

**Table S1 - The top 342 transcripts**

Order	Chromosome Position	Transcript Name	Transcript ID	Score
1	chr19:39292310-39304004	LGALS4	ENSG00000171747.4	0.138
2	chr15:40643233-40648635	PHGR1	ENSG00000233041.4	0.085
3	chr15:45722726-45878488	C15orf48	ENSG00000166920.6	0.067
4	chr7:92817898-92855837	HEPACAM2	ENSG00000188175.5	0.065
5	chr16:56659386-56661024	MT1E	ENSG00000169715.10	0.066
6	chr6:138409641-138428648	PERP	ENSG00000112378.11	0.061
7	chr10:85933493-85945050	C10orf99	ENSG00000188373.4	0.063
8	chr1:45249256-45253377	BEST4	ENSG00000142959.4	0.059
9	chr13:27825445-27830828	RPL21	ENSG00000122026.6	0.054
10	chr2:88422509-88427635	FABP1	ENSG00000163586.5	0.055
11	chr12:39040623-39303394	CPNE8	ENSG00000139117.9	0.054
12	chr12:56544579-56584068	MYL6	ENSG00000092841.14	0.053
13	chr19:40353962-40440533	FCGBP	ENSG00000090920.9	0.052
14	chr20:1290618-1373806	SDCBP2	ENSG00000125775.10	0.053
15	chr16:56700642-56701977	MT1G	ENSG00000125144.9	0.053
16	chr6:31795511-31798031	HSPA1B	ENSG00000204388.5	0.052
17	chr5:179041178-179061785	HNRNPH1	ENSG00000169045.13	0.051
18	chr1:46505811-46651630	TSPAN1	ENSG00000117472.5	0.051
19	chr16:56662970-56667898	MT1M	ENSG00000205364.3	0.051
20	chr14:103985995-103989448	CKB	ENSG00000166165.8	0.051
21	chr17:46952221-47006418	ATP5G1	ENSG00000159199.9	0.05
22	chr2:231729353-231743963	ITM2C	ENSG00000135916.11	0.049
23	chr5:149340299-149432386	SLC26A2	ENSG00000155850.7	0.049
24	chr9:131445702-131458679	SET	ENSG00000119335.12	0.048
25	chr16:29789560-29793096	ZG16	ENSG00000174992.6	0.046
26	chr1:42628361-42630389	GUCA2A	ENSG00000197273.3	0.046
27	chr14:102547074-102771537	HSP90AA1	ENSG00000080824.14	0.045
28	chr17:37004117-37010096	RPL23	ENSG00000125691.8	0.045
29	chr2:169921298-169952677	DHRS9	ENSG00000073737.12	0.044
30	chr13:111530886-111567416	ANKRD10	ENSG00000088448.10	0.043
31	chr1:17393255-17445948	PADI2	ENSG00000117115.8	0.044
32	chr11:307630-315272	IFITM2	ENSG00000185201.12	0.043
33	chr3:42734154-42846023	HIGD1A	ENSG00000181061.9	0.043
34	chr16:23765947-23770272	CHP2	ENSG00000166869.2	0.042
35	chr19:35645632-35660786	FXYD5	ENSG00000089327.10	0.042
36	chr14:21269386-21271437	RNASE1	ENSG00000129538.9	0.042
37	chr1:248902715-248903150	LYPD8	ENSG00000266949.1	0.042
38	chr11:60260250-60274903	MS4A12	ENSG00000071203.5	0.042
39	chrX:24072832-24096088	EIF2S3	ENSG00000130741.6	0.042
40	chr11:67118247-67141648	POLD4	ENSG00000175482.4	0.04
41	chr1:120290618-120311528	HMGCS2	ENSG00000134240.7	0.04
42	chr10:102106880-102124591	SCD	ENSG00000099194.5	0.039
43	chr14:106109388-106115394	IGHG2	ENSG00000211893.3	0.039
44	chr1:212208918-212280742	RPL21P28	ENSG00000220749.3	0.039
45	chr15:51633825-51700210	GLDN	ENSG00000186417.9	0.038
46	chr16:56642110-56643409	MT2A	ENSG00000125148.6	0.038
47	chr13:31710761-31736525	HSPH1	ENSG00000120694.15	0.038
48	chr9:72999502-73029540	KLF9	ENSG00000119138.3	0.038
49	chr7:128095893-128146656	HILPDA	ENSG00000135245.9	0.037
