

Supplementary Table S1 *Number of the SNP markers with genetic variance larger than or equal to 0.001% for milk yield, fat yield, and age at first calving by distance between SNP genotypes and genes in the NCBI database.*

Distance between SNP and gene	Milk yield	Fat yield	Age at first calving
Inside gene	10,263	10,119	10,149
≤ 2500 bp	1,390	1,406	1,360
2500 bp < distance ≤ 5000 bp	855	848	878
5000 bp < distance ≤ 25 000 bp	3,726	3,739	3,713
distance > 25 000 bp	10,342	10,287	10,555
Total	26,576	26,399	26,655

Supplementary Table S2 *Number of genes and total genetic variance for milk yield (MY), fat yield (FY), and age at first calving (AFC) per chromosome identified by SNP markers inside genes or within 2500 bp of genes in the Thai multibreed population.*

Chromosome	Number of genes (n)			Genetic variance (%)		
	MY	FY	AFC	MY	FY	AFC
1	299	296	323	1.46	1.37	1.69
2	322	307	292	1.58	1.49	1.53
3	342	365	347	1.60	1.70	1.66
4	286	282	282	1.91	1.73	2.01
5	393	361	403	2.02	2.07	1.96
6	256	236	241	1.40	1.27	1.39
7	326	342	341	1.57	1.53	1.50
8	271	272	264	1.58	1.49	1.48
9	243	230	230	1.40	1.45	1.29
10	280	304	309	1.75	1.74	1.81
11	327	349	339	1.77	2.09	1.70
12	162	168	157	1.20	1.45	1.39
13	238	263	248	1.33	1.29	1.40
14	195	196	185	1.36	1.40	1.24
15	299	295	299	1.70	1.54	1.66
16	223	237	244	1.38	1.39	1.28
17	224	224	214	1.39	1.29	0.96
18	300	299	286	1.22	1.35	1.25
19	325	317	291	1.67	1.64	1.46
20	141	137	131	0.80	0.64	0.72
21	156	138	151	0.86	0.75	0.79
22	138	134	138	0.73	0.73	0.83
23	140	157	154	0.82	0.83	0.70
24	118	118	125	0.65	0.62	0.72
25	169	177	162	0.84	0.84	0.83

Chromosome	Number of genes (n)			Genetic variance (%)		
	MY	FY	AFC	MY	FY	AFC
26	153	156	159	0.75	0.81	0.87
27	105	109	106	0.66	0.58	0.58
28	146	131	141	0.88	0.85	0.95
29	176	173	171	0.91	1.01	0.93
X	177	186	189	0.87	0.87	0.91
Total	6,930	6,959	6,922	38.04	37.81	37.50

Supplementary Table S3 *Number of genes and total genetic variance for milk yield (MY), fat yield (FY) and age at first calving (AFC) per chromosome in the Thai multibreed population.*

Chromosome	Number of genes (n)	Genetic variance (%)		
		MY	FY	AFC
1	149	1.026	0.917	1.075
2	176	1.103	1.113	1.193
3	159	1.073	1.094	0.964
4	152	1.402	1.356	1.490
5	192	1.406	1.508	1.239
6	135	0.987	0.925	0.957
7	147	0.883	0.928	0.826
8	142	1.165	1.096	0.971
9	118	0.951	1.001	0.873
10	158	1.274	1.243	1.129
11	174	1.191	1.436	1.110
12	94	1.014	1.211	1.109
13	118	0.919	0.862	0.959
14	107	1.015	1.056	0.924
15	137	1.088	0.971	1.060
16	117	0.976	0.964	0.773
17	111	0.990	0.881	0.627
18	108	0.630	0.754	0.712
19	152	1.040	1.043	0.942
20	81	0.605	0.503	0.495
21	65	0.567	0.515	0.488
22	67	0.533	0.565	0.522
23	69	0.563	0.537	0.422
24	62	0.446	0.454	0.436
25	74	0.581	0.529	0.566
26	77	0.520	0.583	0.592
27	55	0.439	0.363	0.419
28	74	0.683	0.672	0.626
29	83	0.599	0.696	0.670
X	83	0.556	0.543	0.526
Total	3436	26.223	26.317	24.693

Supplementary File S1 *Number of connections, number of pathways and percent of genetic variance for milk yield (MY), fat yield (FY), and age at first calving (AFC) explained by single nucleotide polymorphism located inside or within 2,500 bp of genes in the Thai multibreed population.*

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
PLCB1	phospholipase C beta 1	44	12	0.0475	0.0423	0.0674
GNG2	G protein subunit gamma 2	38	5	0.0296	0.0158	0.0067
PLCB4	phosphoinositide phospholipase C	34	12	0.0066	0.0077	0.0227
CAMK2B	calcium/calmodulin dependent protein kinase II beta	32	5	0.0012	0.0014	0.0062
CAMK2D	calcium/calmodulin dependent protein kinase II delta	32	5	0.0199	0.0067	0.0073
MAPK14	mitogen-activated protein kinase 14	29	4	0.0018	0.0026	0.0087
GRB2	growth factor receptor bound protein 2	29	5	0.0107	0.0032	0.0104
ITGB5	integrin subunit beta 5	27	1	0.0012	0.0025	0.0018
PRKCB	protein kinase C beta	25	14	0.0120	0.0091	0.016
FYN	FYN proto-oncogene, Src family tyrosine kinase	24	3	0.0011	0.0033	0.0129
GNGT1	G protein subunit gamma transducin 1	22	5	0.0061	0.0057	0.0026
ADCY8	adenylate cyclase 8	22	10	0.0201	0.0127	0.0167
ADCY2	adenylate cyclase 2	22	10	0.0097	0.0137	0.0215
GNAO1	G protein subunit alpha o1	22	6	0.0047	0.0057	0.0102
MAPK11	mitogen-activated protein kinase 11	22	4	0.0019	0.0027	0.0019
EGFR	epidermal growth factor receptor	22	8	0.0041	0.0098	0.0194
ADCY5	adenylate cyclase 5	21	10	0.0044	0.0011	0.0015
ADCY7	adenylate cyclase 7	21	10	0.0050	0.0149	0.0031
GNAQ	G protein subunit alpha q	21	10	0.0052	0.0063	0.0066

