

Genome-wide association study identifying novel variant for fasting insulin and allelic heterogeneity in known glycemic loci in Chilean adolescents: The Santiago Longitudinal Study

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TABLE S1 Top independent signals in the Santiago Longitudinal Study for homeostatic model of insulin resistance

Gene/ Nearest gene*	SNP	CHR	BP	EA/OA	EAF	β	SE	p
GWAS-significant loci ($p < 5 \times 10^{-8}$)								
<i>CSMD1</i>	rs77465890	8	3628570	C/T	0.10	-0.322	0.057	1.66E-8
Suggestive loci ($p < 5 \times 10^{-6}$)								
<i>RP11-191N8.2*</i>	rs35726538	1	221976039	G/A	0.02	0.693	0.142	1.16E-6
<i>NFIA</i>	rs7535730	1	61871356	G/A	0.18	0.236	0.049	1.50E-6
<i>NCKAP5</i>	rs528181067	2	134374835	A/T	0.01	-0.823	0.175	2.52E-6
<i>RP11-769N22.1*</i>	rs184687999	4	29046057	C/T	0.05	0.415	0.087	1.86E-6
<i>SPEF2</i>	rs2361393	5	35800504	G/A	0.19	0.224	0.047	1.58E-6
<i>MCM9*</i>	rs117381875	6	119134465	C/T	0.02	0.689	0.141	1.12E-6
<i>CSMD1*</i>	rs35051650	8	4859203	A/C	0.13	0.269	0.055	9.49E-7
<i>KIAA1217</i>	rs143654218	10	24319915	G/A	0.01	0.968	0.206	2.54E-6
<i>AKR1C3</i>	rs117400599	10	5143717	G/T	0.04	0.467	0.097	1.55E-6
<i>PTPRO</i>	rs7315300	12	15610293	A/T	0.24	0.223	0.042	1.46E-7
<i>RCOR1</i>	rs12884198	14	103155465	A/G	0.02	0.831	0.157	1.23E-7
<i>MCTP2*</i>	rs12441824	15	94738631	A/G	0.48	-0.240	0.046	1.69E-7
<i>DCC</i>	rs9950187	18	50636401	T/A	0.04	0.453	0.095	1.95E-6
<i>CTA-992D9.7*</i>	rs4820743	22	27512801	T/C	0.78	0.207	0.044	2.26E-6

Abbreviations: SNP, single nucleotide polymorphism; CHR, chromosome; BP, base pair position (hg19 build); EA, effect allele; OA, other allele; EAF, effect allele frequency; β , beta coefficient; SE, standard error; p , p-value.

TABLE S2 Top independent signals in the Santiago Longitudinal Study for fasting glucose, fasting insulin, and homeostatic model assessment of insulin resistance, adjusted for CDC pediatric z-scores of body mass index.

