

Supplemental Table 1. *LPL* SNPs identified by sequencing in this study. PCRs were performed using synthetic oligonucleotide primers prior to sequencing.

Gene Name	SNP ID (rs# or new)	Functional Position	5' Flanking Seq.	Allele	3' Flanking Seq.	5' (forward) PCR Primer	3' (reverse) PCR Primer	PCR Product Size (bp)	MAF
LPL_1	rs11570898	intron2(+155)	cccagtgatgggtccgcacc	C/T	cacatctcacgtggatctcc	GTTCTCTTGCAATCCACATT	GGAGTTCTCATGAACCTGTG	491	0.022
LPL_2	rs3735959	intron3(+20)	ggtaagactgggagaaggag	A/C	cttatgtgtccaaaacagtg	GGACAGACCTGTCTCTGAAC	ACGCTGATTCTGAAGATTG	480	0.043
LPL_3	new	intron3(-54:exon4)	tatattcattttgtttcttt	T/C	agttttatttttggcagaac	ACGGAAAAGTGAAACAAAAG	AGTGAGAGCGTCTGTGTTTT	500	0.022
LPL_4	rs343	intron3(-34:exon4)	tagttttatttttggcagaa	C/A	tgtaagcaccttcattttct	ACGGAAAAGTGAAACAAAAG	AGTGAGAGCGTCTGTGTTTT	500	0.13
LPL_5	rs249	intron4(+74)	tgagagagaatcagaacaaa	T/C	tttgtaataatcccacatgt	ACGGAAAAGTGAAACAAAAG	AGTGAGAGCGTCTGTGTTTT	500	0.087
LPL_6	rs250	intron4(+97~+98)	attttgttaaatacccacat	INS_TG	gtgtggtgttcttcccggag	ACGGAAAAGTGAAACAAAAG	AGTGAGAGCGTCTGTGTTTT	500	0.13
LPL_7	rs254	intron5(+33)	tagaagcgaattaaatgtga	C/G	tcttatccttaacccttatt	TCATTTTAGAAGGAGCCAAG	TGCCCAAATGTGTATATGAA	527	0.217
LPL_8	rs255	intron5(+37)	agcgaataaatgtgactct	T/C	atccttaacccttattgacc	TCATTTTAGAAGGAGCCAAG	TGCCCAAATGTGTATATGAA	527	0.217
LPL_9	rs264	intron5(-171:exon6)	ctcttgaaggtgggtgggccc	G/A	ctaccaccaagaatatctcc	TGCAACTTTCCTCTCTTGA	GTTCCAATGGACAGAATCAG	539	0.087
LPL_10	rs301	intron7(+43)	catcatggcaccagtcctcc	T/C	cctgccataacccttggtct	GAACACTGTGCATGATGAAG	TCAAATAGAGGAAAGACCTCA	443	0.217
LPL_11	rs316	exon8(+25)	gaagtttccacaataagac	C/A	tactccttcctaatttccac	TACTAAATGCCATCGACCTT	AAGGTTTCCTAAAGCTCTCC	461	0.087
LPL_12	rs326	intron8(-187:exon9)	tagcttggtgtgctgaacacc	A/G	ggttaggctctcaaattacc	AACTAGCTTGTTGCTGAAC	CATAAAGCAACAGACCCATT	493	0.239
LPL_13	rs327	intron8(-90:exon9)	ttaccagcatgatcatgta	T/G	tatttaaacagtcctgacag	AACTAGCTTGTTGCTGAAC	CATAAAGCAACAGACCCATT	493	0.239
LPL_14	rs328	exon9(+99)	acaagtcctctgaataagaag	C/G	aggctggtgagcattctggg	AACTAGCTTGTTGCTGAAC	CATAAAGCAACAGACCCATT	493	0.13
LPL_15	rs11570891	intron9(-11:exon10)	aaattgcctttttcctgtg	C/T	tttttctcagaactgggccc	AAAATGATGCACCTTATTGG	ATTTTACTCTGCGCTCAAAC	543	0.13