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
RAP1B	RAP1B, member of RAS oncogene family	21	5	0.0040	0.012	0.0049
IRS1	insulin receptor substrate 1	21	1	0.0123	0.0076	0.0043
PRKCA	protein kinase C alpha	20	15	0.0096	0.0216	0.0064
ITGA6	integrin subunit alpha 6	20	1	0.0076	0.0043	0.003
ITGA9	integrin subunit alpha 9	20	1	0.0072	0.0162	0.0167
ITGA8	integrin subunit alpha 8	20	1	0.0312	0.017	0.0187
PTEN	phosphatase and tensin homolog	20	2	0.0023	0.0043	0.0031
AKT3	AKT serine/threonine kinase 3	20	8	0.0038	0.0042	0.01
ITGA2	integrin subunit alpha 2	19	1	0.0014	0.0019	0.0101
IGF1R	insulin like growth factor 1 receptor	19	3	0.0069	0.0027	0.0048
RASGRF2	RAS protein-specific guanine nucleotide-releasing factor 2	18	2	0.0059	0.0022	0.003
PPP2R5E	protein phosphatase 2 regulatory subunit B'epsilon	18	2	0.007	0.0054	0.0034
PDGFRA	platelet derived growth factor receptor alpha	18	7	0.001	0.0023	0.0032
PDGFRB	platelet derived growth factor receptor beta	18	7	0.0039	0.0078	0.0103
MAPK10	mitogen-activated protein kinase 10	18	6	0.0058	0.0041	0.0168
CACNG2	calcium voltage-gated channel auxiliary subunit gamma 2	18	2	0.0043	0.0039	0.01
SOS1	SOS Ras/Rac guanine nucleotide exchange factor 1	18	5	0.0046	0.005	0.0042
PRKG2	protein kinase, cGMP-dependent, type II	17	3	0.0116	0.0106	0.0022
PRKG1	protein kinase, cGMP-dependent, type I	17	3	0.0366	0.0371	0.0341
ADCY1	adenylate cyclase 1	16	10	0.0021	0.0025	0.0035
LPAR3	lysophosphatidic acid receptor 3	16	2	0.0014	0.004	0.0027
GRM1	glutamate receptor, metabotropic 1	16	4	0.0152	0.0189	0.0128
PLCE1	phospholipase C epsilon 1	16	3	0.0068	0.0094	0.0052
INSR	insulin receptor	16	4	0.0132	0.0303	0.0111

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
SHC3	SHC adaptor protein 3	16	3	0.0029	0.0034	0.0065
CACNG4	calcium voltage-gated channel auxiliary subunit gamma 4	15	2	0.008	0.0014	0.0064
GSK3B	glycogen synthase kinase 3 beta	15	3	0.0119	0.0058	0.0014
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta	14	2	0.0075	0.0015	0.002
CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	14	2	0.0096	0.0124	0.0079
FLT1	fms related tyrosine kinase 1	14	3	0.0092	0.0065	0.0016
GRIA3	glutamate ionotropic receptor AMPA type subunit 3	14	3	0.0118	0.0164	0.0085
MET	MET proto-oncogene, receptor tyrosine kinase	14	3	0.0015	0.0026	0.0041
GRIA1	glutamate receptor, ionotropic, AMPA1	14	3	0.0235	0.0096	0.0123
TEK	TEK receptor tyrosine kinase	14	2	0.007	0.0067	0.0017
RASGRP3	RAS guanyl releasing protein 3	13	3	0.0055	0.0028	0.0024
PLD1	phospholipase D1, phosphatidylcholine-specific	13	4	0.0042	0.0015	0.0339
FGF19	fibroblast growth factor 19	13	3	0.009	0.0025	0.0032
EFNA5	ephrin A5	13	2	0.0085	0.0062	0.0063
CACNB4	calcium voltage-gated channel auxiliary subunit beta 4	13	2	0.0099	0.0038	0.0034
GNA12	G protein subunit alpha 12	13	4	0.0055	0.0023	0.0042
FGF2	BFGF	13	3	0.0081	0.0063	0.0014
TLN1	talin 1	13	2	0.0017	0.0029	0.0032
GRIA2	glutamate ionotropic receptor AMPA type subunit 2	13	3	0.0013	0.0014	0.0105
FLT4	fms related tyrosine kinase 4	13	3	0.0023	0.0076	0.0164
PDE3B	phosphodiesterase 3B	12	1	0.0144	0.0074	0.0013
EDNRB	endothelin receptor type B	12	2	0.0012	0.0015	0.0045
CACNA1A	calcium voltage-gated channel subunit alpha 1 A	12	5	0.0243	0.0255	0.0143

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
GNA13	G protein subunit alpha 13	12	3	0.0037	0.0049	0.0029
GRIA4	glutamate ionotropic receptor AMPA type subunit 4	12	3	0.0342	0.0257	0.029
ITGB2	integrin subunit beta 2	12	1	0.0036	0.004	0.0053
ANGPT1	angiopoietin 1	12	2	0.0248	0.0249	0.0025
PDE3A	phosphodiesterase 3A	11	1	0.012	0.0143	0.0078
CACNA2D4	calcium voltage-gated channel auxiliary subunit alpha2delta 4	11	2	0.0063	0.0095	0.0013
CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3	11	2	0.0302	0.0238	0.0295
FN1	fibronectin 1	11	1	0.0022	0.0039	0.001
BCL2	BCL2, apoptosis regulator	11	2	0.0099	0.0132	0.0015
GRIN2B	glutamate ionotropic receptor NMDA type subunit 2B	11	5	0.0137	0.0243	0.0048
GRIN1	glutamate ionotropic receptor NMDA type subunit 1	11	5	0.002	0.004	0.0069
LRP6	LDL receptor related protein 6	11	1	0.0026	0.0082	0.0066
CACNG5	calcium voltage-gated channel auxiliary subunit gamma 5	10	2	0.0016	0.008	0.0013
FGF12	fibroblast growth factor 12	10	3	0.015	0.0202	0.0198
PDGFD	platelet derived growth factor D	10	5	0.0282	0.0151	0.0331
PDGFC	platelet derived growth factor C	10	5	0.0078	0.003	0.0156
CASP3	caspase 3, apoptosis-related cysteine peptidase	10	1	0.0017	0.0025	0.0011
RAPGEF4	Rap guanine nucleotide exchange factor 4	10	2	0.0036	0.0027	0.0089
FLNB	filamin B	10	2	0.0087	0.0081	0.0044
LRP5	LDL receptor related protein 5	10	1	0.0075	0.0178	0.0046
FIGF	c-fos induced growth factor	10	3	0.0102	0.0121	0.0035
WNT3A	Wnt family member 3A	10	1	0.004	0.0021	0.0022

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
GAB1	GRB2 associated binding protein 1	10	2	0.0057	0.0092	0.002
TACR1	tachykinin receptor 1	9	1	0.0177	0.0214	0.0078
TACR3	tachykinin receptor 3	9	1	0.0049	0.0049	0.004
NTSR1	neurotensin receptor 1	9	1	0.0015	0.0023	0.0022
NSF	N-ethylmaleimide sensitive factor, vesicle fusing ATPase	9	1	0.0055	0.0075	0.0044
PDE1A	phosphodiesterase 1A, calmodulin-dependent	9	1	0.0055	0.0014	0.0017
PDE1C	phosphodiesterase 1C	9	1	0.0273	0.0227	0.011
PDE1B	cam-PDE 1B	9	1	0.0038	0.0056	0.0042
CHRM3	cholinergic receptor muscarinic 3	9	2	0.0164	0.0117	0.006
WNT7A	Wnt family member 7A	9	1	0.0013	0.0084	0.0015
FZD7	frizzled class receptor 7	9	1	0.0046	0.0074	0.0025
TLN2	talin 2	9	2	0.003	0.0078	0.0031
GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A	9	6	0.0054	0.0048	0.0025
VAV3	vav guanine nucleotide exchange factor 3	9	1	0.0033	0.005	0.0104
VAV2	vav guanine nucleotide exchange factor 2	9	1	0.0166	0.0086	0.0074
PPP3CA	protein phosphatase 3 catalytic subunit alpha	9	7	0.0124	0.0101	0.0065
CAMK4	calcium/calmodulin dependent protein kinase IV	8	2	0.0037	0.0114	0.0042
SCTR	secretin receptor	8	1	0.0012	0.0034	0.003
GUCY1B3	guanylate cyclase 1 soluble subunit beta	8	4	0.0033	0.0033	0.0011
GUCY1A2	guanylate cyclase 1 soluble subunit alpha 2	8	4	0.0232	0.0105	0.018
GRM7	glutamate metabotropic receptor 7	8	2	0.0138	0.0334	0.0102
GRM3	glutamate metabotropic receptor 3	8	2	0.0158	0.0152	0.0035
HTR7	5-hydroxytryptamine receptor 7	8	2	0.0076	0.0016	0.0019
CACNA1B	calcium voltage-gated channel subunit alpha 1 B	8	4	0.0062	0.0034	0.0135
MAP3K5	mitogen-activated protein kinase kinase kinase 5	8	2	0.008	0.0148	0.0172

