

SUPPLEMENTARY MATERIAL

Expression analysis of candidate genes for fatty acid composition in adipose tissue and identification of regulatory regions

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Figure S1. GWAS plot of *ELOVL6* and *SLC27A4A* gene expression in adipose tissue. The X-axis represents chromosome positions in Mb relative to *Sscrofa10.2* assembly of the pig genome and the Y-axis shows the $-\log_{10}$ (p -value). Horizontal dashed lines indicate the genome-wide significance level. Plot of eGWAS for (A) *ELOVL6*, and (B) *SLC27A4* gene expression in backfat.

Figure S2. Associations of SNPs from SSC8 and *ELOVL6* polymorphisms for *ELOVL6* gene expression in backfat. The X-axis represents positions of SSC8 in Mb relative to *Sscrofa10.2* assembly of the pig genome and the Y-axis shows the $-\log_{10}$ (p -value). Horizontal dashed lines indicate the chromosome significance level.

Figure S3. Clustered heat map to visualize correlations among gene expression levels (NQ) of the 43 genes and fatty content in adipose tissue. Color legend was adjusted to minimal and maximal values to differentiate the differences.

Figure S4. Clustered heat map to visualize correlations among gene expression levels (NQ) of the 43 genes and fatty content in muscle. Color legend was adjusted to minimal and maximal values to differentiate the differences.

Table S1. List of 44 lipid-related genes selected to study their expression in the present study. The overlapping between categories is labelled by colors.

Table S2. Description of the 193 significant expression-associated SNPs (eSNPs).

Table S3. Transcription factor binding sites for *PPARG* in the *ACSM5* promoter region gene.

Table S4. Transcription factor binding site for *SREBF1* in the *FADS2* promoter region gene.

Table S5. Gene annotation of genes within the eQTL intervals. Annotation was performed by considering for *trans*-eQTLs the eQTL interval ± 1 Mb; whereas for *cis*-eQTLs only the studied gene was selected (*ACSM5*, *FABP4*, and *FADS2*).

Table S6. Mean comparison between males and females of backfat gene expression levels of 43 lipid-related genes.

Table S7. Description of the 393 human orthologous genes.

Table S8. Top functional networks and molecules identified with IPA from the list of annotated genes mapping within the 19 eQTLs.

Table S9. Transcription factor binding sites for the *PPARG* gene.

Table S10. Pearson's correlations of *PPARG* mRNA expression and analyze-related genes.

Table S11. Primers used for the characterization of the 3'UTR of porcine *FABP4* gene.

Table S12. Primers used for the analyses of gene expression of the 48 genes by real-time PCR.

Figure S1. GWAS plot of *ELOVL6* and *SLC27A4* gene expression in adipose tissue. The X-axis represents chromosome positions in Mb relative to *Sscrofa10.2* assembly of the pig genome and the Y-axis shows the $-\log_{10}(p\text{-value})$. Horizontal dashed lines indicate the genome-wide significance level. Plot of eGWAS for (A) *ELOVL6*, and (B) *SLC27A4* gene expression in backfat.

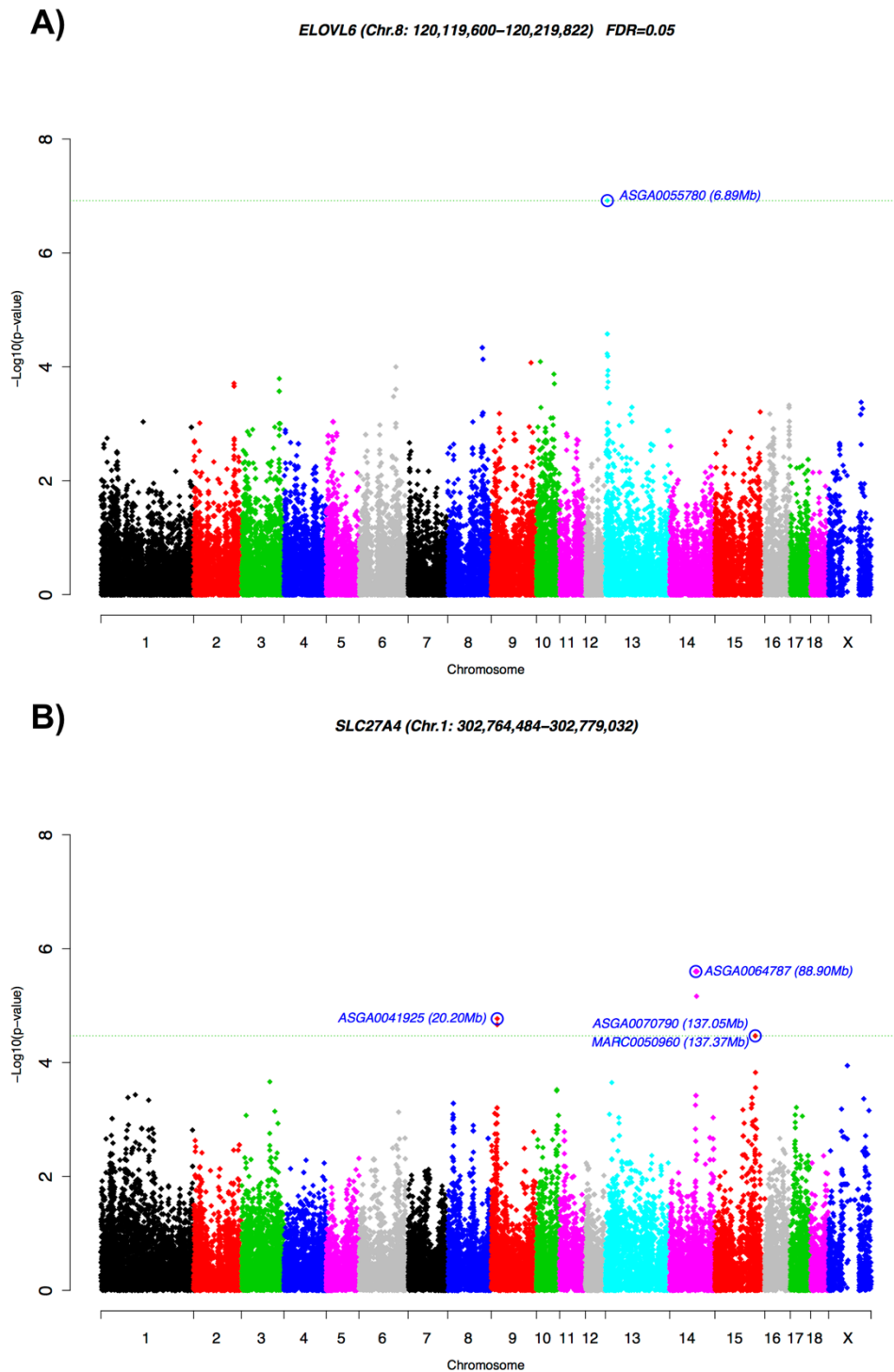


Figure S2. Associations of SNPs from SSC8 and *ELOVL6* polymorphisms for *ELOVL6* gene expression in backfat. The X-axis represents positions of SSC8 in Mb relative to *Sscrofa10.2* assembly of the pig genome and the Y-axis shows the $-\log_{10}(p\text{-value})$. Horizontal dashed lines indicate the chromosome significance level.

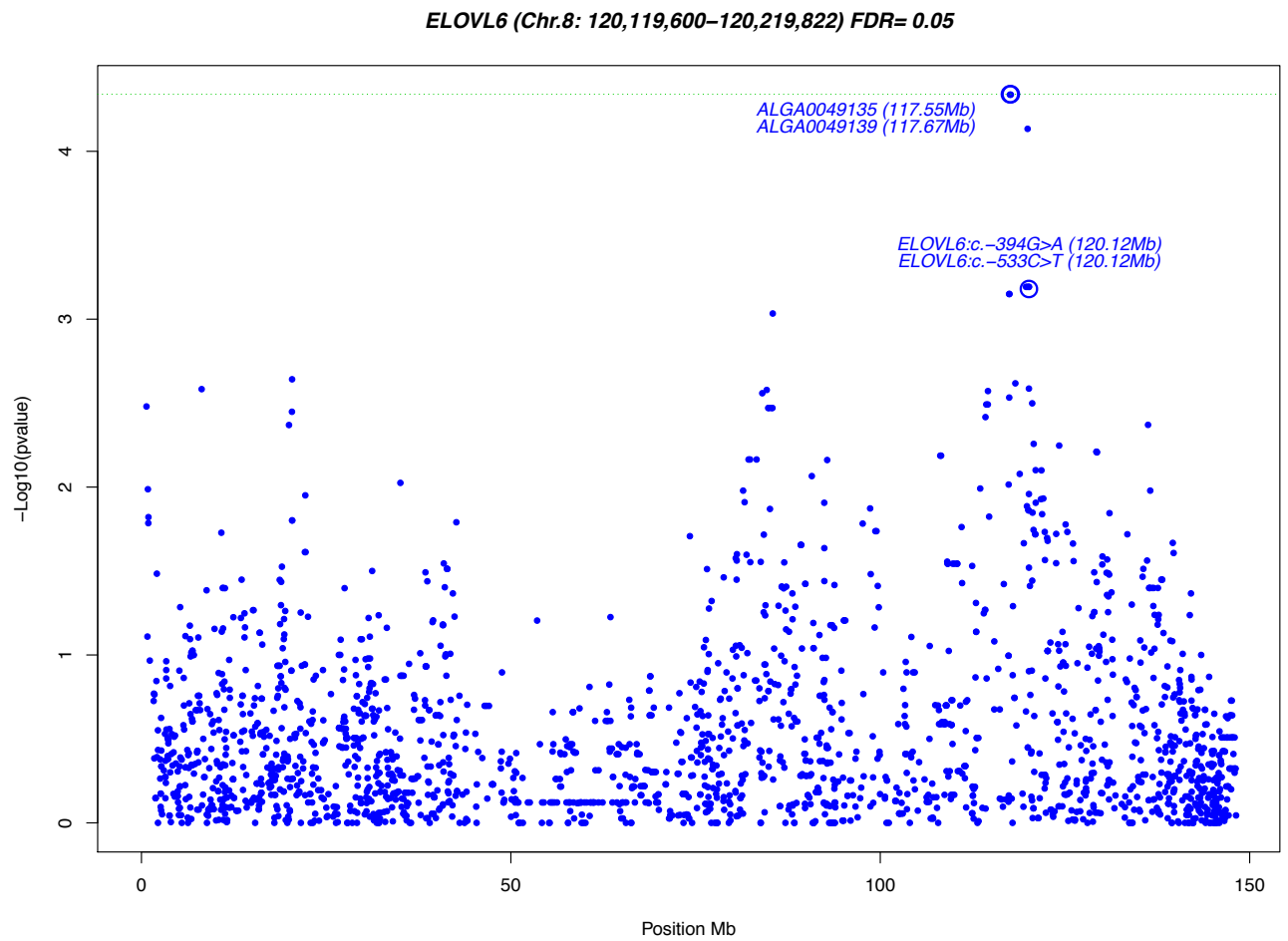


Figure S3. Clustered heat map to visualize correlations among gene expression levels (NQ) of the 43 genes and fatty content in adipose tissue. Color legend was adjusted to minimal and maximal values to differentiate the differences.

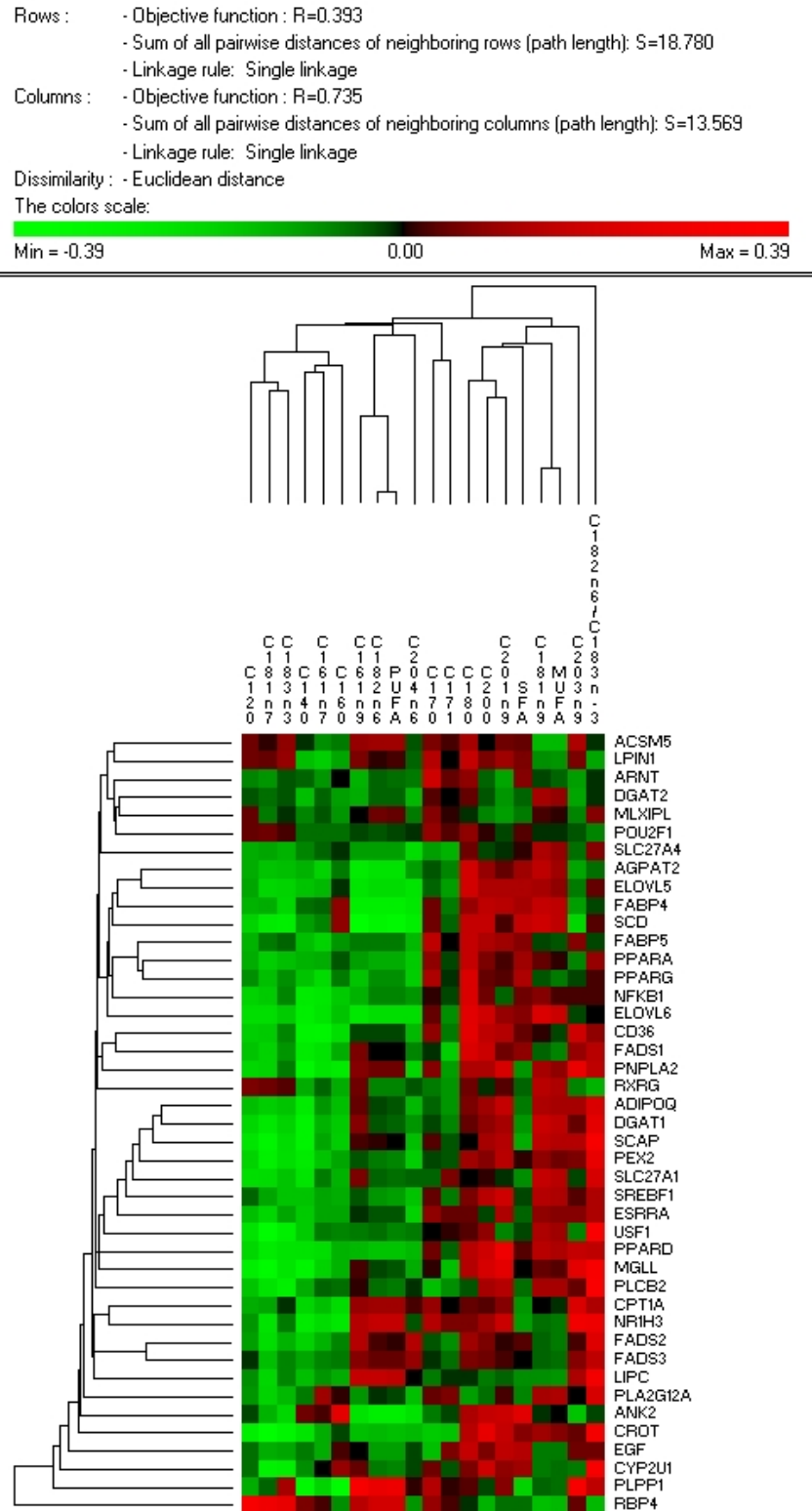


Figure S4. Clustered heat map to visualize correlations among gene expression levels (NQ) of the 43 genes and fatty content in muscle. Color legend was adjusted to minimal and maximal values to differentiate the differences.

