

Supplementary tables and figures

Transcriptome profile of one-month-old lambs' granulosa cells after superstimulation

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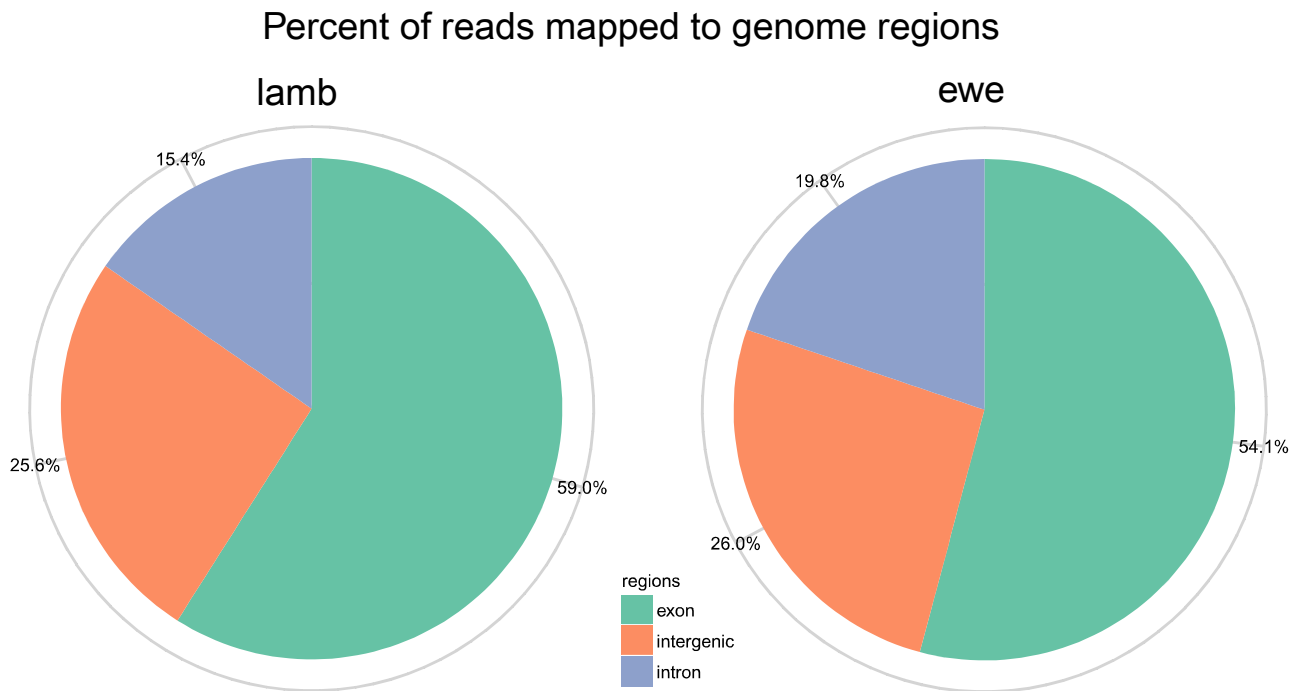
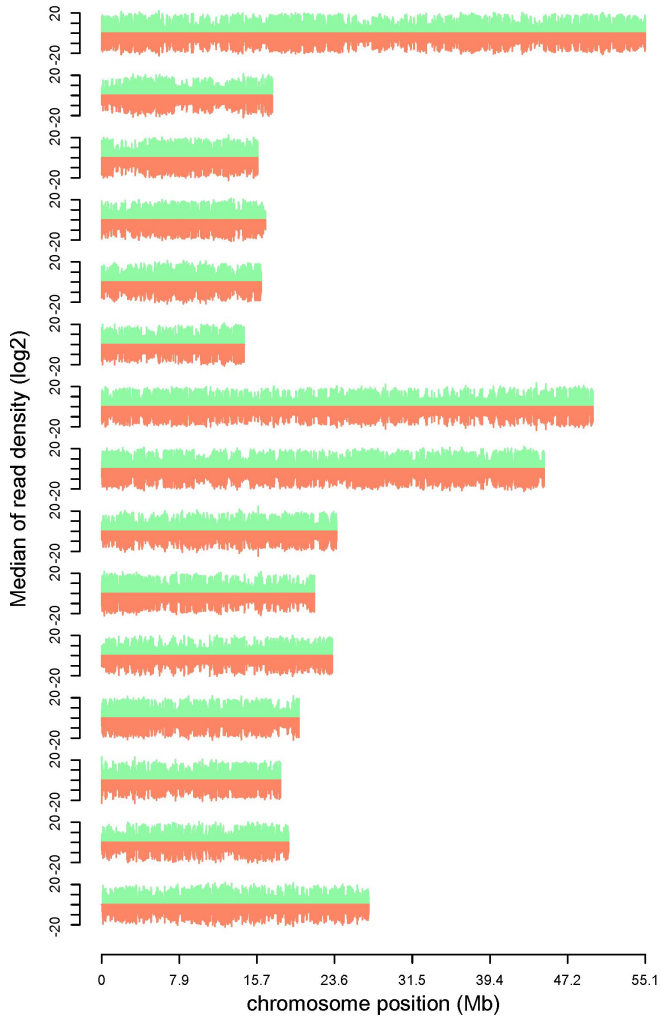


Figure S1. Percent of reads mapped to genome regions.

Reads Density in Chromosomes (ewe)



Reads Density in Chromosomes (lamb)

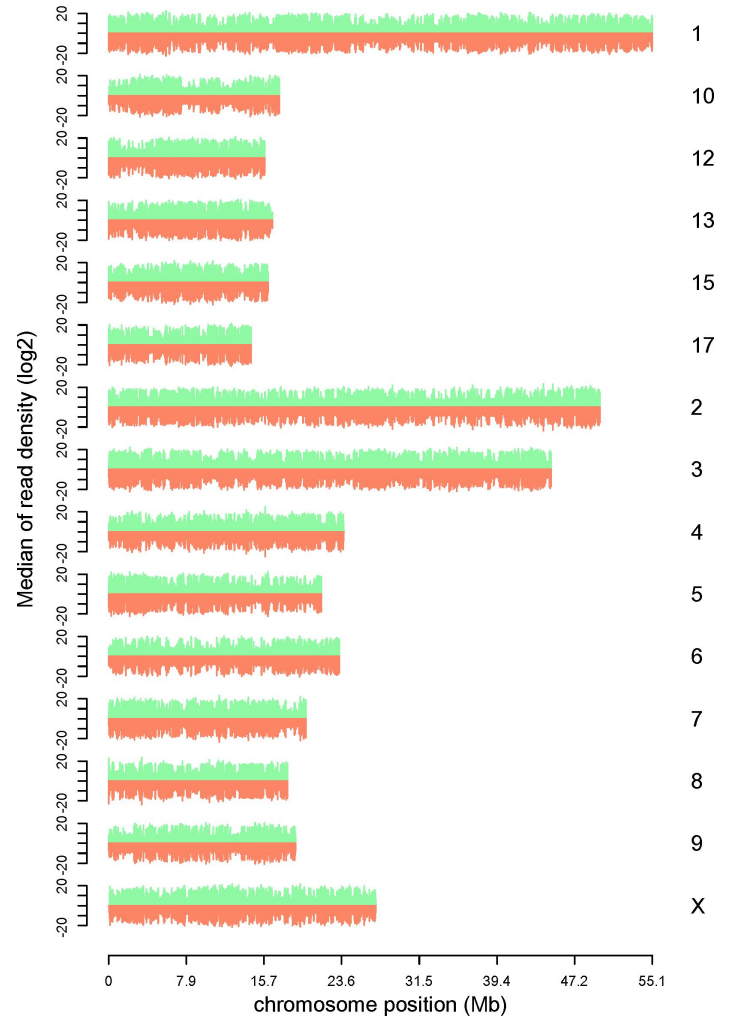


Figure S2. Read density in chromosomes.

Table S1. A summary of the sequencing reads' quality.

Sample name	Raw reads	Clean reads	Clean bases	Error rate (%)	Q20(%)	Q30(%)	GC content(%)
eweGC_1	29627505	25877091	3.23G	0.05	93.55	88.10	47.11
eweGC_2	29627505	25877091	3.23G	0.03	96.27	92.34	47.12
lambGC_1	32774030	28506195	3.56G	0.05	93.54	88.07	47.72
lambGC_2	32774030	28506195	3.56G	0.03	96.28	92.36	47.73

Table S2 A summary of the sequencing reads alignment to the *Ovis aries* genome and reference genes.

	eweGC	lambGC
Total reads	51754182	57012390
Total mapped	44253417 (85.51%)	48875134 (85.73%)
Multiple mapped	1504580 (2.91%)	1487176 (2.61%)
Uniquely mapped	42748837 (82.6%)	47387958 (83.12%)
Read-1	21066433 (40.7%)	23363268 (40.98%)
Read-2	21682404 (41.89%)	24024690 (42.14%)
Reads map to '+'	21378379 (41.31%)	23687012 (41.55%)
Reads map to '-'	21370458 (41.29%)	23700946 (41.57%)
Non-splice reads	31312935 (60.5%)	33305007 (58.42%)
Splice reads	11435902 (22.1%)	14082951 (24.7%)

Table S3. A total list of genes expressed differently between the lamb and ewe in granulosa cells.

Gene_id	FPKM_lamb	FPKM_ewe	log2.Fold_change.	pvalue	qvalue	Associated Gene Name	Description
1	ENSOARG00000000043	64.29093792	185.3679714	-1.5277	4.12E-17	5.80E-15 RAB11FIP2	RAB11 family interacting protein 2 (class I) [Source:HGNC Symbol;Acc:HGNC:29152]
2	ENSOARG00000000117	24.60181768	72.93042958	-1.5678	8.05E-08	4.69E-06 HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3 [Source:HGNC Symbol;Acc:HGNC:4876]
3	ENSOARG00000000345	507.9391861	214.0594483	1.2466	6.18E-24	1.30E-21 GRAMD1B	GRAM domain containing 1B [Source:HGNC Symbol;Acc:HGNC:29214]
4	ENSOARG00000000683	1479.643024	573.4539957	1.3675	9.21E-78	9.90E-75 PTP4A2	protein tyrosine phosphatase type IVA, member 2 [Source:HGNC Symbol;Acc:HGNC:9635]
5	ENSOARG00000000850	22.8348363	53.55241636	-1.2297	9.81E-05	0.0027187 RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4 [Source:HGNC Symbol;Acc:HGNC:16626]
6	ENSOARG00000000908	0	28.46615119	-8.7103	3.35E-07	1.66E-05	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5NRZ8]
7	ENSOARG00000000915	265.0472071	85.77399648	1.6276	7.82E-20	1.30E-17 BAI2	brain-specific angiogenesis inhibitor 2 [Source:HGNC Symbol;Acc:HGNC:944]
8	ENSOARG00000001020	114.5139856	54.75415362	1.0645	3.35E-05	0.0010545 BCOR	BCL6 corepressor [Source:HGNC Symbol;Acc:HGNC:20893]
9	ENSOARG00000001199	257.5035558	710.8275855	-1.4649	1.03E-57	8.57E-55 KIAA1841	KIAA1841 [Source:HGNC Symbol;Acc:HGNC:29387]
10	ENSOARG00000001269	475.9975996	161.032792	1.5636	2.71E-32	8.85E-30 STAR	Ovis aries steroidogenic acute regulatory protein (STAR), nuclear gene encoding mitochondrial protein, mRNA. [Source:RefSeq mRNA;Acc:NM_001009243]
11	ENSOARG00000001301	316.9013145	154.5734542	1.0357	1.74E-11	1.61E-09 RRM1	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HGNC:10451]
12	ENSOARG00000001337	25.5532692	67.59772051	-1.4035	1.62E-06	7.02E-05 CAV1	Ovis aries caveolin 1, caveolae protein, 22kDa (CAV1), mRNA. [Source:RefSeq
13	ENSOARG00000001369	526.6963731	203.243813	1.3738	5.27E-29	1.46E-26 UBE2S	ubiquitin-conjugating enzyme E2S [Source:HGNC Symbol;Acc:HGNC:17895]
14	ENSOARG00000001456	27.93189798	69.40032639	-1.313	3.45E-06	0.0001384 GFPT2	glutamine-fructose-6-phosphate transaminase 2 [Source:HGNC Symbol;Acc:HGNC:4242]
15	ENSOARG00000001504	77.47533746	29.29234556	1.4032	1.28E-05	0.0004546 SREBF1	sterol regulatory element binding transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:11289]
16	ENSOARG00000001626	72.31031496	223.7484549	-1.6296	5.37E-22	1.00E-19 PPM1K	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K [Source:HGNC Symbol;Acc:HGNC:25415]
17	ENSOARG00000001672	826.8793253	2089.445541	-1.3374	6.51E-147	1.70E-143	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5NUA7]
18	ENSOARG00000001811	236.6395834	112.8881933	1.0678	2.21E-09	1.61E-07 TNNI3	troponin I type 3 (cardiac) [Source:HGNC Symbol;Acc:HGNC:11947]
19	ENSOARG00000001834	44.92210356	13.06889263	1.7813	5.70E-05	0.0016677	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5NUT4]
20	ENSOARG00000001908	95.41699455	44.16384407	1.1114	8.10E-05	0.002288 CSPG4	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc:HGNC:2466]
21	ENSOARG00000002051	116.1450454	55.80567371	1.0574	3.29E-05	0.0010399	
22	ENSOARG00000002053	8.019377035	194.5312179	-4.6004	8.21E-48	4.29E-45 EFEMP1	EGF containing fibulin-like extracellular matrix protein 1 [Source:HGNC Symbol;Acc:HGNC:3218]
23	ENSOARG00000002088	224.2027529	82.61943618	1.4403	3.23E-14	3.65E-12 GRK5	G protein-coupled receptor kinase 5 [Source:HGNC Symbol;Acc:HGNC:4544]
24	ENSOARG00000002210	185.6689666	476.2634953	-1.359	1.33E-35	5.17E-33	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5NVY4]
25	ENSOARG00000002223	142.6497661	443.5912637	-1.6368	3.29E-42	1.50E-39 MYOF	myoferlin [Source:HGNC Symbol;Acc:HGNC:3656]
26	ENSOARG00000002225	604.5115146	263.5560014	1.1977	2.39E-26	5.60E-24 HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1 [Source:HGNC Symbol;Acc:HGNC:5210]
27	ENSOARG00000002455	29.69887936	67.07196047	-1.1753	2.42E-05	0.00079463 FAAH	fatty acid amide hydrolase [Source:HGNC Symbol;Acc:HGNC:3553]
28	ENSOARG00000002562	9.92228006	53.02665631	-2.418	2.76E-09	1.99E-07 IL6R	interleukin 6 receptor [Source:HGNC Symbol;Acc:HGNC:6019]
29	ENSOARG00000002590	9.650436771	93.35996289	-3.2741	8.96E-20	1.45E-17 SPP1	osteopontin precursor [Source:RefSeq peptide;Acc:NP_001009224]
30	ENSOARG00000002608	19.36883436	48.06949014	-1.3114	0.00011346	0.0030911 CITED2	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5NX69]
31	ENSOARG00000002610	62.04823079	124.3046972	-1.0024	2.92E-07	1.49E-05 FAM134C	family with sequence similarity 134, member C [Source:HGNC Symbol;Acc:HGNC:27258]
32	ENSOARG00000002665	289.4451423	114.9912335	1.3318	7.17E-16	9.10E-14	
33	ENSOARG00000002703	37.17456981	78.93911585	-1.0864	1.48E-05	0.00051877 VEPH1	ventricular zone expressed PH domain-containing 1 [Source:HGNC Symbol;Acc:HGNC:25735]
34	ENSOARG00000002754	50.97061675	163.1358322	-1.6783	4.82E-17	6.68E-15 PTX3	pentraxin 3, long [Source:HGNC Symbol;Acc:HGNC:9692]
35	ENSOARG00000003100	33.98041117	68.79945777	-1.0177	0.00011455	0.0031161 C20orf194	chromosome 20 open reading frame 194 [Source:HGNC Symbol;Acc:HGNC:17721]
36	ENSOARG00000003230	94.39758222	285.9383578	-1.5989	5.09E-27	1.22E-24 C3orf33	chromosome 3 open reading frame 33 [Source:HGNC Symbol;Acc:HGNC:26434]
37	ENSOARG00000003501	57.15505158	135.2705496	-1.2429	4.45E-10	3.53E-08 PDK4	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC Symbol;Acc:HGNC:8812]
38	ENSOARG00000003518	30.85421334	77.43694428	-1.3276	7.78E-07	3.56E-05 SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) [Source:HGNC Symbol;Acc:HGNC:11169]
39	ENSOARG00000003537	280.6102354	1006.229624	-1.8423	2.32E-108	3.53E-105 SYNE1	spectrin repeat containing, nuclear envelope 1 [Source:HGNC Symbol;Acc:HGNC:17089]
40	ENSOARG00000003547	159.2322067	77.58716144	1.0372	1.80E-06	7.65E-05 MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2 [Source:HGNC Symbol;Acc:HGNC:7548]
41	ENSOARG00000003554	53.41720635	124.15448	-1.2168	3.93E-09	2.79E-07 DSTYK	dual serine/threonine and tyrosine protein kinase [Source:HGNC Symbol;Acc:HGNC:29043]
42	ENSOARG00000003591	109.5528456	222.3213919	-1.021	3.63E-12	3.56E-10 NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive [Source:HGNC Symbol;Acc:HGNC:7774]
43	ENSOARG00000003609	77.54329828	32.52201443	1.2536	7.47E-05	0.0021336	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5P0A0]
44	ENSOARG00000003737	38.73766873	93.13463715	-1.2656	1.59E-07	8.61E-06	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5P0P2]