Trait	Gene/ Nearest Gene*	SNP	CHR	BP	EA/OA	EAF	β	SE	<i>p</i>
FG	<i>RP11-147G16.1*</i>	rs10157848	1	82996068	C/G	0.96	7.233	1.579	5.00E-6
	<i>LOC101927665</i>	rs6748653	2	200528810	T/A	0.21	3.023	0.643	2.60E-6
	<i>AC010149.4*</i>	rs113214710	2	231442593	T/G	0.07	-5.069	1.100	4.03E-6
	<i>AC009223.2*</i>	rs138154342	2	41452492	G/A	0.01	-14.391	2.975	1.31E-6
	<i>TXNRD3</i>	rs78870998	3	126352111	C/A	0.03	7.859	1.719	4.85E-6
	<i>GBA3</i>	rs79399931	4	22714327	A/C	0.02	-11.381	2.300	7.46E-7
	<i>UCHL1-AS1</i>	rs66475765	4	41230618	T/C	0.03	-8.210	1.770	3.53E-6
	<i>CCSER1</i>	rs79947031	4	91829969	C/T	0.11	4.108	0.882	3.22E-6
	<i>RP11-541P9.3*</i>	rs189776108	5	162420388	T/C	0.05	5.905	1.284	4.26E-6
	<i>ZBED3-AS1</i>	rs28589776	5	76406470	T/C	0.01	-11.552	2.492	3.56E-6
	<i>DCBLD1</i>	rs117533208	6	117855911	C/T	0.02	10.528	2.291	4.32E-6
	<i>MAN1A1</i>	rs62418805	6	119508342	C/T	0.32	3.055	0.604	4.19E-7
	<i>AC004535.2*</i>	rs141226872	7	10748548	G/A	0.01	12.046	2.622	4.34E-6
	<i>RPL7*</i>	rs12546395	8	74194405	A/T	0.62	-2.573	0.533	1.40E-6
	<i>SLC24A2</i>	rs79818403	9	19669933	T/C	0.01	15.296	3.100	8.06E-7
	<i>WNK2</i>	rs147515244	9	96046087	A/T	0.05	6.730	1.389	1.26E-6
	<i>RP11-432B10.1*</i>	rs7476984	10	109170924	A/G	0.40	2.825	0.540	1.72E-7
	<i>AL157931.1*</i>	rs117292932	13	23574827	A/T	0.02	9.998	2.067	1.31E-6
	<i>RTN4RL1</i>	rs11656601	17	1924911	T/C	0.25	-3.534	0.732	1.36E-6
	<i>ATP9B</i>	rs7226934	18	76904665	C/T	0.16	3.377	0.730	3.74E-6
	<i>NLRP12*</i>	rs139295665	19	54336151	A/G	0.01	-17.044	3.620	2.50E-6
	<i>RP11-560A15.4*</i>	rs6092424	20	55672544	A/G	0.49	-2.667	0.534	5.82E-7
<i>TAF4*</i>	rs6061420	20	60654074	G/A	0.07	-6.021	1.274	2.29E-6	
<i>RP5-839B4.8*</i>	rs80352176	20	9952118	G/A	0.09	-4.994	1.038	1.52E-6	
<i>PARVG*</i>	rs139198	22	44606772	C/T	0.22	3.040	0.662	4.47E-6	
FI	<i>ENSA*</i>	rs115406107	1	150594155	A/T	0.02	0.508	0.105	1.00E-6
	<i>KAZN</i>	rs80204739	1	15065485	G/C	0.02	0.580	0.127	5.00E-6
	<i>PLD5*</i>	rs61839743	1	242873445	C/T	0.01	-0.883	0.185	2.00E-6
	<i>SMEK2</i>	rs60356354	2	55833911	C/T	0.03	-0.452	0.095	2.06E-6