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
PPAP2B	phosphatidic acid phosphatase type 2B	8	1	0.0055	0.0027	0.0018
CREBBP	CREB binding protein	8	1	0.0049	0.0081	0.0099
BTRC	beta-transducin repeat containing E3 ubiquitin protein ligase	8	1	0.004	0.0136	0.0049
ITGAL	integrin subunit alpha L	8	1	0.0025	0.0044	0.0018
LCP2	lymphocyte cytosolic protein 2 tyrosine phosphoprotein slp-76	8	1	0.0054	0.004	0.0104
CACNA2D1	calcium voltage-gated channel auxiliary subunit alpha2delta 1	7	2	0.0104	0.0071	0.0022
LAMA5	laminin subunit alpha 5	7	1	0.0035	0.0042	0.0045
CACNA1E	calcium voltage-gated channel subunit alpha1 E	7	2	0.0146	0.0107	0.0044
COL9A3	collagen type IX alpha 3 chain	7	1	0.0052	0.005	0.0105
COL2A1	collagen type II alpha 1 chain	7	1	0.0046	0.0026	0.0016
GABBR2	gamma-aminobutyric acid type B receptor subunit 2	7	1	0.0099	0.0063	0.0301
ITPR2	inositol 1,4,5-triphosphate receptor, type 2	7	7	0.0071	0.0083	0.0192
HTR4	5-hydroxytryptamine receptor 4	7	1	0.0098	0.0149	0.0107
COL4A5	collagen type IV alpha 5 chain	7	1	0.0074	0.0037	0.0106
ITPR1	IP3 receptor	7	8	0.0126	0.0084	0.0057
PTK2B	protein tyrosine kinase 2 beta	7	2	0.0015	0.0013	0.0047
LAMC2	laminin subunit gamma 2	7	1	0.0053	0.0044	0.015
AGPAT4	lysophosphatidic acid acyltransferase delta	7	1	0.0141	0.0228	0.0021
LAMA3	laminin subunit alpha 3	7	1	0.0041	0.0014	0.0047
MAP2K6	mitogen-activated protein kinase kinase 6	7	2	0.0019	0.0051	0.0066
WNT11	Wnt family member 11	7	1	0.0013	0.0029	0.0024
CHUK	conserved helix-loop-helix ubiquitous kinase	7	2	0.0017	0.0095	0.0077
ERBB4	erb-b2 receptor tyrosine kinase 4	7	1	0.0229	0.014	0.0271
PPP3CC	protein phosphatase 3 catalytic subunit gamma	7	7	0.0079	0.0028	0.0045

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
PLCL1	phospholipase C like 1	6	1	0.0115	0.014	0.0129
RYR2	ryanodine receptor 2	6	4	0.0083	0.0245	0.0183
GABRB1	gamma-aminobutyric acid type A receptor beta1 subunit	6	1	0.0158	0.0071	0.0046
PTGER3	prostaglandin E receptor 3	6	1	0.002	0.0027	0.0026
TIAM1	T-cell lymphoma invasion and metastasis 1	6	2	0.0114	0.0043	0.0189
COL4A2	collagen type IV alpha 2 chain	6	1	0.004	0.0037	0.0064
COL4A1	collagen type IV alpha 1 chain	6	1	0.0075	0.004	0.0109
WNT10B	Wnt family member 10B	6	1	0.0036	0.0025	0.002
ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	6	1	0.0066	0.0054	0.0049
WIF1	WNT inhibitory factor 1	6	1	0.0013	0.0028	0.0068
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase type 1 beta	6	1	0.0166	0.0115	0.0071
WNT9B	Wnt family member 9B	6	1	0.0032	0.0012	0.0047
LEF1	lymphoid enhancer binding factor 1	6	1	0.0128	0.0067	0.0016
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	6	1	0.0126	0.0096	0.0132
MAP2K4	mitogen-activated protein kinase kinase 4	6	1	0.0016	0.0059	0.0018
APC	APC, WNT signaling pathway regulator	6	1	0.0051	0.0136	0.0054
TSC2	tuberous sclerosis 2	6	1	0.0053	0.0032	0.0028
CHAD	chondroadherin	5	1	0.0018	0.0017	0.0016
CD38	CD38 molecule	5	3	0.004	0.0056	0.0077
DGKH	diacylglycerol kinase eta	5	1	0.0168	0.0149	0.004
LAMA4	laminin subunit alpha 4	5	1	0.0118	0.0095	0.0027
TNR	tenascin R	5	1	0.0144	0.0241	0.0053
GABRA5	gamma-aminobutyric acid type A receptor alpha5 subunit	5	1	0.0195	0.0109	0.0051

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
GABRB2	gamma-aminobutyric acid type A receptor beta2 subunit	5	1	0.0036	0.0053	0.0147
DGKE	diacylglycerol kinase epsilon	5	1	0.0024	0.0018	0.0017
THBS2	thrombospondin 2	5	1	0.011	0.0046	0.0016
PARVA	parvin alpha	5	1	0.0074	0.0092	0.0152
DGKG	diacylglycerol kinase gamma	5	1	0.0025	0.0019	0.0024
DGKB	diacylglycerol kinase beta	5	1	0.0205	0.0188	0.01
DGKI	diacylglycerol kinase iota	5	1	0.0338	0.0218	0.0199
SGMS2	sphingomyelin synthase 2	5	1	0.0011	0.0016	0.0035
GPHN	gephyrin	5	1	0.0337	0.0289	0.0188
SGMS1	sphingomyelin synthase 1	5	1	0.0012	0.0022	0.0058
CERS6	ceramide synthase 6	5	1	0.0096	0.0012	0.0095
DEGS1	delta 4-desaturase, sphingolipid 1	5	1	0.0027	0.0043	0.0117
CERS3	ceramide synthase 3	5	1	0.0047	0.0045	0.0024
TNC	tenascin C	5	1	0.0032	0.0042	0.0084
ARRB1	arrestin beta 1	5	1	0.0066	0.0095	0.006
TCF7L2	transcription factor 7 like 2	5	1	0.0133	0.0098	0.0117
PPP3R1	protein phosphatase 3 regulatory subunit B, alpha	5	6	0.0012	0.0032	0.0011
KIF5A	kinesin family member 5A	4	1	0.0098	0.0216	0.009
KIF5C	kinesin family member 5C	4	1	0.002	0.0017	0.0016
MAP2K5	mitogen-activated protein kinase kinase 5	4	3	0.0147	0.0184	0.0063
MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	4	1	0.0065	0.0047	0.0017
RAPGEF6	Rap guanine nucleotide exchange factor 6	4	1	0.0052	0.0052	0.0094
RAPGEF2	Rap guanine nucleotide exchange factor 2	4	2	0.009	0.0112	0.0019
GRIK3	Glutamate Ionotropic Receptor Kainate Type Subunit 3	4	1	0.0063	0.0061	0.0115