45	ENSOARG00000003804	432.5706341	167.6423469	1.3675	6.11E-24	1.30E-21	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group) [Source:HGNC Symbol;Acc:HGNC:10741]
46	ENSOARG00000003820	135.038154	51.90002764	1.3796	1.35E-08	8.93E-07	NOTCH1	notch 1 [Source:HGNC Symbol;Acc:HGNC:7881]
47	ENSOARG00000003926	184.5136326	542.2839357	-1.5553	5.27E-48	2.83E-45	LRRC16A	leucine rich repeat containing 16A [Source:HGNC Symbol;Acc:HGNC:21581]
48	ENSOARG000000004140	28.06781962	83.97139059	-1.581	7.05E-09	4.79E-07	PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like [Source:HGNC Symbol;Acc:HGNC:29378]
49	ENSOARG000000004162	23.99017028	58.81001685	-1.2936	2.35E-05	0.00077552	FAM222B	family with sequence similarity 222, member B [Source:HGNC Symbol;Acc:HGNC:25563]
50	ENSOARG000000004186	31.73770403	85.92421363	-1.4369	3.93E-08	2.42E-06	FAM13C	family with sequence similarity 13, member C [Source:HGNC Symbol;Acc:HGNC:19371]
51	ENSOARG000000004318	123.4848142	61.28859993	1.0106	4.09E-05	0.0012554	CDC2	Ovis aries cyclin-dependent kinase 1 (CDK1), mRNA. [Source:RefSeq mRNA;Acc:NM_001142508]
52	ENSOARG000000004403	41.59202327	166.5157182	-2.0013	3.06E-21	5.54E-19	ARID5B	AT rich interactive domain 5B (MRF1-like) [Source:HGNC Symbol;Acc:HGNC:17362]
53	ENSOARG000000004429	1022.402611	2660.195628	-1.3796	1.35E-194	4.95E-191	IVNS1ABP	influenza virus NS1A binding protein [Source:HGNC Symbol;Acc:HGNC:16951]
54	ENSOARG000000004495	91.40730603	38.53070069	1.2463	1.88E-05	0.00063529	HELLS	helicase, lymphoid-specific [Source:HGNC Symbol;Acc:HGNC:4861]
55	ENSOARG000000004595	5.572787431	212.7074939	-5.2543	8.26E-54	6.04E-51	OXT	oxytocin-neurophysin 1 precursor [Source:RefSeq peptide;Acc:NP_001009801]
56	ENSOARG000000004819	417.2794491	957.7845911	-1.1987	6.48E-59	5.64E-56	ARHGEF28	Rho guanine nucleotide exchange factor (GEF) 28 [Source:HGNC Symbol;Acc:HGNC:30322]
57	ENSOARG000000004835	115.3295155	55.12969651	1.0649	3.12E-05	0.00099118	BRCA1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5P433]
58	ENSOARG000000004896	18.14553956	46.56731858	-1.3597	9.82E-05	0.0027187	SYTL2	synaptotagmin-like 2 [Source:HGNC Symbol;Acc:HGNC:15585]
59	ENSOARG000000004947	74.5530221	151.1935682	-1.0201	1.01E-08	6.82E-07	ZBED6	zinc finger, BED-type containing 6 [Source:HGNC Symbol;Acc:HGNC:33273]
60	ENSOARG000000005118	22.76687548	119.4226396	-2.3911	7.41E-19	1.16E-16	KCNK12	potassium channel, subfamily K, member 12 [Source:HGNC Symbol;Acc:HGNC:6274]
61	ENSOARG000000005371	242.0764491	116.1178621	1.0599	1.88E-09	1.39E-07	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10862]
62	ENSOARG000000005399	59.80552365	21.25572767	1.4924	5.42E-05	0.0016013	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:7728]
63	ENSOARG000000005456	60.75697516	23.20855071	1.3884	0.00012812	0.0034289	BIRC5	baculoviral IAP repeat containing 5 [Source:HGNC Symbol;Acc:HGNC:593]
64	ENSOARG000000005499	169.2224476	371.2617028	-1.1335	3.56E-22	6.85E-20	EXOC3L4	exocyst complex component 3-like 4 [Source:HGNC Symbol;Acc:HGNC:20120]
65	ENSOARG000000005652	78.42678897	30.11853992	1.3807	1.48E-05	0.00051877	CDC43	cell division cycle associated 3 [Source:HGNC Symbol;Acc:HGNC:14624]
66	ENSOARG000000005706	58.78611132	20.27931615	1.5355	4.20E-05	0.0012837	USP27X	ubiquitin specific peptidase 27, X-linked [Source:HGNC Symbol;Acc:HGNC:13486]
67	ENSOARG000000005709	463.4248475	101.6219065	2.1891	8.22E-51	5.36E-48	COBLL1	cordon-bleu WH2 repeat protein-like 1 [Source:HGNC Symbol;Acc:HGNC:23571]
68	ENSOARG000000005844	183.9019852	77.66227001	1.2437	1.39E-09	1.03E-07	GLCCI1	glucocorticoid induced transcript 1 [Source:HGNC Symbol;Acc:HGNC:18713]
69	ENSOARG000000005888	160.4555015	56.33143376	1.5102	2.45E-11	2.25E-09	PAPPA	pregnancy-associated plasma protein A, pappalysin 1 [Source:HGNC Symbol;Acc:HGNC:8602]
70	ENSOARG000000005997	72.17439332	168.4685412	-1.2229	5.89E-12	5.69E-10	TDP2	tyrosyl-DNA phosphodiesterase 2 [Source:HGNC Symbol;Acc:HGNC:17768]
71	ENSOARG000000006209	373.6486012	179.0588508	1.0612	7.83E-14	8.57E-12	ALAS1	aminolevulinate, delta-, synthase 1 [Source:HGNC Symbol;Acc:HGNC:396]
72	ENSOARG000000006246	14.06789022	44.99003843	-1.6772	1.06E-05	0.00038465	FAP	fibroblast activation protein, alpha [Source:HGNC Symbol;Acc:HGNC:3590]
73	ENSOARG000000006253	43.63084794	87.72681951	-1.0077	1.53E-05	0.00053109	ANG-2	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5P8E6]
74	ENSOARG000000006261	807.850295	402.2064371	1.0062	1.46E-25	3.33E-23	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor [Source:HGNC Symbol;Acc:HGNC:6700]
75	ENSOARG000000006460	747.2972023	268.2127333	1.4783	1.61E-45	7.95E-43	NTRK1	neurotrophic tyrosine kinase, receptor, type 1 [Source:HGNC Symbol;Acc:HGNC:8031]
76	ENSOARG000000006495	747.9768106	326.4969901	1.1959	3.95E-32	1.27E-29	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HGNC Symbol;Acc:HGNC:806]
77	ENSOARG000000006520	179.7563751	72.55488669	1.3089	3.78E-10	3.04E-08	UBE2C	ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;Acc:HGNC:15937]
78	ENSOARG000000006571	121.3780287	52.65111342	1.205	1.72E-06	7.35E-05	TUBA1C	tubulin, alpha 1c [Source:HGNC Symbol;Acc:HGNC:20768]
79	ENSOARG000000006979	82.43647749	36.87831197	1.1605	0.00013819	0.0036717	RHBDFF2	rhomoid 5 homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:20788]
80	ENSOARG000000006991	141.7662754	58.73490827	1.2712	5.90E-08	3.54E-06		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PAN5]
81	ENSOARG000000007049	231.9502866	93.6603972	1.3083	1.15E-12	1.16E-10	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1 [Source:HGNC Symbol;Acc:HGNC:61]
82	ENSOARG000000007070	3421.419639	7475.70702	-1.1276	0	0	GLCL	glutamate-cysteine ligase, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:4311]
83	ENSOARG000000007251	189.6106943	432.324977	-1.1891	3.08E-27	7.52E-25	GPBP1	GC-rich promoter binding protein 1 [Source:HGNC Symbol;Acc:HGNC:29520]
84	ENSOARG000000007278	18.28146121	50.9987247	-1.4801	1.57E-05	0.00054249	ANGPTL5	angiopoietin-like 5 [Source:HGNC Symbol;Acc:HGNC:19705]
85	ENSOARG000000007502	26.36879906	57.30784528	-1.1199	0.00016242	0.0042294	NFKBIA	NF-kappa-B inhibitor alpha [Source:RefSeq peptide;Acc:NP_001159656]
86	ENSOARG000000007721	94.3296214	39.05646074	1.2721	9.63E-06	0.00035189	CKS2	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Symbol;Acc:HGNC:2000]
87	ENSOARG000000007779	545.5894817	218.4908544	1.3202	4.07E-28	1.08E-25	MANF	mesencephalic astrocyte-derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:15461]
88	ENSOARG000000007786	102.8247242	45.36558132	1.1805	1.54E-05	0.00053377	GADD45G	growth arrest and DNA-damage-inducible, gamma [Source:HGNC Symbol;Acc:HGNC:4097]
89	ENSOARG000000007826	1061.616006	436.2306231	1.2831	1.29E-50	8.11E-48	PPAP2B	phosphatidic acid phosphatase type 2B [Source:HGNC Symbol;Acc:HGNC:9229]
90	ENSOARG000000007995	141.2905496	67.59772051	1.0636	4.13E-06	0.00016346	NCAPG2	non-SMC condensin II complex, subunit G2 [Source:HGNC Symbol;Acc:HGNC:21904]
91	ENSOARG000000008116	85.90247943	31.17006002	1.4625	1.96E-06	8.21E-05	NINJ1	ninjurin 1 [Source:HGNC Symbol;Acc:HGNC:7824]

