

ID	NC-1_fpk	NC-2_fpk	NC-3_fpk	DS-1_fpk
novel.1917	0.1276	0.6122	0	1.0464
ENSCHIG00000000115.1	0.3457	0	0	3.7791
ENSCHIG00000016699.1	1.6032	2.2071	0.3962	3.2451
novel.3204	4.1623	3.9928	4.229	0
ENSCHIG00000023889.1	0.4295	0.4709	0.1927	0.9223
novel.4290	0.3205	0.7686	0	2.0436
ENSCHIG00000025535.1	1.5733	2.0563	0.7102	4.1202
novel.1658	1.9551	0.9377	3.6455	0.3339
ENSCHIG00000025448.1	0	0	0.0917	0.9573
ENSCHIG00000018245.1	0.2025	0.3071	0.041	0.5713
ENSCHIG00000007802.1	3.964	1.4625	4.6682	1.7359
ENSCHIG00000024827.1	0.6496	0.7931	0.1854	1.7213
ENSCHIG00000011904.1	0.1143	0	0	1.7706
ENSCHIG00000021439.1	0.6998	0.6221	0.4556	0.4042
ENSCHIG00000022705.1	3.1824	1.7003	0.1265	7.0818
ENSCHIG00000022299.1	0	0.0563	0	1.4972
novel.1637	2.728	1.7446	0.204	4.0232
ENSCHIG00000024872.1	1.3082	2.3188	0.2679	3.3157
ENSCHIG00000022796.1	1.1765	1.0008	0.6274	1.9209
ENSCHIG00000020742.1	4.0041	4.6454	0.6449	9.0092
ENSCHIG00000019198.1	0.947	1.4866	0.3605	2.1174
novel.2096	0.6199	0.3716	0.1217	1.2705
ENSCHIG00000014114.1	0.288	0.4298	0.1005	1.0786
ENSCHIG00000016207.1	0.4192	0.4424	0	1.8712
novel.4601	0.1882	0.7221	0.591	1.3713
novel.4737	0.1139	0.6559	0	0.9342
novel.216	0.3494	0.9497	0.0914	1.1139
ENSCHIG00000025285.1	0.1226	1.2942	0	1.3406
ENSCHIG00000010695.1	0.5166	0.9911	0.0811	2.4939
novel.3612	3.5887	5.8725	0.9944	6.1532
ENSCHIG00000003358.1	0.3016	0.3777	0.0263	0.7403
ENSCHIG00000008359.1	2.4316	1.8661	0	4.8096
novel.2646	0.5582	0.4016	0.2191	1.2711
novel.3802	2.7191	4.9269	5.6927	2.752
novel.1728	0	0.0679	0.2222	0.1289
novel.2063	1.0277	1.0985	0.1383	1.6048
ENSCHIG00000013673.1	2.2753	2.2975	1.3162	0.2182
ENSCHIG00000021795.1	0.9931	0.433	0.5671	1.8915
novel.4505	0.9711	1.3699	0.2691	1.9772
ENSCHIG00000018051.1	4.514	5.1174	1.6109	13.0827
novel.778	0.6461	0.4959	0.1353	0.667
novel.1897	1.2395	2.1402	0.4791	2.6922
novel.652	2.8636	2.1365	0	3.4779
ENSCHIG00000014217.1	2.1278	5.4537	1.0441	3.725
ENSCHIG00000019227.1	1.5037	2.308	0	3.8352
ENSCHIG00000024093.1	5.8274	6.37	2.7663	2.8392
ENSCHIG00000009295.1	0.0769	0.123	0.0805	0.4906
ENSCHIG00000024236.1	1.2158	1.1663	0.1397	2.323

