SUPPLEMENTARY DATA

Supplementary Table 1. Characteristics of the Patients at Baseline in ACCORD-Lipid.

Characteristics	Whites (N=3065)		African-Americans (N=585)	
	Statin (N=1496)	Statin + Fenofibrate (N=1569)	Statin (N=306)	Statin + Fenofibrate (N=279)
Female sex – no. (%)	441 (29.5%)	449 (28.6%)	119 (38.9%)	116 (41.6%)
Age – yr	62.7 ± 6.5	62.9 ± 6.5	62.0 ± 6.8	61.6 ± 6.4
BMI – kg/m^2	33.3 ± 5.2	32.9 ± 5.0	32.4 ± 5.1	32.6 ± 5.0
Waist circumference – cm	110.4 ± 12.8	109.8 ± 12.5	105.6 ± 13.0	105.8 ± 12.5
Systolic BP – mmHg	132.7 ± 17.1	133.2 ± 17.0	136.7 ± 18.1	135.7 ± 18.0
Diastolic BP – mmHg	73.1 ± 10.3	73.4 ± 10.1	75.9 ± 11.0	75.5 ± 10.6
Baseline CVD – no. (%)	547 (36.6%)	584 (37.2%)	100 (32.7%)	93 (33.3%)
Years of Diabetes	10.6 ± 7.4	10.6 ± 7.3	11.4 ± 7.6	10.5 ± 7.4
Glycated hemoglobin – %	8.2 ± 0.9	8.2 ± 0.9	8.5 ± 1.1	8.5 ± 1.1
Triglycerides – mg/dl	198.0 ± 106.9	198.8 ± 105.7	131.5 ± 75.8	140.1 ± 85.4
Total cholesterol – mg/dl	177.0 ± 37.4	174.9 ± 36.4	170.6 ± 32.6	171.6 ± 36.1
HDL-cholesterol – mg/dl	37.5 ± 7.5	37.4 ± 7.4	41.2 ± 8.2	40.4 ± 8.2
LDL-cholesterol – mg/dl	100.6 ± 30.6	98.8 ± 29.8	103.5 ± 27.6	104.0 ± 30.6
Atherogenic dyslipidemia – no. (%)	298 (19.9%)	316 (20.1%)	14 (4.6%)	26 (9.3%)
Serum Creatinine – mg/dl	0.92 ± 0.21	0.92 ± 0.22	0.98 ± 0.22	1.01 ± 0.24

Values are means ± SD or N (%). Atherogenic dyslipidemia is defined by cut off previously used of HDL-c ≤ 34 mg/dL and triglycerides ≥ 204 mg/dL. There were no differences between the groups except for the BMI in Whites (P=0.04). To convert cholesterol values to millimoles per liter, multiply by 0.02586. To convert the values for triglycerides to millimoles per liter, multiply by 0.01129.

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Supplementary Table 2. Top SNPs (with Meta-Analysis P < $1x10^{-2}$) modulating fenofibrate effectiveness in self-reported Whites and African-Americans from ACCORD-Lipid and in a meta-analysis of the two racial groups.

SNP	Hg19 bp position	Allele 1	Allele 2	Whites			African-American			Meta-Analysis			Conditional analysis P value
				P Value	Effect ± S.E.	Allele1 Freq	P Value	Effect ± S.E.	Allele1 Freq	**P value**	**Effect ± S.E.**	**Heterog. P value**	
rs6008845	46525357	c	t	3.7E-04	0.59±0.17	0.40	2.4E-02	1.39±0.62	0.79	**5.6E-05**	0.65±0.16	0.46	ref
rs135557	46541227	g	a	9.3E-04	0.54±0.16	0.44	6.8E-03	1.43±0.53	0.72	**7.3E-05**	0.62±0.16	0.13	3.0E-01
rs135570	46532781	g	a	9.0E-04	0.54±0.16	0.46	5.3E-03	2.16±0.77	0.83	**1.3E-04**	0.61±0.16	0.22	5.4E-01
rs6007904	46521999	g	a	6.4E-04	0.56±0.16	0.42	1.9E-01	0.71±0.54	0.73	**2.6E-04**	0.57±0.16	0.80	9.4E-01
rs2105914	46527955	g	a	1.9E-03	0.50±0.16	0.48	2.7E-02	1.74±0.79	0.83	**5.0E-04**	0.55±0.16	0.48	6.8E-01
rs135577	46526617	a	g	2.2E-03	0.56±0.18	0.28	1.1E-01	0.70±0.44	0.57	**5.8E-04**	0.58±0.17	0.44	6.4E-01
rs11090910	46507670	c	t	8.1E-03	0.49±0.18	0.27	3.5E-02	0.89±0.42	0.41	1.1E-03	0.55±0.17	0.84	**4.2E-02**
rs135562	46539636	t	c	1.0E-02	0.47±0.18	0.29	2.3E-02	0.93±0.41	0.60	1.1E-03	0.54±0.17	0.62	5.2E-01
rs135556	46543485	c	t	6.8E-03	0.49±0.18	0.28	5.1E-02	0.83±0.42	0.51	1.1E-03	0.55±0.17	0.50	3.7E-01
rs135550	46553234	c	t	1.2E-02	0.46±0.18	0.28	2.6E-02	0.88±0.40	0.56	1.3E-03	0.53±0.17	0.34	4.6E-01
rs135542	46556037	c	t	5.8E-03	0.51±0.18	0.28	1.1E-01	0.72±0.46	0.28	1.6E-03	0.54±0.17	0.44	3.4E-01
rs135551	46553021	a	g	1.5E-02	0.45±0.18	0.28	2.8E-02	0.87±0.40	0.53	1.7E-03	0.52±0.17	0.34	4.6E-01
rs4823551	46525916	g	a	8.7E-03	0.44±0.17	0.38	6.2E-02	0.90±0.48	0.75	2.0E-03	0.49±0.16	0.74	3.7E-01
rs9615904	46664741	c	t	1.2E-02	0.46±0.18	0.29	2.9E-02	1.15±0.52	0.81	2.1E-03	0.53±0.17	0.61	**1.3E-02**
rs6007919	46525794	c	t	9.5E-03	0.43±0.17	0.38	6.3E-02	0.90±0.48	0.75	2.2E-03	0.48±0.16	0.75	3.4E-01

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rs4508712	46652959	g	a	1.6E-02	0.43±0.18	0.29	2.1E-02	1.18±0.51	0.81	2.4E-03	0.51±0.17	0.56	**1.2E-02**
rs135553	46552743	c	t	1.9E-02	0.38±0.16	0.43	5.9E-03	1.48±0.54	0.75	2.4E-03	0.47±0.16	0.09	6.9E-01
rs5767213	46526528	a	g	1.8E-02	0.40±0.17	0.36	1.9E-02	1.12±0.48	0.68	2.5E-03	0.48±0.16	0.28	2.2E-01
rs4823547	46523710	g	a	9.8E-03	0.43±0.17	0.38	8.7E-02	0.78±0.45	0.69	2.6E-03	0.47±0.16	0.53	5.7E-01
rs135549	46553308	c	t	1.3E-02	0.40±0.16	0.43	5.5E-02	0.85±0.44	0.63	2.8E-03	0.46±0.15	0.13	8.2E-01
rs2024929	46515210	c	t	3.4E-02	0.45±0.21	0.15	6.5E-03	1.49±0.55	0.74	3.0E-03	0.59±0.20	0.12	4.5E-01
rs9615264	46632589	a	g	2.6E-03	0.95±0.32	0.09	9.6E-01	0.08±1.59	0.02	3.1E-03	0.91±0.31	0.51	**2.3E-03**
rs135563	46536017	c	t	1.7E-02	0.39±0.16	0.48	3.8E-03	2.21±0.76	0.83	3.4E-03	0.47±0.16	0.12	5.3E-01
rs135560	46539655	c	t	2.2E-02	0.41±0.18	0.30	3.6E-02	0.85±0.41	0.60	3.4E-03	0.48±0.16	0.52	7.0E-01
rs9306519	46516140	g	a	1.2E-03	0.54±0.17	0.39	7.7E-01	-0.12±0.42	0.51	3.6E-03	0.45±0.15	0.16	4.5E-01
rs135561	46539639	a	g	2.2E-02	0.41±0.18	0.30	4.4E-02	0.82±0.41	0.60	3.7E-03	0.47±0.16	0.48	7.2E-01
rs135552	46552815	c	t	7.1E-03	0.50±0.18	0.28	2.9E-01	0.49±0.47	0.31	3.9E-03	0.50±0.17	0.99	6.3E-01
rs135539	46559267	c	a	1.3E-02	0.41±0.16	0.44	1.3E-01	0.65±0.43	0.67	4.0E-03	0.44±0.15	0.32	8.5E-01
rs135569	46534187	a	t	1.5E-02	0.39±0.16	0.48	2.9E-02	1.49±0.68	0.80	4.1E-03	0.45±0.16	0.15	4.9E-01
rs5768769	46521225	c	t	1.6E-02	0.40±0.17	0.38	8.1E-02	0.84±0.48	0.75	4.5E-03	0.45±0.16	0.78	3.4E-01
rs135538	46564628	g	c	4.4E-02	0.32±0.16	0.42	9.2E-04	1.88±0.57	0.77	4.5E-03	0.44±0.15	0.04	9.1E-01
rs135567	46534634	g	a	2.4E-02	0.41±0.18	0.30	5.7E-02	0.83±0.44	0.63	4.8E-03	0.47±0.17	0.07	8.9E-01
rs135568	46534601	a	c	2.0E-02	0.42±0.18	0.30	1.1E-01	0.65±0.41	0.58	5.8E-03	0.46±0.17	0.12	8.6E-01
rs58863484	46542393	g	a	9.5E-02	0.39±0.24	0.14	1.1E-02	1.11±0.44	0.34	7.5E-03	0.55±0.21	0.27	3.1E-01
rs135548	46553503	g	a	6.4E-03	0.50±0.18	0.28	7.7E-01	0.15±0.53	0.20	7.6E-	0.46±0.17	0.63	7.0E-01

