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NO.	SOURCE	CATEGORY
1	GOTERM_BP_DIRECT	GO:0070168~negative regulatio
2	GOTERM_BP_DIRECT	GO:0043491~protein kinase B s
3	GOTERM_BP_DIRECT	GO:0042246~tissue regeneratio
4	GOTERM_BP_DIRECT	GO:0006461~protein complex a
5	INTERPRO	IPR023082:Homeo-prospero do
6	GOTERM_BP_DIRECT	GO:0070371~ERK1 and ERK2 c
7	UP_SEQ_FEATURE	region of interest:Prospero-like
8	UP_SEQ_FEATURE	DNA-binding region:Prospero-tyl
9	PIR_SUPERFAMILY	PIRSF036924:sorting nexin, Sn
10	GOTERM_BP_DIRECT	GO:0070384~Harderian gland d
11	INTERPRO	IPR014637:Sorting nexin, Snx5/
12	GOTERM_BP_DIRECT	GO:0060214~endocardium form
13	GOTERM_BP_DIRECT	GO:0006907~pinocytosis
14	GOTERM_BP_DIRECT	GO:0021861~forebrain radial gli
15	UP_SEQ_FEATURE	glycosylation site:O-linked (GalN
16	GOTERM_BP_DIRECT	GO:0048557~embryonic digesti
17	GOTERM_MF_DIRECT	GO:0032393~MHC class I recep
18	INTERPRO	IPR015404:Vps5 C-terminal
19	GOTERM_BP_DIRECT	GO:0085029~extracellular matri
20	BIOCARTA	h_eosinophilsPathway:The Role
21	BIOCARTA	h_pepiPathway:Proepithelin Cor
22	GOTERM_BP_DIRECT	GO:0030916~otic vesicle format
23	GOTERM_BP_DIRECT	GO:0032515~negative regulatio
24	GOTERM_BP_DIRECT	GO:0032808~lacrimal gland dev
25	GOTERM_CC_DIRECT	GO:0032587~ruffle membrane
26	GOTERM_BP_DIRECT	GO:0061098~positive regulation
27	GOTERM_BP_DIRECT	GO:0010837~regulation of kerat
28	INTERPRO	IPR001799:Ephrin
29	INTERPRO	IPR019765:Ephrin, conserved si
30	UP_SEQ_FEATURE	lipid moiety-binding region:GPI- $\alpha$
31	BIOCARTA	h_blymphocytePathway:B Lymph
32	GOTERM_BP_DIRECT	GO:0021915~neural tube develo
33	GOTERM_BP_DIRECT	GO:0007096~regulation of exit f
34	GOTERM_MF_DIRECT	GO:0030296~protein tyrosine ki
35	UP_KEYWORDS	Chylomicron
36	UP_KEYWORDS	GPI-anchor
37	GOTERM_BP_DIRECT	GO:0001946~lymphangiogenesi
38	GOTERM_BP_DIRECT	GO:0060174~limb bud formatior
39	GOTERM_BP_DIRECT	GO:0061564~axon developmen
40	GOTERM_BP_DIRECT	GO:0071364~cellular response t
41	INTERPRO	IPR002957:Keratin, type I
42	GOTERM_BP_DIRECT	GO:0043486~histone exchange
43	INTERPRO	IPR018039:Intermediate filamen
44	UP_SEQ_FEATURE	region of interest:Linker 12
45	UP_SEQ_FEATURE	site:Stutter
46	UP_KEYWORDS	VLDL
47	GOTERM_BP_DIRECT	GO:0043616~keratinocyte prolifi

48	GOTERM_BP_DIRECT	GO:0097320~membrane tubulat
49	GOTERM_BP_DIRECT	GO:1900004~negative regulatio
50	SMART	SM01391:SM01391
51	GOTERM_BP_DIRECT	GO:0006888~ER to Golgi vesicl
52	GOTERM_MF_DIRECT	GO:0001078~transcriptional rep
53	GOTERM_BP_DIRECT	GO:0042157~lipoprotein metabo
