

Supplementary Materials:Genome-wide differential expression profiling of mRNAs and lncRNAs associated with prolificacy in Hu sheep

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Table S1. Details of primer sequences, expected product sizes and Genbank accession numbers of genes used for qRT-PCR

Gene	Primer sequence(5'- 3')	Product size(bp)	Accession number
CCL26	F:GATGTGGCCAAGTTCTGCTG R: TCGGCTGGGCACATACTTTC	148	XM_004020976.3
TSPAN32	F:AAGAAGTGGGTGTGGGCTTT R:CCTGGCCCAATTTGAAGGAC	144	NM_001114667.1
LOC101121 216	F:GCCAACTACAAGGGTGCAGA R: TTGTTAGGCAGGCCAGCAG	257	XM_004019478.3
TYROBP	F:ATGCAACTGCTCCTCGTTGA R:GTGATGTGCTGTTCCGGGT	159	XM_012120538.1
GPNMB	F:CCTGGTATCCCCAGATGCC R:GTCCACGCTGTCCAGTTGTA	120	XM_004007790.3
TCONS_00 025574	F:TGTCCGCTGCTGCCACTTCTA R: TAACGGGCTCCTGCTGGATGAG	132	--
TCONC_00 049541	F:TGCTCAGAGGCTCAGTCGTGTT R: CCTCCCAGGCAGTTCAGTGGTA	194	--
TCONC_00 530192	F:TGAAGCAGCAGAGGACACAGGT R:AGGTTGCTCAGTGGTTCAGAGG	113	--
TCONS_00 560231	F:TGTTGCTGAAGTGGCAGGAACC R:TGTTGCTGAAGTGGCAGGAACC	232	--
TCONC_00 920308	F:ACAAGGGAGGCTTGTTGGTG R: CTGAGTCCACTGCTTGGTGA	107	--
BMPR1B	F: GTGCCGTGAACGCACTAACA R: AGACAAAACGTGCTCCTTCAA	559	NW_011942424.1
CTSB	F: TAGGCTGGGGAGTGGAGAAC R: AGTACTGATGAGTGCACGGC	159	NM_001308587.1
CTSD	F: GCCAGGACCCTGTGTCG R: GCACGTTGTTGACGGAGATG	174	XM_012171958.2
GAPDH	F:GTCAAGGCAGAGAACGGGAA R:GGTTCACGCCCATCACAAAC	232	XM_012166462.1

Table S3 Top20 Biological Process Terms of DE-mRNAs

GO.ID	Term	Annota ted	Signific ant	Expect ed	KS
GO:0009887	organ morphogenesis	2508	5	9.22	3.10E-07
GO:0044763	single-organism cellular process	12940	51	47.59	1.40E-06
GO:0001501	skeletal system development	1683	6	6.19	3.20E-06
GO:0042742	defense response to bacterium	169	7	0.62	3.70E-06
GO:0050896	response to stimulus	9907	50	36.43	1.70E-05
GO:0045654	positive regulation of megakaryocyte differentiation	79	2	0.29	1.90E-05
GO:1901989	positive regulation of cell cycle phase transition	84	1	0.31	2.30E-05
GO:0006958	complement activation, classical pathway	28	2	0.1	2.70E-05
GO:0009888	tissue development	3162	9	11.63	4.50E-05
GO:0044765	single-organism transport	3913	26	14.39	0.00011
GO:0001818	negative regulation of cytokine production	152	6	0.56	0.00026
GO:0002376	immune system process	2537	28	9.33	0.00031
GO:0006950	response to stress	3422	29	12.58	0.00038
GO:0008206	bile acid metabolic process	49	1	0.18	0.00043
GO:0048513	organ development	5586	20	20.54	0.00055
GO:0019882	antigen processing and presentation	106	4	0.39	0.00066
GO:0035095	behavioral response to nicotine	11	1	0.04	0.0008
GO:0071384	cellular response to corticosteroid stimulus	28	1	0.1	0.00084
GO:0050718	positive regulation of interleukin-1 beta secretion	18	1	0.07	0.00087
GO:0016488	farnesol catabolic process	19	1	0.07	0.00098
GO:1900053	negative regulation of retinoic acid	19	1	0.07	0.0009

	biosynthetic process				8
GO:2000224	regulation of testosterone biosynthetic process	19	1	0.07	0.0009
					8
GO:0022604	regulation of cell morphogenesis	449	1	1.65	0.0010
					6
GO:0042448	progesterone metabolic process	27	1	0.1	0.0012
GO:2000353	positive regulation of endothelial cell apoptotic process	27	1	0.1	0.0012

Annotated: all genes annotated to the function of the number of genes; Significant: different expression gene annotated to the function of the number of genes; Expected: to the function of the number of different expression gene expectations; KS: p value of KS test , the smaller the KS value, indicating its enrichment is more significant.