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
LPAR1	lysophosphatidic acid receptor 1	4	3	0.0155	0.0037	0.0057
NTRK2	neurotrophic receptor tyrosine kinase 2	4	1	0.0095	0.0058	0.0011
FBXW11	F-box and WD repeat domain containing 11	4	1	0.0032	0.0012	0.0089
PLA2G16	phospholipase A2, group XVI	4	1	0.0019	0.0029	0.0018
GABRG2	Gamma-Aminobutyric Acid Type A Receptor Gamma2 Subunit	4	1	0.0041	0.0063	0.0142
NFATC2	nuclear factor of activated T-cells 2	4	3	0.0138	0.0106	0.0087
RPS6KA2	ribosomal protein S6 kinase A2	4	1	0.0056	0.01	0.0134
RPS6KA3	ribosomal protein S6 kinase A3	4	1	0.0039	0.0023	0.005
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	4	1	0.0051	0.0031	0.0057
MRVII	murine retrovirus integration site 1 homolog	4	1	0.0049	0.0103	0.0171
SLC8A3	solute carrier family 8 member A3	3	2	0.0142	0.0106	0.0023
SLC8A1	solute carrier family 8 member A1	3	2	0.0126	0.0137	0.0265
PRKD1	protein kinase D1	3	1	0.0077	0.0091	0.0181
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	3	1	0.0131	0.0151	0.0043
STK3	serine/threonine kinase 3	3	1	0.0141	0.0127	0.0102
DKK4	dickkopf WNT signaling pathway inhibitor 4	3	1	0.0044	0.0026	0.0054
BID	BH3 Interacting Domain Death Agonist	3	1	0.0012	0.0031	0.003
CAV2	caveolin 2	3	1	0.0029	0.0019	0.001
ADRA1A	adrenoceptor alpha 1A	3	2	0.006	0.0024	0.0084
SGPP1	sphingosine-1-phosphate phosphatase 1	3	1	0.0013	0.0049	0.003
ITPKB	inositol-trisphosphate 3-kinase B	3	1	0.0068	0.0044	0.0054
PLA2G2F	phospholipase A2 group IIF	3	2	0.0025	0.0018	0.0026
GABRA3	gamma-aminobutyric acid type A receptor alpha3 subunit	3	1	0.0032	0.0021	0.0031

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
FRAT2	FRAT2, WNT signaling pathway regulator	3	1	0.0017	0.0018	0.0016
SKAP1	src kinase associated phosphoprotein 1	3	1	0.0108	0.0077	0.0072
DKK2	dickkopf WNT signaling pathway inhibitor 2	3	1	0.008	0.0063	0.0047
KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2	3	1	0.0055	0.0046	0.0056
KCNMA1	potassium calcium-activated channel subfamily M alpha 1	3	2	0.033	0.0273	0.0221
PRKCE	protein kinase C epsilon	3	2	0.0345	0.0509	0.0184
PLA2G12B	phospholipase A2 group XIIB	3	2	0.001	0.0014	0.01
PTPRR	protein tyrosine phosphatase, receptor type R	3	1	0.0187	0.0024	0.0112
RPS6KA5	ribosomal protein S6 kinase A5	3	2	0.0067	0.0082	0.007
DUSP10	dual specificity phosphatase 10	3	1	0.0302	0.0381	0.0175
NLK	nemo like kinase	3	2	0.0081	0.0111	0.0052
FYB	FYN binding protein	3	1	0.0049	0.0013	0.0075
MKNK1	MAP Kinase Interacting Serine/Threonine Kinase 1	2	1	0.0022	0.0118	0.006
ETS1	ETS proto-oncogene 1, transcription factor	2	1	0.0062	0.0124	0.0022
ATP2B2	ATPase plasma membrane Ca ²⁺ transporting 2	2	3	0.006	0.0104	0.0082
ATP2B4	ATPase plasma membrane Ca ²⁺ transporting 4	2	3	0.0025	0.0034	0.0082
DNM2	dynamamin 2	2	1	0.0027	0.0024	0.0035
STK4	serine/threonine kinase 4	2	2	0.0084	0.004	0.0071
RBX1	Ring-Box 1	2	1	0.0038	0.0017	0.0016
PPP1R12A	protein phosphatase 1 regulatory subunit 12A	2	3	0.0037	0.0023	0.0013
PIK3R6	phosphoinositide-3-kinase regulatory subunit 6	2	3	0.0014	0.0027	0.0014
CTSD	cathepsin D	2	1	0.0028	0.0011	0.0022
TRPC6	transient receptor potential cation channel subfamily C member 6	2	1	0.0227	0.0424	0.0034
LOC529488	glutamate decarboxylase 1	2	1	0.0054	0.0038	0.016

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
GLS	glutaminase	2	2	0.0029	0.0032	0.0015
GAD2	glutamate decarboxylase 2	2	1	0.0045	0.0035	0.0018
FCER1A	Fc fragment of IgE receptor Ia	2	2	0.0037	0.0087	0.0045
MS4A2	Membrane Spanning 4-Domains A2	2	2	0.0031	0.0025	0.0029
ARF1	ADP ribosylation factor 1	2	1	0.0029	0.0012	0.0021
SHANK2	SH3 and multiple ankyrin repeat domains 2	2	1	0.0192	0.0098	0.0255
DLGAP1	DLG associated protein 1	2	1	0.0041	0.0099	0.0028
SHANK1	SH3 and multiple ankyrin repeat domains 1	2	1	0.0054	0.0059	0.0012
TCF7L1	transcription factor 7 like 1	2	1	0.0252	0.017	0.002
ADRBK2	G Protein-Coupled Receptor Kinase 2	2	1	0.0013	0.0012	0.0098
PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1B	1	1	0.0017	0.0013	0.0028
CFTR	ATP-binding cassette sub-family C member 7	1	1	0.0149	0.009	0.0101
DNM3	dynamamin 3	1	1	0.0083	0.0039	0.0037
ARHGAP35	Rho GTPase activating protein 35	1	1	0.0011	0.01	0.0031
IL1R1	interleukin 1 receptor type 1	1	1	0.0128	0.0086	0.0021
SLC17A8	solute carrier family 17 member 8	1	1	0.0026	0.0042	0.0056
SLC18A2	solute carrier family 18 member A2	1	1	0.0021	0.0016	0.0042
MECOM	MDS1 and EVI1 complex locus	1	1	0.0167	0.0178	0.0216
KSR2	kinase suppressor of ras 2	1	1	0.0045	0.0102	0.0094
MYLK3	myosin light chain kinase 3	1	4	0.0031	0.0063	0.0015
PAK7	P21 (RAC1) Activated Kinase 5	1	2	0.0076	0.0026	0.0079
PARD3	par-3 family cell polarity regulator	1	1	0.0014	0.0042	0.0175
DOCK4	dedicator of cytokinesis 4	1	1	0.011	0.0168	0.004
DOCK1	dedicator of cytokinesis 1	1	1	0.0428	0.0386	0.027
TGFB2	transforming growth factor beta 2	1	1	0.0021	0.0023	0.01
MYL12B	myosin, light chain 12B, regulatory	1	1	0.0049	0.0017	0.0103
P2RX1	purinergic receptor P2X 1	1	1	0.0012	0.0011	0.0034