54	GOTERM_BP_DIRECT	GO:0045071~negative regulatio
55	GOTERM_BP_DIRECT	GO:0006518~peptide metabolic
56	GOTERM_BP_DIRECT	GO:0021819~layer formation in
57	GOTERM_BP_DIRECT	GO:0048712~negative regulatio
58	GOTERM_BP_DIRECT	GO:0050730~regulation of pepti
59	GOTERM_BP_DIRECT	GO:1900153~positive regulation
60	UP_SEQ_FEATURE	region of interest:Coil 1A
61	UP_SEQ_FEATURE	region of interest:Coil 1B
62	UP_SEQ_FEATURE	region of interest:Linker 1
63	UP_SEQ_FEATURE	region of interest:Rod
64	GOTERM_CC_DIRECT	GO:0042627~chylomicron
65	BIOCARTA	h_EfpPathway:Estrogen-respons
66	GOTERM_BP_DIRECT	GO:0033700~phospholipid efflu:
67	GOTERM_MF_DIRECT	GO:0000989~transcription facto
68	UP_SEQ_FEATURE	region of interest:Head
69	KEGG_PATHWAY	hsa04640:Hematopoietic cell lin
70	INTERPRO	IPR001664:Intermediate filamen
71	UP_KEYWORDS	Intermediate filament
72	UP_SEQ_FEATURE	region of interest:Tail
73	GOTERM_BP_DIRECT	GO:0030279~negative regulatio
74	GOTERM_BP_DIRECT	GO:0030502~negative regulatio
75	GOTERM_BP_DIRECT	GO:2000117~negative regulatio
76	GOTERM_BP_DIRECT	GO:2000179~positive regulation
77	GOTERM_MF_DIRECT	GO:0008188~neuropeptide rece
78	GOTERM_BP_DIRECT	GO:0001503~ossification
79	SMART	SM00043:CY
80	UP_SEQ_FEATURE	domain:Gla
81	GOTERM_BP_DIRECT	GO:0030949~positive regulation
82	GOTERM_BP_DIRECT	GO:0090280~positive regulation
83	GOTERM_MF_DIRECT	GO:0005543~phospholipid bindi
84	KEGG_PATHWAY	hsa05014:Amyotrophic lateral sc
85	GOTERM_BP_DIRECT	GO:0021542~dentate gyrus dev
86	GOTERM_MF_DIRECT	GO:0005549~odorant binding
87	GOTERM_BP_DIRECT	GO:0071560~cellular response t
88	GOTERM_CC_DIRECT	GO:0005615~extracellular spac
89	GOTERM_MF_DIRECT	GO:0008092~cytoskeletal protei
90	INTERPRO	IPR000010:Proteinase inhibitor
91	GOTERM_CC_DIRECT	GO:0031527~filopodium membr
92	KEGG_PATHWAY	hsa05150:Staphylococcus aureu
93	GOTERM_BP_DIRECT	GO:0030101~natural killer cell a
94	GOTERM_BP_DIRECT	GO:0043691~reverse cholesterc
95	GOTERM_BP_DIRECT	GO:0019886~antigen processin
96	INTERPRO	IPR008972:Cupredoxin
97	GOTERM_CC_DIRECT	GO:0001891~phagocytic cup

98	UP_KEYWORDS	Sialic acid
99	GOTERM_BP_DIRECT	GO:0021772~olfactory bulb dev
100	GOTERM_BP_DIRECT	GO:0032332~positive regulation
101	GOTERM_BP_DIRECT	GO:0046716~muscle cell cellula
102	GOTERM_BP_DIRECT	GO:0071385~cellular response t
103	GOTERM_CC_DIRECT	GO:0014069~postsynaptic dens
104	UP_SEQ_FEATURE	propeptide:Removed in mature f
105	GOTERM_BP_DIRECT	GO:0048146~positive regulation
106	GOTERM_CC_DIRECT	GO:0012507~ER to Golgi transp
107	INTERPRO	IPR020837:Fibrinogen, conserve