ENSCHIG00000014029.1	0.9085	0.8715	0.3566	2.7583
ENSCHIG00000006314.1	0.74	0.3944	0.6456	2.4716

DS-2_fpkm	DS-3_fpkm	DS-4_fpkm	DS-5_fpkm	NC-1_count	NC-2_count
3.7359	5.4909	3.3116	1.1238	1	5
3.0357	1.1017	1.7012	1.522	2	0
5.1093	3.1928	2.4037	3.0654	108	155
0.2866	1.5604	0.4381	0.5879	17	17
0.7902	0.4888	0.8235	1.1133	42	48
3.1894	2.0426	2.4372	2.8219	2	5
4.4437	1.8174	2.0937	4.8956	80	109
0.5722	0	0.6559	0.7825	16	8
0.1367	0.5582	0.3657	1.4021	0	0
0.6807	0.2186	0.3974	0.5961	31	49
1.5172	0.2429	1.6368	0.8542	52	20
1.0601	0.6272	1.3384	2.6469	33	42
0.1339	4.008	0.3069	0.3661	1	0
0.2797	0.0544	0.1527	0.3552	41	38
2.641	2.3105	4.613	11.3497	79	44
0.2062	0	0.2626	1.6915	0	1
6.5397	2.8977	7.4381	3.6393	21	14
2.3971	2.2655	2.4679	3.6648	46	85
1.7152	3.1124	1.8271	2.8784	53	47
7.0116	2.3174	6.6288	10.1628	234	283
3.9982	2.9264	2.131	1.0796	33	54
1.0886	2.2222	1.2478	1.4265	8	5
1.0491	0.3569	0.544	1.4857	9	14
0.6872	0.4008	0.6376	2.7852	10	11
2.6437	5.097	3.7038	1.5062	1	4
2.5347	3.0864	1.4272	0.456	1	6
1.2272	2.2268	1.3546	1.678	6	17
2.8718	4.2991	2.3043	1.1781	1	11
1.391	0.7407	0.9243	3.0597	10	20
10.6271	9.4174	9.8207	7.0966	17	29
0.461	0.2136	0.4797	1.576	36	47
4.4736	1.6604	3.978	4.2819	35	28
1.4703	3.3349	1.3732	0.5026	8	6
1.4148	0	1.3515	1.9346	9	17
0.9111	1.578	1.2025	0.5096	0	1
2.3033	3.6024	1.7076	0.7756	35	39
0.701	0.954	0.9642	0.671	19	20
2.0083	0.7192	1.777	3.252	22	10
1.7388	2.7304	2.3508	1.7374	17	25
9.6085	3.2691	7.3426	11.4961	22	26
3.3788	3.0884	0.4239	0.6551	15	12
3.7282	4.3445	1.9619	1.5263	65	117
6.705	17.2361	3.9852	3.0561	9	7
7.2009	7.2042	8.5367	3.8587	64	171
5.2814	10.0625	2.9597	2.8887	5	8
1.4279	0.8637	3.2736	4.4474	43	49
0.3603	0.4086	0.0229	1.3549	3	5
1.3193	0.8977	1.6449	3.774	41	41

2.1271	0.8443	1.2868	2.6056	12	12
2.4066	0.655	1.7655	2.2377	9	5

NC-3_count	DS-1_count	DS-2_count	DS-3_count	DS-4_count	DS-5_count
0	9	25	27	29	11
0	24	15	4	11	11
17	240	294	135	181	258
11	0	1	4	2	3
12	99	66	30	90	136
0	14	17	8	17	22
23	230	193	58	119	311
19	3	4	0	6	8
1	18	2	6	7	30
4	96	89	21	68	114
39	25	17	2	24	14
6	96	46	20	76	168
0	17	1	22	3	4
17	26	14	2	10	26
2	193	56	36	128	352
0	28	3	0	5	36
1	34	43	14	64	35
6	128	72	50	97	161
18	95	66	88	92	162
24	578	350	85	433	742
8	81	119	64	83	47
1	18	12	18	18	23
2	37	28	7	19	58
0	49	14	6	17	83
2	8	12	17	22	10
0	9	19	17	14	5
1	21	18	24	26	36
0	12	20	22	21	12
1	53	23	9	20	74
3	32	43	28	52	42
2	97	47	16	64	235
0	76	55	15	64	77
2	20	18	30	22	9
12	10	4	0	5	8
2	2	11	14	19	9
3	60	67	77	65	33
7	2	5	5	9	7
8	46	38	10	44	90
3	38	26	30	46	38
5	70	40	10	40	70
2	17	67	45	11	19
16	155	167	143	115	100
0	12	18	34	14	12
20	123	185	136	287	145
0	14	15	21	11	12
13	23	9	4	27	41
2	21	12	10	1	66
3	86	38	19	62	159