50	chr11:124617367-124635832	VSIG2	ENSG00000019102.7	0.037
51	chr4:148999912-149365850	NR3C2	ENSG00000151623.10	0.036
52	chr13:107194020-107220512	ARGLU1	ENSG00000134884.9	0.036
53	chr17:70017991-70216859	SOX9	ENSG00000125398.5	0.036

54	chr16:56691605-56694610	MT1F	ENSG00000198417.5	0.037
55	chr9:123940414-124095121	GSN	ENSG00000148180.12	0.036
56	chr8:86239836-86393722	CA2	ENSG00000104267.5	0.037
57	chr20:44095909-44110172	WFDC2	ENSG00000101443.13	0.036
58	chr14:55590827-55612126	LGALS3	ENSG00000131981.11	0.036
59	chr7:107405911-107443670	SLC26A3	ENSG00000091138.8	0.036
60	chr12:69201955-69365350	CPM	ENSG00000135678.7	0.036
61	chr4:77870855-77961537	SEPT11	ENSG00000138758.7	0.036
62	chr9:69204537-69269662	CBWD6	ENSG00000204790.8	0.036
63	chr8:86239836-86393722	CA1	ENSG00000133742.9	0.036
64	chr7:155266900-155326557	AC008060.5	ENSG00000227365.1	0.036
65	chr7:150521714-150558592	AOC1	ENSG00000002726.15	0.035
66	chr19:51515994-51523431	CTC-518B2.12	ENSG00000268739.1	0.035
67	chr19:42177234-42210895	CEACAM7	ENSG00000007306.10	0.036
68	chr12:76438669-76478813	NAP1L1	ENSG00000187109.9	0.035
69	chr17:34310326-34338658	CCL14	ENSG00000213494.5	0.035
70	chr21:44073745-44195619	PDE9A	ENSG00000160191.13	0.035
71	chr1:207925401-207968858	CD46	ENSG00000117335.14	0.035
72	chr7:19958603-20257027	RPL21P75	ENSG00000213860.3	0.035
73	chr12:20963635-21392180	SLC01B3	ENSG00000111700.8	0.035
74	chr8:145202918-145316843	MROH1	ENSG00000179832.13	0.035
75	chr4:72053002-72437804	SLC4A4	ENSG00000080493.9	0.035
76	chr12:69742120-69748014	RP11-1143G9.4	ENSG00000257764.2	0.035
77	chr17:39077681-39132178	KRT23	ENSG00000108244.12	0.035
78	chr6:134490383-134639250	SGK1	ENSG00000118515.7	0.035
79	chr1:87012760-87158886	CLCA4	ENSG0000016602.8	0.035
80	chr7:116312443-116438440	MET	ENSG00000105976.10	0.034
81	chr22:24198613-24241117	APO00350.10	ENSG00000251357.4	0.035
82	chr17:34310326-34338658	CCL15-CCL14	ENSG00000161574.11	0.034
83	chr14:106202679-106209408	IGHG1	ENSG00000211896.2	0.034
84	chr6:1312674-1314992	FOXQ1	ENSG00000164379.4	0.034
85	chr2:166813908-167232503	SCN9A	ENSG00000169432.10	0.034
86	chr19:35606731-35615228	FXD3	ENSG00000089356.12	0.034
87	chr9:130911349-130915734	LCN2	ENSG00000148346.7	0.034
88	chr5:135364583-135399507	TGFBI	ENSG00000120708.12	0.034
89	chr7:100612903-100662230	MUC12	ENSG00000205277.5	0.034
90	chr1:40798747-40799230	RP1-228H13.1	ENSG00000227311.2	0.034
91	chr15:44019115-44095241	SERF2	ENSG00000140264.15	0.034
92	chr16:23194035-23228204	SCNN1G	ENSG00000166828.2	0.034
93	chr16:66836777-66907159	CA7	ENSG00000168748.9	0.034
94	chr1:26605666-26647014	SH3BGRL3	ENSG00000142669.9	0.033
95	chr12:76419226-76427712	PHLDA1	ENSG00000139289.9	0.033
96	chr16:222845-223709	HBA2	ENSG00000188536.8	0.033
97	chr6:29909036-29913661	HLA-A	ENSG00000206503.7	0.033
98	chr17:72920369-72930007	OTOP2	ENSG00000183034.8	0.033
99	chr1:23884408-23886285	ID3	ENSG00000117318.8	0.033