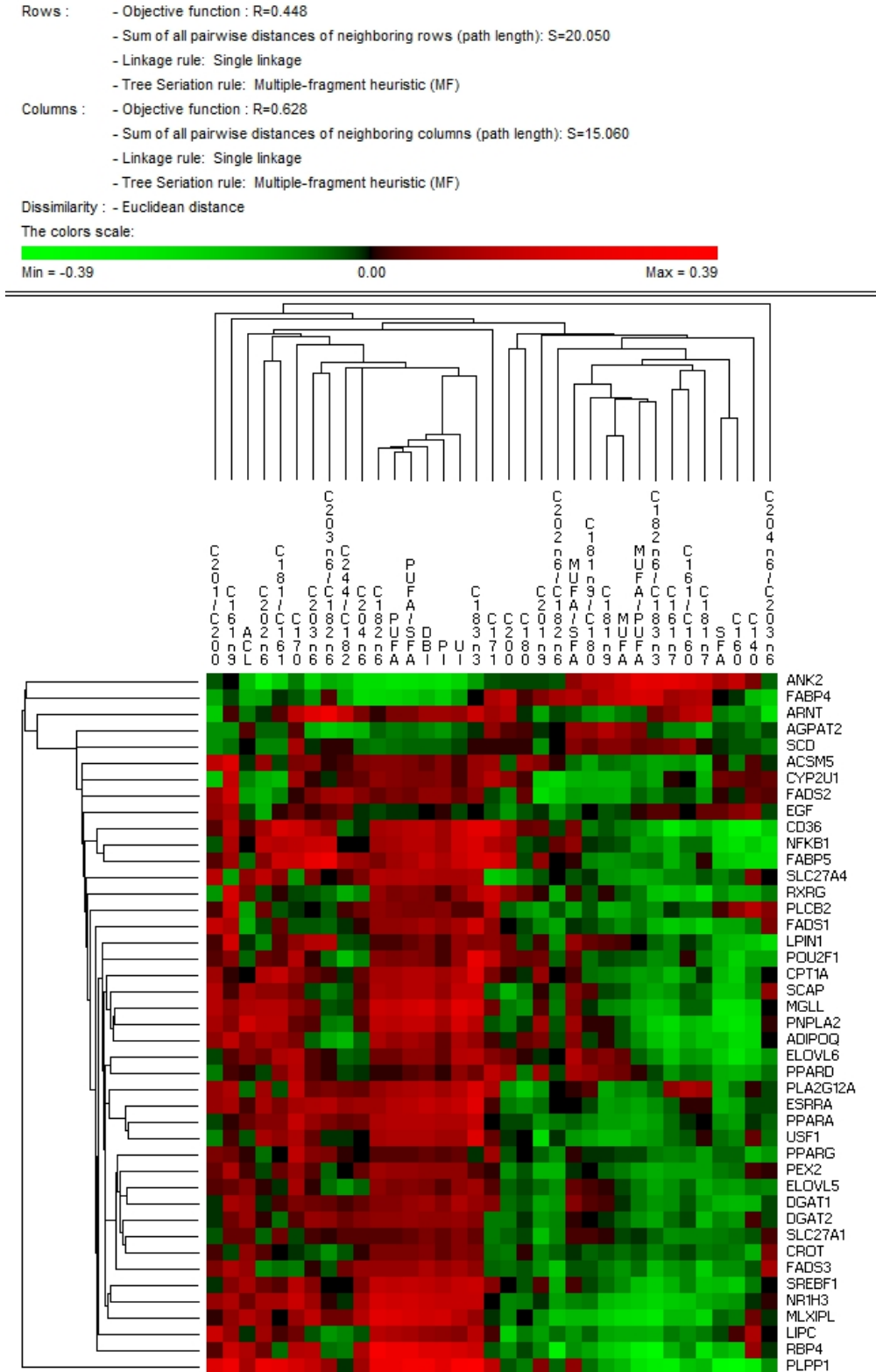


Table S1. List of 44 lipid-related genes selected to study their expression in the present study. The overlapping between categories is labelled by colors.

Description	Bibliographic reference	Genes
Candidate functional and positional genes identified in a GWAS study for intramuscular FA composition in the BC1_LD backcross	[5]	<i>ARNT, CYP2U1, EGF, ELOVL6, FABP4, FABP5, FADS1, FADS2, FADS3, NFKB1, PLA2G12A, PLCB2, PLPP1 and USF1</i>
Genes differentially expressed by RNA-Seq in the adipose tissue of two phenotypically extreme groups of animals for intramuscular FA composition in the BC1_LD backcross	[17]	<i>ELOVL6 and SCD</i>
Candidate positional gene affecting palmitic and palmitoleic FA in pigs	[18]	<i>ELOVL6</i>
Genes related to lipid metabolism identified in gene co-association networks for FA composition in the BC1_LD backcross	[19]	<i>ACSM5, ANK2, ARNT, FABP4, FABP5, MGLL and PPARG</i>
Genes related to lipid metabolism identified in gene co-association networks for fatness and growth related traits in the IBSMAP cross	[20]	<i>ARNT and PPARG</i>
Candidate positional genes identified in a GWAS study for backfat FA composition in the BC1_LD backcross	[21]	<i>FADS1, FADS2 and FADS3</i>
Transporters involved in lipid metabolism		<i>RBP4, SCAP, SLC27A1 and SLC27A4</i>
Enzymes involved in lipid metabolism		<i>AGPAT2, CPT1A, CROT, DGAT1, DGAT2, ELOVL5, LIPC, LPIN1, PEX2 and PNPLA2</i>
Transcriptional factors, cofactors or nuclear receptors involved in lipid metabolism		<i>CD36, ESRRA, MLXIPL, NR1H3, POU2F1, PPARA, PPARD, PPARGC1A, RXRG and SREBF1</i>
Adipokine of white fat tissue	[22]	<i>ADIPOQ</i>

Table S2. Description of the 193 significant expression-associated SNPs (eSNPs).

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I1	2	ASGA0093797	134992155	0.94	0.06	1.55x10 ⁻⁶	5.48x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I2	3	ASGA0089930	16473829	0.74	0.26	4.45x10 ⁻⁶	1.30x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	H3GA0053939	18724340	0.90	0.10	3.75x10 ⁻⁶	1.17x10 ⁻³	ACSM5	intronic	ENSSSCG00000007804	SH2B1	trans
I2	3	ASGA0101457	18742778	0.90	0.10	3.03x10 ⁻⁷	1.22 x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000007805	ATP2A1	trans
I2	3	ALGA0112844	19373384	0.67	0.33	3.66x10 ⁻⁸	1.84x10 ⁻⁵	ACSM5	intronic	ENSSSCG00000022785	GSG1L	trans
I2	3	ASGA0098276	21286903	0.82	0.18	1.69x10 ⁻¹⁴	1.70x10 ⁻¹¹	ACSM5	intergenic	-	-	cis
I2	3	ALGA0017974	21309417	0.77	0.23	1.22x10 ⁻¹⁵	1.51x10 ⁻¹²	ACSM5	intergenic	-	-	cis
I2	3	ASGA0013836	21387300	0.77	0.23	6.97x10 ⁻¹⁰	4.76x10 ⁻⁷	ACSM5	intergenic	-	-	cis
I2	3	ALGA0017987	21528275	0.53	0.47	2.68x10 ⁻⁵	6.75x10 ⁻³	ACSM5	intergenic	-	-	cis
I2	3	ASGA0013852	21562254	0.73	0.27	5.69x10 ⁻⁸	2.79x10 ⁻⁵	ACSM5	intergenic	-	-	cis
I2	3	ALGA0123606	21777886	0.63	0.37	7.13x10 ⁻¹¹	5.66x10 ⁻⁸	ACSM5	intergenic	-	-	cis
I2	3	ASGA0089383	22771385	0.50	0.50	1.19 x10 ⁻¹⁰	8.93x10 ⁻⁸	ACSM5	intronic	ENSSSCG00000007831	CACNG3	cis
I2	3	MARC0101247	22772065	0.88	0.12	1.96x10 ⁻⁶	6.52x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000007831	CACNG3	cis
I2	3	ASGA0094123	22794781	0.84	0.16	7.97x10 ⁻⁶	2.23x10 ⁻³	ACSM5	intronic	ENSSSCG00000007831	CACNG3	cis
I2	3	ALGA0018006	23015607	0.70	0.30	1.08x10 ⁻⁷	4.86x10 ⁻⁵	ACSM5	intergenic	-	-	cis
I2	3	ALGA0018040	23224453	0.66	0.34	3.33x10 ⁻¹⁶	4.39x10 ⁻¹³	ACSM5	intergenic	-	-	cis
I2	3	ASGA0098738	23442184	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	downstream	ENSSSCG00000007836	SCNN1G	cis
I2	3	ALGA0103397	23522898	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	upstream	ENSSSCG000000030424	-	cis
I2	3	ALGA0123533	23592793	0.60	0.40	7.20x10 ⁻¹¹	5.66x10 ⁻⁸	ACSM5	intergenic	-	-	cis
I2	3	MARC0041570	23603118	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	downstream	ENSSSCG00000026544	USP31	cis
I2	3	ASGA0093175	23778733	0.80	0.20	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007837	HS3ST2	cis
I2	3	MARC0003844	23802761	0.80	0.20	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007837	HS3ST2	cis
I2	3	MARC0047020	23961903	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I2	3	ASGA0103399	24010664	0.75	0.25	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	downstream	ENSSSCG00000007838	OTOA	cis
I2	3	ALGA0112358	24025177	0.80	0.20	4.93x10 ⁻¹¹	4.10x10 ⁻⁸	ACSM5	intronic	ENSSSCG00000007838	OTOA	cis
I2	3	ALGA0123020	24042892	0.78	0.22	7.14x10 ⁻¹³	6.50x10 ⁻¹⁰	ACSM5	intronic	ENSSSCG00000007838	OTOA	cis
I2	3	ASGA0094818	24086731	0.33	0.67	2.69x10 ⁻⁰⁵	6.75x10 ⁻³	ACSM5	intergenic	-	-	cis
I2	3	ALGA0115152	24218664	0.53	0.47	2.08x10 ⁻⁰⁷	8.84x10 ⁻⁵	ACSM5	intergenic	-	-	cis
I2	3	ASGA0094620	24288043	0.71	0.29	2.22x10 ⁻¹⁵	2.43x10 ⁻¹²	ACSM5	3_prime_UTR_variant	ENSSSCG00000007839	EEF2K	cis
I2	3	ASGA0089883	24297157	0.71	0.29	2.22x10 ⁻¹⁵	2.43x10 ⁻¹²	ACSM5	intronic	ENSSSCG00000007839	EEF2K	cis
I2	3	ASGA0099261	24299990	0.84	0.16	6.93x10 ⁻¹⁴	6.47x10 ⁻¹¹	ACSM5	intronic	ENSSSCG00000007839	EEF2K	cis
I2	3	ALGA0103433	24365103	0.40	0.60	4.04x10 ⁻⁰⁵	9.20x10 ⁻³	ACSM5	intronic	ENSSSCG00000007839	EEF2K	cis
I2	3	MARC0006151	24387052	0.47	0.53	2.70x10 ⁻⁰⁵	6.75x10 ⁻³	ACSM5	intronic	ENSSSCG00000007839	EEF2K	cis
I2	3	ASGA0101242	24418411	0.77	0.23	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	downstream	ENSSSCG00000007842	SDR42E2	cis
I2	3	ASGA0013894	24602938	0.53	0.47	4.46x10 ⁻⁰⁸	2.22x10 ⁻⁵	ACSM5	upstream	ENSSSCG000000027510	-	cis
I2	3	MARC0110831	25162049	0.84	0.16	6.93x10 ⁻¹⁴	6.47x10 ⁻¹¹	ACSM5	intronic	ENSSSCG00000007847	-	cis
I2	3	MARC0115165	25531453	0.80	0.20	4.93x10 ⁻¹¹	4.10x10 ⁻⁸	ACSM5	upstream	ENSSSCG00000007849	CRYM	cis
I2	3	ASGA0085542	25695049	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	MARC0060700	25794656	0.67	0.33	1.11x10 ⁻¹⁶	1.57x10 ⁻¹³	ACSM5	intergenic	-	-	cis
I2	3	ASGA0013904	25862724	0.74	0.26	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0013906	25939787	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	upstream	ENSSSCG00000007853	LYRM1	cis
I2	3	ALGA0018079	25957412	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0095840	25990903	0.74	0.26	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007855	-	cis
I2	3	MARC0108510	26002460	0.74	0.26	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007855	-	cis
I2	3	ALGA0108097	26045382	0.74	0.26	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007857	ACSM3	cis
I2	3	ASGA0103234	26183486	0.66	0.34	8.18x10 ⁻¹²	7.28x10 ⁻⁹	ACSM5	intronic	ENSSSCG000000026453	ACSM5	cis
I2	3	ASGA0085560	26316304	0.76	0.24	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	H3GA0053928	26392557	0.71	0.29	3.40x10 ⁻¹⁴	3.34x10 ⁻¹¹	ACSM5	intergenic	-	-	cis