3	40	24	7	19	43
5	33	25	5	24	34

log2FoldChange	pvalue	padj	regulated
3.585007271		0.000823995	0.999951577 up
3.938199336		0.001307611	0.999951577 up
1.250614223		0.00131927	0.999951577 up
-3.200445271		0.001459148	0.999951577 down
1.008103305		0.001799478	0.999951577 up
2.618154439		0.002071214	0.999951577 up
1.086779464		0.002195272	0.999951577 up
-2.805566126		0.002636487	0.999951577 down
4.522537224		0.002712119	0.999951577 up
1.314359599		0.003350191	0.999951577 up
-2.035282921		0.003619478	0.999951577 down
1.293986572		0.004906002	0.999951577 up
4.755836582		0.005077294	0.999951577 up
-1.532266317		0.006310987	0.999951577 down
1.70001726		0.006726274	0.999951577 up
4.560341367		0.007069757	0.999951577 up
1.561307831		0.008344071	0.999951577 up
1.067804178		0.008519227	0.999951577 up
1.146262719		0.008528308	0.999951577 up
1.113506095		0.009000521	0.999951577 up
1.352637306		0.011047231	0.999951577 up
1.872177486		0.011248835	0.999951577 up
1.551517307		0.011639884	0.999951577 up
2.029258636		0.012404663	0.999951577 up
2.409847174		0.01311879	0.999951577 up
2.740485802		0.013773712	0.999951577 up
1.6816461		0.014363883	0.999951577 up
2.41352222		0.015253318	0.999951577 up
1.577163249		0.016599228	0.999951577 up
1.238266525		0.017422067	0.999951577 up
1.486409022		0.017474271	0.999951577 up
1.376937342		0.017544139	0.999951577 up
1.982128783		0.017781862	0.999951577 up
-2.013657528		0.018171147	0.999951577 down
2.992376571		0.020898514	0.999951577 up
1.503534749		0.021428083	0.999951577 up
-1.676240401		0.021451407	0.999951577 down
1.25785232		0.022176181	0.999951577 up
1.208404823		0.02220711	0.999951577 up
1.076912149		0.022319187	0.999951577 up
1.990446975		0.022618501	0.999951577 up
1.162831463		0.02292432	0.999951577 up
2.189749281		0.024220149	0.999951577 up
1.085296316		0.026905178	0.999951577 up
2.017042967		0.027510313	0.999951577 up
-1.143460557		0.028080789	0.999951577 down
2.252366616		0.028416904	0.999951577 up
1.152772996		0.029337505	0.999951577 up

1.243326382
1.40966224

0.029560864
0.029650454

0.999951577 up
0.999951577 up

chr	start	end	strand	gene_name
LWLT01000052.1	22	1315504	1316019 .	--
	27	8539523	8540175 +	ENSCHIG00000000115
	11	74783390	74939001 +	ATAD2B
	7	72980	73248 .	--
	1	157281259	157304767 -	ZNF596
		384764	429162 +	--
	12	56510421	56532630 +	USPL1
	2	51248686	51249224 .	--
	8	99188929	99263581 +	ENSCHIG000000025448
	22	51290569	51316051 +	CELSR3
	23	39778060	39778923 +	ENSCHIG000000007802
	2	113946848	113985339 -	GPR155
	28	13806023	13841717 -	LRMDA
	25	25963706	25969255 +	ENSCHIG000000021439
	7	60659810	60662134 -	EGR1
	14	17320783	17387785 +	ENSCHIG000000022299
	2	35139921	35293424 +	--
	1	106625362	106738971 +	IFT80
	11	87633641	87786887 -	ASAP2
	28	37350682	37433283 +	ARID4B
	10	65824172	65831854 -	PLA2G4B
	23	37056118	37056967 .	--
	23	21124943	21142376 -	ZFP57
	23	4832504	4835933 +	ENSCHIG000000016207
LWLT01000684.1		70806	71372 -	--
LWLT01002501.1		8599	9974 +	--
LWLT01000021.1	10	27208820	27209950 .	--
	24	43228273	43235773 +	PRELID3A
	11	93584797	93586071 -	ZBTB6
	9	51190959	51191415 +	--
	24	45836463	45966210 -	EPG5
	12	30726142	30727089 +	SPRY2
	3	69545901	69546844 .	--
		21863102	21863319 .	--
	2	126599619	126600549 .	--
	23	19440209	19445936 +	--
LWLT01000216.1	5	25245892	25252859 +	PPP1R1A
	5	98590580	98634779 +	ENSCHIG000000021795
		20286	26293 -	--
	10	56111955	56112291 +	ENSCHIG000000018051
	14	9000536	9002064 .	--
	21	65229124	65234692 +	--
	13	3033180	3033386 .	--
	6	89589037	89591998 +	ENSCHIG000000014217
	25	22691800	22692185 -	ENSCHIG000000019227
	6	13550431	13550997 -	ENSCHIG000000024093
	29	21906104	21974605 -	ANO5
	5	30690291	30726300 +	CCNT1

25	28031482	28038284 +	KCTD7
12	58086341	58107390 -	N4BP2L1

gene_description

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ATPase family AAA domain containing 2B [Source:HGNC Symbol%3B

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zinc finger protein 596 [Source:HGNC Symbol%3BAcc:HGNC:27268]

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ubiquitin specific peptidase like 1 [Source:HGNC Symbol%3BAcc:HG

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cadherin EGF LAG seven-pass G-type receptor 3 [Source:HGNC Sym