	<i>LINC00290</i>	rs6831952	4	182066235	T/G	0.67	0.164	0.035	3.04E-6
	<i>RP11-434D11.4*</i>	rs1546499	5	126033156	C/A	0.43	0.146	0.031	2.13E-6
	<i>SPEF2</i>	rs2361394	5	35800547	G/A	0.08	0.287	0.056	2.80E-7
	<i>RP11-744I24.2*</i>	rs7795885	7	141251044	G/C	0.03	0.427	0.093	4.20E-6
	<i>DOCK5</i>	rs2709613	8	25212994	C/G	0.97	0.474	0.101	3.03E-6
	<i>CSMD1</i>	rs77465890	8	3628570	C/T	0.10	-0.252	0.047	1.03E-7
	<i>CSMD1*</i>	rs34371265	8	4859170	C/T	0.13	0.216	0.045	1.82E-6
	<i>PRAG1*</i>	rs577483743	8	8376874	A/T	0.02	-0.516	0.111	3.61E-6
	<i>AL157884.1*</i>	rs12337921	9	32735066	A/G	0.02	-0.550	0.117	2.61E-6
	<i>CTD-2507G9.1*</i>	rs11029253	11	26163242	A/T	0.09	0.268	0.058	3.04E-6
	<i>RCOR1</i>	rs12884198	14	103155465	A/G	0.02	0.663	0.130	3.28E-7
	<i>MAP4K5</i>	rs77026144	14	50937785	T/C	0.01	0.942	0.187	4.80E-7
	<i>CIITA</i>	rs45513895	16	10995145	C/T	0.03	-0.419	0.088	2.12E-6
	<i>APBA3</i>	rs10460192	19	3756197	C/T	0.77	0.172	0.037	4.24E-6
	<i>PLXNB2</i>	rs62241209	22	50734392	A/G	0.15	0.213	0.045	2.59E-6
HOMA-IR	<i>ENSA*</i>	rs115406107	1	150594155	A/T	0.02	0.537	0.114	2.00E-6
	<i>KAZN</i>	rs80204739	1	15065485	G/C	0.02	0.643	0.137	3.00E-6
	<i>NFIA</i>	rs2499526	1	61870696	T/C	0.55	-0.150	0.033	4.00E-6
	<i>RP11-434D11.4*</i>	rs1546499	5	126033156	C/A	0.43	0.153	0.033	4.02E-6
	<i>SPEF2</i>	rs2361394	5	35800547	G/A	0.08	0.305	0.060	4.52E-7
	<i>MCM9*</i>	rs117381875	6	119134465	C/T	0.02	0.594	0.126	2.48E-6
	<i>CSMD1</i>	rs77465890	8	3628570	C/T	0.10	-0.275	0.051	7.11E-8
	<i>CSMD1*</i>	rs34371265	8	4859170	C/T	0.13	0.237	0.049	1.21E-6
	<i>PRAG1*</i>	rs577483743	8	8376874	A/T	0.02	-0.554	0.120	4.09E-6
	<i>CTD-2507G9.1*</i>	rs1489506	11	26126773	A/C	0.10	0.258	0.056	4.73E-6
	<i>RCOR1</i>	rs12884198	14	103155465	A/G	0.02	0.692	0.140	8.41E-7
	<i>MAP4K5</i>	rs77026144	14	50937785	T/C	0.01	1.054	0.202	1.75E-7
	<i>RP11-66B24.5*</i>	rs149208997	15	101334196	T/C	0.01	-0.931	0.200	3.44E-6
	<i>DNAH17</i>	rs1530433	17	76559768	C/T	0.56	-0.161	0.033	1.44E-6
	<i>APBA3</i>	rs10460192	19	3756197	C/T	0.77	0.193	0.040	1.59E-6
<i>PLXNB2</i>	rs62241209	22	50734392	A/G	0.15	0.228	0.049	3.08E-6	