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I2	3	MARC0101263	26425965	0.83	0.17	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	MARC0050331	26428824	0.79	0.21	4.44x10 ⁻¹⁶	5.66x10 ⁻¹³	ACSM5	intergenic	-	-	cis
I2	3	MARC0019934	26488381	0.34	0.66	1.36x10 ⁻⁵	3.61x10 ⁻³	ACSM5	intergenic	-	-	cis
I2	3	MARC0007734	26517625	0.66	0.34	1.56x10 ⁻¹⁰	1.15x10 ⁻⁷	ACSM5	intergenic	-	-	cis
I2	3	MARC0052941	26537702	0.73	0.27	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	downstream	ENSSSCG00000007862	GPR139	cis
I2	3	ALGA0018104	26631496	0.49	0.51	1.89x10 ⁻⁶	6.34x10 ⁻⁴	ACSM5	intergenic	-	-	cis
I2	3	M1GA0004189	26724456	0.40	0.60	3.53x10 ⁻⁵	8.24x10 ⁻³	ACSM5	intergenic	-	-	cis
I2	3	MARC0001269	26822485	0.72	0.28	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	ALGA0106209	26913735	0.43	0.57	3.16x10 ⁻⁸	1.61x10 ⁻⁵	ACSM5	intronic	ENSSSCG00000029212	GDE1	cis
I2	3	ALGA0121590	26978899	0.52	0.48	2.66x10 ⁻¹⁵	2.83x10 ⁻¹²	ACSM5	intronic	ENSSSCG00000007866	TMC7	cis
I2	3	ASGA0090088	27058670	0.77	0.23	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007868	TMC5	cis
I2	3	MARC0094635	27083041	0.47	0.53	1.13x10 ⁻⁶	4.12x10 ⁻⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0105223	27200658	0.77	0.23	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000022200	-	cis
I2	3	ALGA0124353	27208947	0.53	0.47	9.98x10 ⁻⁶	2.75x10 ⁻³	ACSM5	intronic	ENSSSCG00000022200	-	cis
I2	3	SIRI0001454	27254477	0.77	0.23	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000022200	-	cis
I2	3	MARC0010219	27473051	0.44	0.56	1.56x10 ⁻⁶	5.48x10 ⁻⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0090426	27551099	0.56	0.44	2.20x10 ⁻⁸	1.17x10 ⁻⁵	ACSM5	intergenic	-	-	cis
I2	3	ALGA0018136	27799603	0.47	0.53	4.95x10 ⁻⁶	1.42x10 ⁻³	ACSM5	intronic	ENSSSCG00000007872	-	cis
I2	3	ALGA0018138	27839633	0.71	0.29	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007872	-	cis
I2	3	MARC0000263	27855477	0.59	0.41	3.32x10 ⁻⁷	1.32x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000007872	-	cis
I2	3	MARC0046257	27878993	0.79	0.21	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intronic	ENSSSCG00000007872	-	cis
I2	3	ALGA0018155	27912117	0.66	0.34	1.37x10 ⁻⁷	6.10x10 ⁻⁵	ACSM5	upstream	ENSSSCG00000007872	-	cis
I2	3	ALGA0018160	27925965	0.66	0.34	2.36x10 ⁻⁷	9.92x10 ⁻⁵	ACSM5	intergenic	-	-	cis
I2	3	ASGA0013982	27941321	0.71	0.29	1.11x10 ⁻¹⁷	1.57x10 ⁻¹⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0013988	27988181	0.65	0.35	1.01x10 ⁻⁵	2.76x10 ⁻³	ACSM5	intergenic	-	-	cis

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I2	3	ALGA0018199	28346892	0.66	0.34	9.35x10 ⁻⁷	3.47x10 ⁻⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0014014	28373428	0.65	0.35	2.85x10 ⁻⁷	1.17x10 ⁻⁴	ACSM5	upstream	ENSSSCG00000019735	5S_rRNA	cis
I2	3	ASGA0014023	28786813	0.67	0.33	2.59x10 ⁻⁶	8.47x10 ⁻⁴	ACSM5	intergenic	-	-	cis
I2	3	ASGA0104499	28886788	0.54	0.46	4.94x10 ⁻⁷	1.93x10 ⁻⁴	ACSM5	downstream	ENSSSCG00000019945	U6	cis
I2	3	ASGA0014039	29752690	0.61	0.39	2.89x10 ⁻⁵	7.18x10 ⁻³	ACSM5	intronic	ENSSSCG00000007878	PARN	cis
I2	3	H3GA0009179	30781487	0.63	0.37	4.30x10 ⁻⁶	1.27x10 ⁻³	ACSM5	intergenic	-	-	cis
I2	3	CASI0006297	32293788	0.54	0.46	2.90x10 ⁻⁷	1.18x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I2	3	M1GA0024387	32474314	0.55	0.45	6.00x10 ⁻⁸	2.83x10 ⁻⁵	ACSM5	intergenic	-	-	trans
I2	3	ALGA0119050	32501522	0.55	0.45	6.00x10 ⁻⁸	2.83x10 ⁻⁵	ACSM5	intergenic	-	-	trans
I2	3	MARC0015229	32509563	0.55	0.45	6.00x10 ⁻⁸	2.83x10 ⁻⁵	ACSM5	upstream	ENSSSCG00000007899	-	trans
I2	3	MARC0031378	32543630	0.55	0.45	1.63x10 ⁻⁷	7.09x10 ⁻⁵	ACSM5	intergenic	-	-	trans
I2	3	MARC0004212	34672106	0.44	0.56	1.18x10 ⁻¹⁰	8.93x10 ⁻⁸	ACSM5	synonymous	ENSSSCG00000007909	ABAT	trans
I2	3	M1GA0004280	34875865	0.62	0.38	1.60x10 ⁻⁶	5.52x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I2	3	ASGA0014213	34921528	0.50	0.50	1.39x10 ⁻⁸	7.71x10 ⁻⁶	ACSM5	intronic	ENSSSCG00000007914	-	trans
I2	3	ALGA0115191	34936811	0.30	0.70	1.16x10 ⁻⁵	3.13x10 ⁻³	ACSM5	intronic	ENSSSCG00000007914	-	trans
I2	3	ALGA0107071	35759334	0.69	0.31	1.06x10 ⁻¹¹	9.22x10 ⁻⁹	ACSM5	intergenic	-	-	trans
I2	3	ALGA0102473	37034994	0.76	0.24	8.97x10 ⁻⁸	4.14x10 ⁻⁵	ACSM5	intergenic	-	-	trans
I2	3	MARC0020793	37234505	0.77	0.23	5.05x10 ⁻⁷	1.95x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I2	3	ASGA0105173	39375927	0.37	0.63	1.52x10 ⁻⁵	3.93x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	ALGA0105074	39433703	0.37	0.63	1.52x10 ⁻⁵	3.93x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	ALGA0114510	39644923	0.37	0.63	1.52x10 ⁻⁵	3.93x10 ⁻³	ACSM5	intronic	ENSSSCG00000007951	CREBBP	trans
I2	3	H3GA0009309	39858459	0.37	0.63	1.52x10 ⁻⁵	3.93x10 ⁻³	ACSM5	downstream	ENSSSCG00000007953	DNASE1	trans
I2	3	ALGA0018568	39881683	0.53	0.47	6.11x10 ⁻⁶	1.73x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	M1GA0004302	39992614	0.53	0.47	6.11x10 ⁻⁶	1.73x10 ⁻³	ACSM5	downstream	ENSSSCG00000007954	SLX4	trans
I2	3	ASGA0093403	46893143	0.75	0.25	7.25x10 ⁻¹¹	5.66x10 ⁻⁸	ACSM5	intergenic	-	-	trans

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I2	3	H3GA0009347	47890224	0.53	0.47	3.38x10 ⁻¹⁰	2.35x10 ⁻⁷	ACSM5	intergenic	-	-	trans
I2	3	ALGA0018674	47957752	0.69	0.31	1.63x10 ⁻⁶	5.52x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000008111	NPHP1	trans
I2	3	ALGA0018683	47979489	0.69	0.31	1.63x10 ⁻⁶	5.52x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000008111	NPHP1	trans
I2	3	H3GA0009368	48216866	0.81	0.19	3.26x10 ⁻⁵	7.75x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	MARC0071874	48324056	0.86	0.14	5.07x10 ⁻⁹	2.90x10 ⁻⁶	ACSM5	intergenic	-	-	trans
I2	3	MARC0041994	48345565	0.86	0.14	2.00x10 ⁻⁹	1.23x10 ⁻⁶	ACSM5	downstream	ENSSSCG00000022826	-	trans
I2	3	ALGA0018791	48500096	0.77	0.23	3.02x10 ⁻¹⁰	2.14x10 ⁻⁷	ACSM5	upstream	ENSSSCG00000008121	GPAT2	trans
I2	3	ALGA0114161	48855083	0.81	0.19	3.26x10 ⁻⁵	7.75x10 ⁻³	ACSM5	intronic	ENSSSCG00000008123	ARID5A	trans
I2	3	ASGA0104566	48856852	0.81	0.19	3.26x10 ⁻⁵	7.75x10 ⁻³	ACSM5	intronic	ENSSSCG00000008123	ARID5A	trans
I2	3	ALGA0018800	49041576	0.81	0.19	3.26x10 ⁻⁵	7.75x10 ⁻³	ACSM5	intronic	ENSSSCG00000008127	-	trans
I2	3	ASGA0014426	49104674	0.81	0.19	3.26x10 ⁻⁵	7.75x10 ⁻³	ACSM5	downstream	ENSSSCG00000008129	-	trans
I2	3	ASGA0103041	49443426	0.86	0.14	2.00x10 ⁻⁹	1.23x10 ⁻⁶	ACSM5	intergenic	-	-	trans
I2	3	ASGA0090160	49528314	0.86	0.14	2.00x10 ⁻⁹	1.23x10 ⁻⁶	ACSM5	intergenic	-	-	trans
I2	3	ALGA0018859	49555848	0.78	0.22	1.80x10 ⁻⁷	7.74x10 ⁻⁵	ACSM5	intergenic	-	-	trans
I2	3	H3GA0009485	50180162	0.85	0.15	6.17x10 ⁻⁷	2.36x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000008140	SLC5A7	trans
I2	3	MARC0024281	50793814	0.43	0.57	4.60x10 ⁻⁶	1.33x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	ASGA0014649	56289772	0.65	0.35	2.41x10 ⁻⁵	6.19x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	M1GA0004378	56459296	0.62	0.38	1.97x10 ⁻¹⁰	1.42x10 ⁻⁷	ACSM5	intronic	ENSSSCG00000008175	CHST10	trans
I2	3	M1GA0004379	56484282	0.73	0.27	2.29x10 ⁻⁶	7.55x10 ⁻⁴	ACSM5	3_prime_UTR_variant	ENSSSCG00000008175	CHST10	trans
I2	3	INRA0010621	56668305	0.86	0.14	3.41x10 ⁻⁶	1.07x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	DRGA0003897	56709945	0.86	0.14	3.41x10 ⁻⁶	1.07x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	ALGA0019110	56746317	0.86	0.14	3.41x10 ⁻⁶	1.07x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	ASGA0014688	56833842	0.67	0.33	4.03x10 ⁻⁹	2.34x10 ⁻⁶	ACSM5	intronic	ENSSSCG00000008177	AFF3	trans
I2	3	ASGA0014690	56857721	0.73	0.27	4.09x10 ⁻⁶	1.22x10 ⁻³	ACSM5	intronic	ENSSSCG00000008177	AFF3	trans
I2	3	ALGA0019116	56885984	0.86	0.14	3.41x10 ⁻⁶	1.07x10 ⁻³	ACSM5	intronic	ENSSSCG00000008177	AFF3	trans

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I2	3	ALGA0019121	57129085	0.73	0.27	4.09x10 ⁻⁶	1.22x10 ⁻³	ACSM5	intronic	ENSSSCG00000008177	AFF3	trans
I2	3	ALGA0108239	57170110	0.73	0.27	4.09x10 ⁻⁶	1.22x10 ⁻³	ACSM5	intronic	ENSSSCG00000008177	AFF3	trans
I2	3	MARC0001937	57187517	0.54	0.46	1.25x10 ⁻⁹	8.25x10 ⁻⁷	ACSM5	intronic	ENSSSCG00000008177	AFF3	trans
I2	3	MARC0034058	57211150	0.40	0.60	2.27x10 ⁻⁹	1.38x10 ⁻⁶	ACSM5	intergenic	-	-	trans
I2	3	ASGA0094631	57219021	0.56	0.44	1.06x10 ⁻⁶	3.90x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I2	3	ALGA0019125	57431333	0.73	0.27	4.09x10 ⁻⁶	1.22x10 ⁻³	ACSM5	intronic	ENSSSCG00000008179	REV1	trans
I2	3	ASGA0082387	57704441	0.73	0.27	4.09x10 ⁻⁶	1.22x10 ⁻³	ACSM5	downstream	ENSSSCG00000008185	MITD1	trans
I2	3	ASGA0014810	60580301	0.18	0.82	3.14x10 ⁻⁵	7.75x10 ⁻³	ACSM5	upstream	ENSSSCG00000008213	CD8B	trans
I2	3	MARC0017871	60850148	0.81	0.19	3.97x10 ⁻⁵	9.10x10 ⁻³	ACSM5	downstream	ENSSSCG00000008217	CD8A	trans
I2	3	ASGA0014871	62719672	0.21	0.79	3.86x10 ⁻⁵	8.90x10 ⁻³	ACSM5	intergenic	-	-	trans
I2	3	ALGA0111911	63248078	0.19	0.81	3.42x10 ⁻⁵	8.03x10 ⁻³	ACSM5	intergenic	-	-	trans
I3	3	MARC0032158	83365626	0.35	0.65	1.63x10 ⁻⁶	5.52x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I4	3	ALGA0020206	100905327	0.70	0.30	9.34x10 ⁻⁶	2.59x10 ⁻³	ACSM5	intergenic	-	-	trans
I4	3	ASGA0015465	101222209	0.68	0.32	1.41x10 ⁻⁶	5.09x10 ⁻⁴	ACSM5	intergenic	-	-	trans
I4	3	ASGA0098441	101461883	0.70	0.30	7.63x10 ⁻⁶	2.15x10 ⁻³	ACSM5	intergenic	-	-	trans
I5	10	H3GA0055101	54839	0.47	0.53	8.11x10 ⁻⁷	3.04x10 ⁻⁴	ACSM5	intronic	ENSSSCG00000010795	NDUFAB1	trans
I5	10	MARC0015344	65922	0.47	0.53	8.11x10 ⁻⁷	3.04x10 ⁻⁴	ACSM5	downstream	ENSSSCG00000010795	NDUFAB1	trans
I5	10	ASGA0082591	120016	0.74	0.26	2.00x10 ⁻⁸	1.08x10 ⁻⁵	ACSM5	downstream	ENSSSCG00000010797	EARS2	trans
I5	10	ASGA0092761	150115	0.65	0.35	2.78x10 ⁻⁹	1.66x10 ⁻⁶	ACSM5	intronic	ENSSSCG00000010798	GGA2	trans
I5	10	H3GA0055120	167126	0.70	0.30	2.89x10 ⁻¹⁵	2.99x10 ⁻¹²	ACSM5	downstream	ENSSSCG00000010798	GGA2	trans
I5	10	ASGA0090778	175359	0.76	0.24	1.44x10 ⁻¹⁵	1.72x10 ⁻¹²	ACSM5	intronic	ENSSSCG00000010799	COG7	trans
I5	10	ASGA0094144	184863	0.71	0.29	1.09x10 ⁻⁸	6.13x10 ⁻⁶	ACSM5	intronic	ENSSSCG00000010799	COG7	trans
I5	10	ASGA0095156	202837	0.74	0.26	2.00x10 ⁻⁸	1.08x10 ⁻⁵	ACSM5	intronic	ENSSSCG00000010799	COG7	trans
I6	16	ALGA0089402	19133382	0.66	0.34	3.83x10 ⁻⁵	8.88x10 ⁻³	ACSM5	intronic	ENSSSCG00000016810	PDZD2	trans
I7	13	ASGA0055780	6891435	0.55	0.45	1.20x10 ⁻⁷	4.74x10 ⁻³	ELOVL6	intergenic	-	-	trans