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G protein-coupled receptor 155 [Source:HGNC Symbol%3BAcc:HGNC

leucine rich melanocyte differentiation associated [Source:HGNC Sy

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early growth response 1 [Source:HGNC Symbol%3BAcc:HGNC:3238]

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intraflagellar transport 80 [Source:HGNC Symbol%3BAcc:HGNC:292

ArfGAP with SH3 domain%2C ankyrin repeat and PH domain 2 [Sou

AT-rich interaction domain 4B [Source:HGNC Symbol%3BAcc:HGNC:

phospholipase A2 group IVB [Source:HGNC Symbol%3BAcc:HGNC:9

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ZFP57 zinc finger protein [Source:HGNC Symbol%3BAcc:HGNC:1879

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PRELI domain containing 3A [Source:HGNC Symbol%3BAcc:HGNC:2

zinc finger and BTB domain containing 6 [Source:HGNC Symbol%3B

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ectopic P-granules autophagy protein 5 homolog [Source:HGNC Syn

sprouty RTK signaling antagonist 2 [Source:HGNC Symbol%3BAcc:H

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protein phosphatase 1 regulatory inhibitor subunit 1A [Source:HGN

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anoctamin 5 [Source:HGNC Symbol%3BAcc:HGNC:27337]

cyclin T1 [Source:NCBI gene (formerly Entrezgene)%3BAcc:1008608

potassium channel tetramerization domain containing 7 [Source:HGNC Symbol;Acc:HGNC:10541]
NEDD4 binding protein 2 like 1 [Source:HGNC Symbol;Acc:HGNC:10542]

真核转录组测序结题报告

KEGG

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K22531 ATPase family AAA domain-containing protein 2 [EC:3.6.1.-]

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K09228 KRAB domain-containing zinc finger protein | (RefSeq) zinc

K04373 ribosomal protein S6 kinase alpha-1/2/3/6 [EC:2.7.11.1] | (RefSeq)

K23008 SUMO-specific isopeptidase USPL1 [EC:3.4.22.-] | (RefSeq) U

K11433 [histone H3]-lysine36 N-dimethyltransferase SETMAR [EC:2.7.1.1]

K16519 A-kinase anchor protein 2 | (RefSeq) AKAP2; A-kinase anchor

K04602 cadherin EGF LAG seven-pass G-type receptor 3 | (RefSeq) C

K02934 large subunit ribosomal protein L6e | (RefSeq) RPL6; 60S rib

K17588 phosphatidylinositol 3,4,5-trisphosphate-dependent Rac ex

K24399 leucine-rich melanocyte differentiation-associated protein |

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K09203 early growth response protein 1 | (RefSeq) EGR1; early gro

K19526 vacuolar protein sorting-associated protein 13B | (RefSeq) V

K18586 ubiquinone biosynthesis protein COQ4 | (RefSeq) COQ4; ub

K19678 intraflagellar transport protein 80 | (RefSeq) IFT80; intraflag

K12488 Arf-GAP with SH3 domain, ANK repeat and PH domain-cont

K19195 AT-rich interactive domain-containing protein 4B | (RefSeq)

K16342 cytosolic phospholipase A2 [EC:3.1.1.4] | (RefSeq) cytosolic

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K09228 KRAB domain-containing zinc finger protein | (RefSeq) ZFP5

K00742 N-acetyllactosaminide beta-1,6-N-acetylglucosaminyltransf

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K09657 beta-1,4-N-acetylgalactosaminyltransferase 4 [EC:2.4.1.244]

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K26544 phosphatidylinositol/phosphatidylcholine transfer protein |

K10493 zinc finger and BTB domain-containing protein 6 | (RefSeq)

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K23883 ectopic P granules protein 5 | (RefSeq) EPG5; ectopic P gran

K17383 protein sprouty homolog 2 | (RefSeq) SPRY2; protein sprout

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K16349 natural cytotoxicity triggering receptor 3 ligand 1 | (RefSeq)

K16349 natural cytotoxicity triggering receptor 3 ligand 1 | (RefSeq)

K09228 KRAB domain-containing zinc finger protein | (RefSeq) zinc

K08050 protein phosphatase 1 regulatory subunit 1A | (RefSeq) PPF

K10072 C-type lectin domain family 2 member D | (RefSeq) C-type I

K10434 microtubule-associated protein 9 | (RefSeq) MAP9; microtu

K00417 ubiquinol-cytochrome c reductase subunit 7 | (RefSeq) cyto

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K05505 C-X-C motif chemokine 1/2/3 | (RefSeq) growth-regulated p

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K14025 selenoprotein S | (RefSeq) VIMP; selenoprotein S (A)

K19480 anoctamin-5 | (RefSeq) ANO5; anoctamin-5 isoform X1 (A)