100	chr13:115047058-115071283	UPF3A	ENSG00000169062.10	0.033
101	chr3:42530790-42579059	VIPR1	ENSG00000114812.8	0.033
102	chr11:27910384-27912580	RP11-1033A18.1	ENSG00000224411.2	0.033
103	chr20:61272070-61317137	SLC04A1	ENSG00000101187.11	0.033
104	chr2:102608305-102645006	IL1R2	ENSG00000115590.9	0.032
105	chr8:74202505-74268696	RPL7	ENSG00000147604.9	0.032
106	chr22:37406899-37425863	TST	ENSG00000128311.9	0.032
107	chr11:2016405-2022700	H19	ENSG00000130600.11	0.032

108	chr7:56119322-56131682	CCT6A	ENSG00000146731.6	0.032
109	chr4:120238404-120243545	FABP2	ENSG00000145384.3	0.032
110	chr1:173832385-173872687	GAS5	ENSG00000234741.3	0.032
111	chr3:172223297-172241297	TNFSF10	ENSG00000121858.6	0.031
112	chr1:22138757-22263790	RP11-26H16.1	ENSG00000232037.2	0.031
113	chr12:94960899-95044338	TMCC3	ENSG00000057704.6	0.031
114	chr16:68670091-68756519	CDH3	ENSG00000062038.9	0.031
115	chr12:69742120-69748014	LYZ	ENSG00000090382.2	0.031
116	chr6:75947390-75960039	COX7A2	ENSG00000112695.7	0.031
117	chr17:28643350-28661077	TMIGD1	ENSG00000182271.8	0.031
118	chr2:110841446-110874143	MALL	ENSG00000144063.3	0.031
119	chr1:203830730-203839678	SNRPE	ENSG00000182004.8	0.031
120	chr1:120454175-120612240	NOTCH2	ENSG00000134250.13	0.03
121	chr17:46799083-46799884	PRAC1	ENSG00000159182.3	0.031
122	chrX:102930423-102946700	MORF4L2	ENSG00000123562.12	0.03
123	chr19:2321515-2355099	LSM7	ENSG00000130332.10	0.03
124	chr2:190744334-191236391	C2orf88	ENSG00000187699.6	0.03
125	chr6:44214823-44221620	HSP90AB1	ENSG00000096384.15	0.03
126	chr16:226678-227521	HBA1	ENSG00000206172.4	0.03
127	chr19:50887460-50934570	SPIB	ENSG00000269404.2	0.03
128	chr17:73584138-73704142	SMIM5	ENSG00000204323.5	0.03
129	chr10:71962585-71993667	PPA1	ENSG00000180817.7	0.03
130	chr9:43064965-43133544	ANKRD20A3	ENSG00000132498.7	0.03
131	chr17:73028669-73061984	ATP5H	ENSG00000167863.7	0.03
132	chr4:84011200-84058228	PLAC8	ENSG00000145287.6	0.03
133	chr10:124320180-124403252	DMBT1	ENSG00000187908.11	0.03
134	chr17:72199720-72209481	RPL38	ENSG00000172809.8	0.03
135	chr13:82264045-82265207	PTMAP5	ENSG00000214182.5	0.029
136	chrY:2709526-2800041	RPS4Y1	ENSG00000129824.11	0.029
137	chr1:80916767-80917689	HNRNPA1P64	ENSG00000213559.4	0.029
138	chr16:67464554-67471456	HSD11B2	ENSG00000176387.6	0.029
139	chr12:106631654-106740793	CKAP4	ENSG00000136026.9	0.029
140	chr6:31654725-31685695	LY6G6D	ENSG00000244355.3	0.029
141	chr1:202300784-202311108	UBE2T	ENSG00000077152.5	0.029
142	chr15:81071683-81282219	KIAA1199	ENSG00000103888.11	0.029
143	chr2:66653866-66801001	MEIS1	ENSG00000143995.15	0.029
144	chr20:49348080-49373332	PARD6B	ENSG00000124171.4	0.029
145	chr17:56378591-56494956	RNF43	ENSG00000108375.8	0.029
146	chr13:45007654-45151283	TSC22D1	ENSG00000102804.10	0.029
147	chr18:55711598-56068772	NEDD4L	ENSG00000049759.12	0.029
148	chr14:74318546-74551196	ENTPD5	ENSG00000187097.8	0.029
149	chr7:157128074-157210133	DNAJB6	ENSG00000105993.10	0.029