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I8	2	ASGA0008719	6094116	0.48	0.52	1.26x10 ⁻⁵	4.75x10 ⁻²	FABP4	intergenic	-	-	trans
I8	2	MARC0018949	8997005	0.59	0.41	1.38x10 ⁻⁵	4.75x10 ⁻²	FABP4	upstream	ENSSSCG00000023090	BEST1	trans
I9	3	ASGA0015643	109404009	0.69	0.31	1.44x10 ⁻⁵	4.75x10 ⁻²	FABP4	3_prime_UTR_variant	ENSSSCG00000020689	CEBPZOS	trans
I9	3	ALGA0020658	113469226	0.91	0.09	6.70x10 ⁻⁶	4.75x10 ⁻²	FABP4	intronic	ENSSSCG00000008510	LTBP1	trans
I9	3	ASGA0016181	119739502	0.66	0.34	8.31x10 ⁻⁶	4.75x10 ⁻²	FABP4	synonymous	ENSSSCG00000008568	DRC1	trans
I10	4	ALGA0024527	36727180	0.57	0.43	1.11x10 ⁻⁵	4.75x10 ⁻²	FABP4	intergenic	-	-	trans
I11	4	ALGA0025158	60566866	0.48	0.52	1.93x10 ⁻⁶	1.95x10 ⁻²	FABP4	intergenic	-	-	cis (FABP5)
I11	4	ALGA0025162	60844160	0.68	0.32	1.32x10 ⁻⁵	4.75x10 ⁻²	FABP4	intergenic	-	-	cis (FABP5)
I11	4	MARC0115316	61059205	0.52	0.48	1.97x10 ⁻⁶	1.95x10 ⁻²	FABP4	intronic	ENSSSCG00000022989	ZNF704	cis (FABP5)
I11	4	INRA0014244	63090979	0.59	0.41	1.19x10 ⁻⁵	4.75x10 ⁻²	FABP4	intronic	ENSSSCG00000006163	PKIA	cis (FABP5)
I11	4	ALGA0025337	65252780	0.77	0.23	8.67x10 ⁻⁷	1.95x10 ⁻²	FABP4	intergenic	-	-	cis (FABP5)
I12	9	ALGA0054847	129178729	0.88	0.12	1.19x10 ⁻⁶	1.95x10 ⁻²	FABP4	intronic	ENSSSCG00000015508	TNR	trans
I13	2	ASGA0008845	7850065	0.61	0.39	9.88x10 ⁻⁶	3.93x10 ⁻²	FADS2	intronic	ENSSSCG00000013056	LGALS12	trans
I13	2	ASGA0104083	8867970	0.78	0.22	5.98x10 ⁻⁸	5.94x10 ⁻⁴	FADS2	intronic	ENSSSCG00000013066	-	cis
I13	2	ASGA0090054	8943379	0.86	0.14	2.03x10 ⁻⁶	1.15x10 ⁻²	FADS2	intergenic	-	-	cis
I13	2	ALGA0011764	9098547	0.89	0.11	1.54x10 ⁻⁵	4.71x10 ⁻²	FADS2	intergenic	-	-	cis
I13	2	ASGA0008884	9139348	0.92	0.08	1.54x10 ⁻⁵	4.71x10 ⁻²	FADS2	intronic	ENSSSCG00000013072	FADS2	cis
I13	2	ASGA0008896	9171685	0.66	0.34	2.58x10 ⁻⁷	1.71x10 ⁻³	FADS2	intronic	ENSSSCG00000013073	FADS3	cis
I13	2	ALGA0011760	9198141	0.86	0.14	1.21x10 ⁻⁵	4.37x10 ⁻²	FADS2	upstream	ENSSSCG00000013074	RAB3IL1	cis
I13	2	ASGA0008874	9218889	0.79	0.21	2.28x10 ⁻⁷	1.71x10 ⁻³	FADS2	intergenic	-	-	cis
I14	6	ALGA0035721	74418977	0.74	0.26	7.50x10 ⁻⁶	3.31x10 ⁻²	FADS2	intergenic	-	-	trans
I15	8	ASGA0100508	59002816	0.35	0.65	1.93x10 ⁻⁵	4.80x10 ⁻²	FADS2	intronic	ENSSSCG00000025792	-	trans
I15	8	MARC0041089	59080961	0.65	0.35	1.93x10 ⁻⁵	4.80x10 ⁻²	FADS2	intronic	ENSSSCG00000008913	IGFBP7	trans
I15	8	H3GA0024926	68676342	0.65	0.35	1.93x10 ⁻⁵	4.80x10 ⁻²	FADS2	intergenic	-	-	trans
I16	10	H3GA0030086	46933533	0.66	0.34	2.40x10 ⁻⁶	1.19x10 ⁻²	FADS2	intergenic	-	-	trans

Interval	Chr	SNP	Position (bp)	fA1	fA2	p-value	q-value	Associated Gene	Consequence	Ensembl_Geneld	Gene Id	Cis/Trans-eSNPs
I17	9	MARC0034587	20183865	0.76	0.24	2.15x10 ⁻⁵	3.42x10 ⁻²	SLC27A4	intergenic	-	-	trans
I17	9	ASGA0041925	20196539	0.79	0.21	1.69x10 ⁻⁵	2.92x10 ⁻²	SLC27A4	intergenic	-	-	trans
I18	14	ASGA0064787	88898693	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0057510	89058255	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intronic	ENSSSCG00000010342	SH2D4B	trans
I18	14	MARC0029597	89073094	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	downstream	ENSSSCG00000010342	SH2D4B	trans
I18	14	ALGA0079330	89521045	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0041088	90286262	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	ASGA0064841	90338701	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	ASGA0064844	90362764	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0088303	90797721	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	ALGA0079375	90925232	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0010015	91126881	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0003938	91360798	0.91	0.09	6.84x10 ⁻⁶	1.24x10 ⁻²	SLC27A4	intergenic	-	-	trans
I18	14	ALGA0079393	91666877	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0056155	91685430	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	ALGA0079399	92014581	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intergenic	-	-	trans
I18	14	MARC0014799	92290727	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intronic	ENSSSCG00000010350	RGR	trans
I18	14	ALGA0079407	92432834	0.95	0.05	2.51x10 ⁻⁶	4.76x10 ⁻³	SLC27A4	intronic	ENSSSCG00000010351	CCSER2	trans
I19	15	ASGA0070790	137054337	0.93	0.07	3.39x10 ⁻⁵	5.00x10 ⁻²	SLC27A4	intergenic	-	-	trans
I19	15	MARC0050960	137365338	0.93	0.07	3.39x10 ⁻⁵	5.00x10 ⁻²	SLC27A4	intergenic	-	-	trans

Table S3. Transcription factor binding sites for *PPARG* in the *ACSM5* promoter region gene.

TF Name	Sequence	Position*	Strand	Score	P-value
PPARG(M00512)	TTTGGGGCCAGAGGTC	3:26,260,381-26,260,365	+	10.16	2.50×10^{-4}
PPARG(M00512)	CTCAGCGTCAAAGGCAA	3:26,260,939-26,260,922	-	6.66	7.50×10^{-4}

* Chromosomal position is given according to *Sscrofa10.2* assembly coordinates

Table S4. Transcription factor binding site for *SREBF1* in the *FADS2* promoter region gene.

TF Name	Sequence	Position*	Strand	Score	P-value
SREBF1(M00220)	CATCAGGTG	2:9,118,880-9,118,889	+	9.23	5.50x10 ⁻⁴

* Chromosomal position is given according to *Sscrofa10.2* assembly coordinates

Table S6. Mean comparison between males and females of backfat gene expression levels of 43 lipid-related genes.

Gene	Mean in Male (SEM^a)	Mean in Female (SEM^a)	P-value
<i>ACSM5</i>	0.5182 (0.1303)	1.7285 (0.2489)	3.13x10 ⁻⁴
<i>ADIPOQ</i>	0.9216 (0.0444)	0.9828 (0.0290)	2.36x10 ⁻¹
<i>AGPAT2</i>	0.8792 (0.0478)	1.1046 (0.0467)	1.37x10 ⁻³
<i>ANK2</i>	0.8480 (0.0357)	1.1495 (0.0379)	2.29x10 ⁻⁷
<i>ARNT</i>	1.0924 (0.0393)	1.1204 (0.0227)	5.19x10 ⁻¹
<i>CD36</i>	0.9962 (0.0380)	0.9262 (0.0255)	1.19x10 ⁻¹
<i>CPT1A</i>	0.9173 (0.0451)	1.0113 (0.0372)	1.12x10 ⁻¹
<i>CROT</i>	0.9526 (0.0487)	1.0587 (0.0456)	1.22x10 ⁻¹
<i>CYP2U1</i>	1.0761 (0.0621)	1.1121 (0.0403)	6.16x10 ⁻¹
<i>DGAT1</i>	1.0078 (0.0818)	1.1463 (0.0575)	1.60x10 ⁻¹
<i>DGAT2</i>	0.8239 (0.0852)	1.2077 (0.1066)	9.35x10 ⁻³
<i>EGF</i>	0.6850 (0.0719)	1.7432 (0.5234)	8.85x10 ⁻²
<i>ELOVL5</i>	0.9596 (0.0657)	1.1672 (0.0642)	2.98x10 ⁻²
<i>ELOVL6</i>	0.7408 (0.0769)	1.2435 (0.1106)	7.89x10 ⁻⁴
<i>ESRRA</i>	1.0523 (0.0441)	1.1324 (0.0547)	2.85x10 ⁻¹
<i>FABP4</i>	0.9172 (0.0298)	0.9783 (0.0361)	2.20x10 ⁻¹
<i>FABP5</i>	0.8709 (0.0395)	0.8328 (0.0288)	4.29x10 ⁻¹
<i>FADS1</i>	0.8151 (0.0421)	0.8192 (0.0286)	9.35x10 ⁻¹
<i>FADS2</i>	1.0317 (0.0630)	0.8606 (0.0388)	1.79x10 ⁻²
<i>FADS3</i>	0.9534 (0.0321)	0.9414 (0.0208)	7.46x10 ⁻¹
<i>LIPC</i>	1.0681 (0.0678)	1.0736 (0.0429)	9.44x10 ⁻¹
<i>LPIN1</i>	0.9895 (0.0544)	0.9046 (0.0408)	2.09x10 ⁻¹
<i>MGLL</i>	0.9194 (0.0456)	1.0508 (0.0376)	2.84x10 ⁻²
<i>MLXIPL</i>	0.9647 (0.0625)	1.2457 (0.0582)	1.65x10 ⁻³
<i>NFKB1</i>	0.9855 (0.0256)	0.8969 (0.0177)	4.24x10 ⁻³
<i>NR1H3</i>	1.0563 (0.0473)	1.0664 (0.0333)	8.59x10 ⁻¹
<i>PEX2</i>	0.8274 (0.0523)	1.1094 (0.0437)	7.24x10 ⁻⁵
<i>PLA2G12A</i>	0.8832 (0.0521)	1.1725 (0.0484)	1.19x10 ⁻⁴
<i>PLCB2</i>	0.9450 (0.0411)	0.9023 (0.0420)	4.85x10 ⁻¹
<i>PLPP1</i>	1.0787 (0.0416)	0.8176 (0.0311)	1.47x10 ⁻⁶
<i>PNPLA2</i>	0.9063 (0.0411)	1.0913 (0.0365)	1.21x10 ⁻³
<i>POU2F1</i>	0.9196 (0.0249)	0.9700 (0.0264)	1.84x10 ⁻¹
<i>PPARA</i>	0.8984 (0.0652)	1.2135 (0.0510)	2.13x10 ⁻⁴
<i>PPARD</i>	0.8802 (0.0451)	1.2035 (0.0500)	1.15x10 ⁻⁵
<i>PPARG</i>	0.9723 (0.0460)	1.0565 (0.0362)	1.51x10 ⁻¹
<i>RBP4</i>	1.1959 (0.0784)	1.2042 (0.0667)	9.36x10 ⁻¹
<i>RXRG</i>	1.1373 (0.0804)	1.1111 (0.0849)	8.30x10 ⁻¹
<i>SCAP</i>	0.9765 (0.0389)	1.1847 (0.0322)	7.55x10 ⁻⁵
<i>SCD</i>	0.4763 (0.6976)	1.0685 (0.1701)	7.40x10 ⁻³
<i>SLC27A1</i>	1.1737 (0.0694)	1.0792 (0.0504)	2.65x10 ⁻¹
<i>SLC27A4</i>	1.1798 (0.0452)	1.1247 (0.0314)	3.09x10 ⁻¹
<i>SREBF1</i>	0.8074 (0.0516)	1.2552 (0.0612)	5.86x10 ⁻⁷
<i>USF1</i>	1.0324 (0.0362)	1.0333 (0.0191)	9.82x10 ⁻¹

^aStandard error of the mean (SEM)

Table S7. Description of the 393 human orthologous genes.