LPL_16	rs4922115	exon10(+10)	ctttttctcagaactgggccc	G/A	aatctacagaacaaagaacg	AAAATGATGCACCTTATTGG	ATTTTACTCTGCGCTCAAAC	543	0.109
LPL_17	rs11570892	exon10(+797)	ctgtaatcctcagctgacac	A/G	taatttgaatggtgcagaaa	CGAAGAAAGGCTCGATAAA	CGGTCCTTGTCTAAAATCTG	476	0.109
LPL_18	rs3208305	exon10(+828)	ggtgcagaaaaaaaaaaga	A/T	accgtaattttattattaga	CGAAGAAAGGCTCGATAAA	CGGTCCTTGTCTAAAATCTG	476	0.239
LPL_19	rs1803924	exon10(+854)	aattttattattagattctc	C/T	aatgattttcatcaattta	CGAAGAAAGGCTCGATAAA	CGGTCCTTGTCTAAAATCTG	476	0.13
LPL_20	rs11570893	exon10(+950)	ttcagttgtacttccagtgcc	G/A	tctcttttgttctctggcttt	CGAAGAAAGGCTCGATAAA	CGGTCCTTGTCTAAAATCTG	476	0.043
LPL_21	rs1059507	exon10(+1143)	atggagtaccatgagggttg	C/T	tatttgtgtttttaacaac	CATAATTTGAATGGTGCAGA	CACACATGCAGAGCTTTCTA	543	0.109
LPL_22	rs3735964	exon10(+1225)	ctatttttcagaatgctctt	C/A	tacgtataaatatgaaatga	CATAATTTGAATGGTGCAGA	CACACATGCAGAGCTTTCTA	543	0.13
LPL_23	rs3200218	exon10(+1251)	ataaatatgaaatgataaag	A/G	tgtcaaatatctcagaggct	CATAATTTGAATGGTGCAGA	CACACATGCAGAGCTTTCTA	543	0.174
LPL_24	rs13702	exon10(+1672)	tctggctccgaaaaactttg	T/C	tatatatatcaaggatgttc	GGCATCCCCTTTATTAATTC	CTCAGAAGCTCTTCGGTTTA	510	0.091
LPL_25	rs1059611	exon10(+1743)	tacatgtgtggatgtgtaaa	T/C	ggagcttgtacatattggaa	GGCATCCCCTTTATTAATTC	CTCAGAAGCTCTTCGGTTTA	510	0.023
LPL_26	rs10645926	exon10(+1806~+1808)	ataaatgtgtggtgctaact	INS_TT	atgtgtctttatcagtgatg	GGCATCCCCTTTATTAATTC	CTCAGAAGCTCTTCGGTTTA	510	0.023
LPL_27	rs15285	exon10(+1847)	atggtctcacagagccaact	C/T	actcttatgaaatgggcttt	GGCATCCCCTTTATTAATTC	CTCAGAAGCTCTTCGGTTTA	510	0.091
LPL_28	rs3866471	exon10(+1849)	ggtctcacagagccaactca	C/A	tcttatgaaatgggctttaa	GGCATCCCCTTTATTAATTC	CTCAGAAGCTCTTCGGTTTA	510	0.062
LPL_29	rs3916027	3'downstream(+99)	accactgtacttagtaaac	G/A	aagagcttctgagaattata	TGAAGAAATGGAATCAGCTT	TGCTACTTGCCTTACAGCTA	419	0.25
LPL_30	rs9644636	3'downstream(+127)	tctgagaattatagtgtacc	T/G	tatagatatttttaacattt	TGAAGAAATGGAATCAGCTT	TGCTACTTGCCTTACAGCTA	419	0.159
LPL_31	rs4921683	3'downstream(+299)	tgtagactaatataaggca	T/A	ctttggccattttatagtg	TGAAGAAATGGAATCAGCTT	TGCTACTTGCCTTACAGCTA	419	0.114

**Supplemental Table 2.** Regression analyses of LPL SNPs with T2DM-related phenotypes while controlling for age, sex, and BMI as covariates in normal controls. Shaded boxes indicate  $p < 0.05$ .