Abbreviations: SNP, single nucleotide polymorphism; CHR, chromosome; BP, base pair position (hg19 build); EA, effect allele; OA, other allele; EAF, effect allele frequency; β , beta coefficient; SE, standard error; *p*, *p*-value; FG, fasting glucose; FI, fasting insulin; HOMA-IR, homeostatic model assessment of insulin resistance.

TABLE S3 Loci reported in other studies to have GWAS-significant associations with fasting glucose that did not generalize in the Santiago Longitudinal Study. Associations either did not reach the nominal significance threshold of $p < 0.05$ or showed a direction of effect inconsistent with other studies. p -values for nominally significant associations are bolded.

Gene/ nearest gene*	SNP	PMID	CHR	BP	EA/ OA	EA AF	β	SE	p	Direction of effect consistent with other studies?
	rs79687284	28270201 ¹ 20081858 ² ,	1	214150821	C/G	0.02	3.430	2.503	0.171	Yes
<i>PROX1-AS1</i>	rs340874	22581228 ³	1	214159256	C/T	0.39	-0.350	0.579	0.545	No
<i>Metazoa_SRP*</i>	rs17407594	25223902 ⁴	1	66170362	A/G	0.19	0.442	0.798	0.541	Yes
	rs477224	28905132 ⁵	2	169750483	T/C	0.73	-0.550	0.627	0.381	Different alleles (EA/OA:A/G) reported in other study.
<i>SPC25*</i>	rs13387347	25187374 ⁶	2	169754846	C/T	0.38	-1.346	0.555	0.015	
<i>AC018712.3*</i>	rs733331	25187374 ⁶	2	173546313	A/G	0.13	-0.580	0.804	0.470	No
<i>DPYSL5</i>	rs1371614	22581228 ³	2	27152874	T/C	0.38	-0.250	0.546	0.647	No
	rs780095	28270201 ¹ 20081858 ² ,	2	277411105	G/A	0.64	0.226	0.564	0.689	Yes
	rs780094	22581228 ³ ,	2	27741237	C/T	0.67	-0.091	0.574	0.874	Other studies inconsistent with one another.
<i>GCKR</i>	rs780094	25187374 ⁶								
<i>MRPL33</i>	rs3736594	22581228 ³								
<i>AC012354.6*</i>	rs895636	25187374 ⁶	2	45188353	T/C	0.27	-0.703	0.614	0.252	No
<i>ADCY5</i>	rs11708067	20081858 ² 22581228 ³	3	123065778	G/A	0.28	-0.410	0.582	0.482	Yes
	rs11920090	20081858 ² 22581228 ³	3	170717521	A/T	0.11	-0.332	0.886	0.708	Other studies inconsistent with one another.
	rs8192675	28270201 ¹								
<i>SLC2A2</i>	rs9873618	28270201 ¹	3	170733076	A/G	0.33	-0.342	0.577	0.554	No
<i>IGF2BP2</i>	rs7651090	22885924 ⁷	3	185513392	G/A	0.32	0.025	0.578	0.965	Yes
<i>AMT</i>	rs11715915	22885924 ⁷	3	49455330	T/C	0.16	-0.508	0.730	0.486	Yes
