	5.8E+05	1.2E+06	2.7E+03	5.0E+01	2.7E+04
HIST2H3D;HIST2H3C;HIST2H3A	6.6E+05	9.4E+04	4.9E+06	2.3E+04	1.3E+02	6.0E+04
BTD	1.5E+06	5.9E+06	5.0E+06	5.0E+01	1.0E+04	1.7E+05
UQCRC2	5.7E+06	4.0E+06	9.8E+06	5.0E+01	5.0E+01	2.9E+05
CPS1	8.1E+05	3.7E+06	4.6E+06	1.0E+02	3.8E+04	1.0E+05
ANXA13	2.3E+05	2.1E+06	6.5E+06	5.0E+01	1.2E+05	3.1E+04
HNRNPL	1.3E+06	5.8E+05	1.5E+06	1.3E+04	5.0E+01	4.7E+04
PROC	5.9E+04	1.2E+06	6.3E+05	5.0E+01	5.0E+01	3.4E+04
APOA4	9.0E+05	7.0E+07	3.5E+07	1.2E+06	4.0E+05	4.4E+05
TST	2.0E+05	2.5E+05	1.3E+06	5.0E+01	6.2E+02	3.4E+04
HRG	6.1E+06	9.4E+06	6.8E+06	4.5E+04	2.8E+05	1.3E+05
NP	1.7E+06	1.6E+06	3.1E+06	1.1E+05	5.0E+01	2.0E+04
LMNA	7.2E+05	5.1E+05	1.2E+06	9.6E+03	5.0E+01	4.3E+04
DEFA5	3.8E+06	3.2E+06	7.0E+06	1.2E+02	1.4E+05	1.7E+05
CNDP1	2.3E+05	1.7E+06	9.5E+05	5.0E+01	2.9E+04	4.6E+04
MYH9	1.8E+06	3.7E+06	1.6E+07	4.5E+05	7.1E+04	4.3E+04
SLC9A3R1	2.7E+06	4.4E+06	3.4E+06	2.0E+04	1.5E+05	1.2E+05
HYOU1	1.2E+06	1.4E+06	1.6E+06	5.0E+01	5.0E+01	1.2E+05
HBG1;HBG2	2.2E+05	8.1E+06	3.6E+06	5.0E+01	1.0E+05	2.4E+05
PRDX5	9.6E+05	1.2E+06	1.2E+06	2.0E+04	5.0E+01	7.8E+04
KRT8	5.8E+06	5.5E+06	1.9E+07	1.3E+05	3.0E+05	4.4E+05
EEF1A1	5.0E+01	5.0E+05	1.5E+06	5.9E+04	5.0E+01	5.0E+01
ACO2	1.2E+06	1.3E+06	2.3E+06	5.0E+01	3.1E+02	1.4E+05
GKN1	4.7E+04	1.4E+02	4.0E+06	8.6E+04	3.5E+04	5.0E+01
HSPA7	6.3E+05	7.6E+05	1.2E+06	5.0E+01	5.0E+01	7.9E+04
AKR7A3	3.0E+05	1.1E+06	1.1E+06	5.3E+04	5.0E+01	2.3E+04
APOC3	5.0E+01	1.4E+06	6.6E+05	1.0E+04	5.0E+01	5.3E+04
REG4	1.7E+05	7.9E+05	2.8E+06	6.5E+04	5.7E+04	5.0E+01
ACAT1	2.2E+06	2.1E+06	4.5E+06	5.0E+01	7.9E+04	2.0E+05
UQCRB	7.1E+05	6.0E+05	9.7E+05	5.0E+01	5.0E+01	7.5E+04
ITIH3	8.8E+05	2.8E+06	3.2E+06	1.8E+02	5.0E+01	2.3E+05

SUPPLEMENTARY DATA

GLUD1	2.6E+06	1.5E+06	1.7E+06	5.0E+01	5.0E+01	2.0E+05
PGC	1.4E+07	1.5E+06	1.0E+07	2.0E+05	4.0E+05	2.8E+05
AGT	3.0E+06	9.5E+06	5.9E+06	1.5E+04	9.5E+01	6.4E+05
CKMT1B;LOC10013362 3;CKMT1A	5.0E+01	1.2E+06	2.1E+06	6.0E+04	5.0E+01	5.7E+04
APOA2	6.0E+04	6.5E+06	3.6E+06	2.8E+04	5.1E+04	2.9E+05
IPI00382440	6.7E+05	8.4E+05	1.2E+06	5.0E+01	5.0E+01	1.0E+05
PCDH24	2.0E+05	2.8E+06	5.0E+05	5.0E+01	1.3E+05	5.0E+01
PDIA3	6.4E+06	4.0E+06	2.5E+06	2.6E+04	5.0E+01	4.8E+05
C8B	2.7E+05	1.9E+06	6.3E+05	5.0E+01	1.1E+05	5.0E+01
CFI	5.7E+06	1.9E+07	1.0E+07	1.2E+05	7.6E+05	5.2E+05
IGFALS	3.2E+05	5.2E+05	4.1E+05	5.0E+01	5.2E+04	5.0E+01
ARCNI	8.6E+05	1.1E+06	1.0E+06	7.6E+04	5.0E+01	5.9E+04
PRDX3	1.4E+06	1.0E+06	2.2E+06	1.6E+03	6.3E+04	1.5E+05
IPI00382489	2.9E+06	7.8E+05	2.8E+05	5.0E+01	4.9E+04	1.3E+05
VNN1	1.7E+05	9.4E+05	7.6E+05	5.0E+01	8.8E+04	5.0E+01
SLC5A1	2.5E+05	3.8E+05	3.5E+05	5.0E+01	5.0E+01	4.7E+04
ETFA	2.9E+06	2.9E+06	1.0E+06	8.5E+03	6.2E+04	2.6E+05
HSP90B1	2.9E+06	3.2E+06	3.7E+06	5.0E+01	2.5E+05	2.2E+05
CD59	6.8E+06	6.5E+06	3.3E+06	5.3E+03	2.9E+05	5.3E+05
IPI00782983	6.9E+05	1.1E+06	8.6E+04	5.0E+01	5.0E+01	9.2E+04
OAT	1.1E+06	1.5E+06	2.7E+06	5.0E+01	1.8E+05	8.6E+04
PCK2	7.5E+05	7.8E+05	7.9E+05	5.0E+01	6.8E+04	5.2E+04
IGJ	3.5E+07	1.0E+07	3.3E+07	2.4E+05	1.9E+06	2.1E+06
MYO1A	2.9E+05	1.9E+05	1.6E+05	5.0E+01	5.0E+01	3.5E+04
LCT	2.8E+05	7.3E+05	2.4E+06	1.5E+04	8.0E+04	9.6E+04
UQCRC1	4.7E+05	7.6E+05	1.8E+06	5.0E+01	1.1E+05	6.4E+04
RAB35	3.7E+05	2.2E+05	8.3E+05	8.1E+04	2.8E+02	5.0E+01
IPI00829624	9.5E+05	3.3E+05	2.3E+05	5.0E+01	5.0E+01	8.6E+04
B2M	6.0E+05	1.4E+05	1.1E+05	3.4E+04	5.0E+01	1.5E+04
KRT4	2.6E+06	1.6E+06	8.9E+06	2.8E+05	3.7E+05	1.3E+05
PPA1	1.5E+06	9.2E+05	1.9E+06	1.4E+05	1.1E+03	1.2E+05
CPN2	1.7E+05	5.0E+05	2.3E+05	5.0E+01	1.3E+02	5.4E+04
IPI00003469	6.8E+05	7.7E+05	5.0E+01	5.0E+01	3.8E+04	5.1E+04
PRB3	4.4E+05	3.1E+02	1.4E+06	8.7E+04	6.1E+02	2.5E+04
NPC2	4.2E+05	2.7E+05	4.8E+05	1.9E+04	5.0E+01	5.5E+04
KNG1	9.8E+06	2.9E+07	2.1E+07	3.2E+05	1.7E+06	1.8E+06
PRSS8	2.3E+05	3.7E+05	4.9E+05	5.1E+02	3.9E+04	3.1E+04
EEF2	1.4E+06	3.0E+06	5.9E+06	3.3E+05	1.9E+05	1.5E+05
ITIH1	9.6E+06	1.6E+07	1.8E+07	5.5E+03	2.6E+05	2.7E+06
ACTN2	7.0E+05	1.1E+02	4.4E+05	2.6E+04	5.0E+01	5.3E+04
PGA3;PGA4;PGA5	1.2E+07	2.5E+06	2.7E+07	1.9E+06	2.3E+05	8.7E+05
ALDOB	1.3E+07	1.4E+07	1.8E+07	7.7E+05	1.2E+06	1.3E+06