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										03			
rs16994874	46515716	c	t	2.8E-02	0.48±0.22	0.16	1.2E-01	0.78±0.50	0.22	8.3E-03	0.53±0.20	0.21	2.2E-01
rs135547	46553650	g	c	5.0E-02	0.35±0.18	0.31	4.6E-02	0.83±0.42	0.58	9.7E-03	0.42±0.16	0.56	8.9E-01
rs135554	46552719	t	a	8.1E-03	0.49±0.18	0.28	7.7E-01	0.14±0.50	0.25	9.8E-03	0.45±0.17	0.67	8.0E-01

Note: The conditional analysis P value is the P value for the SNP by fenofibrate interaction in the entire study population (Whites+African-Americans) after adding the "rs6008845 by fenofibrate" and rs6008845 variables to the model.

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Supplementary Table 3. Characteristics at baseline of self-reported white participants in ACCORD Blood Pressure, ORIGIN and TRIUMPH cohorts on concomitant treatment with statin alone or statin + fibrate.

Characteristics	ACCORD Blood Pressure			ORIGIN			Triumph		
	Statin (N=1320)	Statin + Fibrate (N=87)	P	Statin (N=1162)	Statin + Fibrate (N=82)	P	Statin (N=387)	Statin + Fibrate (N=21)	P
Female sex	546 (41.4%)	15 (17.2%)	<0.001	339 (29.2%)	17 (20.7%)	0.1	132 (34.1%)	6 (28.6%)	0.6
Age – yr	63.2 ± 6.5	61.5 ± 6.6	0.02	63.0 ± 7.7	60.3 ± 7.2	0.002	61.9 ± 11.1	64.1 ± 8.9	0.4
BMI – kg/m^2	32.7 ± 5.2	33.5 ± 4.8	0.2	30.7 ± 5.1	31.2 ± 4.1	0.4	32.4 ± 7.6	34.1 ± 7.5	0.3
Systolic BP – mmHg	137.1 ± 15.0	136.8 ± 13.6	0.9	143.9 ± 21.3	139.0 ± 21.2	0.05	120.5 ± 20.3	126.9 ± 17.1	0.2
Diastolic BP – mmHg	74.5 ± 10.0	73.6 ± 10.2	0.4	83.3 ± 11.8	80.2 ± 13.3	0.02	67.1 ± 11.2	67.8 ± 10.5	0.8
Baseline CVD	504 (38.2%)	53 (60.9%)	<0.001	831 (71.5%)	63 (76.8%)	0.4	100	100	---
Years of Diabetes	11.0 ± 7.6	10.9 ± 7.5	0.9	4.2 ± 4.9	4.5 ± 4.1	0.1	N/A	N/A	---
Glycated hemoglobin (%)	8.2 ± 0.9	8.1 ± 1.0	0.7	6.4 ± 0.9	6.6 ± 1.0	0.6	8.4 ± 3.4	6.8 ± 1.3	0.003
Triglycerides – mg/dl	197 ± 125	277 ± 166	<0.001	163.6 ± 97.7	217.2 ± 139.4	<0.001	187 ± 150	287 ± 283	0.1
Total cholesterol – mg/dl	182.3 ± 37.5	187.6 ± 40.1	0.2	183.0 ± 47.8	189.6 ± 53.9	0.2	170.2 ± 51.6	155.5 ± 47.5	0.2
HDL-cholesterol – mg/dl	44.4 ± 11.7	35.3 ± 8.6	<0.001	45.9 ± 12.3	40.9 ± 9.8	<0.001	37.7 ± 10.5	36.2 ± 11.6	0.5
LDL-cholesterol – mg/dl	99.6 ± 29.8	99.4 ± 33.3	0.9	105.0 ± 41.6	109.8 ± 41.9	0.3	96.8 ± 42.0	75.0 ± 35.2	0.04
Atherogenic dyslipidemia	176 (13.3%)	35 (40.2%)	<0.001	50 (4.3%)	8 (9.9%)	0.04	57 (14.7%)	5 (23.8 %)	0.3
Serum Creatinine – mg/dl	0.90 ± 0.22	1.00 ± 0.24	<0.001	1.00 ± 0.24	1.07 ± 0.29	0.009	1.26 ± 0.91	1.35 ± 0.58	0.5

Values are means ± SD or N (%). Atherogenic dyslipidemia was defined as HDL-c ≤ 34 mg/dL and triglycerides ≥ 204 mg/dL. To convert cholesterol values to millimoles per liter, multiply by 0.02586; to convert triglyceride values to millimoles per liter, multiply by 0.01129.
In ORIGIN, concomitant medications were evaluated at baseline. In ACCORD BP, and TRIUMPH, concomitant medications were evaluated at baseline and every 12 months (subjects were considered to be on a medication if they were reported to be on that medication at baseline and at least once during follow-up, prior to the event or censoring; subjects with follow-up shorter than 1 year were considered to be on a medication only on the basis of the baseline information).

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Supplementary Table 4. Effectiveness of fenofibrate on MACE risk reduction according to presence or absence of ahterogenic dyslipidemia (defined by previously defined cut-off (16)) and rs6008845 genotypes.

Group	rs6008845 Genotype	N/Events	HR for fibrate on MACE (95% C.I.)	rs6008845 by fenofibrate Interaction
Female: HDL<50.3 mg/dl and TG >203.7 mg/dl or Male: HDL<38.7 mg/dl and TG >203.7 mg/dl	ALL	1021/117	0.62 (0.43-0.90)	
	TT	381/47	0.42 (0.22-0.78)	P=0.238
	TC	486/53	0.78 (0.45-1.34)	
	CC	154/17	0.54 (0.19-1.47)	
All others	ALL	2029/205	0.95 (0.72-1.25)	
	TT	715/66	0.52 (0.31-0.86)	P=0.004
	TC	994/105	1.10 (0.65-1.62)	
	CC	320/34	1.68 (0.80-3.53)	

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Supplementary Table 5. Characteristics at baseline of self-reported white participants included or not in the MIND-biomarker study.