Table S4 Top20 Cellular Component Terms of DE-mRNAs

GO.ID	Term	Annot	Signifi	Expe	KS
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		ated	cant	cted	
GO:0044446	intracellular organelle part	7407	16	27.6	2.70E-05
GO:0005765	lysosomal membrane	98	2	0.37	8.60E-05
GO:0005789	endoplasmic reticulum membrane	601	1	2.24	0.00017
GO:0005576	extracellular region	3294	21	12.27	0.00042
GO:0005892	acetylcholine-gated channel complex	15	1	0.06	0.00043
GO:0005634	nucleus	6087	12	22.68	0.00238
GO:0005938	cell cortex	296	2	1.1	0.00252
GO:0044428	nuclear part	2871	5	10.7	0.00285
GO:0043234	protein complex	4474	15	16.67	0.00347
GO:0030670	phagocytic vesicle membrane	32	1	0.12	0.00644
GO:0097458	neuron part	985	3	3.67	0.00912
GO:0043005	neuron projection	663	2	2.47	0.01114
GO:0005829	cytosol	1316	7	4.9	0.01891
GO:0032991	macromolecular complex	5672	16	21.14	0.0196
GO:0012505	endomembrane system	2949	12	10.99	0.02332
GO:0034364	high-density lipoprotein particle	23	1	0.09	0.02334
GO:0044430	cytoskeletal part	1938	2	7.22	0.02398
GO:0043233	organelle lumen	2404	5	8.96	0.02521
GO:0070013	intracellular organelle lumen	2400	5	8.94	0.02752
GO:0031974	membrane-enclosed lumen	2468	5	9.2	0.03234

Table S5 Top20 Molecular Function Terms of DE-mRNAs

GO.ID	Term	Annot ated	Signifi cant	Expec ted	KS
GO:0005044	scavenger receptor activity	68	2	0.26	2.60E-07
GO:0015464	acetylcholine receptor activity	17	1	0.06	0.00028
GO:0004032	alditol:NADP+ 1-oxidoreductase activity	26	1	0.1	0.00032
GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	20	1	0.08	0.00058
GO:0005506	iron ion binding	212	5	0.81	0.00077
GO:0045703	ketoreductase activity	19	1	0.07	0.00084
GO:0047086	ketosteroid monooxygenase activity	19	1	0.07	0.00084

GO:0047020	15-hydroxyprostaglandin-D dehydrogenase (NADP+) activity	19	1	0.07	0.00084
GO:0047042	androsterone dehydrogenase (B-specific) activity	19	1	0.07	0.00084
GO:0047035	testosterone dehydrogenase (NAD+) activity	19	1	0.07	0.00084
GO:0047006	17-alpha,20-alpha-dihydroxypregn-4-en-3-one dehydrogenase activity	19	1	0.07	0.00084
GO:0045550	geranylgeranyl reductase activity	19	1	0.07	0.00084
GO:0047787	delta4-3-oxosteroid 5beta-reductase activity	19	1	0.07	0.00084
GO:0035410	dihydrotestosterone 17-beta-dehydrogenase activity	19	1	0.07	0.00084
GO:0018636	phenanthrene 9,10-monooxygenase activity	19	1	0.07	0.00084
GO:0047017	prostaglandin-F synthase activity	17	1	0.06	0.00177
GO:0036131	prostaglandin D2 11-ketoreductase activity	17	1	0.06	0.00177
GO:0004252	serine-type endopeptidase activity	158	1	0.6	0.00208
GO:0016787	hydrolase activity	2745	20	10.44	0.0024

Table S6 Top20 Cellular Component Terms of the target genes of DE-lncRNAs

GO.ID	Term	Annot ated	Signifi cant	Expe cted	KS
GO:0050896	response to stimulus	9907	5	4.48	6.50E-07
GO:0044763	single-organism cellular process	12940	6	5.86	1.50E-06
GO:0009888	tissue development	3162	1	1.43	4.40E-05
GO:0044765	single-organism transport	3913	1	1.77	9.70E-05
GO:0006950	response to stress	3422	2	1.55	0.00033
GO:0048513	organ development	5586	2	2.53	0.00039
GO:0044711	single-organism biosynthetic process	1265	1	0.57	0.00124