Interval	Human associated gene name
I1	<i>ALDH7A1, C5orf63, CTXN3, LMNB1, MARCH3, MEGF10, PHAX, PRRC1, TEX43, GRAMD3</i>
I2	<i>ACSM5</i>
I3	<i>B3GNT2, CCT4, COMMD1, EHBP1, FAM161A, NUP54, OTX1, USP34, XPO1, MDH1</i>
I4	<i>ATP6V1E2, CAMKMT, EPAS1, PPM1B, PREPL, PRKCE, RHOQ, SIX2, SLC3A1, SRBD1, TMEM247, PIGF</i>
I5	<i>COG7, EARS2, GGA2, NDUFAB1, PALB2, UBF1, DCTN</i>
I6	<i>C5orf22, DROSHA, PDZD2, CDH6</i>
I7	<i>EFHB, KCNH8, SATB1</i>
I8	<i>AHNAK, AP000721.4, AP5B1, ARL2, ASRGL1, ATG2A, ATL3, B3GAT3, B4GAT1, BAD, BANF1, BATF2, BEST1, BRMS1, BSCL2, C11orf68, C11orf84, C11orf95, C11orf98, CAPN1, CATSPER1, CCDC85B, CCDC88B, CD248, CDC42BPG, CDC42EP2, CDCA5, CFL1, CHRM1, CNIH2, CPSF7, CST6, CTSW, CYB561A3, DAGLA, DDB1, DNAJC4, DPF2, DRAP1, EEF1G, EFEMP2, EHD1, EIF1AD, EML3, ESRRA, FADS1, FADS2, FADS3, FAU, FEN1, FERMT3, FIBP, FKBP2, FLRT1, FOSL1, FRMD8, GAL3ST3, GANAB, GPHA2, GPR137, HNRNPUL2, HRASLS5, INCENP, INTS5, KAT5, KCNK4, KCNK7, KLC2, LGALS12, LRR10B, LTBP3, MACROD1, MAP4K2, MARK2, MEN1, METTL12, MRPL49, MTA2, MUS81, MYRF, NAA40, NAALADL1, NRXN2, NUDT22, NXF1, OTUB1, OVOL1, PACS1, PCNXL3, PGA4, PLA2G16, PLCB3, POLA2, POLR2G, PPP1R14B, PPP1R32, PPP2R5B, PRDX5, PYGM, RAB3IL1, RASGRP2, RCOR2, RELA, RIN1, RNASEH2C, ROM1, RPL13A, RPL22, RPS6KA4, RTN3, SAC3D1, SART1, SCGB1A1, SCGB1D2, SCYL1, SDHAF2, SF1, SF3B2, SIPA1, SLC22A10, SLC22A11, SLC22A12, SLC22A6, SLC22A8, SLC25A45, SLC3A2, SNX15, SNX32, SSSCA1, STIP1, STX5, SYT7, SYVN1, TAF6L, TEX40, TIGD3, TKFC, TM7SF2, TMEM138, TMEM151A, TMEM216, TMEM223, TMEM258, TMEM262, TRMT112, TRPT1, TSGA10IP, TTC9C, TUT1, UBXN1, UQCC3, VEGFB, VPS51, VWCE, WDR74, YIF1A, ZBTB3, ZFPL1, ZNHIT2, SCGB2A1, SLC29A2</i>
I9	<i>ABHD1, ADGRF3, AGBL5, ALK, ASXL2, ATRAID, BIRC6, BRE, C2orf16, C2orf70, C2orf71, CAPN14, CCDC121, CDC42EP3, CEBPZ, CEBPZOS, CENPA, CGREF1, CIB4, CLIP4, CRIM1, DNMT3A, DPY30, DPYSL5, DRC1, DTNB, EHD3, EIF2B4, EMILIN1, EPT1, FAM179A, FAM98A, FEZ2, FNDC4, FOSL2, GAREM2, GCKR, GPATCH11, GPN1, HADHA, HADHB, HEATR5B, IFT172, KHK, KIF3C, KRTCAP3, LBH, LCLAT1, LTBP1, MAPRE3, MEMO1, NDUFAF7, NLRC4, NRBP1, PLB1, PPM1G, PPP1CB, PREB, PRKD3, PRR30, QPCT, RAB10, RASGRP3, RBKS, RMDN2, SLC30A6, SLC35F6, SLC4A1AP, SLC5A6, SNX17, SPAST, SPDYA, SRD5A2, STRN, SUPT7L, TCF23, TMEM214, TRMT61B, TTC27, VIT, WDR43, XDH, YPEL5, YWHAE, ZNF512, CYP1B1, GALNT14</i>
I10	<i>ATP6V1C1, AZIN1, BAALC, CTHRC1, DCAF13, FZD6, KLF10, ODF1, RRM2B, SLC25A32, UBR5, RIMS2</i>
I11	<i>FABP5</i>
I12	<i>CACYBP, GPR52, KIAA0040, MRPS14, PAPP2, RABGAP1L, RFWD2, TNN, TNFR, NXPE2</i>
I14	<i>C1orf234, C1QA, C1QB, C1QC, CDC42, CNR2, ECE1, EPHA8, EPHB2, FUCA1, GALE, HMGCL, HSPG2, HTR1D, KDM1A, LACTBL1, LUZP1, ZBTB40</i>
I15	<i>ADGRL3, CENPC, CEP135, CLOCK, EPHA5, EXOC1, IGFBP7, NOA1, PDCL2, POLR2B, PPIC, REST, TECRL, TMEM165, TMSB4X</i>
I16	<i>ARHGAP12, CUBN, EPC1, ERV3-1, KIF5B, PTCHD3, SVIL, ZEB1, ZNF438</i>
I17	<i>ANKRD42, CCDC90B, DLG2, PCF11, PRCP, RAB30</i>
I18	<i>ANXA11, C10orf99, CCSER2, CDHR1, DYDC1, DYDC2, FAM213A, GHITM, GRID1, LRIT1, LRIT2, MAT1A, NRG3, PLAC9, PPIF, RGR, SFTPA1, SFTPD, SH2D4B, TMEM254, TSPAN14, ZMIZ1</i>
I19	<i>EPHA4, FAR5B, MOGAT1, PAX3, SGPP2</i>

Table S8. Top functional networks and molecules identified with IPA from the list of annotated genes mapping within the 19 eQTLs.

ID	Interval	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
1	I1	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking	21	7	ALDH4A1,ALDH7A1,ALDH8A1,APBB3,APP,ARHGAP24,C3orf62,C9orf78,CASC4,CCL26,CREBBP,CXCL12,DPY19L3,EVI2A,Fcr,FRMD8,GIMAP4,GIMAP5,GIMAP8,GPR85,GRAMD3,GRAMD1C,LMNB1,MARCH3,MEGF10,NMNAT2,Oas1b,PHAX,PRRC1,RGL1,RTP4,SYK,TMOD4,VAV1,ZCCHC12
2	I3	Carbohydrate Metabolism, Organ Morphology, Reproductive System Development and Function	30	10	B3GNT2,B3GNT7,B4GAT1,BRCA1,C16orf62,CCT4,COMMD1,DBR1,EHBP1,EXD2,FAM161A,FAM173A,FAM83A,GAREM1,Hd-neuronal intranuclear inclusions,HEATR5B,HTT,LSM14B,MAGEB18,MDH1,MFAP4,NTRK1,NUP54,OTX1,PLEKHA6,POU5F1,PRRT4,Ptpv,RWDD4,TP53,USP29,USP34,WDR91,XPO1,ZC3H7A
3	I4	Connective Tissue Disorders, Organismal Injury and Abnormalities, Cell Death and Survival	29	10	ALKBH7,APP,C11orf52,C11orf71,C2orf49,C9orf64,CAMKMT,CD40LG,CYB561D2,DTWD1,EPA S1,HNF4A,HPF1,Insulin,MCEE,MPV17L,NBPF3,NFkB (complex),NTRK1,omega-muricholic acid,PI3K (complex),PIGF,PPIP5K2,PPM1B,PREPL,PRKCE,PURG,RHOQ,RSPH3,SIX2,SLC3A1,SRBD1,THYN1,TP53,TP53TG5
4	I4	Molecular Transport, Hereditary Disorder, Metabolic Disease	3	1	ATP6V1B1,ATP6V1C2,ATP6V1E2,ATP6V1G1,C9orf16,H+-exporting ATPase,RICTOR,Vacuolar H+ ATPase
5	I5	Cancer, Organismal Injury and Abnormalities, Reproductive System Disease	21	7	ACOT1,AIM1,ANGPTL2,CDC42SE1,CHST2,CNNM4,COG7,CUL3,DCTN5,DDX10,EARS2,ERBB2,ESR1,FAM98B,GGA2,LCN1,MAN1A1,NDUFAB1,NTRK1,PALB2,PCDH8,PCNA,PGM3,PRR15L,PTPRT,RHOBTB2,RTN4RL1,SPAG1,SPAG4,SUPV3L1,THADA,UBAP2,UBFD1,WDR81,ZSWIM8
6	I6	Cellular Development, Embryonic Development, Hair and Skin Development and Function	12	4	BCL9,Bcl9-Cbp/p300-Ctnnb1-Lef/Tcf,C12orf49,C5orf22,CASC4,CDH6,CDH7,CDH8,CDH9,CDH10,CDH15,CDH18,CNMD,CTBS,CTDSPL,CTNNB1,CTNNβ-LEF1,DACT3,DROSHA,DUSP7,ELAVL1,FBXO8,GLIPR1,GPX2,MUM1,MYBPH,MYC,PDZD2,RPL41,TCF4-CTNNβ,TMEM2,Trp53cor1,UST,VEZT,ZXDB
7	I7	Immunological Disease, Inflammatory Disease, Inflammatory Response	4	1	IL1B,KCNH8,PTGER3
8	I7	Cell Cycle, Organ Morphology, Visual System Development and Function	3	1	ABTB1,BTLA,CLEC2B,CORO6,Cux1,ENOSF1,EPSTI1,EVI2A,FAM110A,FAM129A,FAM65B,FOXJ3,Foxp2,GPR18,GPT2,HELZ2,HLA-DOB,HSF5,HVCN1,Ighen,LAG3,LPIN2,LRRN3,MT1A,MYCL,PIK3IP1,POU3F4,QSER1,SATB1, TBX6,TMEM2,TMEM117,TMEM241,ZKSCAN8,ZNF287

ID	Interval	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
9	18	Cell Cycle, DNA Replication, Recombination, and Repair, Developmental Disorder	52	26	26sProteasome,Actin,BANF1,CAPN1,caspase,CD3,CTSW,DDB1,DPF2,EEF1G,ESRRA,FEN1,FERMT3,FKBP2,HISTONE,Histone h3,Histone h4,INCENP,INTS5,KAT5,KCNK4,MAP4K2,MTA2,MUS81,NFkB (complex),OTUB1,POLA2,POLR2G,PRDX5,RNA polymerase II,RPL13A,SF1,SF3B2,TAF6L,UBXN1
10	18	Lipid Metabolism, Small Molecule Biochemistry, Infectious Diseases	42	22	Akt,BSCL2,Calmodulin,CDCA5,CHRM1,Ck2,ERK,estrogen receptor,FADS1,FADS2,FAU,FIBP,FSH,GANAB,Hsp90,Insulin,LGALS12,Lh,Mapk,MYRF,PLA2,PLA2G16,PLC,PLCB3,PPP2R5B,RELA,SCGB1A1,SLC22A8,SLC3A2,STAT5a/b,STIP1,STX5,SYT7,SYVN1,TMEM216
11	18	Lipid Metabolism, Small Molecule Biochemistry, Cellular Assembly and Organization	32	18	AES,AHNAK,ARL2,C11orf68,C20orf194,CCT3,CDC37,CPSF7,DAGLA,DUS3L,EIF1AD,EML3,GPR137,GPR174,HSP90AA1,KCNK7,KLF3,MAP3K1,MAP3K15,MRPL49,MYLK4,NUDT22,NXF1,PDIK1L,PSKH1,RAB3IL1,SSSCA1,STAT4,SUPT5H,TRMT112,TTC9C,TUBB,TUT1,YWHAQ,ZBTB3
12	18	Cellular Assembly and Organization, Cell-To-Cell Signaling and Interaction, Nervous System Development and Function	25	15	14-3-3,Alp,Ap1,BAD,BRMS1,CDC42EP2,CFL1,Creb,ERK1/2,F-Actin,Fibrinogen,FOSL1,Igg3,IgG2a,Igm,Immunoglobulin,KLC2,LDL,LTBP3,MARK2,MEN1,PACS1,PDGF BB,Pka,Pka catalytic subunit,PP2A,Rap1,Ras,RASGRP2,RIN1,Rock,RPS6KA4,Rsk,SIPA1,VEGFB
13	18	Cellular Compromise, Gastrointestinal Disease, Hepatic System Disease	25	15	ABHD2,ATG2A,BRCA1,C11orf84,C11orf98,CDC42BPG,Cyp2d1/Cyp2d5,DNAJB1,Dnajb1-Hsp70,DNAJC4,DNAJC16,EGFR,EHD1,Esr1-Estrogen-Sp1,FAM153A/FAM153B,HLA-C,HNRNPUL2,HSCB,HSPA9,HSPB1,lipid,MACROD1,MDC1,NAA40,PGA5 (includes others),RCOR2,RPL22,SDHAF2,SP1,SUMO2,TMCO3,TMEM223,tretinoin,TSGA10IP,XRCC5
14	18	Nutritional Disease, Cell Morphology, Cell-To-Cell Signaling and Interaction	21	13	APP,ATL3,C15orf39,CACNG2,CACNG3,CACNG8,CNIH2,DRAP1,FRMD8,GORAB,GRIA1,HIST1H2AD,HRASLS5,INIP,MAD2L1,N-acetyl-L-aspartic acid,OLFM1,OLFM3,PDCD7,PPP1R32,RABL3,REEP6,RTN3,SAC3D1,SCYL1,SLC22A6,SLC30A3,SNX1,SNX14,SNX15,SNX32,SP140L,TCP11L1,TRPT1,ZCCHC6
15	18	Cancer, Cell Death and Survival, Organismal Injury and Abnormalities	21	13	ADIRF,AP5B1,ASRGL1,B3GAT3,BCL2,beta-estradiol,CAMK2B,CD248,FADS3,GSK3B,IFNB1,JUNB,PELP1,PHACTR3,PP1 protein complex group,PPP1R11,PPP1R17,PPP1R14B,PPP1R14C,PPP1R14D,PPP2CA,PPP2R3d,PSMC3,PXYLP1,PYGM,REM1,RNASEH2C,SCGB2A1,TGFB2,TKFC,TMEM44,TMEM258,VPS51,WDR74,YAP/TAZ
16	18	Cellular Function and Maintenance, Organ Development, Reproductive System Development and Function	19	12	adenosine,AIFM2,CACNA11,CATSPER,CATSPER1,CATSPER2,CATSPER3,CATSPER4,CYB561A3,EFEMP2,EGF,KCTD11,LSM14A,NRXN2,PPARD,PRPF8,RNU4-1,RNU5A-1,ROM1,SART1,SLC29A2,SLC30A6,SNRNP27,TMED7,TMEM17,TMEM138,TMEM151A,TP53,UBIAD1,UBL5,USO1,voltage-gated calcium channel,YIF1A,ZFPL1,ZNHIT2