<i>ZBED3-AS1</i>	rs7708285	22885924 ⁷	5	76425867	A/G	0.69	-0.850	0.594	0.152	Yes
	rs4869272	22885924 ⁷	5	95539448	T/C	0.81	1.195	0.702	0.089	Yes
<i>LOC101929710</i>	rs13179048	22581228 ³								
<i>CDKAL1</i>	rs9356744	25187374 ⁶	6	20685486	C/T	0.27	-0.235	0.596	0.694	No
	rs17762454	22885924 ⁷	6	7213200	T/C	0.40	0.109	0.569	0.849	Yes
<i>RREB1</i>	rs35742417	25625282 ⁸								
	rs2191349	20081858 ² 22581228 ³	7	15064309	T/G	0.39	0.581	0.559	0.298	Yes
<i>AC006458.3*</i>	rs1974620	25187374 ⁶								
	rs10259649	26132169 ⁹	7	44219705	C/T	0.24	0.597	0.632	0.345	Yes
<i>GCK</i>	rs730497	25187374 ⁶								
	rs1799884	23575436 ¹⁰ 19060907 ¹¹ ,	7	44229068	T/C	0.18	0.446	0.697	0.523	Different effect allele (EA:A) reported in other study.
	rs4607517	20081858 ² 22581228 ³								
<i>GCK*</i>	rs4607517	22581228 ³	7	44235668	A/G	0.18	0.428	0.699	0.540	Yes
<i>YKT6</i>	rs917793	28270201 ¹	7	44245853	T/A	0.29	-0.070	0.602	0.908	No
<i>CAMK2B*</i>	rs878521	26132169 ⁹	7	44255643	A/G	0.33	0.264	0.574	0.645	Yes
	rs10248619	22581228 ³	7	50751090	C/T	0.78	-0.514	0.641	0.422	Yes
<i>GRB10</i>	rs6943153	22885924 ⁷								
	rs13266634	28270201 ¹	8	118184783	T/C	0.21	-1.069	0.637	0.094	No
	rs3802177	25187374 ⁶								
	rs11558471	20081858 ² 21873549 ¹² ,	8	118185733	G/A	0.22	-1.165	0.623	0.062	Other studies inconsistent with one another.
<i>SLC30A8</i>	rs11558471	22581228 ³								
<i>RP11-115J16.1*</i>	rs983309	22885924 ⁷	8	9177732	G/T	0.78	-0.682	0.634	0.282	Yes
<i>LOC157273</i>	rs4841132	22581228 ³	8	9183596	G/A	0.79	-0.459	0.662	0.488	Yes
	rs651007	25631608 ¹³	9	136153875	T/C	0.15	0.494	0.748	0.509	Different alleles (EA/OA:A/G) reported in other study.
<i>ABO*</i>	rs651007	25631608 ¹³								
<i>DNLZ</i>	rs3829109	22885924 ⁷	9	139256766	A/G	0.43	-1.006	0.541	0.063	Yes
<i>CDKN2B-AS1*</i>	rs10811661	25187374 ⁶	9	22134094	C/T	0.14	0.468	0.780	0.548	No
	rs7034200	20081858 ²	9	4289050	A/C	0.53	0.768	0.573	0.180	Yes
<i>GLIS3</i>	rs4237150	25187374 ⁶								
<i>KANK1</i>	rs10815355	25187374 ⁶	9	622523	T/G	0.06	-0.149	1.167	0.898	No
<i>RP11-381K7.1*</i>	rs10885122	20081858 ²	10	113042093	G/T	0.86	-0.378	0.798	0.636	No
	rs4506565	20081858 ²								
	rs7903146	21873549 ¹²								
<i>TCF7L2</i>	rs12243326	22581228 ³	10	114788815	C/T	0.21	-0.035	0.678	0.959	Yes