SUPPLEMENTARY DATA

TUBA4A	1.9E+05	7.7E+05	1.5E+06	2.7E+02	2.5E+02	1.7E+05
PRDX2	1.9E+06	3.7E+06	6.3E+06	1.9E+05	3.3E+04	6.5E+05
TSPAN8	2.1E+05	9.7E+04	8.3E+05	3.1E+04	6.5E+02	5.2E+04
SERPINC1	5.4E+06	2.8E+07	3.2E+07	4.2E+05	1.8E+06	2.7E+06
CLIC1	2.2E+06	2.0E+06	3.4E+06	4.6E+04	1.1E+05	4.0E+05
PGD	2.3E+05	2.5E+05	4.5E+05	5.0E+01	7.1E+04	5.0E+01
RDX	7.6E+05	2.9E+05	9.7E+05	5.0E+01	5.0E+01	1.5E+05
C6	7.7E+05	2.0E+06	2.3E+06	1.0E+05	1.1E+05	1.9E+05
TXN	6.7E+06	6.2E+06	2.0E+07	7.1E+05	4.1E+05	1.5E+06
MANF	1.9E+05	5.0E+01	2.2E+05	5.0E+01	2.6E+02	3.1E+04
HABP2	4.1E+05	5.0E+01	5.0E+01	1.7E+02	5.0E+01	3.3E+04
FBLN1	4.8E+05	7.8E+05	1.1E+05	5.0E+01	5.0E+01	1.1E+05
NT5E	8.9E+04	1.8E+06	1.2E+06	8.5E+04	1.8E+05	5.0E+01
QSOX1	1.7E+06	6.4E+05	3.3E+06	7.1E+04	1.8E+05	2.3E+05
C7	1.7E+06	4.2E+06	2.5E+06	1.4E+05	3.0E+05	2.9E+05
PON1	1.7E+06	4.6E+06	4.3E+06	1.2E+05	3.1E+05	5.1E+05
IPI00386136	1.2E+06	5.0E+01	6.1E+03	2.9E+02	5.0E+01	1.1E+05
C8A	1.3E+06	2.0E+06	1.7E+05	1.8E+02	6.0E+04	2.6E+05
KRT13	1.4E+06	3.4E+05	2.1E+06	1.0E+05	1.4E+05	1.2E+05
SLC25A5	3.7E+06	6.5E+06	6.6E+06	3.4E+04	4.8E+05	1.1E+06
HSP90AB1	8.3E+05	8.4E+05	1.4E+06	5.0E+01	6.5E+04	2.2E+05
ALPP	1.1E+05	1.0E+05	3.0E+05	4.9E+04	5.0E+01	5.0E+01
F2	5.1E+06	1.2E+07	8.5E+06	8.6E+05	6.0E+05	1.0E+06
IPI00783024	9.0E+05	2.1E+06	1.6E+05	1.4E+02	2.3E+04	2.8E+05
EPS8L3	4.3E+05	3.8E+05	8.9E+05	5.0E+01	3.1E+04	1.3E+05
PDCD6IP	2.8E+05	2.0E+05	3.7E+05	5.0E+01	5.0E+01	8.3E+04
CST3	5.9E+06	2.1E+06	2.8E+06	7.1E+05	3.3E+05	5.8E+04
GSN	5.8E+06	1.0E+07	1.1E+07	1.1E+06	4.3E+05	1.4E+06
HNRNPA2B1	8.1E+05	4.3E+05	2.3E+06	9.3E+04	1.9E+05	9.3E+04
FGA	1.4E+07	2.1E+07	2.5E+07	1.5E+05	3.0E+06	3.3E+06
HSPA1A;HSPA1B	6.4E+04	5.0E+01	2.0E+06	5.0E+01	5.1E+04	1.7E+05
HSD17B2	2.2E+06	2.3E+06	1.5E+06	5.0E+01	4.5E+04	6.2E+05
SDHB	4.6E+05	5.0E+01	1.0E+06	1.7E+04	9.7E+04	4.9E+04
RHOC	3.0E+05	3.2E+05	4.0E+05	5.0E+01	5.0E+01	1.2E+05
PPIAP19	1.9E+06	7.2E+05	1.9E+06	5.0E+01	1.0E+05	4.4E+05
IGHG1;IGHG2;IGHV4-31;IGH@	4.9E+05	7.9E+04	2.8E+05	3.5E+02	5.0E+01	1.0E+05
GSTA3	5.0E+06	3.2E+06	2.9E+06	8.3E+04	3.1E+05	9.6E+05
F11R	4.7E+05	7.5E+05	1.7E+06	5.0E+01	1.1E+05	2.6E+05
IPI00019591	8.3E+06	2.4E+07	1.4E+07	4.0E+02	4.0E+05	5.8E+06
HADHA	2.7E+06	3.2E+06	4.0E+06	4.8E+05	2.0E+05	6.5E+05
MDH1	4.7E+05	5.0E+05	1.1E+05	2.4E+02	5.0E+01	1.5E+05
MUC13	4.1E+06	1.9E+06	5.4E+06	1.5E+05	3.4E+05	1.1E+06

SUPPLEMENTARY DATA

CD36	1.6E+06	9.7E+05	2.5E+06	1.1E+04	3.6E+05	3.4E+05
KRT20	1.6E+06	1.7E+06	6.0E+06	2.1E+02	7.1E+04	1.2E+06
IPI00924820	5.9E+05	2.7E+05	6.4E+05	5.0E+01	3.6E+04	1.7E+05
IPI00164838	2.0E+05	2.5E+05	1.0E+05	5.0E+01	5.0E+01	7.6E+04
GSTA5	8.2E+05	5.0E+01	4.4E+05	5.0E+01	5.5E+02	1.8E+05
SOD1	5.9E+05	8.7E+05	3.2E+05	2.1E+05	4.7E+04	5.0E+01
ANXA2	2.2E+06	2.6E+06	4.2E+06	3.8E+04	5.4E+05	7.3E+05
CTSB	1.4E+05	4.1E+05	1.4E+05	5.0E+01	1.0E+05	5.0E+01
OTC	7.6E+05	5.6E+05	6.7E+05	9.8E+04	6.9E+04	1.3E+05
LRG1	1.5E+06	2.7E+06	1.3E+06	5.0E+01	2.3E+05	6.0E+05
CES2	7.9E+05	1.2E+06	1.2E+06	5.0E+01	2.2E+05	2.6E+05
LIPF	6.6E+07	4.0E+06	5.3E+07	1.4E+07	3.8E+06	1.0E+06
ACTA2	1.2E+07	1.6E+07	1.8E+07	6.5E+05	2.3E+06	4.1E+06
OLFM4	1.1E+07	1.1E+06	3.4E+06	8.4E+04	1.2E+06	1.2E+06
ACE2	1.4E+06	1.2E+06	4.2E+06	1.1E+05	9.0E+05	4.8E+04
APOE	2.4E+05	6.4E+06	2.2E+06	9.0E+05	3.3E+05	1.8E+05
PPIB	9.4E+05	7.5E+05	1.2E+06	3.4E+04	1.1E+02	4.5E+05
ECHS1	5.2E+05	1.0E+06	1.9E+06	5.0E+01	1.9E+05	3.8E+05
HPGD	2.0E+05	3.3E+05	5.8E+05	9.7E+04	3.3E+04	5.3E+04
MSMB	1.3E+05	1.0E+05	2.2E+05	7.5E+04	5.0E+01	5.0E+01
HMGCS2	2.8E+05	7.4E+05	4.0E+05	5.7E+04	5.2E+04	1.3E+05
LYZ	4.4E+07	1.5E+07	2.6E+07	6.3E+06	2.7E+06	5.7E+06
MAOA	3.2E+05	2.6E+05	6.8E+05	5.0E+01	2.1E+02	2.2E+05
GPA33	6.3E+05	4.0E+05	1.6E+06	8.5E+04	2.3E+05	1.5E+05
SUCLG1	1.1E+06	1.2E+06	1.3E+06	5.0E+01	4.8E+05	1.6E+05
PIGR	1.0E+08	4.3E+07	7.3E+07	1.4E+07	1.3E+07	1.2E+07
ATP1B3	3.7E+05	2.4E+05	3.3E+05	5.0E+01	7.4E+04	9.4E+04
FABP5L9;FABP5L2;FABP5;FABP5L7	5.0E+01	7.4E+01	1.3E+05	2.4E+04	5.0E+01	5.0E+01
CRISP3	6.1E+05	1.0E+05	1.9E+05	3.5E+04	1.2E+02	1.3E+05
GOLM1	1.5E+06	3.5E+05	3.6E+06	4.7E+05	1.6E+05	3.7E+05
FAM3C	5.8E+05	1.7E+05	1.1E+06	3.9E+04	1.3E+05	1.7E+05
ALDH2	3.9E+06	2.1E+06	3.0E+06	1.6E+05	7.4E+05	7.7E+05
ACAA2	4.8E+05	2.3E+05	6.9E+05	1.3E+05	9.0E+04	4.1E+04
FCN3	6.5E+05	2.0E+06	1.5E+06	5.0E+01	2.6E+05	5.3E+05
PLG	1.5E+07	2.2E+07	1.3E+07	5.5E+05	3.0E+06	5.7E+06
CLU	3.6E+06	2.0E+07	1.8E+07	4.8E+05	5.0E+06	2.5E+06
IGHM	5.6E+07	1.8E+07	2.4E+07	1.1E+06	7.1E+06	1.1E+07
FABP1	1.2E+07	1.1E+07	1.6E+07	8.1E+05	1.9E+06	5.0E+06
GC	2.1E+07	2.7E+07	2.1E+07	2.3E+05	3.6E+06	9.9E+06
GPLD1	6.4E+05	1.2E+06	1.2E+06	5.0E+01	5.0E+01	6.2E+05
CLTC	1.5E+05	1.1E+06	1.1E+06	1.5E+05	1.8E+05	1.5E+05
TUBB	8.0E+04	5.0E+01	9.7E+04	5.0E+01	1.2E+02	3.6E+04

