

#Refseq Gene	Cluster start	Cluster end	Cluster score
NM_001080825	TMEM120B	6800 6842	7.73598845977
NM_001469	XRCC6 1714	1764	1.35919673053
NM_004104	FASN 7168	7216	6.35855227554
NM_004104	FASN 4031	4089	6.58094493279
NM_004104	FASN 3576	3618	5.35453491128
NM_004104	FASN 3157	3210	6.01137889624
NM_004104	FASN 6546	6597	6.58094492524
NM_004104	FASN 2747	2786	5.76957241056
NM_004104	FASN 6159	6209	6.77358327968
NM_004104	FASN 4999	5043	6.49680572341
NM_004104	FASN 3785	3860	6.09551786971
NM_004104	FASN 4552	4654	4.77358327968
NM_004104	FASN 4420	4488	4.77358327968
NM_004104	FASN 5429	5484	4.68945080135
NM_004104	FASN 4917	4995	6.58093820174
NM_007107	SSR3 504	604	6.47528546246
NM_007107	SSR3 607	673	4.73831963238
NM_007107	SSR3 366	494	7.32328236902
NM_007104	RPL10A 513	560	1.05175158419
NM_007104	RPL10A 114	170	1.58628390084
NM_000483	APOC2 465	500	4.17742851716
NM_001682	ATP2B1 2023	2133	9.2754600998
NM_001682	ATP2B1 1728	1750	7.51324898531
NM_001682	ATP2B1 966	1019	8.19132089042
NM_001683	ATP2B2 1218	1268	10.1472446872
NM_001011722	ARHGEF10L	2522 2563	7.54905593197
NM_020199	C5orf15 583	633	8.68375559916
NM_020198	CCDC47 746	792	6.73159028378
NM_020198	CCDC47 695	728	5.08756034369
NM_020198	CCDC47 947	991	5.99462468961
NM_020198	CCDC47 1147	1188	3.08756034369
NM_020198	CCDC47 1557	1604	4.89508901584
NM_020198	CCDC47 1000	1038	3.08772736295
NM_020198	CCDC47 1191	1295	6.67269659473
NM_020198	CCDC47 849	945	4.40966218889
NM_020198	CCDC47 401	503	5.40966218889
NM_020198	CCDC47 514	647	5.89508901606
NM_004818	DDX23 421	502	5.72195463831
NM_020190	OLFML3 1080	1129	11.6903025477
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NM_020190	OLFML3 783	822	10.6061633386
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NM_003688	CASK 2566	2587	8.08118779235
NM_003681	PDXK 4747	4765	5.01646291884
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NM_003685	KHSRP 878	947	4.81837406442
NM_002889	RARRES2 420	470	8.5236058168
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NM_002889	RARRES2	49	161	9.5236058168
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NM_001004067	NOM03	3567	3617	2.81919915033
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NM_005689	ABCB6	2006	2039	6.36024173495
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NM_018050	MANSC1	1497	1586	9.16632000884
NM_001130006	GSPT1	248	297	4.51091392603
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NM_001142355	NIF3L1	596	614	5.97323286678
NM_079834	SCAMP4	575	604	8.05322863404
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NM_014914	AGAP1	541	571	6.73418574377
NM_014916	LMTK2	185	268	10.8764289681
NM_005022	PFN1	713	772	5.17064962553
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NM_001005335	HNRNPL	542	576	3.56328651419
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NM_001853	COL9A3	192	302	9.47546597446
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NM_001853	COL9A3	1708	1754	8.47144837429
NM_001853	COL9A3	1812	1860	8.39132676508
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NM_001852	COL9A2	2302	2337	8.43126800651
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NM_004649	C21orf33		886	906 4.5613959977
NM_032039	ITFG3	710	763	9.90428754881
NM_001144	AMFR	1219	1274	8.44174319428
NM_004315	ASAH1	1149	1193	5.09194240141
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NM_001686	ATP5B	1164	1235	5.42301918941
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NM_025029	MZT2B	515	567	3.98054334459
NM_016454	TMEM85	576	626	7.97642495715
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NM_001689	ATP5G3	269	314	2.01552061978
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NM_006640	SEPT9	4018	4085	5.23493395921
NM_006648	WNK2	2453	2493	10.4903624337
NM_001184781	DGCR2	3236	3271	7.57963861107
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NM_177983	PPM1G	1154	1191	4.11380103669
NM_001080542	FBF1	3187	3209	14.0248167466
NM_001011551	C1GALT1C1		485	528 7.25730110958
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NM_014742	TM9SF4	1454	1518	7.17428766881
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NM_032772	ZNF503	1061	1091	9.68259306241
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NM_001077484	SLC38A1	1383	1414	9.54683644448
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NM_015168	ZC3H4	653	724	8.68299819888
NM_015161	ARL6IP1	529	627	7.39112937927
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NM_001333	CTSL2	650	718	8.48718318146
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NM_004127	GPS1	1061	1103	4.46614656093
NM_001448	GPC4	1649	1678	13.236668479
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NM_001164262	PPIAL4F	534	561	6.76356690503
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NM_000313	PROS1	1370	1411	5.56028658407
NM_000312	PROC	544	588	3.62712261077
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NM_000310	PPT1	435	494	7.32160131404
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NM_138788	TMEM45B	728	810	7.34488666288