	Not included in MIND biomarker study (N=2932)	Included in MIND biomarker study (N=133)	P
Female sex – no. (%)	844 (28.8%)	46 (34.6%)	0.15
Age – yr	62.7 ± 6.5	64.0 ± 6.4	0.03
BMI – kg/m^2	33.1 ± 5.2	33.0 ± 4.5	0.96
Waist circumference – cm	110.2 ± 12.7	109.1 ± 10.9	0.27
Systolic BP – mmHg	133.1 ± 17.1	128.1 ± 16.6	0.001
Diastolic BP – mmHg	73.3 ± 10.3	71.5 ± 9.4	0.06
Baseline CVD – no. (%)	1100 (37.5%)	31 (23.3%)	0.001
Years of Diabetes	10.7 ± 7.4	9.3 ± 6.5	0.05
Glycated hemoglobin – %	8.2 ± 0.9	8.0 ± 0.9	0.02
Triglycerides – mg/dl	198.2 ± 106.2	203.8 ± 107.5	0.55
Total cholesterol – mg/dl	176.1 ± 36.9	171.1 ± 35.9	0.12
HDL-cholesterol – mg/dl	37.4 ± 7.4	38.6 ± 8.1	0.07
LDL-cholesterol – mg/dl	100.0 ± 30.2	93.0 ± 29.9	0.01
Atherogenic dyslipidemia – no. (%)	586 (20.1%)	25 (18.8%)	0.72
Serum Creatinine – mg/dl	0.92 ± 0.22	0.91 ± 0.19	0.44

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Supplementary Table 6. For each **chemokine**, we report the mean ± standard deviation values at baseline and follow-up (log transformed), and the estimated treatment difference (ETD) for fenofibrate use with its standard error (SE), along with the respective p-values. The last column reports the estimate and P value of fenofibrate by rs6008845 interaction, testing whether the fenofibrate effect on chemokine changes across rs6008845 genotypes.

Chemokines	**Placebo (N=64)**		**Fenofibrate (N=69)**			**Fenofibrate effect (SE)**	**P**		**Fenofibrate by rs6008845 interaction**	**P**
	Baseline	**Follow-up**	**Baseline**	**Follow-up**						
CCL2	6.25 ± 0.55	6.23 ± 0.50	6.12 ± 0.65	6.10 ± 0.57		-0.02 (0.05)	0.60		0.03 (0.07)	0.667
CCL3	3.66 ± 1.24	3.77 ± 1.42	4.06 ± 1.12	4.07 ± 1.07		-0.08 (0.13)	0.53		0.19 (0.21)	0.363
CCL4	4.28 ± 0.95	4.30 ± 0.87	4.58 ± 0.98	4.52 ± 0.77		-0.01 (0.09)	0.92		-0.14 (0.14)	0.300
CCL11	**4.72 ± 0.56**	**4.76 ± 0.53**	**4.66 ± 0.58**	**4.71 ± 0.58**		**-0.01 (0.05)**	**0.85**		**0.22 (0.07)**	**0.003**
CXCL8	3.12 ± 0.97	3.20 ± 1.01	3.47 ± 1.10	3.47 ± 1.12		-0.06 (0.12)	0.64		0.30 (0.18)	0.110
CXCL10	4.87 ± 0.56	4.85 ± 0.56	4.84 ± 0.68	4.81 ± 0.68		0.01 (0.07)	0.93		-0.01 (0.10)	0.927
CXC3CR1	4.04 ± 1.92	3.91 ± 1.91	3.85 ± 1.62	3.92 ± 1.73		0.10 (0.18)	0.60		-0.20 (0.29)	0.485

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Supplementary Table 7. For CCL11, we report the mean ± standard deviation log transformed values at baseline and follow-up, and the estimated treatment difference (ETD) for fenofibrate use with its standard error (SE), along with the respective p-values.

	rs6008845 Genotype	**Placebo (N=64)**		**Fenofibrate (N=69)**		**Fenofibrate effect (SE)**	**P**	**Fenofibrate by rs6008845 interaction**	**P**
		Baseline	**Follow-up**	**Baseline**	**Follow-up**				
CCL11	TT (n=39)	4.65 ± 0.33	4.85 ± 0.41	4.63 ± 0.54	4.63 ± 0.59	-0.20 (0.07)	0.01	0.22 (0.07)	0.003
	TC (n=73)	4.67 ± 0.45	4.71 ± 0.45	4.61 ± 0.62	4.69 ± 0.59	0.00 (0.06)	0.99		
	CC (n=21)	4.92 ± 0.92	4.77 ± 0.80	5.01 ± 0.40	5.07 ± 0.40	0.34 (0.19)	0.10		
CCL3	TT (n=39)	3.28 ± 0.97	3.43 ± 1.07	3.96 ± 1.01	3.87 ± 1.09	-0.22 (0.19)	0.27	0.19 (0.21)	0.363
	TC (n=73)	3.54 ± 1.16	3.69 ± 1.37	4.12 ± 1.23	4.12 ± 1.10	-0.17 (0.14)	0.24		
	CC (n=21)	4.39 ± 1.46	4.36 ± 1.78	4.04 ± 0.94	4.40 ± 0.75	0.70 (0.52)	0.21		
CXCL8	TT (n=39)	2.88 ± 0.65	3.03 ± 0.69	3.39 ± 0.92	3.31 ± 0.93	-0.23 (0.26)	0.38	0.30 (0.18)	0.110
	TC (n=73)	2.99 ± 0.95	3.20 ± 1.06	3.50 ± 1.25	3.53 ± 1.27	-0.13 (0.18)	0.47		
	CC (n=21)	3.71 ± 1.14	3.42 ± 1.20	3.53 ± 0.85	3.72 ± 0.75	0.76 (0.41)	0.09		

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Supplementary Table 8. Association between rs6008845 (effect of the T allele) and PPAR-alpha target gene in Skin (Sun exposed and not sun exposed), Skeletal Muscle, Whole blood, Esophagus Mucosae, Vagina and Liver from GtEx. Meta Analysis across tissue done with RE2 random-effect models. Highlighted genes are those with meta-analysis P value surviving a False Discovery Rate of 5%.

