Supplementary Table S1. Animal information

Eartag_Number	Parity	Lactation_period	Milk_yield(breeding value)	Milk_fat(breeding value)	Milk_protein(breeding value)	Milk_solid(breeding value)	305Milk_yield	305Milk_fat	305Milk_protein	305Milk_solid	Milk_yielding_group	Milk_fat_group	Milk_protein_group	Milk_solid_group	RNA-seq	qRT-PCR
2814	3	41	227.5208421	2.782903535	1.541812942	-16.3	7982	331	251	757	HY	HF	HP	LS	O	O
2864	4	270	-181.6561079	-9.927996465	-6.218437058	-16	7116	239	222	631	LY	LF	LP	LS	O	O
2893	4	59	-368.8672079	-4.773246465	-7.871687058	-29.5	7466	313	259	675	LY	LF	LP	LS	O	O
2920	4	168	321.1519921	10.92840353	6.302362942	23.9	10490	374	320	914	HY	HF	HP	HS	O	O
3014	3	268	269.0759421	-10.10944647	6.839412942	20.9	8341	245	276	751	HY	LF	HP	HS	O	O
3057	2	265	459.0590421	-1.839946465	11.13656294	38.2	11547	341	345	1012	HY	LF	HP	HS	O	O
3064	2	220	468.0531921	0.605553535	14.58901294	41.4	11353	338	367	996	HY	HF	HP	HS	O	O
3075	2	101	211.4631921	3.689903535	3.937662942	18	9234	364	284	830	HY	HF	HP	HS	O	O
3135	2	200	-211.1092579	-13.15309647	-7.584487058	7.4	8569	229	257	675	LY	LF	LP	HS	O	O
3161	2	167	-85.19085794	-8.711046465	-3.947237058	-5.7	9051	314	272	776	LY	LF	LP	LS	O	O
3198	2	102	-123.0350079	-9.007296465	-2.572587058	-6.8	7843	305	260	704	LY	LF	LP	LS	O	O
3235	2	176	212.3058421	5.785603535	8.392462942	18.9	9790	400	316	846	HY	HF	HP	HS	O	O
3262	2	65	181.1182421	1.174853535	4.546862942	15.3	10621	382	327	906	HY	HF	HP	HS	O	O
3264	2	223	-70.24255794	-4.109946465	-1.497987058	-3.5	7919	322	252	693	LY	LF	LP	LS	O	O
3272	2	262	-47.84085794	-7.688746465	-0.930837058	-0.8	7319	304	248	659	LY	LF	LP	LS	O	O
3280	2	108	303.7170421	1.678803535	7.984662942	24.4	9857	364	320	853	HY	HF	HP	HS	O	O
3369	2	79	-404.2696079	-12.21764647	-9.370337058	-27.2	8339	322	271	751	LY	LF	LP	LS	O	O
3407	2	52	-364.0948079	-14.37744647	-13.24018706	-29.9	6362	283	204	564	LY	LF	LP	LS	O	O
7598	3	243	-27.52599206	-7.630746465	-0.095987058	-0.7	9552	293	293	824	LY	LF	LP	LS	O	O
7628	3	239	-86.91994206	-2.782246465	1.267662942	8.3	9944	325	302	883	LY	LF	HP	HS	O	O
7643	2	224	-70.47735794	-3.486696465	-0.887587058	-3.9	8115	326	268	719	LY	LF	LP	LS	O	O
3047	2	29	236.3456921	5.6	6.6	21	na	na	na	na	HY	HF	HP	HS	X	O
3059	3	164	260.4742421	8.1	6.2	20.3	na	na	na	na	HY	HF	HP	HS	X	O
3100	2	203	195.3485921	-6.6	-2.6	8	na	na	na	na	HY	LF	LP	HS	X	O
3190	2	na	177.3057421	1.39	4.08	15.2	na	na	na	na	HY	HF	HP	HS	X	O
3328	2	127	-159.0945579	-11.1	-6.8	-10.8	na	na	na	na	LY	LF	LP	LS	X	O

Supplementary Table S2. Significant GO-terms from the DAVID analysis