92	ENSOARG00000008239	80.53357446	183.3400398	-1.1869	2.07E-12	2.08E-10	ZNF692	zinc finger protein 692 [Source:HGNC Symbol;Acc:HGNC:26049]
93	ENSOARG00000008249	96.84417182	194.4561093	-1.0057	1.27E-10	1.08E-08	ASPN	asporin [Source:HGNC Symbol;Acc:HGNC:14872]
94	ENSOARG00000008408	36.97068735	80.89193888	-1.1296	6.54E-06	0.00024734	MAN1A1	mannosidase, alpha, class 1A, member 1 [Source:HGNC Symbol;Acc:HGNC:6821]
95	ENSOARG00000008411	36.76680488	76.53564134	-1.0577	2.87E-05	0.00092077	SLC10A7	solute carrier family 10, member 7 [Source:HGNC Symbol;Acc:HGNC:23088]
96	ENSOARG00000008420	175.950569	84.12160775	1.0646	2.70E-07	1.40E-05	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10 [Source:HGNC Symbol;Acc:HGNC:4800]
97	ENSOARG00000008530	141.2225888	54.67904504	1.3689	7.95E-09	5.38E-07	UHRF1	ubiquitin-like with PHD and ring finger domains 1 [Source:HGNC Symbol;Acc:HGNC:12556]
98	ENSOARG00000008578	16.71836229	53.02665631	-1.6653	1.94E-06	8.15E-05	PTCH	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PFJ2]
99	ENSOARG00000008752	7.611612101	28.84169409	-1.9219	0.00012209	0.0033013	VWF	von Willebrand factor [Source:HGNC Symbol;Acc:HGNC:12726]
100	ENSOARG00000008975	125.9993646	444.2672409	-1.818	4.33E-48	2.40E-45	MYH11	myosin, heavy chain 11, smooth muscle [Source:HGNC Symbol;Acc:HGNC:7569]
101	ENSOARG00000008998	42.47551396	89.67964255	-1.0781	4.41E-06	0.00017266	INADL	InaD-like (Drosophila) [Source:HGNC Symbol;Acc:HGNC:28881]
102	ENSOARG00000009152	26.36879906	0	8.4556	1.22E-06	5.47E-05		Elongation factor 1-alpha [Source:UniProtKB/TrEMBL;Acc:W5PHA3]
103	ENSOARG00000009174	177.3777463	391.9916704	-1.144	1.31E-23	2.69E-21		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PHC7]
104	ENSOARG00000009469	3.941727695	32.597123	-3.0478	1.80E-07	9.67E-06	NOV	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:HGNC:7885]
105	ENSOARG00000009485	30.17460511	68.94967492	-1.1922	1.53E-05	0.00053109	LRRK1	leucine-rich repeat kinase 1 [Source:HGNC Symbol;Acc:HGNC:18608]
106	ENSOARG00000009525	90.72769781	319.4367837	-1.8159	5.14E-35	1.92E-32	MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:13634]
107	ENSOARG00000009544	74.21321799	29.29234556	1.3412	3.96E-05	0.0012216	B4GALT1	Ovis aries UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. [Source:RefSeq mRNA;Acc:NM_001246211]
108	ENSOARG00000009686	144.8245124	40.48352373	1.8389	1.34E-13	1.44E-11	ADAMTS4	ADAM metalloproteinase with thrombospondin type 1 motif, 4 [Source:HGNC Symbol;Acc:HGNC:220]
109	ENSOARG00000009704	59.60164118	22.5325735	1.4033	0.00012918	0.0034524	CHAF1A	chromatin assembly factor 1, subunit A (p150) [Source:HGNC Symbol;Acc:HGNC:1910]
110	ENSOARG00000009808	83.31996818	9.98944092	3.0602	8.49E-15	1.01E-12	APOA2	apolipoprotein A-II [Source:HGNC Symbol;Acc:HGNC:601]
111	ENSOARG00000009868	22.01930644	98.84288911	-2.1664	2.24E-14	2.56E-12		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PJG5]
112	ENSOARG00000009887	271.1636811	133.1675094	1.0259	6.99E-10	5.37E-08	CHST15	carbohydrate (N-acetyl)galactosamine 4-sulfate 6-O) sulfotransferase 15 [Source:HGNC Symbol;Acc:HGNC:18137]
113	ENSOARG00000009949	22.29114972	54.07817641	-1.2786	5.76E-05	0.0016813	SKAP2	src kinase associated phosphoprotein 2 [Source:HGNC Symbol;Acc:HGNC:15687]
114	ENSOARG00000009958	42.06774902	120.9999197	-1.5242	1.17E-11	1.10E-09	NEFM	neurofilament, medium polypeptide [Source:HGNC Symbol;Acc:HGNC:7734]
115	ENSOARG00000009959	65.92199766	152.3201969	-1.2083	8.65E-11	7.53E-09		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PJR1]
116	ENSOARG00000010041	69.72780371	146.3866192	-1.07	5.41E-09	3.76E-07	POSTN	periostin, osteoblast specific factor [Source:HGNC Symbol;Acc:HGNC:16953]
117	ENSOARG00000010042	3.058237005	31.62071149	-3.3701	8.48E-08	4.89E-06	STC1	stanniocalcin 1 [Source:HGNC Symbol;Acc:HGNC:11373]
118	ENSOARG00000010048	234.464837	111.0104788	1.0787	1.85E-09	1.37E-07	OAT	ornithine aminotransferase [Source:HGNC Symbol;Acc:HGNC:8091]
119	ENSOARG00000010118	120.3586163	291.7217183	-1.2773	9.94E-21	1.75E-18	VWA5A	von Willebrand factor A domain containing 5A [Source:HGNC Symbol;Acc:HGNC:6658]
120	ENSOARG00000010127	75.1646695	198.2115383	-1.3989	2.52E-16	3.24E-14	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like) [Source:HGNC Symbol;Acc:HGNC:2359]
121	ENSOARG00000010357	1.019412335	15.39725856	-3.9169	8.37E-05	0.0023567	PIWIL2	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PKY5]
122	ENSOARG00000010614	187.0961439	82.54432761	1.1805	5.49E-09	3.80E-07	MCM6	minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:HGNC:6949]
123	ENSOARG00000010629	76.59184677	29.96832276	1.3538	2.57E-05	0.00083715	POLE	polymerase (DNA directed), epsilon, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:9177]
124	ENSOARG00000010690	301.7460511	642.6289964	-1.0907	2.80E-35	1.07E-32		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PLZ5]
125	ENSOARG00000010719	29.29111442	5.633143376	2.3785	6.89E-05	0.0019783	LPL	Ovis aries lipoprotein lipase (LPL), mRNA. [Source:RefSeq mRNA;Acc:NM_001009394]
126	ENSOARG00000010723	73.05788401	153.6721513	-1.0727	2.12E-09	1.55E-07	WDR19	WD repeat domain 19 [Source:HGNC Symbol;Acc:HGNC:18340]
127	ENSOARG00000010762	11.5533398	38.08004922	-1.7207	3.80E-05	0.0011789		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PM69]
128	ENSOARG00000010776	7.88345539	52.12535337	-2.7251	3.68E-10	2.99E-08		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PM86]
129	ENSOARG00000010904	18.89310861	62.18990287	-1.7188	1.44E-07	7.88E-06	CCDC64	coiled-coil domain containing 64 [Source:HGNC Symbol;Acc:HGNC:28095]
130	ENSOARG00000010930	34.59205857	3.304777447	3.3878	1.53E-07	8.33E-06	CDCP1	CUB domain containing protein 1 [Source:HGNC Symbol;Acc:HGNC:24357]
131	ENSOARG00000010958	70.6112944	27.4146311	1.365	4.71E-05	0.0014166	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 [Source:HGNC Symbol;Acc:HGNC:20663]
132	ENSOARG00000010962	18.82514779	80.8168303	-2.102	1.16E-11	1.09E-09	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9 [Source:HGNC Symbol;Acc:HGNC:13202]
133	ENSOARG00000011014	2.582511249	28.84169409	-3.4813	2.24E-07	1.18E-05	RGS4	Ovis aries regulator of G-protein signaling 4 (RGS4), mRNA. [Source:RefSeq mRNA;Acc:NM_001174111]
134	ENSOARG00000011057	304.6004057	705.8704193	-1.2125	1.44E-44	6.94E-42		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PN27]
135	ENSOARG00000011235	72.85400154	23.43387645	1.6364	1.59E-06	6.98E-05		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PNM3]
136	ENSOARG00000011286	126.9508161	52.65111342	1.2697	2.97E-07	1.50E-05	ABHD2	abhydrolase domain containing 2 [Source:HGNC Symbol;Acc:HGNC:18717]
137	ENSOARG00000011408	38.12602133	81.41769893	-1.0946	9.77E-06	0.00035649	FRY	furry homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:20367]
138	ENSOARG00000011444	126.4750904	498.044983	-1.9774	2.41E-59	2.20E-56	ADM	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]

139	ENSOARG00000011501	25.34938673	3.004343134	3.0768	1.77E-05	0.00060161	GRIK2	glutamate receptor, ionotropic, kainate 2 [Source:HGNC Symbol;Acc:HGNC:4580]
140	ENSOARG00000011565	91.06750192	36.12722619	1.3338	5.87E-06	0.00022345	LIG1	ligase I, DNA, ATP-dependent [Source:HGNC Symbol;Acc:HGNC:6598]
141	ENSOARG00000011840	145.4361598	45.59090706	1.6736	5.13E-12	4.99E-10	ISYNA1	inositol-3-phosphate synthase 1 [Source:HGNC Symbol;Acc:HGNC:29821]
142	ENSOARG00000011869	179.7563751	82.46921903	1.1241	4.58E-08	2.78E-06	AMACR	alpha-methylacyl-CoA racemase [Source:HGNC Symbol;Acc:HGNC:451]
143	ENSOARG00000011895	43.49492629	117.0942736	-1.4288	1.67E-10	1.39E-08	MOSPD2	motile sperm domain containing 2 [Source:HGNC Symbol;Acc:HGNC:28381]
144	ENSOARG00000012051	25.5532692	60.46240557	-1.2425	3.06E-05	0.00097344	MTUS2	microtubule associated tumor suppressor candidate 2 [Source:HGNC Symbol;Acc:HGNC:20595]
145	ENSOARG00000012108	40.91241504	99.51886631	-1.2824	4.54E-08	2.77E-06	ACTB	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PRA1]
146	ENSOARG00000012147	82.23259502	32.9726659	1.3184	2.02E-05	0.00067746	NPR3	natriuretic peptide receptor 3 [Source:HGNC Symbol;Acc:HGNC:7945]
147	ENSOARG00000012206	0	22.5325735	-5.4939	4.72E-07	2.28E-05	CA5A	carbonic anhydrase VA, mitochondrial [Source:HGNC Symbol;Acc:HGNC:1377]
148	ENSOARG00000012362	271.1636811	105.6026612	1.3605	1.82E-15	2.24E-13	TC2N	tandem C2 domains, nuclear [Source:HGNC Symbol;Acc:HGNC:19859]
149	ENSOARG00000012451	108.3295508	53.10176489	1.0286	9.35E-05	0.0026091	GMPPB	GDP-mannose pyrophosphorylase B [Source:HGNC Symbol;Acc:HGNC:22932]
150	ENSOARG00000012475	58.92203296	18.92736174	1.6383	1.56E-05	0.00053993	ABHD6	abhydrolase domain containing 6 [Source:HGNC Symbol;Acc:HGNC:21398]
151	ENSOARG00000012531	846.0442772	397.5497052	1.0896	9.67E-31	2.90E-28	HYOU1	hypoxia up-regulated 1 [Source:HGNC Symbol;Acc:HGNC:16931]
152	ENSOARG00000012666	29.69887936	62.64055434	-1.0767	0.00012642	0.0033936	JARID2	jumonji, AT rich interactive domain 2 [Source:HGNC Symbol;Acc:HGNC:6196]
153	ENSOARG00000012784	23.71832699	2.478583086	3.2584	1.96E-05	0.00065811	HTRA3	Htra serine peptidase 3 [Source:HGNC Symbol;Acc:HGNC:30406]
154	ENSOARG00000012797	140.4750198	55.65545656	1.3357	1.76E-08	1.13E-06	MCM4	minichromosome maintenance complex component 4 [Source:HGNC Symbol;Acc:HGNC:6947]
155	ENSOARG00000012855	1157.304843	484.2250046	1.257	3.90E-53	2.74E-50	ST3GAL4	Ovis aries ST3 beta-galactoside alpha-2,3-sialyltransferase 4 (ST3GAL4), mRNA. [Source:RefSeq mRNA;Acc:NM_001112818]
156	ENSOARG00000012909	88.5529515	30.34386565	1.5451	4.34E-07	2.11E-05	HK2	hexokinase 2 [Source:HGNC Symbol;Acc:HGNC:4923]
157	ENSOARG00000012928	1196.314355	559.1082572	1.0974	2.58E-43	1.21E-40	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) [Source:HGNC Symbol;Acc:HGNC:5238]
158	ENSOARG00000013108	97.3878584	36.87831197	1.401	1.03E-06	4.65E-05	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10 [Source:HGNC Symbol;Acc:HGNC:15559]
159	ENSOARG00000013111	1.019412335	141.8049959	-7.12	9.22E-35	3.31E-32	IL1RL1	interleukin 1 receptor-like 1 [Source:HGNC Symbol;Acc:HGNC:5998]
160	ENSOARG00000013172	22.56299301	67.67282909	-1.5846	1.94E-07	1.03E-05	WDR73	WD repeat domain 73 [Source:HGNC Symbol;Acc:HGNC:25928]
161	ENSOARG00000013611	460.5704929	219.9179174	1.0665	7.73E-17	1.05E-14	JAM3	junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:HGNC:15532]
162	ENSOARG00000013683	100.1742521	47.84416441	1.0661	0.00010207	0.0028143	LMNB2	lamin B2 [Source:HGNC Symbol;Acc:HGNC:6638]
163	ENSOARG00000013756	51.65022497	107.7057014	-1.0602	6.65E-07	3.11E-05	ARHGAP12	Rho GTPase activating protein 12 [Source:HGNC Symbol;Acc:HGNC:16348]
164	ENSOARG00000013771	316.1537455	143.1569503	1.143	1.81E-13	1.92E-11	L3MBTL3	l(3)mbl-like 3 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:23035]
165	ENSOARG00000014063	50.56285181	14.49595562	1.8024	1.64E-05	0.00056391	CDC6	cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
166	ENSOARG00000014126	188.183517	92.00800848	1.0323	2.38E-07	1.25E-05	HMMR	hyaluronan-mediated motility receptor (RHAMM) [Source:HGNC Symbol;Acc:HGNC:5012]
167	ENSOARG00000014143	191.5135973	65.41957174	1.5497	9.38E-14	1.01E-11	MCM3	minichromosome maintenance complex component 3 [Source:HGNC Symbol;Acc:HGNC:6945]
168	ENSOARG00000014176	120.0867731	59.71131979	1.008	5.45E-05	0.0016069	CCNA2	cyclin A2 [Source:HGNC Symbol;Acc:HGNC:1578]
169	ENSOARG00000014188	99.35872225	33.87396884	1.5525	7.73E-08	4.53E-06	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1 [Source:HGNC Symbol;Acc:HGNC:3356]
170	ENSOARG00000014240	88.41702985	37.85472349	1.2239	3.47E-05	0.001091	CTGF	connective tissue growth factor precursor [Source:RefSeq peptide;Acc:NP_001158186]
171	ENSOARG00000014510	16.85428394	46.04155853	-1.4498	5.20E-05	0.0015494	SLC18B1	solute carrier family 18, subfamily B, member 1 [Source:HGNC Symbol;Acc:HGNC:21573]
172	ENSOARG00000014562	908.2963905	429.9215025	1.0791	2.53E-32	8.40E-30	MKI67	marker of proliferation Ki-67 [Source:HGNC Symbol;Acc:HGNC:7107]
173	ENSOARG00000014627	25.89307331	61.36370851	-1.2448	2.60E-05	0.00084266	SNX16	sorting nexin 16 [Source:HGNC Symbol;Acc:HGNC:14980]
174	ENSOARG00000014674	1968.757062	834.6816312	1.238	8.04E-87	1.13E-83	SCD	Ovis aries stearoyl-CoA desaturase (delta-9-desaturase) (SCD), mRNA. [Source:RefSeq mRNA;Acc:NM_001009254]
175	ENSOARG00000014718	26.50472071	1.80260588	3.8781	1.22E-06	5.47E-05	COL6A6	collagen, type VI, alpha 6 [Source:HGNC Symbol;Acc:HGNC:27023]
176	ENSOARG00000014740	43.01920054	104.3258153	-1.278	2.33E-08	1.48E-06	STAMBPL1	STAM binding protein-like 1 [Source:HGNC Symbol;Acc:HGNC:24105]
177	ENSOARG00000014744	86.24228354	259.1997039	-1.5876	1.97E-24	4.28E-22	DHRS3	dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:HGNC:17693]
178	ENSOARG00000014764	37.99009968	128.435669	-1.7574	1.75E-14	2.04E-12	ZNF175	zinc finger protein 175 [Source:HGNC Symbol;Acc:HGNC:12964]
179	ENSOARG00000014849	129.669249	57.08251955	1.1837	1.14E-06	5.13E-05	NEDD9	neural precursor cell expressed, developmentally down-regulated 9 [Source:HGNC]
180	ENSOARG00000014858	106.7664519	41.68526098	1.3568	6.40E-07	3.01E-05	PBK	PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:18282]
181	ENSOARG00000014902	382.0757431	168.693867	1.1795	8.27E-17	1.10E-14		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5PZU9]
182	ENSOARG00000014971	45.46579014	8.787703667	2.3712	7.46E-07	3.43E-05	SERPINA14	Ovis aries serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 14 (SERPINA14), mRNA. [Source:RefSeq mRNA;Acc:NM_001009304]
183	ENSOARG00000015028	72.24235414	30.64429997	1.2372	0.00015756	0.0041204	DNAH9	dynein, axonemal, heavy chain 9 [Source:HGNC Symbol;Acc:HGNC:2953]
184	ENSOARG00000015035	37.99009968	85.92421363	-1.1774	1.71E-06	7.33E-05	PDE7B	phosphodiesterase 7B [Source:HGNC Symbol;Acc:HGNC:8792]
185	ENSOARG00000015133	73.26176647	149.4660709	-1.0287	1.00E-08	6.77E-07	CEP95	centrosomal protein 95kDa [Source:HGNC Symbol;Acc:HGNC:25141]