108	GOTERM_BP_DIRECT	GO:0000132~establishment of r
109	GOTERM_BP_DIRECT	GO:0046697~decidualization
110	SMART	SM00240:FHA
111	UP_KEYWORDS	ER-Golgi transport
112	GOTERM_BP_DIRECT	GO:0071456~cellular response t
113	GOTERM_CC_DIRECT	GO:0034361~very-low-density li
114	GOTERM_BP_DIRECT	GO:0031016~pancreas develop
115	GOTERM_BP_DIRECT	GO:0034394~protein localizati
116	GOTERM_BP_DIRECT	GO:0097150~neuronal stem cel
117	GOTERM_BP_DIRECT	GO:0045665~negative regulatio
118	GOTERM_MF_DIRECT	GO:0008289~lipid binding
119	GOTERM_BP_DIRECT	GO:0010719~negative regulatio
120	GOTERM_BP_DIRECT	GO:0046427~positive regulation
121	GOTERM_CC_DIRECT	GO:0031093~platelet alpha gran
122	GOTERM_MF_DIRECT	GO:0043027~cysteine-type end
123	GOTERM_BP_DIRECT	GO:0045732~positive regulation
124	GOTERM_BP_DIRECT	GO:0050679~positive regulation
125	SMART	SM00186:FBG
126	GOTERM_BP_DIRECT	GO:0007159~leukocyte cell-cell
127	GOTERM_BP_DIRECT	GO:0019433~triglyceride catabc
128	UP_SEQ_FEATURE	compositionally biased region:Gl
129	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1; c
130	UP_KEYWORDS	Lipoprotein
131	GOTERM_BP_DIRECT	GO:0009611~response to woun
132	GOTERM_BP_DIRECT	GO:0000070~mitotic sister chro
133	GOTERM_BP_DIRECT	GO:0033344~cholesterol efflux
134	GOTERM_BP_DIRECT	GO:0048709~oligodendrocyte d
135	GOTERM_MF_DIRECT	GO:0042056~chemoattractant a
136	INTERPRO	IPR014715:Fibrinogen, alpha/be
137	GOTERM_BP_DIRECT	GO:0042632~cholesterol homec
138	SMART	SM00355:ZnF_C2H2
139	KEGG_PATHWAY	hsa00030:Pentose phosphate p
140	GOTERM_BP_DIRECT	GO:0001656~metanephros deve
141	GOTERM_BP_DIRECT	GO:0032148~activation of prote
142	GOTERM_BP_DIRECT	GO:0035987~endodermal cell d
143	GOTERM_BP_DIRECT	GO:0055007~cardiac muscle ce
144	GOTERM_BP_DIRECT	GO:0070328~triglyceride homec
145	GOTERM_BP_DIRECT	GO:0072661~protein targeting to
146	GOTERM_MF_DIRECT	GO:0046875~ephrin receptor bi
147	GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis

148	GOTERM_BP_DIRECT	GO:0016050~vesicle organizatic
149	GOTERM_BP_DIRECT	GO:0032008~positive regulation
150	GOTERM_BP_DIRECT	GO:0032689~negative regulatio
151	GOTERM_BP_DIRECT	GO:0033077~T cell differentiat
152	GOTERM_BP_DIRECT	GO:0035019~somatic stem cell
153	GOTERM_MF_DIRECT	GO:0004864~protein phosphata
154	GOTERM_CC_DIRECT	GO:0046658~anchored compon
155	GOTERM_BP_DIRECT	GO:0032715~negative regulatio
156	GOTERM_BP_DIRECT	GO:0045931~positive regulation
157	GOTERM_BP_DIRECT	GO:0050766~positive regulation
158	UP_SEQ_FEATURE	region of interest:Coil 2