<i>CRY2</i>	rs11605924	20081858 ² , 22581228 ³	11	45873091	C/A	0.57	-0.122	0.526	0.817	Yes
<i>MADD</i>	rs7944584	20081858 ² , 22581228 ³	11	47336320	T/A	0.19	0.672	0.676	0.320	No
<i>OR4S1*</i>	rs1483121	22581228 ³	11	48333360	A/G	0.08	0.139	1.000	0.890	Yes
<i>FADS1</i>	rs174550	20081858 ² , 22581228 ³	11	61571478	C/T	0.62	0.060	0.566	0.915	No
<i>ARAP1</i>	rs11603334	22581228 ³	11	72432985	A/G	0.07	-1.506	1.078	0.162	No
	rs3847554	25187374 ⁶	11	92668826	T/C	0.29	0.590	0.597	0.322	Yes
	rs1387153	19060909 ¹⁴	11	92673828	T/C	0.21	1.251	0.664	0.059	Yes
	rs7936247	23903356 ¹⁵	11	92690032	T/G	0.24	1.054	0.622	0.090	Yes
	rs2166706	19651812 ¹⁶	11	92691532	C/T	0.27	1.046	0.610	0.086	Different alleles (EA/OA:G/A) reported in other study.
<i>RP11-676F20.1*</i>	rs10830962	23575436 ¹⁰	11	92698427	G/C	0.29	0.806	0.598	0.178	
<i>RP11-503G7.2*</i>	rs10747083	22885924 ⁷	12	133041618	A/G	0.72	-0.163	0.588	0.782	No
<i>GLS2</i>	rs2657879	22885924 ⁷	12	56865338	G/A	0.22	0.501	0.642	0.435	Yes
<i>RMST</i>	rs17331697	26132169 ⁹	12	97868906	C/T	0.04	-0.365	1.291	0.777	Yes
<i>PDX1-AS1*</i>	rs2293941	22581228 ³	13	28491198	A/G	0.33	1.071	0.578	0.064	Yes
<i>PDX1</i>	rs7981781	28270201 ¹	13	28499962	A/G	0.33	1.136	0.610	0.063	Yes
<i>WARS</i>	rs3783347	22885924 ⁷	14	100839261	T/G	0.11	-0.566	0.861	0.511	Yes
<i>C2CD4A*</i>	rs7173964	22581228 ³	15	62396942	A/G	0.48	-0.073	0.538	0.892	No
<i>IGF1R</i>	rs2018860	25187374 ⁶	15	99258710	T/A	0.54	-0.528	0.548	0.336	Yes
<i>QPCTL</i>	rs2302593	22885924 ⁷	19	46196634	G/C	0.52	0.693	0.545	0.204	No
<i>LINC00261</i>	rs6113722	22885924 ⁷	20	22557099	A/G	0.04	1.144	1.444	0.428	No
<i>LINC00261*</i>	rs6048205	22581228 ³	20	22559601	G/A	0.04	0.269	1.374	0.845	No
<i>RP4-788L20.3*</i>	rs1209523	20152958 ¹⁷	20	22567942	T/C	0.03	1.741	1.577	0.269	No
<i>LOC101929685</i>	rs6048216	25187374 ⁶	20	22581268	C/T	0.04	1.265	1.371	0.356	No
<i>TOP1</i>	rs6072275	22885924 ⁷	20	39743905	A/G	0.14	0.753	0.805	0.349	Yes