T2DM related phenotype	SNP ID	anova	codominant	dominant	recessive	C/C			C/R			R/R		
		p-value	p-value	p-value	p-value	Freq	mean	S.D	Freq	mean	S.D	Freq	mean	S.D
BMI	rs343	0.431	0.227	0.337	0.221	327	23.226	3.077	131	23.432	3.211	10	24.415	3.503
	rs249	0.144	0.084	0.054	0.974	405	23.203	3.074	57	24.064	3.404	5	23.708	2.988
	rs316	0.134	0.145	0.094	0.535	389	23.225	2.984	76	23.869	3.680	3	21.269	2.921
	rs328	0.464	0.316	0.236	0.862	344	23.218	3.087	101	23.657	3.296	9	23.258	2.746
	rs4922115	0.127	0.129	0.085	0.558	383	23.194	2.964	81	23.839	3.743	3	21.269	2.921
	rs3208305	0.292	0.088	0.180	0.106	289	23.179	2.929	155	23.450	3.363	24	24.124	3.548
	rs3200218	0.260	0.599	0.422	0.259	361	23.381	3.166	104	22.973	2.984	4	25.086	1.145
	rs13702	0.300	0.094	0.192	0.106	288	23.181	2.934	155	23.443	3.364	24	24.124	3.548
	rs9644636	0.515	0.208	0.238	0.469	322	23.408	3.088	133	23.114	3.200	12	22.677	3.375
	WHR	rs343	0.465	0.360	0.254	0.698	327	0.910	0.066	131	0.903	0.065	10	0.925
rs249		0.060	0.084	0.061	0.831	405	0.906	0.067	57	0.927	0.057	5	0.916	0.054
rs316		0.489	0.085	0.098	0.426	389	0.910	0.066	76	0.904	0.060	3	0.875	0.015
rs328		0.208	0.137	0.156	0.432	344	0.905	0.065	101	0.917	0.069	9	0.924	0.049
rs4922115		0.464	0.068	0.076	0.457	383	0.910	0.067	81	0.902	0.059	3	0.875	0.015
rs3208305		0.879	0.865	0.906	0.474	289	0.908	0.067	155	0.911	0.064	24	0.910	0.051
rs3200218		0.009	0.001	0.000	0.847	361	0.903	0.065	104	0.925	0.065	4	0.913	0.049
rs13702		0.885	0.862	0.907	0.468	288	0.908	0.067	155	0.911	0.064	24	0.910	0.051
rs9644636		0.900	0.852	0.882	0.854	322	0.909	0.067	133	0.906	0.064	12	0.907	0.054
BODY_FAT		rs343	0.520	0.220	0.394	0.078	226	26.524	7.393	89	25.806	7.742	5	23.431
	rs249	0.318	0.617	0.505	0.758	274	26.436	7.526	41	24.874	7.382	4	29.534	8.475
	rs316	0.733	0.021	0.021		272	26.346	7.444	49	25.948	7.891	0		
	rs328	0.791	0.750	0.777	0.813	237	26.479	7.581	67	25.761	7.428	7	26.244	9.298
	rs4922115	0.894	0.121	0.121		268	26.274	7.420	52	26.426	8.038	0		
	rs3208305	0.650	0.198	0.276	0.296	203	26.541	7.367	103	25.721	7.765	15	26.704	7.794
	rs3200218	0.877	0.431	0.345	0.511	247	26.389	7.511	72	25.904	7.561	2	27.215	7.916
	rs13702	0.623	0.173	0.237	0.297	202	26.540	7.386	103	25.678	7.747	15	26.704	7.794
	rs9644636	0.237	0.446	0.217	0.388	217	26.759	7.643	90	25.158	6.953	11	26.489	9.225
	SBP	rs343	0.302	0.305	0.188	0.585	327	121.631	17.631	131	119.201	16.149	10	125.067
rs249		0.648	0.911	0.865	0.331	405	121.050	17.421	57	120.468	16.883	5	128.000	12.953
rs316		0.531	0.136	0.129	0.772	389	121.409	17.509	76	118.974	16.176	3	120.000	21.197
rs328		0.653	0.745	0.548	0.472	344	121.353	17.488	101	120.198	17.336	9	125.259	11.597