Category	Term	Count	%	Genes	List Total	Pop Hits	Pop Total	ld Enrichme	PValue
GOTERM_	GO:0006690~icosanoid metabolic process	3	0.131234	ALOX15B, EDN2, LOC782922	132	32	8785	6.239347	0.081895
GOTERM_	GO:0033559~unsaturated fatty acid metabolic process	3	0.131234	ALOX15B, EDN2, LOC782922	132	32	8785	6.239347	0.081895
GOTERM_	GO:0031640~killing of cells of another organism	4	0.174978	CATHL4, LAP, ALB, CATHL6	132	6	8785	44.36869	6.27E-05
GOTERM_	GO:0001906~cell killing	4	0.174978	CATHL4, LAP, ALB, CATHL6	132	12	8785	22.18434	6.46E-04
GOTERM_	GO:0050832~defense response to fungus	3	0.131234	CATHL4, LAP, CATHL6	132	8	8785	24.95739	0.005826
GOTERM_	GO:0009620~response to fungus	3	0.131234	CATHL4, LAP, CATHL6	132	15	8785	13.31061	0.020408
GOTERM_	GO:0006952~defense response	8	0.349956	CATHL4, LAT, TNF, LAP, LOC781146, CAMP, CATHL6, C4BPA	132	223	8785	2.387553	0.049012
GOTERM_	GO:0009617~response to bacterium	7	0.306212	CATHL4, STAT4, TNF, LAP, LOC781146, CAMP, CATHL6	132	88	8785	5.293991	0.001956
GOTERM_	GO:0042742~defense response to bacterium	6	0.262467	CATHL4, TNF, LAP, LOC781146, CAMP, CATHL6	132	55	8785	7.260331	0.001308
GOTERM_	GO:0055080~cation homeostasis	5	0.218723	CAV1, EDN2, LOC525947, ATP6V1B1, CSRP3	132	115	8785	2.89361	0.092664
GOTERM_	GO:0050880~regulation of blood vessel size	3	0.131234	CAV1, EDN2, NOS3	132	31	8785	6.440616	0.07751
GOTERM_	GO:0035150~regulation of tube size	3	0.131234	CAV1, EDN2, NOS3	132	31	8785	6.440616	0.07751
GOTERM_	GO:0003018~vascular process in circulatory system	3	0.131234	CAV1, EDN2, NOS3	132	31	8785	6.440616	0.07751
GOTERM_	GO:0009725~response to hormone stimulus	4	0.174978	CAV1, EIF4EBP1, TNF, FHL2	132	53	8785	5.02287	0.044233
GOTERM_	GO:0009719~response to endogenous stimulus	4	0.174978	CAV1, EIF4EBP1, TNF, FHL2	132	62	8785	4.293744	0.06493
GOTERM_	GO:0031327~negative regulation of cellular biosynthetic process	7	0.306212	CAV1, EIF4EBP1, TNF, FOXA1, HR, LMCD1, CBY1	132	189	8785	2.464927	0.06318
GOTERM_	GO:0009890~negative regulation of biosynthetic process	7	0.306212	CAV1, EIF4EBP1, TNF, FOXA1, HR, LMCD1, CBY1	132	195	8785	2.389083	0.071203
GOTERM_	GO:0060056~mammary gland involution	2	0.087489	CAV1, ELF3	132	2	8785	66.55303	0.029603
GOTERM_	GO:0060443~mammary gland morphogenesis	2	0.087489	CAV1, ELF3	132	2	8785	66.55303	0.029603
GOTERM_	GO:0030879~mammary gland development	3	0.131234	CAV1, ELF3, HOXA9	132	21	8785	9.507576	0.038518
GOTERM_	GO:0048514~blood vessel morphogenesis	6	0.262467	CAV1, HOXA3, CTGF, NOS3, CDH2, CXCL12	132	99	8785	4.033517	0.016008