150	chr3:123304388-123603178	MYLK	ENSG00000065534.14	0.029
151	chr12:104164230-104234975	NT5DC3	ENSG00000111696.7	0.029
152	chr1:26605666-26647014	UBXN11	ENSG00000158062.16	0.029
153	chr9:36190852-36304921	GNE	ENSG00000159921.10	0.029
154	chr1:148003641-148025863	NBPF14	ENSG00000122497.13	0.029
155	chr13:32889610-32973805	BRCA2	ENSG00000139618.10	0.029
156	chr16:67464554-67471456	AC009061.1	ENSG00000203401.4	0.029
157	chr20:33432522-33515769	ACSS2	ENSG00000131069.15	0.029
158	chr6:1610680-1614127	FOXC1	ENSG00000054598.5	0.029
159	chrM:8365-9990	MT-ATP8	ENSG00000228253.1	0.029
160	chr19:35615416-35645204	LGI4	ENSG00000153902.9	0.029
161	chr13:113831890-113919399	CUL4A	ENSG00000139842.10	0.029

162	chr11:114441312-114466484	NXPE4	ENSG00000137634.5	0.029
163	chr2:102313311-102511150	MAP4K4	ENSG00000071054.11	0.028
164	chr9:70856396-70914929	CBWD3	ENSG00000196873.11	0.028
165	chr19:51515994-51523431	KLK10	ENSG00000129451.7	0.028
166	chr20:55743803-55841685	BMP7	ENSG00000101144.8	0.028
167	chr16:14766404-14788526	PLA2G10	ENSG00000069764.5	0.028
168	chr1:86934050-86965972	CLCA1	ENSG00000016490.11	0.028
169	chr19:51525471-51531295	KLK11	ENSG00000167757.9	0.028
170	chr6:33217310-33244287	RPS18	ENSG00000231500.2	0.028
171	chr13:50601268-51423190	DLEU2	ENSG00000231607.4	0.028
172	chr10:18041217-18089855	TMEM236	ENSG00000184040.7	0.028
173	chr16:75145757-75150669	LDHD	ENSG00000166816.9	0.028
174	chr20:52553315-52687304	BCAS1	ENSG00000064787.8	0.028
175	chr1:28832454-28865812	SNHG3	ENSG00000242125.2	0.028
176	chr4:15937191-15940363	FGFBP1	ENSG00000137440.3	0.028
177	chr9:127997131-128003609	HSPA5	ENSG00000044574.7	0.028
178	chr5:83236372-83786583	EDIL3	ENSG00000164176.8	0.028
179	chr1:42619091-42621495	GUCA2B	ENSG00000044012.3	0.028
180	chr2:85788684-85809154	VAMP8	ENSG00000118640.6	0.028
181	chr4:48499377-48782339	FRYL	ENSG00000075539.9	0.027
182	chr12:14956505-15059520	ART4	ENSG00000111339.6	0.027
183	chr1:200374067-200379184	ZNF281	ENSG00000162702.7	0.027
184	chr14:62453802-62568431	SYT16	ENSG00000139973.11	0.027
185	chr6:144606836-145174170	UTRN	ENSG00000152818.14	0.027
186	chr3:108015375-108097132	HHLA2	ENSG00000114455.9	0.027
187	chr13:53602893-53626192	OLFM4	ENSG00000102837.6	0.027
188	chr7:12609750-12693228	SCIN	ENSG00000006747.10	0.027
189	chr8:124864226-125183763	FER1L6	ENSG00000214814.2	0.027
190	chr16:9250218-9250761	RPL21P119	ENSG00000220793.4	0.027
191	chr14:54416453-54425479	BMP4	ENSG00000125378.11	0.027
192	chr9:67926760-67987998	ANKRD20A1	ENSG00000196774.3	0.027
193	chr6:122793075-123047518	PKIB	ENSG00000135549.10	0.027
194	chr22:24105207-24126503	CHCHD10	ENSG00000250479.4	0.027
195	chr1:148250248-148347506	NBPF20	ENSG00000203832.6	0.027
196	chr21:42836477-42903043	TMPRSS2	ENSG00000184012.7	0.027
197	chr16:89627064-89630950	RPL13	ENSG00000167526.9	0.027
198	chr17:34310326-34338658	CCL15	ENSG00000267596.1	0.027