SUPPLEMENTARY DATA

APOB	2.1E+07	6.4E+07	8.2E+07	4.0E+06	6.1E+06	2.4E+07
PRDX1	7.3E+06	7.0E+06	1.2E+07	7.0E+05	3.1E+06	1.6E+06
YWHAЕ	1.1E+06	5.0E+01	3.2E+05	5.0E+01	4.3E+02	2.8E+05
MASP2	4.1E+05	1.4E+05	1.0E+05	5.0E+01	5.0E+01	1.4E+05
HEPACAM	5.0E+01	3.9E+05	5.7E+04	5.9E+04	3.5E+04	5.0E+01
KLKB1	1.9E+06	4.5E+06	1.1E+06	6.0E+05	3.4E+05	6.7E+05
IGHA1	1.8E+06	1.3E+06	2.5E+02	1.1E+02	2.2E+05	4.5E+05
SERPINA7	7.7E+05	6.1E+05	6.5E+05	5.0E+01	7.8E+04	3.7E+05
ALB	3.0E+06	3.1E+06	1.2E+06	5.0E+01	4.0E+04	1.6E+06
CFHR2	1.7E+06	4.8E+06	1.7E+06	5.0E+01	4.1E+05	1.4E+06
ANPEP	2.6E+07	1.1E+07	1.3E+07	4.3E+06	5.5E+06	1.7E+06
GIF	5.6E+05	5.0E+01	1.3E+05	1.3E+05	3.0E+04	5.0E+01
UBC;RPS27A;UBB	2.2E+06	1.6E+06	5.0E+06	1.0E+06	4.6E+05	4.9E+05
ATRN	1.2E+06	1.3E+06	7.5E+05	2.5E+04	2.1E+05	5.2E+05
C8G	1.2E+06	1.8E+06	1.1E+06	2.3E+04	1.6E+05	7.6E+05
IPI00827815	2.2E+06	1.2E+06	3.6E+06	5.0E+01	4.1E+05	1.2E+06
SPINK1	4.3E+05	6.1E+05	7.2E+05	5.0E+01	2.0E+05	2.0E+05
SI	9.8E+06	4.5E+06	1.2E+07	7.3E+05	3.2E+06	2.1E+06
IPI00386137	5.0E+01	3.8E+05	4.4E+05	5.0E+01	8.5E+04	1.0E+05
CDH17	3.7E+06	3.4E+06	1.1E+07	9.8E+05	2.0E+06	1.3E+06
MVP	4.4E+05	7.2E+05	2.6E+06	2.6E+05	4.8E+05	2.0E+05
HSP90AA2	1.6E+05	5.0E+01	1.4E+05	2.1E+02	1.6E+02	7.2E+04
APOD	1.9E+06	2.5E+06	1.9E+06	1.1E+05	3.8E+05	1.0E+06
MUC6	1.1E+08	1.6E+07	6.2E+07	6.6E+06	2.0E+07	2.1E+07
HLA-H	1.3E+05	7.5E+04	5.0E+01	1.5E+02	5.0E+01	5.2E+04
S100A9	2.4E+05	6.3E+05	7.6E+05	1.5E+05	7.1E+04	1.9E+05
LOC100126583;IGHA2	9.0E+05	4.2E+05	4.8E+05	5.0E+01	9.1E+04	3.7E+05
SERPIND1	2.7E+06	7.0E+06	6.7E+06	6.0E+02	1.1E+06	3.2E+06
PTGR1	5.5E+05	8.4E+05	7.0E+05	3.3E+05	1.4E+05	7.9E+04
GDI2	7.8E+05	1.7E+06	3.6E+06	2.7E+05	9.6E+05	3.7E+05
TUBA1C	1.5E+06	1.3E+06	3.4E+06	5.2E+04	5.3E+05	1.0E+06
CD5L	8.6E+06	6.0E+06	5.5E+06	7.7E+04	7.5E+05	4.5E+06
SERPINA1	1.1E+07	2.9E+07	2.9E+07	2.1E+05	6.1E+06	1.2E+07
DAK	1.3E+06	2.2E+06	1.3E+06	1.1E+06	4.7E+04	1.2E+05
SERPINA4	6.3E+05	3.4E+06	5.3E+06	9.1E+04	1.1E+06	1.3E+06
PPP1CC	2.0E+05	2.2E+05	2.6E+05	6.3E+04	7.0E+04	5.1E+04
REG3A	2.9E+06	4.5E+06	6.8E+06	9.1E+05	6.9E+05	2.2E+06
F13B	5.5E+06	3.0E+06	3.0E+06	5.0E+01	4.1E+05	2.7E+06
ACTN4	6.6E+06	4.3E+06	8.0E+06	6.3E+05	9.8E+05	3.6E+06
PDIA6	1.2E+05	5.0E+01	7.6E+04	1.7E+02	8.9E+01	5.4E+04
IPI00382439	8.1E+05	9.4E+05	1.4E+06	5.0E+01	1.5E+05	7.3E+05
IPI00384401	4.3E+06	4.0E+06	4.7E+06	4.1E+04	2.3E+05	3.4E+06
ANXA2P2	1.9E+06	1.6E+06	4.1E+06	9.8E+05	5.7E+05	6.3E+05

SUPPLEMENTARY DATA

PARK7	5.8E+05	5.1E+05	7.1E+05	1.8E+05	5.0E+04	2.9E+05
DPP4	2.3E+05	6.7E+05	6.4E+05	3.6E+04	1.6E+05	2.5E+05
CANX	2.2E+06	1.4E+06	7.2E+06	1.4E+06	1.1E+06	6.1E+05
ACTBL2	5.8E+06	6.2E+06	4.8E+06	4.4E+05	1.8E+06	2.7E+06
ACY1	8.7E+05	2.4E+06	1.2E+06	1.3E+05	9.3E+05	2.3E+05
IPI00385264	8.6E+07	1.1E+07	1.4E+07	3.5E+06	1.2E+07	1.7E+07
IPI00830057	1.6E+05	2.3E+05	4.6E+05	5.0E+01	4.8E+04	2.0E+05
SERPING1	3.8E+06	7.6E+06	7.1E+06	1.0E+05	1.8E+06	3.5E+06
S100A8	1.7E+06	1.1E+06	5.0E+06	1.6E+06	3.5E+05	2.9E+05
ETFDH	1.8E+05	5.0E+01	1.9E+05	5.6E+04	5.2E+04	5.0E+01
P4HB	1.6E+07	9.0E+06	1.2E+07	1.6E+06	5.5E+06	3.7E+06
LOC440786	5.1E+05	5.0E+01	2.5E+05	5.0E+02	3.1E+02	2.2E+05
KRT24	1.9E+05	5.0E+01	4.5E+02	1.7E+02	5.0E+01	5.5E+04
CSTB	1.2E+06	2.8E+06	1.4E+06	1.2E+06	2.9E+05	1.6E+05
COX4I1	5.4E+05	8.0E+05	1.2E+05	3.1E+05	1.1E+05	1.8E+04
IPI00827690	3.1E+05	1.3E+05	3.4E+05	5.0E+01	3.7E+04	2.0E+05
C1R	1.7E+06	5.8E+06	4.4E+06	8.1E+04	9.9E+05	2.6E+06
IGKC	5.8E+05	5.0E+01	2.3E+05	5.0E+01	5.3E+04	2.0E+05
C1S	2.0E+06	6.3E+06	3.1E+06	5.0E+05	1.1E+06	1.9E+06
IPI00854709	3.4E+05	2.0E+05	2.7E+05	5.0E+01	5.0E+01	2.5E+05
RAB1A	1.2E+06	1.3E+06	2.3E+06	6.5E+05	3.8E+05	4.4E+05
EEF1A2	2.2E+06	2.7E+06	5.4E+06	8.7E+05	7.0E+05	1.7E+06
IGKV3D-11	1.7E+06	1.7E+06	1.4E+06	1.5E+04	3.9E+05	1.1E+06
LOC100126583;IGHA2	4.3E+07	1.0E+07	7.6E+06	4.1E+06	8.4E+06	6.8E+06
A1BG	8.0E+06	1.6E+07	1.2E+07	1.2E+05	3.7E+06	7.7E+06
PDIA4	5.5E+05	6.3E+05	7.6E+05	1.8E+05	3.1E+05	1.4E+05
IGKV3-20	1.6E+07	1.9E+07	3.1E+06	4.5E+05	2.8E+06	9.2E+06
IGLV7-43	5.0E+05	2.3E+05	1.6E+05	5.0E+01	1.1E+05	1.8E+05
LOC100126583;IGHA2	1.7E+06	1.6E+06	5.0E+01	5.0E+01	3.5E+05	7.5E+05
PGK1	2.7E+06	1.7E+06	3.2E+06	8.7E+04	7.5E+05	1.7E+06
ACTB	6.8E+06	8.0E+06	1.2E+07	1.7E+05	1.7E+06	7.1E+06
IPI00382494	5.6E+06	3.0E+06	2.2E+06	5.0E+01	9.7E+05	2.7E+06
ORM2	7.2E+06	2.1E+07	8.1E+06	1.8E+05	3.3E+06	8.9E+06
PSMB8	5.5E+05	3.9E+05	2.3E+05	5.0E+01	2.8E+05	1.4E+05
IPI00735451	3.8E+06	3.5E+06	4.7E+06	7.7E+05	8.2E+05	2.7E+06
HADHB	4.1E+06	2.9E+06	3.5E+06	9.9E+05	1.2E+06	1.6E+06
PTGDS	6.1E+05	2.2E+06	7.0E+05	5.0E+01	7.1E+05	5.5E+05
IGHA1	1.1E+07	5.6E+06	5.5E+06	1.1E+06	3.4E+06	3.5E+06
MME	1.7E+06	6.8E+05	1.6E+06	3.1E+05	6.0E+05	5.3E+05
ATP1A1	1.5E+06	9.3E+05	1.5E+06	9.6E+05	1.4E+05	3.1E+05
ACTN1	7.8E+05	1.8E+06	7.7E+05	3.4E+05	3.2E+05	5.8E+05
HSPE1	3.3E+06	1.3E+06	1.9E+06	7.9E+05	9.6E+05	6.8E+05
CAP1	1.5E+06	1.2E+06	1.9E+06	5.0E+01	9.4E+05	7.6E+05