GOTERM_	GO:0001568~blood vessel development	6	0.262467	CAV1, HOXA3, CTGF, NOS3, CDH2, CXCL12	132	118	8785	3.384052	0.031383
GOTERM_	GO:0001944~vasculature development	6	0.262467	CAV1, HOXA3, CTGF, NOS3, CDH2, CXCL12	132	121	8785	3.30015	0.034437
GOTERM_	GO:0048732~gland development	5	0.218723	CAV1, HOXA3, ELF3, FOXA1, HOXA9	132	56	8785	5.942235	0.009536
GOTERM_	GO:0048771~tissue remodeling	4	0.174978	CAV1, HOXA3, ELF3, NOS3	132	27	8785	9.859708	0.007297
GOTERM_	GO:0015674~di-, tri-valent inorganic cation transport	5	0.218723	CAV1, LOC525947, CACNB3, CACNG2, CACNG1	132	104	8785	3.199665	0.069603
GOTERM_	GO:0006937~regulation of muscle contraction	3	0.131234	CAV1, MYL3, EDN2	132	25	8785	7.986364	0.052952
GOTERM_	GO:0003013~circulatory system process	4	0.174978	CAV1, MYL3, EDN2, NOS3	132	71	8785	3.749466	0.08928
GOTERM_	GO:0008015~blood circulation	4	0.174978	CAV1, MYL3, EDN2, NOS3	132	71	8785	3.749466	0.08928
GOTERM_	GO:0044057~regulation of system process	5	0.218723	CAV1, MYL3, EDN2, NOS3, CSRP3	132	89	8785	3.738934	0.043681
GOTERM_	GO:0043085~positive regulation of catalytic activity	6	0.262467	CAV1, TNF, EDN2, NOS3, KIT, CISH	132	149	8785	2.679988	0.071732
GOTERM_	GO:0019915~lipid storage	3	0.131234	CAV1, TNF, PLIN2	132	13	8785	15.35839	0.015458
GOTERM_	GO:0042522~regulation of tyrosine phosphorylation of Stat5 protein	2	0.087489	CSF2, CAV1	132	7	8785	19.01515	0.09986
GOTERM_	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	3	0.131234	CSF2, CAV1, FGFR3	132	31	8785	6.440616	0.07751
GOTERM_	GO:0042127~regulation of cell proliferation	10	0.437445	CSF2, CAV1, HOXA3, TNF, FGFR3, ALOX15B, EDN2, MMP7, KIT, CXADR	132	275	8785	2.42011	0.021608
GOTERM_	GO:0001932~regulation of protein amino acid phosphorylation	4	0.174978	CSF2, CAV1, TNF, FGFR3	132	74	8785	3.597461	0.098136
GOTERM_	GO:0008284~positive regulation of cell proliferation	6	0.262467	CSF2, HOXA3, TNF, FGFR3, EDN2, KIT	132	153	8785	2.609923	0.078365
GOTERM_	GO:0006916~anti-apoptosis	4	0.174978	CSF2, TNF, EEF1A2, NOS3	132	63	8785	4.225589	0.067462
GOTERM_	GO:0032270~positive regulation of cellular protein metabolic process	4	0.174978	CSF2, TNF, FGFR3, KRT17	132	73	8785	3.646741	0.095145
GOTERM_	GO:0051094~positive regulation of developmental process	6	0.262467	CSF2, TNF, FGFR3, KRT17, FOXA1, NOS3	132	113	8785	3.533789	0.026683
GOTERM_	GO:0043067~regulation of programmed cell death	9	0.393701	CSF2, TNF, FGFR3, SNCB, ALB, EEF1A2, NOS3, KIT, TRAF4	132	298	8785	2.009991	0.076977
GOTERM_	GO:0010941~regulation of cell death	9	0.393701	CSF2, TNF, FGFR3, SNCB, ALB, EEF1A2, NOS3, KIT, TRAF4	132	299	8785	2.003268	0.078145