199	chr17:34083267-34122711	MMP28	ENSG00000129270.11	0.027
200	chr4:100226120-100242558	ADH1B	ENSG00000196616.8	0.027
201	chr13:100634025-100639018	ZIC2	ENSG00000043355.6	0.027
202	chr14:92582465-92588261	NDUFB1	ENSG00000183648.5	0.027
203	chr6:31654725-31685695	MEGT1	ENSG00000250641.1	0.027
204	chr6:46761126-46807515	MEP1A	ENSG00000112818.5	0.027
205	chr1:160846328-160854960	ITLN1	ENSG00000179914.4	0.027
206	chr9:75766672-75785309	ANXA1	ENSG00000135046.9	0.027
207	chr5:76506273-76916436	RPL7P23p	ENSG00000244363.2	0.027
208	chr7:100547186-100611410	RP11-395B7.2	ENSG00000225946.1	0.027
209	chr16:4827669-4846533	SMIM22	ENSG00000267795.1	0.027
210	chr16:56716335-56721964	MT1X	ENSG00000187193.8	0.027
211	chr3:185764096-186080026	ETV5	ENSG00000244405.3	0.026
212	chr5:142657495-142815077	RP11-278J6.1	ENSG00000231579.3	0.026
213	chr7:130621222-130624420	RP11-138A9.2	ENSG00000273319.1	0.026
214	chr19:1285889-1378430	EFNA2	ENSG00000099617.2	0.026
215	chr15:45879320-45983492	SQRDL	ENSG00000137767.9	0.026

216	chr7:128095893-128146656	RP11-155G14. 6	ENSG00000240758. 2	0. 026
217	chr3:142168076-142297668	ATR	ENSG00000175054. 10	0. 026
218	chr20:34633543-34638882	LINC00657	ENSG00000260032. 1	0. 026
219	chr10:112629500-112679032	BBIP1	ENSG00000214413. 3	0. 026
220	chr10:122114176-122114718	RP11-572P18. 1	ENSG00000220842. 5	0. 026
221	chr14:106130969-106136180	IGHGP	ENSG00000253755. 1	0. 026
222	chr12:6456008-6500733	SCNN1A	ENSG00000111319. 8	0. 026
223	chr16:25227051-25240261	AQP8	ENSG00000103375. 6	0. 026
224	chr19:36139124-36149763	COX6B1	ENSG00000126267. 4	0. 026
225	chr7:34386123-34917944	NPSR1	ENSG00000187258. 9	0. 026
226	chr2:55401926-55462989	RPS27A	ENSG00000143947. 8	0. 026
227	chr19:31765850-31908700	TSHZ3	ENSG00000121297. 6	0. 026
228	chr13:27998680-28024739	GTF3A	ENSG00000122034. 8	0. 026
229	chr11:61976139-62028021	SCGB2A1	ENSG00000124939. 4	0. 026
230	chr2:9983482-10074545	TAF1B	ENSG00000115750. 12	0. 026
231	chr11:127810807-127811549	RP11-676M6. 1	ENSG00000254612. 2	0. 025
232	chr17:18380050-18398259	LGALS9C	ENSG00000171916. 12	0. 025
233	chr4:128702975-128765195	RP11-50D9. 1	ENSG00000244021. 3	0. 025
234	chr4:39500374-39640710	SMIM14	ENSG00000163683. 7	0. 025
235	chr5:130759613-131132710	FNIP1	ENSG00000217128. 7	0. 025
236	chr7:92759367-92777682	SAMD9L	ENSG00000177409. 7	0. 025
237	chr21:42676138-42729358	FAM3B	ENSG00000183844. 12	0. 025
238	chr10:102133371-102143125	LINC00263	ENSG00000235823. 1	0. 025
239	chr12:104382761-104457961	RP11-490H24. 5	ENSG00000216285. 4	0. 025
240	chr17:16592850-16719854	UPF3AP1	ENSG00000226478. 2	0. 025
241	chr16:14821138-14827204	RP11-719K4. 3	ENSG00000254609. 1	0. 025
242	chr1:24128374-24165110	HMGCL	ENSG00000117305. 10	0. 025
243	chr11:2909009-2946476	SLC22A18AS	ENSG00000254827. 1	0. 025
244	chr12:56119106-56124467	CD63	ENSG00000135404. 7	0. 025
245	chr7:32535037-33102409	FKBP9	ENSG00000122642. 6	0. 025
246	chr7:65216128-65228341	CCT6P1	ENSG00000228409. 1	0. 025
