

Table S5. The list of the 100 top-predicted genes of the KNN model in the Cross-Pop cross-validation scheme

Entrez ID	Mean Test R ²	Gene Symbol	Gene Description
91612	0.67	My015	churchill domain containing 1
158160	0.56	MGC88684	hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2
84288	0.55	RP11-290P14.1	EF-hand calcium binding domain 2
93035	0.51	PKHDL1	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1
94101	0.45	ORMDL1	ORM1-like 1 (<i>S. cerevisiae</i>)
6231	0.44	RPS26	ribosomal protein S26
829	0.41	CAZ1	capping protein (actin filament) muscle Z-line, alpha 1
3117	0.41	HLA-DQA	major histocompatibility complex, class II, DQ alpha 1
3663	0.39	IRF5	interferon regulatory factor 5
91687	0.38	RP3-383J4.1	centromere protein L
3127	0.38	HLA-DRB5	major histocompatibility complex, class II, DR beta 5
3123	0.37	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
55556	0.33	TYMSAS	enolase superfamily member 1
9045	0.33	RPL14	ribosomal protein L14
8904	0.32	MGC1142	copine 1
84833	0.31	USMG5	upregulated during skeletal muscle growth 5 homolog (mouse)
81889	0.31	YISKL	fumarylacetoacetate hydrolase domain containing 1
2635	0.31	GBP3	guanylate binding protein 3
115024	0.29	NT5C3L	5'-nucleotidase, cytosolic III-like
55228	0.29	FLJ10781	hypothetical protein FLJ10781
858	0.29	MGC12294	caveolin 2
10494	0.28	YSK1	serine/threonine kinase 25 (STE20 homolog, yeast)
282991	0.28	RP11-316M21.4	biogenesis of lysosome-related organelles complex-1, subunit 2
11118	0.27	BTN3A2	butyrophilin, subfamily 3, member A2
162394	0.26	SLFN5	schlafen family member 5
3652	0.25	IPP	intracisternal A particle-promoted polypeptide
87769	0.25	RP11-151A6.2	hypothetical protein BC004360
54535	0.25	SBP	coiled-coil alpha-helical rod protein 1
7639	0.25	ZNF85	zinc finger protein 85
84617	0.25	TUBB6	tubulin, beta 6
255403	0.24	ZNF718	zinc finger protein 718
128272	0.24	WGEF	Rho guanine nucleotide exchange factor (GEF) 19
7536	0.23	ZNF162	splicing factor 1
133383	0.23	MGC33648	hypothetical protein MGC33648
54014	0.23	WDR9	bromodomain and WD repeat domain containing 1
80817	0.22	PS1TP3	KIAA1712
23593	0.22	SOUL	heme binding protein 2
219927	0.22	MRPL21	mitochondrial ribosomal protein L21
80008	0.22	TMEM156	transmembrane protein 156
51144	0.21	KAR	hydroxysteroid (17-beta) dehydrogenase 12
113277	0.21	TMEM106A	transmembrane protein 106A
5411	0.21	SDK3	pinin, desmosome associated protein
26519	0.21	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)
3059	0.20	HS1	hematopoietic cell-specific Lyn substrate 1
152815	0.20	THAP6	THAP domain containing 6
6168	0.20	RPL37A	ribosomal protein L37a
25961	0.20	NUDT13	nudix (nucleoside diphosphate linked moiety X)-type motif 13
84314	0.20	TMEM107	transmembrane protein 107
84680	0.20	PHACS	1-aminocyclopropane-1-carboxylate synthase
7311	0.20	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1
10953	0.20	TOMM34	translocase of outer mitochondrial membrane 34
29035	0.20	PRO0149	PRO0149 protein
197322	0.19	LOC197322	hypothetical protein LOC197322
23008	0.19	KIAA0265	KIAA0265 protein
130502	0.19	LOC130502	similar to CG14894-PA
7390	0.19	UROS	uroporphyrinogen III synthase (congenital erythropoietic porphyria)
84516	0.19	p25	dynactin 5 (p25)
10694	0.19	KIAA0002	chaperonin containing TCP1, subunit 8 (theta)
2768	0.19	RMP	guanine nucleotide binding protein (G protein) alpha 12
27102	0.19	KIAA1369	eukaryotic translation initiation factor 2-alpha kinase 1
9179	0.19	MU-ARP2	adaptor-related protein complex 4, mu 1 subunit
7760	0.18	ZNF213	zinc finger protein 213
348094	0.18	MGC120307	ankyrin repeat and death domain containing 1A
283726	0.18	DKFZp666G057	hypothetical protein DKFZp666G057
261726	0.17	TIPRL	TIP41, TOR signalling pathway regulator-like (<i>S. cerevisiae</i>)
57602	0.17	USP36	ubiquitin specific peptidase 36

3105	0.17	HLA-A	major histocompatibility complex, class I, A
9794	0.17	MAML1	mastermind-like 1 (Drosophila)
10412	0.17	YR-29	TGF beta-inducible nuclear protein 1
387338	0.17	RP4-603I14.2	NOL1/NOP2/Sun domain family, member 4
1965	0.16	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
51275	0.16	FLJ39616	chromosome 12 open reading frame 47
1912	0.16	PHC2	polyhomeotic-like 2 (Drosophila)
4552	0.16	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
51101	0.16	CGI-62	chromosome 8 open reading frame 70
10233	0.16	LRRC23	leucine rich repeat containing 23
5037	0.16	RKIP	phosphatidylethanolamine binding protein 1
55755	0.16	MCPH3	CDK5 regulatory subunit associated protein 2
1520	0.16	MGC3886	cathepsin S
8034	0.15	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16
7084	0.15	TK2	thymidine kinase 2, mitochondrial
10645	0.15	MGC15254	calcium/calmodulin-dependent protein kinase kinase 2, beta
3134	0.15	HLAF	major histocompatibility complex, class I, F
8693	0.15	GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)
23042	0.15	LP8165	KIAA0251 protein
10520	0.15	ZNFC25	zinc finger protein 211
2653	0.15	NKH	glycine cleavage system protein H (aminomethyl carrier)
285464	0.15	FLJ34443	hypothetical protein FLJ34443
4925	0.15	NUCB2	nucleobindin 2
81491	0.15	PSP24B	G protein-coupled receptor 63
92070	0.15	MGC21675	hypothetical protein MGC21675
127700	0.15	OSCP1	chromosome 1 open reading frame 102
55666	0.14	NPLOC4	nuclear protein localization 4 homolog (S. cerevisiae)
151963	0.14	C3orf59	chromosome 3 open reading frame 59
4835	0.14	QR2	NAD(P)H dehydrogenase, quinone 2
90416	0.14	MGC20481	coiled-coil domain containing 32
953	0.14	NTPDase-1	ectonucleoside triphosphate diphosphohydrolase 1
439921	0.14	TMAP1	matrix-remodelling associated 7
286354	0.14	NAG12	chromosome 9 open reading frame 130
977	0.14	TSPAN24	CD151 molecule (Raph blood group)