genes	Skin* N=498 β (P value)	Muscle N=361 β (P value)	Blood N=338 β (P value)	Esophagus N=241 β (P value)	Vagina N=79 β (P value)	Liver N=97 β (P value)	Meta-Analysis N=1614 (P value)	Heterogeneity I^2 (pval)
PPARA	**-0.46 (1E-29)**	**-0.09 (2E-02)**	**-0.16 (9E-03)**	**-0.17 (4E-04)**	**-0.24 (3E-03)**	-0.23 (7E-02)		
SLC25A20	**-0.21 (1E-03)**	**-0.12 (2E-02)**	-0.04 (5E-01)	**-0.19 (2E-02)**	0.20 (1E-01)	-0.08 (5E-01)	**4.5E-05**	0.59 (2E-02)
HSD17B4	**-0.13 (6E-04)**	-0.05 (3E-01)	**-0.10 (1E-02)**	-0.06 (2E-01)	-0.04 (8E-01)	-0.03 (7E-01)	**4.6E-05**	0.00 (7E-01)
ETFDH	**-0.22 (9E-08)**	-0.05 (2E-01)	0.03 (5E-01)	-0.01 (8E-01)	0.11 (3E-01)	-0.09 (3E-01)	**5.2E-05**	0.73 (1E-03)
HMGCS2	**-0.25 (1E-03)**	-0.03 (7E-01)	-0.07 (3E-01)	-0.06 (4E-01)	-0.05 (8E-01)	0.02 (8E-01)	**5.3E-04**	0.53 (5E-02)
ACADVL	**-0.13 (5E-04)**	-0.03 (5E-01)	-0.07 (1E-01)	-0.04 (5E-01)	-0.11 (4E-01)	-0.02 (8E-01)	**6.5E-04**	0.00 (7E-01)
FABP3	-0.04 (5E-01)	**-0.16 (6E-04)**	0.01 (9E-01)	-0.03 (7E-01)	-0.02 (8E-01)	**-0.41 (9E-04)**	**7.6E-04**	0.63 (1E-02)
PRKCA	**0.10 (4E-02)**	0.03 (6E-01)	0.09 (8E-02)	0.08 (3E-01)	0.05 (3E-01)	0.10 (5E-01)	**8.0E-04**	0.00 (8E-01)
MLYCD	-0.04 (2E-01)	**-0.15 (1E-02)**	-0.06 (1E-01)	-0.07 (3E-01)	0.11 (3E-01)	**-0.28 (2E-02)**	**2.7E-03**	0.37 (1E-01)
ACAA2	-0.07 (7E-02)	**-0.11 (2E-02)**	0.05 (4E-01)	**-0.18 (1E-02)**	0.11 (4E-01)	-0.14 (2E-01)	**4.9E-03**	0.43 (1E-01)
ACADS	**-0.11 (1E-02)**	-0.04 (3E-01)	-0.01 (8E-01)	-0.01 (8E-01)	0.14 (2E-01)	-0.02 (9E-01)	**5.9E-03**	0.47 (8E-02)
HADHA	**-0.11 (3E-03)**	**-0.10 (3E-02)**	0.01 (8E-01)	-0.06 (3E-01)	0.15 (2E-01)	-0.07 (5E-01)	**7.0E-03**	0.38 (1E-01)
CPT2	**-0.09 (2E-02)**	-0.05 (1E-01)	-0.02 (5E-01)	-0.05 (4E-01)	-0.01 (9E-01)	-0.13 (1E-01)	**7.0E-03**	0.00 (8E-01)
GALNT2	0.03 (7E-01)	0.06 (2E-01)	**-0.06 (1E-02)**	0.01 (9E-01)	0.04 (6E-01)	0.08 (2E-01)	**1.0E-02**	0.69 (3E-03)
CYP4A11	-0.05 (5E-01)	0.05 (5E-01)	-0.10 (7E-02)	N/A	**-0.32 (2E-02)**	-0.16 (7E-02)	**1.7E-02**	0.42 (1E-01)
CYP4X1	**-0.08 (5E-02)**	0.01 (9E-01)	-0.04 (5E-01)	-0.08 (2E-01)	-0.21 (1E-01)	-0.11 (3E-01)	**1.8E-02**	0.00 (7E-01)
ACAA1	-0.02 (7E-01)	**-0.08 (2E-02)**	-0.01 (8E-01)	**-0.11 (2E-02)**	0.06 (4E-01)	-0.02 (8E-01)	**2.3E-02**	0.20 (3E-01)
F3	0.02 (8E-01)	0.06 (3E-01)	**0.13 (4E-02)**	0.02 (7E-01)	**0.21 (4E-02)**	0.07 (4E-01)	**2.4E-02**	0.23 (3E-01)
ECH1	**-0.13 (2E-03)**	-0.03 (5E-01)	-0.01 (8E-01)	-0.07 (3E-01)	0.14 (3E-01)	-0.12 (3E-01)	**3.3E-02**	0.30 (2E-01)
ACSL5	-0.08 (3E-01)	-0.10 (8E-02)	-0.04 (4E-01)	0.00 (1E+00)	0.08 (5E-01)	0.06 (6E-01)	**4.3E-02**	0.33 (2E-01)
CETP	**0.17 (1E-02)**	0.08 (3E-01)	0.04 (4E-01)	-0.03 (7E-01)	-0.24 (7E-02)	0.17 (5E-02)	**4.5E-02**	0.45 (9E-02)
LIPC	-0.14 (5E-02)	N/A	-0.02 (8E-01)	0.00 (1E+00)	-0.02 (9E-01)	0.02 (9E-01)	**4.6E-02**	0.11 (3E-01)
ANGPTL4	0.06 (2E-01)	-0.04 (5E-01)	0.07 (1E-01)	0.07 (2E-01)	0.14 (2E-01)	0.04 (7E-01)	**4.6E-02**	0.00 (7E-01)
CPT1A	**-0.10 (4E-02)**	-0.08 (2E-01)	-0.02 (8E-01)	-0.09 (3E-01)	0.10 (4E-01)	-0.04 (8E-01)	**4.6E-02**	0.00 (8E-01)
SCARB1	**-0.10 (3E-02)**	0.09 (9E-02)	**-0.12 (2E-02)**	-0.02 (8E-01)	0.07 (5E-01)	**0.26 (3E-02)**	**4.7E-02**	0.66 (7E-03)
ETFA	-0.05 (3E-01)	-0.05 (2E-01)	-0.05 (2E-01)	0.01 (9E-01)	0.03 (7E-01)	-0.10 (2E-01)	6.5E-02	0.00 (8E-01)

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SLC16A1	0.06 (2E-01)	0.01 (7E-01)	0.07 (1E-01)	0.03 (4E-01)	-0.07 (5E-01)	0.00 (1E+00)	7.1E-02	0.00 (7E-01)
HNF4A	N/A	N/A	-0.04 (6E-01)	N/A	N/A	**-0.27 (2E-02)**	9.1E-02	0.70 (7E-02)
KLF10	0.02 (7E-01)	-0.02 (8E-01)	-0.07 (1E-01)	-0.12 (6E-02)	-0.09 (5E-01)	-0.23 (1E-01)	1.1E-01	0.05 (4E-01)
ABCC3	-0.05 (5E-01)	-0.10 (1E-01)	-0.01 (8E-01)	-0.08 (2E-01)	0.00 (1E+00)	0.01 (1E+00)	1.2E-01	0.00 (7E-01)
ABCD3	0.01 (8E-01)	-0.02 (5E-01)	-0.05 (9E-02)	-0.01 (8E-01)	-0.19 (6E-02)	-0.09 (4E-01)	1.2E-01	0.29 (2E-01)
VCAM1	0.05 (4E-01)	0.05 (4E-01)	-0.02 (8E-01)	0.08 (1E-01)	0.01 (9E-01)	-0.02 (9E-01)	1.2E-01	0.00 (6E-01)
KLF11	-0.07 (1E-01)	0.06 (3E-01)	0.01 (7E-01)	**-0.16 (2E-02)**	-0.07 (5E-01)	-0.14 (2E-01)	1.3E-01	0.36 (2E-01)
NOS3	**-0.15 (1E-03)**	0.07 (2E-01)	0.05 (4E-01)	-0.04 (5E-01)	0.01 (1E+00)	0.10 (3E-01)	1.3E-01	0.56 (3E-02)
ELOVL3	0.05 (3E-01)	0.04 (6E-01)	0.09 (7E-02)	0.02 (8E-01)	**-0.29 (4E-02)**	N/A	1.4E-01	0.31 (2E-01)
PNPLA2	-0.04 (3E-01)	-0.08 (2E-01)	0.00 (9E-01)	0.03 (5E-01)	**-0.15 (5E-02)**	-0.11 (4E-01)	1.5E-01	0.12 (3E-01)
APOA1	0.04 (6E-01)	0.02 (8E-01)	-0.11 (8E-02)	-0.10 (3E-01)	-0.20 (2E-01)	**0.26 (7E-03)**	1.6E-01	0.59 (2E-02)
ETFB	-0.01 (6E-01)	**-0.07 (3E-02)**	0.02 (5E-01)	-0.07 (2E-01)	0.00 (1E+00)	-0.02 (8E-01)	1.7E-01	0.00 (6E-01)
CPT1B	0.00 (9E-01)	**-0.12 (1E-02)**	-0.02 (7E-01)	0.00 (1E+00)	-0.06 (5E-01)	0.10 (3E-01)	2.0E-01	0.00 (4E-01)
LIPA	0.07 (6E-02)	-0.09 (1E-01)	**-0.09 (4E-02)**	0.06 (2E-01)	0.05 (6E-01)	-0.06 (5E-01)	2.0E-01	0.52 (5E-02)
ABCA1	0.01 (8E-01)	0.07 (2E-01)	-0.01 (9E-01)	0.02 (8E-01)	0.13 (3E-01)	0.10 (3E-01)	2.2E-01	0.00 (8E-01)
HADHB	-0.08 (6E-02)	-0.04 (4E-01)	0.00 (1E+00)	-0.01 (8E-01)	0.09 (5E-01)	-0.02 (9E-01)	2.5E-01	0.00 (7E-01)
PEMT	-0.06 (5E-01)	-0.03 (4E-01)	0.00 (9E-01)	-0.04 (4E-01)	-0.12 (3E-01)	0.02 (8E-01)	2.5E-01	0.00 (4E-01)
SLC27A2	-0.08 (5E-01)	N/A	0.02 (7E-01)	0.01 (9E-01)	-0.04 (7E-01)	-0.19 (6E-02)	2.6E-01	0.49 (8E-02)
AGPAT2	-0.03 (5E-01)	0.01 (8E-01)	**0.05 (3E-02)**	-0.03 (5E-01)	0.06 (6E-01)	-0.07 (5E-01)	2.7E-01	0.00 (5E-01)
CD36	0.05 (3E-01)	-0.01 (9E-01)	0.02 (6E-01)	-0.02 (8E-01)	**0.26 (5E-02)**	0.13 (3E-01)	2.7E-01	0.00 (4E-01)
AQP3	0.05 (5E-01)	-0.01 (9E-01)	0.04 (3E-01)	0.06 (4E-01)	-0.12 (2E-01)	0.15 (3E-01)	2.7E-01	0.20 (3E-01)
ALAS1	0.01 (8E-01)	0.00 (1E+00)	-0.04 (3E-01)	-0.02 (6E-01)	-0.11 (2E-01)	-0.24 (7E-02)	2.9E-01	0.00 (5E-01)
FGF21	N/A	-0.08 (2E-01)	-0.01 (9E-01)	N/A	N/A	-0.09 (5E-01)	3.1E-01	0.00 (7E-01)
G0S2	-0.04 (4E-01)	0.01 (7E-01)	-0.07 (8E-02)	0.03 (6E-01)	-0.08 (5E-01)	0.04 (7E-01)	3.2E-01	0.00 (6E-01)
GPAM	0.00 (1E+00)	0.03 (5E-01)	-0.02 (7E-01)	-0.08 (1E-01)	-0.09 (3E-01)	-0.10 (2E-01)	3.2E-01	0.00 (6E-01)
ABCD2	-0.04 (5E-01)	-0.04 (5E-01)	0.06 (1E-01)	**-0.19 (2E-02)**	0.02 (8E-01)	N/A	3.3E-01	0.45 (1E-01)
FBP1	0.01 (9E-01)	0.03 (6E-01)	0.06 (2E-01)	0.00 (9E-01)	-0.01 (9E-01)	0.07 (6E-01)	3.7E-01	0.00 (8E-01)
CES3	0.08 (1E-01)	0.00 (1E+00)	-0.04 (6E-01)	0.04 (6E-01)	0.06 (6E-01)	0.03 (8E-01)	3.9E-01	0.00 (9E-01)
PLTP	0.05 (3E-01)	0.00 (1E+00)	**-0.10 (3E-02)**	-0.09 (2E-01)	0.07 (4E-01)	0.15 (1E-01)	3.9E-01	0.44 (1E-01)
SREBF1	0.04 (4E-01)	0.06 (3E-01)	-0.01 (9E-01)	0.02 (7E-01)	-0.04 (7E-01)	0.09 (5E-01)	4.1E-01	0.00 (9E-01)
GK	-0.02 (7E-01)	-0.03 (6E-01)	-0.04 (1E-01)	0.09 (7E-02)	-0.13 (3E-01)	-0.09 (4E-01)	4.2E-01	0.12 (3E-01)