GO:0051716	cellular response to stimulus	7400	3	3.35	0.00154
GO:0006508	proteolysis	1261	2	0.57	0.00176
GO:0016043	cellular component organization	6252	3	2.83	0.00196
GO:0006810	transport	4832	1	2.19	0.00209
GO:0006957	complement activation, alternative pathway	16	1	0.01	0.00239
GO:0065008	regulation of biological quality	3641	3	1.65	0.00301
GO:0043170	macromolecule metabolic process	9613	6	4.35	0.00375
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	1119	2	0.51	0.00388
GO:0006464	cellular protein modification process	3089	1	1.4	0.00474
GO:0006996	organelle organization	3561	2	1.61	0.0053
GO:0019538	protein metabolic process	5283	4	2.39	0.00546
GO:0002376	immune system process	2537	1	1.15	0.00862
GO:0030154	cell differentiation	4631	2	2.1	0.011
GO:0010466	negative regulation of peptidase activity	174	1	0.08	0.01208
GO:0048869	cellular developmental process	5001	2	2.26	0.01277

Significant: target gene of DE-lncRNAs that annotated to the function of the number of genes

Table S7 Top20 Biological Process Terms of the target genes of DE-lncRNAs

GO.ID	Term	Annotat ed	Significa nt	Expect ed	KS
GO:0044446	intracellular organelle part	7407	6	3.3	2.20E- 05
GO:0005765	lysosomal membrane	98	1	0.04	0.0001 6
GO:0005576	extracellular region	3294	2	1.47	0.0007 9
GO:0005634	nucleus	6087	5	2.71	0.0021 8
GO:0044428	nuclear part	2871	4	1.28	0.0030 4
GO:0043234	protein complex	4474	4	1.99	0.0034 8
GO:0032991	macromolecular complex	5672	5	2.52	0.0173

GO:0005829	cytosol	1316	1	0.59	0.0189 8
GO:0012505	endomembrane system	2949	2	1.31	0.0218 4
GO:0044430	cytoskeletal part	1938	1	0.86	0.0223 3
GO:0043233	organelle lumen	2404	3	1.07	0.0279 1
GO:0070013	intracellular organelle lumen	2400	3	1.07	0.0304 4
GO:0031300	intrinsic component of organelle membran...	167	0	0.07	0.0308 9
GO:0044422	organelle part	7655	6	3.41	0.0324 6
GO:0031974	membrane-enclosed lumen	2468	3	1.1	0.0354 1
GO:0036128	CatSper complex	14	1	0.01	0.0374 2
GO:0031981	nuclear lumen	2071	2	0.92	0.0374 3
GO:0015630	microtubule cytoskeleton	1336	1	0.59	0.0463 1
GO:0005694	chromosome	909	1	0.4	0.0474 9
GO:0034707	chloride channel complex	41	1	0.02	0.0531 2

Table S8 The pathway enrich in DE-mRNAs

#Kegg_pathway	ko_id	Cluter_frequency	P-value	Corrected_P-value
Lysosome	ko04142	14 out of 47 29.7872340425532%	4.24E-14	1.40E-12
Tuberculosis	ko05152	8 out of 47 17.0212765957447%	2.59E-05	0.000854
Mineral absorption	ko04978	5 out of 47 10.6382978723404%	3.46E-05	0.001141
Staphylococcus aureus infection	ko05150	5 out of 47 10.6382978723404%	0.00011	0.003615
Pertussis	ko05133	5 out of 47 10.6382978723404%	0.00016	0.003835
Phagosome	ko04145	7 out of 47 14.8936170212766%	0.000178	0.005882
Osteoclast differentiation	ko04380	5 out of 47	0.0007	0.025813