186	ENSOARG00000015263	387.1728048	144.5089047	1.4218	5.86E-23	1.16E-20	CTSB	Cathepsin B [Source:UniProtKB/TrEMBL;Acc:W5Q0Z2]
187	ENSOARG00000015285	20.72805081	49.34633598	-1.2514	0.00015358	0.0040279	TMTC2	transmembrane and tetratricopeptide repeat containing 2 [Source:HGNC Symbol;Acc:HGNC:25440]
188	ENSOARG00000015286	8.427141969	38.53070069	-2.1929	1.58E-06	6.94E-05	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A [Source:HGNC Symbol;Acc:HGNC:10723]
189	ENSOARG00000015333	257.8433599	74.5828183	1.7896	3.77E-22	7.17E-20	RRM2	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGNC:10452]
190	ENSOARG00000015347	496.5897288	231.5597471	1.1007	4.97E-19	7.90E-17	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source:HGNC Symbol;Acc:HGNC:6395]
191	ENSOARG00000015536	32.21342978	7.2855321	2.1446	9.72E-05	0.0027041	CEMP1	cell migration inducing protein, hyaluronan binding [Source:HGNC Symbol;Acc:HGNC:29213]
192	ENSOARG00000015588	250.2997086	124.9055658	1.0028	6.73E-09	4.59E-07	ATP6V1C2	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2 [Source:HGNC Symbol;Acc:HGNC:18264]
193	ENSOARG00000015633	59.87348447	19.30290464	1.6331	1.40E-05	0.00049221	FEN1	Ovis aries flap structure-specific endonuclease 1 (FEN1), mRNA. [Source:RefSeq mRNA;Acc:NM_001166196]
194	ENSOARG00000015835	62.59191737	17.80073307	1.814	1.46E-06	6.47E-05	SDF2L1	stromal cell-derived factor 2-like 1 [Source:HGNC Symbol;Acc:HGNC:10676]
195	ENSOARG00000015918	481.7742695	1378.843281	-1.517	2.00E-115	3.32E-112		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5Q300]
196	ENSOARG00000015964	123.552775	57.15762812	1.1121	7.19E-06	0.00026944		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5Q353]
197	ENSOARG00000016272	301.6780903	147.4381393	1.0329	5.91E-11	5.25E-09	GNB2	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5Q438]
198	ENSOARG00000016415	823.1414801	197.6857782	2.0579	9.61E-82	1.25E-78	CDO1	cysteine dioxygenase type 1 [Source:HGNC Symbol;Acc:HGNC:1795]
199	ENSOARG00000016418	116.2130062	57.00741097	1.0276	5.28E-05	0.0015682		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5Q4J3]
200	ENSOARG00000016448	333.551716	157.1271459	1.086	5.43E-13	5.61E-11	TFR2	transferrin receptor 2 [Source:HGNC Symbol;Acc:HGNC:11762]
201	ENSOARG00000016533	59.26183707	131.1395778	-1.1459	6.66E-09	4.56E-07	USP53	ubiquitin specific peptidase 53 [Source:HGNC Symbol;Acc:HGNC:29255]
202	ENSOARG00000016541	328.5226151	759.19751	-1.2085	1.37E-47	6.98E-45	CLK1	CDC-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
203	ENSOARG00000016846	0	20.42953331	-5.9098	1.63E-06	7.06E-05	SV2C	synaptic vesicle glycoprotein 2C [Source:HGNC Symbol;Acc:HGNC:30670]
204	ENSOARG00000016886	191.9893231	93.96083152	1.0309	1.87E-07	1.00E-05	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11 [Source:HGNC Symbol;Acc:HGNC:17422]
205	ENSOARG00000017047	27.9998588	74.05705825	-1.4032	5.19E-07	2.48E-05	ALDH1L2	aldehyde dehydrogenase 1 family, member L2 [Source:HGNC Symbol;Acc:HGNC:26777]
206	ENSOARG00000017123	18.75718696	197.7608868	-3.3982	3.57E-41	1.56E-38		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5Q6N3]
207	ENSOARG00000017129	67.41713575	153.5970427	-1.188	1.21E-10	1.03E-08	ZBED5	zinc finger, BED-type containing 5 [Source:HGNC Symbol;Acc:HGNC:30803]
208	ENSOARG00000017133	178.5330803	85.09801927	1.069	1.99E-07	1.06E-05	PCNA	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:HGNC:8729]
209	ENSOARG00000017339	267.4937967	542.2839357	-1.0195	2.08E-27	5.15E-25	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase [Source:HGNC Symbol;Acc:HGNC:8127]
210	ENSOARG00000017480	43.56288711	143.3071675	-1.7179	1.42E-15	1.78E-13	ELL2	elongation factor, RNA polymerase II, 2 [Source:HGNC Symbol;Acc:HGNC:17064]
211	ENSOARG00000017485	83.86365476	439.4602919	-2.3896	7.14E-65	6.87E-62	NRP1	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]
212	ENSOARG00000017529	15.01934174	41.30971809	-1.4597	0.000118	0.0032004	CRYBG3	beta-gamma crystallin domain containing 3 [Source:HGNC Symbol;Acc:HGNC:34427]
213	ENSOARG00000017599	24.39793522	68.49902345	-1.4893	5.02E-07	2.41E-05	PCSK1	proprotein convertase subtilisin/kexin type 1 [Source:HGNC Symbol;Acc:HGNC:8743]
214	ENSOARG00000017620	62.52395654	24.18496223	1.3703	0.00012192	0.0033013	DTYMK	deoxythymidylate kinase (thymidylate kinase) [Source:HGNC Symbol;Acc:HGNC:3061]
215	ENSOARG00000017639	682.5305387	272.4939223	1.3247	6.00E-35	2.19E-32	LDLR	low density lipoprotein receptor [Source:HGNC Symbol;Acc:HGNC:6547]
216	ENSOARG00000017739	25.34938673	3.530103182	2.8442	3.83E-05	0.0011855	CAPN6	calpain 6 [Source:HGNC Symbol;Acc:HGNC:1483]
217	ENSOARG00000017838	20.45620752	50.24763892	-1.2965	9.03E-05	0.0025246	AMPH	amphiphysin [Source:HGNC Symbol;Acc:HGNC:471]
218	ENSOARG00000017979	27.11636811	60.31218841	-1.1533	7.79E-05	0.0022089	NBEAL1	neurobeachin-like 1 [Source:HGNC Symbol;Acc:HGNC:20681]
219	ENSOARG00000017994	43.15512218	135.7963097	-1.6538	3.38E-14	3.78E-12	LNPEP	leucyl/cystinyl aminopeptidase [Source:HGNC Symbol;Acc:HGNC:6656]
220	ENSOARG00000018127	251.7268859	90.73116265	1.4722	2.63E-16	3.36E-14	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27 [Source:HGNC Symbol;Acc:HGNC:30290]
221	ENSOARG00000018142	304.464484	133.6932695	1.1873	7.54E-14	8.30E-12	LMNB1	lamin B1 [Source:HGNC Symbol;Acc:HGNC:6637]
222	ENSOARG00000018303	26.64064235	68.49902345	-1.3625	2.24E-06	9.21E-05		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5QAA3]
223	ENSOARG00000018305	37.24253064	103.5747295	-1.4756	8.17E-10	6.20E-08		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5QAA4]
224	ENSOARG00000018341	17.33000969	89.90496828	-2.3751	1.76E-14	2.04E-12	MT1A	Metallothionein-1A [Source:UniProtKB/Swiss-Prot;Acc:P67982]
225	ENSOARG00000018385	250.7074736	110.3345016	1.1841	1.29E-11	1.21E-09	PMM1	phosphomannomutase 1 [Source:HGNC Symbol;Acc:HGNC:9114]
226	ENSOARG00000018527	122.4654018	39.05646074	1.6487	3.86E-10	3.10E-08	MCM5	minichromosome maintenance complex component 5 [Source:HGNC Symbol;Acc:HGNC:6948]
227	ENSOARG00000018670	20.45620752	1.201737254	4.0893	1.42E-05	0.00049863	FGL2	fibrinogen-like 2 [Source:HGNC Symbol;Acc:HGNC:3696]
228	ENSOARG00000018796	2.03882467	26.13778527	-3.6803	5.00E-07	2.41E-05		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5QBU5]
229	ENSOARG00000018832	179.6204534	86.52508226	1.0538	2.65E-07	1.37E-05	IL4R	interleukin 4 receptor [Source:HGNC Symbol;Acc:HGNC:6015]
230	ENSOARG00000018879	125.3877172	62.26501145	1.0099	3.62E-05	0.0011317		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5QC30]
231	ENSOARG00000018882	637.7443568	257.4722066	1.3086	4.10E-32	1.29E-29	PDIA4	protein disulfide isomerase family A, member 4 [Source:HGNC Symbol;Acc:HGNC:30167]
232	ENSOARG00000018889	114.7178681	229.9824669	-1.0034	2.92E-12	2.90E-10	ANTXR2	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:HGNC:21732]
233	ENSOARG00000018942	6.932003878	70.52695507	-3.3468	1.48E-15	1.84E-13	CXorf57	chromosome X open reading frame 57 [Source:HGNC Symbol;Acc:HGNC:25486]

234	ENSOARG00000019211	213.6008646	471.5316549	-1.1424	5.10E-28	1.31E-25	KANSL2	KAT8 regulatory NSL complex subunit 2 [Source:HGNC Symbol;Acc:HGNC:26024]
235	ENSOARG00000019338	20.79601163	53.55241636	-1.3646	2.82E-05	0.00090785	IFT172	intraflagellar transport 172 [Source:HGNC Symbol;Acc:HGNC:30391]
236	ENSOARG00000019361	13.45624282	0	5.4851	0.00018808	0.0048629		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:W5QDK1]
237	ENSOARG00000019402	77.33941581	214.8105341	-1.4738	9.79E-19	1.50E-16	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:27281]
238	ENSOARG00000019483	29.97072265	71.50336659	-1.2545	5.01E-06	0.00019322	FOSL2	FOS-like antigen 2 [Source:HGNC Symbol;Acc:HGNC:3798]
239	ENSOARG00000019542	108.1256683	53.17687347	1.0238	0.00010186	0.0028126	CLSPN	claspin [Source:HGNC Symbol;Acc:HGNC:19715]
240	ENSOARG00000019622	75.36855196	201.2158814	-1.4167	8.24E-17	1.10E-14	NELL2	NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:HGNC:7751]
241	ENSOARG00000019646	182.5427688	74.88325261	1.2855	5.20E-10	4.07E-08	CRELD2	cysteine-rich with EGF-like domains 2 [Source:HGNC Symbol;Acc:HGNC:28150]
242	ENSOARG00000019718	14.67953762	52.0502448	-1.8261	5.71E-07	2.70E-05	PRKAG3	Ovis aries protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA. [Source:RefSeq mRNA;Acc:NM_001122692]
243	ENSOARG00000019974	35.20370597	107.5554842	-1.6113	3.25E-11	2.95E-09	TSPYL4	TSPY-like 4 [Source:HGNC Symbol;Acc:HGNC:21559]
244	ENSOARG00000020058	167.931192	337.913494	-1.0088	1.97E-17	2.79E-15	THBS1	thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
245	ENSOARG00000020187	114.5139856	269.4895791	-1.2347	1.89E-18	2.85E-16	RLF	rearranged L-myc fusion [Source:HGNC Symbol;Acc:HGNC:10025]
246	ENSOARG00000020343	131.8439953	371.3368114	-1.4939	9.35E-32	2.85E-29	RECQL	RecQ helicase-like [Source:HGNC Symbol;Acc:HGNC:9948]
247	ENSOARG00000020431	171.6690372	26.43821958	2.6989	2.36E-25	5.27E-23	REG4	regenerating islet-derived family, member 4 [Source:HGNC Symbol;Acc:HGNC:22977]
248	ENSOARG00000020530	175.6107649	74.80814404	1.2311	4.46E-09	3.15E-07	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11 [Source:HGNC Symbol;Acc:HGNC:14889]
249	ENSOARG00000020542	186.8243006	84.34693349	1.1473	1.36E-08	8.94E-07	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723]
250	ENSOARG00000020582	121.3780287	49.04590166	1.3073	2.73E-07	1.41E-05	MGST1	microsomal glutathione S-transferase 1 [Source:HGNC Symbol;Acc:HGNC:7061]
251	ENSOARG00000020648	89.23255972	183.4902569	-1.0401	1.56E-10	1.31E-08	KLHL24	kelch-like family member 24 [Source:HGNC Symbol;Acc:HGNC:25947]
252	ENSOARG00000020756	740.7050026	288.2667237	1.3615	1.60E-39	6.64E-37	PLD1	phospholipase D1, phosphatidylcholine-specific [Source:HGNC Symbol;Acc:HGNC:9067]
253	ENSOARG00000020839	41.25221915	95.23767735	-1.2071	2.94E-07	1.49E-05	RNF111	ring finger protein 111 [Source:HGNC Symbol;Acc:HGNC:17384]
254	ENSOARG00000020892	601.6571601	250.1115659	1.2664	8.60E-29	2.35E-26	SLC20A1	solute carrier family 20 (phosphate transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:10946]
255	ENSOARG00000020902	102.6208417	271.9681622	-1.4061	5.82E-22	1.08E-19	FAM63A	family with sequence similarity 63, member A [Source:HGNC Symbol;Acc:HGNC:25648]
256	ENSOARG00000020976	250.7074736	123.8540457	1.0174	4.05E-09	2.87E-07	GLDN	gliomedin [Source:HGNC Symbol;Acc:HGNC:29514]
257	ENSOARG00000020977	2613.773227	1032.367409	1.3402	2.01E-131	4.59E-128	CYP19A1	Ovis aries cytochrome P450, family 19 (CYP19), mRNA. [Source:RefSeq mRNA;Acc:NM_001123000]
258	ENSOARG00000021009	73.05788401	279.3288029	-1.9349	3.30E-33	1.12E-30	GABARAPL1	GABA(A) receptor-associated protein like 1 [Source:HGNC Symbol;Acc:HGNC:4068]
259	ENSOARG00000021011	2.378628782	45.4406899	-4.2558	4.91E-12	4.80E-10	TMEM52B	transmembrane protein 52B [Source:HGNC Symbol;Acc:HGNC:26438]
260	ENSOARG00000021020	2.310667959	25.16137375	-3.4448	1.45E-06	6.46E-05	CLEC1B	C-type lectin domain family 1, member B [Source:HGNC Symbol;Acc:HGNC:24356]
261	ENSOARG00000021032	240.5813111	119.7230739	1.0068	1.16E-08	7.77E-07	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D [Source:HGNC Symbol;Acc:HGNC:16770]
262	ENSOARG00000021738	45.80559425	94.48659156	-1.0446	4.09E-06	0.0001623		
263	ENSOARG00000024483	153.7953409	335.8104538	-1.1266	4.77E-20	8.15E-18		
264	ENSOARG00000025169	141.154628	47.91927299	1.5586	1.32E-10	1.11E-08	CYCS	Cytochrome c [Source:UniProtKB/Swiss-Prot;Acc:P62896]
265	Novel00015	14.40769433	74.80814404	-2.3764	2.64E-12	2.64E-10	-/-	
266	Novel00031	29.08723196	64.44316022	-1.1476	4.71E-05	0.0014166	-/-	
267	Novel00041	41.18425833	116.0427536	-1.4945	5.51E-11	4.91E-09	-/-	
268	Novel00052	128.6498367	290.5199811	-1.1752	1.52E-18	2.32E-16	-/-	
269	Novel00120	13.45624282	42.96210682	-1.6748	1.71E-05	0.0005824	-/-	
270	Novel00138	24.60181768	61.66414282	-1.3257	1.06E-05	0.00038465	-/-	
271	Novel00145	17.87369627	59.78642837	-1.742	1.97E-07	1.05E-05	-/-	
272	Novel00248	15.49506749	51.44937617	-1.7313	1.53E-06	6.78E-05	-/-	
273	Novel00506	0	15.47236714	-5.8308	2.99E-05	0.00095613	-/-	
274	Novel00511	16.65040147	63.09120581	-1.9219	1.33E-08	8.84E-07	-/-	
275	Novel00532	13.59216447	46.19177568	-1.7649	4.01E-06	0.00015943	-/-	
276	Novel00544	131.1643871	415.2753297	-1.6627	2.09E-40	8.87E-38	-/-	
277	Novel00562	2227.415952	4860.426322	-1.1257	4.20E-267	1.92E-263	-/-	
278	Novel00568	17.46593134	227.5038838	-3.7033	6.03E-50	3.67E-47	-/-	
279	Novel00595	1.563098914	15.84791003	-3.3418	0.00015688	0.0041086	-/-	
280	Novel00608	0	152.8459569	-8.2559	7.00E-34	2.41E-31	-/-	