rs4922115		0.341	0.065	0.059	0.768	383	121.530	17.527	81	118.428	16.146	3	120.000	21.197
rs3208305		0.674	0.201	0.323	0.214	289	121.511	17.596	155	120.378	17.348	24	118.944	13.365
rs3200218		0.874	0.631	0.603	0.957	361	120.796	16.812	104	121.795	19.101	4	121.000	12.806
rs13702		0.579	0.151	0.238	0.215	288	121.627	17.515	155	120.142	17.538	24	118.944	13.365
rs9644636		0.994	0.678	0.630	0.975	322	121.025	17.305	133	121.068	17.520	12	120.500	16.873
DBP		rs343	0.090	0.719	0.358	0.100	327	75.566	9.539	131	74.366	10.509	10	81.067
	rs249	0.813	0.723	0.834	0.538	405	75.274	10.016	57	75.766	9.201	5	77.733	8.036
	rs316	0.742	0.241	0.244	0.715	389	75.517	9.715	76	74.605	10.841	3	74.000	6.928
	rs328	0.614	0.471	0.601	0.374	344	75.283	9.816	101	75.875	10.571	9	78.222	6.912
	rs4922115	0.440	0.092	0.089	0.726	383	75.619	9.735	81	74.099	10.503	3	74.000	6.928
	rs3208305	0.874	0.723	0.977	0.374	289	75.285	9.492	155	75.617	10.856	24	74.583	7.994
	rs3200218	0.939	0.851	0.928	0.620	361	75.391	9.986	104	75.295	9.648	4	73.667	5.696
	rs13702	0.916	0.619	0.840	0.376	288	75.345	9.453	155	75.492	10.947	24	74.583	7.994
	rs9644636	0.112	0.072	0.093	0.295	322	75.936	9.854	133	74.150	9.840	12	72.111	10.110
	log-TG	rs343	0.291	0.270	0.371	0.290	327	2.13	0.18	131	2.14	0.18	10	2.21
rs249		0.284	0.034	0.029	0.537	405	2.14	0.18	57	2.10	0.19	5	2.09	0.06
rs316		0.712	0.647	0.772	0.358	389	2.13	0.18	76	2.15	0.18	3	2.20	0.10
rs328		0.125	0.017	0.022	0.219	344	2.15	0.18	101	2.11	0.19	9	2.07	0.09
rs4922115		0.625	0.537	0.640	0.372	383	2.13	0.18	81	2.15	0.18	3	2.20	0.10
rs3208305		0.539	0.163	0.306	0.140	289	2.14	0.17	155	2.13	0.19	24	2.10	0.14
rs3200218		0.300	0.154	0.195	0.329	361	2.14	0.18	104	2.11	0.17	4	2.08	0.11
rs13702		0.523	0.147	0.274	0.141	288	2.14	0.17	155	2.13	0.19	24	2.10	0.14
rs9644636		0.126	0.614	0.276	0.131	322	2.13	0.19	133	2.15	0.15	12	2.05	0.10
TCHOL		rs343	0.082	0.606	0.939	0.038	327	180.437	31.573	131	178.962	31.904	10	202.300
	rs249	0.910	0.952	0.999	0.829	405	180.202	31.855	57	182.158	32.555	5	180.400	26.159
	rs316	0.723	0.742	0.775	0.771	389	180.470	31.141	76	180.658	35.029	3	165.667	36.747
	rs328	0.938	0.522	0.540	0.735	344	181.195	32.504	101	180.257	30.794	9	178.333	22.814
	rs4922115	0.645	0.963	0.907	0.747	383	180.337	30.960	81	182.148	35.609	3	165.667	36.747
	rs3208305	0.955	0.798	0.919	0.644	289	180.311	31.542	155	180.832	32.257	24	178.792	32.836
	rs3200218	0.023	0.716	0.393	0.032	361	181.341	32.149	104	176.000	29.247	4	216.750	38.586
	rs13702	0.967	0.729	0.833	0.644	288	180.424	31.539	155	180.587	32.361	24	178.792	32.836
	rs9644636	0.938	0.933	0.910	0.958	322	180.770	32.473	133	179.632	30.452	12	179.667	24.344