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NM_138783	ZNF653	130	153	11.8359193115
NM_173514	SLC38A9	1841	1876	8.80425845735
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NM_001174136	TDGF1	238	258	9.22591628447
NM_139322	ATRN	77	147	6.893288276
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NM_001170937	FUS	744	781	3.77133205799
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NM_006435	IFITM2	221	289	8.69283262919
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NM_006432	NPC2	636	698	10.7405003044
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NM_015375	DSTYK	52	87	10.7895697959
NM_018211	RAVER2	4034	4055	8.58172001021
NM_002203	ITGA2	2501	2542	10.0341910452
NM_002203	ITGA2	3263	3310	8.35611240906
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NM_001166114	PNPLA6	756	813	10.4936239917
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NM_033161	SURF4	795	837	7.42074801777
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NM_002951	RPN2	1826	1871	4.65431097598
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NM_002951	RPN2	1935	2022	5.80115236431
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NM_002951	RPN2	302	376	1.846955818
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NM_014681	DHX34	3508	3564	9.57822226703
NM_133631	ROB01	5534	5562	6.50644321864
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NM_133631	ROB01	3247	3274	5.42632160943
NM_133631	ROB01	2261	2320	4.92549831054
NM_014976	PDCD11	4566	4603	6.92777334533
NM_005005	NDUFB9	206	262	3.62962937546
NM_213611	SLC25A3	541	620	4.11328963859
NM_080476	PIGU	1275	1343	9.73715149016
NM_080476	PIGU	1185	1220	8.08490104326
NM_001034852	SMOC1	719	751	5.94084430649
NM_001034852	SMOC1	1253	1289	4.35588180577
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NM_001784	CD97	1007	1047	11.5176783272
NM_001784	CD97	1238	1264	9.51767832725
NM_001784	CD97	2214	2251	9.43755671804
NM_001784	CD97	1705	1773	12.3290508495
NM_182646	CPEB2	1049	1080	10.8391769753
NM_182646	CPEB2	1435	1461	9.83515937508
NM_021977	SLC22A3	19	43	8.32977788342
NM_001024912	CEACAM1	1555	1582	3.41571810333
NM_198310	TTC8	1848	1869	9.03505099556
NM_000784	CYP27A1	956	1044	7.28520291356
NM_000784	CYP27A1	1146	1208	6.47784775559
NM_000784	CYP27A1	780	836	4.97867128284
NM_016306	DNAJB11	417	471	3.47567647651
NM_016306	DNAJB11	1019	1065	2.89054022548
NM_016306	DNAJB11	340	415	4.69806889785
NM_016306	DNAJB11	1255	1317	3.89071397558
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NM_016306	DNAJB11	730	774	3.47566974547
NM_016306	DNAJB11	1132	1187	4.8907139758
NM_016306	DNAJB11	820	946	5.06063897724
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NM_015966	ERGIC3	1219	1276	4.63935724754
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NM_015966	ERGIC3	511	580	3.26084562428
NM_015966	ERGIC3	921	995	3.93891752918
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NM_015966	ERGIC3	326	428	3.74627245146
NM_015965	NDUFA13	319	349	2.64016912084
NM_004566	PFKFB3	259	292	7.92841442179
NM_172251	MRPL54	287	306	6.5031875474
NM_001032281	TFPI	730	775	2.34672937947
NM_001032281	TFPI	843	918	2.56912180835
NM_001032281	TFPI	527	593	3.93169188774
NM_001032281	TFPI	777	816	2.08369498118
NM_031157	HNRNPA1	160	249	2.18279863716
NM_014762	DHCR24	1400	1512	6.9578006418
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NM_014762	DHCR24	1833	1878	4.82029688213
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NM_014762	DHCR24	352	383	4.81627951787
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NM_014762	DHCR24	655	818	7.58583186441
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NM_014765	TOMM20	619	662	1.77801391205
NM_018685	ANLN	1849	1911	8.02498686737
NM_018687	C19orf80		279	339 7.55520059312
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NM_032717	AGPAT9	563	607	10.6078542782
NM_032717	AGPAT9	1486	1527	10.3409760225
NM_015140	TTLL12	3	36	8.87842285508
NM_015149	RGL1	597	618	9.33601133278
NM_170665	ATP2A2	991	1046	6.19987427154
NM_170665	ATP2A2	1779	1845	7.47998219096
NM_170665	ATP2A2	2316	2386	6.56244435115
NM_170665	ATP2A2	2535	2605	7.47998219096
NM_170665	ATP2A2	1641	1697	6.71444744437
NM_170665	ATP2A2	2472	2507	6.85195096834



NM_170665	ATP2A2	2916	2952	6.19987403585
NM_170665	ATP2A2	617	657	5.71444743705
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NM_170665	ATP2A2	927	987	7.47998219096
NM_170665	ATP2A2	2264	2309	6.71444744459
NM_170665	ATP2A2	2613	2740	8.43691346907
NM_170665	ATP2A2	1556	1635	7.85195096834
NM_170665	ATP2A2	3188	3289	8.03637553948
NM_170665	ATP2A2	2070	2120	3.38850174953
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NM_001178115	ZNF185	1403	1421	11.6355824303
NM_015607	CHTOP	932	992	7.51033333136
NM_001100626	ERLIN1	705	754	3.41128967404
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NM_021203	SRPRB	517	569	8.03176733935
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NM_001146158	MOGS	359	463	8.09906932619
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NM_001146152	CYP51A1	1128	1187	7.99080373805
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NM_001146152	CYP51A1	1315	1368	5.5717486386