		10.6382978723404%	82	
Complement and coagulation cascades	ko04610	3 out of 47 6.38297872340426%	0.0113 77	0.375438
Leishmaniasis	ko05140	3 out of 47 6.38297872340426%	0.0130 24	0.429805
Legionellosis	ko05134	3 out of 47 6.38297872340426%	0.0143 45	0.473391
Hematopoietic cell lineage	ko04640	3 out of 47 6.38297872340426%	0.0177 14	0.584572
Prion diseases	ko05020	2 out of 47 4.25531914893617%	0.0186 36	0.614976
Fc gamma R-mediated phagocytosis	ko04666	3 out of 47 6.38297872340426%	0.0192 82	0.636317
Antigen processing and presentation	ko04612	3 out of 47 6.38297872340426%	0.0244 36	0.8064
Nicotine addiction	ko05033	2 out of 47 4.25531914893617%	0.0286 33	0.944905
Natural killer cell mediated cytotoxicity	ko04650	3 out of 47 6.38297872340426%	0.0309 56	1
Systemic lupus erythematosus	ko05322	3 out of 47 6.38297872340426%	0.0517 47	1
Malaria	ko05144	2 out of 47 4.25531914893617%	0.0550 21	1
PPAR signaling pathway	ko03320	2 out of 47 4.25531914893617%	0.0662 72	1
Rheumatoid arthritis	ko05323	2 out of 47 4.25531914893617%	0.1438 66	1
Rap1 signaling pathway	ko04015	3 out of 47 6.38297872340426%	0.1460 46	1
Regulation of actin cytoskeleton	ko04810	3 out of 47 6.38297872340426%	0.1517 28	1
Protein digestion and absorption	ko04974	2 out of 47 4.25531914893617%	0.1627 86	1
Sphingolipid signaling pathway	ko04071	2 out of 47 4.25531914893617%	0.1670 53	1
Leukocyte transendothelial migration	ko04670	2 out of 47 4.25531914893617%	0.1691 93	1
Chagas disease (American trypanosomiasis)	ko05142	2 out of 47 4.25531914893617%	0.1691 93	1
Amoebiasis	ko05146	2 out of 47 4.25531914893617%	0.1734 9	1
Neuroactive ligand-receptor interaction	ko04080	3 out of 47 6.38297872340426%	0.2505 28	1
Influenza A	ko05164	2 out of 47	0.2979	1

		4.25531914893617%	94	
Transcriptional misregulation in cancer	ko05202	2 out of 47	0.3114	1
		4.25531914893617%	32	
Cell adhesion molecules (CAMs)	ko04514	2 out of 47	0.3270	1
		4.25531914893617%	52	
Viral carcinogenesis	ko05203	2 out of 47	0.4183	1
		4.25531914893617%	88	
PI3K-Akt signaling pathway	ko04151	2 out of 47	0.6561	1
		4.25531914893617%	37	

Table S9 The pathway enrich in DE-lncRNAs

#Kegg_pathway	ko_id	Cluter_frequency	P-value	Corrected_P-value
Spliceosome	ko03040	2 out of 6 33.3333333333333%	0.0072 33	0.13743
Other glycan degradation	ko00511	1 out of 6 16.6666666666667%	0.0205 97	0.391341
Aminoacyl-tRNA biosynthesis	ko00970	1 out of 6 16.6666666666667%	0.0363 71	0.691052
Sphingolipid metabolism	ko00600	1 out of 6 16.6666666666667%	0.0371 17	0.705223
Lysine degradation	ko00310	1 out of 6 16.6666666666667%	0.0511 97	0.972741
Complement and coagulation cascades	ko04610	1 out of 6 16.6666666666667%	0.0585 38	1
Staphylococcus aureus infection	ko05150	1 out of 6 16.6666666666667%	0.0600 01	1

RNA degradation	ko03018	1 out of 6 16.6666666666667%	0.0600 01	1
Legionellosis	ko05134	1 out of 6 16.6666666666667%	0.0636 49	1
Estrogen signaling pathway	ko04915	1 out of 6 16.6666666666667%	0.0759 64	1
Antigen processing and presentation	ko04612	1 out of 6 16.6666666666667%	0.0774 04	1
Lysosome	ko04142	1 out of 6 16.6666666666667%	0.0952 47	1
Toxoplasmosis	ko05145	1 out of 6 16.6666666666667%	0.1008 95	1
Measles	ko05162	1 out of 6 16.6666666666667%	0.1030 06	1
Influenza A	ko05164	1 out of 6 16.6666666666667%	0.1314 39	1
Protein processing in endoplasmic reticulum	ko04141	1 out of 6 16.6666666666667%	0.1362 17	1
Epstein-Barr virus infection	ko05169	1 out of 6 16.6666666666667%	0.1564 5	1
Endocytosis	ko04144	1 out of 6 16.6666666666667%	0.1683 98	1
MAPK signaling pathway	ko04010	1 out of 6 16.6666666666667%	0.1867 04	1