GOTERM_	GO:0002573~myeloid leukocyte differentiation	3	0.131234	CSF2, TNF, KIT	132	14	8785	14.26136	0.01786
GOTERM_	GO:0043066~negative regulation of apoptosis	6	0.262467	CSF2, TNF, SNCB, ALB, EEF1A2, NOS3	132	146	8785	2.735056	0.06697
GOTERM_	GO:0060548~negative regulation of cell death	7	0.306212	CSF2, TNF, SNCB, ALB, EEF1A2, NOS3, KIT	132	148	8785	3.147778	0.023136
GOTERM_	GO:0043069~negative regulation of programmed cell death	7	0.306212	CSF2, TNF, SNCB, ALB, EEF1A2, NOS3, KIT	132	148	8785	3.147778	0.023136
GOTERM_	GO:0001503~ossification	4	0.174978	CTGF, FHL2, IGF2, ATP6V1B1	132	54	8785	4.929854	0.046341
GOTERM_	GO:0060348~bone development	4	0.174978	CTGF, FHL2, IGF2, ATP6V1B1	132	54	8785	4.929854	0.046341
GOTERM_	GO:0003100~regulation of systemic arterial blood pressure by endothelin	2	0.087489	EDN2, NOS3	132	3	8785	44.36869	0.044077
GOTERM_	GO:0008543~fibroblast growth factor receptor signaling pathway	2	0.087489	FGFR3, CTGF	132	6	8785	22.18434	0.086224
GOTERM_	GO:0003006~reproductive developmental process	5	0.218723	FOXA1, DMRT1, NOS3, KIT, CXCL12	132	96	8785	3.466304	0.054963
GOTERM_	GO:0001501~skeletal system development	6	0.262467	HOXA3, CTGF, HOXA9, FHL2, IGF2, ATP6V1B1	132	120	8785	3.327652	0.033399
GOTERM_	GO:0008354~germ cell migration	2	0.087489	KIT, CXCL12	132	7	8785	19.01515	0.09986
GOTERM_	GO:0045109~intermediate filament organization	2	0.087489	KRT17, KRT14	132	6	8785	22.18434	0.086224

GOTERM_	GO:0006108~malate metabolic process	2	0.087489	ME1, ME3	132	6	8785	22.18434	0.086224
GOTERM_	GO:0043648~dicarboxylic acid metabolic process	3	0.131234	ME1, ME3, QPRT	132	14	8785	14.26136	0.01786
GOTERM_	GO:0007155~cell adhesion	9	0.393701	MIA, TNF, PKP1, CTGF, PECAM1, FBLIM1, BCAM, CDH2, CXADR	132	306	8785	1.957442	0.086616
GOTERM_	GO:0022610~biological adhesion	9	0.393701	MIA, TNF, PKP1, CTGF, PECAM1, FBLIM1, BCAM, CDH2, CXADR	132	306	8785	1.957442	0.086616
GOTERM_	GO:0048738~cardiac muscle tissue development	4	0.174978	MYL3, CBY1, CXADR, CSRP3	132	29	8785	9.179728	0.008921
GOTERM_	GO:0008016~regulation of heart contraction	3	0.131234	MYL3, EDN2, CSRP3	132	29	8785	6.884796	0.068976
GOTERM_	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	7	0.306212	PLAT, EPHA4, EIF4EBP1, FGFR3, CTGF, KIT, EPHA1	132	92	8785	5.063818	0.002452
GOTERM_	GO:0007167~enzyme linked receptor protein signaling pathway	7	0.306212	PLAT, EPHA4, EIF4EBP1, FGFR3, CTGF, KIT, EPHA1	132	138	8785	3.375878	0.017002
GOTERM_	GO:0006928~cell motion	10	0.437445	PLAT, EPHA4, TNF, CTGF, EDN2, TEKT2, NOS3, CDH2, KIT, CXCL12	132	148	8785	4.496826	3.54E-04