NM_001146152	CYP51A1	263	346	6.99080373051
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NM_021064	HIST1H2AG		283	329 9.30924466807
NM_001142676	CHID1	580	632	8.59030537702
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NM_002127	HLA-G	828	888	8.50432407836
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NM_001166133	FRAS1	1358	1431	10.7128630777

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NM_153615	RGL4	159	177	10.9041912574
NM_004859	CLTC	3188	3234	5.87862087492
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NM_004859	CLTC	4236	4276	5.3970378976
NM_004859	CLTC	4457	4530	4.07126595286
NM_004859	CLTC	4872	4931	5.66007230344
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NM_004501	HNRNPU	613	717	3.93713888179
NM_004501	HNRNPU	1296	1370	2.35217637352
NM_004852	ONECUT2	152	198	9.57728877696
NM_198129	LAMA3	5929	5966	13.1620487486
NM_000999	RPL38	142	234	2.53193383904
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NM_000990	RPL27A	640	701	3.7687881058
NM_000997	RPL37	239	306	1.49211621085
NM_000997	RPL37	188	223	0.492116210853
NM_002046	GAPDH	816	866	2.45332395592
NM_002046	GAPDH	731	805	3.56880790439
NM_002046	GAPDH	686	719	0.864350586078
NM_002046	GAPDH	548	641	2.19028955008
NM_015241	MICAL3	7531	7579	10.2775775705
NM_001163524	ITPRIPL1		849	903 9.47618726245
NM_001025234	TSPAN4	335	388	8.69292377405
NM_001025234	TSPAN4	542	565	7.19210024679
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NM_018279	TMEM19	1082	1137	7.86727074006
NM_001145408	NONO	1642	1682	3.73889398191
NM_015317	PUM2	4669	4689	4.91446012214
NM_012339	TSPAN15	1410	1431	8.49216966467
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NM_014402	UQCRQ	24	73	5.17624336288
NM_005065	SEL1L	2118	2160	6.18534409255
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NM_005063	SCD	980	1061	7.34078275708
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NM_001762	CCT6A	782	814	3.8005458003	
NM_020928	ZSWIM6	419	461	9.71962564676	
NM_001106	ACVR2B	7692	7712	9.73307185548	
NM_001101	ACTB	384	449	4.4140212333	
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NM_198332	STAT2	542	563	7.26268947507	
NM_016142	HSD17B12		589	643	5.19432015454
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NM_016145	C19orf56		500	556	8.6676359899
NM_198335	GANAB	1773	1840	6.17198652554	
NM_198335	GANAB	804	878	7.17198676146	
NM_198335	GANAB	2608	2683	8.04645587938	
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NM_198335	GANAB	752	792	7.39437245175	
NM_198335	GANAB	1919	1985	8.67448710199	
NM_198335	GANAB	119	186	6.90895235562	
NM_198335	GANAB	878	1016	10.2308804505	
NM_198335	GANAB	3155	3190	6.08784755208	
NM_198335	GANAB	3522	3580	6.58300666057	
NM_198335	GANAB	2558	2599	6.16796916129	
NM_198335	GANAB	2018	2153	9.3943791828	
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NM_198335	GANAB	1365	1521	9.8724264796	
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NM_198335	GANAB	1605	1717	8.97934168352	
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NM_198335	GANAB	631	720	8.58702426074	
NM_198335	GANAB	2765	2922	9.54122057113	
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NM_017814	TMEM161A		981	1030	11.591453005
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NM_017811	UBE2R2	1193	1229	5.09088775997	
NM_017813	IMPAD1	201	244	7.53222485202	
NM_138426	GLCCI1	425	448	10.6087762916	
NM_198841	FAM120AOS		2184	2204	10.1003366629
NM_198591	BSG	1250	1291	3.79513504412	
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NM_024334	TMEM43	447	470	8.19227195631	
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NM_178862	STT3B	1620	1687	7.7185150432	
NM_178862	STT3B	2013	2047	6.71449745057	
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NM_178865	SERINC2	765	815	8.78559576656	
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NM_001078175	SLC29A1	1436	1477	9.67255866846	
NM_001078175	SLC29A1	1002	1045	7.26649809525	
NM_006579	EBP	740	837	9.05283758878	
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NM_003051	SLC16A1	1620	1655	5.16703931184	
NM_003051	SLC16A1	799	849	5.65246637493	
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NM_002901	RCN1	791	822	7.50149295788	

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NM_001190836	DCTN1	1642	1662	4.00137628007
NM_014918	CHSY1	1853	1879	8.47222320968
NM_031284	ADPGK	1090	1149	6.70694380584
NM_032737	LMNB2	1019	1080	7.30962349686
NM_001005498	RHBDF2	2373	2423	10.1076665335
NM_015127	CLCC1	754	798	9.08124106381
NM_015127	CLCC1	1261	1316	8.49627855554
NM_033280	SEC11C	470	510	5.83410489825
NM_003262	SEC62	955	1047	5.61691983802
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NM_001031696	PLD3	822	874	9.49113866565
NM_001031696	PLD3	1850	1906	8.61649579742
NM_001031696	PLD3	1358	1406	9.83906196907
NM_001031696	PLD3	772	818	8.61265194757
NM_001031696	PLD3	1232	1276	9.93859764263
NM_001031696	PLD3	1307	1344	9.03170031596
NM_001031696	PLD3	658	704	9.03170704701
NM_001031696	PLD3	2030	2068	8.02768944684
NM_001031696	PLD3	455	511	9.49113866565