159	UP_SEQ_FEATURE	repeat:LRR 3
160	GOTERM_CC_DIRECT	GO:0000922~spindle pole
161	GOTERM_CC_DIRECT	GO:0072562~blood microparticl
162	GOTERM_BP_DIRECT	GO:0035690~cellular response t
163	GOTERM_BP_DIRECT	GO:0044344~cellular response t
164	UP_KEYWORDS	Primary ciliary dyskinesia
165	GOTERM_BP_DIRECT	GO:0006611~protein export fron
166	GOTERM_BP_DIRECT	GO:0097193~intrinsic apoptotic
167	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3
168	GOTERM_BP_DIRECT	GO:0070374~positive regulation
169	GOTERM_BP_DIRECT	GO:0006886~intracellular protei
170	GOTERM_BP_DIRECT	GO:0009953~dorsal/ventral patt
171	GOTERM_BP_DIRECT	GO:0045747~positive regulation
172	UP_KEYWORDS	Protein transport
173	INTERPRO	IPR014716:Fibrinogen, alpha/be
174	UP_KEYWORDS	Protease inhibitor

<b>NUMBER OF CONFIRMED HITS</b>	<b>CONFIRMED HITS (UNIPROTKB ID)</b>
3	P02765, P48436, Q14393
5	P13501, P25713, Q07352, P48436, Q14393
4	P14635, Q6Q788, P17677, O15520
8	P14635, P35612, Q9Y697, Q5TA89, Q997
2	Q92786, Q3B8N5
4	P25713, Q07352, P48436, O15520
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2	Q92786, Q3B8N5
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2	P48436, O15520
2	Q86XE0, Q9Y5X3
2	Q92786, Q9BRP0
2	P02765, Q9Y5X3
2	P10071, Q5TA89
6	P40225, P02765, Q86YL7, Q96PE5, P026
3	P10071, O15520, Q9BRP0
2	Q14943, O95971
2	Q86XE0, Q9Y5X3
2	Q92839, Q14393
2	P01911, P13501
2	P03973, P08217
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2	Q96SB3, Q49AN0
2	P48436, O15520
5	O76039, Q96SB3, Q86YL7, Q86YS7, O76
3	P13501, P25063, Q14393
2	Q07352, Q9BRP0
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4	Q9Y6M0, P20827, Q8NI32, O95971
2	P01911, P05107
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2	P35908, O15520

2	Q9UBW5, Q9NZN4
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6	O95487, Q96FJ2, Q13190, P48444, Q143
5	Q92786, Q5TA89, Q9Y466, Q3B8N5, Q9Y
3	Q9BWW8, Q6Q788, P02656
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2	Q5TA89, Q9Y466
2	P20827, P05107
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2	Q07352, P52823
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3	P10071, Q5TA89, Q9Y466
5	Q9BWW8, Q6Q788, P02656, P56589, Q9
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3	Q96NA2, Q13190, P48436
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2	P04075, P49247
2	P10071, O15520
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2	Q9HCE7, Q14393
2	P20827, O43921
3	P13501, P25089, Q9UBW5



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2	Q9Y2Q5, Q14393