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Genetic variance (%)		
				MY	FY	AFC
P2RX3	purinergic receptor P2X 3	1	1	0.0049	0.0015	0.0012
SIPA1L1	signal induced proliferation associated 1 like 1	1	1	0.0196	0.0343	0.0496
GRIK4	glutamate ionotropic receptor kainate type subunit 4	1	1	0.0101	0.0073	0.0205
MAPT	PHF-tau microtubule associated protein tau neurofibrillary tangle protein paired helical filament-tau	1	1	0.002	0.0013	0.0012
PHKB	phosphorylase kinase regulatory subunit beta	1	1	0.0222	0.0207	0.0049
PHKA2	Phosphorylase Kinase Regulatory Subunit Alpha 2	1	1	0.0034	0.0035	0.0019
RAP1GAP	RAP1 GTPase activating protein	1	1	0.0011	0.0027	0.0016
Total		2,313	625	2.2789	2.2624	2.1223

Supplementary File S1 *Number of connections, number of pathways and predicted SNP value for milk yield (MY), fat yield (FY), and age at first calving (AFC) explained by single nucleotide polymorphism located inside or within 2,500 bp of genes in the Thai multibreed population.*

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
PLCB1	phospholipase C beta 1	44	12	-0.2944	-0.0171	-0.0001
GNG2	G protein subunit gamma 2	38	5	-0.0437	0.0008	-0.0009
PLCB4	phosphoinositide phospholipase C	34	12	-0.1088	-0.0040	0.0024
CAMK2B	calcium/calmodulin dependent protein kinase II beta	32	5	0.0128	-0.0021	-0.0001
CAMK2D	calcium/calmodulin dependent protein kinase II delta	32	5	-0.1764	0.0042	0.0004
MAPK14	mitogen-activated protein kinase 14	29	4	0.1379	0.0040	-0.0007
GRB2	growth factor receptor bound protein 2	29	5	0.0972	0.0030	0.0000
ITGB5	integrin subunit beta 5	27	1	-0.0167	-0.0029	-0.0003
PRKCB	protein kinase C beta	25	14	0.2256	0.0051	-0.0015
FYN	FYN proto-oncogene, Src family tyrosine kinase	24	3	-0.1183	-0.0044	-0.0005
GNGT1	G protein subunit gamma transducin 1	22	5	-0.1447	-0.0039	-0.0004
ADCY8	adenylate cyclase 8	22	10	-0.4131	-0.0050	0.0001
ADCY2	adenylate cyclase 2	22	10	0.0889	-0.0008	0.0003
GNAO1	G protein subunit alpha o1	22	6	0.0117	0.0043	-0.0011
MAPK11	mitogen-activated protein kinase 11	22	4	0.0898	0.0029	0.0004
EGFR	epidermal growth factor receptor	22	8	-0.0384	-0.0041	-0.0008
ADCY5	adenylate cyclase 5	21	10	0.1311	0.0017	0.0003
ADCY7	adenylate cyclase 7	21	10	-0.2207	-0.0109	-0.0004

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
GNAQ	G protein subunit alpha q	21	10	-0.0211	-0.0060	0.0005
RAP1B	RAP1B, member of RAS oncogene family	21	5	0.1595	0.0079	-0.0005
IRS1	insulin receptor substrate 1	21	1	-0.2775	-0.0046	0.0005
PRKCA	protein kinase C alpha	20	15	-0.0481	0.0059	-0.0002
ITGA6	integrin subunit alpha 6	20	1	0.2281	0.0035	-0.0004
ITGA9	integrin subunit alpha 9	20	1	-0.0938	0.0089	-0.0013
ITGA8	integrin subunit alpha 8	20	1	-0.5823	-0.0127	0.0020
PTEN	phosphatase and tensin homolog	20	2	-0.1400	-0.0048	0.0004
AKT3	AKT serine/threonine kinase 3	20	8	-0.0024	0.0022	0.0010
ITGA2	integrin subunit alpha 2	19	1	0.0841	0.0023	0.0011
IGF1R	insulin like growth factor 1 receptor	19	3	-0.1536	-0.0035	-0.0003
RASGRF2	RAS protein-specific guanine nucleotide-releasing factor 2	18	2	-0.2245	-0.0025	0.0001
PPP2R5E	protein phosphatase 2 regulatory subunit B'epsilon	18	2	0.0000	0.0000	0.0000
PDGFRA	platelet derived growth factor receptor alpha	18	7	-0.0728	0.0026	-0.0004
PDGFRB	platelet derived growth factor receptor beta	18	7	-0.1023	-0.0048	0.0011
MAPK10	mitogen-activated protein kinase 10	18	6	-0.2962	-0.0055	0.0018
CACNG2	calcium voltage-gated channel auxiliary subunit gamma 2	18	2	0.2016	0.0034	-0.0009
SOS1	SOS Ras/Rac guanine nucleotide exchange factor 1	18	5	-0.1791	-0.0039	0.0007
PRKG2	protein kinase, cGMP-dependent, type II	17	3	-0.0887	-0.0033	0.0000
PRKG1	protein kinase, cGMP-dependent, type I	17	3	0.1390	-0.0035	0.0008
ADCY1	adenylate cyclase 1	16	10	-0.0846	-0.0026	0.0004
LPAR3	lysophosphatidic acid receptor 3	16	2	0.0617	0.0010	-0.0001
GRM1	glutamate receptor, metabotropic 1	16	4	0.1673	0.0094	-0.0006
PLCE1	phospholipase C epsilon 1	16	3	0.1183	0.0093	0.0010
INSR	insulin receptor	16	4	-0.3107	-0.0131	0.0012

