Table S7. The list of the 100 top-predicted genes of the Single-SNP model in the Cross-Pop cross-validation scheme

Entrez ID	Mean Test R^2	Gene Symbol	Gene Description
3117	0.75	HLA-DQA	major histocompatibility complex, class II, DQ alpha 1
158160	0.70	MGC88684	hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2
27004	0.65	TNG2	T-cell leukemia/lymphoma 6
25902	0.57	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
6168	0.54	RPL37A	ribosomal protein L37a
439921	0.54	TMAP1	matrix-remodelling associated 7
91612	0.53	My015	churchill domain containing 1
4731	0.52	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
282991	0.50	RP11-316M21.4	biogenesis of lysosome-related organelles complex-1, subunit 2
9623	0.49	TML1	T-cell leukemia/lymphoma 1B
829	0.48	CAZ1	capping protein (actin filament) muscle Z-line, alpha 1
84833	0.48	USMG5	upregulated during skeletal muscle growth 5 homolog (mouse)
91687	0.47	RP3-383J4.1	centromere protein L
84641	0.46	MGC117350	hippocampus abundant transcript-like 1
10494	0.45	YSK1	serine/threonine kinase 25 (STE20 homolog, yeast)
7773	0.45	ZNF230	zinc finger protein 230
55755	0.43	MCPH3	CDK5 regulatory subunit associated protein 2
84288	0.43	RP11-290P14.1	EF-hand calcium binding domain 2
4725	0.42	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
115024	0.41	NT5C3L	5'-nucleotidase, cytosolic III-like
7639	0.41	ZNF85	zinc finger protein 85
80008	0.41	TMEM156	transmembrane protein 156
349565	0.41	PNAT3	nicotinamide nucleotide adenylyltransferase 3
151246	0.40	TRIPIN	shugoshin-like 2 (S. pombe)
219927	0.40	MRPL21	mitochondrial ribosomal protein L21
80817	0.40	PS1TP3	KIAA1712
27068	0.39	SID6-306	pyrophosphatase (inorganic) 2
858	0.39	MGC12294	caveolin 2
11118	0.39	BTN3A2	butyrophilin, subfamily 3, member A2
133383	0.39	MGC33648	hypothetical protein MGC33648
155368	0.39	WBSCR27	Williams Beuren syndrome chromosome region 27
91647	0.38	MGC29736	ATP synthase mitochondrial F1 complex assembly factor 2
2944	0.38	MU	glutathione S-transferase M1
8904	0.38	MGC1142	copine I
10694	0.37	KIAA0002	chaperonin containing TCP1, subunit 8 (theta)
7536	0.37	ZNF162	splicing factor 1
55228	0.37	FLJ10781	hypothetical protein FLJ10781
255403	0.37	ZNF718	zinc finger protein 718
2635	0.36	GBP3	guanylate binding protein 3
10320	0.36	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)
26519	0.36	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)
8312	0.35	MGC52315	axin 1
84680	0.35	PHACS	1-aminocyclopropane-1-carboxylate synthase
11116	0.34	FOP	FGFR1 oncogene partner
81889	0.34	YISKL	fumarylacetoacetate hydrolase domain containing 1
93100	0.33	PP3856	nicotinate phosphoribosyltransferase domain containing 1
8878	0.33	ZIP3	sequestosome 1
130502	0.33	LOC130502	similar to CG14894-PA
55871	0.33	CBWD1	COBW domain containing 1
10953	0.33	TOMM34	translocase of outer mitochondrial membrane 34
10267	0.32	RAMP1	receptor (calcitonin) activity modifying protein 1
131076	0.32	FLJ33273	coiled-coil domain containing 58
6434	0.32	TRA2B	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
147138	0.32	TMC8	transmembrane channel-like 8
55588	0.31	MED29	intersex-like (Drosophila)
3118	0.31	HLA-DXA	major histocompatibility complex, class II, DQ alpha 2
7311	0.31	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1
3652	0.31	IPP	intracisternal A particle-promoted polypeptide
51097	0.30	SCCPDH	saccharopine dehydrogenase (putative)
51144	0.30	KAR	hydroxysteroid (17-beta) dehydrogenase 12
1497	0.30	PQLC4	cystinosis, nephropathic
79672	0.29	FN3KRP	fructosamine-3-kinase-related protein
9172	0.29	TTNAP	myomesin (M-protein) 2, 165kDa
87769	0.28	RP11-151A6.2	hypothetical protein BC004360

197322	0.27	LOC197322	hypothetical protein LOC197322
54822	0.27	TRP-PLIK	transient receptor potential cation channel, subfamily M, member 7
115004	0.27	MGC131892	chromosome 6 open reading frame 150
56927	0.27	MGC14393	G protein-coupled receptor 108
51122	0.27	MGC57611	COMM domain containing 2
55957	0.27	MGC9505	protein F25965
10653	0.26	SPINT2	serine peptidase inhibitor, Kunitz type, 2
3105	0.26	HLA-A	major histocompatibility complex, class I, A
128272	0.26	WGEF	Rho guanine nucleotide exchange factor (GEF) 19
1984	0.26	uORF	eukaryotic translation initiation factor 5A
22900	0.26	TUCAN	caspase recruitment domain family, member 8
84617	0.26	TUBB6	tubulin, beta 6
11014	0.25	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
55556	0.25	TYMSAS	enolase superfamily member 1
80221	0.25	FLJ20920	hypothetical protein FLJ20920
80315	0.25	KIAA1673	cytoplasmic polyadenylation element binding protein 4
1429	0.25	FLJ41475	crystallin, zeta (quinone reductase)
93349	0.24	MGC132667	hypothetical protein BC004921
127428	0.24	RP4-758J24.3	chromosome 1 open reading frame 83
9794	0.24	MAML1	mastermind-like 1 (Drosophila)
84284	0.24	RP4-659I19.2	chromosome 1 open reading frame 57
127700	0.24	OSCP1	chromosome 1 open reading frame 102
113277	0.24	TMEM106A	transmembrane protein 106A
64858	0.24	SNM1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)
81544	0.24	PP1665	glycerophosphodiester phosphodiesterase domain containing 5
54475	0.23	Nle	notchless homolog 1 (Drosophila)
8310	0.23	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl
1479	0.23	MGC75122	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
7390	0.23	UROS	uroporphyrinogen III synthase (congenital erythropoietic porphyria)
1776	0.23	LSD	deoxyribonuclease I-like 3
10905	0.23	MAN1B	mannosidase, alpha, class 1A, member 2
54535	0.23	SBP	coiled-coil alpha-helical rod protein 1
147968	0.22	MGC20576	calpain 12
283726	0.22	DKFZp666G057	hypothetical protein DKFZp666G057
26284	0.22	HERA-B	Era G-protein-like 1 (E. coli)
1912	0.22	PHC2	polyhomeotic-like 2 (Drosophila)