SUPPLEMENTARY DATA

PLS1	6.6E+06	2.9E+06	5.5E+06	2.8E+06	1.2E+06	1.6E+06
IGHG1;IGHG2;IGHV4-31;IGH@	3.0E+06	2.4E+06	3.1E+06	6.8E+02	5.0E+05	2.7E+06
IPI00783094	3.3E+05	2.0E+05	6.4E+05	5.0E+01	1.2E+05	3.2E+05
HP	3.9E+07	1.1E+08	5.5E+07	2.6E+06	1.5E+07	5.9E+07
AKR1C4	1.9E+06	1.5E+06	1.6E+06	8.3E+05	1.3E+05	9.1E+05
IPI00382500	1.6E+06	1.8E+06	2.3E+06	3.4E+05	8.0E+05	1.0E+06
PROS1	3.9E+06	5.2E+06	3.9E+06	7.1E+04	1.5E+06	3.4E+06
SPRR1A	7.4E+05	3.4E+05	3.3E+06	1.6E+06	5.8E+04	5.0E+01
IPI00387100	2.5E+05	3.9E+05	3.6E+05	6.6E+04	1.3E+05	1.8E+05
DMBT1	4.3E+07	5.2E+06	6.7E+06	1.6E+07	3.2E+06	1.9E+06
IPI00069693	3.6E+05	5.0E+01	4.7E+05	5.0E+01	6.1E+02	3.2E+05
VIL1	5.8E+06	3.6E+06	7.3E+06	4.1E+05	1.5E+06	4.5E+06
ORM1	3.2E+06	2.4E+07	4.1E+06	5.2E+06	2.5E+06	4.2E+06
CD14	4.5E+04	2.7E+06	6.3E+05	2.4E+05	4.6E+05	6.1E+05
IPI00827944	4.5E+05	2.4E+05	1.6E+05	5.0E+01	8.4E+04	2.5E+05
PREP	3.3E+05	1.5E+05	4.2E+05	9.5E+04	1.1E+05	1.4E+05
SERPINA3	1.8E+07	1.3E+07	1.0E+07	4.4E+05	4.0E+06	1.2E+07
LOC100126583;IGHA2	2.3E+06	8.9E+05	1.3E+05	1.7E+02	5.0E+05	8.3E+05
RBP2	1.6E+06	1.6E+06	1.7E+06	2.6E+05	1.0E+06	7.0E+05
IPI00387026	2.0E+06	6.6E+05	4.4E+05	2.1E+04	4.1E+05	8.1E+05
PPIA	5.0E+01	1.1E+02	1.1E+05	4.4E+04	1.3E+02	5.0E+01
SPRR2C;SPRR2G	4.8E+05	1.2E+02	2.0E+05	2.2E+05	4.6E+04	5.0E+01
PCK2	5.8E+06	3.4E+06	2.4E+06	1.7E+06	1.6E+06	1.3E+06
IPI00382436	4.3E+05	7.3E+05	6.8E+05	5.0E+01	8.1E+04	6.7E+05
CP	2.5E+07	4.4E+07	3.3E+07	3.3E+06	8.8E+06	3.0E+07
RAP1B	1.4E+05	7.1E+04	2.4E+05	4.8E+04	7.5E+04	5.8E+04
CES1	1.4E+05	5.0E+01	2.2E+05	5.0E+01	2.9E+02	1.5E+05
HSPA8	5.6E+06	2.2E+06	6.2E+06	1.8E+06	1.1E+06	2.9E+06
CFHR5	2.3E+05	2.5E+05	4.1E+05	5.0E+01	4.1E+02	3.7E+05
KRT3	6.7E+05	3.0E+05	1.5E+06	7.7E+05	2.9E+02	2.6E+05
LDHAL6A	3.2E+06	3.6E+06	6.8E+05	6.8E+03	1.6E+06	1.5E+06
IPI00384409	3.2E+05	5.0E+05	1.4E+05	5.0E+01	7.2E+04	3.2E+05
IGLL1	4.5E+06	1.3E+06	7.5E+05	3.3E+05	1.0E+06	1.4E+06
ITIH4	1.1E+07	2.0E+07	2.0E+07	1.3E+06	5.9E+06	1.4E+07
PYCARD	5.0E+01	5.0E+01	2.6E+02	5.0E+01	5.0E+01	5.0E+01
LOC284422	2.8E+05	1.3E+05	1.4E+05	5.0E+01	5.0E+01	2.3E+05
TFF1	2.0E+06	4.1E+05	1.8E+06	1.5E+06	2.4E+05	2.0E+04
CAPRIN2	1.6E+05	1.4E+05	6.0E+04	5.0E+01	4.5E+04	1.0E+05
IPI00382420	1.2E+06	8.4E+05	8.9E+04	3.8E+02	5.0E+01	9.1E+05
CPB2	2.2E+05	2.2E+05	2.7E+05	5.0E+01	1.3E+05	1.7E+05
GMDS	1.9E+05	2.9E+05	6.5E+05	1.2E+05	2.9E+05	7.3E+04
ITLN2	1.2E+06	2.0E+06	3.5E+06	1.2E+06	1.2E+06	4.9E+05

SUPPLEMENTARY DATA

CBR1	3.8E+06	5.3E+06	9.0E+06	5.2E+06	1.5E+06	1.1E+06
ATP1B1	1.5E+06	5.0E+05	1.9E+06	4.0E+05	4.5E+05	8.6E+05
VTN	2.1E+06	1.1E+07	9.3E+06	7.6E+05	3.7E+06	5.6E+06
TP53I3	1.7E+05	5.0E+01	5.0E+01	2.3E+02	5.0E+01	7.4E+04
PRKCSH	8.9E+04	5.0E+01	1.9E+05	5.0E+01	7.4E+04	5.2E+04
EPCAM	1.6E+06	5.7E+05	1.7E+06	2.8E+04	6.4E+05	1.0E+06
VDAC1	2.8E+06	1.2E+06	8.6E+06	1.3E+06	2.5E+06	1.8E+06
CPT2	6.1E+05	1.8E+05	5.8E+05	5.0E+01	4.8E+05	1.3E+05
IGKV1-5	3.5E+05	1.6E+05	1.5E+05	5.0E+01	7.4E+04	2.2E+05
AKR1C3	9.0E+04	7.2E+05	1.5E+06	9.8E+05	5.0E+01	5.3E+04
TUBB2C	9.8E+05	4.2E+05	1.8E+06	4.0E+04	5.0E+05	9.0E+05
C5	5.1E+06	9.6E+06	8.2E+06	5.1E+05	3.6E+06	6.3E+06
FN1	1.6E+07	2.2E+07	1.4E+07	4.3E+05	4.6E+06	1.8E+07
ALDH1A1	7.1E+06	8.7E+06	1.6E+07	6.8E+06	5.5E+06	2.6E+06
ANP32B	8.8E+04	9.6E+04	3.6E+02	5.0E+01	8.7E+04	5.0E+01
GDA	6.6E+05	8.1E+05	2.5E+06	7.3E+05	5.0E+05	6.7E+05
IPI00829653	1.2E+05	6.7E+04	5.0E+01	2.5E+02	5.0E+01	9.0E+04
UGT2B17	2.5E+06	6.9E+05	3.4E+06	2.6E+06	1.5E+02	5.9E+05
IPI00829701	9.2E+05	2.5E+05	3.2E+05	1.8E+02	1.3E+05	5.8E+05
IGHA1	1.3E+08	5.4E+07	7.0E+07	2.3E+07	5.1E+07	4.7E+07
VCP	7.6E+05	4.2E+05	1.8E+06	1.4E+05	6.3E+05	6.9E+05
CEACAM5	1.4E+05	1.1E+05	1.1E+05	5.2E+04	3.4E+04	8.9E+04
GSTA1	3.2E+06	1.2E+06	2.7E+06	2.7E+06	1.2E+03	8.5E+05
EEF1G	3.1E+05	1.0E+06	2.3E+06	5.9E+05	9.9E+05	2.8E+05
LCP1	6.4E+05	2.0E+05	3.8E+05	1.3E+05	6.4E+04	4.3E+05
IGLC1;IGLV1-44;IGLV1-40;IGLV3-21;IGLV2-11;IGLV2-14;IGL@;IGLC2;IGLC3	8.6E+06	5.4E+06	5.9E+06	1.0E+05	2.9E+06	7.2E+06
FGG	7.2E+07	4.2E+07	1.8E+07	3.3E+06	1.9E+07	4.5E+07
ALDOA	1.7E+05	6.9E+05	4.5E+05	5.0E+01	6.2E+05	5.6E+04
LGALS3BP	6.1E+06	1.4E+06	1.1E+06	8.2E+05	2.3E+06	1.3E+06
IPI00385253	7.1E+05	3.2E+05	6.4E+05	1.2E+02	2.0E+05	6.7E+05
SDHA	9.7E+05	4.4E+05	9.3E+05	1.6E+05	9.8E+05	6.8E+04
MDH2	2.5E+06	1.1E+06	1.4E+06	1.1E+06	1.2E+06	3.5E+05
IPI00829873	2.1E+05	5.0E+01	1.3E+05	5.0E+01	1.8E+02	1.8E+05
ADH5;ADH5P4	5.0E+01	1.9E+05	3.6E+05	4.5E+04	2.4E+05	5.0E+01
CA2	1.2E+06	3.4E+06	7.0E+06	2.9E+06	2.5E+06	8.8E+05
IPI00101961	7.3E+05	1.2E+05	2.4E+05	1.8E+05	2.2E+05	1.9E+05
IGLV2-18	5.9E+05	1.4E+05	7.5E+04	4.5E+04	3.3E+05	6.0E+04
APOH	4.9E+06	2.8E+07	7.3E+06	1.3E+06	8.4E+06	1.2E+07
LOC390956	5.6E+05	1.1E+02	1.6E+06	3.6E+05	2.5E+05	5.7E+05
IPI00003939	5.2E+05	5.6E+05	1.9E+05	5.0E+01	8.0E+04	6.2E+05
MYL12B	5.0E+01	5.0E+05	1.2E+06	7.6E+05	1.7E+05	5.0E+01