K15188 cyclin T | (RefSeq) CCNT1; cyclin-T1 (A)

K21917 BTB/POZ domain-containing protein KCTD7/14 | (RefSeq) K
K15720 NEDD4-binding protein 2 [EC:3.-.-.] | (RefSeq) NEDD4-bindi

KEGG pathway

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ko05168: Herpes simplex virus 1 infection

ko04010: MAPK signaling pathway; ko04114: Oocyte meiosis; ko04:

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ko00310: Lysine degradation; ko01100: Metabolic pathways

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ko03010: Ribosome; ko05171: Coronavirus disease - COVID-19

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ko04371: Apelin signaling pathway; ko04912: GnRH signaling pathw

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ko04144: Endocytosis; ko04666: Fc gamma R-mediated phagocytos

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ko00564: Glycerophospholipid metabolism; ko00565: Ether lipid me

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ko05168: Herpes simplex virus 1 infection

ko00601: Glycosphingolipid biosynthesis - lacto and neolacto series

--

ko00513: Various types of N-glycan biosynthesis; ko01100: Metabo

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ko05206: MicroRNAs in cancer

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--

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ko05168: Herpes simplex virus 1 infection

ko04261: Adrenergic signaling in cardiomyocytes; ko04720: Long-te

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ko00190: Oxidative phosphorylation; ko01100: Metabolic pathways

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ko04060: Cytokine-cytokine receptor interaction; ko04061: Viral pro

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ko04141: Protein processing in endoplasmic reticulum

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ko03250: Viral life cycle - HIV-1; ko05202: Transcriptional misregula

NR

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intraflagellar transport-associated protein [Ovis aries]

ATPase family AAA domain-containing protein 2B isoform X1 [Ovis aries]

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Craniofacial development protein 2 [Varanus komodoensis]

PREDICTED: LOW QUALITY PROTEIN: ribosomal protein S6 kinase alpha-1 [Capra hircus]

PREDICTED: SUMO-specific isopeptidase USPL1 isoform X1 [Capra hircus]

hypothetical protein AV530_017556 [Patagioenas fasciata monilis]

hypothetical protein JEQ12_008746 [Ovis aries]

PREDICTED: cadherin EGF LAG seven-pass G-type receptor 3 isoform X1 [Ovis aries]

60S ribosomal protein L6 [Ovis aries]

PREDICTED: integral membrane protein GPR155 isoform X1 [Capra hircus]

hypothetical protein MJG53_019141 [Ovis ammon polii x Ovis aries]

PREDICTED: apolipoprotein B receptor [Capra hircus]

PREDICTED: early growth response protein 1 [Capra hircus]

vacuolar protein sorting-associated protein 13B isoform X7 [Bos taurus]

hypothetical protein FD755_017270, partial [Muntiacus reevesi]

PREDICTED: intraflagellar transport protein 80 homolog isoform X1 [Ovis aries]

arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 [Ovis aries]

PREDICTED: AT-rich interactive domain-containing protein 4B isoform X1 [Ovis aries]

PREDICTED: cytosolic phospholipase A2 beta isoform X7 [Capra hircus]

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PREDICTED: zinc finger protein 57 homolog isoform X1 [Capra hircus]

N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase-like 1 [Ovis aries]

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hypothetical protein Celaphus_00004985 [Cervus elaphus hippelaphus]

hypothetical protein MJG53_015733 [Ovis ammon polii x Ovis aries]

PREDICTED: PRELI domain containing protein 3A isoform X2 [Capra hircus]

PREDICTED: zinc finger and BTB domain-containing protein 6 [Capra hircus]

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PREDICTED: ectopic P granules protein 5 homolog isoform X1 [Capra hircus]

PREDICTED: protein sprouty homolog 2 [Capra hircus]

hypothetical protein mRhiFer1_010318 [Rhinolophus ferrumequinum]

hypothetical protein FD754_003310 [Muntiacus muntjak]

hypothetical protein MG293_000479 [Ovis ammon polii]

LOW QUALITY PROTEIN: zinc finger protein with KRAB and SCAN domain [Ovis aries]

PREDICTED: protein phosphatase 1 regulatory subunit 1A isoform X1 [Ovis aries]

C-type lectin domain family 2 member D11-like [Ovis aries]

hypothetical protein FD754_025647 [Muntiacus muntjak]

cytochrome b-c1 complex subunit 7 isoform X2 [Physeter catodon]

hypothetical protein FD755_019938 [Muntiacus reevesi]

uncharacterized protein LOC122419715 isoform X1 [Cervus canadensis]

hypothetical protein FD755_019993, partial [Muntiacus reevesi]