281	Novel00609	0	108.6821129	-7.764	9.89E-26	2.29E-23	-/-
282	Novel00669	39.68912024	98.39223764	-1.3098	3.43E-08	2.14E-06	-/-
283	Novel00678	77.6112591	29.8181056	1.3801	1.66E-05	0.00056594	-/-
284	Novel00701	41.25221915	137.3735898	-1.7356	3.62E-15	4.41E-13	-/-
285	Novel00712	3.466001939	27.71506541	-2.9993	1.77E-06	7.54E-05	-/-
286	Novel00719	3327.090018	1545.734542	1.106	5.07E-119	1.03E-115	-/-
287	Novel00720	111.319827	51.74981048	1.1051	2.28E-05	0.00075805	-/-
288	Novel00763	28.81538867	99.96951778	-1.7946	7.12E-12	6.85E-10	-/-
289	Novel00815	10.60188828	45.74112421	-2.1092	3.14E-07	1.57E-05	-/-
290	Novel00838	81.41706515	253.3412348	-1.6377	7.67E-25	1.69E-22	-/-
291	Novel00860	36.35903995	105.1520097	-1.5321	2.22E-10	1.82E-08	-/-
292	Novel00913	377.1146031	158.9297518	1.2466	3.54E-18	5.26E-16	-/-
293	Novel00945	60.96085763	163.9620265	-1.4274	4.16E-14	4.64E-12	-/-
294	Novel01020	423.8036881	1298.702428	-1.6156	4.26E-118	7.79E-115	-/-
295	Novel01053	24.46589604	67.97326341	-1.4742	6.63E-07	3.11E-05	-/-
296	Novel01094	4.145610162	26.81376247	-2.6933	7.86E-06	0.00029018	-/-
297	Novel01095	4.621335918	47.76905583	-3.3697	4.59E-11	4.14E-09	-/-
298	Novel01096	7.611612101	61.96457714	-3.0252	7.37E-13	7.53E-11	-/-
299	Novel01169	3.737845228	35.97700903	-3.2668	1.66E-08	1.07E-06	-/-
300	Novel01183	19.91252094	54.37861073	-1.4494	1.10E-05	0.00039833	-/-
301	Novel01229	82.70832078	170.4964729	-1.0436	6.24E-10	4.86E-08	-/-
302	Novel01263	118.0479484	273.0947909	-1.21	3.38E-18	5.07E-16	-/-
303	Novel01321	121.5819111	262.7298071	-1.1117	9.52E-16	1.20E-13	-/-
304	Novel01341	34.9998235	106.2786384	-1.6024	4.98E-11	4.46E-09	-/-
305	Novel01366	3.601923584	34.17440315	-3.2461	4.08E-08	2.51E-06	-/-
306	Novel01405	20.9998941	108.2314614	-2.3657	4.70E-17	6.55E-15	-/-
307	Novel01439	401.4445775	194.3058922	1.0469	2.05E-14	2.35E-12	-/-
308	Novel01445	119.8828906	285.3374891	-1.251	8.93E-20	1.45E-17	-/-
309	Novel01581	67.34917493	149.7665052	-1.153	4.83E-10	3.81E-08	-/-
310	Novel01585	47.43665399	98.91799769	-1.0602	1.90E-06	8.01E-05	-/-
311	Novel01623	37.85417804	84.42204206	-1.1572	2.80E-06	0.00011384	-/-

Table S4. GO analysis of the differentially expressed genes.

GO_accession	Description	Term_type	Over_represented_pValue	Corrected_pValue	DEG_item	DEG_list	Bg_item	Bg_list	Up	Up_Gene_names	Down	Down_Gene_names	
1	GO:0006260	DNA replication	biological_process	3.43E-07	0.0014066	36	257	624	17434	14	ENSOARG00000010629, ENSOARG0000001301, ENSOARG00000013771, ENSOARG00000010614, ENSOARG00000018142, ENSOARG00000006261, ENSOARG0000014143, ENSOARG0000012797, ENSOARG0000004318, ENSOARG00000006991, Novel 01439, ENSOARG0000017133, ENSOARG0000012475, ENSOARG00000018527	22	ENSOARG00000010690, Novel 01020, Novel 00701, Novel 01095, ENSOARG0000009485, ENSOARG00000002703, Novel 00608, Novel 01366, Novel 01445, ENSOARG0000001199, ENSOARG0000002223, ENSOARG00000003737, Novel 00945, Novel 00595, Novel 00145, Novel 00609, ENSOARG0000018305, Novel 00568, Novel 00562, Novel 00120, ENSOARG0000009959, ENSOARG00000020343, Novel 00145, Novel 00609, Novel 00701, Novel 01020, Novel 00595, Novel 00945, ENSOARG00000003737, ENSOARG0000010690, ENSOARG0000002223, ENSOARG0000001199, Novel 00120, Novel 00562, ENSOARG0000009959, Novel 01366, Novel 01445, Novel 00568, Novel 00608, Novel 01095, ENSOARG0000002703, ENSOARG0000018305, Novel 01095, Novel 00608, ENSOARG0000002703, ENSOARG0000018305, Novel 00568, Novel 00562, Novel 00120, ENSOARG0000009959, Novel 01445, Novel 010366, ENSOARG0000001199, ENSOARG0000010690, ENSOARG00000003737, Novel 01020, Novel 00945, Novel 00595, Novel 00145, Novel 00701, Novel 00609
2	GO:0003964	RNA-directed DNA polymerase activity	molecular_function	6.30E-05	0.089755	24	257	362	17434	4	ENSOARG00000004318, ENSOARG0000018142, Novel 01439, ENSOARG0000012475	20	Novel 01439, ENSOARG0000012475, ENSOARG0000018142, ENSOARG0000004318
3	GO:0006278	RNA-dependent DNA replication	biological_process	6.56E-05	0.089755	24	257	364	17434	4	Novel 01439, ENSOARG0000012475, ENSOARG0000018142, ENSOARG0000004318	20	Novel 00608, Novel 01095, ENSOARG0000002703, ENSOARG0000009485, Novel 01366, Novel 01445, ENSOARG0000001199, ENSOARG0000010690, ENSOARG0000001672, Novel 01020, ENSOARG0000020187, Novel 00701, ENSOARG00000018305, Novel 00568, ENSOARG0000009959, Novel 00562, Novel 00120, ENSOARG0000020343, ENSOARG0000002223, ENSOARG0000019974, ENSOARG0000011014, ENSOARG00000003737, Novel 00595, Novel 00945, Novel 00609, Novel 00145
4	GO:0006259	DNA metabolic process	biological_process	0.00010484	0.10759	45	257	1245	17434	19	ENSOARG0000001301, ENSOARG0000019361, ENSOARG0000013771, ENSOARG00000010614, ENSOARG0000018142, ENSOARG0000010629, ENSOARG0000011565, ENSOARG0000017133, ENSOARG0000012475, Novel 01439, ENSOARG00000005371, ENSOARG0000018527, ENSOARG0000009686, ENSOARG0000006261, ENSOARG0000015633, ENSOARG0000012797, ENSOARG0000014143, ENSOARG0000004318, ENSOARG0000006991	26	Novel 00120, Novel 00562, ENSOARG0000009959, Novel 01445, Novel 01366, ENSOARG0000001199, Novel 00608, Novel 01095, ENSOARG0000002703, ENSOARG0000018305, Novel 00609, Novel 01020, Novel 00945, Novel 00595, Novel 00945, Novel 00145, Novel 00701, Novel 00609, ENSOARG0000002223, ENSOARG0000010690, ENSOARG00000003737, Novel 01020, Novel 00945, Novel 00595, Novel 00145, Novel 00701, Novel 00609
5	GO:0034061	DNA polymerase activity	molecular_function	0.00018884	0.15503	25	257	433	17434	5	ENSOARG00000018142, Novel 01439, ENSOARG0000012475, ENSOARG0000004318, ENSOARG0000010629	20	Novel 00595, Novel 01020, Novel 00945, Novel 00860, Novel 00145, Novel 00701, Novel 00609, ENSOARG0000002223, ENSOARG0000010690, ENSOARG00000003737, Novel 00562, Novel 00120, ENSOARG0000009959, ENSOARG0000008408, Novel 01445, Novel 01366, ENSOARG0000001199, Novel 00608, Novel 01095, ENSOARG0000002703, ENSOARG00000005118, ENSOARG00000003591, Novel 00544, ENSOARG0000001672, Novel 01020, ENSOARG00000008050, ENSOARG0000021011, ENSOARG0000011057, ENSOARG0000009174, ENSOARG0000002210, ENSOARG0000001626, Novel 00568, Novel 00562, ENSOARG0000011057
6	GO:0016779	nucleotidyl transferase activity	molecular_function	0.0018935	1	29	257	710	17434	7	ENSOARG0000011565, ENSOARG0000004318, ENSOARG0000012451, ENSOARG0000010629, ENSOARG0000018142, Novel 01439, ENSOARG0000012475	22	ENSOARG0000001199, Novel 00608, Novel 01095, ENSOARG0000002703, ENSOARG0000018305, Novel 00568, Novel 01020, Novel 00595, Novel 00945, Novel 00145, Novel 00701, Novel 00609, ENSOARG0000002223, ENSOARG0000010690, ENSOARG0000003737
7	GO:0019012	virion	cellular_component	0.0034803	1	18	257	556	17434	4	ENSOARG0000010629, ENSOARG0000017639, ENSOARG0000018670, ENSOARG0000009704	14	Novel 00595, Novel 01020, Novel 00945, Novel 00860, Novel 00145, Novel 00701, Novel 00609, ENSOARG0000002223, ENSOARG0000010690, ENSOARG00000003737, Novel 00562, Novel 00120, ENSOARG0000009959, ENSOARG0000008408, Novel 01445, Novel 01366, ENSOARG0000001199, Novel 00608, Novel 01095, ENSOARG0000002703, ENSOARG0000018305, Novel 00568
8	GO:0016765	transferase activity, transferring alkyl or aryl (other than methyl) groups	molecular_function	0.003921	1	4	257	46	17434	1	ENSOARG0000004318	3	ENSOARG00000005118, ENSOARG0000003591, Novel 00544, ENSOARG0000001672, Novel 01020, ENSOARG00000008050, ENSOARG0000021011, ENSOARG0000011057, ENSOARG0000009174, ENSOARG0000002210, ENSOARG0000001626, Novel 00568, Novel 00562, ENSOARG0000011057
9	GO:0044423	virion part	cellular_component	0.0042386	1	17	257	531	17434	3	ENSOARG0000018670, ENSOARG0000017639, ENSOARG0000009704	14	ENSOARG00000018305, ENSOARG0000009959, Novel 00544
10	GO:0030269	tetrahydromethanopterin-S-methyltransferase activity	molecular_function	0.0068362	1	3	257	10	17434	0		3	ENSOARG00000021011, Novel 01020, ENSOARG00000008050, Novel 00544, ENSOARG0000001672, ENSOARG00000003591, ENSOARG00000005118, ENSOARG0000011057, Novel 00562, Novel 00568, ENSOARG0000001626, ENSOARG0000015918, ENSOARG0000002210, ENSOARG0000009174
11	GO:0042086	5-methyl-5,6,7,8-tetrahydromethanopterin-dependent methyltransferase activity	molecular_function	0.0068362	1	3	257	10	17434	0		3	ENSOARG0000003537, ENSOARG0000004162, Novel 00120
12	GO:0009061	anaerobic respiration	biological_process	0.010995	1	3	257	22	17434	0		3	Novel 00120, ENSOARG0000004162, ENSOARG00000003537
13	GO:0015947	methane metabolic process	biological_process	0.010995	1	3	257	22	17434	0		3	ENSOARG0000003537, ENSOARG0000010042, ENSOARG00000004162