Abbreviations: SNP, single nucleotide polymorphism; PMID, PubMed ID for previously reported association; CHR, chromosome; BP, base pair position (hg19 build); EA, effect allele; OA, other allele; EAF, effect allele frequency; β , beta coefficient; SE, standard error; p , p-value.

TABLE S4 Loci reported in other studies to have GWAS-significant associations with fasting insulin that did not generalize in the Santiago Longitudinal Study. No associations reached the nominal significance threshold of $p < 0.05$ for this trait.

Gene/ nearest gene*	SNP	PMID	CHR	BP	EA/ OA	EAF	β	SE	p	Direction of effect consistent with other studies?
<i>RP11-95P13.1*</i>	rs2820436	22885924 ⁷	1	219640680	C/A	0.51	0.044	0.034	0.193	Yes
	rs2785980	22581228 ³	1	219700519	C/T	0.54	-0.009	0.036	0.794	Yes
<i>RP11-95P13.2*</i>	rs4846565	22885924 ⁷	1	219722104	A/G	0.54	0.018	0.035	0.612	No
<i>MAP3K19</i>	rs1530559	22885924 ⁷	2	135755629	G/A	0.68	0.005	0.042	0.911	No
<i>LOC101929615</i>	rs10195252	22885924 ⁷	2	165513091	C/T	0.22	0.024	0.044	0.592	No
<i>COBLL1</i>	rs7607980	22581228 ³	2	165551201	C/T	0.07	-0.008	0.068	0.910	Yes
	rs2943634	22581228 ³	2	227068080	C/A	0.83	0.022	0.047	0.643	No
<i>AC068138.1*</i>	rs2943645	22885924 ⁷	2	227099180	T/C	0.82	0.038	0.045	0.399	Yes
		20081858 ² ,								Other studies inconsistent with one another.
<i>GCKR</i>	rs780094	22581228 ³	2	27741237	C/T	0.67	0.062	0.036	0.089	
<i>AY269186.2*</i>	rs9841287	22581228 ³	3	108993	G/A	0.34	-0.034	0.036	0.338	Yes
<i>PPARG</i>	rs17036328	22885924 ⁷	3	12390484	C/T	0.12	-0.016	0.054	0.775	Yes
	rs974801	22885924 ⁷	4	106071064	G/A	0.38	0.001	0.036	0.970	Yes
<i>TET2</i>	rs9884482	22885924 ⁷	4	106081636	C/T	0.38	-0.006	0.036	0.866	No
	rs4691380	22581228 ³	4	157720124	T/C	0.35	0.038	0.035	0.283	Yes
<i>PDGFC</i>	rs6822892	22885924 ⁷	4	157734675	G/A	0.35	0.041	0.035	0.244	No
<i>MSMO1</i>	rs17046216	22791750 ¹⁸	4	166255704	A/T	0.21	0.049	0.044	0.264	Yes
<i>FAM13A</i>	rs3822072	22885924 ⁷	4	89741269	A/G	0.38	0.008	0.036	0.823	Yes
<i>ARL15</i>	rs4865796	22885924 ⁷	5	53272664	A/G	0.84	-0.023	0.049	0.645	No
<i>AC022431.2*</i>	rs459193	22885924 ⁷	5	55806751	G/A	0.79	0.042	0.042	0.320	Yes
<i>RSPO3</i>	rs2745353	22885924 ⁷	6	127452935	T/C	0.61	-0.009	0.036	0.802	No
<i>UHRF1BP1</i>	rs6912327	22885924 ⁷	6	34764922	C/T	0.24	0.059	0.039	0.131	No
<i>UHRF1BP1*</i>	rs4646949	22581228 ³	6	34845449	G/T	0.38	0.033	0.035	0.337	No
<i>HIP1</i>	rs1167800	22885924 ⁷	7	75176196	A/G	0.61	-0.006	0.037	0.880	No
<i>RP11-115J16.1*</i>	rs983309	22885924 ⁷	8	9177732	G/T	0.78	-0.059	0.040	0.141	Yes
	rs4841132	22581228 ³	8	9183596	G/A	0.79	-0.066	0.042	0.115	Yes
<i>LOC157273</i>	rs2126259	22885924 ⁷	8	9185146	C/T	0.73	-0.031	0.039	0.419	Yes
		22581228 ³ ,								Other studies inconsistent with one another.
<i>TCF7L2</i>	rs7903146	22885924 ⁷	10	114758349	T/C	0.24	-0.016	0.042	0.701	
										Different effect allele (EA:T) reported in other study.
<i>MIR378C*</i>	rs7077836	22791750 ¹⁸	10	132751498	A/G	0.11	0.007	0.055	0.896	
<i>IGF1</i>	rs35767	20081858 ²	12	102875569	G/A	0.84	0.038	0.049	0.433	Yes
<i>IGF1*</i>	rs35747	22581228 ³	12	102912558	A/G	0.83	0.035	0.048	0.463	Yes
<i>FTO</i>	rs1421085	22885924 ⁷	16	53800954	C/T	0.23	0.063	0.041	0.122	Yes
<i>PEPD</i>	rs731839	22885924 ⁷	19	33899065	A/G	0.65	0.035	0.036	0.322	No

