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61779	MAPK8IP3	0	2319	MAPK8IP3	0	chr16	1758000
62279	MAPK8IP3	0	1819	MAPK8IP3	0	chr16	1758500
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33712	CTDP1	0	40995	CTDP1	0	chr18	75574500
34212	CTDP1	0	40495	CTDP1	0	chr18	75575000
63522	ELOVL2	0	110	ELOVL2	0	chr6	11152500
23124	CYS1	0	489	CYS1	0	chr2	10137500
11794	UNKL	0	4682	UNKL	0	chr16	1365000
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36708	TCF3	0	4286	TCF3	0	chr19	1597000
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-323954	CDH18	0	1154345	GUSBP1	0	chr5	20341000
-16034	PLCB2	0	7444	C15orf52	0	chr15	38403500
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17663	RUFY1	0	32625	RUFY1	0	chr5	178937000
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-94323	C20orf191	0	2088539	FRG1B	0	chr20	26137000
-94823	C20orf191	0	2088039	FRG1B	0	chr20	26137500
2063	C14orf21	0	3214	C14orf21	0	chr14	23841000
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-950597	C20orf197	0	228953	CDH4	0	chr20	59032000
-951097	C20orf197	0	228453	CDH4	0	chr20	59032500
-558650	OR4A47	0	98262	FOLH1	0	chr11	49026500
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-14188	WWP2	0	401	WWP2	0	chr16	68516000
-98682	SLC5A4	0	871	RFPL3	0	chr22	31080000
-137671	SC5DL	0	1170	SORL1	0	chr11	120827000
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-34859	H19	0	96422	IGF2	0	chr11	2010500
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-28945	ZNF667	0	1523	ZNF471	0	chr19	61709500
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-444	SCN11A	0	101010	WDR48	0	chr3	38967500
-35321	GRIK4	0	2512	TBCEL	0	chr11	120397500
-35821	GRIK4	0	2012	TBCEL	0	chr11	120398000
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174377	KDM4B	0	10108	KDM4B	0	chr19	5094500
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91629	KCTD1	0	1998	KCTD1	0	chr18	22380500
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-8075	OR2C1	0	17085	ZNF434	0	chr16	3355000
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-25485	NOMO1	0	15800	NPIP	0	chr16	14923000
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-156	KRT79	0	4512	KRT78	0	chr12	51514500
-2395	ADRBK1	0	394	ANKRD13D	0	chr11	66813000
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-340170	MYEOV	0	3553	CCND1	0	chr11	69161500
12465	ANKRD11	0	210470	ANKRD11	0	chr16	87874000
-424	RPH3AL	0	57433	C17orf97	0	chr17	203000
-1018	GUCA2A	0	10796	FOXJ3	0	chr1	42404000

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-22696	ST3GAL5	0	129850	LOC90784	0	chr2	85971000
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-9697	ARID3A	0	1827	WDR18	0	chr19	933500
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-8237	ZC3H3	0	8634	GSDMD	0	chr8	144703000
-1616	LEMD2	0	3926	MLN	0	chr6	33866500
-240904	SMOC2	0	306299	THBS2	0	chr6	169051500
-2214	BMS1P4	0	11637	SEC24C	0	chr10	75162500
-264721	CECR1	0	1127	CECR2	0	chr22	16335500
-265221	CECR1	0	627	CECR2	0	chr22	16336000
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548	ZNF276	0	18833	ZNF276	0	chr16	88316000
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-877	SKP1	0	18546	PPP2CA	0	chr5	133541500
118	FOXK2	0	84772	FOXK2	0	chr17	78071000
14623	IGDCC4	0	26963	IGDCC4	0	chr15	63475500
1346	OPLAH	0	8072	OPLAH	0	chr8	145179500
124462	BANP	0	1425	BANP	0	chr16	86667000
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-637274	ERICH1	0	128475	DLGAP2	0	chr8	1308500
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-187161	HTR1B	0	1216907	IRAK1BP1	0	chr6	78417000
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-47193	C17orf87	0	281	RABEP1	0	chr17	5126000
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1609	MLLT1	0	67959	MLLT1	0	chr19	6163000
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26179	ZBTB46	0	34800	ZBTB46	0	chr20	61872500

26679	ZBTB46	0	34300	ZBTB46	0	chr20	61873000
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-259140	EFEMP1	0	1761	CCDC85A	0	chr2	56263000
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24084	SH2D3C	0	16369	SH2D3C	0	chr9	129564500
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-47805	TACC3	0	336	FGFR3	0	chr4	1764500
-100551	C20orf112	0	48822	C20orf203	0	chr20	30635500
-25332	NOMO3	0	11734	PKD1P1	0	chr16	16321500
-26673	CSF2RA	0	8	IL3RA	0	chrX	1415500
-73075	MED13	0	126348	TBC1D3P2	0	chr17	57570500
-340	TSSC1	0	1452	TTC15	0	chr2	3361000
-840	TSSC1	0	952	TTC15	0	chr2	3361500
-17667	ZNF517	0	706	ZNF7	0	chr8	146023000
-18167	ZNF517	0	206	ZNF7	0	chr8	146023500
-1202549	CADM1	0	41100	BUD13	0	chr11	116083000
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-177540	4F16,OR4F29,OR	0	74958	6,OR4F29,OR4F3	0	chr1	536000
-11134	SLC29A1	0	1826	HSP90AB1	0	chr6	44321000
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-713	LOC100131551	0	28188	CPN2	0	chr3	195514000
-8991	SNRPD3	0	2217	GGT1	0	chr22	23307500
-913	CDH24	0	113	ACIN1	0	chr14	22597500
-3624	C9orf50	0	1755	METTL11A	0	chr9	131426500
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248	GPSM1	0	31878	GPSM1	0	chr9	138342000
45492	FGFR1	0	9	FGFR1	0	chr8	38445500
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219	TRNP1	0	6964	TRNP1	0	chr1	27193000
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-167	MAP1D	0	4453	DLX1	0	chr2	172654000
-33268	FGFR4	0	1685	NSD1	0	chr5	176491000
-33768	FGFR4	0	1185	NSD1	0	chr5	176491500
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13333	EFNA2	0	444	EFNA2	0	chr19	1250500
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-674	CAMSAP1	0	25135	UBAC1	0	chr9	137939500
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22604	FBXL19	0	1605	FBXL19	0	chr16	30866000
9473	PLAC4	0	536	PLAC4	0	chr21	41478500
-75127	RASGEF1A	0	29597	FXYD4	0	chr10	43157500
-75627	RASGEF1A	0	29097	FXYD4	0	chr10	43158000
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-14142	SULT1A1	0		87282	EIF3C	0	chr16	28543000
-772	C1orf222	0		24611	KIAA1751	0	chr1	1850000
148	OR11L1	0		821	OR11L1	0	chr1	246071000
-19552	S1PR2	0		1139	MRPL4	0	chr19	10222500
226	MAGEA2	0		3751	MAGEA2	0	chrX	151634000
21337	CDH15	0		2401	CDH15	0	chr16	87787000
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-1687	C19orf29	0		1681	PIP5K1C	0	chr19	3579500
1467	CD248	0		1091	CD248	0	chr11	65840000
-572	PITPNM2	0		45398	MPHOSPH9	0	chr12	122161500
-484	SNORD105B	0		1196	P2RY11	0	chr19	10082000
7647	SRSF9	0		441	SRSF9	0	chr12	119391500
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493	ZDHHC20	0		82423	ZDHHC20	0	chr13	20849000
993	ZDHHC20	0		81923	ZDHHC20	0	chr13	20849500
9455	PRSSL1	0		461	PRSSL1	0	chr19	646000
27962	FBXO32	0		10127	FBXO32	0	chr8	124612500
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9728	LASS2	0		64	LASS2	0	chr1	149214000
901	SEMA6B	0		15003	SEMA6B	0	chr19	4494500
1401	SEMA6B	0		14503	SEMA6B	0	chr19	4495000
6108	INPP5E	0		5077	INPP5E	0	chr9	138449000
12607	MMP17	0		10769	MMP17	0	chr12	130891500
266426	GLI3	0		9643	GLI3	0	chr7	42233500
45	CNTD2	0		4404	CNTD2	0	chr19	45420000
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420781	RPTOR	0		768	RPTOR	0	chr17	76554000
421281	RPTOR	0		268	RPTOR	0	chr17	76554500
-236540	IQSEC1	0		112236	NUP210	0	chr3	13220500
-113806	C22orf34	0		1940	BRD1	0	chr22	48551000
-628	LIG1	0		37154	CARD8	0	chr19	53366000
-1128	LIG1	0		36654	CARD8	0	chr19	53366500
-1628	LIG1	0		36154	CARD8	0	chr19	53367000
3895	SLC39A4	0		581	SLC39A4	0	chr8	145612500
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730	POFUT2	0		23239	POFUT2	0	chr21	45509000
1089	DLX2	0		2224	DLX2	0	chr2	172673500

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-10648	CCDC126	0	24773	C7orf46	0	chr7	23661500
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-27183	ZFP37	0	20826	NCRNA00256B	0	chr9	114886000
-27683	ZFP37	0	20326	NCRNA00256B	0	chr9	114886500
-47647	FAM48B2	0	1798	FAM48B1	0	chrX	24289000
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-143316	NCRNA00168	0	1367251	PFKP	0	chr10	1732500
-1636	ALDH3A1	0	23735	ULK2	0	chr17	19591000
-5402	OTX2	0	391446	EXOC5	0	chr14	56347500
-5902	OTX2	0	390946	EXOC5	0	chr14	56348000
-6402	OTX2	0	390446	EXOC5	0	chr14	56348500
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59335	UNC5A	0	11005	UNC5A	0	chr5	176229500
4001	POLR3K	0	2625	POLR3K	0	chr16	41000
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-19683	---	0	851	SCNN1D	0	chr1	1206500
-20183	---	0	351	SCNN1D	0	chr1	1207000
-215795	NBPF24	0	80145	FLJ39739	0	chr1	146292500
-216295	NBPF24	0	79645	FLJ39739	0	chr1	146293000
463	INTS4L1	0	92534	INTS4L1	0	chr7	64239500
5590	ADAM8	0	8862	ADAM8	0	chr10	134931500
786777	TMEM132D	0	45165	TMEM132D	0	chr12	128909000
10031	PPP2R3B	0	42627	PPP2R3B	0	chrX	225000
-421	ZNF280D	0	152159	LOC145783	0	chr15	54813500
5912	FAM38A	0	15318	FAM38A	0	chr16	87315000
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30288	TBC1D22A	0	380888	TBC1D22A	0	chr22	45567500
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10360	TBC1D17	0	813	TBC1D17	0	chr19	55083000
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20634	C18orf1	0	11253	C18orf1	0	chr18	13631500
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-133058	NHLRC2	0	2295	ADRB1	0	chr10	115791500
-11517	PNMA3	0	457	PNMA6A	0	chrX	151991000
-85664	CRYBB2	0	387	IGLL3	0	chr22	24043500
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-498125	HERC2P4	0	22841	TP53TG3B	0	chr16	32569500
6973	ZNF436	0	1966	ZNF436	0	chr1	23565500
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-47423	ZNF275	0	17974	ZFP92	0	chrX	152319000
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23531	PPP2R3B	0	29127	PPP2R3B	0	chrY	238500
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-373385	FAM92B	0	125529	KIAA0182	0	chr16	84077000
-10957	ZNF217	0	280446	SUMO1P1	0	chr20	51644000
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3140	CYP2W1	0	3302	CYP2W1	0	chr7	992500
3640	CYP2W1	0	2802	CYP2W1	0	chr7	993000
4967	ANO8	0	6638	ANO8	0	chr19	17300000
310990	GNAQ	0	12	GNAQ	0	chr9	79836000
397	PRDM16	0	369045	PRDM16	0	chr1	2976000
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5297	TSEN54	0	2915	TSEN54	0	chr17	71029500
-531	SLC12A4	0	11066	DPEP3	0	chr16	66556000
-30406	CIDEA	0	256	TUBB6	0	chr18	12298000
13787	TMCC2	0	31593	TMCC2	0	chr1	203477500
-260116	QKI	0	1438142	C6orf118	0	chr6	164175000
-260616	QKI	0	1437642	C6orf118	0	chr6	164175500
-261116	QKI	0	1437142	C6orf118	0	chr6	164176000
-84298	LOC654342	0	31094	GGT8P	0	chr2	91296000
-84798	LOC654342	0	30594	GGT8P	0	chr2	91296500
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-674	ENTPD2	0	7399	C9orf140	0	chr9	139069000
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-252505	ANKRD30BL	0	2116	GPR39	0	chr2	132888500
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-2927	AQP12A	0	12356	KIF1A	0	chr2	241289500
-37113	GTPBP6	0	6969	PPP2R3B	0	chrY	208000
-37613	GTPBP6	0	6469	PPP2R3B	0	chrY	208500
2634	SEPT9	0	124773	SEPT9	0	chr17	72883500
472	PITX2	0	19457	PITX2	0	chr4	111758500
972	PITX2	0	18957	PITX2	0	chr4	111759000
34139	UGT1A10	0	102690	UGT1A10	0	chr2	234244000
34639	UGT1A10	0	102190	UGT1A10	0	chr2	234244500
23230	POFUT2	0	739	POFUT2	0	chr21	45531500
49198	PCBP3	0	43296	PCBP3	0	chr21	46143500
40714	TERT	0	1162	TERT	0	chr5	1347000
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19776	CABLES1	0	104932	CABLES1	0	chr18	18989500
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-54484	PIKFYVE	0	46800	PTH2R	0	chr2	208933000
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-20564	OR10H1	0	256	UCA1	0	chr19	15800500
-561	PBX4	0	4465	LPAR2	0	chr19	19591000
-48683	YAF2	0	25154	ZCRB1	0	chr12	40967000
-396	FGF22	0	3525	RNF126	0	chr19	595000
-896	FGF22	0	3025	RNF126	0	chr19	595500
221	OSTalpha	0	16696	OSTalpha	0	chr3	197428000
41047	MAD1L1	0	376109	MAD1L1	0	chr7	1863000
-9303	PKD1P1	0	31182	NOMO2	0	chr16	18387500
440	DCLRE1B	0	8217	DCLRE1B	0	chr1	114250000
87732	APBA1	0	157095	APBA1	0	chr9	71320000
88232	APBA1	0	156595	APBA1	0	chr9	71320500
8643	PMS2L4	0	1341	PMS2L4	0	chr7	66403500
-81280	MRP63	0	116007	ZDHHC20	0	chr13	20732500
-1696	NLRP6	0	2137	ATHL1	0	chr11	277000
-2196	NLRP6	0	1637	ATHL1	0	chr11	277500

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-362316	MAGEB6	0	374	VENTXP1	0	chrX	26486000
-268	SAMD1	0	1006	PRKACA	0	chr19	14062500
81	YAP1	0	122864	YAP1	0	chr11	101486500
12564	PMPCA	0	534	PMPCA	0	chr9	138437500
-2615207	C4orf33	0	1421419	PCDH10	0	chr4	132868500
-2615707	C4orf33	0	1420919	PCDH10	0	chr4	132869000
128	ZBTB12	0	2248	ZBTB12	0	chr6	31975500
628	ZBTB12	0	1748	ZBTB12	0	chr6	31976000
-102895	NGEF	0	1625	NEU2	0	chr2	233604000
2550	HAPLN4	0	4596	HAPLN4	0	chr19	19230000
-1170	PALM	0	1645	C19orf21	0	chr19	700500
-14094	TKTL1	0	4093	FLNA	0	chrX	153226000
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11982	ELK4	0	1623	ELK4	0	chr1	203867000
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34167	SLC9A3	0	17049	SLC9A3	0	chr5	560500
66353	DOT1L	0	2077	DOT1L	0	chr19	2181500
-346348	NCRNA00120	0	225	SPACA1	0	chr6	88814000
-54505	CTDP1	0	54655	KCNG2	0	chr18	75670000
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1227	TPSD1	0	995	TPSD1	0	chr16	1247500
51897	PRDM16	0	317545	PRDM16	0	chr1	3027500
12	TXNDC2	0	2156	TXNDC2	0	chr18	9876000
14964	ARID3A	0	31803	ARID3A	0	chr19	892000
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-28581	CPEB4	0	267	C5orf47	0	chr5	173348500
-698	JAKMIP3	0	1403	DPYSL4	0	chr10	133849000
-1198	JAKMIP3	0	903	DPYSL4	0	chr10	133849500
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16379	C1orf106	0	4486	C1orf106	0	chr1	199147000
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-779989	C5orf38	0	60667	IRX1	0	chr5	3588500
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344	HDGFL1	0	729	HDGFL1	0	chr6	22678000
-51761	PSMG2	0	7979	PTPN2	0	chr18	12767500
172877	KDM4B	0	11608	KDM4B	0	chr19	5093000
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-35341	RRN3	0	266111	MPV17L	0	chr16	15131000
-35841	RRN3	0	265611	MPV17L	0	chr16	15131500
-15714	LOC407835	0	947	TSPAN33	0	chr7	128571000
-324077	FAM21B	0	12361	LOC642826	0	chr10	47793500
-324577	FAM21B	0	11861	LOC642826	0	chr10	47794000
-829	RGS16	0	41414	RGS8	0	chr1	180841000
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-388	LRTM1	0	537282	WNT5A	0	chr3	54937500
-36841	RRN3	0	264611	MPV17L	0	chr16	15132500
15905	TP73	0	27327	TP73	0	chr1	3613000
-15803	RASA3	0	86463	CDC16	0	chr13	113932000
-128158	USP7	0	37	C16orf72	0	chr16	9093000

463	C16orf72	0	27556	C16orf72	0	chr16	9093500
120462	BANP	0	5425	BANP	0	chr16	86663000
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1633	IZUMO4	0	1083	IZUMO4	0	chr19	2049500
21938	ADAP1	0	34815	ADAP1	0	chr7	926000
22438	ADAP1	0	34315	ADAP1	0	chr7	926500
22938	ADAP1	0	33815	ADAP1	0	chr7	927000
557	MGMT	0	299773	MGMT	0	chr10	131156000
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-118	GPS2	0	174	NEURL4	0	chr17	7159500
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-7774	EPS8L2	0	11931	TALDO1	0	chr11	725500
-8274	EPS8L2	0	11431	TALDO1	0	chr11	726000
-8774	EPS8L2	0	10931	TALDO1	0	chr11	726500
8326	C16orf88	0	3493	C16orf88	0	chr16	19633500
175	F2RL3	0	2830	F2RL3	0	chr19	16861000
620547	CDH4	0	64194	CDH4	0	chr20	59881500
-2035	AXIN1	0	12896	MRPL28	0	chr16	344500
-51574	VPREB1	0	962	LOC96610	0	chr22	20981500
1894	MACROD1	0	165661	MACROD1	0	chr11	63524500
-48495	TPO	0	40665	PXDN	0	chr2	1574000
-48995	TPO	0	40165	PXDN	0	chr2	1574500
-49495	TPO	0	39665	PXDN	0	chr2	1575000
-504146	GYPA	0	1122	HHIP	0	chr4	145785500
10057	GRIN2D	0	40000	GRIN2D	0	chr19	53600000
-1124	KRT74	0	10639	KRT72	0	chr12	51255000
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-39957	LOC440040	0	102050	OR4C13	0	chr11	49828500
-40457	LOC440040	0	101550	OR4C13	0	chr11	49829000
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-3496	MGC29506	0	3356	SPATA24	0	chr5	138757000
432	OR7E156P	0	4702	OR7E156P	0	chr13	63210000
-321	PKN1	0	277	PTGER1	0	chr19	14444000
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723	PTGER1	0	2174	PTGER1	0	chr19	14445000
-3	NOVA2	0	21678	CCDC61	0	chr19	51168500
428	DEF6	0	23526	DEF6	0	chr6	35374000
-45471	LOC648740	0	521	AMY2A	0	chr1	103961000
-45971	LOC648740	0	21	AMY2A	0	chr1	103961500
-926	DAPK2	0	25313	FAM96A	0	chr15	62126500
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7991	DACT1	0	2291	DACT1	0	chr14	58182500
3671	KLHL17	0	1458	KLHL17	0	chr1	889500
-207573	FAM182B	0	934	LOC100134868	0	chr20	25937500
-123557	CTBP2	0	422929	LOC100169752	0	chr10	126830000
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74515	STK32C	0	25967	STK32C	0	chr10	133945500
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-1651	JPH4	0	55912	DHRS2	0	chr14	23119500
1618	EGFL8	0	2040	EGFL8	0	chr6	32242000
4551	GAA	0	13774	GAA	0	chr17	75694500
-625	HERC2P4	0	520341	TP53TG3B	0	chr16	32072000
-165616	BARX2	0	197950	TMEM45B	0	chr11	128993000
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-3896	FGF22	0	25	RNF126	0	chr19	598500
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22111	MAP7D1	0	2528	MAP7D1	0	chr1	36416500
19587	NCOR2	0	191602	NCOR2	0	chr12	123394500
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-46571	ZNF519	0	158421	LOC284233	0	chr18	14169000
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4314	PI16	0	6091	PI16	0	chr6	37034500
4814	PI16	0	5591	PI16	0	chr6	37035000
-859	HS6ST1	0	1603404	LOC389033	0	chr2	128793500
8261	AMZ2	0	900	AMZ2	0	chr17	63764000
21366	LMF1	0	95985	LMF1	0	chr16	865000
666	FANCG	0	5513	FANCG	0	chr9	35064500
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-45737	AGR2	0	8554	AGR3	0	chr7	16857000
-46237	AGR2	0	8054	AGR3	0	chr7	16857500
-304558	POTEG	0	94453	POTEM	0	chr14	18959500
3956	RECQL5	0	36360	RECQL5	0	chr17	71138500
-195625	HERC2P4	0	325341	TP53TG3B	0	chr16	32267000
-196125	HERC2P4	0	324841	TP53TG3B	0	chr16	32267500
11618	NDUFS7	0	88	NDUFS7	0	chr19	1346500
-123432	RDH10	0	100894	STAU2	0	chr8	74523500
-975	TAP2	0	971	PSMB8	0	chr6	32915500
-755	C3orf17	0	192064	BOC	0	chr3	114222000
4268	SEMA5B	0	114266	SEMA5B	0	chr3	124115000
-68540	4F16,OR4F29,OR	0	183958	6,OR4F29,OR4F3	0	chr1	427000
7379	OGFR	0	1797	OGFR	0	chr20	60914000
-1348	SNORA47	0	4878	LOC728723	0	chr5	76413500
-37561	NOC4L	0	6369	GALNT9	0	chr12	131240500
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2129	RFPL3	0	4148	RFPL3	0	chr22	31083000
996	STMN3	0	12724	STMN3	0	chr20	61742500
-38679	S3,LIMS3-LOC44	0	2555	LOC440895	0	chr2	110060000
-39179	S3,LIMS3-LOC44	0	2055	LOC440895	0	chr2	110060500
-24936	LOC150381	0	2540	LOC400931	0	chr22	44858000
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4153	C1orf86	0	1074	C1orf86	0	chr1	2115000
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78599	WDR52	0	30	WDR52	0	chr3	114643000
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-22145	GNB1	0	1625	CALML6	0	chr1	1834500
-4306	HPCAL1	0	8458	ODC1	0	chr2	10489500
-4806	HPCAL1	0	7958	ODC1	0	chr2	10490000
293364	FMN1	0	377	FMN1	0	chr15	31147000
-123	FMN1	0	242968	RYR3	0	chr15	31147500
-12461	IRAK1BP1	0	23355	PHIP	0	chr6	79677500
315	NSD1	0	166820	NSD1	0	chr5	176493000
-397	NFIC	0	10404	C19orf77	0	chr19	3415000
-897	NFIC	0	9904	C19orf77	0	chr19	3415500
-515	LMF1	0	10308	SOX8	0	chr16	961500
29541	SNPH	0	13471	SNPH	0	chr20	1224500
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51398	MAST3	0	2499	MAST3	0	chr19	18121000
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10378	PRAME	0	1196	PRAME	0	chr22	21230500
-60891	CBFA2T3	0	91754	ACSF3	0	chr16	87596000
-61391	CBFA2T3	0	91254	ACSF3	0	chr16	87596500
7412	FAM71E2	0	932	FAM71E2	0	chr19	60565500
145	HSPA12B	0	20258	HSPA12B	0	chr20	3661500
394	ADAMTSL2	0	42961	ADAMTSL2	0	chr9	135387500
119774	MBP	0	262	MBP	0	chr18	72973500
10922	CNN1	0	638	CNN1	0	chr19	11521500
29815	THRA	0	1146	THRA	0	chr17	35502500
434	NR1D1	0	7499	NR1D1	0	chr17	35503000
3563	PVR	0	18766	PVR	0	chr19	49842500
-39586	N4BP2	0	1921	RHOH	0	chr4	39873000
-299131	LOC100133612	0	250970	LOC284661	0	chr1	4121000
-299631	LOC100133612	0	250470	LOC284661	0	chr1	4121500
302	DSCAML1	0	369186	DSCAML1	0	chr11	116804000
802	DSCAML1	0	368686	DSCAML1	0	chr11	116804500
35687	NFATC1	0	93311	NFATC1	0	chr18	75297000
36187	NFATC1	0	92811	NFATC1	0	chr18	75297500
-174385	FAM92B	0	324529	KIAA0182	0	chr16	83878000
-174885	FAM92B	0	324029	KIAA0182	0	chr16	83878500
-4868	LMX1B	0	99105	ZBTB43	0	chr9	128508000
11917	DAZAP1	0	16182	DAZAP1	0	chr19	1370500
12417	DAZAP1	0	15682	DAZAP1	0	chr19	1371000
-158150	PDE4B	0	1412	SGIP1	0	chr1	66771000
-12046	DLGAP4	0	810	MYL9	0	chr20	34602500
-12546	DLGAP4	0	310	MYL9	0	chr20	34603000
-25956	INTS1	0	393	MAFK	0	chr7	1536500
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63883	NSL1	0	1762	NSL1	0	chr1	211030000
64383	NSL1	0	1262	NSL1	0	chr1	211030500
-55106	SIX3	0	4828	SIX2	0	chr2	45081000
3851	KIRREL2	0	6388	KIRREL2	0	chr19	41043500
-3985502	LRRTM1	0	816	FUNDC2P2	0	chr2	84370500
17284	GET4	0	2597	GET4	0	chr7	900000
351281	RPTOR	0	70268	RPTOR	0	chr17	76484500
351781	RPTOR	0	69768	RPTOR	0	chr17	76485000
6883	MFSD7	0	473	MFSD7	0	chr4	672500
80271	FBRSL1	0	14344	FBRSL1	0	chr12	131657500
80771	FBRSL1	0	13844	FBRSL1	0	chr12	131658000
22860	RGMA	0	22937	RGMA	0	chr15	91410500
-76328	SV2C	0	1404	IQGAP2	0	chr5	75733500
39389	ENG	0	368	ENG	0	chr9	129656500
-132	ENG	0	11579	AK1	0	chr9	129657000

-437	HSPBP1	0	3345	BRSK1	0	chr19	60484000
9093	NR2E1	0	13704	NR2E1	0	chr6	108603000
4573	LOC678655	0	7944	LOC678655	0	chr12	6423000
28605	STAB1	0	551	STAB1	0	chr3	52533000
76	NT5DC2	0	10633	NT5DC2	0	chr3	52533500
576	NT5DC2	0	10133	NT5DC2	0	chr3	52534000
6440	ZNF280A	0	113	ZNF280A	0	chr22	21204500
15920	CNGB1	0	521	CNGB1	0	chr16	56562000
28361	WDR86	0	557	WDR86	0	chr7	150737500
-41456	ZSWIM4	0	3449	NANOS3	0	chr19	13845500
-41956	ZSWIM4	0	2949	NANOS3	0	chr19	13846000
-36228	MSMP	0	1905	NPR2	0	chr9	35780500
-36728	MSMP	0	1405	NPR2	0	chr9	35781000
16031	PPP2R3B	0	36627	PPP2R3B	0	chrX	231000
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-12082	GPIHBP1	0	17983	ZFP41	0	chr8	144382500
-12582	GPIHBP1	0	17483	ZFP41	0	chr8	144383000
8167	SLC9A3	0	43049	SLC9A3	0	chr5	534500
8667	SLC9A3	0	42549	SLC9A3	0	chr5	535000
-1177	SCRT2	0	82723	C20orf54	0	chr20	606000
-1677	SCRT2	0	82223	C20orf54	0	chr20	606500
-89674	LOC728875	0	378	C1orf152	0	chr1	143323000
122	C1orf152	0	584	C1orf152	0	chr1	143323500
35235	RADIL	0	49361	RADIL	0	chr7	4840500
-708	ZXDA	0	4529331	SPIN4	0	chrX	57954500
-94532	LOC146481	0	10393749	ANKRD26P1	0	chr16	34667000
-63946	TP53TG3	0	136797	SLC6A10P	0	chr16	32659500
-64446	TP53TG3	0	136297	SLC6A10P	0	chr16	32660000
-533	TIMELESS	0	150	MIP	0	chr12	55130000
350	MIP	0	4196	MIP	0	chr12	55130500
7545	ADAMTS2	0	223935	ADAMTS2	0	chr5	178481000
-1518	NRIP2	0	21109	FOXM1	0	chr12	2816000
-1497	RNF19A	0	209175	ANKRD46	0	chr8	101393000
12742	C11orf2	0	2756	C11orf2	0	chr11	64633000
-526	TNFRSF9	0	20300	PARK7	0	chr1	7924000
-3138	PRR25	0	36634	LMF1	0	chr16	807000
-3638	PRR25	0	36134	LMF1	0	chr16	807500
5418	C11orf21	0	219	C11orf21	0	chr11	2279500
77507	SKI	0	4011	SKI	0	chr1	2227500
-1342	GPATCH1	0	337	WDR88	0	chr19	38314500
-244077	---	0	99267	ZNF479	0	chr7	57092000
-11184	ZNF524	0	6418	ZNF784	0	chr19	60817500
-35391	CBFA2T3	0	117254	ACSF3	0	chr16	87570500
4149	CHAD	0	226	CHAD	0	chr17	45901000
-4404	FAM135A	0	1345	C6orf57	0	chr6	71332000
85549	FAM19A5	0	184250	FAM19A5	0	chr22	47349500
31082	APIP	0	3015	APIP	0	chr11	34891500
31582	APIP	0	2515	APIP	0	chr11	34892000
1835	SH2B2	0	31898	SH2B2	0	chr7	101717000
-33861	CHRNA4	0	10985	KCNQ2	0	chr20	61497000
2828	NOTUM	0	5847	NOTUM	0	chr17	77506500
12531	PPP2R3B	0	40127	PPP2R3B	0	chrY	227500
34716	TBX5	0	3086	TBX5	0	chr12	113323000
-1179	CSH2	0	5303	GH2	0	chr17	59306000
14748	GPSM1	0	17378	GPSM1	0	chr9	138356500
15248	GPSM1	0	16878	GPSM1	0	chr9	138357000
141587	NCOR2	0	69602	NCOR2	0	chr12	123516500
142087	NCOR2	0	69102	NCOR2	0	chr12	123517000

3246	C21orf2	0	7213	C21orf2	0	chr21	44576500
3746	C21orf2	0	6713	C21orf2	0	chr21	44577000
57485	LAMA5	0	763	LAMA5	0	chr20	60375000
57985	LAMA5	0	263	LAMA5	0	chr20	60375500
15917	NFIX	0	87110	NFIX	0	chr19	12983500
16417	NFIX	0	86610	NFIX	0	chr19	12984000
5915	KLHL35	0	1881	KLHL35	0	chr11	74817000
-3837	TAF1C	0	223	ADAD2	0	chr16	82782000
-28609	COL6A1	0	64460	COL6A2	0	chr21	46278000
-29109	COL6A1	0	63960	COL6A2	0	chr21	46278500
-90247	TIAF1	0	81000	CRYBA1	0	chr17	24517000
-5833	ESPNL	0	1655	KLHL30	0	chr2	238712500
112	RAVER1	0	17314	RAVER1	0	chr19	10288000
612	RAVER1	0	16814	RAVER1	0	chr19	10288500
1450	C9orf173	0	755	C9orf173	0	chr9	139267000
4062	INTS1	0	30044	INTS1	0	chr7	1480500
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-1363429	TTTY23B,TTTY23	0	1560691	TTTY15	0	chrY	11723000
-1363929	TTTY23B,TTTY23	0	1560191	TTTY15	0	chrY	11723500
52281	ZDHHC11	0	3101	ZDHHC11	0	chr5	901000
5997	C2orf27B	0	704	C2orf27B	0	chr2	132275000
6497	C2orf27B	0	204	C2orf27B	0	chr2	132275500
187716	SLIT1	0	173	SLIT1	0	chr10	98935500
1392	SQSTM1	0	29681	SQSTM1	0	chr5	179168000
-2396	SNORD88A	0	393	SNORD88C	0	chr19	55997000
-14855	PSCA	0	2532	LY6K	0	chr8	143776000
-15355	PSCA	0	2032	LY6K	0	chr8	143776500
56936	GAK	0	26174	GAK	0	chr4	890000
76142	KCNT1	0	14813	KCNT1	0	chr9	137810000
76642	KCNT1	0	14313	KCNT1	0	chr9	137810500
-1989	INSR	0	118998	ARHGEF18	0	chr19	7247000
297	OTUD1	0	2814	OTUD1	0	chr10	23768500
-1965	DDX12	0	145136	KLRB1	0	chr12	9494000
-139892	C10orf108	0	4483	LARP4B	0	chr10	841000
-140392	C10orf108	0	3983	LARP4B	0	chr10	841500
23969	ASMTL	0	25844	ASMTL	0	chrX	1506000
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23647	STEAP3	0	18197	STEAP3	0	chr2	119721500
24147	STEAP3	0	17697	STEAP3	0	chr2	119722000
99	MAGEA9	0	5706	MAGEA9	0	chrX	148671500
26789	PKD1	0	20400	PKD1	0	chr16	2105500
7579	C21orf33	0	4533	C21orf33	0	chr21	44385500
-169946	TP53TG3	0	30797	SLC6A10P	0	chr16	32765500
-25258	CHST12	0	60004	LFNG	0	chr7	2466000
-1219	ACBD7	0	5389	C10orf111	0	chr10	15172000
-101264	TANK	0	2031	PSMD14	0	chr2	161871000
-192620	GGT8P	0	3263899	ANKRD20B	0	chr2	91526500
-1968	TP53AIP1	0	20165	ARHGAP32	0	chr11	128320000
-130599	ITSN2	0	93349	NCOA1	0	chr2	24567500
608	HCN2	0	26659	HCN2	0	chr19	541500
1108	HCN2	0	26159	HCN2	0	chr19	542000
-681	BOLL	0	18777	PLCL1	0	chr2	198359000
11966	PLXNB2	0	7836	PLXNB2	0	chr22	49067500
-837	CD70	0	72565	TNFSF14	0	chr19	6543000
-1337	CD70	0	72065	TNFSF14	0	chr19	6543500
2943	RHBDF1	0	11629	RHBDF1	0	chr16	51000
-33209	UBTFL2	0	10470	TRIM49	0	chr11	89160000

-33709	UBTFL2	0	9970	TRIM49	0	chr11	89160500
605	SLC25A34	0	4471	SLC25A34	0	chr1	15936000
200	TNFRSF25	0	4842	TNFRSF25	0	chr1	6444000
8361	TNFSF12-TNFSF13	0	4149	NFSF12-TNFSF13	0	chr17	7401500
9610	CCDC154	0	491	CCDC154	0	chr16	1434000
-9	CCDC154	0	435	CLCN7	0	chr16	1434500
5435	TNFSF14	0	599	TNFSF14	0	chr19	6621000
610	LOC100240735	0	2374	LOC100240735	0	chr12	52759500
-52248	RCAN1	0	2057	CLIC6	0	chr21	34961500
733	C9orf163	0	1840	C9orf163	0	chr9	138498500
-145	DVL1	0	3433	MXRA8	0	chr1	1274500
32096	POLD1	0	1583	POLD1	0	chr19	55611500
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-62276	BTF3L1	0	559	CLN5	0	chr13	76463500
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-2770997	ALG10	0	153323	ALG10B	0	chr12	36843500
-14600	DTYMK	0	628	ING5	0	chr2	242289500
-15100	DTYMK	0	128	ING5	0	chr2	242290000
-152526	ZNF599	0	1146	ZNF30	0	chr19	40108500
-27085	ETS1	0	144522	FLI1	0	chr11	127924500
-17117	GUCY2D	0	1582	ALOX15B	0	chr17	7881500
-250266	MIMT1	0	21320	USP29	0	chr19	62302000
-250766	MIMT1	0	20820	USP29	0	chr19	62302500
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-1190	OTUD7B	0	55465	VPS45	0	chr1	148250500
-1690	OTUD7B	0	54965	VPS45	0	chr1	148251000
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-1610	SRXN1	0	6740	SCRT2	0	chr20	583500
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-1200	SLC37A4	0	12105	HYOU1	0	chr11	118408000
576	SLC7A5P1	0	39	SLC7A5P1	0	chr16	29532500
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-180225	JAK1	0	819	AK4	0	chr1	65385000
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-151478	LRPAP1	0	82593	ADRA2C	0	chr4	3655500
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-55449	LOC400657	0	406	ZNF407	0	chr18	70471500
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-2820	RPL3L	0	2017	NDUFB10	0	chr16	1947500
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658	PHF13	0	9680	PHF13	0	chr1	6597000
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59473	EMILIN2	0	7590	EMILIN2	0	chr18	2896500
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-32	OTUB1	0	106	MACROD1	0	chr11	63522500
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-616274	ERICH1	0	149475	DLGAP2	0	chr8	1287500
-71018	SLC14A1	0	2042	SIGLEC15	0	chr18	41657500
-93608	ALOX12P2	0	2107	ALOX12	0	chr17	6838000
46281	CASR	0	56534	CASR	0	chr3	123431500
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3035	PCDHGB7	0	92230	PCDHGB7	0	chr5	140780500
3959	C16orf7	0	9895	C16orf7	0	chr16	88305000
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-1322	AOAH	0	128485	ELMO1	0	chr7	36732000
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912	TAS1R3	0	2207	TAS1R3	0	chr1	1257500
1412	TAS1R3	0	1707	TAS1R3	0	chr1	1258000
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-1391	RPL8	0	5064	ZNF517	0	chr8	145990000
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5033	GFRA3	0	17152	GFRA3	0	chr5	137621000
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-20887	TNFRSF14	0	608	C1orf93	0	chr1	2507500
-21387	TNFRSF14	0	108	C1orf93	0	chr1	2508000
-877261	XYLT1	0	9955	PKD1P1	0	chr16	18349500
-877761	XYLT1	0	9455	PKD1P1	0	chr16	18350000
-31109	COL6A1	0	61960	COL6A2	0	chr21	46280500
-31609	COL6A1	0	61460	COL6A2	0	chr21	46281000
299	AVP	0	1870	AVP	0	chr20	3011500
-427	NDUFA13	0	219	YJEFN3	0	chr19	19500500
-138606	RELL1	0	1676	PGM2	0	chr4	37503000
-2507	FOXQ1	0	72567	FOXF2	0	chr6	1262500
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5950	CALHM3	0	487	CALHM3	0	chr10	105228500
3258	SLC17A6	0	38120	SLC17A6	0	chr11	22319500
3758	SLC17A6	0	37620	SLC17A6	0	chr11	22320000
636	CCDC36	0	59041	CCDC36	0	chr3	49211500
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-7765	PRR14	0	278	FBRS	0	chr16	30583000
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2474	TGFB1I1	0	2281	TGFB1I1	0	chr16	31394500
2974	TGFB1I1	0	1781	TGFB1I1	0	chr16	31395000
-1153	TGM5	0	8270	TGM7	0	chr15	41347500
-1718491	COBL	0	342	POM121L12	0	chr7	53070500
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5331	C11orf45	0	802	C11orf45	0	chr11	128280000
9193	PRMT1	0	2016	PRMT1	0	chr19	54881500
-85805	RNF38	0	85904	MELK	0	chr9	36477000
-86305	RNF38	0	85404	MELK	0	chr9	36477500
-12710	TRIM53	0	47726	TRIM49L	0	chr11	89236500
-13210	TRIM53	0	47226	TRIM49L	0	chr11	89237000
-13710	TRIM53	0	46726	TRIM49L	0	chr11	89237500
-14210	TRIM53	0	46226	TRIM49L	0	chr11	89238000
2799	AIRE	0	5038	AIRE	0	chr21	44537500
3299	AIRE	0	4538	AIRE	0	chr21	44538000
10255	ZSCAN1	0	10311	ZSCAN1	0	chr19	63247500
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-7720	MS4A15	0	896	MS4A10	0	chr11	60308500
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-2610147	PABPC4L	0	707021	PCDH18	0	chr4	137952500
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114621	SMOC2	0	111096	SMOC2	0	chr6	168699500
-4296	RANBP1	0	364	ZDHHC8	0	chr22	18499000
5370	C14orf80	0	2629	C14orf80	0	chr14	105034000
-230	KLK8	0	580	KLK9	0	chr19	56197000
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-1700	ST5	0	98776	C11orf17	0	chr11	8790500
94878	ZFYVE28	0	54167	ZFYVE28	0	chr4	2336000
-150381	CEBPB	0	167297	PTPN1	0	chr20	48393000
-150881	CEBPB	0	166797	PTPN1	0	chr20	48393500
-151381	CEBPB	0	166297	PTPN1	0	chr20	48394000
48140	SIM2	0	2380	SIM2	0	chr21	37042000
971	RIC8A	0	5610	RIC8A	0	chr11	199500
4453	C19orf63	0	2420	C19orf63	0	chr19	55676000
123964	EBF3	0	4581	EBF3	0	chr10	131647500
12207	SLC12A9	0	2070	SLC12A9	0	chr7	100300500
12707	SLC12A9	0	1570	SLC12A9	0	chr7	100301000

13207	SLC12A9	0	1070	SLC12A9	0	chr7	100301500
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-941271	NOX3	0	380777	ARID1B	0	chr6	156760000
-20189	NFATC1	0	130288	CTDP1	0	chr18	75410500
-20689	NFATC1	0	129788	CTDP1	0	chr18	75411000
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9064	GRIN3B	0	223	GRIN3B	0	chr19	960500
351	C19orf6	0	11141	C19orf6	0	chr19	961000
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1351	C19orf6	0	10141	C19orf6	0	chr19	962000
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-446	DPPA2	0	9177	DPPA4	0	chr3	110518500
-282414	LOC399744	0	3083819	LOC441666	0	chr10	39063500
1506	PRR23A	0	800	PRR23A	0	chr3	140207000
2006	PRR23A	0	300	PRR23A	0	chr3	140207500
-13678	FAM154B	0	131239	GOLGA6L9	0	chr15	80378000
24151	CDK18	0	4040	CDK18	0	chr1	203764500
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5279	C10orf58	0	19233	C10orf58	0	chr10	82163500
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8525	NTN5	0	3076	NTN5	0	chr19	53865000
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-23457	FLJ40292	0	89561	CACNA1B	0	chr9	139802500
-1693	CGB2	0	637	CGB1	0	chr19	54230000
-8861	MPP2	0	601	C17orf88	0	chr17	39349500
-3649	PANX2	0	1986	TRABD	0	chr22	48964500
-85617	ISG20	0	62177	ACAN	0	chr15	87085500
-86117	ISG20	0	61677	ACAN	0	chr15	87086000
6748	GPSM1	0	25378	GPSM1	0	chr9	138348500
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22819	PIP5K1C	0	47445	PIP5K1C	0	chr19	3604000
2542	TEKT4	0	2795	TEKT4	0	chr2	94903500
3042	TEKT4	0	2295	TEKT4	0	chr2	94904000
6283	C12orf53	0	573	C12orf53	0	chr12	6679500
-31880	LOC441208	0	106302	KBTBD2	0	chr7	32768000
-18741	STXBP2	0	2471	RETN	0	chr19	7637500
-19241	STXBP2	0	1971	RETN	0	chr19	7638000
-33021	SOX8	0	44084	LOC146336	0	chr16	1010000
-1321	KCNJ14	0	1776	CYTH2	0	chr19	53662500
989	FRAT1	0	1662	FRAT1	0	chr10	99070000
9733	CBFA2T3	0	56609	CBFA2T3	0	chr16	87478500
-732	C1orf111	0	1319	C1orf226	0	chr1	160614000
903	RIPK4	0	26818	RIPK4	0	chr21	42033500
94058	BCOR	0	32026	BCOR	0	chrX	39889500
1295	IRF2BP1	0	1216	IRF2BP1	0	chr19	51080000
-122479	SOX1	0	182169	C13orf28	0	chr13	111896500
-122979	SOX1	0	181669	C13orf28	0	chr13	111897000
9848	ZNF672	0	1337	ZNF672	0	chr1	247109000
-741	C7orf64	0	224	MGC16142	0	chr7	92005500
276	MGC16142	0	1013	MGC16142	0	chr7	92006000
36034	C21orf81	0	636	C21orf81	0	chr21	14274000
-1364	C21orf81	0	127005	LIPI	0	chr21	14276000
-1877	DDX11L2	0	7785	RPL23AP7	0	chr2	114077500
-2404	CABIN1	0	443	SUSD2	0	chr22	22907000

-6061	CYB561	0	30165	ACE	0	chr17	58878000
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2347	TIMP2	0	70067	TIMP2	0	chr17	74363000
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9723	GOLGA8B	0	1014	GOLGA8B	0	chr15	32614500
-431750	FAM19A5	0	433793	C22orf34	0	chr22	47965500
1689	TPRX1	0	673	TPRX1	0	chr19	52998000
-18095	BDP1	0	1370	MCCC2	0	chr5	70917500
-18595	BDP1	0	870	MCCC2	0	chr5	70918000
-3106	C6orf114	0	85270	SIRT5	0	chr6	13597500
70587	TBC1D16	0	25242	TBC1D16	0	chr17	75599000
-131	ELF4	0	18518	AIFM1	0	chrX	129072500
-30058	FCGR3A	0	1252	FCGR2C	0	chr1	159816500
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426	MIER2	0	38791	MIER2	0	chr19	257000
926	MIER2	0	38291	MIER2	0	chr19	257500
-51428	IPP	0	1371	MAST2	0	chr1	46040500
-745	KIAA0101	0	5572	TRIP4	0	chr15	62461500
-1935	ZNF295	0	9681	C21orf121	0	chr21	42305500
-31566	RNASE2	0	1804	METT11D1	0	chr14	20526000
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-234	SLC7A5P2	0	78856	METTL9	0	chr16	21439500
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13552	TNRC18	0	103203	TNRC18	0	chr7	5326500
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-126	GOPC	0	72809	NUS1	0	chr6	118030500
-626	GOPC	0	72309	NUS1	0	chr6	118031000
9873	GABRD	0	1552	GABRD	0	chr1	1950500
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16561	C7orf26	0	1880	C7orf26	0	chr7	6613000
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1292	DACT3	0	12235	DACT3	0	chr19	51844000
25006	DNAH10	0	148218	DNAH10	0	chr12	122838000
132	KCNK4	0	8579	KCNK4	0	chr11	63815500
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14825	MTL5	0	564	MTL5	0	chr11	68275000
7346	OPLAH	0	2072	OPLAH	0	chr8	145185500
9618	PRIC285	0	6536	PRIC285	0	chr20	61669500
8164	FGFR3	0	7396	FGFR3	0	chr4	1773000
7642	IRGQ	0	4127	IRGQ	0	chr19	48788000
-1909	MREG	0	22855	PECR	0	chr2	216588500
698	IQSEC3	0	93255	IQSEC3	0	chr12	57500
-624	LOC284837	0	52043	AGPAT3	0	chr21	44057500
-74759	KIAA0754	0	404	BMP8A	0	chr1	39729500
96	BMP8A	0	38128	BMP8A	0	chr1	39730000
22739	TMEM175	0	3443	TMEM175	0	chr4	939000
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19345	KCNG2	0	16804	KCNG2	0	chr18	75744000
6837	LOC285740	0	878	LOC285740	0	chr6	143924000
7337	LOC285740	0	378	LOC285740	0	chr6	143924500
644	C11orf35	0	5279	C11orf35	0	chr11	545500
-1656	DLG1	0	209550	BDH1	0	chr3	198511500
-37362	CEP350	0	2590	QSOX1	0	chr1	178388000

-6374	IL11	0	15	TMEM190	0	chr19	60580000
-76330	NFYB	0	1188	TXNRD1	0	chr12	103132500
5968	SUV420H2	0	2301	SUV420H2	0	chr19	60549000
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6968	SUV420H2	0	1301	SUV420H2	0	chr19	60550000
-33613	GTPBP6	0	10469	PPP2R3B	0	chrX	204500
-34113	GTPBP6	0	9969	PPP2R3B	0	chrX	205000
-69957	FLJ40292	0	43061	CACNA1B	0	chr9	139849000
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105	STAB1	0	29051	STAB1	0	chr3	52504500
-87045	LOC400891	0	131213	POM121L8P	0	chr22	19835500
5474	ZIC4	0	15097	ZIC4	0	chr3	148592000
4636	ERCC2	0	7185	ERCC2	0	chr19	50558500
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-408	BBS7	0	8132	TRPC3	0	chr4	123011500
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7694	WHSC1	0	81732	WHSC1	0	chr4	1872000
350	WHSC1	0	47843	WHSC1	0	chr4	1872500
41732	RNF212	0	582	RNF212	0	chr4	1097000
2366	PCDH7	0	424019	PCDH7	0	chr4	30333500
-236106	C6orf208	0	224346	LOC154449	0	chr6	170181000
93236	GLTSCR1	0	1846	GLTSCR1	0	chr19	52896500
-1106	MPHOSPH9	0	10293	C12orf65	0	chr12	122273500
-1606	MPHOSPH9	0	9793	C12orf65	0	chr12	122274000
-167	FAM65C	0	94487	PARD6B	0	chr20	48687000
-7239	COX19	0	360	CYP2W1	0	chr7	989000
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-89996	TUBA3E	0	49785	CCDC115	0	chr2	130762500
15	KCNQ2	0	66437	KCNQ2	0	chr20	61508000
164047	MAD1L1	0	253109	MAD1L1	0	chr7	1986000
164547	MAD1L1	0	252609	MAD1L1	0	chr7	1986500
8843	FAM9C	0	221	FAM9C	0	chrX	12972500
239	CCDC85A	0	201813	CCDC85A	0	chr2	56265000
-75	BNIP3	0	122802	JAKMIP3	0	chr10	133645500
3641	LRRC4	0	238	LRRC4	0	chr7	127458000
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11193	SEMA3G	0	583	SEMA3G	0	chr3	52453500
-36213	MYOM2	0	663281	CSMD1	0	chr8	2117000
36242	AGAP3	0	21456	AGAP3	0	chr7	150451000
36742	AGAP3	0	20956	AGAP3	0	chr7	150451500
-648	TSPYL5	0	365582	MTDH	0	chr8	98360000
13547	FZR1	0	255	FZR1	0	chr19	3487500
-245	FZR1	0	1262	C19orf28	0	chr19	3488000
-148	ARFGAP3	0	13380	PACSIN2	0	chr22	41583500
565	GPX4	0	2287	GPX4	0	chr19	1055500
-4737	EPT1	0	1287	C2orf39	0	chr2	26477000
-98	TRIML2	0	34091	TRIML1	0	chr4	189263500
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-88	FAM196A	0	353102	NPS	0	chr10	128884500
25352	C7orf50	0	115919	C7orf50	0	chr7	1028500
26352	C7orf50	0	114919	C7orf50	0	chr7	1029500
-166301	TMEM215	0	17107	APTX	0	chr9	32945500
-166801	TMEM215	0	16607	APTX	0	chr9	32946000
-38012	TCP10	0	172069	C6orf123	0	chr6	167756000
-38512	TCP10	0	171569	C6orf123	0	chr6	167756500

50473	LOXHD1	0	41624	LOXHD1	0	chr18	42394000
21246	HDGFRP2	0	8722	HDGFRP2	0	chr19	4444500
-6002	SLC25A6	0	2423	ASMTLAS	0	chrX	1477000
-6502	SLC25A6	0	1923	ASMTLAS	0	chrX	1477500
-7002	SLC25A6	0	1423	ASMTLAS	0	chrX	1478000
-78379	NEDD4	0	95022	RFX7	0	chr15	54075000
-660	OSM	0	17606	GATSL3	0	chr22	28993500
-70	TPN20B,PTPN20	0	425379	AM25G,FAM25C	0	chr10	48448000
-100558	POTEG	0	298453	POTEM	0	chr14	18755500
3608	C2orf16	0	2593	C2orf16	0	chr2	27656500
4718	ZNF324B	0	1511	ZNF324B	0	chr19	63659500
27938	ADAP1	0	28815	ADAP1	0	chr7	932000
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-2070	SIK1	0	20831	C21orf125	0	chr21	43673500
15914	SLC29A4	0	5230	SLC29A4	0	chr7	5305000
16414	SLC29A4	0	4730	SLC29A4	0	chr7	5305500
9307	SCAF1	0	7217	SCAF1	0	chr19	54846500
9807	SCAF1	0	6717	SCAF1	0	chr19	54847000
35829	MAEA	0	14425	MAEA	0	chr4	1309500
-83365	ALLC	0	1938749	SOX11	0	chr2	3811500
5017	A1BG	0	1677	A1BG	0	chr19	63555000
353	A1BGAS	0	2861	A1BGAS	0	chr19	63555500
13854	PEAR1	0	8850	PEAR1	0	chr1	155144000
14354	PEAR1	0	8350	PEAR1	0	chr1	155144500
73685	RARS2	0	1954	RARS2	0	chr6	88354500
74185	RARS2	0	1454	RARS2	0	chr6	88355000
-26871	C14orf80	0	497	TMEM121	0	chr14	105063500
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8881	GLTSCR2	0	2627	GLTSCR2	0	chr19	52949500
9381	GLTSCR2	0	2127	GLTSCR2	0	chr19	52950000
9881	GLTSCR2	0	1627	GLTSCR2	0	chr19	52950500
-307354	PWRN2	0	80896	PWRN1	0	chr15	22273500
8900	GJB6	0	372	GJB6	0	chr13	19703000
-128	GJB6	0	172305	CRYL1	0	chr13	19703500
307801	KSR2	0	207411	KSR2	0	chr12	116683000
308301	KSR2	0	206911	KSR2	0	chr12	116683500
-11184	C21orf70	0	11056	NCRNA00162	0	chr21	45232500
-16878	TSPY3	0	63329	RBMY3AP	0	chrY	9995000
-17378	TSPY3	0	62829	RBMY3AP	0	chrY	9995500
4687	DMRTA2	0	1229	DMRTA2	0	chr1	50660500
11096	LOC389033	0	360	LOC389033	0	chr2	130408000
-1143	PUS1	0	4960	EP400	0	chr12	130995500
1200	BRD4	0	41762	BRD4	0	chr19	15210500
1700	BRD4	0	41262	BRD4	0	chr19	15211000
1200	ZAP70	0	4255	ZAP70	0	chr2	97718500
1214	SEMA6C	0	13728	SEMA6C	0	chr1	149372000
199	SNN	0	10509	SNN	0	chr16	11670000
699	SNN	0	10009	SNN	0	chr16	11670500
-829	AKTIP	0	95818	RPGRIP1L	0	chr16	52095500
-1329	AKTIP	0	95318	RPGRIP1L	0	chr16	52096000
9645	METRNL	0	5511	METRNL	0	chr17	78640500
10145	METRNL	0	5011	METRNL	0	chr17	78641000
-623774	ERICH1	0	141975	DLGAP2	0	chr8	1295000
-1231	CD7	0	2188	SECTM1	0	chr17	77870000
-1731	CD7	0	1688	SECTM1	0	chr17	77870500
-2231	CD7	0	1188	SECTM1	0	chr17	77871000
-41526	SSX2	0	2532	SSX2	0	chrX	52794500
-42026	SSX2	0	2032	SSX2	0	chrX	52795000

-2201	GPR132	0	74120	JAG2	0	chr14	104605000
7204	C2orf64	0	1887	C2orf64	0	chr2	98589500
1251	FAM27B	0	9	FAM27B	0	chr9	67384000
14327	HMHA1	0	5127	HMHA1	0	chr19	1032500
-223	TNK2	0	50689	SDHAP1	0	chr3	197120500
16539	NOP14	0	8916	NOP14	0	chr4	2926000
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17539	NOP14	0	7916	NOP14	0	chr4	2927000
22721	ERBB2	0	5941	ERBB2	0	chr17	35132500
23221	ERBB2	0	5441	ERBB2	0	chr17	35133000
23721	ERBB2	0	4941	ERBB2	0	chr17	35133500
-27941	LOC100130238	0	181729	FBRSL1	0	chr12	131395500
46339	TRIM66	0	459	TRIM66	0	chr11	8636500
53007	MRC2	0	13184	MRC2	0	chr17	58111500
998	FASN	0	18895	FASN	0	chr17	77630500
22885	SETD1A	0	4482	SETD1A	0	chr16	30899000
23385	SETD1A	0	3982	SETD1A	0	chr16	30899500
688	C21orf119	0	135	C21orf119	0	chr21	32688000
-70982	APOH	0	2387	PRKCA	0	chr17	61727000
12626	NCLN	0	11073	NCLN	0	chr19	3149500
13126	NCLN	0	10573	NCLN	0	chr19	3150000
118	PHYHD1	0	19641	PHYHD1	0	chr9	130724500
-121465	DDX12	0	25636	KLRB1	0	chr12	9613500
7679	ZBTB46	0	53300	ZBTB46	0	chr20	61854000
8179	ZBTB46	0	52800	ZBTB46	0	chr20	61854500
1438	DGKZ	0	33680	DGKZ	0	chr11	46325000
979	MMP23A	0	890	MMP23A	0	chr1	1559000
-83864	C21orf81	0	44505	LIPI	0	chr21	14358500
13266	WDR5	0	6915	WDR5	0	chr9	136008000
-534	GRWD1	0	1077	KCNJ14	0	chr19	53649500
-54951	DLGAP2	0	276	CLN8	0	chr8	1699000
-10748	TTYH2	0	1491	DNAI2	0	chr17	69780500
-174536	SLC6A10P	0	133156	TP53TG3B	0	chr16	32978500
-14090	SNORD68	0	176	CPNE7	0	chr16	88169500
324	CPNE7	0	21154	CPNE7	0	chr16	88170000
-7810	DUS3L	0	24817	NRTN	0	chr19	5750000
-8310	DUS3L	0	24317	NRTN	0	chr19	5750500
1476	PDF,COG8	0	499	PDF,COG8	0	chr16	67921500
5901	KCNG1	0	13582	KCNG1	0	chr20	49059500
-5482	LOC645323	0	34314	MEF2C	0	chr5	88015500
-5982	LOC645323	0	33814	MEF2C	0	chr5	88016000
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19410	COL6A1	0	3891	COL6A1	0	chr21	46245500
21410	COL6A1	0	1891	COL6A1	0	chr21	46247500
21910	COL6A1	0	1391	COL6A1	0	chr21	46248000
-30359	H19	0	100922	IGF2	0	chr11	2006000
-30859	H19	0	100422	IGF2	0	chr11	2006500
7137	AMDHD2	0	2232	AMDHD2	0	chr16	2517500
11022	RNFT2	0	104319	RNFT2	0	chr12	115671500
11522	RNFT2	0	103819	RNFT2	0	chr12	115672000
12022	RNFT2	0	103319	RNFT2	0	chr12	115672500
298	EGFL7	0	9451	EGFL7	0	chr9	138677500
19831	ARHGAP23	0	35153	ARHGAP23	0	chr17	33887000
20331	ARHGAP23	0	34653	ARHGAP23	0	chr17	33887500
-15660	LRRK1	0	89954	CHSY1	0	chr15	99443500
-16160	LRRK1	0	89454	CHSY1	0	chr15	99444000
-44086	HTRA1	0	1670	DMBT1	0	chr10	124308500
697	MRPS2	0	3340	MRPS2	0	chr9	137533000

-1717	BACH2	0	217073	MAP3K7	0	chr6	91065000
-96480	GOT1	0	5679	NKX2-3	0	chr10	101277000
-96980	GOT1	0	5179	NKX2-3	0	chr10	101277500
25801	TTBK1	0	18975	TTBK1	0	chr6	43345000
26301	TTBK1	0	18475	TTBK1	0	chr6	43345500
-878261	XYLT1	0	8955	PKD1P1	0	chr16	18350500
-878761	XYLT1	0	8455	PKD1P1	0	chr16	18351000
-43825	SRD5A1	0	1217	PAPD7	0	chr5	6766500
18991	ABR	0	164866	ABR	0	chr17	872500
19491	ABR	0	164366	ABR	0	chr17	873000
4769	AKT1	0	19483	AKT1	0	chr14	104311500
55981	TC2N	0	602	TC2N	0	chr14	91372000
56481	TC2N	0	102	TC2N	0	chr14	91372500
308	CAPS	0	1722	CAPS	0	chr19	5865500
808	CAPS	0	1222	CAPS	0	chr19	5866000
190	FJX1	0	2495	FJX1	0	chr11	35596500
690	FJX1	0	1995	FJX1	0	chr11	35597000
-1739	FAM171A2	0	6575	ITGA2B	0	chr17	39798500
25115	TUBBP5	0	2205	TUBBP5	0	chr9	140189500
-8955	BRPF3	0	1422	PNPLA1	0	chr6	36317500
26093	GNA11	0	954	GNA11	0	chr19	3071500
-46	GNA11	0	14690	GNA15	0	chr19	3072500
4755	NEU4	0	1907	NEU4	0	chr2	242405500
5255	NEU4	0	1407	NEU4	0	chr2	242406000
4852	TTLL10	0	19176	TTLL10	0	chr1	1104000
5352	TTLL10	0	18676	TTLL10	0	chr1	1104500
-25097	TPTE2	0	71879	MPHOSPH8	0	chr13	19034000
-93361	UNCX	0	104020	MICALL2	0	chr7	1336500
-93861	UNCX	0	103520	MICALL2	0	chr7	1337000
-37890	BTBD1	0	2327	TM6SF1	0	chr15	81565000
-38390	BTBD1	0	1827	TM6SF1	0	chr15	81565500
-191005	ANKRD30BL	0	63616	GPR39	0	chr2	132827000
-191505	ANKRD30BL	0	63116	GPR39	0	chr2	132827500
-205324	AKT3	0	2683	ZNF238	0	chr1	242278500
33355	SCN4A	0	1010	SCN4A	0	chr17	59403000
17686	C18orf62	0	77	C18orf62	0	chr18	71268500
-387	TNFRSF14	0	21108	C1orf93	0	chr1	2487000
-887	TNFRSF14	0	20608	C1orf93	0	chr1	2487500
8713	C6orf204	0	151713	C6orf204	0	chr6	118928000
9213	C6orf204	0	151213	C6orf204	0	chr6	118928500
23108	HCN2	0	4159	HCN2	0	chr19	564000
4434	DPEP3	0	453	DPEP3	0	chr16	66571500
640	LASS1,GDF1	0	26953	LASS1,GDF1	0	chr19	18841000
1140	LASS1,GDF1	0	26453	LASS1,GDF1	0	chr19	18841500
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-53378	GEMIN7	0	7000	NKPD1	0	chr19	50340000
-53878	GEMIN7	0	6500	NKPD1	0	chr19	50340500
-92806	C22orf34	0	22940	BRD1	0	chr22	48530000
-93306	C22orf34	0	22440	BRD1	0	chr22	48530500
-1441	NOTCH1	0	115697	EGFL7	0	chr9	138561500
109054	PROM1	0	6721	PROM1	0	chr4	15688000
109554	PROM1	0	6221	PROM1	0	chr4	15688500
1311	GNAS	0	70145	GNAS	0	chr20	56849500
67552	TNRC18	0	49203	TNRC18	0	chr7	5380500
14906	ZNF488	0	3874	ZNF488	0	chr10	47990000
6337	LMNB2	0	22458	LMNB2	0	chr19	2385500
174	LIMD1	0	86259	LIMD1	0	chr3	45611500
-409	ZNF484	0	68921	FGD3	0	chr9	94680500

316490	PTPRN2	0	732243	PTPRN2	0	chr7	157341000
-21473	NKX6-2	0	886	C10orf92	0	chr10	134471000
1228	GPT	0	1863	GPT	0	chr8	145701500
-1408	FBXL14	0	21482	WNT5B	0	chr12	1575000
68321	RYR1	0	85544	RYR1	0	chr19	43684500
68821	RYR1	0	85044	RYR1	0	chr19	43685000
-31639	RAET1L	0	7435	ULBP3	0	chr6	150420000
-23817	GPR17	0	24566	SFT2D3	0	chr2	128150500
4671	DOK2	0	151	DOK2	0	chr8	21827000
9518	WNT5B	0	20638	WNT5B	0	chr12	1606000
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19284	SS18L1	0	19461	SS18L1	0	chr20	60171500
19784	SS18L1	0	18961	SS18L1	0	chr20	60172000
-44845	RCN2	0	19	PSTPIP1	0	chr15	75074500
1975	RNF126	0	13727	RNF126	0	chr19	600500
9392	SQSTM1	0	21681	SQSTM1	0	chr5	179176000
9892	SQSTM1	0	21181	SQSTM1	0	chr5	179176500
3555	SLC43A2	0	50880	SLC43A2	0	chr17	1428000
-1593	NEU4	0	31705	PDCD1	0	chr2	242409000
-619	RAB6B	0	31679	C3orf36	0	chr3	135098000
42675	SIRPA	0	2040	SIRPA	0	chr20	1866500
-245598	AQP9	0	466	LIPC	0	chr15	56511000
34	LIPC	0	136865	LIPC	0	chr15	56511500
19837	CDH15	0	3901	CDH15	0	chr16	87785500
-62202	CTSD	0	8249	SYT8	0	chr11	1804000
48627	ITIH5	0	46940	ITIH5	0	chr10	7702000
49127	ITIH5	0	46440	ITIH5	0	chr10	7702500
356	BCL2L14	0	28394	BCL2L14	0	chr12	12115500
332	BCL2L14	0	27894	BCL2L14	0	chr12	12116000
-36218	RAB10	0	17007	HADHA	0	chr2	26250000
222	TMEM89	0	693	TMEM89	0	chr3	48633500
-50870	LY6H	0	2442	GPIHBP1	0	chr8	144364000
-26673	CSF2RA	0	8	IL3RA	0	chrY	1415500
298	ZNF579	0	3023	ZNF579	0	chr19	60781000
798	ZNF579	0	2523	ZNF579	0	chr19	60781500
5706	B4GALNT4	0	6616	B4GALNT4	0	chr11	365500
6206	B4GALNT4	0	6116	B4GALNT4	0	chr11	366000
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47259	CACNA1H	0	21273	CACNA1H	0	chr16	1190500
384	KIAA1875	0	10206	KIAA1875	0	chr8	145235000
27367	RARRES1	0	469	RARRES1	0	chr3	159932500
-31	RARRES1	0	69605	MFSD1	0	chr3	159933000
86428	NFIC	0	10603	NFIC	0	chr19	3404000
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-693	CGB2	0	1637	CGB1	0	chr19	54229000
135158	SDK1	0	4157	SDK1	0	chr7	4271000
-6469	C21orf84	0	44499	HSF2BP	0	chr21	43729000
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63746	CDH20	0	845	CDH20	0	chr18	57372500
-10269	PDCD1	0	558	C2orf85	0	chr2	242460000
-1732	SSX2IP	0	121173	LPAR3	0	chr1	84930500
-2232	SSX2IP	0	120673	LPAR3	0	chr1	84931000
3383	SIGLEC14	0	944	SIGLEC14	0	chr19	56841000
3883	SIGLEC14	0	444	SIGLEC14	0	chr19	56841500
27148	RAI14	0	148973	RAI14	0	chr5	34719500
27648	RAI14	0	148473	RAI14	0	chr5	34720000
14453	ZDHHC6	0	2162	ZDHHC6	0	chr10	114194500
14953	ZDHHC6	0	1662	ZDHHC6	0	chr10	114195000

-71290	ZNF782	0	2912	FAM22G	0	chr9	98727500
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-270	CELA1	0	5099	GALNT6	0	chr12	50027000
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-827	SCT	0	9304	DRD4	0	chr11	618000
7426	CDHR5	0	1007	CDHR5	0	chr11	614000
7926	CDHR5	0	507	CDHR5	0	chr11	614500
8426	CDHR5	0	7	CDHR5	0	chr11	615000
11368	SBNO2	0	13273	SBNO2	0	chr19	1070000
11021	ZNF74	0	3252	ZNF74	0	chr22	19089500
11521	ZNF74	0	2752	ZNF74	0	chr22	19090000
12021	ZNF74	0	2252	ZNF74	0	chr22	19090500
70377	KDM4B	0	114108	KDM4B	0	chr19	4990500
70877	KDM4B	0	113608	KDM4B	0	chr19	4991000
2070	GNAS	0	56145	GNAS	0	chr20	56863500
2570	GNAS	0	55645	GNAS	0	chr20	56864000
3070	GNAS	0	55145	GNAS	0	chr20	56864500
-9361	CHRNA4	0	35485	KCNQ2	0	chr20	61472500
-9861	CHRNA4	0	34985	KCNQ2	0	chr20	61473000
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27061	CHD5	0	51270	CHD5	0	chr1	6111500
-1396	CD22	0	2784	FFAR1	0	chr19	40531500
144428	HTR4	0	434	HTR4	0	chr5	148013500
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38087	TBC1D16	0	57742	TBC1D16	0	chr17	75566500
-17691	ZNF572	0	1400	SQLE	0	chr8	126078500
-18191	ZNF572	0	900	SQLE	0	chr8	126079000
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-1088	AMY1B,AMY1C	0	52301	AMY1A	0	chr1	104041500
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29358	ELAVL3	0	303	ELAVL3	0	chr19	11452500
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2669	GGN	0	1008	GGN	0	chr19	43569500
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-131376	ZNF99	0	456337	ZNF91	0	chr19	22876000
-138096	MTR	0	324	RYR2	0	chr1	235272000
-38492	CLC	0	73	LEUTX	0	chr19	44959000
-2637707	C4orf33	0	1398919	PCDH10	0	chr4	132891000
-2638207	C4orf33	0	1398419	PCDH10	0	chr4	132891500
-817	PSMD12	0	10385	PITPNC1	0	chr17	62794000
-1317	PSMD12	0	9885	PITPNC1	0	chr17	62794500
-43916	TMEM121	0	343382	KIAA0125	0	chr14	105111500
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-261347	SYK	0	53917	AUH	0	chr9	92962000
-261847	SYK	0	53417	AUH	0	chr9	92962500
-766	LGALS7B	0	9150	LGALS4	0	chr19	43975000
-694170	INSC	0	25071	SOX6	0	chr11	15919500
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-23517	UCK1	0	21977	RAPGEF1	0	chr9	133420000
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-931	CCDC27	0	211	LOC388588	0	chr1	3679000
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16177	MUC6	0	7706	MUC6	0	chr11	1019000
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11756	REXO1	0	21452	REXO1	0	chr19	1778000
12256	REXO1	0	20952	REXO1	0	chr19	1778500
-277	SNORA5B	0	51391	RAMP3	0	chr7	45112500
1741	OR11A1	0	488	OR11A1	0	chr6	29503000
-12	OR11A1	0	12271	OR10C1	0	chr6	29503500
4230	CCDC88B	0	13082	CCDC88B	0	chr11	63868500
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5244	MAD2L1BP	0	6166	MAD2L1BP	0	chr6	43710500
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-157278	NMU	0	26493	LOC644145	0	chr4	56354500
-1303	NBEAL2	0	535	NRADDP	0	chr3	47027500
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-14126	DHX32	0	1097	FANK1	0	chr10	127574000
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-43945	TRIP4	0	171	ZNF609	0	chr15	62578500
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-527	SLC13A4	0	894	FAM180A	0	chr7	135064000
-1027	SLC13A4	0	394	FAM180A	0	chr7	135064500
-15298	LY6E	0	1553	C8orf31	0	chr8	144190500
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-954	ANXA8L1	0	2226	AM25G,FAM25C	0	chr10	46595000
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6151	FAM195A	0	475	FAM195A	0	chr16	638000
15768	PPP1R13L	0	10947	PPP1R13L	0	chr19	50590500
16268	PPP1R13L	0	10447	PPP1R13L	0	chr19	50591000
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-34195	CDC25A	0	865	CAMP	0	chr3	48239000
-143392	FSTL1	0	1817	NDUFB4	0	chr3	121796000
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-176521	GSG1L	0	33316	XPO6	0	chr16	27983500
-190953	NFIA	0	27306	TM2D1	0	chr1	61892000
-191453	NFIA	0	26806	TM2D1	0	chr1	61892500

-1640	C19orf38	0	252	CARM1	0	chr19	10843000
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99009	MRPS27	0	1840	MRPS27	0	chr5	71650000
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113241	KCNQ1	0	274416	KCNQ1	0	chr11	2552500
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-46845	JDP2	0	2536	BATF	0	chr14	75056000
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12112	FURIN	0	2691	FURIN	0	chr15	89225000
1413	GAMT	0	3052	GAMT	0	chr19	1349500
13109	FBXO24	0	1676	FBXO24	0	chr7	100035000
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-15126	DHX32	0	97	FANK1	0	chr10	127575000
-114297	ARGFXP2	0	307	RHBDL3	0	chr17	27617000
-55235	AGAP6	0	2189	FAM21A	0	chr10	51495500
-13626	C3orf10	0	818	VHL	0	chr3	10157500
13555	TSPAN4	0	9116	TSPAN4	0	chr11	848000
-30010	ZNF367	0	1734	HABP4	0	chr9	98250500
20714	C22orf9	0	27814	C22orf9	0	chr22	43987500
4864	CT62	0	393	CT62	0	chr15	69194500
-107	CT62	0	25841	THSD4	0	chr15	69195000
1590	C8orf82	0	1266	C8orf82	0	chr8	145724000
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78869	COL4A2	0	126874	COL4A2	0	chr13	109836500
4627	FGF17	0	1265	FGF17	0	chr8	21961000
5127	FGF17	0	765	FGF17	0	chr8	21961500
27635	AGRN	0	8355	AGRN	0	chr1	973000
-172503	LPHN1	0	2712	CD97	0	chr19	14350500
-173003	LPHN1	0	2212	CD97	0	chr19	14351000
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23247	ACCN2	0	2661	ACCN2	0	chr12	48761000
23747	ACCN2	0	2161	ACCN2	0	chr12	48761500
6417	NFIX	0	96610	NFIX	0	chr19	12974000
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-40003	KLRG2	0	213	CLEC2L	0	chr7	138859000
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-80615	C7orf33	0	2365	CUL1	0	chr7	148024500
-81115	C7orf33	0	1865	CUL1	0	chr7	148025000
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-9310	INF2	0	10078	ADSSL1	0	chr14	104251500
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349283	JAZF1	0	962	JAZF1	0	chr7	28186000
3492	PP14571	0	3790	PP14571	0	chr2	241041000
3992	PP14571	0	3290	PP14571	0	chr2	241041500
-65276	RIC8B	0	1173	C12orf23	0	chr12	105872500
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2212	MAGEL2	0	268	MAGEL2	0	chr15	21442000
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-732	MAGEL2	0	38646	NDN	0	chr15	21443000
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20392	NACC1	0	2459	NACC1	0	chr19	13110500
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-1174	SYT8	0	308	TNNI2	0	chr11	1816500
-503	LOC100144604	0	44682	FAM174B	0	chr15	90917000
-1003	LOC100144604	0	44182	FAM174B	0	chr15	90917500
-27521	IQGAP1	0	201	CRTC3	0	chr15	88874000
299	CRTC3	0	115081	CRTC3	0	chr15	88874500
585	KRT86	0	6714	KRT86	0	chr12	50982500
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1517	TRIM46	0	9569	TRIM46	0	chr1	153414500
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4447	DDT	0	4019	DDT	0	chr22	22648000
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-794	FUT10	0	11226	MAK16	0	chr8	33451000
-2683429	TTTY23B,TTTY23	0	240691	TTTY15	0	chrY	13043000
-1595	PEX11G	0	6944	C19orf45	0	chr19	7461500
-2095	PEX11G	0	6444	C19orf45	0	chr19	7462000
-462	UQCRB	0	3320	MTERFD1	0	chr8	97317500
-40058	POTEG	0	358953	POTEM	0	chr14	18695000
-40558	POTEG	0	358453	POTEM	0	chr14	18695500
-60446	RNMT	0	764	MC5R	0	chr18	13815000
8907	C6orf208	0	3894	C6orf208	0	chr6	169941000

-15515	CBX8	0	20549	CBX4	0	chr17	75401000
224	TMEM8A	0	10951	TMEM8A	0	chr16	361000
-2023	CD93	0	262372	NXT1	0	chr20	23017000
53	PLA2G6	0	70207	PLA2G6	0	chr22	36837500
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-96065	NBPF16	0	73909	LOC645166	0	chr1	147121000
-96565	NBPF16	0	73409	LOC645166	0	chr1	147121500
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218	SPDYC	0	2764	SPDYC	0	chr11	64694500
4259	CACNA1H	0	64273	CACNA1H	0	chr16	1147500
-9561	SCXA,SCXB	0	13577	HSF1	0	chr8	145472500
59076	CRTC1	0	39643	CRTC1	0	chr19	18714500
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192114	SAMD4A	0	29095	SAMD4A	0	chr14	54296500
-6827	GMEB2	0	13004	STMN3	0	chr20	61728500
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12571	ANO9	0	11511	ANO9	0	chr11	420500
7468	MYBPC3	0	13829	MYBPC3	0	chr11	47317000
22812	AMZ1	0	13095	AMZ1	0	chr7	2708500
23312	AMZ1	0	12595	AMZ1	0	chr7	2709000
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-932	POLRMT	0	5425	FGF22	0	chr19	585500
-1432	POLRMT	0	4925	FGF22	0	chr19	586000
-1932	POLRMT	0	4425	FGF22	0	chr19	586500
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8025	CD72	0	424	CD72	0	chr9	35608000
12494	ABCA2	0	9195	ABCA2	0	chr9	139034000
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-21553	FAM47E	0	1200	STBD1	0	chr4	77445500
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-27796	C2orf27B	0	318138	ANKRD30BL	0	chr2	132303500
144602	CELF2	0	174178	CELF2	0	chr10	11244500
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-86298	SPESP1	0	47743	NCRNA00277	0	chr15	67112500
32201	THBS2	0	6062	THBS2	0	chr6	169390000
33201	THBS2	0	5062	THBS2	0	chr6	169391000
-701280	TP53TG3	0	387802	UBE2MP1	0	chr16	33873500
-1367171	RNF144B	0	1595	ID4	0	chr6	19944000
-4646	TFAMP1	0	123132	ELFN1	0	chr7	1627500
-32710	OR5D16	0	10848	SPRYD5	0	chr11	55396500
-33210	OR5D16	0	10348	SPRYD5	0	chr11	55397000
-9368	KIAA0284	0	18731	PLD4	0	chr14	104443500
-9868	KIAA0284	0	18231	PLD4	0	chr14	104444000
82001	JPH3	0	13262	JPH3	0	chr16	86276000
83001	JPH3	0	12262	JPH3	0	chr16	86277000
88	ZNF511	0	4156	ZNF511	0	chr10	134972500
932	GIPC3	0	7038	GIPC3	0	chr19	3537500
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2534	NFKBIA	0	711	NFKBIA	0	chr14	34943000
-745	C3orf67	0	698575	FHIT	0	chr3	59011500
-1245	C3orf67	0	698075	FHIT	0	chr3	59012000
176028	COL5A1	0	27009	COL5A1	0	chr9	136849500
7065	CLCN7	0	23086	CLCN7	0	chr16	1442000
1227	LOC340508	0	5048	LOC340508	0	chr9	98879000

586990	PTPRN2	0	461743	PTPRN2	0	chr7	157611500
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1353	TMC4	0	11756	TMC4	0	chr19	59357000
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-132353	TOP3B	0	129699	VPREB1	0	chr22	20799500
66537	PCNT	0	55110	PCNT	0	chr21	46635000
-91505	ANKRD30BL	0	163116	GPR39	0	chr2	132727500
-92005	ANKRD30BL	0	162616	GPR39	0	chr2	132728000
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12621	ABCA3	0	52248	ABCA3	0	chr16	2278500
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-1639351	EDEM1	0	1926	GRM7	0	chr3	6876000
-1639851	EDEM1	0	1426	GRM7	0	chr3	6876500
-31236	STX2	0	1569	RAN	0	chr12	129921000
-31736	STX2	0	1069	RAN	0	chr12	129921500
39541	SNPH	0	3471	SNPH	0	chr20	1234500
7931	RHBDF2	0	22603	RHBDF2	0	chr17	71986500
2289	RRP7B	0	6461	RRP7B	0	chr22	41301500
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-31	DUS1L	0	12502	FASN	0	chr17	77617000
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22177	MUC6	0	1706	MUC6	0	chr11	1025000
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-343253	OPRK1	0	120667	ATP6V1H	0	chr8	54670000
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-4841	ULK1	0	1241	PUS1	0	chr12	130978500
-24452	C19orf34	0	6446	BTBD2	0	chr19	1930000
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-17335	DEFB130	0	255	ZNF705D	0	chr8	11984000
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-376	DDOST	0	2093	KIF17	0	chr1	20861000
-22374	APTX	0	1208	DNAJA1	0	chr9	33014000
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-1889	TH	0	94803	ASCL2	0	chr11	2151500
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-739	SNORD42B	0	1226	SNORD4A	0	chr17	24072500
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-1005991	PTPRD	0	1074885	TYRP1	0	chr9	11608500
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-97386	ZFATAS	0	536055	LOC286094	0	chr8	135779500
-97886	ZFATAS	0	535555	LOC286094	0	chr8	135780000
5781	PTK6	0	3151	PTK6	0	chr20	61636000
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-940	CTCFL	0	35042	PCK1	0	chr20	55534500
-1440	CTCFL	0	34542	PCK1	0	chr20	55535000
-1940	CTCFL	0	34042	PCK1	0	chr20	55535500
-2440	CTCFL	0	33542	PCK1	0	chr20	55536000
-523966	RHOU	0	501	RAB4A	0	chr1	227473000
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-114	GFPT1	0	8756	NFU1	0	chr2	69468000
-614	GFPT1	0	8256	NFU1	0	chr2	69468500
-27804	C12orf74	0	395	PLEKHG7	0	chr12	91654000
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-240181	UST	0	755	TAB2	0	chr6	149680000
-33306	CDH4	0	4248	TAF4	0	chr20	59979000
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-2057	ISYNA1	0	2473	ELL	0	chr19	18412000
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-193203	C21orf131	0	2003	NCAM2	0	chr21	21290500
-193703	C21orf131	0	1503	NCAM2	0	chr21	21291000
-17271	NADSYN1	0	8460	KRTAP5-7	0	chr11	70907500
-1786	FAM131C	0	48918	EPHA2	0	chr1	16274500
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-29947	BSND	0	807	PCSK9	0	chr1	55277000
-559	C1QL2	0	64353	STEAP3	0	chr2	119633500
-24121	PTPLA	0	2629	STAM	0	chr10	17723500
-59955	SPAG6	0	57271	PIP4K2A	0	chr10	22806500
47241	PAK4	0	6386	PAK4	0	chr19	44355500
-274779	ABHD5	0	244381	C3orf77	0	chr3	44014000
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-1829	RPS6KA3	0	1106400	CNKSR2	0	chrX	20196500
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-74403	VWF	0	1315	CD9	0	chr12	6178500
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-1478	LDB2	0	586117	QDPR	0	chr4	16511000
-1222	C9orf100	0	7414	CA9	0	chr9	35656500
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172047	MAD1L1	0	245109	MAD1L1	0	chr7	1994000
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20915	GRAMD1A	0	5213	GRAMD1A	0	chr19	40204000
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-29359	H19	0	101922	IGF2	0	chr11	2005000
-2365	EPB41L1	0	1360	C20orf4	0	chr20	34286500
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-203169	FOXF2	0	11679	FOXC1	0	chr6	1544000
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-337	TAF1C	0	3723	ADAD2	0	chr16	82778500
-837	TAF1C	0	3223	ADAD2	0	chr16	82779000
-5684	ZFP2	0	2329	ZNF454	0	chr5	178298500
-6184	ZFP2	0	1829	ZNF454	0	chr5	178299000
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-23039	GPR133	0	508	LOC116437	0	chr12	130215000
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-134	ANKRD16	0	219	FBXO18	0	chr10	5972000
-11372	CASP10	0	410	CASP8	0	chr2	201806000
-56710	PMS2L5	0	518	GATSL1	0	chr7	74016500
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217663	VAV2	0	12767	VAV2	0	chr9	135834500
19129	TMEM27	0	18575	TMEM27	0	chrX	15574500
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9031	MKNK2	0	4743	MKNK2	0	chr19	1997500

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-14236	OR2C3	0	1073	C1orf150	0	chr1	245778000
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32959	LPCAT1	0	29576	LPCAT1	0	chr5	1547500
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282	PPP1R3G	0	1454	PPP1R3G	0	chr6	5031000
782	PPP1R3G	0	954	PPP1R3G	0	chr6	5031500
26	FAM108A1	0	8518	FAM108A1	0	chr19	1828000
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-35044	SNORA77	0	406	LAX1	0	chr1	202000500
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-17604	MYOC	0	32782	VAMP4	0	chr1	169906000
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-7545	PAX6	0	272052	RCN1	0	chr11	31797000
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-18695	PRPSAP2	0	2202	SLC5A10	0	chr17	18794000
-29423	SNORA23	0	2588	ZNF143	0	chr11	9436500
-29982	TUBB4Q	0	9516	FRG2	0	chr4	191173000
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-495	HYI	0	76133	PTPRF	0	chr1	43693000
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-5960	GOLGA8C	0	138890	LOC646214	0	chr15	19047000
-2341	LHB	0	3438	CGB	0	chr19	54214500
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1932	TNFRSF4	0	875	TNFRSF4	0	chr1	1138500
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-31682	C19orf21	0	1391	PTBP1	0	chr19	747000
-2382	ZNF644	0	236910	HFM1	0	chr1	91262000
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5366	LMF1	0	111985	LMF1	0	chr16	849000
150889	PRUNE2	0	143823	PRUNE2	0	chr9	78567000
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5526	ASGR1	0	607	ASGR1	0	chr17	7023000
150560	KIAA1671	0	18913	KIAA1671	0	chr22	23904500
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-5274	TDRD7	0	22757	TMOD1	0	chr9	99303500
-13337	SNORA27	0	1463	RASL11A	0	chr13	26741000
130369	COL4A2	0	75374	COL4A2	0	chr13	109888000

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-108222	MC3R	0	889	C20orf108	0	chr20	54366500
23571	IFT140	0	78110	IFT140	0	chr16	1524000
269	TMEM204	0	20744	TMEM204	0	chr16	1524500
2284	NOTCH1	0	49059	NOTCH1	0	chr9	138511000
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-41457	LOC440040	0	100550	OR4C13	0	chr11	49830000
-154792	FTH1	0	1520	INCENP	0	chr11	61646500
-7991	POM121L4P	0	1401	TMEM191A	0	chr22	19384000
31439	ARHGEF7	0	120582	ARHGEF7	0	chr13	110635500
4791	SLC6A19	0	18730	SLC6A19	0	chr5	1259500
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-32755	C1QTNF8	0	24241	CACNA1H	0	chr16	1119000
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-11989	HGFAC	0	1830	DOK7	0	chr4	3433000
-12489	HGFAC	0	1330	DOK7	0	chr4	3433500
-2425	HSPA12A	0	139795	KIAA1598	0	chr10	118494500
-1107	CT62	0	24841	THSD4	0	chr15	69196000
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14901	SEMA6B	0	1003	SEMA6B	0	chr19	4508500
-1526	TCERG1L	0	596449	PPP2R2D	0	chr10	133001500
-2026	TCERG1L	0	595949	PPP2R2D	0	chr10	133002000
8780	MFI2	0	2083	MFI2	0	chr3	198239000
39329	MAEA	0	10925	MAEA	0	chr4	1313000
1247	CPSF1	0	15041	CPSF1	0	chr8	145590500
-13180	ZNF544	0	2129	ZNF8	0	chr19	63480000
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250461	GMDS	0	371345	GMDS	0	chr6	1819500
810	REPIN1	0	2066	REPIN1	0	chr7	149700000
1310	REPIN1	0	1566	REPIN1	0	chr7	149700500
155	KCNA5	0	2710	KCNA5	0	chr12	5023500
87227	CHST8	0	1754	CHST8	0	chr19	38954500
-668	PGBD3	0	84146	CHAT	0	chr10	50403000
-27666	PTPN2	0	35982	SEH1L	0	chr18	12902000
-901042	SVIP	0	766131	LUZP2	0	chr11	23709000
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6268	RAB40B	0	35387	RAB40B	0	chr17	78214500
6768	RAB40B	0	34887	RAB40B	0	chr17	78215000
-7595	SPATA5L1	0	1554	C15orf48	0	chr15	43508500
-944	RWDD2B	0	4308	USP16	0	chr21	29314500
-466	ID2	0	43937	KIDINS220	0	chr2	8742500
-966	ID2	0	43437	KIDINS220	0	chr2	8743000
-1131	ST8SIA4	0	1329590	SLCO4C1	0	chr5	100268000
-14844	NUDT16P1	0	1896	NUDT16	0	chr3	132581500
-637	SLC16A14	0	99389	SP110	0	chr2	230642500

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-4308	ADSSL1	0	1514	SIVA1	0	chr14	104289000
-611579	NLGN4Y	0	2119934	NCRNA00230B	0	chrY	16076500
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-1025	B3GNTL1	0	26855	METRNL	0	chr17	78604000
-1125	SCMH1	0	235535	EDN2	0	chr1	41481500
-2442	FARSA	0	2413	CALR	0	chr19	12908000
-2942	FARSA	0	1913	CALR	0	chr19	12908500
-5910	DMRT1	0	1963	DMRT3	0	chr9	965000
-6410	DMRT1	0	1463	DMRT3	0	chr9	965500
-21727	SBNO2	0	51797	STK11	0	chr19	1105000
-22227	SBNO2	0	51297	STK11	0	chr19	1105500
33165	SLA2	0	472	SLA2	0	chr20	34707500
-1021	GSG1L	0	208816	XPO6	0	chr16	27808000
-1521	GSG1L	0	208316	XPO6	0	chr16	27808500
-4264	PFKFB1	0	2004	APEX2	0	chrX	55041500
-1638	ADAM8	0	1127	TUBGCP2	0	chr10	134942000
-53303	IGFN1	0	1202	PKP1	0	chr1	199518000
-616	C6orf138	0	1361949	MUT	0	chr6	48145000
-1116	C6orf138	0	1361449	MUT	0	chr6	48145500
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-25985	OR2W5	0	6603	LOC148824	0	chr1	245748000
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-94646	TTTY22	0	2906	TTTY23B,TTTY23	0	chrY	10355500
-66633	ENO1	0	508	CA6	0	chr1	8928000
-67133	ENO1	0	8	CA6	0	chr1	8928500
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-87	NCRNA00175	0	30351	COL18A1	0	chr21	45669500
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-103534	TRH	0	363	ALG1L2	0	chr3	131283000
137	ALG1L2	0	16422	ALG1L2	0	chr3	131283500
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9177	MGAT5B	0	68566	MGAT5B	0	chr17	72389500
9677	MGAT5B	0	68066	MGAT5B	0	chr17	72390000
9756	MYO15A	0	61341	MYO15A	0	chr17	17962500
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-1075	ZNF541	0	51264	GLTSCR1	0	chr19	52752000

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-155916	TMEM121	0	231382	KIAA0125	0	chr14	105223500
-102	TSTD1	0	164	USF1	0	chr1	159275500
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-167416	TMEM121	0	219882	KIAA0125	0	chr14	105235000
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-64216	AP3B1	0	1594	SCAMP1	0	chr5	77690500
-29999	SLC1A4	0	2498	CEP68	0	chr2	65134500
-30499	SLC1A4	0	1998	CEP68	0	chr2	65135000
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16472	PITX2	0	3457	PITX2	0	chr4	111774500
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12102	GPR123	0	31669	GPR123	0	chr10	134763500
2333	SIPA1	0	8467	SIPA1	0	chr11	65166500
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7335	LIMS3	0	689	LIMS3	0	chr2	110664500
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35678	LOC100133669	0	682	LOC100133669	0	chr8	144170500
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-75800	HERC2P2	0	356046	MKRN3	0	chr15	21005500
-180429	TTTY23B,TTTY23	0	2743691	TTTY15	0	chrY	10540000
-180929	TTTY23B,TTTY23	0	2743191	TTTY15	0	chrY	10540500
-880405	C13orf16	0	94913	SOX1	0	chr13	111675000
-880905	C13orf16	0	94413	SOX1	0	chr13	111675500
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37006	TCF25	0	793	TCF25	0	chr16	88504500
-10312	ADAMTSL5	0	577	PLK5P	0	chr19	1474500
-2846	NKX2-1	0	57466	NKX2-8	0	chr14	36061500
-3346	NKX2-1	0	56966	NKX2-8	0	chr14	36062000
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-10480	ZIC2	0	91837	PCCA	0	chr13	99447500
-410650	OR4A47	0	246262	FOLH1	0	chr11	48878500
-411150	OR4A47	0	245762	FOLH1	0	chr11	48879000
-20807	PLTP	0	1723	PCIF1	0	chr20	43995000
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-35392	RUFY4	0	490	CXCR2	0	chr2	218698500
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116058	BCOR	0	10026	BCOR	0	chrX	39911500
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9745	LRIT1	0	197	LRIT1	0	chr10	85991000
-85264	DR1	0	426	FNBP1L	0	chr1	93686000
-208129	OR4F5	0	89521	6,OR4F29,OR4F3	0	chr1	268000
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-209129	OR4F5	0	88521	6,OR4F29,OR4F3	0	chr1	269000
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-664	PENK	0	510541	IMPAD1	0	chr8	57522500
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-96035	LOC728819	0	1685	DYNC2LI1	0	chr2	43853000
-96535	LOC728819	0	1185	DYNC2LI1	0	chr2	43853500
-29698	VAX1	0	29489	KCNK18	0	chr10	118917500
-71005	CTDP1	0	38155	KCNG2	0	chr18	75686500
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4599	PNPLA2	0	1717	PNPLA2	0	chr11	813500
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28722	KCNJ4	0	149	KCNJ4	0	chr22	37181000
4442	MPEG1	0	70	MPEG1	0	chr11	58737000
16208	TCF3	0	24786	TCF3	0	chr19	1576500
7221	MMRN2	0	14905	MMRN2	0	chr10	88692500
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2755	LMF2	0	1979	LMF2	0	chr22	49291000
-14884	C1QB	0	34417	EPHB2	0	chr1	22875500
-15384	C1QB	0	33917	EPHB2	0	chr1	22876000
-15884	C1QB	0	33417	EPHB2	0	chr1	22876500
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-27359	HS6ST1	0	1576904	LOC389033	0	chr2	128820000
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-15249	RAC2	0	22940	CYTH4	0	chr22	35985500
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-33162	DEFB131	0	111	LOC650293	0	chr4	9094500
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2858	GALNS	0	40375	GALNS	0	chr16	87410500
3358	GALNS	0	39875	GALNS	0	chr16	87411000
7064	GRIN3B	0	2223	GRIN3B	0	chr19	958500
3824	CPNE7	0	17654	CPNE7	0	chr16	88173500
4324	CPNE7	0	17154	CPNE7	0	chr16	88174000
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58445	ARHGEF10	0	76214	ARHGEF10	0	chr8	1818000
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37372	WLS	0	69841	WLS	0	chr1	68401000
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5683	ARMC5	0	2489	ARMC5	0	chr16	31383500
-5015	EFB106B,DEFB10	0	2402	B104B,DEFB104A	0	chr8	7729000
-5515	EFB106B,DEFB10	0	1902	B104B,DEFB104A	0	chr8	7729500
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33224	LONRF1	0	363	LONRF1	0	chr8	12657000
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-856	RS1	0	17965	PPEF1	0	chrX	18601000
50146	EIF4ENIF1	0	204	EIF4ENIF1	0	chr22	30215500
14699	SLC35E2B	0	16603	SLC35E2B	0	chr1	1597500
15199	SLC35E2B	0	16103	SLC35E2B	0	chr1	1598000
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72	PDLIM2	0	17483	PDLIM2	0	chr8	22494000
-29380	LOC728613	0	134998	MRPL36	0	chr5	1716500
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15167	SLC9A3	0	36049	SLC9A3	0	chr5	541500
639	C1orf83	0	45504	C1orf83	0	chr1	54292500
1139	C1orf83	0	45004	C1orf83	0	chr1	54293000
517	FLJ42627	0	6629	FLJ42627	0	chr16	2629500
-70992	SERPIND1	0	291	SNAP29	0	chr22	19543000
2959	CRYGB	0	622	CRYGB	0	chr2	208718500
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-606	RAB37	0	1357	SLC9A3R1	0	chr17	70255000
86037	COL9A1	0	1007	COL9A1	0	chr6	71068500
-292137	PITX1	0	7969	H2AFY	0	chr5	134690000
7930	CCDC9	0	7548	CCDC9	0	chr19	52459500
392	KLF17	0	15896	KLF17	0	chr1	44357500
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-970	DBNDD1	0	11508	GAS8	0	chr16	88605000
71832	EXD3	0	44535	EXD3	0	chr9	139393000
72332	EXD3	0	44035	EXD3	0	chr9	139393500
-15551	OBP2B	0	30383	ABO	0	chr9	135090000
14772	NDUFS2	0	308	NDUFS2	0	chr1	159450500
-412013	CDK20	0	1616	SPIN1	0	chr9	90191500
-111482	MUC16	0	420	OR1M1	0	chr19	9064500
58796	BRSK2	0	13404	BRSK2	0	chr11	1426500
-38796	CTSL1	0	2649	CTSL3	0	chr9	89575000
-390398	IER5	0	2338	CACNA1E	0	chr1	179717000
-24	H2AFY	0	44302	C5orf20	0	chr5	134763500
-6795	DES	0	1443	SPEG	0	chr2	220006500
-1622	HDAC8	0	4388	PHKA1	0	chrX	71711000

-2122	HDAC8	0	3888	PHKA1	0	chrX	71711500
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34443	SGSM2	0	9098	SGSM2	0	chr17	2222000
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-1535	FAM132A	0	5654	UBE2J2	0	chr1	1173500
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-1075	TOP1MT	0	30668	C8orf51	0	chr8	144489500
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-1379	SNORA72	0	20925	C8orf47	0	chr8	99125000
-152756	MEIS3P1	0	2455	ADORA2B	0	chr17	15786500
-7430	LOC415056	0	19991	C9orf23	0	chr9	34580500
-591	DSCAM	0	293796	C21orf130	0	chr21	41141500
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7801	CHERP	0	16763	CHERP	0	chr19	16497500
13541	KDM6B	0	1343	KDM6B	0	chr17	7697500
-157625	HERC2P4	0	363341	TP53TG3B	0	chr16	32229000
-158125	HERC2P4	0	362841	TP53TG3B	0	chr16	32229500
2858	ELAVL3	0	26803	ELAVL3	0	chr19	11426000
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4596	RBPJL	0	6378	RBPJL	0	chr20	43373500
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-16297	SPI1	0	13626	SLC39A13	0	chr11	47373000
-157441	LOC100130238	0	52229	FBRSL1	0	chr12	131525000
-157941	LOC100130238	0	51729	FBRSL1	0	chr12	131525500
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1259	HDAC10	0	4961	HDAC10	0	chr22	49027000
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3088	EHD2	0	26703	EHD2	0	chr19	52911500
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2456	ZNF219	0	6148	ZNF219	0	chr14	20630500
1191159	AUTS2	0	2821	AUTS2	0	chr7	69893000
1191659	AUTS2	0	2321	AUTS2	0	chr7	69893500
75494	SARDH	0	898	SARDH	0	chr9	135594000
-46420	HECW2	0	600	CCDC150	0	chr2	197212000
-1070	ANGPT1	0	400220	RSPO2	0	chr8	108580500
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-35666	C14orf70	0	18505	DLK1	0	chr14	100244500
-36666	C14orf70	0	17505	DLK1	0	chr14	100245500
-358	CHRNB4	0	117599	ADAMTS7	0	chr15	76721000

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-1961	GDNF	0	416789	EGFLAM	0	chr5	37877500
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-11867	PRSS41	0	164	PRSS21	0	chr16	2807000
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249995	JARID2	0	25732	JARID2	0	chr6	15604500
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-1740	NXN	0	15606	TIMM22	0	chr17	831500
-143	PLD6	0	5751	FLCN	0	chr17	17050500
53421	CORO2A	0	18277	CORO2A	0	chr9	99976500
2896	C20orf166	0	17416	C20orf166	0	chr20	60561000
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23524	SF3A1	0	1413	SF3A1	0	chr22	29081500
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-34113	GTPBP6	0	9969	PPP2R3B	0	chrY	205000
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-82858	TMEM179	0	1987	INF2	0	chr14	104225000
-83358	TMEM179	0	1487	INF2	0	chr14	104225500
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-17102	CRX	0	10034	SULT2A1	0	chr19	53055500
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-2087	NDUFC2	0	18635	ALG8	0	chr11	77471000
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-15473	RP1L1	0	2056	C8orf74	0	chr8	10565500
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22191	ATP2A1	0	3831	ATP2A1	0	chr16	28819500
-450138	LOC285627	0	317	ADRA1B	0	chr5	159276000
-292903	ERBB4	0	168155	IKZF2	0	chr2	213404500
-293403	ERBB4	0	167655	IKZF2	0	chr2	213405000
-520724	MAP2K4	0	1431	MYOCD	0	chr17	12508500
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-4942	FRG2C	0	64718	ZNF717	0	chr3	75804000
-5442	FRG2C	0	64218	ZNF717	0	chr3	75804500
-17674	SCARNA6	0	1047	SAG	0	chr2	233880000
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-19069	SNORA79	0	48661	STON2	0	chr14	80758000
-47097	PDGFB	0	20832	RPL3	0	chr22	38018000
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38289	PKD1	0	8900	PKD1	0	chr16	2117000
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21992	CARKD	0	2343	CARKD	0	chr13	110088000
-5755	C1QTNF8	0	51241	CACNA1H	0	chr16	1092000
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2792	ZBTB45	0	3233	ZBTB45	0	chr19	63719500
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-239	CYP11B2	0	138322	LOC100133669	0	chr8	143996500
51	RGS14	0	14705	RGS14	0	chr5	176717500
-510	SNIP1	0	2106	DNALI1	0	chr1	37793000
20263	CDC42BPG	0	117	CDC42BPG	0	chr11	64368500

-312575	BANP	0	40379	ZNF469	0	chr16	86981000
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869	FLJ40434	0	781	FLJ40434	0	chr1	53677500
11784	NOTCH1	0	39559	NOTCH1	0	chr9	138520500
835	FAM179B	0	111384	FAM179B	0	chr14	44502000
9345	KLHL30	0	2786	KLHL30	0	chr2	238723500
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515	TAS2R5	0	635	TAS2R5	0	chr7	141137000
2897	DMWD	0	6900	DMWD	0	chr19	50981000
20412	FAM38A	0	818	FAM38A	0	chr16	87329500
20912	FAM38A	0	318	FAM38A	0	chr16	87330000
-182	FAM38A	0	67186	CDT1	0	chr16	87330500
-1992	GGN	0	278	SPRED3	0	chr19	43572500
-1426	NCOA2	0	168226	TRAM1	0	chr8	71480000
7949	SLC45A4	0	9855	SLC45A4	0	chr8	142298000
35570	GNAS	0	22645	GNAS	0	chr20	56897000
216	ZFAND3	0	334875	ZFAND3	0	chr6	37895500
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-5831	C1QTNF9	0	92568	PARP4	0	chr13	23800500
71833	ZNF536	0	113805	ZNF536	0	chr19	35627000
11036	AJAP1	0	111714	AJAP1	0	chr1	4626000
11536	AJAP1	0	111214	AJAP1	0	chr1	4626500
-78553	NGRN	0	1480	ZNF774	0	chr15	88695000
-39163	HSPG2	0	504	CELA3B	0	chr1	22175500
12259	TRIM8	0	1566	TRIM8	0	chr10	104406500
-3107	GSTT2,GSTT2B	0	2525	DDTL	0	chr22	22636500
-3607	GSTT2,GSTT2B	0	2025	DDTL	0	chr22	22637000
7394	LPPR2	0	2872	LPPR2	0	chr19	11334500
-49971	UBXN10	0	47498	VWA5B1	0	chr1	20442500
-1564	NCRNA00202	0	60550	ANKRD26	0	chr10	27272500
13495	THOP1	0	14599	THOP1	0	chr19	2750000
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-3921	BMF	0	51001	BUB1B	0	chr15	38189500
-4421	BMF	0	50501	BUB1B	0	chr15	38190000
-70290	ZNF782	0	3912	FAM22G	0	chr9	98726500
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-174365	FOXD4L5	0	23442	)XD4L4,FOXD4L2	0	chr9	69643000
65245	ZNF710	0	14029	ZNF710	0	chr15	88411000
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-138192	FAM150B	0	241472	TMEM18	0	chr2	416500
-138692	FAM150B	0	240972	TMEM18	0	chr2	417000
-116070	RPS6KC1	0	598982	PROX1	0	chr1	211629500
-19540	LOC100129534	0	19573	RER1	0	chr1	2293500
-20040	LOC100129534	0	19073	RER1	0	chr1	2294000
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479	MMP23A	0	1390	MMP23A	0	chr1	1558500
-1564	CD79B	0	4645	SCN4A	0	chr17	59365000
-4578	C16orf90	0	963	CLUAP1	0	chr16	3490000
5919	ABHD14A	0	255	ABHD14A	0	chr3	51990000
-245	ABHD14A	0	2102	ACY1	0	chr3	51990500
53885	LOC400927	0	377	LOC400927	0	chr22	37124500
-347916	KGFLP2	0	798	0A3,ANKRD20A2	0	chr9	42357500
-8837	MDN1	0	1339	CASP8AP2	0	chr6	90595000
-9337	MDN1	0	839	CASP8AP2	0	chr6	90595500
1030	PRR22	0	610	PRR22	0	chr19	5735000
1530	PRR22	0	110	PRR22	0	chr19	5735500

10554	SPERT	0	1694	SPERT	0	chr13	45185000
-20645	AGRN	0	5060	C1orf159	0	chr1	1002000
-21145	AGRN	0	4560	C1orf159	0	chr1	1002500
-21645	AGRN	0	4060	C1orf159	0	chr1	1003000
-117886	RBX1	0	2059	EP300	0	chr22	39816500
-1069	STAT3	0	12993	PTRF	0	chr17	37795000
-1569	STAT3	0	12493	PTRF	0	chr17	37795500
4427	ADORA3	0	266	ADORA3	0	chr1	111848000
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-3973	HSPB2	0	810	C11orf52	0	chr11	111294000
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2052	TNRC18	0	114703	TNRC18	0	chr7	5315000
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851	TBXAS1	0	241092	TBXAS1	0	chr7	139125500
-807774	CHSY3	0	164773	HINT1	0	chr5	130358000
-808274	CHSY3	0	164273	HINT1	0	chr5	130358500
-808774	CHSY3	0	163773	HINT1	0	chr5	130359000
93869	DIP2C	0	321608	DIP2C	0	chr10	404000
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104558	BCOR	0	21526	BCOR	0	chrX	39900000
15592	PQLC1	0	33641	PQLC1	0	chr18	75779000
16092	PQLC1	0	33141	PQLC1	0	chr18	75779500
-21720	C10orf47	0	26026	UPF2	0	chr10	11976000
-22220	C10orf47	0	25526	UPF2	0	chr10	11976500
543	OR1N1	0	393	OR1N1	0	chr9	124329000
6869	RAB1B	0	2039	RAB1B	0	chr11	65799500
2797	TYK2	0	27248	TYK2	0	chr19	10325000
3588	PVRL1	0	64145	PVRL1	0	chr11	119040500
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143878	LASS3	0	448	LASS3	0	chr15	98902000
-312	ABCC4	0	131858	CLDN10	0	chr13	94752000
-812	ABCC4	0	131358	CLDN10	0	chr13	94752500
99394	ZNF516	0	4043	ZNF516	0	chr18	72300000
1435	NFATC4	0	10150	NFATC4	0	chr14	23908500
13512	SLC12A7	0	48172	SLC12A7	0	chr5	1117000
68366	LMF1	0	48985	LMF1	0	chr16	912000
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-260276	TMEM174	0	10840	FOXD1	0	chr5	72767000
-260776	TMEM174	0	10340	FOXD1	0	chr5	72767500
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298	PEPD	0	134641	PEPD	0	chr19	38570000
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419	SLC16A3	0	10658	SLC16A3	0	chr17	77780000
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2656	LONP1	0	25676	LONP1	0	chr19	5645500
890	LOC100132215	0	2850	LOC100132215	0	chr2	63125500
38965	ANKRD11	0	183970	ANKRD11	0	chr16	87900500

39465	ANKRD11	0	183470	ANKRD11	0	chr16	87901000
40178	C20orf203	0	904	C20orf203	0	chr20	30724500
94362	ADRA1A	0	1339	ADRA1A	0	chr8	26777500
94862	ADRA1A	0	839	ADRA1A	0	chr8	26778000
-1238	ICOSLG	0	4150	DNMT3L	0	chr21	44486500
-1738	ICOSLG	0	3650	DNMT3L	0	chr21	44487000
34040	COL6A2	0	691	COL6A2	0	chr21	46376500
34540	COL6A2	0	191	COL6A2	0	chr21	46377000
149377	KDM4B	0	35108	KDM4B	0	chr19	5069500
-15656	FBRSL1	0	17975	P2RX2	0	chr12	131687500
649	COL18A1	0	57562	COL18A1	0	chr21	45700500
15560	MMEL1	0	26789	MMEL1	0	chr1	2527500
9325	HIGD2B	0	1043	HIGD2B	0	chr15	70764500
-25721	CEBPD	0	9221	PRKDC	0	chr8	48839000
-26221	CEBPD	0	8721	PRKDC	0	chr8	48839500
-61087	NCRNA00169	0	313	RUNDC2B	0	chr16	21298500
187	RUNDC2B	0	11915	RUNDC2B	0	chr16	21299000
-88340	BEGAIN	0	857	C14orf70	0	chr14	100192500
-562	RGS12	0	1523	HGFAC	0	chr4	3412000
4088	PRKD2	0	38724	PRKD2	0	chr19	51873500
-100	BCL7C	0	2428	CTF1	0	chr16	30813000
5114	XAGE1D	0	28	XAGE1D	0	chrX	52550000
-472	XAGE1D	0	7278	XAGE1C,XAGE1A	0	chrX	52550500
-814	RLIM	0	117416	KIAA2022	0	chrX	73752000
18597	DPYSL4	0	270	DPYSL4	0	chr10	133869000
-230	DPYSL4	0	1485	STK32C	0	chr10	133869500
11801	PREX1	0	191827	PREX1	0	chr20	46686000
12301	PREX1	0	191327	PREX1	0	chr20	46686500
-3952	SPATA13	0	1715	C1QTNF9	0	chr13	23780000
-1198	SULT1A2	0	7916	SULT1A1	0	chr16	28516500
2498	C19orf22	0	14225	C19orf22	0	chr19	850000
2998	C19orf22	0	13725	C19orf22	0	chr19	850500
-57952	AMTN	0	1589	AMBN	0	chr4	71491000
-58452	AMTN	0	1089	AMBN	0	chr4	71491500
-69776	BCR	0	2791	ZDHHC8P1	0	chr22	22060000
-118464	PLAC4	0	13030	FAM3B	0	chr21	41597500
-118964	PLAC4	0	12530	FAM3B	0	chr21	41598000
16322	TTLL8	0	23182	TTLL8	0	chr22	48812000
1310	SSTR3	0	4799	SSTR3	0	chr22	35933500
-206276	TMEM174	0	64840	FOXD1	0	chr5	72713000
16444	SLC19A1	0	11279	SLC19A1	0	chr21	45775500
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-255	C1QTNF8	0	56741	CACNA1H	0	chr16	1086500
-17801	LCN1	0	1805	OBP2A	0	chr9	137576000
6773	PTOV1	0	2811	PTOV1	0	chr19	55053000
132468	WNK2	0	3175	WNK2	0	chr9	95119500
-2102	VGLL4	0	219418	C3orf31	0	chr3	11587500
-115941	LOC100130238	0	93729	FBRSL1	0	chr12	131483500
-116941	LOC100130238	0	92729	FBRSL1	0	chr12	131484500
-232983	HAND1	0	1654	LARP1	0	chr5	154071000
538	ZNF414	0	3048	ZNF414	0	chr19	8482000
284	ZNF414	0	2548	ZNF414	0	chr19	8482500
-243695	ARHGAP11B	0	21346	FAN1	0	chr15	28962000
-244695	ARHGAP11B	0	20346	FAN1	0	chr15	28963000
5450	RERE	0	65834	RERE	0	chr1	8340500
23740	ZNF362	0	20407	ZNF362	0	chr1	33518500
15418	NLRP2	0	19317	NLRP2	0	chr19	60185000
-2630207	C4orf33	0	1406419	PCDH10	0	chr4	132883500

-2630707	C4orf33	0	1405919	PCDH10	0	chr4	132884000
-16469	LOC644172	0	1494	MGC57346	0	chr17	41052000
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-5785	DYSFIP1	0	2322	P4HB	0	chr17	77392000
-6785	DYSFIP1	0	1322	P4HB	0	chr17	77393000
-77673	C6orf57	0	1199	SMAP1	0	chr6	71433000
-479584	GGTLC1	0	834	TMEM90B	0	chr20	24397000
-294	MUC6	0	37874	MUC2	0	chr11	1027000
-54345	BUB1	0	120	ACOXL	0	chr2	111206500
5982	PTPRS	0	129314	PTPRS	0	chr19	5162500
6982	PTPRS	0	128314	PTPRS	0	chr19	5163500
-301075	BANP	0	51879	ZNF469	0	chr16	86969500
-301575	BANP	0	51379	ZNF469	0	chr16	86970000
-305	RD116-9,SNORD1	0	2276	SNORD116-4	0	chr15	22853500
-100773	PPP2R2C	0	1802	MAN2B2	0	chr4	6626000
-101273	PPP2R2C	0	1302	MAN2B2	0	chr4	6626500
66835	UNC5A	0	3505	UNC5A	0	chr5	176237000
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-12070	GSTM2	0	440	GSTM1	0	chr1	110031500
60	GSTM1	0	5889	GSTM1	0	chr1	110032000
94893	GNG4	0	7416	GNG4	0	chr1	233872500
8783	CSPG4	0	29744	CSPG4	0	chr15	73762500
28667	FLJ42709	0	10759	FLJ42709	0	chr5	92932000
9016	AEBP1	0	1184	AEBP1	0	chr7	44119500
9516	AEBP1	0	684	AEBP1	0	chr7	44120000
1442	TCIRG1	0	10442	TCIRG1	0	chr11	67564500
1548	PALM	0	37830	PALM	0	chr19	661500
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10685	SF3A2	0	1178	SF3A2	0	chr19	2198500
10587	TBC1D16	0	85242	TBC1D16	0	chr17	75539000
6300	THEM5	0	297	THEM5	0	chr1	150092500
-203	THEM5	0	19683	THEM4	0	chr1	150093000
11900	DENND4B	0	5278	DENND4B	0	chr1	152180500
-511	ACYP1	0	5051	FAM164C	0	chr14	74601000
-1011	ACYP1	0	4551	FAM164C	0	chr14	74601500
-2675079	NLGN4Y	0	56434	NCRNA00230B	0	chrY	18140000
989	PCDHGB1	0	161730	PCDHGB1	0	chr5	140711000
24977	MOCS1	0	5232	MOCS1	0	chr6	40005000
74952	TRRAP	0	59802	TRRAP	0	chr7	98389000
4370	BCAT2	0	11613	BCAT2	0	chr19	53994500
4870	BCAT2	0	11113	BCAT2	0	chr19	53995000
58866	LMF1	0	58485	LMF1	0	chr16	902500
59366	LMF1	0	57985	LMF1	0	chr16	903000
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23427	ARHGEF18	0	9370	ARHGEF18	0	chr19	7434000
23927	ARHGEF18	0	8870	ARHGEF18	0	chr19	7434500
35449	RELB	0	1292	RELB	0	chr19	50232000
12098	TOP1MT	0	13425	TOP1MT	0	chr8	144475000
-153067	ZNF92	0	93711	INTS4L2	0	chr7	64656500
-153567	ZNF92	0	93211	INTS4L2	0	chr7	64657000
-1157	APRT	0	642	GALNS	0	chr16	87407000
13879	INPP5K	0	8432	INPP5K	0	chr17	1358500
14379	INPP5K	0	7932	INPP5K	0	chr17	1359000
15784	NOTCH1	0	35559	NOTCH1	0	chr9	138524500
-96048	PRSS54	0	1298	GINS3	0	chr16	56982500
-96548	PRSS54	0	798	GINS3	0	chr16	56983000
39321	FAM196A	0	21412	FAM196A	0	chr10	128863000

39821	FAM196A	0	20912	FAM196A	0	chr10	128863500
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8735	REM1	0	869	REM1	0	chr20	29535500
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868	ELFN1	0	2616	ELFN1	0	chr7	1751500
907	ADRA2C	0	1051	ADRA2C	0	chr4	3739000
7198	MAP1S	0	7824	MAP1S	0	chr19	17698500
7698	MAP1S	0	7324	MAP1S	0	chr19	17699000
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-1519	METRN	0	2158	FAM173A	0	chr16	709000
15631	RBM38	0	2292	RBM38	0	chr20	55415500
-11333	POTEB	0	431395	LOC727924	0	chr15	19348000
-11833	POTEB	0	430895	LOC727924	0	chr15	19348500
15265	SART1	0	3183	SART1	0	chr11	65501000
-114941	NOTCH1	0	2197	EGFL7	0	chr9	138675000
-655	CLIC3	0	10006	ABCA2	0	chr9	139011500
6273	TBCB	0	4689	TBCB	0	chr19	41304000
6773	TBCB	0	4189	TBCB	0	chr19	41304500
32688	KIF26A	0	9488	KIF26A	0	chr14	103707500
33188	KIF26A	0	8988	KIF26A	0	chr14	103708000
-850	ATP5SL	0	2402	C19orf69	0	chr19	46638500
234677	ZNF704	0	1571	ZNF704	0	chr8	81948000
235177	ZNF704	0	1071	ZNF704	0	chr8	81948500
7343	LRRC23	0	2166	LRRC23	0	chr12	6891500
-113386	ZFATAS	0	520055	LOC286094	0	chr8	135795500
-113886	ZFATAS	0	519555	LOC286094	0	chr8	135796000
-114386	ZFATAS	0	519055	LOC286094	0	chr8	135796500
-37875	SNX8	0	2499	EIF3B	0	chr7	2358500
-504	C3orf70	0	37105	EHHADH	0	chr3	186354000
-1004	C3orf70	0	36605	EHHADH	0	chr3	186354500
250	C4BPB	0	10460	C4BPB	0	chr1	205329500
1332	ASPDH	0	1759	ASPDH	0	chr19	55708000
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-2102	CNIH	0	30958	GMFB	0	chr14	53980000
1590	C4orf29	0	64405	C4orf29	0	chr4	129107500
2090	C4orf29	0	63905	C4orf29	0	chr4	129108000
77246	RFX8	0	97	RFX8	0	chr2	101457500
-403	RFX8	0	222919	MAP4K4	0	chr2	101458000
15932	IL17REL	0	2182	IL17REL	0	chr22	48791000
82490	PTPRN2	0	966243	PTPRN2	0	chr7	157107000
-7159	CCDC137	0	128	ARL16	0	chr17	77258500
372	ARL16	0	2359	ARL16	0	chr17	77259000
82160	AP2A2	0	4240	AP2A2	0	chr11	998000
13129	MUC5B	0	25982	MUC5B	0	chr11	1214000
35056	ZMAT5	0	969	ZMAT5	0	chr22	28492000
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-51613	KRTAP10-12	0	19382	UBE2G2	0	chr21	44994000
69797	GPR116	0	32634	GPR116	0	chr6	46998000
6492	PGAM5	0	1825	PGAM5	0	chr12	131804000
249525	ODZ4	0	537843	ODZ4	0	chr11	78291500
250025	ODZ4	0	537343	ODZ4	0	chr11	78292000
-13578	ACTG1	0	2011	FSCN2	0	chr17	77108000
-73	MSLNL	0	1974	RPUSD1	0	chr16	773000
450	NOD2	0	35488	NOD2	0	chr16	49289000
-11865	ANKRD34C	0	1045	TMED3	0	chr15	77389500
423	DKFZP434K028	0	3212	DKFZP434K028	0	chr11	61278500
233547	MAD1L1	0	183609	MAD1L1	0	chr7	2055500