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ACACB	-0.05 (8E-02)	0.00 (9E-01)	-0.02 (8E-01)	0.02 (6E-01)	0.01 (8E-01)	-0.05 (6E-01)	4.3E-01	0.00 (8E-01)
LPCAT3	-0.04 (3E-01)	**-0.12 (4E-02)**	0.01 (7E-01)	-0.01 (9E-01)	0.04 (7E-01)	-0.02 (9E-01)	4.3E-01	0.00 (5E-01)
SLC22A5	-0.01 (9E-01)	-0.02 (5E-01)	0.03 (6E-01)	-0.05 (3E-01)	-0.06 (6E-01)	-0.06 (6E-01)	4.3E-01	0.00 (9E-01)
NFKB1	-0.04 (2E-01)	-0.02 (6E-01)	0.01 (9E-01)	0.03 (4E-01)	**-0.20 (2E-02)**	-0.05 (5E-01)	4.4E-01	0.27 (2E-01)
ABCG2	-0.10 (1E-01)	0.03 (7E-01)	0.02 (7E-01)	-0.02 (8E-01)	-0.06 (4E-01)	-0.03 (7E-01)	4.6E-01	0.00 (6E-01)
VNN1	-0.04 (5E-01)	-0.01 (9E-01)	0.04 (4E-01)	0.09 (2E-01)	-0.03 (8E-01)	0.16 (2E-01)	4.6E-01	0.00 (7E-01)
ACSL1	-0.04 (3E-01)	-0.03 (5E-01)	0.01 (7E-01)	-0.01 (8E-01)	-0.04 (8E-01)	-0.13 (2E-01)	4.8E-01	0.00 (8E-01)
PLIN2	0.05 (1E-01)	-0.06 (2E-01)	0.04 (2E-01)	-0.03 (6E-01)	0.14 (2E-01)	-0.16 (3E-01)	4.9E-01	0.35 (2E-01)
ACOT7	-0.01 (9E-01)	0.01 (9E-01)	**0.06 (4E-02)**	-0.03 (5E-01)	-0.08 (5E-01)	-0.13 (2E-01)	4.9E-01	0.08 (4E-01)
APOA5	N/A	N/A	-0.07 (3E-01)	N/A	N/A	0.08 (5E-01)	5.0E-01	0.15 (3E-01)
ME1	-0.03 (7E-01)	-0.03 (6E-01)	0.06 (3E-01)	-0.04 (3E-01)	0.00 (1E+00)	-0.10 (4E-01)	5.1E-01	0.28 (2E-01)
PEX11A	0.04 (3E-01)	-0.07 (1E-01)	-0.01 (9E-01)	-0.04 (4E-01)	0.00 (1E+00)	-0.04 (8E-01)	5.3E-01	0.00 (8E-01)
NR1H3	0.01 (7E-01)	0.01 (9E-01)	-0.01 (9E-01)	0.03 (6E-01)	0.03 (8E-01)	0.04 (6E-01)	5.5E-01	0.00 (1E+00)
PCK1	0.01 (9E-01)	0.07 (3E-01)	-0.02 (8E-01)	0.01 (9E-01)	0.09 (4E-01)	0.12 (3E-01)	5.6E-01	0.00 (6E-01)
ABCB4	-0.02 (6E-01)	-0.03 (3E-01)	0.09 (1E-01)	-0.07 (4E-01)	-0.16 (2E-01)	0.04 (8E-01)	5.7E-01	0.08 (4E-01)
ACAD8	0.04 (5E-01)	-0.04 (2E-01)	-0.05 (4E-01)	-0.02 (8E-01)	0.04 (8E-01)	-0.09 (5E-01)	5.8E-01	0.00 (5E-01)
KDR	0.02 (5E-01)	-0.03 (7E-01)	-0.05 (4E-01)	-0.14 (5E-02)	-0.06 (4E-01)	0.05 (5E-01)	5.8E-01	0.10 (4E-01)
LPL	-0.01 (9E-01)	-0.04 (3E-01)	0.03 (7E-01)	-0.07 (4E-01)	0.02 (8E-01)	0.07 (7E-01)	5.8E-01	0.00 (9E-01)
ALDH9A1	-0.01 (7E-01)	0.02 (7E-01)	0.03 (5E-01)	0.01 (7E-01)	0.03 (8E-01)	0.02 (8E-01)	6.2E-01	0.00 (1E+00)
ACOX1	-0.06 (2E-01)	-0.04 (3E-01)	0.02 (4E-01)	-0.01 (7E-01)	0.02 (7E-01)	-0.05 (6E-01)	6.2E-01	0.00 (4E-01)
APOC3	0.05 (5E-01)	0.06 (5E-01)	**-0.10 (5E-02)**	0.03 (7E-01)	-0.13 (4E-01)	0.07 (4E-01)	6.6E-01	0.07 (4E-01)
ACADM	0.05 (2E-01)	0.00 (9E-01)	0.00 (9E-01)	-0.02 (7E-01)	0.02 (9E-01)	0.03 (8E-01)	6.6E-01	0.00 (9E-01)
CREB3L3	N/A	N/A	-0.08 (2E-01)	0.01 (1E+00)	N/A	0.04 (6E-01)	7.0E-01	0.00 (5E-01)
PDK4	0.01 (9E-01)	-0.07 (9E-02)	0.04 (4E-01)	0.05 (5E-01)	0.16 (1E-01)	0.18 (1E-01)	7.0E-01	0.33 (2E-01)
TXNIP	0.02 (5E-01)	0.01 (8E-01)	-0.02 (6E-01)	0.01 (8E-01)	-0.01 (1E+00)	0.09 (5E-01)	7.1E-01	0.00 (9E-01)
RETSAT	**-0.09 (3E-02)**	0.03 (5E-01)	0.04 (5E-01)	0.01 (8E-01)	0.02 (8E-01)	-0.08 (4E-01)	7.1E-01	0.08 (4E-01)
SLC27A4	-0.04 (8E-02)	0.03 (2E-01)	0.04 (3E-01)	-0.04 (4E-01)	0.00 (1E+00)	-0.01 (9E-01)	7.3E-01	0.12 (3E-01)
CIDEC	0.01 (9E-01)	0.01 (9E-01)	-0.09 (2E-01)	-0.02 (9E-01)	0.06 (5E-01)	0.17 (9E-02)	7.5E-01	0.00 (5E-01)
ACSL3	-0.07 (2E-01)	0.07 (2E-01)	0.01 (7E-01)	0.04 (5E-01)	0.05 (5E-01)	-0.04 (7E-01)	7.6E-01	0.03 (4E-01)
PEX19	0.00 (9E-01)	0.03 (3E-01)	-0.06 (2E-01)	0.06 (3E-01)	0.08 (3E-01)	-0.12 (2E-01)	7.9E-01	0.18 (3E-01)
PLIN4	0.04 (4E-01)	**-0.08 (4E-02)**	0.03 (4E-01)	0.00 (1E+00)	-0.01 (9E-01)	-0.02 (9E-01)	7.9E-01	0.00 (5E-01)