GOTERM_	GO:0016477~cell migration	8	0.349956	PLAT, TNF, CTGF, EDN2, NOS3, CDH2, KIT, CXCL12	132	114	8785	4.670388	0.001531
GOTERM_	GO:0051674~localization of cell	9	0.393701	PLAT, TNF, CTGF, EDN2, TEKT2, NOS3, CDH2, KIT, CXCL12	132	124	8785	4.830462	5.10E-04
GOTERM_	GO:0048870~cell motility	9	0.393701	PLAT, TNF, CTGF, EDN2, TEKT2, NOS3, CDH2, KIT, CXCL12	132	124	8785	4.830462	5.10E-04
GOTERM_	GO:0007242~intracellular signaling cascade	14	0.612423	RHOJ, CAV1, TNF, FGFR3, EDN2, PECAM1, RAB34, CHN1, RTKN, RHOD, KIT, NEURL2, ASB15, CISH	132	498	8785	1.870969	0.034331
GOTERM_	GO:0008360~regulation of cell shape	3	0.131234	RHOJ, FBLIM1, PALMD	132	24	8785	8.319129	0.049185
GOTERM_	GO:0007266~Rho protein signal transduction	3	0.131234	RHOJ, PECAM1, RTKN	132	14	8785	14.26136	0.01786
GOTERM_	GO:0007265~Ras protein signal transduction	3	0.131234	RHOJ, PECAM1, RTKN	132	27	8785	7.394781	0.06078
GOTERM_	GO:0030036~actin cytoskeleton organization	5	0.218723	RHOJ, PFN2, CNN1, DBN1, EHD2	132	84	8785	3.96149	0.036508
GOTERM_	GO:0030029~actin filament-based process	5	0.218723	RHOJ, PFN2, CNN1, DBN1, EHD2	132	86	8785	3.869362	0.039289
GOTERM_	GO:0007010~cytoskeleton organization	8	0.349956	RHOJ, PFN2, KRT17, KRT14, TEKT2, CNN1, DBN1, EHD2	132	167	8785	3.188169	0.012325
GOTERM_	GO:0014706~striated muscle tissue development	7	0.306212	SRPK3, CAV1, MYL3, CACNG2, CBY1, CXADR, CSRP3	132	65	8785	7.167249	3.94E-04
GOTERM_	GO:0060537~muscle tissue development	7	0.306212	SRPK3, CAV1, MYL3, CACNG2, CBY1, CXADR, CSRP3	132	68	8785	6.851047	5.03E-04
GOTERM_	GO:0007517~muscle organ development	7	0.306212	SRPK3, CAV1, MYL3, CACNG2, CBY1, CXADR, CSRP3	132	86	8785	5.417107	0.001738
GOTERM_	GO:0019221~cytokine-mediated signaling pathway	5	0.218723	STAT4, TNF, EDN2, KRT8, KIT	132	25	8785	13.31061	4.69E-04
GOTERM_	GO:0048584~positive regulation of response to stimulus	7	0.306212	TNF, EDN2, CACNB3, IGF2, C4BPA, CXCL12, NCR3	132	114	8785	4.08659	0.007035
GOTERM_	GO:0051798~positive regulation of hair follicle development	2	0.087489	TNF, KRT17	132	4	8785	33.27652	0.058336
GOTERM_	GO:0042634~regulation of hair cycle	2	0.087489	TNF, KRT17	132	5	8785	26.62121	0.072384
GOTERM_	GO:0045684~positive regulation of epidermis development	2	0.087489	TNF, KRT17	132	5	8785	26.62121	0.072384
GOTERM_	GO:0051797~regulation of hair follicle development	2	0.087489	TNF, KRT17	132	5	8785	26.62121	0.072384
GOTERM_	GO:0033209~tumor necrosis factor-mediated signaling pathway	2	0.087489	TNF, KRT8	132	4	8785	33.27652	0.058336