	HDL	rs343	0.174	0.179	0.403	0.036	327	44.144	9.846	131	44.397	10.041	10	50.100
rs249		0.773	0.443	0.348	0.799	405	44.249	9.860	57	45.193	10.502	5	43.200	11.692
rs316		0.679	0.596	0.575	0.995	389	44.509	10.152	76	43.421	8.907	3	45.000	4.583
rs328		0.563	0.206	0.221	0.535	344	43.971	9.940	101	44.941	9.916	9	46.333	10.712
rs4922115		0.825	0.778	0.768	0.989	383	44.483	10.097	81	43.741	9.367	3	45.000	4.583
rs3208305		0.839	0.410	0.530	0.410	289	44.197	10.124	155	44.426	9.613	24	45.417	9.952
rs3200218		0.378	0.386	0.557	0.128	361	44.161	9.911	104	44.731	9.761	4	50.750	15.283
rs13702		0.851	0.440	0.571	0.414	288	44.226	10.130	155	44.400	9.630	24	45.417	9.952
rs9644636		0.175	0.232	0.107	0.457	322	44.826	10.134	133	43.135	9.304	12	46.833	9.778
LDL		rs343	0.230	0.716	0.421	0.206	323	107.247	27.472	131	104.321	27.937	10	118.620
	rs249	0.599	0.536	0.536	0.806	402	106.043	27.582	56	109.618	29.710	5	112.240	21.399
	rs316	0.536	0.704	0.782	0.555	385	106.651	27.509	76	106.813	28.918	3	88.733	31.916
	rs328	0.982	0.927	0.907	0.966	343	106.864	28.173	98	107.286	27.071	9	108.244	22.629
	rs492													

log-Glu0	rs343	0.896	0.692	0.640	0.930	327	1.87	0.02	131	1.87	0.02	10	1.87	0.02
	rs249	0.225	0.676	0.378	0.173	405	1.87	0.02	57	1.87	0.02	5	1.89	0.02
	rs316	0.001	0.091	0.284	0.001	389	1.87	0.02	76	1.87	0.02	3	1.83	0.02
	rs328	0.924	0.919	0.991	0.750	344	1.87	0.02	101	1.87	0.02	9	1.87	0.03
	rs4922115	0.001	0.264	0.633	0.001	383	1.87	0.02	81	1.87	0.02	3	1.83	0.02
	rs3208305	0.725	0.398	0.528	0.383	289	1.87	0.02	155	1.87	0.02	24	1.87	0.03
	rs3200218	0.252	0.492	0.687	0.137	361	1.87	0.02	104	1.87	0.02	4	1.89	0.01
	rs13702	0.722	0.382	0.502	0.390	288	1.87	0.02	155	1.87	0.02	24	1.87	0.03
	rs9644636	0.817	0.481	0.563	0.519	322	1.87	0.02	133	1.87	0.02	12	1.88	0.02
	rs343	0.326	0.361	0.618	0.100	327	2.08	0.13	131	2.08	0.12	10	2.02	0.17
rs249	0.261	0.585	0.923	0.091	405	2.08	0.13	57	2.07	0.11	5	2.17	0.10	
rs316	0.275	0.377	0.560	0.096	389	2.08	0.13	76	2.08	0.12	3	1.96	0.19	
rs328	0.112	0.518	0.971	0.033	344	2.08	0.13	101	2.07	0.13	9	2.16	0.08	
rs4922115	0.273	0.474	0.680	0.096	383	2.08	0.13	81	2.08	0.12	3	1.96	0.19	
rs3208305	0.823	0.876	0.722	0.712	289	2.07	0.13	155	2.08	0.13	24	2.07	0.12	
rs3200218	0.947	0.797	0.815	0.857	361	2.07	0.13	104	2.08	0.14	4	2.10	0.11	
rs13702	0.803	0.853	0.692	0.705	288	2.07	0.13	155	2.08	0.13	24	2.07	0.12	
rs9644636	0.266	0.178	0.277	0.200	322	2.08	0.13	133	2.07	0.12	12	2.02	0.17	
rs343	0.650	0.620	0.489	0.660	327	1.98	0.10	131	1.97	0.13	10	2.00	0.09	
rs249	0.663	0.907	0.740	0.510	405	1.98	0.11	57	1.98	0.09	5	2.02	0.09	
rs316	0.436	0.847	0.857	0.070	389	1.98	0.11	76	1.98	0.11	3	2.06	0.05	