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NM_003618	MAP4K3	163	191	4.32182348724
NM_033467	MMEL1	665	687	11.2882606744
NM_001376	DYNC1H1	8877	8945	7.47389612955
NM_001376	DYNC1H1	14017	14051	6.47790699867
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NM_001376	DYNC1H1	4760	4799	6.05885863027
NM_001376	DYNC1H1	2777	2808	6.71570261522
NM_001376	DYNC1H1	9066	9138	6.06286949939
NM_001376	DYNC1H1	9754	9843	8.06287623044
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NM_001376	DYNC1H1	12262	12342	6.39377452034
NM_001377	DYNC2H1	1047	1067	13.4261888072
NM_015544	TMEM98	974	1050	4.83033921454
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NM_018317	TBC1D19	575	594	11.4722467605
NM_000355	TCN2	67	88	11.3417683739
NM_000354	SERPINA7		1096	1122 3.6943297507
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NM_000428	LTBP2	2952	3000	11.3426653072
NM_000428	LTBP2	5694	5751	15.0471226255
NM_000428	LTBP2	4016	4054	12.8475061987
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NM_000428	LTBP2	4403	4503	13.3466761763

NM_000428	LTBP2	493	544	12.8475061987
NM_000428	LTBP2	2343	2424	13.6686042712
NM_000428	LTBP2	5245	5300	12.8475061987
NM_006811	SERINC3	659	705	7.17695794451
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NM_006816	LMAN2	1203	1237	4.06458258654
NM_006816	LMAN2	916	966	6.39052827406
NM_006816	LMAN2	693	758	6.06860018671
NM_006816	LMAN2	807	865	6.23852518815
NM_006816	LMAN2	525	552	5.30638907222
NM_006816	LMAN2	334	403	4.06458258654
NM_001190946	FAM193B	13	62	9.6879047674
NM_006815	TMED2	251	309	3.13340279123
NM_006815	TMED2	30	69	0.811474932266
NM_003334	UBA1	29	65	6.41669676991
NM_006744	RBP4	869	925	1.59086153907
NM_006744	RBP4	272	429	5.23873532902
NM_006744	RBP4	691	738	3.17984163975
NM_006744	RBP4	628	667	2.40222733025
NM_006744	RBP4	434	623	4.95243114387
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NM_006745	MSM01	925	955	7.26548255576
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NM_020132	AGPAT3	518	564	5.32567996198
NM_172351	CD46	409	456	7.37908178402
NM_172351	CD46	66	149	7.18661044884
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NM_172351	CD46	302	371	6.70118362922
NM_172351	CD46	1132	1188	7.18661045617
NM_172351	CD46	569	634	7.7011833933
NM_007293	C4A	4642	4687	4.67386023842
NM_007293	C4A	2619	2701	6.89642641008
NM_007293	C4A	1512	1551	5.41099285185
NM_007293	C4A	4288	4363	3.0890712521
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NM_198181	GOLGA6L9		118	138 5.86880358772
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NM_001037637	BTF3	165	186		-0.0288546390345
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NM_004482	GALNT3	1976	2034		12.6712166141
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NM_012201	GLG1	2279	2356		7.05336085486
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NM_001022	RPS19	368	430	3.35968032945
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NM_022338	C11orf24		1077	1125 6.7460633933
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NM_000970	RPL6	861	901	3.57109341936
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NM_000977	RPL13	337	383	1.74676738942
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NM_001206840	TGOLN2 1496	1546		7.04157504019
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NM_020781	ZNF398 179	199		11.2450866207
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NM_032802	SPPL2A 1032	1105		8.68741305334
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NM_001024736	CD276 1654	1710		6.39090285089
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NM_006597	HSPA8 1441	1530		2.16632883132
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NM_173647	RNF149	278	325	7.12813336392
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NM_001889	CRYZ	1858	1878	6.12645799896
NM_001100165	PHACTR2	7903	7923	7.02641552093
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NM_004343	CALR	303	352	3.05319536787
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NM_004343	CALR	1793	1871	3.24583395067
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NM_004616	TSPAN8	508	552	12.7708317223
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NM_004617	TM4SF4	431	624	15.3880580059
NM_004617	TM4SF4	901	973	12.1785979092
NM_004617	TM4SF4	744	901	13.82246083
NM_004615	TSPAN7	463	509	6.15339525948
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NM_134428	RFX3	45	75	7.91374197911
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NM_020531	C20orf3	802	835	6.10754373764
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NM_020531	C20orf3	959	1016	6.27746873909
NM_020531	C20orf3	1148	1231	6.10754373764
NM_172209	TAPBP	919	952	11.785525348
NM_172209	TAPBP	590	644	10.6480285553



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NM_000821	GGCX	630	678	8.58360818388
NM_000821	GGCX	1691	1742	7.41367645138
NM_000821	GGCX	2174	2224	7.99847193284
NM_000821	GGCX	1252	1314	7.99864544724
NM_000821	GGCX	697	736	7.99462808298
NM_000821	GGCX	2096	2132	6.99847193284