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
SHC3	SHC adaptor protein 3	16	3	0.0664	-0.0008	0.0001
CACNG4	calcium voltage-gated channel auxiliary subunit gamma 4	15	2	-0.0842	-0.0021	0.0006
GSK3B	glycogen synthase kinase 3 beta	15	3	-0.3226	-0.0041	0.0003
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta	14	2	0.0603	0.0021	0.0004
CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	14	2	-0.0464	0.0024	-0.0005
FLT1	fms related tyrosine kinase 1	14	3	-0.1673	-0.0024	-0.0003
GRIA3	glutamate ionotropic receptor AMPA type subunit 3	14	3	0.2136	0.0063	-0.0012
MET	MET proto-oncogene, receptor tyrosine kinase	14	3	-0.1268	-0.0027	-0.0005
GRIA1	glutamate receptor, ionotropic, AMPA1	14	3	-0.1594	-0.0024	0.0008
TEK	TEK receptor tyrosine kinase	14	2	-0.0937	-0.0014	-0.0003
RASGRP3	RAS guanyl releasing protein 3	13	3	0.1886	0.0046	-0.0004
PLD1	phospholipase D1, phosphatidylcholine-specific	13	4	0.1959	0.0023	-0.0007
FGF19	fibroblast growth factor 19	13	3	0.1805	0.0027	-0.0004
EFNA5	ephrin A5	13	2	-0.0419	0.0000	0.0004
CACNB4	calcium voltage-gated channel auxiliary subunit beta 4	13	2	0.2408	-0.0035	0.0001
GNA12	G protein subunit alpha 12	13	4	0.2226	0.0025	0.0002
FGF2	BFGF	13	3	-0.0823	-0.0019	0.0003
TLN1	talin 1	13	2	-0.0808	-0.0029	-0.0004
GRIA2	glutamate ionotropic receptor AMPA type subunit 2	13	3	-0.0639	-0.0021	-0.0006
FLT4	fms related tyrosine kinase 4	13	3	0.0666	0.0018	-0.0007
PDE3B	phosphodiesterase 3B	12	1	-0.2859	-0.0064	0.0003
EDNRB	endothelin receptor type B	12	2	-0.0924	-0.0021	0.0008
CACNA1A	calcium voltage-gated channel subunit alpha1 A	12	5	-0.7185	-0.0176	0.0015

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
GNA13	G protein subunit alpha 13	12	3	0.1230	0.0040	-0.0004
GRIA4	glutamate ionotropic receptor AMPA type subunit 4	12	3	0.1124	-0.0015	-0.0010
ITGB2	integrin subunit beta 2	12	1	-0.1126	-0.0033	0.0005
ANGPT1	angiopoietin 1	12	2	0.0392	0.0000	0.0006
PDE3A	phosphodiesterase 3A	11	1	-0.1269	-0.0038	0.0008
CACNA2D4	calcium voltage-gated channel auxiliary subunit alpha2delta 4	11	2	0.0682	0.0031	0.0003
CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3	11	2	-0.0887	-0.0096	-0.0015
FN1	fibronectin 1	11	1	0.0863	0.0048	-0.0003
BCL2	BCL2, apoptosis regulator	11	2	0.0541	-0.0008	0.0003
GRIN2B	glutamate ionotropic receptor NMDA type subunit 2B	11	5	0.1044	-0.0006	0.0002
GRIN1	glutamate ionotropic receptor NMDA type subunit 1	11	5	0.0835	0.0033	-0.0006
LRP6	LDL receptor related protein 6	11	1	-0.0717	-0.0014	-0.0004
CACNG5	calcium voltage-gated channel auxiliary subunit gamma 5	10	2	0.0748	0.0047	0.0003
FGF12	fibroblast growth factor 12	10	3	-0.1499	-0.0133	0.0010
PDGFD	platelet derived growth factor D	10	5	-0.2855	-0.0100	-0.0001
PDGFC	platelet derived growth factor C	10	5	-0.3096	-0.0043	0.0003
CASP3	caspase 3, apoptosis-related cysteine peptidase	10	1	-0.0839	-0.0029	0.0003
RAPGEF4	Rap guanine nucleotide exchange factor 4	10	2	-0.1286	0.0001	-0.0007
FLNB	filamin B	10	2	-0.2384	-0.0063	-0.0001
LRP5	LDL receptor related protein 5	10	1	-0.0695	0.0016	0.0003
FIGF	c-fos induced growth factor	10	3	-0.1949	-0.0059	0.0005
WNT3A	Wnt family member 3A	10	1	0.1754	0.0025	-0.0004

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
GAB1	GRB2 associated binding protein 1	10	2	-0.1477	-0.0071	0.0003
TACR1	tachykinin receptor 1	9	1	-0.2235	-0.0053	-0.0001
TACR3	tachykinin receptor 3	9	1	0.0760	0.0056	-0.0008
NTSR1	neurotensin receptor 1	9	1	-0.0747	-0.0026	-0.0004
NSF	N-ethylmaleimide sensitive factor, vesicle fusing ATPase	9	1	-0.0277	-0.0005	0.0005
PDE1A	phosphodiesterase 1A, calmodulin-dependent	9	1	0.2022	0.0020	0.0003
PDE1C	phosphodiesterase 1C	9	1	0.2922	0.0061	-0.0007
PDE1B	cam-PDE 1B	9	1	-0.1092	-0.0037	0.0005
CHRM3	cholinergic receptor muscarinic 3	9	2	-0.3344	-0.0051	0.0008
WNT7A	Wnt family member 7A	9	1	0.0411	0.0018	0.0004
FZD7	frizzled class receptor 7	9	1	-0.1394	-0.0049	-0.0004
TLN2	talin 2	9	2	-0.2003	-0.0057	-0.0005
GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A	9	6	-0.0682	-0.0011	0.0000
VAV3	vav guanine nucleotide exchange factor 3	9	1	-0.1188	-0.0008	0.0001
VAV2	vav guanine nucleotide exchange factor 2	9	1	-0.1439	-0.0036	-0.0009
PPP3CA	protein phosphatase 3 catalytic subunit alpha	9	7	-0.3663	-0.0125	0.0011
CAMK4	calcium/calmodulin dependent protein kinase IV	8	2	0.0132	0.0028	-0.0006
SCTR	secretin receptor	8	1	0.0417	0.0044	0.0000
GUCY1B3	guanylate cyclase 1 soluble subunit beta	8	4	-0.2392	-0.0053	-0.0003
GUCY1A2	guanylate cyclase 1 soluble subunit alpha 2	8	4	0.3172	0.0096	-0.0011
GRM7	glutamate metabotropic receptor 7	8	2	-0.1710	-0.0019	-0.0012
GRM3	glutamate metabotropic receptor 3	8	2	-0.0206	-0.0048	-0.0007
HTR7	5-hydroxytryptamine receptor 7	8	2	-0.2181	0.0021	-0.0003
CACNA1B	calcium voltage-gated channel subunit alpha1 B	8	4	-0.0744	0.0040	-0.0005
MAP3K5	mitogen-activated protein kinase kinase kinase 5	8	2	0.1774	0.0117	-0.0011