Abbreviations: SNP, single nucleotide polymorphism; PMID, PubMed ID for previously reported association; CHR, chromosome; BP, base pair position (hg19 build); EA, effect allele; OA, other allele; EAF, effect allele frequency; β , beta coefficient; SE, standard error; p , p-value.

TABLE S5 Meta-Analyses of Glucose and Insulin-Related Traits Consortium (MAGIC) and Nonalcoholic Steatohepatitis (NASH) validation results for top independent fasting glucose, fasting insulin, and homeostatic model of insulin resistance results. Variants with minor allele count <10 in these studies not shown.

	Gene/ Nearest gene*	SNP	CHR	BP	EA/OA	MAGIC					Consist. direction of effect?	NASH					Consist. direction of effect?
						EAF	β	SE	<i>p</i>	<i>n</i>		EAF	β	SE	<i>p</i>	<i>n</i>	
FG	<i>LOC101927665</i>	rs6748653	2	200528810	T/A	--	--	--	--	--	--	0.12	1.616	1.393	0.247	207	Yes
	<i>AC010149.4*</i>	rs113214710	2	231442593	T/G	--	--	--	--	--	--	0.05	0.983	1.969	0.618	207	No
	<i>CCSER1</i>	rs79947031	4	91829969	C/T	--	--	--	--	--	--	0.13	0.802	1.270	0.529	207	Yes
	<i>MAN1A1</i>	rs62418805	6	119508342	C/T	--	--	--	--	--	--	0.28	-0.066	1.079	0.951	207	No
	<i>RPL7*</i>	rs12546395	8	74194405	A/T	--	--	--	--	--	--	0.68	0.212	0.981	0.829	207	No
	<i>RP11-432B10.1*</i>	rs7476984	10	109170924	A/G	--	--	--	--	--	--	0.38	0.355	0.927	0.702	207	Yes
	<i>RTN4RL1</i>	rs11656601	17	1924911	T/C	--	--	--	--	--	--	0.23	0.253	1.103	0.819	207	No
	<i>ATP9B</i>	rs7226934	18	76904665	C/T	--	--	--	--	--	--	0.19	1.847	1.145	0.108	207	Yes
	<i>RP5-839B4.8*</i>	rs80352176	20	9952118	G/A	--	--	--	--	--	--	0.12	-0.486	1.362	0.722	207	Yes
	<i>RP11-560A15.4*</i>	rs6092424	20	55672544	A/G	--	--	--	--	--	--	0.41	-0.180	0.878	0.837	207	Yes
	<i>PARVG*</i>	rs139198	22	44606772	C/T	--	--	--	--	--	--	0.20	-0.073	1.117	0.948	207	No
FI	<i>NFIA</i>	rs7535730	1	61871356	G/A	0.78	0.003	0.005	0.501	38,238	Yes	0.18	0.005	0.112	0.967	201	Yes
	<i>IQCB1</i>	rs2331964	3	121542898	C/T	0.66	-0.004	0.004	0.295	38,238	No	0.26	0.016	0.098	0.871	201	Yes
	<i>SPEF2</i>	rs2361394	5	35800547	G/A	0.94	-0.003	0.009	0.768	38,238	No	0.07	-0.166	0.164	0.312	201	No
	<i>CSMD1</i>	rs77465890	8	3628570	C/T	--	--	--	--	--	--	0.10	0.050	0.152	0.741	201	No
	<i>CSMD1*</i>	rs35051650	8	4859203	A/C	--	--	--	--	--	--	0.08	0.059	0.159	0.711	201	Yes
	<i>PTPRO</i>	rs7315300	12	15610293	A/T	--	--	--	--	--	--	0.26	-0.011	0.102	0.917	201	No
	<i>MCTP2*</i>	rs12441824	15	94738631	A/G	0.32	0.005	0.006	0.438	38,238	No	0.41	0.053	0.084	0.526	201	No
	<i>TIAM1*</i>	rs2833275	21	32489757	T/C	0.43	-0.000	0.004	0.933	38,238	Yes	0.34	-0.018	0.095	0.853	201	Yes
	<i>CTA-992D9.7*</i>	rs4820743	22	27512801	T/C	--	--	--	--	--	--	0.39	0.003	0.092	0.974	201	Yes
HOMA-IR	<i>NFIA</i>	rs7535730	1	61871356	G/A	0.78	0.005	0.005	0.273	37,037	--	--	--	--	--	--	--
	<i>RCOR1</i>	rs12884198	14	103155465	A/G	0.04	0.014	0.011	0.189	37,037	--	--	--	--	--	--	--
	<i>MCTP2*</i>	rs12441824	15	94738631	A/G	0.32	0.009	0.006	0.137	37,037	--	--	--	--	--	--	--

Abbreviations: SNP, single nucleotide polymorphism; CHR, chromosome; BP, base pair position (hg19 build); EA, effect allele; OA, other allele; EAF, effect allele frequency; β , beta coefficient; SE, standard error; *p*, *p*-value; Consist, consistent; FG, fasting glucose; FI, fasting insulin, HOMA-IR, homeostatic model of insulin resistance.

TABLE S6 Population Architecture using Genomics and Epidemiology (PAGE) Consortium validation results for rs77465890 and fasting insulin

Ancestry group	EA/OA	Not adjusted for BMI					Adjusted for BMI				
		<i>n</i>	EAF	β	SE	<i>p</i>	<i>n</i>	EAF	β	SE	<i>p</i>
African	C/T	7,696	0.02	-0.100	0.065	0.122	7,683	0.02	-0.113	0.067	0.092
Asian	C/T	1,900	0.14	0.007	0.046	0.885	1,898	0.14	0.027	0.048	0.574
European	C/T	18,656	0.03	0.044	0.054	0.417	18,637	0.03	0.015	0.054	0.787
Hispanic	C/T	14,301	0.07	-0.004	0.024	0.861	14,270	0.07	-0.015	0.024	0.535
Native Hawaiian	C/T	1,398	0.12	0.044	0.062	0.478	1,397	0.12	0.073	0.065	0.257
Overall ^a	C/T	44,349	0.06	-0.003	0.018	0.876	44,280	0.06	-0.006	0.018	0.758

^aAdditional ancestry groups with much smaller sample sizes are not shown individually but are included in the Overall group; thus, the Overall *N* exceeds the total of the shown subgroup sample sizes.

Abbreviations: EA, effect allele; OA, other allele; EAF, effect allele frequency; β , beta coefficient; SE, standard error; *p*, p-value.

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