234047	MAD1L1	0	183109	MAD1L1	0	chr7	2056000
-2523	GPER	0	56569	ZFAND2A	0	chr7	1102500
-305274	ERICH1	0	460475	DLGAP2	0	chr8	976500
-305774	ERICH1	0	459975	DLGAP2	0	chr8	977000
-306274	ERICH1	0	459475	DLGAP2	0	chr8	977500
-306774	ERICH1	0	458975	DLGAP2	0	chr8	978000
-4412	CHRM1	0	50644	SLC22A6	0	chr11	62450000
226	KALRN	0	626226	KALRN	0	chr3	125296500
-7758	PTPN7	0	301	PTPRVP	0	chr1	200403500
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-473	DNMT3L	0	23190	AIRE	0	chr21	44507000
138814	RREB1	0	4691	RREB1	0	chr6	7192000
49375	GPATCH1	0	158	GPATCH1	0	chr19	38313000
4106	PAPOLB	0	151	PAPOLB	0	chr7	4868000
9670	DOK7	0	21507	DOK7	0	chr4	3444500
10170	DOK7	0	21007	DOK7	0	chr4	3445000
125256	JAK2	0	17682	JAK2	0	chr9	5100500
96300	NIN	0	7589	NIN	0	chr14	50360000
96800	NIN	0	7089	NIN	0	chr14	50360500
-71025	SLC25A36	0	932	SPSB4	0	chr3	142252500
-1571429	TTTY23B,TTTY23	0	1352691	TTTY15	0	chrY	11931000
-133312	FRMD1	0	94432	DACT2	0	chr6	168356000
-73903	VWF	0	1815	CD9	0	chr12	6178000
4364	ENTPD8	0	2722	ENTPD8	0	chr9	139453000
-63404	SPTY2D1	0	926	TMEM86A	0	chr11	18676000
-40859	H19	0	90422	IGF2	0	chr11	2016500
-41359	H19	0	89922	IGF2	0	chr11	2017000
38070	OTOP1	0	22	OTOP1	0	chr4	4279500
-2779	PITX3	0	1298	GBF1	0	chr10	103994000
30910	RTEL1	0	7045	RTEL1	0	chr20	61791000
31410	RTEL1	0	6545	RTEL1	0	chr20	61791500
6047	ATP6V0C	0	220	ATP6V0C	0	chr16	2510000
3137	BOP1	0	25928	BOP1	0	chr8	145460000
2216	C10orf125	0	519	C10orf125	0	chr10	135021000
2716	C10orf125	0	19	C10orf125	0	chr10	135021500
483	KLF14	0	900	KLF14	0	chr7	130068500
983	KLF14	0	400	KLF14	0	chr7	130069000
21634	MYH7B	0	5397	MYH7B	0	chr20	33048500
22134	MYH7B	0	4897	MYH7B	0	chr20	33049000
-32040	LOC100129534	0	7073	RER1	0	chr1	2306000
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-14857	SERPINA3	0	1814	SERPINA13	0	chr14	94175000
5653	ASMT	0	41974	ASMT	0	chrY	1680000
6153	ASMT	0	41474	ASMT	0	chrY	1680500
-26	KNCN	0	6177	MKNK1	0	chr1	46789500
27760	C2orf55	0	114616	C2orf55	0	chr2	98804500
28260	C2orf55	0	114116	C2orf55	0	chr2	98805000
181	DOHH	0	9621	DOHH	0	chr19	3442000
7	APOB48R	0	4283	APOB48R	0	chr16	28413500
-7702	CCDC81	0	10297	ME3	0	chr11	85819500
-8702	CCDC81	0	9297	ME3	0	chr11	85820500
-2912	NDUFV1	0	12484	NUDT8	0	chr11	67139500
-3412	NDUFV1	0	11984	NUDT8	0	chr11	67140000
-3912	NDUFV1	0	11484	NUDT8	0	chr11	67140500
-857352	FAM84B	0	38	POU5F1B	0	chr8	128497000
462	POU5F1B	0	1121	POU5F1B	0	chr8	128497500
176794	SLC22A23	0	10792	SLC22A23	0	chr6	3391000
-24231	ACOXL	0	2461	BCL2L11	0	chr2	111592500

35192	PLEC	0	25031	PLEC	0	chr8	145096500
32558	BCOR	0	93526	BCOR	0	chrX	39828000
877	GAL3ST1	0	9376	GAL3ST1	0	chr22	29281500
68079	RSF1	0	86528	RSF1	0	chr11	77123000
68579	RSF1	0	86028	RSF1	0	chr11	77123500
-988416	GALR1	0	741762	SALL3	0	chr18	74099500
-988916	GALR1	0	741262	SALL3	0	chr18	74100000
-703	HERPUD2	0	105151	SEPT7	0	chr7	35702000
-892	FSTL1	0	144317	NDUFB4	0	chr3	121653500
-31669	TRIM38	0	238	HIST1H1A	0	chr6	26125000
-30173	UBE3C	0	37470	DNAJB6	0	chr7	156785000
25165	NR5A1	0	1020	NR5A1	0	chr9	126308500
25665	NR5A1	0	520	NR5A1	0	chr9	126309000
74369	DIP2C	0	341108	DIP2C	0	chr10	384500
17368	PDGFB	0	3903	PDGFB	0	chr22	37967000
17868	PDGFB	0	3403	PDGFB	0	chr22	37967500
-36641	TNIP2	0	47	SH3BP2	0	chr4	2764500
-1913	EPS8L3	0	144755	CSF1	0	chr1	110110000
-2413	EPS8L3	0	144255	CSF1	0	chr1	110110500
-49457	FLJ40292	0	63561	CACNA1B	0	chr9	139828500
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2840	LCN8	0	1052	LCN8	0	chr9	138771500
3340	LCN8	0	552	LCN8	0	chr9	138772000
3840	LCN8	0	52	LCN8	0	chr9	138772500
-39315	PARD6B	0	1873	BCAS4	0	chr20	48843000
1748	GPSM1	0	30378	GPSM1	0	chr9	138343500
2248	GPSM1	0	29878	GPSM1	0	chr9	138344000
-84275	PNLDC1	0	1963	MAS1	0	chr6	160246000
-84775	PNLDC1	0	1463	MAS1	0	chr6	160246500
-10451	SLC9A3	0	77404	CEP72	0	chr5	588000
-10951	SLC9A3	0	76904	CEP72	0	chr5	588500
-18776	SERPINB12	0	1513	SERPINB13	0	chr18	59404000
-49	ELFN2	0	41548	MFNG	0	chr22	36153500
-549	ELFN2	0	41048	MFNG	0	chr22	36154000
-556846	SV2B	0	1441	SLCO3A1	0	chr15	90196500
88153	MYO7B	0	13773	MYO7B	0	chr2	128098000
88653	MYO7B	0	13273	MYO7B	0	chr2	128098500
622	YDJC	0	1340	YDJC	0	chr22	20313000
272442	SRPK2	0	77	SRPK2	0	chr7	104816500
-1065	ADAMTS2	0	204176	RUFY1	0	chr5	178706000
-1565	ADAMTS2	0	203676	RUFY1	0	chr5	178706500
1643	CHST2	0	1502	CHST2	0	chr3	144323000
31469	ASMTL	0	18344	ASMTL	0	chrX	1513500
4287	KIF13B	0	191529	KIF13B	0	chr8	28985000
-53970	CRLF2	0	2200	CSF2RA	0	chrX	1345500
-35445	TLR6	0	2831	FAM114A1	0	chr4	38543000
-35945	TLR6	0	2331	FAM114A1	0	chr4	38543500
1874	CCDC157	0	18318	CCDC157	0	chr22	29084500
139	UGT1A10	0	136690	UGT1A10	0	chr2	234210000
5084	PPP1R16A	0	312	PPP1R16A	0	chr8	145698000
-188	PPP1R16A	0	1772	GPT	0	chr8	145698500
-270228	BOD1	0	1436	CPEB4	0	chr5	173246500
-270728	BOD1	0	936	CPEB4	0	chr5	173247000
-3949	ARAP1	0	28421	STARD10	0	chr11	72115000
-4449	ARAP1	0	27921	STARD10	0	chr11	72115500
172	C17orf105	0	4080	C17orf105	0	chr17	39213500
672	C17orf105	0	3580	C17orf105	0	chr17	39214000
-928	ATF7	0	63210	ATP5G2	0	chr12	52282000

375	LRRC14B	0	3468	LRRC14B	0	chr5	245000
-56616	QKI	0	1641642	C6orf118	0	chr6	163971500
-57116	QKI	0	1641142	C6orf118	0	chr6	163972000
-467751	OR4N3P	0	1335	TUBGCP5	0	chr15	20383500
1627	SCN1B	0	8193	SCN1B	0	chr19	40215000
4653	ASMT	0	42974	ASMT	0	chrX	1679000
322	TPSAB1	0	1556	TPSAB1	0	chr16	1231000
-20672	ADAMTS7	0	40726	MORF4L1	0	chr15	76911500
-248385	FAM92B	0	250529	KIAA0182	0	chr16	83952000
-566	TRIM45	0	21231	VTCN1	0	chr1	117466500
-1066	TRIM45	0	20731	VTCN1	0	chr1	117467000
688	NANOS2	0	876	NANOS2	0	chr19	51109000
331	ARHGAP23	0	54653	ARHGAP23	0	chr17	33867500
43	MAPK12	0	8716	MAPK12	0	chr22	49033500
197658	INPP5A	0	47974	INPP5A	0	chr10	134399000
297	SRPK3	0	4381	SRPK3	0	chrX	152700000
-1561	HK3	0	4111	UIMC1	0	chr5	176260500
1174	PQLC2	0	15881	PQLC2	0	chr1	19512500
11685	SF3A2	0	178	SF3A2	0	chr19	2199500
-2221	SLC19A1	0	305302	PCBP3	0	chr21	45789000
9315	ARHGEF19	0	5191	ARHGEF19	0	chr1	16406500
13251	PDLIM4	0	2544	PDLIM4	0	chr5	131634500
13751	PDLIM4	0	2044	PDLIM4	0	chr5	131635000
-125941	LOC100130238	0	83729	FBRSL1	0	chr12	131493500
-126441	LOC100130238	0	83229	FBRSL1	0	chr12	131494000
-802	ZNF83	0	12783	ZNF611	0	chr19	57886500
19192	PLEC	0	41031	PLEC	0	chr8	145080500
19692	PLEC	0	40531	PLEC	0	chr8	145081000
20192	PLEC	0	40031	PLEC	0	chr8	145081500
-103425	CRTAC1	0	370	C10orf28	0	chr10	99884000
-515	SOX10	0	72207	PICK1	0	chr22	36711000
-1015	SOX10	0	71707	PICK1	0	chr22	36711500
160023	RAPGEF1	0	746	RAPGEF1	0	chr9	133602000
160523	RAPGEF1	0	246	RAPGEF1	0	chr9	133602500
2073	MAPK8IP2	0	6345	MAPK8IP2	0	chr22	49390500
2573	MAPK8IP2	0	5845	MAPK8IP2	0	chr22	49391000
-63783	RGAG1	0	195	TDGF3	0	chrX	109650000
305	TDGF3	0	2405	TDGF3	0	chrX	109650500
10654	ODF3L2	0	983	ODF3L2	0	chr19	425000
-121828	TAGAP	0	2416	FNDC1	0	chr6	159508000
20964	ARID3A	0	25803	ARID3A	0	chr19	898000
21464	ARID3A	0	25303	ARID3A	0	chr19	898500
21964	ARID3A	0	24803	ARID3A	0	chr19	899000
-99480	GOT1	0	2679	NKX2-3	0	chr10	101280000
-99980	GOT1	0	2179	NKX2-3	0	chr10	101280500
-1413	CDC34	0	526	GZMM	0	chr19	494500
2610	CCDC154	0	7491	CCDC154	0	chr16	1427000
25281	XIST	0	6813	XIST	0	chrX	72982500
14719	KDM2B	0	136747	KDM2B	0	chr12	120366000
-91	C11orf94	0	2296	PEX16	0	chr11	45885500
68797	GPR116	0	33634	GPR116	0	chr6	46997000
69297	GPR116	0	33134	GPR116	0	chr6	46997500
5944	ANAPC2	0	7878	ANAPC2	0	chr9	139195000
-83073	TOPBP1	0	1424	TF	0	chr3	134946500
-83573	TOPBP1	0	924	TF	0	chr3	134947000
714	TERT	0	41162	TERT	0	chr5	1307000
-131130	SLC35F5	0	2006	ACTR3	0	chr2	114362000
-94505	ANKRD30BL	0	160116	GPR39	0	chr2	132730500

-95005	ANKRD30BL	0	159616	GPR39	0	chr2	132731000
-5713	TMEM8C	0	1606	ADAMTSL2	0	chr9	135385500
-1507	BSG	0	4892	HCN2	0	chr19	536000
8339	ADAMTS4	0	969	ADAMTS4	0	chr1	159434500
-26290	INPP5F	0	775	INPP5F	0	chr10	121568000
7668	ZP4	0	558	ZP4	0	chr1	236120000
8168	ZP4	0	58	ZP4	0	chr1	236120500
-83589	NKX6-1	0	1080	CDS1	0	chr4	85722000
-9297	TRIB3	0	1208	RBCK1	0	chr20	335500
354	PIM3	0	3223	PIM3	0	chr22	48740500
1509	LOC441956	0	330	LOC441956	0	chr21	13975000
-170	LOC441956	0	161825	C21orf15	0	chr21	13975500
-670	LOC441956	0	161325	C21orf15	0	chr21	13976000
3009	PCDHGC5	0	20730	PCDHGC5	0	chr5	140852000
69609	CDYL	0	179776	CDYL	0	chr6	4721000
70109	CDYL	0	179276	CDYL	0	chr6	4721500
801	OR2A20P	0	129	OR2A20P	0	chr7	143579500
-5388	GPR77	0	1885	DHX34	0	chr19	52542500
-205774	NBPF4	0	426	NBPF6	0	chr1	108794000
-160954	SIX2	0	218323	SRBD1	0	chr2	45251000
-161454	SIX2	0	217823	SRBD1	0	chr2	45251500
-34530	LOC400931	0	2162	PPARA	0	chr22	44923000
-45	F8A3,F8A2	0	773	H2AFB3,H2AFB1	0	chrX	154341500
119187	NFATC1	0	9811	NFATC1	0	chr18	75380500
-47681	BAG3	0	598	INPP5F	0	chr10	121475000
-48181	BAG3	0	98	INPP5F	0	chr10	121475500
95827	ARHGEF7	0	23082	ARHGEF7	0	chr13	110733000
96327	ARHGEF7	0	22582	ARHGEF7	0	chr13	110733500
37909	SLC8A2	0	6119	SLC8A2	0	chr19	52661000
-1075	MTHFS	0	736	ST20	0	chr15	77977500
-18497	MOBKL1B	0	1197	MTHFD2	0	chr2	74278000
3968	EPS8L1	0	8103	EPS8L1	0	chr19	60283000
-832	C6orf186	0	33075	DDO	0	chr6	110787000
40515	DAGLA	0	26049	DAGLA	0	chr11	61245000
-20458	DIO3	0	146526	NCRNA00239	0	chr14	101120000
-8057	ZNF578	0	2720	ZNF808	0	chr19	57720000
-8557	ZNF578	0	2220	ZNF808	0	chr19	57720500
-5255	KRTAP6-3	0	375	KRTAP6-2	0	chr21	30892500
125	KRTAP6-2	0	64	KRTAP6-2	0	chr21	30893000
-16311	RBM44	0	425	RAMP1	0	chr2	238432500
-1544	SNTB2	0	787	VPS4A	0	chr16	67902000
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132587	NCOR2	0	78602	NCOR2	0	chr12	123507500
12616	WNT4	0	13106	WNT4	0	chr1	22329000
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5648	ZCCHC14	0	79961	ZCCHC14	0	chr16	86003000
-31949	ARAP1	0	421	STARD10	0	chr11	72143000
79	STARD10	0	38898	STARD10	0	chr11	72143500
286461	SYN3	0	259377	SYN3	0	chr22	31525000
4422	ADSSL1	0	18692	ADSSL1	0	chr14	104266000
-1921	ZNF461	0	20641	ZNF567	0	chr19	41851500
23531	PPP2R3B	0	29127	PPP2R3B	0	chrX	238500
24031	PPP2R3B	0	28627	PPP2R3B	0	chrX	239000
24531	PPP2R3B	0	28127	PPP2R3B	0	chrX	239500
-214373	ELAVL4	0	1313	DMRTA2	0	chr1	50654500
-214873	ELAVL4	0	813	DMRTA2	0	chr1	50655000
-2202	RNPS1	0	5879	ABCA3	0	chr16	2260000
-2702	RNPS1	0	5379	ABCA3	0	chr16	2260500

-17310	INF2	0	2078	ADSSL1	0	chr14	104259500
-145049	PTPN18	0	636	CFC1B	0	chr2	130994500
-1080	P2RY14	0	14565	GPR87	0	chr3	152480000
-23359	H19	0	107922	IGF2	0	chr11	1999000
-266932	PTCH1	0	22190	C9orf130	0	chr9	97586000
-267432	PTCH1	0	21690	C9orf130	0	chr9	97586500
19677	MUC6	0	4206	MUC6	0	chr11	1022500
-20730	LCN12	0	1276	PTGDS	0	chr9	138990500
-21230	LCN12	0	776	PTGDS	0	chr9	138991000
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429	MEN1	0	6611	MEN1	0	chr11	64328000
929	MEN1	0	6111	MEN1	0	chr11	64328500
1429	MEN1	0	5611	MEN1	0	chr11	64329000
-26364	CRYBA4	0	483	MIAT	0	chr22	25383000
-14734	GNA15	0	265	S1PR4	0	chr19	3129500
235	S1PR4	0	1330	S1PR4	0	chr19	3130000
-16336	RBP7	0	602	UBE4B	0	chr1	10015000
-51623	LOC285370	0	416	SLC6A11	0	chr3	10832500
9168	LEPREL2	0	2279	LEPREL2	0	chr12	6817000
13416	LOC146336	0	1232	LOC146336	0	chr16	1067500
2496	PCNXL2	0	309082	PCNXL2	0	chr1	231189000
49885	OCA2	0	294553	OCA2	0	chr15	25723500
57587	LPCAT2	0	20082	LPCAT2	0	chr16	54158000
416	CAPNS2	0	593	CAPNS2	0	chr16	54158500
-13056	EFNA2	0	41975	MUM1	0	chr19	1264000
-13556	EFNA2	0	41475	MUM1	0	chr19	1264500
-15916	TMEM121	0	371382	KIAA0125	0	chr14	105083500
-16916	TMEM121	0	370382	KIAA0125	0	chr14	105084500
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-37145	SEC62	0	2428	GPR160	0	chr3	171236000
5166	NXN	0	175260	NXN	0	chr17	654500
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-166308	CNGA2	0	1016	MAGEA4	0	chrX	150831000
-166808	CNGA2	0	516	MAGEA4	0	chrX	150831500
-167308	CNGA2	0	16	MAGEA4	0	chrX	150832000
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-36808	PTGDR	0	765	PTGER2	0	chr14	51850000
-70575	GRIN2A	0	176225	ATF7IP2	0	chr16	10254000
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-32	HGC6.3	0	40901	KIF25	0	chr6	168120500
-532	HGC6.3	0	40401	KIF25	0	chr6	168121000
-1032	HGC6.3	0	39901	KIF25	0	chr6	168121500
-1532	HGC6.3	0	39401	KIF25	0	chr6	168122000
6227	C15orf39	0	4063	C15orf39	0	chr15	73287500
6727	C15orf39	0	3563	C15orf39	0	chr15	73288000
-199372	ZNF267	0	34609	HERC2P4	0	chr16	32035500
-212	MAMSTR	0	653	RASIP1	0	chr19	53915000

2277	GPR162	0	3344	GPR162	0	chr12	6803500
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31692	PLEC	0	28531	PLEC	0	chr8	145093000
-40178	ERN2	0	948	CHP2	0	chr16	23672500
-40678	ERN2	0	448	CHP2	0	chr16	23673000
4397	SLC45A3	0	18253	SLC45A3	0	chr1	203898000
-55337	LMBR1	0	1177	NOM1	0	chr7	156434000
-55837	LMBR1	0	677	NOM1	0	chr7	156434500
-82121	PDE4DIP	0	19263	SEC22B	0	chr1	143788500
-82621	PDE4DIP	0	18763	SEC22B	0	chr1	143789000
7284	NOTCH1	0	44059	NOTCH1	0	chr9	138516000
44716	SLIT1	0	143173	SLIT1	0	chr10	98792500
45216	SLIT1	0	142673	SLIT1	0	chr10	98793000
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152	SLC25A11	0	2563	SLC25A11	0	chr17	4781500
20013	AZI1	0	13346	AZI1	0	chr17	76798000
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39507	MRC2	0	26684	MRC2	0	chr17	58098000
-63056	IGFBPL1	0	133584	FAM201A	0	chr9	38477500
-63556	IGFBPL1	0	133084	FAM201A	0	chr9	38478000
12181	MAP2K2	0	21626	MAP2K2	0	chr19	4053500
-114889	EPHA6	0	1284	ARL6	0	chr3	98965000
8683	BCL3	0	2641	BCL3	0	chr19	49952500
9183	BCL3	0	2141	BCL3	0	chr19	49953000
-13578	COLEC11	0	160	ALLC	0	chr2	3683500
317	DEF8	0	18968	DEF8	0	chr16	88543000
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43903	METT10D	0	51950	METT10D	0	chr17	2310000
44403	METT10D	0	51450	METT10D	0	chr17	2310500
-177838	MGC45800	0	1630	ODZ3	0	chr4	183480500
-1626	PNPLA8	0	34406	THAP5	0	chr7	107955500
-47323	AP3S1	0	1049	AQPEP	0	chr5	115325000
1806	APLF	0	110797	APLF	0	chr2	68550000
1008	ISM2	0	23463	ISM2	0	chr14	77011500
1508	ISM2	0	22963	ISM2	0	chr14	77012000
-384	ACSS1	0	16098	VSX1	0	chr20	24988000
1348	DUS3L	0	4690	DUS3L	0	chr19	5737500
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-9862	UBA2	0	2219	WTIP	0	chr19	39662500
1817	TDGF1	0	2956	TDGF1	0	chr3	46596000
-69561	LOC348840	0	2133	FAM157A	0	chr3	199361500
43486	ZFPM1	0	38075	ZFPM1	0	chr16	87091000
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-228	PLXND1	0	40824	TMCC1	0	chr3	130808500
85874	SCARB1	0	472	SCARB1	0	chr12	123914000
-28	SCARB1	0	47644	UBC	0	chr12	123914500
471	KLHL34	0	2369	KLHL34	0	chrX	21584000
971	KLHL34	0	1869	KLHL34	0	chrX	21584500
-59691	SP3	0	47420	OLA1	0	chr2	174598000
-60191	SP3	0	46920	OLA1	0	chr2	174598500
-60691	SP3	0	46420	OLA1	0	chr2	174599000
-1018	BEND7	0	82944	PRPF18	0	chr10	13586000
230	CASS4	0	46243	CASS4	0	chr20	54421000
3185	PITPNM1	0	10419	PITPNM1	0	chr11	67019000
5996	LFNG	0	3336	LFNG	0	chr7	2532000
6496	LFNG	0	2836	LFNG	0	chr7	2532500
-37512	TCP10	0	172569	C6orf123	0	chr6	167755500
2264	C9orf139	0	7055	C9orf139	0	chr9	139044000

489	UGT1A3	0	43684	UGT1A3	0	chr2	234303000
-789	NUP133	0	7451	ABCB10	0	chr1	227711500
-83180	PIGG	0	2862	PDE6B	0	chr4	606500
-83680	PIGG	0	2362	PDE6B	0	chr4	607000
92	CASQ1	0	11298	CASQ1	0	chr1	158427000
-268776	TMEM174	0	2340	FOXD1	0	chr5	72775500
-269276	TMEM174	0	1840	FOXD1	0	chr5	72776000
6490	ZNF628	0	1666	ZNF628	0	chr19	60686000
1681	SNAP47	0	44555	SNAP47	0	chr1	225991000
47781	ZDHHC11	0	7601	ZDHHC11	0	chr5	896500
72890	FLJ43860	0	512	FLJ43860	0	chr8	142586000
73390	FLJ43860	0	12	FLJ43860	0	chr8	142586500
-488	FLJ43860	0	690623	NCRNA00051	0	chr8	142587000
1037	MGC16025	0	1090	MGC16025	0	chr2	239781000
1537	MGC16025	0	590	MGC16025	0	chr2	239781500
133523	RAPGEF1	0	27246	RAPGEF1	0	chr9	133575500
6631	GALNT9	0	3026	GALNT9	0	chr12	131253500
7631	GALNT9	0	2026	GALNT9	0	chr12	131254500
8104	TMEM184A	0	6092	TMEM184A	0	chr7	1556500
8604	TMEM184A	0	5592	TMEM184A	0	chr7	1557000
9104	TMEM184A	0	5092	TMEM184A	0	chr7	1557500
23428	ADARB2	0	528218	ADARB2	0	chr10	1241500
-217	TRIM7	0	17911	TRIM41	0	chr5	180565000
-717	TRIM7	0	17411	TRIM41	0	chr5	180565500
1486	C14orf174	0	12340	C14orf174	0	chr14	76915000
5925	SOHLH1	0	195	SOHLH1	0	chr9	137731000
-3980	ZIC2	0	98337	PCCA	0	chr13	99441000
-27209	TMEM183B	0	433	PPFIA4	0	chr1	201286500
51991	ABR	0	131866	ABR	0	chr17	905500
-9384	B4GALNT4	0	2716	PKP3	0	chr11	381500
-9884	B4GALNT4	0	2216	PKP3	0	chr11	382000
-10384	B4GALNT4	0	1716	PKP3	0	chr11	382500
-1853	GALE	0	453	HMGCL	0	chr1	24000500
47	HMGCL	0	23536	HMGCL	0	chr1	24001000
66233	CBFA2T3	0	109	CBFA2T3	0	chr16	87535000
-391	CBFA2T3	0	152254	ACSF3	0	chr16	87535500
-891	CBFA2T3	0	151754	ACSF3	0	chr16	87536000
-1349	PTK6	0	2106	SRMS	0	chr20	61640500
-24788	IRF8	0	384456	LOC732275	0	chr16	84538500
-25788	IRF8	0	383456	LOC732275	0	chr16	84539500
24918	C6orf147	0	11309	C6orf147	0	chr6	74065500
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28035	XKR7	0	2417	XKR7	0	chr20	30047500
28535	XKR7	0	1917	XKR7	0	chr20	30048000
-66701	SCUBE1	0	1963	MPPED1	0	chr22	42136000
-67201	SCUBE1	0	1463	MPPED1	0	chr22	42136500
-121231	LOC100133920	0	389526	FOXD4L5	0	chr9	69076000
-121731	LOC100133920	0	389026	FOXD4L5	0	chr9	69076500
-122231	LOC100133920	0	388526	FOXD4L5	0	chr9	69077000
-843	SNX3	0	32790	LACE1	0	chr6	108690000
20976	TTC38	0	5069	TTC38	0	chr22	45063500
-806	LRRN4	0	19991	FERMT1	0	chr20	5983500
1205	ALPPL2	0	2669	ALPPL2	0	chr2	232981000
-1830	PSG7	0	68648	PSG11	0	chr19	48135000
17509	TMIGD1	0	191	TMIGD1	0	chr17	25685000
-309	TMIGD1	0	44609	CPD	0	chr17	25685500
4192	CDC37	0	8271	CDC37	0	chr19	10367000
4692	CDC37	0	7771	CDC37	0	chr19	10367500

5192	CDC37	0	7271	CDC37	0	chr19	10368000
746	C16orf79	0	1012	C16orf79	0	chr16	2200000
1246	C16orf79	0	512	C16orf79	0	chr16	2200500
1746	C16orf79	0	12	C16orf79	0	chr16	2201000
5653	ASMT	0	41974	ASMT	0	chrX	1680000
6153	ASMT	0	41474	ASMT	0	chrX	1680500
2412	RUNX3	0	28357	RUNX3	0	chr1	25101000
2912	RUNX3	0	27857	RUNX3	0	chr1	25101500
-37713	C10orf57	0	2237	PLAC9	0	chr10	81880000
96877	KDM4B	0	87608	KDM4B	0	chr19	5017000
60119	LRRC2	0	4576	LRRC2	0	chr3	46592000
-47	MRPL12	0	4775	SLC25A10	0	chr17	77285000
19784	NOTCH1	0	31559	NOTCH1	0	chr9	138528500
20284	NOTCH1	0	31059	NOTCH1	0	chr9	138529000
-16515	CBX8	0	19549	CBX4	0	chr17	75402000
-1088	C9	0	6036	DAB2	0	chr5	39401500
13851	NLRX1	0	1436	NLRX1	0	chr11	118558500
-6897	SLC35E2B	0	237	MMP23A	0	chr1	1621000
263	MMP23A	0	1607	MMP23A	0	chr1	1621500
-30210	FLJ42393	0	1914	LPP	0	chr3	189411500
-5493	DOK7	0	12587	LRPAP1	0	chr4	3471500
-5993	DOK7	0	12087	LRPAP1	0	chr4	3472000
3180	TRIM35	0	23251	TRIM35	0	chr8	27201500
16991	ABR	0	166866	ABR	0	chr17	870500
-155	C1orf127	0	48265	TARDBP	0	chr1	10947000
59058	ADARB1	0	92902	ADARB1	0	chr21	45378000
59558	ADARB1	0	92402	ADARB1	0	chr21	45378500
-108619	RNF4	0	956	FAM193A	0	chr4	2596000
-92280	TP53TG3	0	996802	UBE2MP1	0	chr16	33264500
-9742	CXCR2P1	0	2284	RUFY4	0	chr2	218644000
-10242	CXCR2P1	0	1784	RUFY4	0	chr2	218644500
-792	WDR85	0	2351	ZMYND19	0	chr9	139594000
6177	HSPG2	0	108837	HSPG2	0	chr1	22027500
6677	HSPG2	0	108337	HSPG2	0	chr1	22028000
1928	PEG10	0	11442	PEG10	0	chr7	94125500
118361	PRDM11	0	12979	PRDM11	0	chr11	45190500
118861	PRDM11	0	12479	PRDM11	0	chr11	45191000
306	PTPN6	0	9740	PTPN6	0	chr12	6931000
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-16648	ASB10	0	3355	ABCF2	0	chr7	150532500
2798	EGFL7	0	6951	EGFL7	0	chr9	138680000
-9	LMAN2	0	5949	RGS14	0	chr5	176711500
-509	LMAN2	0	5449	RGS14	0	chr5	176712000
48015	ARHGEF3	0	303876	ARHGEF3	0	chr3	56784500
48515	ARHGEF3	0	303376	ARHGEF3	0	chr3	56785000
-310	TMED6	0	3533	TERF2	0	chr16	67943500
-148	C2orf81	0	3892	WDR54	0	chr2	74498500
-156255	KRTAP11-1	0	348	KRTAP19-8	0	chr21	31332000
2228	LOC148413	0	288	LOC148413	0	chr1	1327000
-90480	GOT1	0	11679	NKX2-3	0	chr10	101271000
7858	ASAP3	0	47837	ASAP3	0	chr1	23635500
8358	ASAP3	0	47337	ASAP3	0	chr1	23636000
882	PDIA2	0	3210	PDIA2	0	chr16	274000
1382	PDIA2	0	2710	PDIA2	0	chr16	274500
-252131	LOC643955	0	651015	ZNF735	0	chr7	62654000
-252631	LOC643955	0	650515	ZNF735	0	chr7	62654500
-38145	DUSP22	0	2251	IRF4	0	chr6	334500

1560	PTX4	0	969	PTX4	0	chr16	1477500
33491	SAFB2	0	2438	SAFB2	0	chr19	5571500
90236	GLTSCR1	0	4846	GLTSCR1	0	chr19	52893500
90736	GLTSCR1	0	4346	GLTSCR1	0	chr19	52894000
18548	PALM	0	20830	PALM	0	chr19	678500
19048	PALM	0	20330	PALM	0	chr19	679000
5289	KAZ	0	138738	KAZ	0	chr1	15128500
618	KAZ	0	137738	KAZ	0	chr1	15129500
-32398	TC2N	0	507	FBLN5	0	chr14	91405000
3273	NPTX1	0	6499	NPTX1	0	chr17	76058500
-13560	TCL6	0	1015	TCL1B	0	chr14	95221500
-57564	PTCD2	0	26489	ZNF366	0	chr5	71748500
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25047	FBXL18	0	12925	FBXL18	0	chr7	5507000
56866	BAHCC1	0	2953	BAHCC1	0	chr17	77045000
57366	BAHCC1	0	2453	BAHCC1	0	chr17	77045500
-107067	ZNF92	0	139711	INTS4L2	0	chr7	64610500
-107567	ZNF92	0	139211	INTS4L2	0	chr7	64611000
-108067	ZNF92	0	138711	INTS4L2	0	chr7	64611500
64	ARHGAP25	0	51961	ARHGAP25	0	chr2	68855500
2520	LTBP4	0	30065	LTBP4	0	chr19	45797500
3020	LTBP4	0	29565	LTBP4	0	chr19	45798000
26165	OTOA	0	56051	OTOA	0	chr16	21623500
5899	ABCA7	0	19570	ABCA7	0	chr19	997000
6399	ABCA7	0	19070	ABCA7	0	chr19	997500
6899	ABCA7	0	18570	ABCA7	0	chr19	998000
77622	BAI1	0	3370	BAI1	0	chr8	143620000
78122	BAI1	0	2870	BAI1	0	chr8	143620500
14301	CHERP	0	10263	CHERP	0	chr19	16504000
14801	CHERP	0	9763	CHERP	0	chr19	16504500
-63079	GRM4	0	40054	HMGA1	0	chr6	34272500
-2037	DNMT3A	0	32615	DTNB	0	chr2	25421000
-11150	LOC650623	0	219913	MBL1P	0	chr10	81450000
7035	BICD2	0	46404	BICD2	0	chr9	94520500
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27088	SMAD3	0	30086	SMAD3	0	chr15	65244500
1314	CDT1	0	4167	CDT1	0	chr16	87399000
1814	CDT1	0	3667	CDT1	0	chr16	87399500
1384	GPR39	0	228639	GPR39	0	chr2	132892000
-23354	SPG20	0	61966	CCNA1	0	chr13	35842000
-942280	TP53TG3	0	146802	UBE2MP1	0	chr16	34114500
-942780	TP53TG3	0	146302	UBE2MP1	0	chr16	34115000
-6488	TNNT3	0	2077	MRPL23	0	chr11	1923000
-45056	TSNARE1	0	14878	BAI1	0	chr8	143527500
17954	C9orf64	0	483	C9orf64	0	chr9	85761000
1837	ADAL	0	16906	ADAL	0	chr15	41412000
10636	ZDHHC8	0	3974	ZDHHC8	0	chr22	18510000
11136	ZDHHC8	0	3474	ZDHHC8	0	chr22	18510500
11636	ZDHHC8	0	2974	ZDHHC8	0	chr22	18511000
-453862	ATG4C	0	4817	FOXD3	0	chr1	63556500
15626	NCLN	0	8073	NCLN	0	chr19	3152500
16512	ZNF331	0	42835	ZNF331	0	chr19	58732500
-119169	FOXF2	0	95679	FOXC1	0	chr6	1460000
-119669	FOXF2	0	95179	FOXC1	0	chr6	1460500
-610	GCC1	0	2252	ARF5	0	chr7	127013500
-37775	TGM3	0	2053	TGM6	0	chr20	2307500
85760	CLIP2	0	30709	CLIP2	0	chr7	73427500

86760	CLIP2	0	29709	CLIP2	0	chr7	73428500
1105	SCAMP3	0	5319	SCAMP3	0	chr1	153493500
-1432	TSPAN3	0	35525	SGK269	0	chr15	75152000
7479	ADAMTSL4	0	1847	ADAMTSL4	0	chr1	148796000
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26887	PLCH2	0	2324	PLCH2	0	chr1	2424500
-1256	PRKCQ	0	580754	SFMBT2	0	chr10	6663500
-1756	PRKCQ	0	580254	SFMBT2	0	chr10	6664000
1062	C6orf201	0	50498	C6orf201	0	chr6	4025500
1516	C16orf90	0	422	C16orf90	0	chr16	3485000
-78	C16orf90	0	5463	CLUAP1	0	chr16	3485500
-112113	SLC44A5	0	1130	ACADM	0	chr1	75961500
-344	TGFB1	0	161	B9D2	0	chr19	46552000
339	B9D2	0	9418	B9D2	0	chr19	46552500
-7795	DES	0	443	SPEG	0	chr2	220007500
3239	TRMT61A	0	4663	TRMT61A	0	chr14	103068500
3739	TRMT61A	0	4163	TRMT61A	0	chr14	103069000
62700	HDAC4	0	290080	HDAC4	0	chr2	239697500
7058	IL17F	0	757	IL17F	0	chr6	52216500
7558	IL17F	0	257	IL17F	0	chr6	52217000
9748	GPSM1	0	22378	GPSM1	0	chr9	138351500
-141433	SSBP3	0	488	ACOT11	0	chr1	54786000
-56394	USP40	0	29	UGT1A8	0	chr2	234191000
471	UGT1A8	0	155184	UGT1A8	0	chr2	234191500
8414	CC2D2A	0	123278	CC2D2A	0	chr4	15089000
25907	ZMYM5	0	276	ZMYM5	0	chr13	19335500
-70831	LDOC1L	0	382	NCRNA00207	0	chr22	43343500
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16093	GNA11	0	10954	GNA11	0	chr19	3061500
-198083	ANKRD10	0	2124	ARHGEF7	0	chr13	110563500
-142416	TMEM121	0	244882	KIAA0125	0	chr14	105210000
249791	DPP6	0	686428	DPP6	0	chr7	153630500
250291	DPP6	0	685928	DPP6	0	chr7	153631000
250791	DPP6	0	685428	DPP6	0	chr7	153631500
25679	ZBTB46	0	35300	ZBTB46	0	chr20	61872000
19609	MLLT1	0	49959	MLLT1	0	chr19	6181000
20109	MLLT1	0	49459	MLLT1	0	chr19	6181500
-9583	STK11IP	0	1535	SLC4A3	0	chr2	220199000
1253	C9orf69	0	3052	C9orf69	0	chr9	138147500
1753	C9orf69	0	2552	C9orf69	0	chr9	138148000
69401	KIAA1529	0	69390	KIAA1529	0	chr9	99110000
507	PRM2	0	338	PRM2	0	chr16	11277500
78076	CRTC1	0	20643	CRTC1	0	chr19	18733500
78576	CRTC1	0	20143	CRTC1	0	chr19	18734000
79076	CRTC1	0	19643	CRTC1	0	chr19	18734500
1354	MGAT1	0	18243	MGAT1	0	chr5	180151500
1854	MGAT1	0	17743	MGAT1	0	chr5	180152000
-382	GK5	0	80638	XRN1	0	chr3	143427500
2456	SLC25A6	0	3498	SLC25A6	0	chrX	1467500
-2080	TRPV1	0	13304	SHPK	0	chr17	3445000
-11628	LIG1	0	26154	CARD8	0	chr19	53377000
-12128	LIG1	0	25654	CARD8	0	chr19	53377500
-4676	FAM20B	0	734	TOR3A	0	chr1	177317000
-668604	LOC339788	0	36563	ID2	0	chr2	8703000
-279	CFC1B	0	80092	C2orf14	0	chr2	131074000
-779	CFC1B	0	79592	C2orf14	0	chr2	131074500
8717	STRA6	0	5924	STRA6	0	chr15	72282500
-949	CH25H	0	5305	LIPA	0	chr10	90958000

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50603	C4orf22	0	577426	C4orf22	0	chr4	81526500
917990	PTPRN2	0	130743	PTPRN2	0	chr7	157942500
918490	PTPRN2	0	130243	PTPRN2	0	chr7	157943000
-25145	AGRN	0	560	C1orf159	0	chr1	1006500
-25645	AGRN	0	60	C1orf159	0	chr1	1007000
1485	PHLDB1	0	48951	PHLDB1	0	chr11	117985000
128	PLEKHG4B	0	49587	PLEKHG4B	0	chr5	193500
70430	SVOPL	0	14330	SVOPL	0	chr7	138000000
-1278	C14orf176	0	49935	OR5AU1	0	chr14	20643000
-36794	MUC6	0	1374	MUC2	0	chr11	1063500
-37294	MUC6	0	874	MUC2	0	chr11	1064000
26548	PALM	0	12830	PALM	0	chr19	686500
27548	PALM	0	11830	PALM	0	chr19	687500
4015	ST6GALNAC4	0	5126	ST6GALNAC4	0	chr9	129714000
4515	ST6GALNAC4	0	4626	ST6GALNAC4	0	chr9	129714500
-2250	---	0	227	CTBP1	0	chr4	1195000
-43109	SNTG2	0	2741	TPO	0	chr2	1393500
69976	ACVR1C	0	818	ACVR1C	0	chr2	158161500
341897	PRDM16	0	27545	PRDM16	0	chr1	3317500
-877	PON3	0	7609	PON2	0	chr7	94864500
-2176	HDAC6	0	1726	ERAS	0	chrX	48570500
-2676	HDAC6	0	1226	ERAS	0	chrX	48571000
131651	LOC91948	0	163	LOC91948	0	chr15	96218500
-1842	TBXA2R	0	2126	C19orf29	0	chr19	3559500
3316	C5orf40	0	807	C5orf40	0	chr5	156704500
3816	C5orf40	0	307	C5orf40	0	chr5	156705000
3590	XAB2	0	6439	XAB2	0	chr19	7594000
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-5496	NNAT	0	164847	CTNNBL1	0	chr20	35591000
-5996	NNAT	0	164347	CTNNBL1	0	chr20	35591500
-169303	VEZT	0	1952	METAP2	0	chr12	94390000
17907	SIGLEC5	0	1039	SIGLEC5	0	chr19	56824500
-567	C10orf113	0	347426	C10orf114	0	chr10	21476000
-119301	ORC5L	0	1339	LHFPL3	0	chr7	103755000
-119801	ORC5L	0	839	LHFPL3	0	chr7	103755500
-62891	EIF2AK3	0	1290	RPIA	0	chr2	88771000
1985	PHLDB1	0	48451	PHLDB1	0	chr11	117985500
2485	PHLDB1	0	47951	PHLDB1	0	chr11	117986000
617	KIAA0467	0	28891	KIAA0467	0	chr1	43662000
3869	UCKL1	0	12712	UCKL1	0	chr20	62045500
4369	UCKL1	0	12212	UCKL1	0	chr20	62046000
4869	UCKL1	0	11712	UCKL1	0	chr20	62046500
12738	SALL3	0	5181	SALL3	0	chr18	74854000
13238	SALL3	0	4681	SALL3	0	chr18	74854500
2734	LOC283731	0	172	LOC283731	0	chr15	72208500
-108408	GRIP2	0	1256	C3orf19	0	chr3	14667000
-1648	ARFGAP3	0	11880	PACSIN2	0	chr22	41585000
-534	PLCB2	0	22944	C15orf52	0	chr15	38388000
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-1245	TPSG1	0	1836	TPSB2	0	chr16	1216500
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-20939	PHF21A	0	135303	CREB3L1	0	chr11	46120500
6460	SLC35E2	0	7291	SLC35E2	0	chr1	1660000
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595	AVPR1B	0	6605	AVPR1B	0	chr1	204391500

41001	JPH3	0	54262	JPH3	0	chr16	86235000
-19043	DUSP23	0	796	FCRL6	0	chr1	158038000
-224737	LHX2	0	63	NEK6	0	chr9	126060000
-2896	FGF22	0	1025	RNF126	0	chr19	597500
-59791	COMMD1	0	265	B3GNT2	0	chr2	62276500
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545547	CDH4	0	139194	CDH4	0	chr20	59806500
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-32638	PRR25	0	7134	LMF1	0	chr16	836500
-2119	THUMPD2	0	330789	SLC8A1	0	chr2	39862000
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1800	PSRC1	0	1794	PSRC1	0	chr1	109625500
2300	PSRC1	0	1294	PSRC1	0	chr1	109626000
-100026	DSCR8	0	33	KCNJ15	0	chr21	38550500
-307827	FHIT	0	2282	PTPRG	0	chr3	61520000
-308327	FHIT	0	1782	PTPRG	0	chr3	61520500
1561	ABHD8	0	9782	ABHD8	0	chr19	17265500
28917	NFIX	0	74110	NFIX	0	chr19	12996500
29417	NFIX	0	73610	NFIX	0	chr19	12997000
23922	ADAMTS15	0	926	ADAMTS15	0	chr11	129848000
24422	ADAMTS15	0	426	ADAMTS15	0	chr11	129848500
-2048	TNFRSF18	0	2568	TNFRSF4	0	chr1	1134000
-84447	DMRT2	0	873341	SMARCA2	0	chr9	1132000
472	CSNK1D	0	28862	CSNK1D	0	chr17	77796000
972	CSNK1D	0	28362	CSNK1D	0	chr17	77796500
13540	COL6A2	0	21191	COL6A2	0	chr21	46356000
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66687	NFATC1	0	62311	NFATC1	0	chr18	75328000
-23506	CYP1A2	0	1977	CSK	0	chr15	72859500
-24006	CYP1A2	0	1477	CSK	0	chr15	72860000
300	GALP	0	9456	GALP	0	chr19	61379500
-27933	MRAS	0	1104	ESYT3	0	chr3	139635000
13910	TRIM62	0	22758	TRIM62	0	chr1	33397500
14410	TRIM62	0	22258	TRIM62	0	chr1	33398000
49748	CARM1	0	1448	CARM1	0	chr19	10893000
39282	IQSEC1	0	30960	IQSEC1	0	chr3	12953000
177	C1orf177	0	36025	C1orf177	0	chr1	55044500
-8395	FADS1	0	2788	FADS2	0	chr11	61349500
-1340	GALC	0	10248	GPR65	0	chr14	87531000
397281	RPTOR	0	24268	RPTOR	0	chr17	76530500
68892	SMC1B	0	664	SMC1B	0	chr22	44187500
987	RRP7A	0	6252	RRP7A	0	chr22	41239500
1487	RRP7A	0	5752	RRP7A	0	chr22	41240000
1826	RFX2	0	115664	RFX2	0	chr19	5946000
1827	METRN	0	481	METRN	0	chr16	707000
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7684	PLXNA3	0	7678	PLXNA3	0	chrX	153347500
8184	PLXNA3	0	7178	PLXNA3	0	chrX	153348000
-778	CHM	0	100110	DACH2	0	chrX	85190000
-12334	ZNF469	0	514	ZFPM1	0	chr16	87047000
-12834	ZNF469	0	14	ZFPM1	0	chr16	87047500
59852	C7orf50	0	81419	C7orf50	0	chr7	1063000
20649	COL18A1	0	37562	COL18A1	0	chr21	45720500
-17515	CBX8	0	18549	CBX4	0	chr17	75403000
-4324	DIRC2	0	1049	LOC100129550	0	chr3	124087000
-4824	DIRC2	0	549	LOC100129550	0	chr3	124087500
5784	DPEP1	0	19340	DPEP1	0	chr16	88213000

2506	CTRB2	0	573	CTRB2	0	chr16	73798000
3006	CTRB2	0	73	CTRB2	0	chr16	73798500
3220	PGLYRP1	0	663	PGLYRP1	0	chr19	51217500
-341366	SLC30A8	0	2645	MED30	0	chr8	118599500
-341866	SLC30A8	0	2145	MED30	0	chr8	118600000
-1078083	SOX2	0	984	ATP11B	0	chr3	183993000
14372	CXorf48	0	917	CXorf48	0	chrX	134132500
14872	CXorf48	0	417	CXorf48	0	chrX	134133000
43698	FCGBP	0	42873	FCGBP	0	chr19	45089500
44198	FCGBP	0	42373	FCGBP	0	chr19	45090000
-148791	CCDC74A	0	40033	C2orf27A	0	chr2	132156500
54073	SNED1	0	41316	SNED1	0	chr2	241641000
9856	UBA1	0	11471	UBA1	0	chrX	46948000
-657	AK1	0	6921	ST6GALNAC6	0	chr9	129680500
17613	FAM26D	0	12224	FAM26D	0	chr6	116974500
18113	FAM26D	0	11724	FAM26D	0	chr6	116975000
-2369	ICMT	0	5848	HES3	0	chr1	6221000
-9089	TTTY5	0	893	RBMY2FP	0	chrY	22863500
9655	C1QTNF1	0	15965	C1QTNF1	0	chr17	74541500
10155	C1QTNF1	0	15465	C1QTNF1	0	chr17	74542000
6167	PCDHA6	0	178113	PCDHA6	0	chr5	140194000
348	PCDHA7	0	177613	PCDHA7	0	chr5	140194500
-89187	XIST	0	2383	NCRNA00183	0	chrX	73078500
-89687	XIST	0	1883	NCRNA00183	0	chrX	73079000
1829	FAM123A	0	1357	FAM123A	0	chr13	24642500
-19051	EEF1A2	0	2576	PPDPF	0	chr20	61620000
-19551	EEF1A2	0	2076	PPDPF	0	chr20	61620500
144	CASZ1	0	149294	CASZ1	0	chr1	10630000
644	CASZ1	0	148794	CASZ1	0	chr1	10630500
166465	ANKRD11	0	56470	ANKRD11	0	chr16	88028000
-42140	CXorf49,CXorf49	0	2864	Xorf49,CXorf49B	0	chrX	70897000
-42640	CXorf49,CXorf49	0	2364	Xorf49,CXorf49B	0	chrX	70897500
408	MESP2	0	1986	MESP2	0	chr15	88121000
34727	ZSWIM4	0	2044	ZSWIM4	0	chr19	13802000
35227	ZSWIM4	0	1544	ZSWIM4	0	chr19	13802500
121450	STAT4	0	170	STAT4	0	chr2	191724000
279	VAV1	0	84371	VAV1	0	chr19	6724000
-398012	KIF26A	0	2100	C14orf180	0	chr14	104115000
-398512	KIF26A	0	1600	C14orf180	0	chr14	104115500
-301	SNORA54	0	36734	CARS	0	chr11	2942000
-2818	C12orf34	0	9776	TRPV4	0	chr12	108695500
3305	NCKAP5L	0	33975	NCKAP5L	0	chr12	48474500
3805	NCKAP5L	0	33475	NCKAP5L	0	chr12	48475000
227	ATP2B3	0	46581	ATP2B3	0	chrX	152455000
143	ZACN	0	3480	ZACN	0	chr17	71587000
1227	SH3BP5L	0	14277	SH3BP5L	0	chr1	247072500
1727	SH3BP5L	0	13777	SH3BP5L	0	chr1	247073000
7298	EGFL7	0	2451	EGFL7	0	chr9	138684500
-63530	POU2F2	0	2591	DEDD2	0	chr19	47392000
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-1831	---	0	48717	SFTPA1	0	chr10	80992000
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11634	SH3GL1	0	28471	SH3GL1	0	chr19	4323000
-137	GPT	0	1859	MFSD3	0	chr8	145703500
64155	FAT2	0	698	FAT2	0	chr5	150928000
4926	GLI3	0	271143	GLI3	0	chr7	41972000
-4006	NR2F2	0	439182	SPATA8	0	chr15	94688500
-4506	NR2F2	0	438682	SPATA8	0	chr15	94689000

8142	DECR2	0	2488	DECR2	0	chr16	400000
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-241968	LOC100192426	0	442	RAB12	0	chr18	8599000
12161	CROCCP2	0	488	CROCCP2	0	chr1	16829500
-46334	RCOR1	0	568	TRAF3	0	chr14	102313000
22872	SPPL2B	0	3600	SPPL2B	0	chr19	2302500
24372	SPPL2B	0	2100	SPPL2B	0	chr19	2304000
-14280	GATA2	0	367	LOC90246	0	chr3	129709000
133	LOC90246	0	2617	LOC90246	0	chr3	129709500
-2540	C9orf86	0	687	C9orf172	0	chr9	138858000
-3040	C9orf86	0	187	C9orf172	0	chr9	138858500
1313	C9orf172	0	1618	C9orf172	0	chr9	138860000
-348	PRSS8	0	2748	PRSS36	0	chr16	31055000
-98359	PEPD	0	1700	CHST8	0	chr19	38803000
-98859	PEPD	0	1200	CHST8	0	chr19	38803500
-1577429	TTTY23B,TTTY23	0	1346691	TTTY15	0	chrY	11937000
6606	TFIP11	0	13937	TFIP11	0	chr22	25224500
-21408	FBXL14	0	1482	WNT5B	0	chr12	1595000
-175762	CACNG3	0	1408	RBBP6	0	chr16	24457000
-1688	PPP1R16A	0	272	GPT	0	chr8	145700000
-1452916	GALR1	0	277262	SALL3	0	chr18	74564000
-1453416	GALR1	0	276762	SALL3	0	chr18	74564500
96718	C11orf80	0	2063	C11orf80	0	chr11	66365500
-75375	ANGPTL7	0	1841	UBIAD1	0	chr1	11254000
-75875	ANGPTL7	0	1341	UBIAD1	0	chr1	11254500
7161	GMFG	0	566	GMFG	0	chr19	44518000
7661	GMFG	0	66	GMFG	0	chr19	44518500
20312	AMZ1	0	15595	AMZ1	0	chr7	2706000
4579	ADRM1	0	1313	ADRM1	0	chr20	60316000
3232	MAPK11	0	3406	MAPK11	0	chr22	49047500
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-16338	FAM120B	0	113629	PSMB1	0	chr6	170572500
36649	COL18A1	0	21562	COL18A1	0	chr21	45736500
-13086	C9orf167	0	3903	NRARP	0	chr9	139310000
-1821	LOC728024	0	12758	PROSC	0	chr8	37726500
-1856	RCC2	0	99416	ARHGEF10L	0	chr1	17639500
-2356	RCC2	0	98916	ARHGEF10L	0	chr1	17640000
10582	GFI1B	0	2404	GFI1B	0	chr9	134854500
11082	GFI1B	0	1904	GFI1B	0	chr9	134855000
67751	TRAK1	0	66772	TRAK1	0	chr3	42175500
68251	TRAK1	0	66272	TRAK1	0	chr3	42176000
51	NANOS3	0	3571	NANOS3	0	chr19	13849000
5144	WNT3	0	49081	WNT3	0	chr17	42202000
5644	WNT3	0	48581	WNT3	0	chr17	42202500
-4257	C19orf24	0	2667	EFNA2	0	chr19	1234500
-1615	FAM106A	0	54946	CCDC144B	0	chr17	18372500
32705	ADAMTSL2	0	7961	ADAMTSL2	0	chr9	135422500
54547	MAD1L1	0	362609	MAD1L1	0	chr7	1876500
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-91234	TM4SF20	0	1631	AGFG1	0	chr2	228043500

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-47404	SLC7A10	0	26681	CEBPA	0	chr19	38456000
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-9756	CSPG4	0	1373	ODF3L1	0	chr15	73802000
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-88328	SLC12A7	0	1209	SLC6A19	0	chr5	1253500
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-197993	UBE2V2	0	455026	EFCAB1	0	chr8	49335000
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-23349	PAPOLB	0	20645	MMD2	0	chr7	4891500
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-1116	C10orf119	0	18712	SEC23IP	0	chr10	121623500
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1793	FBXW5	0	2494	FBXW5	0	chr9	138956500
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29809	PLXNA1	0	18920	PLXNA1	0	chr3	128220000
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29129	MUC5B	0	9982	MUC5B	0	chr11	1230000
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-141816	NCRNA00168	0	1368751	PFKP	0	chr10	1731000
-891	TFR2	0	661	ACTL6B	0	chr7	100078000
-1942	FRG2C	0	67718	ZNF717	0	chr3	75801000
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2758	DKK4	0	331	DKK4	0	chr8	42353500
2741	NFATC1	0	69665	NFATC1	0	chr18	75259500
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-53143	KCNG4	0	1901	WFDC1	0	chr16	82884000
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-104254	ZNF770	0	144818	LOC723972	0	chr15	33172000
-104754	ZNF770	0	144318	LOC723972	0	chr15	33172500
-38523	AFF3	0	129184	LONRF2	0	chr2	100127000
-1706	CASZ1	0	148119	C1orf127	0	chr1	10781000
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-206624	ZNF184	0	127735	HIST1H2BL	0	chr6	27755500
-207124	ZNF184	0	127235	HIST1H2BL	0	chr6	27756000
-285243	THSD7B	0	1277	HNMT	0	chr2	138437000
-285743	THSD7B	0	777	HNMT	0	chr2	138437500
-714	A3GALT2	0	1810	PHC2	0	chr1	33560000
-89864	C21orf81	0	38505	LIPI	0	chr21	14364500
-90364	C21orf81	0	38005	LIPI	0	chr21	14365000
38647	STEAP3	0	3197	STEAP3	0	chr2	119736500
-1380	LOC728613	0	162998	MRPL36	0	chr5	1688500
7154	LOC154449	0	1082	LOC154449	0	chr6	170412500

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42	DGKE	0	34533	DGKE	0	chr17	52266500
10692	PLEC	0	49531	PLEC	0	chr8	145072000
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-455	CCDC144NL	0	102997	USP22	0	chr17	20740500
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7083	TUBA3C	0	936	TUBA3C	0	chr13	18653000
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-102621	INSIG1	0	108084	EN2	0	chr7	154835500
35	HS3ST6	0	6732	HS3ST6	0	chr16	1901500
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785	MEG3	0	34121	MEG3	0	chr14	100363000
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61759	CACNA1H	0	6773	CACNA1H	0	chr16	1205000
62259	CACNA1H	0	6273	CACNA1H	0	chr16	1205500
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860	ASFMR1	0	11868	ASFMR1	0	chrX	146799500
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-270058	POTEG	0	128953	POTEM	0	chr14	18925000
-33727	OLFM1	0	347968	KIAA0649	0	chr9	137163500
-15523	GPER	0	43569	ZFAND2A	0	chr7	1115500
31695	CRYL1	0	90512	CRYL1	0	chr13	19907500
32195	CRYL1	0	90012	CRYL1	0	chr13	19908000
3299	ISL2	0	2371	ISL2	0	chr15	74419500
3799	ISL2	0	1871	ISL2	0	chr15	74420000
-911	PRSS42	0	22860	MYL3	0	chr3	46851500
-125754	DENND1B	0	1399	C1orf53	0	chr1	196137000
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46062	C6orf176	0	2517	C6orf176	0	chr6	166319000
6819	PIP5K1C	0	63445	PIP5K1C	0	chr19	3588000
7319	PIP5K1C	0	62945	PIP5K1C	0	chr19	3588500
-406	KRTAP2-1	0	17393	KRTAP2-4	0	chr17	36457500
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21372	SPPL2B	0	5100	SPPL2B	0	chr19	2301000
15107	PRDM15	0	63160	PRDM15	0	chr21	42109500
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643	DOK3	0	5464	DOK3	0	chr5	176864000
25102	FYCO1	0	52811	FYCO1	0	chr3	45959500
4367	CALHM1	0	1138	CALHM1	0	chr10	105207500
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17792	OBSL1	0	2755	OBSL1	0	chr2	220141500
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-30646	TFAMP1	0	97132	ELFN1	0	chr7	1653500
-2055	GPR56	0	1157	GPR97	0	chr16	56258500
-1226	C2CD4B	0	470664	MGC15885	0	chr15	60246000
72990	PTPRN2	0	975743	PTPRN2	0	chr7	157097500
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-3770	SNORD15A	0	112	SNORD15B	0	chr11	74793000
1714	RAB35	0	19982	RAB35	0	chr12	119019000
2171	KLHL17	0	2958	KLHL17	0	chr1	888000
2671	KLHL17	0	2458	KLHL17	0	chr1	888500
3171	KLHL17	0	1958	KLHL17	0	chr1	889000
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-1572	TNNT2	0	1588	LAD1	0	chr1	199615000
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257616	ATP9B	0	51270	ATP9B	0	chr18	75188000
258116	ATP9B	0	50770	ATP9B	0	chr18	75188500
258616	ATP9B	0	50270	ATP9B	0	chr18	75189000
6233	CBFA2T3	0	60109	CBFA2T3	0	chr16	87475000
-18144	WDR91	0	2270	STRA8	0	chr7	134565000
1087	NCOR2	0	210102	NCOR2	0	chr12	123376000
36381	PON3	0	123	PON3	0	chr7	94863500
-236796	C2orf27B	0	109138	ANKRD30BL	0	chr2	132512500
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5383	MFSD7	0	1973	MFSD7	0	chr4	671000
5883	MFSD7	0	1473	MFSD7	0	chr4	671500
-1929	C8orf73	0	97	NAPRT1	0	chr8	144728000
403	NAPRT1	0	3156	NAPRT1	0	chr8	144728500
-995	AVPI1	0	25470	MARVELD1	0	chr10	99438000
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-1666	WSB2	0	782	VSIG10	0	chr12	116985000
-359	HS6ST1	0	1603904	LOC389033	0	chr2	128793000
-11470	DBNDD1	0	1008	GAS8	0	chr16	88615500
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-4103	PCDHB10	0	31	PCDHB11	0	chr5	140559500
-1152	TCEA3	0	2642	ASAP3	0	chr1	23625000
13172	C14orf86	0	8471	C14orf86	0	chr14	93454000
219	MEST	0	19867	MEST	0	chr7	129913500
11603	ZFYVE21	0	6252	ZFYVE21	0	chr14	103263500
23966	MOBKL2A	0	1269	MOBKL2A	0	chr19	2046000
4809	SF3B3	0	49071	SF3B3	0	chr16	69120000
-7902	ZNF548	0	1840	ZNF17	0	chr19	62612500
-78251	PRKAG2	0	943	GALNTL5	0	chr7	151283500
-404	SERPINC1	0	13474	RC3H1	0	chr1	172153500
-700	KIAA0100	0	2733	SDF2	0	chr17	23997000
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790	C16orf55	0	12676	C16orf55	0	chr16	88252500
-425	JTB	0	3251	RAB13	0	chr1	152217500
-925	JTB	0	2751	RAB13	0	chr1	152218000
19789	PKD1	0	27400	PKD1	0	chr16	2098500
18520	ADRBK1	0	1605	ADRBK1	0	chr11	66809000
-96452	PRO0628	0	2074	PLCG1	0	chr20	39197500
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91076	CRTC1	0	7643	CRTC1	0	chr19	18746500
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-1745	MAGEA2B	0	5889	CSAG3,CSAG2	0	chrX	151672500
1614	C17orf70	0	10848	C17orf70	0	chr17	77119000
4746	C21orf2	0	5713	C21orf2	0	chr21	44578000
5246	C21orf2	0	5213	C21orf2	0	chr21	44578500
-108040	IQSEC1	0	240736	NUP210	0	chr3	13092000
98114	C10orf92	0	20989	C10orf92	0	chr10	134570000
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-584	GNG4	0	10468	LYST	0	chr1	233880500
-1084	GNG4	0	9968	LYST	0	chr1	233881000
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-55970	CRLF2	0	200	CSF2RA	0	chrY	1347500
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-1742	GSTTP1	0	24116	LOC391322	0	chr22	22679000
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141	MEG8	0	12058	MEG8	0	chr14	100431000
641	MEG8	0	11558	MEG8	0	chr14	100431500
-41521	SOX8	0	35584	LOC146336	0	chr16	1018500
-26766	CDC42EP5	0	2824	LAIR2	0	chr19	59703000
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-3	TKTL2	0	20622	C4orf43	0	chr4	164614500
22555	SLC2A7	0	491	SLC2A7	0	chr1	9008500
-32798	FAM35A	0	1184	FAM22A	0	chr10	88974000
-33298	FAM35A	0	684	FAM22A	0	chr10	88974500
-33798	FAM35A	0	184	FAM22A	0	chr10	88975000
-24106	DNAJB6	0	97510	PTPRN2	0	chr7	156927000
-24606	DNAJB6	0	97010	PTPRN2	0	chr7	156927500
-25106	DNAJB6	0	96510	PTPRN2	0	chr7	156928000
-16684	KIR2DL3	0	76	KIR2DL1	0	chr19	59973000
19143	PFKL	0	8184	PFKL	0	chr21	44563500
6626	TNNT3	0	12512	TNNT3	0	chr11	1904000
33374	VIPR2	0	83410	VIPR2	0	chr7	158547000
33874	VIPR2	0	82910	VIPR2	0	chr7	158547500
5169	ZNF526	0	2693	ZNF526	0	chr19	47421500
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-1518	BEND7	0	82444	PRPF18	0	chr10	13586500
-2018	BEND7	0	81944	PRPF18	0	chr10	13587000
9413	LRPAP1	0	10522	LRPAP1	0	chr4	3493500
-22190	TET3	0	5035	BOLA3	0	chr2	74211000
1705	DDAH2	0	1518	DDAH2	0	chr6	31804500
-12053	KCNH2	0	1079	NOS3	0	chr7	150318000
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22645	ARHGAP30	0	384	ARHGAP30	0	chr1	159306000
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5881	EPS8L2	0	15726	EPS8L2	0	chr11	702000
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-348606	C6orf208	0	111846	LOC154449	0	chr6	170293500
121314	RREB1	0	22191	RREB1	0	chr6	7174500
5731	RP1L1	0	43027	RP1L1	0	chr8	10507000
-120501	SOSTDC1	0	13436	ANKMY2	0	chr7	16592500
-121001	SOSTDC1	0	12936	ANKMY2	0	chr7	16593000
-1967	FABP5L3	0	256	CCT8L1	0	chr7	151773000
-348	GPRC5B	0	146543	GPR139	0	chr16	19804000
-1033	EDNRB	0	679230	POU4F1	0	chr13	77392000
-497	PITRM1	0	605738	KLF6	0	chr10	3205500
-859	PQLC1	0	12069	HSBP1L1	0	chr18	75813500
-1112	CFDP1	0	12423	TMEM170A	0	chr16	74026000
-26923	MANBAL	0	501	SRC	0	chr20	35406000
22480	SETD1B	0	5444	SETD1B	0	chr12	120749500
22980	SETD1B	0	4944	SETD1B	0	chr12	120750000
10640	C12orf72	0	11281	C12orf72	0	chr12	31702000
65527	MUC5AC	0	47302	MUC5AC	0	chr11	1198000
372	C16orf81	0	4084	C16orf81	0	chr16	87753500
107	CABP4	0	3763	CABP4	0	chr11	66979500
-6008	NAGLU	0	1509	HSD17B1	0	chr17	37956000
-6508	NAGLU	0	1009	HSD17B1	0	chr17	37956500
-1674	CAMSAP1	0	24135	UBAC1	0	chr9	137940500
21485	LAMA5	0	36763	LAMA5	0	chr20	60339000
21985	LAMA5	0	36263	LAMA5	0	chr20	60339500
14212	CTDP1	0	60495	CTDP1	0	chr18	75555000
14712	CTDP1	0	59995	CTDP1	0	chr18	75555500
14196	C1orf113	0	3573	C1orf113	0	chr1	36559500
14696	C1orf113	0	3073	C1orf113	0	chr1	36560000
282	FAM176B	0	1842	FAM176B	0	chr1	36560500
5480	C1orf70	0	103	C1orf70	0	chr1	1465500
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-1629	MTMR12	0	39712	ZFR	0	chr5	32350500
-2129	MTMR12	0	39212	ZFR	0	chr5	32351000
12460	SLC34A1	0	1955	SLC34A1	0	chr5	176756500
19956	PAX8	0	42968	PAX8	0	chr2	113710000
8957	FAM70B	0	43873	FAM70B	0	chr13	113608000
10017	SAMD11	0	8824	SAMD11	0	chr1	861000
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133	OR4F4	0	785	OR4F4	0	chr15	100280000
-89442	FAM178B	0	96049	FAHD2B	0	chr2	97017000
9126	TNNT3	0	10012	TNNT3	0	chr11	1906500
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1243	TNFRSF25	0	842	TNFRSF25	0	chr1	6448000
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-17308	SLC39A14	0	1040	PPP3CC	0	chr8	22353500
-26375	C2orf54	0	80427	SNED1	0	chr2	241506500
-26875	C2orf54	0	79927	SNED1	0	chr2	241507000
-6257	C19orf24	0	667	EFNA2	0	chr19	1236500
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-109858	CHRNB4	0	8099	ADAMTS7	0	chr15	76830500
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556	KCNAB1	0	395621	KCNAB1	0	chr3	157344000
1970	GREB1	0	46306	GREB1	0	chr2	11599500
920	NLRP3	0	32027	NLRP3	0	chr1	245647000
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-53421	BMF	0	1501	BUB1B	0	chr15	38239000
-1492	KCNK10	0	113264	SPATA7	0	chr14	87808500
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-642809	FERMT1	0	1744	BMP2	0	chr20	6695000
-83332	ZNF496	0	1080	NLRP3	0	chr1	245645000
-42642	C14orf169	0	1180	ACOT1	0	chr14	73072500
24248	GPSM1	0	7878	GPSM1	0	chr9	138366000
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33854	TRERF1	0	193261	TRERF1	0	chr6	42334500
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21853	TBC1D24	0	6489	TBC1D24	0	chr16	2487000
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1615	ARHGDIA	0	2027	ARHGDIA	0	chr17	77420500
31341	LOC145783	0	989	LOC145783	0	chr15	54997000
-397	SEMA3C	0	782379	HGF	0	chr7	80387000
-12973	NKX6-2	0	9386	C10orf92	0	chr10	134462500
-333624	ZNF184	0	735	HIST1H2BL	0	chr6	27882500
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10965	ANKRD11	0	211970	ANKRD11	0	chr16	87872500
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-2155	C1orf127	0	46265	TARDBP	0	chr1	10949000
-6261	AHNAK2	0	1660	C14orf79	0	chr14	104522000
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24143	PFKL	0	3184	PFKL	0	chr21	44568500
24643	PFKL	0	2684	PFKL	0	chr21	44569000
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18406	PDGFRB	0	23615	PDGFRB	0	chr5	149492000
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-298	LARP4B	0	102348	GTPBP4	0	chr10	922000
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93161	DYSF	0	126900	DYSF	0	chr2	71640500
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20390	PIGZ	0	2101	PIGZ	0	chr3	198178000
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-308442	RAPGEF5	0	61790	IL6	0	chr7	22671500
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-105539	ASAP1IT1	0	378228	ADCY8	0	chr8	131483500
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-11311	SP140L	0	1114	SP100	0	chr2	230988000
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-1100	DMWD	0	1807	RSPH6A	0	chr19	50989000
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17630	ITGB4	0	15494	ITGB4	0	chr17	71250000
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2178	C2orf90	0	1011	C2orf90	0	chr2	895000
2678	C2orf90	0	511	C2orf90	0	chr2	895500
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575	FGF22	0	3104	FGF22	0	chr19	591500
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-168483	HAND1	0	66154	LARP1	0	chr5	154006500
-168983	HAND1	0	65654	LARP1	0	chr5	154007000
588	TMEM159	0	21438	TMEM159	0	chr16	21078000
20318	SLC25A18	0	10147	SLC25A18	0	chr22	16443500
4724	TMEM8A	0	6451	TMEM8A	0	chr16	365500
5224	TMEM8A	0	5951	TMEM8A	0	chr16	366000
30799	C9orf86	0	2460	C9orf86	0	chr9	138853000
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-86802	BCL2A1	0	1575	ZFAND6	0	chr15	78137500
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-218772	SKOR1	0	1625	PIAS1	0	chr15	66132000
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-859	RNF183	0	15751	WDR31	0	chr9	115102000
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-8846	CT45A1	0	379	CT45A4,CT45A2	0	chrX	134693500
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-759	SFTA3	0	1852	NKX2-1	0	chr14	36053500
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-2026	GGT3P	0	112235	DGCR6	0	chr22	17161500
27816	NFYA	0	1623	NFYA	0	chr6	41176500
7832	PARVG	0	26367	PARVG	0	chr22	42908000
1436	DND1	0	1355	DND1	0	chr5	140032000
-147218	FKSG29	0	2228	TM9SF2	0	chr13	98949500
49400	MEGF8	0	3761	MEGF8	0	chr19	47571000
1009	LOC441956	0	830	LOC441956	0	chr21	13974500
-1527	ARSA	0	44935	SHANK3	0	chr22	49415000
-4874	SNORA36A	0	1466	SNORA56	0	chrX	153655000
1445	KIAA1324	0	87877	KIAA1324	0	chr1	109459500
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3053	KCNH2	0	25447	KCNH2	0	chr7	150280500
125	RNF151	0	1977	RNF151	0	chr16	1957000
292	ZBTB45	0	5733	ZBTB45	0	chr19	63717000
19142	PCNXL3	0	1986	PCNXL3	0	chr11	65159500
19642	PCNXL3	0	1486	PCNXL3	0	chr11	65160000
62119	LRRC2	0	2576	LRRC2	0	chr3	46594000
317	TDGF1	0	4456	TDGF1	0	chr3	46594500
106	OR12D2	0	927	OR12D2	0	chr6	29472500
606	P2RY6	0	25812	P2RY6	0	chr11	72661500
-172147	ANKRD57	0	1623	RGPD5,RGPD6	0	chr2	109906000
1808	NME4	0	1755	NME4	0	chr16	389000
8473	LGR6	0	107512	LGR6	0	chr1	200448000
67959	BAIAP2	0	7407	BAIAP2	0	chr17	76691500
68459	BAIAP2	0	6907	BAIAP2	0	chr17	76692000
-1933	EXOSC3	0	13789	DCAF10	0	chr9	37777000
63877	KDM4B	0	120608	KDM4B	0	chr19	4984000
-26075	BANP	0	326879	ZNF469	0	chr16	86694500
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7371	CT45A5	0	660	CT45A5	0	chrX	134781000
74858	ANO6	0	149454	ANO6	0	chr12	43971000
75358	ANO6	0	148954	ANO6	0	chr12	43971500
-23680	CD177	0	1602	TEX101	0	chr19	48583000
-24180	CD177	0	1102	TEX101	0	chr19	48583500
31135	MEGF6	0	92419	MEGF6	0	chr1	3425500
31635	MEGF6	0	91919	MEGF6	0	chr1	3426000
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-123791	CCDC74A	0	65033	C2orf27A	0	chr2	132131500
-124291	CCDC74A	0	64533	C2orf27A	0	chr2	132132000
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36481	PSTPIP1	0	5726	PSTPIP1	0	chr15	75111000
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34188	KIF26A	0	7988	KIF26A	0	chr14	103709000
-1306	C22orf34	0	114440	BRD1	0	chr22	48438500
-1936	KCNA4	0	212138	FSHB	0	chr11	29997000
-1060	HECTD1	0	83244	HEATR5A	0	chr14	30747500
-1560	HECTD1	0	82744	HEATR5A	0	chr14	30748000
-112	NXF2	0	41765	TMSB15A	0	chrX	101613500
-64707	LOC100129387	0	1370	USP8	0	chr15	48502500
-65207	LOC100129387	0	870	USP8	0	chr15	48503000
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10693	PRMT1	0	516	PRMT1	0	chr19	54883000
11193	PRMT1	0	16	PRMT1	0	chr19	54883500

247	C19orf76	0	2059	C19orf76	0	chr19	54884000
2724	TMEM8A	0	8451	TMEM8A	0	chr16	363500
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-12629	TSPAN14	0	2637	SH2D4B	0	chr10	82285000
71369	DIP2C	0	344108	DIP2C	0	chr10	381500
438	SLC4A11	0	9873	SLC4A11	0	chr20	3156500
-2225102	NRXN1	0	1097121	ASB3	0	chr2	52653500
-139029	ZSCAN5A	0	779	ZNF542	0	chr19	61570500
63	RTN4R	0	26816	RTN4R	0	chr22	18609000
-12473	NKX6-2	0	9886	C10orf92	0	chr10	134462000
3391	PAF1	0	2019	PAF1	0	chr19	44571500
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-77251	PRKAG2	0	1943	GALNTL5	0	chr7	151282500
-5342	NRF1	0	70730	UBE2H	0	chr7	129189500
-21941	FAM20C	0	177424	PDGFA	0	chr7	326000
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664490	PTPRN2	0	384243	PTPRN2	0	chr7	157689000
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-459	TMEM163	0	119155	ACMSD	0	chr2	135193500
-794887	RD20A3,ANKRD2	0	15063	PGM5P2	0	chr9	68355000
13054	BTBD2	0	17202	BTBD2	0	chr19	1949500
13554	BTBD2	0	16702	BTBD2	0	chr19	1950000
-20761	OR2T33	0	40	OR2T12	0	chr1	246524500
460	OR2T12	0	503	OR2T12	0	chr1	246525000
-23295	AKR1B10	0	772	AKR1B15	0	chr7	133900000
-7348	RAD54L2	0	261	TEX264	0	chr3	51680000
5440	MAP2K3	0	25144	MAP2K3	0	chr17	21134000
21862	C6orf52	0	1516	C6orf52	0	chr6	10801500
3271	CARD9	0	6454	CARD9	0	chr9	138381500
3771	CARD9	0	5954	CARD9	0	chr9	138382000
1941	PYCR1	0	2759	PYCR1	0	chr17	77485500
-614274	ERICH1	0	151475	DLGAP2	0	chr8	1285500
-614774	ERICH1	0	150975	DLGAP2	0	chr8	1286000
-615274	ERICH1	0	150475	DLGAP2	0	chr8	1286500
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-51	CASQ2	0	67521	NHLH2	0	chr1	116113000
-11242	ADRBK2	0	1619	MYO18B	0	chr22	24466500
55052	TNRC18	0	61703	TNRC18	0	chr7	5368000
233655	CLEC16A	0	4045	CLEC16A	0	chr16	11179500
234155	CLEC16A	0	3545	CLEC16A	0	chr16	11180000
21990	GLT25D1	0	5465	GLT25D1	0	chr19	17549500
13042	NEK8	0	911	NEK8	0	chr17	24093000
-1186	LRP8	0	109131	FLJ40434	0	chr1	53567500
116462	BANP	0	9425	BANP	0	chr16	86659000
-10590	TIMM17A	0	1388	RNPEP	0	chr1	200217000
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3750	TIE1	0	18366	TIE1	0	chr1	43543000
4250	TIE1	0	17866	TIE1	0	chr1	43543500
-714	SLC6A16	0	9488	CD37	0	chr19	54521000
-1214	SLC6A16	0	8988	CD37	0	chr19	54521500
4026	ACP5	0	301	ACP5	0	chr19	11550500
-1446	C10orf93	0	143898	GPR123	0	chr10	134607500
13259	CACNA1H	0	55273	CACNA1H	0	chr16	1156500
14259	CACNA1H	0	54273	CACNA1H	0	chr16	1157500
-1333	OR7A17	0	58800	OR7C2	0	chr19	14854500
667047	CDH4	0	17694	CDH4	0	chr20	59928000
667547	CDH4	0	17194	CDH4	0	chr20	59928500

4440	MAP2K3	0	26144	MAP2K3	0	chr17	21133000
34355	SCN4A	0	10	SCN4A	0	chr17	59404000
3475	RNF126	0	12227	RNF126	0	chr19	602000
-50356	WDR60	0	11805	LOC154822	0	chr7	158482000
-50856	WDR60	0	11305	LOC154822	0	chr7	158482500
-1637	KRCC1	0	10496	SMYD1	0	chr2	88138000
570	RAGE	0	75784	RAGE	0	chr14	101765500
-63609	CYP46A1	0	2497	EML1	0	chr14	99327000
-124759	XAGE2B	0	985	XAGE1D	0	chrX	52527500
-125259	XAGE2B	0	485	XAGE1D	0	chrX	52528000
-892135	ST3GAL1	0	13712	ZFAT	0	chr8	135545500
-892635	ST3GAL1	0	13212	ZFAT	0	chr8	135546000
-893135	ST3GAL1	0	12712	ZFAT	0	chr8	135546500
-893635	ST3GAL1	0	12212	ZFAT	0	chr8	135547000
-894135	ST3GAL1	0	11712	ZFAT	0	chr8	135547500
-894635	ST3GAL1	0	11212	ZFAT	0	chr8	135548000
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208945	SNX29	0	313147	SNX29	0	chr16	12262500
209445	SNX29	0	312647	SNX29	0	chr16	12263000
-2029	FGFR2	0	147114	ATE1	0	chr10	123345500
1481	NCRNA00245	0	3745	NCRNA00245	0	chr10	76835000
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104039	ADCY10	0	577	ADCY10	0	chr1	166149500
104539	ADCY10	0	77	ADCY10	0	chr1	166150000
4769	NRN1	0	4632	NRN1	0	chr6	5948000
-598	FAM83H	0	56577	SCRIB	0	chr8	144888500
20087	NCOR2	0	191102	NCOR2	0	chr12	123395000
41479	HRNBP3	0	351658	HRNBP3	0	chr17	74638500
41979	HRNBP3	0	351158	HRNBP3	0	chr17	74639000
-24727	SBNO2	0	48797	STK11	0	chr19	1108000
-4648	SLC7A2	0	1985	PDGFRL	0	chr8	17477000
-5148	SLC7A2	0	1485	PDGFRL	0	chr8	17477500
-1469	C21orf84	0	49499	HSF2BP	0	chr21	43724000
164	XGPY2	0	22537	XGPY2	0	chrY	2680500
-456	SRD5A2	0	286397	MEMO1	0	chr2	31660000
16195	LOC154822	0	1689	LOC154822	0	chr7	158510000
27555	HPS4	0	4820	HPS4	0	chr22	25205000
3055	GAD1	0	23015	GAD1	0	chr2	171384500
3555	GAD1	0	22515	GAD1	0	chr2	171385000
-4431	WDR18	0	1436	GRIN3B	0	chr19	950000
74475	TTLL11	0	197206	TTLL11	0	chr9	123698500
74975	TTLL11	0	196706	TTLL11	0	chr9	123699000
40798	EIF2AK2	0	469	EIF2AK2	0	chr2	37228000
-5305	HIST1H1D	0	132	HIST1H4F	0	chr6	26348500
98751	ANKRD26P1	0	1010	ANKRD26P1	0	chr16	45159500
-3753	FAM22F	0	42153	HIATL1	0	chr9	96134500
-928	ZNF239	0	30860	ZNF485	0	chr10	43391000
22545	ATG16L1	0	21559	ATG16L1	0	chr2	233847500
-231	CD7	0	3188	SECTM1	0	chr17	77869000
32759	CACNA1H	0	35773	CACNA1H	0	chr16	1176000
-49036	GRTP1	0	8760	ADPRHL1	0	chr13	113115500
-49536	GRTP1	0	8260	ADPRHL1	0	chr13	113116000
4770	LRRC27	0	44500	LRRC27	0	chr10	134000500
-91479	LAMA4	0	1224	RFPL4B	0	chr6	112774000
-91979	LAMA4	0	724	RFPL4B	0	chr6	112774500
-39086	N4BP2	0	2421	RHOH	0	chr4	39872500
39935	UHRF1	0	11665	UHRF1	0	chr19	4901500
-70	POU5F1	0	2990	PSORS1C3	0	chr6	31246500

224	OR2T33	0	739	OR2T33	0	chr1	246503000
509	LOC441956	0	1330	LOC441956	0	chr21	13974000
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1460	SIX3	0	1894	SIX3	0	chr2	45024000
-137	CCDC11	0	2213	MBD1	0	chr18	46047000
-637	CCDC11	0	1713	MBD1	0	chr18	46047500
-201	GPR132	0	76120	JAG2	0	chr14	104603000
-1675	TMPRSS13	0	55315	IL10RA	0	chr11	117307000
-2175	TMPRSS13	0	54815	IL10RA	0	chr11	117307500
119769	WDR27	0	125084	WDR27	0	chr6	169719000
-110687	LAMA1	0	2636	LRRC30	0	chr18	7218500
-111187	LAMA1	0	2136	LRRC30	0	chr18	7219000
18025	HK3	0	439	HK3	0	chr5	176258500
-651	MAP3K5	0	29394	PEX7	0	chr6	137156000
29051	H6PD	0	7481	H6PD	0	chr1	9246500
29551	H6PD	0	6981	H6PD	0	chr1	9247000
30051	H6PD	0	6481	H6PD	0	chr1	9247500
27076	KIAA0182	0	35811	KIAA0182	0	chr16	84231500
27576	KIAA0182	0	35311	KIAA0182	0	chr16	84232000
-110891	CBFA2T3	0	41754	ACSF3	0	chr16	87646000
-105689	NFATC1	0	44788	CTDP1	0	chr18	75496000
4963	PCDHGA2	0	169230	PCDHGA2	0	chr5	140703500
216	PCDHGA3	0	168730	PCDHGA3	0	chr5	140704000
-118941	LOC100130238	0	90729	FBRSL1	0	chr12	131486500
5881	KRT9	0	336	KRT9	0	chr17	36981500
1034	C1QL4	0	3738	C1QL4	0	chr12	48013500
5150	CLDN19	0	2012	CLDN19	0	chr1	42976500
10800	RPS6KA4	0	2263	RPS6KA4	0	chr11	63894000
-1488	POM121L1P	0	281	GGTLC2	0	chr22	21318500
-26270	SH3TC1	0	2391	HTRA3	0	chr4	8320000
5698	FAM86A	0	7790	FAM86A	0	chr16	5080000
6198	FAM86A	0	7290	FAM86A	0	chr16	5080500
-14966	NQO1	0	274	NOB1	0	chr16	68333000
226	NOB1	0	12830	NOB1	0	chr16	68333500
726	NOB1	0	12330	NOB1	0	chr16	68334000
-849	CDK11A	0	7040	SLC35E2	0	chr1	1646500
58	OR2T8	0	881	OR2T8	0	chr1	246151000
-43527	ARSA	0	2935	SHANK3	0	chr22	49457000
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37149	COL18A1	0	21062	COL18A1	0	chr21	45737000
3957	FAM70B	0	48873	FAM70B	0	chr13	113603000
4457	FAM70B	0	48373	FAM70B	0	chr13	113603500
-87692	CBX4	0	12913	TBC1D16	0	chr17	75515500
-88192	CBX4	0	12413	TBC1D16	0	chr17	75516000
-65620	IRX4	0	797780	IRX2	0	chr5	2001500
-66120	IRX4	0	797280	IRX2	0	chr5	2002000
2955	SYT3	0	13114	SYT3	0	chr19	55820000
-701	GPR132	0	75620	JAG2	0	chr14	104603500
-1201	GPR132	0	75120	JAG2	0	chr14	104604000
41675	SIRPA	0	3040	SIRPA	0	chr20	1865500
42175	SIRPA	0	2540	SIRPA	0	chr20	1866000
7754	MIB2	0	7348	MIB2	0	chr1	1548500
940	CSDE1	0	40147	CSDE1	0	chr1	115062000
1440	CSDE1	0	39647	CSDE1	0	chr1	115062500
3269	TMEM204	0	17744	TMEM204	0	chr16	1527500
3769	TMEM204	0	17244	TMEM204	0	chr16	1528000

20733	CBFA2T3	0	45609	CBFA2T3	0	chr16	87489500
29929	LOC646982	0	143	LOC646982	0	chr13	39953000
-34925	SRPX	0	13366	RPGR	0	chrX	38000000
-35425	SRPX	0	12866	RPGR	0	chrX	38000500
1589	ARC	0	1835	ARC	0	chr8	143691000
2089	ARC	0	1335	ARC	0	chr8	143691500
2589	ARC	0	835	ARC	0	chr8	143692000
-221555	CNKSR3	0	1203	RBM16	0	chr6	155095000
-77939	GRAP	0	2506	GRAPL	0	chr17	18969000
-78439	GRAP	0	2006	GRAPL	0	chr17	18969500
14845	MCF2L	0	104363	MCF2L	0	chr13	112696500
-1304	ATPBD4	0	1032103	C15orf41	0	chr15	33627000
-1804	ATPBD4	0	1031603	C15orf41	0	chr15	33627500
-757	PTPRN2	0	42763	NCAPG2	0	chr7	158074000
68866	LMF1	0	48485	LMF1	0	chr16	912500
-698	CYP2W1	0	6648	C7orf50	0	chr7	996500
6	FOXI1	0	3807	FOXI1	0	chr5	169465500
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-4761	ESPNP	0	29988	MST1P9	0	chr1	16924000
14145	METRNL	0	1011	METRNL	0	chr17	78645000
-54717	CROCCP3	0	16498	NBPF1	0	chr1	16746500
-55217	CROCCP3	0	15998	NBPF1	0	chr1	16747000
-33871	FLJ42627	0	2495	KCTD5	0	chr16	2670000
-34371	FLJ42627	0	1995	KCTD5	0	chr16	2670500
17337	GNAS	0	2145	GNAS	0	chr20	56917500
17837	GNAS	0	1645	GNAS	0	chr20	56918000
-80280	MRP63	0	117007	ZDHHC20	0	chr13	20731500
-80780	MRP63	0	116507	ZDHHC20	0	chr13	20732000
39214	TERT	0	2662	TERT	0	chr5	1345500
25237	PLVAP	0	637	PLVAP	0	chr19	17348500
-1047	KCNC1	0	9171	SERGEF	0	chr11	17757000
90372	TPN20B,PTPN20	0	509	PN20B,PTPN20A	0	chr10	46060500
-2728	LOC126536	0	2285	FLJ25328	0	chr19	16002000
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-1635	ETFA	0	23701	ISL2	0	chr15	74392500
58223	SUN1	0	65	SUN1	0	chr7	881000
-18717	FAT3	0	54436	MTNR1B	0	chr11	92288000
909	ALPP	0	3343	ALPP	0	chr2	232952500
-1871	25B,FAM25G,FA	0	1230	ANXA8	0	chr10	47874000
35650	RAB11FIP3	0	11981	RAB11FIP3	0	chr16	500500
36150	RAB11FIP3	0	11481	RAB11FIP3	0	chr16	501000
36650	RAB11FIP3	0	10981	RAB11FIP3	0	chr16	501500
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35704	SPTBN2	0	446	SPTBN2	0	chr11	66245000
-54	SPTBN2	0	23282	C11orf80	0	chr11	66245500
796	GLYR1	0	43304	GLYR1	0	chr16	4794000
1	NCRNA00221	0	13074	NCRNA00221	0	chr14	106009500
3943	RHBDF1	0	10629	RHBDF1	0	chr16	52000
4443	RHBDF1	0	10129	RHBDF1	0	chr16	52500
4943	RHBDF1	0	9629	RHBDF1	0	chr16	53000
40407	KIF17	0	13404	KIF17	0	chr1	20903500
30087	TTC25	0	694	TTC25	0	chr17	37370500
30587	TTC25	0	194	TTC25	0	chr17	37371000
5435	UHRF1	0	46165	UHRF1	0	chr19	4867000
5935	UHRF1	0	45665	UHRF1	0	chr19	4867500
-453003	MCTP2	0	576825	LOC145820	0	chr15	93200500
-3283	20B,PRR20A,PRR	0	266	,PRR20D,PRR20E	0	chr13	56632500
-197	PTCHD3	0	89754	RAB18	0	chr10	27743500

-1961	TRPV3	0	5489	TRPV1	0	chr17	3410000
-707916	GALR1	0	1022262	SALL3	0	chr18	73819000
-708416	GALR1	0	1021762	SALL3	0	chr18	73819500
-708916	GALR1	0	1021262	SALL3	0	chr18	73820000
47561	RGS7	0	534101	RGS7	0	chr1	239053000
-68637	NRXN2	0	14958	RASGRP2	0	chr11	64236000
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-200075	BANP	0	152879	ZNF469	0	chr16	86868500
-200575	BANP	0	152379	ZNF469	0	chr16	86869000
-201075	BANP	0	151879	ZNF469	0	chr16	86869500
-364558	POTEG	0	34453	POTEM	0	chr14	19019500
-365058	POTEG	0	33953	POTEM	0	chr14	19020000
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8491	ATP13A1	0	10003	ATP13A1	0	chr19	19625500
54260	PRRX2	0	2772	PRRX2	0	chr9	131522000
54760	PRRX2	0	2272	PRRX2	0	chr9	131522500
52309	SEPT9	0	128773	SEPT9	0	chr17	72879500
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-507685	LOC400940	0	352401	CMPK2	0	chr2	6553500
1804	COX4I1	0	5608	COX4I1	0	chr16	84392500
2304	COX4I1	0	5108	COX4I1	0	chr16	84393000
78106	CELSR1	0	98231	CELSR1	0	chr22	45213500
78606	CELSR1	0	97731	CELSR1	0	chr22	45214000
485	THOC4	0	3258	THOC4	0	chr17	77439500
378399	CUX1	0	54064	CUX1	0	chr7	101626000
10057	SPEG	0	48598	SPEG	0	chr2	220018000
-316	AGXT2L1	0	50420	COL25A1	0	chr4	109904000
21284	SS18L1	0	17461	SS18L1	0	chr20	60173500
21784	SS18L1	0	16961	SS18L1	0	chr20	60174000
-375945	FAM43A	0	3301	C3orf21	0	chr3	196267000
-376445	FAM43A	0	2801	C3orf21	0	chr3	196267500
-2160	YDJC	0	585	CCDC116	0	chr22	20316500
-2660	YDJC	0	85	CCDC116	0	chr22	20317000
80316	TTC7B	0	195514	TTC7B	0	chr14	90157000
80816	TTC7B	0	195014	TTC7B	0	chr14	90157500
4294	ATP2B2	0	177268	ATP2B2	0	chr3	10345000
4794	ATP2B2	0	176768	ATP2B2	0	chr3	10345500
19038	ZAP70	0	7255	ZAP70	0	chr2	97715500
37031	PPP2R3B	0	15627	PPP2R3B	0	chrY	252000
39469	ASMTL	0	10344	ASMTL	0	chrX	1521500
39969	ASMTL	0	9844	ASMTL	0	chrX	1522000
40469	ASMTL	0	9344	ASMTL	0	chrX	1522500
6662	DLL4	0	3029	DLL4	0	chr15	39015500
7162	DLL4	0	2529	DLL4	0	chr15	39016000
2770	LRRC27	0	46500	LRRC27	0	chr10	133998500
922	ST8SIA5	0	77037	ST8SIA5	0	chr18	42514000
-24527	PEG3AS	0	2581	MIMT1	0	chr19	62041500
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91832	EXD3	0	24535	EXD3	0	chr9	139413000
-3683	ZNF613	0	14904	ZNF350	0	chr19	57144500
278	POLRMT	0	16068	POLRMT	0	chr19	568500
778	POLRMT	0	15568	POLRMT	0	chr19	569000
6447	EEF2	0	2961	EEF2	0	chr19	3933500
-1535	GLIS1	0	31975	TMEM48	0	chr1	53974000
-2035	GLIS1	0	31475	TMEM48	0	chr1	53974500

-11847	MYLK4	0	2664	WRNIP1	0	chr6	2708000
-12347	MYLK4	0	2164	WRNIP1	0	chr6	2708500
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93087	NCOR2	0	118102	NCOR2	0	chr12	123468000
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-75870	FAM27L	0	1688	FLJ36000	0	chr17	21826500
-76370	FAM27L	0	1188	FLJ36000	0	chr17	21827000
-76870	FAM27L	0	688	FLJ36000	0	chr17	21827500
-77370	FAM27L	0	188	FLJ36000	0	chr17	21828000
6531	SLC6A18	0	14304	SLC6A18	0	chr5	1285000
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6615	ZNF843	0	849	ZNF843	0	chr16	31361000
26353	DOT1L	0	42077	DOT1L	0	chr19	2141500
26853	DOT1L	0	41577	DOT1L	0	chr19	2142000
27353	DOT1L	0	41077	DOT1L	0	chr19	2142500
-984	SNORD105B	0	696	P2RY11	0	chr19	10082500
-1484	SNORD105B	0	196	P2RY11	0	chr19	10083000
23928	ADARB2	0	527718	ADARB2	0	chr10	1242000
24428	ADARB2	0	527218	ADARB2	0	chr10	1242500
-110957	FLJ40292	0	2061	CACNA1B	0	chr9	139890000
171877	KDM4B	0	12608	KDM4B	0	chr19	5092000
172377	KDM4B	0	12108	KDM4B	0	chr19	5092500
-108618	TLN2	0	89390	TPM1	0	chr15	61032500
-1916	C16orf81	0	6163	CDH15	0	chr16	87759500
-2416	C16orf81	0	5663	CDH15	0	chr16	87760000
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110866	LMF1	0	6485	LMF1	0	chr16	954500
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-72075	MED13	0	127348	TBC1D3P2	0	chr17	57569500
-1494	LRRC34	0	7903	LRRIQ4	0	chr3	171014500
33416	ARHGAP22	0	125644	ARHGAP22	0	chr10	49357500
33916	ARHGAP22	0	125144	ARHGAP22	0	chr10	49358000
-31	SLC12A4	0	11566	DPEP3	0	chr16	66555500
-99182	SLC5A4	0	371	RFPL3	0	chr22	31080500
-424	NTN5	0	22539	FUT2	0	chr19	53868500
-924	NTN5	0	22039	FUT2	0	chr19	53869000
-1424	NTN5	0	21539	FUT2	0	chr19	53869500
-1924	NTN5	0	21039	FUT2	0	chr19	53870000
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1904	NAP1L5	0	46	NAP1L5	0	chr4	89838000
-18301	LCN1	0	1305	OBP2A	0	chr9	137576500
-18801	LCN1	0	805	OBP2A	0	chr9	137577000
-52441	LOC100130238	0	157229	FBRSL1	0	chr12	131420000
-52941	LOC100130238	0	156729	FBRSL1	0	chr12	131420500
-564	CD79B	0	5645	SCN4A	0	chr17	59364000
-12918	DENND3	0	2051	SLC45A4	0	chr8	142288000
-13418	DENND3	0	1551	SLC45A4	0	chr8	142288500
8957	PLIN5	0	3708	PLIN5	0	chr19	4482500

-361116	BARX2	0	2450	TMEM45B	0	chr11	129188500
-361616	BARX2	0	1950	TMEM45B	0	chr11	129189000
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-28	CKLF	0	294	CMTM1	0	chr16	65157500
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-671	PSG6	0	5623	PSG7	0	chr19	48114500
-1171	PSG6	0	5123	PSG7	0	chr19	48115000
-444	RWDD2B	0	4808	USP16	0	chr21	29314000
6187	NFATC1	0	122811	NFATC1	0	chr18	75267500
119685	CACNB2	0	281194	CACNB2	0	chr10	18589500
126759	TPO	0	2505	TPO	0	chr2	1523000
127259	TPO	0	2005	TPO	0	chr2	1523500
84660	AP2A2	0	1740	AP2A2	0	chr11	1000500
22492	CARKD	0	1843	CARKD	0	chr13	110088500
22992	CARKD	0	1343	CARKD	0	chr13	110089000
114205	RASA3	0	36697	RASA3	0	chr13	113879500
114705	RASA3	0	36197	RASA3	0	chr13	113880000
36918	SHC2	0	7496	SHC2	0	chr19	404500
37418	SHC2	0	6996	SHC2	0	chr19	405000
-638	CSNK1D	0	40534	CD7	0	chr17	77825500
-1138	CSNK1D	0	40034	CD7	0	chr17	77826000
-1638	CSNK1D	0	39534	CD7	0	chr17	77826500
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60707	RPH3AL	0	79576	RPH3AL	0	chr17	123000
20678	MUM1	0	1430	MUM1	0	chr19	1328000
21178	MUM1	0	930	MUM1	0	chr19	1328500
-241404	SMOC2	0	305799	THBS2	0	chr6	169052000
-241904	SMOC2	0	305299	THBS2	0	chr6	169052500
-372885	FAM92B	0	126029	KIAA0182	0	chr16	84076500
-23	NDUFB10	0	62	RPS2	0	chr16	1952000
-32	SNORA10	0	474	SNORA64	0	chr16	1952500
-59026	ZNF599	0	94646	ZNF30	0	chr19	40015000
-59526	ZNF599	0	94146	ZNF30	0	chr19	40015500
-8033	ZNF57	0	6715	ZNF77	0	chr19	2877500
-8533	ZNF57	0	6215	ZNF77	0	chr19	2878000
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-1545	KLF6	0	863377	LOC100216001	0	chr10	3819000
78369	COL4A2	0	127374	COL4A2	0	chr13	109836000
1154	LOC154449	0	7082	LOC154449	0	chr6	170406500
1654	LOC154449	0	6582	LOC154449	0	chr6	170407000
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-278490	DAZL	0	955	PLCL2	0	chr3	16900500
12324	CPNE7	0	9154	CPNE7	0	chr16	88182000
19867	P2RX1	0	209	P2RX1	0	chr17	3766500
-855	GNAS	0	69205	TH1L	0	chr20	56920500
37012	PIGG	0	3320	PIGG	0	chr4	520000
-1913	CDC34	0	26	GZMM	0	chr19	495000
474	GZMM	0	5419	GZMM	0	chr19	495500
22918	SMTNL2	0	863	SMTNL2	0	chr17	4457500
7046	NFKBIB	0	1874	NFKBIB	0	chr19	44089500
7546	NFKBIB	0	1374	NFKBIB	0	chr19	44090000

2019	H19	0	641	H19	0	chr11	1975000
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575	GAS6	0	14919	GAS6	0	chr13	113575500
1075	GAS6	0	14419	GAS6	0	chr13	113576000
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35281	SLC47A2	0	3135	SLC47A2	0	chr17	19557500
-5060	SAG	0	2391	DGKD	0	chr2	233925500
-5560	SAG	0	1891	DGKD	0	chr2	233926000
-6060	SAG	0	1391	DGKD	0	chr2	233926500
-6560	SAG	0	891	DGKD	0	chr2	233927000
25867	PTPN14	0	167765	PTPN14	0	chr1	212623500
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-40640	CLDN5	0	152	LOC150185	0	chr22	17933500
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11980	SETD1B	0	15944	SETD1B	0	chr12	120739000
1472	PITX2	0	18457	PITX2	0	chr4	111759500
172106	CELSR1	0	4231	CELSR1	0	chr22	45307500
29714	TERT	0	12162	TERT	0	chr5	1336000
-30182	C19orf21	0	2891	PTBP1	0	chr19	745500
42177	HSPG2	0	72837	HSPG2	0	chr1	22063500
-284997	PITRM1	0	321238	KLF6	0	chr10	3490000
-285497	PITRM1	0	320738	KLF6	0	chr10	3490500
541	CECR7	0	21682	CECR7	0	chr22	15898000
-3464	PRIC285	0	9898	GMEB2	0	chr20	61679500
-3964	PRIC285	0	9398	GMEB2	0	chr20	61680000
-30712	MLYCD	0	2172	OSGIN1	0	chr16	82538000
67962	BANP	0	57925	BANP	0	chr16	86610500
254490	PTPRN2	0	794243	PTPRN2	0	chr7	157279000
254990	PTPRN2	0	793743	PTPRN2	0	chr7	157279500
41501	JPH3	0	53762	JPH3	0	chr16	86235500
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-140	CXorf49,CXorf49B	0	44864	Xorf49,CXorf49B	0	chrX	70855000
-640	CXorf49,CXorf49B	0	44364	Xorf49,CXorf49B	0	chrX	70855500
-147	FAM48B2	0	49298	FAM48B1	0	chrX	24241500
16621	CT45A4,CT45A2	0	8685	CT45A4,CT45A2	0	chrX	134710500
17121	CT45A4,CT45A2	0	8185	CT45A4,CT45A2	0	chrX	134711000
347	CT45A3	0	7685	CT45A3	0	chrX	134711500
574	PCSK4	0	8407	PCSK4	0	chr19	1433000
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-16175	EXD2	0	1667	GALNTL1	0	chr14	68795000
-16675	EXD2	0	1167	GALNTL1	0	chr14	68795500
754	RAX	0	5605	RAX	0	chr18	55086000
-145565	NBPF16	0	24409	LOC645166	0	chr1	147170500
-163831	C6orf155	0	302370	RIMS1	0	chr6	72351000
-164331	C6orf155	0	301870	RIMS1	0	chr6	72351500
198047	MAD1L1	0	219109	MAD1L1	0	chr7	2020000
34792	PHF21B	0	93973	PHF21B	0	chr22	43690500
35292	PHF21B	0	93473	PHF21B	0	chr22	43691000
851	FAM171A1	0	158564	FAM171A1	0	chr10	15294500
1351	FAM171A1	0	158064	FAM171A1	0	chr10	15295000
5972	CSNK1D	0	23362	CSNK1D	0	chr17	77801500
12149	TEAD3	0	11339	TEAD3	0	chr6	35561500
12649	TEAD3	0	10839	TEAD3	0	chr6	35562000

97945	ANO1	0	13299	ANO1	0	chr11	69700000
874	NPBWR2	0	128	NPBWR2	0	chr20	62208500
315490	PTPRN2	0	733243	PTPRN2	0	chr7	157340000
315990	PTPRN2	0	732743	PTPRN2	0	chr7	157340500
90953	TRIM2	0	43924	TRIM2	0	chr4	154436000
91453	TRIM2	0	43424	TRIM2	0	chr4	154436500
-168274	ERICH1	0	597475	DLGAP2	0	chr8	839500
-1283	POU6F1	0	39274	DAZAP2	0	chr12	49879500
-1783	POU6F1	0	38774	DAZAP2	0	chr12	49880000
10816	NFE2L1	0	2406	NFE2L1	0	chr17	43491500
21383	NT5C1B	0	5319	NT5C1B	0	chr2	18629000
21883	NT5C1B	0	4819	NT5C1B	0	chr2	18629500
-75974	GALNT9	0	29549	LOC100130238	0	chr12	131332500
-490560	ANKRD30BP2	0	1368	POTED	0	chr21	13903000
-491060	ANKRD30BP2	0	868	POTED	0	chr21	13903500
-491560	ANKRD30BP2	0	368	POTED	0	chr21	13904000
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-643	LOC100133050	0	146522	FAM174A	0	chr5	99752500
-1143	LOC100133050	0	146022	FAM174A	0	chr5	99753000
-1643	LOC100133050	0	145522	FAM174A	0	chr5	99753500
30510	TSC2	0	10214	TSC2	0	chr16	2068500
31010	TSC2	0	9714	TSC2	0	chr16	2069000
-52113	KRTAP10-12	0	18882	UBE2G2	0	chr21	44994500
-3418	IL3RA	0	44	SLC25A6	0	chrY	1465000
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-1015	LMF1	0	9808	SOX8	0	chr16	962000
10316	NFE2L1	0	2906	NFE2L1	0	chr17	43491000
395	OLFML2B	0	40268	OLFML2B	0	chr1	160220000
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43215	C18orf1	0	390753	C18orf1	0	chr18	13252000
43715	C18orf1	0	390253	C18orf1	0	chr18	13252500
44215	C18orf1	0	389753	C18orf1	0	chr18	13253000
1340	PHYHIP	0	11296	PHYHIP	0	chr8	22134500
1840	PHYHIP	0	10796	PHYHIP	0	chr8	22135000
25386	ABCG5	0	962	ABCG5	0	chr2	43918500
11432	CNKSR1	0	962	CNKSR1	0	chr1	26388000
9593	NR2E1	0	13204	NR2E1	0	chr6	108603500
10093	NR2E1	0	12704	NR2E1	0	chr6	108604000
407	CORO1B	0	5059	CORO1B	0	chr11	66962500
15444	LDLR	0	29005	LDLR	0	chr19	11076500
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-50885	FAM92B	0	448029	KIAA0182	0	chr16	83754500
200028	COL5A1	0	3009	COL5A1	0	chr9	136873500
200528	COL5A1	0	2509	COL5A1	0	chr9	136874000
26201	SLC27A1	0	9477	SLC27A1	0	chr19	17468500
26701	SLC27A1	0	8977	SLC27A1	0	chr19	17469000
14052	TNRC18	0	102703	TNRC18	0	chr7	5327000
-853113	LOC730811	0	8748	TSSC1	0	chr2	3163000
-853613	LOC730811	0	8248	TSSC1	0	chr2	3163500
-22525	B3GNTL1	0	5355	METRNL	0	chr17	78625500
-23025	B3GNTL1	0	4855	METRNL	0	chr17	78626000
-1035112	TBC1D22A	0	280451	FAM19A5	0	chr22	46983500
-1035612	TBC1D22A	0	279951	FAM19A5	0	chr22	46984000
18872	SPPL2B	0	7600	SPPL2B	0	chr19	2298500
-671280	TP53TG3	0	417802	UBE2MP1	0	chr16	33843500
-671780	TP53TG3	0	417302	UBE2MP1	0	chr16	33844000

1723	PHB2	0	3652	PHB2	0	chr12	6946500
67845	MCF2L	0	51363	MCF2L	0	chr13	112749500
68345	MCF2L	0	50863	MCF2L	0	chr13	112750000
-1460	SSR1	0	11885	CAGE1	0	chr6	7260000
-1960	SSR1	0	11385	CAGE1	0	chr6	7260500
-11364	OBP2A	0	424	PAEP	0	chr9	137593000
76	PAEP	0	4943	PAEP	0	chr9	137593500
14005	KCTD5	0	12530	KCTD5	0	chr16	2686500
14505	KCTD5	0	12030	KCTD5	0	chr16	2687000
-62391	EIF2AK3	0	1790	RPIA	0	chr2	88770500
-126075	BANP	0	226879	ZNF469	0	chr16	86794500
-126575	BANP	0	226379	ZNF469	0	chr16	86795000
11850	DNMT3L	0	4027	DNMT3L	0	chr21	44502500
621047	CDH4	0	63694	CDH4	0	chr20	59882000
621547	CDH4	0	63194	CDH4	0	chr20	59882500
-8077	ABCG1	0	6731	TFF3	0	chr21	42598500
-8577	ABCG1	0	6231	TFF3	0	chr21	42599000
-321	KCNJ14	0	2776	CYTH2	0	chr19	53661500
-821	KCNJ14	0	2276	CYTH2	0	chr19	53662000
1296	ZNF238	0	2903	ZNF238	0	chr1	242284500
1796	ZNF238	0	2403	ZNF238	0	chr1	242285000
20712	MVP	0	6842	MVP	0	chr16	29760000
21212	MVP	0	6342	MVP	0	chr16	29760500
1378	CHTF18	0	8075	CHTF18	0	chr16	780000
1878	CHTF18	0	7575	CHTF18	0	chr16	780500
18527	ELL	0	60937	ELL	0	chr19	18433000
19027	ELL	0	60437	ELL	0	chr19	18433500
18031	PPP2R3B	0	34627	PPP2R3B	0	chrY	233000
18531	PPP2R3B	0	34127	PPP2R3B	0	chrY	233500
-127648	FGG	0	3612	LRAT	0	chr4	155881000
5569	CUL4A	0	49893	CUL4A	0	chr13	112917500
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14055	TSPAN4	0	8616	TSPAN4	0	chr11	848500
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-1264483	IRX1	0	168471	LOC340094	0	chr5	4919000
-1264983	IRX1	0	167971	LOC340094	0	chr5	4919500
1089	SBK2	0	5473	SBK2	0	chr19	60734000
6966	PLXNB2	0	12836	PLXNB2	0	chr22	49062500
7466	PLXNB2	0	12336	PLXNB2	0	chr22	49063000
7966	PLXNB2	0	11836	PLXNB2	0	chr22	49063500
225212	KIF5C	0	17019	KIF5C	0	chr2	149574500
225712	KIF5C	0	16519	KIF5C	0	chr2	149575000
135784	DLGAP4	0	96954	DLGAP4	0	chr20	34493500
15510	TSC2	0	25214	TSC2	0	chr16	2053500
16010	TSC2	0	24714	TSC2	0	chr16	2054000
16510	TSC2	0	24214	TSC2	0	chr16	2054500
4171	KLHL17	0	958	KLHL17	0	chr1	890000
4671	KLHL17	0	458	KLHL17	0	chr1	890500
-42	KLHL17	0	739	PLEKHN1	0	chr1	891000
-125120	IRX4	0	738280	IRX2	0	chr5	2061000
-125620	IRX4	0	737780	IRX2	0	chr5	2061500
20171	PGS1	0	25734	PGS1	0	chr17	73906500
20671	PGS1	0	25234	PGS1	0	chr17	73907000
-247	SLC6A12	0	7051	SLC6A13	0	chr12	193000
1775	PNPLA7	0	88807	PNPLA7	0	chr9	139476000
212422	GALNT2	0	2498	GALNT2	0	chr1	228482000
212922	GALNT2	0	1998	GALNT2	0	chr1	228482500

15794	XRCC3	0	2076	XRCC3	0	chr14	103249500
8180	RNF213	0	48173	RNF213	0	chr17	75936500
561	PRAM1	0	11995	PRAM1	0	chr19	8461500
6213	TUBA3E	0	504	TUBA3E	0	chr2	130672000
6713	TUBA3E	0	4	TUBA3E	0	chr2	130672500
-2862207	C4orf33	0	1174419	PCDH10	0	chr4	133115500
-2862707	C4orf33	0	1173919	PCDH10	0	chr4	133116000
-8095	SPATA5L1	0	1054	C15orf48	0	chr15	43509000
1019	H19	0	1641	H19	0	chr11	1974000
89037	PCNT	0	32610	PCNT	0	chr21	46657500
12422	PDZD7	0	1369	PDZD7	0	chr10	102779500
12922	PDZD7	0	869	PDZD7	0	chr10	102780000
9470	NCRNA00111	0	8565	NCRNA00111	0	chr21	41982000
9970	NCRNA00111	0	8065	NCRNA00111	0	chr21	41982500
4455	PRSSL1	0	5461	PRSSL1	0	chr19	641000
4955	PRSSL1	0	4961	PRSSL1	0	chr19	641500
5455	PRSSL1	0	4461	PRSSL1	0	chr19	642000
4941	USP36	0	39064	USP36	0	chr17	74309500
5441	USP36	0	38564	USP36	0	chr17	74310000
-1845	PSORS1C3	0	18015	HCG27	0	chr6	31255500
92995	CELF4	0	229998	CELF4	0	chr18	33170000
31407	BEND7	0	30482	BEND7	0	chr10	13554500
31907	BEND7	0	29982	BEND7	0	chr10	13555000
32407	BEND7	0	29482	BEND7	0	chr10	13555500
344897	PRDM16	0	24545	PRDM16	0	chr1	3320500
345397	PRDM16	0	24045	PRDM16	0	chr1	3321000
-643	PUS1	0	5460	EP400	0	chr12	130995000
395	GAMT	0	2552	GAMT	0	chr19	1350000
895	GAMT	0	2052	GAMT	0	chr19	1350500
-39	PRSSL1	0	13452	PALM	0	chr19	646500
-539	PRSSL1	0	12952	PALM	0	chr19	647000
39469	ASMTL	0	10344	ASMTL	0	chrY	1521500
72869	DIP2C	0	342608	DIP2C	0	chr10	383000
73869	DIP2C	0	341608	DIP2C	0	chr10	384000
-2140	CXorf49,CXorf49	0	42864	Xorf49,CXorf49B	0	chrX	70857000
-17	ODF3L2	0	21489	MADCAM1	0	chr19	426000
-517	ODF3L2	0	20989	MADCAM1	0	chr19	426500
20188	FRMD1	0	3188	FRMD1	0	chr6	168219500
311	EIF3G	0	4599	EIF3G	0	chr19	10087000
811	EIF3G	0	4099	EIF3G	0	chr19	10087500
705490	PTPRN2	0	343243	PTPRN2	0	chr7	157730000
-60892	C10orf108	0	83483	LARP4B	0	chr10	762000
66639	TEKT5	0	803	TEKT5	0	chr16	10695500
4730	ZNF629	0	4024	ZNF629	0	chr16	30702000
3083	TUBA3C	0	4936	TUBA3C	0	chr13	18649000
199047	MAD1L1	0	218109	MAD1L1	0	chr7	2021000
-1371	TMEM80	0	619	EPS8L2	0	chr11	695500
331869	DIP2C	0	83608	DIP2C	0	chr10	642000
332369	DIP2C	0	83108	DIP2C	0	chr10	642500
20462	ADCK5	0	261	ADCK5	0	chr8	145589000
247	CPSF1	0	16041	CPSF1	0	chr8	145589500
747	CPSF1	0	15541	CPSF1	0	chr8	145590000
4426	MIER2	0	34791	MIER2	0	chr19	261000
4926	MIER2	0	34291	MIER2	0	chr19	261500
8761	AMZ2	0	400	AMZ2	0	chr17	63764500
-100	AMZ2	0	1917	ARSG	0	chr17	63765000
-100393	TPTE2P1	0	27275	PABPC3	0	chr13	24541000
13766	WDR5	0	6415	WDR5	0	chr9	136008500

-28303	RASA3	0	73963	CDC16	0	chr13	113944500
-28803	RASA3	0	73463	CDC16	0	chr13	113945000
6379	OGFR	0	2797	OGFR	0	chr20	60913000
333	JMJD8	0	2440	JMJD8	0	chr16	672000
337990	PTPRN2	0	710743	PTPRN2	0	chr7	157362500
338490	PTPRN2	0	710243	PTPRN2	0	chr7	157363000
-625	SCMH1	0	236035	EDN2	0	chr1	41481000
110805	CSMD2	0	541030	CSMD2	0	chr1	33863000
111305	CSMD2	0	540530	CSMD2	0	chr1	33863500
3300	FAM109B	0	1888	FAM109B	0	chr22	40803500
29242	SLC7A9	0	10023	SLC7A9	0	chr19	38042500
3455	SYT3	0	12614	SYT3	0	chr19	55820500
-32743	GADD45B	0	217	GNG7	0	chr19	2462000
283	GNG7	0	191246	GNG7	0	chr19	2462500
588	GAL3ST2	0	26875	GAL3ST2	0	chr2	242365500
10615	LOC652276	0	16496	LOC652276	0	chr16	2604000
11115	LOC652276	0	15996	LOC652276	0	chr16	2604500
63584	FNDC1	0	39130	FNDC1	0	chr6	159574000
27889	KIAA1751	0	22636	KIAA1751	0	chr1	1902500
6879	OGFR	0	2297	OGFR	0	chr20	60913500
-131624	FLJ35776	0	1414671	LOC642597	0	chr18	3719000
14259	SLCO4A1	0	15592	SLCO4A1	0	chr20	60758500
14759	SLCO4A1	0	15092	SLCO4A1	0	chr20	60759000
66867	PTPRF	0	25930	PTPRF	0	chr1	43836000
2526	RPUSD1	0	884	RPUSD1	0	chr16	777500
-155793	ZNF716	0	4696104	LOC643955	0	chr7	57693000
-156293	ZNF716	0	4695604	LOC643955	0	chr7	57693500
-1772	C19orf25	0	426	PCSK4	0	chr19	1432000
74	PCSK4	0	8907	PCSK4	0	chr19	1432500
8369	GDPD3	0	379	GDPD3	0	chr16	30032000
5669	ZNF526	0	2193	ZNF526	0	chr19	47422000
8083	ATAD3A	0	14427	ATAD3A	0	chr1	1445500
-102080	RPS17	0	106827	Q2P2,UBE2Q2P3	0	chr15	80714000
-166872	ZNF267	0	67109	HERC2P4	0	chr16	32003000
-167372	ZNF267	0	66609	HERC2P4	0	chr16	32003500
-167872	ZNF267	0	66109	HERC2P4	0	chr16	32004000
664	C6orf81	0	11163	C6orf81	0	chr6	35813500
54	FUT7	0	2613	FUT7	0	chr9	139044500
554	FUT7	0	2113	FUT7	0	chr9	139045000
24469	ASMTL	0	25344	ASMTL	0	chrX	1506500
1949	FAM20C	0	14059	FAM20C	0	chr7	290000
2449	FAM20C	0	13559	FAM20C	0	chr7	290500
2949	FAM20C	0	13059	FAM20C	0	chr7	291000
-468251	OR4N3P	0	835	TUBGCP5	0	chr15	20384000
-84604	IRX5	0	305471	IRX6	0	chr16	53610500
86260	CLIP2	0	30209	CLIP2	0	chr7	73428000
1005	LOC92659	0	1919	LOC92659	0	chr17	77480000
2189	TPRX1	0	173	TPRX1	0	chr19	52998500
-327	TPRX1	0	17910	CRX	0	chr19	52999000
81830	DMBT1	0	1242	DMBT1	0	chr10	124392000
82330	DMBT1	0	742	DMBT1	0	chr10	124392500
-15214	LOC407835	0	1447	TSPAN33	0	chr7	128570500
-26088	TNFRSF19	0	34827	MIPEP	0	chr13	23167500
-26588	TNFRSF19	0	34327	MIPEP	0	chr13	23168000
3605	ZSCAN10	0	362	ZSCAN10	0	chr16	3082500
-91872	BTNL9	0	1548	OR2V2	0	chr5	180513000
-92372	BTNL9	0	1048	OR2V2	0	chr5	180513500
-5577	DYNLRB1	0	352	MAP1LC3A	0	chr20	32598000