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FADS1	0.06 (1E-01)	0.00 (1E+00)	-0.09 (1E-01)	-0.07 (3E-01)	0.02 (8E-01)	-0.10 (5E-01)	8.1E-01	0.07 (4E-01)
SCD	0.04 (5E-01)	0.09 (2E-01)	-0.03 (5E-01)	0.06 (4E-01)	-0.06 (6E-01)	-0.21 (1E-01)	8.3E-01	0.15 (3E-01)
HSD17B10	0.03 (4E-01)	-0.04 (3E-01)	0.01 (6E-01)	-0.06 (3E-01)	0.04 (6E-01)	0.02 (8E-01)	8.4E-01	0.00 (7E-01)
FABP1	0.00 (9E-01)	0.05 (5E-01)	-0.01 (8E-01)	0.01 (9E-01)	0.09 (6E-01)	-0.22 (6E-02)	8.6E-01	0.00 (7E-01)
G6PC	N/A	N/A	-0.01 (9E-01)	N/A	N/A	0.00 (1E+00)	9.2E-01	0.00 (9E-01)
PLIN1	0.00 (9E-01)	0.04 (6E-01)	-0.10 (2E-01)	0.03 (8E-01)	0.07 (5E-01)	0.09 (5E-01)	9.4E-01	0.00 (8E-01)
APOA2	0.05 (5E-01)	0.10 (2E-01)	-0.07 (2E-01)	0.06 (6E-01)	-0.15 (4E-01)	0.03 (7E-01)	9.4E-01	0.00 (6E-01)
SLC25A42	0.02 (5E-01)	-0.01 (8E-01)	0.00 (1E+00)	0.01 (9E-01)	-0.08 (2E-01)	-0.02 (8E-01)	9.9E-01	0.00 (9E-01)
LIPG	0.00 (9E-01)	-0.02 (8E-01)	0.11 (1E-01)	-0.01 (8E-01)	0.01 (9E-01)	-0.22 (7E-02)	9.9E-01	0.13 (3E-01)
PCTP	-0.01 (8E-01)	-0.05 (4E-01)	0.00 (1E+00)	0.08 (2E-01)	0.10 (3E-01)	-0.15 (1E-01)	9.9E-01	0.23 (3E-01)
VLDLR	-0.05 (3E-01)	-0.01 (8E-01)	0.09 (3E-01)	0.06 (3E-01)	-0.01 (9E-01)	-0.06 (6E-01)	1.0E+00	0.00 (6E-01)

Note: Nominally significant associations are in bold. eQTL effect size (beta) represents the slope of the linear regression of normalized expression data versus the three genotype categories using single-tissue eQTL analysis. The normalized expression values are based on quantile normalization within each tissue, followed by inverse quantile normalization for each gene across samples. P-values were generated for each variant-gene pair by testing the alternative hypothesis that the slope of a linear regression model between genotype and expression deviates from 0. *Skin is the random effect meta-analysis of N=302 samples from Skin-Sun Exposed (lower leg) and N=196 samples from Skin-Not Sun Exposed (Suprapubic).

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Supplementary Table 9. Annotation of regulatory function of rs6008845, from RegulomeDB[1] and HaploReg[2], summarizing Encode and Roadmap Epigenomics projects data.

SNP	Position	Promoter Histone Marks	Enhancer Histone Marks	DNase	Protein Bound[1]	Motif Altered[1]
rs6008845 Allele T/C	Intergenic 22kb 5' of PPARA	Primary monocytes, B Cells and neutrophils from peripheral blood, Primary hematopoietic stem cells G-CSF-mobilized Male, Foreskin Melanocyte Primary Cells, Liver, Colonic and Rectal Mucosa, Rectal Smooth Muscle, GM12878 Lymphoblastoid Cells, HepG2 Hepatocellular Carcinoma Cell Line, Monocytes-CD14+ RO01746 Primary Cells	H1 Derived Mesenchymal Stem Cells, Primary B cells from cord blood, Primary hematopoietic stem cells, Primary Natural Killer cells from peripheral blood, Primary hematopoietic stem cells G-CSF-mobilized Female, Muscle Satellite Cultured Cells, Foreskin Fibroblast Primary Cells, Adipose Nuclei, Duodenum Mucosa, Esophagus, Fetal Adrenal Gland, Fetal Muscle Trunk, Fetal Muscle Leg, Placenta, Fetal Stomach, Fetal Thymus, Left Ventricle, Lung, Ovary, Pancreas, Rectal Mucosa, Right Atrium, Right Ventricle, Skeletal Muscle, Stomach Smooth Muscle, Spleen, HSMM Skeletal Muscle Myoblasts Cells, NHDF-Ad Adult Dermal Fibroblast Primary Cells	Primary monocyte, B Cells from peripheral blood, Primary T cells from cord blood, Primary hematopoietic stem cells G-CSF-mobilized Female, Fetal Adrenal Gland, Fetal Heart, Fetal Kidney, Fetal Lung, Fetal Muscle Trunk, Fetal Muscle Leg, Placenta, Fetal Stomach, Ovary, Pancreas, Psoas Muscle, GM12878 Lymphoblastoid Cells, HepG2 Hepatocellular Carcinoma Cell Line, Monocytes-CD14+ RO01746 Primary Cells	GABPB1, PAX5*, POLR2A*, GABPA, ELF1*, FOXP2, SPI1* ; ELF1*, PAX5C20*, PU1*, POL2*	VDR*-CAR-PXR ; BCL, ERalpha-a, EWSR1-FLI1, KAP1, NRSF, VDR*

Note: [1]Data on protein bound and motif altered are separated by semicolons, before are from RegulomeDb and after from HaploReg database. Asterisk marks repeated sites at both datasets.