SUPPLEMENTARY DATA

CFH	1.6E+07	2.3E+07	2.4E+07	1.2E+06	8.8E+06	2.4E+07
DECR1	4.0E+05	5.0E+01	2.9E+05	7.1E+04	2.2E+05	8.2E+04
LOC401847	1.8E+06	8.2E+05	4.0E+05	5.0E+01	3.4E+05	1.4E+06
PRSS7	5.9E+06	2.8E+06	8.2E+06	5.0E+06	1.6E+06	2.6E+06
NUDT21	2.6E+05	1.0E+05	2.8E+05	2.1E+05	1.4E+05	1.9E+04
LOC652128	1.0E+07	4.3E+06	3.2E+06	3.5E+02	3.6E+06	6.6E+06
IGLC1;IGLV1-44;IGLV1-40;IGLV3-21;IGLV2-11;IGLV2-14;IGL@;IGLC2;IGLC3	3.6E+07	1.7E+07	2.0E+07	1.1E+06	1.4E+07	2.7E+07
A2M	9.7E+07	1.0E+08	1.1E+08	8.6E+06	6.1E+07	1.1E+08
TFF3	2.0E+06	1.4E+06	4.8E+06	2.0E+06	1.9E+06	8.6E+05
ENO1	4.9E+06	3.9E+06	4.9E+06	1.5E+06	2.8E+06	3.8E+06
TCN1	1.5E+05	3.0E+05	6.8E+05	4.0E+04	1.1E+05	5.1E+05
IGLC1;IGLV1-44;IGLV1-40;IGLV3-21;IGLV2-11;IGLV2-14;IGL@;IGLC2;IGLC3	5.0E+01	5.0E+01	9.6E+05	2.0E+02	1.2E+03	5.8E+05
C20orf114	2.0E+06	1.5E+05	3.8E+05	7.4E+05	1.9E+05	6.0E+05
IPI00382478	5.0E+06	2.6E+06	1.4E+06	1.4E+02	1.7E+06	3.8E+06
IGHG1;IGHG2;IGHV4-31;IGH@	5.0E+01	5.5E+05	1.6E+06	5.0E+01	1.3E+06	5.0E+01
IPI00760721	9.6E+05	6.4E+05	1.0E+05	3.0E+04	4.4E+05	5.8E+05
MUC2	2.2E+07	4.1E+06	1.2E+07	4.3E+06	1.1E+07	8.6E+06
FH	8.4E+05	4.8E+05	1.2E+06	7.9E+05	6.3E+05	1.3E+05
AZGP1	7.0E+06	1.2E+07	4.9E+06	4.1E+06	4.3E+06	6.6E+06
HDGF	3.7E+06	1.9E+05	1.9E+05	5.0E+01	5.0E+01	2.6E+06
SELENBP1	6.2E+04	6.5E+05	4.8E+05	5.0E+01	1.0E+05	6.5E+05
IPI00383732	2.8E+06	2.5E+06	1.3E+06	6.2E+02	1.3E+06	3.0E+06
IGHA1	1.0E+06	8.0E+05	1.1E+06	5.0E+01	2.4E+05	1.6E+06
BCHE	5.1E+05	6.2E+05	1.0E+06	3.2E+04	5.3E+05	7.9E+05
DLD	6.5E+05	1.7E+05	5.3E+05	2.3E+05	5.4E+05	8.3E+04
IGLV8-61	7.5E+05	1.6E+05	2.0E+05	3.7E+02	1.9E+05	5.2E+05
WDR1	2.0E+06	1.4E+06	1.5E+06	9.4E+05	1.1E+06	1.1E+06
GALNT7	2.9E+05	1.4E+05	5.2E+05	4.2E+05	8.3E+04	1.1E+05
LAP3	9.7E+05	8.3E+05	6.2E+05	1.1E+05	7.6E+05	6.9E+05
HEBP1	2.0E+06	1.2E+06	1.4E+06	2.2E+05	2.1E+06	6.8E+05
HSPA5	6.1E+06	5.9E+06	8.2E+06	6.4E+06	4.1E+06	2.7E+06
NME1;NME2	1.0E+06	5.0E+01	6.3E+05	1.1E+05	4.4E+05	5.4E+05
ADH6	1.4E+05	5.9E+05	1.3E+06	1.7E+05	9.7E+05	2.2E+05
C4BPA	5.2E+06	6.9E+06	4.7E+06	4.0E+05	3.3E+06	7.5E+06
IPI00550731	5.3E+07	5.7E+07	6.6E+07	2.7E+07	3.4E+07	5.6E+07
HBZ	2.0E+06	1.3E+06	1.9E+06	5.0E+01	6.3E+05	2.9E+06
IPI00830122	1.2E+05	9.6E+04	5.0E+01	5.0E+01	4.0E+04	1.0E+05
CNDP2	9.8E+05	1.4E+06	1.8E+06	1.8E+06	5.4E+05	5.5E+05

SUPPLEMENTARY DATA

ACADVL	1.2E+06	8.4E+05	2.3E+05	2.3E+05	1.2E+06	1.2E+05
IGKV4-1	4.0E+06	4.3E+06	6.1E+06	1.5E+06	2.4E+06	5.9E+06
TF	8.8E+07	1.4E+08	8.4E+07	1.2E+07	8.1E+07	1.2E+08
IGHG4	1.0E+07	2.5E+07	1.6E+07	8.1E+05	5.7E+06	2.8E+07
HPR	7.9E+06	1.4E+07	9.0E+06	8.8E+05	5.3E+06	1.5E+07
IPI00382486	3.3E+05	8.6E+04	6.2E+04	5.0E+01	7.7E+04	2.5E+05
ACE	8.3E+05	1.4E+05	7.1E+05	1.5E+05	3.4E+05	6.9E+05
IPI00007899	4.3E+06	8.7E+05	4.5E+05	1.5E+05	1.2E+06	2.5E+06
MYL6B	1.9E+06	6.8E+05	1.2E+06	1.6E+05	1.5E+06	1.0E+06
SERPINA1	4.1E+07	8.3E+07	5.0E+07	1.6E+07	3.6E+07	7.3E+07
AKR1A1	3.6E+05	7.9E+05	8.1E+05	6.1E+05	7.5E+05	5.8E+04
TTR	1.5E+07	1.6E+07	5.1E+06	2.0E+06	6.3E+06	1.8E+07
ALB	5.9E+08	7.8E+08	5.3E+08	1.0E+08	4.0E+08	8.9E+08
HPR;HP	1.5E+07	2.2E+07	1.1E+07	1.3E+06	9.8E+06	2.4E+07
CALR	4.1E+06	2.7E+06	4.5E+06	4.7E+06	2.7E+06	9.8E+05
PGM2	4.3E+05	2.5E+05	4.4E+05	3.5E+05	3.1E+05	1.7E+05
UGT2B15	2.3E+05	2.7E+05	1.5E+06	1.4E+06	3.0E+02	1.1E+05
IPI00029863	1.9E+06	4.0E+06	1.7E+06	1.7E+06	2.5E+06	1.5E+06
HBB	9.4E+06	1.8E+07	3.1E+07	4.0E+05	2.0E+07	2.4E+07
IPI00003470	1.8E+06	1.9E+05	2.1E+05	7.5E+02	1.6E+05	1.5E+06
ADA	1.1E+07	7.1E+06	5.5E+06	3.8E+06	7.6E+06	6.7E+06
CLCA1	3.9E+07	1.5E+07	4.1E+07	3.8E+06	4.5E+07	2.5E+07
SLPI	1.1E+07	1.8E+05	8.1E+06	1.4E+07	2.9E+05	7.2E+05
IGHG1;IGHG2;IGHV4-31;IGH@	3.6E+05	3.5E+05	2.0E+05	1.4E+05	2.0E+05	3.6E+05
SERPINA6	1.3E+06	2.4E+06	6.6E+05	5.0E+01	1.2E+06	2.2E+06
CS	3.0E+05	3.1E+02	5.0E+01	1.2E+05	5.0E+01	1.1E+05
GOT2	2.3E+05	1.9E+05	3.8E+05	1.9E+05	1.9E+05	2.5E+05
HSPB1	2.3E+05	5.0E+01	6.5E+05	1.2E+05	4.8E+05	8.2E+04
KRT6B	7.7E+05	3.2E+03	2.2E+06	1.2E+06	4.0E+05	7.2E+05
IPI00384397	7.1E+06	1.5E+06	1.4E+06	7.3E+04	2.3E+06	5.6E+06
LOC651751	5.0E+01	3.4E+05	3.6E+05	3.6E+05	2.0E+05	5.0E+01
HPX	2.7E+07	4.1E+07	1.2E+07	1.6E+06	2.0E+07	4.2E+07
IPI00386131	2.7E+05	8.5E+04	5.0E+01	8.2E+02	5.0E+01	2.9E+05
IGHG1;IGHG2;IGHV4-31;IGH@	5.1E+07	3.1E+07	3.8E+07	4.2E+06	2.3E+07	7.2E+07
PEBP1	6.2E+06	6.3E+06	6.9E+06	1.8E+06	2.4E+06	1.2E+07
PCK1	3.6E+05	6.2E+05	1.0E+06	4.5E+05	8.8E+05	3.5E+05
IPI00383887	1.7E+05	9.3E+04	5.0E+01	5.0E+01	5.8E+04	1.6E+05
GSR	8.2E+05	5.3E+05	8.5E+05	5.5E+05	7.5E+05	5.3E+05
ITLN1	3.3E+06	2.5E+06	1.2E+06	4.4E+05	3.0E+06	2.4E+06
C3	6.1E+07	8.0E+07	8.8E+07	9.4E+06	6.8E+07	1.2E+08
LOC653879	2.1E+07	2.7E+07	2.3E+07	5.3E+06	1.9E+07	3.8E+07
IPI00890703	3.0E+05	1.2E+05	2.8E+05	2.1E+02	5.9E+04	5.4E+05