14	G0:0015948	methanogenesis energy derivation by	biological_process	0.010995	1	3	257	22	17434	0		3	ENSOARG00000003537, ENSOARG00000004162, ENSOARG00000010042
15	G0:0015975	oxidation of reduced inorganic compounds	biological_process	0.010995	1	3	257	22	17434	0		3	ENSOARG00000003537, ENSOARG00000004162, ENSOARG00000010042
16	G0:0043446	cellular alkalane metabolic process	biological_process	0.010995	1	3	257	22	17434	0		3	ENSOARG00000004162, ENSOARG00000010042, ENSOARG00000003537
17	G0:0043447	alkane biosynthetic process	biological_process	0.010995	1	3	257	22	17434	0		3	ENSOARG00000003537, ENSOARG00000004162, ENSOARG00000010042
18	G0:0004615	phosphomannomutase activity	molecular_function	0.014465	1	1	257	2	17434	1	ENSOARG00000018385	0	
19	G0:0019307	mannose biosynthetic process	biological_process	0.014465	1	1	257	2	17434	1	ENSOARG00000018385	0	
20	G0:0033180	proton-transporting V-type ATPase, V1 domain	cellular_component	0.015654	1	3	257	32	17434	2	ENSOARG00000015347, ENSOARG00000015588	1	ENSOARG00000014510
21	G0:0004651	polynucleotide 5'-phosphatase activity	molecular_function	0.017847	1	1	257	1	17434	1	Novel 01439	0	
22	G0:0019204	nucleotide phosphatase activity	molecular_function	0.017847	1	1	257	1	17434	1	Novel 01439	0	
23	G0:0007610	behavior	biological_process	0.01794	1	3	257	24	17434	1	ENSOARG00000007779	2	Novel 01229, ENSOARG00000003591
24	G0:0018342	protein prenylation	biological_process	0.019153	1	2	257	16	17434	0		2	ENSOARG00000018305, ENSOARG00000009959
25	G0:0097354	prenylation	biological_process	0.019153	1	2	257	16	17434	0		2	ENSOARG00000018305, ENSOARG00000009959
26	G0:0008172	S-methyltransferase activity	molecular_function	0.019803	1	3	257	19	17434	0		3	ENSOARG00000003537, Novel 00120, ENSOARG00000004162
											ENSOARG00000015964, ENSOARG00000015347, ENSOARG00000018879, ENSOARG00000017133, ENSOARG0000001811, ENSOARG00000006991, ENSOARG0000007995, ENSOARG00000015588, ENSOARG00000015028, ENSOARG00000006261, ENSOARG0000000915, ENSOARG00000013683, ENSOARG00000018142, ENSOARG0000003547, ENSOARG00000007779, ENSOARG00000006495, ENSOARG00000002051, ENSOARG00000018670, ENSOARG00000004835	Novel 00562, ENSOARG00000003926, ENSOARG00000010723, Novel 00609, Novel 00860, Novel 00595, ENSOARG00000014510, ENSOARG00000009958, ENSOARG000019338, ENSOARG00000006246, ENSOARG00000001199, ENSOARG00000007251, ENSOARG00000008752, ENSOARG00000005499, Novel 01623, ENSOARG000000020839, ENSOARG00000002703, ENSOARG00000019483, ENSOARG00000003501, ENSOARG00000017480, ENSOARG00000020187, ENSOARG00000004429, ENSOARG00000008975	
27	G0:0043234	protein complex	cellular_component	0.020641	1	42	257	1827	17434	19		23	ENSOARG00000008752, ENSOARG00000005499, Novel 01623, ENSOARG000000020839, ENSOARG00000002703, ENSOARG00000019483, ENSOARG00000003501, ENSOARG00000017480, ENSOARG00000020187, ENSOARG00000004429, ENSOARG00000008975
28	G0:0008318	protein prenyltransferase activity	molecular_function	0.022335	1	2	257	17	17434	0		2	ENSOARG00000009959, ENSOARG00000018305
29	G0:0006013	mannose metabolic process	biological_process	0.022725	1	2	257	15	17434	1	ENSOARG00000018385	1	ENSOARG00000010776
30	G0:0006334	nucleosome assembly	biological_process	0.023848	1	3	257	54	17434	2	ENSOARG00000009686, ENSOARG00000019361	1	ENSOARG00000019974
31	G0:0031497	chromatin assembly	biological_process	0.023848	1	3	257	54	17434	2	ENSOARG00000019361, ENSOARG00000009686	1	ENSOARG00000019974
32	G0:0034728	nucleosome organization	biological_process	0.023848	1	3	257	54	17434	2	ENSOARG00000009686, ENSOARG00000019361	1	ENSOARG00000019974
33	G0:0004512	inositol-3-phosphate synthase activity	molecular_function	0.024627	1	1	257	2	17434	1	ENSOARG00000011840	0	
34	G0:0006021	inositol biosynthetic process	biological_process	0.024627	1	1	257	2	17434	1	ENSOARG00000011840	0	
35	G0:0016872	intramolecular lyase activity	molecular_function	0.024627	1	1	257	2	17434	1	ENSOARG00000011840	0	
36	G0:0046173	polyol biosynthetic process	biological_process	0.024627	1	1	257	2	17434	1	ENSOARG00000011840	0	
37	G0:0006333	chromatin assembly or disassembly	biological_process	0.026415	1	3	257	56	17434	2	ENSOARG00000009686, ENSOARG00000019361	1	ENSOARG00000019974
38	G0:0008373	sialyltransferase activity	molecular_function	0.026436	1	2	257	23	17434	2	ENSOARG00000012855, ENSOARG00000005371	0	
39	G0:0016851	magnesium chelatase activity	molecular_function	0.028076	1	5	257	67	17434	5	ENSOARG00000006991, ENSOARG00000010614, ENSOARG00000014143, ENSOARG00000012797, ENSOARG00000018527	0	
40	G0:0051002	ligase activity, forming nitrogen-metal bonds	molecular_function	0.028076	1	5	257	67	17434	5	ENSOARG00000006991, ENSOARG00000010614, ENSOARG00000014143, ENSOARG00000012797, ENSOARG00000018527	0	
41	G0:0051003	ligase activity, forming nitrogen-metal bonds, forming coordination complexes	molecular_function	0.028076	1	5	257	67	17434	5	ENSOARG00000014143, ENSOARG00000012797, ENSOARG00000018527, ENSOARG00000006991, ENSOARG00000010614	0	
42	G0:0006323	DNA packaging	biological_process	0.028236	1	4	257	72	17434	2	ENSOARG00000009686, ENSOARG00000019361	2	ENSOARG00000019974, Novel 01020
43	G0:0016879	ligase activity, forming carbon-nitrogen bonds	molecular_function	0.028395	1	11	257	307	17434	6	ENSOARG0000000345, ENSOARG00000006520, ENSOARG00000001369, ENSOARG00000004835, ENSOARG00000014849, ENSOARG000000005399	5	ENSOARG000000020839, ENSOARG000000007070, ENSOARG00000000117, ENSOARG00000011408, ENSOARG00000002455

44	G0:0016874	ligase activity	molecular_function	0.029354	1	17	257	554	17434	12	ENSOARG00000006520, ENSOARG00000001369, ENSOARG00000004835, ENSOARG000000014849, ENSOARG000000011565, ENSOARG00000006991, ENSOARG0000012797, ENSOARG000000014143, ENSOARG000000010614, ENSOARG00000000345, ENSOARG000000018527, ENSOARG000000005399	5	ENSOARG000000007070, ENSOARG000000020839, ENSOARG000000000117, ENSOARG0000011408, ENSOARG000000002455
45	G0:0009888	tissue development	biological_process	0.029944	1	2	257	21	17434	1	ENSOARG00000008116	1	ENSOARG000000020839
46	G0:0033644	host cell membrane	cellular_component	0.030075	1	3	257	42	17434	0		3	ENSOARG00000009174, Novel 00669, ENSOARG000000004403
47	G0:0044218	other organism cell membrane	cellular_component	0.030075	1	3	257	42	17434	0		3	ENSOARG00000004403, Novel 00669, ENSOARG000000009174
48	G0:0044279	other organism membrane	cellular_component	0.030075	1	3	257	42	17434	0		3	Novel 00669, ENSOARG00000009174, ENSOARG000000004403
49	G0:0006534	cysteine metabolic process	biological_process	0.030419	1	1	257	4	17434	1	ENSOARG000000016415	0	
50	G0:0017172	cysteine dioxygenase activity	molecular_function	0.030419	1	1	257	4	17434	1	ENSOARG000000016415	0	
51	G0:0046439	L-cysteine metabolic process	biological_process	0.030419	1	1	257	4	17434	1	ENSOARG000000016415	0	
52	G0:0015833	peptide transport	biological_process	0.030475	1	1	257	2	17434	1	ENSOARG00000002225	0	
53	G0:0003824	catalytic activity	molecular_function	0.030687	1	132	257	6975	17434	73	ENSOARG000000010629, ENSOARG00000007049, ENSOARG000000008420, ENSOARG000000012855, ENSOARG00000002051, ENSOARG00000009887, ENSOARG0000007779, ENSOARG00000001908, ENSOARG000000014562, ENSOARG000000015263, ENSOARG000000012797, ENSOARG000000017739, ENSOARG000000000345, ENSOARG000000010048, Novel 00719, ENSOARG000000018527, ENSOARG00000006209, ENSOARG000000025169, ENSOARG000000005706, ENSOARG000000005888, ENSOARG000000018882, ENSOARG000000013771, ENSOARG000000018385, ENSOARG000000012909, ENSOARG00000004495, ENSOARG000000014188, ENSOARG000000020756, ENSOARG000000018142, ENSOARG000000018127, ENSOARG000000012784, ENSOARG00000006991, ENSOARG000000014143, ENSOARG000000015347, ENSOARG000000014718, ENSOARG000000018879, ENSOARG000000005371, ENSOARG000000012475, ENSOARG000000014858, ENSOARG000000000683, ENSOARG000000012928, ENSOARG00000009686, ENSOARG000000020977, ENSOARG00000004835, ENSOARG000000011565, ENSOARG000000011286, ENSOARG000000010614, ENSOARG00000006460, ENSOARG000000011869, ENSOARG000000013683, ENSOARG000000015633, ENSOARG000000011840, ENSOARG000000001369, ENSOARG000000014063, Novel 01439, ENSOARG000000005456, ENSOARG00000009152, ENSOARG000000011235, ENSOARG000000016448, ENSOARG000000012797, ENSOARG000000018527, ENSOARG000000014143, ENSOARG000000010614, ENSOARG00000006991	59	ENSOARG000000016541, Novel 01020, ENSOARG000000010776, ENSOARG000000020839, ENSOARG000000004162, ENSOARG00000002703, ENSOARG00000009485, ENSOARG000000006246, ENSOARG000000019338, Novel 01445, ENSOARG000000016846, ENSOARG000000014740, ENSOARG000000003737, ENSOARG000000002223, Novel 00945, ENSOARG000000018305, ENSOARG000000018796, Novel 00562, ENSOARG000000020343, ENSOARG00000003554, ENSOARG000000015285, ENSOARG000000010690, Novel 00701, Novel 00041, Novel 01095, ENSOARG000000000908, ENSOARG000000001199, ENSOARG000000011014, ENSOARG000000016533, ENSOARG000000017994, ENSOARG000000007070, ENSOARG000000011408, ENSOARG000000009959, ENSOARG000000003591, ENSOARG000000014744, ENSOARG000000000117, Novel 00608, ENSOARG00000008408, ENSOARG000000002455, ENSOARG000000017838, Novel 00145, Novel 00860, Novel 00595, ENSOARG00000003537, Novel 00568, ENSOARG000000001626, Novel 00138, ENSOARG000000015035, ENSOARG000000008975, ENSOARG000000005118, ENSOARG000000010962, ENSOARG000000017047, Novel 01366, Novel 00544, ENSOARG000000014510, Novel 00609, ENSOARG000000017599, ENSOARG000000014764, Novel 00120
54	G0:0015995	chlorophyll biosynthetic process	biological_process	0.031831	1	5	257	71	17434	5	ENSOARG000000013683, ENSOARG000000018142, ENSOARG000000010629, ENSOARG000000018882, ENSOARG000000016448	0	
55	G0:0009186	deoxyribonucleoside diphosphate metabolic process	biological_process	0.032028	1	1	257	2	17434	1	ENSOARG000000015333	0	
56	G0:0004659	prenyltransferase activity	molecular_function	0.03225	1	2	257	22	17434	0		2	ENSOARG000000018305, ENSOARG000000009959
57	G0:0006020	inositol metabolic process	biological_process	0.032461	1	1	257	3	17434	1	ENSOARG000000011840	0	
58	G0:0033176	proton-transporting V-type ATPase complex	cellular_component	0.033312	1	5	257	128	17434	2	ENSOARG000000015588, ENSOARG000000015347	3	ENSOARG000000014510, ENSOARG000000019483, ENSOARG000000004429
59	G0:0047800	cysteine dioxygenase activity	molecular_function	0.03385	1	1	257	3	17434	1	ENSOARG000000016415	0	
60	G0:0005198	structural molecule activity	molecular_function	0.033961	1	24	257	1104	17434	5	ENSOARG000000013683, ENSOARG000000018142, ENSOARG000000010629, ENSOARG000000018882, ENSOARG000000016448	19	Novel 00568, ENSOARG000000015918, ENSOARG000000010723, ENSOARG000000002210, ENSOARG000000009174, ENSOARG000000011057, ENSOARG000000019338, ENSOARG000000009958, ENSOARG00000006246, Novel 00562, ENSOARG000000001672, Novel 00544, ENSOARG000000003591, ENSOARG000000010762, ENSOARG000000008975, ENSOARG000000011895, Novel 00145, Novel 00609, Novel 01020
61	G0:0033013	tetrapyrrole metabolic process	biological_process	0.035191	1	7	257	157	17434	6	ENSOARG000000010614, ENSOARG00000006991, ENSOARG000000012797, ENSOARG000000018527, ENSOARG00000006209, ENSOARG000000014143	1	Novel 00544
62	G0:0008521	acetyl-CoA transporter activity	molecular_function	0.035636	1	1	257	2	17434	0		1	ENSOARG000000004140
63	G0:0051185	coenzyme transporter activity	molecular_function	0.035636	1	1	257	2	17434	0		1	ENSOARG000000004140
64	G0:0004418	hydroxymethylblane synthase activity	molecular_function	0.036915	1	1	257	2	17434	0		1	Novel 00544