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
PPAP2B	phosphatidic acid phosphatase type 2B	8	1	-0.0689	-0.0029	0.0003
CREBBP	CREB binding protein	8	1	-0.0574	-0.0029	0.0002
BTRC	beta-transducin repeat containing E3 ubiquitin protein ligase	8	1	0.0313	0.0008	-0.0005
ITGAL	integrin subunit alpha L	8	1	-0.1526	-0.0051	0.0003
LCP2	lymphocyte cytosolic protein 2 tyrosine phosphoprotein slp-76	8	1	0.1013	-0.0010	0.0007
CACNA2D1	calcium voltage-gated channel auxiliary subunit alpha2delta 1	7	2	0.1799	0.0065	0.0004
LAMA5	laminin subunit alpha 5	7	1	-0.1147	-0.0035	0.0005
CACNA1E	calcium voltage-gated channel subunit alpha1 E	7	2	0.0402	-0.0007	-0.0001
COL9A3	collagen type IX alpha 3 chain	7	1	0.1454	0.0040	-0.0008
COL2A1	collagen type II alpha 1 chain	7	1	-0.1334	-0.0028	-0.0003
GABBR2	gamma-aminobutyric acid type B receptor subunit 2	7	1	-0.5772	-0.0079	0.0001
ITPR2	inositol 1,4,5-triphosphate receptor, type 2	7	7	-0.1070	-0.0069	-0.0004
HTR4	5-hydroxytryptamine receptor 4	7	1	0.2680	0.0092	-0.0008
COL4A5	collagen type IV alpha 5 chain	7	1	0.2224	0.0044	0.0002
ITPR1	IP3 receptor	7	8	0.0568	-0.0005	-0.0001
PTK2B	protein tyrosine kinase 2 beta	7	2	-0.0314	0.0020	-0.0004
LAMC2	laminin subunit gamma 2	7	1	-0.1495	-0.0040	-0.0004
AGPAT4	lysophosphatidic acid acyltransferase delta	7	1	0.1965	0.0089	0.0004
LAMA3	laminin subunit alpha 3	7	1	-0.1197	-0.0020	-0.0005
MAP2K6	mitogen-activated protein kinase kinase 6	7	2	-0.0432	-0.0053	0.0008
WNT11	Wnt family member 11	7	1	-0.0676	-0.0029	0.0004
CHUK	conserved helix-loop-helix ubiquitous kinase	7	2	-0.0794	-0.0052	0.0007
ERBB4	erb-b2 receptor tyrosine kinase 4	7	1	-0.4089	-0.0075	0.0008
PPP3CC	protein phosphatase 3 catalytic subunit gamma	7	7	0.2263	0.0028	-0.0005

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
PLCL1	phospholipase C like 1	6	1	-0.1320	-0.0029	-0.0004
RYR2	ryanodine receptor 2	6	4	-0.5329	-0.0123	0.0009
GABRB1	gamma-aminobutyric acid type A receptor beta1 subunit	6	1	-0.1689	-0.0016	-0.0001
PTGER3	prostaglandin E receptor 3	6	1	0.0961	0.0031	-0.0004
TIAM1	T-cell lymphoma invasion and metastasis 1	6	2	0.0936	0.0018	-0.0009
COL4A2	collagen type IV alpha 2 chain	6	1	-0.0612	-0.0014	0.0009
COL4A1	collagen type IV alpha 1 chain	6	1	-0.3017	-0.0021	-0.0005
WNT10B	Wnt family member 10B	6	1	-0.1215	-0.0028	0.0004
ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	6	1	0.0337	0.0005	-0.0005
WIF1	WNT inhibitory factor 1	6	1	0.0732	0.0030	-0.0007
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase type 1 beta	6	1	-0.2155	-0.0055	0.0012
WNT9B	Wnt family member 9B	6	1	0.1068	0.0018	-0.0005
LEF1	lymphoid enhancer binding factor 1	6	1	0.2246	0.0030	0.0004
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	6	1	-0.2206	-0.0054	0.0009
MAP2K4	mitogen-activated protein kinase kinase 4	6	1	0.0579	0.0063	-0.0004
APC	APC, WNT signaling pathway regulator	6	1	-0.1126	-0.0056	0.0002
TSC2	tuberous sclerosis 2	6	1	-0.1447	-0.0031	0.0004
CHAD	chondroadherin	5	1	-0.0792	-0.0021	0.0003
CD38	CD38 molecule	5	3	0.0133	0.0002	-0.0002
DGKH	diacylglycerol kinase eta	5	1	-0.3457	-0.0089	0.0005
LAMA4	laminin subunit alpha 4	5	1	0.0531	0.0022	0.0000
TNR	tenascin R	5	1	-0.2861	-0.0101	0.0008
GABRA5	gamma-aminobutyric acid type A receptor alpha5 subunit	5	1	0.3057	0.0073	0.0008

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
GABRB2	gamma-aminobutyric acid type A receptor beta2 subunit	5	1	-0.0758	-0.0055	0.0007
DGKE	diacylglycerol kinase epsilon	5	1	0.1128	0.0027	-0.0004
THBS2	thrombospondin 2	5	1	0.1985	0.0036	-0.0003
PARVA	parvin alpha	5	1	0.0972	0.0020	-0.0012
DGKG	diacylglycerol kinase gamma	5	1	0.1202	0.0024	-0.0004
DGKB	diacylglycerol kinase beta	5	1	0.1431	0.0091	-0.0003
DGKI	diacylglycerol kinase iota	5	1	-0.3973	-0.0149	0.0015
SGMS2	sphingomyelin synthase 2	5	1	-0.0663	-0.0022	0.0005
GPHN	gephyrin	5	1	-0.2153	-0.0089	0.0005
SGMS1	sphingomyelin synthase 1	5	1	-0.1802	0.0002	0.0001
CERS6	ceramide synthase 6	5	1	0.1091	0.0027	0.0007
DEGS1	delta 4-desaturase, sphingolipid 1	5	1	-0.0989	-0.0035	0.0008
CERS3	ceramide synthase 3	5	1	0.0488	0.0055	0.0004
TNC	tenascin C	5	1	-0.1908	-0.0050	0.0009
ARRB1	arrestin beta 1	5	1	-0.2640	-0.0096	0.0010
TCF7L2	transcription factor 7 like 2	5	1	0.3306	0.0073	-0.0007
PPP3R1	protein phosphatase 3 regulatory subunit B, alpha	5	6	0.1239	0.0036	-0.0003
KIF5A	kinesin family member 5A	4	1	0.1263	0.0062	-0.0014
KIF5C	kinesin family member 5C	4	1	0.1169	0.0026	0.0003
MAP2K5	mitogen-activated protein kinase kinase 5	4	3	0.0041	0.0036	0.0008
MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	4	1	0.1537	0.0036	-0.0003
RAPGEF6	Rap guanine nucleotide exchange factor 6	4	1	0.1269	0.0062	0.0001
RAPGEF2	Rap guanine nucleotide exchange factor 2	4	2	-0.1135	-0.0018	-0.0003
GRIK3	Glutamate Ionotropic Receptor Kainate Type Subunit 3	4	1	-0.1952	-0.0061	0.0007

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
LPAR1	lysophosphatidic acid receptor 1	4	3	0.3706	0.0044	0.0000
NTRK2	neurotrophic receptor tyrosine kinase 2	4	1	-0.0573	-0.0025	-0.0003
FBXW11	F-box and WD repeat domain containing 11	4	1	-0.1434	-0.0017	0.0012
PLA2G16	phospholipase A2, group XVI	4	1	-0.0862	-0.0029	0.0003
GABRG2	Gamma-Aminobutyric Acid Type A Receptor Gamma2 Subunit	4	1	-0.0310	0.0022	0.0005
NFATC2	nuclear factor of activated T-cells 2	4	3	0.2549	0.0052	-0.0002
RPS6KA2	ribosomal protein S6 kinase A2	4	1	-0.1595	-0.0050	0.0009
RPS6KA3	ribosomal protein S6 kinase A3	4	1	0.1632	0.0025	-0.0005
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	4	1	0.1493	-0.0005	-0.0008
MRVI1	murine retrovirus integration site 1 homolog	4	1	0.1175	0.0071	-0.0017
SLC8A3	solute carrier family 8 member A3	3	2	0.1401	-0.0004	0.0000
SLC8A1	solute carrier family 8 member A1	3	2	0.1290	-0.0007	0.0011
PRKD1	protein kinase D1	3	1	0.0053	0.0001	0.0005
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	3	1	-0.1226	-0.0041	0.0007
STK3	serine/threonine kinase 3	3	1	0.0143	-0.0045	0.0000
DKK4	dickkopf WNT signaling pathway inhibitor 4	3	1	0.1295	0.0028	-0.0006
BID	BH3 Interacting Domain Death Agonist	3	1	0.0682	0.0031	-0.0004
CAV2	caveolin 2	3	1	0.1084	0.0025	-0.0003
ADRA1A	adrenoceptor alpha 1A	3	2	0.1735	0.0031	-0.0008
SGPP1	sphingosine-1-phosphate phosphatase 1	3	1	-0.0695	-0.0038	0.0004
ITPKB	inositol-trisphosphate 3-kinase B	3	1	0.0341	0.0009	-0.0002
PLA2G2F	phospholipase A2 group IIF	3	2	-0.1150	-0.0027	0.0005
GABRA3	gamma-aminobutyric acid type A receptor alpha3 subunit	3	1	-0.0760	-0.0027	0.0004
FRAT2	FRAT2, WNT signaling pathway regulator	3	1	-0.0787	-0.0023	0.0003