173606	CELSR1	0	2731	CELSR1	0	chr22	45309000
174106	CELSR1	0	2231	CELSR1	0	chr22	45309500
12527	MUC5AC	0	100302	MUC5AC	0	chr11	1145000
13027	MUC5AC	0	99802	MUC5AC	0	chr11	1145500
-305097	ADAM6	0	194999	NCRNA00221	0	chr14	105814500
-1589	SNORD105	0	424	SNORD105B	0	chr19	10081000
126	WBP2	0	9596	WBP2	0	chr17	71353500
626	WBP2	0	9096	WBP2	0	chr17	71354000
9626	NCLN	0	14073	NCLN	0	chr19	3146500
10126	NCLN	0	13573	NCLN	0	chr19	3147000
1310	GGTLC1	0	2416	GGTLC1	0	chr20	23915000
-2023	GPER	0	57069	ZFAND2A	0	chr7	1102000
-240577	---	0	102767	ZNF479	0	chr7	57088500
30854	BRI3BP	0	1302	BRI3BP	0	chr12	124075000
31354	BRI3BP	0	802	BRI3BP	0	chr12	124075500
26266	FAM182B	0	5427	FAM182B	0	chr20	25724500
26766	FAM182B	0	4927	FAM182B	0	chr20	25725000
2319	HRNR	0	9793	HRNR	0	chr1	150453500
2819	HRNR	0	9293	HRNR	0	chr1	150454000
29057	NOTCH3	0	12292	NOTCH3	0	chr19	15160500
29557	NOTCH3	0	11792	NOTCH3	0	chr19	15161000
4583	MICAL3	0	232325	MICAL3	0	chr22	16655000
25093	SPIRE2	0	17728	SPIRE2	0	chr16	88447500
-2826	C4B,C4A	0	60	CYP21A2	0	chr6	32114000
440	CYP21A2	0	2898	CYP21A2	0	chr6	32114500
25372	SPPL2B	0	1100	SPPL2B	0	chr19	2305000
25872	SPPL2B	0	600	SPPL2B	0	chr19	2305500
345	MCF2L	0	118863	MCF2L	0	chr13	112682000
4708	RBM12	0	11252	RBM12	0	chr20	33705000
37031	PPP2R3B	0	15627	PPP2R3B	0	chrX	252000
102499	KAZ	0	19738	KAZ	0	chr1	15247500
102999	KAZ	0	19238	KAZ	0	chr1	15248000
-25931	LSP1	0	1374	TNNT3	0	chr11	1896000
-22690	TET3	0	4535	BOLA3	0	chr2	74211500
8130	KLHL21	0	4016	KLHL21	0	chr1	6581500
8630	KLHL21	0	3516	KLHL21	0	chr1	6582000
20296	BRSK2	0	51904	BRSK2	0	chr11	1388000
22232	PRKCZ	0	112694	PRKCZ	0	chr1	1994000
1835	CLSTN1	0	93637	CLSTN1	0	chr1	9713500
2335	CLSTN1	0	93137	CLSTN1	0	chr1	9714000
-12123	APH1B	0	2282	CA12	0	chr15	61400500
-12623	APH1B	0	1782	CA12	0	chr15	61401000
7132	SEC16A	0	35828	SEC16A	0	chr9	138461500
-31182	C19orf21	0	1891	PTBP1	0	chr19	746500
16284	GET4	0	3597	GET4	0	chr7	899000
16784	GET4	0	3097	GET4	0	chr7	899500
1727	TPSD1	0	495	TPSD1	0	chr16	1248000
182537	PDE3A	0	129148	PDE3A	0	chr12	20596000
183037	PDE3A	0	128648	PDE3A	0	chr12	20596500
183537	PDE3A	0	128148	PDE3A	0	chr12	20597000
23235	ASB2	0	20	ASB2	0	chr14	93493500
10418	SHC2	0	33996	SHC2	0	chr19	378000
-1549	IL28B	0	21996	IL28A	0	chr19	44429000
61677	HSPG2	0	53337	HSPG2	0	chr1	22083000
62677	HSPG2	0	52337	HSPG2	0	chr1	22084000
-281	FOXO3B	0	48626	TRIM16L	0	chr17	18517500
23969	ASMTL	0	25844	ASMTL	0	chrY	1506000
-132478	LOC284233	0	2955	CXADRP3	0	chr18	14465000

-9491	SNRPD3	0	1717	GGT1	0	chr22	23308000
-291	P2RX1	0	6917	ATP2A3	0	chr17	3767000
6092	ZBTB4	0	14168	ZBTB4	0	chr17	7309500
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-15060	PKD1P1	0	736681	XYLT1	0	chr16	16367000
1306	ALKBH4	0	7293	ALKBH4	0	chr7	101885000
1159	PDZRN3	0	241262	PDZRN3	0	chr3	73515500
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12629	CBS	0	10109	CBS	0	chr21	43359000
13129	CBS	0	9609	CBS	0	chr21	43359500
1706	YBX2	0	4600	YBX2	0	chr17	7134000
2206	YBX2	0	4100	YBX2	0	chr17	7134500
-55598	FAM83H	0	1577	SCRIB	0	chr8	144943500
11316	NFE2L1	0	1906	NFE2L1	0	chr17	43492000
30047	MAD1L1	0	387109	MAD1L1	0	chr7	1852000
3462	TBX2	0	6109	TBX2	0	chr17	56835500
3962	TBX2	0	5609	TBX2	0	chr17	56836000
7680	RNF213	0	48673	RNF213	0	chr17	75936000
725	PRKACG	0	859	PRKACG	0	chr9	70818000
1225	PRKACG	0	359	PRKACG	0	chr9	70818500
43969	CROCC	0	7061	CROCC	0	chr1	17165000
44469	CROCC	0	6561	CROCC	0	chr1	17165500
2372	SPPL2B	0	24100	SPPL2B	0	chr19	2282000
21858	GALNS	0	21375	GALNS	0	chr16	87429500
22358	GALNS	0	20875	GALNS	0	chr16	87430000
37	OR10Q1	0	923	OR10Q1	0	chr11	57752000
537	OR10Q1	0	423	OR10Q1	0	chr11	57752500
-87192	CBX4	0	13413	TBC1D16	0	chr17	75515000
-1581	ZNF423	0	196689	TMEM188	0	chr16	48420000
6708	GRK6	0	9456	GRK6	0	chr5	176793000
7208	GRK6	0	8956	GRK6	0	chr5	176793500
53425	USP42	0	3220	USP42	0	chr7	6164500
53925	USP42	0	2720	USP42	0	chr7	6165000
-520224	MAP2K4	0	1931	MYOCD	0	chr17	12508000
-8803	PKD1P1	0	31682	NOMO2	0	chr16	18387000
41553	CACNA1G	0	3832	CACNA1G	0	chr17	46035000
5423	MGC2752	0	3574	MGC2752	0	chr19	63784000
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1550	ZBTB17	0	32714	ZBTB17	0	chr1	16142500
522	LSP1	0	23069	LSP1	0	chr11	1847000
1022	LSP1	0	22569	LSP1	0	chr11	1847500
5160	PPP1R13B	0	108680	PPP1R13B	0	chr14	103275000
24416	TECTA	0	63725	TECTA	0	chr11	120503000
50385	OCA2	0	294053	OCA2	0	chr15	25724000
79045	FOXK1	0	10100	FOXK1	0	chr7	4767500
-25391	CBFA2T3	0	127254	ACSF3	0	chr16	87560500
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4590	TNXB	0	63629	TNXB	0	chr6	32121500
4079	ADRM1	0	1813	ADRM1	0	chr20	60315500
907	CORO1B	0	4559	CORO1B	0	chr11	66963000
100475	PLEKHA5	0	70598	PLEKHA5	0	chr12	19350000
5488	ALDH4A1	0	25659	ALDH4A1	0	chr1	19076000
5988	ALDH4A1	0	25159	ALDH4A1	0	chr1	19076500
-854113	LOC730811	0	7748	TSSC1	0	chr2	3164000
42677	HSPG2	0	72337	HSPG2	0	chr1	22064000
4336	SLC7A2	0	27352	SLC7A2	0	chr8	17445000
295	SLC7A2	0	26852	SLC7A2	0	chr8	17445500

1837	COX7A1	0	111	COX7A1	0	chr19	41335500
85214	GABRB3	0	144344	GABRB3	0	chr15	24425000
85714	GABRB3	0	143844	GABRB3	0	chr15	24425500
2061	ABHD8	0	9282	ABHD8	0	chr19	17266000
15643	PMEPA1	0	47447	PMEPA1	0	chr20	55672500
16143	PMEPA1	0	46947	PMEPA1	0	chr20	55673000
67335	UNC5A	0	3005	UNC5A	0	chr5	176237500
25894	PON1	0	320	PON1	0	chr7	94791500
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4252	GPER	0	1477	GPER	0	chr7	1098500
4752	GPER	0	977	GPER	0	chr7	1099000
1489	SHBG	0	3925	SHBG	0	chr17	7473500
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7928	PEG10	0	5442	PEG10	0	chr7	94131500
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62971	WDR60	0	26644	WDR60	0	chr7	158405000
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398	PARVG	0	25867	PARVG	0	chr22	42908500
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7126	TNNT3	0	12012	TNNT3	0	chr11	1904500
5784	NOTCH1	0	45559	NOTCH1	0	chr9	138514500
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7251	LOC100129637	0	291	LOC100129637	0	chr16	86296500
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-1523	ACHE	0	117083	MUC17	0	chr7	100333000
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-82671	F11	0	161302	MTNR1A	0	chr4	187530500
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-179	CSH2	0	6303	GH2	0	chr17	59305000
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705	DDAH2	0	2518	DDAH2	0	chr6	31803500
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8621	ZNF469	0	4666	ZNF469	0	chr16	87030000
29512	SLC12A7	0	32172	SLC12A7	0	chr5	1133000
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21476	TTC38	0	4569	TTC38	0	chr22	45064000
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26132	SEC16A	0	16828	SEC16A	0	chr9	138480500
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636	MAGEA4	0	8298	MAGEA4	0	chrX	150836000
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-8293	CYTSA	0	1529	ADORA2A	0	chr22	23152000
125623	RIN3	0	49587	RIN3	0	chr14	92175500
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-392	C10orf108	0	143983	LARP4B	0	chr10	701500
-892	C10orf108	0	143483	LARP4B	0	chr10	702000
-23875	POLR3D	0	254	PIWIL2	0	chr8	22188500

-4341	ULK1	0	1741	PUS1	0	chr12	130978000
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878530	CAMTA1	0	105851	CAMTA1	0	chr1	7646500
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-510	AQP12B	0	8434	AQP12A	0	chr2	241271500
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2667	SLC9A3	0	48549	SLC9A3	0	chr5	529000
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16188	FRMD1	0	7188	FRMD1	0	chr6	168215500
16688	FRMD1	0	6688	FRMD1	0	chr6	168216000
4598	KNCN	0	974	KNCN	0	chr1	46788500
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21141	CHID1	0	21874	CHID1	0	chr11	879000
33737	DNAH2	0	80283	DNAH2	0	chr17	7597500
34237	DNAH2	0	79783	DNAH2	0	chr17	7598000
138	RPL29P2	0	511	RPL29P2	0	chr17	7598500
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-1027278	FLJ40330	0	1273935	LOC654342	0	chr2	89914500
-68971	TPI1P2	0	60	LOC407835	0	chr7	128553500
3108	INPP5E	0	8077	INPP5E	0	chr9	138446000
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273	SNRPN,SNURF	0	23322	SNRPN,SNURF	0	chr15	22751500
14555	TSPAN4	0	8116	TSPAN4	0	chr11	849000
46859	FOXP4	0	9100	FOXP4	0	chr6	41669000
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-61392	C10orf108	0	82983	LARP4B	0	chr10	762500
66245	ZNF710	0	13029	ZNF710	0	chr15	88412000
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3059	LIF	0	3296	LIF	0	chr22	28969500
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-121	GDPD3	0	426	MAPK3	0	chr16	30032500
3923	BEND3	0	45329	BEND3	0	chr6	107497000
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36539	DNAJC5	0	2339	DNAJC5	0	chr20	62033500
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-1150	CPN2	0	2771	LRRC15	0	chr3	195554500
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-4932	POLRMT	0	1425	FGF22	0	chr19	589500
-4531	SLC12A4	0	7066	DPEP3	0	chr16	66560000
-8255	C1QTNF8	0	48741	CACNA1H	0	chr16	1094500
-8755	C1QTNF8	0	48241	CACNA1H	0	chr16	1095000
-894097	C20orf197	0	285453	CDH4	0	chr20	58975500
-894597	C20orf197	0	284953	CDH4	0	chr20	58976000
-11918	LOC154449	0	7718	DLL1	0	chr6	170425500
-12418	LOC154449	0	7218	DLL1	0	chr6	170426000
18898	TEX101	0	11107	TEX101	0	chr19	48603500
19398	TEX101	0	10607	TEX101	0	chr19	48604000
19898	TEX101	0	10107	TEX101	0	chr19	48604500
21416	LMNA	0	1781	LMNA	0	chr1	154372500
-747	FDPSL2A	0	4762	DTX2	0	chr7	75943000
-1247	FDPSL2A	0	4262	DTX2	0	chr7	75943500
21509	AP2A1	0	18681	AP2A1	0	chr19	54983500
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7120	CT45A6	0	910	CT45A6	0	chrX	134798000
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1340	ZBTB22	0	2197	ZBTB22	0	chr6	33391500
1840	ZBTB22	0	1697	ZBTB22	0	chr6	33392000
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-574274	MARCH1	0	9108	ANP32C	0	chr4	165328500
-700	SLC37A4	0	12605	HYOU1	0	chr11	118407500
16582	ACOT7	0	78091	ACOT7	0	chr1	6263500
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-1873	PPP2R3B	0	235578	SHOX	0	chrY	269500
-9812	ADAMTSL5	0	1077	PLK5P	0	chr19	1474000
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23211	GGA3	0	1772	GGA3	0	chr17	70767500
18729	BRD3	0	18962	BRD3	0	chr9	135904000
1159	PCDHGA12	0	81230	PCDHGA12	0	chr5	140791500

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35552	PDCL2	0	136	PDCL2	0	chr4	56153000
-2880	LY6G5C	0	3714	BAT5	0	chr6	31759000
-101461	RRN3P2	0	73041	RUNDC2C	0	chr16	29137000
6592	ACOX3	0	67852	ACOX3	0	chr4	8425500
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-29241	TAPT1	0	245761	LDB2	0	chr4	15866500
-29741	TAPT1	0	245261	LDB2	0	chr4	15867000
353	ASPHD1	0	4878	ASPHD1	0	chr16	29820000
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32437	NISCH	0	5128	NISCH	0	chr3	52497000
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210	LCN6	0	4301	LCN6	0	chr9	138758500
710	LCN6	0	3801	LCN6	0	chr9	138759000
-73837	LOC286135	0	35672	TMEM66	0	chr8	30004500
65540	KNDC1	0	406	KNDC1	0	chr10	134889500
-462148	CWH43	0	3183032	DCUN1D4	0	chr4	49221000
5418	SHC2	0	38996	SHC2	0	chr19	373000
7565	CLCN7	0	22586	CLCN7	0	chr16	1442500
6284	DPEP1	0	18840	DPEP1	0	chr16	88213500
-16808	SLC39A14	0	1540	PPP3CC	0	chr8	22353000
-1562929	TTTY23B,TTTY23	0	1361191	TTTY15	0	chrY	11922500
-1563429	TTTY23B,TTTY23	0	1360691	TTTY15	0	chrY	11923000
19205	RASA3	0	131697	RASA3	0	chr13	113784500
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135284	DLGAP4	0	97454	DLGAP4	0	chr20	34493000
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-239519	FAT1	0	1032418	ZFP42	0	chr4	188121500
-240019	FAT1	0	1031918	ZFP42	0	chr4	188122000
-149651	ZNF117	0	537	INTS4L1	0	chr7	64238500
-150151	ZNF117	0	37	INTS4L1	0	chr7	64239000
-1663869	CA10	0	237	KIF2B	0	chr17	49255000
263	KIF2B	0	2072	KIF2B	0	chr17	49255500
60352	C7orf50	0	80919	C7orf50	0	chr7	1063500
334	GPR146	0	1423	GPR146	0	chr7	1064000
834	GPR146	0	923	GPR146	0	chr7	1064500
29214	TERT	0	12662	TERT	0	chr5	1335500
47	FZR1	0	13755	FZR1	0	chr19	3474000
-781	MOSC2	0	1661	MOSC1	0	chr1	219025000
86537	COL9A1	0	507	COL9A1	0	chr6	71069000
17786	ASPSCR1	0	22071	ASPSCR1	0	chr17	77546500
345	FGF21	0	1894	FGF21	0	chr19	53951500
37872	WLS	0	69341	WLS	0	chr1	68401500
-1645	GNB1	0	22125	CALML6	0	chr1	1814000
3453	C19orf63	0	3420	C19orf63	0	chr19	55675000
28531	PPP2R3B	0	24127	PPP2R3B	0	chrX	243500
29031	PPP2R3B	0	23627	PPP2R3B	0	chrX	244000
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23562	INTS1	0	10544	INTS1	0	chr7	1500000
6545	ADAMTS2	0	224935	ADAMTS2	0	chr5	178480000
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57852	C7orf50	0	83419	C7orf50	0	chr7	1061000
-96212	C1orf192	0	41328	FCGR2A	0	chr1	159700500
-96712	C1orf192	0	40828	FCGR2A	0	chr1	159701000
-97212	C1orf192	0	40328	FCGR2A	0	chr1	159701500
-97712	C1orf192	0	39828	FCGR2A	0	chr1	159702000
-98212	C1orf192	0	39328	FCGR2A	0	chr1	159702500
-98712	C1orf192	0	38828	FCGR2A	0	chr1	159703000
-99212	C1orf192	0	38328	FCGR2A	0	chr1	159703500
-99712	C1orf192	0	37828	FCGR2A	0	chr1	159704000
-361793	ZNF716	0	4490104	LOC643955	0	chr7	57899000
-362293	ZNF716	0	4489604	LOC643955	0	chr7	57899500
-138579	GFPT2	0	2522	CNOT6	0	chr5	179851500
-139079	GFPT2	0	2022	CNOT6	0	chr5	179852000
54219	FAM19A5	0	128750	FAM19A5	0	chr22	47405000
54719	FAM19A5	0	128250	FAM19A5	0	chr22	47405500
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-2408	GRIP2	0	107256	C3orf19	0	chr3	14561000
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2568	GNPTG	0	8853	GNPTG	0	chr16	1344500
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24495	THOP1	0	3599	THOP1	0	chr19	2761000
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-1000986	C1orf87	0	2533	NFIA	0	chr1	61313000
-36166	C14orf70	0	18005	DLK1	0	chr14	100245000
-125441	LOC100130238	0	84229	FBRSL1	0	chr12	131493000
23399	ABCA7	0	2070	ABCA7	0	chr19	1014500
23899	ABCA7	0	1570	ABCA7	0	chr19	1015000
251047	MAD1L1	0	166109	MAD1L1	0	chr7	2073000
251547	MAD1L1	0	165609	MAD1L1	0	chr7	2073500
-110645	SLC45A4	0	1329	LOC731779	0	chr8	142418500
8865	TFCP2L1	0	59748	TFCP2L1	0	chr2	121699500
9365	TFCP2L1	0	59248	TFCP2L1	0	chr2	121700000
25506	DNAH10	0	147718	DNAH10	0	chr12	122838500
-2061	CYB561	0	34165	ACE	0	chr17	58874000
6357	LRRC47	0	9928	LRRC47	0	chr1	3693000
-818	TTLL8	0	3946	MLC1	0	chr22	48836000
4573	MEX3A	0	5413	MEX3A	0	chr1	154313000
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1266	CHRFAM7A	0	31156	CHRFAM7A	0	chr15	28442000
28472	PSMD9	0	654	PSMD9	0	chr12	120839500
28972	PSMD9	0	154	PSMD9	0	chr12	120840000
-8523	GPER	0	50569	ZFAND2A	0	chr7	1108500
-9523	GPER	0	49569	ZFAND2A	0	chr7	1109500
705990	PTPRN2	0	342743	PTPRN2	0	chr7	157730500
-78	XAGE1D	0	105709	SSX8	0	chrX	52563000
-578	XAGE1D	0	105209	SSX8	0	chrX	52563500
-1061	CYB561	0	35165	ACE	0	chr17	58873000
-699	SRMS	0	4816	C20orf195	0	chr20	61650000
1067	LOC650623	0	4850	LOC650623	0	chr10	81434000
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12579	RFPL2	0	1718	RFPL2	0	chr22	30929000
5857	ATP11A	0	190983	ATP11A	0	chr13	112398500
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10065	GRM6	0	6730	GRM6	0	chr5	178348000

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152047	MAD1L1	0	265109	MAD1L1	0	chr7	1974000
152547	MAD1L1	0	264609	MAD1L1	0	chr7	1974500
20366	LMF1	0	96985	LMF1	0	chr16	864000
78834	ACTN4	0	4010	ACTN4	0	chr19	43909000
79334	ACTN4	0	3510	ACTN4	0	chr19	43909500
33705	ADAMTSL2	0	6961	ADAMTSL2	0	chr9	135423500
1796	GLYR1	0	42304	GLYR1	0	chr16	4795000
-372101	SNORD114-31	0	186812	DIO3OS	0	chr14	100901500
6961	FUT2	0	3003	FUT2	0	chr19	53898000
7461	FUT2	0	2503	FUT2	0	chr19	53898500
5959	LPCAT1	0	56576	LPCAT1	0	chr5	1520500
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6316	CASKIN1	0	12966	CASKIN1	0	chr16	2173500
6816	CASKIN1	0	12466	CASKIN1	0	chr16	2174000
-24174	CAMSAP1	0	1635	UBAC1	0	chr9	137963000
-24674	CAMSAP1	0	1135	UBAC1	0	chr9	137963500
-320	TACR2	0	34231	TSPAN15	0	chr10	70847000
82501	JPH3	0	12762	JPH3	0	chr16	86276500
3994	ABCA2	0	17695	ABCA2	0	chr9	139025500
4494	ABCA2	0	17195	ABCA2	0	chr9	139026000
-71082	PTENP1	0	2014	PRSS3	0	chr9	33738500
-5548	LPPR3	0	330	AZU1	0	chr19	778500
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2409	ALPP	0	1843	ALPP	0	chr2	232954000
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-168	PGBD3	0	84646	CHAT	0	chr10	50402500
128982	PTPRS	0	6314	PTPRS	0	chr19	5285500
129482	PTPRS	0	5814	PTPRS	0	chr19	5286000
-2446	C10orf93	0	142898	GPR123	0	chr10	134608500
679	GRAMD4	0	52352	GRAMD4	0	chr22	45402000
241	SEPT9	0	124273	SEPT9	0	chr17	72884000
-52870	LY6H	0	442	GPIHBP1	0	chr8	144366000
20607	PRDM15	0	57660	PRDM15	0	chr21	42115000
-168946	TP53TG3	0	31797	SLC6A10P	0	chr16	32764500
-169446	TP53TG3	0	31297	SLC6A10P	0	chr16	32765000
1000	NTN3	0	1647	NTN3	0	chr16	2462500
6606	LOC642852	0	2696	LOC642852	0	chr21	45539000
4153	ASMT	0	43474	ASMT	0	chrX	1678500
10391	ZNF707	0	543	ZNF707	0	chr8	144849000
10891	ZNF707	0	43	ZNF707	0	chr8	144849500
-1658	STK24	0	160057	SLC15A1	0	chr13	97974000
4644	C11orf35	0	1279	C11orf35	0	chr11	549500
-6285	DYSFIP1	0	1822	P4HB	0	chr17	77392500
-19521	SOX8	0	57584	LOC146336	0	chr16	996500
-20021	SOX8	0	57084	LOC146336	0	chr16	997000
119	C3orf77	0	90093	C3orf77	0	chr3	44258500
2022	LSP1	0	21569	LSP1	0	chr11	1848500
1975	C19orf34	0	48	C19orf34	0	chr19	1905500
2560	BRD1	0	48956	BRD1	0	chr22	48555500
-29587	NCRNA00175	0	851	COL18A1	0	chr21	45699000
-140639	IER5L	0	2115	C9orf106	0	chr9	131121000
-96227	RTN1	0	364881	C14orf135	0	chr14	59263500
-96727	RTN1	0	364381	C14orf135	0	chr14	59264000
-46597	PDGFB	0	21332	RPL3	0	chr22	38017500
3689	MRPL12	0	453	MRPL12	0	chr17	77284500
3079	LOC619207	0	11443	LOC619207	0	chr10	135120500

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-36117	ZNF624	0	363	CCDC144A	0	chr17	16534000
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23282	FLNC	0	5564	FLNC	0	chr7	128281000
24282	FLNC	0	4564	FLNC	0	chr7	128282000
9047	FZR1	0	4755	FZR1	0	chr19	3483000
-51370	LY6H	0	1942	GPIHBP1	0	chr8	144364500
-51870	LY6H	0	1442	GPIHBP1	0	chr8	144365000
37965	ANKRD11	0	184970	ANKRD11	0	chr16	87899500
-52074	VPREB1	0	462	LOC96610	0	chr22	20982000
533	GPR35	0	1342	GPR35	0	chr2	241218000
-7035	FAM132A	0	154	UBE2J2	0	chr1	1179000
346	UBE2J2	0	19597	UBE2J2	0	chr1	1179500
1346	UBE2J2	0	18597	UBE2J2	0	chr1	1180500
-123678	FAM196B	0	1494	FOXI1	0	chr5	169464000
-124178	FAM196B	0	994	FOXI1	0	chr5	169464500
27259	CACNA1H	0	41273	CACNA1H	0	chr16	1170500
-310272	SHH	0	417945	NCRNA00244	0	chr7	155608000
-310772	SHH	0	417445	NCRNA00244	0	chr7	155608500
2060	TCEB3B	0	986	TCEB3B	0	chr18	42815000
-1020253	GOT2	0	1898735	CDH8	0	chr16	58346000
-1020753	GOT2	0	1898235	CDH8	0	chr16	58346500
-3646	TFAMP1	0	124132	ELFN1	0	chr7	1626500
-4146	TFAMP1	0	123632	ELFN1	0	chr7	1627000
6126	TNNT3	0	13012	TNNT3	0	chr11	1903500
98445	ANO1	0	12799	ANO1	0	chr11	69700500
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21015	STK32C	0	79467	STK32C	0	chr10	133892000
11961	NDUFA13	0	573	NDUFA13	0	chr19	19499500
12461	NDUFA13	0	73	NDUFA13	0	chr19	19500000
3304	C19orf28	0	10071	C19orf28	0	chr19	3498500
13742	C11orf2	0	1756	C11orf2	0	chr11	64634000
1867	PRR23C	0	924	PRR23C	0	chr3	140245500
41	SH3TC1	0	41730	SH3TC1	0	chr4	8252000
541	SH3TC1	0	41230	SH3TC1	0	chr4	8252500
5708	TCF3	0	35286	TCF3	0	chr19	1566000
6208	TCF3	0	34786	TCF3	0	chr19	1566500
22688	FRMD1	0	688	FRMD1	0	chr6	168222000
23188	FRMD1	0	188	FRMD1	0	chr6	168222500
-1442	FRG2C	0	68218	ZNF717	0	chr3	75800500
33759	CACNA1H	0	34773	CACNA1H	0	chr16	1177000
5892	CHRNA4	0	12139	CHRNA4	0	chr20	61451000
27522	PI4KA	0	123570	PI4KA	0	chr22	19419500
4669	ZNF526	0	3193	ZNF526	0	chr19	47421000
52369	DIP2C	0	363108	DIP2C	0	chr10	362500
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14025	KCNQ2	0	24937	KCNQ2	0	chr20	61549500
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-129	E2F1	0	16210	PXMP4	0	chr20	31738000
-1766	GNG13	0	2943	PRR25	0	chr16	792500
13105	TBC1D14	0	110246	TBC1D14	0	chr4	6975500
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-303058	POTEG	0	95953	POTEM	0	chr14	18958000
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-304058	POTEG	0	94953	POTEM	0	chr14	18959000
87232	FAM120B	0	11162	FAM120B	0	chr6	170545000
-48036	GRTP1	0	9760	ADPRHL1	0	chr13	113114500

-48536	GRTP1	0	9260	ADPRHL1	0	chr13	113115000
-289	NUP133	0	7951	ABCB10	0	chr1	227711000
163	WDR88	0	43543	WDR88	0	chr19	38315000
23729	BRD3	0	13962	BRD3	0	chr9	135909000
-432	C2CD2	0	32508	ZNF295	0	chr21	42247500
-932	C2CD2	0	32008	ZNF295	0	chr21	42248000
88537	PCNT	0	33110	PCNT	0	chr21	46657000
11099	ANK1	0	232437	ANK1	0	chr8	41641000
11599	ANK1	0	231937	ANK1	0	chr8	41641500
-301954	SIX2	0	77323	SRBD1	0	chr2	45392000
50973	LOXHD1	0	41124	LOXHD1	0	chr18	42394500
-453274	ERICH1	0	312475	DLGAP2	0	chr8	1124500
-453774	ERICH1	0	311975	DLGAP2	0	chr8	1125000
-454274	ERICH1	0	311475	DLGAP2	0	chr8	1125500
22944	SLC19A1	0	4779	SLC19A1	0	chr21	45782000
93893	GNG4	0	8416	GNG4	0	chr1	233871500
94393	GNG4	0	7916	GNG4	0	chr1	233872000
894	SIRT7	0	5332	SIRT7	0	chr17	77464000
25491	CPNE9	0	592	CPNE9	0	chr3	9746000
-20529	BTBD6	0	43125	PACS2	0	chr14	104809000
5126	SCARF2	0	8146	SCARF2	0	chr22	19114000
-8202	CCDC81	0	9797	ME3	0	chr11	85820000
8591	CECR5	0	19177	CECR5	0	chr22	16007000
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24428	PCGF3	0	40427	PCGF3	0	chr4	714000
24928	PCGF3	0	39927	PCGF3	0	chr4	714500
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62177	HSPG2	0	52837	HSPG2	0	chr1	22083500
-21723	POTED	0	15991	LOC441956	0	chr21	13957500
-22223	POTED	0	15491	LOC441956	0	chr21	13958000
-371101	SNORD114-31	0	187812	DIO3OS	0	chr14	100900500
-582	LOC100127888	0	41633	NTSR1	0	chr20	60769000
-108614	C7orf28B	0	247770	C1GALT1	0	chr7	6941000
-109114	C7orf28B	0	247270	C1GALT1	0	chr7	6941500
4064	GRIN3B	0	5223	GRIN3B	0	chr19	955500
3688	C21orf128	0	2713	C21orf128	0	chr21	42399000
87362	LTBP2	0	26787	LTBP2	0	chr14	74122000
87862	LTBP2	0	26287	LTBP2	0	chr14	74122500
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101369	DIP2C	0	314108	DIP2C	0	chr10	411500
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-358	MBD1	0	210	CXXC1	0	chr18	46062500
-744410	MGC16025	0	22328	NDUFA10	0	chr2	240526500
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-364274	ERICH1	0	401475	DLGAP2	0	chr8	1035500
-2859	H19	0	128422	IGF2	0	chr11	1978500
701	LY6D	0	1010	LY6D	0	chr8	143864000
1201	LY6D	0	510	LY6D	0	chr8	143864500
8211	KIAA0415	0	7925	KIAA0415	0	chr7	4790000
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76007	SKI	0	5511	SKI	0	chr1	2226000
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15352	C7orf50	0	125919	C7orf50	0	chr7	1018500
15852	C7orf50	0	125419	C7orf50	0	chr7	1019000
1871	LYPD2	0	454	LYPD2	0	chr8	143830500
18407	CSNK1A1P1	0	999	CSNK1A1P1	0	chr15	34897000
-1	CSNK1A1P1	0	45935	LOC145845	0	chr15	34898000
-5204	ZNF586	0	21261	ZNF552	0	chr19	62989000
-5704	ZNF586	0	20761	ZNF552	0	chr19	62989500
60685	TMEM51	0	6060	TMEM51	0	chr1	15413500
-36624	IMPA2	0	186817	CIDEA	0	chr18	12057500
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-29689	NFATC1	0	120788	CTDP1	0	chr18	75420000
-30189	NFATC1	0	120288	CTDP1	0	chr18	75420500
-801	LHPP	0	4352	FAM53B	0	chr10	126293500
-1301	LHPP	0	3852	FAM53B	0	chr10	126294000
-28087	NCRNA00175	0	2351	COL18A1	0	chr21	45697500
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63	KCNQ3	0	351686	KCNQ3	0	chr8	133210500
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4846	OPLAH	0	4572	OPLAH	0	chr8	145183000
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2653	ASMT	0	44974	ASMT	0	chrY	1677000
2371	KIFC3	0	37430	KIFC3	0	chr16	56352000
2871	KIFC3	0	36930	KIFC3	0	chr16	56352500
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-1640	CXorf49,CXorf49B	0	43364	Xorf49,CXorf49B	0	chrX	70856500
-8119	IFT122	0	171	RHO	0	chr3	130730000
-961	MYO5A	0	17223	ARPP19	0	chr15	50609500
-900042	SVIP	0	767131	LUZP2	0	chr11	23708000
-900542	SVIP	0	766631	LUZP2	0	chr11	23708500
217163	VAV2	0	13267	VAV2	0	chr9	135834000
-479	SYT10	0	581982	ALG10	0	chr12	33484500
-17246	C17orf91	0	9379	SERPINF2	0	chr17	1583500
-17746	C17orf91	0	8879	SERPINF2	0	chr17	1584000
51	RASSF7	0	2524	RASSF7	0	chr11	551500
551	RASSF7	0	2024	RASSF7	0	chr11	552000
198547	MAD1L1	0	218609	MAD1L1	0	chr7	2020500
16835	PXDN	0	95798	PXDN	0	chr2	1631500
33364	RXRA	0	80753	RXRA	0	chr9	136391500
-26296	C2orf27B	0	319638	ANKRD30BL	0	chr2	132302000
-26796	C2orf27B	0	319138	ANKRD30BL	0	chr2	132302500
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-22493	PDGFA	0	7412	PRKAR1B	0	chr7	548500
759	C16orf42	0	1874	C16orf42	0	chr16	1340000
1259	C16orf42	0	1374	C16orf42	0	chr16	1340500
-917	MFI2	0	11827	DLG1	0	chr3	198242000
-21049	IL28B	0	2496	IL28A	0	chr19	44448500
-122129	KIAA1267	0	773	LRRC37A	0	chr17	41727500
-122629	KIAA1267	0	273	LRRC37A	0	chr17	41728000
227	LRRC37A	0	42418	LRRC37A	0	chr17	41728500
-1545	GMIP	0	9	ATP13A1	0	chr19	19617000
25495	THOP1	0	2599	THOP1	0	chr19	2762000

25995	THOP1	0	2099	THOP1	0	chr19	2762500
26495	THOP1	0	1599	THOP1	0	chr19	2763000
222	SPRED3	0	5711	SPRED3	0	chr19	43573000
7435	GIGYF1	0	2306	GIGYF1	0	chr7	100122500
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3468	C3orf27	0	619	C3orf27	0	chr3	129777000
3968	C3orf27	0	119	C3orf27	0	chr3	129777500
630026	AGAP1	0	1359	AGAP1	0	chr2	236697500
975	CPA1	0	6684	CPA1	0	chr7	129808500
7881	GLTSCR2	0	3627	GLTSCR2	0	chr19	52948500
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15406	ZNF488	0	3374	ZNF488	0	chr10	47990500
15906	ZNF488	0	2874	ZNF488	0	chr10	47991000
46283	SIN3B	0	4664	SIN3B	0	chr19	16847500
46783	SIN3B	0	4164	SIN3B	0	chr19	16848000
501	NCRNA00221	0	12574	NCRNA00221	0	chr14	106010000
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-57145	SLC45A4	0	54829	LOC731779	0	chr8	142365000
-4804	LOC642852	0	103024	COL18A1	0	chr21	45546500
-5304	LOC642852	0	102524	COL18A1	0	chr21	45547000
-5804	LOC642852	0	102024	COL18A1	0	chr21	45547500
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-245	C9orf173	0	1579	COBRA1	0	chr9	139268000
198	JAKMIP3	0	79802	JAKMIP3	0	chr10	133768500
89142	KCNT1	0	1813	KCNT1	0	chr9	137823000
89642	KCNT1	0	1313	KCNT1	0	chr9	137823500
3153	ASMT	0	44474	ASMT	0	chrX	1677500
3653	ASMT	0	43974	ASMT	0	chrX	1678000
32962	BANP	0	92925	BANP	0	chr16	86575500
337490	PTPRN2	0	711243	PTPRN2	0	chr7	157362000
892	SQSTM1	0	30181	SQSTM1	0	chr5	179167500
751	HPN	0	25315	HPN	0	chr19	40224000
70146	MYO1E	0	166363	MYO1E	0	chr15	57286000
167	LDHAL6B	0	1501	LDHAL6B	0	chr15	57286500
8426	JD7,JMJD7-PLA2G	0	1077	,JMJD7-PLA2G4B	0	chr15	39916000
8926	JD7,JMJD7-PLA2G	0	577	,JMJD7-PLA2G4B	0	chr15	39916500
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-75474	GALNT9	0	30049	LOC100130238	0	chr12	131332000
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19426	PMS2L11	0	23512	PMS2L11	0	chr7	76467500
2682	DCAF15	0	6256	DCAF15	0	chr19	13927000
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34141	RRP1B	0	2388	RRP1B	0	chr21	43938000
34641	RRP1B	0	1888	RRP1B	0	chr21	43938500
749	PRKCDBP	0	816	PRKCDBP	0	chr11	6297500
34450	FBXW10	0	887	FBXW10	0	chr17	18622500
34950	FBXW10	0	387	FBXW10	0	chr17	18623000
26416	ADPRHL1	0	4840	ADPRHL1	0	chr13	113151000
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-100586	SOCS6	0	2105894	CBLN2	0	chr18	66249000
-165774	ERICH1	0	599975	DLGAP2	0	chr8	837000
-166274	ERICH1	0	599475	DLGAP2	0	chr8	837500

6099	SPTB	0	50619	SPTB	0	chr14	64309000
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396281	RPTOR	0	25268	RPTOR	0	chr17	76529500
396781	RPTOR	0	24768	RPTOR	0	chr17	76530000
26588	PRKAR1B	0	136159	PRKAR1B	0	chr7	582500
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6482	PTPRS	0	128814	PTPRS	0	chr19	5163000
-2670	PALM	0	145	C19orf21	0	chr19	702000
-1129	KLHL38	0	26714	ANXA13	0	chr8	124735500
-61	HK3	0	5611	UIMC1	0	chr5	176259000
-18630	BAI1	0	47411	ARC	0	chr8	143642000
-19130	BAI1	0	46911	ARC	0	chr8	143642500
19418	SHC2	0	24996	SHC2	0	chr19	387000
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25902	ACRC	0	9658	ACRC	0	chrX	70740500
13916	LOC146336	0	732	LOC146336	0	chr16	1068000
14416	LOC146336	0	232	LOC146336	0	chr16	1068500
378281	RPTOR	0	43268	RPTOR	0	chr17	76511500
-17505	CTDP1	0	91655	KCNG2	0	chr18	75633000
-18005	CTDP1	0	91155	KCNG2	0	chr18	75633500
463301	FHOD3	0	19016	FHOD3	0	chr18	32595000
-61	CYB561	0	36165	ACE	0	chr17	58872000
-561	CYB561	0	35665	ACE	0	chr17	58872500
-292637	PITX1	0	7469	H2AFY	0	chr5	134690500
-293137	PITX1	0	6969	H2AFY	0	chr5	134691000
105	SLC25A34	0	4971	SLC25A34	0	chr1	15935500
-755	C1QTNF8	0	56241	CACNA1H	0	chr16	1087000
-1255	C1QTNF8	0	55741	CACNA1H	0	chr16	1087500
-481	C10orf125	0	3976	ECHS1	0	chr10	135022000
-981	C10orf125	0	3476	ECHS1	0	chr10	135022500
1152	SLC25A11	0	1563	SLC25A11	0	chr17	4782500
-895	AKT2	0	34810	C19orf47	0	chr19	45484000
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-226417	HIVEP3	0	8178	GUCA2B	0	chr1	42383500
-226917	HIVEP3	0	7678	GUCA2B	0	chr1	42384000
228	PNKP	0	6130	PNKP	0	chr19	55056500
2127	SCN1B	0	7693	SCN1B	0	chr19	40215500
-97531	KIAA0087	0	1514	C7orf71	0	chr7	26642500
-396314	AQP7P2	0	7249	FAM27B	0	chr9	67375500
-396814	AQP7P2	0	6749	FAM27B	0	chr9	67376000
28531	PPP2R3B	0	24127	PPP2R3B	0	chrY	243500
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-925	HSPA12A	0	141295	KIAA1598	0	chr10	118493000
1077	MUC20	0	15711	MUC20	0	chr3	196934500
2571	KIAA0664	0	19677	KIAA0664	0	chr17	2542000
1159	POLE3	0	2350	POLE3	0	chr9	115210500
5704	SPTBN2	0	30446	SPTBN2	0	chr11	66215000
6204	SPTBN2	0	29946	SPTBN2	0	chr11	66215500
6392	CHRNA4	0	11639	CHRNA4	0	chr20	61451500
11677	MUC6	0	12206	MUC6	0	chr11	1014500
12177	MUC6	0	11706	MUC6	0	chr11	1015000
229655	CLEC16A	0	8045	CLEC16A	0	chr16	11175500
5166	PANK4	0	12895	PANK4	0	chr1	2435000
5666	PANK4	0	12395	PANK4	0	chr1	2435500
5850	UNC93B1	0	7169	UNC93B1	0	chr11	67521000
6350	UNC93B1	0	6669	UNC93B1	0	chr11	67521500
2852	C7orf50	0	138419	C7orf50	0	chr7	1006000

3352	C7orf50	0	137919	C7orf50	0	chr7	1006500
7317	BTBD12	0	23086	BTBD12	0	chr16	3578500
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-39644	GRHL1	0	1632	KLF11	0	chr2	10099500
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24916	TECTA	0	63225	TECTA	0	chr11	120503500
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338781	RPTOR	0	82768	RPTOR	0	chr17	76472000
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53345	MCF2L	0	65863	MCF2L	0	chr13	112735000
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-21439	PHF21A	0	134803	CREB3L1	0	chr11	46121000
-12587	MRPL23	0	14015	LOC100133545	0	chr11	1947000
-490	FAM116B	0	28125	PPP6R2	0	chr22	49100500
-16416	TMEM121	0	370882	KIAA0125	0	chr14	105084000
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77997	EVL	0	826	EVL	0	chr14	99679500
9080	LRTM1	0	612	LRTM1	0	chr3	54936500
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-30563	LOC401010	0	635	TUBA3D	0	chr2	131949500
-31063	LOC401010	0	135	TUBA3D	0	chr2	131950000
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-170762	FZD10	0	1566	PIWIL1	0	chr12	129387000
-171262	FZD10	0	1066	PIWIL1	0	chr12	129387500
-36727	SBNO2	0	36797	STK11	0	chr19	1120000
-458112	TBC1D22A	0	857451	FAM19A5	0	chr22	46406500
3214	RAB35	0	18482	RAB35	0	chr12	119020500
-3033	IKZF3	0	980	ZPBP2	0	chr17	35277000
-3533	IKZF3	0	480	ZPBP2	0	chr17	35277500
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67574	CYTSB	0	82575	CYTSB	0	chr17	19998500
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621	SLC25A2	0	796	SLC25A2	0	chr5	140663000
1121	SLC25A2	0	296	SLC25A2	0	chr5	140663500
7273	PTOV1	0	2311	PTOV1	0	chr19	55053500
-12036	SLC30A3	0	292	DNAJC5G	0	chr2	27351500
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-4046	LOC650368	0	213289	TRPC2	0	chr11	3391000
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3532	SPG4P1Y,CSPG4P2	0	266	G4P1Y,CSPG4P2Y	0	chrY	24742500
-234	SPG4P1Y,CSPG4P2	0	22502	P3Y,GOLGA2P2Y	0	chrY	24743000
-734	SPG4P1Y,CSPG4P2	0	22002	P3Y,GOLGA2P2Y	0	chrY	24743500
298	WDR24	0	5401	WDR24	0	chr16	675000
6594	RHOBTB2	0	13653	RHOBTB2	0	chr8	22920000
7094	RHOBTB2	0	13153	RHOBTB2	0	chr8	22920500
-44547	ITPRIPL2	0	2138	SYT17	0	chr16	19085000
-45047	ITPRIPL2	0	1638	SYT17	0	chr16	19085500
-38441	LOC100130238	0	171229	FBRSL1	0	chr12	131406000
-38941	LOC100130238	0	170729	FBRSL1	0	chr12	131406500
36741	CARS2	0	27964	CARS2	0	chr13	110128500
37241	CARS2	0	27464	CARS2	0	chr13	110129000

37741	CARS2	0	26964	CARS2	0	chr13	110129500
-2166	SMYD3	0	120990	TFB2M	0	chr1	244649500
-6524	GLI4	0	7933	ZNF696	0	chr8	144437000
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32525	KCNQ2	0	6437	KCNQ2	0	chr20	61568000
12400	DENND4B	0	4778	DENND4B	0	chr1	152181000
1669	GGN	0	2008	GGN	0	chr19	43568500
498	CHST1	0	16248	CHST1	0	chr11	45627500
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-19330	SUZ12	0	767	LRRC37B	0	chr17	27371500
-19830	SUZ12	0	267	LRRC37B	0	chr17	27372000
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8824	CPNE7	0	12654	CPNE7	0	chr16	88178500
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6510	TSC2	0	34214	TSC2	0	chr16	2044500
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7510	TSC2	0	33214	TSC2	0	chr16	2045500
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-24990	NEU2	0	279	INPP5D	0	chr2	233633000
-592	KRT17	0	63652	EIF1	0	chr17	37035000
-1404	STIP1	0	727	FERMT3	0	chr11	63730000
-1904	STIP1	0	227	FERMT3	0	chr11	63730500
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3474	TGFB1I1	0	1281	TGFB1I1	0	chr16	31395500
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13018	PHRF1	0	22720	PHRF1	0	chr11	579500
13518	PHRF1	0	22220	PHRF1	0	chr11	580000
41554	CCDC144B	0	570	CCDC144B	0	chr17	18469000
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13072	MSLNL	0	427	MSLNL	0	chr16	772500
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36965	ANKRD11	0	185970	ANKRD11	0	chr16	87898500
16637	WDR90	0	1830	WDR90	0	chr16	656000
17137	WDR90	0	1330	WDR90	0	chr16	656500
94547	MAD1L1	0	322609	MAD1L1	0	chr7	1916500
95047	MAD1L1	0	322109	MAD1L1	0	chr7	1917000
3360	IRF3	0	2944	IRF3	0	chr19	54858000
3860	IRF3	0	2444	IRF3	0	chr19	54858500
7826	C16orf88	0	3993	C16orf88	0	chr16	19633000
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3404	EFNB2	0	41838	EFNB2	0	chr13	105943500
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126756	JAK2	0	16182	JAK2	0	chr9	5102000
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29979	ZFR2	0	35027	ZFR2	0	chr19	3785000
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121	CNTD1	0	12631	CNTD1	0	chr17	38204500
48332	RAB11FIP3	0	48481	RAB11FIP3	0	chr16	464000
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21088	PRKAR1B	0	141659	PRKAR1B	0	chr7	577000
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-136845	C2orf85	0	78516	LOC728323	0	chr2	242601000
-969	C21orf84	0	49999	HSF2BP	0	chr21	43723500
11900	SBF1	0	16320	SBF1	0	chr22	49244000
13400	SBF1	0	14820	SBF1	0	chr22	49245500
15701	THBS2	0	22562	THBS2	0	chr6	169373500
-20570	UVRAG	0	21517	WNT11	0	chr11	75553500
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23782	FLNC	0	5064	FLNC	0	chr7	128281500
64874	VIPR2	0	51910	VIPR2	0	chr7	158578500
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-338	KRT34	0	11002	KRT31	0	chr17	36792500
14607	PRDM15	0	63660	PRDM15	0	chr21	42109000
-30682	C19orf21	0	2391	PTBP1	0	chr19	746000
5417	NFIX	0	97610	NFIX	0	chr19	12973000
-927	CTRB2	0	10884	CTRB1	0	chr16	73799500
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45819	PIP5K1C	0	24445	PIP5K1C	0	chr19	3627000
46319	PIP5K1C	0	23945	PIP5K1C	0	chr19	3627500
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11134	SH3GL1	0	28971	SH3GL1	0	chr19	4322500
91205	RASA3	0	59697	RASA3	0	chr13	113856500
91705	RASA3	0	59197	RASA3	0	chr13	113857000
85	KRT86	0	7214	KRT86	0	chr12	50982000
45489	COLEC11	0	3922	COLEC11	0	chr2	3666000
505	CAV3	0	12451	CAV3	0	chr3	8751000
9052	PSME3	0	1303	PSME3	0	chr17	38248000
79857	ATP11A	0	116983	ATP11A	0	chr13	112472500
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-247885	FAM92B	0	251029	KIAA0182	0	chr16	83951500
-178338	MGC45800	0	1130	ODZ3	0	chr4	183481000
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-17961	STON1	0	951	GTF2A1L	0	chr2	48697500
-18461	STON1	0	451	GTF2A1L	0	chr2	48698000
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728	GPT	0	2363	GPT	0	chr8	145701000
-99592	CALCA	0	1721	CALCB	0	chr11	15050000
-100092	CALCA	0	1221	CALCB	0	chr11	15050500
2215	FAM78A	0	16227	FAM78A	0	chr9	133125500
2715	FAM78A	0	15727	FAM78A	0	chr9	133126000
57457	AGPAT3	0	64903	AGPAT3	0	chr21	44167000
57957	AGPAT3	0	64403	AGPAT3	0	chr21	44167500
16107	MMP17	0	7269	MMP17	0	chr12	130895000
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-341	SLC26A9	0	141033	FAM72A	0	chr1	204164500
2198	CCDC17	0	1816	CCDC17	0	chr1	45860500
2698	CCDC17	0	1316	CCDC17	0	chr1	45861000
-23957	FLJ40292	0	89061	CACNA1B	0	chr9	139803000
1422	ST8SIA5	0	76537	ST8SIA5	0	chr18	42514500
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-7245	DCAF12	0	45010	UBAP1	0	chr9	34124000
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25593	SPIRE2	0	17228	SPIRE2	0	chr16	88448000
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-1051	EEF1A2	0	20576	PPDPF	0	chr20	61602000
-1551	EEF1A2	0	20076	PPDPF	0	chr20	61602500
747	C19orf76	0	1559	C19orf76	0	chr19	54884500
-699280	TP53TG3	0	389802	UBE2MP1	0	chr16	33871500
-699780	TP53TG3	0	389302	UBE2MP1	0	chr16	33872000
52781	ZDHHC11	0	2601	ZDHHC11	0	chr5	901500
-1329	CIRBP	0	1019	C19orf24	0	chr19	1225500
-666	NTAN1	0	3379	RRN3	0	chr16	15058000
-1166	NTAN1	0	2879	RRN3	0	chr16	15058500
-27597	TPTE2	0	69379	MPHOSPH8	0	chr13	19036500
-28097	TPTE2	0	68879	MPHOSPH8	0	chr13	19037000
24539	DNAJC5	0	14339	DNAJC5	0	chr20	62021500
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40540	KNDC1	0	25406	KNDC1	0	chr10	134864500
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10569	ATAD3C	0	9901	ATAD3C	0	chr1	1385500
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13155	PLIN3	0	16176	PLIN3	0	chr19	4802500
13655	PLIN3	0	15676	PLIN3	0	chr19	4803000
21959	LPCAT1	0	40576	LPCAT1	0	chr5	1536500
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-13578	ZBTB1	0	1938	HSPA2	0	chr14	64075000
306	KRTAP17-1	0	473	KRTAP17-1	0	chr17	36725000
219	GGTLC2	0	1368	GGTLC2	0	chr22	21319000
-553050	FOXD2	0	107973	SKINTL	0	chr1	48232000
-553550	FOXD2	0	107473	SKINTL	0	chr1	48232500
-1849	TTTY23B,TTTY23	0	763	TSPY2	0	chrY	6173500
-2349	TTTY23B,TTTY23	0	263	TSPY2	0	chrY	6174000
7531	PPP2R3B	0	45127	PPP2R3B	0	chrY	222500
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67037	PCNT	0	54610	PCNT	0	chr21	46635500
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1755	NEU4	0	4907	NEU4	0	chr2	242402500
2255	NEU4	0	4407	NEU4	0	chr2	242403000
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6468	MYBPC3	0	14829	MYBPC3	0	chr11	47316000
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-53681	FRA10AC1	0	1555	LGI1	0	chr10	95506000
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6775	PNPLA7	0	83807	PNPLA7	0	chr9	139481000
7783	CSPG4	0	30744	CSPG4	0	chr15	73761500
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158005	SHROOM2	0	4981	SHROOM2	0	chrX	9872500
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10783	ASB10	0	1352	ASB10	0	chr7	150514500
872	ARL16	0	1859	ARL16	0	chr17	77259500
21076	BPHL	0	13429	BPHL	0	chr6	3085000
21576	BPHL	0	12929	BPHL	0	chr6	3085500
-42113	GTPBP6	0	1969	PPP2R3B	0	chrX	213000
14645	METRNL	0	511	METRNL	0	chr17	78645500
15145	METRNL	0	11	METRNL	0	chr17	78646000
1114	C17orf70	0	11348	C17orf70	0	chr17	77118500
8082	TRIM3	0	17281	TRIM3	0	chr11	6434500
-2455	MUC4	0	48632	TNK2	0	chr3	197026000
43741	PAK4	0	9886	PAK4	0	chr19	44352000
28179	ATXN1	0	434200	ATXN1	0	chr6	16435500

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27179	ATXN1	0	435200	ATXN1	0	chr6	16434500
13759	CACNA1H	0	54773	CACNA1H	0	chr16	1157000
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4130	DTX3	0	850	DTX3	0	chr12	56289000
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-967	LAIR1	0	48946	TTYH1	0	chr19	59569500
-9245	PGA4	0	244	PGA5	0	chr11	60765000
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-6106	DNAJB6	0	115510	PTPRN2	0	chr7	156909000
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13995	THOP1	0	14099	THOP1	0	chr19	2750500
11681	MAP2K2	0	22126	MAP2K2	0	chr19	4053000
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15776	DEAF1	0	35740	DEAF1	0	chr11	650000
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378	CHTF18	0	9075	CHTF18	0	chr16	779000
878	CHTF18	0	8575	CHTF18	0	chr16	779500
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20154	RPL23AP53	0	3818	RPL23AP53	0	chr8	168500
20654	RPL23AP53	0	3318	RPL23AP53	0	chr8	169000
23319	PIP5K1C	0	46945	PIP5K1C	0	chr19	3604500
-33255	C1QTNF8	0	23741	CACNA1H	0	chr16	1119500
-453	GCK	0	11102	YKT6	0	chr7	44196000
6866	ZNF213	0	805	ZNF213	0	chr16	3132000
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7314	PI16	0	3091	PI16	0	chr6	37037500
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52986	ZFPM1	0	28575	ZFPM1	0	chr16	87100500
-863905	C13orf16	0	111413	SOX1	0	chr13	111658500
-227887	RD20A3,ANKRD2	0	582063	PGM5P2	0	chr9	67788000
-18278	LOC254559	0	54643	RHCG	0	chr15	87761000
-1369	ICMT	0	6848	HES3	0	chr1	6220000
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7131	GALNT9	0	2526	GALNT9	0	chr12	131254000
-25701	WNT9A	0	33374	WNT3A	0	chr1	226228000
1694	PRPF38A	0	12080	PRPF38A	0	chr1	52644500
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7869	GDPD3	0	879	GDPD3	0	chr16	30031500
500	NTN3	0	2147	NTN3	0	chr16	2462000
73369	DIP2C	0	342108	DIP2C	0	chr10	383500
832	C8orf51	0	1180	C8orf51	0	chr8	144521000
245490	PTPRN2	0	803243	PTPRN2	0	chr7	157270000
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-20092	CDC7	0	89155	HSP90B3P	0	chr1	91784000
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32916	ARHGAP22	0	126144	ARHGAP22	0	chr10	49357000
-25293	UPK1A	0	9169	ZBTB32	0	chr19	40886500

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23065	LOC654342	0	202	LOC654342	0	chr2	91211500
366	DNAJB3	0	900	DNAJB3	0	chr2	234316500
-2952	C19orf34	0	27946	BTBD2	0	chr19	1908500
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-9023	GPER	0	50069	ZFAND2A	0	chr7	1109000
38242	C20orf117	0	44190	C20orf117	0	chr20	34877500
17965	ANKRD11	0	204970	ANKRD11	0	chr16	87879500
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6618	PRIC285	0	9536	PRIC285	0	chr20	61666500
7118	PRIC285	0	9036	PRIC285	0	chr20	61667000
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29252	PIAS4	0	1067	PIAS4	0	chr19	3988000
29752	PIAS4	0	567	PIAS4	0	chr19	3988500
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7618	PRIC285	0	8536	PRIC285	0	chr20	61667500
-946070	FAM75A7	0	38588	LOC442421	0	chr9	66195500
-946570	FAM75A7	0	38088	LOC442421	0	chr9	66196000
2587	TBC1D16	0	93242	TBC1D16	0	chr17	75531000
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-19794	MUC6	0	18374	MUC2	0	chr11	1046500
3724	TMEM8A	0	7451	TMEM8A	0	chr16	364500
-1254	OTOS	0	293787	GPC1	0	chr2	240730000
17531	PPP2R3B	0	35127	PPP2R3B	0	chrX	232500
-108	CD164L2	0	9238	GPR3	0	chr1	27582500
27135	AGRN	0	8855	AGRN	0	chr1	972500
-19016	ZNF480	0	493	ZNF610	0	chr19	57540000
7	ZNF610	0	21423	ZNF610	0	chr19	57540500
9467	ANO8	0	2138	ANO8	0	chr19	17304500
35007	AP3D1	0	15556	AP3D1	0	chr19	2087000
16356	ZNF331	0	25835	ZNF331	0	chr19	58749500
8017	OBSCN	0	145074	OBSCN	0	chr1	226470500
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7714	GJB1	0	2290	GJB1	0	chrX	70359500
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-265277	RASSF10	0	1400	ARNTL	0	chr11	13254500
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-1232	C1orf111	0	819	C1orf226	0	chr1	160614500
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5607	CANT1	0	12433	CANT1	0	chr17	74505000
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13960	EEF1D	0	3988	EEF1D	0	chr8	144747000
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3346	ICAM5	0	3454	ICAM5	0	chr19	10265000
-75432	C13orf31	0	52970	NCRNA00284	0	chr13	43441500
-4379	ZNF212	0	2194	ZNF783	0	chr7	148588000
-10933	CCDC77	0	6803	B4GALNT3	0	chr12	433000
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11109	PTBP1	0	3827	PTBP1	0	chr19	759500
-220072	LOC116437	0	278087	SFRS8	0	chr12	130483500
-13184	C21orf70	0	9056	NCRNA00162	0	chr21	45234500
-13684	C21orf70	0	8556	NCRNA00162	0	chr21	45235000
-75712	C1orf192	0	61828	FCGR2A	0	chr1	159680000
-76212	C1orf192	0	61328	FCGR2A	0	chr1	159680500
-76712	C1orf192	0	60828	FCGR2A	0	chr1	159681000
-77212	C1orf192	0	60328	FCGR2A	0	chr1	159681500
-77712	C1orf192	0	59828	FCGR2A	0	chr1	159682000
-78212	C1orf192	0	59328	FCGR2A	0	chr1	159682500
8298	C21orf29	0	205423	C21orf29	0	chr21	44750500
4974	ZIC4	0	15597	ZIC4	0	chr3	148591500
178	UGT1A7	0	91184	UGT1A7	0	chr2	234255500
-38714	MGC12916	0	885320	PMP22	0	chr17	14188500
-39714	MGC12916	0	884320	PMP22	0	chr17	14189500
-1800	WDR45L	0	6732	RAB40B	0	chr17	78201500
12837	BAIAP3	0	1943	BAIAP3	0	chr16	1337500
13337	BAIAP3	0	1443	BAIAP3	0	chr16	1338000
16354	FIBCD1	0	20276	FIBCD1	0	chr9	132784000
16854	FIBCD1	0	19776	FIBCD1	0	chr9	132784500
-2723579	NLGN4Y	0	7934	NCRNA00230B	0	chrY	18188500
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-87942	FAM178B	0	97549	FAHD2B	0	chr2	97015500
10347	CAMSAP1	0	88326	CAMSAP1	0	chr9	137850500
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2436	DIRAS1	0	4390	DIRAS1	0	chr19	2668000
2936	DIRAS1	0	3890	DIRAS1	0	chr19	2668500
45366	LMF1	0	71985	LMF1	0	chr16	889000
45866	LMF1	0	71485	LMF1	0	chr16	889500
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68991	ABR	0	114866	ABR	0	chr17	922500
-372192	FAM150B	0	7472	TMEM18	0	chr2	650500
-1670	PALM	0	1145	C19orf21	0	chr19	701000
2449	GPS1	0	3135	GPS1	0	chr17	77605500
-239577	---	0	103767	ZNF479	0	chr7	57087500
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6572	CHST5	0	69	CHST5	0	chr16	74126500
250961	GMDS	0	370845	GMDS	0	chr6	1820000
-1425	HSPA12A	0	140795	KIAA1598	0	chr10	118493500
-1925	HSPA12A	0	140295	KIAA1598	0	chr10	118494000
-13033	CEACAM19	0	1697	CEACAM16	0	chr19	49892500
-879	SNORA72	0	21425	C8orf47	0	chr8	99124500
22418	SMTNL2	0	1363	SMTNL2	0	chr17	4457000
38198	FCGBP	0	48373	FCGBP	0	chr19	45084000
38698	FCGBP	0	47873	FCGBP	0	chr19	45084500
-2069	STAT3	0	11993	PTRF	0	chr17	37796000
-587	NCRNA00175	0	29851	COL18A1	0	chr21	45670000
894	ZNF513	0	2597	ZNF513	0	chr2	27454500
1394	ZNF513	0	2097	ZNF513	0	chr2	27455000
4966	MOBKL2A	0	20269	MOBKL2A	0	chr19	2027000
40214	TERT	0	1662	TERT	0	chr5	1346500
6075	GTPBP6	0	3387	GTPBP6	0	chrX	167500
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10181	MAP2K2	0	23626	MAP2K2	0	chr19	4051500
456	SLC25A6	0	5498	SLC25A6	0	chrY	1465500
-806	PTGIR	0	8172	GNG8	0	chr19	51821000
2924	ALPI	0	986	ALPI	0	chr2	233032000
275801	VPS13D	0	6185	VPS13D	0	chr1	12488500
276301	VPS13D	0	5685	VPS13D	0	chr1	12489000
1669	APCDD1L	0	53855	APCDD1L	0	chr20	56469500
32701	THBS2	0	5562	THBS2	0	chr6	169390500
11102	GPR123	0	32669	GPR123	0	chr10	134762500
-5777	TWF2	0	1264	PPM1M	0	chr3	52254000
4792	OBSL1	0	15755	OBSL1	0	chr2	220128500
15661	LMTK3	0	12258	LMTK3	0	chr19	53696000
16161	LMTK3	0	11758	LMTK3	0	chr19	53696500
35507	AP3D1	0	15056	AP3D1	0	chr19	2087500
36007	AP3D1	0	14556	AP3D1	0	chr19	2088000
344	PACSIN3	0	8534	PACSIN3	0	chr11	47156000
2990	ARSD	0	22392	ARSD	0	chrX	2835000
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-1294	FUT10	0	10726	MAK16	0	chr8	33451500
-1794	FUT10	0	10226	MAK16	0	chr8	33452000
-7793	CYTSA	0	2029	ADORA2A	0	chr22	23151500
112156	ASAP2	0	86767	ASAP2	0	chr2	9376500
112656	ASAP2	0	86267	ASAP2	0	chr2	9377000
416025	ODZ4	0	371343	ODZ4	0	chr11	78458000
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-3418	IL3RA	0	44	SLC25A6	0	chrX	1465000
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-605	ARHGAP29	0	180020	ABCD3	0	chr1	94476500
84	IGFALS	0	3235	IGFALS	0	chr16	1780500
2854	PIM3	0	723	PIM3	0	chr22	48743000
11292	OBSL1	0	9255	OBSL1	0	chr2	220135000
11792	OBSL1	0	8755	OBSL1	0	chr2	220135500
879030	CAMTA1	0	105351	CAMTA1	0	chr1	7647000
879530	CAMTA1	0	104851	CAMTA1	0	chr1	7647500
-5183	ZFP37	0	42826	NCRNA00256B	0	chr9	114864000
119857	ATP11A	0	76983	ATP11A	0	chr13	112512500
-4142	NCRNA00092	0	209409	HSD17B3	0	chr9	97828000
-4642	NCRNA00092	0	208909	HSD17B3	0	chr9	97828500
-243598	AQP9	0	2466	LIPC	0	chr15	56509000
93558	BCOR	0	32526	BCOR	0	chrX	39889000
-150478	LRPAP1	0	83593	ADRA2C	0	chr4	3654500

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34678	LOC100133669	0	1682	LOC100133669	0	chr8	144169500
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-130464	PLAC4	0	1030	FAM3B	0	chr21	41609500
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-964	ANGEL1	0	12477	C14orf166B	0	chr14	76350000
794	CGB8	0	680	CGB8	0	chr19	54243500
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-2921	VAMP3	0	349	PER3	0	chr1	7767000
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2657	RPS6KA2	0	450261	RPS6KA2	0	chr6	166745500
3157	RPS6KA2	0	449761	RPS6KA2	0	chr6	166746000
885	STUB1	0	1769	STUB1	0	chr16	671000
1385	STUB1	0	1269	STUB1	0	chr16	671500
94207	RPH3AL	0	46076	RPH3AL	0	chr17	156500
94707	RPH3AL	0	45576	RPH3AL	0	chr17	157000
703	ZNF581	0	1301	ZNF581	0	chr19	60847500
1203	ZNF581	0	801	ZNF581	0	chr19	60848000
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-10061	SCXA,SCXB	0	13077	HSF1	0	chr8	145473000
582	HMHB1	0	7977	HMHB1	0	chr5	143172500
-1058916	GALR1	0	671262	SALL3	0	chr18	74170000
-1059416	GALR1	0	670762	SALL3	0	chr18	74170500
7564	GRIN3B	0	1723	GRIN3B	0	chr19	959000
8064	GRIN3B	0	1223	GRIN3B	0	chr19	959500
-17309	RREB1	0	12286	SSR1	0	chr6	7214000
-136693	RMI1	0	137411	SLC28A3	0	chr9	85945500
-8998	ATP4B	0	97	GRK1	0	chr13	113369500
-35484	PAX4	0	937	SND1	0	chr7	127078500
-988	POM121L1P	0	781	GGTLC2	0	chr22	21318000
95877	KDM4B	0	88608	KDM4B	0	chr19	5016000
96377	KDM4B	0	88108	KDM4B	0	chr19	5016500
22651	SNAPC4	0	210	SNAPC4	0	chr9	138412500
-22039	GPR133	0	1508	LOC116437	0	chr12	130214000
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29264	NCK2	0	13160	NCK2	0	chr2	105864000
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43	OR1N1	0	893	OR1N1	0	chr9	124328500
336	USF1	0	6381	USF1	0	chr1	159276000
33607	PRDM15	0	44660	PRDM15	0	chr21	42128000
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13088	EHD2	0	16703	EHD2	0	chr19	52921500
51679	GRAMD4	0	1352	GRAMD4	0	chr22	45453000
52179	GRAMD4	0	852	GRAMD4	0	chr22	45453500
92587	NCOR2	0	118602	NCOR2	0	chr12	123467500
31604	FAM73A	0	67169	FAM73A	0	chr1	78049500
32104	FAM73A	0	66669	FAM73A	0	chr1	78050000
140428	ADARB2	0	411218	ADARB2	0	chr10	1358500
2118	EGFL8	0	1540	EGFL8	0	chr6	32242500
2618	EGFL8	0	1040	EGFL8	0	chr6	32243000
98394	ZNF516	0	5043	ZNF516	0	chr18	72299000
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-204	TCEB3CL,TCEB3C	0	4070	TCEB3CL,TCEB3C	0	chr18	42804500
-704	TCEB3CL,TCEB3C	0	3570	TCEB3CL,TCEB3C	0	chr18	42805000
-1204	TCEB3CL,TCEB3C	0	3070	TCEB3CL,TCEB3C	0	chr18	42805500
-1704	TCEB3CL,TCEB3C	0	2570	TCEB3CL,TCEB3C	0	chr18	42806000
-2204	TCEB3CL,TCEB3C	0	2070	TCEB3CL,TCEB3C	0	chr18	42806500
174606	CELSR1	0	1731	CELSR1	0	chr22	45310000
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777	ZFP64	0	39931	ZFP64	0	chr20	50202000
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-731	CD7	0	2688	SECTM1	0	chr17	77869500
-254195	FOXL1	0	493444	FBXO31	0	chr16	85427000
308217	IGF1R	0	6782	IGF1R	0	chr15	97318500
24733	CBFA2T3	0	41609	CBFA2T3	0	chr16	87493500
25233	CBFA2T3	0	41109	CBFA2T3	0	chr16	87494000
-49263	PPP2R5C	0	8617	DYNC1H1	0	chr14	101492000
-228900	PSAPL1	0	90216	AFAP1AS	0	chr4	7716500
-229400	PSAPL1	0	89716	AFAP1AS	0	chr4	7717000
-19620	RAB12	0	58368	KIAA0802	0	chr18	8649000
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700	ZAP70	0	4755	ZAP70	0	chr2	97718000
8618	NDUFS7	0	3088	NDUFS7	0	chr19	1343500
9118	NDUFS7	0	2588	NDUFS7	0	chr19	1344000
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-111145	SLC45A4	0	829	LOC731779	0	chr8	142419000
-1570	ANGPT1	0	399720	RSPO2	0	chr8	108581000
-106575	BANP	0	246379	ZNF469	0	chr16	86775000
-107075	BANP	0	245879	ZNF469	0	chr16	86775500
-963	NKX2-8	0	74032	PAX9	0	chr14	36122500
9129	MUC5B	0	29982	MUC5B	0	chr11	1210000
9629	MUC5B	0	29482	MUC5B	0	chr11	1210500
-21403	RFX1	0	516	RLN3	0	chr19	13999500
-21903	RFX1	0	16	RLN3	0	chr19	14000000
-63630	PEX10	0	113	PLCH2	0	chr1	2397500
13927	ATP8B3	0	16270	ATP8B3	0	chr19	1747000
14427	ATP8B3	0	15770	ATP8B3	0	chr19	1747500
39	UBE2S	0	6637	UBE2S	0	chr19	60604500
23240	ZNF362	0	20907	ZNF362	0	chr1	33518000
-1578	NPPA	0	8107	NPPB	0	chr1	11832000
18407	SIGLEC5	0	539	SIGLEC5	0	chr19	56825000
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-12625	CASP8AP2	0	7408	GJA10	0	chr6	90653500
43	ISLR	0	2265	ISLR	0	chr15	72254000
12964	ARID3A	0	33803	ARID3A	0	chr19	890000
-186661	HTR1B	0	1217407	IRAK1BP1	0	chr6	78416500
-76300	HERC2P2	0	355546	MKRN3	0	chr15	21006000
-76800	HERC2P2	0	355046	MKRN3	0	chr15	21006500
6464	ARID3A	0	40303	ARID3A	0	chr19	883500
-124120	IRX4	0	739280	IRX2	0	chr5	2060000
-124620	IRX4	0	738780	IRX2	0	chr5	2060500
4326	RFX2	0	113164	RFX2	0	chr19	5948500
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-8768	AGPAT2	0	16344	FAM69B	0	chr9	138710500
45	PRLH	0	557	PRLH	0	chr2	238140000
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16291	SLC6A19	0	7230	SLC6A19	0	chr5	1271000
37374	SCARB1	0	48972	SCARB1	0	chr12	123865500
70297	GPR116	0	32134	GPR116	0	chr6	46998500
12021	FSCN1	0	1812	FSCN1	0	chr7	5611000
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76545	FOXK1	0	12600	FOXK1	0	chr7	4765000
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12466	PLXNB2	0	7336	PLXNB2	0	chr22	49068000
12074	KCNH6	0	10834	KCNH6	0	chr17	58966500
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3535	PDE6B	0	14180	PDE6B	0	chr4	640500
4035	PDE6B	0	13680	PDE6B	0	chr4	641000
4202	AMPD2	0	7200	AMPD2	0	chr1	109969000
4702	AMPD2	0	6700	AMPD2	0	chr1	109969500
-16023	GPER	0	43069	ZFAND2A	0	chr7	1116000
74507	SKI	0	7011	SKI	0	chr1	2224500
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-21690	TET3	0	5535	BOLA3	0	chr2	74210500
-1034	USP28	0	28298	HTR3B	0	chr11	113252500
182219	FAM19A5	0	750	FAM19A5	0	chr22	47533000
27048	PALM	0	12330	PALM	0	chr19	687000
13527	MUC5AC	0	99302	MUC5AC	0	chr11	1146000
-39679	S3,LIMS3-LOC44	0	1555	LOC440895	0	chr2	110061000
20289	PKD1	0	26900	PKD1	0	chr16	2099000
20789	PKD1	0	26400	PKD1	0	chr16	2099500
10023	PLOD3	0	1731	PLOD3	0	chr7	100646000
10660	LAMB3	0	25802	LAMB3	0	chr1	207865500
10223	GOLGA8B	0	514	GOLGA8B	0	chr15	32615000
-1752	RASL10A	0	10168	AP1B1	0	chr22	28043500
-2252	RASL10A	0	9668	AP1B1	0	chr22	28044000
-2669	HEATR7A	0	2004	SCXA,SCXB	0	chr8	145391500
-3169	HEATR7A	0	1504	SCXA,SCXB	0	chr8	145392000
-32147	CCNY	0	1343	GJD4	0	chr10	35933000
-33147	CCNY	0	343	GJD4	0	chr10	35934000
157	GJD4	0	3369	GJD4	0	chr10	35934500
-81263	C3orf32	0	495	CAV3	0	chr3	8750000
5	CAV3	0	12951	CAV3	0	chr3	8750500
-156416	TMEM121	0	230882	KIAA0125	0	chr14	105224000
-156916	TMEM121	0	230382	KIAA0125	0	chr14	105224500
6466	PLXNB2	0	13336	PLXNB2	0	chr22	49062000
214	TERT	0	41662	TERT	0	chr5	1306500
42310	AATK	0	6467	AATK	0	chr17	76748000
12010	PLCXD1	0	15020	PLCXD1	0	chrY	145000
12510	PLCXD1	0	14520	PLCXD1	0	chrY	145500
56530	SRC	0	2735	SRC	0	chr20	35464500
57030	SRC	0	2235	SRC	0	chr20	35465000
-151526	ZNF599	0	2146	ZNF30	0	chr19	40107500
-152026	ZNF599	0	1646	ZNF30	0	chr19	40108000
-669	MFNG	0	3345	CARD10	0	chr22	36213000
108979	HRNBP3	0	284158	HRNBP3	0	chr17	74706000
9208	GRK6	0	6956	GRK6	0	chr5	176795500
9708	GRK6	0	6456	GRK6	0	chr5	176796000
894	ARHGDIG	0	1504	ARHGDIG	0	chr16	271500
255436	FAM107B	0	902	FAM107B	0	chr10	14856000
255936	FAM107B	0	402	FAM107B	0	chr10	14856500
-98	FAM107B	0	44256	CDNF	0	chr10	14857000
9296	RAB11B	0	4817	RAB11B	0	chr19	8370500
9796	RAB11B	0	4317	RAB11B	0	chr19	8371000

111583	VIT	0	6434	VIT	0	chr2	36889000
112083	VIT	0	5934	VIT	0	chr2	36889500
355897	PRDM16	0	13545	PRDM16	0	chr1	3331500
17123	MAG	0	4547	MAG	0	chr19	40492000
17623	MAG	0	4047	MAG	0	chr19	40492500
18123	MAG	0	3547	MAG	0	chr19	40493000
12429	---	0	750	---	0	chr4	1192000
-1250	---	0	1227	CTBP1	0	chr4	1194000
2060	PTX4	0	469	PTX4	0	chr16	1478000
147479	ZNF423	0	188919	ZNF423	0	chr16	48229500
2621	ACVRL1	0	8412	ACVRL1	0	chr12	50595000
3121	ACVRL1	0	7912	ACVRL1	0	chr12	50595500
-25288	IRF8	0	383956	LOC732275	0	chr16	84539000
-6140	GALNT11	0	6442	MLL3	0	chr7	151456500
20237	DNAH2	0	93783	DNAH2	0	chr17	7584000
20737	DNAH2	0	93283	DNAH2	0	chr17	7584500
21237	DNAH2	0	92783	DNAH2	0	chr17	7585000
2336	SNX8	0	57125	SNX8	0	chr7	2263500
-1387	TNFRSF14	0	20108	C1orf93	0	chr1	2488000
20599	TFAP2A	0	2283	TFAP2A	0	chr6	10525500
-99	WDR24	0	2005	FBXL16	0	chr16	680500
-599	WDR24	0	1505	FBXL16	0	chr16	681000
-131	LOC643955	0	903015	ZNF735	0	chr7	62402000
4922	ADSSL1	0	18192	ADSSL1	0	chr14	104266500
-32882	NPHP4	0	966	KCNAB2	0	chr1	6008000
8517	OBSCN	0	144574	OBSCN	0	chr1	226471000
5936	TBL3	0	752	TBL3	0	chr16	1968000
7	PRM2	0	838	PRM2	0	chr16	11277000
14289	PKD1	0	32900	PKD1	0	chr16	2093000
14789	PKD1	0	32400	PKD1	0	chr16	2093500
-64069	KRTAP9-4	0	194	KRTAP17-1	0	chr17	36724500
15695	LOC154822	0	2189	LOC154822	0	chr7	158509500
15225	LSP1	0	24069	LSP1	0	chr11	1846000
-99819	LRRC8C	0	1660	LRRC8D	0	chr1	90057500
-100319	LRRC8C	0	1160	LRRC8D	0	chr1	90058000
767	SPANXE,SPANXD	0	321	SPANXE,SPANXD	0	chrX	140614000
31506	DDB1	0	2242	DDB1	0	chr11	60855000
11255	TUBB3	0	1506	TUBB3	0	chr16	88528500
11755	TUBB3	0	1006	TUBB3	0	chr16	88529000
12255	TUBB3	0	506	TUBB3	0	chr16	88529500
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-25406	GTF2IRD2P1	0	6161	NSUN5	0	chr7	72349000
-25906	GTF2IRD2P1	0	5661	NSUN5	0	chr7	72349500
-26406	GTF2IRD2P1	0	5161	NSUN5	0	chr7	72350000
980	EGLN2	0	7177	EGLN2	0	chr19	45999000
39486	ZFPM1	0	42075	ZFPM1	0	chr16	87087000
39986	ZFPM1	0	41575	ZFPM1	0	chr16	87087500
-94	KNDC1	0	3767	UTF1	0	chr10	134890000
-105938	MST1P9	0	51531	CROCC	0	chr1	17069500
-106438	MST1P9	0	51031	CROCC	0	chr1	17070000
-106938	MST1P9	0	50531	CROCC	0	chr1	17070500
7763	KRT8	0	135	KRT8	0	chr12	51585000
130200	HDAC4	0	222580	HDAC4	0	chr2	239765000
4897	SLC45A3	0	17753	SLC45A3	0	chr1	203898500
5397	SLC45A3	0	17253	SLC45A3	0	chr1	203899000
1360	RGMA	0	44437	RGMA	0	chr15	91389000
1860	RGMA	0	43937	RGMA	0	chr15	91389500
12612	FURIN	0	2191	FURIN	0	chr15	89225500

13112	FURIN	0	1691	FURIN	0	chr15	89226000
246	PIWIL2	0	80529	PIWIL2	0	chr8	22189000
476	PIWIL2	0	80029	PIWIL2	0	chr8	22189500
18167	SLC9A3	0	33049	SLC9A3	0	chr5	544500
101691	GFRA2	0	6792	GFRA2	0	chr8	21695500
102191	GFRA2	0	6292	GFRA2	0	chr8	21696000
102691	GFRA2	0	5792	GFRA2	0	chr8	21696500
-1485019	NDST4	0	484657	TRAM1L1	0	chr4	117739500
-1485519	NDST4	0	484157	TRAM1L1	0	chr4	117740000
70087	TBC1D16	0	25742	TBC1D16	0	chr17	75598500
64537	PCNT	0	57110	PCNT	0	chr21	46633000
65037	PCNT	0	56610	PCNT	0	chr21	46633500
2308	NME4	0	1255	NME4	0	chr16	389500
2808	NME4	0	755	NME4	0	chr16	390000
3308	NME4	0	255	NME4	0	chr16	390500
531	MKNK2	0	13243	MKNK2	0	chr19	1989000
1031	MKNK2	0	12743	MKNK2	0	chr19	1989500
8935	GIGYF1	0	806	GIGYF1	0	chr7	100124000
9435	GIGYF1	0	306	GIGYF1	0	chr7	100124500
-1307	PRM1	0	62811	C16orf75	0	chr16	11284000
-432	TSPAN3	0	36525	SGK269	0	chr15	75151000
-932	TSPAN3	0	36025	SGK269	0	chr15	75151500
-300954	SIX2	0	78323	SRBD1	0	chr2	45391000
-301454	SIX2	0	77823	SRBD1	0	chr2	45391500
76615	MED15	0	3419	MED15	0	chr22	19268500
-24097	TPTE2	0	72879	MPHOSPH8	0	chr13	19033000
-24597	TPTE2	0	72379	MPHOSPH8	0	chr13	19033500
12537	TACR2	0	180	TACR2	0	chr10	70846500
148	MAP1LC3A	0	13310	MAP1LC3A	0	chr20	32598500
220	C20orf144	0	1381	C20orf144	0	chr20	31714000
39783	PAPD7	0	2661	PAPD7	0	chr5	6807500
40283	PAPD7	0	2161	PAPD7	0	chr5	6808000
-66620	IRX4	0	796780	IRX2	0	chr5	2002500
38938	ADAP1	0	17815	ADAP1	0	chr7	943000
121705	RASA3	0	29197	RASA3	0	chr13	113887000
122205	RASA3	0	28697	RASA3	0	chr13	113887500
-20363	ACTR3	0	463368	DPP10	0	chr2	114453000
-20863	ACTR3	0	462868	DPP10	0	chr2	114453500
-21363	ACTR3	0	462368	DPP10	0	chr2	114454000
17900	SBF1	0	10320	SBF1	0	chr22	49250000
-759620	IRX4	0	103780	IRX2	0	chr5	2695500
-760120	IRX4	0	103280	IRX2	0	chr5	2696000
58835	UNC5A	0	11505	UNC5A	0	chr5	176229000
811895	SDK1	0	155657	SDK1	0	chr7	4119500
812395	SDK1	0	155157	SDK1	0	chr7	4120000
812895	SDK1	0	154657	SDK1	0	chr7	4120500
5313	SOX7	0	1432	SOX7	0	chr8	10624000
141700	HDAC4	0	211080	HDAC4	0	chr2	239776500
-103364	C21orf81	0	25005	LIPI	0	chr21	14378000
-103864	C21orf81	0	24505	LIPI	0	chr21	14378500
-882	GK5	0	80138	XRN1	0	chr3	143428000
1068	GNPTG	0	10353	GNPTG	0	chr16	1343000
811	GNAS	0	70645	GNAS	0	chr20	56849000
-753307	PLSCR5	0	26526	ZIC4	0	chr3	148560000
28333	NKD2	0	1425	NKD2	0	chr5	1090500
28833	NKD2	0	925	NKD2	0	chr5	1091000
29333	NKD2	0	425	NKD2	0	chr5	1091500
26406	PHLDB3	0	3325	PHLDB3	0	chr19	48697500

26906	PHLDB3	0	2825	PHLDB3	0	chr19	48698000
-52944	FGFR1OP	0	18284	CCR6	0	chr6	167427000
-53444	FGFR1OP	0	17784	CCR6	0	chr6	167427500
14317	GGT7	0	13822	GGT7	0	chr20	32910500
14817	GGT7	0	13322	GGT7	0	chr20	32911000
9117	C15orf51	0	7655	C15orf51	0	chr15	98157000
68192	MKX	0	4784	MKX	0	chr10	28070000
68692	MKX	0	4284	MKX	0	chr10	28070500
97345	MCF2L	0	21863	MCF2L	0	chr13	112779000
49353	DOT1L	0	19077	DOT1L	0	chr19	2164500
49853	DOT1L	0	18577	DOT1L	0	chr19	2165000
-91380	LOC728613	0	72998	MRPL36	0	chr5	1778500
-37789	SLC25A28	0	1252	ENTPD7	0	chr10	101408000
191869	APBA2	0	4808	APBA2	0	chr15	27193000
192369	APBA2	0	4308	APBA2	0	chr15	27193500
11177	MUC6	0	12706	MUC6	0	chr11	1014000
-452	CCDC9	0	2481	PRR24	0	chr19	52467500
-577	PHF2P1	0	54917	TUBA3C	0	chr13	18591000
-10433	CCDC77	0	7303	B4GALNT3	0	chr12	432500
506	PHYHD1	0	20641	PHYHD1	0	chr9	130723500
1006	PHYHD1	0	20141	PHYHD1	0	chr9	130724000
109200	VWF	0	66597	VWF	0	chr12	6037500
-15170	LOC441956	0	146825	C21orf15	0	chr21	13990500
1211	PSORS1C2	0	606	PSORS1C2	0	chr6	31214500
3626	NCLN	0	20073	NCLN	0	chr19	3140500
4126	NCLN	0	19573	NCLN	0	chr19	3141000
2555	SLC43A2	0	51880	SLC43A2	0	chr17	1427000
3055	SLC43A2	0	51380	SLC43A2	0	chr17	1427500
9626	TNNT3	0	9512	TNNT3	0	chr11	1907000
3253	MAGED4	0	4104	MAGED4	0	chrX	51948000
22221	PTDSS2	0	18887	PTDSS2	0	chr11	462500
22721	PTDSS2	0	18387	PTDSS2	0	chr11	463000
-60724	ZNF562	0	21650	ZNF846	0	chr19	9707500
-2031	PTX4	0	2852	TELO2	0	chr16	1480500
21312	AMZ1	0	14595	AMZ1	0	chr7	2707000
6300	FAM83C	0	639	FAM83C	0	chr20	33343000
57256	JAK2	0	85682	JAK2	0	chr9	5032500
57756	JAK2	0	85182	JAK2	0	chr9	5033000
-94608	ALOX12P2	0	1107	ALOX12	0	chr17	6839000
8118	C21orf70	0	28816	C21orf70	0	chr21	45192500
8618	C21orf70	0	28316	C21orf70	0	chr21	45193000
-1309	TAF12	0	4198	RNU11	0	chr1	28843500
12756	REXO1	0	20452	REXO1	0	chr19	1779000
652	SLC25A11	0	2063	SLC25A11	0	chr17	4782000
9780	RASSF1	0	1371	RASSF1	0	chr3	50352000
-58858	BEX5	0	435	NXF2B,NXF2	0	chrX	101356500
65	NXF2B,NXF2	0	111290	NXF2B,NXF2	0	chrX	101357000
1460	CST11	0	982	CST11	0	chr20	23380500
1960	CST11	0	482	CST11	0	chr20	23381000
-117	WIF1	0	48137	LEMD3	0	chr12	63801500
-617	WIF1	0	47637	LEMD3	0	chr12	63802000
-431	SPDEF	0	30547	C6orf106	0	chr6	34632500
-931	SPDEF	0	30047	C6orf106	0	chr6	34633000
8454	HEXIM2	0	689	HEXIM2	0	chr17	40602500
8954	HEXIM2	0	189	HEXIM2	0	chr17	40603000
358686	C9orf3	0	1762	C9orf3	0	chr9	96887500
359686	C9orf3	0	762	C9orf3	0	chr9	96888500
-1349	TTTY23B,TTTY23	0	1263	TSPY2	0	chrY	6173000

111026	NXF2	0	388	NXF2	0	chrX	101613000

	..peak value /window and probe (mean is count > 1)						
	Astro 2	Astro 3	Astro 4	HNSCNanog 1	HNSCNanog 3	HNSCNanog 4	p-value t-test over peak scores
	3.24	3.23	3.24	0.0103	0.0105	0.0109	6.88E-12
	3.24	3.23	3.24	0.0103	0.0105	0.0109	6.88E-12
	3.24	3.23	3.24	0.0103	0.0105	0.0109	6.88E-12
	2.84	2.84	2.82	0.0103	0.0105	0.0109	1.87E-10
	2.84	2.84	2.82	0.0103	0.0105	0.0109	1.87E-10
	2.4	2.38	2.39	0.0103	0.0105	0.0109	2.08E-10
	2.4	2.38	2.39	0.0103	0.0105	0.0109	2.08E-10
	2.65	2.66	2.68	0.0103	0.0105	0.0109	7.33E-10
	2.65	2.66	2.68	0.0103	0.0105	0.0109	7.33E-10
	2.54	2.52	2.51	0.0103	0.0105	0.0109	9.11E-10
	3.32	3.36	3.33	0.0103	0.0105	0.0109	1.02E-09
	4.05	4.1	4.09	0.0103	0.0105	0.0109	1.19E-09
	2.99	3.01	2.97	0.0103	0.0105	0.0109	1.35E-09
	5.07	5.01	5.01	0.0103	0.0105	0.0109	1.51E-09
	5.07	5.01	5.01	0.0103	0.0105	0.0109	1.51E-09
	2.5	2.5	2.47	0.0103	0.0105	0.0109	1.59E-09
	2.43	2.46	2.46	0.0103	0.0105	0.0109	1.70E-09
	2.41	2.41	2.44	0.0103	0.0105	0.0109	1.78E-09
	2.41	2.41	2.44	0.0103	0.0105	0.0109	1.78E-09
	2.63	2.66	2.62	0.0103	0.0105	0.0109	2.63E-09
	2.5	2.46	2.48	0.0103	0.0105	0.0109	2.87E-09
	2.48	2.46	2.5	0.0103	0.0105	0.0109	2.87E-09
	2.75	2.78	2.8	0.0103	0.0105	0.0109	4.57E-09
	2.75	2.78	2.8	0.0103	0.0105	0.0109	4.57E-09
	2.72	2.69	2.67	0.0103	0.0105	0.0109	5.16E-09
	4.22	4.3	4.28	0.0103	0.0105	0.0109	6.10E-09
	4.09	4.01	4.04	0.0103	0.0105	0.0109	6.70E-09
	3.05	3.03	3.09	0.0103	0.0105	0.0109	6.75E-09
	4.15	4.13	4.07	0.0103	0.0105	0.0109	7.05E-09
	3.92	4	3.99	0.0103	0.0105	0.0109	9.79E-09
	3.92	4	3.99	0.0103	0.0105	0.0109	9.79E-09
	3.92	4	3.99	0.0103	0.0105	0.0109	9.79E-09
	3.52	3.55	3.47	0.0103	0.0105	0.0109	1.18E-08
	0.011	0.012	0.0117	2.74	2.69	2.68	1.36E-08
	0.011	0.012	0.0117	2.74	2.69	2.68	1.36E-08
	2.67	2.68	2.73	0.0103	0.0105	0.0109	1.37E-08
	2.67	2.68	2.73	0.0103	0.0105	0.0109	1.37E-08
	4.76	4.85	4.87	0.0103	0.0105	0.0109	1.46E-08
	3.29	3.32	3.37	0.0103	0.0105	0.0109	1.47E-08
	3.29	3.32	3.37	0.0103	0.0105	0.0109	1.47E-08
	3.29	3.32	3.37	0.0103	0.0105	0.0109	1.47E-08
	2.93	2.99	3	0.0103	0.0105	0.0109	1.78E-08
	2.93	2.99	3	0.0103	0.0105	0.0109	1.78E-08
	2.93	2.99	3	0.0103	0.0105	0.0109	1.78E-08
	2.24	2.29	2.24	0.0103	0.0105	0.0109	1.82E-08
	2.24	2.29	2.24	0.0103	0.0105	0.0109	1.82E-08
	2.51	2.52	2.46	0.0103	0.0105	0.0109	1.86E-08
	2.51	2.52	2.46	0.0103	0.0105	0.0109	1.86E-08
	2.37	2.35	2.31	0.0103	0.0105	0.0109	1.96E-08
	2.29	2.35	2.33	0.0103	0.0105	0.0109	2.03E-08
	2.29	2.35	2.33	0.0103	0.0105	0.0109	2.03E-08
	2.7	2.66	2.63	0.0103	0.0105	0.0109	2.05E-08
	2.7	2.66	2.63	0.0103	0.0105	0.0109	2.05E-08

3.12	3.14	3.06	0.0103	0.0105	0.0109	2.18E-08
2.96	3.04	2.99	0.0103	0.0105	0.0109	2.24E-08
2.96	3.04	2.99	0.0103	0.0105	0.0109	2.24E-08
2.25	2.27	2.21	0.0103	0.0105	0.0109	2.34E-08
2.25	2.27	2.21	0.0103	0.0105	0.0109	2.34E-08
0.011	0.012	0.0117	2.75	2.74	2.68	2.53E-08
0.011	0.012	0.0117	2.75	2.74	2.68	2.53E-08
3.03	3.04	3.11	0.0103	0.0105	0.0109	2.78E-08
3.03	3.04	3.11	0.0103	0.0105	0.0109	2.78E-08
0.011	0.012	0.0117	2.41	2.41	2.47	2.81E-08
0.011	0.012	0.0117	2.41	2.41	2.47	2.81E-08
2.56	2.51	2.49	0.0103	0.0105	0.0109	2.84E-08
3.44	3.49	3.54	0.0103	0.0105	0.0109	2.84E-08
4.26	4.35	4.38	0.0103	0.0105	0.0109	2.91E-08
4.26	4.35	4.38	0.0103	0.0105	0.0109	2.91E-08
2.65	2.58	2.64	0.0103	0.0105	0.0109	2.94E-08
2.65	2.58	2.64	0.0103	0.0105	0.0109	2.94E-08
2.42	2.42	2.36	0.0103	0.0105	0.0109	2.94E-08
2.42	2.42	2.36	0.0103	0.0105	0.0109	2.94E-08
2.43	2.37	2.37	0.0103	0.0105	0.0109	2.99E-08
2.41	2.43	2.48	0.0103	0.0105	0.0109	3.23E-08
2.74	2.66	2.71	0.0103	0.0105	0.0109	3.38E-08
2.74	2.66	2.71	0.0103	0.0105	0.0109	3.38E-08
2.34	2.38	2.31	0.0103	0.0105	0.0109	3.42E-08
2.34	2.38	2.31	0.0103	0.0105	0.0109	3.42E-08
2.52	2.45	2.46	0.0103	0.0105	0.0109	3.70E-08
2.52	2.45	2.46	0.0103	0.0105	0.0109	3.70E-08
0.011	0.012	0.0117	3.37	3.27	3.34	3.83E-08
2.3	2.26	2.23	0.0103	0.0105	0.0109	3.94E-08
2.3	2.26	2.23	0.0103	0.0105	0.0109	3.94E-08
2.87	2.9	2.96	0.0103	0.0105	0.0109	4.16E-08
2.87	2.9	2.96	0.0103	0.0105	0.0109	4.16E-08
2.93	2.84	2.9	0.0103	0.0105	0.0109	4.27E-08
2.93	2.84	2.9	0.0103	0.0105	0.0109	4.27E-08
2.16	2.23	2.19	0.0103	0.0105	0.0109	4.47E-08
2.16	2.23	2.19	0.0103	0.0105	0.0109	4.47E-08
3.32	3.41	3.42	0.0103	0.0105	0.0109	4.74E-08
3.32	3.41	3.42	0.0103	0.0105	0.0109	4.74E-08
3.32	3.41	3.42	0.0103	0.0105	0.0109	4.74E-08
2.72	2.81	2.76	0.0103	0.0105	0.0109	4.80E-08
2.72	2.81	2.76	0.0103	0.0105	0.0109	4.80E-08
2.8	2.89	2.87	0.0103	0.0105	0.0109	5.09E-08
3.9	3.89	4.01	0.0103	0.0105	0.0109	5.53E-08
3.2	3.21	3.11	0.0103	0.0105	0.0109	6.13E-08
0.011	0.012	0.0117	2.99	3.07	3.09	6.13E-08
4.39	4.25	4.27	0.0103	0.0105	0.0109	6.45E-08
2.48	2.41	2.4	0.0103	0.0105	0.0109	7.02E-08
2.48	2.41	2.4	0.0103	0.0105	0.0109	7.02E-08
2.58	2.65	2.67	0.0103	0.0105	0.0109	7.02E-08
2.22	2.3	2.28	0.0103	0.0105	0.0109	7.73E-08
4.02	4.09	3.94	0.0103	0.0105	0.0109	8.21E-08
4.02	4.09	3.94	0.0103	0.0105	0.0109	8.21E-08
4.02	4.09	3.94	0.0103	0.0105	0.0109	8.21E-08
0.011	0.012	0.0117	4.21	4.07	4.2	8.37E-08
3.48	3.57	3.44	0.0103	0.0105	0.0109	8.86E-08
2.41	2.35	2.44	0.0103	0.0105	0.0109	9.01E-08
2.12	2.15	2.07	0.0103	0.0105	0.0109	9.09E-08
2.76	2.68	2.78	0.0103	0.0105	0.0109	9.41E-08

2.76	2.68	2.78	0.0103	0.0105	0.0109	9.41E-08
2.56	2.48	2.57	0.0103	0.0105	0.0109	9.69E-08
2.56	2.48	2.57	0.0103	0.0105	0.0109	9.69E-08
3.25	3.3	3.38	0.0103	0.0105	0.0109	1.04E-07
2.27	2.36	2.3	0.0103	0.0105	0.0109	1.05E-07
0.011	0.012	0.0117	2.75	2.81	2.7	1.08E-07
0.011	0.012	0.0117	2.75	2.81	2.7	1.08E-07
3.61	3.62	3.49	0.0103	0.0105	0.0109	1.13E-07
3.61	3.62	3.49	0.0103	0.0105	0.0109	1.13E-07
2.33	2.35	2.26	0.0103	0.0105	0.0109	1.18E-07
0.011	0.012	0.0117	2.55	2.52	2.45	1.19E-07
4.18	4.04	4.03	0.0103	0.0105	0.0109	1.20E-07
4.18	4.04	4.03	0.0103	0.0105	0.0109	1.20E-07
2.93	3.03	2.92	0.0103	0.0105	0.0109	1.20E-07
2.25	2.32	2.23	0.0103	0.0105	0.0109	1.28E-07
0.011	0.012	0.0117	2.4	2.36	2.46	1.30E-07
0.011	0.012	0.0117	2.4	2.36	2.46	1.30E-07
0.011	0.012	0.0117	3.22	3.19	3.32	1.31E-07
0.011	0.012	0.0117	2.7	2.59	2.63	1.34E-07
3.1	3.09	3.21	0.0103	0.0105	0.0109	1.38E-07
2.4	2.37	2.47	0.0103	0.0105	0.0109	1.39E-07
2.4	2.37	2.47	0.0103	0.0105	0.0109	1.39E-07
0.011	0.012	0.0117	2.68	2.71	2.6	1.41E-07
2.13	2.07	2.16	0.0103	0.0105	0.0109	1.48E-07
2.13	2.07	2.16	0.0103	0.0105	0.0109	1.48E-07
2.28	2.38	2.32	0.0103	0.0105	0.0109	1.49E-07
2.5	2.61	2.57	0.0103	0.0105	0.0109	1.52E-07
3.09	3	2.96	0.0103	0.0105	0.0109	1.60E-07
3.09	3	2.96	0.0103	0.0105	0.0109	1.60E-07
3.09	2.98	2.97	0.0103	0.0105	0.0109	1.61E-07
3.09	2.98	2.97	0.0103	0.0105	0.0109	1.61E-07
3.47	3.37	3.52	0.0103	0.0105	0.0109	1.61E-07
0.011	0.012	0.0117	2.86	2.99	2.91	1.72E-07
2.96	2.83	2.89	0.0103	0.0105	0.0109	1.73E-07
2.46	2.53	2.42	0.0103	0.0105	0.0109	1.75E-07
3.02	2.91	2.9	0.0103	0.0105	0.0109	1.77E-07
3.02	2.91	2.9	0.0103	0.0105	0.0109	1.77E-07
2.55	2.44	2.47	0.0103	0.0105	0.0109	1.85E-07
2.79	2.87	2.92	0.0103	0.0105	0.0109	1.87E-07
2.79	2.87	2.92	0.0103	0.0105	0.0109	1.87E-07
2.73	2.85	2.83	0.0103	0.0105	0.0109	1.87E-07
2.73	2.85	2.83	0.0103	0.0105	0.0109	1.87E-07
3.01	2.88	2.91	0.0103	0.0105	0.0109	1.96E-07
3.01	2.88	2.91	0.0103	0.0105	0.0109	1.96E-07
3.01	2.88	2.91	0.0103	0.0105	0.0109	1.96E-07
2.72	2.85	2.78	0.0103	0.0105	0.0109	2.02E-07
2.72	2.85	2.78	0.0103	0.0105	0.0109	2.02E-07
2.15	2.25	2.18	0.0103	0.0105	0.0109	2.03E-07
3.2	3.14	3.29	0.0103	0.0105	0.0109	2.06E-07
3.78	3.96	3.9	0.0103	0.0105	0.0109	2.10E-07
0.011	0.012	0.0117	3.26	3.13	3.13	2.11E-07
3.95	3.79	3.79	0.0103	0.0105	0.0109	2.25E-07
0.011	0.012	0.0117	3.21	3.32	3.17	2.25E-07
0.011	0.012	0.0117	3.21	3.32	3.17	2.25E-07
2.38	2.49	2.4	0.0103	0.0105	0.0109	2.32E-07
2.54	2.42	2.49	0.0103	0.0105	0.0109	2.35E-07
2.54	2.42	2.49	0.0103	0.0105	0.0109	2.35E-07
2.62	2.72	2.6	0.0103	0.0105	0.0109	2.36E-07

0.011	0.012	0.0117	2.66	2.79	2.7	2.44E-07
0.011	0.012	0.0117	2.66	2.79	2.7	2.44E-07
3.51	3.38	3.35	0.0103	0.0105	0.0109	2.60E-07
3.34	3.51	3.41	0.0103	0.0105	0.0109	2.63E-07
0.011	0.012	0.0117	2.68	2.69	2.57	2.71E-07
0.011	0.012	0.0117	3.16	3.16	3.3	2.73E-07
3.8	3.63	3.79	0.0103	0.0105	0.0109	2.85E-07
3.8	3.63	3.79	0.0103	0.0105	0.0109	2.85E-07
0.011	0.012	0.0117	2.75	2.87	2.88	2.88E-07
2.52	2.52	2.41	0.0103	0.0105	0.0109	2.90E-07
2.22	2.22	2.32	0.0103	0.0105	0.0109	2.92E-07
2.22	2.22	2.32	0.0103	0.0105	0.0109	2.92E-07
3.93	3.86	4.06	0.0103	0.0105	0.0109	2.93E-07
0.011	0.012	0.0117	2.01	2.11	2.03	3.02E-07
2.84	2.83	2.71	0.0103	0.0105	0.0109	3.04E-07
2.84	2.83	2.71	0.0103	0.0105	0.0109	3.04E-07
0.011	0.012	0.0117	2.33	2.26	2.38	3.08E-07
2.77	2.64	2.66	0.0103	0.0105	0.0109	3.10E-07
2.74	2.61	2.72	0.0103	0.0105	0.0109	3.10E-07
2.74	2.61	2.72	0.0103	0.0105	0.0109	3.10E-07
0.011	0.012	0.0117	3.44	3.54	3.36	3.16E-07
2.54	2.45	2.58	0.0103	0.0105	0.0109	3.28E-07
2.54	2.45	2.58	0.0103	0.0105	0.0109	3.28E-07
3.29	3.23	3.12	0.0103	0.0105	0.0109	3.50E-07
2.12	2.23	2.21	0.0103	0.0105	0.0109	3.50E-07
2.73	2.87	2.85	0.0103	0.0105	0.0109	3.53E-07
2.18	2.1	2.07	0.0103	0.0105	0.0109	3.54E-07
2.15	2.27	2.21	0.0103	0.0105	0.0109	3.69E-07
2.15	2.27	2.21	0.0103	0.0105	0.0109	3.69E-07
2.36	2.27	2.24	0.0103	0.0105	0.0109	3.75E-07
0.011	0.012	0.0117	3.37	3.19	3.28	3.83E-07
2.47	2.6	2.58	0.0103	0.0105	0.0109	3.84E-07
2.47	2.6	2.58	0.0103	0.0105	0.0109	3.84E-07
2.7	2.6	2.56	0.0103	0.0105	0.0109	3.88E-07
2.7	2.6	2.56	0.0103	0.0105	0.0109	3.88E-07
2.66	2.67	2.54	0.0103	0.0105	0.0109	3.91E-07
2.99	2.93	2.83	0.0103	0.0105	0.0109	3.98E-07
2.99	2.93	2.83	0.0103	0.0105	0.0109	3.98E-07
2.41	2.35	2.28	0.0103	0.0105	0.0109	4.00E-07
3.06	2.91	3.05	0.0103	0.0105	0.0109	4.09E-07
3.06	2.91	3.05	0.0103	0.0105	0.0109	4.09E-07
3.01	2.88	2.86	0.0103	0.0105	0.0109	4.11E-07
3.71	3.64	3.51	0.0103	0.0105	0.0109	4.16E-07
3.71	3.64	3.51	0.0103	0.0105	0.0109	4.16E-07
3.99	3.96	4.17	0.0103	0.0105	0.0109	4.20E-07
2.49	2.42	2.56	0.0103	0.0105	0.0109	4.23E-07
2.24	2.15	2.27	0.0103	0.0105	0.0109	4.25E-07
0.011	0.012	0.0117	3.29	3.19	3.11	4.28E-07
2.57	2.72	2.63	0.0103	0.0105	0.0109	4.52E-07
2.57	2.72	2.63	0.0103	0.0105	0.0109	4.52E-07
2.57	2.72	2.63	0.0103	0.0105	0.0109	4.52E-07
2.54	2.4	2.49	0.0103	0.0105	0.0109	4.56E-07
3	2.91	2.83	0.0103	0.0105	0.0109	4.90E-07
3	2.91	2.83	0.0103	0.0105	0.0109	4.90E-07
2.48	2.55	2.63	0.0103	0.0105	0.0109	5.05E-07
4.08	3.95	4.19	0.0103	0.0105	0.0109	5.09E-07
0.011	0.012	0.0117	3.24	3.09	3.07	5.22E-07
3.55	3.75	3.58	0.0103	0.0105	0.0109	5.27E-07

3.19	3.14	3.01	0.0103	0.0105	0.0109	5.35E-07
3.19	3.14	3.01	0.0103	0.0105	0.0109	5.35E-07
0.011	0.012	0.0117	2.49	2.39	2.35	5.44E-07
3.1	3.29	3.22	0.0103	0.0105	0.0109	5.46E-07
2.78	2.63	2.65	0.0103	0.0105	0.0109	5.71E-07
2.78	2.63	2.65	0.0103	0.0105	0.0109	5.71E-07
3.3	3.11	3.17	0.0103	0.0105	0.0109	5.77E-07
3.3	3.11	3.17	0.0103	0.0105	0.0109	5.77E-07
2.54	2.57	2.69	0.0103	0.0105	0.0109	5.87E-07
2.54	2.57	2.69	0.0103	0.0105	0.0109	5.87E-07
3.27	3.45	3.45	0.0103	0.0105	0.0109	5.95E-07
3.05	3.04	3.21	0.0103	0.0105	0.0109	6.05E-07
3.05	3.04	3.21	0.0103	0.0105	0.0109	6.05E-07
2.22	2.35	2.24	0.0103	0.0105	0.0109	6.13E-07
2.83	2.91	3.01	0.0103	0.0105	0.0109	6.17E-07
4	3.77	3.95	0.0103	0.0105	0.0109	6.18E-07
4.74	4.62	4.7	2.47	2.53	2.5	6.25E-07
4.74	4.62	4.7	2.47	2.53	2.5	6.25E-07
0.011	0.012	0.0117	2.87	2.78	2.96	6.54E-07
4.76	4.98	4.69	0.0103	0.0105	0.0109	6.57E-07
2.97	2.86	2.79	0.0103	0.0105	0.0109	6.71E-07
0.011	0.012	0.0117	4.1	3.85	4.01	6.85E-07
0.011	0.012	0.0117	4.1	3.85	4.01	6.85E-07
0.011	0.012	0.0117	4.1	3.85	4.01	6.85E-07
2.34	2.39	2.49	0.0103	0.0105	0.0109	6.87E-07
2.34	2.39	2.49	0.0103	0.0105	0.0109	6.87E-07
0.011	0.012	0.0117	2.86	2.93	2.75	6.98E-07
2.66	2.74	2.57	0.0103	0.0105	0.0109	7.10E-07
4.48	4.29	4.57	0.0103	0.0105	0.0109	7.17E-07
3.76	3.88	4.01	0.0103	0.0105	0.0109	7.23E-07
3.03	2.89	2.85	0.0103	0.0105	0.0109	7.37E-07
2.35	2.24	2.21	0.0103	0.0105	0.0109	7.58E-07
2.8	2.64	2.79	0.0103	0.0105	0.0109	7.70E-07
2.8	2.64	2.79	0.0103	0.0105	0.0109	7.70E-07
0.011	0.012	0.0117	2.97	3.17	3.09	7.74E-07
2.51	2.39	2.36	0.0103	0.0105	0.0109	7.83E-07
3.74	3.51	3.57	0.0103	0.0105	0.0109	8.06E-07
2.38	2.54	2.49	0.0103	0.0105	0.0109	8.16E-07
3	2.82	2.85	0.0103	0.0105	0.0109	8.37E-07
3	2.82	2.85	0.0103	0.0105	0.0109	8.37E-07
3	2.82	2.85	0.0103	0.0105	0.0109	8.37E-07
2.18	2.1	2.04	0.0103	0.0105	0.0109	8.38E-07
2.18	2.1	2.04	0.0103	0.0105	0.0109	8.38E-07
2.11	2.03	2.17	0.0103	0.0105	0.0109	8.44E-07
2.11	2.03	2.17	0.0103	0.0105	0.0109	8.44E-07
2.3	2.2	2.35	0.0103	0.0105	0.0109	8.48E-07
2.3	2.2	2.35	0.0103	0.0105	0.0109	8.48E-07
2.61	2.44	2.53	0.0103	0.0105	0.0109	8.68E-07
2.02	2.02	2.14	0.0103	0.0105	0.0109	8.69E-07
2.67	2.52	2.52	0.0103	0.0105	0.0109	8.72E-07
2.46	2.63	2.57	0.0103	0.0105	0.0109	8.79E-07
2.75	2.72	2.58	0.0103	0.0105	0.0109	8.83E-07
2.81	2.92	2.73	0.0103	0.0105	0.0109	8.84E-07
2.44	2.37	2.28	0.0103	0.0105	0.0109	8.98E-07
2.44	2.37	2.28	0.0103	0.0105	0.0109	8.98E-07
3.31	3.11	3.29	0.0103	0.0105	0.0109	9.04E-07
3.31	3.11	3.29	0.0103	0.0105	0.0109	9.04E-07
3.13	3.18	3.34	0.0103	0.0105	0.0109	9.11E-07

3.13	3.18	3.34	0.0103	0.0105	0.0109	9.11E-07
3.13	3.18	3.34	0.0103	0.0105	0.0109	9.11E-07
5.06	4.82	4.74	0.0103	0.0105	0.0109	9.15E-07
0.011	0.012	0.0117	3.85	3.66	3.91	9.30E-07
0.011	0.012	0.0117	3.85	3.66	3.91	9.30E-07
0.011	0.012	0.0117	2.67	2.66	2.51	9.37E-07
0.011	0.012	0.0117	2.67	2.66	2.51	9.37E-07
4.98	4.68	4.96	0.0103	0.0105	0.0109	9.41E-07
2.39	2.25	2.39	0.0103	0.0105	0.0109	9.58E-07
2.11	2.01	2.15	0.0103	0.0105	0.0109	9.62E-07
2.43	2.47	2.31	0.0103	0.0105	0.0109	9.75E-07
0.011	0.012	0.0117	2.89	2.81	3.01	9.76E-07
2.83	3.03	2.9	0.0103	0.0105	0.0109	9.84E-07
3.04	3.15	3.26	0.0103	0.0105	0.0109	1.00E-06
3.04	3.15	3.26	0.0103	0.0105	0.0109	1.00E-06
2.2	2.25	2.1	0.0103	0.0105	0.0109	1.02E-06
2.2	2.25	2.1	0.0103	0.0105	0.0109	1.02E-06
2.51	2.34	2.43	0.0103	0.0105	0.0109	1.02E-06
2.51	2.34	2.43	0.0103	0.0105	0.0109	1.02E-06
2.39	2.27	2.43	0.0103	0.0105	0.0109	1.04E-06
0.011	0.012	0.0117	2.56	2.72	2.56	1.06E-06
3.02	3.23	3.19	0.0103	0.0105	0.0109	1.06E-06
3.02	3.23	3.19	0.0103	0.0105	0.0109	1.06E-06
0.011	0.012	0.0117	3.48	3.48	3.27	1.08E-06
4.38	4.12	4.39	0.0103	0.0105	0.0109	1.08E-06
0.011	0.012	0.0117	3.1	3.32	3.27	1.10E-06
2.3	2.35	2.19	0.0103	0.0105	0.0109	1.12E-06
2.3	2.35	2.19	0.0103	0.0105	0.0109	1.12E-06
0.011	0.012	0.0117	3.28	3.07	3.1	1.14E-06
0.011	0.012	0.0117	3.28	3.07	3.1	1.14E-06
2.29	2.18	2.34	0.0103	0.0105	0.0109	1.15E-06
2.37	2.31	2.48	0.0103	0.0105	0.0109	1.15E-06
3.2	3.41	3.21	0.0103	0.0105	0.0109	1.16E-06
2.16	2.31	2.29	0.0103	0.0105	0.0109	1.16E-06
2.16	2.31	2.29	0.0103	0.0105	0.0109	1.16E-06
2.24	2.19	2.35	0.0103	0.0105	0.0109	1.17E-06
2.15	2	2.09	0.0103	0.0105	0.0109	1.18E-06
2.15	2	2.09	0.0103	0.0105	0.0109	1.18E-06
2.06	2.19	2.2	0.0103	0.0105	0.0109	1.18E-06
2.06	2.19	2.2	0.0103	0.0105	0.0109	1.18E-06
2.06	2.19	2.2	0.0103	0.0105	0.0109	1.18E-06
3.25	3.25	3.46	0.0103	0.0105	0.0109	1.20E-06
4.11	3.94	4.24	0.0103	0.0105	0.0109	1.22E-06
2.99	2.83	2.79	0.0103	0.0105	0.0109	1.25E-06
2.26	2.17	2.1	0.0103	0.0105	0.0109	1.25E-06
3.67	3.67	3.44	0.0103	0.0105	0.0109	1.25E-06
3.23	3.11	3	0.0103	0.0105	0.0109	1.26E-06
3.23	3.11	3	0.0103	0.0105	0.0109	1.26E-06
3.12	2.94	3.15	0.0103	0.0105	0.0109	1.26E-06
3.12	2.94	3.15	0.0103	0.0105	0.0109	1.26E-06
2.21	2.3	2.38	0.0103	0.0105	0.0109	1.27E-06
2.18	2.29	2.13	0.0103	0.0105	0.0109	1.30E-06
0.011	0.012	0.0117	3.56	3.75	3.83	1.31E-06
2.5	2.32	2.41	0.0103	0.0105	0.0109	1.32E-06
2.5	2.32	2.41	0.0103	0.0105	0.0109	1.32E-06
0.011	0.012	0.0117	2.66	2.86	2.81	1.33E-06
0.011	0.012	0.0117	2.66	2.86	2.81	1.33E-06
3.33	3.31	3.54	0.0103	0.0105	0.0109	1.34E-06