ID	Interval	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
17	18	Cell Death and Survival, Gastrointestinal Disease, Organismal Injury and Abnormalities	17	11	ADGRA1,ADGRG6,Akr1c19,B4GAT1,BEST1,Ca2+,CCDC85B,CPQ,CST6,FLRT1,FPR3,GAL3ST3,GPHA2,GPHB5,GPR19,GPR21,GPR85,GPR108,GPR146,GPR156,HNF1A,NPFFR2,NPS,OSM,P2RY10,PCNX3,PTH1R,SLC22A11,SLC22A12,SOX9,TGFB1,TM7SF2,TRPM5,TSHR,UGT2A3 BATF2,CCDC88B,Ctla2a/Ctla2b,CYP4Z1,Egfr-ErbB2,ESR2,Granzyme,IkB-NfκB,IKK (complex),IL12 (complex),IL12 (family),IL22R1-IL10R2,IRS1/2,isoleucine,Jnk,MIP1,miR-146a-5p (and other miRNAs w/seed GAGAACU),N-arachidonylglycine,OVOL1,P38 MAPK,p85 (pik3r),PI3K (complex),Pkc(s),POU6F1,Rap1-gp91-p22 phox-p40 phox-p47 phox-p67 phox,Sh2b3,SHISA2,TCR,TIGD3,TLR2/TLR4,TPST1,TRAF1-TRAF2-TRAF3,Vegf,Vegfr dimer,VWCE
18	18	Organ Morphology, Organismal Injury and Abnormalities, Reproductive System Development and Function	6	5	
19	18	Developmental Disorder, Hereditary Disorder, Metabolic Disease	2	1	PHLDA3,UQCC3
20	18	Cancer, Organismal Injury and Abnormalities, Reproductive System Disease	2	1	SCGB1D2,SCGB2A2
21	18	Hereditary Disorder, Nephrosis, Organismal Injury and Abnormalities	2	1	METTL12,NT5DC2,XPNPEP3
22	19	Developmental Disorder, Hereditary Disorder, Metabolic Disease	58	25	26sProteasome,ALK,BIRC6,BRE,caspase,CENPA,Cg,CGREF1,CYP1B1,DNMT3A,DPY30,EMILIN1,ERK1/2,FOSL2,GCKR,GPN1,HADHA,HADHB,Histone h3,Jnk,KHK,mediator,MEMO1,NFκB (complex),NLRC4,Pkc(s),PRKD3,RASGRP3,RNA polymerase II,SPAST,SPDYA,SRD5A2,SUPT7L,XDH,YWHAE
23	19	Auditory and Vestibular System Development and Function, Cell Death and Survival, Nervous System Development and Function	32	16	APP,ASXL2,ATRAID,CEBPZ,CIART,CLIP4,CREB1,CRIM1,DPY19L3,FBXO6,FNDCA,GIMAP8,GPR85,IGSF10,KCNC4,MT-ND5,NAGA,NDUFAF7,NMNAT2,NPM1,OCIAD2,PPM1G,PRKACA,QPCT,RAB10,RMDN2,SLC4A1AP,SLC9A6,SNX17,TMEM214,TTC27,WARS2,ZDHHC23,ZNF35,ZNF512
24	19	Cellular Assembly and Organization, Cancer, Cell Morphology	30	15	24R,25-dihydroxyvitamin D3,ABCA1,AGPAT5,ANGPT4,C3orf52,CYP4Z1,DTNB,ELAVL1,ERBB2,FAM20B,FAM98A,GALNT4,GALNT14,HEATR5B,IFT172,LBH,LCLAT1,LPCAT4,MAPK3,norepinephrine,NRBP1,NUDC,PDE7B,PRES,PRKCD,SELENOI,SLC35F6,STRN,TAS1R1,TC2N,TCF23,Vegf,VHL,WDR43,YPEL5
25	19	Cell Morphology, Cellular Assembly and Organization, Nervous System Development and Function	20	11	ACTB,ADGRA1,ADGRF3,AGBL5,CDC42EP3,Clip1,DLG4,DPYSL5,EHD3,FEZ2,FOS,GPR63,GPR137,GPR146,GPR160,HNF4A,KBTBD4,KIF3C,MAPRE3,MSRB2,NGF,NUDT11,ornithine decarboxylase,PCNX1,PTEN,Ptprt,QRFPR,RBKS,SLC30A6,SORCS3,SSTR4,SSU72,TRMT61B,Uba52,VN1R1

ID	Interval	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
26	I9	Amino Acid Metabolism, Carbohydrate Metabolism, Molecular Transport	18	10	Akt,ANGPTL1,ARTN,BMP3,CCDC121,CD38,CLEC4A,CLEC4C,Cyp2j9,DEFB1,DRC1,EIF2B4,ERK,GAREM2,GPATCH11,IFNA2,Insulin,KDM1A,LTBP1,Na+,NANOG,NMN,NMUR2,NRG4,PLB1,PPP1CB,PRR30,S100a7a,SCD5,SLC2A9,SLC5A6,SLC8B1,SLC9A5,THEMIS2,VTCN1
27	I9	Cell Cycle, DNA Replication, Recombination, and Repair, Cellular Development	2	1	ABHD1,CCDC155
28	I9	Neurological Disease, Organismal Injury and Abnormalities, Psychological Disorders	2	1	CIB4,UBB,ZNHIT2
29	I10	Cell Morphology, Cellular Function and Maintenance, Cardiovascular Disease	36	12	ADAT1,ATMIN,ATP6V1C1,AZIN1,BAALC,C9orf64,CA5B,CDK5,CHEK2,CTHRC1,D-glucose,DCAF13,DZANK1,EED,ELAVL1,FZD6,GPR137,GPR180,GUF1,HCN3,HNF4A,KIAA0895,KLF10,ODF1,RIMS2,RRM2B,SLC16A5,SLC25A32,SLC43A2,SMIM7,SMIM12,TMEM101,TNF,UBR5,VN1R1
30	I12	Cell Cycle, Cellular Growth and Proliferation, Tissue Morphology	22	8	ADGRD1,ADGRD2,ADGRF2,ADGRF3,ADGRF4,ADGRG5,CACYBP,DEFB114,ERK1/2,Gpccr,GP R52,GPR61,GPR62,GPR82,GPR149,GPR150,GPR152,GPR157,GPR162,GPR137C,MAS1L,MR PS14,NPFFR1,PAPPA2,RABGAP1L,RB1,RFWD2,RRH,TNF,TNN,TNR,TP53,tretinoin,VN1R1,V N1R2
31	I12	Connective Tissue Development and Function, Connective Tissue Disorders, Nervous System Development and Function	3	1	KIAA0040,KRTAP10-3,MDF1
32	I12	Infectious Diseases, Immunological Disease, Hematological System Development and Function	3	1	AHR,IL10RA,NXPE2
33	I14	Developmental Disorder, Hereditary Disorder, Immunological Disease	26	10	5-oxo-6-8-11-14-(e,z,z,z)-eicosatetraenoic acid,ADGRG6,ALK3-BMPR2,C1q,C1QA,C1QB,C1QC,CDC42,CNR2,CR,CYP4Z1,ECE1,EPHA8,EPHB2,ERK,ERK1/2,Focal adhesion kinase,ganglioside GD2,GPR171,HSPG2,KDM1A,LAIR2,Mapk,N-arachidonylglycine,NMUR1,noladin ether,P38 MAPK,PI3K (complex),PIK3R6,Pka,RXFP3,SCARF1,STYX,TAS1R1,tetraiodothyroacetic acid
34	I14	Cell Signaling, Nucleic Acid Metabolism, Small Molecule Biochemistry	11	5	ADCY4,ADRA2C,ADRB2,APP,BACE2,CPLX1,Dstn/Dstnl1,endocannabinoid,F2RL3,FUCA1,FZD 3,GALE,GPR3,GPR6,GPR12,GPR15,GPR61,GPR78,GPR85,GPRC5B,HMGCL,HTR1B,HTR1D, LPAR3,LUZP1,MRAP2,PIK3R5,PTGDR,RXFP3,S1PR1,SCTR,SLC52A2,SNURF,SP1,VIPR2

ID	Interval	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
35	I14	Cellular Assembly and Organization, Developmental Disorder, Hereditary Disorder	2	1	CDC37,DLG4,FHL1,FOXB1,IER2,ZBTB40
36	I15	Cellular Development, Cellular Growth and Proliferation, Cell Death and Survival	27	10	BCL2,CENPC,CLOCK,DCTPP1,Defb8,EPHA5,ERMAP,HRAS,IGDCC3,IGF1,Igf1-Igfbp,IGFBP7,I11bos,miR-1195 (miRNAs w/seed GAGUUCG),miR-153-3p (miRNAs w/seed UGCAUAG),Mucl1/Mucl2,NOA1,PCDHAC2,POLR2B,POLR2J2/POLR2J3,PPIC,RDM1,REST,RN A Pol-II-TFIIA-TFIIB-TFIID-TFIIF,RNA polymerase II,SCG3,SLC9A8,SNORD118,SPAG7,SPP1,STAT3,TMEM165,TMSB10/TMSB4X,tretinoin,ZNF74
37	I15	Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair	6	3	ADGRL3,CCDC14,CCDC18,CCDC61,CCDC77,CENPJ,CEP72,CEP120,CEP131,CEP135,CEP162,CEP290,CEP295,CEP350,CTNND1,CYLD,EXOC1,FGFR1OP,FOPNL,GYS1,KIAA0753,LUZP1,MAPRE1,MIB1,MTNR1A,NEDD1,PIBF1,PRKAR2A,PRKD1,RALA,SIPA1L1,SIPA1L2,SPATA2,TBC1D31,TMEFF1
38	I15	Cancer, Endocrine System Disorders, Neurological Disease	3	1	CXorf56,GOLGA1,PDCL2
39	I16	Cancer, Hematological Disease, Immunological Disease	17	6	ARHGAP12,beta-estradiol,Crip2,CUBN,CUL7,DNPH1,EPC1,ER- α -Estradiol,FMO1,Gm13194,GPX2,Hmgn2 (includes others),Jnk dimer,JUN,KIF5B,Magea3 (includes others),mir-383,mir-99,MYC,PADI1,PGLYRP2,Ppp1r15a,PRDM2,SCPEP1,SDK1,Snrpc,Sprr2b,Sprr2g,SVIL,TP53,TRIM6,TSKU,UBL3,YY2,ZEB1
40	I16	Cell Cycle, Cancer, Developmental Disorder	3	1	ERV3-1,HECW2
41	I17	Hair and Skin Development and Function, Cellular Compromise, Cell Morphology	18	6	ADGRG6,ANKRD42,B4GALT6,C10orf10,CCDC90B,DEFB114,DLG2,EMCN,FAM132A,FUT3,goralatide,GPR37L1,GUF1,HNF4A,MAPK3,NUDT6,NUDT11,ORM2,PAFAH2,PCF11,PFKFB4,PPP1CA,PPP1R11,PPP1R14D,PRCP,RAB30,RASGRP4,SSTR4,TMEM176B,TNF,ULBP3,UTP11,ZBTB11,ZCCHC9,ZNF300
42	I18	Drug Metabolism, Molecular Transport, Cellular Function and Maintenance	28	11	ADAM10,AFM,ANGPTL7,ANXA11,APP,C2orf57,CALML4,CCSER2,CDHR1,DEF6,DEFA4,DYDC1,DYDC2,ethanol,EZH2,FAM213A,Fcna,FLRT1,GIMAP6,GPR21,GRID1,KIAA0513,MAT1A,MPV17L,NME5,NRG3,OARD1,SLC13A3,TGFB1,THSD4,tretinoin,TSPAN14,TSPAN33,VAT1L,ZMIZ1,ADGRD1,ADGRD2,ADGRF2,ADGRF3,ADGRF4,ADGRG5,EPO,GHITM,Gpcr,GPR27,GPR61,GP R62,GPR75,GPR82,GPR139,GPR148,GPR149,GPR150,GPR152,GPR157,GPR162,GPR137C,HNF4A,LRIT1,MAS1L,NFkB
43	I18	Cell Morphology, Cellular Function and Maintenance, Organismal Development	13	6	(complex),NPFFR1,OXGR1,PPIF,RGR,RRH,SFTPA1,SFTPD,VN1R1,VN1R2

ID	Interval	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
44	I18	Cardiovascular Disease, Hereditary Disorder, Neurological Disease	2	1	CCDC14,EMILIN1,PLAC9,RAPGEF5,RNF213
45	I19	Post-Translational Modification, Gene Expression, Cellular Development	11	4	Calcineurin B,CD6,DUSP2,DUSP8,DUSP16,EPHA1,EPHA4,EYA2,FARSB,FZD10,G0S2,glycochenodeoxycholate,GSTA2,GSTM2,HNF4α dimer,IL36B,Jnk,mir-101,MKP2/5,NUDT1,PAX3,PPP1R16B,PPP2R5B,PRAM1,PTPRH,RLBP1,S1PR4,S1PR5,SGPP2,SH2D3C,sphingosine-1-phosphate,sphingosine-1-phosphate phosphatase,SRGN,TFF2,tretinoin
46	I19	Cell-mediated Immune Response, Cellular Movement, Hematological System Development and Function	3	1	2-acylglycerol O-acyltransferase,AGPAT2,BSCL2,Ccl2,CD44,CXCL10,diacylglycerol O-acyltransferase,MOGAT1,TIMP1,triacylglycerol

Table S9. Transcription factor binding sites for the *PPARG* gene.