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2	P10071, Q07352
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2	Q96SB3, Q8TAP8
2	P20827, O95971
2	Q86UT6, Q14393
2	P14635, O15520
2	P02765, Q14393
3	Q15323, P35908, O76011
7	Q8WXI7, Q8N6Y2, Q8N1G4, Q15345, Q86
4	P14635, Q8IYA6, Q8TDX7, O43264
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2	O14727, P25063
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5	P40225, P13501, P25713, O15520, Q1439
6	O95487, O60343, Q13190, Q99747, P484
2	P10071, Q9BRP0
2	Q5TA89, O15520
12	Q86XE0, P49321, O95487, Q96NA2, Q96
2	Q8N539, Q15485
4	O95428, P03973, Q6IE38, P01036

<b>CONFIRMED HITS (GENE SYMBOL)</b>	<b>P-VALUE</b>	<b>ENRICHMENT SCORE</b>
AHSG, SOX9, GAS6	0.0000015	5.82
CCL5, MT3, ZFP36L1, SOX9, GAS6	0.0000331	4.48
CCNB1, APOA5, GAP43, FGF10	0.0000439	4.36
CCNB1, ADD2, NFS1, HES5, NAPG, SOX	0.0000506	4.30
PROX1, PROX2	0.0001419	3.85
MT3, ZFP36L1, SOX9, FGF10	0.0001445	3.84
PROX1, PROX2	0.0001447	3.84
PROX1, PROX2	0.0001447	3.84
SNX32, SNX5	0.0001792	3.75
SOX9, FGF10	0.0003839	3.42
SNX32, SNX5	0.0004223	3.37
PROX1, OVOL2	0.000762	3.12
AHSG, SNX5	0.000762	3.12
GLI3, HES5	0.000762	3.12
THPO, AHSG, PDPN, OPALIN, APOC3, C	0.0009138	3.04
GLI3, FGF10, OVOL2	0.0010442	2.98
KIR3DS1, CD160	0.0012745	2.89
SNX32, SNX5	0.0013856	2.86
HAS1, GAS6	0.0018765	2.73
HLA-DRB1, CCL5	0.0026027	2.58
SLPI, CELA2A	0.0026027	2.58
SOX9, FGF10	0.0026075	2.58
PPP1R9B, CRY2	0.0026075	2.58
SOX9, FGF10	0.0026075	2.58
CDKL5, PPP1R9B, PDPN, C2CD5, PDE9A	0.0028562	2.54
CCL5, CD24, GAS6	0.0031122	2.51
ZFP36L1, OVOL2	0.0034507	2.46
EFNA1, EFNA2	0.0037889	2.42
EFNA1, EFNA2	0.0037889	2.42
PRSS21, EFNA1, LYPD6B, CD160	0.0040588	2.39
HLA-DRB1, ITGB2	0.0041336	2.38
PROX1, ZFP36L1, HES5	0.004266	2.37
PPP1R9B, ZW10	0.0044034	2.36
CD24, GAS6	0.0044519	2.35
APOA5, APOC3	0.0048817	2.31
CD24, PRSS21, EFNA1, LYPD6B, EFNA2	0.0052145	2.28
PROX1, PDPN	0.0054632	2.26
SOX9, FGF10	0.0054632	2.26
NEFM, GAP43	0.0054632	2.26
PPP1R9B, ZFP36L1, SOX9	0.0061615	2.21
NEFM, KRT31, KRT34	0.0064477	2.19
NASP, ANP32D	0.0066275	2.18
NEFM, KRT31, KRT2, KRT34	0.0067872	2.17
NEFM, KRT31, KRT2, KRT34	0.0070298	2.15
KRT31, KRT2, KRT34	0.0072271	2.14
APOA5, APOC3	0.0073413	2.13
KRT2, FGF10	0.0078938	2.10

<i>BIN2, EHD2</i>	0.0078938	2.10
<i>ANXA8, SPINK14</i>	0.0078938	2.10
<i>NEFM, KRT31, KRT2, KRT34</i>	0.008371	2.08
<i>SEC24B, DYNLL2, STX5, ARCN1, GAS6,</i>	0.0084079	2.08
<i>PROX1, HES5, NR2E1, PROX2, PAXBP1</i>	0.0086642	2.06
<i>APO16, APOA5, APOC3</i>	0.0091402	2.04