NM_000821	GGCX	742	845	7.99864568316
NM_000821	GGCX	1775	1832	7.41368318243
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NM_002972	SBF1	2336	2433	7.23045664032
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NM_031479	INHBE	1331	1367	7.02058003725
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NM_031479	INHBE	158	206	7.52140333613
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NM_001136153	ATF6B	1538	1588	8.67469986338
NM_021814	ELOVL5	450	514	7.74268068198
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NM_001961	EEF2	2711	2766	1.75628652628
NM_001961	EEF2	2091	2132	-0.0550859959398
NM_001961	EEF2	445	515	2.27085969912
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NM_001961	EEF2	834	883	1.94893160423
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NM_001961	EEF2	689	739	0.948931596684
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NM_014718	CLSTN3	1875	1962	7.10363928559
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NM_005996	TBX3	59	102	8.12946370334
NM_152924	ABHD2	555	632	9.83418243721
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NM_001097620	TMEM184A		478	562 10.2079577959
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NM_014345	ZNF318	6762	6782	5.29713974608
NM_020854	KIAA1468		567	588 8.87899371033
NM_016657	KDELR3	505	540	9.60929093973
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NM_194463	RNF128	1223	1258	4.25750948343
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NM_007138	ZNF90	326	350	12.91838525
NM_030665	RAI1	6358	6377	9.76246702416
NM_030666	SERPINB1		882	931 4.87292602937
NM_015833	ADARB1	19	49	8.54775967594
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NM_000120	EPHX1	1164	1215	9.25061311513
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NM_000120	EPHX1	722	747	7.16647390575
NM_000120	EPHX1	535	574	7.25043936481
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NM_144650	ADHFE1	684	702	10.3809588202
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NM_006405	TM9SF1	1016	1081	7.46271931322
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NM_006405	TM9SF1	1548	1616	7.78464717219
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NM_003164	STX5	109	136	6.53545572414

NM_006407	ARL6IP5	511	582	7.28332840434
NM_006406	PRDX4	665	717	7.02402421181
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NM_006408	AGR2	728	798	11.2577384973
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NM_001202470	RPS10-NUDT3		333	378 3.9184390198
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NM_000701	ATP1A1	1212	1262	5.71277783783
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NM_005698	SCAMP3	1060	1141	9.02909348023
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NM_001122752	SERPINI1		1274	1314 7.53449864721
NM_001142364	ALG5	894	953	7.12917128042

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NM_005030	PLK1	1086	1119	6.05496921435
NM_017847	C1orf27	1195	1224	8.92926732061
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NM_001862	COX5B	168	211	3.69329911078
NM_001861	COX4I1	672	714	2.2943118589
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NM_004638	PRRC2A	4317	4368	6.34174043518
NM_004327	BCR	211	251	6.16517945578
NM_004324	BAX	274	340	6.32887110835
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NM_025250	TTYH3	1445	1483	6.54813786102
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NM_025250	TTYH3	1115	1199	7.77053701341
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NM_001146333	SUMF2	336	410	9.87019382317
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NM_001164468	TMED7-TICAM2		840	895 7.26933923721
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NM_031450	C11orf68		30	67 8.62673414414
NM_031453	FAM107B	2058	2080	4.30544995845
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NM_001184796	ESYT1	651	705	8.28048425403
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NM_001184796	ESYT1	728	807	10.0878391763
NM_001184796	ESYT1	1966	2015	8.78130754559
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NM_001184796	ESYT1	1667	1705	9.00369996692
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NM_002950	RPN1	1428	1476	6.40612649876
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NM_024612	DHX40	1966	1987	5.55694164338
NM_175066	DDX51	2294	2315	9.02805089311
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NM_006098	GNB2L1	211	295	-0.0981086509032
NM_006098	GNB2L1	679	735	0.303352717201
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NM_015173	TBC1D1	3750	3768	6.6171475171
NM_001177387	ATXN7	149	175	8.3572815977
NM_019059	TOMM7	248	321	2.91011839156
NM_019050	USP53	140	161	7.57398574767
NM_205845	AKR1C2	1144	1185	1.54468523573
NM_001456	FLNA	6486	6544	7.0059090648
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NM_007114	TMF1	2008	2029	6.40548233948

NM_007118	TRIO	2280	2314	7.64680596936	
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NM_000146	FTL	123	176	3.31163289813	
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NM_000146	FTL	376	484	3.96370959472	