ID	Target Name	Interval	Cis/Trans-eQTL	Associated Gene
1	ABHD1	19	<i>trans</i>	<i>FABP4</i>
2	ADIPOQ			
3	AGPAT2			
4	AHNAK	18	<i>trans</i>	<i>FABP4</i>
5	ALK	19	<i>trans</i>	<i>FABP4</i>
6	ATL3	18	<i>trans</i>	<i>FABP4</i>
7	ATP6V1C1	110	<i>trans</i>	<i>FABP4</i>
8	AZIN1	110	<i>trans</i>	<i>FABP4</i>
9	B3GNT2	13	<i>trans</i>	<i>ACSM5</i>
10	BAD	18	<i>trans</i>	<i>FABP4</i>
11	BATF2	18	<i>trans</i>	<i>FABP4</i>
12	BEST1	18	<i>trans</i>	<i>FABP4</i>
13	C1QA	114	<i>trans</i>	<i>FADS2</i>
14	C2orf16	19	<i>trans</i>	<i>FABP4</i>
15	C2orf71	19	<i>trans</i>	<i>FABP4</i>
16	CAPN14	19	<i>trans</i>	<i>FABP4</i>
17	CD248	18	<i>trans</i>	<i>FABP4</i>
18	CD36			
19	CDC42BPG	18	<i>trans</i>	<i>FABP4</i>
20	CDC42EP2	18	<i>trans</i>	<i>FABP4</i>
21	CDC42EP3	19	<i>trans</i>	<i>FABP4</i>
22	CDH6	16	<i>trans</i>	<i>ACSM5</i>
23	CDHR1	118	<i>trans</i>	<i>SLC27A4</i>
24	CENPA	19	<i>trans</i>	<i>FABP4</i>
25	CEP135	115	<i>trans</i>	<i>FADS2</i>
26	CHRM1	18	<i>trans</i>	<i>FABP4</i>
27	CIB4	19	<i>trans</i>	<i>FABP4</i>
28	CLOCK	115	<i>trans</i>	<i>FADS2</i>
29	CPSF7	18	<i>trans</i>	<i>FABP4</i>
30	CPT1A			
31	CRIM1	19	<i>trans</i>	<i>FABP4</i>
32	CST6	18	<i>trans</i>	<i>FABP4</i>
33	CTHRC1	110	<i>trans</i>	<i>FABP4</i>
34	CTXN3	11	<i>trans</i>	<i>ACSM5</i>
35	CUBN	116	<i>trans</i>	<i>FADS2</i>
36	CYP2U1			
37	DAGLA	18	<i>trans</i>	<i>FABP4</i>
38	DDB1	18	<i>trans</i>	<i>FABP4</i>
39	DGAT1			
40	DGAT2			

ID	Target Name	Interval	Cis/Trans-eQTL	Associated Gene
41	<i>DLG2</i>	117	<i>trans</i>	<i>SLC27A4</i>
42	<i>DNMT3A</i>	19	<i>trans</i>	<i>FABP4</i>
43	<i>ECE1</i>	114	<i>trans</i>	<i>FADS2</i>
44	<i>EHBP1</i>	13	<i>trans</i>	<i>ACSM5</i>
45	<i>EHD3</i>	19	<i>trans</i>	<i>FABP4</i>
46	<i>ELOVL5</i>			
47	<i>EMILIN1</i>	19	<i>trans</i>	<i>FABP4</i>
48	<i>EML3</i>	18	<i>trans</i>	<i>FABP4</i>
49	<i>EPAS1</i>	14	<i>trans</i>	<i>ACSM5</i>
50	<i>EPC1</i>	116	<i>trans</i>	<i>FADS2</i>
51	<i>EPHA8</i>	114	<i>trans</i>	<i>FADS2</i>
52	<i>EPT1</i>	19	<i>trans</i>	<i>FABP4</i>
53	<i>ESRRA</i>	18	<i>trans</i>	<i>FABP4</i>
54	<i>FABP4</i>			
55	<i>FADS1</i>	18	<i>trans</i>	<i>FABP4</i>
56	<i>FADS2</i>	18.113	<i>trans/cis</i>	<i>FABP4/FADS2</i>
57	<i>FADS3</i>	18	<i>trans</i>	<i>FABP4</i>
58	<i>FAM179A</i>	19	<i>trans</i>	<i>FABP4</i>
59	<i>FKBP2</i>	18	<i>trans</i>	<i>FABP4</i>
60	<i>FLRT1</i>	18	<i>trans</i>	<i>FABP4</i>
61	<i>FNDC4</i>	19	<i>trans</i>	<i>FABP4</i>
62	<i>FOSL1</i>	18	<i>trans</i>	<i>FABP4</i>
63	<i>FOSL2</i>	19	<i>trans</i>	<i>FABP4</i>
64	<i>FRMD8</i>	18	<i>trans</i>	<i>FABP4</i>
65	<i>GAL3ST3</i>	18	<i>trans</i>	<i>FABP4</i>
66	<i>GALNT14</i>	19	<i>trans</i>	<i>FABP4</i>
67	<i>GCKR</i>	19	<i>trans</i>	<i>FABP4</i>
68	<i>GGA2</i>	15	<i>trans</i>	<i>ACSM5</i>
69	<i>GPR52</i>	112	<i>trans</i>	<i>FABP4</i>
70	<i>GRID1</i>	118	<i>trans</i>	<i>SLC27A4</i>
71	<i>HADHA</i>	19	<i>trans</i>	<i>FABP4</i>
72	<i>HSPG2</i>	114	<i>trans</i>	<i>FADS2</i>
73	<i>IGFBP7</i>	115	<i>trans</i>	<i>FADS2</i>
74	<i>KCNH8</i>	17	<i>trans</i>	<i>ELOVL6</i>
75	<i>KHK</i>	19	<i>trans</i>	<i>FABP4</i>
76	<i>KIAA0040</i>	112	<i>trans</i>	<i>FABP4</i>
77	<i>KIF5B</i>	116	<i>trans</i>	<i>FADS2</i>
78	<i>KLC2</i>	18	<i>trans</i>	<i>FABP4</i>
79	<i>KLF10</i>	110	<i>trans</i>	<i>FABP4</i>
80	<i>LBH</i>	19	<i>trans</i>	<i>FABP4</i>

ID	Target Name	Interval	Cis/Trans-eQTL	Associated Gene
81	<i>LCLAT1</i>	19	<i>trans</i>	<i>FABP4</i>
82	<i>LIPC</i>			
83	<i>LMNB1</i>	11	<i>trans</i>	<i>ACSM5</i>
84	<i>LPIN1</i>			
85	<i>LRRC10B</i>	18	<i>trans</i>	<i>FABP4</i>
86	<i>LTBP1</i>	19	<i>trans</i>	<i>FABP4</i>
87	<i>LTBP3</i>	18	<i>trans</i>	<i>FABP4</i>
88	<i>LUZP1</i>	114	<i>trans</i>	<i>FADS2</i>
89	<i>MACROD1</i>	18	<i>trans</i>	<i>FABP4</i>
90	<i>MAP4K2</i>	18	<i>trans</i>	<i>FABP4</i>
91	<i>MAPRE3</i>	19	<i>trans</i>	<i>FABP4</i>
92	<i>MARCH3</i>	11	<i>trans</i>	<i>ACSM5</i>
93	<i>MARK2</i>	18	<i>trans</i>	<i>FABP4</i>
94	<i>MDH1</i>	13	<i>trans</i>	<i>ACSM5</i>
95	<i>MEGF10</i>	11	<i>trans</i>	<i>ACSM5</i>
96	<i>MGLL</i>			
97	<i>MIR194-2</i>	18	<i>trans</i>	<i>FABP4</i>
98	<i>MLXIPL</i>			
99	<i>MOGAT1</i>	119	<i>trans</i>	<i>SLC27A4</i>
100	<i>MRPL49</i>	18	<i>trans</i>	<i>FABP4</i>
101	<i>NR1H3</i>			
102	<i>NRXN2</i>	18	<i>trans</i>	<i>FABP4</i>
103	<i>NUDT22</i>	18	<i>trans</i>	<i>FABP4</i>
104	<i>OVOL1</i>	18	<i>trans</i>	<i>FABP4</i>
105	<i>PAPPA2</i>	112	<i>trans</i>	<i>FABP4</i>
106	<i>PCNXL3</i>	18	<i>trans</i>	<i>FABP4</i>
107	<i>PDZD2</i>	16	<i>trans</i>	<i>ACSM5</i>
108	<i>PEX2</i>			
109	<i>PLA2G16</i>	18	<i>trans</i>	<i>FABP4</i>
110	<i>PLAC9</i>	118	<i>trans</i>	<i>SLC27A4</i>
111	<i>PLCB2</i>			
112	<i>PLCB3</i>	18	<i>trans</i>	<i>FABP4</i>
113	<i>PNPLA2</i>			
114	<i>POU2F1</i>			
115	<i>PPARA</i>			
116	<i>PPARG</i>			
117	<i>PPIF</i>	118	<i>trans</i>	<i>SLC27A4</i>
118	<i>PPM1B</i>	14	<i>trans</i>	<i>ACSM5</i>
119	<i>PPP1R14B</i>	18	<i>trans</i>	<i>FABP4</i>
120	<i>PRKCE</i>	14	<i>trans</i>	<i>ACSM5</i>

ID	Target Name	Interval	Cis/Trans-eQTL	Associated Gene
121	<i>PRKD3</i>	19	<i>trans</i>	<i>FABP4</i>
122	<i>PRRC1</i>	11	<i>trans</i>	<i>ACSM5</i>
123	<i>PYGM</i>	18	<i>trans</i>	<i>FABP4</i>
124	<i>RAB30</i>	117	<i>trans</i>	<i>SLC27A4</i>
125	<i>RAB3IL1</i>	18	<i>trans</i>	<i>FABP4</i>
126	<i>RABGAP1L</i>	112	<i>trans</i>	<i>FABP4</i>
127	<i>RASGRP2</i>	18	<i>trans</i>	<i>FABP4</i>
128	<i>RASGRP3</i>	19	<i>trans</i>	<i>FABP4</i>
129	<i>RBP4</i>			
130	<i>RCOR2</i>	18	<i>trans</i>	<i>FABP4</i>
131	<i>REST</i>	115	<i>trans</i>	<i>FADS2</i>
132	<i>RHOQ</i>	14	<i>trans</i>	<i>ACSM5</i>
133	<i>RIMS2</i>	110	<i>trans</i>	<i>FABP4</i>
134	<i>RTN3</i>	18	<i>trans</i>	<i>FABP4</i>
135	<i>RXRG</i>			
136	<i>SATB1</i>	17	<i>trans</i>	<i>ELOVL6</i>
137	<i>SCD</i>			
138	<i>SF3B2</i>	18	<i>trans</i>	<i>FABP4</i>
139	<i>SH2D4B</i>	118	<i>trans</i>	<i>SLC27A4</i>
140	<i>SLC22A11</i>	18	<i>trans</i>	<i>FABP4</i>
141	<i>SLC22A12</i>	18	<i>trans</i>	<i>FABP4</i>
142	<i>SLC25A45</i>	18	<i>trans</i>	<i>FABP4</i>
143	<i>SLC27A1</i>			
144	<i>SLC27A4</i>			
145	<i>SLC5A6</i>	19	<i>trans</i>	<i>FABP4</i>
146	<i>SNX15</i>	18	<i>trans</i>	<i>FABP4</i>
147	<i>SNX17</i>	19	<i>trans</i>	<i>FABP4</i>
148	<i>SREBF1</i>			
149	<i>STRN</i>	19	<i>trans</i>	<i>FABP4</i>
150	<i>SYT7</i>	18	<i>trans</i>	<i>FABP4</i>
151	<i>TAF6L</i>	18	<i>trans</i>	<i>FABP4</i>
152	<i>TCF23</i>	19	<i>trans</i>	<i>FABP4</i>
153	<i>TMEM138</i>	18	<i>trans</i>	<i>FABP4</i>
154	<i>TMEM165</i>	115	<i>trans</i>	<i>FADS2</i>
155	<i>TNN</i>	112	<i>trans</i>	<i>FABP4</i>
156	<i>TNR</i>	112	<i>trans</i>	<i>FABP4</i>
157	<i>TRPT1</i>	18	<i>trans</i>	<i>FABP4</i>
158	<i>TSPAN14</i>	118	<i>trans</i>	<i>SLC27A4</i>
159	<i>TUT1</i>	18	<i>trans</i>	<i>FABP4</i>
160	<i>UBR5</i>	110	<i>trans</i>	<i>FABP4</i>

ID	Target Name	Interval	Cis/Trans-eQTL	Associated Gene
161	<i>VIT</i>	19	<i>trans</i>	<i>FABP4</i>
162	<i>VWCE</i>	18	<i>trans</i>	<i>FABP4</i>
163	<i>XDH</i>	19	<i>trans</i>	<i>FABP4</i>
164	<i>ZBTB40</i>	114	<i>trans</i>	<i>FADS2</i>
165	<i>ZEB1</i>	116	<i>trans</i>	<i>FADS2</i>
166	<i>ZMIZ1</i>	118	<i>trans</i>	<i>SLC27A4</i>
167	<i>ZNF438</i>	116	<i>trans</i>	<i>FADS2</i>

Table S10. Pearson's correlations of *PPARG* mRNA expression and analyze-related genes.