<i>CCL5, PROX1, SLPI</i>	0.0091402	2.04
<i>THOP1, CPN1</i>	0.0092597	2.03
<i>GLI3, NR2E1</i>	0.0092597	2.03
<i>HES5, NR2E1</i>	0.0092597	2.03
<i>EFNA1, ITGB2</i>	0.0092597	2.03
<i>TNRC6B, ZFP36L1</i>	0.0092597	2.03
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0096493	2.02
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0096493	2.02
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0096493	2.02
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0101396	1.99
<i>APOA5, APOC3</i>	0.0101755	1.99
<i>SMURF1, CCNB1</i>	0.0106384	1.97
<i>APOA5, APOC3</i>	0.0107227	1.97
<i>MLXIP, CRY2</i>	0.0108384	1.97
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0111679	1.95
<i>HLA-DRB1, THPO, CD24, EPOR</i>	0.0116937	1.93
<i>NEFM, KRT31, KRT2, KRT34</i>	0.011851	1.93
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0120652	1.92
<i>NEFM, KRT31, KRT2, KRT34</i>	0.0122612	1.91
<i>SMURF1, SOX9</i>	0.0122805	1.91
<i>AHSG, SOX9</i>	0.0122805	1.91
<i>MT3, CST4</i>	0.0122805	1.91
<i>PROX1, NR2E1</i>	0.0122805	1.91
<i>NPBWR2, SORCS2</i>	0.0124124	1.91
<i>LRRC17, AHSG, STC1, SOX9</i>	0.0125898	1.90
<i>AHSG, CST4</i>	0.0136843	1.86
<i>GAS6, PMF1</i>	0.013705	1.86
<i>MT3, FGF10</i>	0.0139307	1.86
<i>STC1, CASK</i>	0.0139307	1.86
<i>SMURF1, APOA5, APOC3, BIN2</i>	0.0145484	1.84
<i>APAF1, NEFM, GRIN2C</i>	0.0147149	1.83
<i>PROX1, NR2E1</i>	0.0156712	1.80
<i>OR8U8, OR10W1, OR5P2, OR5M10</i>	0.0157711	1.80
<i>APAF1, ZFP36L1, SOX9</i>	0.0163106	1.79
<i>THPO, CCL5, LRRC17, AHSG, CELA2A, /</i>	0.0164546	1.78
<i>DYNLL2, ALDOA, KRT2</i>	0.0165547	1.78
<i>AHSG, CST4</i>	0.0171501	1.77
<i>GAP43, PDPN</i>	0.0171949	1.76
<i>HLA-DRB1, FPR3, ITGB2</i>	0.0172599	1.76
<i>KIR3DS1, ITGB2</i>	0.0174995	1.76
<i>APOA5, APOC3</i>	0.0174995	1.76
<i>HLA-DRB1, SEC24B, DYNLL2, RILP</i>	0.0187557	1.73
<i>EFNA1, EFNA2</i>	0.019144	1.72
<i>SNX5, BIN2</i>	0.0191938	1.72

<i>PDPN, APOC3</i>	0.019328	1.71
<i>NR2E1, EFNA2</i>	0.0194136	1.71
<i>GLI3, SOX9</i>	0.0194136	1.71
<i>LARGE, ALDOA</i>	0.0194136	1.71
<i>ZFP36L1, STC1</i>	0.0194136	1.71
<i>PPP1R9B, MT3, ADD2, GAP43, GRIN2C,</i>	0.0197707	1.70
<i>CD24, PRSS21, RAB37, EFNA1, LYPD6B</i>	0.0200017	1.70
<i>CCNB1, FGF10, GAS6</i>	0.0202698	1.69
<i>HLA-DRB1, SEC24B, STX5</i>	0.0207404	1.68
<i>FIBCD1, FCN2</i>	0.0212301	1.67
<i>FGF10, ZW10</i>	0.0214113	1.67
<i>EPOR, STC1</i>	0.0214113	1.67
<i>KIF1A, AGGF1</i>	0.0230878	1.64
<i>SEC24B, NAPG, ARCN1, ZW10</i>	0.0231315	1.64
<i>CCNB1, MT3, ZFP36L1, STC1</i>	0.023216	1.63