3.33	3.31	3.54	0.0103	0.0105	0.0109	1.34E-06
3.33	3.31	3.54	0.0103	0.0105	0.0109	1.34E-06
2.33	2.46	2.29	0.0103	0.0105	0.0109	1.36E-06
2.33	2.46	2.29	0.0103	0.0105	0.0109	1.36E-06
2.96	2.78	2.77	0.0103	0.0105	0.0109	1.36E-06
0.011	0.012	0.0117	2.89	2.79	2.68	1.36E-06
2.45	2.33	2.51	0.0103	0.0105	0.0109	1.37E-06
2.76	2.61	2.57	0.0103	0.0105	0.0109	1.39E-06
3.06	2.92	2.84	0.0103	0.0105	0.0109	1.39E-06
3.06	2.92	2.84	0.0103	0.0105	0.0109	1.39E-06
2.58	2.41	2.57	0.0103	0.0105	0.0109	1.39E-06
2.73	2.55	2.72	0.0103	0.0105	0.0109	1.40E-06
2.73	2.55	2.72	0.0103	0.0105	0.0109	1.40E-06
2.26	2.41	2.42	0.0103	0.0105	0.0109	1.40E-06
2.26	2.41	2.42	0.0103	0.0105	0.0109	1.40E-06
2.64	2.58	2.45	0.0103	0.0105	0.0109	1.41E-06
2.64	2.58	2.45	0.0103	0.0105	0.0109	1.41E-06
2.54	2.41	2.36	0.0103	0.0105	0.0109	1.43E-06
2.54	2.41	2.36	0.0103	0.0105	0.0109	1.43E-06
2.14	2.31	2.24	0.0103	0.0105	0.0109	1.46E-06
2.14	2.31	2.24	0.0103	0.0105	0.0109	1.46E-06
2.35	2.35	2.51	0.0103	0.0105	0.0109	1.48E-06
0.011	0.012	0.0117	3.54	3.72	3.45	1.48E-06
4.9	4.88	4.57	0.0103	0.0105	0.0109	1.50E-06
2.26	2.1	2.23	0.0103	0.0105	0.0109	1.52E-06
2.26	2.1	2.23	0.0103	0.0105	0.0109	1.52E-06
2.26	2.1	2.23	0.0103	0.0105	0.0109	1.52E-06
2.75	2.69	2.9	0.0103	0.0105	0.0109	1.55E-06
2.75	2.69	2.9	0.0103	0.0105	0.0109	1.55E-06
3.47	3.63	3.36	0.0103	0.0105	0.0109	1.55E-06
0.011	0.012	0.0117	2.23	2.31	2.41	1.56E-06
0.011	0.012	0.0117	2.23	2.31	2.41	1.56E-06
2.58	2.51	2.71	0.0103	0.0105	0.0109	1.57E-06
2.58	2.51	2.71	0.0103	0.0105	0.0109	1.57E-06
2.18	2.11	2.28	0.0103	0.0105	0.0109	1.57E-06
3.32	3.22	3.48	0.0103	0.0105	0.0109	1.60E-06
3.14	3.32	3.39	0.0103	0.0105	0.0109	1.60E-06
2.55	2.44	2.64	0.0103	0.0105	0.0109	1.63E-06
2.55	2.44	2.64	0.0103	0.0105	0.0109	1.63E-06
2.32	2.43	2.51	0.0103	0.0105	0.0109	1.63E-06
2.32	2.43	2.51	0.0103	0.0105	0.0109	1.63E-06
3.83	3.57	3.59	0.0103	0.0105	0.0109	1.64E-06
3.51	3.25	3.33	0.0103	0.0105	0.0109	1.65E-06
2.48	2.68	2.62	0.0103	0.0105	0.0109	1.66E-06
3.1	2.87	2.94	0.0103	0.0105	0.0109	1.67E-06
2.51	2.35	2.34	0.0103	0.0105	0.0109	1.69E-06
2.51	2.35	2.34	0.0103	0.0105	0.0109	1.69E-06
2.76	2.63	2.55	0.0103	0.0105	0.0109	1.74E-06
2.76	2.63	2.55	0.0103	0.0105	0.0109	1.74E-06
2.4	2.6	2.49	0.0103	0.0105	0.0109	1.75E-06
2.3	2.49	2.37	0.0103	0.0105	0.0109	1.78E-06
3.33	3.09	3.13	0.0103	0.0105	0.0109	1.79E-06
3.33	3.09	3.13	0.0103	0.0105	0.0109	1.79E-06
3.33	3.09	3.13	0.0103	0.0105	0.0109	1.79E-06
2.69	2.85	2.91	0.0103	0.0105	0.0109	1.79E-06
2.69	2.85	2.91	0.0103	0.0105	0.0109	1.79E-06
2.72	2.51	2.6	0.0103	0.0105	0.0109	1.79E-06
3.14	2.93	3.15	0.0103	0.0105	0.0109	1.80E-06

3.14	2.93	3.15	0.0103	0.0105	0.0109	1.80E-06
2.72	2.78	2.94	0.0103	0.0105	0.0109	1.80E-06
2.49	2.7	2.6	0.0103	0.0105	0.0109	1.81E-06
2.49	2.7	2.6	0.0103	0.0105	0.0109	1.81E-06
2.57	2.77	2.6	0.0103	0.0105	0.0109	1.86E-06
2.57	2.77	2.6	0.0103	0.0105	0.0109	1.86E-06
2.23	2.42	2.35	0.0103	0.0105	0.0109	1.95E-06
2.87	3.08	3.09	0.0103	0.0105	0.0109	1.95E-06
2.87	3.08	3.09	0.0103	0.0105	0.0109	1.95E-06
2.89	3.07	2.84	0.0103	0.0105	0.0109	1.95E-06
2.89	3.07	2.84	0.0103	0.0105	0.0109	1.95E-06
2.46	2.6	2.4	0.0103	0.0105	0.0109	1.96E-06
2.46	2.6	2.4	0.0103	0.0105	0.0109	1.96E-06
0.011	0.012	0.0117	2.9	2.7	2.91	2.05E-06
2.55	2.38	2.57	0.0103	0.0105	0.0109	2.05E-06
3.83	3.53	3.75	0.0103	0.0105	0.0109	2.08E-06
3.72	3.57	3.42	0.0103	0.0105	0.0109	2.09E-06
3.21	2.96	3.15	0.0103	0.0105	0.0109	2.10E-06
3.21	2.96	3.15	0.0103	0.0105	0.0109	2.10E-06
3.21	2.96	3.15	0.0103	0.0105	0.0109	2.10E-06
3.21	2.96	3.15	0.0103	0.0105	0.0109	2.10E-06
3.4	3.15	3.18	0.0103	0.0105	0.0109	2.11E-06
3.4	3.15	3.18	0.0103	0.0105	0.0109	2.11E-06
2.74	2.52	2.66	0.0103	0.0105	0.0109	2.14E-06
0.011	0.012	0.0117	2.3	2.49	2.34	2.14E-06
0.011	0.012	0.0117	2.3	2.49	2.34	2.14E-06
2.84	2.61	2.72	0.0103	0.0105	0.0109	2.15E-06
2.64	2.82	2.86	0.0103	0.0105	0.0109	2.15E-06
2.64	2.82	2.86	0.0103	0.0105	0.0109	2.15E-06
2.64	2.82	2.86	0.0103	0.0105	0.0109	2.15E-06
3.32	3.29	3.07	0.0103	0.0105	0.0109	2.15E-06
3.32	3.29	3.07	0.0103	0.0105	0.0109	2.15E-06
0.011	0.012	0.0117	2.52	2.52	2.34	2.16E-06
0.011	0.012	0.0117	2.52	2.52	2.34	2.16E-06
3.04	3.09	2.85	0.0103	0.0105	0.0109	2.16E-06
2.93	2.73	2.95	0.0103	0.0105	0.0109	2.18E-06
2.16	2.35	2.24	0.0103	0.0105	0.0109	2.19E-06
3.14	2.93	3.17	0.0103	0.0105	0.0109	2.19E-06
0.011	0.012	0.0117	2.71	2.59	2.82	2.20E-06
3.07	3.18	2.92	0.0103	0.0105	0.0109	2.24E-06
3.07	3.18	2.92	0.0103	0.0105	0.0109	2.24E-06
3.04	3.3	3.11	0.0103	0.0105	0.0109	2.24E-06
3.04	3.3	3.11	0.0103	0.0105	0.0109	2.24E-06
2.97	2.79	2.74	0.0103	0.0105	0.0109	2.24E-06
2.97	2.79	2.74	0.0103	0.0105	0.0109	2.24E-06
2.56	2.79	2.67	0.0103	0.0105	0.0109	2.31E-06
2.56	2.79	2.67	0.0103	0.0105	0.0109	2.31E-06
0.011	0.012	0.0117	2.35	2.2	2.17	2.33E-06
3.99	3.66	3.82	0.0103	0.0105	0.0109	2.33E-06
0.011	0.012	0.0117	2.6	2.68	2.46	2.35E-06
0.011	0.012	0.0117	2.6	2.68	2.46	2.35E-06
2.44	2.53	2.32	0.0103	0.0105	0.0109	2.39E-06
0.011	0.012	0.0117	3.1	3.34	3.1	2.43E-06
0.011	0.012	0.0117	3.1	3.34	3.1	2.43E-06
2.63	2.52	2.41	0.0103	0.0105	0.0109	2.45E-06
2.63	2.52	2.41	0.0103	0.0105	0.0109	2.45E-06
3.67	3.39	3.65	0.0103	0.0105	0.0109	2.46E-06
3.67	3.39	3.65	0.0103	0.0105	0.0109	2.46E-06

3.67	3.39	3.65	0.0103	0.0105	0.0109	2.46E-06
3.93	3.91	3.63	0.0103	0.0105	0.0109	2.49E-06
3.93	3.91	3.63	0.0103	0.0105	0.0109	2.49E-06
2.28	2.19	2.39	0.0103	0.0105	0.0109	2.49E-06
2.72	2.5	2.67	0.0103	0.0105	0.0109	2.49E-06
2.72	2.5	2.67	0.0103	0.0105	0.0109	2.49E-06
2.16	2.08	2.27	0.0103	0.0105	0.0109	2.53E-06
2.16	2.08	2.27	0.0103	0.0105	0.0109	2.53E-06
2.88	3.12	2.91	0.0103	0.0105	0.0109	2.53E-06
2.2	2.15	2.34	0.0103	0.0105	0.0109	2.57E-06
2.38	2.23	2.19	0.0103	0.0105	0.0109	2.58E-06
2.41	2.41	2.23	0.0103	0.0105	0.0109	2.58E-06
2.48	2.47	2.29	0.0103	0.0105	0.0109	2.60E-06
0.011	0.012	0.0117	2.63	2.49	2.41	2.62E-06
2.37	2.47	2.26	0.0103	0.0105	0.0109	2.62E-06
2.99	3.25	3.21	0.0103	0.0105	0.0109	2.62E-06
2.88	2.64	2.81	0.0103	0.0105	0.0109	2.63E-06
2.88	2.64	2.81	0.0103	0.0105	0.0109	2.63E-06
2.88	2.64	2.81	0.0103	0.0105	0.0109	2.63E-06
4.94	5.32	4.92	0.0103	0.0105	0.0109	2.63E-06
4.94	5.32	4.92	0.0103	0.0105	0.0109	2.63E-06
4.94	5.32	4.92	0.0103	0.0105	0.0109	2.63E-06
3.14	2.96	2.88	0.0103	0.0105	0.0109	2.64E-06
0.011	0.012	0.0117	2.15	2.32	2.15	2.65E-06
0.011	0.012	0.0117	2.15	2.32	2.15	2.65E-06
2.15	2.23	2.04	0.0103	0.0105	0.0109	2.67E-06
2.15	2.23	2.04	0.0103	0.0105	0.0109	2.67E-06
2.02	2.04	2.19	0.0103	0.0105	0.0109	2.68E-06
2.02	2.04	2.19	0.0103	0.0105	0.0109	2.68E-06
4.49	4.22	4.12	0.0103	0.0105	0.0109	2.69E-06
4.91	4.63	5.06	0.0103	0.0105	0.0109	2.71E-06
4.91	4.63	5.06	0.0103	0.0105	0.0109	2.71E-06
0.011	0.012	0.0117	2.74	2.92	2.68	2.75E-06
0.011	0.012	0.0117	2.74	2.92	2.68	2.75E-06
2.43	2.28	2.49	0.0103	0.0105	0.0109	2.79E-06
3.3	3.61	3.43	0.0103	0.0105	0.0109	2.80E-06
3.71	3.58	3.39	0.0103	0.0105	0.0109	2.80E-06
3.71	3.58	3.39	0.0103	0.0105	0.0109	2.80E-06
2.51	2.31	2.34	0.0103	0.0105	0.0109	2.82E-06
0.011	0.012	0.0117	2.5	2.69	2.72	2.83E-06
0.011	0.012	0.0117	2.5	2.69	2.72	2.83E-06
3.78	3.5	3.8	0.0103	0.0105	0.0109	2.86E-06
3.78	3.5	3.8	0.0103	0.0105	0.0109	2.86E-06
0.011	0.012	0.0117	2.78	2.54	2.64	2.88E-06
0.011	0.012	0.0117	2.49	2.56	2.72	2.90E-06
2.28	2.29	2.47	0.0103	0.0105	0.0109	2.91E-06
2.66	2.44	2.49	0.0103	0.0105	0.0109	2.91E-06
2.66	2.44	2.49	0.0103	0.0105	0.0109	2.91E-06
2.97	3.09	2.82	0.0103	0.0105	0.0109	2.94E-06
2.62	2.73	2.87	0.0103	0.0105	0.0109	2.95E-06
4.25	4.07	4.46	0.0103	0.0105	0.0109	2.95E-06
2.57	2.78	2.79	0.0103	0.0105	0.0109	2.96E-06
2.96	2.81	3.08	0.0103	0.0105	0.0109	2.98E-06
2.96	2.81	3.08	0.0103	0.0105	0.0109	2.98E-06
0.011	0.012	0.0117	2.51	2.42	2.29	3.02E-06
4.5	4.56	4.9	0.0103	0.0105	0.0109	3.09E-06
3.6	3.85	3.94	0.0103	0.0105	0.0109	3.11E-06
3.6	3.85	3.94	0.0103	0.0105	0.0109	3.11E-06

3.6	3.85	3.94	0.0103	0.0105	0.0109	3.11E-06
2.58	2.37	2.4	0.0103	0.0105	0.0109	3.12E-06
0.011	0.012	0.0117	2.63	2.42	2.44	3.14E-06
3.78	3.75	3.47	0.0103	0.0105	0.0109	3.17E-06
2.24	2.04	2.14	0.0103	0.0105	0.0109	3.23E-06
2.45	2.51	2.68	0.0103	0.0105	0.0109	3.25E-06
2.59	2.38	2.58	0.0103	0.0105	0.0109	3.31E-06
2.36	2.2	2.41	0.0103	0.0105	0.0109	3.36E-06
2.36	2.2	2.41	0.0103	0.0105	0.0109	3.36E-06
3.12	2.94	3.23	0.0103	0.0105	0.0109	3.36E-06
3.12	2.94	3.23	0.0103	0.0105	0.0109	3.36E-06
0.011	0.012	0.0117	3.26	3.36	3.06	3.38E-06
2.36	2.57	2.56	0.0103	0.0105	0.0109	3.42E-06
2.88	3.12	3.14	0.0103	0.0105	0.0109	3.42E-06
3.14	3.2	2.92	0.0103	0.0105	0.0109	3.50E-06
3.14	3.2	2.92	0.0103	0.0105	0.0109	3.50E-06
3.14	3.2	2.92	0.0103	0.0105	0.0109	3.50E-06
0.011	0.012	0.0117	2.53	2.44	2.3	3.54E-06
2.25	2.47	2.41	0.0103	0.0105	0.0109	3.54E-06
2.61	2.4	2.41	0.0103	0.0105	0.0109	3.55E-06
3.15	2.98	3.28	0.0103	0.0105	0.0109	3.56E-06
2.2	2.34	2.42	0.0103	0.0105	0.0109	3.59E-06
4.32	4.24	4.64	0.0103	0.0105	0.0109	3.59E-06
3.03	3.02	2.78	0.0103	0.0105	0.0109	3.60E-06
2.69	2.46	2.5	0.0103	0.0105	0.0109	3.64E-06
3.52	3.32	3.2	0.0103	0.0105	0.0109	3.66E-06
2.96	2.91	2.7	0.0103	0.0105	0.0109	3.66E-06
2.96	2.91	2.7	0.0103	0.0105	0.0109	3.66E-06
3.36	3.51	3.7	0.0103	0.0105	0.0109	3.67E-06
0.011	0.012	0.0117	2.25	2.48	2.37	3.78E-06
0.011	0.012	0.0117	2.74	2.9	3.02	3.78E-06
3.24	3.12	2.94	0.0103	0.0105	0.0109	3.78E-06
3.24	3.12	2.94	0.0103	0.0105	0.0109	3.78E-06
2.79	2.97	2.7	0.0103	0.0105	0.0109	3.80E-06
2.68	2.5	2.75	0.0103	0.0105	0.0109	3.82E-06
2.68	2.5	2.75	0.0103	0.0105	0.0109	3.82E-06
3.23	3.52	3.52	0.0103	0.0105	0.0109	3.84E-06
3.23	3.52	3.52	0.0103	0.0105	0.0109	3.84E-06
2.34	2.45	2.58	0.0103	0.0105	0.0109	3.86E-06
2.34	2.45	2.58	0.0103	0.0105	0.0109	3.86E-06
2.41	2.26	2.49	0.0103	0.0105	0.0109	3.87E-06
2.41	2.26	2.49	0.0103	0.0105	0.0109	3.87E-06
4.31	4.01	3.93	0.0103	0.0105	0.0109	3.88E-06
2.45	2.57	2.33	0.0103	0.0105	0.0109	3.88E-06
3.2	2.91	3.13	0.0103	0.0105	0.0109	3.92E-06
3.2	2.91	3.13	0.0103	0.0105	0.0109	3.92E-06
3.05	3.11	2.83	0.0103	0.0105	0.0109	3.94E-06
3.05	3.11	2.83	0.0103	0.0105	0.0109	3.94E-06
0.011	0.012	0.0117	3.69	3.41	3.74	3.94E-06
2.48	2.28	2.28	0.0103	0.0105	0.0109	3.96E-06
2.48	2.28	2.28	0.0103	0.0105	0.0109	3.96E-06
0.011	0.012	0.0117	2.15	2.12	1.96	3.97E-06
0.011	0.012	0.0117	2.15	2.12	1.96	3.97E-06
0.011	0.012	0.0117	4.46	4.54	4.89	3.99E-06
2.31	2.42	2.55	0.0103	0.0105	0.0109	4.05E-06
2.62	2.6	2.84	0.0103	0.0105	0.0109	4.07E-06
3.95	4.27	4.34	0.0103	0.0105	0.0109	4.07E-06
2.23	2.32	2.46	0.0103	0.0105	0.0109	4.09E-06

2.23	2.32	2.46	0.0103	0.0105	0.0109	4.09E-06
2.24	2.42	2.21	0.0103	0.0105	0.0109	4.09E-06
2.24	2.42	2.21	0.0103	0.0105	0.0109	4.09E-06
4.23	4.37	3.96	0.0103	0.0105	0.0109	4.11E-06
4.13	4.32	3.91	0.0103	0.0105	0.0109	4.12E-06
4.13	4.32	3.91	0.0103	0.0105	0.0109	4.12E-06
4.13	4.32	3.91	0.0103	0.0105	0.0109	4.12E-06
2.2	2.31	2.43	0.0103	0.0105	0.0109	4.13E-06
2.61	2.38	2.42	0.0103	0.0105	0.0109	4.13E-06
2.53	2.36	2.3	0.0103	0.0105	0.0109	4.14E-06
2.53	2.36	2.3	0.0103	0.0105	0.0109	4.14E-06
2.53	2.36	2.3	0.0103	0.0105	0.0109	4.14E-06
3.63	3.29	3.52	0.0103	0.0105	0.0109	4.15E-06
2.58	2.85	2.74	0.0103	0.0105	0.0109	4.16E-06
0.011	0.012	0.0117	3.12	3.36	3.06	4.18E-06
2.7	2.5	2.75	0.0103	0.0105	0.0109	4.18E-06
2.7	2.5	2.75	0.0103	0.0105	0.0109	4.18E-06
2.55	2.8	2.6	0.0103	0.0105	0.0109	4.18E-06
2.5	2.39	2.64	0.0103	0.0105	0.0109	4.19E-06
2.5	2.39	2.64	0.0103	0.0105	0.0109	4.19E-06
2.5	2.39	2.64	0.0103	0.0105	0.0109	4.19E-06
0.011	0.012	0.0117	3.37	3.07	3.33	4.21E-06
3.06	2.77	2.89	0.0103	0.0105	0.0109	4.25E-06
4.18	4.26	3.87	0.0103	0.0105	0.0109	4.25E-06
2.85	2.58	2.69	0.0103	0.0105	0.0109	4.26E-06
3.1	2.85	2.84	0.0103	0.0105	0.0109	4.30E-06
2.71	2.45	2.58	0.0103	0.0105	0.0109	4.34E-06
3.13	2.97	2.83	0.0103	0.0105	0.0109	4.35E-06
3.13	2.97	2.83	0.0103	0.0105	0.0109	4.35E-06
3.13	2.97	2.83	0.0103	0.0105	0.0109	4.35E-06
0.011	0.012	0.0117	2.92	2.8	2.64	4.35E-06
2.36	2.51	2.61	0.0103	0.0105	0.0109	4.37E-06
0.011	0.012	0.0117	2.66	2.59	2.41	4.39E-06
0.011	0.012	0.0117	3.05	2.78	2.82	4.39E-06
3.02	2.77	2.77	0.0103	0.0105	0.0109	4.41E-06
3.02	2.77	2.77	0.0103	0.0105	0.0109	4.41E-06
2.76	2.92	2.64	0.0103	0.0105	0.0109	4.43E-06
2.76	2.92	2.64	0.0103	0.0105	0.0109	4.43E-06
2.38	2.61	2.41	0.0103	0.0105	0.0109	4.45E-06
2.33	2.56	2.37	0.0103	0.0105	0.0109	4.48E-06
2.26	2.5	2.36	0.0103	0.0105	0.0109	4.49E-06
2.26	2.5	2.36	0.0103	0.0105	0.0109	4.49E-06
2.26	2.5	2.36	0.0103	0.0105	0.0109	4.49E-06
2.33	2.47	2.58	0.0103	0.0105	0.0109	4.54E-06
2.49	2.74	2.54	0.0103	0.0105	0.0109	4.59E-06
0.011	0.012	0.0117	3.41	3.18	3.09	4.60E-06
0.011	0.012	0.0117	3.41	3.18	3.09	4.60E-06
2.17	2.33	2.4	0.0103	0.0105	0.0109	4.66E-06
2.15	2.38	2.3	0.0103	0.0105	0.0109	4.67E-06
3.24	3.4	3.59	0.0103	0.0105	0.0109	4.68E-06
2.76	2.49	2.62	0.0103	0.0105	0.0109	4.73E-06
3.63	3.32	3.64	0.0103	0.0105	0.0109	4.73E-06
0.011	0.012	0.0117	2.35	2.12	2.24	4.73E-06
3.11	3.11	2.84	0.0103	0.0105	0.0109	4.77E-06
2.13	2.25	2.03	0.0103	0.0105	0.0109	4.77E-06
3.05	2.98	2.76	0.0103	0.0105	0.0109	4.78E-06
3.05	2.98	2.76	0.0103	0.0105	0.0109	4.78E-06
3.05	2.98	2.76	0.0103	0.0105	0.0109	4.78E-06

3.05	2.98	2.76	0.0103	0.0105	0.0109	4.78E-06
3.05	2.98	2.76	0.0103	0.0105	0.0109	4.78E-06
0.011	0.012	0.0117	3.58	3.23	3.38	4.80E-06
2.46	2.72	2.54	0.0103	0.0105	0.0109	4.83E-06
3.09	2.8	2.87	0.0103	0.0105	0.0109	4.85E-06
0.011	0.012	0.0117	2.78	2.75	3.02	4.90E-06
0.011	0.012	0.0117	2.25	2.48	2.45	5.03E-06
2.48	2.69	2.74	0.0103	0.0105	0.0109	5.05E-06
2.48	2.69	2.74	0.0103	0.0105	0.0109	5.05E-06
2.59	2.83	2.85	0.0103	0.0105	0.0109	5.11E-06
2.59	2.83	2.85	0.0103	0.0105	0.0109	5.11E-06
2.32	2.52	2.29	0.0103	0.0105	0.0109	5.17E-06
4.47	4.61	4.95	0.0103	0.0105	0.0109	5.19E-06
4.47	4.61	4.95	0.0103	0.0105	0.0109	5.19E-06
2.45	2.53	2.28	0.0103	0.0105	0.0109	5.22E-06
3.42	3.66	3.8	0.0103	0.0105	0.0109	5.29E-06
3.04	2.75	2.99	0.0103	0.0105	0.0109	5.29E-06
2.22	2.22	2.43	0.0103	0.0105	0.0109	5.30E-06
2.55	2.5	2.76	0.0103	0.0105	0.0109	5.31E-06
2.87	2.93	3.17	0.0103	0.0105	0.0109	5.34E-06
2.57	2.38	2.64	0.0103	0.0105	0.0109	5.39E-06
2.57	2.38	2.64	0.0103	0.0105	0.0109	5.39E-06
3.36	3.05	3.09	0.0103	0.0105	0.0109	5.40E-06
0.011	0.012	0.0117	3.67	3.46	3.3	5.45E-06
3.71	3.86	3.47	0.0103	0.0105	0.0109	5.47E-06
0.011	0.012	0.0117	2.83	3	3.15	5.51E-06
0.011	0.012	0.0117	2.83	3	3.15	5.51E-06
2.52	2.38	2.65	0.0103	0.0105	0.0109	5.58E-06
2.52	2.38	2.65	0.0103	0.0105	0.0109	5.58E-06
4.09	3.77	3.7	0.0103	0.0105	0.0109	5.68E-06
4.26	4.74	4.44	0.0103	0.0105	0.0109	5.74E-06
2.43	2.47	2.23	0.0103	0.0105	0.0109	5.78E-06
2.43	2.47	2.23	0.0103	0.0105	0.0109	5.78E-06
2.3	2.07	2.14	0.0103	0.0105	0.0109	5.88E-06
2.62	2.37	2.41	0.0103	0.0105	0.0109	5.92E-06
0.011	0.012	0.0117	2.43	2.71	2.59	5.96E-06
0.011	0.012	0.0117	2.66	2.55	2.84	5.97E-06
2.23	2.45	2.46	0.0103	0.0105	0.0109	6.00E-06
2.64	2.7	2.43	0.0103	0.0105	0.0109	6.04E-06
3.62	3.96	4.01	0.0103	0.0105	0.0109	6.09E-06
0.011	0.012	0.0117	2.67	2.72	2.45	6.15E-06
2.97	2.82	2.66	0.0103	0.0105	0.0109	6.17E-06
2.97	2.82	2.66	0.0103	0.0105	0.0109	6.17E-06
0.011	0.012	0.0117	2.8	2.7	2.51	6.24E-06
2.69	2.74	2.98	0.0103	0.0105	0.0109	6.29E-06
0.011	0.012	0.0117	2.82	3.1	2.82	6.38E-06
0.011	0.012	0.0117	2.82	3.1	2.82	6.38E-06
3.58	3.51	3.22	0.0103	0.0105	0.0109	6.38E-06
3.58	3.51	3.22	0.0103	0.0105	0.0109	6.38E-06
3.58	3.51	3.22	0.0103	0.0105	0.0109	6.38E-06
3.58	3.51	3.22	0.0103	0.0105	0.0109	6.38E-06
3.58	3.51	3.22	0.0103	0.0105	0.0109	6.38E-06
3.11	3.11	2.82	0.0103	0.0105	0.0109	6.40E-06
3.11	3.11	2.82	0.0103	0.0105	0.0109	6.40E-06
3.11	3.11	2.82	0.0103	0.0105	0.0109	6.40E-06
0.011	0.012	0.0117	2.48	2.53	2.75	6.41E-06
3.32	3.16	2.97	0.0103	0.0105	0.0109	6.42E-06
0.011	0.012	0.0117	3.98	4.09	3.67	6.43E-06

0.011	0.012	0.0117	2.73	2.74	2.48	6.43E-06
3.42	3.08	3.15	0.0103	0.0105	0.0109	6.51E-06
2.41	2.18	2.4	0.0103	0.0105	0.0109	6.53E-06
2.41	2.18	2.4	0.0103	0.0105	0.0109	6.53E-06
0.011	0.012	0.0117	3.07	3.14	2.82	6.56E-06
0.011	0.012	0.0117	3.07	3.14	2.82	6.56E-06
2.92	2.88	2.63	0.0103	0.0105	0.0109	6.58E-06
2.36	2.31	2.12	0.0103	0.0105	0.0109	6.61E-06
2.86	3.11	2.8	0.0103	0.0105	0.0109	6.72E-06
2.86	3.11	2.8	0.0103	0.0105	0.0109	6.72E-06
3.99	3.96	3.6	0.0103	0.0105	0.0109	6.76E-06
2.92	3.25	3.19	0.0103	0.0105	0.0109	6.76E-06
2.92	3.25	3.19	0.0103	0.0105	0.0109	6.76E-06
2.69	2.9	2.6	0.0103	0.0105	0.0109	6.80E-06
2.69	2.9	2.6	0.0103	0.0105	0.0109	6.80E-06
3.32	3.64	3.69	0.0103	0.0105	0.0109	6.85E-06
2.78	2.74	2.5	0.0103	0.0105	0.0109	6.92E-06
2.78	2.74	2.5	0.0103	0.0105	0.0109	6.92E-06
2.51	2.45	2.25	0.0103	0.0105	0.0109	6.94E-06
2.55	2.31	2.32	0.0103	0.0105	0.0109	6.98E-06
2.48	2.22	2.41	0.0103	0.0105	0.0109	7.00E-06
2.25	2.01	2.11	0.0103	0.0105	0.0109	7.02E-06
2.47	2.37	2.65	0.0103	0.0105	0.0109	7.02E-06
3.01	2.76	2.71	0.0103	0.0105	0.0109	7.02E-06
3.01	2.76	2.71	0.0103	0.0105	0.0109	7.02E-06
3.16	2.82	2.98	0.0103	0.0105	0.0109	7.06E-06
0.011	0.012	0.0117	3.6	4.03	3.77	7.07E-06
2.42	2.7	2.64	0.0103	0.0105	0.0109	7.10E-06
2.42	2.7	2.64	0.0103	0.0105	0.0109	7.10E-06
2.8	2.74	2.51	0.0103	0.0105	0.0109	7.12E-06
2.8	2.74	2.51	0.0103	0.0105	0.0109	7.12E-06
4.82	4.32	4.72	0.0103	0.0105	0.0109	7.18E-06
4.82	4.32	4.72	0.0103	0.0105	0.0109	7.18E-06
2.76	2.79	2.51	0.0103	0.0105	0.0109	7.21E-06
2.76	2.79	2.51	0.0103	0.0105	0.0109	7.21E-06
2.55	2.8	2.53	0.0103	0.0105	0.0109	7.24E-06
3.27	3.3	2.97	0.0103	0.0105	0.0109	7.27E-06
3.27	3.3	2.97	0.0103	0.0105	0.0109	7.27E-06
0.011	0.012	0.0117	3.47	3.36	3.1	7.29E-06
3.05	2.73	2.98	0.0103	0.0105	0.0109	7.40E-06
3.05	2.73	2.98	0.0103	0.0105	0.0109	7.40E-06
2.23	2.5	2.34	0.0103	0.0105	0.0109	7.42E-06
2.23	2.5	2.34	0.0103	0.0105	0.0109	7.42E-06
2.39	2.67	2.61	0.0103	0.0105	0.0109	7.44E-06
2.39	2.67	2.61	0.0103	0.0105	0.0109	7.44E-06
0.011	0.012	0.0117	2.24	2.48	2.48	7.50E-06
0.011	0.012	0.0117	2.65	2.62	2.38	7.64E-06
3.54	3.32	3.73	0.0103	0.0105	0.0109	7.64E-06
3.62	4.06	3.78	0.0103	0.0105	0.0109	7.73E-06
2.36	2.41	2.63	0.0103	0.0105	0.0109	7.74E-06
2.36	2.41	2.63	0.0103	0.0105	0.0109	7.74E-06
2.42	2.61	2.33	0.0103	0.0105	0.0109	7.76E-06
2.99	3.18	2.83	0.0103	0.0105	0.0109	7.81E-06
2.99	3.18	2.83	0.0103	0.0105	0.0109	7.81E-06
2.9	2.62	2.63	0.0103	0.0105	0.0109	7.86E-06
0.011	0.012	0.0117	3.36	3.15	2.99	7.92E-06
2.52	2.8	2.55	0.0103	0.0105	0.0109	7.93E-06
2.52	2.8	2.55	0.0103	0.0105	0.0109	7.93E-06

0.011	0.012	0.0117	2.39	2.68	2.6	7.94E-06
3.99	3.55	3.83	0.0103	0.0105	0.0109	7.98E-06
0.011	0.012	0.0117	2.55	2.42	2.72	7.99E-06
3.77	4.22	4.13	0.0103	0.0105	0.0109	8.07E-06
3.77	4.22	4.13	0.0103	0.0105	0.0109	8.07E-06
3.77	4.22	4.13	0.0103	0.0105	0.0109	8.07E-06
0.011	0.012	0.0117	3.24	2.88	3.05	8.09E-06
0.011	0.012	0.0117	2.89	2.57	2.71	8.10E-06
2.08	2.23	2.34	0.0103	0.0105	0.0109	8.10E-06
3.03	2.94	2.7	0.0103	0.0105	0.0109	8.15E-06
3.03	2.94	2.7	0.0103	0.0105	0.0109	8.15E-06
2.53	2.4	2.7	0.0103	0.0105	0.0109	8.23E-06
2.53	2.4	2.7	0.0103	0.0105	0.0109	8.23E-06
3.01	2.72	3.03	0.0103	0.0105	0.0109	8.36E-06
3.01	2.72	3.03	0.0103	0.0105	0.0109	8.36E-06
2.36	2.26	2.54	0.0103	0.0105	0.0109	8.41E-06
2.36	2.26	2.54	0.0103	0.0105	0.0109	8.41E-06
2.29	2.58	2.44	0.0103	0.0105	0.0109	8.45E-06
2.29	2.58	2.44	0.0103	0.0105	0.0109	8.45E-06
0.011	0.012	0.0117	2.68	2.86	2.54	8.47E-06
0.011	0.012	0.0117	2.68	2.86	2.54	8.47E-06
2.76	2.59	2.92	0.0103	0.0105	0.0109	8.63E-06
2.76	2.59	2.92	0.0103	0.0105	0.0109	8.63E-06
2.63	2.38	2.37	0.0103	0.0105	0.0109	8.65E-06
0.011	0.012	0.0117	2.88	3.23	3.16	8.66E-06
3.67	3.27	3.38	0.0103	0.0105	0.0109	8.72E-06
2.29	2.57	2.51	0.0103	0.0105	0.0109	8.73E-06
2.29	2.57	2.51	0.0103	0.0105	0.0109	8.73E-06
0.011	0.012	0.0117	3.48	3.13	3.48	8.74E-06
0.011	0.012	0.0117	3.48	3.13	3.48	8.74E-06
3.2	2.84	2.99	0.0103	0.0105	0.0109	8.74E-06
2.8	2.78	2.51	0.0103	0.0105	0.0109	8.74E-06
0.011	0.012	0.0117	2.63	2.37	2.64	8.79E-06
3.55	4	3.73	0.0103	0.0105	0.0109	8.81E-06
0.011	0.012	0.0117	2.66	2.82	2.5	8.81E-06
2.63	2.92	2.93	0.0103	0.0105	0.0109	8.86E-06
2.63	2.92	2.93	0.0103	0.0105	0.0109	8.86E-06
3.22	2.86	2.99	0.0103	0.0105	0.0109	8.86E-06
3.68	3.27	3.41	0.0103	0.0105	0.0109	8.88E-06
2.77	3.09	2.81	0.0103	0.0105	0.0109	8.89E-06
3.97	3.62	3.55	0.0103	0.0105	0.0109	9.02E-06
2.57	2.29	2.36	0.0103	0.0105	0.0109	9.04E-06
3.07	2.95	3.32	0.0103	0.0105	0.0109	9.06E-06
2.78	3.06	3.12	0.0103	0.0105	0.0109	9.14E-06
0.011	0.012	0.0117	3.01	2.79	3.15	9.19E-06
2.14	2.39	2.17	0.0103	0.0105	0.0109	9.40E-06
0.011	0.012	0.0117	2.46	2.2	2.44	9.42E-06
0.011	0.012	0.0117	2.46	2.2	2.44	9.42E-06
2.2	2.18	2.43	0.0103	0.0105	0.0109	9.45E-06
2.72	2.86	2.53	0.0103	0.0105	0.0109	9.46E-06
2.21	2.44	2.48	0.0103	0.0105	0.0109	9.51E-06
3.14	2.85	2.81	0.0103	0.0105	0.0109	9.53E-06
0.011	0.012	0.0117	2.64	2.92	2.96	9.55E-06
0.011	0.012	0.0117	3.37	3.03	3.04	9.59E-06
2.3	2.04	2.23	0.0103	0.0105	0.0109	9.60E-06
2.3	2.04	2.23	0.0103	0.0105	0.0109	9.60E-06
2.54	2.49	2.79	0.0103	0.0105	0.0109	9.71E-06
2.54	2.49	2.79	0.0103	0.0105	0.0109	9.71E-06

2.57	2.28	2.37	0.0103	0.0105	0.0109	9.74E-06
2.57	2.28	2.37	0.0103	0.0105	0.0109	9.74E-06
2.37	2.33	2.11	0.0103	0.0105	0.0109	9.74E-06
2.37	2.33	2.11	0.0103	0.0105	0.0109	9.74E-06
3.47	3.17	3.09	0.0103	0.0105	0.0109	9.75E-06
3.47	3.17	3.09	0.0103	0.0105	0.0109	9.75E-06
0.011	0.012	0.0117	2.76	2.45	2.54	9.77E-06
2.4	2.62	2.33	0.0103	0.0105	0.0109	9.79E-06
2.74	2.57	2.91	0.0103	0.0105	0.0109	9.95E-06
2.74	2.57	2.91	0.0103	0.0105	0.0109	9.95E-06
2.77	3.12	3.05	0.0103	0.0105	0.0109	1.00E-05
3.14	2.78	3.04	0.0103	0.0105	0.0109	1.00E-05
2.55	2.48	2.79	0.0103	0.0105	0.0109	1.02E-05
2.55	2.48	2.79	0.0103	0.0105	0.0109	1.02E-05
4	4.23	4.53	0.0103	0.0105	0.0109	1.02E-05
3.21	2.97	2.84	0.0103	0.0105	0.0109	1.02E-05
3.21	2.97	2.84	0.0103	0.0105	0.0109	1.02E-05
3.21	2.97	2.84	0.0103	0.0105	0.0109	1.02E-05
2.45	2.19	2.44	0.0103	0.0105	0.0109	1.02E-05
2.45	2.19	2.44	0.0103	0.0105	0.0109	1.02E-05
3.15	2.79	2.9	0.0103	0.0105	0.0109	1.03E-05
2.94	3.33	3.1	0.0103	0.0105	0.0109	1.04E-05
2.94	3.33	3.1	0.0103	0.0105	0.0109	1.04E-05
4.33	4.33	4.82	0.0103	0.0105	0.0109	1.05E-05
2.78	2.81	3.11	0.0103	0.0105	0.0109	1.05E-05
2.78	2.45	2.63	0.0103	0.0105	0.0109	1.06E-05
0.011	0.012	0.0117	2.45	2.78	2.63	1.06E-05
0.011	0.012	0.0117	2.45	2.78	2.63	1.06E-05
3.21	2.92	3.3	0.0103	0.0105	0.0109	1.07E-05
3.7	3.96	4.2	0.0103	0.0105	0.0109	1.07E-05
3.7	3.96	4.2	0.0103	0.0105	0.0109	1.07E-05
0.011	0.012	0.0117	2.43	2.66	2.75	1.07E-05
2.39	2.48	2.7	0.0103	0.0105	0.0109	1.07E-05
2.45	2.69	2.39	0.0103	0.0105	0.0109	1.08E-05
2.57	2.55	2.29	0.0103	0.0105	0.0109	1.08E-05
2.57	2.55	2.29	0.0103	0.0105	0.0109	1.08E-05
3.62	4.11	3.9	0.0103	0.0105	0.0109	1.08E-05
3.62	4.11	3.9	0.0103	0.0105	0.0109	1.08E-05
3.24	3.62	3.26	0.0103	0.0105	0.0109	1.08E-05
3.24	3.62	3.26	0.0103	0.0105	0.0109	1.08E-05
3.24	3.63	3.28	0.0103	0.0105	0.0109	1.08E-05
2.36	2.67	2.59	0.0103	0.0105	0.0109	1.08E-05
2.44	2.61	2.3	0.0103	0.0105	0.0109	1.08E-05
3.35	2.95	3.17	0.0103	0.0105	0.0109	1.09E-05
2.1	2.32	2.37	0.0103	0.0105	0.0109	1.09E-05
0.011	0.012	0.0117	2.73	2.42	2.49	1.12E-05
0.011	0.012	0.0117	2.96	3.35	3.26	1.13E-05
2.6	2.31	2.36	0.0103	0.0105	0.0109	1.13E-05
0.011	0.012	0.0117	2.9	2.56	2.67	1.13E-05
2.39	2.38	2.66	0.0103	0.0105	0.0109	1.14E-05
2.8	2.47	2.58	0.0103	0.0105	0.0109	1.14E-05
2.8	2.47	2.58	0.0103	0.0105	0.0109	1.14E-05
2.96	2.61	2.73	0.0103	0.0105	0.0109	1.15E-05
3.4	3.34	3.01	0.0103	0.0105	0.0109	1.17E-05
3.36	3.01	3.01	0.0103	0.0105	0.0109	1.17E-05
3.36	3.01	3.01	0.0103	0.0105	0.0109	1.17E-05
4.64	4.09	4.27	0.0103	0.0105	0.0109	1.17E-05
3.22	2.9	2.87	0.0103	0.0105	0.0109	1.18E-05

3.22	2.9	2.87	0.0103	0.0105	0.0109	1.18E-05
3.05	3.21	2.82	0.0103	0.0105	0.0109	1.18E-05
2.73	2.78	2.46	0.0103	0.0105	0.0109	1.18E-05
3.54	3.91	3.47	0.0103	0.0105	0.0109	1.19E-05
3.55	3.16	3.2	0.0103	0.0105	0.0109	1.19E-05
3.55	3.16	3.2	0.0103	0.0105	0.0109	1.19E-05
2.62	2.84	2.5	0.0103	0.0105	0.0109	1.20E-05
2.5	2.41	2.2	0.0103	0.0105	0.0109	1.20E-05
0.011	0.012	0.0117	2.66	3.02	2.78	1.20E-05
2.39	2.22	2.1	0.0103	0.0105	0.0109	1.21E-05
2.24	2.15	2.44	0.0103	0.0105	0.0109	1.22E-05
2.47	2.79	2.75	0.0103	0.0105	0.0109	1.22E-05
2.47	2.79	2.75	0.0103	0.0105	0.0109	1.22E-05
2.47	2.79	2.75	0.0103	0.0105	0.0109	1.22E-05
0.011	0.012	0.0117	3.22	3.54	3.13	1.22E-05
0.011	0.012	0.0117	3.11	2.76	2.81	1.23E-05
0.011	0.012	0.0117	3.11	2.76	2.81	1.23E-05
2.82	3.19	2.9	0.0103	0.0105	0.0109	1.24E-05
2.65	3.02	2.88	0.0103	0.0105	0.0109	1.24E-05
3.32	3.21	2.92	0.0103	0.0105	0.0109	1.24E-05
3.32	3.21	2.92	0.0103	0.0105	0.0109	1.24E-05
0.011	0.012	0.0117	3.52	3.59	3.17	1.24E-05
0.011	0.012	0.0117	3.22	3.2	3.59	1.26E-05
2.93	2.85	2.58	0.0103	0.0105	0.0109	1.26E-05
2.67	2.77	3.03	0.0103	0.0105	0.0109	1.26E-05
2.67	2.77	3.03	0.0103	0.0105	0.0109	1.26E-05
2.15	2.42	2.18	0.0103	0.0105	0.0109	1.26E-05
2.15	2.42	2.18	0.0103	0.0105	0.0109	1.26E-05
4.27	4.83	4.38	0.0103	0.0105	0.0109	1.27E-05
2.74	2.43	2.72	0.0103	0.0105	0.0109	1.27E-05
0.011	0.012	0.0117	2.19	2.19	2.45	1.27E-05
0.011	0.012	0.0117	2.04	2.31	2.1	1.28E-05
0.011	0.012	0.0117	2.04	2.31	2.1	1.28E-05
3.35	3.04	2.96	0.0103	0.0105	0.0109	1.28E-05
0.011	0.012	0.0117	2.56	2.79	2.92	1.28E-05
0.011	0.012	0.0117	2.56	2.79	2.92	1.28E-05
0.011	0.012	0.0117	2.47	2.81	2.58	1.29E-05
0.011	0.012	0.0117	2.47	2.81	2.58	1.29E-05
0.011	0.012	0.0117	3.1	3.44	3.05	1.30E-05
0.011	0.012	0.0117	3.1	3.44	3.05	1.30E-05
2.41	2.27	2.11	0.0103	0.0105	0.0109	1.30E-05
2.41	2.27	2.11	0.0103	0.0105	0.0109	1.30E-05
0.011	0.012	0.0117	3	2.63	2.88	1.32E-05
2.24	2.41	2.11	0.0103	0.0105	0.0109	1.34E-05
4.19	3.68	4.07	0.0103	0.0105	0.0109	1.34E-05
0.011	0.012	0.0117	3.66	4.03	3.55	1.36E-05
0.011	0.012	0.0117	3.66	4.03	3.55	1.36E-05
4.05	4	4.06	2.39	2.21	2.41	1.37E-05
3.16	3.29	2.88	0.0103	0.0105	0.0109	1.38E-05
2.22	2.54	2.37	0.0103	0.0105	0.0109	1.38E-05
2.22	2.54	2.37	0.0103	0.0105	0.0109	1.38E-05
2.1	2.39	2.18	0.0103	0.0105	0.0109	1.39E-05
2.1	2.39	2.18	0.0103	0.0105	0.0109	1.39E-05
0.011	0.012	0.0117	2.8	2.59	2.45	1.39E-05
2.96	3.15	2.75	0.0103	0.0105	0.0109	1.41E-05
2.96	3.15	2.75	0.0103	0.0105	0.0109	1.41E-05
3.09	2.8	2.72	0.0103	0.0105	0.0109	1.42E-05
3.09	2.8	2.72	0.0103	0.0105	0.0109	1.42E-05

2.77	2.43	2.53	0.0103	0.0105	0.0109	1.42E-05
0.011	0.012	0.0117	2.5	2.8	2.49	1.42E-05
0.011	0.012	0.0117	2.5	2.86	2.74	1.43E-05
2.79	2.77	3.12	0.0103	0.0105	0.0109	1.43E-05
2.4	2.11	2.18	0.0103	0.0105	0.0109	1.43E-05
2.4	2.11	2.18	0.0103	0.0105	0.0109	1.43E-05
2.44	2.78	2.71	0.0103	0.0105	0.0109	1.43E-05
3.02	2.69	2.69	0.0103	0.0105	0.0109	1.44E-05
2.37	2.08	2.16	0.0103	0.0105	0.0109	1.44E-05
2.37	2.08	2.16	0.0103	0.0105	0.0109	1.44E-05
0.011	0.012	0.0117	2.59	2.26	2.44	1.44E-05
2.33	2.41	2.11	0.0103	0.0105	0.0109	1.44E-05
2.33	2.41	2.11	0.0103	0.0105	0.0109	1.44E-05
2.85	2.49	2.73	0.0103	0.0105	0.0109	1.45E-05
0.011	0.012	0.0117	2.67	3.05	2.95	1.45E-05
2.97	2.64	2.65	0.0103	0.0105	0.0109	1.45E-05
2.54	2.24	2.29	0.0103	0.0105	0.0109	1.45E-05
2.54	2.24	2.29	0.0103	0.0105	0.0109	1.45E-05
2.68	2.56	2.34	0.0103	0.0105	0.0109	1.46E-05
2	2.19	2.29	0.0103	0.0105	0.0109	1.46E-05
2	2.19	2.29	0.0103	0.0105	0.0109	1.46E-05
2.5	2.84	2.8	0.0103	0.0105	0.0109	1.47E-05
2.5	2.84	2.8	0.0103	0.0105	0.0109	1.47E-05
2.5	2.84	2.8	0.0103	0.0105	0.0109	1.47E-05
2.5	2.84	2.8	0.0103	0.0105	0.0109	1.47E-05
2.71	2.45	2.8	0.0103	0.0105	0.0109	1.48E-05
2.71	2.45	2.8	0.0103	0.0105	0.0109	1.48E-05
2.71	2.45	2.8	0.0103	0.0105	0.0109	1.48E-05
4.29	3.76	4.18	0.0103	0.0105	0.0109	1.48E-05
0.011	0.012	0.0117	2.73	2.58	2.38	1.48E-05
0.011	0.012	0.0117	3.36	3.69	3.85	1.49E-05
2.77	3.17	3.06	0.0103	0.0105	0.0109	1.51E-05
2.77	3.17	3.06	0.0103	0.0105	0.0109	1.51E-05
0.011	0.012	0.0117	3.15	3.58	3.23	1.51E-05
2.51	2.78	2.87	0.0103	0.0105	0.0109	1.51E-05
0.011	0.012	0.0117	3.26	2.89	2.91	1.51E-05
0.011	0.012	0.0117	2.61	2.62	2.94	1.51E-05
2.75	3.13	2.83	0.0103	0.0105	0.0109	1.52E-05
0.011	0.012	0.0117	3.4	3.05	3.48	1.52E-05
3.97	3.52	3.54	0.0103	0.0105	0.0109	1.53E-05
3.7	4.24	3.9	0.0103	0.0105	0.0109	1.53E-05
3.7	4.24	3.9	0.0103	0.0105	0.0109	1.53E-05
2.9	2.56	2.6	0.0103	0.0105	0.0109	1.53E-05
0.011	0.012	0.0117	2.94	3.1	3.37	1.54E-05
2.66	2.45	2.32	0.0103	0.0105	0.0109	1.54E-05
2.66	2.45	2.32	0.0103	0.0105	0.0109	1.54E-05
5.5	5.09	4.79	0.0103	0.0105	0.0109	1.55E-05
3.04	3.48	3.18	0.0103	0.0105	0.0109	1.56E-05
3.04	3.48	3.18	0.0103	0.0105	0.0109	1.56E-05
3.51	3.31	3.8	0.0103	0.0105	0.0109	1.57E-05
3.51	3.31	3.8	0.0103	0.0105	0.0109	1.57E-05
3.51	3.31	3.8	0.0103	0.0105	0.0109	1.57E-05
2.96	3.37	3.04	0.0103	0.0105	0.0109	1.57E-05
3.12	2.72	3	0.0103	0.0105	0.0109	1.58E-05
2.65	2.42	2.78	0.0103	0.0105	0.0109	1.58E-05
2.65	2.42	2.78	0.0103	0.0105	0.0109	1.58E-05
2.73	3.14	2.94	0.0103	0.0105	0.0109	1.59E-05
2.73	3.14	2.94	0.0103	0.0105	0.0109	1.59E-05

2	2.3	2.18	0.0103	0.0105	0.0109	1.61E-05
2	2.3	2.18	0.0103	0.0105	0.0109	1.61E-05
2.29	2.33	2.6	0.0103	0.0105	0.0109	1.62E-05
2.29	2.33	2.6	0.0103	0.0105	0.0109	1.62E-05
3.56	3.89	3.39	0.0103	0.0105	0.0109	1.63E-05
3.56	3.89	3.39	0.0103	0.0105	0.0109	1.63E-05
2.68	2.36	2.4	0.0103	0.0105	0.0109	1.64E-05
2.97	3.42	3.22	0.0103	0.0105	0.0109	1.64E-05
0.011	0.012	0.0117	2.65	3.04	2.78	1.64E-05
2.86	3.04	2.64	0.0103	0.0105	0.0109	1.64E-05
3.91	3.54	3.42	0.0103	0.0105	0.0109	1.65E-05
3.91	3.54	3.42	0.0103	0.0105	0.0109	1.65E-05
0.011	0.012	0.0117	2.52	2.69	2.9	1.65E-05
0.011	0.012	0.0117	2.52	2.69	2.9	1.65E-05
2.58	2.97	2.76	0.0103	0.0105	0.0109	1.65E-05
2.58	2.97	2.76	0.0103	0.0105	0.0109	1.65E-05
2.84	3.24	3.19	0.0103	0.0105	0.0109	1.65E-05
2.84	3.24	3.19	0.0103	0.0105	0.0109	1.65E-05
3.06	2.68	2.76	0.0103	0.0105	0.0109	1.67E-05
3.06	2.68	2.76	0.0103	0.0105	0.0109	1.67E-05
0.011	0.012	0.0117	2.5	2.59	2.86	1.68E-05
2.29	2.64	2.46	0.0103	0.0105	0.0109	1.71E-05
2.29	2.64	2.46	0.0103	0.0105	0.0109	1.71E-05
2.22	2.39	2.56	0.0103	0.0105	0.0109	1.72E-05
4.19	4.03	4.62	0.0103	0.0105	0.0109	1.72E-05
2.61	2.7	2.35	0.0103	0.0105	0.0109	1.72E-05
2.61	2.7	2.35	0.0103	0.0105	0.0109	1.72E-05
2.71	3.12	2.87	0.0103	0.0105	0.0109	1.72E-05
2.71	3.12	2.87	0.0103	0.0105	0.0109	1.72E-05
2.71	3.12	2.87	0.0103	0.0105	0.0109	1.72E-05
2.71	3.12	2.87	0.0103	0.0105	0.0109	1.72E-05
3.25	2.9	3.32	0.0103	0.0105	0.0109	1.72E-05
3.25	2.9	3.32	0.0103	0.0105	0.0109	1.72E-05
3.6	3.12	3.36	0.0103	0.0105	0.0109	1.74E-05
3.03	2.67	3.03	0.0103	0.0105	0.0109	1.74E-05
0.011	0.012	0.0117	2.52	2.61	2.27	1.75E-05
2.03	2.34	2.23	0.0103	0.0105	0.0109	1.75E-05
2.5	2.23	2.2	0.0103	0.0105	0.0109	1.76E-05
0.011	0.012	0.0117	2.61	2.67	2.33	1.76E-05
0.011	0.012	0.0117	2.61	2.67	2.33	1.76E-05
2.4	2.11	2.39	0.0103	0.0105	0.0109	1.76E-05
2.16	2.16	2.44	0.0103	0.0105	0.0109	1.78E-05
4.44	3.98	3.89	0.0103	0.0105	0.0109	1.78E-05
3.99	4.55	4.07	0.0103	0.0105	0.0109	1.79E-05
3.62	3.21	3.67	0.0103	0.0105	0.0109	1.80E-05
3.62	3.21	3.67	0.0103	0.0105	0.0109	1.80E-05
3.62	3.21	3.67	0.0103	0.0105	0.0109	1.80E-05
0.011	0.012	0.0117	2.72	2.39	2.71	1.80E-05
2.24	2.57	2.51	0.0103	0.0105	0.0109	1.81E-05
3.53	3.1	3.15	0.0103	0.0105	0.0109	1.81E-05
3.53	3.1	3.15	0.0103	0.0105	0.0109	1.81E-05
3.53	3.1	3.15	0.0103	0.0105	0.0109	1.81E-05
2.43	2.15	2.15	0.0103	0.0105	0.0109	1.81E-05
2.8	2.97	2.57	0.0103	0.0105	0.0109	1.82E-05
3.5	3.21	3.71	0.0103	0.0105	0.0109	1.82E-05
2.4	2.3	2.08	0.0103	0.0105	0.0109	1.85E-05
3.13	3.62	3.38	0.0103	0.0105	0.0109	1.85E-05
3.13	3.62	3.38	0.0103	0.0105	0.0109	1.85E-05

3.13	3.62	3.38	0.0103	0.0105	0.0109	1.85E-05
3.13	3.62	3.38	0.0103	0.0105	0.0109	1.85E-05
2.52	2.21	2.25	0.0103	0.0105	0.0109	1.85E-05
3.43	3.04	3.48	0.0103	0.0105	0.0109	1.86E-05
3.43	3.04	3.48	0.0103	0.0105	0.0109	1.86E-05
3.95	4.57	4.3	0.0103	0.0105	0.0109	1.86E-05
2.95	2.69	2.56	0.0103	0.0105	0.0109	1.86E-05
2.95	2.69	2.56	0.0103	0.0105	0.0109	1.86E-05
2.95	2.69	2.56	0.0103	0.0105	0.0109	1.86E-05
2.95	2.69	2.56	0.0103	0.0105	0.0109	1.86E-05
2.95	2.69	2.56	0.0103	0.0105	0.0109	1.86E-05
2.95	2.69	2.56	0.0103	0.0105	0.0109	1.86E-05
4.95	4.39	5.03	0.0103	0.0105	0.0109	1.87E-05
2.61	2.84	3.02	0.0103	0.0105	0.0109	1.88E-05
2.25	2.5	2.18	0.0103	0.0105	0.0109	1.89E-05
2.61	2.5	2.26	0.0103	0.0105	0.0109	1.89E-05
2.61	2.5	2.26	0.0103	0.0105	0.0109	1.89E-05
2.42	2.72	2.78	0.0103	0.0105	0.0109	1.91E-05
2.34	2.36	2.66	0.0103	0.0105	0.0109	1.91E-05
2.34	2.36	2.66	0.0103	0.0105	0.0109	1.91E-05
2.25	2.6	2.49	0.0103	0.0105	0.0109	1.92E-05
0.011	0.012	0.0117	2.46	2.25	2.13	1.94E-05
3.06	2.76	3.19	0.0103	0.0105	0.0109	1.94E-05
3.06	2.76	3.19	0.0103	0.0105	0.0109	1.94E-05
2.29	2.03	2.33	0.0103	0.0105	0.0109	1.96E-05
2.29	2.03	2.33	0.0103	0.0105	0.0109	1.96E-05
3.65	3.26	3.19	0.0103	0.0105	0.0109	1.96E-05
4.4	3.88	4.44	0.0103	0.0105	0.0109	1.96E-05
0.011	0.012	0.0117	3.14	3.35	2.89	1.97E-05
3.02	3.44	3.05	0.0103	0.0105	0.0109	1.99E-05
3.36	2.91	3.25	0.0103	0.0105	0.0109	1.99E-05
3.36	2.91	3.25	0.0103	0.0105	0.0109	1.99E-05
3.23	2.88	3.32	0.0103	0.0105	0.0109	2.00E-05
0.011	0.012	0.0117	2.8	2.44	2.76	2.01E-05
3.93	3.74	3.39	0.0103	0.0105	0.0109	2.03E-05
2.61	2.69	2.33	0.0103	0.0105	0.0109	2.04E-05
2.61	2.69	2.33	0.0103	0.0105	0.0109	2.04E-05
2.39	2.12	2.44	0.0103	0.0105	0.0109	2.04E-05
0.011	0.012	0.0117	2.63	2.3	2.34	2.05E-05
2.36	2.74	2.58	0.0103	0.0105	0.0109	2.07E-05
2.36	2.74	2.58	0.0103	0.0105	0.0109	2.07E-05
2.05	2.21	2.38	0.0103	0.0105	0.0109	2.07E-05
4.37	5.03	4.94	0.0103	0.0105	0.0109	2.09E-05
0.011	0.012	0.0117	2.8	2.62	2.41	2.10E-05
3.17	3.22	2.8	0.0103	0.0105	0.0109	2.10E-05
0.011	0.012	0.0117	3.37	3.88	3.48	2.11E-05
4.52	4.19	4.87	0.0103	0.0105	0.0109	2.12E-05
2.64	3.06	2.94	0.0103	0.0105	0.0109	2.13E-05
2.21	2.11	2.44	0.0103	0.0105	0.0109	2.13E-05
2.4	2.44	2.12	0.0103	0.0105	0.0109	2.14E-05
2.4	2.44	2.12	0.0103	0.0105	0.0109	2.14E-05
2.58	2.44	2.22	0.0103	0.0105	0.0109	2.14E-05
0.011	0.012	0.0117	2.98	2.8	3.25	2.14E-05
0.011	0.012	0.0117	2.98	2.8	3.25	2.14E-05
3.56	4.12	3.99	0.0103	0.0105	0.0109	2.14E-05
3.56	4.12	3.99	0.0103	0.0105	0.0109	2.14E-05
2.78	3.17	2.8	0.0103	0.0105	0.0109	2.15E-05
3.16	2.74	2.84	0.0103	0.0105	0.0109	2.15E-05

2.73	2.43	2.38	0.0103	0.0105	0.0109	2.15E-05
5.41	5.33	4.7	0.0103	0.0105	0.0109	2.16E-05
3.92	3.37	3.7	0.0103	0.0105	0.0109	2.17E-05
3.92	3.37	3.7	0.0103	0.0105	0.0109	2.17E-05
3.58	3.58	4.07	0.0103	0.0105	0.0109	2.17E-05
2.36	2.62	2.74	0.0103	0.0105	0.0109	2.17E-05
3.7	3.48	3.18	0.0103	0.0105	0.0109	2.18E-05
0.011	0.012	0.0117	3.03	2.83	3.29	2.19E-05
0.011	0.012	0.0117	3.03	2.83	3.29	2.19E-05
0.011	0.012	0.0117	2.79	3.23	3.13	2.19E-05
2.9	2.5	2.79	0.0103	0.0105	0.0109	2.19E-05
3.06	2.63	2.89	0.0103	0.0105	0.0109	2.20E-05
0.011	0.012	0.0117	2.52	2.4	2.78	2.20E-05
2.16	2.48	2.46	0.0103	0.0105	0.0109	2.21E-05
2.47	2.83	2.51	0.0103	0.0105	0.0109	2.21E-05
2.47	2.83	2.51	0.0103	0.0105	0.0109	2.21E-05
0.011	0.012	0.0117	2.5	2.74	2.36	2.22E-05
0.011	0.012	0.0117	2.49	2.71	2.33	2.24E-05
0.011	0.012	0.0117	3.05	3.12	2.7	2.24E-05
0.011	0.012	0.0117	3.61	3.41	3.1	2.25E-05
0.011	0.012	0.0117	3.61	3.41	3.1	2.25E-05
0.011	0.012	0.0117	3.61	3.41	3.1	2.25E-05
3.02	3	2.63	0.0103	0.0105	0.0109	2.25E-05
2.78	2.65	2.39	0.0103	0.0105	0.0109	2.25E-05
0.011	0.012	0.0117	2.99	2.68	2.59	2.26E-05
5.35	4.59	5	0.0103	0.0105	0.0109	2.26E-05
5.35	4.59	5	0.0103	0.0105	0.0109	2.26E-05
2.71	2.48	2.33	0.0103	0.0105	0.0109	2.27E-05
0.011	0.012	0.0117	2.42	2.24	2.61	2.28E-05
0.011	0.012	0.0117	2.42	2.24	2.61	2.28E-05
2.66	3.09	2.81	0.0103	0.0105	0.0109	2.29E-05
2.66	3.09	2.81	0.0103	0.0105	0.0109	2.29E-05
2.66	3.09	2.81	0.0103	0.0105	0.0109	2.29E-05
3.2	3.03	3.52	0.0103	0.0105	0.0109	2.29E-05
3.2	3.03	3.52	0.0103	0.0105	0.0109	2.29E-05
3.2	3.03	3.52	0.0103	0.0105	0.0109	2.29E-05
2.4	2.54	2.18	0.0103	0.0105	0.0109	2.29E-05
2.9	3.38	3.19	0.0103	0.0105	0.0109	2.29E-05
2.34	2.67	2.69	0.0103	0.0105	0.0109	2.30E-05
2.34	2.67	2.69	0.0103	0.0105	0.0109	2.30E-05
2.46	2.31	2.11	0.0103	0.0105	0.0109	2.30E-05
2.44	2.34	2.71	0.0103	0.0105	0.0109	2.31E-05
3.72	3.21	3.62	0.0103	0.0105	0.0109	2.32E-05
2.73	3.11	2.73	0.0103	0.0105	0.0109	2.32E-05
3.12	3.09	2.71	0.0103	0.0105	0.0109	2.33E-05
0.011	0.012	0.0117	3.2	3.1	3.58	2.33E-05
4.62	4.21	3.97	0.0103	0.0105	0.0109	2.34E-05
3.1	3	2.67	0.0103	0.0105	0.0109	2.34E-05
2.46	2.42	2.13	0.0103	0.0105	0.0109	2.36E-05
2.46	2.42	2.13	0.0103	0.0105	0.0109	2.36E-05
2.34	2.73	2.58	0.0103	0.0105	0.0109	2.37E-05
2.34	2.73	2.58	0.0103	0.0105	0.0109	2.37E-05
3.09	2.69	3.08	0.0103	0.0105	0.0109	2.38E-05
0.011	0.012	0.0117	2.26	2.33	2.61	2.38E-05
0.011	0.012	0.0117	2.26	2.33	2.61	2.38E-05
2.62	2.51	2.25	0.0103	0.0105	0.0109	2.38E-05
0.011	0.012	0.0117	2.94	3.41	3.07	2.38E-05
0.011	0.012	0.0117	3.17	3.7	3.41	2.40E-05

2.43	2.76	2.81	0.0103	0.0105	0.0109	2.40E-05
2.73	2.34	2.5	0.0103	0.0105	0.0109	2.44E-05
4.11	4.53	3.89	0.0103	0.0105	0.0109	2.44E-05
4.11	4.53	3.89	0.0103	0.0105	0.0109	2.44E-05
4.11	4.53	3.89	0.0103	0.0105	0.0109	2.44E-05
2.31	2.24	2.59	0.0103	0.0105	0.0109	2.45E-05
2.31	2.24	2.59	0.0103	0.0105	0.0109	2.45E-05
2.5	2.42	2.8	0.0103	0.0105	0.0109	2.46E-05
3.87	3.37	3.87	0.0103	0.0105	0.0109	2.46E-05
2.6	2.23	2.49	0.0103	0.0105	0.0109	2.46E-05
3.05	2.98	2.63	0.0103	0.0105	0.0109	2.46E-05
2	2.33	2.24	0.0103	0.0105	0.0109	2.47E-05
0.011	0.012	0.0117	2.36	2.7	2.72	2.48E-05
2.42	2.24	2.07	0.0103	0.0105	0.0109	2.48E-05
2.42	2.24	2.07	0.0103	0.0105	0.0109	2.48E-05
0.011	0.012	0.0117	2.36	2.76	2.56	2.49E-05
3.42	3	3.47	0.0103	0.0105	0.0109	2.50E-05
3.42	3	3.47	0.0103	0.0105	0.0109	2.50E-05
0.011	0.012	0.0117	2.82	3.3	3.09	2.52E-05
0.011	0.012	0.0117	2.82	3.3	3.09	2.52E-05
2.39	2.45	2.76	0.0103	0.0105	0.0109	2.52E-05
0.011	0.012	0.0117	3.18	3.11	2.74	2.54E-05
3.08	2.65	3	0.0103	0.0105	0.0109	2.54E-05
2.46	2.69	2.88	0.0103	0.0105	0.0109	2.55E-05
0.011	0.012	0.0117	2.94	2.85	3.3	2.55E-05
0.011	0.012	0.0117	2.94	2.85	3.3	2.55E-05
0.011	0.012	0.0117	2.99	2.89	3.35	2.55E-05
3.25	2.85	3.3	0.0103	0.0105	0.0109	2.56E-05
3.25	2.85	3.3	0.0103	0.0105	0.0109	2.56E-05
3.25	2.85	3.3	0.0103	0.0105	0.0109	2.56E-05
2.95	2.67	2.53	0.0103	0.0105	0.0109	2.56E-05
2.53	2.72	2.96	0.0103	0.0105	0.0109	2.57E-05
3.96	3.48	3.45	0.0103	0.0105	0.0109	2.57E-05
3.96	3.48	3.45	0.0103	0.0105	0.0109	2.57E-05
3.02	2.85	2.58	0.0103	0.0105	0.0109	2.57E-05
2.53	2.35	2.75	0.0103	0.0105	0.0109	2.57E-05
2.53	2.78	2.38	0.0103	0.0105	0.0109	2.58E-05
3.41	3.69	3.15	0.0103	0.0105	0.0109	2.60E-05
2.45	2.86	2.75	0.0103	0.0105	0.0109	2.60E-05
2.45	2.86	2.75	0.0103	0.0105	0.0109	2.60E-05
3.54	3.09	3.57	0.0103	0.0105	0.0109	2.60E-05
2.41	2.34	2.71	0.0103	0.0105	0.0109	2.61E-05
2.41	2.34	2.71	0.0103	0.0105	0.0109	2.61E-05
0.011	0.012	0.0117	3.2	3.65	3.71	2.62E-05
3.73	3.81	3.28	0.0103	0.0105	0.0109	2.62E-05
3.73	3.81	3.28	0.0103	0.0105	0.0109	2.62E-05
2.11	2.45	2.4	0.0103	0.0105	0.0109	2.62E-05
2.61	2.35	2.24	0.0103	0.0105	0.0109	2.63E-05
0.011	0.012	0.0117	2.75	3.15	3.18	2.64E-05
0.011	0.012	0.0117	3.45	3.14	2.95	2.65E-05
2.37	2.52	2.15	0.0103	0.0105	0.0109	2.65E-05
2.37	2.52	2.15	0.0103	0.0105	0.0109	2.65E-05
2.92	2.85	2.51	0.0103	0.0105	0.0109	2.66E-05
2.92	2.85	2.51	0.0103	0.0105	0.0109	2.66E-05
2.73	2.64	2.34	0.0103	0.0105	0.0109	2.66E-05
2.73	2.64	2.34	0.0103	0.0105	0.0109	2.66E-05
2.89	3.19	2.73	0.0103	0.0105	0.0109	2.67E-05
2.89	3.19	2.73	0.0103	0.0105	0.0109	2.67E-05

3.67	3.88	3.31	0.0103	0.0105	0.0109	2.67E-05
2.51	2.35	2.14	0.0103	0.0105	0.0109	2.68E-05
3.52	3.07	3.08	0.0103	0.0105	0.0109	2.69E-05
3.52	3.07	3.08	0.0103	0.0105	0.0109	2.69E-05
3.52	3.07	3.08	0.0103	0.0105	0.0109	2.69E-05
0.011	0.012	0.0117	2.57	3	2.9	2.70E-05
3.19	2.72	3.01	0.0103	0.0105	0.0109	2.70E-05
2.83	3.24	2.83	0.0103	0.0105	0.0109	2.70E-05
4.73	4.72	4.1	0.0103	0.0105	0.0109	2.70E-05
0.011	0.012	0.0117	3.94	4.56	4.52	2.71E-05
3.43	3.06	2.95	0.0103	0.0105	0.0109	2.72E-05
3.1	2.78	2.66	0.0103	0.0105	0.0109	2.72E-05
3.1	2.78	2.66	0.0103	0.0105	0.0109	2.72E-05
0.011	0.012	0.0117	2.37	2.21	2.59	2.72E-05
3.48	3.02	3.06	0.0103	0.0105	0.0109	2.72E-05
3.48	3.02	3.06	0.0103	0.0105	0.0109	2.72E-05
2.43	2.15	2.1	0.0103	0.0105	0.0109	2.73E-05
2.43	2.15	2.1	0.0103	0.0105	0.0109	2.73E-05
4.41	3.76	4.18	0.0103	0.0105	0.0109	2.73E-05
2.65	2.38	2.79	0.0103	0.0105	0.0109	2.73E-05
3.38	3.1	3.64	0.0103	0.0105	0.0109	2.73E-05
3.38	3.1	3.64	0.0103	0.0105	0.0109	2.73E-05
3.37	3.15	2.87	0.0103	0.0105	0.0109	2.74E-05
3.37	3.15	2.87	0.0103	0.0105	0.0109	2.74E-05
0.011	0.012	0.0117	2.7	3.15	2.83	2.74E-05
0.011	0.012	0.0117	2.7	3.15	2.83	2.74E-05
2.01	2.21	2.36	0.0103	0.0105	0.0109	2.75E-05
2.01	2.21	2.36	0.0103	0.0105	0.0109	2.75E-05
3.44	3.55	3.04	0.0103	0.0105	0.0109	2.76E-05
3.44	3.55	3.04	0.0103	0.0105	0.0109	2.76E-05
3.44	3.55	3.04	0.0103	0.0105	0.0109	2.76E-05
2.32	2.71	2.44	0.0103	0.0105	0.0109	2.77E-05
2.44	2.73	2.86	0.0103	0.0105	0.0109	2.78E-05
2.44	2.73	2.86	0.0103	0.0105	0.0109	2.78E-05
2.8	3.27	3.17	0.0103	0.0105	0.0109	2.78E-05
2.8	3.27	3.17	0.0103	0.0105	0.0109	2.78E-05
2.92	3.16	2.69	0.0103	0.0105	0.0109	2.79E-05
2.43	2.62	2.23	0.0103	0.0105	0.0109	2.79E-05
2.43	2.62	2.23	0.0103	0.0105	0.0109	2.79E-05
0.011	0.012	0.0117	2.73	2.84	3.18	2.79E-05
2.59	2.25	2.27	0.0103	0.0105	0.0109	2.81E-05
3.74	3.91	3.83	2.34	2.15	2.21	2.83E-05
3.32	2.89	3.35	0.0103	0.0105	0.0109	2.83E-05
3.32	2.89	3.35	0.0103	0.0105	0.0109	2.83E-05
4.54	3.87	4.34	0.0103	0.0105	0.0109	2.85E-05
2.7	2.34	2.37	0.0103	0.0105	0.0109	2.86E-05
2.63	2.25	2.55	0.0103	0.0105	0.0109	2.86E-05
2.63	2.25	2.55	0.0103	0.0105	0.0109	2.86E-05
0.011	0.012	0.0117	2.88	3.07	2.61	2.88E-05
0.011	0.012	0.0117	2.88	3.07	2.61	2.88E-05
2.6	3.05	2.92	0.0103	0.0105	0.0109	2.88E-05
2.6	3.05	2.92	0.0103	0.0105	0.0109	2.88E-05
2.87	2.45	2.59	0.0103	0.0105	0.0109	2.89E-05
5.52	5.41	5.32	3.44	3.5	3.25	2.89E-05
5.52	5.41	5.32	3.44	3.5	3.25	2.89E-05
5.52	5.41	5.32	3.44	3.5	3.25	2.89E-05
0.011	0.012	0.0117	2.64	3.06	2.7	2.89E-05
0.011	0.012	0.0117	2.64	3.06	2.7	2.89E-05

3.72	3.6	4.19	0.0103	0.0105	0.0109	2.90E-05
0.011	0.012	0.0117	2.75	3.2	2.84	2.91E-05
2.79	2.59	2.37	0.0103	0.0105	0.0109	2.92E-05
4.05	4.21	3.59	0.0103	0.0105	0.0109	2.93E-05
2.13	2.49	2.42	0.0103	0.0105	0.0109	2.93E-05
3.25	3.17	3.68	0.0103	0.0105	0.0109	2.93E-05
3.25	3.17	3.68	0.0103	0.0105	0.0109	2.93E-05
3.25	3.17	3.68	0.0103	0.0105	0.0109	2.93E-05
4.59	4.54	3.95	0.0103	0.0105	0.0109	2.95E-05
4.59	4.54	3.95	0.0103	0.0105	0.0109	2.95E-05
4.59	4.54	3.95	0.0103	0.0105	0.0109	2.95E-05
2.42	2.74	2.36	0.0103	0.0105	0.0109	2.95E-05
0.011	0.012	0.0117	2.73	2.93	3.21	2.95E-05
3.24	3.34	3.77	0.0103	0.0105	0.0109	2.95E-05
2.52	2.57	2.92	0.0103	0.0105	0.0109	2.96E-05
3.24	3.02	2.75	0.0103	0.0105	0.0109	2.97E-05
3.24	3.02	2.75	0.0103	0.0105	0.0109	2.97E-05
0.011	0.012	0.0117	2.56	2.92	2.99	2.98E-05
0.011	0.012	0.0117	2.97	3.46	3.07	2.98E-05
2.68	2.92	2.48	0.0103	0.0105	0.0109	2.99E-05
2.68	2.92	2.48	0.0103	0.0105	0.0109	2.99E-05
3.68	3.65	4.21	0.0103	0.0105	0.0109	2.99E-05
2.1	2.21	2.46	0.0103	0.0105	0.0109	2.99E-05
3.1	2.8	2.64	0.0103	0.0105	0.0109	3.02E-05
3.1	2.8	2.64	0.0103	0.0105	0.0109	3.02E-05
0.011	0.012	0.0117	3.36	2.85	3.14	3.02E-05
2.63	2.55	2.97	0.0103	0.0105	0.0109	3.03E-05
2.72	2.41	2.83	0.0103	0.0105	0.0109	3.03E-05
3.23	3.77	3.35	0.0103	0.0105	0.0109	3.03E-05
3.68	3.14	3.3	0.0103	0.0105	0.0109	3.04E-05
2.29	2.27	2.62	0.0103	0.0105	0.0109	3.04E-05
3.24	2.78	3.19	0.0103	0.0105	0.0109	3.04E-05
2.91	2.47	2.75	0.0103	0.0105	0.0109	3.04E-05
2.4	2.62	2.83	0.0103	0.0105	0.0109	3.04E-05
2.4	2.62	2.83	0.0103	0.0105	0.0109	3.04E-05
2.51	2.96	2.77	0.0103	0.0105	0.0109	3.05E-05
2.51	2.96	2.77	0.0103	0.0105	0.0109	3.05E-05
2.56	2.34	2.76	0.0103	0.0105	0.0109	3.06E-05
2.36	2.6	2.21	0.0103	0.0105	0.0109	3.07E-05
4.3	4.65	3.94	0.0103	0.0105	0.0109	3.09E-05
4.3	4.65	3.94	0.0103	0.0105	0.0109	3.09E-05
4.3	4.65	3.94	0.0103	0.0105	0.0109	3.09E-05
2.95	2.61	2.53	0.0103	0.0105	0.0109	3.12E-05
2.95	2.61	2.53	0.0103	0.0105	0.0109	3.12E-05
2.95	2.61	2.53	0.0103	0.0105	0.0109	3.12E-05
3.15	2.67	2.97	0.0103	0.0105	0.0109	3.12E-05
3.15	2.67	2.97	0.0103	0.0105	0.0109	3.12E-05
3.07	2.77	2.61	0.0103	0.0105	0.0109	3.15E-05
2.95	2.5	2.79	0.0103	0.0105	0.0109	3.17E-05
2.95	2.5	2.79	0.0103	0.0105	0.0109	3.17E-05
2.95	2.5	2.79	0.0103	0.0105	0.0109	3.17E-05
3.14	2.66	2.97	0.0103	0.0105	0.0109	3.20E-05
2.74	2.37	2.39	0.0103	0.0105	0.0109	3.20E-05
2.74	2.37	2.39	0.0103	0.0105	0.0109	3.20E-05
3.24	2.79	2.84	0.0103	0.0105	0.0109	3.22E-05
3.24	2.79	2.84	0.0103	0.0105	0.0109	3.22E-05
0.011	0.012	0.0117	3.56	3.71	3.15	3.23E-05
3.56	3.32	3.01	0.0103	0.0105	0.0109	3.25E-05

0.011	0.012	0.0117	3.03	3.22	3.57	3.26E-05
2.99	2.82	2.53	0.0103	0.0105	0.0109	3.27E-05
2.99	2.82	2.53	0.0103	0.0105	0.0109	3.27E-05
2.63	2.28	2.66	0.0103	0.0105	0.0109	3.28E-05
2.63	2.28	2.66	0.0103	0.0105	0.0109	3.28E-05
2.44	2.25	2.66	0.0103	0.0105	0.0109	3.28E-05
2.44	2.25	2.66	0.0103	0.0105	0.0109	3.28E-05
2.41	2.2	2.04	0.0103	0.0105	0.0109	3.29E-05
3.31	3.35	2.87	0.0103	0.0105	0.0109	3.29E-05
3.31	3.35	2.87	0.0103	0.0105	0.0109	3.29E-05
4.23	3.58	3.85	0.0103	0.0105	0.0109	3.31E-05
2.32	2.04	2.4	0.0103	0.0105	0.0109	3.31E-05
2.32	2.04	2.4	0.0103	0.0105	0.0109	3.31E-05
3.24	2.94	3.48	0.0103	0.0105	0.0109	3.31E-05
3.24	2.94	3.48	0.0103	0.0105	0.0109	3.31E-05
2.38	2.76	2.41	0.0103	0.0105	0.0109	3.31E-05
2.38	2.76	2.41	0.0103	0.0105	0.0109	3.31E-05
0.011	0.012	0.0117	2.57	3.04	2.86	3.32E-05
2.18	2.41	2.58	0.0103	0.0105	0.0109	3.32E-05
0.011	0.012	0.0117	2.75	2.88	2.44	3.33E-05
2.67	3.11	2.73	0.0103	0.0105	0.0109	3.33E-05
2.67	3.11	2.73	0.0103	0.0105	0.0109	3.33E-05
2.84	2.96	2.51	0.0103	0.0105	0.0109	3.34E-05
2.84	2.96	2.51	0.0103	0.0105	0.0109	3.34E-05
2.9	2.72	3.21	0.0103	0.0105	0.0109	3.35E-05
2.9	2.72	3.21	0.0103	0.0105	0.0109	3.35E-05
2.77	3.12	2.66	0.0103	0.0105	0.0109	3.36E-05
3.66	3.61	3.13	0.0103	0.0105	0.0109	3.37E-05
3.66	3.61	3.13	0.0103	0.0105	0.0109	3.37E-05
2.9	2.53	2.97	0.0103	0.0105	0.0109	3.39E-05
2.9	2.53	2.97	0.0103	0.0105	0.0109	3.39E-05
2.83	2.39	2.66	0.0103	0.0105	0.0109	3.40E-05
2.83	2.39	2.66	0.0103	0.0105	0.0109	3.40E-05
2.44	2.87	2.79	0.0103	0.0105	0.0109	3.43E-05
3.35	3.02	3.58	0.0103	0.0105	0.0109	3.45E-05
0.011	0.012	0.0117	3.83	3.74	3.26	3.45E-05
3.46	3.91	4.09	0.0103	0.0105	0.0109	3.45E-05
3.46	3.91	4.09	0.0103	0.0105	0.0109	3.45E-05
0.011	0.012	0.0117	2.95	2.5	2.65	3.46E-05
0.011	0.012	0.0117	2.95	2.5	2.65	3.46E-05
2.63	2.22	2.48	0.0103	0.0105	0.0109	3.47E-05
2.52	2.21	2.16	0.0103	0.0105	0.0109	3.47E-05
2.64	3.06	2.66	0.0103	0.0105	0.0109	3.48E-05
2.64	3.06	2.66	0.0103	0.0105	0.0109	3.48E-05
3.21	2.73	3.13	0.0103	0.0105	0.0109	3.48E-05
3.21	2.73	3.13	0.0103	0.0105	0.0109	3.48E-05
3.21	2.73	3.13	0.0103	0.0105	0.0109	3.48E-05
2.75	3.02	2.55	0.0103	0.0105	0.0109	3.48E-05
2.75	3.02	2.55	0.0103	0.0105	0.0109	3.48E-05
3.19	2.93	2.69	0.0103	0.0105	0.0109	3.50E-05
0.011	0.012	0.0117	2.87	3.06	2.58	3.52E-05
0.011	0.012	0.0117	2.87	3.06	2.58	3.52E-05
2.745	2.57	3.04	0.0103	0.0105	0.0109	3.52E-05
2.84	2.84	2.44	0.0103	0.0105	0.0109	3.53E-05
3.47	3.89	3.3	0.0103	0.0105	0.0109	3.54E-05
4.34	4.86	4.12	0.0103	0.0105	0.0109	3.55E-05
2.57	2.27	2.19	0.0103	0.0105	0.0109	3.57E-05
0.011	0.012	0.0117	3.06	2.79	2.58	3.59E-05

3.99	4.4	4.74	0.0103	0.0105	0.0109	3.59E-05
2.73	2.39	2.82	0.0103	0.0105	0.0109	3.59E-05
3.21	3.48	2.93	0.0103	0.0105	0.0109	3.60E-05
0.011	0.012	0.0117	2.33	2.36	2.71	3.60E-05
2.63	2.23	2.55	0.0103	0.0105	0.0109	3.60E-05
2.63	2.23	2.55	0.0103	0.0105	0.0109	3.60E-05
2.88	2.46	2.53	0.0103	0.0105	0.0109	3.61E-05
2.53	2.13	2.35	0.0103	0.0105	0.0109	3.61E-05
0.011	0.012	0.0117	2.41	2.11	2.49	3.61E-05
3.6	3.07	3.55	0.0103	0.0105	0.0109	3.62E-05
3.6	3.07	3.55	0.0103	0.0105	0.0109	3.62E-05
3.13	3.42	2.88	0.0103	0.0105	0.0109	3.63E-05
3.13	3.42	2.88	0.0103	0.0105	0.0109	3.63E-05
3.1	2.61	2.91	0.0103	0.0105	0.0109	3.64E-05
2.6	3.09	2.85	0.0103	0.0105	0.0109	3.65E-05
2.19	2.58	2.29	0.0103	0.0105	0.0109	3.67E-05
2.19	2.58	2.29	0.0103	0.0105	0.0109	3.67E-05
2.99	3.51	3.09	0.0103	0.0105	0.0109	3.69E-05
2.5	2.37	2.8	0.0103	0.0105	0.0109	3.69E-05
0.011	0.012	0.0117	3.67	3.47	3.09	3.70E-05
4.44	3.77	3.93	0.0103	0.0105	0.0109	3.70E-05
0.011	0.012	0.0117	2.62	2.95	3.11	3.71E-05
0.011	0.012	0.0117	2.62	2.95	3.11	3.71E-05
2.76	2.37	2.4	0.0103	0.0105	0.0109	3.73E-05
3.35	2.87	2.92	0.0103	0.0105	0.0109	3.74E-05
0.011	0.012	0.0117	3.74	3.22	3.24	3.75E-05
0.011	0.012	0.0117	3.74	3.22	3.24	3.75E-05
0.011	0.012	0.0117	2.76	2.88	2.43	3.76E-05
0.011	0.012	0.0117	2.76	2.88	2.43	3.76E-05
2.08	2.05	2.39	0.0103	0.0105	0.0109	3.76E-05
2.75	2.8	2.38	0.0103	0.0105	0.0109	3.78E-05
3.5	3.12	2.96	0.0103	0.0105	0.0109	3.78E-05
0.011	0.012	0.0117	2.84	2.57	3.06	3.80E-05
2.24	2.57	2.2	0.0103	0.0105	0.0109	3.81E-05
2.24	2.57	2.2	0.0103	0.0105	0.0109	3.81E-05
3.15	2.74	2.7	0.0103	0.0105	0.0109	3.81E-05
3.15	2.74	2.7	0.0103	0.0105	0.0109	3.81E-05
3.15	2.74	2.7	0.0103	0.0105	0.0109	3.81E-05
3.15	2.74	2.7	0.0103	0.0105	0.0109	3.81E-05
3.25	3.24	3.76	0.0103	0.0105	0.0109	3.81E-05
2.04	2.4	2.36	0.0103	0.0105	0.0109	3.84E-05
2.04	2.4	2.36	0.0103	0.0105	0.0109	3.84E-05
3.57	3.01	3.2	0.0103	0.0105	0.0109	3.87E-05
3.57	3.01	3.2	0.0103	0.0105	0.0109	3.87E-05
3.02	3.57	3.17	0.0103	0.0105	0.0109	3.87E-05
3.75	3.35	3.99	0.0103	0.0105	0.0109	3.88E-05
3.16	3.67	3.17	0.0103	0.0105	0.0109	3.89E-05
3.16	3.67	3.17	0.0103	0.0105	0.0109	3.89E-05
2.55	2.38	2.14	0.0103	0.0105	0.0109	3.90E-05
3.11	2.75	3.27	0.0103	0.0105	0.0109	3.90E-05
0.011	0.012	0.0117	2.74	3.24	3.15	3.91E-05
0.011	0.012	0.0117	2.74	3.24	3.15	3.91E-05
3.34	3.3	3.85	0.0103	0.0105	0.0109	3.92E-05
3.34	3.3	3.85	0.0103	0.0105	0.0109	3.92E-05
2.81	3.32	2.94	0.0103	0.0105	0.0109	3.92E-05
2.81	3.32	2.94	0.0103	0.0105	0.0109	3.92E-05
0.011	0.012	0.0117	2.68	2.74	3.14	3.93E-05
0.011	0.012	0.0117	2.68	2.74	3.14	3.93E-05

0.011	0.012	0.0117	2.65	3.14	2.8	3.94E-05
0.011	0.012	0.0117	2.65	3.14	2.8	3.94E-05
0.011	0.012	0.0117	2.65	3.14	2.8	3.94E-05
2.51	2.49	2.9	0.0103	0.0105	0.0109	3.95E-05
2.13	2.5	2.48	0.0103	0.0105	0.0109	3.96E-05
3.22	3.01	2.7	0.0103	0.0105	0.0109	3.96E-05
3.22	3.01	2.7	0.0103	0.0105	0.0109	3.96E-05
3.22	3.02	2.7	0.0103	0.0105	0.0109	3.99E-05
3.22	3.02	2.7	0.0103	0.0105	0.0109	3.99E-05
3.22	3.02	2.7	0.0103	0.0105	0.0109	3.99E-05
3.72	3.12	3.5	0.0103	0.0105	0.0109	3.99E-05
3.95	3.43	4.06	0.0103	0.0105	0.0109	4.02E-05
3.95	3.43	4.06	0.0103	0.0105	0.0109	4.02E-05
3.95	3.43	4.06	0.0103	0.0105	0.0109	4.02E-05
2.32	2.03	2.41	0.0103	0.0105	0.0109	4.03E-05
2.32	2.03	2.41	0.0103	0.0105	0.0109	4.03E-05
3.115	2.62	2.795	0.0103	0.0105	0.0109	4.04E-05
3.115	2.62	2.795	0.0103	0.0105	0.0109	4.04E-05
3.115	2.62	2.795	0.0103	0.0105	0.0109	4.04E-05
4.72	4.69	4.02	0.0103	0.0105	0.0109	4.04E-05
4.72	4.69	4.02	0.0103	0.0105	0.0109	4.04E-05
4.72	4.69	4.02	0.0103	0.0105	0.0109	4.04E-05
2.56	2.2	2.21	0.0103	0.0105	0.0109	4.05E-05
0.011	0.012	0.0117	2.62	3.12	2.97	4.06E-05
2.48	2.46	2.11	0.0103	0.0105	0.0109	4.10E-05
2.34	2.74	2.38	0.0103	0.0105	0.0109	4.11E-05
2.34	2.74	2.38	0.0103	0.0105	0.0109	4.11E-05
0.011	0.012	0.0117	2.78	3.19	3.3	4.11E-05
0.011	0.012	0.0117	2.78	3.19	3.3	4.11E-05
2.34	2.4	2.75	0.0103	0.0105	0.0109	4.12E-05
2.34	2.4	2.75	0.0103	0.0105	0.0109	4.12E-05
3.06	2.56	2.84	0.0103	0.0105	0.0109	4.15E-05
3.06	2.56	2.84	0.0103	0.0105	0.0109	4.15E-05
3.33	2.83	3.3	0.0103	0.0105	0.0109	4.15E-05
0.011	0.012	0.0117	2.48	2.89	2.92	4.17E-05
0.011	0.012	0.0117	2.48	2.89	2.92	4.17E-05
2.47	2.18	2.6	0.0103	0.0105	0.0109	4.18E-05
2.47	2.18	2.6	0.0103	0.0105	0.0109	4.18E-05
2.12	2.52	2.43	0.0103	0.0105	0.0109	4.19E-05
0.011	0.012	0.0117	2.45	2.89	2.85	4.20E-05
2.77	2.91	2.44	0.0103	0.0105	0.0109	4.20E-05
3.49	2.92	3.28	0.0103	0.0105	0.0109	4.21E-05
3.49	2.92	3.28	0.0103	0.0105	0.0109	4.21E-05
3.45	3.07	3.67	0.0103	0.0105	0.0109	4.23E-05
2.2	2.63	2.4	0.0103	0.0105	0.0109	4.24E-05
2.73	2.42	2.3	0.0103	0.0105	0.0109	4.25E-05
2	2.35	2.34	0.0103	0.0105	0.0109	4.25E-05
0.011	0.012	0.0117	3.13	3.6	3.72	4.26E-05
2.82	2.74	3.23	0.0103	0.0105	0.0109	4.30E-05
2.82	2.74	3.23	0.0103	0.0105	0.0109	4.30E-05
0.011	0.012	0.0117	2.44	2.61	2.91	4.31E-05
0.011	0.012	0.0117	2.44	2.61	2.91	4.31E-05
2.82	2.93	2.46	0.0103	0.0105	0.0109	4.33E-05
2.6	2.33	2.79	0.0103	0.0105	0.0109	4.33E-05
2.6	2.33	2.79	0.0103	0.0105	0.0109	4.33E-05
3.06	3.6	3.13	0.0103	0.0105	0.0109	4.35E-05
3.06	3.6	3.13	0.0103	0.0105	0.0109	4.35E-05
2.69	2.31	2.73	0.0103	0.0105	0.0109	4.36E-05

2.04	2.43	2.34	0.0103	0.0105	0.0109	4.37E-05
3.71	3.5	3.1	0.0103	0.0105	0.0109	4.38E-05
3.71	3.5	3.1	0.0103	0.0105	0.0109	4.38E-05
3.41	2.85	3.09	0.0103	0.0105	0.0109	4.38E-05
3.41	2.85	3.09	0.0103	0.0105	0.0109	4.38E-05
3.41	2.85	3.09	0.0103	0.0105	0.0109	4.38E-05
2.96	2.47	2.72	0.0103	0.0105	0.0109	4.40E-05
2.59	2.32	2.17	0.0103	0.0105	0.0109	4.41E-05
2.16	2.15	2.51	0.0103	0.0105	0.0109	4.41E-05
2.09	2.5	2.26	0.0103	0.0105	0.0109	4.42E-05
2.09	2.5	2.26	0.0103	0.0105	0.0109	4.42E-05
2.63	2.96	3.15	0.0103	0.0105	0.0109	4.42E-05
2.55	2.57	2.18	0.0103	0.0105	0.0109	4.42E-05
2.55	2.57	2.18	0.0103	0.0105	0.0109	4.42E-05
2.76	2.33	2.71	0.0103	0.0105	0.0109	4.45E-05
3.34	2.97	3.56	0.0103	0.0105	0.0109	4.47E-05
3.34	2.97	3.56	0.0103	0.0105	0.0109	4.47E-05
3.34	2.97	3.56	0.0103	0.0105	0.0109	4.47E-05
3.78	3.21	3.28	0.0103	0.0105	0.0109	4.51E-05
3.78	3.21	3.28	0.0103	0.0105	0.0109	4.51E-05
0.011	0.012	0.0117	3.08	3.08	2.62	4.51E-05
0.011	0.012	0.0117	2.62	2.78	2.32	4.52E-05
0.011	0.012	0.0117	2.62	2.78	2.32	4.52E-05
2.6	2.63	3.05	0.0103	0.0105	0.0109	4.59E-05
2.6	2.63	3.05	0.0103	0.0105	0.0109	4.59E-05
0.011	0.012	0.0117	2.58	2.16	2.3	4.60E-05
2.41	2.39	2.8	0.0103	0.0105	0.0109	4.61E-05
3.98	4.08	3.43	0.0103	0.0105	0.0109	4.61E-05
3.98	4.08	3.43	0.0103	0.0105	0.0109	4.61E-05
3.98	4.08	3.43	0.0103	0.0105	0.0109	4.61E-05
3.55	3.51	3	0.0103	0.0105	0.0109	4.63E-05
3.55	3.51	3	0.0103	0.0105	0.0109	4.63E-05
0.011	0.012	0.0117	2.67	2.78	3.17	4.65E-05
2.67	3.17	3.11	0.0103	0.0105	0.0109	4.65E-05
2.26	2.7	2.6	0.0103	0.0105	0.0109	4.67E-05
3.05	2.67	2.57	0.0103	0.0105	0.0109	4.69E-05
0.011	0.012	0.0117	2.91	3.45	3.4	4.70E-05
0.011	0.012	0.0117	2.91	3.45	3.4	4.70E-05
0.011	0.012	0.0117	3.47	3.4	2.92	4.70E-05
0.011	0.012	0.0117	3.47	3.4	2.92	4.70E-05
0.011	0.012	0.0117	2.4	2.38	2.03	4.72E-05
2.13	2.56	2.34	0.0103	0.0105	0.0109	4.72E-05
0.011	0.012	0.0117	3.66	3.16	3.11	4.73E-05
3.45	2.98	2.93	0.0103	0.0105	0.0109	4.74E-05
3.45	2.98	2.93	0.0103	0.0105	0.0109	4.74E-05
3.45	2.98	2.93	0.0103	0.0105	0.0109	4.74E-05
3.4	3.2	2.83	0.0103	0.0105	0.0109	4.75E-05
3.4	3.2	2.83	0.0103	0.0105	0.0109	4.75E-05
0.011	0.012	0.0117	2.27	2.4	2.71	4.75E-05
0.011	0.012	0.0117	2.57	3.06	2.69	4.79E-05
0.011	0.012	0.0117	2.57	3.06	2.69	4.79E-05
0.011	0.012	0.0117	2.7	3.02	2.52	4.81E-05
2.64	2.84	2.36	0.0103	0.0105	0.0109	4.82E-05
2.76	2.78	2.35	0.0103	0.0105	0.0109	4.82E-05
2.76	2.78	2.35	0.0103	0.0105	0.0109	4.82E-05
0.011	0.012	0.0117	3.25	2.77	3.28	4.82E-05
2.77	3.2	2.71	0.0103	0.0105	0.0109	4.83E-05
2.77	3.2	2.71	0.0103	0.0105	0.0109	4.83E-05

2.04	2.4	2.41	0.0103	0.0105	0.0109	4.84E-05
3.14	2.84	3.42	0.0103	0.0105	0.0109	4.87E-05
3.14	2.84	3.42	0.0103	0.0105	0.0109	4.87E-05
2.12	2.23	2.53	0.0103	0.0105	0.0109	4.88E-05
2.49	2.34	2.07	0.0103	0.0105	0.0109	4.89E-05
2.49	2.34	2.07	0.0103	0.0105	0.0109	4.89E-05
3.39	3.9	3.29	0.0103	0.0105	0.0109	4.90E-05
2.69	2.85	2.37	0.0103	0.0105	0.0109	4.91E-05
0.011	0.012	0.0117	4.61	3.83	4.18	4.92E-05
0.011	0.012	0.0117	4.61	3.83	4.18	4.92E-05
0.011	0.012	0.0117	3.23	2.97	2.68	4.96E-05
0.011	0.012	0.0117	3.23	2.97	2.68	4.96E-05
0.011	0.012	0.0117	3.23	2.97	2.68	4.96E-05
2.63	2.55	2.2	0.0103	0.0105	0.0109	4.97E-05
2.64	2.25	2.67	0.0103	0.0105	0.0109	4.97E-05
2.61	3.03	3.12	0.0103	0.0105	0.0109	5.01E-05
0.011	0.012	0.0117	2.54	2.57	2.99	5.02E-05
0.011	0.012	0.0117	2.54	2.57	2.99	5.02E-05
2.47	2.51	2.11	0.0103	0.0105	0.0109	5.03E-05
2.56	2.14	2.26	0.0103	0.0105	0.0109	5.03E-05
2.57	2.21	2.64	0.0103	0.0105	0.0109	5.04E-05
2.57	2.21	2.64	0.0103	0.0105	0.0109	5.04E-05
0.011	0.012	0.0117	2.79	2.32	2.65	5.04E-05
2.77	2.31	2.46	0.0103	0.0105	0.0109	5.05E-05
2.77	2.31	2.46	0.0103	0.0105	0.0109	5.05E-05
3.51	3.11	3.75	0.0103	0.0105	0.0109	5.07E-05
4.62	4.2	3.83	0.0103	0.0105	0.0109	5.10E-05
3.45	2.88	3.34	0.0103	0.0105	0.0109	5.13E-05
3.45	2.88	3.34	0.0103	0.0105	0.0109	5.13E-05
2.26	2.7	2.37	0.0103	0.0105	0.0109	5.13E-05
2.63	2.19	2.34	0.0103	0.0105	0.0109	5.13E-05
0.011	0.012	0.0117	2.87	3.15	2.61	5.16E-05
3.44	2.93	2.94	0.0103	0.0105	0.0109	5.17E-05
4.21	4.77	5.08	0.0103	0.0105	0.0109	5.17E-05
0.011	0.012	0.0117	2.59	2.23	2.67	5.17E-05
3.07	3.03	2.58	0.0103	0.0105	0.0109	5.19E-05
2.59	2.79	2.31	0.0103	0.0105	0.0109	5.20E-05
2.59	2.79	2.31	0.0103	0.0105	0.0109	5.20E-05
2.22	2.46	2.04	0.0103	0.0105	0.0109	5.22E-05
4.06	4.5	3.73	0.0103	0.0105	0.0109	5.22E-05
4.06	4.5	3.73	0.0103	0.0105	0.0109	5.22E-05
3.19	2.65	2.85	0.0103	0.0105	0.0109	5.23E-05
3.19	2.65	2.85	0.0103	0.0105	0.0109	5.23E-05
3.02	2.74	3.31	0.0103	0.0105	0.0109	5.24E-05
0.011	0.012	0.0117	2.69	2.65	3.13	5.26E-05
0.011	0.012	0.0117	2.69	2.65	3.13	5.26E-05
2.58	3.12	2.87	0.0103	0.0105	0.0109	5.31E-05
2.58	3.12	2.87	0.0103	0.0105	0.0109	5.31E-05
2.53	3.06	2.81	0.0103	0.0105	0.0109	5.33E-05
2.53	3.06	2.81	0.0103	0.0105	0.0109	5.33E-05
2.82	2.42	2.9	0.0103	0.0105	0.0109	5.36E-05
2.82	2.42	2.9	0.0103	0.0105	0.0109	5.36E-05
0.011	0.012	0.0117	2.29	2.77	2.56	5.36E-05
2.54	2.11	2.26	0.0103	0.0105	0.0109	5.37E-05
0.011	0.012	0.0117	2.3	2.38	2.74	5.37E-05
0.011	0.012	0.0117	3.32	2.78	3.26	5.37E-05
0.011	0.012	0.0117	3.32	2.78	3.26	5.37E-05
0.011	0.012	0.0117	3.32	2.78	3.26	5.37E-05

5.29	4.38	4.76	0.0103	0.0105	0.0109	5.37E-05
0.011	0.012	0.0117	2.71	2.51	2.24	5.39E-05
2.24	2.48	2.71	0.0103	0.0105	0.0109	5.39E-05
3.37	4	3.45	0.0103	0.0105	0.0109	5.41E-05
3.37	4	3.45	0.0103	0.0105	0.0109	5.41E-05
3.37	4	3.45	0.0103	0.0105	0.0109	5.41E-05
0.011	0.012	0.0117	2.32	2.51	2.8	5.43E-05
2.37	2.45	2.04	0.0103	0.0105	0.0109	5.43E-05
2.84	2.47	2.38	0.0103	0.0105	0.0109	5.43E-05
2.84	2.47	2.38	0.0103	0.0105	0.0109	5.43E-05
0.011	0.012	0.0117	3.08	3.52	2.94	5.44E-05
2.81	3.38	2.99	0.0103	0.0105	0.0109	5.45E-05
2.81	3.38	2.99	0.0103	0.0105	0.0109	5.45E-05
3.1	3.63	3.08	0.0103	0.0105	0.0109	5.48E-05
3.29	3.8	3.19	0.0103	0.0105	0.0109	5.50E-05
2.13	2.58	2.37	0.0103	0.0105	0.0109	5.51E-05
2.4	2.8	2.88	0.0103	0.0105	0.0109	5.52E-05
2.4	2.8	2.88	0.0103	0.0105	0.0109	5.52E-05
2.4	2.8	2.88	0.0103	0.0105	0.0109	5.52E-05
2.4	2.8	2.88	0.0103	0.0105	0.0109	5.52E-05
4.09	3.49	4.18	0.0103	0.0105	0.0109	5.54E-05
4.09	3.49	4.18	0.0103	0.0105	0.0109	5.54E-05
4.09	3.49	4.18	0.0103	0.0105	0.0109	5.54E-05
2.56	2.58	3.02	0.0103	0.0105	0.0109	5.54E-05
2.56	2.58	3.02	0.0103	0.0105	0.0109	5.54E-05
0.011	0.012	0.0117	3.35	4.01	3.93	5.55E-05
0.011	0.012	0.0117	3.35	4.01	3.93	5.55E-05
2.41	2.01	2.11	0.0103	0.0105	0.0109	5.57E-05
2.41	2.01	2.11	0.0103	0.0105	0.0109	5.57E-05
4.12	3.75	3.4	0.0103	0.0105	0.0109	5.57E-05
2.42	2.55	2.11	0.0103	0.0105	0.0109	5.60E-05
3.14	2.67	2.67	0.0103	0.0105	0.0109	5.63E-05
3.82	3.98	3.3	0.0103	0.0105	0.0109	5.63E-05
3.82	3.98	3.3	0.0103	0.0105	0.0109	5.63E-05
3.82	3.98	3.3	0.0103	0.0105	0.0109	5.63E-05
0.011	0.012	0.0117	2.77	3.36	3.09	5.66E-05
2.85	2.35	2.6	0.0103	0.0105	0.0109	5.67E-05
0.011	0.012	0.0117	3.77	4.23	3.5	5.68E-05
0.011	0.012	0.0117	2.76	3.18	2.66	5.70E-05
0.011	0.012	0.0117	2.76	3.18	2.66	5.70E-05
0.011	0.012	0.0117	2.76	3.18	2.66	5.70E-05
3.19	2.67	3.15	0.0103	0.0105	0.0109	5.71E-05
3.19	2.67	3.15	0.0103	0.0105	0.0109	5.71E-05
2.23	2.55	2.7	0.0103	0.0105	0.0109	5.71E-05
2.41	2.07	2.03	0.0103	0.0105	0.0109	5.71E-05
0.011	0.012	0.0117	2.75	3.23	2.74	5.72E-05
0.011	0.012	0.0117	3.13	2.69	3.24	5.72E-05
2.65	2.2	2.56	0.0103	0.0105	0.0109	5.74E-05
2.65	2.2	2.56	0.0103	0.0105	0.0109	5.74E-05
0.011	0.012	0.0117	2.53	3.07	2.8	5.74E-05
2.55	2.27	2.11	0.0103	0.0105	0.0109	5.75E-05
0.011	0.012	0.0117	2.18	2.37	2.64	5.76E-05
0.011	0.012	0.0117	2.18	2.37	2.64	5.76E-05
0.011	0.012	0.0117	2.1	2.55	2.35	5.81E-05
3.34	3.47	3.39	2.26	2.14	2.32	5.82E-05
3.34	3.47	3.39	2.26	2.14	2.32	5.82E-05
0.011	0.012	0.0117	3.36	4	3.44	5.82E-05
0.011	0.012	0.0117	2.25	2.38	2.71	5.87E-05

2.67	2.88	2.37	0.0103	0.0105	0.0109	5.89E-05
2.93	3.56	3.32	0.0103	0.0105	0.0109	5.91E-05
0.011	0.012	0.0117	3.03	3.06	2.56	5.93E-05
2.98	3.14	2.59	0.0103	0.0105	0.0109	5.97E-05
4.62	3.96	4.78	0.0103	0.0105	0.0109	5.98E-05
2.34	2.8	2.42	0.0103	0.0105	0.0109	6.00E-05
2.34	2.8	2.42	0.0103	0.0105	0.0109	6.00E-05
2.34	2.8	2.42	0.0103	0.0105	0.0109	6.00E-05
4.21	4.41	3.64	0.0103	0.0105	0.0109	6.03E-05
2.78	3.06	3.38	0.0103	0.0105	0.0109	6.03E-05
3.23	2.68	3.14	0.0103	0.0105	0.0109	6.05E-05
2.68	3.07	2.55	0.0103	0.0105	0.0109	6.07E-05
2.68	3.07	2.55	0.0103	0.0105	0.0109	6.07E-05
2.4	2.77	2.31	0.0103	0.0105	0.0109	6.07E-05
2.06	2.47	2.14	0.0103	0.0105	0.0109	6.07E-05
4.65	4.46	3.84	0.0103	0.0105	0.0109	6.11E-05
4.65	4.46	3.84	0.0103	0.0105	0.0109	6.11E-05
2.94	2.46	2.53	0.0103	0.0105	0.0109	6.14E-05
5	4.19	4.29	0.0103	0.0105	0.0109	6.15E-05
2.42	2.11	2.01	0.0103	0.0105	0.0109	6.15E-05
2.42	2.11	2.01	0.0103	0.0105	0.0109	6.15E-05
3.28	2.93	2.7	0.0103	0.0105	0.0109	6.19E-05
2.88	3.08	2.53	0.0103	0.0105	0.0109	6.20E-05
2.88	3.08	2.53	0.0103	0.0105	0.0109	6.20E-05
2.88	3.08	2.53	0.0103	0.0105	0.0109	6.20E-05
2.51	2.06	2.3	0.0103	0.0105	0.0109	6.21E-05
2.51	2.06	2.3	0.0103	0.0105	0.0109	6.21E-05
0.011	0.012	0.0117	2.86	2.53	2.36	6.23E-05
2.84	2.6	2.33	0.0103	0.0105	0.0109	6.25E-05
2.84	2.6	2.33	0.0103	0.0105	0.0109	6.25E-05
0.011	0.012	0.0117	2.45	2.48	2.91	6.25E-05
3.84	3.5	3.15	0.0103	0.0105	0.0109	6.26E-05
3.26	3.73	3.09	0.0103	0.0105	0.0109	6.26E-05
0.011	0.012	0.0117	3.26	2.83	2.71	6.26E-05
0.011	0.012	0.0117	3.26	2.83	2.71	6.26E-05
3.17	3.06	2.62	0.0103	0.0105	0.0109	6.27E-05
2.48	2.13	2.58	0.0103	0.0105	0.0109	6.27E-05
2.48	2.13	2.58	0.0103	0.0105	0.0109	6.27E-05
3.14	3.18	2.65	0.0103	0.0105	0.0109	6.28E-05
3.14	3.18	2.65	0.0103	0.0105	0.0109	6.28E-05
3.39	2.78	3.1	0.0103	0.0105	0.0109	6.29E-05
0.011	0.012	0.0117	2.29	2.68	2.77	6.35E-05
4.11	3.78	4.6	0.0103	0.0105	0.0109	6.36E-05
2.37	2.89	2.69	0.0103	0.0105	0.0109	6.36E-05
2.37	2.89	2.69	0.0103	0.0105	0.0109	6.36E-05
3.34	3.39	2.82	0.0103	0.0105	0.0109	6.39E-05
3.34	3.39	2.82	0.0103	0.0105	0.0109	6.39E-05
3.72	3.11	3.19	0.0103	0.0105	0.0109	6.41E-05
3.72	3.11	3.19	0.0103	0.0105	0.0109	6.41E-05
3.16	3.17	2.65	0.0103	0.0105	0.0109	6.44E-05
3.48	4.11	3.47	0.0103	0.0105	0.0109	6.45E-05
3.48	4.11	3.47	0.0103	0.0105	0.0109	6.45E-05
2.5	2.07	2.18	0.0103	0.0105	0.0109	6.46E-05
2.36	2.27	2.73	0.0103	0.0105	0.0109	6.47E-05
2.36	2.27	2.73	0.0103	0.0105	0.0109	6.47E-05
3.21	3.3	2.73	0.0103	0.0105	0.0109	6.48E-05
3.81	3.53	3.12	0.0103	0.0105	0.0109	6.48E-05
2.96	2.66	3.25	0.0103	0.0105	0.0109	6.56E-05

3.23	3.2	2.69	0.0103	0.0105	0.0109	6.57E-05
3.23	3.2	2.69	0.0103	0.0105	0.0109	6.57E-05
3.19	2.61	2.92	0.0103	0.0105	0.0109	6.58E-05
3.19	2.61	2.92	0.0103	0.0105	0.0109	6.58E-05
2.57	2.15	2.57	0.0103	0.0105	0.0109	6.58E-05
2.57	2.15	2.57	0.0103	0.0105	0.0109	6.58E-05
2.91	2.81	2.4	0.0103	0.0105	0.0109	6.58E-05
4.3	3.53	4.09	0.0103	0.0105	0.0109	6.64E-05
4.3	3.53	4.09	0.0103	0.0105	0.0109	6.64E-05
4.3	3.53	4.09	0.0103	0.0105	0.0109	6.64E-05
2.24	2.73	2.59	0.0103	0.0105	0.0109	6.67E-05
2.24	2.73	2.59	0.0103	0.0105	0.0109	6.67E-05
2.24	2.73	2.59	0.0103	0.0105	0.0109	6.67E-05
2.24	2.73	2.59	0.0103	0.0105	0.0109	6.67E-05
2.56	3.13	2.91	0.0103	0.0105	0.0109	6.69E-05
3.76	3.23	3.13	0.0103	0.0105	0.0109	6.70E-05
3.76	3.23	3.13	0.0103	0.0105	0.0109	6.70E-05
3.02	2.48	2.88	0.0103	0.0105	0.0109	6.70E-05
3.26	2.87	3.51	0.0103	0.0105	0.0109	6.71E-05
3.17	2.82	2.6	0.0103	0.0105	0.0109	6.72E-05
3.17	2.82	2.6	0.0103	0.0105	0.0109	6.72E-05
3.17	2.82	2.6	0.0103	0.0105	0.0109	6.72E-05
3.02	2.75	3.36	0.0103	0.0105	0.0109	6.73E-05
0.011	0.012	0.0117	3.17	2.78	3.4	6.77E-05
0.011	0.012	0.0117	3.17	2.78	3.4	6.77E-05
0.011	0.012	0.0117	2.93	3.43	3.56	6.77E-05
0.011	0.012	0.0117	2.93	3.43	3.56	6.77E-05
2.42	2.04	2.46	0.0103	0.0105	0.0109	6.77E-05
2.81	3.06	3.43	0.0103	0.0105	0.0109	6.77E-05
2.4	2.77	2.93	0.0103	0.0105	0.0109	6.80E-05
2.4	2.77	2.93	0.0103	0.0105	0.0109	6.80E-05
3.4	3.35	2.82	0.0103	0.0105	0.0109	6.81E-05
3.4	3.35	2.82	0.0103	0.0105	0.0109	6.81E-05
3.6	3.32	2.94	0.0103	0.0105	0.0109	6.81E-05
3.6	3.32	2.94	0.0103	0.0105	0.0109	6.81E-05
2.25	2.74	2.42	0.0103	0.0105	0.0109	6.83E-05
2.94	3.59	3.2	0.0103	0.0105	0.0109	6.84E-05
2.78	2.91	3.36	0.0103	0.0105	0.0109	6.85E-05
2.26	2.68	2.73	0.0103	0.0105	0.0109	6.89E-05
2.74	2.77	2.3	0.0103	0.0105	0.0109	6.91E-05
2.74	2.77	2.3	0.0103	0.0105	0.0109	6.91E-05
2.6	2.17	2.6	0.0103	0.0105	0.0109	6.91E-05
2.6	2.17	2.6	0.0103	0.0105	0.0109	6.91E-05
0.011	0.012	0.0117	3.04	2.54	2.59	6.93E-05
2.86	2.35	2.75	0.0103	0.0105	0.0109	6.93E-05
2.86	2.35	2.75	0.0103	0.0105	0.0109	6.93E-05
3.14	3.07	3.68	0.0103	0.0105	0.0109	6.94E-05
3.14	3.07	3.68	0.0103	0.0105	0.0109	6.94E-05
4.17	3.52	3.51	0.0103	0.0105	0.0109	6.94E-05
4.17	3.52	3.51	0.0103	0.0105	0.0109	6.94E-05
3.83	4.35	3.57	0.0103	0.0105	0.0109	6.96E-05
3.83	4.35	3.57	0.0103	0.0105	0.0109	6.96E-05
2.99	3.62	3.54	0.0103	0.0105	0.0109	6.97E-05
2.99	3.62	3.54	0.0103	0.0105	0.0109	6.97E-05
3.63	3.04	3.08	0.0103	0.0105	0.0109	6.99E-05
3.63	3.04	3.08	0.0103	0.0105	0.0109	6.99E-05
3.7	3.15	3.09	0.0103	0.0105	0.0109	7.00E-05
3.7	3.15	3.09	0.0103	0.0105	0.0109	7.00E-05

3.7	3.15	3.09	0.0103	0.0105	0.0109	7.00E-05
2.73	2.56	2.23	0.0103	0.0105	0.0109	7.01E-05
2.73	2.56	2.23	0.0103	0.0105	0.0109	7.01E-05
2.48	2.82	3.04	0.0103	0.0105	0.0109	7.02E-05
0.011	0.012	0.0117	2.93	2.52	2.43	7.03E-05
0.011	0.012	0.0117	3.03	2.48	2.69	7.05E-05
2.37	2.79	2.88	0.0103	0.0105	0.0109	7.05E-05
3.23	2.67	3.17	0.0103	0.0105	0.0109	7.07E-05
3.74	4.21	4.59	0.0103	0.0105	0.0109	7.09E-05
0.011	0.012	0.0117	2.65	2.16	2.43	7.10E-05
2.58	2.15	2.2	0.0103	0.0105	0.0109	7.13E-05
2.97	2.73	3.34	0.0103	0.0105	0.0109	7.15E-05
0.011	0.012	0.0117	2.88	3.53	3.31	7.16E-05
0.011	0.012	0.0117	2.88	3.53	3.31	7.16E-05
2.71	2.21	2.44	0.0103	0.0105	0.0109	7.18E-05
2.45	2.09	2.04	0.0103	0.0105	0.0109	7.18E-05
3	2.59	3.17	0.0103	0.0105	0.0109	7.18E-05
3	2.59	3.17	0.0103	0.0105	0.0109	7.18E-05
0.011	0.012	0.0117	2.01	2.44	2.12	7.20E-05
0.011	0.012	0.0117	3.51	4.21	3.58	7.24E-05
0.011	0.012	0.0117	3.51	4.21	3.58	7.24E-05
0.011	0.012	0.0117	2.66	2.83	3.24	7.29E-05
2.745	2.74	3.26	0.0103	0.0105	0.0109	7.29E-05
3.22	2.97	2.62	0.0103	0.0105	0.0109	7.33E-05
3.39	2.78	3.27	0.0103	0.0105	0.0109	7.34E-05
2.31	2.81	2.73	0.0103	0.0105	0.0109	7.35E-05
4.77	4.04	4.92	0.0103	0.0105	0.0109	7.36E-05
4.77	4.04	4.92	0.0103	0.0105	0.0109	7.36E-05
2.39	2.77	2.93	0.0103	0.0105	0.0109	7.40E-05
2.94	2.9	2.43	0.0103	0.0105	0.0109	7.41E-05
0.011	0.012	0.0117	2.96	2.45	2.93	7.44E-05
0.011	0.012	0.0117	2.71	3.09	2.53	7.44E-05
0.011	0.012	0.0117	2.71	3.09	2.53	7.44E-05
2.78	2.56	2.26	0.0103	0.0105	0.0109	7.46E-05
2.84	3.04	3.47	0.0103	0.0105	0.0109	7.51E-05
2.84	3.04	3.47	0.0103	0.0105	0.0109	7.51E-05
3.85	3.8	3.18	0.0103	0.0105	0.0109	7.53E-05
3.09	3.54	2.9	0.0103	0.0105	0.0109	7.56E-05
3.09	3.54	2.9	0.0103	0.0105	0.0109	7.56E-05
2.66	3.2	2.72	0.0103	0.0105	0.0109	7.58E-05
2.66	3.2	2.72	0.0103	0.0105	0.0109	7.58E-05
2.66	3.2	2.72	0.0103	0.0105	0.0109	7.58E-05
2.13	2.49	2.06	0.0103	0.0105	0.0109	7.65E-05
0.011	0.012	0.0117	3.47	2.84	3.03	7.67E-05
0.011	0.012	0.0117	2.96	2.48	2.49	7.68E-05
2.97	2.44	2.9	0.0103	0.0105	0.0109	7.71E-05
4.21	4.33	3.55	0.0103	0.0105	0.0109	7.76E-05
4.21	4.33	3.55	0.0103	0.0105	0.0109	7.76E-05
3.45	3.05	2.81	0.0103	0.0105	0.0109	7.77E-05
3.45	3.05	2.81	0.0103	0.0105	0.0109	7.77E-05
2.67	2.34	2.18	0.0103	0.0105	0.0109	7.82E-05
2.67	2.34	2.18	0.0103	0.0105	0.0109	7.82E-05
0.011	0.012	0.0117	2.38	2.75	2.93	7.86E-05
0.011	0.012	0.0117	2.38	2.75	2.93	7.86E-05
3.51	4.25	3.63	0.0103	0.0105	0.0109	7.88E-05
2.95	2.96	2.45	0.0103	0.0105	0.0109	7.92E-05
2.95	2.96	2.45	0.0103	0.0105	0.0109	7.92E-05
0.011	0.012	0.0117	3.65	4.09	3.32	7.94E-05