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NM_173054	RELN	127	159	7.11207430715	
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NM_000021	PSEN1	640	675	8.32206691474	
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NM_001174126	SLC11A2	1215	1255	8.87879014898	
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NM_001002029	C4B	4854	4901	5.15635052406	
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NM_004925	AQP3	616	647	9.50542784792
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NM_016147	PPME1	352	371	5.94048746504
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NM_001145201	PRAP1	218	303	11.9245312748
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NM_002216	ITIH2	1723	1767	2.95972777868
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NM_002216	ITIH2	2301	2362	2.71871967918
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NM_012325	MAPRE1	64	111	2.3506968582
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NM_001190328	YJEFN3	517	538	11.3273221915
NM_014944	CLSTN1	3698	3745	6.17083257534
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NM_001645	APOC1	90	161	6.4411707837
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NM_052972	LRG1	490	574	10.0396627295
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NM_013279	C11orf9	3088	3141	6.81137088735
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NM_006575	MAP4K5	66	95	5.84515414066
NM_021095	SLC5A6	889	978	7.95621462056
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NM_000185	SERPIND1		994	1021 0.773886687893

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NM_002076	GNS	760	796	7.47763422426
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NM_174936	PCSK9	414	488	10.2051054151
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NM_001679	ATP1B3	1158	1244	7.57154290618	
NM_001679	ATP1B3	695	763	7.30850873625	
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NM_032121	MAGT1	714	792	9.35276753973	
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NM_012232	PTRF	1543	1562	7.19715314937
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NM_004753	DHRS3	576	634	5.25242435622
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NM_001505	GPER	743	764	8.6498938275
NM_022365	DNAJC1	1064	1104	6.98445252394
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NM_006885	ZFH3	11210	11253	9.83432527251
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NM_006315	PCGF3	1324	1348	6.90795705006	
NM_052853	ADCK2	330	358	9.22055452343	
NM_032333	C10orf58		492	533	5.93800105936
NM_032333	C10orf58		686	752	6.2010352295
NM_032333	C10orf58		342	390	5.61205536453
NM_032333	C10orf58		591	654	6.78599123509
NM_032333	C10orf58		409	479	6.20103546542
NM_002414	CD99	545	603	3.19976783231	
NM_002415	MIF	52	107	3.22860744883	
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NM_177524	MEST	782	849	9.86731482987	
NM_138349	TP53I13	1165	1187	7.69168553329	
NM_138340	ABHD3	474	524	9.43576424708	
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NM_138346	KIAA2013		1256	1292	8.03255961612
NM_001268	RCBTB2	363	382	11.333612261	
NM_001142298	SQSTM1	468	516	3.94240985233	
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NM_013995	LAMP2	867	917	6.97507124614	
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NM_145061	SKA3	174	192	7.50889880453
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NM_203463	CERS6	1065	1106	8.83133842287
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NM_004924	ACTN4	3740	3784	3.79655939878
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NM_004924	ACTN4	1392	1470	3.29171850727
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NM_004922	SEC24C	2948	2969	6.35540203498
NM_022821	ELOVL1	587	631	9.41679410571
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NM_014256	B3GNT3	904	954	12.1431673917
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NM_001031	RPS28	101	156	3.496887427
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NM_001520	GTF3C1	39	98	8.52308763277
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NM_001031847	CPT1A	2045	2138	6.91666240059
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NM_178148	SLC35B2	1316	1381	6.47112651122
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NM_003963	TM4SF5	532	573	6.63066614688
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NM_052831	C6orf192		1319	1356 10.7795791117
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NM_022117	TSPYL2	2190	2209	4.28296784605
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NM_019088	PAF1	1566	1595	6.13985624437
NM_148170	CTSC	358	401	8.92552967973
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NM_017623	CNNM3	261	282	7.25457038353
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NM_004491	ARHGAP35		6272	6305 6.30871565931
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NM_181521	CMTM4	72	114	8.69018125702
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NM_003204	NFE2L1	2673	2764	7.24753927171
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NM_013336	SEC61A1	772	819	7.40448376014