65	G0:0016043	cellular component organization	biological_process	0.038992	1	26	257	1114	17434	14	ENSOARG00000018879, ENSOARG00000019361, ENSOARG00000017133, ENSOARG00000015964, ENSOARG00000009686, ENSOARG00000014562, ENSOARG00000012928, ENSOARG0000001504, ENSOARG00000007049, ENSOARG00000006991, ENSOARG00000018670, ENSOARG00000012531, ENSOARG00000000251, ENSOARG00000012797	Novel 00568, ENSOARG00000002210, Novel 01169, ENSOARG00000001199, ENSOARG00000009469, Novel 01445, ENSOARG000000021009, ENSOARG00000019974, ENSOARG00000021011, ENSOARG00000019483, Novel 00532, Novel 01020
66	G0:0000105	histidine biosynthetic process	biological_process	0.039085	1	2	257	16	17434	0		2 ENSOARG00000014764, Novel 00120
67	G0:0006547	histidine metabolic process	biological_process	0.039085	1	2	257	16	17434	0		2 Novel 00120, ENSOARG00000014764
68	G0:0052803	imidazole-containing compound metabolic process	biological_process	0.039085	1	2	257	16	17434	0		2 Novel 00120, ENSOARG00000014764
69	G0:0015994	chlorophyll metabolic process	biological_process	0.03967	1	5	257	80	17434	5	ENSOARG00000012797, ENSOARG00000018527, ENSOARG00000014143, ENSOARG00000010614, ENSOARG00000006991	0
70	G0:0016881	acid-amino acid ligase activity	molecular_function	0.040008	1	9	257	257	17434	5	ENSOARG00000005399, ENSOARG00000014849, ENSOARG00000006520, ENSOARG00000001369, ENSOARG00000004835	4 ENSOARG00000011408, ENSOARG00000020839, ENSOARG00000007070, ENSOARG0000000117
71	G0:0006778	porphyrin-containing compound metabolic process	biological_process	0.040369	1	6	257	120	17434	6	ENSOARG00000010614, ENSOARG00000006991, ENSOARG00000018527, ENSOARG00000012797, ENSOARG00000014143, ENSOARG00000006209	0
72	G0:0030117	membrane coat	cellular_component	0.040778	1	6	257	140	17434	2	ENSOARG00000015347, ENSOARG00000007995	4 ENSOARG00000006246, ENSOARG00000019338, ENSOARG00000003501, ENSOARG0000010723
73	G0:0048475	coated membrane	cellular_component	0.040778	1	6	257	140	17434	2	ENSOARG00000007995, ENSOARG00000015347	4 ENSOARG00000010723, ENSOARG00000003501, ENSOARG00000006246, ENSOARG0000019338
74	G0:0008134	transcription factor binding	molecular_function	0.040873	1	7	257	166	17434	7	ENSOARG00000006991, ENSOARG00000010614, ENSOARG00000014143, ENSOARG00000012797, ENSOARG00000018670, ENSOARG00000015028, ENSOARG0000018527	0
75	G0:0042555	MCM complex	cellular_component	0.040981	1	1	257	2	17434	1	ENSOARG00000006991	0
76	G0:0005179	hormone activity	molecular_function	0.0411	1	7	257	168	17434	0		7 ENSOARG00000011444, Novel 00532, ENSOARG00000010042, Novel 00838, Novel 01169, ENSOARG00000003591, ENSOARG00000004595
77	G0:0019207	kinase regulator activity	molecular_function	0.043265	1	2	257	25	17434	2	ENSOARG00000003547, ENSOARG00000007721	0
78	G0:0019887	protein kinase regulator activity	molecular_function	0.043265	1	2	257	25	17434	2	ENSOARG00000007721, ENSOARG00000003547	0
79	G0:0000902	cell morphogenesis	biological_process	0.044317	1	3	257	43	17434	2	ENSOARG00000012531, ENSOARG00000012928	1 Novel 01445
80	G0:0032989	cellular component morphogenesis	biological_process	0.044317	1	3	257	43	17434	2	ENSOARG00000012531, ENSOARG00000012928	1 Novel 01445
81	G0:0015074	DNA integration	biological_process	0.044573	1	4	257	67	17434	0		4 ENSOARG00000011014, ENSOARG00000001672, Novel 00562, Novel 00595
82	G0:0031342	negative regulation of cell killing	biological_process	0.046359	1	1	257	4	17434	1	ENSOARG00000007779	0
83	G0:0019031	viral envelope	cellular_component	0.046527	1	7	257	224	17434	0		7 ENSOARG00000001626, ENSOARG00000009174, Novel 00562, ENSOARG00000001672, Novel 00544, ENSOARG00000021011, ENSOARG00000003591
84	G0:0036338	viral membrane	cellular_component	0.046527	1	7	257	224	17434	0		7 Novel 00562, ENSOARG00000009174, ENSOARG00000001626, ENSOARG000000021011, ENSOARG00000003591, ENSOARG00000001672, Novel 00544
85	G0:0032801	receptor catabolic process	biological_process	0.046536	1	2	257	18	17434	0		2 Novel 00669, ENSOARG00000009174
86	G0:0003870	5-aminolevulinic acid synthase activity	molecular_function	0.047204	1	1	257	3	17434	1	ENSOARG00000006209	0
87	G0:0016748	succinyl transferase activity	molecular_function	0.047204	1	1	257	3	17434	1	ENSOARG00000006209	0
88	G0:0016749	N-succinyl transferase activity	molecular_function	0.047204	1	1	257	3	17434	1	ENSOARG00000006209	0
89	G0:0045333	cellular respiration	biological_process	0.047278	1	4	257	79	17434	1	ENSOARG00000012928	3 ENSOARG00000004162, ENSOARG00000010042, ENSOARG00000003537

Table S5. A total list of Ingenuity canonical pathways by IPA analysis.

Ingenuity Canonical Pathways	-log(p-value)	zScore	Ratio	Molecules
BER pathway	5.15	NaN	0.33	LIG1,PCNA,POLE,FEN1
Cell Cycle Control of Chromosomal Replication	4.95	NaN	0.19	MCM3,MCM5,MCM6,CDC6,MCM4
GADD45 Signaling	4.28	NaN	0.21	PCNA,GADD45G,BRCA1,CDK1
Protein Ubiquitination Pathway	3.20	NaN	0.04	CDC20,USP27X,USP53,DNAJB11,DNAJC27,UBE2S,NEDD4L,BRCA1,HSPA5,UBE2C
Granzyme B Signaling	3.16	NaN	0.19	LMNB2,CYCS,LMNB1
Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I	2.74	NaN	0.14	RRM2,DTYMK,RRM1
GDP-mannose Biosynthesis	2.74	NaN	0.33	GMPPB,PMM1
Triacylglycerol Degradation	2.63	NaN	0.13	FAAH,ABHD6,LPL
LXR/RXR Activation	2.61	NaN	0.05	SCD,LDLR,IL1RL1,SREBF1,APOA2,LPL
Role of CHK Proteins in Cell Cycle Checkpoint Control	2.47	NaN	0.07	PCNA,CLSPN,BRCA1,CDK1
Axonal Guidance Signaling	2.43	NaN	0.03	SEMA3A,SEMA6D,PAPPA,NFAT5,PTCH1,NTRK1,GNB2,TUBA1C,ADAMTS9,ADAMTS4,NRP1,SEMA7A
ATM Signaling	2.36	NaN	0.07	NFKBIA,GADD45G,BRCA1,CDK1
p53 Signaling	2.31	NaN	0.05	PCNA,THBS1,GADD45G,BRCA1,BIRC5
Estrogen Biosynthesis	2.06	NaN	0.08	HSD17B10,CYP19A1,HSD17B1
Colanic Acid Building Blocks Biosynthesis	1.98	NaN	0.14	GMPPB,PMM1
DNA Double-Strand Break Repair by Homologous Recombination	1.98	NaN	0.14	LIG1,BRCA1
Mechanisms of Viral Exit from Host Cells	1.96	NaN	0.07	ACTB,LMNB2,LMNB1
LPS/IL-1 Mediated Inhibition of RXR Function	1.92	NaN	0.03	MGST1,ALDH1L2,IL1RL1,SREBF1,CHST11,ALAS1,CHST15
Mismatch Repair in Eukaryotes	1.87	NaN	0.13	PCNA,FEN1
Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency	1.83	NaN	0.07	SPP1,JARID2,BRCA1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.76	NaN	0.06	CKS2,BRCA1,CDK1
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1.76	NaN	0.03	IL4R,CTGF,IL1RL1,IL6R,MYH11,COL6A6
Apoptosis Signaling	1.75	1.00	0.04	CAPN6,NFKBIA,CYCS,CDK1
DNA damage-induced 14-3-3 σ Signaling	1.72	NaN	0.11	BRCA1,CDK1
Semaphorin Signaling in Neurons	1.67	NaN	0.06	SEMA3A,NRP1,SEMA7A
Anandamide Degradation	1.65	NaN	0.50	FAAH,
Taurine Biosynthesis	1.65	NaN	0.50	CDO1,
Amyotrophic Lateral Sclerosis Signaling	1.61	NaN	0.04	CAPN6,NEFM,CYCS,GRIK2
Regulation of Cellular Mechanics by Calpain Protease	1.58	NaN	0.05	CCNA2,CAPN6,CDK1
Estrogen-mediated S-phase Entry	1.53	NaN	0.08	CCNA2,CDK1
Glutathione Biosynthesis	1.48	NaN	0.33	GCLC,
Estrogen-Dependent Breast Cancer Signaling	1.47	NaN	0.05	HSD17B10,CYP19A1,HSD17B1
Hypoxia Signaling in the Cardiovascular System	1.44	NaN	0.05	NFKBIA,UBE2S,UBE2C
Angiopoietin Signaling	1.42	NaN	0.05	ANGPT2,NFKBIA,BIRC5
IL-10 Signaling	1.39	NaN	0.04	IL4R,NFKBIA,IL1RL1
IL-6 Signaling	1.38	-1.00	0.03	NFKBIA,IL1RL1,CYP19A1,IL6R
Arginine Degradation I (Arginase Pathway)	1.36	NaN	0.25	OAT,
L-cysteine Degradation I	1.36	NaN	0.25	CDO1,
Myo-inositol Biosynthesis	1.36	NaN	0.25	ISYNA1,
Huntington's Disease Signaling	1.35	NaN	0.03	CAPN6,NTRK1,GNB2,CYCS,UBE2S,HSPA5
Sonic Hedgehog Signaling	1.35	NaN	0.07	PTCH1,CDK1
Gai Signaling	1.33	NaN	0.03	NPR3,CAV1,GNB2,RGS4

Table S6. A total list of functions with their predicted activation state by IPA analysis.

Categories	Functions	Diseases or Functions Annotation	p-Value	Predicted Activation State	Activation z-score	Bias-corrected z-score	Molecules	# Molecules
Cellular Growth and Proliferation	proliferation	proliferation of cells	3.88E-10	Activated	3.602	3.565	CTGF,HMMR,GCLC,MKI67,SKAP2,RECQL,PTP4A2,CAV1,JARID2,AMACR,CAPN6,IL4R,PTCH1,RRM2,GRK5,PLD1,NINJ1,OXT,PCNA,NPR3,ZBED6,CTSB,CLSPN,NOTCH1,UBE2C,NRP1,ADM,IL1RL1,MYH11,OGT,HK2,NTRK1,GRIK2,FAP,CITED2,ENPP1,ACTB,CDC6,CDK1,RRM1,MCM3,SEMA3A,NOV,SREBF1,FEN1,NEDD9,SEMA7A,LIG1,CDCP1,FGL2,HSPA5,PBK,LMNB1,GABARAPL1,PIWIL2,POSTN,CHST11,KPNA2,MYBL2,NEDD4L,FOSL2,BRCA1,IIFT172,ADAMTS4,PKK4,MCM5,CLEC1B,PTX3,PAPPA,SPP1,IL6R,RGS4,HELLS,MYOF,STC1,LMNB2,SCD,ANGPT2,CDC20,GADD45G,DTYMK,MCM4,CCNA2,CCNA2,NFAT5,CLK1,NFKBIA,CYP19A1,THBS1,CSPG4,MANF,SLC20A1,ARID5B,CKS2,UHRF1,VWF,MT1A,BIRC5,IVNS1ABP,B4GALT1,RNF111,EFEMP1	101
Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities	digestive system cancer	digestive system cancer	2.18E-12	Activated	2.804	2.811	SNTB2,MCM6,CTGF,L3MBTL3,SYTL2,PCSK1,TFR2,HMMR,GCLC,MKI67,CHAF1A,RECQL,JARID2,CAV1,TDP2,HSD17B1,AMACR,BCOR,PTCH1,LRRC16A,GRAMD1B,RRM2,GRK5,UBE2S,PLD1,PCNA,NPR3,ST3GAL1,CTSB,ARHGEF28,FAM13C,TSPYL4,CEP95,CLSPN,LRP8,NOTCH1,NRP1,UBE2C,CHCHD10,IL1RL1,USP53,ZBED5,HYOU1,MYH11,CRYBG3,REG4,OGT,ISYNA1,AMN1,HK2,PPAP2B,NTRK1,ANTXR2,ABHD2,DSTYK,LNPEP,GRIK2,FAP,VEPH1,CITED2,ADGRB2,STAMBPL1,ENPP1,PMM1,NELL2,ACTB,FAM63A,CDC6,POLE,RRM1,MCM3,SEMA3A,SDF2L1,NOV,LDLR,GPBP1,SREBF1,MAN1A1,FEN1,INADL,NEDD9,KANSL2,WDR19,COBLL1,SEMA7A,LIG1,CDCP1,SERPINA12,KIAA1841,C3orf33,SYNE1,HSPA5,LMNB1,PBK,CHST15,SEMA6D,TMTC2,PIWIL2,LPL,AMPH,POSTN,PDIA4,CHST11,KPNA2,TUBA1C,MYBL2,CDCA3,BRCA1,CCDC64,PKK4,ADAMTS4,IIFT172,PTX3,DNAH9,PHYHIPL,MCM5,NBEAL1,ATP6V1C2,PAPPA,SPP1,IL6R,MTUS2,RGS4,HELLS,FAM222B,KCNK12,ADAMTS9,MYOF,RHBD2,RLF,JAM3,LMNB2,ELL2,C20orf194,GMPPB,ABCD1,SCD,ANGPT2,CDC20,TC2N,RAPGEF4,ALAS1,LRRK1,COL6A6,MCM4,ZNF175,GFPT2,CCNA2,SNX16,CLK1,NFAT5,CSPG4,THBS1,MANF,ASPN,ARID5B,CKS2,KLHL24,FRY,WDR73,UHRF1,NEFM,VWF,BIRC5,ATP1B3,ANGPTL5,IVNS1ABP,CREL2,D2,B4GALT1,RNF111,DNAJB11,EFEMP1,CEMIP	173
Cancer, Organismal Injury and Abnormalities	abdominal neoplasm	abdominal neoplasm	3.33E-15	Activated	2.671	2.679	SNTB2,SYTL2,HMMR,PCSK1,GCLC,JARID2,CAV1,AMACR,IL4R,BCOR,RRM2,GRAMD1B,LRRC16A,PLD1,NPR3,ST3GAL1,CTSB,TSPYL4,ARHGEF28,CEP95,CXorf57,UBE2C,HSD17B10,CHCHD10,IL1RL1,ZBED5,CRYBG3,AMN1,ISYNA1,OGT,NTRK1,ANTXR2,LNPEP,FAP,PMM1,MCM3,SEMA3A,SDF2L1,LDLR,NOV,GPBP1,INADL,KANSL2,LIG1,CDCP1,FGL2,HSPA5,TMTC2,PIWIL2,LPL,PDIA4,MYBL2,TUBA1C,CCDC64,IIFT172,PHYHIPL,PAPPA,MGST1,ATP6V1C2,NBEAL1,IL6R,MTUS2,HELLS,KCNK12,ADAMTS9,RLF,JAM3,LMNB2,ELL2,ABCD1,SCD,CDC20,TC2N,ALAS1,RAPGEF4,COL6A6,GFPT2,CCNA2,SNX16,NFAT5,CYP19A1,SLC20A1,FRY,BIRC5,IVNS1ABP,ANGPTL5,CREL2,RNF111,DNAJB11,MCM6,L3MBTL3,CTGF,TFR2,MKI67,RECQL,CHAF1A,TDP2,CRIM1,HSD17B1,CAPN6,OAT,PTCH1,GRK5,UBE2S,NINJ1,PCNA,GNB2,FAM13C,LRP8,CLSPN,NOTCH1,NRP1,ADM,USP53,HYOU1,MYH11,REG4,HK2,USP27X,PPAP2B,ABHD2,DSTYK,GRIK2,SV2C,VEPH1,ADGRB2,CITED2,ENPP1,STAMBPL1,NELL2,FAM63A,ACTB,POLE,CDC6,CDK1,RRM1,ABHD6,SREBF1,MAN1A1,FEN1,NEDD9,WDR19,SEMA7A,COBLL1,SERPINA12,KIAA1841,APOA2,C3orf33,SYNE1,PBK,LMNB1,CHST15,SEMA6D,PDE7B,AMPH,POSTN,CHST11,KPNA2,CDCA3,BRCA1,ADAMTS4,PKK4,DNAH9,MCM5,PTX3,SPP1,RGS4,TNNI3,FAM222B,MYOF,STC1,C20orf194,GMPPB,ANGPT2,SLC10A7,LRRK1,MCM4,ZNF175,CLK1,NFKBIA,THBS1,CSPG4,MANF,ASPN,FAAH,ARID5B,CKS2,WDR73,K	197
DNA Replication, Recombination, and Repair	replication	DNA replication	4.96E-04	Activated	2.605	2.592	LIG1,CCNA2,PCNA,CKS2,GADD45G,CDC6,POLE,CAV1,FEN1,BRCA1,CDK1	11
DNA Replication, Recombination, and Repair	metabolism	metabolism of DNA	4.67E-05	Activated	2.434	2.423	ADM,HSD17B10,LIG1,CKS2,GADD45G,POLE,CDC6,BIRC5,CDK1,CCNA2,PCNA,NFKBIA,CAV1,CYCS,KPNA2,FEN1,BRCA1	17
Cancer, Organismal Injury and Abnormalities	abdominal cancer	abdominal cancer	2.65E-15	Activated	2.376	2.382	SNTB2,SYTL2,HMMR,PCSK1,GCLC,JARID2,CAV1,AMACR,IL4R,BCOR,RRM2,GRAMD1B,LRRC16A,PLD1,NPR3,ST3GAL1,CTSB,TSPYL4,ARHGEF28,CEP95,CXorf57,UBE2C,CHCHD10,IL1RL1,ZBED5,CRYBG3,AMN1,ISYNA1,OGT,NTRK1,ANTXR2,LNPEP,FAP,PMM1,MCM3,SEMA3A,SDF2L1,LDLR,NOV,GPBP1,INADL,KANSL2,LIG1,CDCP1,FGL2,HSPA5,TMTC2,PIWIL2,LPL,PDIA4,MYBL2,TUBA1C,CCDC64,IIFT172,PHYHIPL,PAPPA,MGST1,ATP6V1C2,NBEAL1,IL6R,MTUS2,HELLS,KCNK12,ADAMTS9,RLF,JAM3,LMNB2,ELL2,ABCD1,SCD,CDC20,TC2N,ALAS1,RAPGEF4,COL6A6,GFPT2,CCNA2,SNX16,NFAT5,CYP19A1,SLC20A1,FRY,BIRC5,IVNS1ABP,ANGPTL5,CREL2,RNF111,DNAJB11,MCM6,L3MBTL3,CTGF,TFR2,MKI67,RECQL,CHAF1A,TDP2,CRIM1,HSD17B1,CAPN6,OAT,PTCH1,GRK5,UBE2S,NINJ1,PCNA,GNB2,FAM13C,LRP8,CLSPN,NOTCH1,NRP1,ADM,USP53,HYOU1,MYH11,REG4,HK2,USP27X,PPAP2B,ABHD2,DSTYK,GRIK2,SV2C,VEPH1,ADGRB2,CITED2,ENPP1,STAMBPL1,NELL2,FAM63A,ACTB,POLE,CDC6,CDK1,RRM1,ABHD6,SREBF1,MAN1A1,FEN1,NEDD9,WDR19,SEMA7A,COBLL1,SERPINA12,KIAA1841,APOA2,C3orf33,SYNE1,PBK,LMNB1,CHST15,SEMA6D,PDE7B,AMPH,POSTN,CHST11,KPNA2,CDCA3,BRCA1,ADAMTS4,PKK4,MCM5,DNAH9,PTX3,SPP1,RGS4,TNNI3,FAM222B,MYOF,STC1,C20orf194,GMPPB,ANGPT2,SLC10A7,LRRK1,MCM4,ZNF175,CLK1,NFKBIA,THBS1,CSPG4,MANF,ASPN,FAAH,ARID5B,CKS2,WDR73,KLHL24,UHRF	196
Cellular Development, Cellular Growth and Proliferation	proliferation	proliferation of tumor cell lines	4.72E-08	Activated	2.311	2.291	LIG1,CTGF,CDCP1,HMMR,MKI67,HSPA5,PBK,CAV1,POSTN,KPNA2,BRCA1,ADAMTS4,PKK4,AMACR,CAPN6,SPP1,IL6R,PTCH1,RRM2,PLD1,OXT,PCNA,ZBED6,CTSB,NOTCH1,UBE2C,NRP1,ADM,SCD,ANGPT2,GADD45G,CCNA2,OGT,HK2,NFKBIA,CYP19A1,THBS1,CSPG4,NTRK1,UHRF1,ACTB,MT1A,BIRC5,CDK1,RRM1,NOV,RNF111,SREBF1,FEN1,EFEMP1,NEDD9	51