2.25	2.26	2.69	0.0103	0.0105	0.0109	7.95E-05
2.25	2.26	2.69	0.0103	0.0105	0.0109	7.95E-05
4.01	3.35	4.07	0.0103	0.0105	0.0109	7.95E-05
0.011	0.012	0.0117	3.58	3.17	2.91	7.99E-05
3.03	2.57	3.15	0.0103	0.0105	0.0109	8.01E-05
2.96	3.46	3.64	0.0103	0.0105	0.0109	8.03E-05
2.96	3.46	3.64	0.0103	0.0105	0.0109	8.03E-05
2.41	2.8	2.3	0.0103	0.0105	0.0109	8.03E-05
2.27	2.76	2.37	0.0103	0.0105	0.0109	8.03E-05
2.45	2.84	2.33	0.0103	0.0105	0.0109	8.03E-05
2.69	3.25	2.76	0.0103	0.0105	0.0109	8.09E-05
2.69	3.25	2.76	0.0103	0.0105	0.0109	8.09E-05
3.54	2.95	2.98	0.0103	0.0105	0.0109	8.10E-05
3.54	2.95	2.98	0.0103	0.0105	0.0109	8.10E-05
3.8	3.08	3.56	0.0103	0.0105	0.0109	8.11E-05
2.46	3.04	2.77	0.0103	0.0105	0.0109	8.12E-05
3.63	3.78	3.08	0.0103	0.0105	0.0109	8.13E-05
3.63	3.78	3.08	0.0103	0.0105	0.0109	8.13E-05
2.46	2.99	2.56	0.0103	0.0105	0.0109	8.18E-05
0.011	0.012	0.0117	2.86	2.54	3.14	8.18E-05
0.011	0.012	0.0117	2.86	2.54	3.14	8.18E-05
2.52	2.98	3.09	0.0103	0.0105	0.0109	8.21E-05
0.011	0.012	0.0117	3.1	3.5	2.84	8.22E-05
0.011	0.012	0.0117	3.1	3.5	2.84	8.22E-05
3.5	2.83	3.22	0.0103	0.0105	0.0109	8.23E-05
2.52	2.48	2.07	0.0103	0.0105	0.0109	8.26E-05
2.52	2.48	2.07	0.0103	0.0105	0.0109	8.26E-05
2.08	2.04	2.46	0.0103	0.0105	0.0109	8.27E-05
2.58	3.08	3.15	0.0103	0.0105	0.0109	8.28E-05
4.13	3.84	3.34	0.0103	0.0105	0.0109	8.30E-05
2.6	3.21	2.86	0.0103	0.0105	0.0109	8.30E-05
2.6	3.21	2.86	0.0103	0.0105	0.0109	8.30E-05
3.22	2.97	3.66	0.0103	0.0105	0.0109	8.44E-05
3.22	2.97	3.66	0.0103	0.0105	0.0109	8.44E-05
3.22	2.97	3.66	0.0103	0.0105	0.0109	8.44E-05
3.22	2.97	3.66	0.0103	0.0105	0.0109	8.44E-05
3.22	2.97	3.66	0.0103	0.0105	0.0109	8.44E-05
2.7	2.46	2.18	0.0103	0.0105	0.0109	8.47E-05
2.9	2.48	3.06	0.0103	0.0105	0.0109	8.48E-05
0.011	0.012	0.0117	3.9	3.32	3.21	8.52E-05
0.011	0.012	0.0117	3.9	3.32	3.21	8.52E-05
0.011	0.012	0.0117	2.61	2.77	3.2	8.56E-05
0.011	0.012	0.0117	2.61	2.77	3.2	8.56E-05
2.92	2.42	2.94	0.0103	0.0105	0.0109	8.57E-05
2.26	2.14	2.62	0.0103	0.0105	0.0109	8.60E-05
2.75	2.23	2.62	0.0103	0.0105	0.0109	8.61E-05
2.3	2.17	2.66	0.0103	0.0105	0.0109	8.61E-05
2.3	2.17	2.66	0.0103	0.0105	0.0109	8.61E-05
2.74	2.5	2.21	0.0103	0.0105	0.0109	8.62E-05
0.011	0.012	0.0117	2.97	3.37	2.73	8.63E-05
2.27	2.48	2	0.0103	0.0105	0.0109	8.66E-05
2.79	2.26	2.65	0.0103	0.0105	0.0109	8.66E-05
0.011	0.012	0.0117	2.46	3.01	2.59	8.67E-05
0.011	0.012	0.0117	2.46	3.01	2.59	8.67E-05
3.19	2.6	2.76	0.0103	0.0105	0.0109	8.67E-05
0.011	0.012	0.0117	2.64	2.29	2.15	8.67E-05
2.41	2.56	2.07	0.0103	0.0105	0.0109	8.67E-05
2.41	2.56	2.07	0.0103	0.0105	0.0109	8.67E-05

2.19	2.26	2.66	0.0103	0.0105	0.0109	8.67E-05
2.19	2.26	2.66	0.0103	0.0105	0.0109	8.67E-05
0.011	0.012	0.0117	3.02	2.89	2.45	8.72E-05
0.011	0.012	0.0117	3.02	2.89	2.45	8.72E-05
2.82	2.73	3.32	0.0103	0.0105	0.0109	8.80E-05
0.011	0.012	0.0117	2.61	3.22	2.82	8.81E-05
2.46	2.88	2.36	0.0103	0.0105	0.0109	8.82E-05
2.21	2.18	2.63	0.0103	0.0105	0.0109	8.84E-05
2.67	3.27	2.81	0.0103	0.0105	0.0109	8.84E-05
2.67	3.27	2.81	0.0103	0.0105	0.0109	8.84E-05
2.98	3.2	2.58	0.0103	0.0105	0.0109	8.85E-05
2.94	2.49	2.42	0.0103	0.0105	0.0109	8.93E-05
3.62	2.92	3.22	0.0103	0.0105	0.0109	8.94E-05
2.76	3.35	3.35	0.0103	0.0105	0.0109	8.97E-05
3.01	2.89	2.44	0.0103	0.0105	0.0109	9.00E-05
3.01	2.89	2.44	0.0103	0.0105	0.0109	9.00E-05
0.011	0.012	0.0117	2.41	2.79	2.27	9.02E-05
2.47	2.77	3.07	0.0103	0.0105	0.0109	9.07E-05
2.47	2.77	3.07	0.0103	0.0105	0.0109	9.07E-05
2.47	2.77	3.07	0.0103	0.0105	0.0109	9.07E-05
0.011	0.012	0.0117	2.25	2.77	2.4	9.07E-05
0.011	0.012	0.0117	3.46	2.79	3.07	9.07E-05
3.07	2.84	2.47	0.0103	0.0105	0.0109	9.09E-05
2.88	3.28	2.65	0.0103	0.0105	0.0109	9.15E-05
3.77	3.15	3.13	0.0103	0.0105	0.0109	9.15E-05
2.54	2.69	2.17	0.0103	0.0105	0.0109	9.16E-05
0.011	0.012	0.0117	2.62	3.07	2.51	9.17E-05
3.64	3.97	3.19	0.0103	0.0105	0.0109	9.19E-05
3.64	3.97	3.19	0.0103	0.0105	0.0109	9.19E-05
4.64	4.46	4.77	2.27	1.96	2.37	9.21E-05
4.64	4.46	4.77	2.27	1.96	2.37	9.21E-05
2.73	2.38	2.21	0.0103	0.0105	0.0109	9.21E-05
2.73	2.2	2.42	0.0103	0.0105	0.0109	9.22E-05
2.37	2.95	2.71	0.0103	0.0105	0.0109	9.27E-05
3.32	2.67	2.97	0.0103	0.0105	0.0109	9.27E-05
3.32	2.67	2.97	0.0103	0.0105	0.0109	9.27E-05
0.011	0.012	0.0117	3.15	2.98	2.54	9.29E-05
2.64	2.41	2.99	0.0103	0.0105	0.0109	9.30E-05
3	2.48	3.03	0.0103	0.0105	0.0109	9.31E-05
3	2.48	3.03	0.0103	0.0105	0.0109	9.31E-05
0.011	0.012	0.0117	2.83	2.28	2.5	9.38E-05
0.011	0.012	0.0117	2.83	2.28	2.5	9.38E-05
0.011	0.012	0.0117	3.74	3.07	3.73	9.39E-05
0.011	0.012	0.0117	3.74	3.07	3.73	9.39E-05
4.63	3.72	4.14	0.0103	0.0105	0.0109	9.39E-05
3.71	3.22	4.01	0.0103	0.0105	0.0109	9.39E-05
3.71	3.22	4.01	0.0103	0.0105	0.0109	9.39E-05
2.29	2.83	2.46	0.0103	0.0105	0.0109	9.41E-05
2.29	2.83	2.46	0.0103	0.0105	0.0109	9.41E-05
2.62	2.48	3.05	0.0103	0.0105	0.0109	9.42E-05
0.011	0.012	0.0117	2.89	2.85	2.36	9.43E-05
2.45	3.04	2.88	0.0103	0.0105	0.0109	9.43E-05
3.13	3.87	3.72	0.0103	0.0105	0.0109	9.44E-05
3.14	2.54	2.73	0.0103	0.0105	0.0109	9.44E-05
3.34	3.54	2.85	0.0103	0.0105	0.0109	9.44E-05
3.66	3.07	3.02	0.0103	0.0105	0.0109	9.46E-05
3.66	3.07	3.02	0.0103	0.0105	0.0109	9.46E-05
3.21	2.65	3.24	0.0103	0.0105	0.0109	9.48E-05

2.78	2.54	2.23	0.0103	0.0105	0.0109	9.51E-05
2.78	2.54	2.23	0.0103	0.0105	0.0109	9.51E-05
2.3	2.79	2.34	0.0103	0.0105	0.0109	9.62E-05
0.011	0.012	0.0117	2.72	2.43	3.03	9.68E-05
0.011	0.012	0.0117	2.72	2.43	3.03	9.68E-05
0.011	0.012	0.0117	2.87	3.15	3.57	9.72E-05
0.011	0.012	0.0117	2.87	3.15	3.57	9.72E-05
2.44	2.04	2.52	0.0103	0.0105	0.0109	9.75E-05
2.44	2.04	2.52	0.0103	0.0105	0.0109	9.75E-05
2.53	2.92	2.36	0.0103	0.0105	0.0109	9.76E-05
2.53	2.92	2.36	0.0103	0.0105	0.0109	9.76E-05
3.14	2.52	2.79	0.0103	0.0105	0.0109	9.77E-05
2.3	2.66	2.87	0.0103	0.0105	0.0109	9.81E-05
0.011	0.012	0.0117	3.1	3.55	2.86	9.82E-05
0.011	0.012	0.0117	3.1	3.55	2.86	9.82E-05
3.61	4.1	4.51	0.0103	0.0105	0.0109	9.82E-05
0.011	0.012	0.0117	2.69	3.27	3.29	9.83E-05
0.011	0.012	0.0117	2.69	3.27	3.29	9.83E-05
2.67	2.48	2.14	0.0103	0.0105	0.0109	9.84E-05
2.67	2.48	2.14	0.0103	0.0105	0.0109	9.84E-05
0.011	0.012	0.0117	2.09	2.61	2.39	9.85E-05
2.06	2.54	2.18	0.0103	0.0105	0.0109	9.87E-05
3.44	3.6	2.9	0.0103	0.0105	0.0109	9.87E-05
3.44	3.6	2.9	0.0103	0.0105	0.0109	9.87E-05
2.2	2.2	2.65	0.0103	0.0105	0.0109	9.87E-05
2.32	2.87	2.48	0.0103	0.0105	0.0109	9.89E-05
0.011	0.012	0.0117	3.6	2.89	3.18	9.90E-05
0.011	0.012	0.0117	2.12	2.63	2.29	9.92E-05
2.65	2.53	3.11	0.0103	0.0105	0.0109	9.93E-05
3.2	3.42	3.96	0.0103	0.0105	0.0109	9.93E-05
3.2	3.42	3.96	0.0103	0.0105	0.0109	9.93E-05
3.29	2.73	2.73	0.0103	0.0105	0.0109	9.94E-05
0.011	0.012	0.0117	2.7	2.88	2.31	9.95E-05
0.011	0.012	0.0117	2.7	2.88	2.31	9.95E-05
3.15	2.57	2.67	0.0103	0.0105	0.0109	9.95E-05
3.63	2.91	3.4	0.0103	0.0105	0.0109	9.97E-05
3.2	2.56	2.94	0.0103	0.0105	0.0109	9.99E-05
3.2	2.56	2.94	0.0103	0.0105	0.0109	9.99E-05
3.29	2.64	3.1	0.0103	0.0105	0.0109	1.00E-04
3.29	2.64	3.1	0.0103	0.0105	0.0109	1.00E-04
0.011	0.012	0.0117	2.9	3.53	2.96	1.00E-04
4.26	3.99	4.94	0.0103	0.0105	0.0109	1.01E-04
0.011	0.012	0.0117	2.43	2.43	2.93	1.01E-04
4.29	4.4	4.31	2.6	2.41	2.78	1.01E-04
0.011	0.012	0.0117	2.74	2.51	2.19	1.02E-04
0.011	0.012	0.0117	2.74	2.51	2.19	1.02E-04
2.98	3.66	3.62	0.0103	0.0105	0.0109	1.02E-04
2.98	3.66	3.62	0.0103	0.0105	0.0109	1.02E-04
3.43	3.18	3.95	0.0103	0.0105	0.0109	1.02E-04
2.71	2.18	2.59	0.0103	0.0105	0.0109	1.02E-04
0.011	0.012	0.0117	3.15	3.53	3.94	1.02E-04
0.011	0.012	0.0117	3.15	3.53	3.94	1.02E-04
3	2.43	2.93	0.0103	0.0105	0.0109	1.02E-04
2.81	2.46	3.08	0.0103	0.0105	0.0109	1.02E-04
2.81	2.46	3.08	0.0103	0.0105	0.0109	1.02E-04
2.19	2.66	2.22	0.0103	0.0105	0.0109	1.03E-04
2.54	2.68	2.15	0.0103	0.0105	0.0109	1.03E-04
4.09	3.46	3.33	0.0103	0.0105	0.0109	1.04E-04

3.48	3.05	2.79	0.0103	0.0105	0.0109	1.04E-04
2.51	3.13	2.74	0.0103	0.0105	0.0109	1.04E-04
3.18	3.81	3.95	0.0103	0.0105	0.0109	1.05E-04
3.18	3.81	3.95	0.0103	0.0105	0.0109	1.05E-04
0.011	0.012	0.0117	2.46	2.51	3	1.05E-04
4.48	3.97	3.58	0.0103	0.0105	0.0109	1.05E-04
4.48	3.97	3.58	0.0103	0.0105	0.0109	1.05E-04
2.26	2.82	2.47	0.0103	0.0105	0.0109	1.05E-04
2.26	2.82	2.47	0.0103	0.0105	0.0109	1.05E-04
3.28	2.62	2.91	0.0103	0.0105	0.0109	1.06E-04
3.28	2.62	2.91	0.0103	0.0105	0.0109	1.06E-04
2.86	2.28	2.6	0.0103	0.0105	0.0109	1.06E-04
2.55	2.61	2.11	0.0103	0.0105	0.0109	1.06E-04
3.08	2.88	2.46	0.0103	0.0105	0.0109	1.06E-04
0.011	0.012	0.0117	3.41	3.26	4.02	1.07E-04
0.011	0.012	0.0117	3.74	3.44	2.98	1.07E-04
2.4	2.69	3.01	0.0103	0.0105	0.0109	1.07E-04
0.011	0.012	0.0117	2.77	2.68	3.29	1.07E-04
3.07	2.7	3.39	0.0103	0.0105	0.0109	1.07E-04
3.07	2.7	3.39	0.0103	0.0105	0.0109	1.07E-04
3.43	3.07	3.85	0.0103	0.0105	0.0109	1.08E-04
3.43	3.07	3.85	0.0103	0.0105	0.0109	1.08E-04
4.79	3.99	3.93	0.0103	0.0105	0.0109	1.08E-04
0.011	0.012	0.0117	2.47	2.87	2.31	1.08E-04
0.011	0.012	0.0117	2.47	2.87	2.31	1.08E-04
2.67	2.49	2.13	0.0103	0.0105	0.0109	1.08E-04
0.011	0.012	0.0117	2.45	2.94	3.05	1.09E-04
0.011	0.012	0.0117	2.45	2.94	3.05	1.09E-04
2.46	2.57	2.06	0.0103	0.0105	0.0109	1.10E-04
4.24	3.75	3.38	0.0103	0.0105	0.0109	1.10E-04
3.23	4.05	3.57	0.0103	0.0105	0.0109	1.10E-04
0.011	0.012	0.0117	3.01	2.66	2.4	1.11E-04
0.011	0.012	0.0117	3.01	2.66	2.4	1.11E-04
0.011	0.012	0.0117	2.28	2.86	2.53	1.11E-04
3.49	4.38	4.1	0.0103	0.0105	0.0109	1.11E-04
2.99	3.74	3.26	0.0103	0.0105	0.0109	1.11E-04
2.92	3.08	2.46	0.0103	0.0105	0.0109	1.12E-04
3	3.06	2.99	2.57	2.54	2.49	1.12E-04
3	3.06	2.99	2.57	2.54	2.49	1.12E-04
2.58	3.08	2.51	0.0103	0.0105	0.0109	1.12E-04
2.74	3.26	2.65	0.0103	0.0105	0.0109	1.12E-04
2.68	2.42	2.13	0.0103	0.0105	0.0109	1.12E-04
2.68	2.42	2.13	0.0103	0.0105	0.0109	1.12E-04
3.28	2.61	2.91	0.0103	0.0105	0.0109	1.13E-04
2.32	2.92	2.68	0.0103	0.0105	0.0109	1.13E-04
0.011	0.012	0.0117	4.31	3.45	3.73	1.13E-04
2.77	2.7	2.23	0.0103	0.0105	0.0109	1.13E-04
3.5	3.61	2.9	0.0103	0.0105	0.0109	1.13E-04
0.011	0.012	0.0117	2.77	2.23	2.7	1.13E-04
2.51	3.16	2.9	0.0103	0.0105	0.0109	1.13E-04
2.51	3.16	2.9	0.0103	0.0105	0.0109	1.13E-04
0.011	0.012	0.0117	3.13	3.46	3.93	1.13E-04
0.011	0.012	0.0117	4.11	4.17	3.37	1.14E-04
2.18	2.7	2.29	0.0103	0.0105	0.0109	1.14E-04
2.18	2.7	2.29	0.0103	0.0105	0.0109	1.14E-04
0.011	0.012	0.0117	3.45	2.74	3.09	1.14E-04
0.011	0.012	0.0117	3.05	3.05	3.7	1.14E-04
0.011	0.012	0.0117	2.55	2.06	2.16	1.15E-04

2.52	2.01	2.2	0.0103	0.0105	0.0109	1.15E-04
3.08	2.94	2.46	0.0103	0.0105	0.0109	1.15E-04
3.08	2.94	2.46	0.0103	0.0105	0.0109	1.15E-04
2.61	3.26	2.81	0.0103	0.0105	0.0109	1.15E-04
2.57	2.57	2.09	0.0103	0.0105	0.0109	1.15E-04
2.57	2.57	2.09	0.0103	0.0105	0.0109	1.15E-04
0.011	0.012	0.0117	3.17	3.76	3.98	1.15E-04
0.011	0.012	0.0117	2.58	2.67	2.14	1.16E-04
0.011	0.012	0.0117	2.58	2.67	2.14	1.16E-04
0.011	0.012	0.0117	2.87	3.62	3.29	1.16E-04
0.011	0.012	0.0117	2.87	3.62	3.29	1.16E-04
2.73	2.89	2.3	0.0103	0.0105	0.0109	1.17E-04
2.73	2.89	2.3	0.0103	0.0105	0.0109	1.17E-04
3.05	2.71	2.42	0.0103	0.0105	0.0109	1.18E-04
0.011	0.012	0.0117	3.49	2.81	2.96	1.18E-04
0.011	0.012	0.0117	3.49	2.81	2.96	1.18E-04
0.011	0.012	0.0117	3.14	2.53	2.66	1.18E-04
2.97	2.43	2.46	0.0103	0.0105	0.0109	1.18E-04
0.011	0.012	0.0117	2.43	3.01	2.54	1.18E-04
0.011	0.012	0.0117	2.52	3.08	2.55	1.19E-04
0.011	0.012	0.0117	2.52	3.08	2.55	1.19E-04
0.011	0.012	0.0117	3.1	2.69	2.47	1.20E-04
2.82	2.31	2.33	0.0103	0.0105	0.0109	1.20E-04
2.82	2.31	2.33	0.0103	0.0105	0.0109	1.20E-04
3.64	3.29	2.88	0.0103	0.0105	0.0109	1.20E-04
2.74	2.6	2.18	0.0103	0.0105	0.0109	1.20E-04
2.74	2.6	2.18	0.0103	0.0105	0.0109	1.20E-04
0.011	0.012	0.0117	2.48	3.13	2.91	1.21E-04
3.11	2.81	2.46	0.0103	0.0105	0.0109	1.21E-04
0.011	0.012	0.0117	2.75	3.47	3.07	1.21E-04
0.011	0.012	0.0117	2.75	3.47	3.07	1.21E-04
2.47	2.85	2.27	0.0103	0.0105	0.0109	1.21E-04
2.35	2.73	2.97	0.0103	0.0105	0.0109	1.21E-04
0.011	0.012	0.0117	3.23	2.73	2.6	1.21E-04
0.011	0.012	0.0117	3.23	2.73	2.6	1.21E-04
2.83	3.24	3.58	0.0103	0.0105	0.0109	1.22E-04
2.83	3.24	3.58	0.0103	0.0105	0.0109	1.22E-04
2.83	3.24	3.58	0.0103	0.0105	0.0109	1.22E-04
2.97	3.15	2.5	0.0103	0.0105	0.0109	1.22E-04
2.97	3.15	2.5	0.0103	0.0105	0.0109	1.22E-04
0.011	0.012	0.0117	2.08	2.58	2.55	1.22E-04
3.74	3.14	3.02	0.0103	0.0105	0.0109	1.22E-04
3.74	3.14	3.02	0.0103	0.0105	0.0109	1.22E-04
3.06	3.65	2.95	0.0103	0.0105	0.0109	1.22E-04
3.53	3.23	2.79	0.0103	0.0105	0.0109	1.22E-04
3.37	2.68	3.21	0.0103	0.0105	0.0109	1.23E-04
0.011	0.012	0.0117	3.39	2.81	2.76	1.24E-04
0.011	0.012	0.0117	3.39	2.81	2.76	1.24E-04
2.57	3.02	3.25	0.0103	0.0105	0.0109	1.25E-04
3.2	3.44	2.72	0.0103	0.0105	0.0109	1.25E-04
3.2	3.44	2.72	0.0103	0.0105	0.0109	1.25E-04
3.34	3.34	4.07	0.0103	0.0105	0.0109	1.25E-04
3.34	3.34	4.07	0.0103	0.0105	0.0109	1.25E-04
2.26	2.13	2.66	0.0103	0.0105	0.0109	1.26E-04
2.26	2.13	2.66	0.0103	0.0105	0.0109	1.26E-04
2.78	3.17	2.51	0.0103	0.0105	0.0109	1.26E-04
2.17	2.55	2.04	0.0103	0.0105	0.0109	1.26E-04
0.011	0.012	0.0117	2.16	2.67	2.67	1.27E-04

0.011	0.012	0.0117	3	3.38	3.8	1.27E-04
3.5	3.68	2.92	0.0103	0.0105	0.0109	1.27E-04
0.011	0.012	0.0117	3.61	3.21	2.85	1.27E-04
3.18	3.09	2.54	0.0103	0.0105	0.0109	1.27E-04
2.96	2.35	2.56	0.0103	0.0105	0.0109	1.28E-04
2.96	2.35	2.56	0.0103	0.0105	0.0109	1.28E-04
0.011	0.012	0.0117	2.41	2.93	3.02	1.28E-04
0.011	0.012	0.0117	2.41	2.93	3.02	1.28E-04
0.011	0.012	0.0117	3.07	3.86	3.71	1.28E-04
0.011	0.012	0.0117	3.07	3.86	3.71	1.28E-04
3.21	2.65	3.33	0.0103	0.0105	0.0109	1.29E-04
3.21	2.65	3.33	0.0103	0.0105	0.0109	1.29E-04
3.21	2.65	3.33	0.0103	0.0105	0.0109	1.29E-04
2.61	3.25	3.21	0.0103	0.0105	0.0109	1.30E-04
2.65	2.21	2.14	0.0103	0.0105	0.0109	1.30E-04
3.21	2.53	2.96	0.0103	0.0105	0.0109	1.30E-04
0.011	0.012	0.0117	2.53	2.55	3.1	1.30E-04
0.011	0.012	0.0117	2.54	3.15	3.14	1.30E-04
3.48	4.38	4.21	0.0103	0.0105	0.0109	1.30E-04
2.7	3.38	3.3	0.0103	0.0105	0.0109	1.31E-04
3.11	3.63	3.95	0.0103	0.0105	0.0109	1.31E-04
2.27	2.71	2.18	0.0103	0.0105	0.0109	1.31E-04
3.77	3.05	3.13	0.0103	0.0105	0.0109	1.31E-04
3.06	3.3	2.6	0.0103	0.0105	0.0109	1.32E-04
3	2.62	2.37	0.0103	0.0105	0.0109	1.32E-04
3	2.62	2.37	0.0103	0.0105	0.0109	1.32E-04
0.011	0.012	0.0117	2.03	2.58	2.34	1.32E-04
0.011	0.012	0.0117	2.03	2.58	2.34	1.32E-04
2.14	2.33	2.7	0.0103	0.0105	0.0109	1.33E-04
2.14	2.33	2.7	0.0103	0.0105	0.0109	1.33E-04
4.78	4.27	3.76	0.0103	0.0105	0.0109	1.33E-04
2.17	2.7	2.26	0.0103	0.0105	0.0109	1.33E-04
3.18	2.74	2.52	0.0103	0.0105	0.0109	1.33E-04
3.55	3.11	2.8	0.0103	0.0105	0.0109	1.34E-04
3.44	3.92	3.09	0.0103	0.0105	0.0109	1.34E-04
2.96	2.93	3.6	0.0103	0.0105	0.0109	1.34E-04
2.96	2.93	3.6	0.0103	0.0105	0.0109	1.34E-04
3.68	3.31	4.2	0.0103	0.0105	0.0109	1.35E-04
2.58	2.18	2.06	0.0103	0.0105	0.0109	1.35E-04
0.011	0.012	0.0117	2.33	2.95	2.56	1.36E-04
4	3.43	3.17	0.0103	0.0105	0.0109	1.36E-04
4	3.43	3.17	0.0103	0.0105	0.0109	1.36E-04
2.67	2.1	2.36	0.0103	0.0105	0.0109	1.37E-04
2.36	2.98	2.86	0.0103	0.0105	0.0109	1.37E-04
2.36	2.98	2.86	0.0103	0.0105	0.0109	1.37E-04
0.011	0.012	0.0117	3.1	2.44	2.72	1.38E-04
3.5	2.88	2.84	0.0103	0.0105	0.0109	1.38E-04
0.011	0.012	0.0117	3.51	3.44	2.8	1.38E-04
0.011	0.012	0.0117	3.51	3.44	2.8	1.38E-04
0.011	0.012	0.0117	3.6	3.91	3.07	1.38E-04
0.011	0.012	0.0117	3.6	3.91	3.07	1.38E-04
0.011	0.012	0.0117	2.27	2.03	2.58	1.38E-04
2.16	2.75	2.54	0.0103	0.0105	0.0109	1.38E-04
3.35	2.96	3.77	0.0103	0.0105	0.0109	1.38E-04
3.35	2.96	3.77	0.0103	0.0105	0.0109	1.38E-04
3.35	2.96	3.77	0.0103	0.0105	0.0109	1.38E-04
0.011	0.012	0.0117	3.56	2.83	3.46	1.38E-04
0.011	0.012	0.0117	3.56	2.83	3.46	1.38E-04

3.38	2.96	2.66	0.0103	0.0105	0.0109	1.38E-04
3.38	2.96	2.66	0.0103	0.0105	0.0109	1.38E-04
0.011	0.012	0.0117	2.73	3.36	3.42	1.38E-04
0.011	0.012	0.0117	2.73	3.36	3.42	1.38E-04
0.011	0.012	0.0117	2.83	2.86	2.29	1.39E-04
2.59	2.08	2.58	0.0103	0.0105	0.0109	1.39E-04
2.94	3.14	3.7	0.0103	0.0105	0.0109	1.39E-04
0.011	0.012	0.0117	2.94	2.9	2.35	1.40E-04
0.011	0.012	0.0117	2.94	2.9	2.35	1.40E-04
3.27	3.32	2.65	0.0103	0.0105	0.0109	1.41E-04
3.6	4.1	3.22	0.0103	0.0105	0.0109	1.41E-04
0.011	0.012	0.0117	2.71	3.03	3.45	1.41E-04
3.21	3.83	3.06	0.0103	0.0105	0.0109	1.41E-04
3.36	3.62	2.84	0.0103	0.0105	0.0109	1.42E-04
3.38	2.65	3.12	0.0103	0.0105	0.0109	1.42E-04
0.011	0.012	0.0117	2.52	2.46	3.05	1.42E-04
3.39	2.79	3.53	0.0103	0.0105	0.0109	1.42E-04
3.02	2.57	3.28	0.0103	0.0105	0.0109	1.43E-04
3.02	2.57	3.28	0.0103	0.0105	0.0109	1.43E-04
3.33	2.71	2.72	0.0103	0.0105	0.0109	1.43E-04
3.33	2.71	2.72	0.0103	0.0105	0.0109	1.43E-04
2.51	2.64	2.08	0.0103	0.0105	0.0109	1.44E-04
0.011	0.012	0.0117	3.4	3.69	2.89	1.44E-04
2.59	3.25	2.73	0.0103	0.0105	0.0109	1.44E-04
2.72	2.14	2.36	0.0103	0.0105	0.0109	1.44E-04
0.011	0.012	0.0117	2.99	2.34	2.68	1.44E-04
2.56	2.02	2.45	0.0103	0.0105	0.0109	1.44E-04
0.011	0.012	0.0117	3.53	2.77	3.09	1.45E-04
3.42	3.04	3.88	0.0103	0.0105	0.0109	1.45E-04
3.01	2.62	3.35	0.0103	0.0105	0.0109	1.45E-04
2.71	2.75	3.35	0.0103	0.0105	0.0109	1.45E-04
2.71	2.75	3.35	0.0103	0.0105	0.0109	1.45E-04
2.71	2.75	3.35	0.0103	0.0105	0.0109	1.45E-04
3.53	2.78	3.04	0.0103	0.0105	0.0109	1.46E-04
2.06	2.44	2.63	0.0103	0.0105	0.0109	1.46E-04
2.06	2.44	2.63	0.0103	0.0105	0.0109	1.46E-04
2.61	2.09	2.6	0.0103	0.0105	0.0109	1.46E-04
3.85	3.1	3.88	0.0103	0.0105	0.0109	1.47E-04
2.3	2.94	2.71	0.0103	0.0105	0.0109	1.47E-04
2.5	3.12	2.59	0.0103	0.0105	0.0109	1.47E-04
2.5	3.12	2.59	0.0103	0.0105	0.0109	1.47E-04
2.17	2.72	2.69	0.0103	0.0105	0.0109	1.47E-04
2.63	2.96	3.36	0.0103	0.0105	0.0109	1.47E-04
2.63	2.96	3.36	0.0103	0.0105	0.0109	1.47E-04
4.26	3.33	3.92	0.0103	0.0105	0.0109	1.48E-04
0.011	0.012	0.0117	2.71	2.57	3.23	1.48E-04
2.27	2.55	2.9	0.0103	0.0105	0.0109	1.48E-04
0.011	0.012	0.0117	2.77	3.49	2.94	1.48E-04
0.011	0.012	0.0117	2.32	2.94	2.51	1.49E-04
0.011	0.012	0.0117	2.23	2.74	2.23	1.49E-04
2.37	2.5	2.98	0.0103	0.0105	0.0109	1.49E-04
2.94	3.76	3.31	0.0103	0.0105	0.0109	1.50E-04
2.94	3.76	3.31	0.0103	0.0105	0.0109	1.50E-04
3.27	3.03	3.84	0.0103	0.0105	0.0109	1.50E-04
3.47	3.91	4.44	0.0103	0.0105	0.0109	1.50E-04
3.47	3.91	4.44	0.0103	0.0105	0.0109	1.50E-04
3.47	3.91	4.44	0.0103	0.0105	0.0109	1.50E-04
3.47	3.91	4.44	0.0103	0.0105	0.0109	1.50E-04

2.6	3.29	2.79	0.0103	0.0105	0.0109	1.51E-04
2.67	3.01	2.35	0.0103	0.0105	0.0109	1.51E-04
3.31	3.74	2.92	0.0103	0.0105	0.0109	1.51E-04
3	2.42	2.46	0.0103	0.0105	0.0109	1.52E-04
3	2.42	2.46	0.0103	0.0105	0.0109	1.52E-04
0.011	0.012	0.0117	2.31	2.36	2.87	1.52E-04
0.011	0.012	0.0117	2.31	2.36	2.87	1.52E-04
2.59	2.07	2.15	0.0103	0.0105	0.0109	1.52E-04
2.59	2.07	2.15	0.0103	0.0105	0.0109	1.52E-04
3.3	2.63	2.75	0.0103	0.0105	0.0109	1.52E-04
3.3	2.63	2.75	0.0103	0.0105	0.0109	1.52E-04
3.43	4	4.4	0.0103	0.0105	0.0109	1.52E-04
0.011	0.012	0.0117	3.14	2.59	2.52	1.52E-04
0.011	0.012	0.0117	3.14	2.59	2.52	1.52E-04
2.73	2.24	2.2	0.0103	0.0105	0.0109	1.53E-04
4.91	5.03	5.16	3.11	3.44	3.37	1.53E-04
4.91	5.03	5.16	3.11	3.44	3.37	1.53E-04
2.99	3.62	2.9	0.0103	0.0105	0.0109	1.53E-04
3.54	4.5	4.32	0.0103	0.0105	0.0109	1.53E-04
3.32	2.65	3.31	0.0103	0.0105	0.0109	1.55E-04
2.24	2.52	2.87	0.0103	0.0105	0.0109	1.55E-04
2.24	2.52	2.87	0.0103	0.0105	0.0109	1.55E-04
3.15	2.68	2.48	0.0103	0.0105	0.0109	1.56E-04
3.29	2.57	3.08	0.0103	0.0105	0.0109	1.56E-04
3.29	2.57	3.08	0.0103	0.0105	0.0109	1.56E-04
0.011	0.012	0.0117	3.78	2.96	3.58	1.56E-04
0.011	0.012	0.0117	3.78	2.96	3.58	1.56E-04
4.65	3.88	4.97	0.0103	0.0105	0.0109	1.56E-04
2.58	2.29	2.01	0.0103	0.0105	0.0109	1.57E-04
0.011	0.012	0.0117	2.28	2.74	2.18	1.57E-04
0.011	0.012	0.0117	2.28	2.74	2.18	1.57E-04
0.011	0.012	0.0117	2.65	3.39	3.2	1.58E-04
0.011	0.012	0.0117	3.04	3.91	3.53	1.59E-04
3.24	2.84	3.65	0.0103	0.0105	0.0109	1.59E-04
2.1	2.34	2.69	0.0103	0.0105	0.0109	1.59E-04
3.07	3.95	3.57	0.0103	0.0105	0.0109	1.59E-04
2.98	2.64	3.39	0.0103	0.0105	0.0109	1.60E-04
2.98	2.64	3.39	0.0103	0.0105	0.0109	1.60E-04
2.81	2.25	2.83	0.0103	0.0105	0.0109	1.61E-04
3.43	3.49	2.76	0.0103	0.0105	0.0109	1.62E-04
3.43	3.49	2.76	0.0103	0.0105	0.0109	1.62E-04
3.08	3.52	2.74	0.0103	0.0105	0.0109	1.62E-04
3.08	3.52	2.74	0.0103	0.0105	0.0109	1.62E-04
3.08	3.52	2.74	0.0103	0.0105	0.0109	1.62E-04
3.22	2.92	2.5	0.0103	0.0105	0.0109	1.62E-04
3.22	2.92	2.5	0.0103	0.0105	0.0109	1.62E-04
2.77	3.49	3.46	0.0103	0.0105	0.0109	1.63E-04
2.77	3.49	3.46	0.0103	0.0105	0.0109	1.63E-04
2.85	3.6	3.55	0.0103	0.0105	0.0109	1.63E-04
0.011	0.012	0.0117	3.19	2.95	2.48	1.63E-04
0.011	0.012	0.0117	3.22	2.94	2.5	1.63E-04
3.03	3.13	2.46	0.0103	0.0105	0.0109	1.64E-04
2.48	2.22	2.85	0.0103	0.0105	0.0109	1.64E-04
0.011	0.012	0.0117	2.99	2.68	2.32	1.65E-04
4.17	3.26	3.98	0.0103	0.0105	0.0109	1.65E-04
0.011	0.012	0.0117	2.9	3.72	3.51	1.65E-04
0.011	0.012	0.0117	3.16	2.45	2.85	1.66E-04
2.8	2.87	2.26	0.0103	0.0105	0.0109	1.66E-04

2.8	2.87	2.26	0.0103	0.0105	0.0109	1.66E-04
2.41	2.99	3.06	0.0103	0.0105	0.0109	1.67E-04
2.41	2.99	3.06	0.0103	0.0105	0.0109	1.67E-04
2.24	2.75	2.21	0.0103	0.0105	0.0109	1.67E-04
2.24	2.75	2.21	0.0103	0.0105	0.0109	1.67E-04
2.64	3.14	2.47	0.0103	0.0105	0.0109	1.68E-04
3.82	3.06	3.12	0.0103	0.0105	0.0109	1.68E-04
3.75	3.29	2.91	0.0103	0.0105	0.0109	1.69E-04
2.49	3.12	2.56	0.0103	0.0105	0.0109	1.69E-04
2.49	3.12	2.56	0.0103	0.0105	0.0109	1.69E-04
2.93	2.76	2.28	0.0103	0.0105	0.0109	1.69E-04
2.88	2.88	2.29	0.0103	0.0105	0.0109	1.70E-04
0.011	0.012	0.0117	2.53	3.15	3.21	1.70E-04
4.37	3.4	3.77	0.0103	0.0105	0.0109	1.71E-04
2.81	3.2	2.48	0.0103	0.0105	0.0109	1.72E-04
2.81	3.2	2.48	0.0103	0.0105	0.0109	1.72E-04
2.44	3.05	3.09	0.0103	0.0105	0.0109	1.72E-04
2.44	3.05	3.09	0.0103	0.0105	0.0109	1.72E-04
2	2.39	2.58	0.0103	0.0105	0.0109	1.72E-04
2	2.39	2.58	0.0103	0.0105	0.0109	1.72E-04
0.011	0.012	0.0117	2.48	2.72	3.18	1.72E-04
0.011	0.012	0.0117	3.56	3.59	2.84	1.72E-04
3.01	3.66	3.87	0.0103	0.0105	0.0109	1.73E-04
0.011	0.012	0.0117	2.15	2.68	2.18	1.73E-04
2.61	2.42	3.09	0.0103	0.0105	0.0109	1.73E-04
2.67	2.09	2.58	0.0103	0.0105	0.0109	1.73E-04
2.67	2.09	2.58	0.0103	0.0105	0.0109	1.73E-04
3.72	4.37	3.41	0.0103	0.0105	0.0109	1.73E-04
2.83	2.3	2.27	0.0103	0.0105	0.0109	1.74E-04
2.83	2.3	2.27	0.0103	0.0105	0.0109	1.74E-04
2.62	3.33	2.78	0.0103	0.0105	0.0109	1.75E-04
2.62	3.33	2.78	0.0103	0.0105	0.0109	1.75E-04
3.23	3.24	4.01	0.0103	0.0105	0.0109	1.75E-04
3.23	3.24	4.01	0.0103	0.0105	0.0109	1.75E-04
3.23	3.24	4.01	0.0103	0.0105	0.0109	1.75E-04
3.02	3.63	2.86	0.0103	0.0105	0.0109	1.76E-04
3.02	3.63	2.86	0.0103	0.0105	0.0109	1.76E-04
3.02	2.82	2.34	0.0103	0.0105	0.0109	1.76E-04
3.02	2.82	2.34	0.0103	0.0105	0.0109	1.76E-04
4.36	3.53	4.52	0.0103	0.0105	0.0109	1.77E-04
4.36	3.53	4.52	0.0103	0.0105	0.0109	1.77E-04
4.36	3.53	4.52	0.0103	0.0105	0.0109	1.77E-04
2.91	2.38	3.06	0.0103	0.0105	0.0109	1.77E-04
2.58	2.52	3.16	0.0103	0.0105	0.0109	1.77E-04
2.96	2.31	2.51	0.0103	0.0105	0.0109	1.77E-04
2.96	2.31	2.51	0.0103	0.0105	0.0109	1.77E-04
2.96	2.31	2.51	0.0103	0.0105	0.0109	1.77E-04
4.16	3.75	3.21	0.0103	0.0105	0.0109	1.78E-04
4.16	3.75	3.21	0.0103	0.0105	0.0109	1.78E-04
2.9	2.47	3.2	0.0103	0.0105	0.0109	1.78E-04
2.81	3.62	3.42	0.0103	0.0105	0.0109	1.78E-04
0.011	0.012	0.0117	3.07	3.97	3.68	1.78E-04
0.011	0.012	0.0117	2.87	2.22	2.66	1.78E-04
0.011	0.012	0.0117	2.87	2.22	2.66	1.78E-04
0.011	0.012	0.0117	3.65	4.27	3.32	1.79E-04
3.38	3.95	3.07	0.0103	0.0105	0.0109	1.79E-04
3.38	3.95	3.07	0.0103	0.0105	0.0109	1.79E-04
0.011	0.012	0.0117	2.89	2.23	2.59	1.79E-04

0.011	0.012	0.0117	3.85	4.02	3.13	1.79E-04
0.011	0.012	0.0117	3.85	4.02	3.13	1.79E-04
0.011	0.012	0.0117	2.9	3.05	2.37	1.80E-04
2.54	3	2.34	0.0103	0.0105	0.0109	1.80E-04
2.54	3	2.34	0.0103	0.0105	0.0109	1.80E-04
3.32	2.66	2.69	0.0103	0.0105	0.0109	1.80E-04
0.011	0.012	0.0117	2.48	3.11	3.15	1.81E-04
0.011	0.012	0.0117	2.53	3.26	3.09	1.81E-04
3.79	2.94	3.59	0.0103	0.0105	0.0109	1.81E-04
3.18	3.52	4.1	0.0103	0.0105	0.0109	1.81E-04
2.91	2.64	3.4	0.0103	0.0105	0.0109	1.81E-04
0.011	0.012	0.0117	2.97	2.99	2.36	1.82E-04
3.37	2.68	3.4	0.0103	0.0105	0.0109	1.82E-04
3.37	2.68	3.4	0.0103	0.0105	0.0109	1.82E-04
2.99	2.78	2.31	0.0103	0.0105	0.0109	1.82E-04
2.89	3.18	2.45	0.0103	0.0105	0.0109	1.83E-04
0.011	0.012	0.0117	2.19	2.79	2.74	1.83E-04
2.88	2.29	2.35	0.0103	0.0105	0.0109	1.84E-04
2.88	2.29	2.35	0.0103	0.0105	0.0109	1.84E-04
3.13	2.41	2.81	0.0103	0.0105	0.0109	1.84E-04
3.13	2.41	2.81	0.0103	0.0105	0.0109	1.84E-04
3.13	2.41	2.81	0.0103	0.0105	0.0109	1.84E-04
0.011	0.012	0.0117	2.78	2.87	2.24	1.84E-04
2.29	2.76	2.17	0.0103	0.0105	0.0109	1.84E-04
3.32	2.63	3.33	0.0103	0.0105	0.0109	1.84E-04
3.48	3.22	4.13	0.0103	0.0105	0.0109	1.85E-04
0.011	0.012	0.0117	2.55	3.15	2.52	1.85E-04
4.29	3.31	3.99	0.0103	0.0105	0.0109	1.85E-04
4.16	3.51	3.24	0.0103	0.0105	0.0109	1.86E-04
2.5	3.05	3.23	0.0103	0.0105	0.0109	1.86E-04
2.5	3.05	3.23	0.0103	0.0105	0.0109	1.86E-04
4.02	3.11	3.46	0.0103	0.0105	0.0109	1.86E-04
2.51	2.37	3.02	0.0103	0.0105	0.0109	1.86E-04
2.51	2.37	3.02	0.0103	0.0105	0.0109	1.86E-04
0.011	0.012	0.0117	4.01	3.09	3.52	1.86E-04
3.12	2.49	2.53	0.0103	0.0105	0.0109	1.86E-04
3.12	2.49	2.53	0.0103	0.0105	0.0109	1.86E-04
3.29	2.97	2.53	0.0103	0.0105	0.0109	1.87E-04
3.29	2.97	2.53	0.0103	0.0105	0.0109	1.87E-04
3.29	2.97	2.53	0.0103	0.0105	0.0109	1.87E-04
0.011	0.012	0.0117	2.08	2.58	2.67	1.87E-04
3.2	3.12	2.5	0.0103	0.0105	0.0109	1.88E-04
0.011	0.012	0.0117	2.89	3.39	3.76	1.89E-04
2.85	3.08	3.66	0.0103	0.0105	0.0109	1.89E-04
3.09	2.7	3.51	0.0103	0.0105	0.0109	1.90E-04
3.09	2.7	3.51	0.0103	0.0105	0.0109	1.90E-04
3.09	2.7	3.51	0.0103	0.0105	0.0109	1.90E-04
4.96	4.4	3.81	0.0103	0.0105	0.0109	1.91E-04
2.1	2.73	2.4	0.0103	0.0105	0.0109	1.91E-04
2.1	2.73	2.4	0.0103	0.0105	0.0109	1.91E-04
3.23	2.8	2.49	0.0103	0.0105	0.0109	1.91E-04
3.23	2.8	2.49	0.0103	0.0105	0.0109	1.91E-04
2.46	2.26	2.91	0.0103	0.0105	0.0109	1.92E-04
2.46	2.26	2.91	0.0103	0.0105	0.0109	1.92E-04
0.011	0.012	0.0117	2.6	3.25	2.62	1.92E-04
2.73	2.98	2.29	0.0103	0.0105	0.0109	1.92E-04
0.011	0.012	0.0117	2.73	2.52	2.1	1.92E-04
2.38	1.87	2.36	0.0103	0.0105	0.0109	1.93E-04

3.22	3.06	2.49	0.0103	0.0105	0.0109	1.93E-04
2.09	2.5	2.72	0.0103	0.0105	0.0109	1.94E-04
2.77	3.22	3.61	0.0103	0.0105	0.0109	1.94E-04
2.66	2.49	3.19	0.0103	0.0105	0.0109	1.94E-04
0.011	0.012	0.0117	3.15	3.9	3.11	1.94E-04
4.4	3.63	4.72	0.0103	0.0105	0.0109	1.96E-04
4.4	3.63	4.72	0.0103	0.0105	0.0109	1.96E-04
0.011	0.012	0.0117	3.56	3.46	2.77	1.96E-04
3.08	2.93	2.38	0.0103	0.0105	0.0109	1.96E-04
3.64	3.24	2.79	0.0103	0.0105	0.0109	1.97E-04
3.64	3.24	2.79	0.0103	0.0105	0.0109	1.97E-04
3.64	3.24	2.79	0.0103	0.0105	0.0109	1.97E-04
2.76	3.6	3.28	0.0103	0.0105	0.0109	1.97E-04
0.011	0.012	0.0117	2.27	2.72	2.12	1.97E-04
3.06	2.47	3.19	0.0103	0.0105	0.0109	1.98E-04
2.48	2.1	1.92	0.0103	0.0105	0.0109	1.98E-04
2.13	2.71	2.7	0.0103	0.0105	0.0109	1.99E-04
3.08	2.39	2.59	0.0103	0.0105	0.0109	1.99E-04
3.08	2.39	2.59	0.0103	0.0105	0.0109	1.99E-04
2.85	2.47	2.19	0.0103	0.0105	0.0109	2.00E-04
5.41	4.85	4.14	0.0103	0.0105	0.0109	2.00E-04
5.41	4.85	4.14	0.0103	0.0105	0.0109	2.00E-04
3.07	3.64	4.01	0.0103	0.0105	0.0109	2.00E-04
0.011	0.012	0.0117	3.74	2.95	3.05	2.00E-04
2.12	2.64	2.11	0.0103	0.0105	0.0109	2.01E-04
0.011	0.012	0.0117	2.76	3.23	2.49	2.01E-04
0.011	0.012	0.0117	2.76	3.23	2.49	2.01E-04
3.35	3.61	2.77	0.0103	0.0105	0.0109	2.01E-04
3.74	3.68	2.92	0.0103	0.0105	0.0109	2.01E-04
3.19	2.62	3.41	0.0103	0.0105	0.0109	2.01E-04
3.94	3.14	3.17	0.0103	0.0105	0.0109	2.01E-04
3.94	3.14	3.17	0.0103	0.0105	0.0109	2.01E-04
0.011	0.012	0.0117	3.28	2.51	2.98	2.02E-04
0.011	0.012	0.0117	3.28	2.51	2.98	2.02E-04
2.82	2.85	2.23	0.0103	0.0105	0.0109	2.02E-04
2.82	2.85	2.23	0.0103	0.0105	0.0109	2.02E-04
2.17	2.64	2.07	0.0103	0.0105	0.0109	2.03E-04
3.4	4.4	3.72	0.0103	0.0105	0.0109	2.03E-04
3.4	4.4	3.72	0.0103	0.0105	0.0109	2.03E-04
1.97	2.46	2.54	0.0103	0.0105	0.0109	2.03E-04
1.97	2.46	2.54	0.0103	0.0105	0.0109	2.03E-04
2.68	3.45	2.88	0.0103	0.0105	0.0109	2.04E-04
4.09	3.14	3.53	0.0103	0.0105	0.0109	2.04E-04
4.09	3.14	3.53	0.0103	0.0105	0.0109	2.04E-04
4.09	3.14	3.53	0.0103	0.0105	0.0109	2.04E-04
2.63	2.55	2.04	0.0103	0.0105	0.0109	2.04E-04
2.63	2.55	2.04	0.0103	0.0105	0.0109	2.04E-04
2.63	2.55	2.04	0.0103	0.0105	0.0109	2.04E-04
0.011	0.012	0.0117	2.5	2.62	3.19	2.04E-04
2.88	2.36	2.26	0.0103	0.0105	0.0109	2.05E-04
2.86	3.03	2.33	0.0103	0.0105	0.0109	2.05E-04
2.86	3.03	2.33	0.0103	0.0105	0.0109	2.05E-04
2.3	2.08	2.7	0.0103	0.0105	0.0109	2.05E-04
2.81	2.91	3.57	0.0103	0.0105	0.0109	2.05E-04
2.62	3.38	2.83	0.0103	0.0105	0.0109	2.06E-04
2.62	3.38	2.83	0.0103	0.0105	0.0109	2.06E-04
4	3.18	4.09	0.0103	0.0105	0.0109	2.06E-04
4	3.18	4.09	0.0103	0.0105	0.0109	2.06E-04

3.49	2.71	2.91	0.0103	0.0105	0.0109	2.06E-04
2.4	2.71	3.13	0.0103	0.0105	0.0109	2.06E-04
2.4	2.71	3.13	0.0103	0.0105	0.0109	2.06E-04
2.4	2.71	3.13	0.0103	0.0105	0.0109	2.06E-04
0.011	0.012	0.0117	2.63	3.43	3.2	2.06E-04
0.011	0.012	0.0117	3.4	3.47	2.7	2.06E-04
0.011	0.012	0.0117	3.4	3.47	2.7	2.06E-04
0.011	0.012	0.0117	3.46	2.65	3.01	2.07E-04
0.011	0.012	0.0117	3.46	2.65	3.01	2.07E-04
0.011	0.012	0.0117	2.35	3.03	2.53	2.08E-04
0.011	0.012	0.0117	2.58	3.37	2.93	2.08E-04
2.83	2.17	2.44	0.0103	0.0105	0.0109	2.09E-04
2.83	2.17	2.44	0.0103	0.0105	0.0109	2.09E-04
3.04	2.45	2.41	0.0103	0.0105	0.0109	2.10E-04
3.04	2.45	2.41	0.0103	0.0105	0.0109	2.10E-04
0.011	0.012	0.0117	3.12	2.72	3.56	2.10E-04
3.68	3.13	2.83	0.0103	0.0105	0.0109	2.10E-04
3.68	3.13	2.83	0.0103	0.0105	0.0109	2.10E-04
3.68	3.13	2.83	0.0103	0.0105	0.0109	2.10E-04
3.19	2.96	2.44	0.0103	0.0105	0.0109	2.11E-04
0.011	0.012	0.0117	2.76	2.26	2.95	2.11E-04
3.16	2.49	3.19	0.0103	0.0105	0.0109	2.11E-04
2.87	3.34	2.56	0.0103	0.0105	0.0109	2.12E-04
2.87	3.34	2.56	0.0103	0.0105	0.0109	2.12E-04
2.87	3.34	2.56	0.0103	0.0105	0.0109	2.12E-04
2.07	2.32	2.7	0.0103	0.0105	0.0109	2.12E-04
3.08	2.89	3.72	0.0103	0.0105	0.0109	2.13E-04
3.08	2.89	3.72	0.0103	0.0105	0.0109	2.13E-04
2.82	2.91	2.25	0.0103	0.0105	0.0109	2.13E-04
2.82	2.91	2.25	0.0103	0.0105	0.0109	2.13E-04
0.011	0.012	0.0117	2.9	3.42	2.63	2.13E-04
3.71	3.87	2.98	0.0103	0.0105	0.0109	2.14E-04
3.43	2.68	2.81	0.0103	0.0105	0.0109	2.14E-04
3.28	3.99	3.11	0.0103	0.0105	0.0109	2.15E-04
3.28	3.99	3.11	0.0103	0.0105	0.0109	2.15E-04
2.22	2.88	2.77	0.0103	0.0105	0.0109	2.15E-04
0.011	0.012	0.0117	3.04	2.35	2.95	2.16E-04
0.011	0.012	0.0117	3.04	2.35	2.95	2.16E-04
3.44	3.06	4	0.0103	0.0105	0.0109	2.16E-04
2.46	2.54	3.13	0.0103	0.0105	0.0109	2.16E-04
2.58	2.64	3.27	0.0103	0.0105	0.0109	2.16E-04
4.14	4.89	5.44	0.0103	0.0105	0.0109	2.16E-04
4.14	4.89	5.44	0.0103	0.0105	0.0109	2.16E-04
2.7	3.53	3.31	0.0103	0.0105	0.0109	2.17E-04
2.7	3.53	3.31	0.0103	0.0105	0.0109	2.17E-04
0.011	0.012	0.0117	2.16	2.72	2.79	2.17E-04
0.011	0.012	0.0117	2.16	2.72	2.79	2.17E-04
2.99	3.23	3.87	0.0103	0.0105	0.0109	2.17E-04
2.99	3.23	3.87	0.0103	0.0105	0.0109	2.17E-04
2.52	2.66	2.04	0.0103	0.0105	0.0109	2.17E-04
0.011	0.012	0.0117	4.31	4.77	3.63	2.17E-04
2.97	2.9	2.3	0.0103	0.0105	0.0109	2.17E-04
2.01	2.64	2.39	0.0103	0.0105	0.0109	2.18E-04
2.01	2.64	2.39	0.0103	0.0105	0.0109	2.18E-04
3.08	2.7	3.54	0.0103	0.0105	0.0109	2.18E-04
3.08	2.7	3.54	0.0103	0.0105	0.0109	2.18E-04
2.29	2.15	2.77	0.0103	0.0105	0.0109	2.18E-04
2.78	3.63	3.43	0.0103	0.0105	0.0109	2.19E-04

2.78	3.63	3.43	0.0103	0.0105	0.0109	2.19E-04
2.53	3.18	2.54	0.0103	0.0105	0.0109	2.19E-04
0.011	0.012	0.0117	3.51	3.59	2.78	2.19E-04
0.011	0.012	0.0117	3.51	3.59	2.78	2.19E-04
2.72	2.6	2.09	0.0103	0.0105	0.0109	2.19E-04
2.72	2.6	2.09	0.0103	0.0105	0.0109	2.19E-04
2.66	2.4	3.13	0.0103	0.0105	0.0109	2.19E-04
2.66	2.4	3.13	0.0103	0.0105	0.0109	2.19E-04
3.18	2.43	2.98	0.0103	0.0105	0.0109	2.20E-04
3.97	3.05	3.35	0.0103	0.0105	0.0109	2.20E-04
4	3.05	3.47	0.0103	0.0105	0.0109	2.20E-04
2.41	2.12	2.78	0.0103	0.0105	0.0109	2.21E-04
0.011	0.012	0.0117	3.32	3.28	2.58	2.22E-04
3.52	2.77	2.84	0.0103	0.0105	0.0109	2.23E-04
3.52	2.77	2.84	0.0103	0.0105	0.0109	2.23E-04
0.011	0.012	0.0117	3.25	3.42	2.62	2.23E-04
0.011	0.012	0.0117	3.25	3.42	2.62	2.23E-04
0.011	0.012	0.0117	2.29	3.01	2.64	2.23E-04
3.22	3.62	2.75	0.0103	0.0105	0.0109	2.23E-04
2.52	3.17	3.27	0.0103	0.0105	0.0109	2.24E-04
0.011	0.012	0.0117	3.58	2.8	2.91	2.24E-04
4.29	4.49	4.52	3.15	3.01	3.26	2.24E-04
4.29	4.49	4.52	3.15	3.01	3.26	2.24E-04
0.011	0.012	0.0117	2.76	2.78	3.48	2.25E-04
3.8	3.22	2.91	0.0103	0.0105	0.0109	2.25E-04
3.8	3.22	2.91	0.0103	0.0105	0.0109	2.25E-04
3.82	2.9	3.4	0.0103	0.0105	0.0109	2.25E-04
3.82	2.9	3.4	0.0103	0.0105	0.0109	2.25E-04
3.4	3.19	4.12	0.0103	0.0105	0.0109	2.26E-04
0.011	0.012	0.0117	3.44	3.52	2.72	2.26E-04
3.24	2.48	3.08	0.0103	0.0105	0.0109	2.26E-04
3.24	2.48	3.08	0.0103	0.0105	0.0109	2.26E-04
0.011	0.012	0.0117	3.34	2.56	3.19	2.26E-04
0.011	0.012	0.0117	3.34	2.56	3.19	2.26E-04
3.11	2.68	2.37	0.0103	0.0105	0.0109	2.26E-04
2.06	2.6	2.67	0.0103	0.0105	0.0109	2.27E-04
2.06	2.6	2.67	0.0103	0.0105	0.0109	2.27E-04
3.26	2.51	2.72	0.0103	0.0105	0.0109	2.27E-04
3.27	2.56	2.65	0.0103	0.0105	0.0109	2.27E-04
2.58	3.02	3.4	0.0103	0.0105	0.0109	2.27E-04
3.77	3.68	2.91	0.0103	0.0105	0.0109	2.27E-04
3.77	3.68	2.91	0.0103	0.0105	0.0109	2.27E-04
3.38	2.59	2.85	0.0103	0.0105	0.0109	2.28E-04
3.76	3.83	3.63	2.75	2.87	2.88	2.28E-04
3.2	4.17	3.5	0.0103	0.0105	0.0109	2.28E-04
2.89	2.22	2.42	0.0103	0.0105	0.0109	2.29E-04
2.95	2.65	3.47	0.0103	0.0105	0.0109	2.30E-04
0.011	0.012	0.0117	3.69	2.8	3.23	2.31E-04
0.011	0.012	0.0117	3.69	2.8	3.23	2.31E-04
0.011	0.012	0.0117	3.19	2.44	3.04	2.31E-04
2.54	2.16	2.85	0.0103	0.0105	0.0109	2.31E-04
2.54	2.16	2.85	0.0103	0.0105	0.0109	2.31E-04
3.31	2.91	2.51	0.0103	0.0105	0.0109	2.32E-04
3.31	2.91	2.51	0.0103	0.0105	0.0109	2.32E-04
3.57	2.77	2.92	0.0103	0.0105	0.0109	2.33E-04
3.62	2.89	2.86	0.0103	0.0105	0.0109	2.34E-04
3.15	3.59	2.72	0.0103	0.0105	0.0109	2.35E-04
2.3	2.12	2.76	0.0103	0.0105	0.0109	2.35E-04

2.3	2.12	2.76	0.0103	0.0105	0.0109	2.35E-04
0.011	0.012	0.0117	2.9	2.56	3.37	2.37E-04
0.011	0.012	0.0117	2.9	2.56	3.37	2.37E-04
2.84	3.43	2.64	0.0103	0.0105	0.0109	2.37E-04
2.84	3.43	2.64	0.0103	0.0105	0.0109	2.37E-04
0.011	0.012	0.0117	2.45	2.75	2.08	2.38E-04
0.011	0.012	0.0117	2.4	3.09	3.08	2.39E-04
3.06	2.92	3.76	0.0103	0.0105	0.0109	2.39E-04
2	2.52	2.61	0.0103	0.0105	0.0109	2.40E-04
2.8	2.71	3.47	0.0103	0.0105	0.0109	2.40E-04
2.8	2.71	3.47	0.0103	0.0105	0.0109	2.40E-04
2.47	2.98	2.29	0.0103	0.0105	0.0109	2.41E-04
2.47	2.98	2.29	0.0103	0.0105	0.0109	2.41E-04
0.011	0.012	0.0117	3.41	3.58	2.73	2.41E-04
0.011	0.012	0.0117	2.47	3.03	2.35	2.41E-04
0.011	0.012	0.0117	2.47	3.03	2.35	2.41E-04
2.79	3.42	2.65	0.0103	0.0105	0.0109	2.41E-04
2.79	3.42	2.65	0.0103	0.0105	0.0109	2.41E-04
2.95	2.46	2.26	0.0103	0.0105	0.0109	2.41E-04
2.95	2.46	2.26	0.0103	0.0105	0.0109	2.41E-04
3.72	4.59	3.57	0.0103	0.0105	0.0109	2.42E-04
2.9	3.84	3.45	0.0103	0.0105	0.0109	2.42E-04
3.24	3.16	2.49	0.0103	0.0105	0.0109	2.42E-04
3	3.42	3.96	0.0103	0.0105	0.0109	2.42E-04
3	3.42	3.96	0.0103	0.0105	0.0109	2.42E-04
3.18	2.54	3.33	0.0103	0.0105	0.0109	2.42E-04
3.08	3.69	4.08	0.0103	0.0105	0.0109	2.44E-04
3.08	3.69	4.08	0.0103	0.0105	0.0109	2.44E-04
3.02	2.37	3.08	0.0103	0.0105	0.0109	2.45E-04
3.01	2.36	2.41	0.0103	0.0105	0.0109	2.46E-04
2.56	3.39	2.97	0.0103	0.0105	0.0109	2.46E-04
2.56	3.39	2.97	0.0103	0.0105	0.0109	2.46E-04
5.15	4.86	3.91	0.0103	0.0105	0.0109	2.46E-04
0.011	0.012	0.0117	2.7	2.56	3.31	2.46E-04
0.011	0.012	0.0117	2.7	2.56	3.31	2.46E-04
3.59	2.75	2.98	0.0103	0.0105	0.0109	2.47E-04
3.54	2.9	2.73	0.0103	0.0105	0.0109	2.47E-04
0.011	0.012	0.0117	2.26	2.6	2.99	2.47E-04
2.92	3.87	3.52	0.0103	0.0105	0.0109	2.47E-04
2.4	2.65	3.15	0.0103	0.0105	0.0109	2.47E-04
2.4	2.65	3.15	0.0103	0.0105	0.0109	2.47E-04
3.31	2.79	2.52	0.0103	0.0105	0.0109	2.47E-04
3.31	2.79	2.52	0.0103	0.0105	0.0109	2.47E-04
5.11	4.09	4	0.0103	0.0105	0.0109	2.48E-04
0.011	0.012	0.0117	2.88	2.38	2.21	2.49E-04
2.84	3.07	2.32	0.0103	0.0105	0.0109	2.49E-04
2.84	3.07	2.32	0.0103	0.0105	0.0109	2.49E-04
2.71	3.59	3.3	0.0103	0.0105	0.0109	2.49E-04
3.65	2.75	3.27	0.0103	0.0105	0.0109	2.50E-04
3.08	2.65	2.33	0.0103	0.0105	0.0109	2.50E-04
3.08	2.65	2.33	0.0103	0.0105	0.0109	2.50E-04
3.38	2.65	2.7	0.0103	0.0105	0.0109	2.50E-04
2.7	2.52	3.28	0.0103	0.0105	0.0109	2.50E-04
2.7	2.52	3.28	0.0103	0.0105	0.0109	2.50E-04
3.23	4.28	3.72	0.0103	0.0105	0.0109	2.51E-04
0.011	0.012	0.0117	4.21	3.24	3.45	2.52E-04
0.011	0.012	0.0117	4.21	3.24	3.45	2.52E-04
2.99	2.53	3.36	0.0103	0.0105	0.0109	2.52E-04

2.99	2.53	3.36	0.0103	0.0105	0.0109	2.52E-04
2.99	2.53	3.36	0.0103	0.0105	0.0109	2.52E-04
3.8	2.95	3.07	0.0103	0.0105	0.0109	2.52E-04
3.6	2.97	2.76	0.0103	0.0105	0.0109	2.53E-04
3.6	2.97	2.76	0.0103	0.0105	0.0109	2.53E-04
2.19	2.77	2.19	0.0103	0.0105	0.0109	2.53E-04
3.96	3.14	3.12	0.0103	0.0105	0.0109	2.53E-04
3.96	3.14	3.12	0.0103	0.0105	0.0109	2.53E-04
3.96	3.14	3.12	0.0103	0.0105	0.0109	2.53E-04
0.011	0.012	0.0117	2.47	2.63	3.21	2.53E-04
0.011	0.012	0.0117	2.47	2.63	3.21	2.53E-04
2.66	3.23	3.53	0.0103	0.0105	0.0109	2.54E-04
2.45	2.8	2.11	0.0103	0.0105	0.0109	2.54E-04
2.45	2.8	2.11	0.0103	0.0105	0.0109	2.54E-04
3.39	2.61	3.35	0.0103	0.0105	0.0109	2.55E-04
3.14	2.38	2.97	0.0103	0.0105	0.0109	2.56E-04
2.94	2.31	3.02	0.0103	0.0105	0.0109	2.57E-04
3.22	2.49	2.61	0.0103	0.0105	0.0109	2.57E-04
3.22	2.49	2.61	0.0103	0.0105	0.0109	2.57E-04
2.66	2.03	2.21	0.0103	0.0105	0.0109	2.57E-04
2.66	2.03	2.21	0.0103	0.0105	0.0109	2.57E-04
0.011	0.012	0.0117	3.12	2.55	2.4	2.58E-04
2.02	2.64	2.18	0.0103	0.0105	0.0109	2.58E-04
2.02	2.64	2.18	0.0103	0.0105	0.0109	2.58E-04
0.011	0.012	0.0117	2.89	3.03	3.74	2.60E-04
0.011	0.012	0.0117	4.12	3.36	3.17	2.60E-04
0.011	0.012	0.0117	4.12	3.36	3.17	2.60E-04
0.011	0.012	0.0117	4.12	3.36	3.17	2.60E-04
2.26	2.34	2.91	0.0103	0.0105	0.0109	2.61E-04
2.3	2.69	3.06	0.0103	0.0105	0.0109	2.61E-04
2.3	2.69	3.06	0.0103	0.0105	0.0109	2.61E-04
0.011	0.012	0.0117	2.32	3.01	2.99	2.61E-04
0.011	0.012	0.0117	2.66	2.06	2.67	2.63E-04
2.93	2.27	2.36	0.0103	0.0105	0.0109	2.64E-04
2.93	2.27	2.36	0.0103	0.0105	0.0109	2.64E-04
2.56	2.55	3.24	0.0103	0.0105	0.0109	2.64E-04
2.56	2.55	3.24	0.0103	0.0105	0.0109	2.64E-04
0.011	0.012	0.0117	3.57	3.93	2.95	2.65E-04
0.011	0.012	0.0117	3.57	3.93	2.95	2.65E-04
2.32	2.93	2.3	0.0103	0.0105	0.0109	2.66E-04
0.011	0.012	0.0117	3.24	2.78	2.44	2.66E-04
3.83	4.42	3.32	0.0103	0.0105	0.0109	2.67E-04
3.83	4.42	3.32	0.0103	0.0105	0.0109	2.67E-04
3.4	2.65	2.71	0.0103	0.0105	0.0109	2.68E-04
2.22	2.53	2.95	0.0103	0.0105	0.0109	2.69E-04
0.011	0.012	0.0117	2.35	3.1	2.97	2.69E-04
0.011	0.012	0.0117	2.39	2.31	2.98	2.71E-04
4.49	4.92	4.44	2.38	2.06	2.44	2.71E-04
0.011	0.012	0.0117	3.97	3.14	3.11	2.72E-04
3.04	2.94	2.31	0.0103	0.0105	0.0109	2.72E-04
3.81	3.17	2.89	0.0103	0.0105	0.0109	2.72E-04
3.81	3.17	2.89	0.0103	0.0105	0.0109	2.72E-04
3.07	3.58	2.69	0.0103	0.0105	0.0109	2.73E-04
3.43	3.3	2.6	0.0103	0.0105	0.0109	2.74E-04
0.011	0.012	0.0117	3.05	3.97	3.95	2.75E-04
0.011	0.012	0.0117	2.14	2.83	2.37	2.76E-04
3.01	2.26	2.58	0.0103	0.0105	0.0109	2.77E-04
4	4.14	3.14	0.0103	0.0105	0.0109	2.77E-04

4	4.14	3.14	0.0103	0.0105	0.0109	2.77E-04
3.29	3.74	4.38	0.0103	0.0105	0.0109	2.77E-04
3.84	3.13	4.18	0.0103	0.0105	0.0109	2.78E-04
3.84	3.13	4.18	0.0103	0.0105	0.0109	2.78E-04
3.84	3.13	4.18	0.0103	0.0105	0.0109	2.78E-04
3.84	3.13	4.18	0.0103	0.0105	0.0109	2.78E-04
0.011	0.012	0.0117	3.05	2.97	2.32	2.79E-04
3.57	4.16	3.12	0.0103	0.0105	0.0109	2.79E-04
3.52	2.63	3.15	0.0103	0.0105	0.0109	2.79E-04
3.52	2.63	3.15	0.0103	0.0105	0.0109	2.79E-04
2.85	2.18	2.32	0.0103	0.0105	0.0109	2.80E-04
2.09	2.74	2.69	0.0103	0.0105	0.0109	2.81E-04
0.011	0.012	0.0117	2.6	3.05	2.29	2.82E-04
3.27	2.9	2.44	0.0103	0.0105	0.0109	2.85E-04
2.41	2.68	2	0.0103	0.0105	0.0109	2.85E-04
2.41	2.68	2	0.0103	0.0105	0.0109	2.85E-04
3.91	2.92	3.4	0.0103	0.0105	0.0109	2.86E-04
0.011	0.012	0.0117	2.82	2.92	2.21	2.86E-04
0.011	0.012	0.0117	2.82	2.92	2.21	2.86E-04
2.73	2.22	2.97	0.0103	0.0105	0.0109	2.86E-04
3.92	2.94	3.68	0.0103	0.0105	0.0109	2.88E-04
2.85	2.31	3.09	0.0103	0.0105	0.0109	2.88E-04
0.011	0.012	0.0117	2.41	2.97	2.27	2.88E-04
2.54	3.13	3.4	0.0103	0.0105	0.0109	2.89E-04
0.011	0.012	0.0117	3.43	2.59	3.3	2.90E-04
2.49	2.31	3.04	0.0103	0.0105	0.0109	2.90E-04
2.49	2.31	3.04	0.0103	0.0105	0.0109	2.90E-04
2.21	2.51	2.95	0.0103	0.0105	0.0109	2.91E-04
0.011	0.012	0.0117	2.99	2.29	2.98	2.92E-04
2.29	3.07	2.81	0.0103	0.0105	0.0109	2.92E-04
2.29	3.07	2.81	0.0103	0.0105	0.0109	2.92E-04
3.51	3.99	2.97	0.0103	0.0105	0.0109	2.94E-04
3.09	2.5	3.35	0.0103	0.0105	0.0109	2.94E-04
2.7	3.07	3.61	0.0103	0.0105	0.0109	2.96E-04
2.7	3.07	3.61	0.0103	0.0105	0.0109	2.96E-04
2.04	2.23	2.7	0.0103	0.0105	0.0109	2.96E-04
2.04	2.23	2.7	0.0103	0.0105	0.0109	2.96E-04
2.67	2.72	3.44	0.0103	0.0105	0.0109	2.96E-04
2.67	2.72	3.44	0.0103	0.0105	0.0109	2.96E-04
3.79	2.88	3.09	0.0103	0.0105	0.0109	2.96E-04
3.79	2.88	3.09	0.0103	0.0105	0.0109	2.96E-04
0.011	0.012	0.0117	2.53	2.85	2.12	2.97E-04
2.88	2.25	2.26	0.0103	0.0105	0.0109	2.98E-04
2.88	2.25	2.26	0.0103	0.0105	0.0109	2.98E-04
3.58	4.7	3.81	0.0103	0.0105	0.0109	2.98E-04
2.34	3.08	2.51	0.0103	0.0105	0.0109	2.99E-04
2.34	3.08	2.51	0.0103	0.0105	0.0109	2.99E-04
2.39	3.21	2.94	0.0103	0.0105	0.0109	3.00E-04
0.011	0.012	0.0117	2.44	2.33	3.04	3.00E-04
3.51	2.95	2.63	0.0103	0.0105	0.0109	3.01E-04
3.51	2.95	2.63	0.0103	0.0105	0.0109	3.01E-04
3.36	2.67	3.57	0.0103	0.0105	0.0109	3.02E-04
3.36	2.67	3.57	0.0103	0.0105	0.0109	3.02E-04
3.36	2.67	3.57	0.0103	0.0105	0.0109	3.02E-04
2.76	3.56	2.81	0.0103	0.0105	0.0109	3.03E-04
2.76	3.56	2.81	0.0103	0.0105	0.0109	3.03E-04
0.011	0.012	0.0117	4.18	3.48	3.14	3.03E-04
0.011	0.012	0.0117	3.04	3.1	2.35	3.04E-04

2.84	2.11	2.58	0.0103	0.0105	0.0109	3.05E-04
3.22	2.83	2.39	0.0103	0.0105	0.0109	3.06E-04
3.23	3.12	3.02	2.36	2.39	2.3	3.06E-04
2.47	3.33	2.98	0.0103	0.0105	0.0109	3.07E-04
2.47	3.33	2.98	0.0103	0.0105	0.0109	3.07E-04
3.46	2.62	2.82	0.0103	0.0105	0.0109	3.08E-04
3.46	2.62	2.82	0.0103	0.0105	0.0109	3.08E-04
0.011	0.012	0.0117	2.63	2.85	2.12	3.09E-04
0.011	0.012	0.0117	2.92	2.99	2.26	3.09E-04
0.011	0.012	0.0117	4.32	5.77	4.82	3.09E-04
2.28	2.99	2.98	0.0103	0.0105	0.0109	3.10E-04
3	2.47	2.26	0.0103	0.0105	0.0109	3.10E-04
3	2.47	2.26	0.0103	0.0105	0.0109	3.10E-04
3.24	2.82	3.79	0.0103	0.0105	0.0109	3.10E-04
2.34	2.33	2.99	0.0103	0.0105	0.0109	3.11E-04
2.34	2.33	2.99	0.0103	0.0105	0.0109	3.11E-04
2.92	2.22	2.36	0.0103	0.0105	0.0109	3.11E-04
2.41	3.15	2.52	0.0103	0.0105	0.0109	3.12E-04
2.41	3.15	2.52	0.0103	0.0105	0.0109	3.12E-04
2.5	2.73	3.32	0.0103	0.0105	0.0109	3.13E-04
2.5	2.73	3.32	0.0103	0.0105	0.0109	3.13E-04
3.66	2.89	3.87	0.0103	0.0105	0.0109	3.13E-04
3.66	2.89	3.87	0.0103	0.0105	0.0109	3.13E-04
3.66	2.89	3.87	0.0103	0.0105	0.0109	3.13E-04
0.011	0.012	0.0117	2.81	2.22	2.17	3.13E-04
2.15	2.39	2.87	0.0103	0.0105	0.0109	3.13E-04
2.15	2.39	2.87	0.0103	0.0105	0.0109	3.13E-04
0.011	0.012	0.0117	3.06	3.14	3.97	3.14E-04
0.011	0.012	0.0117	3.06	3.14	3.97	3.14E-04
2.55	2.85	3.41	0.0103	0.0105	0.0109	3.14E-04
2.55	2.85	3.41	0.0103	0.0105	0.0109	3.14E-04
0.011	0.012	0.0117	2.53	3.17	3.4	3.15E-04
3.02	3.89	3.05	0.0103	0.0105	0.0109	3.15E-04
3.02	3.89	3.05	0.0103	0.0105	0.0109	3.15E-04
0.011	0.012	0.0117	3.4	4.59	4.17	3.16E-04
3.35	3.31	2.54	0.0103	0.0105	0.0109	3.16E-04
3.35	3.31	2.54	0.0103	0.0105	0.0109	3.16E-04
2.67	2.22	3	0.0103	0.0105	0.0109	3.17E-04
2.71	2.01	2.49	0.0103	0.0105	0.0109	3.18E-04
0.011	0.012	0.0117	3.99	3.2	3.04	3.18E-04
0.011	0.012	0.0117	3.99	3.2	3.04	3.18E-04
2.65	2.03	2.11	0.0103	0.0105	0.0109	3.19E-04
2.15	2.77	2.17	0.0103	0.0105	0.0109	3.19E-04
2.17	2.68	2.03	0.0103	0.0105	0.0109	3.20E-04
0.011	0.012	0.0117	2.73	2.16	2.1	3.21E-04
0.011	0.012	0.0117	2.85	2.15	2.79	3.22E-04
0.011	0.012	0.0117	2.85	2.15	2.79	3.22E-04
0.011	0.012	0.0117	3.69	3.36	2.73	3.23E-04
0.011	0.012	0.0117	2.8	3.76	3.16	3.23E-04
2.6	2.3	3.09	0.0103	0.0105	0.0109	3.24E-04
2.6	2.3	3.09	0.0103	0.0105	0.0109	3.24E-04
0.011	0.012	0.0117	3.28	3.71	2.74	3.25E-04
0.011	0.012	0.0117	3.28	3.71	2.74	3.25E-04
3.59	2.69	2.95	0.0103	0.0105	0.0109	3.30E-04
3.59	2.69	2.95	0.0103	0.0105	0.0109	3.30E-04
0.011	0.012	0.0117	3.81	3.96	2.96	3.32E-04
0.011	0.012	0.0117	3.81	3.96	2.96	3.32E-04
0.011	0.012	0.0117	3.27	3.59	2.65	3.32E-04

3.16	2.5	2.42	0.0103	0.0105	0.0109	3.33E-04
3.22	3.49	2.58	0.0103	0.0105	0.0109	3.33E-04
3.22	3.49	2.58	0.0103	0.0105	0.0109	3.33E-04
0.011	0.012	0.0117	4.1	3.05	3.89	3.34E-04
3.27	4.35	3.54	0.0103	0.0105	0.0109	3.34E-04
5.34	4.33	4.02	0.0103	0.0105	0.0109	3.35E-04
3.91	2.95	3.86	0.0103	0.0105	0.0109	3.36E-04
3.42	2.52	3.1	0.0103	0.0105	0.0109	3.38E-04
2.47	3.26	3.25	0.0103	0.0105	0.0109	3.38E-04
0.011	0.012	0.0117	2.39	3.24	2.79	3.40E-04
0.011	0.012	0.0117	2.39	3.24	2.79	3.40E-04
2.95	3.97	3.31	0.0103	0.0105	0.0109	3.40E-04
2	2.66	2.61	0.0103	0.0105	0.0109	3.41E-04
3.62	3.05	2.68	0.0103	0.0105	0.0109	3.42E-04
4.08	3.03	3.4	0.0103	0.0105	0.0109	3.42E-04
2.38	2.93	2.2	0.0103	0.0105	0.0109	3.43E-04
0.011	0.012	0.0117	2.45	2.89	3.33	3.46E-04
0.011	0.012	0.0117	2.83	2.49	2.08	3.47E-04
3.17	2.37	3.08	0.0103	0.0105	0.0109	3.48E-04
3.24	3.41	2.53	0.0103	0.0105	0.0109	3.48E-04
2.84	2.15	2.84	0.0103	0.0105	0.0109	3.49E-04
3.61	2.65	3.23	0.0103	0.0105	0.0109	3.50E-04
3.61	2.65	3.23	0.0103	0.0105	0.0109	3.50E-04
4.33	3.64	3.2	0.0103	0.0105	0.0109	3.51E-04
4.33	3.64	3.2	0.0103	0.0105	0.0109	3.51E-04
0.011	0.012	0.0117	2.18	2.92	2.83	3.51E-04
3.09	3.75	2.79	0.0103	0.0105	0.0109	3.52E-04
3.09	3.75	2.79	0.0103	0.0105	0.0109	3.52E-04
3.09	3.75	2.79	0.0103	0.0105	0.0109	3.52E-04
0.011	0.012	0.0117	2.56	3.44	2.83	3.54E-04
2.86	3.69	3.85	0.0103	0.0105	0.0109	3.54E-04
2.86	3.69	3.85	0.0103	0.0105	0.0109	3.54E-04
0.011	0.012	0.0117	2.54	3.31	2.59	3.54E-04
0.011	0.012	0.0117	2.54	3.31	2.59	3.54E-04
2.58	3.51	3.22	0.0103	0.0105	0.0109	3.55E-04
2.58	3.51	3.22	0.0103	0.0105	0.0109	3.55E-04
0.011	0.012	0.0117	3.75	3.47	2.76	3.55E-04
0.011	0.012	0.0117	3.75	3.47	2.76	3.55E-04
4.36	3.83	5.19	0.0103	0.0105	0.0109	3.57E-04
0.011	0.012	0.0117	2.54	2.93	2.15	3.58E-04
4.06	3.39	3	0.0103	0.0105	0.0109	3.59E-04
4.06	3.39	3	0.0103	0.0105	0.0109	3.59E-04
4.06	3.39	3	0.0103	0.0105	0.0109	3.59E-04
3.51	2.85	3.89	0.0103	0.0105	0.0109	3.61E-04
3.51	2.85	3.89	0.0103	0.0105	0.0109	3.61E-04
3.75	4.18	5.06	0.0103	0.0105	0.0109	3.61E-04
2.91	2.3	2.21	0.0103	0.0105	0.0109	3.62E-04
0.011	0.012	0.0117	3.77	3.38	2.76	3.63E-04
3.9	5.19	4.16	0.0103	0.0105	0.0109	3.64E-04
4.06	2.97	3.6	0.0103	0.0105	0.0109	3.64E-04
0.011	0.012	0.0117	3.97	3.14	3.01	3.64E-04
0.011	0.012	0.0117	3.97	3.14	3.01	3.64E-04
3.24	2.41	2.65	0.0103	0.0105	0.0109	3.65E-04
0.011	0.012	0.0117	2.87	2.53	3.43	3.65E-04
0.011	0.012	0.0117	2.87	2.53	3.43	3.65E-04
2.82	2.38	3.25	0.0103	0.0105	0.0109	3.65E-04
0.011	0.012	0.0117	2.68	2.08	2.81	3.65E-04
2.88	2.78	2.14	0.0103	0.0105	0.0109	3.66E-04

2.88	2.78	2.14	0.0103	0.0105	0.0109	3.66E-04
0.011	0.012	0.0117	2.65	2.98	2.18	3.66E-04
3.34	2.48	2.74	0.0103	0.0105	0.0109	3.66E-04
3.12	2.46	2.37	0.0103	0.0105	0.0109	3.66E-04
3.19	2.55	2.4	0.0103	0.0105	0.0109	3.67E-04
0.011	0.012	0.0117	2.6	3.04	2.23	3.67E-04
0.011	0.012	0.0117	2.6	3.04	2.23	3.67E-04
0.011	0.012	0.0117	3.24	2.47	2.54	3.70E-04
0.011	0.012	0.0117	2.51	2.26	3.05	3.71E-04
2.66	2.07	2.04	0.0103	0.0105	0.0109	3.71E-04
5.31	5.65	5.5	3.83	4.1	3.76	3.71E-04
5.31	5.65	5.5	3.83	4.1	3.76	3.71E-04
5.31	5.65	5.5	3.83	4.1	3.76	3.71E-04
3.18	2.58	3.53	0.0103	0.0105	0.0109	3.71E-04
2	2.68	2.17	0.0103	0.0105	0.0109	3.72E-04
2	2.68	2.17	0.0103	0.0105	0.0109	3.72E-04
4.23	3.19	3.36	0.0103	0.0105	0.0109	3.72E-04
0.011	0.012	0.0117	2.03	2.77	2.37	3.72E-04
0.011	0.012	0.0117	2.49	2.76	3.36	3.72E-04
4.07	4.59	3.35	0.0103	0.0105	0.0109	3.74E-04
4.07	4.59	3.35	0.0103	0.0105	0.0109	3.74E-04
0.011	0.012	0.0117	2.82	3.35	3.86	3.75E-04
4.37	3.93	3.19	0.0103	0.0105	0.0109	3.76E-04
0.011	0.012	0.0117	3	2.27	3.03	3.76E-04
2	2.73	2.32	0.0103	0.0105	0.0109	3.78E-04
2	2.73	2.32	0.0103	0.0105	0.0109	3.78E-04
3.38	4.22	3.16	0.0103	0.0105	0.0109	3.78E-04
3.38	4.22	3.16	0.0103	0.0105	0.0109	3.78E-04
2.59	3.19	3.55	0.0103	0.0105	0.0109	3.79E-04
0.011	0.012	0.0117	2.64	3.09	3.61	3.79E-04
0.011	0.012	0.0117	2.57	2.85	2.08	3.80E-04
2.92	2.35	3.22	0.0103	0.0105	0.0109	3.81E-04
0.011	0.012	0.0117	2.92	3.1	3.89	3.81E-04
3.11	2.28	2.9	0.0103	0.0105	0.0109	3.82E-04
2.9	2.77	2.14	0.0103	0.0105	0.0109	3.82E-04
0.011	0.012	0.0117	3.03	3.47	2.53	3.82E-04
0.011	0.012	0.0117	3.03	3.47	2.53	3.82E-04
0.011	0.012	0.0117	2.59	3.19	2.37	3.83E-04
0.011	0.012	0.0117	2.59	3.19	2.37	3.83E-04
0.011	0.012	0.0117	2.71	3.53	2.73	3.84E-04
0.011	0.012	0.0117	3	3.04	2.27	3.85E-04
2.69	1.96	2.41	0.0103	0.0105	0.0109	3.86E-04
2.69	1.96	2.41	0.0103	0.0105	0.0109	3.86E-04
4.01	3.36	2.94	0.0103	0.0105	0.0109	3.87E-04
3.27	2.4	2.73	0.0103	0.0105	0.0109	3.88E-04
3.27	2.4	2.73	0.0103	0.0105	0.0109	3.88E-04
3.1	2.61	2.27	0.0103	0.0105	0.0109	3.88E-04
3.1	2.61	2.27	0.0103	0.0105	0.0109	3.88E-04
0.011	0.012	0.0117	3.52	2.57	3	3.90E-04
4.36	3.42	3.3	0.0103	0.0105	0.0109	3.90E-04
0.011	0.012	0.0117	2.99	3.86	2.95	3.93E-04
3.7	2.73	3.03	0.0103	0.0105	0.0109	3.94E-04
3.7	2.73	3.03	0.0103	0.0105	0.0109	3.94E-04
3.7	2.73	3.03	0.0103	0.0105	0.0109	3.94E-04
0.011	0.012	0.0117	3.11	3.2	2.37	3.94E-04
0.011	0.012	0.0117	3.11	3.2	2.37	3.94E-04
0.011	0.012	0.0117	2.41	3.03	2.27	3.94E-04
0.011	0.012	0.0117	2.41	3.03	2.27	3.94E-04

0.011	0.012	0.0117	3.26	2.55	2.47	3.96E-04
0.011	0.012	0.0117	2.82	2.38	3.27	3.96E-04
0.011	0.012	0.0117	2.93	2.13	2.62	3.96E-04
3.71	2.8	3.76	0.0103	0.0105	0.0109	3.97E-04
3.03	2.32	2.34	0.0103	0.0105	0.0109	3.97E-04
3.03	2.32	2.34	0.0103	0.0105	0.0109	3.97E-04
2.36	2.97	3.24	0.0103	0.0105	0.0109	3.97E-04
2.07	2.7	2.81	0.0103	0.0105	0.0109	4.00E-04
2.07	2.7	2.81	0.0103	0.0105	0.0109	4.00E-04
4.82	3.51	4.44	0.0103	0.0105	0.0109	4.00E-04
3.51	3	4.12	0.0103	0.0105	0.0109	4.00E-04
3.51	3	4.12	0.0103	0.0105	0.0109	4.00E-04
3.51	3	4.12	0.0103	0.0105	0.0109	4.00E-04
2.02	2.72	2.67	0.0103	0.0105	0.0109	4.01E-04
2.79	2.08	2.23	0.0103	0.0105	0.0109	4.01E-04
2.79	2.08	2.23	0.0103	0.0105	0.0109	4.01E-04
2.46	2.99	3.39	0.0103	0.0105	0.0109	4.02E-04
2.78	2.05	2.27	0.0103	0.0105	0.0109	4.03E-04
3.08	4.03	4.18	0.0103	0.0105	0.0109	4.03E-04
3.65	2.84	2.77	0.0103	0.0105	0.0109	4.03E-04
3	2.78	3.74	0.0103	0.0105	0.0109	4.03E-04
4.05	3.11	3.11	0.0103	0.0105	0.0109	4.03E-04
0.011	0.012	0.0117	3.55	2.99	2.59	4.04E-04
0.011	0.012	0.0117	3.55	2.99	2.59	4.04E-04
3.57	3.12	2.59	0.0103	0.0105	0.0109	4.04E-04
3.57	3.12	2.59	0.0103	0.0105	0.0109	4.04E-04
3.48	2.53	2.98	0.0103	0.0105	0.0109	4.05E-04
3.48	2.53	2.98	0.0103	0.0105	0.0109	4.05E-04
2.91	2.22	2.25	0.0103	0.0105	0.0109	4.05E-04
2.91	2.22	2.25	0.0103	0.0105	0.0109	4.05E-04
3.11	2.43	3.33	0.0103	0.0105	0.0109	4.06E-04
2.73	3.77	3.34	0.0103	0.0105	0.0109	4.12E-04
0.011	0.012	0.0117	2.87	3.46	2.53	4.13E-04
3.09	2.56	2.26	0.0103	0.0105	0.0109	4.14E-04
3.09	2.56	2.26	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
2.88	3.97	3.4	0.0103	0.0105	0.0109	4.14E-04
0.011	0.012	0.0117	3.53	2.56	3.22	4.15E-04
4.48	3.39	3.48	0.0103	0.0105	0.0109	4.17E-04
3.95	2.87	3.34	0.0103	0.0105	0.0109	4.17E-04
3.95	2.87	3.34	0.0103	0.0105	0.0109	4.17E-04
3.32	3.06	2.41	0.0103	0.0105	0.0109	4.19E-04
3.32	3.06	2.41	0.0103	0.0105	0.0109	4.19E-04
3.32	3.06	2.41	0.0103	0.0105	0.0109	4.19E-04
3.32	3.06	2.41	0.0103	0.0105	0.0109	4.19E-04
3.33	2.81	2.42	0.0103	0.0105	0.0109	4.19E-04
3.33	2.81	2.42	0.0103	0.0105	0.0109	4.19E-04
4.14	3.35	3.05	0.0103	0.0105	0.0109	4.21E-04
3.99	4.63	3.35	0.0103	0.0105	0.0109	4.21E-04

2.96	2.73	3.69	0.0103	0.0105	0.0109	4.22E-04
2.96	2.73	3.69	0.0103	0.0105	0.0109	4.22E-04
3.1	3.63	2.63	0.0103	0.0105	0.0109	4.22E-04
0.011	0.012	0.0117	2.24	3.04	2.46	4.22E-04
0.011	0.012	0.0117	2.24	3.04	2.46	4.22E-04
3.49	2.93	4.05	0.0103	0.0105	0.0109	4.23E-04
2.06	2.18	2.76	0.0103	0.0105	0.0109	4.25E-04
2.06	2.18	2.76	0.0103	0.0105	0.0109	4.25E-04
0.011	0.012	0.0117	2.54	3.24	2.43	4.26E-04
0.011	0.012	0.0117	2.54	3.24	2.43	4.26E-04
2.29	2.14	2.88	0.0103	0.0105	0.0109	4.26E-04
4.72	3.5	3.76	0.0103	0.0105	0.0109	4.27E-04
4.72	3.5	3.76	0.0103	0.0105	0.0109	4.27E-04
4.72	3.5	3.76	0.0103	0.0105	0.0109	4.27E-04
5.97	4.31	5.19	0.0103	0.0105	0.0109	4.27E-04
2.89	2.14	2.31	0.0103	0.0105	0.0109	4.28E-04
2.89	2.14	2.31	0.0103	0.0105	0.0109	4.28E-04
3.48	3.08	2.51	0.0103	0.0105	0.0109	4.32E-04
2.84	2.1	2.8	0.0103	0.0105	0.0109	4.33E-04
2.84	2.1	2.8	0.0103	0.0105	0.0109	4.33E-04
4.62	3.93	3.34	0.0103	0.0105	0.0109	4.34E-04
0.011	0.012	0.0117	2.67	3.69	3.4	4.35E-04
2.37	3.28	2.8	0.0103	0.0105	0.0109	4.36E-04
2.37	3.28	2.8	0.0103	0.0105	0.0109	4.36E-04
0.011	0.012	0.0117	2.86	3.95	3.66	4.37E-04
2.31	2.22	2.96	0.0103	0.0105	0.0109	4.38E-04
2.31	2.22	2.96	0.0103	0.0105	0.0109	4.38E-04
3.36	3.6	2.61	0.0103	0.0105	0.0109	4.38E-04
3.36	3.6	2.61	0.0103	0.0105	0.0109	4.38E-04
0.011	0.012	0.0117	4.11	3.17	3.11	4.39E-04
0.011	0.012	0.0117	2.25	2.49	3.07	4.41E-04
0.011	0.012	0.0117	3.56	2.59	2.94	4.41E-04
0.011	0.012	0.0117	2.9	2.3	3.19	4.44E-04
2.16	2.89	2.26	0.0103	0.0105	0.0109	4.45E-04
2.16	2.89	2.26	0.0103	0.0105	0.0109	4.45E-04
0.011	0.012	0.0117	2.67	2.45	3.33	4.47E-04
2.96	3.42	4.09	0.0103	0.0105	0.0109	4.47E-04
2.96	3.42	4.09	0.0103	0.0105	0.0109	4.47E-04
0.011	0.012	0.0117	2.63	3.17	2.3	4.48E-04
0.011	0.012	0.0117	2.22	3.08	2.81	4.48E-04
0.011	0.012	0.0117	2.33	3.21	3.03	4.48E-04
2.45	3.25	2.51	0.0103	0.0105	0.0109	4.49E-04
2.45	3.25	2.51	0.0103	0.0105	0.0109	4.49E-04
3.33	2.4	2.84	0.0103	0.0105	0.0109	4.49E-04
2.31	3.17	2.59	0.0103	0.0105	0.0109	4.52E-04
2.31	3.17	2.59	0.0103	0.0105	0.0109	4.52E-04
3.55	2.7	2.71	0.0103	0.0105	0.0109	4.54E-04
3.55	2.7	2.71	0.0103	0.0105	0.0109	4.54E-04
4.18	3	3.67	0.0103	0.0105	0.0109	4.56E-04
4.18	3	3.67	0.0103	0.0105	0.0109	4.56E-04
4.18	3	3.67	0.0103	0.0105	0.0109	4.56E-04
0.011	0.012	0.0117	2.32	3.1	2.41	4.57E-04
0.011	0.012	0.0117	2.65	3.67	3.42	4.58E-04
2.52	2.23	3.07	0.0103	0.0105	0.0109	4.58E-04
2.52	2.23	3.07	0.0103	0.0105	0.0109	4.58E-04
2.52	2.23	3.07	0.0103	0.0105	0.0109	4.58E-04
4.24	3.95	3.06	0.0103	0.0105	0.0109	4.59E-04
3.57	4.43	3.24	0.0103	0.0105	0.0109	4.59E-04

0.011	0.012	0.0117	3.66	3.4	2.64	4.60E-04
3.15	3.22	3.29	2.36	2.53	2.31	4.60E-04
2.47	2.9	3.43	0.0103	0.0105	0.0109	4.60E-04
2.47	2.9	3.43	0.0103	0.0105	0.0109	4.60E-04
0.011	0.012	0.0117	2.5	2.41	3.22	4.60E-04
3.86	2.77	3.47	0.0103	0.0105	0.0109	4.61E-04
3.86	2.77	3.47	0.0103	0.0105	0.0109	4.61E-04
3.16	2.31	3.07	0.0103	0.0105	0.0109	4.62E-04
2.13	2.63	2.97	0.0103	0.0105	0.0109	4.62E-04
2.9	2.08	2.58	0.0103	0.0105	0.0109	4.62E-04
3.4	2.45	2.86	0.0103	0.0105	0.0109	4.62E-04
3.4	2.45	2.86	0.0103	0.0105	0.0109	4.62E-04
3.4	2.45	2.86	0.0103	0.0105	0.0109	4.62E-04
3.53	3.14	2.53	0.0103	0.0105	0.0109	4.65E-04
3.53	3.14	2.53	0.0103	0.0105	0.0109	4.65E-04
0.011	0.012	0.0117	3.21	2.3	2.84	4.67E-04
3.64	2.62	3.37	0.0103	0.0105	0.0109	4.68E-04
3.64	2.62	3.37	0.0103	0.0105	0.0109	4.68E-04
2.77	3.13	3.82	0.0103	0.0105	0.0109	4.68E-04
2.77	3.13	3.82	0.0103	0.0105	0.0109	4.68E-04
2.77	3.13	3.82	0.0103	0.0105	0.0109	4.68E-04
5.48	5.58	4.09	0.0103	0.0105	0.0109	4.69E-04
0.011	0.012	0.0117	2.97	4.1	3.36	4.73E-04
0.011	0.012	0.0117	2.97	4.1	3.36	4.73E-04
0.011	0.012	0.0117	2.99	3.5	4.16	4.74E-04
3.24	2.39	3.23	0.0103	0.0105	0.0109	4.74E-04
3.7	2.82	3.9	0.0103	0.0105	0.0109	4.76E-04
0.011	0.012	0.0117	3.64	2.61	3.33	4.78E-04
3.32	2.61	2.45	0.0103	0.0105	0.0109	4.81E-04
2.69	2.73	3.57	0.0103	0.0105	0.0109	4.81E-04
2.69	2.73	3.57	0.0103	0.0105	0.0109	4.81E-04
2.69	2.73	3.57	0.0103	0.0105	0.0109	4.81E-04
0.011	0.012	0.0117	2.98	3.9	2.94	4.82E-04
0.011	0.012	0.0117	2.98	3.9	2.94	4.82E-04
2.99	4.1	4	0.0103	0.0105	0.0109	4.83E-04
2.99	4.1	4	0.0103	0.0105	0.0109	4.83E-04
2.99	4.1	4	0.0103	0.0105	0.0109	4.83E-04
3.37	2.42	3.13	0.0103	0.0105	0.0109	4.85E-04
3.79	2.89	2.86	0.0103	0.0105	0.0109	4.85E-04
3.79	2.89	2.86	0.0103	0.0105	0.0109	4.85E-04
3.42	2.45	3.14	0.0103	0.0105	0.0109	4.86E-04
3.42	2.45	3.14	0.0103	0.0105	0.0109	4.86E-04
3.69	3.04	2.66	0.0103	0.0105	0.0109	4.88E-04
3.69	3.04	2.66	0.0103	0.0105	0.0109	4.88E-04
0.011	0.012	0.0117	3.82	2.95	2.85	4.88E-04
0.011	0.012	0.0117	3.82	2.95	2.85	4.88E-04
2.16	2.98	2.42	0.0103	0.0105	0.0109	4.88E-04
2.16	2.98	2.42	0.0103	0.0105	0.0109	4.88E-04
2.16	2.98	2.42	0.0103	0.0105	0.0109	4.88E-04
3.23	3.2	2.37	0.0103	0.0105	0.0109	4.88E-04
4.56	3.3	3.71	0.0103	0.0105	0.0109	4.89E-04
0.011	0.012	0.0117	3.26	2.96	2.33	4.90E-04
3.08	3.78	4.32	0.0103	0.0105	0.0109	4.91E-04
2.17	2.99	2.89	0.0103	0.0105	0.0109	4.92E-04
0.011	0.012	0.0117	3.26	2.61	3.66	4.93E-04
0.011	0.012	0.0117	3.26	2.61	3.66	4.93E-04
3.9	3.07	4.3	0.0103	0.0105	0.0109	4.93E-04
3.9	3.07	4.3	0.0103	0.0105	0.0109	4.93E-04

3.9	3.07	4.3	0.0103	0.0105	0.0109	4.93E-04
3.49	2.67	2.62	0.0103	0.0105	0.0109	4.94E-04
3.49	2.67	2.62	0.0103	0.0105	0.0109	4.94E-04
3.49	2.67	2.62	0.0103	0.0105	0.0109	4.94E-04
3.17	2.26	2.82	0.0103	0.0105	0.0109	4.94E-04
3.17	2.26	2.82	0.0103	0.0105	0.0109	4.94E-04
2.25	3.03	2.35	0.0103	0.0105	0.0109	4.94E-04
2.25	3.03	2.35	0.0103	0.0105	0.0109	4.94E-04
2.13	2.79	2.96	0.0103	0.0105	0.0109	4.95E-04
2.36	3.31	2.97	0.0103	0.0105	0.0109	4.96E-04
0.011	0.012	0.0117	3.21	4.22	3.18	4.99E-04
3.8	2.71	3.25	0.0103	0.0105	0.0109	5.00E-04
2.92	2.13	2.87	0.0103	0.0105	0.0109	5.02E-04
2.92	2.13	2.87	0.0103	0.0105	0.0109	5.02E-04
2.96	2.88	2.15	0.0103	0.0105	0.0109	5.02E-04
0.011	0.012	0.0117	2.83	2.8	3.72	5.03E-04
3.45	3.34	2.5	0.0103	0.0105	0.0109	5.04E-04
4.66	3.66	3.42	0.0103	0.0105	0.0109	5.05E-04
4.66	3.66	3.42	0.0103	0.0105	0.0109	5.05E-04
0.011	0.012	0.0117	2.96	4.16	3.72	5.06E-04
2.23	2.04	2.8	0.0103	0.0105	0.0109	5.06E-04
2.23	2.04	2.8	0.0103	0.0105	0.0109	5.06E-04
3.39	2.64	2.5	0.0103	0.0105	0.0109	5.10E-04
5.37	3.82	4.6	0.0103	0.0105	0.0109	5.11E-04
0.011	0.012	0.0117	2.17	3.02	2.86	5.12E-04
3.47	2.65	3.7	0.0103	0.0105	0.0109	5.13E-04
3.47	2.65	3.7	0.0103	0.0105	0.0109	5.13E-04
2.46	2.27	3.11	0.0103	0.0105	0.0109	5.14E-04
3.23	2.55	2.36	0.0103	0.0105	0.0109	5.14E-04
0.011	0.012	0.0117	3.28	2.34	2.76	5.14E-04
0.011	0.012	0.0117	3.28	2.34	2.76	5.14E-04
5.03	3.61	4.77	0.0103	0.0105	0.0109	5.17E-04
4.44	3.21	4.31	0.0103	0.0105	0.0109	5.22E-04
4.44	3.21	4.31	0.0103	0.0105	0.0109	5.22E-04
3.77	3.6	2.71	0.0103	0.0105	0.0109	5.22E-04
2.35	3.31	2.82	0.0103	0.0105	0.0109	5.28E-04
2.35	3.31	2.82	0.0103	0.0105	0.0109	5.28E-04
3.99	2.83	3.6	0.0103	0.0105	0.0109	5.28E-04
4.15	3.95	4.07	2.4	2.82	2.42	5.29E-04
4.15	3.95	4.07	2.4	2.82	2.42	5.29E-04
2.96	2.37	2.14	0.0103	0.0105	0.0109	5.30E-04
2.2	3	2.34	0.0103	0.0105	0.0109	5.31E-04
2.73	3.59	2.68	0.0103	0.0105	0.0109	5.36E-04
2.73	3.59	2.68	0.0103	0.0105	0.0109	5.36E-04
0.011	0.012	0.0117	2.97	3.67	4.2	5.38E-04
0.011	0.012	0.0117	2.97	3.67	4.2	5.38E-04
0.011	0.012	0.0117	2.88	3.95	3.1	5.39E-04
3.53	2.95	2.51	0.0103	0.0105	0.0109	5.39E-04
0.011	0.012	0.0117	3.04	2.8	2.16	5.39E-04
3.65	4.34	3.08	0.0103	0.0105	0.0109	5.41E-04
2.87	3.93	3.93	0.0103	0.0105	0.0109	5.42E-04
3.66	2.98	2.62	0.0103	0.0105	0.0109	5.43E-04
3.66	2.98	2.62	0.0103	0.0105	0.0109	5.43E-04
3.35	2.45	3.36	0.0103	0.0105	0.0109	5.44E-04
3.35	2.45	3.36	0.0103	0.0105	0.0109	5.44E-04
2.91	2.21	3.1	0.0103	0.0105	0.0109	5.44E-04
2.91	2.21	3.1	0.0103	0.0105	0.0109	5.44E-04
0.011	0.012	0.0117	2.37	3.24	3.25	5.44E-04

3.77	3.22	4.53	0.0103	0.0105	0.0109	5.44E-04
0.011	0.012	0.0117	2.93	2.14	2.93	5.44E-04
3.34	2.55	2.48	0.0103	0.0105	0.0109	5.45E-04
3.34	2.55	2.48	0.0103	0.0105	0.0109	5.45E-04
2.26	3.04	3.14	0.0103	0.0105	0.0109	5.46E-04
2.26	3.04	3.14	0.0103	0.0105	0.0109	5.46E-04
4.16	3.58	2.94	0.0103	0.0105	0.0109	5.46E-04
4.16	3.58	2.94	0.0103	0.0105	0.0109	5.46E-04
0.011	0.012	0.0117	2.44	3.31	2.55	5.46E-04
3.9	3.12	2.81	0.0103	0.0105	0.0109	5.47E-04
0.011	0.012	0.0117	2.34	2.18	2.99	5.49E-04
4.21	2.97	3.7	0.0103	0.0105	0.0109	5.51E-04
4.21	2.97	3.7	0.0103	0.0105	0.0109	5.51E-04
4.21	2.97	3.7	0.0103	0.0105	0.0109	5.51E-04
3.64	2.57	3.14	0.0103	0.0105	0.0109	5.52E-04
2.75	2.64	3.58	0.0103	0.0105	0.0109	5.53E-04
2.75	2.64	3.58	0.0103	0.0105	0.0109	5.53E-04
3.54	2.58	2.76	0.0103	0.0105	0.0109	5.60E-04
3.54	2.58	2.76	0.0103	0.0105	0.0109	5.60E-04
3.54	2.58	2.76	0.0103	0.0105	0.0109	5.60E-04
3.61	2.66	2.77	0.0103	0.0105	0.0109	5.60E-04
2.87	2.53	3.54	0.0103	0.0105	0.0109	5.60E-04
2.87	2.53	3.54	0.0103	0.0105	0.0109	5.60E-04
0.011	0.012	0.0117	3.56	2.52	3.28	5.61E-04
2.75	3.87	3.63	0.0103	0.0105	0.0109	5.61E-04
2.75	3.87	3.63	0.0103	0.0105	0.0109	5.61E-04
2.75	3.87	3.63	0.0103	0.0105	0.0109	5.61E-04
3.9	3.34	2.75	0.0103	0.0105	0.0109	5.62E-04
3.9	3.34	2.75	0.0103	0.0105	0.0109	5.62E-04
2.63	3.56	2.72	0.0103	0.0105	0.0109	5.63E-04
2.63	3.56	2.72	0.0103	0.0105	0.0109	5.63E-04
3.09	2.57	2.19	0.0103	0.0105	0.0109	5.64E-04
0.011	0.012	0.0117	2.27	2.03	2.83	5.67E-04
3.39	2.72	2.43	0.0103	0.0105	0.0109	5.67E-04
3.45	2.51	2.69	0.0103	0.0105	0.0109	5.68E-04
3.45	2.51	2.69	0.0103	0.0105	0.0109	5.68E-04
3.77	3.13	4.44	0.0103	0.0105	0.0109	5.69E-04
2.36	2.66	3.3	0.0103	0.0105	0.0109	5.69E-04
2.36	2.66	3.3	0.0103	0.0105	0.0109	5.69E-04
2.3	3.27	2.86	0.0103	0.0105	0.0109	5.71E-04
0.011	0.012	0.0117	2.25	3	2.25	5.72E-04
3.15	2.67	2.22	0.0103	0.0105	0.0109	5.75E-04
3.15	2.67	2.22	0.0103	0.0105	0.0109	5.75E-04
0.011	0.012	0.0117	2.25	3.19	2.69	5.76E-04
3.06	2.2	2.43	0.0103	0.0105	0.0109	5.77E-04
0.011	0.012	0.0117	2.01	2.71	2.81	5.78E-04
0.011	0.012	0.0117	2.09	2.19	2.85	5.80E-04
3.84	4.22	2.97	0.0103	0.0105	0.0109	5.82E-04
3.84	4.22	2.97	0.0103	0.0105	0.0109	5.82E-04
3.84	4.22	2.97	0.0103	0.0105	0.0109	5.82E-04
0.011	0.012	0.0117	2.31	2.9	2.08	5.83E-04
2.43	2.23	3.09	0.0103	0.0105	0.0109	5.84E-04
3.38	3.28	2.42	0.0103	0.0105	0.0109	5.85E-04
3.72	2.76	2.81	0.0103	0.0105	0.0109	5.86E-04
3.72	2.76	2.81	0.0103	0.0105	0.0109	5.86E-04
0.011	0.012	0.0117	2.46	2.75	3.44	5.89E-04
0.011	0.012	0.0117	3.12	2.35	2.32	5.90E-04
4.03	3.21	4.58	0.0103	0.0105	0.0109	5.91E-04

4.03	3.21	4.58	0.0103	0.0105	0.0109	5.91E-04
0.011	0.012	0.0117	3.79	2.82	2.85	5.92E-04
0.011	0.012	0.0117	2.88	4.09	3.42	5.93E-04
4.23	4.69	3.29	0.0103	0.0105	0.0109	5.95E-04
4.23	4.69	3.29	0.0103	0.0105	0.0109	5.95E-04
3.9	2.77	3.72	0.0103	0.0105	0.0109	5.96E-04
0.011	0.012	0.0117	2.44	2.83	3.45	5.97E-04
0.011	0.012	0.0117	2.44	2.83	3.45	5.97E-04
0.011	0.012	0.0117	2.84	2.47	1.99	5.98E-04
3.75	2.81	3.97	0.0103	0.0105	0.0109	5.99E-04
3.75	2.81	3.97	0.0103	0.0105	0.0109	5.99E-04
0.011	0.012	0.0117	2.08	2.97	2.62	6.00E-04
3.05	2.93	2.17	0.0103	0.0105	0.0109	6.02E-04
3.05	2.93	2.17	0.0103	0.0105	0.0109	6.02E-04
3.43	3.01	2.4	0.0103	0.0105	0.0109	6.03E-04
2.54	2.77	3.53	0.0103	0.0105	0.0109	6.04E-04
2.54	2.77	3.53	0.0103	0.0105	0.0109	6.04E-04
3.48	2.49	2.76	0.0103	0.0105	0.0109	6.05E-04
0.011	0.012	0.0117	2.54	3.63	3.23	6.06E-04
0.011	0.012	0.0117	2.54	3.63	3.23	6.06E-04
2.86	2.42	3.44	0.0103	0.0105	0.0109	6.07E-04
2.62	3.74	3.38	0.0103	0.0105	0.0109	6.07E-04
0.011	0.012	0.0117	2.39	3.09	3.41	6.08E-04
0.011	0.012	0.0117	2.39	3.09	3.41	6.08E-04
0.011	0.012	0.0117	2.48	3.25	2.38	6.09E-04
2.24	2.87	2.07	0.0103	0.0105	0.0109	6.10E-04
0.011	0.012	0.0117	3.08	3.38	2.37	6.10E-04
0.011	0.012	0.0117	3.08	3.38	2.37	6.10E-04
3.9	3.91	2.82	0.0103	0.0105	0.0109	6.15E-04
0.011	0.012	0.0117	2.97	4.01	3.01	6.19E-04
2.8	2.15	3.07	0.0103	0.0105	0.0109	6.19E-04
0.011	0.012	0.0117	3.97	2.82	3.18	6.20E-04
0.011	0.012	0.0117	3.97	2.82	3.18	6.20E-04
0.011	0.012	0.0117	3.97	2.82	3.18	6.20E-04
3.45	3.18	2.42	0.0103	0.0105	0.0109	6.20E-04
3.32	2.32	2.83	0.0103	0.0105	0.0109	6.22E-04
3.32	2.32	2.83	0.0103	0.0105	0.0109	6.22E-04
0.011	0.012	0.0117	3.77	2.67	3.04	6.22E-04
2.95	2.86	2.1	0.0103	0.0105	0.0109	6.22E-04
2.95	2.86	2.1	0.0103	0.0105	0.0109	6.22E-04
0.011	0.012	0.0117	2.75	2.86	2.03	6.22E-04
4.18	2.94	3.91	0.0103	0.0105	0.0109	6.23E-04
3.91	2.73	3.34	0.0103	0.0105	0.0109	6.24E-04
3.91	2.73	3.34	0.0103	0.0105	0.0109	6.24E-04
3.91	2.73	3.34	0.0103	0.0105	0.0109	6.24E-04
3.27	2.74	2.29	0.0103	0.0105	0.0109	6.24E-04
3.27	2.74	2.29	0.0103	0.0105	0.0109	6.24E-04
0.011	0.012	0.0117	2.4	3.36	2.65	6.30E-04
4.63	3.86	3.24	0.0103	0.0105	0.0109	6.32E-04
0.011	0.012	0.0117	3.34	3.76	2.62	6.33E-04
3.36	3.19	2.37	0.0103	0.0105	0.0109	6.34E-04
3.36	3.19	2.37	0.0103	0.0105	0.0109	6.34E-04
0.011	0.012	0.0117	5	3.73	3.71	6.35E-04
3.49	3.2	2.44	0.0103	0.0105	0.0109	6.35E-04
0.011	0.012	0.0117	2.78	2.7	3.68	6.37E-04
0.011	0.012	0.0117	2.78	2.7	3.68	6.37E-04
2.67	2.8	3.67	0.0103	0.0105	0.0109	6.39E-04
0.011	0.012	0.0117	2.97	2.75	2.08	6.40E-04

3.28	2.69	3.86	0.0103	0.0105	0.0109	6.40E-04
3.28	2.69	3.86	0.0103	0.0105	0.0109	6.40E-04
5.01	5.08	5.21	4.18	3.88	4.11	6.40E-04
5.01	5.08	5.21	4.18	3.88	4.11	6.40E-04
3.5	2.44	2.96	0.0103	0.0105	0.0109	6.42E-04
3.5	2.44	2.96	0.0103	0.0105	0.0109	6.42E-04
3.08	2.19	2.44	0.0103	0.0105	0.0109	6.43E-04
2.96	2.57	3.65	0.0103	0.0105	0.0109	6.43E-04
2.58	3.71	3.31	0.0103	0.0105	0.0109	6.47E-04
0.011	0.012	0.0117	2.09	2.97	2.41	6.48E-04
3.7	2.72	2.78	0.0103	0.0105	0.0109	6.49E-04
3.7	2.72	2.78	0.0103	0.0105	0.0109	6.49E-04
2.61	3.6	3.66	0.0103	0.0105	0.0109	6.49E-04
2.61	3.6	3.66	0.0103	0.0105	0.0109	6.49E-04
4.69	4.82	3.42	0.0103	0.0105	0.0109	6.51E-04
4.69	4.82	3.42	0.0103	0.0105	0.0109	6.51E-04
4.41	3.07	4	0.0103	0.0105	0.0109	6.51E-04
0.011	0.012	0.0117	2.61	3.17	3.75	6.54E-04
2.78	3.44	2.42	0.0103	0.0105	0.0109	6.56E-04
2.89	4.15	3.79	0.0103	0.0105	0.0109	6.56E-04
0.011	0.012	0.0117	3.39	2.43	3.38	6.59E-04
4.39	4.05	3.06	0.0103	0.0105	0.0109	6.63E-04
4.39	4.05	3.06	0.0103	0.0105	0.0109	6.63E-04
0.011	0.012	0.0117	2.39	3.1	2.23	6.63E-04
3.09	2.2	3.04	0.0103	0.0105	0.0109	6.63E-04
0.011	0.012	0.0117	2.64	2.57	3.51	6.65E-04
0.011	0.012	0.0117	2.64	2.57	3.51	6.65E-04
3.29	2.43	2.45	0.0103	0.0105	0.0109	6.65E-04
3.29	2.43	2.45	0.0103	0.0105	0.0109	6.65E-04
0.011	0.012	0.0117	2.64	3.71	2.91	6.66E-04
0.011	0.012	0.0117	2.64	3.71	2.91	6.66E-04
0.011	0.012	0.0117	3.05	2.57	2.12	6.67E-04
3.69	2.72	3.87	0.0103	0.0105	0.0109	6.67E-04
0.011	0.012	0.0117	2.53	3.43	3.6	6.68E-04
0.011	0.012	0.0117	3.42	2.5	3.54	6.68E-04
0.011	0.012	0.0117	3.42	2.5	3.54	6.68E-04
0.011	0.012	0.0117	4.54	4.47	3.23	6.68E-04
3.08	2.18	2.44	0.0103	0.0105	0.0109	6.69E-04
3.08	2.18	2.44	0.0103	0.0105	0.0109	6.69E-04
2.68	2.98	3.78	0.0103	0.0105	0.0109	6.71E-04
2.75	3.6	2.6	0.0103	0.0105	0.0109	6.72E-04
2.75	3.6	2.6	0.0103	0.0105	0.0109	6.72E-04
2.75	3.6	2.6	0.0103	0.0105	0.0109	6.72E-04
3.41	3.69	2.57	0.0103	0.0105	0.0109	6.72E-04
3.41	3.69	2.57	0.0103	0.0105	0.0109	6.72E-04
0.011	0.012	0.0117	2.36	3.38	3.16	6.75E-04
0.011	0.012	0.0117	3.03	3.65	2.54	6.76E-04
0.011	0.012	0.0117	2.41	2.39	3.24	6.77E-04
2.66	3.81	3.57	0.0103	0.0105	0.0109	6.78E-04
3.6	2.49	3.19	0.0103	0.0105	0.0109	6.82E-04
3.6	2.49	3.19	0.0103	0.0105	0.0109	6.82E-04
4.33	3.23	3.18	0.0103	0.0105	0.0109	6.82E-04
4.33	3.23	3.18	0.0103	0.0105	0.0109	6.82E-04
3.58	3.52	2.54	0.0103	0.0105	0.0109	6.85E-04
5	5.04	5.12	3.08	3.65	3.49	6.86E-04
5	5.04	5.12	3.08	3.65	3.49	6.86E-04
5	5.04	5.12	3.08	3.65	3.49	6.86E-04
3.27	2.26	2.84	0.0103	0.0105	0.0109	6.86E-04