SUPPLEMENTARY DATA

MTTP	6.5E+06	2.1E+06	3.6E+06	3.1E+06	5.9E+06	1.6E+06
AMBP	1.0E+06	2.9E+06	2.8E+06	7.7E+04	3.1E+06	2.7E+06
IPI00382499	1.1E+06	8.5E+05	2.4E+06	1.6E+06	6.3E+05	1.5E+06
LTF	2.3E+06	3.0E+06	3.3E+06	3.8E+06	3.3E+06	5.9E+05
CFHR3	7.3E+05	5.3E+05	1.2E+05	1.8E+05	2.6E+05	8.0E+05
PEPD	2.3E+06	2.7E+05	6.3E+05	1.8E+06	5.0E+01	1.1E+06
UBA1	5.0E+01	5.0E+01	7.0E+04	5.0E+01	9.2E+01	6.3E+04
IPI00829980	7.3E+05	2.7E+05	4.5E+05	5.0E+01	2.3E+05	1.1E+06
KRT14	4.5E+05	2.4E+05	7.8E+05	7.2E+05	4.1E+05	2.3E+05
ITGB1	9.0E+05	2.7E+05	1.7E+05	4.7E+05	5.0E+05	2.7E+05
IPI00007906	6.2E+05	5.8E+05	2.2E+05	1.1E+05	3.9E+05	8.1E+05
GOT1	2.6E+05	2.8E+05	8.5E+04	6.8E+04	3.1E+05	2.0E+05
SERPINA5	2.0E+06	1.3E+06	1.1E+06	2.0E+05	1.3E+06	2.6E+06
LDHA	6.5E+05	3.5E+05	5.4E+05	1.1E+02	7.9E+05	6.6E+05
IPI00384404	1.2E+05	8.4E+04	2.6E+05	5.0E+01	1.1E+05	3.4E+05
IPI00384391	2.3E+06	4.4E+05	5.7E+05	4.2E+04	8.1E+05	2.4E+06
GNB2	5.7E+05	5.0E+01	9.6E+04	1.5E+05	3.2E+05	1.9E+05
PZP	1.1E+07	1.3E+07	1.1E+07	5.0E+06	9.4E+06	2.1E+07
CKMT1B;LOC100133623;CKMT1A	6.5E+05	2.4E+05	4.4E+05	6.3E+05	5.6E+05	1.4E+05
C6orf58	3.5E+06	5.9E+05	4.3E+06	2.1E+06	3.4E+06	3.0E+06
GNB1	5.0E+01	1.2E+05	2.6E+05	3.3E+05	5.5E+04	5.0E+01
IGHG1;IGHG2;IGHV4-31;IGH@	1.4E+05	5.0E+01	5.0E+01	4.1E+02	5.0E+01	1.4E+05
LOC652113	2.1E+05	5.0E+01	1.2E+06	9.8E+05	3.9E+05	8.9E+04
ANXA5	7.5E+05	5.0E+01	1.6E+05	2.0E+05	3.0E+05	4.4E+05
HBD	1.1E+07	1.4E+07	2.9E+07	4.0E+05	1.9E+07	3.6E+07
EFHD2	1.9E+05	5.0E+01	1.5E+05	2.6E+05	1.6E+04	8.2E+04
ZG16B	2.1E+06	2.4E+06	4.5E+06	5.4E+06	1.6E+06	2.5E+06
IGKV1D-8	2.5E+06	1.7E+06	1.3E+06	3.5E+05	1.6E+06	3.8E+06
UGT2B10	6.9E+05	2.1E+05	6.6E+05	1.5E+06	5.0E+01	1.6E+05
FGB	6.2E+07	2.6E+07	1.6E+07	6.8E+06	4.9E+07	5.6E+07
ANXA4	5.4E+05	7.0E+05	1.3E+06	1.8E+06	5.6E+05	3.5E+05
GSTP1	2.6E+06	2.6E+06	6.4E+06	9.5E+06	1.7E+06	1.3E+06
ALDOC	5.2E+05	5.2E+05	9.7E+05	1.7E+06	2.8E+05	2.0E+05
FLNB	4.0E+06	1.4E+06	3.0E+06	2.7E+06	3.7E+06	2.9E+06
MASP1	3.5E+05	2.1E+05	1.1E+05	3.0E+04	1.5E+02	7.1E+05
UGCGL1	2.3E+05	1.2E+05	7.2E+04	5.0E+01	1.0E+05	3.5E+05
CNDP2	6.3E+05	7.0E+05	1.1E+06	1.2E+06	4.7E+05	1.0E+06
DEFA1;LOC728358	3.2E+06	4.2E+06	2.2E+06	1.0E+07	1.3E+05	2.0E+05
IGHG3	8.3E+07	7.6E+07	4.8E+07	1.5E+07	5.2E+07	1.6E+08
IGLV3-12	2.3E+05	5.0E+01	5.0E+01	5.0E+01	5.0E+01	2.6E+05
SCARB2	4.6E+05	2.0E+05	8.2E+05	1.1E+06	5.1E+05	1.2E+05
TPI1;RCTPI1	6.8E+05	3.3E+05	4.9E+05	1.6E+05	8.9E+05	6.6E+05

SUPPLEMENTARY DATA

OGDH	3.5E+05	7.1E+05	1.1E+06	1.4E+06	9.4E+05	1.4E+05
C4A	1.9E+07	4.4E+07	2.8E+07	3.4E+06	4.5E+07	5.9E+07
UGT1A1;UGT1A8	4.5E+05	5.5E+05	5.0E+05	6.6E+05	3.6E+05	7.5E+05
PIP	5.0E+01	2.8E+05	8.6E+05	1.2E+06	1.4E+05	5.0E+01
VDAC2	3.0E+05	8.7E+04	6.2E+05	6.1E+05	5.9E+05	5.0E+01
CBR3	1.9E+06	1.9E+06	1.5E+06	4.5E+06	1.2E+06	6.6E+05
MUC5AC	4.1E+07	6.1E+06	5.7E+07	1.0E+08	1.5E+07	7.3E+06
C1QB	1.8E+05	1.6E+05	2.3E+04	3.6E+02	5.0E+01	4.4E+05
UGT2A3	9.1E+05	2.0E+05	9.1E+04	8.1E+05	3.7E+05	2.9E+05
IPI00743194	1.9E+06	3.7E+05	4.1E+05	3.5E+05	6.2E+05	2.4E+06
MAOB	3.1E+05	6.0E+04	3.1E+05	1.9E+05	3.3E+05	3.3E+05
RBP4	4.5E+06	5.9E+06	2.6E+06	2.5E+05	6.1E+06	1.0E+07
CA1	1.1E+06	2.7E+06	4.2E+06	4.8E+05	5.3E+06	4.4E+06
PSMA6	4.6E+05	1.6E+05	1.6E+06	2.2E+05	1.8E+06	7.8E+05
ANO10	5.0E+01	1.1E+05	1.5E+05	1.4E+05	1.9E+05	5.0E+01
HLA-DRB3;HLA-DRB5;LOC649783;LOC100133484;LOC100133661;HLA-DRB4;LOC100133811;HLA-DRB1	5.0E+01	1.4E+05	8.9E+04	9.1E+04	2.1E+05	5.0E+01
IPI00384407	1.8E+06	4.5E+05	5.5E+05	2.3E+02	8.8E+05	2.7E+06
FKBP1A	1.3E+05	1.7E+05	3.0E+05	4.2E+04	2.2E+05	5.3E+05
ENPP7	1.9E+05	5.0E+01	5.0E+01	4.9E+04	1.7E+05	3.1E+04
ACADS	6.8E+05	3.5E+05	6.2E+05	4.9E+05	1.5E+06	1.8E+05
GKN2	5.0E+01	5.0E+01	1.8E+05	9.1E+04	1.5E+05	5.0E+01
GPI	2.0E+06	1.1E+06	1.1E+06	2.9E+06	1.7E+06	9.9E+05
DDT	6.1E+05	3.9E+05	1.1E+06	1.1E+06	7.6E+05	9.6E+05
IGHG1;IGHG2;IGHV4-31;IGH@	5.4E+05	6.8E+04	1.1E+05	3.1E+02	1.4E+05	8.4E+05
ESD	9.7E+04	5.0E+01	1.7E+05	6.9E+04	1.5E+05	1.6E+05
TKT	1.5E+06	7.3E+05	1.8E+06	1.8E+06	2.6E+06	1.5E+06
IGHG1;IGHG2;IGHV4-31;IGH@	1.1E+07	1.7E+07	7.9E+06	4.2E+06	1.7E+07	3.2E+07
IGLC1;IGLV1-44;IGLV1-40;IGLV3-21;IGLV2-11;IGLV2-14;IGL@;IGLC2;IGLC3	1.7E+05	5.0E+01	5.0E+01	5.0E+01	3.7E+04	2.1E+05
TGM3	3.8E+06	2.7E+05	1.3E+06	7.8E+06	1.4E+05	1.4E+05
KRT10	4.9E+06	4.0E+06	1.2E+06	1.0E+06	8.1E+06	6.4E+06
IPI00385252	1.1E+05	5.0E+01	5.0E+01	4.8E+02	5.0E+01	1.7E+05
NDUFAB1	5.5E+04	5.0E+01	1.5E+05	1.8E+05	1.6E+05	5.0E+01
IPI00829827	1.8E+06	2.0E+05	2.2E+05	5.1E+04	8.7E+05	2.6E+06
KRT5	2.4E+06	6.7E+05	1.5E+06	4.7E+06	1.5E+06	1.2E+06
ADH4	1.3E+06	1.0E+06	2.1E+06	1.7E+06	4.7E+06	8.9E+05
IGKV2-40	1.5E+06	4.6E+05	6.7E+05	8.3E+05	9.8E+05	2.5E+06

SUPPLEMENTARY DATA

HSD17B4	1.2E+06	4.0E+05	9.2E+05	2.3E+06	1.2E+06	6.3E+05
CAT	2.0E+06	1.2E+06	1.2E+06	1.3E+06	3.0E+06	3.1E+06
ADH1A	6.7E+06	4.7E+06	9.5E+06	4.1E+06	2.0E+07	1.0E+07
FGL1	8.8E+04	4.5E+05	1.1E+05	5.9E+04	6.3E+05	4.0E+05
CMBL	2.2E+06	1.5E+06	2.4E+06	4.3E+06	3.9E+06	2.0E+06
PSCA	1.1E+05	4.6E+03	1.4E+06	2.0E+06	4.1E+04	5.5E+05
CKMT2	2.0E+05	3.2E+05	1.1E+06	4.4E+05	2.1E+06	2.5E+05
IGHG1;IGHG2;IGHV4-31;IGH@	2.0E+05	1.8E+05	1.6E+05	1.9E+05	2.6E+05	4.9E+05
REG1A	9.7E+06	3.5E+06	1.0E+07	1.1E+07	2.1E+07	8.7E+06
AKR1C2	1.9E+06	3.3E+06	4.5E+06	1.3E+07	2.3E+06	2.0E+06
LOC652694	3.5E+06	1.5E+06	1.2E+06	1.0E+06	3.4E+06	6.4E+06
KRT16	1.1E+06	8.4E+04	4.8E+04	1.9E+06	1.9E+05	1.4E+05
LOC100133944	6.8E+05	8.5E+05	1.9E+06	3.9E+05	4.6E+06	1.1E+06
LOC652493	9.4E+04	5.0E+01	1.2E+05	1.8E+02	6.5E+04	3.2E+05
CTSD	1.2E+06	5.7E+05	1.3E+06	3.1E+06	1.8E+06	6.4E+05
FCGBP	3.4E+07	1.6E+07	2.4E+07	3.4E+07	6.6E+07	3.4E+07
HBA1;HBA2	2.8E+07	2.3E+07	4.5E+07	2.5E+06	5.6E+07	1.1E+08
GDI1	2.6E+05	1.7E+05	6.7E+05	2.6E+05	3.8E+05	1.4E+06
ADH1C	4.0E+05	8.0E+05	1.4E+06	2.6E+06	1.7E+06	4.1E+05
CD163L1	6.8E+05	5.0E+01	3.2E+03	6.7E+05	5.0E+05	8.0E+04
AKR1B10	5.8E+06	3.4E+06	8.2E+06	1.3E+07	1.3E+07	7.0E+06
LTA4H	4.4E+05	1.5E+05	5.0E+05	1.1E+06	5.3E+05	4.3E+05
GAPDH	7.9E+06	4.1E+06	1.1E+07	2.2E+07	1.3E+07	9.6E+06
CFHR1	1.8E+05	3.9E+05	7.0E+05	5.7E+04	6.9E+05	1.7E+06
IPI00914985	1.7E+05	5.0E+01	5.0E+01	5.0E+01	7.8E+04	2.6E+05
LCN2	2.6E+06	2.0E+05	4.1E+05	6.3E+06	2.1E+05	6.5E+04
PGRMC2	2.2E+05	5.0E+01	5.0E+01	2.9E+05	1.6E+05	5.0E+01
PGLS	5.6E+05	1.4E+05	7.8E+04	7.1E+05	6.4E+05	2.6E+05
SYCN	8.0E+05	1.5E+05	3.8E+03	1.5E+06	2.6E+05	1.8E+05
DNASE1	1.8E+06	2.5E+04	5.0E+01	2.2E+06	7.3E+05	9.0E+05
IPI00784773	2.4E+06	3.9E+05	4.1E+05	1.4E+05	2.5E+06	4.2E+06
ACADM	2.9E+05	1.0E+05	1.8E+05	4.8E+04	9.8E+05	2.3E+05
LGALS3	1.2E+06	7.9E+05	1.7E+06	4.7E+06	3.0E+06	5.5E+05
MSRA	1.1E+05	5.0E+01	5.0E+01	8.9E+04	1.0E+05	6.5E+04
IGHD	2.4E+05	7.4E+04	2.4E+05	5.0E+01	9.9E+05	2.9E+05
TFF2	3.3E+06	2.5E+05	8.7E+05	8.5E+06	1.0E+06	6.9E+05
HPR	3.3E+06	1.0E+06	6.9E+06	2.6E+06	1.2E+07	1.2E+07
NAPRT1	3.8E+05	9.1E+04	1.7E+05	1.0E+06	2.7E+05	3.3E+05
RNPEP	9.5E+05	4.1E+05	8.4E+05	4.2E+06	1.2E+06	4.9E+05
IPI00387024	2.4E+06	3.5E+05	1.2E+05	9.4E+04	3.5E+06	4.1E+06
GAPDHS	2.8E+05	5.0E+01	1.7E+05	7.8E+04	6.6E+05	5.0E+05
SERPINB6	1.6E+05	5.0E+01	1.1E+05	3.0E+05	3.1E+05	1.5E+05