Gene	Pearson correlation coefficient	p-value
<i>ACSM5</i>	0.08	3.86x10 ⁻¹
<i>ADIPOQ</i>	0.66	1.78x10 ⁻¹⁵
<i>AGPAT2</i>	0.54	6.98x10 ⁻¹⁰
<i>ANK2</i>	0.27	3.93x10 ⁻³
<i>ARNT</i>	0.30	1.42x10 ⁻³
<i>CD36</i>	0.70	2.22x10 ⁻¹⁶
<i>CPT1A</i>	0.03	7.33x10 ⁻¹
<i>CROT</i>	0.50	1.71x10 ⁻⁸
<i>CYP2U1</i>	0.54	6.01x10 ⁻¹⁰
<i>DGAT1</i>	0.62	2.53x10 ⁻¹³
<i>DGAT2</i>	0.61	1.09x10 ⁻¹²
<i>EGF</i>	0.08	4.00x10 ⁻¹
<i>ELOVL5</i>	0.75	2.22x10 ⁻¹⁶
<i>ELOVL6</i>	0.68	2.22x10 ⁻¹⁶
<i>ESRRA</i>	0.43	2.41x10 ⁻⁶
<i>FABP4</i>	0.51	9.27x10 ⁻⁹
<i>FABP5</i>	0.40	1.27x10 ⁻⁵
<i>FADS1</i>	0.12	1.95x10 ⁻¹
<i>FADS2</i>	0.18	5.92x10 ⁻²
<i>FADS3</i>	0.17	7.71x10 ⁻²
<i>LIPC</i>	0.27	3.55x10 ⁻³
<i>LPIN1</i>	0.69	2.22x10 ⁻¹⁶
<i>MGLL</i>	0.43	1.90x10 ⁻⁶
<i>MLXIPL</i>	0.61	5.55x10 ⁻¹³
<i>NFKB1</i>	0.58	2.49x10 ⁻¹¹
<i>NR1H3</i>	0.56	1.56x10 ⁻¹⁰
<i>PEX2</i>	0.60	1.69x10 ⁻¹²
<i>PLA2G12A</i>	0.61	9.13x10 ⁻¹³
<i>PLCB2</i>	0.13	1.71x10 ⁻¹
<i>PLPP1</i>	0.27	4.16x10 ⁻³
<i>PNPLA2</i>	0.55	3.09x10 ⁻¹⁰
<i>POU2F1</i>	0.25	7.75x10 ⁻³
<i>PPARA</i>	0.63	1.01x10 ⁻¹³
<i>PPARD</i>	0.48	8.61x10 ⁻⁸
<i>RBP4</i>	0.36	1.11x10 ⁻⁴
<i>RXRG</i>	0.41	7.83x10 ⁻⁶
<i>SCAP</i>	0.45	4.59x10 ⁻⁷
<i>SCD</i>	0.59	1.01x10 ⁻¹¹
<i>SLC27A1</i>	0.23	1.23x10 ⁻²
<i>SLC27A4</i>	0.23	1.60x10 ⁻²
<i>SREBF1</i>	0.55	2.63x10 ⁻¹⁰
<i>USF1</i>	0.33	4.15x10 ⁻⁴

Table S11. Primers used for the characterization of the 3'UTR of porcine *FABP4* gene.

Gene	Full name	Primer Name	Type	Primer Sequence¹
<i>FABP4</i>	<i>Fatty acid binding protein 4</i>	oligo(dT)-UAP	mRNA 3' UTR amplification	5'-GGCCACGCGTCGACTAGTAC(T)30VN-3'
<i>FABP4</i>	<i>Fatty acid binding protein 4</i>	UAP	mRNA 3' UTR amplification	5'-GGCCACGCGTCGACTAGTAC-3'
<i>FABP4</i>	<i>Fatty acid binding protein 4</i>	FABP4-3NC-1-Fw	mRNA 3' UTR sequencing	5'-TTGGATCGAACTCTACAACACTCTG-3'
<i>FABP4</i>	<i>Fatty acid binding protein 4</i>	FABP4-3NC-2-Fw	mRNA 3' UTR sequencing	5'-TGTTTATGGATCTTCCATTATCTTAGG-3'

¹Primers were designed from the GenBank Y16039 sequence

Table S12. Primers used for the analyses of gene expression of the 48 genes by real-time PCR.

Gene	Full name	Type	Primer sequence	
			Forward	Reverse
<i>ACSM5</i>	Acyl-CoA synthetase medium-chain family member 5	Target	5'-TGTAATCTGTGCCAATCCCAA-3'	5'-CATCATCTACGATCTGCACCTCAT-3'
<i>ACTB</i>	Actin, Beta	Reference	5'-CAAGGACCTCTACGCCAACAC-3'	5'-TGGAGGCGCGATGATCTT-3'
<i>ADIPOQ</i>	Adiponectin, C1Q and collagen domain containing	Target	5'-GTACCCAGGCCGTGATG-3'	5'-CCCTTAGGACCAGTAAGACCTGTATCT-
<i>AGPAT2</i>	1-acylglycerol-3-phosphate O-acyltransferase 2	Target	5'-CATGGTCAGGAGAAGCTCAA-3'	5'-GCCAGGTAGAAGGCACCTTTC-3'
<i>ANK2</i>	Ankyrin 2	Target	5'-GTGGATTCTGCTACGAAGAAAGG-3'	5'-AAGGACTTTGACAACCTTCTGCTTGT-3'
<i>ARNT</i>	Aryl hydrocarbon receptor nuclear translocator	Target	5'-TCTAATGATAAGGAGCGGTTTGC-3'	5'-TATGATTTTCCCTGGCGAGTCT-3'
<i>B2M</i>	Beta-2-microglobulin	Reference	5'-ACCTTCTGGTCCACACTGAGTTC-3'	5'-GGTCTCGATCCCCTTAACCTATCTTG-3'
<i>CD36</i>	CD36 molecule	Target	5'-GGTCCTTACACGTACAGAGTTCGTT-3'	5'-CCATTGGGCTGTAGGAAAGAGA-3'
<i>CPT1A</i>	Carnitine palmitoyltransferase 1A	Target	5'-CCTGAAGGTGCTGCTCTCCTA-3'	5'-CTCACCATCATCATCCAGATCTTG-3'
<i>CROT</i>	Carnitine O-octanoyltransferase	Target	5'-GGGAAACGAAATTGGTTGGA-3'	5'-CGCAAAGTTGACATTCAGTTGTG-3'
<i>CYP2U1</i>	Cytochrome P450, family 2, subfamily U, member 1	Target	5'-AGAGAAAACAGTGCTCCAAGGGTAT-3'	5'-TGGCTGGGTCTCTGTGTACTGA-3'
<i>DGAT1</i>	Diacylglycerol O-acyltransferase 1	Target	5'-CCTGAATTGGTGTGTGGTCATG-3'	5'-GATGCCGTACTTGATGAGGTTCTC-3'
<i>DGAT2</i>	Diacylglycerol O-acyltransferase 2	Target	5'-GGAACACGCCCAAGAAAGGT-3'	5'-GGATGGGAAAGTAGTCTCGAAAGTAG-3'
<i>EGF</i>	Epidermal growth factor	Target	5'-AACGGGAATGCCACTTGTGT-3'	5'-CCTTCCAAGTCAATCCTAAAGATACTG-3'
<i>ELOVL5</i>	ELOVL fatty acid elongase 5	Target	5'-CCTCTCGGCTGGCTGTACTT-3'	5'-CCTTCTTGGTTGAGGTCTGGATGTAG-3'
<i>ELOVL6</i>	ELOVL fatty acid elongase 6	Target	5'-AGCAGTTCAACGAGAACGAAGCC-3'	5'-TGCCGACCGCCAAAGATAAAG-3'
<i>ESRRA</i>	Estrogen-related receptor alpha	Target	5'-CAAGAGCATCCCAGGCTTCTC-3'	5'-CACCCAACACCAATACCTCCAT-3'
<i>FABP4</i>	Fatty acid binding protein 4	Target	5'-TAAGTTGGTGGTGAATGTATCATG-3'	5'-AGAGTGTGTAGAGTTCGATCCAAAC-3'
<i>FABP5</i>	Fatty acid binding protein 5	Target	5'-CCAATGGAGAATTGGTTCAACA-3'	5'-GTTTCATGACGCATACCACCACTA-3'
<i>FADS1</i>	Fatty acid desaturase 1	Target	5'-CCTTGTGAGGAAGTATATGAGCTCTCT-3'	5'-TCATCTGTCAGCTCTTTATTCTTAGTCG-3'
<i>FADS2</i>	Fatty acid desaturase 2	Target	5'-TCCACCGCGACCTTGATTTA-3'	5'-TCGGTGATCTCAGAGTTCTTGGT-3'
<i>FADS3</i>	Fatty acid desaturase 3	Target	5'-CCAGCACCTCTACTTCTTCTGAT-3'	5'-CATGTATGCCAGATTTTCCACTTC-3'

Gene	Full name	Type	Primer sequence	
			Forward	Reverse
<i>HPRT1</i>	Hypoxanthine phosphoribosyltransferase 1	Reference	5'- TCATTATGCCGAGGATTTGGA-3'	5'- CTCTTTCATCACATCTCGAGCAA-3'
<i>LIPC</i>	Lipase C, hepatic type	Target	5'- CGTTACAGCAGTGTGGCTTCA-3'	5'- CCAGCAAGCCATCCATCAA-3'
<i>LPIN1</i>	Lipin 1	Target	5'- CCGAGAGAAGGTGGTGGACAT-3'	5'- CTCTCCATTGTCTCCCAGTTTCA-3'
<i>MGLL</i>	Monoglyceride lipase	Target	5'-GTGTTTCGCCACGACCAT-3'	5'-CCTGACGAACACCTGGAAGTC-3'
<i>MLXIPL</i>	MLX Interacting Protein-Like	Target	5'-CCCAAGTGAAGAATTTCAAAGG-3'	5'-CTTCCTCCGCTCCACATACTG-3'
<i>NFKB1</i>	Nuclear factor kappa B subunit 1	Target	5'-CCCACAGACGTTTCATAGACAATTT-3'	5'-GAGGCTGGTTTTGTAAATGTTGACA-3'
<i>NR1H3</i>	Nuclear Receptor Subfamily 1, Group H, Member 3	Target	5'-CTGGGCATGATCGAGAAGCT-3'	5'-TGGGCCAAGGCGTGACT-3'
<i>PEX2</i>	Peroxisomal biogenesis factor 2	Target	5'-CTCAGACTCCTAAGAAACCTTCAGAGA-3'	5'-ACTGATTCTGAGCACTCTGTTTGC-3'
<i>PLA2G12A</i>	Phospholipase A2, group XIIA	Target	5'-CCCCTCTTTGGTGTTCATCTTAA-3'	5'-ATAGCACCTGTGCTGCTGGTT-3'
<i>PLCB2</i>	Phospholipase C, beta 2	Target	5'- AGATCTTCACCTCCTACCACTCCAA-3'	5'- GCGCTGTTTCTGGTTGATGA-3'
<i>PLPP1</i>	Phospholipid phosphatase 1	Target	5'-GGCCACTCTTCATTCTCCATGTAC-3'	5'-AGGCCACGTAATGGATACAG-3'
<i>PNPLA2</i>	Patatin-like phospholipase domain containing 2	Target	5'-CTTCACCGTCCGCTTGCT-3'	5'-GCATCACCAGGACTGGCAGAT-3'
<i>POU2F1</i>	POU class 2 homeobox 1	Target	5'- CCCATACAGATCGCACAGGAT-3'	5'- GATGATAAACTGTGCTGGTTGCA-3'
<i>PPARA</i>	Peroxisome proliferator-activated receptor alpha	Target	5'-GGCACTGAACATCGAATGTAGAATC-3'	5'-CCGAAAGAAGCCCTTGCAA-3'
<i>PPARD</i>	Peroxisome proliferator-activated receptor delta	Target	5'-GCATGTCTCA CAACGCCATT-3'	5'-GCTGACTCCCCTCGTTTGC-3'
<i>PPARG</i>	Peroxisome proliferator-activated receptor gamma	Target	5'-TTGTGAAGGATGCAAGGGTTT-3'	5'-ATCCGACAGTTAAGATCGCACCTA-3'
<i>PPARGC1A</i>	Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	Target	5'-CTCTGGAAGTGCAGGCCTAA-3'	5'-TGGAGAAGCCCTAAAAGGGTTAT-3'
<i>RBP4</i>	Retinol binding protein 4	Target	5'-GGGTCGAGTCCGTCTTTTAAATAACT-3'	5'-GGTCCTCGGTGTCTGTAAAGGT-3'
<i>RXRG</i>	Retinoid X receptor, gamma	Target	5'-GAGGATTCTGGAAGCTGAACTTG-3'	5'-TCATTCGTCGAATTCTCCATGT-3'
<i>SCAP</i>	SREBF chaperone	Target	5'- AGATATCTCAGGCCTTCTACAACCA-3'	5'- AGTTTCAACAGTGGGTAGCAGC-3'
<i>SCD</i>	Stearoyl-CoA Desaturase	Target	5'- GGTGATGTTCCAGAGGAGGTACTAC-3'	5'- CAGCAATACCAGGGCAGAT-3'
<i>SLC27A1</i>	Solute carrier family 27, member 1	Target	5'-TCACTCGGCAGGGAACATC-3'	5'-CGGCTGGCTGAAAACCTTCTT-3'
<i>SLC27A4</i>	Solute carrier family 27, member 4	Target	5'-GCTGCATAAAACAGGGACTTTCA-3'	5'-AACAGCGGGTCTTTCACGACT-3'

Gene	Full name	Type	Primer sequence	
			Forward	Reverse
<i>SREBF1</i>	Sterol Regulatory Element Binding Transcription Factor 1	Target	5'-CACGGAGGCGAAGCTGAATA-3'	5'-GCTTCTGGTTGCTCTGCTGAA-3'
<i>TBP</i>	TATA-Box Binding Protein	Reference	5'-CAGAATGATCAAACCGAGAATTGT-3'	5'-CTGCTCTGACTTTAGCACCTGTTAA-3'
<i>USF1</i>	Upstream transcription factor 1	Target	5'- CCCTTATTCCCCGAAGTCAGA-3'	5'- GCGGCGTTCCACTTCATTAT-3'