rs328	0.154	0.139	0.259	0.098	344	1.98	0.11	101	1.99	0.11	9	2.04	0.07	
rs4922115	0.457	0.540	0.794	0.062	383	1.98	0.11	81	1.98	0.11	3	2.06	0.05	
rs3208305	0.132	0.053	0.091	0.149	289	1.98	0.11	155	1.99	0.11	24	2.02	0.09	
rs3200218	0.625	0.846	0.970	0.442	361	1.98	0.12	104	1.98	0.10	4	2.03	0.05	
rs13702	0.134	0.055	0.096	0.146	288	1.98	0.11	155	1.99	0.11	24	2.02	0.09	
rs9644636	0.152	0.133	0.259	0.094	322	1.99	0.11	133	1.98	0.11	12	1.93	0.17	
rs343	0.566	0.370	0.535	0.230	327	2.32	0.08	131	2.32	0.08	10	2.29	0.09	
rs249	0.180	0.778	0.821	0.075	405	2.32	0.08	57	2.31	0.08	5	2.38	0.05	
rs316	0.552	0.454	0.560	0.323	389	2.32	0.08	76	2.31	0.08	3	2.26	0.11	
rs328	0.069	0.368	0.800	0.019	344	2.32	0.08	101	2.31	0.08	9	2.38	0.05	
rs4922115	0.559	0.638	0.767	0.332	383	2.32	0.09	81	2.32	0.08	3	2.26	0.11	
rs3208305	0.669	0.542	0.463	0.989	289	2.31	0.09	155	2.32	0.08	24	2.32	0.08	
rs3200218	0.839	0.680	0.732	0.664	361	2.32	0.08	104	2.32	0.09	4	2.34	0.06	
rs13702	0.661	0.533	0.452	0.992	288	2.31	0.09	155	2.32	0.08	24	2.32	0.08	
rs9644636	0.131	0.082	0.145	0.138	322	2.32	0.08	133	2.31	0.08	12	2.28	0.11	
rs343	0.972	0.975	0.962	0.970	327	0.72	0.32	131	0.72	0.38	10	0.74	0.47	
rs249	0.463	0.510	0.636	0.384	405	0.71	0.35	57	0.74	0.27	5	0.87	0.15	
rs316	0.085	0.352	0.542	0.078	389	0.72	0.33	76	0.72	0.36	3	0.28	1.12	
rs328	0.716	0.373	0.295	0.898	344	0.72	0.35	101	0.69	0.33	9	0.74	0.24	
rs4922115	0.074	0.678	0.942	0.077	383	0.72	0.33	81	0.74	0.35	3	0.28	1.12	
rs3208305	0.716	0.281	0.317	0.497	289	0.73	0.32	155	0.70	0.36	24	0.69	0.42	
rs3200218	0.513	0.148	0.134	0.865	361	0.71	0.35	104	0.75	0.30	4	0.78	0.26	
rs13702	0.723	0.287	0.325	0.498	288	0.73	0.32	155	0.70	0.36	24	0.69	0.42	
rs9644636	0.740	0.305	0.271	0.856	322	0.71	0.33	133	0.74	0.34	12	0.72	0.49	
rs343	0.643	0.714	0.548	0.543	327	1.29	0.43	131	1.33	0.46	10	1.24	0.35	
rs249	0.558	0.822	0.602	0.375	405	1.30	0.44	57	1.27	0.37	5	1.48	0.21	
rs316	0.370	0.723	0.560	0.329	389	1.30	0.44	76	1.35	0.42	3	1.04	0.45	
rs328	0.130	0.669	0.322	0.118	344	1.31	0.45	101	1.25	0.40	9	1.53	0.24	
rs4922115	0.398	0.778	0.616	0.324	383	1.30	0.44	81	1.34	0.42	3	1.04	0.45	
rs3208305	0.747	0.653	0.531	0.858	289	1.31	0.45	155	1.28	0.42	24	1.34	0.37	
rs3200218	0.578	0.277	0.293	0.641	361	1.29	0.44	104	1.33	0.43	4	1.42	0.23	
rs13702	0.746	0.653	0.532	0.859	288	1.31	0.45	155	1.28	0.42	24	1.34	0.37	
rs9644636	0.817	0.942	0.911	0.569	322	1.30	0.41	133	1.31	0.49	12	1.22	0.35	
rs343	0.199	0.928	0.700	0.123	327	1.18	0.40	131	1.15	0.40	10	1.39	0.49	
rs249	0.240	0.450	0.242	0.288	405	1.18	0.41	57	1.12	0.35	5	1.40	0.22	
rs316	0.423	0.308	0.458	0.112	389	1.17	0.41	76	1.21	0.37	3	1.44	0.34	