SUPPLEMENTARY DATA

ZG16	2.3E+06	1.7E+05	8.7E+05	1.4E+06	5.0E+06	3.1E+06
VSIG1	5.0E+01	5.0E+01	8.0E+05	2.3E+06	9.1E+02	5.0E+01
TPI1;RCTPI1	3.0E+06	5.0E+06	1.6E+06	1.2E+07	1.2E+07	4.3E+06
NPM1	1.1E+05	2.6E+05	1.4E+05	4.8E+05	9.3E+05	6.7E+04
AKR1C1	5.7E+05	7.4E+04	4.0E+05	1.7E+06	6.9E+05	8.6E+05
IPI00387109	5.0E+01	5.0E+01	4.2E+04	5.0E+01	1.3E+05	5.0E+01
EPHX1	6.2E+05	4.6E+05	9.8E+05	5.5E+06	7.7E+05	2.6E+05
ANXA1	2.2E+05	2.8E+05	6.6E+05	3.6E+06	4.7E+04	1.4E+05
FN1	2.3E+05	5.0E+01	3.9E+02	1.3E+03	3.6E+04	6.9E+05
C1RL	1.5E+05	3.7E+05	3.9E+04	1.9E+05	9.8E+05	6.5E+05
KRT2	2.9E+06	1.2E+06	5.8E+05	1.4E+06	8.3E+06	5.8E+06
LGALS4	3.6E+06	9.8E+05	1.6E+06	1.2E+07	7.1E+06	3.0E+06
LOC100130811	5.3E+04	5.0E+01	5.0E+01	5.4E+02	5.0E+01	2.0E+05
C1QC	3.1E+05	1.8E+05	1.4E+05	6.4E+04	4.3E+05	1.9E+06
MUC5B	6.5E+06	2.3E+06	4.5E+06	4.9E+07	1.4E+06	7.3E+05
FTH1	1.3E+05	5.0E+01	5.0E+01	5.0E+01	3.1E+05	1.8E+05
KRT71	5.9E+05	5.0E+01	5.0E+01	5.0E+01	1.3E+06	1.0E+06
IPI00384395	8.1E+04	5.0E+01	5.0E+01	5.0E+01	1.8E+05	1.6E+05
REG1B	5.7E+04	4.7E+04	2.0E+05	3.5E+05	7.3E+05	2.4E+05
GP2	8.6E+05	2.2E+04	5.0E+01	1.9E+05	1.8E+06	1.9E+06
RBKS	5.0E+01	5.0E+01	6.7E+04	1.7E+05	6.5E+04	5.6E+04
CPA4	8.9E+05	1.2E+05	7.1E+04	2.1E+06	1.3E+06	1.5E+06
IGHV1OR15-1	2.8E+06	1.4E+06	3.1E+05	2.5E+04	9.1E+06	1.1E+07
SERPINB1	1.7E+06	9.7E+05	2.0E+06	1.8E+07	2.7E+06	2.8E+06
IPI00383629	7.7E+05	1.5E+05	5.0E+01	9.2E+04	1.5E+06	3.0E+06
PRSS3	1.9E+06	3.3E+05	1.2E+05	7.1E+06	1.7E+06	2.8E+06
KRT1	4.0E+06	2.8E+06	2.1E+06	7.1E+06	2.3E+07	1.5E+07
APCS	5.2E+05	3.5E+05	2.9E+05	1.2E+05	1.5E+06	4.3E+06
MUC1	1.4E+05	1.1E+02	4.7E+04	7.7E+05	1.7E+05	4.4E+04
IPI00829752	1.3E+05	5.0E+01	5.0E+01	5.0E+01	2.2E+05	4.4E+05
IPI00748265	7.8E+04	5.0E+01	4.7E+04	4.7E+02	1.1E+05	5.8E+05
TAGLN2	1.1E+06	1.1E+05	2.5E+05	6.9E+06	6.8E+05	9.7E+05
CUZD1	2.6E+06	4.7E+06	1.3E+06	1.6E+07	2.4E+07	9.6E+06
CLPS	2.9E+05	3.7E+05	2.2E+05	1.6E+06	6.1E+05	3.0E+06
PNLIPRP2	1.5E+07	5.9E+06	8.2E+05	4.3E+07	6.1E+07	3.6E+07
IL1RN	8.5E+04	1.2E+03	5.0E+01	4.6E+05	5.0E+01	9.2E+04
KRT6A	7.5E+04	1.3E+03	5.0E+01	4.9E+05	5.0E+01	5.0E+01
KLK1	9.5E+05	6.9E+05	6.8E+05	9.1E+06	5.8E+06	5.0E+05
IPI00382442	4.5E+05	5.0E+01	5.0E+01	1.6E+05	7.9E+05	2.2E+06
KRT9	2.5E+06	4.1E+05	1.5E+05	3.8E+06	8.5E+06	8.9E+06
HBE1	8.5E+05	3.6E+05	3.1E+05	2.2E+04	5.9E+06	5.1E+06
IGK@	6.8E+04	5.0E+01	5.0E+01	5.0E+01	1.2E+05	4.0E+05
CELA2B	9.5E+05	8.5E+05	5.6E+05	1.4E+07	7.6E+06	1.3E+06



SUPPLEMENTARY DATA

CST2	5.0E+01	1.1E+05	5.0E+01	1.1E+06	5.7E+03	5.0E+01
HEXA	6.7E+04	5.0E+01	5.0E+01	4.2E+05	1.8E+05	8.9E+04
IPI00827637	7.2E+04	5.0E+01	5.0E+01	5.0E+01	3.6E+05	4.4E+05
RNASE1	6.9E+05	1.3E+06	2.5E+06	2.9E+07	2.0E+07	2.9E+06
CPA2	7.9E+06	4.2E+06	3.8E+06	1.6E+08	2.4E+07	1.4E+07
PSMB1	1.6E+05	5.0E+01	5.0E+01	9.1E+05	7.7E+05	3.3E+05
S100A7	4.3E+04	1.4E+05	1.6E+05	4.8E+06	5.5E+04	1.1E+05
LY6D	5.0E+01	6.4E+04	5.0E+01	9.1E+05	4.0E+04	5.0E+01
CEL	1.4E+07	5.8E+06	3.6E+06	1.1E+08	2.1E+08	3.1E+07
CTRB1	1.0E+07	2.7E+06	1.5E+06	4.9E+07	1.4E+08	3.2E+07
CTRL	4.1E+05	4.2E+05	1.3E+05	6.7E+06	6.1E+06	1.9E+06
PRSS1	9.4E+06	4.2E+06	3.5E+06	1.5E+08	9.1E+07	3.3E+07
PSMA1	1.3E+05	5.0E+01	4.4E+04	1.5E+06	9.9E+05	4.6E+05
CTRL	2.0E+05	5.0E+01	5.0E+01	4.6E+05	2.3E+06	6.5E+05
CPA1	1.8E+07	4.5E+06	5.6E+06	2.9E+08	1.5E+08	4.3E+07
IPI00385254	7.4E+04	5.0E+01	5.0E+01	3.7E+04	8.4E+05	4.4E+05
KRT76	2.1E+05	5.0E+01	5.9E+04	1.1E+06	2.5E+06	1.2E+06
NME1	2.2E+05	5.0E+01	5.0E+01	2.6E+06	8.3E+05	5.8E+05
CELA3B	1.6E+06	2.4E+04	7.8E+05	3.1E+07	1.1E+07	4.4E+06
PNLIPRP1	3.1E+06	3.0E+05	4.7E+05	4.9E+07	2.2E+07	6.7E+06
FASN	1.5E+05	7.6E+04	5.5E+04	2.8E+04	1.7E+06	4.7E+06
CELA2A	2.3E+06	9.2E+05	3.9E+05	4.3E+07	3.3E+07	1.3E+07
IPI00219910	2.3E+05	8.1E+04	1.4E+05	5.1E+06	5.7E+06	6.1E+05
IPI00827829	6.4E+04	5.7E+04	3.2E+02	3.3E+06	5.0E+01	5.0E+01
PNLIP	2.8E+07	3.5E+06	7.6E+06	7.0E+08	2.7E+08	9.1E+07
PRSS2	2.6E+06	2.7E+05	6.5E+05	5.3E+07	3.6E+07	1.1E+07
CLC	5.0E+01	4.3E+04	5.0E+01	7.0E+05	3.7E+05	2.1E+05
CELA3A	4.4E+06	1.1E+06	2.2E+06	1.3E+08	7.7E+07	2.7E+07
CTRC	2.0E+06	1.2E+06	4.9E+05	4.4E+07	5.6E+07	1.2E+07
MPO	5.0E+01	7.1E+04	3.5E+04	3.4E+06	2.2E+05	5.0E+01
GP2	8.7E+04	2.3E+05	1.1E+05	1.0E+07	2.6E+06	2.2E+06
GP2	9.5E+05	8.4E+04	4.8E+05	1.4E+07	2.8E+07	1.4E+07
CPB1	4.0E+06	1.5E+06	9.4E+05	1.3E+08	8.8E+07	2.4E+07
AMY1C;AMY2A;AMY1A;AMY1B	2.1E+06	3.3E+05	5.1E+05	7.7E+07	3.3E+07	4.6E+06
AMY2B	1.0E+07	4.9E+06	3.9E+06	4.3E+08	3.2E+08	4.6E+07
SERPINI2	5.0E+01	6.7E+04	5.0E+01	3.6E+06	3.3E+06	2.9E+05
PLA2G1B	3.7E+05	4.9E+04	7.6E+04	4.0E+07	1.5E+07	3.8E+06
HMGCL	5.0E+01	5.0E+01	5.0E+01	5.0E+01	4.1E+04	5.0E+01
CD302;LY75	5.0E+01	2.7E+02	5.0E+01	1.1E+05	5.0E+01	5.0E+01
HPN	5.0E+01	8.8E+02	5.0E+01	3.4E+05	5.0E+01	5.0E+01
SCFV	5.0E+01	5.0E+01	5.0E+01	1.5E+02	5.0E+01	5.4E+04
IPI00884092	5.0E+01	5.0E+01	5.0E+01	5.0E+01	3.0E+04	3.5E+04