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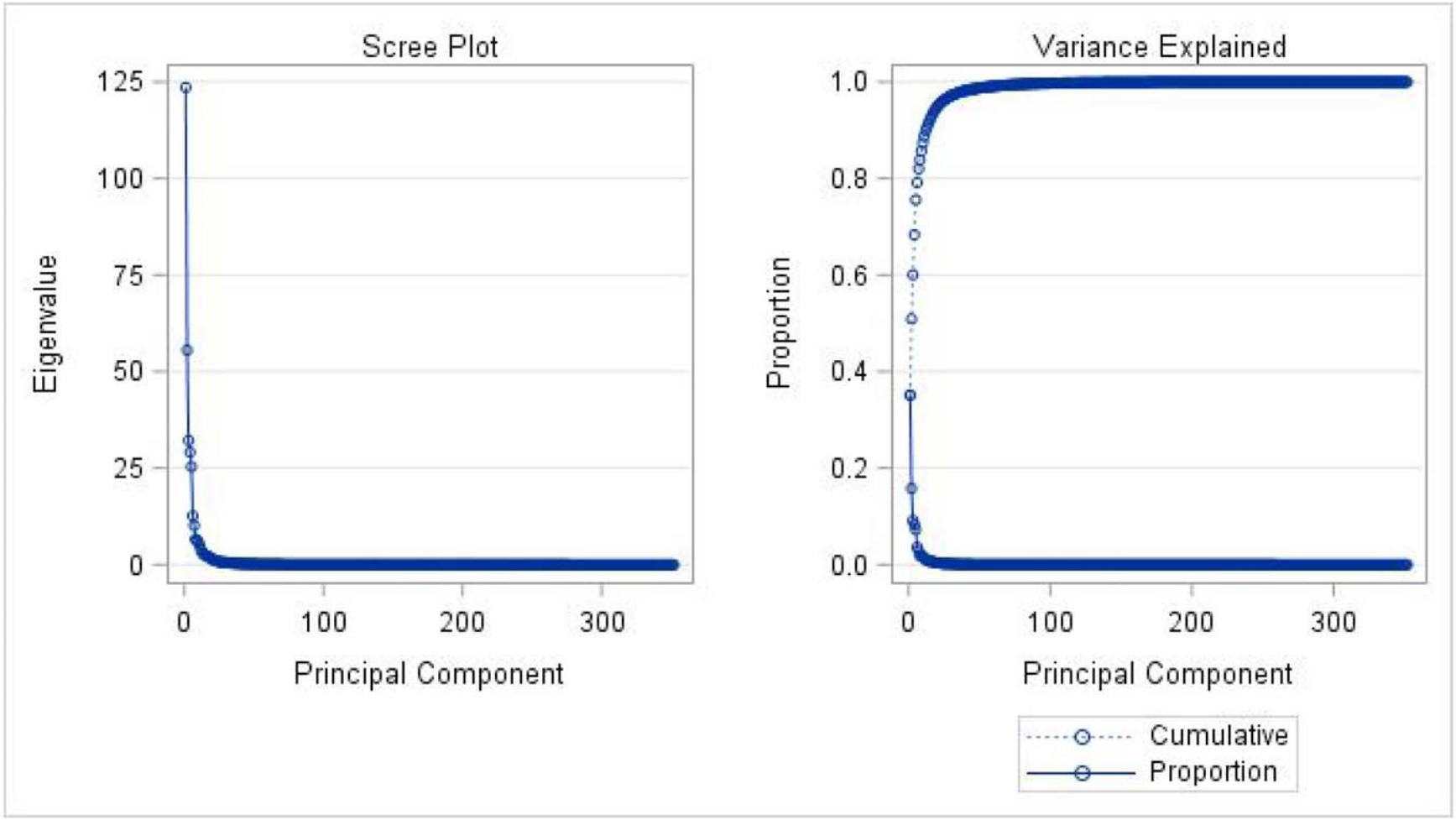
Supplementary Figure 1. Graphical representation of the Principal Component (PC) Analysis to estimate the number of Independent comparisons, that correspond to the number of PCs derived to explain 99.5% of trait variance among the 360 SNPs analyzed. Note: in post-imputation QC an IMPUTE-info threshold of 0.8 was used to filter out poorly imputed SNPs[3]**.**



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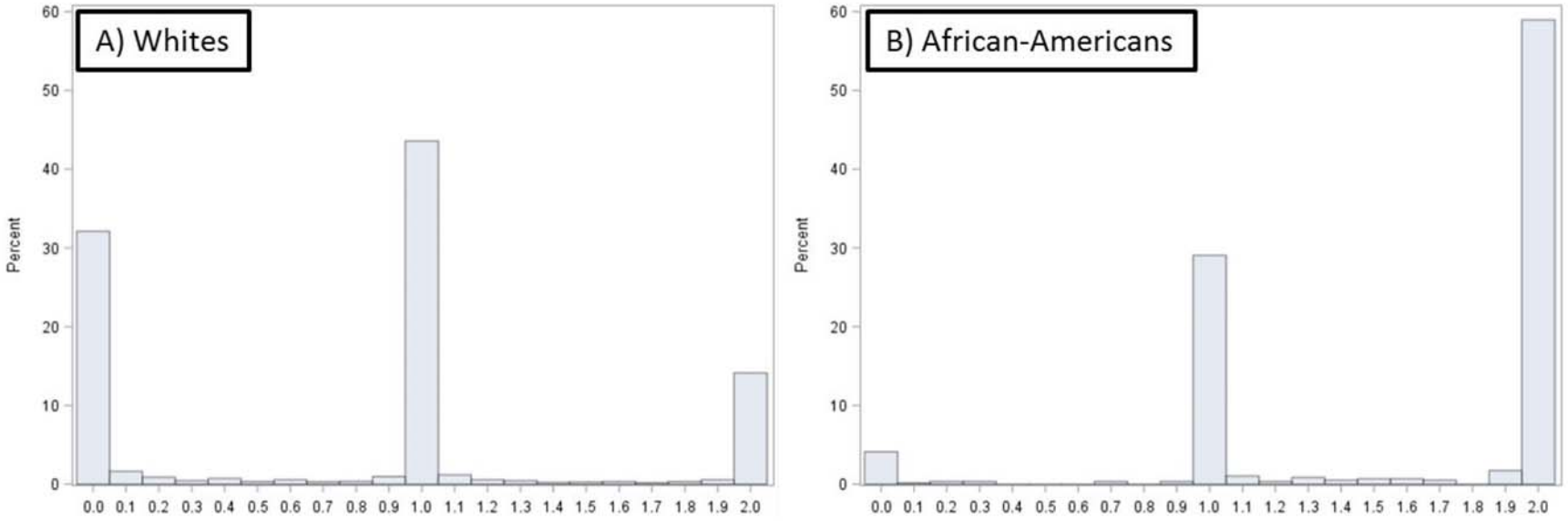
Supplementary Figure 2. Distribution of rs6008845 C allele dosage in whites (A) and African-Americans (B) in ACCORD-Lipid. According to this distribution, for graphical and representation purposes, subjects were considered as major allele homozygotes if the minor allele dosage was <0.5, heterozygotes if the minor allele dosage was ≥0.5 and <1.5, and minor allele homozygotes if the minor allele dosage was ≥ 1.5.



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Supplementary Figure 3. **eQTL association of rs6008845 with PPAR-alpha expression in 44 different tissues from GtEx.** Box plot show the normalized PPARA gene expression levels according to rs6008845 genotypes in Skin (lower leg) - figures adapted from http://www.gtexportal.org/home/snp/rs6008845