rs328	0.020	0.662	0.217	0.022	344	1.19	0.41	101	1.12	0.38	9	1.49	0.24	
rs4922115	0.413	0.310	0.458	0.112	383	1.17	0.41	81	1.21	0.36	3	1.44	0.34	
rs3208305	0.659	0.686	0.865	0.479	289	1.17	0.42	155	1.18	0.36	24	1.25	0.41	
rs3200218	0.780	0.488	0.531	0.619	361	1.17	0.41	104	1.19	0.39	4	1.31	0.50	
rs13702	0.653	0.761	0.961	0.477	288	1.18	0.42	155	1.17	0.36	24	1.25	0.41	
rs9644636	0.164	0.443	0.227	0.326	322	1.20	0.39	133	1.13	0.44	12	1.28	0.40	
rs343	0.761	0.566	0.559	0.862	327	1.53	0.32	131	1.55	0.33	10	1.58	0.28	
rs249	0.211	0.246	0.117	0.379	405	1.55	0.32	57	1.48	0.30	5	1.68	0.17	
rs316	0.558	0.506	0.471	0.941	389	1.53	0.32	76	1.57	0.30	3	1.48	0.32	
rs328	0.018	0.252	0.058	0.063	344	1.55	0.33	101	1.48	0.30	9	1.74	0.18	
rs4922115	0.599	0.564	0.531	0.929	383	1.53	0.32	81	1.57	0.31	3	1.48	0.32	
rs3208305	0.641	0.456	0.354	0.958	289	1.55	0.33	155	1.52	0.30	24	1.56	0.30	
rs3200218	0.602	0.262	0.278	0.635	361	1.53	0.32	104	1.56	0.32	4	1.64	0.22	
rs13702	0.619	0.440	0.337	0.959	288	1.55	0.33	155	1.52	0.30	24	1.56	0.30	
rs9644636	0.903	0.779	0.676	0.770	322	1.54	0.32	133	1.55	0.34	12	1.50	0.29	
rs343	0.067	0.090	0.254	0.018	327	0.74	0.02	131	0.74	0.02	10	0.72	0.03	
rs249	0.435	0.359	0.298	0.962	405	0.74	0.02	57	0.74	0.02	5	0.74	0.02	
rs316	0.004	0.009	0.032	0.005	389	0.74	0.02	76	0.73	0.02	3	0.70	0.04	
rs328	0.437	0.259	0.340	0.328	344	0.74	0.02	101	0.74	0.02	9	0.74	0.01	
rs4922115	0.006	0.031	0.091	0.004	383	0.74	0.02	81	0.74	0.02	3	0.70	0.04	
rs3208305	0.116	0.575	0.851	0.055	289	0.74	0.02	155	0.74	0.02	24	0.73	0.03	
rs3200218	0.614	0.912	0.954	0.423	361	0.74	0.02	104	0.74	0.02	4	0.75	0.01	
rs13702	0.121	0.549	0.887	0.054	288	0.74	0.02	155	0.74	0.02	24	0.73	0.03	
rs9644636	0.686	0.423	0.468	0.596	322	0.74	0.02	133	0.74	0.02	12	0.73	0.03	
rs343	0.969	0.955	0.939	0.966	327	-0.02	0.32	131	-0.02	0.38	10	0.01	0.47	
rs249	0.444	0.532	0.681	0.343	405	-0.03	0.35	57	0.00	0.27	5	0.15	0.16	
rs316	0.054	0.304	0.502	0.050	389	-0.01	0.33	76	-0.02	0.37	3	-0.49	1.12	
rs328	0.734	0.375	0.300	0.916	344	-0.01	0.35	101	-0.04	0.33	9	0.00	0.25	
rs4922115	0.047	0.629	0.918	0.049	383	-0.02	0.33	81	0.00	0.36	3	-0.49	1.12	
rs3208305	0.700	0.263	0.304	0.467	289	-0.01	0.33	155	-0.03	0.36	24	-0.05	0.43	
rs3200218	0.501	0.140	0.132	0.793	361	-0.03	0.35	104	0.01	0.31	4	0.06	0.25	
rs13702	0.706	0.267	0.309	0.468	288	-0.01	0.33	155	-0.03	0.36	24	-0.05	0.43	
rs9644636	0.731	0.289	0.260	0.826	322	-0.03	0.34	133	0.00	0.35	12	-0.01	0.49	

**Supplemental Table 3.** Regression analyses of LPL haplotypes with T2DM-related phenotypes while controlling for age, sex, and BMI as covariates in normal controls. Shaded boxes indicate  $p < 0.05$ .