4.64	4.17	3.21	0.0103	0.0105	0.0109	6.86E-04
0.011	0.012	0.0117	3.5	3	2.42	6.88E-04
2.25	3.23	2.65	0.0103	0.0105	0.0109	6.88E-04
2.59	3.67	3.57	0.0103	0.0105	0.0109	6.91E-04
2.98	2.75	2.07	0.0103	0.0105	0.0109	6.91E-04
2.98	2.75	2.07	0.0103	0.0105	0.0109	6.91E-04
3.22	2.85	4.05	0.0103	0.0105	0.0109	6.91E-04
3.22	2.85	4.05	0.0103	0.0105	0.0109	6.91E-04
3.24	2.33	3.28	0.0103	0.0105	0.0109	6.92E-04
0.011	0.012	0.0117	2.88	4.02	3.09	6.93E-04
2.31	3.31	3.12	0.0103	0.0105	0.0109	6.94E-04
3.08	2.86	4	0.0103	0.0105	0.0109	6.97E-04
3.08	2.86	4	0.0103	0.0105	0.0109	6.97E-04
2.86	3.1	4.01	0.0103	0.0105	0.0109	6.97E-04
0.011	0.012	0.0117	2.48	3.2	2.28	6.98E-04
0.011	0.012	0.0117	2.48	3.2	2.28	6.98E-04
3.14	4.53	3.76	0.0103	0.0105	0.0109	6.99E-04
4.48	3.14	3.58	0.0103	0.0105	0.0109	7.02E-04
4.48	3.14	3.58	0.0103	0.0105	0.0109	7.02E-04
2.02	2.82	2.84	0.0103	0.0105	0.0109	7.02E-04
2.02	2.82	2.84	0.0103	0.0105	0.0109	7.02E-04
3.4	2.46	2.57	0.0103	0.0105	0.0109	7.04E-04
3.01	2.99	2.14	0.0103	0.0105	0.0109	7.06E-04
2.86	3.65	2.58	0.0103	0.0105	0.0109	7.07E-04
2.86	3.65	2.58	0.0103	0.0105	0.0109	7.07E-04
3.16	2.37	3.42	0.0103	0.0105	0.0109	7.09E-04
3.16	2.37	3.42	0.0103	0.0105	0.0109	7.09E-04
3.16	2.37	3.42	0.0103	0.0105	0.0109	7.09E-04
4.19	3.78	2.89	0.0103	0.0105	0.0109	7.12E-04
0.011	0.012	0.0117	4.04	2.92	3.05	7.13E-04
0.011	0.012	0.0117	4.04	2.92	3.05	7.13E-04
2.97	3.37	2.32	0.0103	0.0105	0.0109	7.14E-04
0.011	0.012	0.0117	2.59	3.62	3.65	7.14E-04
2.43	2.5	3.34	0.0103	0.0105	0.0109	7.16E-04
2.43	2.5	3.34	0.0103	0.0105	0.0109	7.16E-04
3.49	3.45	2.47	0.0103	0.0105	0.0109	7.22E-04
3.22	2.34	2.41	0.0103	0.0105	0.0109	7.23E-04
2.36	2.26	3.13	0.0103	0.0105	0.0109	7.25E-04
0.011	0.012	0.0117	2.42	3.5	2.89	7.27E-04
0.011	0.012	0.0117	2.95	2.03	2.51	7.27E-04
3.71	2.87	2.63	0.0103	0.0105	0.0109	7.30E-04
3.39	2.33	2.89	0.0103	0.0105	0.0109	7.32E-04
3.72	4.15	3.66	2.35	2.16	2.35	7.34E-04
3.72	4.15	3.66	2.35	2.16	2.35	7.34E-04
3.52	2.8	2.46	0.0103	0.0105	0.0109	7.34E-04
3.33	2.54	2.38	0.0103	0.0105	0.0109	7.35E-04
3.41	2.79	2.36	0.0103	0.0105	0.0109	7.35E-04
4.14	3.58	2.84	0.0103	0.0105	0.0109	7.37E-04
4.14	3.58	2.84	0.0103	0.0105	0.0109	7.37E-04
0.011	0.012	0.0117	2.66	3.86	3.21	7.38E-04
2.05	2.19	2.87	0.0103	0.0105	0.0109	7.39E-04
2.05	2.19	2.87	0.0103	0.0105	0.0109	7.39E-04
4.4	4.1	4.4	3	2.99	2.65	7.39E-04
3.76	2.78	2.75	0.0103	0.0105	0.0109	7.43E-04
2.96	2.03	2.55	0.0103	0.0105	0.0109	7.44E-04
0.011	0.012	0.0117	2.36	3.44	3.08	7.48E-04
0.011	0.012	0.0117	2.36	3.44	3.08	7.48E-04
3.84	3.5	2.64	0.0103	0.0105	0.0109	7.48E-04

3.47	2.59	3.76	0.0103	0.0105	0.0109	7.52E-04
3.47	2.59	3.76	0.0103	0.0105	0.0109	7.52E-04
3.7	2.55	3.04	0.0103	0.0105	0.0109	7.55E-04
0.011	0.012	0.0117	3.5	4.23	2.91	7.56E-04
0.011	0.012	0.0117	3.5	4.23	2.91	7.56E-04
2.81	3.2	2.19	0.0103	0.0105	0.0109	7.57E-04
0.011	0.012	0.0117	3.07	2.25	2.26	7.57E-04
0.011	0.012	0.0117	3.07	2.25	2.26	7.57E-04
3.09	2.21	2.34	0.0103	0.0105	0.0109	7.60E-04
3.09	2.21	2.34	0.0103	0.0105	0.0109	7.60E-04
2.28	3.04	2.19	0.0103	0.0105	0.0109	7.61E-04
3.03	2.12	2.95	0.0103	0.0105	0.0109	7.61E-04
3.2	3.24	4.39	0.0103	0.0105	0.0109	7.67E-04
0.011	0.012	0.0117	2.94	2.43	2.02	7.71E-04
0.011	0.012	0.0117	2.8	4.1	3.64	7.75E-04
0.011	0.012	0.0117	2.8	4.1	3.64	7.75E-04
3.37	3.58	2.47	0.0103	0.0105	0.0109	7.78E-04
4.5	3.24	3.36	0.0103	0.0105	0.0109	7.79E-04
3.84	2.69	2.99	0.0103	0.0105	0.0109	7.81E-04
3.84	2.69	2.99	0.0103	0.0105	0.0109	7.81E-04
0.011	0.012	0.0117	3.17	3.51	2.4	7.81E-04
0.011	0.012	0.0117	3.17	3.51	2.4	7.81E-04
0.011	0.012	0.0117	2.48	3.63	3.26	7.82E-04
0.011	0.012	0.0117	2.48	3.63	3.26	7.82E-04
3.45	2.48	2.58	0.0103	0.0105	0.0109	7.84E-04
2.71	2.55	3.58	0.0103	0.0105	0.0109	7.84E-04
2.71	2.55	3.58	0.0103	0.0105	0.0109	7.84E-04
2.75	3.43	2.37	0.0103	0.0105	0.0109	7.89E-04
2.75	3.43	2.37	0.0103	0.0105	0.0109	7.89E-04
4.1	3.97	2.85	0.0103	0.0105	0.0109	7.93E-04
3.78	3.44	4.9	0.0103	0.0105	0.0109	7.97E-04
3.78	3.44	4.9	0.0103	0.0105	0.0109	7.97E-04
2.94	3.27	2.23	0.0103	0.0105	0.0109	7.97E-04
3.2	2.35	3.42	0.0103	0.0105	0.0109	7.98E-04
3.2	2.35	3.42	0.0103	0.0105	0.0109	7.98E-04
0.011	0.012	0.0117	3.29	2.58	2.29	8.03E-04
4.32	3	3.4	0.0103	0.0105	0.0109	8.03E-04
4.09	4.01	4.04	2.17	2.75	2.54	8.04E-04
4.09	4.01	4.04	2.17	2.75	2.54	8.04E-04
0.011	0.012	0.0117	3.63	3.64	2.56	8.05E-04
0.011	0.012	0.0117	3.65	2.54	2.86	8.05E-04
2.36	3.44	2.8	0.0103	0.0105	0.0109	8.06E-04
2.36	3.44	2.8	0.0103	0.0105	0.0109	8.06E-04
3.83	3.46	2.61	0.0103	0.0105	0.0109	8.06E-04
3.5	2.99	2.38	0.0103	0.0105	0.0109	8.09E-04
3.13	2.24	2.34	0.0103	0.0105	0.0109	8.11E-04
3.13	2.24	2.34	0.0103	0.0105	0.0109	8.11E-04
3.34	2.86	2.27	0.0103	0.0105	0.0109	8.12E-04
3.41	2.65	2.38	0.0103	0.0105	0.0109	8.12E-04
3.41	2.65	2.38	0.0103	0.0105	0.0109	8.12E-04
0.011	0.012	0.0117	3.09	3.25	2.24	8.13E-04
0.011	0.012	0.0117	3.09	3.25	2.24	8.13E-04
3.54	2.47	3.48	0.0103	0.0105	0.0109	8.15E-04
3.21	2.19	2.94	0.0103	0.0105	0.0109	8.17E-04
0.011	0.012	0.0117	3.9	3.03	2.72	8.17E-04
3.22	2.54	2.23	0.0103	0.0105	0.0109	8.18E-04
0.011	0.012	0.0117	3.21	2.26	2.45	8.24E-04
0.011	0.012	0.0117	3.21	2.26	2.45	8.24E-04

2.81	2.04	2.06	0.0103	0.0105	0.0109	8.27E-04
2.81	2.04	2.06	0.0103	0.0105	0.0109	8.27E-04
2.35	3.1	2.19	0.0103	0.0105	0.0109	8.29E-04
3.11	2.65	2.11	0.0103	0.0105	0.0109	8.29E-04
4.26	3.37	2.94	0.0103	0.0105	0.0109	8.30E-04
3.56	2.43	3.3	0.0103	0.0105	0.0109	8.32E-04
3.56	2.43	3.3	0.0103	0.0105	0.0109	8.32E-04
0.011	0.012	0.0117	2.6	3.76	2.96	8.33E-04
0.011	0.012	0.0117	2.6	3.76	2.96	8.33E-04
3.1	2.13	2.48	0.0103	0.0105	0.0109	8.35E-04
3.1	2.13	2.48	0.0103	0.0105	0.0109	8.35E-04
3.1	2.13	2.48	0.0103	0.0105	0.0109	8.35E-04
0.011	0.012	0.0117	3.02	2.35	2.1	8.35E-04
0.011	0.012	0.0117	2.04	2.67	3.01	8.38E-04
0.011	0.012	0.0117	2.04	2.67	3.01	8.38E-04
3.11	3.01	2.15	0.0103	0.0105	0.0109	8.39E-04
3.22	3.41	4.54	0.0103	0.0105	0.0109	8.40E-04
0.011	0.012	0.0117	3.08	3.91	2.7	8.41E-04
0.011	0.012	0.0117	2.67	3.93	3.58	8.42E-04
3.21	3.48	2.37	0.0103	0.0105	0.0109	8.42E-04
2.66	3.13	2.12	0.0103	0.0105	0.0109	8.44E-04
2.66	3.13	2.12	0.0103	0.0105	0.0109	8.44E-04
0.011	0.012	0.0117	2.33	3.44	2.92	8.45E-04
3.56	2.48	2.75	0.0103	0.0105	0.0109	8.45E-04
3.56	2.48	2.75	0.0103	0.0105	0.0109	8.45E-04
2.78	2.37	3.46	0.0103	0.0105	0.0109	8.45E-04
2.78	2.37	3.46	0.0103	0.0105	0.0109	8.45E-04
4.3	3.06	3.21	0.0103	0.0105	0.0109	8.47E-04
4.11	4.11	4.6	2.74	2.83	2.79	8.48E-04
3.33	2.33	2.55	0.0103	0.0105	0.0109	8.49E-04
3.37	3.16	3.31	2.73	2.71	2.7	8.49E-04
3.37	3.16	3.31	2.73	2.71	2.7	8.49E-04
3.43	2.92	2.32	0.0103	0.0105	0.0109	8.52E-04
3.43	2.92	2.32	0.0103	0.0105	0.0109	8.52E-04
4.44	4.53	5.24	2.15	2.44	2.01	8.56E-04
2.31	1.99	2.9	0.0103	0.0105	0.0109	8.56E-04
0.011	0.012	0.0117	2.41	2.89	3.54	8.57E-04
0.011	0.012	0.0117	2.6	3.68	2.77	8.57E-04
0.011	0.012	0.0117	2.6	3.68	2.77	8.57E-04
2.91	3.01	2.86	2.5	2.52	2.45	8.60E-04
2.91	3.01	2.86	2.5	2.52	2.45	8.60E-04
0.011	0.012	0.0117	2.98	4.36	3.5	8.62E-04
0.011	0.012	0.0117	2.98	4.36	3.5	8.62E-04
2.83	2.28	3.37	0.0103	0.0105	0.0109	8.62E-04
3.24	2.42	2.3	0.0103	0.0105	0.0109	8.63E-04
3.24	2.42	2.3	0.0103	0.0105	0.0109	8.63E-04
3.24	2.3	2.42	0.0103	0.0105	0.0109	8.63E-04
0.011	0.012	0.0117	2.58	2.23	3.25	8.66E-04
3.08	3.08	4.24	0.0103	0.0105	0.0109	8.66E-04
3.72	3.58	5.02	0.0103	0.0105	0.0109	8.68E-04
3.72	3.58	5.02	0.0103	0.0105	0.0109	8.68E-04
3.72	3.58	5.02	0.0103	0.0105	0.0109	8.68E-04
3.2	2.39	2.27	0.0103	0.0105	0.0109	8.68E-04
2.94	2.26	3.35	0.0103	0.0105	0.0109	8.68E-04
2.94	2.26	3.35	0.0103	0.0105	0.0109	8.68E-04
2.41	2.75	3.5	0.0103	0.0105	0.0109	8.69E-04
3.38	2.28	2.9	0.0103	0.0105	0.0109	8.70E-04
0.011	0.012	0.0117	2.83	2.7	3.8	8.70E-04

3.49	3.28	2.38	0.0103	0.0105	0.0109	8.70E-04
2.8	3.15	4.05	0.0103	0.0105	0.0109	8.71E-04
2.8	3.15	4.05	0.0103	0.0105	0.0109	8.71E-04
3.54	3.56	4.89	0.0103	0.0105	0.0109	8.72E-04
3.54	3.56	4.89	0.0103	0.0105	0.0109	8.72E-04
3.54	3.56	4.89	0.0103	0.0105	0.0109	8.72E-04
3.53	2.38	3.09	0.0103	0.0105	0.0109	8.72E-04
3.58	2.45	3.41	0.0103	0.0105	0.0109	8.75E-04
2.78	3.06	2.07	0.0103	0.0105	0.0109	8.76E-04
2.49	3.66	3.42	0.0103	0.0105	0.0109	8.77E-04
2.49	3.66	3.42	0.0103	0.0105	0.0109	8.77E-04
4.25	3	4.34	0.0103	0.0105	0.0109	8.77E-04
2.25	3.02	2.14	0.0103	0.0105	0.0109	8.87E-04
2.25	3.02	2.14	0.0103	0.0105	0.0109	8.87E-04
3.44	2.52	2.47	0.0103	0.0105	0.0109	8.89E-04
3.44	2.52	2.47	0.0103	0.0105	0.0109	8.89E-04
0.011	0.012	0.0117	4.48	3.16	4.58	8.90E-04
4.72	4.24	3.18	0.0103	0.0105	0.0109	8.92E-04
0.011	0.012	0.0117	2.64	3.56	3.91	8.93E-04
3	2.93	4.09	0.0103	0.0105	0.0109	8.94E-04
3.59	2.81	4.18	0.0103	0.0105	0.0109	8.95E-04
3.59	2.81	4.18	0.0103	0.0105	0.0109	8.95E-04
0.011	0.012	0.0117	3.35	2.47	2.39	8.96E-04
3.56	2.47	3.54	0.0103	0.0105	0.0109	9.08E-04
4.21	2.83	3.77	0.0103	0.0105	0.0109	9.09E-04
4.21	2.83	3.77	0.0103	0.0105	0.0109	9.09E-04
3.07	4.27	3.11	0.0103	0.0105	0.0109	9.10E-04
0.011	0.012	0.0117	3.31	2.24	2.69	9.13E-04
0.011	0.012	0.0117	3.17	2.14	2.92	9.17E-04
0.011	0.012	0.0117	2.39	3.46	2.66	9.22E-04
0.011	0.012	0.0117	3.76	2.53	3.11	9.25E-04
3.37	2.32	3.31	0.0103	0.0105	0.0109	9.28E-04
0.011	0.012	0.0117	2.52	3.39	2.39	9.29E-04
3.58	2.4	3.02	0.0103	0.0105	0.0109	9.31E-04
3.54	2.47	3.58	0.0103	0.0105	0.0109	9.34E-04
2.34	2.62	3.4	0.0103	0.0105	0.0109	9.39E-04
2.31	2.51	3.32	0.0103	0.0105	0.0109	9.39E-04
2.31	2.51	3.32	0.0103	0.0105	0.0109	9.39E-04
3.3	2.21	2.79	0.0103	0.0105	0.0109	9.39E-04
3.3	2.21	2.79	0.0103	0.0105	0.0109	9.39E-04
0.011	0.012	0.0117	2.5	3.71	3.02	9.42E-04
0.011	0.012	0.0117	3.31	2.36	2.42	9.44E-04
2.71	2.99	3.92	0.0103	0.0105	0.0109	9.45E-04
0.011	0.012	0.0117	3.15	2.96	2.13	9.47E-04
0.011	0.012	0.0117	3.15	2.96	2.13	9.47E-04
2.54	2.43	3.44	0.0103	0.0105	0.0109	9.49E-04
2.23	3.24	3.2	0.0103	0.0105	0.0109	9.53E-04
2.23	3.24	3.2	0.0103	0.0105	0.0109	9.53E-04
5.17	4.15	3.49	0.0103	0.0105	0.0109	9.54E-04
3.82	2.58	3.6	0.0103	0.0105	0.0109	9.62E-04
3.82	2.58	3.6	0.0103	0.0105	0.0109	9.62E-04
4.2	3.88	2.82	0.0103	0.0105	0.0109	9.67E-04
4.2	3.88	2.82	0.0103	0.0105	0.0109	9.67E-04
0.011	0.012	0.0117	2.96	2.26	2.04	9.68E-04
0.011	0.012	0.0117	2.47	3.43	2.47	9.68E-04
3.6	2.54	2.65	0.0103	0.0105	0.0109	9.71E-04
3.6	2.54	2.65	0.0103	0.0105	0.0109	9.71E-04
3.52	2.45	2.64	0.0103	0.0105	0.0109	9.71E-04

3.31	3.11	2.23	0.0103	0.0105	0.0109	9.78E-04
3.56	2.66	2.48	0.0103	0.0105	0.0109	9.83E-04
3.56	2.66	2.48	0.0103	0.0105	0.0109	9.83E-04
2.67	3.97	3.72	0.0103	0.0105	0.0109	9.85E-04
2.67	3.97	3.72	0.0103	0.0105	0.0109	9.85E-04
2.67	3.97	3.72	0.0103	0.0105	0.0109	9.85E-04
4.51	5.19	5.13	2.81	3.09	2.81	9.94E-04
0.011	0.012	0.0117	2.78	3.74	2.61	9.96E-04
0.011	0.012	0.0117	2.78	3.74	2.61	9.96E-04
4.2	3.02	3.01	0.0103	0.0105	0.0109	1.00E-03
4.2	3.02	3.01	0.0103	0.0105	0.0109	1.00E-03
3.29	3.33	2.28	0.0103	0.0105	0.0109	1.00E-03
3.29	3.33	2.28	0.0103	0.0105	0.0109	1.00E-03
4.69	3.53	3.24	0.0103	0.0105	0.0109	1.00E-03
4.69	3.53	3.24	0.0103	0.0105	0.0109	1.00E-03
4.69	3.53	3.24	0.0103	0.0105	0.0109	1.00E-03
2.44	2.25	3.25	0.0103	0.0105	0.0109	1.01E-03
3.83	2.61	3.75	0.0103	0.0105	0.0109	1.01E-03
4.04	3.24	2.71	0.0103	0.0105	0.0109	1.01E-03
3.98	4.05	3.62	2.7	2.76	2.73	1.01E-03
3.98	4.05	3.62	2.7	2.76	2.73	1.01E-03
2.38	3.57	3.27	0.0103	0.0105	0.0109	1.02E-03
0.011	0.012	0.0117	2.28	3.43	2.86	1.02E-03
3.88	2.84	2.73	0.0103	0.0105	0.0109	1.02E-03
3.1	3.37	3.27	2.46	2.36	2.53	1.02E-03
3.1	3.37	3.27	2.46	2.36	2.53	1.02E-03
2.88	2.27	3.42	0.0103	0.0105	0.0109	1.02E-03
4.42	4.36	4.28	2.93	2.97	2.41	1.02E-03
4.42	4.36	4.28	2.93	2.97	2.41	1.02E-03
3.55	2.42	3.49	0.0103	0.0105	0.0109	1.02E-03
4.54	4.69	4.22	2.11	2.78	2.27	1.02E-03
0.011	0.012	0.0117	2.92	2.13	3.2	1.03E-03
0.011	0.012	0.0117	2.92	2.13	3.2	1.03E-03
0.011	0.012	0.0117	2.92	2.13	3.2	1.03E-03
0.011	0.012	0.0117	2.32	3.47	2.79	1.04E-03
4.33	3.18	3.03	0.0103	0.0105	0.0109	1.04E-03
4.33	3.18	3.03	0.0103	0.0105	0.0109	1.04E-03
3.54	2.56	2.51	0.0103	0.0105	0.0109	1.04E-03
3.14	2.11	2.99	0.0103	0.0105	0.0109	1.04E-03
4.24	4.58	3.05	0.0103	0.0105	0.0109	1.05E-03
0.011	0.012	0.0117	3.21	2.81	4.15	1.05E-03
2.97	2.14	2.11	0.0103	0.0105	0.0109	1.05E-03
4.4	4.83	4.59	2.33	3	2.6	1.05E-03
4.4	4.83	4.59	2.33	3	2.6	1.05E-03
0.011	0.012	0.0117	3.41	3.36	2.32	1.05E-03
0.011	0.012	0.0117	3.31	2.42	2.32	1.05E-03
0.011	0.012	0.0117	3.31	2.42	2.32	1.05E-03
3.555	2.365	3.285	0.0103	0.0105	0.0109	1.06E-03
0.011	0.012	0.0117	2.51	2.92	3.73	1.06E-03
0.011	0.012	0.0117	2.51	2.92	3.73	1.06E-03
0.011	0.012	0.0117	3.33	3.36	2.29	1.06E-03
0.011	0.012	0.0117	3.33	3.36	2.29	1.06E-03
0.011	0.012	0.0117	2.27	2.93	3.44	1.07E-03
3.82	3.25	2.52	0.0103	0.0105	0.0109	1.07E-03
3.82	3.25	2.52	0.0103	0.0105	0.0109	1.07E-03
3.75	3	2.5	0.0103	0.0105	0.0109	1.07E-03
0.011	0.012	0.0117	2.43	3.67	3.34	1.07E-03
2.8	3.02	4.06	0.0103	0.0105	0.0109	1.08E-03

2.31	3.29	2.39	0.0103	0.0105	0.0109	1.08E-03
2.31	3.29	2.39	0.0103	0.0105	0.0109	1.08E-03
0.011	0.012	0.0117	2.64	3.45	2.34	1.08E-03
3.15	2.83	2.08	0.0103	0.0105	0.0109	1.08E-03
2.8	2.59	3.76	0.0103	0.0105	0.0109	1.08E-03
2.8	2.59	3.76	0.0103	0.0105	0.0109	1.08E-03
2.8	2.59	3.76	0.0103	0.0105	0.0109	1.08E-03
0.011	0.012	0.0117	4.22	3.47	2.79	1.08E-03
0.011	0.012	0.0117	4.22	3.47	2.79	1.08E-03
3.14	2.56	2.08	0.0103	0.0105	0.0109	1.09E-03
3.14	2.56	2.08	0.0103	0.0105	0.0109	1.09E-03
4.05	4.62	3.04	0.0103	0.0105	0.0109	1.09E-03
3.16	2.33	2.19	0.0103	0.0105	0.0109	1.09E-03
3.16	2.33	2.19	0.0103	0.0105	0.0109	1.09E-03
3.16	2.33	2.19	0.0103	0.0105	0.0109	1.09E-03
3.86	2.76	4.16	0.0103	0.0105	0.0109	1.09E-03
0.011	0.012	0.0117	2.94	4.42	3.53	1.09E-03
2.4	3.18	3.65	0.0103	0.0105	0.0109	1.09E-03
0.011	0.012	0.0117	3.99	3.32	2.63	1.09E-03
3.01	4.41	3.32	0.0103	0.0105	0.0109	1.10E-03
3.01	4.41	3.32	0.0103	0.0105	0.0109	1.10E-03
3.21	2.77	2.11	0.0103	0.0105	0.0109	1.10E-03
3.21	2.77	2.11	0.0103	0.0105	0.0109	1.10E-03
0.011	0.012	0.0117	2.94	3.55	4.43	1.10E-03
0.011	0.012	0.0117	2.94	3.55	4.43	1.10E-03
3.25	2.44	2.22	0.0103	0.0105	0.0109	1.11E-03
3.25	2.44	2.22	0.0103	0.0105	0.0109	1.11E-03
3.38	3.08	2.23	0.0103	0.0105	0.0109	1.11E-03
0.011	0.012	0.0117	3.91	3.78	2.62	1.12E-03
0.011	0.012	0.0117	3.91	3.78	2.62	1.12E-03
2.75	2.62	3.77	0.0103	0.0105	0.0109	1.12E-03
2.75	2.62	3.77	0.0103	0.0105	0.0109	1.12E-03
2.75	2.62	3.77	0.0103	0.0105	0.0109	1.12E-03
2.75	2.62	3.77	0.0103	0.0105	0.0109	1.12E-03
3.72	2.44	3.12	0.0103	0.0105	0.0109	1.13E-03
3.72	2.44	3.12	0.0103	0.0105	0.0109	1.13E-03
4.36	3.15	3.05	0.0103	0.0105	0.0109	1.13E-03
0.011	0.012	0.0117	2.25	3.31	3.31	1.13E-03
0.011	0.012	0.0117	2.25	3.31	3.31	1.13E-03
0.011	0.012	0.0117	2.01	3.02	2.87	1.13E-03
3.02	2.21	2.09	0.0103	0.0105	0.0109	1.14E-03
0.011	0.012	0.0117	2.2	3.26	3.22	1.15E-03
3.54	3.86	2.54	0.0103	0.0105	0.0109	1.15E-03
4.02	2.63	3.54	0.0103	0.0105	0.0109	1.15E-03
4.02	2.63	3.54	0.0103	0.0105	0.0109	1.15E-03
4.11	3.07	2.8	0.0103	0.0105	0.0109	1.15E-03
4.11	3.07	2.8	0.0103	0.0105	0.0109	1.15E-03
0.011	0.012	0.0117	3.23	2.34	2.25	1.15E-03
0.011	0.012	0.0117	2.16	2.5	3.23	1.15E-03
0.011	0.012	0.0117	2.16	2.5	3.23	1.15E-03
0.011	0.012	0.0117	3.71	2.43	3.33	1.16E-03
2.42	2.85	3.64	0.0103	0.0105	0.0109	1.16E-03
2.42	2.85	3.64	0.0103	0.0105	0.0109	1.16E-03
0.011	0.012	0.0117	2.21	3.13	3.35	1.17E-03
3.69	3.53	3.49	3.07	3.01	2.98	1.17E-03
3.69	3.53	3.49	3.07	3.01	2.98	1.17E-03
2.39	2.87	3.62	0.0103	0.0105	0.0109	1.18E-03
3.91	3.2	2.56	0.0103	0.0105	0.0109	1.18E-03

3.48	2.35	2.62	0.0103	0.0105	0.0109	1.18E-03
3.48	2.35	2.62	0.0103	0.0105	0.0109	1.18E-03
3.66	2.57	3.9	0.0103	0.0105	0.0109	1.19E-03
3.4	2.59	2.28	0.0103	0.0105	0.0109	1.19E-03
0.011	0.012	0.0117	3.25	2.4	2.22	1.19E-03
3.32	2.5	2.24	0.0103	0.0105	0.0109	1.19E-03
3.32	2.5	2.24	0.0103	0.0105	0.0109	1.19E-03
4.61	3.09	3.51	0.0103	0.0105	0.0109	1.19E-03
2.01	3.06	2.46	0.0103	0.0105	0.0109	1.20E-03
2.55	2.4	3.49	0.0103	0.0105	0.0109	1.20E-03
2.55	2.4	3.49	0.0103	0.0105	0.0109	1.20E-03
2.48	3.81	3.23	0.0103	0.0105	0.0109	1.20E-03
2.48	3.81	3.23	0.0103	0.0105	0.0109	1.20E-03
3.41	2.22	2.89	0.0103	0.0105	0.0109	1.20E-03
0.011	0.012	0.0117	2.71	4.16	3.69	1.20E-03
3.55	4.09	2.66	0.0103	0.0105	0.0109	1.20E-03
3.55	4.09	2.66	0.0103	0.0105	0.0109	1.20E-03
0.011	0.012	0.0117	2.61	3.97	3.17	1.20E-03
2.81	1.86	2.68	0.0103	0.0105	0.0109	1.20E-03
3.63	3.32	3.64	2.35	2.43	2.61	1.21E-03
3.63	3.32	3.64	2.35	2.43	2.61	1.21E-03
3.63	3.32	3.64	2.35	2.43	2.61	1.21E-03
2.86	3.16	4.23	0.0103	0.0105	0.0109	1.21E-03
0.011	0.012	0.0117	2.19	3.37	2.91	1.21E-03
3.41	3.86	2.51	0.0103	0.0105	0.0109	1.21E-03
0.011	0.012	0.0117	2.61	3.97	3.72	1.21E-03
0.011	0.012	0.0117	2.61	3.97	3.72	1.21E-03
4.29	4.69	4.68	2.92	3.12	3.32	1.21E-03
4.29	4.69	4.68	2.92	3.12	3.32	1.21E-03
4.29	4.69	4.68	2.92	3.12	3.32	1.21E-03
3.24	2.69	2.11	0.0103	0.0105	0.0109	1.22E-03
0.011	0.012	0.0117	3.15	3.11	2.11	1.22E-03
3.8	5.05	3.39	0.0103	0.0105	0.0109	1.23E-03
2.73	3.66	2.47	0.0103	0.0105	0.0109	1.24E-03
3.89	2.52	3.39	0.0103	0.0105	0.0109	1.24E-03
2.25	2.18	3.14	0.0103	0.0105	0.0109	1.24E-03
3.15	2.04	2.67	0.0103	0.0105	0.0109	1.25E-03
3.15	2.04	2.67	0.0103	0.0105	0.0109	1.25E-03
2.73	2.85	3.96	0.0103	0.0105	0.0109	1.27E-03
2.73	2.85	3.96	0.0103	0.0105	0.0109	1.27E-03
0.011	0.012	0.0117	2.35	2.92	3.61	1.27E-03
0.011	0.012	0.0117	2.35	2.92	3.61	1.27E-03
0.011	0.012	0.0117	2.22	3.04	3.43	1.27E-03
3.36	3.05	2.18	0.0103	0.0105	0.0109	1.28E-03
0.011	0.012	0.0117	2.09	2.99	3.2	1.28E-03
0.011	0.012	0.0117	2.09	2.99	3.2	1.28E-03
0.011	0.012	0.0117	2.64	3.17	4.03	1.28E-03
2.65	3.8	4.06	0.0103	0.0105	0.0109	1.29E-03
0.011	0.012	0.0117	3.21	2.35	2.18	1.29E-03
3.15	4.25	2.86	0.0103	0.0105	0.0109	1.29E-03
3.29	2.6	2.15	0.0103	0.0105	0.0109	1.29E-03
2.87	4.08	2.86	0.0103	0.0105	0.0109	1.29E-03
2.22	3.44	3.05	0.0103	0.0105	0.0109	1.30E-03
0.011	0.012	0.0117	2.73	2.09	3.24	1.30E-03
0.011	0.012	0.0117	2.77	3.61	2.38	1.31E-03
0.011	0.012	0.0117	2.16	3.24	2.43	1.32E-03
0.011	0.012	0.0117	3.14	2.29	2.13	1.32E-03
2.26	2.77	3.48	0.0103	0.0105	0.0109	1.33E-03

2.26	2.77	3.48	0.0103	0.0105	0.0109	1.33E-03
0.011	0.012	0.0117	2.52	3.83	2.94	1.33E-03
0.011	0.012	0.0117	2.52	3.83	2.94	1.33E-03
3.94	2.53	3.41	0.0103	0.0105	0.0109	1.33E-03
3.6	3.46	2.36	0.0103	0.0105	0.0109	1.34E-03
3.06	2.13	3.28	0.0103	0.0105	0.0109	1.34E-03
3.38	3.8	3.64	2.63	2.54	2.44	1.34E-03
2.99	2.55	1.92	0.0103	0.0105	0.0109	1.34E-03
0.011	0.012	0.0117	2.51	3.08	3.87	1.34E-03
0.011	0.012	0.0117	4.08	2.7	3.08	1.35E-03
0.011	0.012	0.0117	4.08	2.7	3.08	1.35E-03
5.13	3.34	4.86	0.0103	0.0105	0.0109	1.35E-03
2.29	3.57	3.02	0.0103	0.0105	0.0109	1.35E-03
0.011	0.012	0.0117	2.7	2.67	3.84	1.36E-03
0.011	0.012	0.0117	2.7	2.67	3.84	1.36E-03
3.79	2.53	2.81	0.0103	0.0105	0.0109	1.36E-03
3.79	2.53	2.81	0.0103	0.0105	0.0109	1.36E-03
2.65	3.96	2.92	0.0103	0.0105	0.0109	1.37E-03
4.07	2.66	3.14	0.0103	0.0105	0.0109	1.37E-03
3.57	3.33	2.31	0.0103	0.0105	0.0109	1.38E-03
3.57	3.33	2.31	0.0103	0.0105	0.0109	1.38E-03
3.16	3.94	2.54	0.0103	0.0105	0.0109	1.38E-03
3.57	3.49	3.63	2.62	2.37	2.77	1.38E-03
0.011	0.012	0.0117	3.63	2.43	2.67	1.38E-03
0.011	0.012	0.0117	2.52	3.83	2.9	1.39E-03
0.011	0.012	0.0117	2.52	3.83	2.9	1.39E-03
0.011	0.012	0.0117	2.52	3.83	2.9	1.39E-03
3.96	3.6	3.6	2.59	2.76	2.72	1.39E-03
3.96	3.6	3.6	2.59	2.76	2.72	1.39E-03
0.011	0.012	0.0117	3.25	2.51	2.12	1.39E-03
2.2	3.42	3.14	0.0103	0.0105	0.0109	1.40E-03
2.2	3.42	3.14	0.0103	0.0105	0.0109	1.40E-03
0.011	0.012	0.0117	3.43	2.37	3.67	1.41E-03
0.011	0.012	0.0117	2.73	4.13	3.09	1.41E-03
0.011	0.012	0.0117	2.73	4.13	3.09	1.41E-03
2.25	3.13	3.52	0.0103	0.0105	0.0109	1.41E-03
0.011	0.012	0.0117	2.96	4.09	2.76	1.41E-03
3.88	3.14	2.49	0.0103	0.0105	0.0109	1.41E-03
4.53	4.65	5.02	3.45	3.5	3.22	1.41E-03
4.53	4.65	5.02	3.45	3.5	3.22	1.41E-03
4.53	4.65	5.02	3.45	3.5	3.22	1.41E-03
3.09	3.56	2.27	0.0103	0.0105	0.0109	1.42E-03
0.011	0.012	0.0117	3.64	2.32	3.15	1.42E-03
0.011	0.012	0.0117	3.64	2.32	3.15	1.42E-03
0.011	0.012	0.0117	3.64	2.32	3.15	1.42E-03
5.57	4.22	3.65	0.0103	0.0105	0.0109	1.42E-03
5.57	4.22	3.65	0.0103	0.0105	0.0109	1.42E-03
5.57	4.22	3.65	0.0103	0.0105	0.0109	1.42E-03
2.2	2.39	3.28	0.0103	0.0105	0.0109	1.42E-03
3.75	3.93	2.55	0.0103	0.0105	0.0109	1.42E-03
4.34	3.73	4.01	2.62	2.28	2.3	1.44E-03
3.16	2.01	2.75	0.0103	0.0105	0.0109	1.45E-03
3.16	2.01	2.75	0.0103	0.0105	0.0109	1.45E-03
4.13	4.6	4.29	3.09	2.69	2.66	1.45E-03
2.26	2.39	3.34	0.0103	0.0105	0.0109	1.46E-03
2.26	2.39	3.34	0.0103	0.0105	0.0109	1.46E-03
3.78	2.49	3.78	0.0103	0.0105	0.0109	1.48E-03
0.011	0.012	0.0117	3.71	2.69	2.48	1.48E-03

0.011	0.012	0.0117	2.32	3.1	3.66	1.49E-03
0.011	0.012	0.0117	2.32	3.1	3.66	1.49E-03
3.8	2.48	3.73	0.0103	0.0105	0.0109	1.49E-03
3.91	4.51	3.88	2.56	2.45	2.44	1.50E-03
4.72	3.01	4.34	0.0103	0.0105	0.0109	1.50E-03
0.011	0.012	0.0117	3.24	3.05	2.08	1.50E-03
4.48	4.37	2.91	0.0103	0.0105	0.0109	1.51E-03
3.15	2.05	2.38	0.0103	0.0105	0.0109	1.52E-03
2.17	2.87	3.43	0.0103	0.0105	0.0109	1.52E-03
3.17	3.97	2.53	0.0103	0.0105	0.0109	1.52E-03
3.17	3.97	2.53	0.0103	0.0105	0.0109	1.52E-03
3.72	2.69	2.48	0.0103	0.0105	0.0109	1.53E-03
3.88	2.48	3.06	0.0103	0.0105	0.0109	1.53E-03
2.57	2.19	3.38	0.0103	0.0105	0.0109	1.53E-03
2.48	3.35	2.2	0.0103	0.0105	0.0109	1.53E-03
2.48	3.35	2.2	0.0103	0.0105	0.0109	1.53E-03
0.011	0.012	0.0117	3.66	2.47	2.6	1.54E-03
3.71	2.42	3.67	0.0103	0.0105	0.0109	1.54E-03
0.011	0.012	0.0117	3.48	3.01	4.63	1.55E-03
3.5	2.43	3.83	0.0103	0.0105	0.0109	1.55E-03
2.81	4.17	4.38	0.0103	0.0105	0.0109	1.55E-03
0.011	0.012	0.0117	3.09	4.35	2.93	1.55E-03
0.011	0.012	0.0117	2.55	2.59	3.72	1.55E-03
2.65	2.5	3.72	0.0103	0.0105	0.0109	1.55E-03
2.65	2.5	3.72	0.0103	0.0105	0.0109	1.55E-03
0.011	0.012	0.0117	3.65	2.35	2.8	1.56E-03
4.46	3	3.16	0.0103	0.0105	0.0109	1.58E-03
3.78	4.53	2.85	0.0103	0.0105	0.0109	1.58E-03
3.44	2.41	3.82	0.0103	0.0105	0.0109	1.59E-03
0.011	0.012	0.0117	4.05	2.73	2.86	1.59E-03
0.011	0.012	0.0117	4.05	2.73	2.86	1.59E-03
0.011	0.012	0.0117	2.12	2.39	3.24	1.59E-03
2.3	3.63	3.35	0.0103	0.0105	0.0109	1.60E-03
2.3	3.63	3.35	0.0103	0.0105	0.0109	1.60E-03
2.6	2.23	3.45	0.0103	0.0105	0.0109	1.60E-03
2.6	2.23	3.45	0.0103	0.0105	0.0109	1.60E-03
2.33	2.46	3.47	0.0103	0.0105	0.0109	1.60E-03
2.33	2.46	3.47	0.0103	0.0105	0.0109	1.60E-03
2.33	2.46	3.47	0.0103	0.0105	0.0109	1.60E-03
4	3.41	2.51	0.0103	0.0105	0.0109	1.60E-03
4	3.41	2.51	0.0103	0.0105	0.0109	1.60E-03
3.95	2.55	2.98	0.0103	0.0105	0.0109	1.60E-03
3.95	2.55	2.98	0.0103	0.0105	0.0109	1.60E-03
0.011	0.012	0.0117	3.06	3.11	4.48	1.60E-03
0.011	0.012	0.0117	3.06	3.11	4.48	1.60E-03
3.29	2.56	4.06	0.0103	0.0105	0.0109	1.61E-03
3.78	2.4	2.97	0.0103	0.0105	0.0109	1.62E-03
2.38	3.62	3.68	0.0103	0.0105	0.0109	1.62E-03
3.27	2.25	2.25	0.0103	0.0105	0.0109	1.62E-03
3.27	2.25	2.25	0.0103	0.0105	0.0109	1.62E-03
0.011	0.012	0.0117	3.27	2.56	4.06	1.62E-03
0.011	0.012	0.0117	2.41	3.35	2.22	1.62E-03
3.56	2.79	2.26	0.0103	0.0105	0.0109	1.63E-03
4.51	5.19	5.13	2.81	3.09	2.45	1.64E-03
3.16	2.2	3.5	0.0103	0.0105	0.0109	1.64E-03
3.16	2.2	3.5	0.0103	0.0105	0.0109	1.64E-03
3.1	2.24	3.58	0.0103	0.0105	0.0109	1.64E-03
3.1	2.24	3.58	0.0103	0.0105	0.0109	1.64E-03

4.25	2.73	3.21	0.0103	0.0105	0.0109	1.65E-03
3.05	2.08	2.11	0.0103	0.0105	0.0109	1.65E-03
2.16	2.94	3.46	0.0103	0.0105	0.0109	1.67E-03
2.16	2.94	3.46	0.0103	0.0105	0.0109	1.67E-03
3.61	2.38	2.59	0.0103	0.0105	0.0109	1.69E-03
4.02	2.53	3.72	0.0103	0.0105	0.0109	1.69E-03
0.011	0.012	0.0117	3.17	4.08	5.06	1.69E-03
3.57	2.36	2.55	0.0103	0.0105	0.0109	1.69E-03
3.57	2.36	2.55	0.0103	0.0105	0.0109	1.69E-03
3.24	2.02	2.83	0.0103	0.0105	0.0109	1.70E-03
3.45	2.32	2.41	0.0103	0.0105	0.0109	1.70E-03
3.45	2.32	2.41	0.0103	0.0105	0.0109	1.70E-03
0.011	0.012	0.0117	2.52	2.44	3.62	1.71E-03
0.011	0.012	0.0117	2.52	2.44	3.62	1.71E-03
0.011	0.012	0.0117	2.21	3.55	3.06	1.71E-03
0.011	0.012	0.0117	3.34	2.51	2.14	1.71E-03
0.011	0.012	0.0117	3.81	3.23	2.37	1.72E-03
0.011	0.012	0.0117	2.33	3.57	3.63	1.72E-03
0.011	0.012	0.0117	2.3	2.67	3.58	1.72E-03
3.61	2.76	2.29	0.0103	0.0105	0.0109	1.74E-03
3.61	2.76	2.29	0.0103	0.0105	0.0109	1.74E-03
4.4	2.77	3.43	0.0103	0.0105	0.0109	1.74E-03
4.4	2.77	3.43	0.0103	0.0105	0.0109	1.74E-03
0.011	0.012	0.0117	2.55	3.74	2.56	1.74E-03
0.011	0.012	0.0117	3.34	2.51	4.04	1.75E-03
0.011	0.012	0.0117	2.01	3.15	2.37	1.76E-03
3.03	4.88	4.02	0.0103	0.0105	0.0109	1.76E-03
3.03	4.88	4.02	0.0103	0.0105	0.0109	1.76E-03
4.76	3.85	2.96	0.0103	0.0105	0.0109	1.78E-03
3.13	4.65	3.21	0.0103	0.0105	0.0109	1.78E-03
3.83	3.53	3.75	2.54	2.34	2.78	1.79E-03
3.83	3.53	3.75	2.54	2.34	2.78	1.79E-03
3.9	4.92	3.07	0.0103	0.0105	0.0109	1.79E-03
3.9	4.92	3.07	0.0103	0.0105	0.0109	1.79E-03
3.9	4.92	3.07	0.0103	0.0105	0.0109	1.79E-03
0.011	0.012	0.0117	2.14	3.33	3.32	1.79E-03
3.86	2.49	2.82	0.0103	0.0105	0.0109	1.80E-03
3.86	2.49	2.82	0.0103	0.0105	0.0109	1.80E-03
0.011	0.012	0.0117	2.29	3.31	2.22	1.81E-03
3.88	2.9	2.47	0.0103	0.0105	0.0109	1.81E-03
3.1	2.18	2.05	0.0103	0.0105	0.0109	1.81E-03
4.04	4.1	4.04	3.48	3.23	3.13	1.82E-03
4.04	4.1	4.04	3.48	3.23	3.13	1.82E-03
4.37	2.72	3.47	0.0103	0.0105	0.0109	1.82E-03
3.24	2.18	2.23	0.0103	0.0105	0.0109	1.82E-03
3.24	2.18	2.23	0.0103	0.0105	0.0109	1.82E-03
0.011	0.012	0.0117	3.57	2.27	2.67	1.83E-03
2.33	2.32	3.42	0.0103	0.0105	0.0109	1.83E-03
2.33	2.32	3.42	0.0103	0.0105	0.0109	1.83E-03
2.33	2.23	3.35	0.0103	0.0105	0.0109	1.84E-03
0.011	0.012	0.0117	2.7	4.29	3.26	1.86E-03
0.011	0.012	0.0117	2.41	3.6	2.48	1.86E-03
5.4	5.32	5.28	1.93	0.0105	0.0109	1.86E-03
0.011	0.012	0.0117	3.02	4.35	2.89	1.87E-03
3.65	2.26	2.91	0.0103	0.0105	0.0109	1.88E-03
4.08	3.95	2.57	0.0103	0.0105	0.0109	1.88E-03
4.08	3.95	2.57	0.0103	0.0105	0.0109	1.88E-03
4.08	3.95	2.57	0.0103	0.0105	0.0109	1.88E-03

3.32	2.54	2.08	0.0103	0.0105	0.0109	1.89E-03
3.32	2.04	2.76	0.0103	0.0105	0.0109	1.89E-03
3.4	2.29	3.7	0.0103	0.0105	0.0109	1.90E-03
2.86	2.44	3.85	0.0103	0.0105	0.0109	1.90E-03
2.86	2.44	3.85	0.0103	0.0105	0.0109	1.90E-03
2.78	2.52	3.89	0.0103	0.0105	0.0109	1.90E-03
2.78	2.52	3.89	0.0103	0.0105	0.0109	1.90E-03
2.78	2.52	3.89	0.0103	0.0105	0.0109	1.90E-03
0.011	0.012	0.0117	2.8	3.75	2.37	1.91E-03
0.011	0.012	0.0117	2.17	3.07	3.54	1.92E-03
0.011	0.012	0.0117	2.17	3.07	3.54	1.92E-03
3.75	4.14	2.55	0.0103	0.0105	0.0109	1.92E-03
3.75	4.14	2.55	0.0103	0.0105	0.0109	1.92E-03
3.65	2.49	2.45	0.0103	0.0105	0.0109	1.92E-03
2.44	3.68	2.54	0.0103	0.0105	0.0109	1.94E-03
2.44	3.68	2.54	0.0103	0.0105	0.0109	1.94E-03
2.28	3.35	3.71	0.0103	0.0105	0.0109	1.95E-03
2.28	3.35	3.71	0.0103	0.0105	0.0109	1.95E-03
2.68	4.36	3.95	0.0103	0.0105	0.0109	1.95E-03
2.68	4.36	3.95	0.0103	0.0105	0.0109	1.95E-03
3.14	2.57	4.12	0.0103	0.0105	0.0109	1.96E-03
4.17	2.75	2.89	0.0103	0.0105	0.0109	1.96E-03
4.17	2.75	2.89	0.0103	0.0105	0.0109	1.96E-03
4.64	4.66	4.05	2.26	2.33	2.85	1.96E-03
3.35	2.08	3.17	0.0103	0.0105	0.0109	1.97E-03
0.011	0.012	0.0117	2.26	3.67	2.89	1.99E-03
0.011	0.012	0.0117	2.28	2.58	3.57	1.99E-03
2.21	2.37	2.56	3.29	3.19	3.11	1.99E-03
2.21	2.37	2.56	3.29	3.19	3.11	1.99E-03
3.26	3.08	2.02	0.0103	0.0105	0.0109	2.00E-03
0.011	0.012	0.0117	2.68	2.29	3.63	2.00E-03
3.72	3.78	3.67	2.19	2.34	2.78	2.02E-03
3.72	3.78	3.67	2.19	2.34	2.78	2.02E-03
0.011	0.012	0.0117	3.59	2.36	2.48	2.03E-03
4.13	3.57	2.51	0.0103	0.0105	0.0109	2.03E-03
3.51	2.43	2.3	0.0103	0.0105	0.0109	2.04E-03
0.011	0.012	0.0117	4.05	2.5	3.12	2.05E-03
3.47	2.5	2.21	0.0103	0.0105	0.0109	2.05E-03
3.64	2.38	3.86	0.0103	0.0105	0.0109	2.06E-03
3.64	2.38	3.86	0.0103	0.0105	0.0109	2.06E-03
2.65	3.95	4.34	0.0103	0.0105	0.0109	2.06E-03
2.65	3.95	4.34	0.0103	0.0105	0.0109	2.06E-03
4.63	2.91	4.59	0.0103	0.0105	0.0109	2.06E-03
0.011	0.012	0.0117	2.46	3.64	2.43	2.07E-03
0.011	0.012	0.0117	4.34	3.5	2.64	2.08E-03
4.49	4.13	4.85	2.53	2.98	2.55	2.09E-03
4.49	4.13	4.85	2.53	2.98	2.55	2.09E-03
4.76	4.46	4.56	3.22	3.34	2.71	2.10E-03
4.76	4.46	4.56	3.22	3.34	2.71	2.10E-03
3.2	5.29	4.37	0.0103	0.0105	0.0109	2.11E-03
3.2	5.29	4.37	0.0103	0.0105	0.0109	2.11E-03
0.011	0.012	0.0117	2.28	3.74	2.96	2.11E-03
3.7	2.69	4.45	0.0103	0.0105	0.0109	2.12E-03
3.33	3.41	5.03	0.0103	0.0105	0.0109	2.12E-03
3.33	3.41	5.03	0.0103	0.0105	0.0109	2.12E-03
0.011	0.012	0.0117	4.44	2.88	3.08	2.13E-03
0.011	0.012	0.0117	4.44	2.88	3.08	2.13E-03
0.011	0.012	0.0117	2.09	3.15	2.13	2.14E-03

4.05	4.3	4.61	2.64	2.89	2.26	2.14E-03
3.4	4.32	2.63	0.0103	0.0105	0.0109	2.14E-03
0.011	0.012	0.0117	2.25	3.35	3.71	2.15E-03
0.011	0.012	0.0117	2.21	2.35	3.4	2.15E-03
2.75	2.35	3.76	0.0103	0.0105	0.0109	2.18E-03
2.75	2.35	3.76	0.0103	0.0105	0.0109	2.18E-03
0.011	0.012	0.0117	2.06	3.12	3.39	2.18E-03
3.42	2.57	2.11	0.0103	0.0105	0.0109	2.18E-03
3.42	2.57	2.11	0.0103	0.0105	0.0109	2.18E-03
2.27	3.46	3.73	0.0103	0.0105	0.0109	2.18E-03
2.27	3.46	3.73	0.0103	0.0105	0.0109	2.18E-03
0.011	0.012	0.0117	3.57	2.37	2.4	2.18E-03
0.011	0.012	0.0117	3.57	2.37	2.4	2.18E-03
3.43	3.33	2.12	0.0103	0.0105	0.0109	2.19E-03
2.65	3.75	4.41	0.0103	0.0105	0.0109	2.19E-03
3.7	4.17	4.36	2.19	2.32	2.66	2.20E-03
3.7	4.17	4.36	2.19	2.32	2.66	2.20E-03
3.21	2.01	2.33	0.0103	0.0105	0.0109	2.21E-03
3.21	2.01	2.33	0.0103	0.0105	0.0109	2.21E-03
4.58	2.84	3.38	0.0103	0.0105	0.0109	2.21E-03
5.34	5.45	5.57	2.79	3.49	2.21	2.22E-03
5.34	5.45	5.57	2.79	3.49	2.21	2.22E-03
3.55	2.38	3.95	0.0103	0.0105	0.0109	2.23E-03
3.3	2.22	2.18	0.0103	0.0105	0.0109	2.23E-03
3.3	2.22	2.18	0.0103	0.0105	0.0109	2.23E-03
3.3	2.28	2.13	0.0103	0.0105	0.0109	2.24E-03
0.011	0.012	0.0117	2.47	4.11	3.64	2.24E-03
0.011	0.012	0.0117	2.14	3.57	3.06	2.24E-03
0.011	0.012	0.0117	2.64	3.48	2.13	2.24E-03
0.011	0.012	0.0117	2.64	3.48	2.13	2.24E-03
0.011	0.012	0.0117	3.39	2.3	3.83	2.25E-03
0.011	0.012	0.0117	3.39	2.3	3.83	2.25E-03
4.14	5.44	3.32	0.0103	0.0105	0.0109	2.25E-03
0.011	0.012	0.0117	2.36	3.09	3.91	2.26E-03
0.011	0.012	0.0117	2.09	2.92	3.49	2.26E-03
0.011	0.012	0.0117	2.09	2.92	3.49	2.26E-03
3.2	3.62	2.17	0.0103	0.0105	0.0109	2.27E-03
3.2	3.62	2.17	0.0103	0.0105	0.0109	2.27E-03
0.011	0.012	0.0117	3.62	2.17	2.95	2.28E-03
0.011	0.012	0.0117	3.62	2.17	2.95	2.28E-03
3.85	3.59	3.76	2.52	2.86	2.89	2.28E-03
3.85	3.59	3.76	2.52	2.86	2.89	2.28E-03
3.85	3.59	3.76	2.52	2.86	2.89	2.28E-03
4.11	2.53	4.02	0.0103	0.0105	0.0109	2.29E-03
4.11	2.53	4.02	0.0103	0.0105	0.0109	2.29E-03
4.8	5.04	4.64	3.68	3.5	3.9	2.30E-03
2.4	3.86	2.8	0.0103	0.0105	0.0109	2.30E-03
2.4	3.86	2.8	0.0103	0.0105	0.0109	2.30E-03
2.4	3.86	2.8	0.0103	0.0105	0.0109	2.30E-03
4.66	2.78	3.93	0.0103	0.0105	0.0109	2.30E-03
4.66	2.78	3.93	0.0103	0.0105	0.0109	2.30E-03
3.79	2.31	3.63	0.0103	0.0105	0.0109	2.32E-03
3.79	2.31	3.63	0.0103	0.0105	0.0109	2.32E-03
4.37	4.08	2.64	0.0103	0.0105	0.0109	2.32E-03
0.011	0.012	0.0117	2.11	3.33	2.33	2.35E-03
4.14	2.69	2.8	0.0103	0.0105	0.0109	2.36E-03
5.01	3.25	3.39	0.0103	0.0105	0.0109	2.37E-03
5.01	3.25	3.39	0.0103	0.0105	0.0109	2.37E-03

5.01	3.25	3.39	0.0103	0.0105	0.0109	2.37E-03
2.29	2.1	3.3	0.0103	0.0105	0.0109	2.37E-03
2.29	2.1	3.3	0.0103	0.0105	0.0109	2.37E-03
2.58	3.41	2.07	0.0103	0.0105	0.0109	2.37E-03
3.83	2.5	2.57	0.0103	0.0105	0.0109	2.39E-03
3.83	2.5	2.57	0.0103	0.0105	0.0109	2.39E-03
3.89	3.12	2.32	0.0103	0.0105	0.0109	2.39E-03
3.89	3.12	2.32	0.0103	0.0105	0.0109	2.39E-03
0.011	0.012	0.0117	3.68	3.63	2.26	2.40E-03
0.011	0.012	0.0117	3.68	3.63	2.26	2.40E-03
0.011	0.012	0.0117	2.16	3.38	2.32	2.42E-03
3.79	2.25	3.08	0.0103	0.0105	0.0109	2.43E-03
3.94	2.49	2.74	0.0103	0.0105	0.0109	2.43E-03
3.94	2.49	2.74	0.0103	0.0105	0.0109	2.43E-03
3.77	4.34	2.57	0.0103	0.0105	0.0109	2.44E-03
3.77	4.34	2.57	0.0103	0.0105	0.0109	2.44E-03
0.011	0.012	0.0117	2.09	3.42	2.52	2.44E-03
0.011	0.012	0.0117	2.22	2.45	3.52	2.46E-03
0.011	0.012	0.0117	4.13	2.5	3.09	2.48E-03
0.011	0.012	0.0117	4.13	2.5	3.09	2.48E-03
4.08	3.96	3.61	2.15	2.71	2.23	2.49E-03
4.08	3.96	3.61	2.15	2.71	2.23	2.49E-03
3.63	3.32	2.16	0.0103	0.0105	0.0109	2.49E-03
4.11	2.92	2.55	0.0103	0.0105	0.0109	2.49E-03
4.11	2.92	2.55	0.0103	0.0105	0.0109	2.49E-03
0.011	0.012	0.0117	2.47	2.72	3.92	2.50E-03
0.011	0.012	0.0117	2.47	2.72	3.92	2.50E-03
3.23	2.5	1.93	0.0103	0.0105	0.0109	2.50E-03
0.011	0.012	0.0117	3.45	2.1	2.54	2.50E-03
0.011	0.012	0.0117	2.11	3.47	3.4	2.52E-03
0.011	0.012	0.0117	2.11	3.47	3.4	2.52E-03
0.011	0.012	0.0117	2.64	3.82	2.41	2.52E-03
0.011	0.012	0.0117	2.64	3.82	2.41	2.52E-03
0.011	0.012	0.0117	2.64	3.82	2.41	2.52E-03
0.011	0.012	0.0117	2.4	3.95	2.91	2.52E-03
0.011	0.012	0.0117	2.4	3.95	2.91	2.52E-03
4.81	3.21	3.11	0.0103	0.0105	0.0109	2.56E-03
3.51	3.25	3.33	2.29	2.66	2.34	2.57E-03
3.55	3.58	3.88	2.51	2.87	2.64	2.59E-03
3.55	3.58	3.88	2.51	2.87	2.64	2.59E-03
3.66	2.37	2.43	0.0103	0.0105	0.0109	2.61E-03
3.66	2.37	2.43	0.0103	0.0105	0.0109	2.61E-03
0.011	0.012	0.0117	3.1	4.93	3.39	2.61E-03
3.66	2.32	3.9	0.0103	0.0105	0.0109	2.61E-03
4.07	2.74	2.6	0.0103	0.0105	0.0109	2.62E-03
4.07	2.74	2.6	0.0103	0.0105	0.0109	2.62E-03
3.75	2.53	4.32	0.0103	0.0105	0.0109	2.62E-03
3.88	3	2.3	0.0103	0.0105	0.0109	2.62E-03
0.011	0.012	0.0117	2.38	3.83	2.67	2.65E-03
3.73	2.96	4.96	0.0103	0.0105	0.0109	2.66E-03
3.73	2.96	4.96	0.0103	0.0105	0.0109	2.66E-03
0.011	0.012	0.0117	3.65	2.78	2.17	2.66E-03
3.15	3.55	2.08	0.0103	0.0105	0.0109	2.66E-03
3.15	3.55	2.08	0.0103	0.0105	0.0109	2.66E-03
0.011	0.012	0.0117	3.51	3.28	2.08	2.67E-03
4.23	2.54	3.13	0.0103	0.0105	0.0109	2.67E-03
4.23	2.54	3.13	0.0103	0.0105	0.0109	2.67E-03
0.011	0.012	0.0117	2.5	3.48	2.12	2.68E-03

3.73	2.19	3.38	0.0103	0.0105	0.0109	2.69E-03
0.011	0.012	0.0117	2.17	3	3.71	2.69E-03
3.68	2.35	2.46	0.0103	0.0105	0.0109	2.71E-03
3.57	4.16	4.25	2.56	2.25	2.52	2.71E-03
4.61	2.71	4.24	0.0103	0.0105	0.0109	2.72E-03
3.99	2.47	2.77	0.0103	0.0105	0.0109	2.74E-03
3.8	2.72	4.67	0.0103	0.0105	0.0109	2.74E-03
5.31	5.65	5.5	3.83	4.1	3.26	2.74E-03
0.011	0.012	0.0117	1.7	2.67	2.89	2.75E-03
3	4.26	2.61	0.0103	0.0105	0.0109	2.75E-03
0.011	0.012	0.0117	2.31	3.83	3.8	2.76E-03
4.78	4.6	4.6	2.39	2.41	3.28	2.78E-03
4.78	4.6	4.6	2.39	2.41	3.28	2.78E-03
3.23	3.85	2.23	0.0103	0.0105	0.0109	2.80E-03
3.59	2.71	2.12	0.0103	0.0105	0.0109	2.81E-03
3.95	3.77	3.77	2.54	2.6	3.04	2.82E-03
3.95	3.77	3.77	2.54	2.6	3.04	2.82E-03
0.011	0.012	0.0117	2.49	4.22	3.18	2.84E-03
0.011	0.012	0.0117	2.49	4.22	3.18	2.84E-03
0.011	0.012	0.0117	2.54	3.85	2.46	2.86E-03
2.53	4.34	4	0.0103	0.0105	0.0109	2.88E-03
0.011	0.012	0.0117	2.11	3.65	2.96	2.89E-03
3.88	3.94	2.35	0.0103	0.0105	0.0109	2.90E-03
0.011	0.012	0.0117	2.55	3.62	4.42	2.90E-03
3.46	2.62	2.03	0.0103	0.0105	0.0109	2.91E-03
3.46	2.62	2.03	0.0103	0.0105	0.0109	2.91E-03
3.92	3.85	2.33	0.0103	0.0105	0.0109	2.94E-03
4.21	2.42	3.62	0.0103	0.0105	0.0109	2.94E-03
3.58	3.89	3.51	2.72	2.22	2.33	2.96E-03
3.58	3.89	3.51	2.72	2.22	2.33	2.96E-03
3.75	3.6	3.95	2.27	2.56	2.82	2.96E-03
0.011	0.012	0.0117	2.28	3.62	2.4	3.00E-03
0.011	0.012	0.0117	2.28	3.62	2.4	3.00E-03
0.011	0.012	0.0117	2.09	3.65	3.08	3.02E-03
0.011	0.012	0.0117	2.09	3.65	3.08	3.02E-03
3.03	2.33	4	0.0103	0.0105	0.0109	3.02E-03
3.03	2.33	4	0.0103	0.0105	0.0109	3.02E-03
0.011	0.012	0.0117	2.69	4.48	3.17	3.02E-03
4.11	2.35	3.42	0.0103	0.0105	0.0109	3.04E-03
4.11	2.35	3.42	0.0103	0.0105	0.0109	3.04E-03
4.28	4.95	4.2	2.03	2.79	2.11	3.06E-03
4.28	4.95	4.2	2.03	2.79	2.11	3.06E-03
0.011	0.012	0.0117	3.63	2.2	3.75	3.08E-03
4.03	5.08	2.91	0.0103	0.0105	0.0109	3.10E-03
2.8	2.45	4.05	0.0103	0.0105	0.0109	3.13E-03
2.8	2.45	4.05	0.0103	0.0105	0.0109	3.13E-03
3.71	3.75	2.21	0.0103	0.0105	0.0109	3.17E-03
0.011	0.012	0.0117	2.05	3.47	3.45	3.18E-03
0.011	0.012	0.0117	2.34	4.11	3.64	3.18E-03
0.011	0.012	0.0117	2.06	3.63	3.1	3.19E-03
0.011	0.012	0.0117	2.06	3.63	3.1	3.19E-03
0.011	0.012	0.0117	3.1	2.94	4.71	3.21E-03
0.011	0.012	0.0117	3.44	2.42	2.05	3.21E-03
0.011	0.012	0.0117	3.44	2.42	2.05	3.21E-03
0.011	0.012	0.0117	4.41	3.24	2.57	3.22E-03
0.011	0.012	0.0117	4.41	3.24	2.57	3.22E-03
4.19	4.03	4.62	3.13	3.2	3.15	3.22E-03
4.19	4.03	4.62	3.13	3.2	3.15	3.22E-03

4.19	4.03	4.62	3.13	3.2	3.15	3.22E-03
4.98	4.14	4.98	2.69	3	2.56	3.22E-03
4.98	4.14	4.98	2.69	3	2.56	3.22E-03
3.88	3	2.22	0.0103	0.0105	0.0109	3.24E-03
4.62	3.96	4.78	2.89	2.36	2.51	3.25E-03
3.63	2.38	4.21	0.0103	0.0105	0.0109	3.26E-03
4.87	2.75	4.21	0.0103	0.0105	0.0109	3.28E-03
0.011	0.012	0.0117	2.01	3.56	3	3.29E-03
3.88	2.32	2.69	0.0103	0.0105	0.0109	3.29E-03
5.4	5.32	5.28	1.93	3.41	2.34	3.31E-03
0.011	0.012	0.0117	3.66	2.09	2.8	3.33E-03
0.011	0.012	0.0117	3.66	2.09	2.8	3.33E-03
0.011	0.012	0.0117	2.23	3.61	2.38	3.36E-03
3.66	3.98	2.26	0.0103	0.0105	0.0109	3.38E-03
4.33	2.59	2.97	0.0103	0.0105	0.0109	3.40E-03
3.45	2.21	2.18	0.0103	0.0105	0.0109	3.40E-03
3.73	3.35	4.1	2.25	2.29	2.45	3.42E-03
3.73	3.35	4.1	2.25	2.29	2.45	3.42E-03
0.011	0.012	0.0117	2.15	3.78	2.88	3.43E-03
3.67	2.22	2.47	0.0103	0.0105	0.0109	3.44E-03
4.52	2.63	3.24	0.0103	0.0105	0.0109	3.44E-03
4.52	2.63	3.24	0.0103	0.0105	0.0109	3.44E-03
3.9	4.33	4.49	2.94	2.5	2.23	3.45E-03
3.9	4.33	4.49	2.94	2.5	2.23	3.45E-03
2.14	3.33	2.09	0.0103	0.0105	0.0109	3.46E-03
3.89	4.11	2.34	0.0103	0.0105	0.0109	3.51E-03
4.13	2.9	2.42	0.0103	0.0105	0.0109	3.51E-03
0.011	0.012	0.0117	2.2	3.87	3.65	3.52E-03
3.45	2.31	2.08	0.0103	0.0105	0.0109	3.56E-03
3.45	2.31	2.08	0.0103	0.0105	0.0109	3.56E-03
4.15	3.58	2.31	0.0103	0.0105	0.0109	3.58E-03
4.29	3.76	4.18	3.03	3.12	2.9	3.64E-03
4.29	3.76	4.18	3.03	3.12	2.9	3.64E-03
4.29	3.76	4.18	3.03	3.12	2.9	3.64E-03
4.29	3.76	4.18	3.03	3.12	2.9	3.64E-03
0.011	0.012	0.0117	3.8	2.51	2.3	3.66E-03
0.011	0.012	0.0117	2.7	4.51	3.02	3.67E-03
2.17	3.16	3.91	0.0103	0.0105	0.0109	3.67E-03
4.61	3.1	2.75	0.0103	0.0105	0.0109	3.67E-03
3.13	2.73	4.61	0.0103	0.0105	0.0109	3.69E-03
3.13	2.73	4.61	0.0103	0.0105	0.0109	3.69E-03
4.62	2.82	3.01	0.0103	0.0105	0.0109	3.69E-03
3.88	2.4	2.49	0.0103	0.0105	0.0109	3.70E-03
0.011	0.012	0.0117	4.37	3.25	2.47	3.70E-03
3.59	2.04	2.63	0.0103	0.0105	0.0109	3.72E-03
0.011	0.012	0.0117	2.55	4.62	3.79	3.75E-03
0.011	0.012	0.0117	2.55	4.62	3.79	3.75E-03
3.97	2.88	2.26	0.0103	0.0105	0.0109	3.76E-03
3.97	2.88	2.26	0.0103	0.0105	0.0109	3.76E-03
0.011	0.012	0.0117	2.04	3.67	2.85	3.79E-03
0.011	0.012	0.0117	2.04	3.67	2.85	3.79E-03
3.82	2.23	3.94	0.0103	0.0105	0.0109	3.83E-03
4.15	4.19	3.56	2.46	2.67	2.76	3.85E-03
2.48	4.31	3.02	0.0103	0.0105	0.0109	3.87E-03
2.48	4.31	3.02	0.0103	0.0105	0.0109	3.87E-03
0.011	0.012	0.0117	2.16	2.8	3.83	3.88E-03
4.71	5.09	5.3	0.0103	2.11	0.0109	3.89E-03
4.71	5.09	5.3	0.0103	2.11	0.0109	3.89E-03

4.13	2.9	2.37	0.0103	0.0105	0.0109	3.91E-03
3.35	3.02	3.58	2.18	2.09	2.38	3.91E-03
3.69	2.11	3.69	0.0103	0.0105	0.0109	3.92E-03
3.65	2.04	2.72	0.0103	0.0105	0.0109	3.92E-03
3.65	2.04	2.72	0.0103	0.0105	0.0109	3.92E-03
0.011	0.012	0.0117	2.16	3.95	3.28	3.95E-03
4.11	2.89	2.35	0.0103	0.0105	0.0109	3.96E-03
2.69	2.46	3	4.46	3.82	4.27	3.97E-03
4.88	4.65	4.34	3.66	3.67	3.44	3.99E-03
4.88	4.65	4.34	3.66	3.67	3.44	3.99E-03
5.79	6.15	5.79	3	3.99	4.11	4.01E-03
5.79	6.15	5.79	3	3.99	4.11	4.01E-03
5.79	6.15	5.79	3	3.99	4.11	4.01E-03
5.79	6.15	5.79	3	3.99	4.11	4.01E-03
5.79	6.15	5.79	3	3.99	4.11	4.01E-03
5.79	6.15	5.79	3	3.99	4.11	4.01E-03
3.77	2.5	2.23	0.0103	0.0105	0.0109	4.01E-03
5.54	5.82	5.56	2.79	4.06	3.29	4.02E-03
5.54	5.82	5.56	2.79	4.06	3.29	4.02E-03
0.011	0.012	0.0117	3.18	3.89	2.12	4.04E-03
4.38	2.41	4.08	0.0103	0.0105	0.0109	4.14E-03
4.38	2.41	4.08	0.0103	0.0105	0.0109	4.14E-03
0.011	0.012	0.0117	4.16	2.38	2.85	4.24E-03
0.011	0.012	0.0117	4.16	2.38	2.85	4.24E-03
0.011	0.012	0.0117	3.83	3	2.08	4.25E-03
2.17	2.29	3.6	0.0103	0.0105	0.0109	4.28E-03
4.47	4.61	4.95	0.0103	2.02	0.0109	4.30E-03
4.74	5.28	5.02	2.62	3.6	3.18	4.38E-03
4.74	5.28	5.02	2.62	3.6	3.18	4.38E-03
4.51	2.68	2.89	0.0103	0.0105	0.0109	4.41E-03
0.011	0.012	0.0117	3.11	3.79	2.03	4.43E-03
0.011	0.012	0.0117	3.11	3.79	2.03	4.43E-03
4.03	3.51	4.06	2.81	2.86	2.84	4.54E-03
0.011	0.012	0.0117	2.39	4.36	4.22	4.55E-03
4.16	4.38	4.06	3.6	3.52	3.32	4.63E-03
4.77	4.23	4.82	2.03	3.09	2.54	4.65E-03
0.011	0.012	0.0117	2.09	3.67	3.85	4.66E-03
4.27	4.18	2.34	0.0103	0.0105	0.0109	4.67E-03
4.27	4.18	2.34	0.0103	0.0105	0.0109	4.67E-03
2.4	4.52	4.01	0.0103	0.0105	0.0109	4.72E-03
2.25	4.18	3.12	0.0103	0.0105	0.0109	4.73E-03
2.25	4.18	3.12	0.0103	0.0105	0.0109	4.73E-03
0.011	0.012	0.0117	2.3	4.16	4.19	4.80E-03
0.011	0.012	0.0117	2.22	3.92	2.61	4.83E-03
3.83	2.57	4.87	0.0103	0.0105	0.0109	4.89E-03
2.99	3.62	3.54	2.26	2.28	2.27	4.93E-03
0.011	0.012	0.0117	2.88	4.93	3.12	4.95E-03
0.011	0.012	0.0117	2.48	2.81	4.33	4.96E-03
5.52	5.41	5.32	0.0103	2.46	0.0109	4.97E-03
4.93	4.23	4.47	3.21	2.97	2.49	4.97E-03
4.96	5.05	4.52	2.68	2.38	3.45	4.99E-03
4.96	5.05	4.52	2.68	2.38	3.45	4.99E-03
0.011	0.012	0.0117	4.77	4.17	2.5	5.00E-03
0.011	0.012	0.0117	2.39	3.92	4.58	5.06E-03
0.011	0.012	0.0117	2.39	3.92	4.58	5.06E-03
3.09	2.78	2.96	3.6	4.03	3.77	5.11E-03
4.1	3.85	3.91	3	2.19	2.57	5.12E-03
0.011	0.012	0.0117	3.86	2.4	2.27	5.14E-03

4.07	4.53	4.68	2.87	3.36	2.79	5.15E-03
5.31	5.65	5.5	2.88	4.1	3.26	5.16E-03
4.29	3.97	3.53	2.32	2.64	2.69	5.18E-03
4.29	3.97	3.53	2.32	2.64	2.69	5.18E-03
3.04	2.7	4.73	0.0103	0.0105	0.0109	5.18E-03
0.011	0.012	0.0117	2.8	4.7	2.87	5.19E-03
0.011	0.012	0.0117	2.66	4.44	2.69	5.24E-03
0.011	0.012	0.0117	2.66	4.44	2.69	5.24E-03
3.72	3.6	4.19	2.66	2.61	2.12	5.29E-03
0.011	0.012	0.0117	4.23	2.79	2.36	5.30E-03
0.011	0.012	0.0117	4.23	2.79	2.36	5.30E-03
5.41	5.33	4.7	0.0103	0.0105	2.3	5.34E-03
0.011	0.012	0.0117	2.21	2.88	4.11	5.36E-03
0.011	0.012	0.0117	2.21	2.88	4.11	5.36E-03
0.011	0.012	0.0117	5.12	3.89	2.66	5.46E-03
0.011	0.012	0.0117	3.97	2.04	3.23	5.48E-03
5.45	4.4	5.37	3.19	3.13	2.61	5.49E-03
5.45	4.4	5.37	3.19	3.13	2.61	5.49E-03
5.45	4.4	5.37	3.19	3.13	2.61	5.49E-03
4.51	5.23	5.43	3.52	3.16	2.8	5.52E-03
4.51	5.23	5.43	3.52	3.16	2.8	5.52E-03
4.48	3.14	2.39	0.0103	0.0105	0.0109	5.54E-03
2.29	4.41	3.32	0.0103	0.0105	0.0109	5.54E-03
0.011	0.012	0.0117	2.17	4.24	3.53	5.55E-03
0.011	0.012	0.0117	2.17	4.24	3.53	5.55E-03
5.11	2.87	3.27	0.0103	0.0105	0.0109	5.61E-03
3.72	2.07	2.41	0.0103	0.0105	0.0109	5.64E-03
2.73	5.37	4.42	0.0103	0.0105	0.0109	5.72E-03
2.05	2.58	3.81	0.0103	0.0105	0.0109	5.78E-03
3.8	2.16	2.36	0.0103	0.0105	0.0109	5.89E-03
3.59	3.18	3.7	2.61	2.68	2.49	5.89E-03
4.54	4.01	4.51	0.0103	0.0105	2.01	5.92E-03
3.33	3.07	3.36	2.57	2.62	2.78	5.93E-03
3.33	3.07	3.36	2.57	2.62	2.78	5.93E-03
4.26	4.68	4.68	3.84	3.6	3.6	5.95E-03
4.26	4.68	4.68	3.84	3.6	3.6	5.95E-03
4.26	4.68	4.68	3.84	3.6	3.6	5.95E-03
3.25	3.7	3.37	2.35	2.72	2.38	5.95E-03
3.98	4.36	4.4	2.26	3.08	2.9	6.05E-03
2.36	4.64	3.51	0.0103	0.0105	0.0109	6.06E-03
2.36	4.64	3.51	0.0103	0.0105	0.0109	6.06E-03
4.44	4.53	5.24	2.15	0.0105	0.0109	6.07E-03
4.37	4.35	4.33	3.59	2.89	3.33	6.18E-03
4.37	4.35	4.33	3.59	2.89	3.33	6.18E-03
3.84	3.91	4.73	2.51	2.74	2.58	6.18E-03
3.84	3.91	4.73	2.51	2.74	2.58	6.18E-03
3.34	3.24	2.98	2.43	2.65	2.5	6.24E-03
3.34	3.24	2.98	2.43	2.65	2.5	6.24E-03
4.81	4.04	4.95	0.0103	2.07	0.0109	6.27E-03
3.72	3.6	4.19	2.66	2.61	2.05	6.28E-03
3.72	3.6	4.19	2.66	2.61	2.05	6.28E-03
4.44	3.77	3.93	2.46	2.89	2.89	6.30E-03
4.44	3.77	3.93	2.46	2.89	2.89	6.30E-03
4.13	2.42	2.43	0.0103	0.0105	0.0109	6.30E-03
0.011	0.012	0.0117	2.67	2.83	4.68	6.33E-03
0.011	0.012	0.0117	2.67	2.83	4.68	6.33E-03
4.39	4.25	4.27	0.0103	2.07	0.0109	6.33E-03
4.39	4.25	4.27	0.0103	2.07	0.0109	6.33E-03

5.01	2.61	3.46	0.0103	0.0105	0.0109	6.33E-03
2.93	3.23	2.83	4.04	4.1	3.67	6.46E-03
4.52	3.76	3.74	2.53	2.74	2.64	6.55E-03
4.52	3.76	3.74	2.53	2.74	2.64	6.55E-03
3.83	2.49	2.05	0.0103	0.0105	0.0109	6.55E-03
3.83	2.49	2.05	0.0103	0.0105	0.0109	6.55E-03
3.83	2.49	2.05	0.0103	0.0105	0.0109	6.55E-03
0.011	0.012	0.0117	2.67	4.24	2.32	6.55E-03
3.29	2.66	3.26	4.21	4.07	4.2	6.57E-03
3.29	2.66	3.26	4.21	4.07	4.2	6.57E-03
4.27	4.08	4.32	2.85	3.45	2.73	6.62E-03
0.011	0.012	0.0117	2.61	2.15	4.03	6.71E-03
0.011	0.012	0.0117	2.61	2.15	4.03	6.71E-03
2.09	2.98	4.14	0.0103	0.0105	0.0109	6.72E-03
4.14	4.89	5.44	0.0103	0.0105	2.12	6.74E-03
3.89	2.02	2.63	0.0103	0.0105	0.0109	6.74E-03
4.24	4.25	4.2	2.31	3.02	3.19	6.75E-03
4.24	4.25	4.2	2.31	3.02	3.19	6.75E-03
4.8	3.95	4.3	2.03	2.58	2.92	6.78E-03
4.31	3.88	3.92	1.95	0.0105	0.0109	6.91E-03
3.57	3.51	4.3	2.51	2.53	2.37	6.92E-03
3.57	3.51	4.3	2.51	2.53	2.37	6.92E-03
2.76	2.7	2.67	3.23	3.64	3.28	6.94E-03
2.76	2.7	2.67	3.23	3.64	3.28	6.94E-03
4.79	5.05	4.75	4.2	4.41	4.26	7.09E-03
4.79	5.05	4.75	4.2	4.41	4.26	7.09E-03
4.5	4.56	4.9	0.0103	0.0105	2.28	7.14E-03
4.5	4.56	4.9	0.0103	0.0105	2.28	7.14E-03
3.71	3.58	3.39	2.74	2.75	3.06	7.17E-03
3.59	4.03	3.35	2.65	2.21	2.52	7.35E-03
4.53	2.45	2.78	0.0103	0.0105	0.0109	7.36E-03
3.12	3.24	2.85	2.39	2.51	2.49	7.45E-03
3.71	3.87	4.2	2.72	3.19	2.85	7.46E-03
3.71	3.87	4.2	2.72	3.19	2.85	7.46E-03
0.011	0.012	0.0117	2.85	2.45	4.59	7.49E-03
0.011	0.012	0.0117	4.3	2.66	2.3	7.51E-03
4.95	4.39	5.03	0.0103	2.34	0.0109	7.54E-03
3.89	3.79	4.29	2.94	3.01	2.42	7.57E-03
3.87	3.34	3.44	0.0103	0.0105	1.73	7.60E-03
4.2	3.67	3.9	2.98	3.13	2.7	7.66E-03
4.2	3.67	3.9	2.98	3.13	2.7	7.66E-03
4.2	3.67	3.9	2.98	3.13	2.7	7.66E-03
4.78	4.94	4.72	4.01	3.27	3.77	7.68E-03
4.78	4.94	4.72	4.01	3.27	3.77	7.68E-03
4.78	4.94	4.72	4.01	3.27	3.77	7.68E-03
5.31	5.85	4.59	2.91	2.99	3.58	7.73E-03
4.29	3.97	3.53	2.32	2.82	2.69	7.73E-03
4.64	4.09	4.27	3.53	3.34	3.1	7.78E-03
4.64	4.09	4.27	3.53	3.34	3.1	7.78E-03
4.64	4.09	4.27	3.53	3.34	3.1	7.78E-03
5.41	4.21	4.61	2.98	2.94	2.41	7.79E-03
0.011	0.012	0.0117	2.89	2.65	4.86	7.84E-03
0.011	0.012	0.0117	2.89	2.65	4.86	7.84E-03
3.82	3.18	3.4	2.31	2.62	2.36	7.96E-03
3.82	3.18	3.4	2.31	2.62	2.36	7.96E-03
4.75	3.85	4.2	2.05	0.0105	0.0109	7.99E-03
5.19	4.57	5.1	3.86	3.87	3.36	8.04E-03
4.25	5.07	4.41	0.0103	2.23	0.0109	8.06E-03

4.6	4.45	2.23	0.0103	0.0105	0.0109	8.08E-03
5.67	4.73	5.55	3.91	3.78	3.89	8.12E-03
5.67	4.73	5.55	3.91	3.78	3.89	8.12E-03
5.67	4.73	5.55	3.91	3.78	3.89	8.12E-03
3	3.35	3.24	2.53	2.05	2.41	8.13E-03
3.25	3.73	3.8	2.06	2.63	2.51	8.20E-03
4.06	3.16	3.61	5.79	4.95	5.29	8.26E-03
4.06	3.16	3.61	5.79	4.95	5.29	8.26E-03
4.06	3.16	3.61	5.79	4.95	5.29	8.26E-03
4.06	3.16	3.61	5.79	4.95	5.29	8.26E-03
5.12	4.81	5.13	0.0103	2.56	0.0109	8.29E-03
5.12	4.81	5.13	0.0103	2.56	0.0109	8.29E-03
3.38	3.42	3.45	2.85	2.25	2.6	8.33E-03
3.38	3.42	3.45	2.85	2.25	2.6	8.33E-03
3.34	3.89	3.53	2.33	2.52	2.81	8.37E-03
3.34	3.89	3.53	2.33	2.52	2.81	8.37E-03
0.011	0.012	0.0117	4.11	2.64	2.08	8.38E-03
4.55	4.17	4.09	2.31	3.25	2.81	8.46E-03
4.55	4.17	4.09	2.31	3.25	2.81	8.46E-03
4.98	4.98	5.08	2.5	3.82	3.18	8.48E-03
4.98	4.98	5.08	2.5	3.82	3.18	8.48E-03
0.011	0.012	0.0117	2.35	4.54	2.8	8.52E-03
0.011	0.012	0.0117	2.35	4.54	2.8	8.52E-03
4.92	5	4.17	0.0103	2.32	0.0109	8.58E-03
4.92	5	4.17	0.0103	2.32	0.0109	8.58E-03
5.6	4.42	5.6	3.09	3.08	2.12	8.59E-03
5.55	5.55	5.73	2.93	4.09	2.33	8.68E-03
4.55	3.68	4.26	2.81	2.87	2.29	8.77E-03
0.011	0.012	0.0117	2.36	2.58	4.41	8.78E-03
5.19	4.6	4.4	3.34	3.41	2.68	8.79E-03
5.19	4.6	4.4	3.34	3.41	2.68	8.79E-03
3.9	4.54	4.45	0.0103	0.0105	2.17	8.82E-03
3.9	4.54	4.45	0.0103	0.0105	2.17	8.82E-03
4.18	3.84	4.02	2.17	3.04	2.83	8.88E-03
4.18	3.84	4.02	2.17	3.04	2.83	8.88E-03
4.2	4.52	4.17	5.03	4.83	4.86	8.90E-03
4.2	4.52	4.17	5.03	4.83	4.86	8.90E-03
4.73	4.26	4.01	2.19	0.0105	0.0109	8.95E-03
4.73	4.26	4.01	2.19	0.0105	0.0109	8.95E-03
4.54	3.87	4.34	3.1	2.72	3.27	8.95E-03
4.75	3.76	4.75	2.45	2.93	2.78	9.08E-03
3.87	5.18	5	0.0103	2.19	0.0109	9.10E-03
3.87	5.18	5	0.0103	2.19	0.0109	9.10E-03
3.87	5.18	5	0.0103	2.19	0.0109	9.10E-03
4.2	4.56	4.42	0.0103	2.29	0.0109	9.15E-03
4.2	4.56	4.42	0.0103	2.29	0.0109	9.15E-03
0.011	0.012	0.0117	4.77	4.17	2.18	9.17E-03
4.25	4.04	3.69	2.04	2.13	2.98	9.17E-03
4.77	4.04	4.92	0.0103	2.29	0.0109	9.19E-03
4.77	4.04	4.92	0.0103	2.29	0.0109	9.19E-03
5.08	5.79	4.67	2.43	3.03	3.56	9.29E-03
5.08	5.79	4.67	2.43	3.03	3.56	9.29E-03
0.011	0.012	0.0117	4.91	2.72	2.71	9.34E-03
4.05	4.3	4.61	2.24	0.0105	0.0109	9.38E-03
4.05	4.3	4.61	2.24	0.0105	0.0109	9.38E-03
3.89	3.34	4.26	2.58	2.61	2.31	9.40E-03
0.011	0.012	0.0117	4.58	3.31	2.12	9.44E-03
0.011	0.012	0.0117	4.58	3.31	2.12	9.44E-03

3.39	2.97	3.5	2.31	2.6	2.33	9.45E-03
3.39	2.97	3.5	2.31	2.6	2.33	9.45E-03
5.56	4.55	4.93	2.98	3.65	2.71	9.45E-03
5.56	4.55	4.93	2.98	3.65	2.71	9.45E-03
5.48	4.71	4.73	2.54	0.0105	0.0109	9.45E-03
5.09	5.05	4.44	3.61	3.85	3.23	9.46E-03
5.09	5.05	4.44	3.61	3.85	3.23	9.46E-03
5.09	5.05	4.44	3.61	3.85	3.23	9.46E-03
5.09	5.05	4.44	3.61	3.85	3.23	9.46E-03
5.09	5.05	4.44	3.61	3.85	3.23	9.46E-03
2.53	2.76	2.84	2.26	2.2	2.02	9.47E-03
2.53	2.76	2.84	2.26	2.2	2.02	9.47E-03
3.67	3.63	3.83	2.36	2.98	2.13	9.50E-03
3.67	3.63	3.83	2.36	2.98	2.13	9.50E-03
3.81	3.08	3.56	2.36	2.54	2.46	9.50E-03
3.81	3.08	3.56	2.36	2.54	2.46	9.50E-03
5.39	4.54	4.89	3.5	3.87	3.69	9.57E-03
5.39	4.54	4.89	3.5	3.87	3.69	9.57E-03
5.39	4.54	4.89	3.5	3.87	3.69	9.57E-03
4.9	4.88	4.57	3.52	3.43	2.47	9.58E-03
4.9	4.88	4.57	3.52	3.43	2.47	9.58E-03
5.48	5.58	4.09	2.35	0.0105	0.0109	9.66E-03
5.48	5.58	4.09	2.35	0.0105	0.0109	9.66E-03
4.14	4.03	4.16	3.73	3.64	3.87	9.68E-03
3.2	2.91	3.13	2.44	2.61	2.66	9.71E-03
3.2	2.91	3.13	2.44	2.61	2.66	9.71E-03
4.53	4.26	3.86	2.37	3.2	2.37	9.72E-03
4.49	4.5	4.79	3.34	3.36	2.38	9.77E-03
4.49	4.5	4.79	3.34	3.36	2.38	9.77E-03
5.05	4.45	4.22	2.35	0.0105	0.0109	9.85E-03
0.011	0.012	0.0117	2.24	4.59	2.9	9.89E-03
4.57	4.19	4.23	3.34	3.76	3.35	9.93E-03
4.57	4.19	4.23	3.34	3.76	3.35	9.93E-03
4.57	4.19	4.23	3.34	3.76	3.35	9.93E-03
4.57	4.19	4.23	3.34	3.76	3.35	9.93E-03
4.57	4.19	4.23	3.34	3.76	3.35	9.93E-03
0.011	0.012	0.0117	2.33	2.08	4.01	9.94E-03
2.86	3.03	2.9	2.45	2.64	2.36	1.01E-02
2.95	3.31	3.32	2.45	2.67	2.36	1.01E-02
3.66	4.03	4.42	2.61	3.03	2.31	1.02E-02
3.66	4.03	4.42	2.61	3.03	2.31	1.02E-02
3.16	3.14	3.64	2.63	2.49	2.41	1.02E-02
3.78	3.96	3.9	2.09	0.0105	0.0109	1.03E-02
3.99	3.96	4.17	3.39	2.79	2.62	1.03E-02
3.99	3.96	4.17	3.39	2.79	2.62	1.03E-02
3.99	3.96	4.17	3.39	2.79	2.62	1.03E-02
3.99	3.96	4.17	3.39	2.79	2.62	1.03E-02
4.18	5.17	4.39	0.0103	2.34	0.0109	1.04E-02
4.18	5.17	4.39	0.0103	2.34	0.0109	1.04E-02
4.18	5.17	4.39	0.0103	2.34	0.0109	1.04E-02
3.76	3.83	3.63	2.75	2.87	2.06	1.04E-02
3.76	3.83	3.63	2.75	2.87	2.06	1.04E-02
5.06	4.82	4.74	0.0103	2.63	0.0109	1.05E-02
5.06	4.82	4.74	0.0103	2.63	0.0109	1.05E-02
0.011	0.012	0.0117	4.59	2.62	2.37	1.06E-02
4.9	4.84	4.12	3.36	2.97	3.5	1.06E-02
4.9	4.84	4.12	3.36	2.97	3.5	1.06E-02
2.66	4.54	2.29	0.0103	0.0105	0.0109	1.06E-02

4.98	4.25	4.62	2.72	3.6	2.94	1.06E-02
4.98	4.25	4.62	2.72	3.6	2.94	1.06E-02
4.72	4.84	4.22	3.06	3.71	3	1.07E-02
4.72	4.84	4.22	3.06	3.71	3	1.07E-02
4.33	5.02	4.94	3.48	3.72	3.83	1.08E-02
4.33	5.02	4.94	3.48	3.72	3.83	1.08E-02
3.97	4.44	4.23	3.21	2.07	2.27	1.08E-02
3.97	4.44	4.23	3.21	2.07	2.27	1.08E-02
2.63	2.55	2.83	4.11	4.17	3.37	1.09E-02
3.93	3.48	4.13	2.8	2.57	3.03	1.10E-02
0.011	0.012	0.0117	2.08	4.8	3.88	1.10E-02
5.38	4.32	5.35	2.83	3.6	2.95	1.11E-02
5.38	4.32	5.35	2.83	3.6	2.95	1.11E-02
5.15	4.55	4.19	3.21	3.47	2.95	1.11E-02
4.96	4.4	3.81	0.0103	2.24	0.0109	1.11E-02
4.96	4.4	3.81	0.0103	2.24	0.0109	1.11E-02
4.7	4.73	5.1	2.62	3.82	2.78	1.12E-02
4.7	4.73	5.1	2.62	3.82	2.78	1.12E-02
3.72	3.12	3.31	2.67	2.51	2.47	1.13E-02
3.72	3.12	3.31	2.67	2.51	2.47	1.13E-02
5.14	3.96	5.01	2.46	3.03	3.03	1.13E-02
5.14	3.96	5.01	2.46	3.03	3.03	1.13E-02
5.14	3.96	5.01	2.46	3.03	3.03	1.13E-02
4.27	4.24	4.2	3.38	3.5	2.76	1.13E-02
4.27	4.24	4.2	3.38	3.5	2.76	1.13E-02
4.97	5.14	4.72	2.7	3.93	2.96	1.14E-02
4.97	5.14	4.72	2.7	3.93	2.96	1.14E-02
4.76	4.98	4.69	2.65	0.0105	0.0109	1.14E-02
4.76	4.98	4.69	2.65	0.0105	0.0109	1.14E-02
3.93	3.91	3.63	0.0103	2.1	0.0109	1.14E-02
4.13	3.84	3.34	2.23	2.79	2.07	1.14E-02
4.13	3.84	3.34	2.23	2.79	2.07	1.14E-02
4.33	3.99	3.19	2.13	2.49	2.12	1.14E-02
4.33	3.99	3.19	2.13	2.49	2.12	1.14E-02
5.01	4.9	3.66	2.6	2.43	2.7	1.15E-02
5.01	4.9	3.66	2.6	2.43	2.7	1.15E-02
3.43	3.54	3.02	2.68	2.56	2.6	1.15E-02
3.43	3.54	3.02	2.68	2.56	2.6	1.15E-02
3.74	3.5	3.21	2.57	2.87	2.53	1.15E-02
4.29	4.4	4.31	0.0103	2.41	0.0109	1.17E-02
0.011	0.012	0.0117	2.26	4.49	2.54	1.17E-02
4.06	4.5	3.73	0.0103	2.2	0.0109	1.17E-02
4.67	4.58	5.15	3.71	2.71	2.48	1.17E-02
4.67	4.58	5.15	3.71	2.71	2.48	1.17E-02
4.26	4.62	4.54	0.0103	2.48	0.0109	1.18E-02
4.26	4.62	4.54	0.0103	2.48	0.0109	1.18E-02
3.94	4.21	3.67	0.0103	2.16	0.0109	1.19E-02
4.24	3.52	4.77	2.6	2.61	2.56	1.19E-02
4.52	3.93	3.94	2.25	0.0105	0.0109	1.20E-02
3.19	3.58	3.25	2.79	2.37	2.3	1.20E-02
3.76	3.46	4.47	2.73	2.35	2.37	1.20E-02
0.011	0.012	0.0117	1.86	4.41	3.57	1.21E-02
5.02	4.3	3.96	2.13	3.12	2.45	1.21E-02
3.75	4.18	5.06	2.2	0.0105	0.0109	1.22E-02
3.75	4.18	5.06	2.2	0.0105	0.0109	1.22E-02
3.5	4.26	3.61	2.65	2.62	2.86	1.23E-02
4.72	3.62	4.09	0.0103	2.17	0.0109	1.23E-02
4.72	3.62	4.09	0.0103	2.17	0.0109	1.23E-02

4.275	3.88	2.98	1.82	0.0105	0.0109	1.23E-02
3.7	3.43	4	0.0103	0.0105	2.05	1.25E-02
5.17	4.7	4.88	3.09	4.06	3.57	1.25E-02
5.17	4.7	4.88	3.09	4.06	3.57	1.25E-02
5.17	4.7	4.88	3.09	4.06	3.57	1.25E-02
5.17	4.7	4.88	3.09	4.06	3.57	1.25E-02
5.17	4.7	4.88	3.09	4.06	3.57	1.25E-02
3.89	3.25	3.99	2.51	2.8	2.31	1.26E-02
3.89	3.25	3.99	2.51	2.8	2.31	1.26E-02
5.11	4.29	4.64	2.59	3.59	2.6	1.27E-02
3.58	3.03	3.13	2.52	2.51	2.25	1.27E-02
4.04	3.68	3.73	2.8	3.19	3.21	1.27E-02
4.04	3.68	3.73	2.8	3.19	3.21	1.27E-02
4.04	3.68	3.73	2.8	3.19	3.21	1.27E-02
4.04	3.68	3.73	2.8	3.19	3.21	1.27E-02
3.99	4.31	5.11	3.18	2.86	2.87	1.27E-02
3.99	4.31	5.11	3.18	2.86	2.87	1.27E-02
4.89	4.23	4.31	2.92	3.49	3.45	1.28E-02
4.89	4.23	4.31	2.92	3.49	3.45	1.28E-02
3.25	4.45	3.88	2.42	2.22	2.41	1.28E-02
4.91	4.63	5.06	2.75	0.0105	0.0109	1.29E-02
5.11	4.29	4.64	2.59	0.0105	0.0109	1.29E-02
4.16	3.69	5.06	2.78	2.29	2.21	1.30E-02
4.26	3.99	4.94	2.39	0.0105	0.0109	1.30E-02
4.77	5.34	4.82	2.8	0.0105	0.0109	1.31E-02
4.56	4.49	5.06	3.54	3.86	3.11	1.31E-02
4.56	4.49	5.06	3.54	3.86	3.11	1.31E-02
4.26	3.48	4.22	2.08	2.92	2.48	1.31E-02
5.22	5.27	4.55	0.0103	2.8	0.0109	1.32E-02
5.22	5.27	4.55	0.0103	2.8	0.0109	1.32E-02
3.63	4.02	3.6	3.08	2.77	2.42	1.32E-02
4.32	3.71	4.28	0.0103	0.0105	2.29	1.32E-02
4.98	4.68	4.96	0.0103	2.78	0.0109	1.32E-02
4.98	4.68	4.96	0.0103	2.78	0.0109	1.32E-02
4.64	4.17	3.21	2	0.0105	0.0109	1.32E-02
4.64	4.17	3.21	2	0.0105	0.0109	1.32E-02
3.66	4.16	4.78	0.0103	2.25	0.0109	1.34E-02
3.66	4.16	4.78	0.0103	2.25	0.0109	1.34E-02
4.12	3.69	4.35	0.0103	0.0105	2.27	1.34E-02
3.82	3.45	3.82	2.46	2.75	3.09	1.34E-02
3.82	3.45	3.82	2.46	2.75	3.09	1.34E-02
3.82	3.45	3.82	2.46	2.75	3.09	1.34E-02
3.68	3.31	4.2	0.0103	0.0105	2.03	1.34E-02
3.68	3.31	4.2	0.0103	0.0105	2.03	1.34E-02
0.011	0.012	0.0117	2.96	4.57	2	1.35E-02
0.011	0.012	0.0117	2.96	4.57	2	1.35E-02
3.7	3.81	4	3.11	3.36	2.84	1.35E-02
5.11	4.67	4.56	2.72	0.0105	0.0109	1.36E-02
4.52	4.42	4.17	3.42	2.67	3.48	1.36E-02
4.52	4.42	4.17	3.42	2.67	3.48	1.36E-02
4.55	3.49	4.55	2.23	0.0105	0.0109	1.37E-02
3.01	3.33	3.64	2.61	2.52	2.53	1.37E-02
3.01	3.33	3.64	2.61	2.52	2.53	1.37E-02
5.25	5.56	4.87	3.61	3.99	2.72	1.38E-02
5.25	5.56	4.87	3.61	3.99	2.72	1.38E-02
3.12	2.69	2.93	2.14	2.41	2.33	1.38E-02
4.33	4.22	3.76	0.0103	2.33	0.0109	1.38E-02
4.33	4.22	3.76	0.0103	2.33	0.0109	1.38E-02

4.71	4.54	4.7	0.0103	2.69	0.0109	1.38E-02
4.13	4.81	4.28	3.01	3.48	3.48	1.39E-02
3.99	4.4	4.74	0.0103	2.47	0.0109	1.39E-02
3.99	4.4	4.74	0.0103	2.47	0.0109	1.39E-02
4.63	5.12	4.55	2.22	3.64	2.82	1.39E-02
4.63	5.12	4.55	2.22	3.64	2.82	1.39E-02
4.71	2.04	4.94	0.0103	0.0105	0.0109	1.40E-02
4.27	4.05	4.31	2.38	3.43	2.89	1.40E-02
4.27	4.05	4.31	2.38	3.43	2.89	1.40E-02
4.94	3.45	4.59	2.23	2.49	2.52	1.41E-02
4.58	3.31	3.87	0.0103	2.06	0.0109	1.42E-02
4.58	3.31	3.87	0.0103	2.06	0.0109	1.42E-02
4.63	4.47	4.42	0.0103	2.62	0.0109	1.42E-02
3.8	3.73	3.79	3.03	3.35	3.42	1.42E-02
3.8	3.73	3.79	3.03	3.35	3.42	1.42E-02
3.8	3.73	3.79	3.03	3.35	3.42	1.42E-02
4.52	4.19	4.87	0.0103	2.59	0.0109	1.43E-02
4.52	4.19	4.87	0.0103	2.59	0.0109	1.43E-02
4.52	4.19	4.87	0.0103	2.59	0.0109	1.43E-02
4.93	4.34	4.81	3.19	3.91	3.11	1.44E-02
4.93	4.34	4.81	3.19	3.91	3.11	1.44E-02
4.93	4.34	4.81	3.19	3.91	3.11	1.44E-02
5.05	5.4	4.22	3.49	2.55	3.12	1.44E-02
5.05	5.4	4.22	3.49	2.55	3.12	1.44E-02
4.49	4.92	4.44	2.38	2.06	0.0109	1.44E-02
4.93	4.53	4.68	0.0103	2.74	0.0109	1.44E-02
4.93	4.53	4.68	0.0103	2.74	0.0109	1.44E-02
3.99	3.96	3.6	0.0103	2.23	0.0109	1.45E-02
4.94	3.45	4.59	2.23	0.0105	0.0109	1.45E-02
4.79	5.06	4.84	2.29	2.49	0.0109	1.45E-02
4.79	5.06	4.84	2.29	2.49	0.0109	1.45E-02
4.59	4.61	4.57	0.0103	2.69	0.0109	1.45E-02
4.59	4.61	4.57	0.0103	2.69	0.0109	1.45E-02
4.59	4.61	4.57	0.0103	2.69	0.0109	1.45E-02
4.93	4.98	4.7	0.0103	2.85	0.0109	1.46E-02
4.93	4.98	4.7	0.0103	2.85	0.0109	1.46E-02
2.99	3.71	3.44	2.59	2.46	2.29	1.48E-02
4.84	4.67	4.16	2.97	2.49	3.58	1.48E-02
3.99	3.55	3.83	3	3.3	3.16	1.48E-02
3.99	3.55	3.83	3	3.3	3.16	1.48E-02
4.01	3.57	4.1	2.25	0.0105	0.0109	1.48E-02
4.5	4.47	4.95	0.0103	2.7	0.0109	1.48E-02
4.5	4.47	4.95	0.0103	2.7	0.0109	1.48E-02
4.85	5.43	4.65	3.86	3.04	2.57	1.48E-02
4.12	3.92	3.91	2.34	0.0105	0.0109	1.48E-02
4.12	3.92	3.91	2.34	0.0105	0.0109	1.48E-02
4.58	3.84	4.37	3.46	2.98	2.91	1.49E-02
4.58	3.84	4.37	3.46	2.98	2.91	1.49E-02
5.35	4.59	5	0.0103	2.15	2.6	1.49E-02
5.35	4.61	4.87	2.86	0.0105	0.0109	1.50E-02
5.35	4.61	4.87	2.86	0.0105	0.0109	1.50E-02
3.97	3.85	3.8	2.52	3.33	2.78	1.50E-02
3.97	3.85	3.8	2.52	3.33	2.78	1.50E-02
4.2	4.57	3.72	2.4	3.22	2.61	1.51E-02
4.2	4.57	3.72	2.4	3.22	2.61	1.51E-02
4.49	4.41	4.1	3.46	3.06	2.39	1.51E-02
3.36	2.91	3.51	2.15	2.58	2.37	1.51E-02
3.36	2.91	3.51	2.15	2.58	2.37	1.51E-02

3.98	4.03	4.3	3.32	2.2	2.4	1.51E-02
3.8	4.27	3.82	0.0103	2.31	0.0109	1.51E-02
3.8	4.27	3.82	0.0103	2.31	0.0109	1.51E-02
3.4	3.75	3.95	0.0103	2.15	0.0109	1.52E-02
3.4	3.75	3.95	0.0103	2.15	0.0109	1.52E-02
4.19	3.36	3.6	2.71	2.71	2.72	1.52E-02
4.19	3.36	3.6	2.71	2.71	2.72	1.52E-02
5.55	4.42	5.16	3.6	3.72	3.05	1.53E-02
5.55	4.42	5.16	3.6	3.72	3.05	1.53E-02
0.011	2.14	0.0117	4.54	4.47	3.23	1.53E-02
5.06	5.04	4.25	3.73	2.88	2.71	1.54E-02
5.06	5.04	4.25	3.73	2.88	2.71	1.54E-02
3.76	3.88	4.01	0.0103	0.0105	2.3	1.54E-02
4.18	4.26	3.87	0.0103	2.42	0.0109	1.55E-02
4.18	4.26	3.87	0.0103	2.42	0.0109	1.55E-02
4.81	4.73	4.22	3.44	3.92	3.5	1.55E-02
4.81	4.73	4.22	3.44	3.92	3.5	1.55E-02
4.37	5.03	4.94	0.0103	2.79	0.0109	1.55E-02
4.37	5.03	4.94	0.0103	2.79	0.0109	1.55E-02
4.07	3.76	3.68	2.7	3.29	3	1.56E-02
4.07	3.76	3.68	2.7	3.29	3	1.56E-02
4.1	3.71	4.44	0.0103	0.0105	2.37	1.57E-02
4.1	3.71	4.44	0.0103	0.0105	2.37	1.57E-02
4.08	4.71	3.73	2.97	3.09	2.66	1.57E-02
4.08	4.71	3.73	2.97	3.09	2.66	1.57E-02
3.44	3.43	3.91	2.69	2.83	2.17	1.58E-02
3.44	3.43	3.91	2.69	2.83	2.17	1.58E-02
4.49	4.51	4.03	2.25	2.86	3.42	1.58E-02
4.49	4.51	4.03	2.25	2.86	3.42	1.58E-02
3.89	3.49	3.81	2.63	3.2	2.88	1.58E-02
4.38	4.99	5.09	2.9	3.84	3.47	1.58E-02
4.38	4.99	5.09	2.9	3.84	3.47	1.58E-02
4.21	4.77	5.08	0.0103	0.0105	2.72	1.59E-02
4.51	3.85	4.77	2.36	3.33	2.66	1.59E-02
4.51	3.85	4.77	2.36	3.33	2.66	1.59E-02
4.83	4.08	5.03	2.14	3.4	2.8	1.59E-02
4.83	4.08	5.03	2.14	3.4	2.8	1.59E-02
3.59	3.58	3.66	3.35	3	2.96	1.60E-02
4.29	4.4	4.31	2.6	0.0105	0.0109	1.61E-02
4.29	4.4	4.31	2.6	0.0105	0.0109	1.61E-02
4.29	4.4	4.31	2.6	0.0105	0.0109	1.61E-02
3.8	4.06	4.56	2.13	3.05	2.9	1.62E-02
3.8	4.06	4.56	2.13	3.05	2.9	1.62E-02
3.65	4.14	4.29	0.0103	2.37	0.0109	1.63E-02
4.63	3.72	4.14	2.99	3.19	3.09	1.63E-02
4.63	3.72	4.14	2.99	3.19	3.09	1.63E-02
4.63	3.72	4.14	2.99	3.19	3.09	1.63E-02
3.63	3.32	3.64	2.11	0.0105	0.0109	1.63E-02
3.63	3.32	3.64	2.11	0.0105	0.0109	1.63E-02
3.63	3.32	3.64	2.11	0.0105	0.0109	1.63E-02
4.12	4.79	3.8	2.53	3.22	2.6	1.64E-02
4.12	4.79	3.8	2.53	3.22	2.6	1.64E-02
5.61	4.75	4.79	3.16	3.87	2.6	1.64E-02
5.61	4.75	4.79	3.16	3.87	2.6	1.64E-02
3.4	4.49	4	0.0103	0.0105	2.24	1.65E-02
4.01	3.62	3.45	2.15	2.44	2.98	1.65E-02
5.05	5.56	5.31	4.12	3.88	2.81	1.65E-02
5.05	5.56	5.31	4.12	3.88	2.81	1.65E-02

3.55	3.27	3.47	3.05	3.13	3.08	1.65E-02
5.5	5.09	4.79	0.0103	3.05	0.0109	1.66E-02
5.04	4.66	4.73	3.09	4.07	3.03	1.67E-02
5.17	5.69	4.82	3.73	3.93	2.75	1.67E-02
5.17	5.69	4.82	3.73	3.93	2.75	1.67E-02
4.15	3.57	4.24	2.92	2.96	2.18	1.68E-02
4.15	3.57	4.24	2.92	2.96	2.18	1.68E-02
2.04	0.012	0.0117	3.13	3.46	3.93	1.69E-02
4.275	3.695	3.285	0.0103	0.0105	2.15	1.70E-02
4.24	5.38	3.86	2.39	2.38	2.92	1.70E-02
3.83	3.74	4.21	2.36	0.0105	0.0109	1.70E-02
3.83	3.74	4.21	2.36	0.0105	0.0109	1.70E-02
4.54	3.94	4.15	3.25	3.49	3.55	1.70E-02
4.54	3.94	4.15	3.25	3.49	3.55	1.70E-02
4.85	4.96	4.73	2.6	3.99	3.1	1.72E-02
4.85	4.96	4.73	2.6	3.99	3.1	1.72E-02
4.85	4.96	4.73	2.6	3.99	3.1	1.72E-02
3.7	3.19	3.74	0.0103	2.11	0.0109	1.72E-02
3.7	3.19	3.74	0.0103	2.11	0.0109	1.72E-02
4.96	5.58	4.78	3.99	3.12	2.57	1.72E-02
4.07	3.95	4.12	2.47	0.0105	0.0109	1.73E-02
5.28	5.44	4.35	3.11	3.85	2.93	1.74E-02
5.28	5.44	4.35	3.11	3.85	2.93	1.74E-02
5.28	5.44	4.35	3.11	3.85	2.93	1.74E-02
3.57	3.35	4.05	0.0103	0.0105	2.17	1.74E-02
3.57	3.35	4.05	0.0103	0.0105	2.17	1.74E-02
3.74	3.91	3.83	2.34	0.0105	0.0109	1.74E-02
4.62	4.2	3.83	2.51	0.0105	0.0109	1.75E-02
4.62	4.2	3.83	2.51	0.0105	0.0109	1.75E-02
3.47	3.63	3.36	0.0103	0.0105	2.13	1.76E-02
3.47	3.63	3.36	0.0103	0.0105	2.13	1.76E-02
4.21	5.18	5.15	0.0103	2.85	0.0109	1.76E-02
4.62	3.96	4.78	0.0103	2.65	0.0109	1.76E-02
4.62	3.96	4.78	0.0103	2.65	0.0109	1.76E-02
3.66	4.16	4.78	2.43	0.0105	0.0109	1.77E-02
4.36	3.83	5.19	3	2.93	2.53	1.77E-02
4.36	3.83	5.19	3	2.93	2.53	1.77E-02
5.56	4.55	4.93	2.98	0.0105	0.0109	1.78E-02
4.82	4.57	4.81	2.4	2.42	0.0109	1.78E-02
4.82	4.57	4.81	2.4	2.42	0.0109	1.78E-02
4.56	4.73	3.69	0.0103	0.0105	2.52	1.78E-02
5.07	5.26	5.14	3.17	0.0105	0.0109	1.78E-02
4.12	3.74	3.97	0.0103	2.41	0.0109	1.78E-02
4.86	4.67	4.43	2.72	3.85	2.66	1.79E-02
3.95	5.17	5.07	2.66	3.41	2.45	1.79E-02
4.55	3.49	4.55	0.0103	2.41	0.0109	1.80E-02
3.02	3.6	3.78	2.05	0.0105	0.0109	1.80E-02
4.86	5.65	5.16	2.66	2.57	0.0109	1.80E-02
4.86	5.65	5.16	2.66	2.57	0.0109	1.80E-02
3.23	4.05	3.57	0.0103	2.14	0.0109	1.80E-02
3.23	4.05	3.57	0.0103	2.14	0.0109	1.80E-02
3.23	4.05	3.57	0.0103	2.14	0.0109	1.80E-02
5.21	3.98	4.41	3.31	2.92	2.94	1.81E-02
5.21	3.98	4.41	3.31	2.92	2.94	1.81E-02
2.13	0.012	0.0117	3.67	3.46	3.3	1.81E-02
2.13	0.012	0.0117	3.67	3.46	3.3	1.81E-02
4.39	4.04	3.65	2.06	3.12	2.58	1.82E-02
3.23	3.77	3.35	2.09	0.0105	0.0109	1.82E-02

4.15	4.17	3.58	2.29	2.78	3.16	1.83E-02
4.15	4.17	3.58	2.29	2.78	3.16	1.83E-02
3.62	3.96	4.01	0.0103	2.37	0.0109	1.83E-02
5.05	4.45	4.22	3.03	3.49	2.31	1.83E-02
3.18	4.23	3.56	2.34	2.45	2.56	1.83E-02
3.18	4.23	3.56	2.34	2.45	2.56	1.83E-02
0.011	2.16	0.0117	3.17	3.76	3.98	1.83E-02
4.89	3.76	4.44	0.0103	2.56	0.0109	1.84E-02
4.89	3.76	4.44	0.0103	2.56	0.0109	1.84E-02
4	3.77	3.95	0.0103	2.42	0.0109	1.85E-02
3.48	4.21	4.41	0.0103	2.39	0.0109	1.85E-02
4.81	4.04	4.95	2.44	2.07	0.0109	1.86E-02
3.7	3.63	4.17	0.0103	2.34	0.0109	1.86E-02
3.7	3.63	4.17	0.0103	2.34	0.0109	1.86E-02
3.57	4.23	3.85	0.0103	2.36	0.0109	1.86E-02
4.9	5.07	5.25	2.72	4.19	3.22	1.86E-02
4.9	5.07	5.25	2.72	4.19	3.22	1.86E-02
4.26	4.62	4.54	0.0103	2.48	2.08	1.88E-02
4.75	4.27	5.86	0.0103	0.0105	2.83	1.89E-02
3.62	3.96	4.01	2.39	0.0105	0.0109	1.89E-02
3.59	2.95	3.37	2.24	2.48	2.65	1.89E-02
4.01	3.35	4.07	0.0103	2.3	0.0109	1.90E-02
4.01	3.35	4.07	0.0103	2.3	0.0109	1.90E-02
3.83	4.35	3.57	0.0103	2.37	0.0109	1.90E-02
5.07	4.6	5.31	0.0103	3.07	0.0109	1.90E-02
5.34	4.37	4.77	3.05	3.66	2.33	1.90E-02
5.34	4.37	4.77	3.05	3.66	2.33	1.90E-02
3.68	3.31	4.2	0.0103	2.23	0.0109	1.91E-02
3.68	3.31	4.2	0.0103	2.23	0.0109	1.91E-02
4.54	4.69	4.22	0.0103	2.78	0.0109	1.91E-02
4.13	4.6	4.29	0.0103	2.69	0.0109	1.91E-02
3.04	3.62	3.19	2.65	1.97	2.22	1.91E-02
2.88	2.86	2.92	2.26	2.56	2.6	1.91E-02
3.75	4.14	3.87	2.38	2.89	3.27	1.91E-02
3.75	4.14	3.87	2.38	2.89	3.27	1.91E-02
3.75	4.14	3.87	2.38	2.89	3.27	1.91E-02
3.4	3.95	3.4	0.0103	2.19	0.0109	1.91E-02
3.57	4.43	3.24	0.0103	0.0105	2.15	1.92E-02
3.57	4.43	3.24	0.0103	0.0105	2.15	1.92E-02
3.62	4.11	3.9	0.0103	2.4	0.0109	1.92E-02
4.17	4.63	3.69	0.0103	2.51	0.0109	1.93E-02
4.17	4.63	3.69	0.0103	2.51	0.0109	1.93E-02
4.17	4.63	3.69	0.0103	2.51	0.0109	1.93E-02
2.15	0.012	0.0117	4.1	3.05	3.89	1.94E-02
4.03	4.1	4.54	0.0103	2.62	0.0109	1.94E-02
4.03	3.21	4.58	0.0103	2.24	0.0109	1.94E-02
4.36	4	3.86	0.0103	2.53	0.0109	1.95E-02
3.7	3.48	3.18	2.78	2.96	2.69	1.95E-02
3.7	3.48	3.18	2.78	2.96	2.69	1.95E-02
4.3	4.42	4.25	3.51	3.21	2.38	1.95E-02
4.3	4.42	4.25	3.51	3.21	2.38	1.95E-02
0.011	0.012	2.26	3.69	3.41	3.74	1.96E-02
3.67	3.67	3.44	0.0103	2.26	0.0109	1.98E-02
3.67	3.67	3.44	0.0103	2.26	0.0109	1.98E-02
4.21	4.76	3.99	2.09	3.37	2.56	1.98E-02
3.32	3.67	3.13	2.53	2.64	2.86	1.99E-02
3.32	3.67	3.13	2.53	2.64	2.86	1.99E-02
4.45	4.42	4.88	0.0103	2.87	0.0109	1.99E-02

5.11	4.29	4.64	2.2	3.59	2.99	1.99E-02
5.11	4.29	4.64	2.2	3.59	2.99	1.99E-02
4.61	3.92	4.98	3.43	2.85	2.41	2.00E-02
4.61	3.92	4.98	3.43	2.85	2.41	2.00E-02
5.18	4.6	4.97	2.22	3.9	2.58	2.00E-02
4.9	4.88	4.57	3.54	3.72	2.44	2.01E-02
4.7	3.72	4.33	3.29	3.02	3.11	2.01E-02
4.7	3.72	4.33	3.29	3.02	3.11	2.01E-02
4.27	3.66	5.05	2.88	2.74	2.1	2.01E-02
4.27	3.66	5.05	2.88	2.74	2.1	2.01E-02
3.31	3.5	4.13	2.47	2.86	2.43	2.01E-02
3.29	3.74	4.38	0.0103	0.0105	2.26	2.01E-02
4.43	4.23	4.08	0.0103	2.68	0.0109	2.02E-02
3.99	4.58	4.11	0.0103	2.64	0.0109	2.03E-02
3.99	4.58	4.11	0.0103	2.64	0.0109	2.03E-02
4.69	4.5	4.43	3.7	3.79	2.92	2.03E-02
4.69	4.5	4.43	3.7	3.79	2.92	2.03E-02
5.25	5.12	5.42	3.62	4.66	3.91	2.03E-02
5.25	5.12	5.42	3.62	4.66	3.91	2.03E-02
3.94	4.56	3.72	0.0103	0.0105	2.5	2.03E-02
3.94	4.56	3.72	0.0103	0.0105	2.5	2.03E-02
4.47	4.58	3.62	2.56	0.0105	0.0109	2.03E-02
4.38	4.89	4.13	2.78	0.0105	0.0109	2.05E-02
3.36	3.84	3.98	2.89	3.05	3.06	2.06E-02
3.36	3.84	3.98	2.89	3.05	3.06	2.06E-02
3.56	3.52	3.8	0.0103	2.3	0.0109	2.06E-02
3.56	3.52	3.8	0.0103	2.3	0.0109	2.06E-02
4.78	4.09	4.09	3.49	2.89	2.52	2.06E-02
2.52	0.012	0.0117	3.48	4.74	4.97	2.06E-02
4.7	3.62	4.86	2.62	3.16	2.44	2.06E-02
5.21	4.57	4.68	2.63	3.94	3.08	2.06E-02
5.21	4.57	4.68	2.63	3.94	3.08	2.06E-02
4.43	3.06	3.53	0.0103	2.09	0.0109	2.07E-02
3.91	4.51	3.88	2.56	0.0105	0.0109	2.07E-02
4.69	4.52	4.2	2.88	3.66	2.35	2.07E-02
4.69	4.52	4.2	2.88	3.66	2.35	2.07E-02
4.64	4.66	4.05	2.26	2.33	0.0109	2.08E-02
3.88	4.06	3.99	2.36	3.39	2.82	2.08E-02
4.61	3.77	4.11	2.26	3.3	2.34	2.09E-02
4.61	3.77	4.11	2.26	3.3	2.34	2.09E-02
4.45	4.63	3.07	0.0103	2.24	0.0109	2.09E-02
4.45	4.63	3.07	0.0103	2.24	0.0109	2.09E-02
4.87	5.07	4.57	2.21	3.69	3.37	2.09E-02
4.26	3.99	4.94	0.0103	0.0105	2.71	2.09E-02
3.62	4.06	3.78	2.42	0.0105	0.0109	2.09E-02
3.62	4.06	3.78	2.42	0.0105	0.0109	2.09E-02
3.36	3.51	3.7	0.0103	2.24	0.0109	2.09E-02
5.63	4.94	5.68	3.34	4.52	3.45	2.09E-02
5.63	4.94	5.68	3.34	4.52	3.45	2.09E-02
5.63	4.94	5.68	3.34	4.52	3.45	2.09E-02
4.6	3.9	3.45	0.0103	2.39	0.0109	2.10E-02
3.92	2.97	3.95	0.0103	2.15	0.0109	2.10E-02
2.92	3.22	3.11	3.44	3.73	3.93	2.10E-02
4.66	3.95	4.86	0.0103	2.78	0.0109	2.10E-02
4.66	3.95	4.86	0.0103	2.78	0.0109	2.10E-02
2.01	0.012	0.0117	3.08	3.1	3.25	2.10E-02
4.36	4.06	3.76	0.0103	2.56	0.0109	2.10E-02
5.34	5.45	5.57	0.0103	3.49	0.0109	2.11E-02