247	chr10:63661058-63856703	ARID5B	ENSG00000150347. 10	0. 025
248	chr4:75230859-75254468	EREG	ENSG00000124882. 3	0. 025
249	chr16:11641852-11730237	LITAF	ENSG00000189067. 8	0. 025
250	chr17:74620842-74639920	ST6GALNAC1	ENSG00000070526. 10	0. 025
251	chr6:5102826-5261172	LYRM4	ENSG00000214113. 6	0. 025
252	chr4:89011415-89152474	ABCG2	ENSG00000118777. 6	0. 025
253	chr17:1614804-1641893	MIR22HG	ENSG00000186594. 8	0. 025
254	chrM:8365-9990	MT-ATP6	ENSG00000198899. 2	0. 025
255	chr19:22235253-22274282	ZNF257	ENSG00000197134. 7	0. 024
256	chr19:17970684-17974962	RPL18A	ENSG00000105640. 8	0. 024
257	chr12:69201955-69365350	MDM2	ENSG00000135679. 17	0. 024
258	chr18:61143993-61172318	RP11-635N19. 3	ENSG00000269989. 1	0. 024
259	chrX:99929487-99987110	SYTL4	ENSG00000102362. 11	0. 024
260	chr7:155755325-155759037	AC021218. 2	ENSG00000204876. 4	0. 024
261	chr10:105239359-105615301	NEURL	ENSG00000107954. 6	0. 024
262	chr2:89246818-89247475	IGKV1-5	ENSG00000243466. 1	0. 024
263	chr22:24198613-24241117	AP000350. 4	ENSG00000218537. 1	0. 024
264	chr1:55446464-55457966	TMEM61	ENSG00000143001. 4	0. 024
265	chr5:21616370-22853731	HSPD1P1	ENSG00000213430. 5	0. 024
266	chr10:105239359-105615301	RP11-416N2. 4	ENSG00000273108. 1	0. 024
267	chr16:56651387-56652730	MT1L	ENSG00000260549. 1	0. 024
268	chr4:100010007-100222513	ADH1A	ENSG00000187758. 3	0. 024
269	chr1:168338291-168338839	RP5-1059H15. 1	ENSG00000227722. 1	0. 024

270	chr1:144811743-144830413	NBPF9	ENSG00000168614.13	0.024
271	chr1:200890121-200935658	MROH3P	ENSG00000233217.1	0.024
272	chr10:7830091-7849778	ATP5C1	ENSG00000165629.15	0.024
273	chr18:9708161-9862548	RAB31	ENSG00000168461.8	0.024
274	chr2:10085340-10142411	GRHL1	ENSG00000134317.13	0.024
275	chr20:60877148-60942368	LAMA5	ENSG00000130702.9	0.024
276	chrX:129757349-130037208	ENOX2	ENSG00000165675.12	0.024
277	chr12:67663060-67713731	CAND1	ENSG00000111530.8	0.024
278	chr19:42901279-43156507	CEACAM1	ENSG00000079385.17	0.024
279	chr9:127019884-127115586	NEK6	ENSG00000119408.12	0.023
280	chr9:136336216-136344259	SLC2A6	ENSG00000160326.9	0.023
281	chrX:106045909-106243474	CLDN2	ENSG00000165376.6	0.023
282	chr9:21802541-22121096	CDKN2B-AS1	ENSG00000240498.2	0.023
283	chr21:15608526-15735075	ABCC13	ENSG00000243064.4	0.023
284	chr4:4269427-4291896	LYAR	ENSG00000145220.9	0.023
285	chr10:1034337-1095110	GTPBP4	ENSG00000107937.14	0.023
286	chr12:54624723-54745633	HNRNPA1	ENSG00000135486.13	0.023
287	chrX:70835765-70838367	CXCR3	ENSG00000186810.7	0.023
288	chr19:49375648-49379314	PPP1R15A	ENSG00000087074.7	0.023
289	chr8:141667998-142012315	PTK2	ENSG00000169398.15	0.023
290	chr17:7465191-7536700	SNORD10	ENSG00000238917.1	0.023
291	chr13:42614175-42830714	DGKH	ENSG00000102780.12	0.023
292	chr11:94883702-94967268	SESN3	ENSG00000149212.6	0.023
293	chr2:235401684-235405697	ARL4C	ENSG00000188042.5	0.023
294	chr6:100956069-101329248	ASCC3	ENSG00000112249.9	0.023