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NM_002844	PTPRK	2321	2358	5.80070455674
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NM_002335	LRP5	1510	1551	4.07564020757
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NM_002335	LRP5	3567	3689	5.39774205278
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NM_005319	HIST1H1C		31	91 10.9012207188
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NM_199141	CARM1	13	70	6.10218316404
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NM_024541	C10orf76		3075	3098 9.57174923006
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NM_000214	JAG1	2399	2444	5.44412478781
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NM_017780	CHD7	0	48	5.77064313126
NM_001042678	RHOC	514	539	4.43067294747
NM_199337	TMEM179B		535	602 9.46473677568
NM_001080434	LMTK3	4342	4369	13.2223208574
NM_001135208	FKBP2	278	349	7.98007051932
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NM_033049	MUC13	920	964	14.2399829392
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NM_001142276	APLP2	1505	1607	4.62518742242
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NM_032832	LRP11	1264	1295	8.08531623909
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NM_183416	KIF1B	5596	5623	7.38996980431
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NM_002117	HLA-C	623	688	6.98957081584
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NM_002116	HLA-A	642	711	7.87802184374
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NM_178454	DRAM2	616	670	5.26855113672
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NM_018335	ZNF839	1784	1813	7.6907037874	
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NM_147187	TNFRSF10B		1195	1266	6.2275142407
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NM_201442	C1S	1407	1474	10.095298028	
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NM_006948	HSPA13	1085	1135	7.23545719603	
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NM_203355	CTAGE5	730	775	3.68787464874
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NM_003840	TNFRSF10D		506	591 6.74357023238
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NM_000253	MTTP	2867	2907	6.42389782904
NM_000253	MTTP	1852	1885	5.68693223487
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NM_148923	CYB5A	102	144	3.75761652987
NM_207380	C15orf52		5130	5168 14.4485002728
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NM_001080472	FITM2	66	118	6.36990819327
NM_000876	IGF2R	4453	4503	6.6740481023
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NM_000876	IGF2R	3291	3337	4.7995789846
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NM_000876	IGF2R	4882	4907	4.71543977522
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NM_000876	IGF2R	6149	6200	7.46254399733
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NM_000876	IGF2R	3454	3490	6.21461624796
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NM_000876	IGF2R	3894	3952	5.53653784772
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NM_000876	IGF2R	1633	1687	6.67404810252
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NM_000875	IGF1R	3773	3793	7.35134775772
NM_024640	YRDC	615	636	7.05806787618
NM_025231	ZSCAN16	431	452	6.71786072816
NM_178557	NAT8L	4084	4108	12.927150608
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NM_025232	REEP4	1176	1218	11.414818813
NM_015274	MAN2B2	2918	2958	11.9282556658
NM_178126	FAM134C	720	774	8.42252998719
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NM_004415	DSP	7268	7310	0.771014225574
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NM_001397	ECE1	1233	1286	7.19138860134
NM_001397	ECE1	1906	1937	5.86946050645
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NM_001428	EN01	1182	1283	0.0572690427642
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NM_022731	NUCKS1	2655	2675	3.22869431981
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NM_018976	SLC38A2	1250	1292	5.47471644331
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NM_001643	APOA2	382	443	2.11410077683
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NM_022551	RPS18	203	258	0.701341464034
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NM_144970	CXorf38	3725	3765	8.83438708261
NM_001164280	SLC37A4	904	939	8.66043675164
NM_006260	DNAJC3	1040	1102	7.23631650091
NM_001205206	SLC19A1	1117	1155	7.23330085122
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NM_001024401	SBK1	4055	4124	12.6787860963
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NM_014044	UNC50	570	627	7.24301145058
NM_014044	UNC50	280	300	5.57390974048
NM_014045	LRP10	1764	1860	9.81299577033
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NM_004800	TM9SF2	877	960	8.07332648418
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NM_003641	IFITM1	358	403	8.90413533911
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NM_014992	DAAM1	1373	1481	8.94939369014
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NM_001040716	PC	1018	1036	8.29577245186