Haplotype ID	reg			reg			reg			reg		
	co-dom	dom	rec	co-dom	dom	rec	co-dom	dom	rec	co-dom	dom	rec
	<b>bmi</b>			<b>whr</b>			<b>body_fat</b>			<b>sbp</b>		
H1	0.1442	0.1632	0.2873	0.0203	0.1901	0.0239	0.6171	0.7460	0.3946	0.2754	0.1716	0.5557
H2	0.6293	0.4475	0.2581	0.0009	0.0003	0.8444	0.2931	0.2216	0.5106	0.5755	0.5449	0.9577
H3	0.1212	0.0770	0.5489	0.0970	0.1097	0.4592	0.0449	0.0449		0.1544	0.1486	0.7654
H4	0.1556	0.1054	0.9946	0.1413	0.1302	0.6152	0.5836	0.4713	0.7580	0.7990	0.9891	0.4040
H5	0.5068	0.6070	0.2580	0.8305	0.7904	0.7643	0.8603	0.7128	0.3349	0.7264	0.7755	0.6149

Haplotype ID	<b>dbp</b>			<b>log-tg</b>			<b>tchol</b>			<b>hdl</b>		
H1	0.5332	0.1677	0.9687	0.0832	0.0475	0.4377	0.5409	0.7932	0.5172	0.2528	0.2081	0.4670
H2	0.9142	0.9960	0.6179	0.1583	0.2	0.3282	0.7827	0.4459	0.0316	0.3244	0.4769	0.1274
H3	0.2795	0.2857	0.7154	0.8462	0.7666	0.1151	0.7979	0.8379	0.7548	0.6847	0.6683	0.9938
H4	0.4863	0.5908	0.4380	0.0384	0.0329	0.5364	0.9955	0.9745	0.9080	0.3875	0.2907	0.8352
H5	0.5619	0.5768	0.7905	0.1929	0.2222	0.4036	0.7579	0.8135	0.5853	0.3581	0.4988	0.0709

Haplotype ID	<b>ldlc</b>			<b>log-glucose 0</b>			<b>log-glucose 60</b>			<b>log-glucose 120</b>		
H1	0.9686	0.6056	0.7052	0.4144	0.5282	0.4888	0.4023	0.4243	0.5847	0.8556	0.397	0.544
H2	0.9822	0.6146	0.0159	0.3136	0.4583	0.136	0.6592	0.6684	0.8572	0.784	0.9029	0.4423
H3	0.7236	0.8066	0.5431	0.845	0.9375	0.3611	0.2934	0.4001	0.2917	0.2871	0.2576	0.8289
H4	0.5622	0.5660	0.7894	0.6074	0.3218	0.1759	0.7095	0.9176	0.088	0.8616	0.9964	0.5133
H5	0.7346	0.8400	0.3335	0.1683	0.2132	0.2175	0.6406	0.7471	0.245	0.9099	0.8504	0.586

Haplotype ID	<b>log-acuglu</b>			<b>log-insulin 0</b>			<b>log-insulin 60</b>			<b>log-insulin 120</b>		
H1	0.4914	0.5831	0.572	0.7342	0.6908	0.8871	0.7864	0.863	0.7876	0.9583	0.316	0.3207
H2	0.5283	0.5663	0.6636	0.1474	0.1336	0.8652	0.3028	0.3213	0.6442	0.4928	0.5357	0.6222
H3	0.1656	0.2027	0.3721	0.7839	0.6355	0.6169	0.7111	0.8099	0.5873	0.8842	0.639	0.3531
H4	0.8689	0.7165	0.0727	0.516	0.6355	0.4053	0.7098	0.4929	0.3808	0.5879	0.3515	0.2903
H5	0.6039	0.6853	0.3469	0.6442	0.7597	0.2118	0.4779	0.4005	0.3912	0.3902	0.4829	0.1835

Haplotype ID	<b>log-aucins</b>			<b>log-hba1c</b>			<b>log-homa_ir</b>		
H1	0.8127	0.846	0.8502	0.4221	0.2617	0.8886	0.6983	0.6647	0.8537
H2	0.2687	0.2846	0.6381	0.7446	0.8652	0.4236	0.1344	0.1258	0.7929
H3	0.8245	0.7466	0.8252	0.3501	0.3968	0.5252	0.7767	0.6428	0.6623
H4	0.2155	0.098	0.3885	0.445	0.3818	0.9543	0.5421	0.6849	0.3633
H5	0.259	0.2548	0.9028	0.0057	0.0244	<.0001	0.712	0.8232	0.2476