295	chr11:104896169-104972158	CARD16	ENSG00000204397.3	0.023
296	chrX:151121595-151143152	GABRE	ENSG00000102287.12	0.023
297	chr20:19867164-19983101	RIN2	ENSG00000132669.8	0.023
298	chr10:70975088-71027904	RP11-227H15.4	ENSG00000229261.1	0.023
299	chrX:17755587-17773105	SCML1	ENSG00000047634.10	0.023
300	chr1:211916798-212027045	LPGAT1	ENSG00000123684.8	0.023
301	chr5:149546357-149564120	CDX1	ENSG00000113722.12	0.023
302	chr1:161475219-161648444	HSPA6	ENSG00000173110.6	0.023
303	chr7:127937737-127983962	RBM28	ENSG00000106344.4	0.023
304	chr13:95226307-95248511	TGDS	ENSG00000088451.6	0.023
305	chr10:135093134-135166187	ZNF511	ENSG00000198546.10	0.022
306	chr11:14665268-14892350	PDE3B	ENSG00000152270.4	0.022
307	chr3:142315228-142432506	PLS1	ENSG00000120756.8	0.022
308	chr7:95034174-95064510	PON2	ENSG00000105854.8	0.022
309	chr7:75931860-75933612	HSPB1	ENSG00000106211.8	0.022
310	chr3:149086808-149104370	TM4SF1	ENSG00000169908.6	0.022
311	chr12:6643092-6647537	RP5-940J5.9	ENSG00000269968.1	0.022
312	chr7:100951626-100954266	RP11-132A1.4	ENSG00000232445.1	0.022
313	chr2:62759717-62760194	AC092155.1	ENSG00000229503.1	0.022
314	chr10:112836789-112840658	ADRA2A	ENSG00000150594.5	0.022
315	chr16:66968346-67009051	CES3	ENSG00000172828.8	0.022
316	chrM:8365-9990	MT-CO3	ENSG00000198938.2	0.022
317	chr5:473350-524447	CTD-2228K2.7	ENSG00000225138.3	0.022
318	chr16:14860258-14863932	RP11-680G24.1	ENSG00000255037.1	0.022
319	chr13:72012097-72441330	H3F3BP1	ENSG00000236534.1	0.022
320	chr11:102391238-102401484	MMP7	ENSG00000137673.4	0.022
321	chr1:144146807-144224481	NBPF8	ENSG00000162825.12	0.022
322	chr1:20808883-20812713	CAMK2N1	ENSG00000162545.5	0.022
323	chr5:85913720-85916779	COX7C	ENSG00000127184.6	0.022

324	chr3:22423309-22424420	HMGB1P5	ENSG00000132967.9	0.022
325	chr22:24198613-24241117	MIF	ENSG00000240972.1	0.022
326	chr17:29224353-29286340	TEFM	ENSG00000172171.6	0.022
327	chr7:73007523-73038873	MLXIPL	ENSG00000009950.11	0.022
328	chr8:29952913-30041156	RPS15AP24	ENSG00000241511.1	0.022
329	chr7:87462882-87538856	DBF4	ENSG00000006634.3	0.022
330	chr5:27472398-27496508	LINC01021	ENSG00000250337.1	0.022
331	chr20:56884751-56942563	RAB22A	ENSG00000124209.3	0.022
332	chr16:54952774-54963101	CRNDE	ENSG00000245694.4	0.022
333	chr2:103236165-103327777	SLC9A2	ENSG00000115616.2	0.022
334	chr2:41370919-41384695	HNRNPA1P57	ENSG00000237442.3	0.022
335	chr20:47835883-47905797	ZFAS1	ENSG00000177410.8	0.022
336	chr16:89642175-89663654	CPNE7	ENSG00000178773.10	0.022
337	chr5:92953774-93447404	NPM1P27	ENSG00000249353.2	0.022
338	chrX:73164158-73513409	RP3-368A4.5	ENSG00000271430.1	0.022
339	chrX:118722299-118739858	NKRF	ENSG00000186416.8	0.022
340	chr19:12305829-12405702	ZNF44	ENSG00000197857.9	0.022
341	chr11:67351065-67354131	GSTP1	ENSG00000084207.11	0.022
342	chr16:2089815-2185899	PKD1	ENSG00000008710.13	0.022

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