PREDICTED: growth-regulated protein homolog gamma isoform X1 [Ovis aries]

protein CEBPZOS isoform X2 [Balaenoptera acutorostrata scammon]

selenoprotein S isoform X2 [Ovis aries]

PREDICTED: anoctamin-5 isoform X1 [Capra hircus]

cyclin-T1 [Capra hircus]

PREDICTED: BTB/POZ domain-containing protein KCTD7 [Capra hircus]
NEDD4-binding protein 2-like 1 isoform X1 [Ovis aries]

Swissprot

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IFTAP_BOVIN RecName: Full=Intraflagellar transport-associated pro

ATD2B_HUMAN RecName: Full=ATPase family AAA domain-contain

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CFDP2_BOVIN RecName: Full=Craniofacial development protein 2; /

KS6A6_HUMAN RecName: Full=Ribosomal protein S6 kinase alpha-t

USPL1_HUMAN RecName: Full=SUMO-specific isopeptidase USPL1;

SETMR_HUMAN RecName: Full=Histone-lysine N-methyltransferase

PALM2_HUMAN RecName: Full=Paralemmin-2; Flags: Precursor;

CEL3_HUMAN RecName: Full=Cadherin EGF LAG seven-pass G-typ

RL6_BOVIN RecName: Full=60S ribosomal protein L6;

GP155_PONAB RecName: Full=Integral membrane protein GPR155;

LRMDA_MOUSE RecName: Full=Leucine-rich melanocyte differentia

APOBR_HUMAN RecName: Full=Apolipoprotein B receptor {ECO:00

EGR1_BOVIN RecName: Full=Early growth response protein 1; Short

VP13B_MOUSE RecName: Full=Intermembrane lipid transfer protei

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IFT80_HUMAN RecName: Full=Intraflagellar transport protein 80 hc

ASAP2_HUMAN RecName: Full=Arf-GAP with SH3 domain, ANK rep

ARI4B_HUMAN RecName: Full=AT-rich interactive domain-containir

PA24B_HUMAN RecName: Full=Cytosolic phospholipase A2 beta {E

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ZFP57_HUMAN RecName: Full=Zinc finger protein 57 homolog {ECC

GCNT2_MOUSE RecName: Full=N-acetyllactosaminide beta-1,6-N-a

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B4GN4_HUMAN RecName: Full=N-acetyl-beta-glucosaminyl-glycop

LORF2_HUMAN RecName: Full=LINE-1 retrotransposable element C

PLD3A_HUMAN RecName: Full=PRELI domain containing protein 3A

ZBTB6_BOVIN RecName: Full=Zinc finger and BTB domain-containin

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EPG5_HUMAN RecName: Full=Ectopic P granules protein 5 homolog

SPY2_CHLAE RecName: Full=Protein sprouty homolog 2; Short=Spry

LORF2_HUMAN RecName: Full=LINE-1 retrotransposable element C

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PPR1A_CANLF RecName: Full=Protein phosphatase 1 regulatory sub

CLC2H_MOUSE RecName: Full=C-type lectin domain family 2 memb

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QCR7_BOVIN RecName: Full=Cytochrome b-c1 complex subunit 7; /

YSM6_CAEEL RecName: Full=Putative uncharacterized transposon-c

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GROA_SHEEP RecName: Full=Growth-regulated alpha protein; AltN

CEBOS_HUMAN RecName: Full=Protein CEBPZOS {ECO:0000305}; A

SELS_BOVIN RecName: Full=Selenoprotein S {ECO:0000250|UniProt

ANO5_HUMAN RecName: Full=Anoctamin-5; AltName: Full=Gnatho

CCNT1_BOVIN RecName: Full=Cyclin-T1; Short=CycT1;

KCTD7_BOVIN RecName: Full=BTB/POZ domain-containing protein |

N42L1_HUMAN RecName: Full=NEDD4-binding protein 2-like 1;

Tremble

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A0A452DK09_CAPHI SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452EWP4_CAPHI SubName: Full=ATPase family AAA domain containing

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A0A8B9XA5_BOSMU SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A5F9DNY0_RABIT RecName: Full=Protein kinase domain-containing

A0A452G356_CAPHI SubName: Full=Ubiquitin specific peptidase like

A0A1V4JVU1_PATFA RecName: Full=HTH_48 domain-containing protein

A0A452G2W9_CAPHI SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452F4Q0_CAPHI SubName: Full=Cadherin EGF LAG seven-pass type I

A0A452DV36_CAPHI RecName: Full=60S ribosomal protein L6 {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452FZX6_CAPHI SubName: Full=G protein-coupled receptor 155

A0A452EA65_CAPHI SubName: Full=Leucine rich melanocyte differentiation

W5NYTO_SHEEP SubName: Full=Apolipoprotein B receptor {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452FQ14_CAPHI RecName: Full=Early growth response protein