2.18	0.012	0.0117	3.48	3.48	3.27	2.11E-02
3.76	3.46	4.47	0.0103	0.0105	2.37	2.11E-02
4.12	3.14	3.32	2.12	0.0105	0.0109	2.13E-02
4.12	3.14	3.32	2.12	0.0105	0.0109	2.13E-02
5.35	5.11	4.44	0.0103	3.11	0.0109	2.14E-02
4.17	3.52	3.51	0.0103	2.33	0.0109	2.14E-02
4.52	4.79	4.12	2.3	3.62	2.48	2.14E-02
4.52	4.79	4.12	2.3	3.62	2.48	2.14E-02
3.66	3.98	3.84	0.0103	2.45	0.0109	2.14E-02
3.66	3.98	3.84	0.0103	2.45	0.0109	2.14E-02
3.8	4.92	4.06	0.0103	2.59	0.0109	2.14E-02
3.8	4.92	4.06	0.0103	2.59	0.0109	2.14E-02
3.58	3.81	3.56	2.34	0.0105	0.0109	2.14E-02
4.94	3.45	4.59	0.0103	0.0105	2.52	2.15E-02
4.42	3.76	3.94	2.55	0.0105	0.0109	2.15E-02
2.41	0.012	0.0117	3.77	4.23	3.5	2.17E-02
2.41	0.012	0.0117	3.77	4.23	3.5	2.17E-02
5.5	5.09	4.79	0.0103	3.05	2.17	2.17E-02
4.26	3.56	4.23	2.9	3.3	2.72	2.17E-02
4.26	3.56	4.23	2.9	3.3	2.72	2.17E-02
4	3.8	4.09	0.0103	2.55	0.0109	2.18E-02
4	3.8	4.09	0.0103	2.55	0.0109	2.18E-02
4.37	4.1	4.53	0.0103	0.0105	2.78	2.18E-02
3.61	4.1	4.51	0.0103	2.54	0.0109	2.18E-02
3.61	4.1	4.51	0.0103	2.54	0.0109	2.18E-02
3.44	4.37	4.25	0.0103	2.48	0.0109	2.18E-02
3.44	4.37	4.25	0.0103	2.48	0.0109	2.18E-02
3.84	3.91	4.73	0.0103	0.0105	2.58	2.18E-02
2.26	0.012	0.0117	4.37	3.53	3.31	2.18E-02
3.24	3.51	3.92	0.0103	2.24	0.0109	2.19E-02
3.24	3.51	3.92	0.0103	2.24	0.0109	2.19E-02
4.96	4.65	4.83	2.44	2.54	3.97	2.19E-02
4.96	4.65	4.83	2.44	2.54	3.97	2.19E-02
0.011	2.18	0.0117	4.01	3.09	3.52	2.19E-02
4.25	4.07	4.46	0.0103	2.74	0.0109	2.19E-02
3.67	4.12	4.35	3.23	3.22	2.64	2.19E-02
4.81	3.93	4.67	0.0103	2.8	0.0109	2.19E-02
4.81	3.93	4.67	0.0103	2.8	0.0109	2.19E-02
4.81	3.93	4.67	0.0103	2.8	0.0109	2.19E-02
3.85	2.83	3.86	0.0103	0.0105	2.09	2.20E-02
3.99	3.69	3.25	2.91	2.81	2.49	2.21E-02
3.99	3.69	3.25	2.91	2.81	2.49	2.21E-02
3.98	3.89	3.57	0.0103	2.45	0.0109	2.21E-02
5.28	4.45	4.35	0.0103	2.94	0.0109	2.21E-02
4.05	3.11	3.11	0.0103	2.06	0.0109	2.21E-02
4.98	4.96	4.44	2.54	3.95	2.88	2.22E-02
3.38	3.36	3.43	0.0103	2.2	0.0109	2.22E-02
3.38	3.36	3.43	0.0103	2.2	0.0109	2.22E-02
3.45	4.49	4.4	0.0103	2.52	0.0109	2.22E-02
4.11	4.11	4.6	2.74	0.0105	0.0109	2.22E-02
4.01	3.57	4.1	0.0103	0.0105	2.49	2.22E-02
4.14	3.73	4.47	0.0103	2.61	0.0109	2.22E-02
4.71	3.39	4.47	0.0103	2.5	0.0109	2.22E-02
4.71	3.39	4.47	0.0103	2.5	0.0109	2.22E-02
5.35	4.61	4.87	2.86	2.25	0.0109	2.23E-02
4.77	5.34	4.82	2.8	2.42	0.0109	2.23E-02
4.72	4.62	5.48	3.35	4.04	3.01	2.23E-02
4.72	4.62	5.48	3.35	4.04	3.01	2.23E-02

2.76	3.22	3.02	2.48	2.57	2.36	2.24E-02
3.67	4.18	4.36	0.0103	0.0105	2.59	2.24E-02
3.67	4.18	4.36	0.0103	0.0105	2.59	2.24E-02
3.14	4.53	3.76	2.24	0.0105	0.0109	2.24E-02
3.66	3.66	4.58	0.0103	2.45	0.0109	2.24E-02
3.66	3.66	4.58	0.0103	2.45	0.0109	2.24E-02
2.79	3.42	2.65	2.09	2.12	2.08	2.25E-02
3.96	4.03	3.28	2.27	2.52	3	2.25E-02
3.51	4.25	3.63	2.5	3.06	2.79	2.25E-02
3.1	3.09	3.21	0.0103	0.0105	2.04	2.26E-02
4.99	4.2	4.19	0.0103	0.0105	2.82	2.26E-02
5.57	4.84	5.2	3.56	2.63	4.14	2.26E-02
5.57	4.84	5.2	3.56	2.63	4.14	2.26E-02
3.68	3.49	3.49	3.04	2.94	2.39	2.27E-02
3.68	3.49	3.49	3.04	2.94	2.39	2.27E-02
3.68	3.49	3.49	3.04	2.94	2.39	2.27E-02
4.24	3.95	3.06	0.0103	2.26	0.0109	2.27E-02
4.24	3.95	3.06	0.0103	2.26	0.0109	2.27E-02
3.59	4.01	3.87	2.56	3.31	2.52	2.27E-02
4	3.18	4.09	0.0103	2.33	0.0109	2.27E-02
5.11	4.09	4	2.45	3.06	3.16	2.28E-02
4.19	4.55	5.53	0.0103	2.92	0.0109	2.28E-02
4.22	3.47	4.21	3.06	3.13	3	2.28E-02
4.22	3.47	4.21	3.06	3.13	3	2.28E-02
0.011	2.16	0.0117	2.92	4.43	3.92	2.28E-02
4.47	3.04	4.27	0.0103	2.28	0.0109	2.28E-02
4.47	3.04	4.27	0.0103	2.28	0.0109	2.28E-02
4.9	4.18	4.72	2.83	3.85	3.01	2.30E-02
4.9	4.18	4.72	2.83	3.85	3.01	2.30E-02
5.13	4.04	4.14	2.66	3.39	2.82	2.30E-02
5.13	4.04	4.14	2.66	3.39	2.82	2.30E-02
5.13	4.04	4.14	2.66	3.39	2.82	2.30E-02
0.011	2.15	0.0117	3.47	3.06	3.45	2.30E-02
5.29	4.38	4.76	0.0103	3.07	0.0109	2.30E-02
3.23	3.34	3.38	2.17	0.0105	0.0109	2.30E-02
3.23	3.34	3.38	2.17	0.0105	0.0109	2.30E-02
3.87	3.81	3.84	2.75	2.74	3.46	2.31E-02
3.87	3.81	3.84	2.75	2.74	3.46	2.31E-02
5.19	4.34	3.76	0.0103	2.69	0.0109	2.32E-02
5.19	4.34	3.76	0.0103	2.69	0.0109	2.32E-02
5.19	4.34	3.76	0.0103	2.69	0.0109	2.32E-02
4.61	4.85	5.28	0.0103	3.18	0.0109	2.32E-02
4.61	4.85	5.28	0.0103	3.18	0.0109	2.32E-02
4.34	4.5	4.53	0.0103	0.0105	2.92	2.32E-02
3.57	4.16	4.25	2.56	0.0105	0.0109	2.33E-02
3.57	4.16	4.25	2.56	0.0105	0.0109	2.33E-02
3.52	3.66	3.21	2.36	2.43	3	2.33E-02
0.011	2.22	0.0117	2.98	3.85	4.01	2.34E-02
0.011	2.22	0.0117	2.98	3.85	4.01	2.34E-02
3.49	4.38	4.1	0.0103	0.0105	2.53	2.34E-02
3.49	4.38	4.1	0.0103	0.0105	2.53	2.34E-02
5.69	4.73	5.05	4.2	2.91	3.08	2.34E-02
5.69	4.73	5.05	4.2	2.91	3.08	2.34E-02
3.57	4.68	4.28	2.61	0.0105	0.0109	2.35E-02
3.94	2.98	3.69	0.0103	2.2	0.0109	2.35E-02
3.94	2.98	3.69	0.0103	2.2	0.0109	2.35E-02
3.89	3.17	3.69	0.0103	2.29	0.0109	2.35E-02
5.35	5.11	4.44	3.72	3.11	4.01	2.36E-02

5.35	5.11	4.44	3.72	3.11	4.01	2.36E-02
5.35	5.11	4.44	3.72	3.11	4.01	2.36E-02
5.35	5.11	4.44	3.72	3.11	4.01	2.36E-02
3.95	4.27	4.34	2.74	0.0105	0.0109	2.36E-02
3.95	4.27	4.34	2.74	0.0105	0.0109	2.36E-02
5.35	5.39	5.35	2.44	3.25	0.0109	2.36E-02
5.35	5.39	5.35	2.44	3.25	0.0109	2.36E-02
3.57	4.23	3.85	2.51	0.0105	0.0109	2.37E-02
3.57	4.23	3.85	2.51	0.0105	0.0109	2.37E-02
3.57	4.23	3.85	2.51	0.0105	0.0109	2.37E-02
3.77	3.13	4.44	2.25	2.48	2.49	2.37E-02
4.1	5.08	4.99	3.22	3.8	3.1	2.38E-02
4.1	5.08	4.99	3.22	3.8	3.1	2.38E-02
3.76	4.09	4.24	3.11	3.47	2.7	2.38E-02
3.76	4.09	4.24	3.11	3.47	2.7	2.38E-02
2.99	3.23	3.87	0.0103	2.11	0.0109	2.38E-02
4.26	3.33	3.92	0.0103	2.43	0.0109	2.38E-02
3.8	3.08	3.56	0.0103	2.23	0.0109	2.39E-02
4.51	3.85	4.25	0.0103	2.73	0.0109	2.39E-02
4.51	3.85	4.25	0.0103	2.73	0.0109	2.39E-02
4.34	3.73	4.01	2.62	0.0105	0.0109	2.39E-02
3.54	3.02	3.42	0.0103	2.16	0.0109	2.39E-02
3.54	3.02	3.42	0.0103	2.16	0.0109	2.39E-02
4.97	4.35	4.16	0.0103	2.9	0.0109	2.40E-02
4	3.11	4.56	2.32	0.0105	0.0109	2.40E-02
4	3.11	4.56	2.32	0.0105	0.0109	2.40E-02
3.9	4.36	4.92	2.8	0.0105	0.0109	2.40E-02
3.32	3.64	3.69	2.44	2.81	3.08	2.41E-02
3.32	3.64	3.69	2.44	2.81	3.08	2.41E-02
0.011	0.012	2.17	3.37	3.19	3.28	2.42E-02
4.84	4.67	4.16	2.97	0.0105	0.0109	2.42E-02
3.91	3.13	3.89	0.0103	2.32	0.0109	2.43E-02
3.78	3.75	3.47	0.0103	2.42	0.0109	2.43E-02
3.07	3.18	2.92	2.02	0.0105	0.0109	2.43E-02
4.4	4.31	4.45	2.91	0.0105	0.0109	2.43E-02
4.4	4.31	4.45	2.91	0.0105	0.0109	2.43E-02
3.47	3.04	3.77	2.47	2.73	2.08	2.44E-02
3.47	3.04	3.77	2.47	2.73	2.08	2.44E-02
3.22	3.62	3.51	2.27	0.0105	0.0109	2.44E-02
0.011	2.73	0.0117	4.61	3.83	4.18	2.44E-02
4.37	4.66	4.31	2.94	0.0105	0.0109	2.44E-02
3.62	3.9	4.59	3.07	3	2.56	2.44E-02
3.62	3.9	4.59	3.07	3	2.56	2.44E-02
4.78	4.27	3.34	2.51	0.0105	0.0109	2.45E-02
4.78	4.27	3.34	2.51	0.0105	0.0109	2.45E-02
4.24	4.58	3.05	0.0103	2.33	0.0109	2.45E-02
4.24	4.58	3.05	0.0103	2.33	0.0109	2.45E-02
2.87	3.9	4.15	0.0103	0.0105	2.19	2.45E-02
2.87	3.9	4.15	0.0103	0.0105	2.19	2.45E-02
4.27	3.75	4.07	2.65	0.0105	0.0109	2.45E-02
3.07	3.95	3.57	2.25	0.0105	0.0109	2.45E-02
4.53	4.34	4.28	0.0103	2.91	0.0109	2.46E-02
4.53	4.34	4.28	0.0103	2.91	0.0109	2.46E-02
4.53	4.34	4.28	0.0103	2.91	0.0109	2.46E-02
4.13	4.65	3.89	2.41	3.45	2.85	2.46E-02
4.13	4.65	3.89	2.41	3.45	2.85	2.46E-02
3.3	3.22	3	0.0103	2.1	0.0109	2.46E-02
3.3	3.22	3	0.0103	2.1	0.0109	2.46E-02

5.6	4.42	5.6	0.0103	3.08	2.12	2.46E-02
4.62	3.96	4.78	2.89	0.0105	0.0109	2.47E-02
3.8	3.42	3.11	2.85	2.24	2.24	2.47E-02
4.64	3.74	3.47	0.0103	0.0105	2.46	2.47E-02
4.64	3.74	3.47	0.0103	0.0105	2.46	2.47E-02
4.75	4.35	3.94	0.0103	2.83	0.0109	2.47E-02
4.75	4.35	3.94	0.0103	2.83	0.0109	2.47E-02
3.46	3.7	3.43	2.52	3.13	2.4	2.48E-02
3.46	3.7	3.43	2.52	3.13	2.4	2.48E-02
2.31	0.012	0.0117	3.2	3.65	3.71	2.48E-02
4.72	4.24	3.18	0.0103	2.42	0.0109	2.48E-02
4.72	4.24	3.18	0.0103	2.42	0.0109	2.48E-02
3.62	3.71	3.64	0.0103	2.44	0.0109	2.49E-02
3.62	3.71	3.64	0.0103	2.44	0.0109	2.49E-02
4.83	3.62	4.16	0.0103	2.65	0.0109	2.49E-02
4.28	3.6	3.93	3.37	3.03	3.04	2.50E-02
4.28	3.6	3.93	3.37	3.03	3.04	2.50E-02
4.28	3.6	3.93	3.37	3.03	3.04	2.50E-02
4.27	3.91	4.52	0.0103	2.22	2.33	2.50E-02
4.27	3.91	4.52	0.0103	2.22	2.33	2.50E-02
3.91	3.45	3.58	0.0103	2.41	0.0109	2.50E-02
5.08	5.39	4.83	0.0103	3.38	0.0109	2.50E-02
5.08	5.39	4.83	0.0103	3.38	0.0109	2.50E-02
5.08	5.39	4.83	0.0103	3.38	0.0109	2.50E-02
4.72	3.01	4.34	0.0103	2.32	0.0109	2.50E-02
4.72	3.01	4.34	0.0103	2.32	0.0109	2.50E-02
3.09	2.86	2.92	1.97	0.0105	0.0109	2.51E-02
3.09	2.86	2.92	1.97	0.0105	0.0109	2.51E-02
3.42	3	3.47	0.0103	0.0105	2.17	2.51E-02
3.88	4.06	3.99	2.26	3.39	2.82	2.51E-02
3.88	4.06	3.99	2.26	3.39	2.82	2.51E-02
3.67	3.5	3.9	2.45	0.0105	0.0109	2.51E-02
3.67	3.5	3.9	2.45	0.0105	0.0109	2.51E-02
3.67	3.5	3.9	2.45	0.0105	0.0109	2.51E-02
4.29	3.89	3.19	0.0103	2.39	0.0109	2.51E-02
4.29	3.89	3.19	0.0103	2.39	0.0109	2.51E-02
3.38	3.74	3.67	0.0103	2.39	0.0109	2.52E-02
3.38	3.74	3.67	0.0103	2.39	0.0109	2.52E-02
4.01	3.57	4.1	0.0103	2.57	0.0109	2.52E-02
4.01	3.57	4.1	0.0103	2.57	0.0109	2.52E-02
5.16	4.02	4.96	3.19	3.47	2.32	2.52E-02
3.29	3.8	3.19	0.0103	2.24	0.0109	2.52E-02
3.71	4.32	3.98	0.0103	2.64	0.0109	2.52E-02
3.96	3.66	2.98	0.0103	2.24	0.0109	2.52E-02
4.79	3.66	3.83	0.0103	0.0105	2.58	2.53E-02
3.4	3.48	3.62	2.34	0.0105	0.0109	2.53E-02
3.4	3.48	3.62	2.34	0.0105	0.0109	2.53E-02
3.64	3.82	3.54	3.38	3	3.19	2.53E-02
3.64	3.82	3.54	3.38	3	3.19	2.53E-02
4.88	4.65	4.34	3.66	3.67	2.65	2.54E-02
4.01	3.62	3.45	0.0103	2.44	0.0109	2.55E-02
4.19	4.55	5.53	3.52	2.92	2.33	2.55E-02
4.19	4.55	5.53	3.52	2.92	2.33	2.55E-02
3.97	3.62	3.55	0.0103	2.47	0.0109	2.55E-02
3.97	3.62	3.55	0.0103	2.47	0.0109	2.55E-02
4.04	4.08	4.03	0.0103	2.72	0.0109	2.55E-02
3.24	3.63	3.28	2.25	0.0105	0.0109	2.56E-02
4.28	4.48	4.28	2.8	3.82	2.78	2.56E-02

4.28	4.48	4.28	2.8	3.82	2.78	2.56E-02
4.28	4.48	4.28	2.8	3.82	2.78	2.56E-02
5.08	4.77	5.01	3.06	4.33	3.42	2.57E-02
5.08	4.77	5.01	3.06	4.33	3.42	2.57E-02
4.275	3.695	2.82	0.0103	0.0105	2.15	2.57E-02
3.72	4.37	3.41	0.0103	0.0105	2.47	2.58E-02
4.76	4.85	4.87	2.39	4	2.25	2.58E-02
4.76	4.85	4.87	2.39	4	2.25	2.58E-02
3.63	4.63	4.03	2.65	0.0105	0.0109	2.58E-02
5.26	4.61	4.09	3.27	3.6	3.44	2.58E-02
5.26	4.61	4.09	3.27	3.6	3.44	2.58E-02
3.34	3.25	3.45	0.0103	2.25	0.0109	2.58E-02
3.34	3.25	3.45	0.0103	2.25	0.0109	2.58E-02
2.52	2.49	2.49	3.3	3.66	2.88	2.59E-02
3.9	2.75	3.7	0.0103	2.13	0.0109	2.59E-02
3.9	2.75	3.7	0.0103	2.13	0.0109	2.59E-02
4.72	5.05	4.32	2.6	3.91	2.71	2.59E-02
4.72	5.05	4.32	2.6	3.91	2.71	2.59E-02
3.79	3.91	3.43	3.23	2.81	2.55	2.59E-02
3.54	3.52	3.48	0.0103	2.37	0.0109	2.60E-02
3.54	3.52	3.48	0.0103	2.37	0.0109	2.60E-02
3.54	3.35	3.9	2.39	0.0105	0.0109	2.60E-02
3.54	3.35	3.9	2.39	0.0105	0.0109	2.60E-02
2.08	0.012	0.0117	3.69	2.8	3.23	2.60E-02
3.48	3.22	4.13	2.33	0.0105	0.0109	2.60E-02
3.48	3.22	4.13	2.33	0.0105	0.0109	2.60E-02
4.01	3.65	4.09	2.44	3.38	2.53	2.61E-02
4.01	3.65	4.09	2.44	3.38	2.53	2.61E-02
3.7	4.24	3.9	0.0103	2.17	2.12	2.61E-02
3.4	3.35	2.82	0.0103	2.1	0.0109	2.62E-02
4.91	4.14	4.98	0.0103	0.0105	3.08	2.62E-02
4.13	3.79	3.31	2.5	2.72	3.05	2.62E-02
3.61	2.96	3.4	0.0103	2.19	0.0109	2.62E-02
3.61	2.96	3.4	0.0103	2.19	0.0109	2.62E-02
3.61	2.96	3.4	0.0103	2.19	0.0109	2.62E-02
3.72	3.35	2.97	2.66	2.6	2.48	2.63E-02
3.72	3.35	2.97	2.66	2.6	2.48	2.63E-02
4.56	3.3	3.71	0.0103	2.42	0.0109	2.63E-02
4.56	3.3	3.71	0.0103	2.42	0.0109	2.63E-02
4.12	3.21	3.7	0.0103	2.39	0.0109	2.63E-02
4.12	3.21	3.7	0.0103	2.39	0.0109	2.63E-02
4.12	3.21	3.7	0.0103	2.39	0.0109	2.63E-02
4.12	3.21	3.7	0.0103	2.39	0.0109	2.63E-02
5.17	4.15	3.49	2.59	0.0105	0.0109	2.64E-02
5.17	4.15	3.49	2.59	0.0105	0.0109	2.64E-02
4.58	5.38	4.15	3.03	3.07	3.69	2.64E-02
4.58	5.38	4.15	3.03	3.07	3.69	2.64E-02
4.58	5.38	4.15	3.03	3.07	3.69	2.64E-02
2.88	3.97	3.4	2.16	0.0105	0.0109	2.64E-02
2.88	3.97	3.4	2.16	0.0105	0.0109	2.64E-02
2.88	3.97	3.4	2.16	0.0105	0.0109	2.64E-02
3.88	4.42	3.25	0.0103	2.45	0.0109	2.64E-02
2.89	2.93	3.89	0.0103	2.02	0.0109	2.65E-02
3.49	4.35	4.19	2.63	0.0105	0.0109	2.66E-02
3.49	4.35	4.19	2.63	0.0105	0.0109	2.66E-02
3.66	4	4.49	2.59	3.28	2.2	2.67E-02
3.66	4	4.49	2.59	3.28	2.2	2.67E-02
3.11	3.81	3.21	2.22	0.0105	0.0109	2.67E-02

3.63	3.04	3.08	0.0103	2.15	0.0109	2.67E-02
3.13	3.31	2.86	2.43	2.71	2.26	2.68E-02
3.55	4.06	3.91	0.0103	2.58	0.0109	2.68E-02
3.55	4.06	3.91	0.0103	2.58	0.0109	2.68E-02
4.69	4.19	4.44	2.62	2.23	0.0109	2.69E-02
4.69	4.19	4.44	2.62	2.23	0.0109	2.69E-02
2.94	2.97	3.33	0.0103	2.07	0.0109	2.69E-02
2.94	2.97	3.33	0.0103	2.07	0.0109	2.69E-02
4.07	3.95	4.12	0.0103	2.75	0.0109	2.69E-02
3.27	3.84	3.1	0.0103	2.24	0.0109	2.69E-02
2.45	0.012	0.0117	3.96	3.59	3.41	2.69E-02
3.74	4.21	4.59	0.0103	2.77	0.0109	2.69E-02
4.4	4.12	4.25	0.0103	2.89	0.0109	2.70E-02
5.41	4.37	4.56	3.45	3.61	2.53	2.70E-02
5.15	4.73	4.71	0.0103	3.29	0.0109	2.70E-02
4.3	3.82	4.59	3.58	3.23	3.38	2.70E-02
4.3	3.82	4.59	3.58	3.23	3.38	2.70E-02
4.26	4.56	3.6	0.0103	0.0105	2.72	2.71E-02
4.53	4.4	4.78	0.0103	3.1	0.0109	2.71E-02
4.87	4.74	4.63	0.0103	3.23	0.0109	2.71E-02
3.09	3.74	3.69	2.74	2.88	2.54	2.71E-02
3.09	3.74	3.69	2.74	2.88	2.54	2.71E-02
3.9	3.89	4.01	3.45	3.14	2.58	2.72E-02
3.72	3.11	3.81	0.0103	2.35	0.0109	2.72E-02
3.72	3.11	3.81	0.0103	2.35	0.0109	2.72E-02
3.29	2.72	3.32	2.06	0.0105	0.0109	2.73E-02
3.29	2.72	3.32	2.06	0.0105	0.0109	2.73E-02
3.58	4.7	3.81	0.0103	2.6	0.0109	2.73E-02
3.58	4.7	3.81	0.0103	2.6	0.0109	2.73E-02
3.42	3.53	3.47	0.0103	2.37	0.0109	2.73E-02
4.24	4.4	3.88	3.4	3.57	3.72	2.73E-02
4.24	4.4	3.88	3.4	3.57	3.72	2.73E-02
4.24	4.4	3.88	3.4	3.57	3.72	2.73E-02
5.37	3.82	4.6	2.34	2.75	3.31	2.73E-02
5.37	3.82	4.6	2.34	2.75	3.31	2.73E-02
5.37	3.82	4.6	2.34	2.75	3.31	2.73E-02
4.87	5.01	5.13	0.0103	2.49	3.02	2.73E-02
4.87	5.01	5.13	0.0103	2.49	3.02	2.73E-02
5.4	5.32	5.28	0.0103	3.41	2.34	2.73E-02
4.21	5.18	5.15	0.0103	2.85	2.27	2.73E-02
4.21	5.18	5.15	0.0103	2.85	2.27	2.73E-02
3.76	3.47	3.01	0.0103	2.26	0.0109	2.74E-02
3.76	3.47	3.01	0.0103	2.26	0.0109	2.74E-02
4.62	3.92	4.35	0.0103	2.89	0.0109	2.75E-02
3.81	3.78	3.68	2.57	0.0105	0.0109	2.76E-02
3.15	3.09	3.09	0.0103	0.0105	2.13	2.76E-02
3.23	2.67	3.17	0.0103	2.02	0.0109	2.78E-02
4.64	4.21	4.52	3.37	3.56	2.32	2.78E-02
4.64	4.21	4.52	3.37	3.56	2.32	2.78E-02
2.99	3.74	3.26	0.0103	2.21	0.0109	2.78E-02
4.21	4.77	5.08	2.35	0.0105	2.72	2.78E-02
5.35	5.33	3.88	2.32	3.38	3.01	2.79E-02
5.35	5.33	3.88	2.32	3.38	3.01	2.79E-02
5.07	5.26	5.14	3.17	2.52	0.0109	2.79E-02
3.4	4.4	3.72	0.0103	2.52	0.0109	2.79E-02
3.4	4.4	3.72	0.0103	2.52	0.0109	2.79E-02
2.96	3.34	3.33	2.18	0.0105	0.0109	2.79E-02
3.85	4.03	2.9	2.29	0.0105	0.0109	2.79E-02

3.85	4.03	2.9	2.29	0.0105	0.0109	2.79E-02
4.29	3.72	3.38	2.48	3.06	2.3	2.80E-02
4.29	3.72	3.38	2.48	3.06	2.3	2.80E-02
5.03	3.61	4.77	2.77	3.18	2.87	2.80E-02
5.03	3.61	4.77	2.77	3.18	2.87	2.80E-02
3.15	3.44	3.83	0.0103	2.33	0.0109	2.80E-02
3.15	3.44	3.83	0.0103	2.33	0.0109	2.80E-02
4.23	3.15	3.15	0.0103	2.22	0.0109	2.80E-02
4.23	3.15	3.15	0.0103	2.22	0.0109	2.80E-02
4.54	4.69	4.22	2.11	2.78	0.0109	2.80E-02
4.55	4.16	4.67	2.92	3.64	2.12	2.81E-02
5.05	4.48	5.21	0.0103	3.33	0.0109	2.82E-02
5.05	4.48	5.21	0.0103	3.33	0.0109	2.82E-02
5.05	4.48	5.21	0.0103	3.33	0.0109	2.82E-02
3.75	2.81	3.97	0.0103	2.23	0.0109	2.83E-02
4.36	4.16	3.56	2.7	0.0105	0.0109	2.83E-02
4.36	4.16	3.56	2.7	0.0105	0.0109	2.83E-02
4.36	4.16	3.56	2.7	0.0105	0.0109	2.83E-02
0.011	0.012	2.78	3.71	4.18	4.5	2.83E-02
3.41	3.12	3.72	2.85	2.61	2.86	2.83E-02
3.41	3.12	3.72	2.85	2.61	2.86	2.83E-02
3.01	2.9	3.18	2.08	0.0105	0.0109	2.85E-02
4.12	4.83	3.8	3.12	3.14	2.26	2.85E-02
4.12	4.83	3.8	3.12	3.14	2.26	2.85E-02
4.26	2.95	4.33	0.0103	0.0105	2.38	2.85E-02
4.26	2.95	4.33	0.0103	0.0105	2.38	2.85E-02
2.79	3.09	3.17	0.0103	2.06	0.0109	2.85E-02
2.79	3.09	3.17	0.0103	2.06	0.0109	2.85E-02
3.85	3.93	4.65	2.78	0.0105	0.0109	2.85E-02
3.85	3.93	4.65	2.78	0.0105	0.0109	2.85E-02
3.85	3.93	4.65	2.78	0.0105	0.0109	2.85E-02
3.24	4.62	3.36	2.31	0.0105	0.0109	2.86E-02
4.73	5.68	4.6	2.41	3.97	2.84	2.86E-02
4.73	5.68	4.6	2.41	3.97	2.84	2.86E-02
5.02	5.11	3.75	2.76	3.36	3.02	2.87E-02
5.02	5.11	3.75	2.76	3.36	3.02	2.87E-02
0.011	0.012	2.21	2.99	3.24	3.51	2.87E-02
3.46	3.23	4.03	0.0103	2.39	0.0109	2.87E-02
3.46	3.23	4.03	0.0103	2.39	0.0109	2.87E-02
3.46	3.23	4.03	0.0103	2.39	0.0109	2.87E-02
3.43	3.32	3.36	0.0103	2.33	0.0109	2.88E-02
0.011	2.03	0.0117	2.77	2.94	3.79	2.88E-02
3.84	5.09	5.55	3.06	0.0105	0.0109	2.88E-02
3.84	5.09	5.55	3.06	0.0105	0.0109	2.88E-02
3.84	5.09	5.55	3.06	0.0105	0.0109	2.88E-02
3.84	5.09	5.55	3.06	0.0105	0.0109	2.88E-02
3.74	3.51	3.57	0.0103	2.49	0.0109	2.88E-02
3.74	3.51	3.57	0.0103	2.49	0.0109	2.88E-02
3.71	3.58	2.98	2.47	2.81	2.46	2.89E-02
2.19	0.012	0.0117	3.1	3.44	3.05	2.89E-02
4.17	3	3.41	0.0103	0.0105	2.27	2.89E-02
4.62	3.96	4.78	0.0103	2.36	2.51	2.90E-02
2.65	3.82	3.54	0.0103	2.12	0.0109	2.90E-02
3.44	3.92	3.09	0.0103	2.33	0.0109	2.90E-02
3.04	2.77	3	3.85	4.19	3.35	2.90E-02
3.04	2.77	3	3.85	4.19	3.35	2.90E-02
3.92	3.82	3.54	0.0103	2.59	0.0109	2.91E-02
5.7	4.55	5.55	4.22	3.96	3.85	2.91E-02

5.7	4.55	5.55	4.22	3.96	3.85	2.91E-02
5.7	4.55	5.55	4.22	3.96	3.85	2.91E-02
3.44	3.6	2.9	0.0103	2.23	0.0109	2.91E-02
3.92	2.97	3.95	2.36	0.0105	0.0109	2.91E-02
3.04	2.65	3.67	0.0103	2.02	0.0109	2.91E-02
2.63	2.86	2.54	3.51	3.52	2.99	2.91E-02
2.63	2.86	2.54	3.51	3.52	2.99	2.91E-02
3.35	2.7	2.98	2.38	2.39	2.38	2.91E-02
4.81	4.42	4.62	3.3	3.87	2.47	2.92E-02
5.15	5.02	5.4	4.26	4.02	2.87	2.93E-02
5.15	5.02	5.4	4.26	4.02	2.87	2.93E-02
3.79	3.91	3.43	0.0103	0.0105	2.55	2.93E-02
4.15	4.13	4.07	0.0103	2.86	0.0109	2.93E-02
4.15	4.13	4.07	0.0103	2.86	0.0109	2.93E-02
3.2	3.37	3.33	0.0103	2.29	0.0109	2.93E-02
3.2	3.37	3.33	0.0103	2.29	0.0109	2.93E-02
3.46	3.76	3.47	2.06	3.07	2.05	2.94E-02
4.21	4.28	3.59	0.0103	2.74	0.0109	2.94E-02
5.19	4.65	5.05	2.05	3.98	3.08	2.94E-02
3.76	3.23	3.13	2.29	0.0105	0.0109	2.94E-02
3.76	3.23	3.13	2.29	0.0105	0.0109	2.94E-02
3.62	2.92	3.22	0.0103	2.2	0.0109	2.94E-02
4.89	5.08	3.19	0.0103	2.62	0.0109	2.95E-02
3.33	3.09	3.03	2.28	2.83	2.51	2.95E-02
4.23	3.55	3.49	0.0103	2.54	0.0109	2.95E-02
3.81	3.53	3.12	0.0103	2.37	0.0109	2.95E-02
3.84	3.5	2.64	2.12	0.0105	0.0109	2.96E-02
2.48	0.012	0.0117	3.17	4.08	5.06	2.96E-02
4.09	3.72	3.41	2.97	3.16	2.66	2.96E-02
4.09	3.72	3.41	2.97	3.16	2.66	2.96E-02
3.36	3.04	4	2.3	0.0105	0.0109	2.97E-02
3.36	3.04	4	2.3	0.0105	0.0109	2.97E-02
3.65	4.14	4.29	0.0103	2.37	2.08	2.97E-02
3.81	3.66	3.87	2.09	0.0105	2.18	2.97E-02
3.31	3.23	3.08	0.0103	2.23	0.0109	2.98E-02
3.31	3.23	3.08	0.0103	2.23	0.0109	2.98E-02
3.04	3.09	2.85	2.08	0.0105	0.0109	2.98E-02
3.04	3.09	2.85	2.08	0.0105	0.0109	2.98E-02
4.31	4.36	4.64	3.28	4.05	3.4	2.98E-02
4.31	4.36	4.64	3.28	4.05	3.4	2.98E-02
4.4	4.1	4.4	0.0103	2.99	0.0109	2.99E-02
4.4	4.1	4.4	0.0103	2.99	0.0109	2.99E-02
4.4	4.1	4.4	0.0103	2.99	0.0109	2.99E-02
4.16	3.69	5.06	0.0103	2.29	2.21	2.99E-02
3.05	3.21	3.54	2.25	0.0105	0.0109	2.99E-02
2.41	0.012	0.0117	3.55	3.16	3.96	2.99E-02
0.011	0.012	2.35	3.04	3.91	3.53	3.00E-02
3.61	3.29	3.71	0.0103	2.45	0.0109	3.00E-02
3.94	3.55	3.62	2.57	0.0105	0.0109	3.00E-02
3.31	3.74	2.92	0.0103	0.0105	2.24	3.01E-02
4.75	4.18	5.12	3.78	3.36	2.63	3.01E-02
3.5	3.21	3.71	0.0103	2.4	0.0109	3.01E-02
3.48	4.38	4.21	2.72	0.0105	0.0109	3.01E-02
3.48	4.38	4.21	2.72	0.0105	0.0109	3.01E-02
4.76	4.37	3.72	0.0103	2.89	0.0109	3.02E-02
4.76	4.37	3.72	0.0103	2.89	0.0109	3.02E-02
3.2	2.84	2.99	2.09	0.0105	0.0109	3.02E-02
3.2	2.84	2.99	2.09	0.0105	0.0109	3.02E-02

4.4	4.1	4.4	3	0.0105	0.0109	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.08	4.77	5.01	2.91	4.33	3.42	3.03E-02
5.45	4.66	4.95	2.34	4.14	2.68	3.03E-02
5.45	4.66	4.95	2.34	4.14	2.68	3.03E-02
3.58	3.18	3.33	2.98	2.48	2.79	3.03E-02
3.58	3.18	3.33	2.98	2.48	2.79	3.03E-02
4.67	3.57	4.33	2.81	0.0105	0.0109	3.04E-02
4.67	3.57	4.33	2.81	0.0105	0.0109	3.04E-02
3.26	3.68	4.09	2.5	0.0105	0.0109	3.04E-02
3.83	3.57	3.59	2.56	0.0105	0.0109	3.04E-02
3.83	3.57	3.59	2.56	0.0105	0.0109	3.04E-02
4.3	3.49	3.93	0.0103	2.67	0.0109	3.04E-02
4.36	4	3.86	3.45	2.53	3.18	3.05E-02
4.36	4	3.86	3.45	2.53	3.18	3.05E-02
3.74	3.8	4.19	2.72	0.0105	0.0109	3.06E-02
3.74	3.8	4.19	2.72	0.0105	0.0109	3.06E-02
3.01	3.06	3.29	0.0103	2.18	0.0109	3.06E-02
3.01	3.06	3.29	0.0103	2.18	0.0109	3.06E-02
0.011	0.012	2.26	3.14	3.45	3.13	3.06E-02
3.38	3.95	3.07	0.0103	2.34	0.0109	3.06E-02
4.33	3.64	3.2	0.0103	2.47	0.0109	3.06E-02
3.47	3.06	3.34	0.0103	2.29	0.0109	3.06E-02
3.47	3.06	3.34	0.0103	2.29	0.0109	3.06E-02
3.65	3.18	3.32	0.0103	2.35	0.0109	3.07E-02
3.65	3.18	3.32	0.0103	2.35	0.0109	3.07E-02
3.88	3.19	3.09	0.0103	0.0105	2.29	3.07E-02
3.83	3.54	4.39	3.27	2.61	2.7	3.07E-02
3.83	3.54	4.39	3.27	2.61	2.7	3.07E-02
2.9	3.38	3.19	0.0103	0.0105	2.19	3.08E-02
4.37	4.05	4.65	3.04	3.8	2.78	3.08E-02
3.46	3.41	2.96	2.68	2.84	2.56	3.08E-02
3.55	2.92	3.45	0.0103	2.27	0.0109	3.08E-02
3.4	3.37	3.62	0.0103	2.43	0.0109	3.09E-02
3.4	3.37	3.62	0.0103	2.43	0.0109	3.09E-02
3.4	3.37	3.62	0.0103	2.43	0.0109	3.09E-02
4.17	4.09	4.39	0.0103	2.96	0.0109	3.09E-02
0.011	2.47	0.0117	3.29	3.51	3.92	3.09E-02
0.011	2.47	0.0117	3.29	3.51	3.92	3.09E-02
5.15	4.68	4.48	0.0103	3.32	0.0109	3.10E-02
5.15	4.68	4.48	0.0103	3.32	0.0109	3.10E-02
4.56	4.73	3.69	0.0103	2.16	2.52	3.10E-02
4.32	4.1	4.24	2.79	3.79	2.85	3.10E-02
4.32	4.1	4.24	2.79	3.79	2.85	3.10E-02
4.37	4.05	4.65	3.04	3.8	2.77	3.11E-02
3.12	3.14	3.06	0.0103	2.19	0.0109	3.11E-02
5.26	4.83	4.55	3.79	4.22	3.27	3.11E-02
5.26	4.83	4.55	3.79	4.22	3.27	3.11E-02
3.4	3.74	4.29	2.6	0.0105	0.0109	3.11E-02
3.48	2.9	3.16	0.0103	0.0105	2.2	3.11E-02
3.48	2.9	3.16	0.0103	0.0105	2.2	3.11E-02
4.2	3.74	4.53	2.87	0.0105	0.0109	3.12E-02

4.2	3.74	4.53	2.87	0.0105	0.0109	3.12E-02
4.59	5.42	4.7	3.88	3.38	2.34	3.12E-02
4.59	5.42	4.7	3.88	3.38	2.34	3.12E-02
3.71	3.86	3.47	2.58	0.0105	0.0109	3.12E-02
3.48	2.81	3.87	2.25	0.0105	0.0109	3.13E-02
3.48	2.81	3.87	2.25	0.0105	0.0109	3.13E-02
3.08	3.08	4.24	2.23	0.0105	0.0109	3.13E-02
5.31	5.85	4.59	0.0103	0.0105	3.58	3.13E-02
3.75	4.1	3.16	2.49	0.0105	0.0109	3.13E-02
4.33	5.43	4.42	0.0103	3.21	0.0109	3.14E-02
4.33	5.43	4.42	0.0103	3.21	0.0109	3.14E-02
3.32	3.45	3.38	0.0103	2.39	0.0109	3.14E-02
3.32	3.45	3.38	0.0103	2.39	0.0109	3.14E-02
4.38	3.67	4.19	0.0103	2.83	0.0109	3.14E-02
4.38	3.67	4.19	0.0103	2.83	0.0109	3.14E-02
3.76	4.36	4.37	2.32	3.51	2.74	3.15E-02
3.76	4.36	4.37	2.32	3.51	2.74	3.15E-02
2.19	0.012	0.0117	3.93	3.08	2.91	3.15E-02
3.72	3.11	3.19	2.31	0.0105	0.0109	3.15E-02
4.63	3.76	4.59	2.97	0.0105	0.0109	3.16E-02
4.63	3.76	4.59	2.97	0.0105	0.0109	3.16E-02
3.72	3.94	3.36	2.36	3.18	2.38	3.16E-02
3.27	2.68	3.81	0.0103	2.14	0.0109	3.16E-02
3.27	2.68	3.81	0.0103	2.14	0.0109	3.16E-02
3.05	2.72	3.9	0.0103	2.09	0.0109	3.16E-02
3.61	4.48	3.68	0.0103	2.68	0.0109	3.16E-02
3.61	4.48	3.68	0.0103	2.68	0.0109	3.16E-02
2.63	0.012	0.0117	4.31	3.45	3.73	3.16E-02
3.54	3.53	3.3	2.44	0.0105	0.0109	3.17E-02
3.54	3.53	3.3	2.44	0.0105	0.0109	3.17E-02
4.15	4.19	3.56	0.0103	0.0105	2.76	3.17E-02
5.33	5.14	5.59	0.0103	3.78	0.0109	3.18E-02
4.49	4.22	4.12	0.0103	3.02	0.0109	3.19E-02
3.35	3.04	2.96	0.0103	2.19	0.0109	3.19E-02
4.9	4.37	4.22	3.12	3.78	2.51	3.19E-02
3.35	2.95	3.17	0.0103	2.22	0.0109	3.19E-02
3.35	2.95	3.17	0.0103	2.22	0.0109	3.19E-02
3.81	3.66	3.87	2.09	2.24	0.0109	3.19E-02
4.35	4.01	3.97	0.0103	2.9	0.0109	3.19E-02
5.34	4.33	4.02	0.0103	0.0105	3.07	3.21E-02
4.15	3.3	4.11	2.18	2.56	3.1	3.22E-02
4.15	3.3	4.11	2.18	2.56	3.1	3.22E-02
3.88	4.47	3.7	0.0103	2.79	0.0109	3.22E-02
3.69	3.45	4.02	0.0103	2.61	0.0109	3.22E-02
2.84	3.43	2.64	0.0103	2.02	0.0109	3.22E-02
3.25	2.55	3.94	0.0103	2.06	0.0109	3.22E-02
3.25	2.55	3.94	0.0103	2.06	0.0109	3.22E-02
4.12	3.85	3.53	0.0103	0.0105	2.69	3.22E-02
3.99	3.69	3.25	2.91	2.81	2.18	3.23E-02
3.5	2.96	2.54	2.01	0.0105	0.0109	3.24E-02
3.37	2.68	3.21	2.13	0.0105	0.0109	3.24E-02
4	4.04	3.47	0.0103	2.69	0.0109	3.24E-02
3.11	2.74	3.15	2.11	0.0105	0.0109	3.24E-02
3.49	3.44	2.99	2.32	0.0105	0.0109	3.25E-02
3.49	3.44	2.99	2.32	0.0105	0.0109	3.25E-02
2.85	3.08	3.66	0.0103	0.0105	2.19	3.25E-02
3.8	2.71	3.25	0.0103	2.17	0.0109	3.25E-02
2.75	3.61	2.93	0.0103	2.1	0.0109	3.25E-02

2.75	3.61	2.93	0.0103	2.1	0.0109	3.25E-02
3.47	3.37	3.52	2.51	3.1	2.22	3.26E-02
3.47	3.37	3.52	2.51	3.1	2.22	3.26E-02
5.35	4.78	5.04	3.58	0.0105	0.0109	3.26E-02
5.35	4.78	5.04	3.58	0.0105	0.0109	3.26E-02
2.87	2.93	3.17	0.0103	2.12	0.0109	3.26E-02
3.5	3.12	2.96	0.0103	2.24	0.0109	3.26E-02
3.5	3.12	2.96	0.0103	2.24	0.0109	3.26E-02
4.71	3.63	3.43	0.0103	0.0105	2.6	3.26E-02
3.1	2.85	2.84	0.0103	2.08	0.0109	3.27E-02
3.96	3.24	2.92	0.0103	2.27	0.0109	3.27E-02
4.26	4.31	4.1	0.0103	3.01	0.0109	3.27E-02
4.26	4.31	4.1	0.0103	3.01	0.0109	3.27E-02
4.26	4.31	4.1	0.0103	3.01	0.0109	3.27E-02
4.24	4.25	4.2	0.0103	3.02	0.0109	3.27E-02
4.24	4.25	4.2	0.0103	3.02	0.0109	3.27E-02
4.48	2.9	4.31	0.0103	0.0105	2.46	3.27E-02
3.86	4.79	4.22	3.43	2.73	3.35	3.28E-02
3.86	4.79	4.22	3.43	2.73	3.35	3.28E-02
4.97	4.2	3.9	0.0103	3	0.0109	3.28E-02
3.77	4.89	4.16	3.38	3.07	2.71	3.29E-02
3.77	4.89	4.16	3.38	3.07	2.71	3.29E-02
4.11	3.78	4.6	0.0103	2.91	0.0109	3.29E-02
4.11	3.78	4.6	0.0103	2.91	0.0109	3.29E-02
4.34	3.73	4.01	0.0103	2.28	2.3	3.29E-02
4.71	4.54	4.7	2.68	2.69	0.0109	3.30E-02
4.71	4.54	4.7	2.68	2.69	0.0109	3.30E-02
4.03	4.47	3.92	0.0103	2.93	0.0109	3.30E-02
2.97	3.42	3.22	2.82	2.79	2.63	3.30E-02
2.97	3.42	3.22	2.82	2.79	2.63	3.30E-02
3.71	3.26	3.17	0.0103	0.0105	2.38	3.30E-02
3.55	4	3.73	2.67	0.0105	0.0109	3.31E-02
2.83	3.38	2.79	2.09	0.0105	0.0109	3.31E-02
3.68	3.21	2.49	0.0103	0.0105	2.05	3.31E-02
3.68	3.21	2.49	0.0103	0.0105	2.05	3.31E-02
3.29	3.83	3.12	2.84	2.28	2.55	3.31E-02
3.29	3.83	3.12	2.84	2.28	2.55	3.31E-02
4.43	3.04	4.26	2.46	2.55	2.52	3.31E-02
4.43	3.04	4.26	2.46	2.55	2.52	3.31E-02
3.98	4.05	3.62	0.0103	2.76	0.0109	3.31E-02
4.93	4.23	4.47	3.21	0.0105	0.0109	3.32E-02
4	3.71	3.17	0.0103	2.52	0.0109	3.32E-02
3.36	4.28	4.66	0.0103	2.76	0.0109	3.32E-02
4.13	4.6	4.29	3.09	0.0105	0.0109	3.32E-02
3.88	5.06	4.56	2.75	3.62	3.05	3.33E-02
3.88	5.06	4.56	2.75	3.62	3.05	3.33E-02
3.87	3.37	3.87	0.0103	2.62	0.0109	3.33E-02
3.87	3.37	3.87	0.0103	2.62	0.0109	3.33E-02
3.25	2.77	2.9	2.1	0.0105	0.0109	3.33E-02
3.58	4.44	3.38	0.0103	2.59	0.0109	3.33E-02
4.8	5.3	4.52	3.67	3.51	4.29	3.33E-02
4.8	5.3	4.52	3.67	3.51	4.29	3.33E-02
4.8	5.3	4.52	3.67	3.51	4.29	3.33E-02
4.09	3.77	3.7	3.21	3.53	3.05	3.34E-02
4.09	3.77	3.7	3.21	3.53	3.05	3.34E-02
4.09	3.77	3.7	3.21	3.53	3.05	3.34E-02
3.79	3.51	3.33	2.86	3.18	2.66	3.34E-02
4.96	5.05	4.52	0.0103	0.0105	3.45	3.34E-02

4.96	5.05	4.52	0.0103	0.0105	3.45	3.34E-02
3.15	3.22	3.29	0.0103	0.0105	2.31	3.34E-02
2.77	3.09	2.81	0.0103	0.0105	2.06	3.35E-02
4.29	3.33	3.85	2.65	0.0105	0.0109	3.36E-02
3.25	3.11	3.77	2.37	0.0105	0.0109	3.36E-02
3.25	3.11	3.77	2.37	0.0105	0.0109	3.36E-02
4.24	5.38	3.86	2.39	2.38	0.0109	3.37E-02
3.32	3.73	3.4	2.99	3.05	2.59	3.38E-02
3.32	3.73	3.4	2.99	3.05	2.59	3.38E-02
4.49	4.34	5.14	0.0103	0.0105	3.29	3.38E-02
3.67	3.88	3.31	2.57	0.0105	0.0109	3.38E-02
5.78	5.61	5.33	2.15	4.31	3.87	3.39E-02
5.78	5.61	5.33	2.15	4.31	3.87	3.39E-02
5.78	5.61	5.33	2.15	4.31	3.87	3.39E-02
3.4	4.32	2.63	2.14	0.0105	0.0109	3.39E-02
3.72	4.59	3.57	0.0103	2.73	0.0109	3.39E-02
3.72	4.59	3.57	0.0103	2.73	0.0109	3.39E-02
4.27	3.78	4.83	3.17	3.43	2.63	3.39E-02
3.27	3.23	2.85	0.0103	2.22	0.0109	3.40E-02
4.63	3.47	4.06	2.99	3.01	2.32	3.40E-02
3.27	3.45	3.45	2.44	0.0105	0.0109	3.40E-02
3.51	2.95	2.63	0.0103	0.0105	2.08	3.40E-02
3.25	3.43	3.17	0.0103	2.36	0.0109	3.41E-02
3.25	3.43	3.17	0.0103	2.36	0.0109	3.41E-02
5	4.53	5.12	0.0103	3.49	0.0109	3.41E-02
5	4.53	5.12	0.0103	3.49	0.0109	3.41E-02
5	4.53	5.12	0.0103	3.49	0.0109	3.41E-02
4.66	3.95	4.86	0.0103	2.78	2.23	3.41E-02
3.62	4.28	4.1	0.0103	2.84	0.0109	3.41E-02
3.62	4.28	4.1	0.0103	2.84	0.0109	3.41E-02
3.75	4.1	3.16	0.0103	2.55	0.0109	3.41E-02
3.92	3.25	4.14	0.0103	2.63	0.0109	3.42E-02
4.58	3.46	3.77	0.0103	2.08	2.23	3.42E-02
4.58	3.46	3.77	0.0103	2.08	2.23	3.42E-02
3.77	3.05	3.13	2.32	0.0105	0.0109	3.42E-02
4.56	4.81	5.26	0.0103	3.48	0.0109	3.42E-02
3.98	3.17	3.24	0.0103	2.41	0.0109	3.43E-02
3.98	3.17	3.24	0.0103	2.41	0.0109	3.43E-02
4.5	4.64	4.47	3.94	3.41	4.14	3.44E-02
4.5	4.64	4.47	3.94	3.41	4.14	3.44E-02
5.01	4.54	4.54	0.0103	3.37	0.0109	3.44E-02
5.01	4.54	4.54	0.0103	3.37	0.0109	3.44E-02
2.6	2.75	3.39	0.0103	0.0105	2.01	3.44E-02
5.38	4.85	4.69	3.63	3.95	2.37	3.44E-02
3.78	4.21	3.69	3.4	2.71	2.41	3.44E-02
2.73	5.37	4.42	0.0103	0.0105	2.28	3.45E-02
2.73	5.37	4.42	0.0103	0.0105	2.28	3.45E-02
0.011	0.012	2.19	3.3	3.6	2.66	3.45E-02
3.64	3.6	3.47	0.0103	2.58	0.0109	3.45E-02
3.64	3.6	3.47	0.0103	2.58	0.0109	3.45E-02
3.56	2.79	2.84	0.0103	0.0105	2.12	3.45E-02
4.2	4.79	4.77	0.0103	3.28	0.0109	3.45E-02
3.6	3.1	3.37	2.4	0.0105	0.0109	3.45E-02
3.6	3.1	3.37	2.4	0.0105	0.0109	3.45E-02
3.19	3.93	3.13	0.0103	2.38	0.0109	3.45E-02
3.19	3.93	3.13	0.0103	2.38	0.0109	3.45E-02
3.68	3.27	3.41	0.0103	2.48	0.0109	3.45E-02
2.24	0.012	0.0117	3.44	3.52	2.72	3.46E-02

3.29	2.97	3.2	2.27	0.0105	0.0109	3.46E-02
3.21	2.97	2.84	0.0103	0.0105	2.16	3.47E-02
4.67	2.86	3.93	0.0103	0.0105	2.41	3.47E-02
4.67	2.86	3.93	0.0103	0.0105	2.41	3.47E-02
2.99	3.62	2.9	2.22	0.0105	0.0109	3.47E-02
4.02	4	3.5	0.0103	2.75	0.0109	3.49E-02
4.02	4	3.5	0.0103	2.75	0.0109	3.49E-02
3.46	2.99	2.97	0.0103	2.24	0.0109	3.49E-02
3.46	2.99	2.97	0.0103	2.24	0.0109	3.49E-02
3.85	4.57	4.03	2.28	3.29	3.21	3.49E-02
2.92	2.58	2.89	2.01	0.0105	0.0109	3.49E-02
3.13	4.65	3.21	0.0103	0.0105	2.33	3.49E-02
3.88	3.59	3.73	2.22	2.42	3.31	3.49E-02
3.88	3.59	3.73	2.22	2.42	3.31	3.49E-02
3.88	3.59	3.73	2.22	2.42	3.31	3.49E-02
4.97	4.67	4.3	2.84	0.0105	2.5	3.50E-02
4.97	4.67	4.3	2.84	0.0105	2.5	3.50E-02
4	4.04	3.47	2.62	2.44	3.34	3.50E-02
2.89	3.26	3.49	0.0103	2.29	0.0109	3.51E-02
2.89	3.26	3.49	0.0103	2.29	0.0109	3.51E-02
3.97	4.53	4.36	3.13	3.61	2.36	3.51E-02
3.97	4.53	4.36	3.13	3.61	2.36	3.51E-02
3.33	4.15	4.11	0.0103	2.72	0.0109	3.51E-02
3.33	4.15	4.11	0.0103	2.72	0.0109	3.51E-02
5.11	4.09	4	0.0103	3.06	0.0109	3.51E-02
2.79	3.84	3.56	2.33	0.0105	0.0109	3.51E-02
2.79	3.84	3.56	2.33	0.0105	0.0109	3.51E-02
4.44	3.98	3.89	0.0103	2.95	0.0109	3.52E-02
4.44	3.98	3.89	0.0103	2.95	0.0109	3.52E-02
3.66	4.16	4.78	2.43	2.25	0.0109	3.53E-02
3.66	4.16	4.78	2.43	2.25	0.0109	3.53E-02
4.04	4.9	4.47	2.96	3.77	2.51	3.53E-02
3.49	3.01	3.3	0.0103	2.35	0.0109	3.53E-02
3.5	3.61	2.9	2.36	0.0105	0.0109	3.53E-02
3.5	3.61	2.9	2.36	0.0105	0.0109	3.53E-02
3.34	3.54	2.85	0.0103	2.3	0.0109	3.53E-02
0.011	0.012	2.38	3.22	3.54	3.13	3.54E-02
3.97	3.12	4.27	0.0103	2.61	0.0109	3.55E-02
3.97	3.12	4.27	0.0103	2.61	0.0109	3.55E-02
3	3.04	2.51	2.03	0.0105	0.0109	3.55E-02
3	3.04	2.51	2.03	0.0105	0.0109	3.55E-02
4.55	3.49	4.55	2.23	2.41	0.0109	3.56E-02
5.2	3.14	3.85	0.0103	0.0105	2.52	3.56E-02
2.8	3.43	3.66	0.0103	2.31	0.0109	3.56E-02
3.26	3.73	3.09	2.4	0.0105	0.0109	3.56E-02
3.26	3.73	3.09	2.4	0.0105	0.0109	3.56E-02
3.26	3.73	3.09	2.4	0.0105	0.0109	3.56E-02
5.23	4.39	4.39	3.16	3.95	2.82	3.56E-02
5.23	4.39	4.39	3.16	3.95	2.82	3.56E-02
4.7	3.91	3.38	2.74	0.0105	0.0109	3.57E-02
4.7	3.91	3.38	2.74	0.0105	0.0109	3.57E-02
2.51	2.63	2.81	2.95	3.63	3.61	3.58E-02
2.45	2.39	2.89	3.13	4.44	4.17	3.58E-02
4.52	3.64	4.28	3.15	3.45	2.76	3.58E-02
4.52	3.64	4.28	3.15	3.45	2.76	3.58E-02
4.52	3.64	4.28	3.15	3.45	2.76	3.58E-02
3.11	3.03	2.76	0.0103	2.15	0.0109	3.58E-02
4.17	3.88	3.34	0.0103	2.7	0.0109	3.58E-02

4.17	3.88	3.34	0.0103	2.7	0.0109	3.58E-02
4.17	3.88	3.34	0.0103	2.7	0.0109	3.58E-02
2.76	3.6	3.28	2.26	0.0105	0.0109	3.59E-02
4.8	3.83	4.25	3.05	0.0105	0.0109	3.59E-02
4.8	3.83	4.25	3.05	0.0105	0.0109	3.59E-02
2.66	2.47	2.06	3.19	2.84	3.39	3.59E-02
4.26	3	4.1	0.0103	2.57	0.0109	3.60E-02
4.26	3	4.1	0.0103	2.57	0.0109	3.60E-02
2.91	4.54	4.19	0.0103	0.0105	2.53	3.60E-02
3.63	3.32	4.61	0.0103	2.63	0.0109	3.60E-02
3.44	3.55	3.04	2.39	2.94	2.63	3.60E-02
4.41	4.81	3.13	0.0103	0.0105	2.71	3.61E-02
3.03	4.88	4.02	0.0103	2.56	0.0109	3.61E-02
3.03	4.88	4.02	0.0103	2.56	0.0109	3.61E-02
3.47	3.89	3.3	0.0103	2.56	0.0109	3.61E-02
3.47	3.89	3.3	0.0103	2.56	0.0109	3.61E-02
3.37	3.03	3.09	0.0103	2.3	0.0109	3.61E-02
3.37	3.03	3.09	0.0103	2.3	0.0109	3.61E-02
4.29	3.97	3.53	0.0103	2.82	0.0109	3.62E-02
4.13	4.1	4.1	0.0103	3.01	0.0109	3.62E-02
4.05	3.17	4.33	2.67	0.0105	0.0109	3.63E-02
3.43	3.88	3.67	2.66	0.0105	0.0109	3.63E-02
3.7	3.45	3.35	0.0103	2.55	0.0109	3.63E-02
3.7	3.45	3.35	0.0103	2.55	0.0109	3.63E-02
3.7	3.45	3.35	0.0103	2.55	0.0109	3.63E-02
4	4.23	4.53	0.0103	3.09	0.0109	3.63E-02
4	4.23	4.53	0.0103	3.09	0.0109	3.63E-02
4.17	4.16	4.56	3.13	0.0105	0.0109	3.63E-02
2.62	3.12	3.67	2.16	0.0105	0.0109	3.63E-02
2.62	3.12	3.67	2.16	0.0105	0.0109	3.63E-02
5.34	4.33	4.02	2.95	3.57	3.07	3.64E-02
5.34	4.33	4.02	2.95	3.57	3.07	3.64E-02
5.2	4.67	4.42	0.0103	3.44	0.0109	3.64E-02
3.18	4.23	3.56	0.0103	0.0105	2.56	3.64E-02
2.78	2.81	3.11	0.0103	2.11	0.0109	3.64E-02
4.08	3.67	3.85	2.82	0.0105	0.0109	3.65E-02
5.29	5.21	5.22	3.71	4.41	4.75	3.65E-02
5.29	5.21	5.22	3.71	4.41	4.75	3.65E-02
4.06	3.32	4.41	0.0103	2.76	0.0109	3.65E-02
4.06	3.32	4.41	0.0103	2.76	0.0109	3.65E-02
4.06	3.32	4.41	0.0103	2.76	0.0109	3.65E-02
4.63	4.47	4.42	2.69	2.62	0.0109	3.65E-02
4.64	4.7	4.5	3.17	4.23	3.32	3.65E-02
4.64	4.7	4.5	3.17	4.23	3.32	3.65E-02
4.64	4.7	4.5	3.17	4.23	3.32	3.65E-02
4.46	4.69	3.47	2.4	2.25	0.0109	3.66E-02
4.46	4.69	3.47	2.4	2.25	0.0109	3.66E-02
4.46	4.69	3.47	2.4	2.25	0.0109	3.66E-02
4.31	4.54	3.63	0.0103	2.97	0.0109	3.66E-02
4.31	4.54	3.63	0.0103	2.97	0.0109	3.66E-02
3.99	3.41	3.64	0.0103	2.21	2.06	3.66E-02
2.63	2.84	3.07	3.15	3.57	3.55	3.66E-02
2.63	2.84	3.07	3.15	3.57	3.55	3.66E-02
2.66	2.81	2.33	3.56	3.12	3.07	3.67E-02
2.66	2.81	2.33	3.56	3.12	3.07	3.67E-02
4.05	3.64	4.08	2.54	3.44	2.28	3.67E-02
3.28	3.32	2.62	0.0103	2.18	0.0109	3.67E-02
3.28	3.32	2.62	0.0103	2.18	0.0109	3.67E-02

3.34	3.51	3.41	0.0103	2.51	0.0109	3.67E-02
3.34	3.51	3.41	0.0103	2.51	0.0109	3.67E-02
3.71	2.87	2.63	0.0103	2.09	0.0109	3.67E-02
3.71	2.87	2.63	0.0103	2.09	0.0109	3.67E-02
5.36	5.34	5.27	0.0103	3.91	0.0109	3.67E-02
5.36	5.34	5.27	0.0103	3.91	0.0109	3.67E-02
5.36	5.34	5.27	0.0103	3.91	0.0109	3.67E-02
2.8	2.71	3.47	0.0103	2.11	0.0109	3.67E-02
2.88	3.12	3.14	2.23	0.0105	0.0109	3.68E-02
0.011	2.25	0.0117	3.72	3.03	2.85	3.68E-02
0.011	0.012	2.21	5.12	3.89	2.66	3.68E-02
4.31	4.16	4.75	0.0103	2.65	2.49	3.68E-02
4.31	4.16	4.75	0.0103	2.65	2.49	3.68E-02
4.06	2.49	3.61	0.0103	2.18	0.0109	3.68E-02
4.06	2.49	3.61	0.0103	2.18	0.0109	3.68E-02
3.6	3.22	4.03	0.0103	2.59	0.0109	3.69E-02
3.65	2.84	2.77	0.0103	2.15	0.0109	3.69E-02
3.65	2.84	2.77	0.0103	2.15	0.0109	3.69E-02
4.12	3.74	3.98	0.0103	2.89	0.0109	3.69E-02
4.36	4.57	4.33	3.28	3.59	2.08	3.70E-02
4.36	4.57	4.33	3.28	3.59	2.08	3.70E-02
4.58	4.12	3.21	2.73	0.0105	0.0109	3.70E-02
4.37	4.05	4.65	3.32	3.8	2.77	3.70E-02
4.37	4.05	4.65	3.32	3.8	2.77	3.70E-02
3.24	2.84	3.65	2.31	0.0105	0.0109	3.70E-02
3.24	2.84	3.65	2.31	0.0105	0.0109	3.70E-02
3.05	3.21	2.82	2.21	0.0105	0.0109	3.70E-02
3.38	2.59	2.85	0.0103	2.08	0.0109	3.70E-02
3.38	2.59	2.85	0.0103	2.08	0.0109	3.70E-02
2.7	3.07	3.61	0.0103	2.2	0.0109	3.71E-02
2.7	3.07	3.61	0.0103	2.2	0.0109	3.71E-02
5.97	4.31	5.19	0.0103	3.59	0.0109	3.71E-02
0.011	2.12	0.0117	3.04	3.67	2.56	3.72E-02
0.011	2.12	0.0117	3.04	3.67	2.56	3.72E-02
3.32	3.37	3.55	0.0103	2.51	0.0109	3.72E-02
3.32	3.37	3.55	0.0103	2.51	0.0109	3.72E-02
4.24	4.73	3.5	2.92	0.0105	0.0109	3.72E-02
3.27	4.35	3.54	0.0103	2.61	0.0109	3.72E-02
0.011	0.012	2.06	2.38	3.68	3.23	3.72E-02
3.95	3.72	4.03	2.99	3.43	2.4	3.72E-02
3.95	3.72	4.03	2.99	3.43	2.4	3.72E-02
3.54	4.5	4.32	2.94	0.0105	0.0109	3.72E-02
3.54	4.5	4.32	2.94	0.0105	0.0109	3.72E-02
4.79	3.99	3.93	0.0103	2.24	2.59	3.72E-02
4.12	4.55	4.08	3.11	0.0105	0.0109	3.73E-02
3.25	3.3	3.38	2.44	0.0105	0.0109	3.73E-02
0.011	0.012	2.58	3.17	3.8	3.73	3.73E-02
3.82	3.25	2.92	0.0103	2.36	0.0109	3.73E-02
3.82	3.25	2.92	0.0103	2.36	0.0109	3.73E-02
4	3.71	3.17	2.6	0.0105	0.0109	3.73E-02
4.12	4.62	2.9	0.0103	2.54	0.0109	3.73E-02
4.12	4.62	2.9	0.0103	2.54	0.0109	3.73E-02
5.15	4.73	4.71	0.0103	3.29	2.27	3.73E-02
3.53	3.01	2.69	0.0103	2.18	0.0109	3.73E-02
3.53	3.01	2.69	0.0103	2.18	0.0109	3.73E-02
3.49	2.88	4.84	0.0103	0.0105	2.32	3.73E-02
3.49	2.88	4.84	0.0103	0.0105	2.32	3.73E-02
3.43	4.34	3.26	0.0103	0.0105	2.57	3.73E-02

3.43	4.34	3.26	0.0103	0.0105	2.57	3.73E-02
2.7	3.38	3.3	0.0103	2.24	0.0109	3.74E-02
2.7	3.38	3.3	0.0103	2.24	0.0109	3.74E-02
3.88	3.96	4.09	3.33	3.43	2.55	3.74E-02
3.88	3.96	4.09	3.33	3.43	2.55	3.74E-02
2.94	3.01	4.23	0.0103	2.26	0.0109	3.75E-02
2.94	3.01	4.23	0.0103	2.26	0.0109	3.75E-02
5.28	4.45	4.35	0.0103	2.94	2.41	3.75E-02
5.28	4.45	4.35	0.0103	2.94	2.41	3.75E-02
3.85	3.86	2.65	0.0103	2.33	0.0109	3.75E-02
3.85	3.86	2.65	0.0103	2.33	0.0109	3.75E-02
4.19	4.03	4.62	3.13	0.0105	0.0109	3.76E-02
5.53	4.88	5.38	3.4	2.71	0.0109	3.76E-02
5.53	4.88	5.38	3.4	2.71	0.0109	3.76E-02
5.53	4.88	5.38	3.4	2.71	0.0109	3.76E-02
3.58	3.52	2.54	0.0103	2.21	0.0109	3.76E-02
2.87	2.63	3.09	2.09	0.0105	0.0109	3.77E-02
3.52	3.83	2.83	2.39	0.0105	0.0109	3.77E-02
3.48	2.53	2.98	2.1	0.0105	0.0109	3.77E-02
4.07	4.23	4.44	0.0103	0.0105	3.13	3.77E-02
4.07	4.23	4.44	0.0103	0.0105	3.13	3.77E-02
4.26	4.44	4.45	0.0103	3.24	0.0109	3.78E-02
0.011	3.41	0.0117	4.46	4.54	4.89	3.78E-02
0.011	3.41	0.0117	4.46	4.54	4.89	3.78E-02
4.76	4.68	4.9	3.14	2.46	0.0109	3.78E-02
4.76	4.68	4.9	3.14	2.46	0.0109	3.78E-02
4.76	4.68	4.9	3.14	2.46	0.0109	3.78E-02
2.81	2.78	2.98	0.0103	2.11	0.0109	3.78E-02
2.81	2.78	2.98	0.0103	2.11	0.0109	3.78E-02
3.32	3.38	2.74	2.27	0.0105	0.0109	3.79E-02
4.05	4	4.06	2.39	0.0105	2.41	3.79E-02
4.4	4.31	4.45	2.91	0.0105	2.22	3.79E-02
2.06	0.012	0.0117	2.63	2.79	2.99	3.79E-02
2.06	0.012	0.0117	2.63	2.79	2.99	3.79E-02
4.35	4.52	3.91	3.12	0.0105	0.0109	3.79E-02
0.011	0.012	3.18	4.51	4.02	4.45	3.79E-02
0.011	0.012	3.18	4.51	4.02	4.45	3.79E-02
3.13	2.6	3.18	3.66	3.44	3.9	3.79E-02
3.13	2.6	3.18	3.66	3.44	3.9	3.79E-02
3.16	3.13	3.14	0.0103	2.33	0.0109	3.80E-02
3.16	3.13	3.14	0.0103	2.33	0.0109	3.80E-02
3.2	4.17	3.5	0.0103	2.58	0.0109	3.80E-02
3.72	4	3.4	0.0103	2.71	0.0109	3.80E-02
3.72	4	3.4	0.0103	2.71	0.0109	3.80E-02
4.15	3.95	4.07	2.4	0.0105	2.42	3.80E-02
4.4	3.63	4.72	0.0103	2.41	2.42	3.80E-02
3.62	2.29	3.19	0.0103	2.01	0.0109	3.81E-02
3.62	2.29	3.19	0.0103	2.01	0.0109	3.81E-02
3.62	2.29	3.19	0.0103	2.01	0.0109	3.81E-02
3.39	3.9	3.29	0.0103	2.57	0.0109	3.81E-02
3.58	4.02	3.51	2.31	0.0105	2.02	3.81E-02
3.58	4.02	3.51	2.31	0.0105	2.02	3.81E-02
2.3	0.012	0.0117	3.07	3.61	2.89	3.82E-02
2.3	0.012	0.0117	3.07	3.61	2.89	3.82E-02
4.32	4.58	2.47	0.0103	2.24	0.0109	3.82E-02
4.32	4.58	2.47	0.0103	2.24	0.0109	3.82E-02
3.7	3.72	4.52	3.16	2.94	3.24	3.82E-02
3.7	3.72	4.52	3.16	2.94	3.24	3.82E-02

3.7	3.72	4.52	3.16	2.94	3.24	3.82E-02
2.51	3.13	2.74	2.02	0.0105	0.0109	3.82E-02
3.06	2.56	2.84	0.0103	2.06	0.0109	3.82E-02
4.13	3.57	2.51	0.0103	0.0105	2.21	3.82E-02
4.13	3.57	2.51	0.0103	0.0105	2.21	3.82E-02
5.15	4.86	3.91	0.0103	2.3	2.89	3.82E-02
3.49	2.92	3.28	2.36	0.0105	0.0109	3.83E-02
5.33	4.45	4.29	0.0103	3.38	0.0109	3.83E-02
5.33	4.45	4.29	0.0103	3.38	0.0109	3.83E-02
5.33	4.45	4.29	0.0103	3.38	0.0109	3.83E-02
5.33	4.45	4.29	0.0103	3.38	0.0109	3.83E-02
4.63	3.76	3.47	2.37	3.04	2.8	3.83E-02
4.63	3.76	3.47	2.37	3.04	2.8	3.83E-02
4.63	3.76	3.47	2.37	3.04	2.8	3.83E-02
2.49	2.72	3.43	0.0103	2.01	0.0109	3.83E-02
4.03	3.36	4.73	0.0103	2.82	0.0109	3.83E-02
3.88	4.42	3.25	3	2.45	2.69	3.83E-02
3.6	3.39	3.57	2.61	0.0105	0.0109	3.83E-02
3.6	3.39	3.57	2.61	0.0105	0.0109	3.83E-02
0.011	0.012	2.18	2.83	2.8	3.72	3.84E-02
4.91	4.14	4.98	0.0103	2.24	3.08	3.85E-02
4.09	3.35	4.12	2.79	0.0105	0.0109	3.85E-02
4.09	3.35	4.12	2.79	0.0105	0.0109	3.85E-02
4.09	3.35	4.12	2.79	0.0105	0.0109	3.85E-02
4.29	4.27	4.72	0.0103	3.27	0.0109	3.85E-02
4.29	4.27	4.72	0.0103	3.27	0.0109	3.85E-02
4.29	4.27	4.72	0.0103	3.27	0.0109	3.85E-02
4.32	3.71	4.28	2.66	3.61	2.76	3.85E-02
4.06	3.82	4.14	0.0103	0.0105	2.97	3.85E-02
3.23	4.85	4.45	0.0103	2.84	0.0109	3.86E-02
3.45	4.49	4.4	2.11	2.52	0.0109	3.86E-02
0.011	0.012	2.03	2.49	2.76	3.36	3.86E-02
4.31	3.88	3.39	2.87	3.13	3.06	3.86E-02
4.28	3.74	4.42	3.04	0.0105	0.0109	3.87E-02
4.35	4.03	3.61	3.41	3.35	3.2	3.87E-02
4.35	4.03	3.61	3.41	3.35	3.2	3.87E-02
2.8	3.18	3.45	2.29	0.0105	0.0109	3.87E-02
3.06	2.68	2.76	2.09	0.0105	0.0109	3.88E-02
3.06	2.68	2.76	2.09	0.0105	0.0109	3.88E-02
4.94	4.9	5.1	0.0103	3.5	2.17	3.88E-02
4.94	4.9	5.1	0.0103	3.5	2.17	3.88E-02
4.11	4.1	4.26	2.84	3.44	3.74	3.88E-02
4.11	4.1	4.26	2.84	3.44	3.74	3.88E-02
3.43	3.3	2.6	0.0103	0.0105	2.22	3.88E-02
2.81	3.38	2.99	0.0103	2.24	0.0109	3.89E-02
2.81	3.38	2.99	0.0103	2.24	0.0109	3.89E-02
4.71	3.63	3.43	0.0103	2.74	0.0109	3.90E-02
4.97	4.64	4.63	3.87	3.94	2.73	3.90E-02
4.97	4.64	4.63	3.87	3.94	2.73	3.90E-02
3.24	2.59	2.65	0.0103	2.04	0.0109	3.90E-02
3.24	2.59	2.65	0.0103	2.04	0.0109	3.90E-02
4.54	3.03	4.35	0.0103	2.7	0.0109	3.91E-02
4.54	3.03	4.35	0.0103	2.7	0.0109	3.91E-02
2.42	0.012	0.0117	3.37	3.07	3.33	3.91E-02
3.22	3.56	3.26	3.03	2.53	2.84	3.91E-02
4.31	4.33	3.04	0.0103	2.69	0.0109	3.92E-02
4.31	4.33	3.04	0.0103	2.69	0.0109	3.92E-02
2.96	2.61	2.73	0.0103	2.05	0.0109	3.92E-02

3.33	3.41	5.03	2.56	0.0105	0.0109	3.92E-02
5.41	4.21	4.61	2.98	0.0105	2.41	3.93E-02
3.9	5.19	4.16	3.14	0.0105	0.0109	3.93E-02
3.9	5.19	4.16	3.14	0.0105	0.0109	3.93E-02
4.01	3.36	2.94	2.44	0.0105	0.0109	3.93E-02
4.01	3.36	2.94	2.44	0.0105	0.0109	3.93E-02
3.91	2.92	3.4	0.0103	2.44	0.0109	3.93E-02
5.26	3.76	4.18	0.0103	3.08	0.0109	3.93E-02
4.05	3.17	4.33	2.67	2.96	2.25	3.93E-02
3.83	3.1	4.31	2.28	2.33	2.93	3.94E-02
2.92	2.69	2.72	0.0103	2.07	0.0109	3.94E-02
2.92	2.69	2.72	0.0103	2.07	0.0109	3.94E-02
4.82	3.51	4.44	2.5	2.27	0.0109	3.95E-02
4.82	3.51	4.44	2.5	2.27	0.0109	3.95E-02
3.23	4.28	3.72	0.0103	2.69	0.0109	3.95E-02
3.82	4.09	4.47	3.35	3.39	2.49	3.96E-02
3.92	4.82	4.32	0.0103	3.19	0.0109	3.96E-02
3.92	4.82	4.32	0.0103	3.19	0.0109	3.96E-02
3.92	4.82	4.32	0.0103	3.19	0.0109	3.96E-02
3.68	3.96	4.43	0.0103	2.96	0.0109	3.96E-02
3.68	3.96	4.43	0.0103	2.96	0.0109	3.96E-02
3.68	3.96	4.43	0.0103	2.96	0.0109	3.96E-02
2.72	2.81	2.76	0.0103	2.07	0.0109	3.96E-02
4.03	3.51	4.06	0.0103	2.86	0.0109	3.97E-02
4.36	3.4	4.52	0.0103	2.93	0.0109	3.97E-02
4.36	3.4	4.52	0.0103	2.93	0.0109	3.97E-02
4.84	3.97	3.89	3.53	2.46	2.7	3.97E-02
3.9	4.36	4.92	2.8	2.24	0.0109	3.97E-02
3.9	4.36	4.92	2.8	2.24	0.0109	3.97E-02
5.35	4.78	5.04	3.58	0.0105	2.12	3.97E-02
3.62	2.96	3.43	0.0103	2.45	0.0109	3.98E-02
3.62	2.96	3.43	0.0103	2.45	0.0109	3.98E-02
5.54	4.8	5.85	4.1	4.67	3.82	3.98E-02
5.54	4.8	5.85	4.1	4.67	3.82	3.98E-02
5.54	4.8	5.85	4.1	4.67	3.82	3.98E-02
5.54	4.8	5.85	4.1	4.67	3.82	3.98E-02
3.36	3.55	3.1	2.48	0.0105	0.0109	3.98E-02
2.39	2.87	3.62	2.02	0.0105	0.0109	3.99E-02
4.26	3.99	4.94	2.39	0.0105	2.71	3.99E-02
2.82	3.19	2.9	2.21	0.0105	0.0109	3.99E-02
3.47	3.92	3.76	2.77	3.32	2.42	3.99E-02
3.47	3.92	3.76	2.77	3.32	2.42	3.99E-02
3.37	2.35	3.4	0.0103	2.1	0.0109	3.99E-02
3.37	2.35	3.4	0.0103	2.1	0.0109	3.99E-02
3.9	3.91	2.82	0.0103	2.49	0.0109	3.99E-02
3.9	3.91	2.82	0.0103	2.49	0.0109	3.99E-02
4.26	3.48	4.22	0.0103	2.92	0.0109	4.00E-02
3.68	3.91	4.03	3.62	3.28	3.14	4.00E-02
3.54	2.47	3.48	2.2	0.0105	0.0109	4.00E-02
5.1	5.36	4.75	3.37	4.54	3.86	4.00E-02
5.1	5.36	4.75	3.37	4.54	3.86	4.00E-02
4.12	3.75	3.4	0.0103	2.77	0.0109	4.01E-02
2.76	2.54	3.22	0.0103	0.0105	2.07	4.01E-02
5.16	3.61	5.25	0.0103	3.23	0.0109	4.01E-02
2.02	0.012	0.0117	2.79	2.9	2.47	4.03E-02
4.52	4.32	4.99	0.0103	3.43	0.0109	4.03E-02
4.52	4.32	4.99	0.0103	3.43	0.0109	4.03E-02
2.78	4.04	3.17	2.09	2.33	2.17	4.03E-02

2.78	4.04	3.17	2.09	2.33	2.17	4.03E-02
3.84	3.74	4.82	0.0103	2.98	0.0109	4.04E-02
3.84	3.74	4.82	0.0103	2.98	0.0109	4.04E-02
4.37	2.19	4.21	0.0103	2.03	0.0109	4.04E-02
3.48	3.05	2.79	2.28	0.0105	0.0109	4.04E-02
3.02	2.69	2.69	2.52	2.36	2.45	4.04E-02
2.28	0.012	0.0117	3.99	3.32	2.63	4.04E-02
2.28	0.012	0.0117	3.99	3.32	2.63	4.04E-02
2.47	3.26	3.25	0.0103	0.0105	2.15	4.04E-02
2.47	3.26	3.25	0.0103	0.0105	2.15	4.04E-02
0.011	0.012	2.47	4.11	3.17	3.11	4.04E-02
4.24	3.75	3.38	0.0103	2.78	0.0109	4.04E-02
3.95	4.7	5	0.0103	2.89	2.35	4.04E-02
3.95	4.7	5	0.0103	2.89	2.35	4.04E-02
3.95	4.7	5	0.0103	2.89	2.35	4.04E-02
3.76	3.82	3.58	3.29	2.21	2.79	4.05E-02
3.76	3.82	3.58	3.29	2.21	2.79	4.05E-02
3.21	3.48	2.93	0.0103	2.38	0.0109	4.05E-02
4.97	4.91	4.16	2.15	3.88	2.96	4.05E-02
4.97	4.91	4.16	2.15	3.88	2.96	4.05E-02
5.49	4.31	5.3	0.0103	3.67	0.0109	4.05E-02
5.49	4.31	5.3	0.0103	3.67	0.0109	4.05E-02
3.95	4.57	4.3	0.0103	2.71	2.35	4.05E-02
3.95	4.57	4.3	0.0103	2.71	2.35	4.05E-02
3.59	3.11	2.87	0.0103	2.34	0.0109	4.05E-02
3.59	3.11	2.87	0.0103	2.34	0.0109	4.05E-02
4.99	4.2	4.19	2.15	2.97	0.0109	4.05E-02
3.65	3.19	3.26	0.0103	2.51	0.0109	4.06E-02
3.65	3.19	3.26	0.0103	2.51	0.0109	4.06E-02
3.65	3.26	3.19	0.0103	0.0105	2.51	4.06E-02
4.25	4.04	3.69	0.0103	0.0105	2.98	4.06E-02
2.71	4.63	3.94	2.44	0.0105	0.0109	4.06E-02
2.71	4.63	3.94	2.44	0.0105	0.0109	4.06E-02
4.79	5.05	4.75	4.2	4.41	3.57	4.06E-02
4.33	4.61	3.59	0.0103	3.05	0.0109	4.07E-02
3.13	2.8	2.71	0.0103	0.0105	2.15	4.09E-02
3.13	2.8	2.71	0.0103	0.0105	2.15	4.09E-02
3.94	2.53	3.41	0.0103	0.0105	2.25	4.09E-02
4.38	4.89	4.13	2.78	3.81	2.24	4.09E-02
4.38	4.89	4.13	2.78	3.81	2.24	4.09E-02
3.32	3.59	4.22	3.01	2.51	2.88	4.09E-02
3.32	3.59	4.22	3.01	2.51	2.88	4.09E-02
4.19	4.03	4.62	0.0103	3.2	0.0109	4.09E-02
3.39	2.78	3.1	0.0103	2.29	0.0109	4.10E-02
3.39	2.78	3.1	0.0103	2.29	0.0109	4.10E-02
3.15	2.79	2.9	2.21	0.0105	0.0109	4.10E-02
4.65	3.26	4.57	2.92	0.0105	0.0109	4.10E-02
2.67	0.012	0.0117	3.26	3.56	4.73	4.10E-02
2.67	0.012	0.0117	3.26	3.56	4.73	4.10E-02
3.31	4.15	4.04	2.27	2.2	0.0109	4.10E-02
3.31	4.15	4.04	2.27	2.2	0.0109	4.10E-02
3.69	3.69	2.82	2.41	2.7	2.22	4.10E-02
3.69	3.69	2.82	2.41	2.7	2.22	4.10E-02
2.82	3.03	2.63	2.19	2.57	2.17	4.12E-02
2.82	3.03	2.63	2.19	2.57	2.17	4.12E-02
2.99	0.012	0.0117	3.81	3.85	4.31	4.12E-02
3.79	4.72	2.65	0.0103	2.36	0.0109	4.12E-02
3.79	4.72	2.65	0.0103	2.36	0.0109	4.12E-02

2.42	4.03	4.2	0.0103	2.26	0.0109	4.13E-02
2.42	4.03	4.2	0.0103	2.26	0.0109	4.13E-02
4.41	4.26	4.09	0.0103	3.21	0.0109	4.13E-02
4.41	4.26	4.09	0.0103	3.21	0.0109	4.13E-02
3.36	3.13	3.6	2.52	2.46	3.05	4.13E-02
4.87	3.41	4.96	2.64	3.22	2.49	4.13E-02
3.59	3.18	3.7	2.61	0.0105	0.0109	4.13E-02
5.15	2.35	4.39	0.0103	2.13	0.0109	4.13E-02
5.15	2.35	4.39	0.0103	2.13	0.0109	4.13E-02
3.03	3.16	2.88	0.0103	2.28	0.0109	4.13E-02
3.03	3.16	2.88	0.0103	2.28	0.0109	4.13E-02
3.82	4.5	3.47	3.19	2.85	2.44	4.13E-02
3.82	4.5	3.47	3.19	2.85	2.44	4.13E-02
2.91	2.81	2.4	0.0103	2.01	0.0109	4.13E-02
3.79	4.33	3.58	3.24	3.29	3.15	4.14E-02
3.79	4.33	3.58	3.24	3.29	3.15	4.14E-02
3.8	3.32	3.88	2.74	0.0105	0.0109	4.14E-02
4.37	4.1	4.53	0.0103	2.41	2.78	4.14E-02
4.37	4.1	4.53	0.0103	2.41	2.78	4.14E-02
3.84	3.25	3.72	0.0103	2.69	0.0109	4.14E-02
3.84	3.25	3.72	0.0103	2.69	0.0109	4.14E-02
3.75	2.58	3.91	2.35	0.0105	0.0109	4.14E-02
3.75	2.58	3.91	2.35	0.0105	0.0109	4.14E-02
2.76	2.58	3.55	0.0103	2.11	0.0109	4.15E-02
2.76	2.58	3.55	0.0103	2.11	0.0109	4.15E-02
3.54	2.43	3.08	0.0103	2.13	0.0109	4.15E-02
3.4	3.15	3.18	2.45	0.0105	0.0109	4.15E-02
4.64	3.75	3.76	3.21	3.01	2.26	4.15E-02
4.64	3.75	3.76	3.21	3.01	2.26	4.15E-02
5	4.19	4.29	0.0103	2.46	2.83	4.15E-02
5	4.19	4.29	0.0103	2.46	2.83	4.15E-02
4.98	4.1	4.64	2.17	3.86	2.72	4.16E-02
2.95	0.012	0.0117	3.98	4.09	3.67	4.16E-02
2.95	0.012	0.0117	3.98	4.09	3.67	4.16E-02
2.62	3.74	3.38	0.0103	2.31	0.0109	4.16E-02
3.12	3.09	2.71	0.0103	2.23	0.0109	4.16E-02
3.12	3.09	2.71	0.0103	2.23	0.0109	4.16E-02
2.94	4.44	3.7	0.0103	0.0105	2.57	4.17E-02
2.96	2.66	3.25	0.0103	0.0105	2.2	4.17E-02
0.011	0.012	2.34	3.49	2.8	3.18	4.17E-02
4.19	5.08	4.83	3.5	0.0105	0.0109	4.17E-02
4.19	5.08	4.83	3.5	0.0105	0.0109	4.17E-02
2.9	3.84	3.45	0.0103	2.48	0.0109	4.17E-02
2.9	3.84	3.45	0.0103	2.48	0.0109	4.17E-02
4.1	4.27	2.67	0.0103	2.47	0.0109	4.17E-02
4.1	4.27	2.67	0.0103	2.47	0.0109	4.17E-02
3.29	3.67	3.67	2.67	0.0105	0.0109	4.18E-02
3.83	4.42	3.32	2.81	0.0105	0.0109	4.18E-02
3.88	4.55	4.14	0.0103	2.37	2.62	4.18E-02
3.88	4.55	4.14	0.0103	2.37	2.62	4.18E-02
3.57	3.15	3.91	2.63	0.0105	0.0109	4.18E-02
4.31	3.88	3.92	1.95	3.4	2.83	4.18E-02
4.31	3.88	3.92	1.95	3.4	2.83	4.18E-02
4.07	2.66	3.14	0.0103	2.26	0.0109	4.18E-02
3.31	3.14	3.28	2.46	0.0105	0.0109	4.18E-02
4.15	4.07	5.07	0.0103	0.0105	3.26	4.18E-02
3.14	4.48	3.99	2.76	0.0105	0.0109	4.18E-02
4.51	5.19	5.13	2.81	3.09	0.0109	4.18E-02

4.51	5.19	5.13	2.81	3.09	0.0109	4.18E-02
3.21	2.41	3.76	2.15	0.0105	0.0109	4.18E-02
4.51	5.19	5.13	0.0103	3.09	2.81	4.19E-02
2.48	4.31	3.02	0.0103	2.06	0.0109	4.19E-02
3.57	3.38	2.63	0.0103	2.31	0.0109	4.19E-02
3.57	3.38	2.63	0.0103	2.31	0.0109	4.19E-02
2.96	3.89	2.98	2.36	0.0105	0.0109	4.19E-02
2.96	3.89	2.98	2.36	0.0105	0.0109	4.19E-02
3.32	3.6	3.18	3.01	3.03	2.83	4.19E-02
0.011	0.012	2.03	3.36	2.9	2.32	4.19E-02
0.011	0.012	2.03	3.36	2.9	2.32	4.19E-02
2.82	3.8	3.72	0.0103	2.49	0.0109	4.19E-02
2.82	3.8	3.72	0.0103	2.49	0.0109	4.19E-02
3.53	2.38	3.09	0.0103	2.11	0.0109	4.19E-02
3.54	2.25	3.05	0.0103	2.02	0.0109	4.19E-02
3.54	2.25	3.05	0.0103	2.02	0.0109	4.19E-02
4.18	3.84	4.02	0.0103	3.04	0.0109	4.20E-02
4	3.93	3.7	0.0103	2.94	0.0109	4.21E-02
4	3.93	3.7	0.0103	2.94	0.0109	4.21E-02
4	3.93	3.7	0.0103	2.94	0.0109	4.21E-02
3.94	3.14	3.17	0.0103	2.51	0.0109	4.21E-02
4.62	3.93	3.34	0.0103	2.86	0.0109	4.21E-02
3.57	2.82	2.97	2.3	0.0105	0.0109	4.22E-02
3.21	3.3	2.73	0.0103	0.0105	2.3	4.22E-02
4.12	4.72	5.22	2.72	2.63	3.97	4.22E-02
4.12	4.72	5.22	2.72	2.63	3.97	4.22E-02
4.08	4.71	3.73	0.0103	3.09	0.0109	4.23E-02
4.08	4.71	3.73	0.0103	3.09	0.0109	4.23E-02
0.011	0.012	2.37	2.88	4.02	3.09	4.23E-02
5.33	4.04	4.78	2.59	3.89	2.88	4.24E-02
5.33	4.04	4.78	2.59	3.89	2.88	4.24E-02
3.93	3.74	3.39	0.0103	2.78	0.0109	4.24E-02
3.07	2.7	3.39	0.0103	2.27	0.0109	4.24E-02
3.08	2.93	2.77	2.22	0.0105	0.0109	4.25E-02
4.7	4.63	4.97	0.0103	3.15	2.58	4.25E-02
4.7	4.63	4.97	0.0103	3.15	2.58	4.25E-02
2.65	3.02	2.53	0.0103	0.0105	2.05	4.25E-02
2.65	3.02	2.53	0.0103	0.0105	2.05	4.25E-02
3.08	3.64	3.29	2.46	2.26	2.96	4.26E-02
3.86	3.35	3.91	2.79	0.0105	0.0109	4.26E-02
3.93	3.86	4.06	0.0103	3.01	0.0109	4.26E-02
3.07	4.36	3.89	0.0103	2.71	0.0109	4.26E-02
3.37	3.58	2.47	0.0103	2.23	0.0109	4.26E-02
3.37	3.58	2.47	0.0103	2.23	0.0109	4.26E-02
3.64	2.62	3.37	2.32	0.0105	0.0109	4.26E-02
3.03	2.91	2.85	2.4	2.57	2.77	4.27E-02
0.011	0.012	2.26	2.56	4.09	3.29	4.27E-02
0.011	0.012	2.26	2.56	4.09	3.29	4.27E-02
4.54	4.69	4.22	2.64	2.78	0.0109	4.27E-02
3.81	2.2	3.87	2.09	0.0105	0.0109	4.27E-02
4.62	3.96	4.78	2.65	2.65	0.0109	4.27E-02
3.46	2.63	3.51	0.0103	2.33	0.0109	4.27E-02
3.4	2.48	3.07	0.0103	2.17	0.0109	4.27E-02
3.4	2.48	3.07	0.0103	2.17	0.0109	4.27E-02
4.76	3.76	4.13	0.0103	3.13	0.0109	4.27E-02
4.76	3.76	4.13	0.0103	3.13	0.0109	4.27E-02
3.66	4.03	4.42	0.0103	3.03	0.0109	4.28E-02
2.94	3.14	3.7	0.0103	2.42	0.0109	4.28E-02

2.94	3.14	3.7	0.0103	2.42	0.0109	4.28E-02
3	3.38	2.95	0.0103	0.0105	2.35	4.28E-02
4.47	3.92	4.68	2.3	3.52	3.35	4.28E-02
2.57	3.87	4.21	0.0103	0.0105	2.39	4.28E-02
2.57	3.87	4.21	0.0103	0.0105	2.39	4.28E-02
5.15	4.68	4.48	0.0103	3.32	2.24	4.28E-02
2.94	3.59	3.2	0.0103	2.43	0.0109	4.28E-02
3.93	3.85	5.13	0.0103	3.11	0.0109	4.29E-02
3.93	3.85	5.13	0.0103	3.11	0.0109	4.29E-02
3.93	3.85	5.13	0.0103	3.11	0.0109	4.29E-02
5.32	5.21	5.1	4.71	3.69	3.13	4.29E-02
5.32	5.21	5.1	4.71	3.69	3.13	4.29E-02
4.73	4.72	4.1	3.54	4.07	3.49	4.29E-02
4.73	4.72	4.1	3.54	4.07	3.49	4.29E-02
4.73	4.72	4.1	3.54	4.07	3.49	4.29E-02
3.72	2.6	3.62	2.36	0.0105	0.0109	4.30E-02
3.72	2.6	3.62	2.36	0.0105	0.0109	4.30E-02
4.38	4.24	3.7	2.23	3.55	2.13	4.30E-02
4.27	4.68	3.83	2.88	3.72	3.09	4.30E-02
3.59	2.98	3.5	0.0103	2.52	0.0109	4.30E-02
3.59	2.98	3.5	0.0103	2.52	0.0109	4.30E-02
3.71	3.76	3.15	0.0103	2.66	0.0109	4.30E-02
3.71	3.76	3.15	0.0103	2.66	0.0109	4.30E-02
3.71	3.76	3.15	0.0103	2.66	0.0109	4.30E-02
3	3.2	2.56	0.0103	2.18	0.0109	4.30E-02
3	3.2	2.56	0.0103	2.18	0.0109	4.30E-02
3	3.2	2.56	0.0103	2.18	0.0109	4.30E-02
3	3.2	2.56	0.0103	2.18	0.0109	4.30E-02
5.07	4.33	4.37	3.27	3.81	3.93	4.30E-02
5.07	4.33	4.37	3.27	3.81	3.93	4.30E-02
5.07	4.33	4.37	3.27	3.81	3.93	4.30E-02
3.72	3.21	3.62	0.0103	2.66	0.0109	4.30E-02
3.98	3.71	4.61	2.48	3.51	2.4	4.31E-02
3.98	3.71	4.61	2.48	3.51	2.4	4.31E-02
4.58	4.22	4.23	0.0103	3.31	0.0109	4.31E-02
4.58	4.22	4.23	0.0103	3.31	0.0109	4.31E-02
0.011	0.012	2.28	2.77	3.49	2.94	4.32E-02
4.63	5.2	4.14	2.58	2.91	0.0109	4.32E-02
4.63	5.2	4.14	2.58	2.91	0.0109	4.32E-02
4.98	4.14	4.98	0.0103	3	2.56	4.32E-02
3.52	3.57	3.8	3.08	3.37	2.79	4.32E-02
4.55	4.17	4.09	0.0103	3.25	0.0109	4.33E-02
3.15	2.71	2.88	0.0103	0.0105	2.21	4.35E-02
3.02	2.74	3.31	0.0103	2.28	0.0109	4.35E-02
0.011	0.012	2.2	3.21	2.46	3.42	4.35E-02
0.011	0.012	2.2	3.21	2.46	3.42	4.35E-02
5.09	3.47	4.76	0.0103	3.16	0.0109	4.36E-02
4.87	4.74	4.63	0.0103	3.23	2.48	4.36E-02
5.32	4.49	3.72	0.0103	0.0105	3.25	4.36E-02
3.82	3.19	4.04	0.0103	0.0105	2.75	4.36E-02
3.16	2.82	2.98	2.28	0.0105	0.0109	4.37E-02
4.84	4.67	4.16	2.97	2.49	0.0109	4.37E-02
3.25	2.93	2.94	0.0103	2.32	0.0109	4.38E-02
3.25	2.93	2.94	0.0103	2.32	0.0109	4.38E-02
4.16	3.38	4.6	2.73	3.25	2.56	4.38E-02
0.011	0.012	2.3	2.67	3.14	4.06	4.38E-02
0.011	0.012	2.3	2.67	3.14	4.06	4.38E-02
4.64	4.21	3.8	2.57	2.47	0.0109	4.38E-02

4.64	4.21	3.8	2.57	2.47	0.0109	4.38E-02
3.39	4.45	2.43	0.0103	2.17	0.0109	4.38E-02
3.39	4.45	2.43	0.0103	2.17	0.0109	4.38E-02
2.72	0.012	0.0117	3.37	3.88	3.48	4.38E-02
2.72	0.012	0.0117	3.37	3.88	3.48	4.38E-02
2.97	3.45	4.14	0.0103	2.56	0.0109	4.38E-02
2.97	3.45	4.14	0.0103	2.56	0.0109	4.38E-02
4.33	4.03	5.12	3.35	0.0105	0.0109	4.39E-02
4.33	4.03	5.12	3.35	0.0105	0.0109	4.39E-02
3.64	2.57	3.14	0.0103	2.26	0.0109	4.39E-02
3.53	2.32	3.12	0.0103	2.11	0.0109	4.39E-02
3.5	4.44	4.77	2.57	3.1	3.26	4.39E-02
3.5	4.44	4.77	2.57	3.1	3.26	4.39E-02
3.87	3.6	3.2	0.0103	2.69	0.0109	4.40E-02
4.08	3.32	3.3	2.24	2.98	2.57	4.40E-02
0.011	2.16	0.0117	2.54	3.67	2.86	4.41E-02
3.91	3.28	2.81	2.51	2.34	2.33	4.41E-02
3.19	2.77	3.05	0.0103	0.0105	2.29	4.41E-02
3.19	2.77	3.05	0.0103	0.0105	2.29	4.41E-02
2.51	2.65	2.85	2.04	0.0105	0.0109	4.41E-02
4.35	3.91	4.33	0.0103	2.84	2.19	4.41E-02
4.35	3.91	4.33	0.0103	2.84	2.19	4.41E-02
4.69	5.35	4.97	2.92	4.39	3.65	4.41E-02
4.69	5.35	4.97	2.92	4.39	3.65	4.41E-02
4.69	5.35	4.97	2.92	4.39	3.65	4.41E-02
4.69	5.35	4.97	2.92	4.39	3.65	4.41E-02
4.69	5.35	4.97	2.92	4.39	3.65	4.41E-02
4.69	5.35	4.97	2.92	4.39	3.65	4.41E-02
4.23	4.01	3.93	0.0103	2.58	2.37	4.41E-02
4.33	3.47	3.17	2.36	2.7	2.72	4.41E-02
0.011	0.012	2.63	3.09	4.13	3.47	4.42E-02
4.05	3.47	4.7	0.0103	3	0.0109	4.42E-02
4.05	3.47	4.7	0.0103	3	0.0109	4.42E-02
4.21	4.44	4.26	0.0103	3.31	0.0109	4.42E-02
2.85	2.85	3.31	2.28	0.0105	0.0109	4.42E-02
2.85	2.85	3.31	2.28	0.0105	0.0109	4.42E-02
4.02	4.54	4.22	2.63	2.55	0.0109	4.43E-02
4.02	4.54	4.22	2.63	2.55	0.0109	4.43E-02
3.97	4.13	5.05	2.95	3.65	2.64	4.43E-02
3.97	4.13	5.05	2.95	3.65	2.64	4.43E-02
3.97	4.13	5.05	2.95	3.65	2.64	4.43E-02
3.33	2.98	3.38	2.8	2.7	2.17	4.43E-02
3.59	2.98	3.5	0.0103	0.0105	2.54	4.43E-02
3.24	2.95	3	2.35	0.0105	0.0109	4.43E-02
3.24	2.95	3	2.35	0.0105	0.0109	4.43E-02
4.88	5.05	4.16	0.0103	3.55	0.0109	4.43E-02
4.88	5.05	4.16	0.0103	3.55	0.0109	4.43E-02
4.17	3.82	4.22	0.0103	3.12	0.0109	4.43E-02
4.17	3.82	4.22	0.0103	3.12	0.0109	4.43E-02
4.17	3.82	4.22	0.0103	3.12	0.0109	4.43E-02
4.37	4.66	4.31	2.94	2.46	0.0109	4.44E-02
0.011	0.012	2.04	2.95	2.3	3	4.44E-02
2.88	3.12	3.14	0.0103	2.34	0.0109	4.44E-02
3.57	4.68	4.28	2.61	3.46	2.23	4.44E-02
4.43	4.23	4.08	2.51	2.68	0.0109	4.44E-02
4.43	4.23	4.08	2.51	2.68	0.0109	4.44E-02
3.7	2.72	2.78	0.0103	2.22	0.0109	4.44E-02
3.7	2.72	2.78	0.0103	2.22	0.0109	4.44E-02

4.68	3.64	3.22	2.72	2.57	2.4	4.45E-02
2.74	3.26	2.65	0.0103	2.17	0.0109	4.45E-02
4.79	3.99	3.93	2.76	2.24	0.0109	4.45E-02
4.79	3.99	3.93	2.76	2.24	0.0109	4.45E-02
2.04	0.012	0.0117	2.74	2.95	2.4	4.45E-02
0.011	2.09	0.0117	2.48	2.72	3.18	4.45E-02
3.5	4.26	3.61	0.0103	0.0105	2.86	4.45E-02
3.43	3.32	3.7	2.75	3.18	2.46	4.46E-02
3.43	3.32	3.7	2.75	3.18	2.46	4.46E-02
0.011	2.38	0.0117	3.4	3.47	2.7	4.46E-02
2.83	3.24	3.58	0.0103	2.42	0.0109	4.46E-02
2.71	5.2	4.03	0.0103	2.47	0.0109	4.47E-02
2.71	5.2	4.03	0.0103	2.47	0.0109	4.47E-02
3.24	2.81	3.4	0.0103	0.0105	2.39	4.47E-02
3.71	3.58	3.39	2.74	0.0105	0.0109	4.47E-02
4.65	3.79	3.9	0.0103	3.1	0.0109	4.47E-02
4.65	3.79	3.9	0.0103	3.1	0.0109	4.47E-02
4.62	3.93	3.34	2.91	0.0105	0.0109	4.48E-02
4.93	4.53	4.68	3.02	2.74	0.0109	4.48E-02
4.8	3.22	4.43	2.84	2.8	2.65	4.48E-02
4.13	3.82	2.66	0.0103	2.48	0.0109	4.48E-02
3.4	3.4	2.92	0.0103	2.47	0.0109	4.48E-02
3.4	3.4	2.92	0.0103	2.47	0.0109	4.48E-02
3.4	4.08	4.08	0.0103	2.92	0.0109	4.48E-02
3.14	3.18	2.65	2.42	2.17	2.58	4.48E-02
4.44	4.19	3.81	0.0103	3.17	0.0109	4.48E-02
3.49	3.28	2.38	0.0103	2.19	0.0109	4.49E-02
5.1	4.24	3.98	0.0103	3.32	0.0109	4.49E-02
3.58	2.63	3.39	2.36	0.0105	0.0109	4.50E-02
3.58	2.63	3.39	2.36	0.0105	0.0109	4.50E-02
4.87	4.74	4.63	2.53	3.23	0.0109	4.50E-02
4.87	4.74	4.63	2.53	3.23	0.0109	4.50E-02
4.39	3.72	3.42	0.0103	0.0105	2.88	4.50E-02
3.36	2.56	2.52	0.0103	2.06	0.0109	4.50E-02
3.36	2.56	2.52	0.0103	2.06	0.0109	4.50E-02
0.011	2.13	0.0117	2.53	3.07	2.8	4.50E-02
0.011	2.13	0.0117	2.53	3.07	2.8	4.50E-02
2.89	2.93	3.89	2.36	0.0105	0.0109	4.51E-02
3.76	3.76	3.09	2.73	3.04	2.68	4.51E-02
3.76	3.76	3.09	2.73	3.04	2.68	4.51E-02
4.34	4.13	3.59	0.0103	2.34	2.5	4.51E-02
4.34	4.13	3.59	0.0103	2.34	2.5	4.51E-02
5.29	4.38	4.76	2.71	3.07	0.0109	4.51E-02
5.29	4.38	4.76	2.71	3.07	0.0109	4.51E-02
0.011	0.012	2.43	2.75	3.34	3.79	4.52E-02
3.25	2.99	2.72	2.28	0.0105	0.0109	4.52E-02
4.41	3.4	3.19	0.0103	2.67	0.0109	4.52E-02
5.42	3.99	4.36	0.0103	3.38	0.0109	4.52E-02
5.42	3.99	4.36	0.0103	3.38	0.0109	4.52E-02
5.41	4.37	4.56	0.0103	3.61	0.0109	4.52E-02
5.41	4.37	4.56	0.0103	3.61	0.0109	4.52E-02
4.53	4.36	4.13	3.35	0.0105	0.0109	4.53E-02
4.58	2.84	3.38	0.0103	0.0105	2.46	4.53E-02
4.2	3.68	3.99	2.41	2.42	0.0109	4.53E-02
4.2	3.68	3.99	2.41	2.42	0.0109	4.53E-02
3.63	3.16	2.87	0.0103	0.0105	2.43	4.53E-02
2.64	3.06	2.94	2.21	0.0105	0.0109	4.54E-02
4.19	3.68	4.07	3.06	0.0105	0.0109	4.54E-02

4.19	3.68	4.07	3.06	0.0105	0.0109	4.54E-02
3.11	3.63	3.95	0.0103	2.69	0.0109	4.54E-02
3.11	3.63	3.95	0.0103	2.69	0.0109	4.54E-02
2.19	0.012	0.0117	2.48	3.11	3.15	4.54E-02
2.59	0.012	0.0117	3.5	3.21	3.34	4.54E-02
0.011	0.012	2.58	3.8	2.85	3.83	4.54E-02
4.91	3.99	5.13	3.47	3.6	2.3	4.54E-02
4.91	3.99	5.13	3.47	3.6	2.3	4.54E-02
3.21	3.83	3.06	2.54	0.0105	0.0109	4.54E-02
3.21	3.83	3.06	2.54	0.0105	0.0109	4.54E-02
3.51	3.19	2.67	0.0103	2.34	0.0109	4.55E-02
3.51	3.19	2.67	0.0103	2.34	0.0109	4.55E-02
5.05	4.45	4.22	0.0103	3.49	0.0109	4.55E-02
5.05	4.45	4.22	0.0103	3.49	0.0109	4.55E-02
3.32	3.62	3.67	0.0103	2.73	0.0109	4.55E-02
3.32	3.62	3.67	0.0103	2.73	0.0109	4.55E-02
4.63	3.28	3.36	0.0103	2.69	0.0109	4.55E-02
4.63	3.28	3.36	0.0103	2.69	0.0109	4.55E-02
4.63	3.28	3.36	0.0103	2.69	0.0109	4.55E-02
3.23	2.68	3.14	0.0103	2.3	0.0109	4.55E-02
2.56	0.012	0.0117	3.87	3.42	2.95	4.56E-02
3.29	2.67	2.33	0.0103	2.02	0.0109	4.56E-02
3.29	2.67	2.33	0.0103	2.02	0.0109	4.56E-02
3.27	3.03	3.84	2.55	0.0105	0.0109	4.56E-02
3.27	3.03	3.84	2.55	0.0105	0.0109	4.56E-02
4.83	3.62	4.16	0.0103	2.65	2.26	4.56E-02
0.011	0.012	2.46	3.91	3.16	2.9	4.56E-02
3.58	2.45	3.41	0.0103	2.27	0.0109	4.56E-02
0.011	2.37	0.0117	3.3	3.6	2.66	4.57E-02
3.59	3.18	3.7	0.0103	2.68	0.0109	4.57E-02
2.36	3.31	2.97	0.0103	2.12	0.0109	4.57E-02
2.36	3.31	2.97	0.0103	2.12	0.0109	4.57E-02
4.12	3.1	3.73	0.0103	2.73	0.0109	4.57E-02
3.71	3.22	4.01	0.0103	2.77	0.0109	4.57E-02
3.71	3.22	4.01	0.0103	2.77	0.0109	4.57E-02
4.04	4.66	3.65	0.0103	2.38	2.52	4.57E-02
4.04	4.66	3.65	0.0103	2.38	2.52	4.57E-02
0.011	0.012	2.24	2.9	3.42	2.63	4.57E-02
2.44	0.012	0.0117	3.61	3.21	2.85	4.57E-02
4.36	3.95	4.58	3.13	3.82	2.68	4.58E-02
4.36	3.95	4.58	3.13	3.82	2.68	4.58E-02
3.76	4.09	4.24	3.11	0.0105	0.0109	4.58E-02
4.28	5.32	3.94	0.0103	3.34	0.0109	4.58E-02
4.28	5.32	3.94	0.0103	3.34	0.0109	4.58E-02
4.28	5.32	3.94	0.0103	3.34	0.0109	4.58E-02
3.29	2.9	2.65	0.0103	2.24	0.0109	4.58E-02
3.29	2.9	2.65	0.0103	2.24	0.0109	4.58E-02
5.48	4.71	4.73	2.54	4.32	2.96	4.58E-02
3.07	3.03	2.97	0.0103	2.35	0.0109	4.59E-02
3.07	3.03	2.97	0.0103	2.35	0.0109	4.59E-02
4.6	2.73	4.13	0.0103	2.6	0.0109	4.59E-02
3.09	2.8	2.87	0.0103	2.26	0.0109	4.59E-02
3.09	2.8	2.87	0.0103	2.26	0.0109	4.59E-02
3.44	3.06	4	0.0103	2.63	0.0109	4.59E-02
3.44	3.06	4	0.0103	2.63	0.0109	4.59E-02
4.51	3.85	4.77	0.0103	3.33	0.0109	4.59E-02
3.25	2.99	2.72	0.0103	2.29	0.0109	4.60E-02
0.011	2.19	0.0117	3	2.63	2.88	4.60E-02

5.35	5.23	4.96	3.24	4.68	3.92	4.60E-02
5.35	5.23	4.96	3.24	4.68	3.92	4.60E-02
5.35	5.23	4.96	3.24	4.68	3.92	4.60E-02
5.35	5.23	4.96	3.24	4.68	3.92	4.60E-02
5.35	5.23	4.96	3.24	4.68	3.92	4.60E-02
5.11	4.29	4.64	0.0103	3.59	0.0109	4.60E-02
5.11	4.29	4.64	0.0103	3.59	0.0109	4.60E-02
4.93	4.73	3.56	2.35	2.72	0.0109	4.61E-02
4.93	4.73	3.56	2.35	2.72	0.0109	4.61E-02
5.52	5.41	5.32	3.44	0.0105	3.25	4.61E-02
3.91	4.98	4.53	3.42	3.56	2.46	4.61E-02
5.74	5.8	4.41	0.0103	3.97	0.0109	4.61E-02
3.14	3.82	3.55	0.0103	2.68	0.0109	4.61E-02
3.14	3.82	3.55	0.0103	2.68	0.0109	4.61E-02
3.64	3.87	2.76	2.52	0.0105	0.0109	4.61E-02
4.67	5.2	4.64	2.98	4.19	3.87	4.62E-02
4.67	5.2	4.64	2.98	4.19	3.87	4.62E-02
4.33	4.56	3.99	2.98	3.8	2.45	4.62E-02
4.33	4.56	3.99	2.98	3.8	2.45	4.62E-02
3.32	3.16	2.97	0.0103	2.44	0.0109	4.62E-02
3.32	3.16	2.97	0.0103	2.44	0.0109	4.62E-02
4.46	4.71	4.07	3.92	2.72	3.22	4.62E-02
4.46	4.71	4.07	3.92	2.72	3.22	4.62E-02
4.54	3.87	4.34	2.45	2.72	0.0109	4.62E-02
4.85	4.96	4.74	2.66	3.28	0.0109	4.62E-02
4.85	4.96	4.74	2.66	3.28	0.0109	4.62E-02
4.85	4.96	4.74	2.66	3.28	0.0109	4.62E-02
3.88	3.19	3.09	0.0103	2.56	0.0109	4.62E-02
2.7	0.012	0.0117	3.07	3.97	3.68	4.63E-02
4.88	4.54	4.39	2.96	4.17	2.84	4.63E-02
4.88	4.54	4.39	2.96	4.17	2.84	4.63E-02
5.01	3.25	3.39	0.0103	0.0105	2.66	4.63E-02
3.24	2.71	3.03	0.0103	2.3	0.0109	4.63E-02
3.24	2.71	3.03	0.0103	2.3	0.0109	4.63E-02
3.22	3.49	4.23	2.49	2.86	2.82	4.63E-02
3.22	3.49	4.23	2.49	2.86	2.82	4.63E-02
3.57	2.82	2.97	0.0103	2.36	0.0109	4.64E-02
3.08	2.84	2.56	2.17	0.0105	0.0109	4.64E-02
3.08	2.84	2.56	2.17	0.0105	0.0109	4.64E-02
3.55	4.06	3.91	2.08	2.58	0.0109	4.64E-02
3.62	2.89	2.86	0.0103	2.35	0.0109	4.64E-02
0.011	2.5	0.0117	3.04	3.43	3.21	4.64E-02
3.69	2.72	3.87	0.0103	2.51	0.0109	4.64E-02
3.69	2.72	3.87	0.0103	2.51	0.0109	4.64E-02
2.85	3.21	3.31	0.0103	2.41	0.0109	4.65E-02
3.43	3.18	3.95	2.91	2.92	2.65	4.65E-02
5.03	5.12	4.06	0.0103	3.59	0.0109	4.65E-02
2.75	2.72	2.58	2.09	0.0105	0.0109	4.65E-02
3.06	3.3	2.6	0.0103	2.27	0.0109	4.65E-02
3.06	3.3	2.6	0.0103	2.27	0.0109	4.65E-02
2.4	3.6	2.88	0.0103	2.13	0.0109	4.65E-02
4.12	4.79	3.8	0.0103	3.22	0.0109	4.66E-02
4.12	4.79	3.8	0.0103	3.22	0.0109	4.66E-02
4.25	3.51	3.04	0.0103	2.66	0.0109	4.66E-02
3.42	2.63	3.2	2.33	0.0105	0.0109	4.66E-02
3.42	2.63	3.2	2.33	0.0105	0.0109	4.66E-02
3.17	2.44	4.24	2.19	0.0105	0.0109	4.66E-02
3.17	2.44	4.24	2.19	0.0105	0.0109	4.66E-02