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
SKAP1	src kinase associated phosphoprotein 1	3	1	0.1007	0.0047	0.0007
DKK2	dickkopf WNT signaling pathway inhibitor 2	3	1	0.2370	0.0062	-0.0005
KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2	3	1	-0.0245	-0.0024	0.0006
KCNMA1	potassium calcium-activated channel subfamily M alpha 1	3	2	-0.1482	-0.0047	0.0004
PRKCE	protein kinase C epsilon	3	2	0.6961	0.0250	0.0001
PLA2G12B	phospholipase A2 group XIIB	3	2	0.0602	0.0020	-0.0008
PTPRR	protein tyrosine phosphatase, receptor type R	3	1	0.0227	0.0035	0.0006
RPS6KA5	ribosomal protein S6 kinase A5	3	2	-0.0029	-0.0017	-0.0002
DUSP10	dual specificity phosphatase 10	3	1	0.0818	0.0023	-0.0004
NLK	nemo like kinase	3	2	0.0044	0.0010	0.0000
FYB	FYN binding protein	3	1	0.1952	0.0020	-0.0011
MKNK1	MAP Kinase Interacting Serine/Threonine Kinase 1	2	1	-0.1395	-0.0081	0.0006
ETS1	ETS proto-oncogene 1, transcription factor	2	1	-0.1685	-0.0060	0.0004
ATP2B2	ATPase plasma membrane Ca ²⁺ transporting 2	2	3	-0.0144	0.0010	-0.0007
ATP2B4	ATPase plasma membrane Ca ²⁺ transporting 4	2	3	0.0709	0.0043	-0.0010
DNM2	dynamamin 2	2	1	-0.1009	-0.0027	0.0005
STK4	serine/threonine kinase 4	2	2	0.2030	0.0048	0.0006
RBX1	Ring-Box 1	2	1	-0.1248	-0.0023	-0.0003
PPP1R12A	protein phosphatase 1 regulatory subunit 12A	2	3	-0.1472	-0.0028	-0.0003
PIK3R6	phosphoinositide-3-kinase regulatory subunit 6	2	3	-0.0859	-0.0026	-0.0003
CTSD	cathepsin D	2	1	-0.0841	-0.0019	0.0003
TRPC6	transient receptor potential cation channel subfamily C member 6	2	1	0.1704	0.0066	-0.0007
LOC529488	glutamate decarboxylase 1	2	1	-0.0682	-0.0010	0.0002
GLS	glutaminase	2	2	0.1185	0.0035	0.0003

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
GAD2	glutamate decarboxylase 2	2	1	0.0231	0.0002	0.0003
FCER1A	Fc fragment of IgE receptor 1a	2	2	-0.1174	-0.0050	0.0005
MS4A2	Membrane Spanning 4-Domains A2	2	2	-0.1083	-0.0027	0.0004
ARF1	ADP ribosylation factor 1	2	1	0.1142	0.0021	0.0004
SHANK2	SH3 and multiple ankyrin repeat domains 2	2	1	0.2879	0.0045	-0.0019
DLGAP1	DLG associated protein 1	2	1	-0.1384	-0.0029	0.0008
SHANK1	SH3 and multiple ankyrin repeat domains 1	2	1	0.1503	0.0044	-0.0003
TCF7L1	transcription factor 7 like 1	2	1	0.2505	0.0056	-0.0003
ADRBK2	G Protein-Coupled Receptor Kinase 2	2	1	-0.0983	-0.0019	-0.0011
PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1B	1	1	0.0792	0.0019	-0.0004
CFTR	ATP-binding cassette sub-family C member 7	1	1	0.2142	0.0067	-0.0008
DNM3	dynamamin 3	1	1	0.2789	0.0047	0.0006
ARHGAP35	Rho GTPase activating protein 35	1	1	0.0212	0.0008	0.0000
IL1R1	interleukin 1 receptor type 1	1	1	0.4206	0.0096	0.0003
SLC17A8	solute carrier family 17 member 8	1	1	-0.0982	-0.0034	0.0006
SLC18A2	solute carrier family 18 member A2	1	1	-0.0805	-0.0023	-0.0006
MECOM	MDS1 and EVI1 complex locus	1	1	-0.4502	-0.0107	-0.0001
KSR2	kinase suppressor of ras 2	1	1	-0.1042	-0.0044	-0.0001
MYLK3	myosin light chain kinase 3	1	4	-0.0749	-0.0022	0.0003
PAK7	P21 (RAC1) Activated Kinase 5	1	2	0.2659	0.0046	0.0002
PARD3	par-3 family cell polarity regulator	1	1	0.1968	0.0051	-0.0002
DOCK4	dedicator of cytokinesis 4	1	1	0.1897	0.0068	0.0007
DOCK1	dedicator of cytokinesis 1	1	1	-0.3004	-0.0127	-0.0011
TGFB2	transforming growth factor beta 2	1	1	0.1360	0.0038	-0.0011
MYL12B	myosin, light chain 12B, regulatory	1	1	-0.1608	-0.0021	0.0010
P2RX1	purinergic receptor P2X 1	1	1	-0.0748	-0.0020	0.0005

Gene name	Gene description	Number of Connections (n)	Number of pathways (n)	Predicted SNP value		
				MY	FY	AFC
P2RX3	purinergic receptor P2X 3	1	1	-0.0956	0.0019	0.0003
SIPA1L1	signal induced proliferation associated 1 like 1	1	1	0.0693	0.0043	0.0005
GRIK4	glutamate ionotropic receptor kainate type subunit 4	1	1	-0.3617	-0.0093	0.0008
MAPT	PHF-tau microtubule associated protein tau neurofibrillary tangle protein paired helical filament-tau	1	1	0.0848	0.0019	-0.0003
PHKB	phosphorylase kinase regulatory subunit beta	1	1	-0.1028	-0.0029	0.0002
PHKA2	Phosphorylase Kinase Regulatory Subunit Alpha 2	1	1	0.1117	0.0032	-0.0003
RAP1GAP	RAP1 GTPase activating protein	1	1	0.0637	0.0002	0.0003
Total		2,313	625	-5.6150	-0.1404	0.0067