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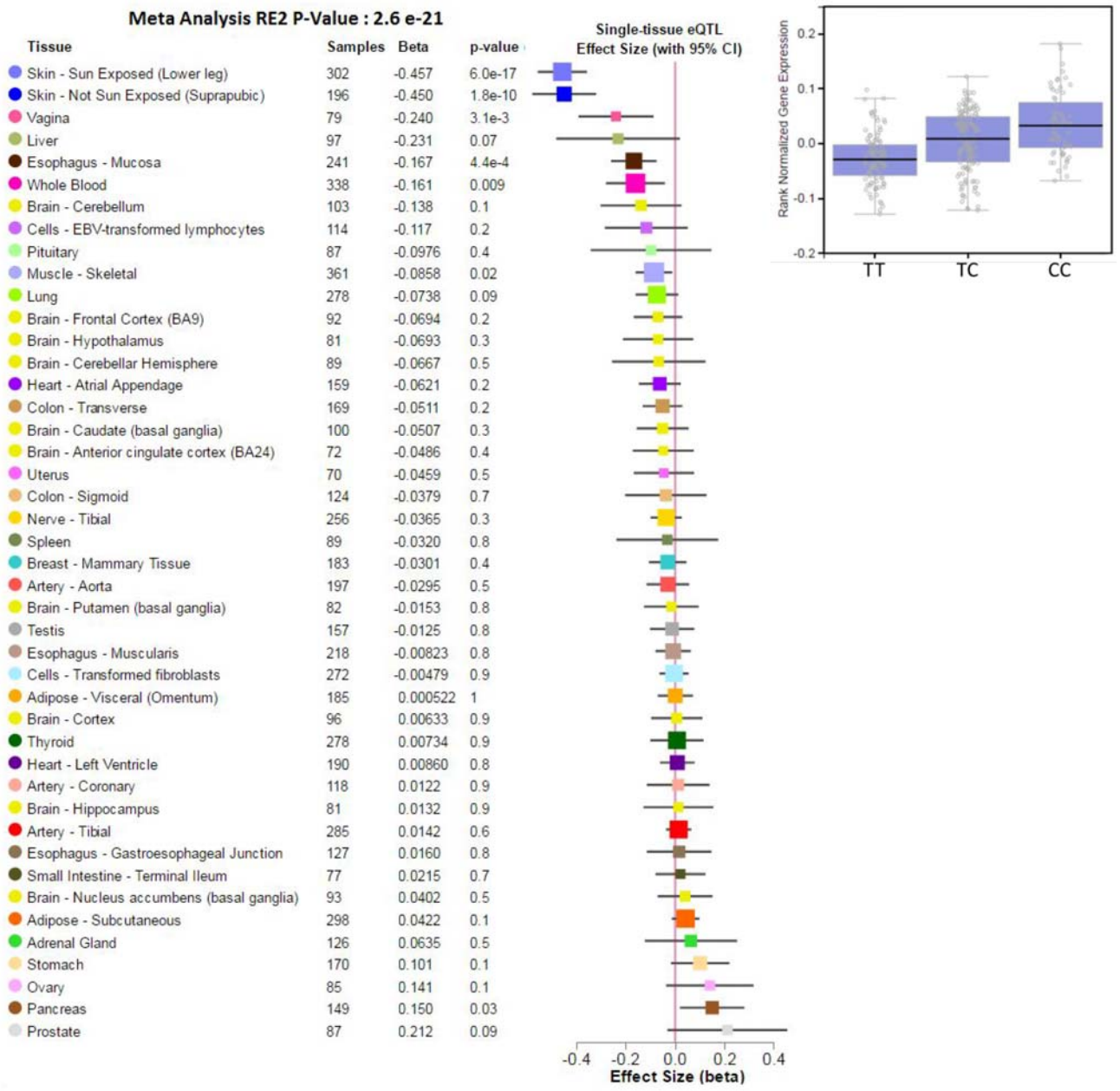

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Note: As described in http://www.gtexportal.org/home/documentationPage meta-analysis of all tissues was computed by means of Han and Eskin's Random Effects model (RE2). eQTL effect size (beta) represent, for each tissue with at least 70 sample genotyped and with RNA-seq data available, the slope of the linear regression of normalized expression data versus the three genotype categories using single-tissue eQTL analysis (effect size was referred to the T allele). The normalized expression values are based on quantile normalization within each tissue, followed by inverse quantile normalization for each gene across samples.

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Supplementary Figure 4. RegulomeDB output showing the transcription factors whose binding is likely to be affected by rs6008845 in different cell types.

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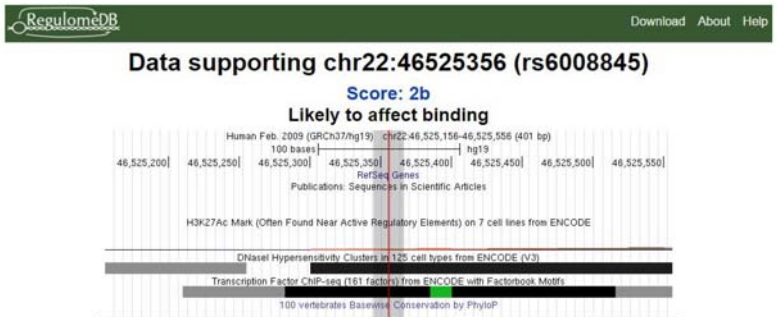

Protein Binding Filter:

Method	Location	Bound Protein	Cell Type	Additional Info	Reference
ChIP-seq	chr22:46525267..46525583	GABPB1	HepG2		ENCODE
ChIP-seq	chr22:46525261..46525525	PAX5	GM12878		ENCODE
ChIP-seq	chr22:46525217..46525527	PAX5	GM12878		ENCODE
ChIP-seq	chr22:46525242..46525722	POLR2A	GM12892		ENCODE
ChIP-seq	chr22:46525237..46525717	POLR2A	GM19099		ENCODE
ChIP-seq	chr22:46525210..46525740	POLR2A	GM19193		ENCODE
ChIP-seq	chr22:46525240..46525595	GABPA	CD34+CD133+HPC		21139080
ChIP-seq	chr22:46525337..46525507	ELF1	GM12878		ENCODE
ChIP-seq	chr22:46525289..46525565	ELF1	HepG2		ENCODE
ChIP-seq	chr22:46525348..46525652	FOXP2	PFSK-1		ENCODE
ChIP-seq	chr22:46525282..46525516	SPI1	GM12878		ENCODE
ChIP-seq	chr22:46525314..46525493	SPI1	GM12891		ENCODE
ChIP-seq	chr22:46525290..46525494	SPI1	K562		ENCODE

Motifs Filter:

Method	Location	Motif	Cell Type	PWM	Reference
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Chorion		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Gm12878		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Gm12891		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Gm12892		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Gm18507		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Gm19238		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Gm19239		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	H1hesc		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Hepatocytes		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Hsmm		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	LncapAndro		21106904
Footprinting	chr22:46525345..46525366	VDR=CAR=PXR	Lncap		21106904
PWM	chr22:46525345..46525366	VDR=CAR=PXR			16381825

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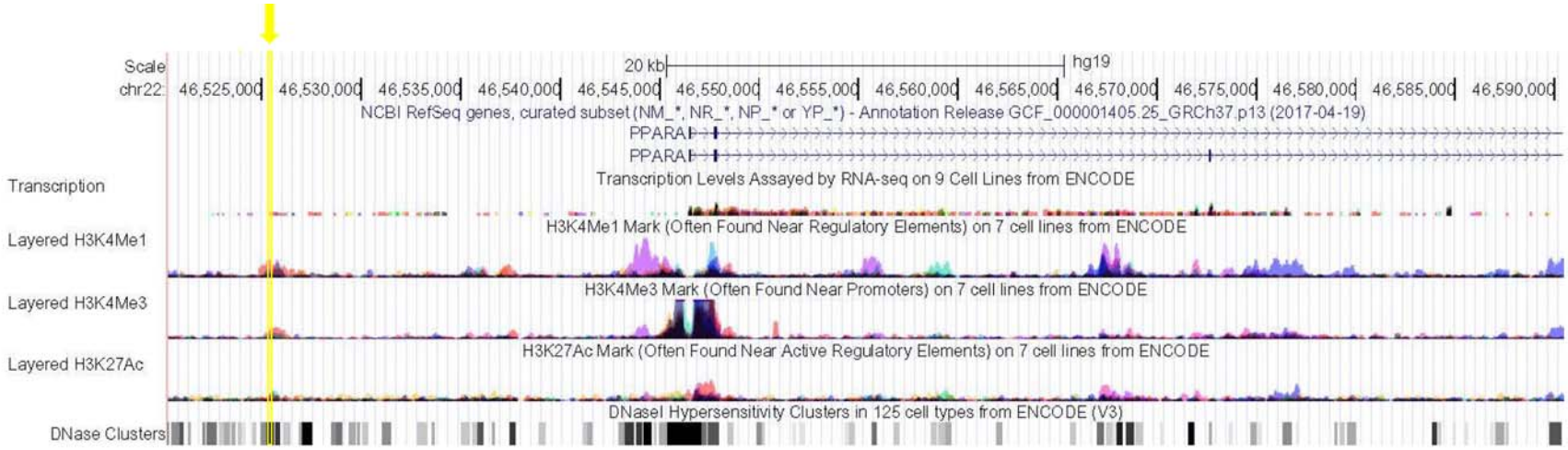
Supplementary Figure 5. *PPARA* region with detail on rs6008845 (yellow-line). rs6008845 is located inside epigenetic peaks for Histone 3 (H3K4Me1, H3K4Me1 and H3K27Ac). Figure generated with freely available bionformatic resources from University of Santa Cruz (UCSC) genome browser gateway http://genome.ucsc.edu [4] (based on assembly GRCh37/hg19)..



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