A0A452FM56_CAPHI SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A5N3X9I9_MUNRE SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452FZR9_CAPHI SubName: Full=Intraflagellar transport 80 {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452FQK8_CAPHI SubName: Full=ArfGAP with SH3 domain, ankyrin

A0A452FF77_CAPHI SubName: Full=AT-rich interaction domain 4B {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452F8A4_CAPHI RecName: Full=Phospholipase A2 {ECO:0000256|Rule:0000256|ARBA:0000256}

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A0A452EJQ8_CAPHI SubName: Full=ZFP57 zinc finger protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452EUB3_CAPHI SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A8C6FNN3_MOSMO RecName: Full=Deoxyribonuclease-1 {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A8C2XXK8_CAPHI RecName: Full=Beta-1,4-N-acetylgalactosaminidase

A0A4W2CTC1_BOBOX SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452G1U0_CAPHI SubName: Full=PRELI domain containing 3A {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452E4T3_CAPHI SubName: Full=Zinc finger and BTB domain containing

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A0A452DQ00_CAPHI SubName: Full=Ectopic P-granules autophagy

A0A452DWT1_CAPHI RecName: Full=Protein sprouty homolog 2 {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A7J7X5I7_RHIFE RecName: Full=DUF1725 domain-containing protein

A0A8C6E1K0_MOSMO SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A5N3VWF6_MUNRE RecName: Full=RNA helicase {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A6P7D7Y5_SHEEP SubName: Full=LOW QUALITY PROTEIN: zinc finger

A0A452EHL1_CAPHI SubName: Full=Protein phosphatase 1 regulatory

A0A452FK01_CAPHI RecName: Full=C-type lectin domain-containing

A0A4W2G8A3_BOBOX SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452F316_CAPHI RecName: Full=Cytochrome b-c1 complex subunit

A0A8C0A1B8_BOSMU RecName: Full=Reverse transcriptase domain

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A0A5N3X217_MUNRE RecName: Full=RNA-directed DNA polymerase

A0A452EK68_CAPHI RecName: Full=C-X-C motif chemokine {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452F8N5_CAPHI SubName: Full=Uncharacterized protein {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452FWA4_CAPHI RecName: Full=Selenoprotein S {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452DZX8_CAPHI RecName: Full=Anoctamin {ECO:0000256|Rule:0000256|ARBA:0000256}

A0A452FX03_CAPHI RecName: Full=Cyclin-T1 {ECO:0000256|ARBA:0000256}

A0A452EJC2_CAPHI SubName: Full=Potassium channel tetramerizat

A0A6P3EGL5_SHEEP SubName: Full=NEDD4-binding protein 2-like 1

KOG

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AAA+-type ATPase containing the bromodomain

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FOG: Zn-finger

Ribosomal protein S6 kinase

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Cadherin EGF LAG seven-pass G-type receptor

60s ribosomal protein L6

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U2-associated snRNP A' protein

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FOG: Zn-finger

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WD40 repeat-containing protein CHE-2

Putative GTPase activating proteins (GAPs)

Dosage compensation regulatory complex/histone acetyltransferase

Lysophospholipase

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FOG: Zn-finger

Branching enzyme

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Chondroitin synthase 1

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Predicted member of the intramitochondrial sorting protein family

FOG: Zn-finger

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Uncharacterized conserved protein

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FOG: Zn-finger

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C-type lectin

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Ubiquinol cytochrome c reductase, subunit QCR7

FOG: Reverse transcriptase

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Uncharacterized conserved protein

CDK9 kinase-activating protein cyclin T

Uncharacterized conserved protein, contains BTB/POZ domain
Predicted MutS-related protein involved in mismatch repair

GO

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GO:0097731,9+0 non-motile cilium; GO:0005829,cytosol; GO:0120:
GO:0005654,nucleoplasm; GO:0005634,nucleus; GO:0005524,ATP l

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GO:0005737,cytoplasm; GO:0005634,nucleus; GO:0003824,catalyti
GO:0005737,cytoplasm; GO:0005829,cytosol; GO:0001650,fibrillar
GO:0015030,Cajal body; GO:0005615,extracellular space; GO:00169
GO:0005730,nucleolus; GO:0005634,nucleus; GO:0035861,site of d
GO:0005654,nucleoplasm; GO:0005886,plasma membrane; GO:000
GO:0016021,integral component of membrane; GO:0005886,plasm
GO:0022625,cytosolic large ribosomal subunit; GO:0031090,organe
GO:0016021,integral component of membrane; GO:0035556,intrac
GO:0030318,melanocyte differentiation; GO:0008150,biological_pr
GO:0042627,chylomicron; GO:0034362,low-density lipoprotein par
GO:0005737,cytoplasm; GO:0005634,nucleus; GO:0000981,DNA-bi
GO:0002080,acrosomal membrane; GO:0033106,cis-Golgi network
GO:0008168,methyltransferase activity; GO:0003674,molecular_fui
GO:0097731,9+0 non-motile cilium; GO:0005813,centrosome; GO:(
GO:0032580,Golgi cisterna membrane; GO:0005886,plasma membi
GO:0005829,cytosol; GO:0005739,mitochondrion; GO:0005654,nuc
GO:0005829,cytosol; GO:0031901,early endosome membrane; GO:

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GO:0005634,nucleus; GO:0003682,chromatin binding; GO:0000981
GO:0005794,Golgi apparatus; GO:0000139,Golgi membrane; GO:00
GO:0005635,nuclear envelope; GO:0042588,zymogen granule; GO:(
GO:0032580,Golgi cisterna membrane; GO:0016021,integral compo
GO:0046872,metal ion binding; GO:0003964,RNA-directed DNA pol
GO:0005758,mitochondrial intermembrane space; GO:1990050,pho
GO:0005654,nucleoplasm; GO:0001227,DNA-binding transcription i

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GO:0005737,cytoplasm; GO:0005764,lysosome; GO:0048471,perini
GO:0005737,cytoplasm; GO:0005874,microtubule; GO:0032587,ruf
GO:0046872,metal ion binding; GO:0003964,RNA-directed DNA pol
GO:0046855,inositol phosphate dephosphorylation; GO:0005975,ca
GO:0005524,ATP binding; GO:0016787,hydrolase activity; GO:0003
GO:0005634,nucleus; GO:0005575,cellular_component; GO:000562
GO:0005737,cytoplasm; GO:0004864,protein phosphatase inhibitor
GO:0009986,cell surface; GO:0005783,endoplasmic reticulum; GO:(

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GO:0005750,mitochondrial respiratory chain complex III; GO:00061

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GO:0005615,extracellular space; GO:0008009,chemokine activity; G
GO:0016021,integral component of membrane; GO:0031966,mitoc
GO:0005881,cytoplasmic microtubule; GO:0036513,Derlin-1 retrotr
GO:0005789,endoplasmic reticulum membrane; GO:0016021,integ
GO:0008024,cyclin/CDK positive transcription elongation factor con

GO:0005829,cytosol; GO:0005886,plasma membrane; GO:0060081

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Pfam	TF-Family
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PF17722.4:Intraflagellar transport-associated protein	--
PF00004.32:ATPase family associated with various cellular activities	AF-4
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PF00078.30:Reverse transcriptase (RNA-dependent DNA polymeras	zf-C2H2
PF00069.28:Protein kinase domain	bHLH
PF15509.9:Domain of unknown function (DUF4650)	--
PF17906.4:HTH domain in Mos1 transposase	TF_others
PF03285.18:Paralemmmin	--
PF00028.20:Cadherin domain	IRF
PF01159.22:Ribosomal protein L6e	--
PF03547.21:Membrane transport protein	--
PF14580.9:Leucine-rich repeat	--
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PF11914.11:Domain of unknown function (DUF3432)	zf-C2H2
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PF00400.35:WD domain, G-beta repeat	--
PF01412.21:Putative GTPase activating protein for Arf	zf-C2H2
PF01388.24:ARID/BRIGHT DNA binding domain	ARID
PF01735.21:Lysophospholipase catalytic domain	--
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PF01352.30:KRAB box	zf-C2H2
PF02485.24:Core-2/I-Branching enzyme	--
--	--
PF02709.17:N-terminal domain of galactosyltransferase	--
--	HSF
PF04707.17:PRELI-like family	--
PF00651.34:BTB/POZ domain	ZBTB
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--	--
PF05210.16:Sprouty protein (Spry)	--
--	--
--	zf-C2H2
--	ETS
--	zf-C2H2
PF05395.15:Protein phosphatase inhibitor 1/DARPP-32	--
PF00059.24:Lectin C-type domain	THAP
--	THAP
PF02271.19:Ubiquinol-cytochrome C reductase complex 14kD subu	--
PF00078.30:Reverse transcriptase (RNA-dependent DNA polymeras	THAP
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PF00048.23:Small cytokines (intecrine/chemokine), interleukin-8 lik	--
--	--
PF06936.14:Selenoprotein S (SelS)	--
PF04547.15:Calcium-activated chloride channel	--
PF00134.26:Cyclin, N-terminal domain	--

PF02214.25:BTB/POZ domain

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PF13671.9:AAA domain

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