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NM_002743	PRKCSH	276	355	6.90040859596
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NM_001130046	CCL20	658	695	5.21022661185
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NM_001005	RPS3	129	210	1.40659434766
NM_001005	RPS3	226	309	0.947162493105
NM_001006	RPS3A	255	300	0.740065013171
NM_001007	RPS4X	571	655	2.49307914999
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NM_000578	SLC11A1	3098	3117	11.3845327954
NM_000973	RPL8	765	826	3.03977914569
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NM_138571	HINT3	24	43	6.08474765841
NM_138578	BCL2L1	168	217	3.42338586637
NM_000979	RPL18	506	544	4.25423056606
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NM_017896	C20orf11		2	22 4.01469850388
NM_001893	CSNK1D	1123	1213	7.21341213205
NM_004217	AURKB	1035	1077	7.3826845438
NM_004355	CD74	677	741	7.81523524139
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NM_001195532	SPTAN1	7529	7611	6.12347071106
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NM_000271	NPC1	984	1029	5.96910867667
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NM_001128325	SPON2	880	927	7.70936240664
NM_001128325	SPON2	1080	1163	8.7133800068
NM_001128325	SPON2	735	811	8.71338000681
NM_001128325	SPON2	517	628	9.58784912473
NM_032815	NFATC2IP		73	106 7.97222619092
NM_172230	SYVN1	665	707	10.1233592799
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NM_001098210	CTNNB1	2322	2370	4.49051781253
NM_172236	POFUT1	344	381	8.00100686807
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NM_002720	PPP4C	839	878	5.12181262517
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NM_023935	DDRKG1	330	378	5.43056934902
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NM_001042371	PGP	18	45	11.792594839
NM_005984	SLC25A1	948	997	6.33839101373
NM_019107	C19orf10		799	853 6.25537697091
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NM_001197026	PLEKHA8	6820	6839	8.73720545609
NM_019027	RBM47	938	1005	8.39487625867
NM_019026	TMC01	487	514	2.75834451157
NM_019026	TMC01	342	413	4.75817749231
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NM_019026	TMC01	102	177	4.56570615713
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NM_152243	CDC42EP1		957	1015 9.42868244987
NM_018950	HLA-F	1070	1116	10.2160793456
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NM_018955	UBB	825	893	0.529895130339
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NM_016626	MEX3C	890	920	6.91160667288
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NM_001409	MEGF6	4963	4986	11.027905534
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NM_001404	EEF1G	546	616	2.45714155263
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NM_007126	VCP	631	662	4.02267690036
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NM_014230	SRP68	59	87	3.32926519161
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NM_001205228	SORT1	2363	2406	5.5607833214
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NM_182983	HPN	1893	1967	7.00591041936
NM_006293	TYR03	1376	1457	7.39282597927
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NM_003403	YY1	326	347	5.60586582868
NM_005667	RNF103	1558	1587	5.73507661782
NM_006471	MYL12A	335	395	2.91440823109
NM_002569	FURIN	2451	2499	10.2112461919
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NM_152744	SDK1	4696	4716	9.91112626191
NM_032256	TMEM117	226	245	10.4411140519
NM_152743	BRAT1	420	474	11.9619067552
NM_001017995	SH3PXD2B		13	42 9.61103665029
NM_001007468	SMARCB1	1065	1107	3.02558736571
NM_014399	TSPAN13	570	610	10.1403045447
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NM_014931	PPP6R1	2228	2295	5.20824869236
NM_017877	C2orf18	16	35	9.61572895759
NM_001873	CPE	1279	1318	3.87552884154
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NM_030801	MAGED4B	1797	1846	5.93307526171
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NM_004339	PTTG1IP	470	500	2.32304263288
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NM_022965	FGFR3	635	735	5.8139933755
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NM_001037283	EIF3B	1987	2036	3.52106363468
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NM_020524	PBXIP1	860	923	8.72470017136
NM_172210	CSF1	803	833	9.95602796126
NM_006667	PGRMC1	612	647	7.39898345786
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NM_138821	PAM	1108	1164	6.53800720461
NM_006088	TUBB2C	289	336	6.02186830186
NM_006080	SEMA3A	570	600	13.2733810062
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NM_005216	DDOST	768	835	7.43434801102
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NM_001143760	EIF5A	505	557	2.03256412441
NM_001007073	RPL32	88	119	4.7426870456
NM_001037738	NPM1	237	285	0.350088271173
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NM_001206954	AGER	1100	1118	8.32835956188
NM_019044	CCDC93	29	58	3.05047493484
NM_003270	TSPAN6	400	429	4.68252612283
NM_003270	TSPAN6	777	818	5.92433260851
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NM_020860	STIM2	1464	1511	8.40568858258
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