<i>APOA5, APOC3</i>	0.0234666	1.63
<i>PROX1, FGF10</i>	0.0234904	1.63
<i>SMURF1, FGF10</i>	0.0234904	1.63
<i>PROX1, HES5</i>	0.0234904	1.63
<i>GLI3, HES5, NR2E1</i>	0.0247112	1.61
<i>APOL6, APOA5, APOC3, PEX3, ACBD6</i>	0.025043	1.60
<i>EFNA1, OVOL2</i>	0.0256488	1.59
<i>CCL5, HES5</i>	0.0256488	1.59
<i>AHSG, ALDOA, GAS6</i>	0.0280441	1.55
<i>MT3, GAS6</i>	0.0281747	1.55
<i>RILP, STX5, SOX9</i>	0.0296344	1.53
<i>CCL5, SOX9, FGF10</i>	0.0296344	1.53
<i>FIBCD1, FCN2</i>	0.0296878	1.53
<i>CCL5, ITGB2</i>	0.0301956	1.52
<i>APOA5, APOC3</i>	0.0301956	1.52
<i>NASP, SH3BGR</i>	0.031008	1.51
<i>ZNF45, ZNF234, ZNF44, ZNF563</i>	0.0318648	1.50
<i>APOL6, PRSS21, KCNA3, GAP43, RAB37</i>	0.0319538	1.50
<i>GAP43, ZFP36L1, GRIN2C</i>	0.0322759	1.49
<i>KIF25, ZW10</i>	0.0325799	1.49
<i>APOA5, APOC3</i>	0.0325799	1.49
<i>GLI3, SOX9</i>	0.0325799	1.49
<i>CCL5, FGF10</i>	0.0329162	1.48
<i>FIBCD1, FCN2</i>	0.0329609	1.48
<i>APOA5, CD24, APOC3</i>	0.0336413	1.47
<i>ZKSCAN7, MECOM, GLI3, ZNF44, ZNF27</i>	0.0343525	1.46
<i>ALDOA, RPIA</i>	0.0348677	1.46
<i>GLI3, FGF10</i>	0.0350355	1.46
<i>MT3, GAS6</i>	0.0350355	1.46
<i>MIXL1, ITGB2</i>	0.0350355	1.46
<i>PROX1, PROX2</i>	0.0350355	1.46
<i>APOA5, APOC3</i>	0.0350355	1.46
<i>SMURF1, GAS6</i>	0.0350355	1.46
<i>EFNA1, EFNA2</i>	0.0353957	1.45
<i>CCL5, FPR3, BIN2</i>	0.0364609	1.44

<i>SNX32, SNX5</i>	0.0375606	1.43
<i>LAMTOR2, GAS6</i>	0.0375606	1.43
<i>HLA-DRB1, GAS6</i>	0.0375606	1.43
<i>GLI3, ZFP36L1</i>	0.0375606	1.43
<i>SOX9, NR2E1, FGF10</i>	0.037915	1.42
<i>PPP1R9B, PPP1R35</i>	0.0379451	1.42
<i>EFNA1, CD160</i>	0.0383127	1.42
<i>NLRX1, GAS6</i>	0.0401532	1.40
<i>CCNB1, FGF10</i>	0.0401532	1.40
<i>AHSG, GAS6</i>	0.0401532	1.40
<i>KRT31, KRT2, KRT34</i>	0.0404881	1.39
<i>MUC16, LRRC17, LRRC47, LRRC41, NLF</i>	0.0406557	1.39
<i>CCNB1, CKAP2L, NEK7, ZW10</i>	0.0406869	1.39
<i>APOA5, AHSG, FCN2, AFM</i>	0.041857	1.38
<i>PPP1R9B, MT3, GAS6</i>	0.0424523	1.37
<i>CCL5, ZFP36L1</i>	0.0428115	1.37
<i>CCDC103, C21orf59</i>	0.0441691	1.35
<i>SMURF1, XPO5</i>	0.0455337	1.34
<i>APAF1, CD24</i>	0.0455337	1.34
<i>ZNF45, ZKSCAN7, MECOM, ZNF691, GLI</i>	0.0459881	1.34
<i>THPO, CCL5, MT3, FGF10, GAS6</i>	0.0460363	1.34
<i>SEC24B, TBC1D4, STX5, NAPG, ARCN1,</i>	0.0472719	1.33
<i>GLI3, OVOL2</i>	0.048318	1.32
<i>HES5, FGF10</i>	0.048318	1.32
<i>SNX32, NASP, SEC24B, RILP, RAB37, NI</i>	0.0491567	1.31
<i>FIBCD1, FCN2</i>	0.0495964	1.30
<i>PAPLN, SLPI, SPINK14, CST4</i>	0.0498504	1.30









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