Cellular Movement	migration	migration of cells	5.47E-10	Activated	2.276	2.227	CTGF, CDCP1, HMMR, HSPA5, LMNB1, SKAP2, SEMA6D, PTP4A2, CAV1, POSTN, TDP2, KPNA2, BRCA1, CLEC1B, PTX3, PAPP, IL4R, SPP1, IL6R, LRRC16A, RGS4, PLD1, NINJ1, STC1, RHBD2, JAM3, CTSS, LMNB2, ARHGFE28, LRP8, NOTCH1, NRP1, ADM, ANGPT2, IL1RL1, HYOU1, MYH11, CCNA2, NFKBIA, NFAT5, CSPG4, CYP19A1, THBS1, PPAP2B, ABHD2, FAP, CITED2, FAAH, ARID5B, ACTB, VWF, CDK1, RRM1, MCM3, SEMA3A, ABHD6, LDLR, NOV, B4GALT1, SREBF1, CEMIP, INADL, NEDD9, ST3GAL4	64
Cancer, Endocrine System Disorders, Gastrointestinal Disease, Organismal Injury and Abnormalities	growth	growth of pancreatic tumor	4.19E-05	Activated	2.219	2.213	CTGF, THBS1, HMMR, CTSS, NRP1	5
Cardiovascular System Development and Function, Cellular Development, Cellular Growth and Proliferation	proliferation	proliferation of endothelial cell lines	1.11E-04	Activated	2.219	2.202	ADM, PTX3, THBS1, RGS4, MYH11, PLD1, CDK1	7
Skeletal and Muscular System Development and Function	thickness	thickness of bone	1.26E-04	Activated	2.219	2.204	STC1, CTGF, SPP1, CAV1, BRCA1, LRRK1, PDK4	7
Cellular Assembly and Organization	association	association of chromosome components	1.35E-05	Activated	2.2	2.187	CDC6, HELLS, BRCA1, BIRC5, MCM4	5
Cancer, Organismal Injury and Abnormalities	growth	growth of tumor	1.98E-07	Activated	2.176	2.158	ADM, ANGPT2, CTGF, IL1RL1, HMMR, HYOU1, MKI67, HSPA5, OGT, NFKBIA, CYP19A1, THBS1, CAV1, POSTN, MYBL2, BRCA1, FAP, IL4R, SPP1, IL6R, PTC1, RRM2, BIRC5, PLD1, NOV, RNF111, JAM3, CTSS, NEDD9, NOTCH1, UBE2C, NRP1	32
Cell Death and Survival	apoptosis	apoptosis of pancreatic cancer cell lines	6.32E-05	Activated	2.158	2.164	OGT, NFKBIA, SREBF1, ZBED6, HMMR, TDP2, EFEMP1, NOTCH1	8
Carbohydrate Metabolism	metabolism	metabolism of carbohydrate	1.58E-05	Activated	2.011	1.973	GMPPB, SCD, CTGF, ENPP1, SPP1, PMM1, APOA2, RGS4, GCLC, PRKAG3, GRK5, CHST15, PLD1, GFPT2, OXT, HK2, B4GALT1, SREBF1, NTRK1, LPL, CTSS, ASPN, CHST11, CEMIP	24
Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities	gastrointestinal tract cancer	gastrointestinal tract cancer	3.32E-12	Activated	2	2.009	SNTB2, L3MBTL3, CTGF, SYTL2, PCSK1, TFR2, HMMR, MKI67, CHAF1A, RECQL, JARID2, CAV1, TDP2, HSD17B1, AMACR, BCOR, PTCH1, RRM2, GRK5, UBE2S, PLD1, PCNA, NRP3, ST3GAL1, CTSS, FAM13C, CEP95, CLSPN, LRP8, NOTCH1, UBE2C, NRP1, IL1RL1, USP53, MYH11, JSYNA1, OGT, HK2, PPAP2B, NTRK1, ANTXR2, ABHD2, DSTYK, LNPEP, GRIK2, VEPH1, CITED2, ADGRB2, ENPP1, STAMBPL1, PMM1, CDC6, POLE, RRM1, MCM3, SEMA3A, SDF2L1, LDLR, NOV, GPBP1, FEN1, INADL, NEDD9, COBLL1, SEMA7A, LIG1, SERPINA12, CDCP1, KIAA1841, SYNE1, LMNB1, PBK, CHST15, SEMA6D, TMTC2, LPL, AMPH1, POSTN, CHST11, KPNA2, MYBL2, TUBA1C, BRCA1, PDK4, ADAMTS4, IFT172, DNAH9, PHYHIP, MCM5, PTX3, NBEAL1, ATP6V1C2, PAPP, SPP1, IL6R, MTUS2, RGS4, HELLS, ADAMTS9, MYOF, RHBD2, JAM3, ELL2, GMPPB, ANGPT2, CDC20, TC2N, ALAS1, LRRK1, COL6A6, MCM4, GFPT2, CCNA2, SNX16, CSPG4, THBS1, ASPN, ARID5B, WDR73, FRY, KLHL24, UHRF1, NEFM, VWF, BIRC5, IVNS1ABP, ANGPTL5, CRELD2, B4GALT1, RNF111, DNAJB11, EFEMP1, CEMIP	133
Skeletal and Muscular System Development and Function	thickness	thickness of trabecular bone	6.06E-04	Activated	2	1.999	CTGF, SPP1, CAV1, LRRK1, PDK4	5
Cancer, Gastrointestinal Disease, Hepatic System Disease, Organismal Injury and Abnormalities	cancer	liver cancer	1.11E-06		1.982	1.987	MCM6, L3MBTL3, SYTL2, PCSK1, TFR2, HMMR, GCLC, MKI67, RECQL, JARID2, RRM2, LRRC16A, GRAMD1B, UBE2S, PLD1, ST3GAL1, TSPYL4, ARHGFE28, LRP8, NOTCH1, UBE2C, CHCHD10, ZBED5, CRYBG3, AMN1, OGT, HK2, NTRK1, ANTXR2, LNPEP, GRIK2, FAP, ENPP1, STAMBPL1, NELL2, FAM63A, ACTB, POLE, RRM1, MCM3, LDLR, NOV, SREBF1, MAN1A1, INADL, WDR19, KANS12, SEMA7A, COBLL1, CDCP1, C3orf33, SYNE1, HSPA5, TMTC2, PIWIL2, AMPH, PDIA4, POSTN, CDCA3, BRCA1, CCDC64, PDK4, ADAMTS4, DNAH9, PTX3, PAPP, ATP6V1C2, SPP1, IL6R, RGS4, MTUS2, KCNK12, MYOF, RLF, LMNB2, C20orf194, ELL2, ABCD1, SCD, ANGPT2, CDC20, RAPGEF4, LRRK1, COL6A6, MCM4, ZNF175, CCNA2, SNX16, NFAT5, CLK1, THBS1, ASPN, ARID5B, CKS2, FRY, KLHL24, VWF, BIRC5, IVNS1ABP, ATP1B3, CRELD2, B4GALT1, RNF111, EFEMP1	104
Cellular Movement	cell movement	cell movement	7.90E-11		1.975	1.923	CTGF, CDCP1, FGL2, HMMR, HSPA5, LMNB1, PBK, SKAP2, SEMA6D, PTP4A2, POSTN, CAV1, TDP2, KPNA2, TUBA1C, BRCA1, FOSL2, CLEC1B, PTX3, IL4R, PAPP, SPP1, IL6R, LRRC16A, RGS4, PLD1, NINJ1, STC1, RHBD2, JAM3, GNB2, CTSS, LMNB2, ARHGFE28, LRP8, NOTCH1, NRP1, ADM, ANGPT2, IL1RL1, HYOU1, RAPGEF4, MYH11, CCNA2, NFKBIA, NFAT5, CSPG4, THBS1, CYP19A1, PPAP2B, ABHD2, FAP, CITED2, FAAH, ARID5B, ACTB, VWF, CDK1, RRM1, MCM3, ABHD6, SEMA3A, LDLR, NOV, B4GALT1, SREBF1, EFEMP1, CEMIP, INADL, NEDD9, ST3GAL4	71
Cancer, Organismal Injury and Abnormalities	benign neoplasia	benign neoplasia	3.57E-04		1.974	1.99	HSD17B10, LIG1, SCD, ANGPT2, CTGF, HMMR, MKI67, CYP19A1, THBS1, ANTXR2, MYBL2, PDK4, CAPN6, MGST1, SPP1, IL6R, PTCH1, RRM2, UBE2S, BIRC5, PCNA, NOV, CTSS, LRP8, NOTCH1	25
Cellular Assembly and Organization	association	association of chromatin	4.16E-05		1.969	1.943	CDC6, HELLS, BRCA1, MCM4	4
Developmental Disorder	metaplasia	metaplasia	1.96E-05		1.964	1.962	IL4R, NFKBIA, SPP1, THBS1, CYP19A1, BIRC5	6
Cell Death and Survival	cell death	cell death of pancreatic cancer cell lines	4.92E-07		1.941	1.949	OGT, NFKBIA, SPP1, SREBF1, ZBED6, HMMR, CTSS, TDP2, EFEMP1, NOTCH1, UBE2C	11
Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities	growth	growth of digestive organ tumor	1.72E-04		1.937	1.925	CTGF, THBS1, HMMR, CTSS, RRM2, NOTCH1, NRP1	7
Cell Death and Survival	apoptosis	apoptosis of brain cancer cell lines	5.96E-05		-1.607	-1.607	SEMA3A, SPP1, CSPG4, NTRK1, BIRC5, NOTCH1, CDK1, NRP1	8

Cellular Movement, Connective Tissue Development and Function	migration	migration of fibroblasts	3.40E-04	-1.697	-1.71	CCNA2,ARID5B,SPP1,THBS1,ACTB,POSTN,CAV1,SKAP2	8
Cell Death and Survival	apoptosis	apoptosis of carcinoma cell lines	1.77E-04	-1.705	-1.703	OGT,NFKBIA,HK2,SPP1,CDCP1,RRM2,HSPA5,BIRC5,NOTCH1,RRM1	10
Cellular Movement, Connective Tissue Development and Function	cell movement	cell movement of fibroblasts	1.93E-05	-1.72	-1.742	CCNA2,ARID5B,ANGPT2,NOV,SPP1,THBS1,ACTB,HMMR,POSTN,CAV1,SKAP2	11
Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry	efflux	efflux of cholesterol	5.85E-07	-1.824	-1.838	SCD,PAPPA,NFKBIA,LDLR,SREBF1,APOA2,PTCH1,LPL,CAV1,PLD1	10
Dermatological Diseases and Conditions, Organismal Injury and Abnormalities	formation	formation of skin lesion	1.16E-05	-1.951	-1.954	NFKBIA,LDLR,B4GALT1,CDCP1,PTCH1,NTRK1,CRIM1,BIRC5	8
Cancer, Dermatological Diseases and Conditions, Organismal Injury and Abnormalities	tumorigenesis	tumorigenesis of skin tumor	6.14E-04	-1.951	-1.956	NFKBIA,CDCP1,PTCH1,BIRC5	4
Cardiovascular Disease	aortic disorder	aortic disorder	2.76E-05	-1.959	-1.949	ADM,SCD,ANGPT2,LDLR,ENPP1,SREBF1,IL6R,VWF,MYH11,CITED2,NRP1	11
Cardiovascular Disease, Organismal Injury and Abnormalities	interstitial fibrosis	interstitial fibrosis of heart	2.21E-04	-1.98	-1.984	PTX3,ANGPT2,LPL,POSTN	4