SUPPLEMENTARY DATA

AZU1	5.0E+01	2.3E+03	5.0E+01	1.4E+06	3.4E+05	5.0E+01
TPM3	5.0E+01	5.0E+01	5.0E+01	5.0E+01	3.5E+04	7.6E+04
LOC100132635	5.0E+01	4.2E+03	5.0E+01	3.1E+06	6.2E+04	5.0E+01
ERO1L	5.0E+01	5.0E+01	5.0E+01	9.8E+04	6.0E+04	5.0E+01
IPI00827580	5.0E+01	5.0E+01	5.0E+01	5.0E+01	4.5E+04	1.2E+05
TTN	5.0E+01	5.0E+01	5.0E+01	4.4E+04	4.1E+04	8.1E+04
PGAM4;LOC728188	5.0E+01	5.0E+01	5.0E+01	1.3E+05	6.4E+04	5.0E+01
IPI00398220	5.0E+01	5.0E+01	5.0E+01	5.2E+02	5.0E+01	1.9E+05
BPI	5.0E+01	1.4E+03	5.0E+01	2.9E+06	5.0E+01	5.0E+01
CTRB2	5.0E+01	5.0E+01	5.0E+01	2.7E+05	1.2E+05	5.0E+01
C1QA	5.0E+01	5.0E+01	5.0E+01	3.8E+05	8.5E+04	5.0E+01
GLO1	5.0E+01	9.9E+01	5.0E+01	4.5E+05	2.2E+05	5.0E+01
AMY1C;AMY2A;AMY1A;AMY1B	5.0E+01	9.4E+02	5.0E+01	2.7E+06	1.3E+06	5.0E+01
GALM	5.0E+01	5.0E+01	5.0E+01	3.0E+05	2.9E+05	5.0E+01
GC	5.0E+01	5.0E+01	5.0E+01	5.0E+01	6.7E+05	5.0E+01
CNP	5.0E+01	5.0E+01	5.0E+01	7.9E+05	5.8E+04	5.0E+01
LCN1	5.0E+01	1.2E+02	5.0E+01	1.4E+06	5.0E+01	5.0E+01
MBL2	5.0E+01	5.0E+01	5.0E+01	1.1E+06	2.6E+04	5.0E+01
CDH1	5.0E+01	5.0E+01	5.0E+01	7.4E+05	4.2E+05	4.2E+04
IGLC1;IGLV1-44;IGLV1-40;IGLV3-21;IGLV2-11;IGLV2-14;IGL@;IGLC2;IGLC3	5.0E+01	5.0E+01	5.0E+01	5.0E+01	9.6E+05	6.5E+05
PRSS1	5.0E+01	5.0E+01	5.0E+01	2.9E+06	3.0E+05	4.2E+05
GFPT1	5.0E+01	5.0E+01	5.0E+01	4.6E+06	7.8E+05	1.0E+05

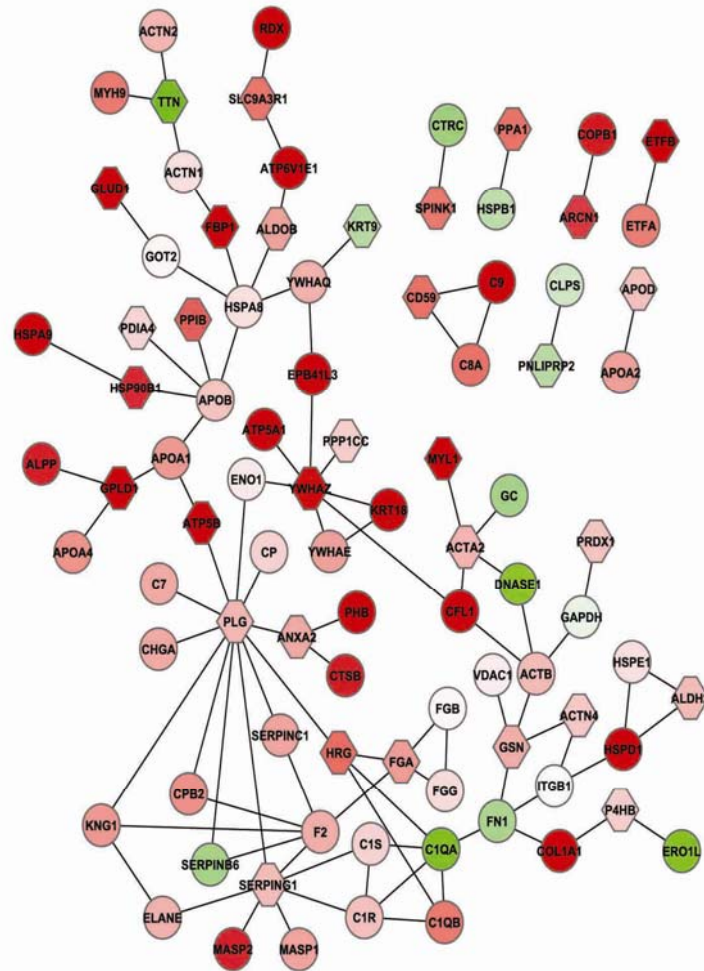
SUPPLEMENTARY DATA

**Supplementary Table 3.** PubMed IDs documenting the literature support of pathways involved in the MAPK-targeted proteins based on the output from the Biobase Explain tool.

Map	PMID
A1	15542607
A2	11274345
A3	11606045
A4	12205041
B1	10791986
B2	16611744
B3	16122376
B4	10880430
B5	11950845
B6	16614236
B7	11368003
C1	17915332
C2	10339425
C3	12049736
C4	9164868
C5	11389839
C6	11505407
C7	Gerhard Michal: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology
D1	15071501
D2	15716280
D3	9054461
D4	7925482
D5	Gerhard Michal: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology
E1	12235123

## SUPPLEMENTARY DATA

**Supplementary Figure 1.** Protein-protein interaction modeling of upregulated pancreatic juice proteins in CEL mutation carriers. Using Cytoscape, the figure shows major protein-protein interactions among the proteins identified in pancreatic juice based on Gene Network Enrichment Analysis. Note the direct interaction between *YWHAZ* and *KRT18*, two proteins that were identified in the pancreatic juice protein analyses. More generally, the immediate set of protein-protein interactors to the *YWHAZ*-encoded protein, comprising the proteins encoded by *YWHAE*, *ATP5A1*, *EPB41L3*, *PPP1CC*, *ENO1*, and *KRT18* was together highly significant (Fisher's p-value = 0.00028).



### References

1. Ræder H, Johansson S, Holm PI, Haldorsen IS, Mas E, Sbarra V, Nerموen I, Eide SA, Grevle L, Bjørkhaug L, Sagen JV, Aksnes L, Søvik O, Lombardo D, Molven A, Njølstad PR: Mutations in the CEL VNTR cause a syndrome of diabetes and pancreatic exocrine dysfunction. *Nat Genet* 2006;38:54-62
2. Villen J, Gygi SP: The SCX/IMAC enrichment approach for global phosphorylation analysis by mass spectrometry. *Nature protocols* 2008;3:1630-1638
3. Ting L, Rad R, Gygi SP, Haas W: MS3 eliminates ratio distortion in isobaric multiplexed quantitative proteomics. *Nature methods* 2011;
4. Huttlin EL, Jedrychowski MP, Elias JE, Goswami T, Rad R, Beausoleil SA, Villen J, Haas W, Sowa ME, Gygi SP: A tissue-specific atlas of mouse protein phosphorylation and expression. *Cell* 2010;143:1174-1189
5. Eng JK, McCormack AL, Yates JR, 3rd: An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database. *J Am Soc Mass Spectrom*. 1994;5:976-989
6. Elias JE, Gygi SP: Target-decoy search strategy for increased confidence in large-scale protein identifications by mass spectrometry. *Nature methods* 2007;4:207-214
7. Kubota K, Anjum R, Yu Y, Kunz RC, Andersen JN, Kraus M, Keilhack H, Nagashima K, Krauss S, Paweletz C, Hendrickson RC, Feldman AS, Wu CL, Rush J, Villen J, Gygi SP: Sensitive multiplexed analysis of kinase activities and activity-based kinase identification. *Nat Biotechnol* 2009;27:933-940