3.77	3.58	2.92	0.0103	2.59	0.0109	4.67E-02
3.54	3.12	3.84	0.0103	2.68	0.0109	4.67E-02
0.011	0.012	2.56	3.97	3.14	3.11	4.67E-02
3.59	2.84	3.34	0.0103	2.48	0.0109	4.67E-02
3.59	2.84	3.34	0.0103	2.48	0.0109	4.67E-02
3.47	2.68	3.04	0.0103	0.0105	2.32	4.67E-02
3.47	2.68	3.04	0.0103	0.0105	2.32	4.67E-02
3.4	3.34	3.01	0.0103	2.52	0.0109	4.67E-02
3.65	3.59	4.09	2.91	3.33	3.31	4.67E-02
3.65	3.59	4.09	2.91	3.33	3.31	4.67E-02
3.85	3.1	4	0.0103	2.76	0.0109	4.67E-02
3.85	3.1	4	0.0103	2.76	0.0109	4.67E-02
3.95	3.79	3.79	0.0103	3	0.0109	4.68E-02
3.95	3.79	3.79	0.0103	3	0.0109	4.68E-02
3.54	3.86	2.54	0.0103	2.38	0.0109	4.68E-02
2.89	3.34	3.32	2.46	0.0105	0.0109	4.68E-02
2.89	3.34	3.32	2.46	0.0105	0.0109	4.68E-02
3.91	4.51	3.88	2.56	0.0105	2.44	4.69E-02
2.46	2.12	2.36	2.77	2.75	3.38	4.69E-02
4.11	3.4	2.72	2.46	0.0105	0.0109	4.69E-02
2.61	3.6	3.66	0.0103	0.0105	2.42	4.69E-02
4.61	3.92	4.98	3.43	0.0105	0.0109	4.70E-02
2.72	2.36	2.33	2.82	3.1	2.82	4.70E-02
5.13	3.34	4.86	0.0103	3.17	0.0109	4.70E-02
5.13	3.34	4.86	0.0103	3.17	0.0109	4.70E-02
2.69	4.06	3.31	0.0103	2.42	0.0109	4.71E-02
3.7	2.69	4.45	0.0103	2.51	0.0109	4.71E-02
3.58	3.58	4.07	0.0103	0.0105	2.9	4.71E-02
2.23	2.43	2.21	2.46	2.51	2.62	4.71E-02
2.23	2.43	2.21	2.46	2.51	2.62	4.71E-02
3.92	3.29	3.8	2.83	0.0105	0.0109	4.71E-02
3.92	3.29	3.8	2.83	0.0105	0.0109	4.71E-02
0.011	0.012	2.78	3.05	4.07	4.02	4.72E-02
0.011	0.012	2.78	3.05	4.07	4.02	4.72E-02
0.011	0.012	2.78	3.05	4.07	4.02	4.72E-02
5.16	3.61	5.25	2.58	3.23	3.29	4.72E-02
5.16	3.61	5.25	2.58	3.23	3.29	4.72E-02
3.5	3.68	2.92	0.0103	2.57	0.0109	4.72E-02
3.5	3.68	2.92	0.0103	2.57	0.0109	4.72E-02
4.29	4.4	4.31	2.6	0.0105	2.78	4.72E-02
2.82	2.38	3.25	0.0103	2.11	0.0109	4.72E-02
2.82	4.6	3.21	0.0103	0.0105	2.41	4.73E-02
2.85	3.29	2.77	0.0103	2.29	0.0109	4.73E-02
2.85	3.29	2.77	0.0103	2.29	0.0109	4.73E-02
5.15	4.06	4.83	2.68	2.94	0.0109	4.73E-02
5.15	4.06	4.83	2.68	2.94	0.0109	4.73E-02
4.27	4.83	4.38	0.0103	3.12	2.31	4.74E-02
4.27	4.83	4.38	0.0103	3.12	2.31	4.74E-02
0.011	0.012	2.03	3.28	2.39	2.55	4.74E-02
4.17	2.88	4.97	2.73	0.0105	0.0109	4.74E-02
4.36	3.15	3.05	2.54	0.0105	0.0109	4.74E-02
4.36	3.15	3.05	2.54	0.0105	0.0109	4.74E-02
2.61	2.42	3.09	0.0103	2.06	0.0109	4.74E-02
4.96	5.35	4.49	3.73	4.11	2.62	4.74E-02
4.96	5.35	4.49	3.73	4.11	2.62	4.74E-02
4.96	5.35	4.49	3.73	4.11	2.62	4.74E-02
3.23	3.38	3.69	0.0103	0.0105	2.67	4.74E-02
3.23	3.38	3.69	0.0103	0.0105	2.67	4.74E-02

3.42	3.04	3.88	0.0103	2.63	0.0109	4.74E-02
3.42	3.04	3.88	0.0103	2.63	0.0109	4.74E-02
3.81	3.86	3.4	2.87	0.0105	0.0109	4.75E-02
4.55	3.44	4.14	0.0103	3.06	0.0109	4.75E-02
4.55	3.44	4.14	0.0103	3.06	0.0109	4.75E-02
4.55	3.44	4.14	0.0103	3.06	0.0109	4.75E-02
4.41	5.18	4	0.0103	3.44	0.0109	4.75E-02
4.41	5.18	4	0.0103	3.44	0.0109	4.75E-02
3.77	3.22	4.53	0.0103	2.85	0.0109	4.75E-02
4.93	2.99	4.24	2.67	2.28	2.27	4.76E-02
4.41	3.08	3.55	0.0103	2.71	0.0109	4.76E-02
4.41	3.08	3.55	0.0103	2.71	0.0109	4.76E-02
3.79	2.89	2.86	0.0103	2.37	0.0109	4.76E-02
3.07	4.16	3.3	0.0103	2.62	0.0109	4.76E-02
2.95	3.96	3.63	0.0103	2.65	0.0109	4.76E-02
2.95	3.96	3.63	0.0103	2.65	0.0109	4.76E-02
2.95	3.96	3.63	0.0103	2.65	0.0109	4.76E-02
3.6	3.57	3.19	2.69	0.0105	0.0109	4.76E-02
3.46	3.91	4.09	2.96	0.0105	0.0109	4.76E-02
3.26	3.68	4.09	0.0103	2.82	0.0109	4.76E-02
4.47	4.76	4.63	4.22	3.2	2.81	4.77E-02
4.47	4.76	4.63	4.22	3.2	2.81	4.77E-02
0.011	2.36	0.0117	2.73	3.23	3.19	4.77E-02
4.36	3.42	3.3	0.0103	0.0105	2.77	4.77E-02
0.011	2.58	0.0117	4.13	2.8	3.63	4.77E-02
3.82	3.19	4.04	2.25	3.08	2.75	4.77E-02
2.44	2.78	2.71	2.06	0.0105	0.0109	4.77E-02
4.18	2.94	3.91	2.24	2.59	2.76	4.78E-02
3.09	2.79	2.68	0.0103	2.22	0.0109	4.78E-02
3.09	2.79	2.68	0.0103	2.22	0.0109	4.78E-02
4.87	3.41	4.96	0.0103	3.22	0.0109	4.78E-02
4.77	4.23	4.82	0.0103	3.09	2.54	4.78E-02
3.99	3.69	3.25	0.0103	2.81	0.0109	4.79E-02
0.011	0.012	2.73	3.22	4.23	3.4	4.80E-02
0.011	0.012	2.73	3.22	4.23	3.4	4.80E-02
3.14	2.93	3.24	0.0103	2.43	0.0109	4.80E-02
0.011	0.012	2.26	2.79	3.09	2.79	4.80E-02
3.94	4.39	3.69	3.54	3.3	3.34	4.80E-02
3.94	4.39	3.69	3.54	3.3	3.34	4.80E-02
3.94	4.39	3.69	3.54	3.3	3.34	4.80E-02
2.01	0.012	0.0117	2.25	2.67	3.3	4.81E-02
3.68	3.44	3.32	3.27	2.92	2.92	4.81E-02
3.68	3.44	3.32	3.27	2.92	2.92	4.81E-02
3.68	3.44	3.32	3.27	2.92	2.92	4.81E-02
3.39	2.79	3.53	0.0103	2.48	0.0109	4.81E-02
3.72	3.29	4.1	2.6	3.23	2.43	4.81E-02
3.72	3.29	4.1	2.6	3.23	2.43	4.81E-02
4.89	5.08	3.19	0.0103	2.62	2.1	4.81E-02
4.76	4.11	4.87	4.01	3.86	3.8	4.81E-02
4.76	4.11	4.87	4.01	3.86	3.8	4.81E-02
4.76	4.11	4.87	4.01	3.86	3.8	4.81E-02
2.92	2.82	3.46	0.0103	2.36	0.0109	4.82E-02
4.53	4.23	3.7	3.21	0.0105	0.0109	4.82E-02
3.49	2.93	4.05	0.0103	0.0105	2.62	4.82E-02
3.49	2.93	4.05	0.0103	0.0105	2.62	4.82E-02
3.74	3.68	3.12	0.0103	2.72	0.0109	4.82E-02
3.74	3.68	3.12	0.0103	2.72	0.0109	4.82E-02
3.51	3.11	3.75	0.0103	2.68	0.0109	4.82E-02

3.51	3.11	3.75	0.0103	2.68	0.0109	4.82E-02
3.11	3.81	3.21	0.0103	2.6	0.0109	4.83E-02
3.11	3.81	3.21	0.0103	2.6	0.0109	4.83E-02
3.82	3.06	3.12	0.0103	0.0105	2.55	4.83E-02
3.4	3.78	3.69	0.0103	2.84	0.0109	4.83E-02
3.4	3.78	3.69	0.0103	2.84	0.0109	4.83E-02
3.4	3.78	3.69	0.0103	2.84	0.0109	4.83E-02
4.44	3.76	4.03	2.56	0.0105	2.45	4.83E-02
4.44	3.76	4.03	2.56	0.0105	2.45	4.83E-02
2.9	2.5	2.79	0.0103	2.13	0.0109	4.83E-02
3.66	4.42	4.51	2.51	3.65	2.6	4.84E-02
3.66	4.42	4.51	2.51	3.65	2.6	4.84E-02
3.88	3.94	2.35	0.0103	2.32	0.0109	4.84E-02
3.88	3.94	2.35	0.0103	2.32	0.0109	4.84E-02
3.88	3.94	2.35	0.0103	2.32	0.0109	4.84E-02
2.62	2.68	3.07	2.17	0.0105	0.0109	4.84E-02
2.62	2.68	3.07	2.17	0.0105	0.0109	4.84E-02
3.55	4.3	4.02	3.34	2.82	3.35	4.84E-02
3.55	4.3	4.02	3.34	2.82	3.35	4.84E-02
2.81	2.5	2.77	0.0103	2.11	0.0109	4.85E-02
0.011	0.012	2.58	2.88	4.09	3.42	4.85E-02
0.011	0.012	2.58	2.88	4.09	3.42	4.85E-02
4.49	4.34	5.14	2.26	0.0105	3.29	4.85E-02
4.49	4.34	5.14	2.26	0.0105	3.29	4.85E-02
4.81	4.03	5.17	3.58	0.0105	0.0109	4.85E-02
2.77	3.12	2.66	0.0103	0.0105	2.22	4.85E-02
2.77	3.12	2.66	0.0103	0.0105	2.22	4.85E-02
0.011	2.48	0.0117	3.93	3.08	2.91	4.85E-02
4.45	4.42	4.88	2.82	2.87	0.0109	4.85E-02
2.82	3.98	3.17	2.47	0.0105	0.0109	4.86E-02
3.42	3.9	3.16	0.0103	0.0105	2.7	4.86E-02
3.42	3.9	3.16	0.0103	0.0105	2.7	4.86E-02
3.34	3.24	2.98	0.0103	0.0105	2.5	4.86E-02
4.35	4.36	4.03	3.34	0.0105	0.0109	4.86E-02
4.18	4.98	5.68	2.63	0.0105	3.19	4.87E-02
4.18	4.98	5.68	2.63	0.0105	3.19	4.87E-02
4.44	3.71	3.14	0.0103	2.81	0.0109	4.87E-02
4.44	3.71	3.14	0.0103	2.81	0.0109	4.87E-02
4.44	3.71	3.14	0.0103	2.81	0.0109	4.87E-02
4.04	4.08	4.03	2.32	2.72	0.0109	4.87E-02
3.63	2.62	3.05	0.0103	2.33	0.0109	4.87E-02
3.63	2.62	3.05	0.0103	2.33	0.0109	4.87E-02
2.74	2.52	2.66	2.08	0.0105	0.0109	4.88E-02
4.35	2.96	3.66	0.0103	2.7	0.0109	4.88E-02
4.35	2.96	3.66	0.0103	2.7	0.0109	4.88E-02
4.35	2.96	3.66	0.0103	2.7	0.0109	4.88E-02
2.21	0.012	0.0117	2.58	2.84	3.09	4.88E-02
3.56	3.28	3.61	0.0103	2.74	0.0109	4.88E-02
3.83	2.42	4.04	0.0103	2.38	0.0109	4.89E-02
3.83	2.42	4.04	0.0103	2.38	0.0109	4.89E-02
0.011	0.012	2.09	2.4	3.36	2.65	4.89E-02
3.74	3.8	4.19	0.0103	3.07	0.0109	4.90E-02
2.745	2.53	3.26	0.0103	0.0105	2.18	4.90E-02
4.63	5.26	5.45	3.87	4.05	2.29	4.90E-02
2.6	3.35	3.53	2.39	0.0105	0.0109	4.90E-02
2.6	3.35	3.53	2.39	0.0105	0.0109	4.90E-02
2.6	3.35	3.53	2.39	0.0105	0.0109	4.90E-02
3.41	3.52	3.84	0.0103	2.82	0.0109	4.90E-02

3.41	3.52	3.84	0.0103	2.82	0.0109	4.90E-02
3.46	3.11	2.48	0.0103	0.0105	2.27	4.90E-02
3.46	3.11	2.48	0.0103	0.0105	2.27	4.90E-02
3.54	4.67	3.65	2.06	2.57	0.0109	4.90E-02
3.54	4.67	3.65	2.06	2.57	0.0109	4.90E-02
4.5	3.68	4.22	3.21	0.0105	0.0109	4.90E-02
3.63	3.75	3.96	0.0103	2.98	0.0109	4.91E-02
3.63	3.75	3.96	0.0103	2.98	0.0109	4.91E-02
3.18	2.74	2.52	0.0103	2.17	0.0109	4.91E-02
2.71	3.11	2.64	0.0103	2.2	0.0109	4.91E-02
2.71	3.11	2.64	0.0103	2.2	0.0109	4.91E-02
4.57	4.27	4.82	2.26	4.04	2.56	4.91E-02
3.18	2.83	4.2	0.0103	2.48	0.0109	4.92E-02
3.65	4.36	2.52	0.0103	2.42	0.0109	4.92E-02
3.65	4.36	2.52	0.0103	2.42	0.0109	4.92E-02
4.12	4.62	2.9	2.78	0.0105	0.0109	4.92E-02
2.72	3.27	3.28	2.4	0.0105	0.0109	4.92E-02
2.88	3.65	3.83	0.0103	2.63	0.0109	4.92E-02
3.91	3.28	2.81	2.51	0.0105	0.0109	4.93E-02
3.68	3.65	4.21	0.0103	3.01	0.0109	4.93E-02
3.68	3.65	4.21	0.0103	3.01	0.0109	4.93E-02
3.47	2.98	3.27	0.0103	2.54	0.0109	4.93E-02
4.64	3.7	4.38	0.0103	3.28	0.0109	4.93E-02
4.81	2.91	3.44	2.57	0.0105	0.0109	4.93E-02
2.52	2.79	3.03	0.0103	2.17	0.0109	4.93E-02
2.52	2.79	3.03	0.0103	2.17	0.0109	4.93E-02
2.99	3.51	3.09	0.0103	2.5	0.0109	4.94E-02
2.99	3.51	3.09	0.0103	2.5	0.0109	4.94E-02
3.56	2.79	2.26	2.06	0.0105	0.0109	4.94E-02
5.24	4.14	4.67	0.0103	3.62	0.0109	4.94E-02
3.58	3.7	3	0.0103	2.66	0.0109	4.95E-02
3.58	3.7	3	0.0103	2.66	0.0109	4.95E-02
2.91	4.43	4.93	0.0103	2.85	0.0109	4.95E-02
2.87	4.18	3.48	2.61	0.0105	0.0109	4.96E-02
4.3	3.06	3.21	2.61	0.0105	0.0109	4.96E-02
4.06	3.01	3.48	0.0103	2.68	0.0109	4.97E-02
3.59	2.42	2.6	0.0103	0.0105	2.08	4.97E-02
3.59	2.42	2.6	0.0103	0.0105	2.08	4.97E-02
3.1	3.29	3.22	3.36	3.69	3.85	4.97E-02
4.24	3.66	3.29	3.04	2.64	2.98	4.98E-02
4.24	3.66	3.29	3.04	2.64	2.98	4.98E-02
0.011	0.012	2.25	3.81	3.23	2.37	4.98E-02
3.78	3.21	3.28	2.68	0.0105	0.0109	4.98E-02
5.97	4.31	5.19	2.28	3.59	0.0109	4.99E-02
3.36	2.99	3.67	2.38	2.95	2.51	4.99E-02
0.011	0.012	2.46	2.89	3.1	4.51	4.99E-02
0.011	0.012	2.46	2.89	3.1	4.51	4.99E-02
2.76	0.012	0.0117	3.5	3.23	3.82	4.99E-02
2.76	0.012	0.0117	3.5	3.23	3.82	4.99E-02
2.58	3.12	2.93	0.0103	2.25	0.0109	4.99E-02
2.58	3.12	2.93	0.0103	2.25	0.0109	4.99E-02
4.34	4.5	4.53	3.05	4.14	2.92	5.00E-02
4.34	4.5	4.53	3.05	4.14	2.92	5.00E-02
3.77	2.66	4.15	0.0103	2.56	0.0109	5.00E-02
3.77	2.66	4.15	0.0103	2.56	0.0109	5.00E-02
3.42	3.26	4.43	0.0103	2.79	0.0109	5.00E-02
3.42	3.26	4.43	0.0103	2.79	0.0109	5.00E-02
3.03	3.16	3.73	2.57	0.0105	0.0109	5.00E-02

0.011	0.012	2.46	3.1	2.94	4.71	5.00E-02

		..peak count / window and probe			
fold-change(Astro/Nanog)	log2(fold-change)	up_gene_description	down_gene_symbol	up_gene_acc	down_gene_acc
3.09E+02	8.27E+00	scribbled homolo	poly-U binding sp	NM_182706,NM	NM_182706,NM_015356
3.09E+02	8.27E+00	poly-U binding sp	poly-U binding sp	NM_001136033	NM_001136033
3.09E+02	8.27E+00	poly-U binding sp	poly-U binding sp	NM_001136033	NM_001136033
2.70E+02	8.08E+00	death inducer-ob	death inducer-ob	NM_022105,NM	NM_022105,NM_080796
2.70E+02	8.08E+00	death inducer-ob	death inducer-ob	NM_022105,NM	NM_022105,NM_080796
2.28E+02	7.83E+00	huntingtin intera	huntingtin intera	NM_005338	NM_005338
2.28E+02	7.83E+00	huntingtin intera	huntingtin intera	NM_005338	NM_005338
2.53E+02	7.98E+00	mitogen-activate	mitogen-activate	NM_015133,NM	NM_015133,NM_001040439
2.53E+02	7.98E+00	mitogen-activate	mitogen-activate	NM_015133,NM	NM_015133,NM_001040439
2.40E+02	7.91E+00	dual specificity p	dual specificity p	NM_001003892	NM_001003892
3.17E+02	8.31E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
3.90E+02	8.61E+00	---	sodium channel,	NR_027361	NR_027361
2.85E+02	8.15E+00	hypothetical pro	hypothetical pro	NR_024607	NR_024607
4.77E+02	8.90E+00	CTD (carboxy-ter	CTD (carboxy-ter	NM_048368,NM	NM_048368,NM_004715
4.77E+02	8.90E+00	CTD (carboxy-ter	CTD (carboxy-ter	NM_048368,NM	NM_048368,NM_004715
2.38E+02	7.90E+00	elongation of ver	elongation of ver	NM_017770	NM_017770
2.34E+02	7.87E+00	cystin 1	cystin 1	NM_001037160	NM_001037160
2.30E+02	7.84E+00	unkempt homolo	unkempt homolo	NM_023076	NM_023076
2.30E+02	7.84E+00	unkempt homolo	unkempt homolo	NM_023076	NM_023076
2.50E+02	7.97E+00	solute carrier fan	solute carrier fan	NM_182632	NM_182632
2.36E+02	7.88E+00	WD repeat doma	zinc and ring fing	NM_030581	NM_030581
2.36E+02	7.88E+00	SPO11 meiotic pr	RAE1 RNA export	NM_012444,NM	NM_012444,NM_198265
2.65E+02	8.05E+00	presenilin 1	papilin, proteogl	NM_000021,NM	NM_000021,NM_007318
2.65E+02	8.05E+00	papilin, proteogl	papilin, proteogl	NM_173462	NM_173462
2.56E+02	8.00E+00	melanoma antige	melanoma antige	NM_004988	NM_004988
4.08E+02	8.67E+00	Lck interacting tr	Lck interacting tr	NM_017806	NM_017806
3.85E+02	8.59E+00	kinesin family me	chromosome 14	NM_015656	NM_015656
2.90E+02	8.18E+00	short stature hor	cytokine recepto	NM_006883,NM	NM_006883,NM_000451
3.93E+02	8.62E+00	transmembrane	LIM domain bind	NM_153365	NM_153365
3.80E+02	8.57E+00	unkempt homolo	unkempt homolo	NM_023076	NM_023076
3.80E+02	8.57E+00	unkempt homolo	unkempt homolo	NM_023076	NM_023076
3.80E+02	8.57E+00	unkempt homolo	unkempt homolo	NM_023076	NM_023076
3.35E+02	8.39E+00	solute carrier fan	solute carrier fan	NM_152346	NM_152346
4.35E-03	-7.84E+00	FERM domain co	FERM domain co	NM_018027	NM_018027
4.35E-03	-7.84E+00	FERM domain co	FERM domain co	NM_018027	NM_018027
2.55E+02	8.00E+00	FERM and PDZ d	RNA (guanine-9-)	NM_014907	NM_014907
2.55E+02	8.00E+00	FERM and PDZ d	RNA (guanine-9-)	NM_014907	NM_014907
4.62E+02	8.85E+00	hypothetical pro	hypothetical pro	NR_024609	NR_024609
3.16E+02	8.30E+00	hexosaminidase	hexosaminidase	NM_173620	NM_173620
3.16E+02	8.30E+00	hexosaminidase	hexosaminidase	NM_173620	NM_173620
3.16E+02	8.30E+00	hexosaminidase	hexosaminidase	NM_173620	NM_173620
2.85E+02	8.15E+00	tubulin tyrosine l	tubulin tyrosine l	NM_015140	NM_015140
2.85E+02	8.15E+00	tubulin tyrosine l	tubulin tyrosine l	NM_015140	NM_015140
2.85E+02	8.15E+00	tubulin tyrosine l	tubulin tyrosine l	NM_015140	NM_015140
2.13E+02	7.74E+00	ovarian tumor su	hypermethylated	NM_080822	NM_080822
2.13E+02	7.74E+00	ovarian tumor su	hypermethylated	NM_080822	NM_080822
2.39E+02	7.90E+00	LIM homeobox 2	LIM homeobox 2	NM_004789	NM_004789
2.39E+02	7.90E+00	LIM homeobox 2	LIM homeobox 2	NM_004789	NM_004789
2.24E+02	7.81E+00	CREB binding pro	CREB binding pro	NM_001079846,	NM_001079846,NM_004380
2.22E+02	7.79E+00	CDC42 binding pr	chromosome 14	NM_006035	NM_006035
2.22E+02	7.79E+00	CDC42 binding pr	chromosome 14	NM_006035	NM_006035
2.53E+02	7.98E+00	mindbomb homo	mindbomb homo	NM_080875	NM_080875
2.53E+02	7.98E+00	mindbomb homo	mindbomb homo	NM_080875	NM_080875

2.97E+02	8.22E+00	src-related kinas	chromosome 20	NM_080823	NM_080823
2.85E+02	8.15E+00	phosphatidylinos	phosphatidylinos	NM_033198	NM_033198
2.85E+02	8.15E+00	phosphatidylinos	phosphatidylinos	NM_033198	NM_033198
2.14E+02	7.74E+00	fibroblast growtl	fibroblast growtl	NM_005247	NM_005247
2.14E+02	7.74E+00	fibroblast growtl	fibroblast growtl	NM_005247	NM_005247
4.27E-03	-7.87E+00	ubiquitin B	transient recepto	NM_018955	NM_018955
4.27E-03	-7.87E+00	ubiquitin B	transient recepto	NM_018955	NM_018955
2.90E+02	8.18E+00	pregnancy specif	pregnancy specif	NM_002781,NM	NM_002781,NM_001130014
2.90E+02	8.18E+00	pregnancy specif	pregnancy specif	NM_002781,NM	NM_002781,NM_001130014
4.85E-03	-7.69E+00	aldehyde dehydr	leucine-rich repe	NM_000693	NM_000693
4.85E-03	-7.69E+00	aldehyde dehydr	leucine-rich repe	NM_000693	NM_000693
2.39E+02	7.90E+00	carbohydrate (ch	carbohydrate (ch	NM_004273	NM_004273
3.32E+02	8.38E+00	solute carrier fan	solute carrier fan	NM_025257	NM_025257
4.14E+02	8.69E+00	transcription fact	transcription fact	NM_001136139,	NM_001136139,NM_003200
4.14E+02	8.69E+00	transcription fact	transcription fact	NM_001136139,	NM_001136139,NM_003200
2.51E+02	7.97E+00	CASK interacting	CASK interacting	NM_001142643,	NM_001142643,NM_020753
2.51E+02	7.97E+00	CASK interacting	CASK interacting	NM_001142643,	NM_001142643,NM_020753
2.30E+02	7.85E+00	small optic lobes	chromosome 16	NM_005632	NM_005632
2.30E+02	7.85E+00	chromosome 16	chromosome 16	NM_145270	NM_145270
2.26E+02	7.82E+00	cadherin 18, type	glucuronidase, b	NM_004934	NM_004934
2.31E+02	7.85E+00	phospholipase C,	chromosome 15	NM_004573	NM_004573
2.58E+02	8.01E+00	matrix metallope	matrix metallope	NM_002428	NM_002428
2.58E+02	8.01E+00	matrix metallope	matrix metallope	NM_002428	NM_002428
2.23E+02	7.80E+00	RUN and FYVE dc	RUN and FYVE dc	NM_001040452,	NM_001040452,NM_001040451
2.23E+02	7.80E+00	RUN and FYVE dc	RUN and FYVE dc	NM_001040452,	NM_001040452,NM_001040451
2.34E+02	7.87E+00	nuclear receptor	FSHD region gen	NR_003678	NR_003678
2.34E+02	7.87E+00	nuclear receptor	FSHD region gen	NR_003678	NR_003678
3.50E-03	-8.16E+00	chromosome 14	chromosome 14	NM_174913	NM_174913
2.15E+02	7.75E+00	metastasis assoc	metastasis assoc	NM_004689	NM_004689
2.15E+02	7.75E+00	metastasis assoc	metastasis assoc	NM_004689	NM_004689
2.76E+02	8.11E+00	IgLON family me	IgLON family me	NM_001101372	NM_001101372
2.76E+02	8.11E+00	IgLON family me	IgLON family me	NM_001101372	NM_001101372
2.76E+02	8.11E+00	chromosome 20	cadherin 4, type	NM_173644	NM_173644
2.76E+02	8.11E+00	chromosome 20	cadherin 4, type	NM_173644	NM_173644
2.09E+02	7.70E+00	olfactory recepto	folate hydrolase	NM_001005512	NM_001005512
2.09E+02	7.70E+00	olfactory recepto	folate hydrolase	NM_001005512	NM_001005512
3.25E+02	8.34E+00	CDC42 binding pi	zinc finger protei	NM_014826,NM	NM_014826,NM_003607
3.25E+02	8.34E+00	CDC42 binding pi	zinc finger protei	NM_014826,NM	NM_014826,NM_003607
3.25E+02	8.34E+00	CDC42 binding pi	zinc finger protei	NM_014826,NM	NM_014826,NM_003607
2.63E+02	8.04E+00	chromosome 2 o	hypothetical LOC	NM_173821	NM_173821
2.63E+02	8.04E+00	chromosome 2 o	hypothetical LOC	NM_173821	NM_173821
2.73E+02	8.09E+00	major facilitator	major facilitator	NM_001146069,	NM_001146069,NM_001120
3.71E+02	8.54E+00	fms-related tyros	fms-related tyros	NM_002020	NM_002020
3.05E+02	8.25E+00	zinc finger protei	zinc finger protei	NM_033273	NM_033273
3.81E-03	-8.04E+00	hypothetical LOC	family with sequ	NR_024397	NR_024397
4.07E+02	8.67E+00	transmembrane	transmembrane	NM_024600	NM_024600
2.30E+02	7.84E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.30E+02	7.84E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.52E+02	7.98E+00	kinase non-catal	kinase non-catal	NM_152643	NM_152643
2.17E+02	7.76E+00	autocrine motilit	autocrine motilit	NM_001144	NM_001144
3.83E+02	8.58E+00	NLR family, pyrin	ATH1, acid treha	NM_138329	NM_138329
3.83E+02	8.58E+00	ATH1, acid treha	ATH1, acid treha	NM_025092	NM_025092
3.83E+02	8.58E+00	ATH1, acid treha	ATH1, acid treha	NM_025092	NM_025092
2.79E-03	-8.49E+00	GRB2-related ad	GRB2-related ad	NM_006613	NM_006613
3.31E+02	8.37E+00	inositol monoph	chromosome 8 o	NM_017813	NM_017813
2.30E+02	7.84E+00	neurotensin rece	neurotensin rece	NM_002531	NM_002531
2.02E+02	7.66E+00	zinc finger protei	zinc finger protei	NM_001130022	NM_001130022
2.63E+02	8.04E+00	BH3 interacting c	BH3 interacting c	NM_001196,NM	NM_001196,NM_197967,NM_197

2.63E+02	8.04E+00	BH3 interacting	BH3 interacting	NM_001196,NM	NM_001196,NM_197967,NM_197
2.44E+02	7.93E+00	poly(A) binding	poly(A) binding	NM_002568	NM_002568
2.44E+02	7.93E+00	poly(A) binding	poly(A) binding	NM_002568	NM_002568
3.14E+02	8.30E+00	KIAA0664	KIAA0664	NM_015229	NM_015229
2.19E+02	7.78E+00	tyrosylprotein su	tyrosylprotein su	NM_003595,NM	NM_003595,NM_001008566
4.25E-03	-7.88E+00	triple functional	family with sequ	NM_007118	NM_007118
4.25E-03	-7.88E+00	triple functional	family with sequ	NM_007118	NM_007118
3.44E+02	8.43E+00	family with sequ	family with sequ	NM_145253	NM_145253
3.44E+02	8.43E+00	family with sequ	family with sequ	NM_145253	NM_145253
2.22E+02	7.79E+00	chaperonin cont	hypothetical LO	NM_001029866	NM_001029866
4.64E-03	-7.75E+00	chromosome 14	pellino homolog	NR_026797,NR_	NR_026797,NR_026796
3.85E+02	8.59E+00	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165
3.85E+02	8.59E+00	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165
2.79E+02	8.12E+00	complement con	complement con	NM_000606	NM_000606
2.14E+02	7.74E+00	UTP6, small sub	suppressor of ze	NM_018428	NM_018428
4.88E-03	-7.68E+00	WD repeat dom	WD repeat dom	NM_015131	NM_015131
4.88E-03	-7.68E+00	small nucleolar R	small nucleolar R	NR_003074	NR_003074
3.63E-03	-8.10E+00	dynein, axonem	dynein, axonem	NM_023036	NM_023036
4.45E-03	-7.81E+00	solute carrier fa	solute carrier fa	NM_003055	NM_003055
2.95E+02	8.21E+00	goosecoid hom	dicer 1, ribonucl	NM_173849	NM_173849
2.29E+02	7.84E+00	SH3 and multiple	C-type lectin do	NM_016148	NM_016148
2.29E+02	7.84E+00	SH3 and multiple	C-type lectin do	NM_016148	NM_016148
4.37E-03	-7.84E+00	ubiquitin specific	Thy-1 cell surfac	NM_171997,NM	NM_171997,NM_004205
2.03E+02	7.66E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
2.03E+02	7.66E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
2.21E+02	7.79E+00	oncomodulin	oncomodulin	NM_001097622	NM_001097622
2.45E+02	7.94E+00	GLI family zinc fi	zinc finger prote	NM_138465	NM_138465
2.86E+02	8.16E+00	EPH receptor B4	EPH receptor B4	NM_004444	NM_004444
2.86E+02	8.16E+00	EPH receptor B4	EPH receptor B4	NM_004444	NM_004444
2.84E+02	8.15E+00	espin pseudogen	espin pseudogen	NR_026567	NR_026567
2.84E+02	8.15E+00	espin pseudogen	espin pseudogen	NR_026567	NR_026567
3.30E+02	8.37E+00	zinc finger prote	coiled-coil doma	NM_020787	NM_020787
4.02E-03	-7.96E+00	pleckstrin homol	leucine rich repe	NR_024386	NR_024386
2.75E+02	8.10E+00	adenylate cyclas	adenylate cyclas	NM_001116	NM_001116
2.34E+02	7.87E+00	caspase recruitm	caspase recruitm	NM_032415	NM_032415
2.77E+02	8.11E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
2.77E+02	8.11E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
2.35E+02	7.88E+00	tripartite motif-c	tripartite motif-c	NM_001136486	NM_001136486
2.73E+02	8.09E+00	glycoprotein VI (	glycoprotein VI (	NM_001083899,	NM_001083899,NM_016363
2.73E+02	8.09E+00	glycoprotein VI (	glycoprotein VI (	NM_001083899,	NM_001083899,NM_016363
2.70E+02	8.07E+00	apolipoprotein D	succinate dehyd	NM_001647	NM_001647
2.70E+02	8.07E+00	apolipoprotein D	succinate dehyd	NM_001647	NM_001647
2.77E+02	8.11E+00	scavenger recep	scavenger recep	NM_001144950	NM_001144950
2.77E+02	8.11E+00	scavenger recep	scavenger recep	NM_001144950	NM_001144950
2.77E+02	8.11E+00	scavenger recep	scavenger recep	NM_001144950	NM_001144950
2.65E+02	8.05E+00	myosin binding	myosin binding	NM_004533	NM_004533
2.65E+02	8.05E+00	myosin binding	myosin binding	NM_004533	NM_004533
2.08E+02	7.70E+00	chromosome 22	chromosome 22	NM_001123225	NM_001123225
3.05E+02	8.25E+00	WW domain con	WW domain con	NM_199423,NM	NM_199423,NM_007014
3.71E+02	8.54E+00	solute carrier fa	ret finger protei	NM_014227	NM_014227
3.74E-03	-8.06E+00	sterol-C5-desat	sortilin-related r	NM_001024956	NM_001024956
3.61E+02	8.50E+00	adenosine mono	adenosine mono	NM_203404	NM_203404
3.64E-03	-8.10E+00	transmembrane	ADAMTS-like 2	NM_001080483	NM_001080483
3.64E-03	-8.10E+00	transmembrane	ADAMTS-like 2	NM_001080483	NM_001080483
2.29E+02	7.84E+00	neuroblastoma	hypothetical FLJ	NM_001101663	NM_001101663
2.37E+02	7.89E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_00
2.37E+02	7.89E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_00
2.50E+02	7.96E+00	chromosome 22	chromosome 22	NM_182520	NM_182520

4.33E-03	-7.85E+00	microseminopro	natriuretic pepti	NM_001044264	NM_001044264
4.33E-03	-7.85E+00	microseminopro	natriuretic pepti	NM_001044264	NM_001044264
3.22E+02	8.33E+00	H19, imprinted n	insulin-like grow	NR_002196	NR_002196
3.25E+02	8.34E+00	spectrin, beta, er	spectrin, beta, er	NM_000347	NM_000347
4.37E-03	-7.84E+00	signal transducer	low density lipop	NM_003153	NM_003153
3.70E-03	-8.08E+00	zinc finger protei	zinc finger protei	NM_022103	NM_022103
3.61E+02	8.50E+00	single stranded	single stranded	NM_032627,NM	NM_032627,NM_001009998
3.61E+02	8.50E+00	inositol-3-phosp	inositol-3-phosp	NM_016368	NM_016368
4.08E-03	-7.94E+00	lipocalin 1 (tear	odorant binding	NM_002297	NM_002297
2.40E+02	7.91E+00	active BCR-relat	tumor suppresso	NM_001159746	NM_001159746
2.11E+02	7.72E+00	lemur tyrosine ki	lemur tyrosine ki	NM_001080434	NM_001080434
2.11E+02	7.72E+00	lemur tyrosine ki	lemur tyrosine ki	NM_001080434	NM_001080434
3.74E+02	8.55E+00	ankyrin repeat d	phosphoglucom	NM_001012419,	NM_001012419,NM_032250
5.76E-03	-7.44E+00	G protein-couple	zinc finger protei	NM_017986,NM	NM_017986,NM_001104577
2.70E+02	8.07E+00	speedy homolog	speedy homolog	NM_001146210	NM_001146210
2.70E+02	8.07E+00	speedy homolog	speedy homolog	NM_001146210	NM_001146210
5.02E-03	-7.64E+00	phosphoinositid	netrin 1	NM_014308,NM	NM_014308,NM_001142633
2.53E+02	7.98E+00	tudor domain co	asparaginase ho	NM_153046	NM_153046
2.59E+02	8.02E+00	tripartite motif-c	upstream bindin	NM_001146208,	NM_001146208,NM_001145126
2.59E+02	8.02E+00	tripartite motif-c	upstream bindin	NM_001146208,	NM_001146208,NM_001145126
3.40E-03	-8.20E+00	profilin 3	coagulation fact	NM_001029886	NM_001029886
2.42E+02	7.92E+00	cytoskeleton-ass	cytoskeleton-ass	NM_006825	NM_006825
2.42E+02	7.92E+00	cytoskeleton-ass	cytoskeleton-ass	NM_006825	NM_006825
3.08E+02	8.27E+00	ATP synthase, H	zinc finger protei	NM_001003713,	NM_001003713,NM_001003714,
2.10E+02	7.72E+00	SH3-domain GR	SH3-domain GR	NM_020145	NM_020145
2.71E+02	8.08E+00	zinc finger and B	chromosome 20	NM_025224	NM_025224
2.00E+02	7.64E+00	sodium channel,	WD repeat dom	NM_014139	NM_014139
2.10E+02	7.72E+00	glutamate recep	tubulin folding c	NM_014619	NM_014619
2.10E+02	7.72E+00	glutamate recep	tubulin folding c	NM_014619	NM_014619
2.16E+02	7.76E+00	pellino homolog	pellino homolog	NM_001098510,	NM_001098510,NM_145065
3.57E-03	-8.13E+00	acetylcholineste	mucin 17, cell su	NM_015831,NM	NM_015831,NM_000665
2.46E+02	7.94E+00	pericentrin	pericentrin	NM_006031	NM_006031
2.46E+02	7.94E+00	pericentrin	pericentrin	NM_006031	NM_006031
2.48E+02	7.95E+00	lysine (K)-specifi	lysine (K)-specifi	NM_015015	NM_015015
2.48E+02	7.95E+00	lysine (K)-specifi	lysine (K)-specifi	NM_015015	NM_015015
2.53E+02	7.98E+00	hydatidiform mo	hydatidiform mo	NR_002768	NR_002768
2.79E+02	8.12E+00	potassium chann	potassium chann	NM_001142730,	NM_001142730,NM_001136205,
2.79E+02	8.12E+00	potassium chann	potassium chann	NM_001142730,	NM_001142730,NM_001136205,
2.24E+02	7.81E+00	acyl-CoA thioest	acyl-CoA thioest	NM_006821	NM_006821
2.90E+02	8.18E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
2.90E+02	8.18E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
2.74E+02	8.10E+00	5-oxoprolinase (	5-oxoprolinase (	NM_017570	NM_017570
3.47E+02	8.44E+00	olfactory recept	zinc finger protei	NM_012368	NM_012368
3.47E+02	8.44E+00	olfactory recept	zinc finger protei	NM_012368	NM_012368
3.80E+02	8.57E+00	netrin 5	netrin 5	NM_145807	NM_145807
2.37E+02	7.89E+00	NODAL modulat	nuclear pore co	NM_014287	NM_014287
2.13E+02	7.74E+00	stem-loop bindin	stem-loop bindin	NM_006527	NM_006527
3.67E-03	-8.09E+00	kaptin (actin bin	N-ethylmaleimid	NM_007059	NM_007059
2.50E+02	7.97E+00	keratin 79	keratin 79	NM_175834	NM_175834
2.50E+02	7.97E+00	keratin 79	keratin 79	NM_175834	NM_175834
2.50E+02	7.97E+00	keratin 79	keratin 78	NM_175834	NM_175834
2.37E+02	7.89E+00	adrenergic, beta,	ankyrin repeat d	NM_001619	NM_001619
2.77E+02	8.11E+00	tubulin, gamma	tubulin, gamma	NM_006659	NM_006659
2.77E+02	8.11E+00	tubulin, gamma	tubulin, gamma	NM_006659	NM_006659
2.43E+02	7.92E+00	myeloma overex	cyclin D1	NM_138768	NM_138768
3.89E+02	8.60E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
3.79E-03	-8.04E+00	rabphilin 3A-like	chromosome 17	NM_006987	NM_006987
3.41E+02	8.41E+00	guanylate cyclas	forkhead box J3	NM_033553	NM_033553

2.99E+02	8.22E+00	sperm acrosome	ribosomal protei	NM_133498	NM_133498
2.99E+02	8.22E+00	sperm acrosome	ribosomal protei	NM_133498	NM_133498
4.90E-03	-7.67E+00	ST3 beta-galacto	hypothetical pro	NM_001042437	NM_001042437
3.07E+02	8.26E+00	arachidonate 12-	arachidonate 12-	NR_002710	NR_002710
2.52E+02	7.98E+00	kinesin family m	kinesin family m	NM_015656	NM_015656
2.52E+02	7.98E+00	kinesin family m	kinesin family m	NM_015656	NM_015656
3.02E+02	8.24E+00	UDP-N-acetyl-al	hypothetical LO	NM_021808,NM	NM_021808,NM_001122636
3.02E+02	8.24E+00	UDP-N-acetyl-al	hypothetical LO	NM_021808,NM	NM_021808,NM_001122636
2.45E+02	7.94E+00	pleckstrin homol	pleckstrin homol	NM_015164	NM_015164
2.45E+02	7.94E+00	pleckstrin homol	pleckstrin homol	NM_015164	NM_015164
3.29E+02	8.36E+00	scavenger recept	scavenger recept	NM_153334,NM	NM_153334,NM_182895
2.90E+02	8.18E+00	deoxythymidylat	inhibitor of grow	NM_012145	NM_012145
2.90E+02	8.18E+00	deoxythymidylat	inhibitor of grow	NM_012145	NM_012145
2.13E+02	7.74E+00	AT rich interactiv	WD repeat dom	NM_005224	NM_005224
2.77E+02	8.11E+00	insulin-like grow	ribosomal protei	NM_006547	NM_006547
3.76E+02	8.56E+00	family with sequ	family with sequ	NM_001002034	NM_001002034
1.88E+00	9.11E-01	zinc finger CCCH-	gasdermin D	NM_015117	NM_015117
1.88E+00	9.11E-01	zinc finger CCCH-	gasdermin D	NM_015117	NM_015117
4.08E-03	-7.94E+00	LEM domain con	motilin	NM_181336,NM	NM_181336,NM_001143944
4.53E+02	8.82E+00	SPARC related m	thrombospondin	NM_022138	NM_022138
2.72E+02	8.09E+00	BMS1 pseudoge	SEC24 family, m	NR_026592	NR_026592
2.92E-03	-8.42E+00	cat eye syndrom	cat eye syndrom	NM_017424	NM_017424
2.92E-03	-8.42E+00	cat eye syndrom	cat eye syndrom	NM_017424	NM_017424
2.92E-03	-8.42E+00	cat eye syndrom	cat eye syndrom	NM_017424	NM_017424
2.28E+02	7.83E+00	zinc finger protei	zinc finger protei	NM_001080409	NM_001080409
2.28E+02	7.83E+00	zinc finger protei	zinc finger protei	NM_001080409	NM_001080409
4.09E-03	-7.93E+00	chromosome 15	syntaxin binding	NR_003954	NR_003954
2.53E+02	7.98E+00	family with sequ	keratinocyte gro	NM_001145196	NM_001145196
4.27E+02	8.74E+00	serum/glucocort	serum/glucocort	NM_170693	NM_170693
3.70E+02	8.53E+00	DNA (cytosine-5-	DNA (cytosine-5-	NM_013369,NM	NM_013369,NM_175867
2.75E+02	8.10E+00	chromosome 19	cell division cycl	NM_033513	NM_033513
2.13E+02	7.74E+00	forkhead box F2	forkhead box C1	NM_001452	NM_001452
2.66E+02	8.05E+00	zinc finger protei	zinc finger protei	NM_001113525	NM_001113525
2.66E+02	8.05E+00	zinc finger protei	zinc finger protei	NM_001113525	NM_001113525
3.79E-03	-8.04E+00	S-phase kinase-a	protein phospha	NM_006930,NM	NM_006930,NM_170679
2.28E+02	7.83E+00	forkhead box K2	forkhead box K2	NM_004514	NM_004514
3.40E+02	8.41E+00	immunoglobulin	immunoglobulin	NM_020962	NM_020962
2.37E+02	7.89E+00	5-oxoprolinase (	5-oxoprolinase (	NM_017570	NM_017570
2.71E+02	8.08E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
2.71E+02	8.08E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
2.71E+02	8.08E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
2.00E+02	7.64E+00	serpin peptidase	chromosome 18	NM_001031848,	NM_001031848,NM_198833,NM_
2.00E+02	7.64E+00	serpin peptidase	chromosome 18	NM_001031848,	NM_001031848,NM_198833,NM_
2.01E+02	7.65E+00	megakaryoblasti	megakaryoblasti	NM_020831	NM_020831
2.01E+02	7.65E+00	megakaryoblasti	megakaryoblasti	NM_020831	NM_020831
2.19E+02	7.78E+00	nuclear receptor	nuclear receptor	NM_004959	NM_004959
2.19E+02	7.78E+00	nuclear receptor	nuclear receptor	NM_004959	NM_004959
2.41E+02	7.91E+00	coenzyme Q4 ho	solute carrier fa	NM_016035	NM_016035
1.92E+02	7.59E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
2.40E+02	7.91E+00	frizzled homolog	ankyrin repeat d	NM_031866	NM_031866
2.45E+02	7.94E+00	F-box and leucin	F-box and leucin	NM_022824	NM_022824
2.59E+02	8.02E+00	5-hydroxytrypta	interleukin-1 rec	NM_000863	NM_000863
2.68E+02	8.06E+00	null	golgin A8 family,	null	null
2.26E+02	7.82E+00	chromosome 17	rabaptin, RAB GT	NM_207103	NM_207103
2.26E+02	7.82E+00	rabaptin, RAB GT	rabaptin, RAB GT	NM_001083585,	NM_001083585,NM_004703
3.13E+02	8.29E+00	myeloid/lymphoi	myeloid/lymphoi	NM_005934	NM_005934
3.13E+02	8.29E+00	myeloid/lymphoi	myeloid/lymphoi	NM_005934	NM_005934
3.03E+02	8.24E+00	zinc finger and B	zinc finger and B	NM_025224	NM_025224

3.03E+02	8.24E+00	zinc finger and B	zinc finger and B	NM_025224	NM_025224
3.03E+02	8.24E+00	zinc finger and B	zinc finger and B	NM_025224	NM_025224
4.59E+02	8.84E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.04E-03	-8.36E+00	EGF-containing fi	coiled-coil domai	NM_004105,NM	NM_004105,NM_001039349,NM_
3.04E-03	-8.36E+00	EGF-containing fi	coiled-coil domai	NM_004105,NM	NM_004105,NM_001039349,NM_
4.40E-03	-7.83E+00	SH2 domain cont	SH2 domain cont	NM_170600,NM	NM_170600,NM_005489,NM_001
4.40E-03	-7.83E+00	SH2 domain cont	SH2 domain cont	NM_170600,NM	NM_170600,NM_005489,NM_001
4.72E+02	8.88E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.28E+02	7.83E+00	transforming, aci	fibroblast growth	NM_006342	NM_006342
2.01E+02	7.65E+00	chromosome 20	chromosome 20	NM_080616	NM_080616
2.31E+02	7.85E+00	NODAL modulato	polycystic kidney	NM_001004067	NM_001004067
4.05E-03	-7.95E+00	colony stimulatir	interleukin 3 rece	NM_172247	NM_172247
2.76E+02	8.11E+00	mediator comple	TBC1 domain fan	NM_005121	NM_005121
3.00E+02	8.23E+00	tumor suppressir	tetratricopeptide	NM_003310	NM_003310
3.00E+02	8.23E+00	tumor suppressir	tetratricopeptide	NM_003310	NM_003310
2.10E+02	7.71E+00	zinc finger protei	zinc finger protei	NM_213605	NM_213605
2.10E+02	7.71E+00	zinc finger protei	zinc finger protei	NM_213605	NM_213605
2.31E+02	7.85E+00	cell adhesion mo	BUD13 homolog	NM_014333,NM	NM_014333,NM_001098517
2.31E+02	7.85E+00	cell adhesion mo	BUD13 homolog	NM_014333,NM	NM_014333,NM_001098517
2.28E+02	7.83E+00	olfactory recepto	olfactory recepto	NM_001005277,	NM_001005277,NM_001005221,N
4.57E-03	-7.77E+00	solute carrier fan	heat shock prote	NM_001078177	NM_001078177
3.04E+02	8.25E+00	hypothetical LOC	carboxypeptidase	NR_024480	NR_024480
3.04E+02	8.25E+00	hypothetical LOC	carboxypeptidase	NR_024480	NR_024480
3.36E-03	-8.22E+00	small nuclear rib	gamma-glutamyl	NM_004175	NM_004175
4.17E+02	8.70E+00	cadherin 24, type	apoptotic chrom	NM_022478,NM	NM_022478,NM_144985
3.58E-03	-8.13E+00	chromosome 9 o	methyltransferas	NM_199350	NM_199350
2.19E+02	7.78E+00	hypothetical LOC	hypothetical LOC	NR_026964	NR_026964
2.19E+02	7.78E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
3.77E-03	-8.05E+00	fibroblast growth	fibroblast growth	NM_023107,NM	NM_023107,NM_023108
3.77E-03	-8.05E+00	fibroblast growth	chromosome 8 o	NM_023107,NM	NM_023107,NM_023108
2.18E+02	7.77E+00	TMF1-regulated	TMF1-regulated	NM_001013642	NM_001013642
2.26E+02	7.82E+00	golgin A3	golgin A3	NM_005895	NM_005895
3.06E+02	8.26E+00	methionine amir	distal-less home	NM_199227	NM_199227
2.18E+02	7.77E+00	fibroblast growth	nuclear receptor	NM_022963	NM_022963
2.18E+02	7.77E+00	fibroblast growth	nuclear receptor	NM_022963	NM_022963
2.13E+02	7.74E+00	transcription fact	NFAT activating p	NM_005650,NM	NM_005650,NM_181492
1.99E+02	7.64E+00	ephrin-A2	ephrin-A2	NM_001405	NM_001405
1.99E+02	7.64E+00	ephrin-A2	melanoma assoc	NM_001405	NM_001405
2.09E+02	7.70E+00	calmodulin regul	calmodulin regul	NM_015447	NM_015447
2.09E+02	7.70E+00	calmodulin regul	UBA domain con	NM_015447	NM_015447
2.09E+02	7.70E+00	calmodulin regul	UBA domain con	NM_015447	NM_015447
3.10E+02	8.27E+00	transmembrane	lipase, member H	NM_080652	NM_080652
3.91E+02	8.61E+00	coiled-coil domai	coiled-coil domai	NM_001136505	NM_001136505
2.70E+02	8.07E+00	zinc finger RNA b	zinc finger RNA b	NM_015174	NM_015174
2.07E+02	7.69E+00	proteasome (pro	colony stimulatir	NM_002809	NM_002809
3.50E+02	8.45E+00	tumor necrosis fa	mitochondrial int	NM_018647	NM_018647
2.96E+02	8.21E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
2.96E+02	8.21E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
2.97E+02	8.22E+00	alkaline phospha	alkaline phospha	NM_031313	NM_031313
2.97E+02	8.22E+00	alkaline phospha	alkaline phospha	NM_031313	NM_031313
2.19E+02	7.78E+00	runt-related tran	runt-related tran	NM_001754,NM	NM_001754,NM_001001890
2.08E+02	7.70E+00	F-box and leucine	F-box and leucine	NM_001099784	NM_001099784
3.12E-03	-8.32E+00	placenta-specific	placenta-specific	NM_182832	NM_182832
2.30E+02	7.84E+00	RasGEF domain f	FXYD domain cor	NM_145313	NM_145313
2.30E+02	7.84E+00	RasGEF domain f	FXYD domain cor	NM_145313	NM_145313
4.16E-03	-7.91E+00	zinc finger protei	zinc finger protei	NM_021915	NM_021915
4.16E-03	-7.91E+00	zinc finger protei	zinc finger protei	NM_021915	NM_021915
3.17E+02	8.31E+00	potassium voltag	potassium voltag	NM_172109	NM_172109

3.17E+02	8.31E+00	potassium voltag	potassium voltag	NM_172109	NM_172109
3.17E+02	8.31E+00	potassium voltag	potassium voltag	NM_172109	NM_172109
2.22E+02	7.79E+00	sulfotransferase	eukaryotic transl	NM_001055,NM	NM_001055,NM_177529,NM_177
2.22E+02	7.79E+00	sulfotransferase	eukaryotic transl	NM_001055,NM	NM_001055,NM_177529,NM_177
2.65E+02	8.05E+00	chromosome 1 o	KIAA1751	NM_001003808	NM_001003808
4.19E-03	-7.90E+00	olfactory recept	olfactory recept	NM_001001959	NM_001001959
2.33E+02	7.87E+00	sphingosine-1-ph	mitochondrial rib	NM_004230	NM_004230
2.49E+02	7.96E+00	melanoma antige	melanoma antige	NM_175743,NM	NM_175743,NM_175742,NM_005
2.78E+02	8.12E+00	cadherin 15, type	cadherin 15, type	NM_004933	NM_004933
2.78E+02	8.12E+00	cadherin 15, type	cadherin 15, type	NM_004933	NM_004933
2.45E+02	7.94E+00	Theg homolog (n	C2 calcium-depe	NM_199202,NM	NM_199202,NM_016585
2.59E+02	8.02E+00	TBC1 domain fan	TBC1 domain fan	NM_019020	NM_019020
2.59E+02	8.02E+00	TBC1 domain fan	TBC1 domain fan	NM_019020	NM_019020
2.30E+02	7.84E+00	solute carrier fan	solute carrier fan	NM_033125	NM_033125
2.30E+02	7.84E+00	solute carrier fan	solute carrier fan	NM_033125	NM_033125
2.46E+02	7.94E+00	ribosomal RNA p	pyridoxal (pyrido	NM_015056	NM_015056
2.46E+02	7.94E+00	ribosomal RNA p	pyridoxal (pyrido	NM_015056	NM_015056
2.30E+02	7.84E+00	MAX dimerizatio	lectin, mannose-	NM_031300	NM_031300
2.30E+02	7.84E+00	lectin, mannose-	lectin, mannose-	NM_006816	NM_006816
2.13E+02	7.74E+00	chromosome 19	phosphatidylinos	NM_021231	NM_021231
2.13E+02	7.74E+00	chromosome 19	phosphatidylinos	NM_021231	NM_021231
2.24E+02	7.81E+00	CD248 molecule,	CD248 molecule,	NM_020404	NM_020404
3.31E-03	-8.24E+00	phosphatidylinos	M-phase phosph	NM_020845	NM_020845
4.65E+02	8.86E+00	small nucleolar R	purinergic recept	NR_003688	NR_003688
2.12E+02	7.73E+00	serine/arginine-r	serine/arginine-r	NM_003769	NM_003769
2.12E+02	7.73E+00	serine/arginine-r	dynein, light chai	NM_003769	NM_003769
2.12E+02	7.73E+00	dynein, light chai	dynein, light chai	NM_001037494	NM_001037494
2.62E+02	8.03E+00	zinc finger, DHH	zinc finger, DHH	NM_153251	NM_153251
2.62E+02	8.03E+00	zinc finger, DHH	zinc finger, DHH	NM_153251	NM_153251
3.30E+02	8.37E+00	protease, serine-	protease, serine-	NM_214710	NM_214710
5.06E-03	-7.63E+00	F-box protein 32	F-box protein 32	NM_058229,NM	NM_058229,NM_148177
5.06E-03	-7.63E+00	F-box protein 32	F-box protein 32	NM_058229,NM	NM_058229,NM_148177
2.46E+02	7.94E+00	PR domain conta	null	NM_052996,NM	NM_052996,NM_001098173
2.46E+02	7.94E+00	PR domain conta	null	NM_052996,NM	NM_052996,NM_001098173
2.08E+02	7.70E+00	ADAM metallope	ADAM metallope	NM_030957	NM_030957
3.16E+02	8.30E+00	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
3.16E+02	8.30E+00	MACRO domain	MACRO domain	NM_014067	NM_014067
2.43E+02	7.92E+00	LAG1 homolog, c	LAG1 homolog, c	NM_022075,NM	NM_022075,NM_181746
2.43E+02	7.92E+00	LAG1 homolog, c	LAG1 homolog, c	NM_022075,NM	NM_022075,NM_181746
2.31E+02	7.85E+00	sema domain, tr	sema domain, tr	NM_032108	NM_032108
2.31E+02	7.85E+00	sema domain, tr	sema domain, tr	NM_032108	NM_032108
3.42E+02	8.42E+00	inositol polyphos	inositol polyphos	NM_019892	NM_019892
3.17E+02	8.31E+00	matrix metallope	matrix metallope	NM_016155	NM_016155
2.50E+02	7.96E+00	GLI family zinc fi	GLI family zinc fi	NM_000168	NM_000168
2.80E+02	8.13E+00	cyclin N-terminal	cyclin N-terminal	NM_024877	NM_024877
2.24E+02	7.81E+00	solute carrier fan	solute carrier fan	NM_022082	NM_022082
2.24E+02	7.81E+00	solute carrier fan	solute carrier fan	NM_022082	NM_022082
2.50E+02	7.97E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
2.50E+02	7.97E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
2.37E+02	7.89E+00	IQ motif and Sec	nucleoporin 210l	NM_014869,NM	NM_014869,NM_001134382
2.26E+02	7.82E+00	chromosome 22	bromodomain cc	NR_026997	NR_026997
2.98E+02	8.22E+00	ligase I, DNA, ATI	caspase recruitm	NM_000234	NM_000234
2.98E+02	8.22E+00	ligase I, DNA, ATI	caspase recruitm	NM_000234	NM_000234
2.98E+02	8.22E+00	ligase I, DNA, ATI	caspase recruitm	NM_000234	NM_000234
2.71E+02	8.08E+00	solute carrier fan	solute carrier fan	NM_130849,NM	NM_130849,NM_017767
2.71E+02	8.08E+00	solute carrier fan	solute carrier fan	NM_130849,NM	NM_130849,NM_017767
2.48E+02	7.95E+00	protein O-fucosy	protein O-fucosy	NR_004858,NM_	NR_004858,NM_133635,NM_015
2.99E+02	8.22E+00	distal-less home	distal-less home	NM_004405	NM_004405

2.99E+02	8.22E+00	distal-less home	distal-less home	NM_004405	NM_004405
2.65E+02	8.05E+00	solute carrier fa	solute carrier fa	NM_004174	NM_004174
2.48E+02	7.95E+00	coiled-coil doma	chromosome 7 o	NM_138771	NM_138771
2.48E+02	7.95E+00	coiled-coil doma	chromosome 7 o	NM_138771	NM_138771
2.48E+02	7.95E+00	zinc finger, DHH	zinc finger, DHH	NM_153746,NM	NM_153746,NM_024630
2.48E+02	7.95E+00	zinc finger, DHH	zinc finger, DHH	NM_153746,NM	NM_153746,NM_024630
2.24E+02	7.81E+00	perilipin 2	DENN/MADD do	NM_001122	NM_001122
2.93E+02	8.20E+00	active BCR-relat	active BCR-relat	NM_001159746	NM_001159746
2.93E+02	8.20E+00	active BCR-relat	active BCR-relat	NM_001159746	NM_001159746
2.75E+02	8.10E+00	KN motif and an	KN motif and an	NM_015493,NM	NM_015493,NM_001136191
2.75E+02	8.10E+00	KN motif and an	KN motif and an	NM_015493,NM	NM_015493,NM_001136191
2.34E+02	7.87E+00	zinc finger protei	non-protein codi	NM_003408	NM_003408
2.34E+02	7.87E+00	zinc finger protei	non-protein codi	NM_003408	NM_003408
4.03E-03	-7.95E+00	family with sequ	family with sequ	NM_001136233	NM_001136233
2.43E+02	7.92E+00	non-protein codi	non-protein codi	NR_026873	NR_026873
3.57E+02	8.48E+00	non-protein codi	phosphofructoki	NM_001098830	NM_001098830
3.40E+02	8.41E+00	aldehyde dehydr	unc-51-like kinas	NM_001135168,	NM_001135168,NM_001135167,
3.00E+02	8.23E+00	orthodenticle ho	exocyst complex	NM_172337,NM	NM_172337,NM_021728
3.00E+02	8.23E+00	orthodenticle ho	exocyst complex	NM_172337,NM	NM_172337,NM_021728
3.00E+02	8.23E+00	orthodenticle ho	exocyst complex	NM_172337,NM	NM_172337,NM_021728
3.00E+02	8.23E+00	orthodenticle ho	exocyst complex	NM_172337,NM	NM_172337,NM_021728
3.03E+02	8.24E+00	E4F transcription	E4F transcription	NM_004424	NM_004424
3.03E+02	8.24E+00	E4F transcription	E4F transcription	NM_004424	NM_004424
2.53E+02	7.98E+00	unc-5 homolog	unc-5 homolog	NM_133369	NM_133369
5.00E-03	-7.64E+00	polymerase (RN	polymerase (RN	NM_016310	NM_016310
5.00E-03	-7.64E+00	polymerase (RN	polymerase (RN	NM_016310	NM_016310
2.59E+02	8.02E+00	Smith-Magenis s	sterol regulatory	NR_024007	NR_024007
2.69E+02	8.07E+00	receptor-associa	receptor-associa	NM_005055,NM	NM_005055,NM_032645
2.69E+02	8.07E+00	receptor-associa	receptor-associa	NM_005055,NM	NM_005055,NM_032645
2.69E+02	8.07E+00	receptor-associa	CUGBP, Elav-like	NM_005055,NM	NM_005055,NM_032645
3.13E+02	8.29E+00	---	sodium channel,	NR_027361	NR_027361
3.13E+02	8.29E+00	---	sodium channel,	NR_027361	NR_027361
4.64E-03	-7.75E+00	neuroblastoma	hypothetical FLJ	NM_001101663	NM_001101663
4.64E-03	-7.75E+00	neuroblastoma	hypothetical FLJ	NM_001101663	NM_001101663
2.90E+02	8.18E+00	integrator compl	integrator compl	NR_027393	NR_027393
2.79E+02	8.12E+00	ADAM metallop	ADAM metallop	NM_001109	NM_001109
2.13E+02	7.74E+00	transmembrane	transmembrane	NM_133448	NM_133448
2.99E+02	8.22E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
4.32E-03	-7.86E+00	zinc finger protei	hypothetical LO	NM_001002844	NM_001002844
2.92E+02	8.19E+00	family with sequ	family with sequ	NM_001142864	NM_001142864
2.92E+02	8.19E+00	family with sequ	family with sequ	NM_001142864	NM_001142864
2.96E+02	8.21E+00	TBC1 domain fa	TBC1 domain fa	NM_014346	NM_014346
2.96E+02	8.21E+00	TBC1 domain fa	TBC1 domain fa	NM_014346	NM_014346
2.66E+02	8.05E+00	TBC1 domain fa	TBC1 domain fa	NM_024682	NM_024682
2.66E+02	8.05E+00	TBC1 domain fa	TBC1 domain fa	NM_024682	NM_024682
2.54E+02	7.99E+00	chromosome 18	chromosome 18	NM_004338,NM	NM_004338,NM_181483
2.54E+02	7.99E+00	chromosome 18	chromosome 18	NM_004338,NM	NM_004338,NM_181483
5.32E-03	-7.55E+00	NHL repeat conta	adrenergic, beta-	NM_198514	NM_198514
3.64E+02	8.51E+00	paraneoplastic a	paraneoplastic a	NM_013364	NM_013364
4.50E-03	-7.80E+00	crystallin, beta B	immunoglobulin	NM_000496	NM_000496
4.50E-03	-7.80E+00	immunoglobulin	immunoglobulin	NM_001013618	NM_001013618
2.32E+02	7.86E+00	hect domain and	TP53 target 3B	NR_002827	NR_002827
3.77E-03	-8.05E+00	zinc finger protei	zinc finger protei	NM_030634,NM	NM_030634,NM_001077195
3.77E-03	-8.05E+00	zinc finger protei	zinc finger protei	NM_030634,NM	NM_030634,NM_001077195
2.40E+02	7.91E+00	zinc finger protei	zinc finger protei	NM_001080485	NM_001080485
2.40E+02	7.91E+00	zinc finger protei	zinc finger protei	NM_001080485	NM_001080485
3.48E+02	8.44E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
3.48E+02	8.44E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326

3.48E+02	8.44E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
3.72E+02	8.54E+00	family with sequ	KIAA0182	NM_198491	NM_198491
3.72E+02	8.54E+00	family with sequ	KIAA0182	NM_198491	NM_198491
2.17E+02	7.76E+00	zinc finger protei	SUMO1 pseudog	NM_006526	NM_006526
2.54E+02	7.99E+00	DENN/MADD do	transmembrane	NM_015213	NM_015213
2.54E+02	7.99E+00	DENN/MADD do	transmembrane	NM_015213	NM_015213
2.06E+02	7.68E+00	cytochrome P45	cytochrome P45	NM_017781	NM_017781
2.06E+02	7.68E+00	cytochrome P45	cytochrome P45	NM_017781	NM_017781
2.77E+02	8.11E+00	anoctamin 8	anoctamin 8	NM_020959	NM_020959
2.10E+02	7.71E+00	guanine nucleoti	guanine nucleoti	NM_002072	NM_002072
2.12E+02	7.73E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
2.30E+02	7.84E+00	contactin 3 (plas	family with sequ	NM_020872	NM_020872
2.35E+02	7.88E+00	tRNA splicing en	tRNA splicing en	NM_207346	NM_207346
4.70E-03	-7.73E+00	solute carrier fa	dipeptidase 3	NM_001145963,	NM_001145963,NM_001145964,
2.26E+02	7.82E+00	cell death-induci	tubulin, beta 6	NM_198289	NM_198289
3.06E+02	8.26E+00	transmembrane	transmembrane	NM_014858	NM_014858
2.68E+02	8.06E+00	quaking homolo	chromosome 6 o	NM_006775,NM	NM_006775,NM_206855,NM_20
2.68E+02	8.06E+00	quaking homolo	chromosome 6 o	NM_006775,NM	NM_006775,NM_206855,NM_20
2.68E+02	8.06E+00	quaking homolo	chromosome 6 o	NM_006775,NM	NM_006775,NM_206855,NM_20
4.70E+02	8.88E+00	lymphocyte-spec	gamma-glutamyl	NR_027238	NR_027238
4.70E+02	8.88E+00	lymphocyte-spec	gamma-glutamyl	NR_027238	NR_027238
4.70E+02	8.88E+00	lymphocyte-spec	gamma-glutamyl	NR_027238	NR_027238
2.82E+02	8.14E+00	ectonucleoside t	chromosome 9 o	NM_203468,NM	NM_203468,NM_001246
5.44E-03	-7.52E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
5.44E-03	-7.52E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
2.05E+02	7.68E+00	aquaporin 12A	kinesin family m	NM_198998	NM_198998
2.05E+02	7.68E+00	aquaporin 12A	kinesin family m	NM_198998	NM_198998
1.94E+02	7.60E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
1.94E+02	7.60E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
4.02E+02	8.65E+00	septin 9	septin 9	NM_001113493	NM_001113493
4.68E+02	8.87E+00	paired-like home	paired-like home	NM_153426,NM	NM_153426,NM_153427,NM_00
4.68E+02	8.87E+00	paired-like home	paired-like home	NM_153426,NM	NM_153426,NM_153427,NM_00
4.27E-03	-7.87E+00	UDP glucuronos	UDP glucuronos	NM_019075	NM_019075
4.27E-03	-7.87E+00	UDP glucuronos	UDP glucuronos	NM_019075	NM_019075
2.31E+02	7.85E+00	protein O-fucosy	protein O-fucosy	NR_004858,NM_	NR_004858,NM_133635,NM_015
3.27E+02	8.35E+00	poly(rC) binding	poly(rC) binding	NM_001130141,	NM_001130141,NM_020528
3.41E+02	8.41E+00	telomerase reve	telomerase reve	NM_198253,NM	NM_198253,NM_198255
3.41E+02	8.41E+00	telomerase reve	telomerase reve	NM_198253,NM	NM_198253,NM_198255
2.23E+02	7.80E+00	HCC-related HCC	chromosome 8 o	NR_024479	NR_024479
4.35E-03	-7.84E+00	Cdk5 and Abl en	Cdk5 and Abl en	NM_001100619	NM_001100619
4.35E-03	-7.84E+00	Cdk5 and Abl en	Cdk5 and Abl en	NM_138375	NM_138375
3.60E+02	8.49E+00	phosphoinositid	parathyroid hor	NM_152671,NM	NM_152671,NM_015040
3.60E+02	8.49E+00	phosphoinositid	parathyroid hor	NM_152671,NM	NM_152671,NM_015040
4.43E-03	-7.82E+00	olfactory recept	urothelial cancer	NM_013940	NM_013940
4.57E-03	-7.77E+00	pre-B-cell leuke	lysophosphatidic	NM_025245	NM_025245
2.18E+02	7.77E+00	YY1 associated f	zinc finger CCHC	NM_005748	NM_005748
2.37E+02	7.89E+00	fibroblast growt	ring finger protei	NM_020637	NM_020637
2.37E+02	7.89E+00	fibroblast growt	ring finger protei	NM_020637	NM_020637
2.83E+02	8.14E+00	organic solute tr	organic solute tr	NM_152672	NM_152672
2.60E+02	8.02E+00	MAD1 mitotic a	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
4.05E+02	8.66E+00	polycystic kidney	NODAL modulat	NM_178541	NM_178541
2.65E+02	8.05E+00	DNA cross-link r	DNA cross-link r	NM_022836	NM_022836
2.82E+02	8.14E+00	amyloid beta (A4	amyloid beta (A4	NM_001163	NM_001163
2.82E+02	8.14E+00	amyloid beta (A4	amyloid beta (A4	NM_001163	NM_001163
4.83E-03	-7.69E+00	postmeiotic segr	postmeiotic segr	NR_022007	NR_022007
4.34E+02	8.76E+00	mitochondrial ri	zinc finger, DHH	NM_024026	NM_024026
3.67E+02	8.52E+00	NLR family, pyrin	ATH1, acid treha	NM_138329	NM_138329
3.67E+02	8.52E+00	NLR family, pyrin	ATH1, acid treha	NM_138329	NM_138329

3.67E+02	8.52E+00	NLR family, pyrin	ATH1, acid treha	NM_138329	NM_138329
2.29E+02	7.84E+00	actin filament as	actin filament as	NM_001134647,	NM_001134647,NM_198595
4.80E-03	-7.70E+00	deoxynucleotidyl	deoxynucleotidyl	NM_052951	NM_052951
3.57E+02	8.48E+00	melanoma antige	VENT homeobox	NM_173523	NM_173523
2.04E+02	7.67E+00	sterile alpha mot	protein kinase, c	NM_138352	NM_138352
2.39E+02	7.90E+00	Yes-associated p	Yes-associated p	NM_006106,NM	NM_006106,NM_001130145
2.46E+02	7.94E+00	peptidase (mitoc	peptidase (mitoc	NM_015160	NM_015160
2.25E+02	7.81E+00	chromosome 4 o	protocadherin 1	NM_001099783	NM_001099783
2.25E+02	7.81E+00	chromosome 4 o	protocadherin 1	NM_001099783	NM_001099783
2.97E+02	8.22E+00	zinc finger and B	zinc finger and B	NM_181842	NM_181842
2.97E+02	8.22E+00	zinc finger and B	zinc finger and B	NM_181842	NM_181842
3.59E-03	-8.12E+00	neuronal guanine	sialidase 2 (cytos	NM_001114090,	NM_001114090,NM_019850
2.44E+02	7.93E+00	hyaluronan and	hyaluronan and	NM_023002	NM_023002
2.97E+02	8.22E+00	paralemmin	chromosome 19	NM_001040134,	NM_001040134,NM_002579
2.99E+02	8.22E+00	transketolase-lik	filamin A, alpha	NM_001145934	NM_001145934
2.99E+02	8.22E+00	transketolase-lik	filamin A, alpha	NM_001145934	NM_001145934
2.99E+02	8.22E+00	transketolase-lik	filamin A, alpha	NM_001145934	NM_001145934
4.80E-03	-7.70E+00	UDP-Gal:betaGlc	UDP-Gal:betaGlc	NM_033173,NM	NM_033173,NM_033172,NM_03
2.30E+02	7.84E+00	ELK4, ETS-domai	ELK4, ETS-domai	NM_021795	NM_021795
2.30E+02	7.84E+00	NK6 homeobox 1	NK6 homeobox 1	NM_006168	NM_006168
3.00E+02	8.23E+00	coiled-coil domai	coiled-coil domai	NM_013301	NM_013301
2.23E+02	7.80E+00	embigin pseudog	hypothetical FLJ	NR_003955	NR_003955
4.11E+02	8.68E+00	solute carrier fa	solute carrier fa	NM_004174	NM_004174
2.88E+02	8.17E+00	DOT1-like, histor	DOT1-like, histor	NM_032482	NM_032482
2.38E+02	7.90E+00	non-protein codi	sperm acrosome	NR_002767	NR_002767
3.16E+02	8.30E+00	CTD (carboxy-ter	potassium voltag	NM_048368,NM	NM_048368,NM_004715
2.77E+02	8.11E+00	plexin B2	plexin B2	NM_012401	NM_012401
2.77E+02	8.11E+00	plexin B2	plexin B2	NM_012401	NM_012401
3.34E+02	8.38E+00	tryptase delta 1	tryptase delta 1	NM_012217	NM_012217
4.94E-03	-7.66E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
4.03E-03	-7.95E+00	thioredoxin dom	thioredoxin dom	NM_001098530	NM_001098530
2.97E+02	8.22E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
2.97E+02	8.22E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
2.66E+02	8.05E+00	cytoplasmic poly	chromosome 5 o	NM_030627	NM_030627
2.55E+02	8.00E+00	Janus kinase and	dihydropyrimidi	NM_001105521	NM_001105521
2.55E+02	8.00E+00	Janus kinase and	dihydropyrimidi	NM_001105521	NM_001105521
3.35E+02	8.39E+00	TEL2, telomere n	TEL2, telomere n	NM_016111	NM_016111
3.35E+02	8.39E+00	TEL2, telomere n	TEL2, telomere n	NM_016111	NM_016111
2.33E+02	7.87E+00	chromosome 1 o	chromosome 1 o	NM_001142569	NM_001142569
2.33E+02	7.87E+00	chromosome 1 o	chromosome 1 o	NM_001142569	NM_001142569
2.30E+02	7.84E+00	chromosome 5 o	iroquois homeob	NM_178569	NM_178569
2.30E+02	7.84E+00	chromosome 5 o	iroquois homeob	NM_178569	NM_178569
3.82E+02	8.58E+00	hepatoma derive	hepatoma derive	NM_138574	NM_138574
2.33E+02	7.87E+00	proteasome (pro	protein tyrosine	NM_020232	NM_020232
2.98E+02	8.22E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
2.98E+02	8.22E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
2.90E+02	8.18E+00	RRN3 RNA polym	MPV17 mitochon	NM_018427	NM_018427
2.90E+02	8.18E+00	RRN3 RNA polym	MPV17 mitochon	NM_018427	NM_018427
3.17E-03	-8.30E+00	mitogen-activate	tetraspanin 33	NR_002144	NR_002144
2.17E+02	7.76E+00	family with sequ	hypothetical LOC	NM_018232	NM_018232
2.17E+02	7.76E+00	family with sequ	hypothetical LOC	NM_018232	NM_018232
5.52E-03	-7.50E+00	regulator of G-pr	regulator of G-pr	NM_002928	NM_002928
5.52E-03	-7.50E+00	regulator of G-pr	regulator of G-pr	NM_002928	NM_002928
2.58E-03	-8.60E+00	leucine-rich repe	wingless-type MI	NM_020678	NM_020678
2.30E+02	7.85E+00	RRN3 RNA polym	MPV17 mitochon	NM_018427	NM_018427
2.50E+02	7.96E+00	tumor protein p7	tumor protein p7	NM_001126240,	NM_001126240,NM_001126242,
4.07E+02	8.67E+00	RAS p21 protein	cell division cycle	NM_007368	NM_007368
2.21E+02	7.79E+00	ubiquitin specific	chromosome 16	NM_003470	NM_003470

2.21E+02	7.79E+00	chromosome 16	chromosome 16	NM_014117	NM_014117
2.13E+02	7.74E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
2.13E+02	7.74E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
4.03E+02	8.65E+00	IZUMO family m	IZUMO family m	NM_001039846,	NM_001039846,NM_001031735
3.93E+02	8.62E+00	ArfGAP with dua	ArfGAP with dua	NM_006869	NM_006869
3.93E+02	8.62E+00	ArfGAP with dua	ArfGAP with dua	NM_006869	NM_006869
3.93E+02	8.62E+00	ArfGAP with dua	ArfGAP with dua	NM_006869	NM_006869
2.20E+02	7.78E+00	O-6-methylguani	O-6-methylguani	NM_002412	NM_002412
2.30E+02	7.85E+00	cysteine-rich PA	family with sequ	NM_175918	NM_175918
2.25E+02	7.81E+00	cartilage interme	cartilage interme	NM_153221	NM_153221
2.25E+02	7.81E+00	cartilage interme	cartilage interme	NM_153221	NM_153221
2.25E+02	7.81E+00	cartilage interme	cartilage interme	NM_153221	NM_153221
3.35E+02	8.39E+00	G protein pathwa	neuralized homo	NM_004489	NM_004489
2.61E+02	8.03E+00	RAN binding prot	coiled-coil doma	NM_005493	NM_005493
3.75E-03	-8.06E+00	neuronal guanin	sialidase 2 (cytos	NM_001114090,	NM_001114090,NM_019850
2.57E+02	8.01E+00	olfactory recepto	null	NM_001005224,	NM_001005224,NM_001005221,
2.57E+02	8.01E+00	olfactory recepto	null	NM_001005224,	NM_001005224,NM_001005221,
2.48E+02	7.95E+00	patatin-like phos	variable charge,	NM_001142389,	NM_001142389,NM_004650
2.38E+02	7.90E+00	EPS8-like 2	transaldolase 1	NM_022772	NM_022772
2.38E+02	7.90E+00	EPS8-like 2	transaldolase 1	NM_022772	NM_022772
2.38E+02	7.90E+00	EPS8-like 2	transaldolase 1	NM_022772	NM_022772
3.51E-03	-8.15E+00	chromosome 16	chromosome 16	NM_001012991	NM_001012991
2.75E+02	8.10E+00	coagulation facto	coagulation facto	NM_003950	NM_003950
3.98E+02	8.64E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794
2.56E+02	8.00E+00	axin 1	mitochondrial ri	NM_181050,NM	NM_181050,NM_003502
2.71E+02	8.08E+00	pre-B lymphocyt	BMS1 homolog,	NM_007128	NM_007128
2.46E+02	7.94E+00	MACRO domain	MACRO domain	NM_014067	NM_014067
2.83E+02	8.14E+00	thyroid peroxida	peroxidasin hom	NM_000547,NM	NM_000547,NM_175719,NM_17
2.83E+02	8.14E+00	thyroid peroxida	peroxidasin hom	NM_000547,NM	NM_000547,NM_175719,NM_17
2.83E+02	8.14E+00	thyroid peroxida	peroxidasin hom	NM_000547,NM	NM_000547,NM_175719,NM_17
4.18E-03	-7.90E+00	glycophorin A (	hedgehog intera	NM_002099	NM_002099
2.39E+02	7.90E+00	glutamate recep	glutamate recep	NM_000836	NM_000836
4.52E-03	-7.79E+00	keratin 74	keratin 72	NM_175053	NM_175053
4.15E-03	-7.91E+00	cerebellin 3 prec	cerebellin 3 prec	NM_001039771	NM_001039771
2.64E+02	8.04E+00	glutamate recep	olfactory recepto	NR_027044	NR_027044
2.64E+02	8.04E+00	glutamate recep	olfactory recepto	NR_027044	NR_027044
2.63E+02	8.04E+00	2'-5'-oligoadenyl	deltex homolog	NM_001032731,	NM_001032731,NM_002535,NM_
2.63E+02	8.04E+00	deltex homolog	deltex homolog	NM_004416	NM_004416
2.30E+02	7.84E+00	plasma cell-indu	spermatogenesis	NM_016459	NM_016459
2.26E+02	7.82E+00	olfactory recepto	olfactory recepto	NR_002171	NR_002171
2.25E+02	7.81E+00	protein kinase N	prostaglandin E r	NM_213560	NM_213560
2.25E+02	7.81E+00	prostaglandin E r	prostaglandin E r	NM_000955	NM_000955
2.25E+02	7.81E+00	prostaglandin E r	prostaglandin E r	NM_000955	NM_000955
2.35E+02	7.88E+00	neuro-oncologica	coiled-coil doma	NM_002516	NM_002516
2.42E+02	7.92E+00	differentially exp	differentially exp	NM_022047	NM_022047
3.68E-03	-8.09E+00	actin, beta pseu	amylase, alpha 2	NR_024438	NR_024438
3.68E-03	-8.09E+00	actin, beta pseu	amylase, alpha 2	NR_024438	NR_024438
2.22E+02	7.79E+00	death-associated	family with sequ	NM_014326	NM_014326
2.19E+02	7.78E+00	F-box and WD re	F-box and WD re	NM_022039	NM_022039
3.24E+02	8.34E+00	zinc finger protei	zinc finger protei	NM_001042428,	NM_001042428,NM_003456
2.50E+02	7.96E+00	dapper, antagoni	dapper, antagoni	NM_001079520,	NM_001079520,NM_016651
3.46E+02	8.43E+00	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
5.22E-03	-7.58E+00	family with sequ	hypothetical LOC	NR_026714	NR_026714
2.96E+02	8.21E+00	C-terminal bindi	hypothetical LOC	NM_022802,NM	NM_022802,NM_001329,NM_001
2.03E+02	7.66E+00	claudin 15	claudin 15	NM_014343	NM_014343
2.84E+02	8.15E+00	serine/threonine	serine/threonine	NM_173575	NM_173575
2.84E+02	8.15E+00	serine/threonine	serine/threonine	NM_173575	NM_173575
2.84E+02	8.15E+00	serine/threonine	serine/threonine	NM_173575	NM_173575

2.84E+02	8.15E+00	TBC1 domain fa	TBC1 domain fa	NM_019020	NM_019020
2.84E+02	8.15E+00	TBC1 domain fa	TBC1 domain fa	NM_019020	NM_019020
3.46E-03	-8.17E+00	apolipoprotein B	ATPase family, A	NM_000384	NM_000384
2.42E+02	7.92E+00	junctophilin 4	dehydrogenase/	NM_032452,NM	NM_032452,NM_001146028
2.73E+02	8.09E+00	EGF-like-domain,	EGF-like-domain,	NM_030652	NM_030652
4.21E-03	-7.89E+00	glucosidase, alph	glucosidase, alph	NM_000152,NM	NM_000152,NM_001079804,NM_
4.78E-03	-7.71E+00	hect domain and	TP53 target 3B	NR_002827	NR_002827
2.56E+02	8.00E+00	BARX homeobox	transmembrane	NM_003658	NM_003658
2.56E+02	8.00E+00	BARX homeobox	transmembrane	NM_003658	NM_003658
2.70E+02	8.07E+00	fibroblast growt	ring finger protei	NM_020637	NM_020637
2.70E+02	8.07E+00	ring finger protei	ring finger protei	NM_194460	NM_194460
2.21E+02	7.79E+00	MAP7 domain c	MAP7 domain c	NM_018067	NM_018067
4.39E+02	8.78E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
4.39E+02	8.78E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
2.33E+02	7.87E+00	zinc finger protei	hypothetical LOC	NM_145287	NM_145287
3.49E+02	8.45E+00	tubulin, gamma	tubulin, gamma	NM_006322	NM_006322
2.85E+02	8.15E+00	hypothetical LOC	COBW domain c	NR_015377	NR_015377
2.11E+02	7.72E+00	null	family with sequ	null	null
2.43E+02	7.92E+00	ADP-ribosylation	protein kinase C	NM_001142293,	NM_001142293,NM_014570
2.79E+02	8.12E+00	fizzy/cell division	fizzy/cell division	NM_001136197,	NM_001136197,NM_001136198
2.45E+02	7.94E+00	peptidase inhibit	peptidase inhibit	NM_153370	NM_153370
2.45E+02	7.94E+00	peptidase inhibit	peptidase inhibit	NM_153370	NM_153370
2.94E+02	8.20E+00	heparan sulfate	placenta-specific	NM_004807	NM_004807
3.38E-03	-8.21E+00	archaelysin famil	archaelysin famil	NM_001033569,	NM_001033569,NM_001033570,
3.53E+02	8.46E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.90E-03	-8.00E+00	Fanconi anemia,	Fanconi anemia,	NM_004629	NM_004629
3.90E-03	-8.00E+00	Fanconi anemia,	Fanconi anemia,	NM_004629	NM_004629
2.40E+02	7.91E+00	anterior gradient	anterior gradient	NM_006408	NM_006408
2.40E+02	7.91E+00	anterior gradient	anterior gradient	NM_006408	NM_006408
3.59E+02	8.49E+00	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
4.23E+02	8.72E+00	RecQ protein-lik	RecQ protein-lik	NM_004259	NM_004259
2.31E+02	7.85E+00	hect domain and	TP53 target 3B	NR_002827	NR_002827
2.31E+02	7.85E+00	hect domain and	TP53 target 3B	NR_002827	NR_002827
2.04E+02	7.67E+00	NADH dehydrog	NADH dehydrog	NM_024407	NM_024407
2.30E+02	7.84E+00	retinol dehydrog	staufen, RNA bin	NM_172037	NM_172037
4.52E-03	-7.79E+00	transporter 2, AT	proteasome (pro	NM_000544	NM_000544
4.40E-03	-7.83E+00	chromosome 3 o	Boc homolog (m	NM_001025072,	NM_001025072,NM_015412,NM_
2.33E+02	7.87E+00	sema domain, se	sema domain, se	NM_001031702	NM_001031702
2.51E+02	7.97E+00	olfactory recept	olfactory recept	NM_001005277,	NM_001005277,NM_001005221,
3.77E+02	8.56E+00	opioid growth f	opioid growth f	NM_007346	NM_007346
4.38E-03	-7.83E+00	small nucleolar R	hypothetical LOC	NR_003014	NR_003014
2.69E+02	8.07E+00	nucleolar compl	UDP-N-acetyl-al	NM_024078	NM_024078
2.69E+02	8.07E+00	nucleolar compl	UDP-N-acetyl-al	NM_024078	NM_024078
4.33E-03	-7.85E+00	ret finger protei	ret finger protei	NM_006604	NM_006604
2.61E+02	8.03E+00	stathmin-like 3	stathmin-like 3	NM_015894	NM_015894
4.15E-03	-7.91E+00	LIM and senesce	LIM and senesce	NM_033514,NR_	NM_033514,NR_027144,NR_0271
4.15E-03	-7.91E+00	LIM and senesce	LIM and senesce	NM_033514,NR_	NM_033514,NR_027144,NR_0271
3.34E+02	8.38E+00	hypothetical LOC	hypothetical LOC	NR_027034	NR_027034
3.34E+02	8.38E+00	hypothetical LOC	hypothetical LOC	NR_027034	NR_027034
3.34E+02	8.38E+00	hypothetical LOC	hypothetical LOC	NR_027034	NR_027034
3.34E+02	8.38E+00	hypothetical LOC	hypothetical LOC	NR_027034	NR_027034
3.34E+02	8.38E+00	hypothetical LOC	hypothetical LOC	NR_027034	NR_027034
2.96E+02	8.21E+00	chromosome 1 o	chromosome 1 o	NM_182533	NM_182533
2.96E+02	8.21E+00	chromosome 1 o	chromosome 1 o	NM_182533	NM_182533
2.96E+02	8.21E+00	chromosome 1 o	chromosome 1 o	NM_182533	NM_182533
4.62E-03	-7.76E+00	WD repeat dom	WD repeat dom	NM_018338	NM_018338
3.01E+02	8.23E+00	null	phosphatidylinos	null	null
2.94E-03	-8.41E+00	fragile site, folic	leucine-rich, glio	NM_145246	NM_145246

4.29E-03	-7.87E+00	zinc finger protei	similar to GLI-Kru	NM_173680	NM_173680
3.00E+02	8.23E+00	guanine nucleoti	calmodulin-like 6	NM_002074	NM_002074
2.29E+02	7.84E+00	hippocalcin-like	ornithine decarb	NM_134421	NM_134421
2.29E+02	7.84E+00	hippocalcin-like	ornithine decarb	NM_134421	NM_134421
3.81E-03	-8.04E+00	formin 1	formin 1	NM_001103184	NM_001103184
3.81E-03	-8.04E+00	formin 1	ryanodine recept	NM_001103184	NM_001103184
2.74E+02	8.10E+00	interleukin-1 rec	pleckstrin homol	NM_001010844	NM_001010844
2.20E+02	7.78E+00	nuclear receptor	nuclear receptor	NM_172349	NM_172349
2.72E+02	8.09E+00	nuclear factor I/	chromosome 19	NM_005597	NM_005597
2.72E+02	8.09E+00	nuclear factor I/	chromosome 19	NM_005597	NM_005597
3.77E+02	8.56E+00	lipase maturatio	SRY (sex determi	NM_022773	NM_022773
3.04E+02	8.25E+00	syntaphilin	syntaphilin	NM_014723	NM_014723
3.04E+02	8.25E+00	syntaphilin	syntaphilin	NM_014723	NM_014723
2.56E+02	8.00E+00	microtubule assc	microtubule assc	NM_015016	NM_015016
2.56E+02	8.00E+00	microtubule assc	microtubule assc	NM_015016	NM_015016
3.47E+02	8.44E+00	preferentially ex	preferentially ex	NM_206953,NM	NM_206953,NM_006115,NM_206
2.61E+02	8.03E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
2.61E+02	8.03E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
2.33E+02	7.87E+00	family with sequ	family with sequ	NM_001145402	NM_001145402
2.21E+02	7.79E+00	heat shock 70kD	heat shock 70kD	NM_052970	NM_052970
2.30E+02	7.84E+00	ADAMTS-like 2	ADAMTS-like 2	NM_001145320	NM_001145320
2.01E+02	7.65E+00	myelin basic prot	myelin basic prot	NM_001025100	NM_001025100
2.35E+02	7.88E+00	calponin 1, basic,	calponin 1, basic,	NM_001299	NM_001299
2.63E+02	8.04E+00	thyroid hormone	thyroid hormone	NM_003250	NM_003250
2.63E+02	8.04E+00	nuclear receptor	nuclear receptor	NM_021724	NM_021724
2.84E+02	8.15E+00	poliovirus recept	poliovirus recept	NM_001135768,	NM_001135768,NM_001135769,N
3.10E-03	-8.33E+00	NEDD4 binding p	ras homolog gen	NM_018177	NM_018177
2.51E+02	7.97E+00	similar to hCG18	hypothetical LOC	NR_024455	NR_024455
2.51E+02	7.97E+00	similar to hCG18	hypothetical LOC	NR_024455	NR_024455
2.61E+02	8.03E+00	Down syndrome	Down syndrome	NM_020693	NM_020693
2.61E+02	8.03E+00	Down syndrome	Down syndrome	NM_020693	NM_020693
4.50E+02	8.81E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
4.50E+02	8.81E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
2.63E+02	8.04E+00	family with sequ	KIAA0182	NM_198491	NM_198491
2.63E+02	8.04E+00	family with sequ	KIAA0182	NM_198491	NM_198491
2.43E+02	7.92E+00	LIM homeobox t	zinc finger and B	NM_002316	NM_002316
3.11E+02	8.28E+00	DAZ associated p	DAZ associated p	NM_018959,NM	NM_018959,NM_170711
3.11E+02	8.28E+00	DAZ associated p	DAZ associated p	NM_018959,NM	NM_018959,NM_170711
3.48E-03	-8.17E+00	phosphodiestera	SH3-domain GRB	NM_001037339	NM_001037339
2.84E+02	8.15E+00	discs, large (Dros	myosin, light cha	NM_183006	NM_183006
2.84E+02	8.15E+00	discs, large (Dros	myosin, light cha	NM_183006	NM_183006
2.23E+02	7.80E+00	integrator compl	v-maf musculoap	NM_001080453	NM_001080453
2.23E+02	7.80E+00	v-maf musculoap	v-maf musculoap	NM_002360	NM_002360
2.49E+02	7.96E+00	NSL1, MIND kine	NSL1, MIND kine	NM_015471,NM	NM_015471,NM_001042549
2.49E+02	7.96E+00	NSL1, MIND kine	NSL1, MIND kine	NM_015471,NM	NM_015471,NM_001042549
4.72E-03	-7.73E+00	SIX homeobox 3	SIX homeobox 2	NM_005413	NM_005413
4.47E-03	-7.81E+00	kin of IRRE like 2	kin of IRRE like 2	NM_199180,NM	NM_199180,NM_032123,NM_19
3.37E+02	8.40E+00	leucine rich repe	FUN14 domain c	NM_178839	NM_178839
3.60E+02	8.49E+00	golgi to ER traffic	golgi to ER traffic	NM_015949	NM_015949
2.30E+02	7.84E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
2.30E+02	7.84E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
2.30E+02	7.85E+00	major facilitator	major facilitator	NM_032219	NM_032219
2.85E+02	8.15E+00	fibrosin-like 1	fibrosin-like 1	NM_001142641	NM_001142641
2.85E+02	8.15E+00	fibrosin-like 1	fibrosin-like 1	NM_001142641	NM_001142641
2.50E+02	7.97E+00	RGM domain fan	RGM domain fan	NM_020211	NM_020211
3.71E-03	-8.07E+00	synaptic vesicle g	IQ motif containi	NM_014979	NM_014979
2.43E+02	7.92E+00	endoglin	endoglin	NM_001114753,	NM_001114753,NM_000118
2.43E+02	7.92E+00	endoglin	adenylate kinase	NM_001114753,	NM_001114753,NM_000118

4.50E-03	-7.80E+00	HSPA (heat shocl	BR serine/threon	NM_001130106,	NM_001130106,NM_012267
3.65E+02	8.51E+00	nuclear receptor	nuclear receptor	NM_003269	NM_003269
4.59E-03	-7.77E+00	hypothetical locu	hypothetical locu	NR_015382	NR_015382
3.93E+02	8.62E+00	stabilin 1	stabilin 1	NM_015136	NM_015136
3.93E+02	8.62E+00	5'-nucleotidase c	5'-nucleotidase c	NM_022908,NM	NM_022908,NM_001134231
3.93E+02	8.62E+00	5'-nucleotidase c	5'-nucleotidase c	NM_022908,NM	NM_022908,NM_001134231
3.84E-03	-8.03E+00	zinc finger protei	zinc finger protei	NM_080740	NM_080740
4.32E-03	-7.86E+00	cyclic nucleotide	cyclic nucleotide	NM_001135639	NM_001135639
2.12E+02	7.73E+00	WD repeat doma	WD repeat doma	NM_198285	NM_198285
2.80E+02	8.13E+00	zinc finger, SWIN	nanos homolog 3	NM_023072	NM_023072
2.80E+02	8.13E+00	zinc finger, SWIN	nanos homolog 3	NM_023072	NM_023072
2.41E+02	7.91E+00	microseminopro	natriuretic peptic	NM_001044264	NM_001044264
2.41E+02	7.91E+00	microseminopro	natriuretic peptic	NM_001044264	NM_001044264
2.87E+02	8.16E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
2.87E+02	8.16E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
2.25E+02	7.81E+00	glycosylphospha	zinc finger protei	NM_178172	NM_178172
2.25E+02	7.81E+00	glycosylphospha	zinc finger protei	NM_178172	NM_178172
2.32E+02	7.86E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
2.32E+02	7.86E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
4.37E-03	-7.84E+00	scratch homolog	chromosome 20	NM_033129	NM_033129
4.37E-03	-7.84E+00	scratch homolog	chromosome 20	NM_033129	NM_033129
2.63E+02	8.04E+00	hypothetical LOC	profilin 1 pseudo	NR_024584	NR_024584
2.63E+02	8.04E+00	profilin 1 pseudo	profilin 1 pseudo	NR_003242	NR_003242
2.27E+02	7.82E+00	Ras association a	Ras association a	NM_018059	NM_018059
3.70E-03	-8.08E+00	zinc finger, X-link	spindlin family, n	NM_007156	NM_007156
3.22E+02	8.33E+00	FSHD region gen	ankyrin repeat d	NR_026980	NR_026980
2.39E+02	7.90E+00	TP53 target 3	solute carrier fan	NM_016212	NM_016212
2.39E+02	7.90E+00	TP53 target 3	solute carrier fan	NM_016212	NM_016212
3.36E-03	-8.22E+00	timeless homolo	major intrinsic p	NM_003920	NM_003920
3.36E-03	-8.22E+00	major intrinsic p	major intrinsic p	NM_012064	NM_012064
2.85E+02	8.15E+00	ADAM metallope	ADAM metallope	NM_014244	NM_014244
2.65E+02	8.05E+00	nuclear receptor	forkhead box M1	NM_031474	NM_031474
4.45E-03	-7.81E+00	ring finger protei	ankyrin repeat d	NM_183419,NM	NM_183419,NM_015435
3.55E+02	8.47E+00	chromosome 11	chromosome 11	NM_013265	NM_013265
4.40E-03	-7.83E+00	tumor necrosis f	Parkinson diseas	NM_001561	NM_001561
2.78E+02	8.12E+00	proline rich 25	lipase maturatio	NM_001013638	NM_001013638
2.78E+02	8.12E+00	proline rich 25	lipase maturatio	NM_001013638	NM_001013638
2.85E+02	8.15E+00	chromosome 11	chromosome 11	NM_001142946,	NM_001142946,NR_024621
3.25E+02	8.34E+00	v-ski sarcoma vir	v-ski sarcoma vir	NM_003036	NM_003036
2.68E+02	8.06E+00	G patch domain	WD repeat doma	NM_018025	NM_018025
3.45E+02	8.43E+00	---	zinc finger protei	NR_027050	NR_027050
2.25E+02	7.81E+00	zinc finger protei	zinc finger protei	NM_153219	NM_153219
2.92E+02	8.19E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
2.91E+02	8.19E+00	chondroadherin	chondroadherin	NM_001267	NM_001267
3.89E-03	-8.01E+00	family with sequ	chromosome 6 o	NM_001105531,	NM_001105531,NM_020819
2.07E+02	7.69E+00	family with sequ	family with sequ	NM_001082967	NM_001082967
4.80E-03	-7.70E+00	APAF1 interactin	APAF1 interactin	NM_015957	NM_015957
4.80E-03	-7.70E+00	APAF1 interactin	APAF1 interactin	NM_015957	NM_015957
2.10E+02	7.71E+00	SH2B adaptor pr	SH2B adaptor pr	NM_020979	NM_020979
2.59E+02	8.02E+00	cholinergic recep	potassium voltag	NM_000744	NM_000744
2.32E+02	7.86E+00	notum pectinace	notum pectinace	NM_178493	NM_178493
2.71E+02	8.08E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
4.01E-03	-7.96E+00	T-box 5	T-box 5	NM_080718	NM_080718
3.85E-03	-8.02E+00	chorionic somato	growth hormone	NM_022644	NM_022644
2.12E+02	7.73E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
2.12E+02	7.73E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
2.42E+02	7.92E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
2.42E+02	7.92E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261

2.26E+02	7.82E+00	chromosome 21	chromosome 21	NM_004928	NM_004928
2.26E+02	7.82E+00	chromosome 21	chromosome 21	NM_004928	NM_004928
2.22E+02	7.79E+00	laminin, alpha 5	laminin, alpha 5	NM_005560	NM_005560
2.22E+02	7.79E+00	laminin, alpha 5	laminin, alpha 5	NM_005560	NM_005560
3.02E+02	8.24E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
3.02E+02	8.24E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
4.61E-03	-7.76E+00	kelch-like 35 (Dr	kelch-like 35 (Dr	NM_001039548	NM_001039548
2.29E+02	7.84E+00	TATA box bindin	adenosine deami	NM_139353,NM	NM_139353,NM_005679
2.61E+02	8.03E+00	collagen, type VI	collagen, type VI	NM_001848	NM_001848
2.61E+02	8.03E+00	collagen, type VI	collagen, type VI	NM_001848	NM_001848
2.90E+02	8.18E+00	TGFB1-induced a	crystallin, beta A	NM_004740	NM_004740
2.90E+02	8.18E+00	espin-like	kelch-like 30 (Dr	NM_194312	NM_194312
2.43E+02	7.92E+00	ribonucleoprotei	ribonucleoprotei	NM_133452	NM_133452
2.43E+02	7.92E+00	ribonucleoprotei	ribonucleoprotei	NM_133452	NM_133452
4.03E+02	8.65E+00	chromosome 9 o	chromosome 9 o	NM_001004353	NM_001004353
2.83E+02	8.14E+00	integrator compl	integrator compl	NM_001080453	NM_001080453
2.83E+02	8.14E+00	integrator compl	integrator compl	NM_001080453	NM_001080453
2.83E+02	8.14E+00	integrator compl	integrator compl	NM_001080453	NM_001080453
2.32E+02	7.86E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
2.32E+02	7.86E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
2.76E+02	8.11E+00	zinc finger, DHH	zinc finger, DHH	NM_024786	NM_024786
2.95E+02	8.21E+00	chromosome 2 o	chromosome 2 o	NM_214461	NM_214461
2.95E+02	8.21E+00	chromosome 2 o	chromosome 2 o	NM_214461	NM_214461
4.12E+02	8.69E+00	slit homolog 1 (D	slit homolog 1 (D	NM_003061	NM_003061
2.68E+02	8.06E+00	sequestosome 1	sequestosome 1	NM_001142299	NM_001142299
2.50E+02	7.97E+00	small nucleolar R	small nucleolar R	NR_003067	NR_003067
4.45E-03	-7.81E+00	prostate stem ce	lymphocyte anti	NM_005672	NM_005672
4.45E-03	-7.81E+00	prostate stem ce	lymphocyte anti	NM_005672	NM_005672
3.06E+02	8.26E+00	cyclin G associat	cyclin G associat	NM_005255	NM_005255
3.77E+02	8.56E+00	potassium chann	potassium chann	NM_020822	NM_020822
3.77E+02	8.56E+00	potassium chann	potassium chann	NM_020822	NM_020822
4.40E-03	-7.83E+00	insulin receptor	Rho/Rac guanine	NM_001079817,	NM_001079817,NM_000208
2.36E+02	7.88E+00	OTU domain con	OTU domain con	NM_001145373	NM_001145373
2.33E+02	7.87E+00	DEAD/H (Asp-Glu	killer cell lectin-li	NM_004400	NM_004400
2.43E+02	7.92E+00	chromosome 10	La ribonucleopro	NR_027152,NR_	NR_027152,NR_027151
2.43E+02	7.92E+00	chromosome 10	La ribonucleopro	NR_027152,NR_	NR_027152,NR_027151
3.71E+02	8.54E+00	acetylserotonin	acetylserotonin	NM_004192	NM_004192
3.71E+02	8.54E+00	acetylserotonin	acetylserotonin	NM_004192	NM_004192
3.10E+02	8.28E+00	STEAP family me	STEAP family me	NM_018234,NM	NM_018234,NM_182915,NM_001
3.10E+02	8.28E+00	STEAP family me	STEAP family me	NM_018234,NM	NM_018234,NM_182915,NM_001
3.12E+02	8.29E+00	melanoma antig	melanoma antig	NM_005365	NM_005365
2.47E+02	7.95E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
2.32E+02	7.86E+00	chromosome 21	chromosome 21	NM_198155,NM	NM_198155,NM_004649
3.02E+02	8.24E+00	TP53 target 3	solute carrier fa	NM_016212	NM_016212
2.21E+02	7.79E+00	carbohydrate (ch	LFNG O-fucosylp	NM_018641	NM_018641
4.70E-03	-7.73E+00	acyl-CoA binding	chromosome 10	NM_001039844	NM_001039844
3.59E-03	-8.12E+00	TRAF family me	proteasome (pro	NM_133484,NM	NM_133484,NM_004180
2.25E+02	7.81E+00	gamma-glutamyl	ankyrin repeat d	NR_003503	NR_003503
4.38E-03	-7.83E+00	tumor protein p5	Rho GTPase activ	NM_022112	NM_022112
2.28E+02	7.83E+00	intersectin 2	nuclear receptor	NM_147152	NM_147152
2.46E+02	7.94E+00	hyperpolarizatio	hyperpolarizatio	NM_001194	NM_001194
2.46E+02	7.94E+00	hyperpolarizatio	hyperpolarizatio	NM_001194	NM_001194
2.60E+02	8.02E+00	bol, boule-like (D	phospholipase C-	NM_033030,NM	NM_033030,NM_197970
3.18E+02	8.31E+00	plexin B2	plexin B2	NM_012401	NM_012401
2.87E+02	8.16E+00	CD70 molecule	tumor necrosis f	NM_001252	NM_001252
2.87E+02	8.16E+00	CD70 molecule	tumor necrosis f	NM_001252	NM_001252
4.07E+02	8.67E+00	rhomboid 5 hom	rhomboid 5 hom	NM_022450	NM_022450
2.76E+02	8.11E+00	upstream bindin	tripartite motif-c	NM_001101321	NM_001101321

2.76E+02	8.11E+00	upstream binding	tripartite motif-c	NM_001101321	NM_001101321
2.90E+02	8.18E+00	solute carrier fan	solute carrier fan	NM_207348	NM_207348
2.60E+02	8.02E+00	tumor necrosis fa	tumor necrosis fa	NM_148970,NM	NM_148970,NM_148967,NM_148
3.37E+02	8.40E+00	TNFSF12-TNFSF1	TNFSF12-TNFSF1	NM_172089	NM_172089
3.05E+02	8.25E+00	coiled-coil domai	coiled-coil domai	NM_001143980	NM_001143980
3.05E+02	8.25E+00	coiled-coil domai	chloride channel	NM_001143980	NM_001143980
2.50E+02	7.96E+00	tumor necrosis fa	tumor necrosis fa	NM_172014,NM	NM_172014,NM_003807
2.30E+02	7.84E+00	hypothetical LOC	hypothetical LOC	NR_026658	NR_026658
4.21E-03	-7.89E+00	regulator of calci	chloride intracell	NM_004414,NM	NM_004414,NM_203417,NM_203
2.11E+02	7.72E+00	chromosome 9 o	chromosome 9 o	NM_152571	NM_152571
2.13E+02	7.74E+00	dishevelled, dsh	matrix-remodelli	NM_004421	NM_004421
2.62E+02	8.03E+00	polymerase (DNA	polymerase (DNA	NM_002691	NM_002691
2.62E+02	8.03E+00	polymerase (DNA	polymerase (DNA	NM_002691	NM_002691
2.62E+02	8.03E+00	polymerase (DNA	Spi-B transcriptic	NM_002691	NM_002691
3.63E-03	-8.10E+00	synaptotagmin X	asparagine-linke	NM_198992	NM_198992
4.16E-03	-7.91E+00	Fc fragment of Ig	Fc fragment of Ig	NM_000570	NM_000570
4.16E-03	-7.91E+00	Fc fragment of Ig	Fc fragment of Ig	NM_000570	NM_000570
2.76E+02	8.11E+00	nuclear factor I/X	nuclear factor I/X	NM_002501	NM_002501
2.74E+02	8.10E+00	ring finger protei	oligonucleotide/	NM_005785,NM	NM_005785,NM_194358,NM_194
3.06E+02	8.26E+00	metastasis assoc	metastasis assoc	NM_004689	NM_004689
3.06E+02	8.26E+00	metastasis assoc	metastasis assoc	NM_004689	NM_004689
3.32E-03	-8.23E+00	basic transcriptic	ceroid-lipofuscin	NR_026983	NR_026983
3.63E-03	-8.10E+00	cannabinoid rece	pleckstrin	NM_015463	NM_015463
2.71E+02	8.08E+00	hypothetical LOC	FXYD domain cor	NR_024561	NR_024561
2.64E+02	8.04E+00	asparagine-linke	asparagine-linke	NM_032834	NM_032834
2.64E+02	8.04E+00	asparagine-linke	asparagine-linke	NM_032834	NM_032834
2.08E+02	7.70E+00	deoxythymidylat	inhibitor of grow	NM_012145	NM_012145
2.08E+02	7.70E+00	deoxythymidylat	inhibitor of grow	NM_012145	NM_012145
4.17E+02	8.70E+00	zinc finger protei	zinc finger protei	NM_001007248	NM_001007248
2.59E+02	8.02E+00	v-ets erythroblas	Friend leukemia	NM_005238,NM	NM_005238,NM_001143820
5.34E-03	-7.55E+00	guanylate cyclase	arachidonate 15-	NM_000180	NM_000180
5.57E-03	-7.49E+00	MER1 repeat cor	ubiquitin specific	NR_024059	NR_024059
5.57E-03	-7.49E+00	MER1 repeat cor	ubiquitin specific	NR_024059	NR_024059
2.90E+02	8.18E+00	glycosylphospha	glycosylphospha	NM_178172	NM_178172
4.19E-03	-7.90E+00	OTU domain con	vacuolar protein	NM_020205	NM_020205
4.19E-03	-7.90E+00	OTU domain con	vacuolar protein	NM_020205	NM_020205
4.53E-03	-7.78E+00	sulfiredoxin 1	scratch homolog	NM_080725	NM_080725
4.53E-03	-7.78E+00	sulfiredoxin 1	scratch homolog	NM_080725	NM_080725
3.77E-03	-8.05E+00	solute carrier fan	hypoxia up-regul	NM_001467	NM_001467
3.77E-03	-8.05E+00	solute carrier fan	hypoxia up-regul	NM_001467	NM_001467
2.16E+02	7.76E+00	solute carrier fan	solute carrier fan	NR_002593	NR_002593
2.16E+02	7.76E+00	solute carrier fan	sialophorin	NR_002593	NR_002593
4.06E-03	-7.94E+00	Janus kinase 1	adenylate kinase	NM_002227	NM_002227
2.13E+02	7.74E+00	grainyhead-like 2	grainyhead-like 2	NM_024915	NM_024915
3.88E+02	8.60E+00	low density lipop	adrenergic, alpha	NM_002337	NM_002337
3.20E-03	-8.29E+00	hypothetical LOC	zinc finger protei	NR_024484	NR_024484
3.20E-03	-8.29E+00	hypothetical LOC	zinc finger protei	NR_024484	NR_024484
1.69E+00	7.61E-01	TBC1 domain fan	family with sequ	NM_014346	NM_014346
3.01E+02	8.23E+00	clathrin, heavy cl	clathrin, heavy cl	NM_007098	NM_007098
2.26E+02	7.82E+00	ribosomal protei	NADH dehydroge	NM_005061	NM_005061
2.26E+02	7.82E+00	ribosomal protei	NADH dehydroge	NM_005061	NM_005061
2.08E+02	7.70E+00	lipocalin 6	lipocalin 6	NM_198946	NM_198946
2.08E+02	7.70E+00	lipocalin 6	lipocalin 6	NM_198946	NM_198946
4.52E-03	-7.79E+00	fatty acid binding	threonine syntha	NM_001443	NM_001443
2.82E+02	8.14E+00	solute carrier fan	solute carrier fan	NM_003041	NM_003041
2.82E+02	8.14E+00	solute carrier fan	solute carrier fan	NM_003041	NM_003041
2.67E+02	8.06E+00	dipeptidase 3	dipeptidase 2	NM_022357,NM	NM_022357,NM_001129758
2.67E+02	8.06E+00	dipeptidase 3	dipeptidase 2	NM_022357,NM	NM_022357,NM_001129758

2.41E+02	7.91E+00	N-acetylneurami	zinc finger protei	NM_152667	NM_152667
4.68E-03	-7.74E+00	coiled-coil domai	chromosome 7 o	NM_194300	NM_194300
4.27E-03	-7.87E+00	anterior gradient	anterior gradient	NM_006408	NM_006408
2.66E+02	8.05E+00	syndecan binding	syndecan binding	NM_080489,NM	NM_080489,NM_015685
2.08E+02	7.70E+00	family with sequ	FSHD region gen	NR_024241	NR_024241
2.08E+02	7.70E+00	family with sequ	FSHD region gen	NR_024241	NR_024241
2.58E+02	8.01E+00	transducin (beta)	transducin (beta)	NM_006453	NM_006453
2.56E+02	8.00E+00	acidic repeat con	acidic repeat con	NM_052957	NM_052957
2.06E+02	7.68E+00	KN motif and ank	KN motif and ank	NM_198471	NM_198471
2.06E+02	7.68E+00	KN motif and ank	KN motif and ank	NM_198471	NM_198471
4.80E-03	-7.70E+00	glycosyltransfera	lipocalin 9	NM_182974	NM_182974
2.22E+02	7.79E+00	cannabinoid rece	RNA guanylyltran	NM_033181,NM	NM_033181,NM_016083
2.22E+02	7.79E+00	cannabinoid rece	RNA guanylyltran	NM_033181,NM	NM_033181,NM_016083
2.60E+02	8.02E+00	glycogen synthas	glycogen synthas	NM_002103	NM_002103
3.97E-03	-7.98E+00	solute carrier fan	zinc finger protei	NM_024628	NM_024628
2.52E+02	7.98E+00	hypothetical LOC	zinc finger protei	NR_024497	NR_024497
2.18E+02	7.77E+00	SWI/SNF related,	SWI/SNF related,	NM_001128846,	NM_001128846,NM_001128848,
2.18E+02	7.77E+00	SWI/SNF related,	SWI/SNF related,	NM_001128846,	NM_001128846,NM_001128848,
2.44E+02	7.93E+00	PHD finger prote	PHD finger prote	NM_153812	NM_153812
2.09E+02	7.70E+00	elastin microfibri	elastin microfibri	NM_032048	NM_032048
2.09E+02	7.70E+00	elastin microfibri	elastin microfibri	NM_032048	NM_032048
2.67E+02	8.06E+00	immunoglobulin	immunoglobulin	NM_014987	NM_014987
2.67E+02	8.06E+00	immunoglobulin	immunoglobulin	NM_014987	NM_014987
2.67E+02	8.06E+00	immunoglobulin	immunoglobulin	NM_014987	NM_014987
2.67E+02	8.06E+00	immunoglobulin	immunoglobulin	NM_014987	NM_014987
2.58E+02	8.01E+00	OTU domain, ubi	MACRO domain	NM_017670,NR_	NM_017670,NR_003089
2.58E+02	8.01E+00	MACRO domain	MACRO domain	NM_014067	NM_014067
2.58E+02	8.01E+00	MACRO domain	MACRO domain	NM_014067	NM_014067
3.98E+02	8.64E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
4.53E-03	-7.78E+00	solute carrier fan	sialic acid binding	NM_001146037	NM_001146037
3.17E-03	-8.30E+00	arachidonate 12-	arachidonate 12-	NR_002710	NR_002710
2.91E+02	8.19E+00	calcium-sensing	calcium-sensing	NM_000388	NM_000388
2.91E+02	8.19E+00	calcium-sensing	calcium-sensing	NM_000388	NM_000388
3.62E-03	-8.11E+00	protocadherin ga	protocadherin ga	NM_018927,NM	NM_018927,NM_032101
2.65E+02	8.05E+00	chromosome 16	chromosome 16	NM_004913	NM_004913
4.02E-03	-7.96E+00	protein phospha	galanin preprope	NM_018312	NM_018312
4.47E-03	-7.81E+00	acyloxyacyl hydr	engulfment and	NM_001637	NM_001637
2.70E+02	8.07E+00	chromosome 12	chromosome 12	NM_032848	NM_032848
3.44E-03	-8.18E+00	regulatory factor	regulatory factor	NM_213594	NM_213594
3.37E+02	8.40E+00	chromosome 1 o	tubulin tyrosine l	NM_017891	NM_017891
3.71E+02	8.54E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
3.71E+02	8.54E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
2.48E+02	7.95E+00	notum pectinace	alveolar soft part	NM_178493	NM_178493
3.77E-03	-8.05E+00	sec1 family doma	coagulation facto	NM_016106,NM	NM_016106,NM_182835
2.33E+02	7.87E+00	null	golgin A8 family,	null	null
2.33E+02	7.87E+00	null	golgin A8 family,	null	null
4.85E+02	8.92E+00	ring finger protei	ring finger protei	NM_020914	NM_020914
3.03E+02	8.24E+00	arginine vasopre	arginine vasopre	NR_027419	NR_027419
3.03E+02	8.24E+00	arginine vasopre	arginine vasopre	NR_027419	NR_027419
3.34E+02	8.38E+00	taste receptor, ty	taste receptor, ty	NM_152228	NM_152228
3.34E+02	8.38E+00	taste receptor, ty	taste receptor, ty	NM_152228	NM_152228
3.34E+02	8.38E+00	taste receptor, ty	taste receptor, ty	NM_152228	NM_152228
2.90E+02	8.18E+00	apoptosis-associ	apoptosis-associ	NM_001080395	NM_001080395
2.86E+02	8.16E+00	ribosomal protei	zinc finger protei	NM_000973,NM	NM_000973,NM_033301
2.52E+02	7.98E+00	integrin beta 1 bi	death-associated	NM_170678	NM_170678
2.52E+02	7.98E+00	death-associated	death-associated	NM_001348	NM_001348
2.80E+02	8.13E+00	GDNF family rece	GDNF family rece	NM_001496	NM_001496
2.80E+02	8.13E+00	GDNF family rece	GDNF family rece	NM_001496	NM_001496

2.08E+02	7.70E+00	tumor necrosis fa	chromosome 1 o	NM_003820	NM_003820
2.08E+02	7.70E+00	tumor necrosis fa	chromosome 1 o	NM_003820	NM_003820
2.22E+02	7.79E+00	xylosyltransferas	polycystic kidney	NM_022166	NM_022166
2.22E+02	7.79E+00	xylosyltransferas	polycystic kidney	NM_022166	NM_022166
3.39E+02	8.41E+00	collagen, type VI,	collagen, type VI,	NM_001848	NM_001848
3.39E+02	8.41E+00	collagen, type VI,	collagen, type VI,	NM_001848	NM_001848
2.29E+02	7.84E+00	arginine vasopres	arginine vasopres	NM_000490	NM_000490
3.07E+02	8.26E+00	NADH dehydroge	YjeF N-terminal d	NM_015965	NM_015965
4.21E-03	-7.89E+00	RELT-like 1	phosphoglucomu	NM_001085400	NM_001085400
2.72E+02	8.09E+00	forkhead box Q1	forkhead box F2	NM_033260	NM_033260
3.37E+02	8.40E+00	calcium homeost	calcium homeost	NM_001129742	NM_001129742
3.37E+02	8.40E+00	calcium homeost	calcium homeost	NM_001129742	NM_001129742
4.35E-03	-7.84E+00	solute carrier fam	solute carrier fam	NM_020346	NM_020346
4.35E-03	-7.84E+00	solute carrier fam	solute carrier fam	NM_020346	NM_020346
2.63E+02	8.04E+00	coiled-coil domai	coiled-coil domai	NM_178173	NM_178173
2.63E+02	8.04E+00	coiled-coil domai	coiled-coil domai	NM_001135197	NM_001135197
3.04E+02	8.25E+00	proline rich 14	fibrosin	NM_024031	NM_024031
3.04E+02	8.25E+00	fibrosin	fibrosin	NM_001105079	NM_001105079
2.63E+02	8.04E+00	transforming gro	transforming gro	NM_015927	NM_015927
2.63E+02	8.04E+00	transforming gro	transforming gro	NM_015927	NM_015927
4.52E-03	-7.79E+00	transglutaminase	transglutaminase	NM_201631,NM	NM_201631,NM_004245
2.34E+02	7.87E+00	cordon-bleu hom	POM121 membr	NM_015198	NM_015198
2.34E+02	7.87E+00	POM121 membr	POM121 membr	NM_182595	NM_182595
2.28E+02	7.83E+00	chromosome 11	chromosome 11	NM_145013	NM_145013
3.99E+02	8.64E+00	protein arginine	protein arginine	NM_198318,NM	NM_198318,NM_198319,NM_001
2.49E+02	7.96E+00	ring finger protei	maternal embryo	NM_194330,NM	NM_194330,NM_194332,NM_194
2.49E+02	7.96E+00	ring finger protei	maternal embryo	NM_194330,NM	NM_194330,NM_194332,NM_194
2.73E+02	8.09E+00	tripartite motif-c	tripartite motif-c	NM_001146208,	NM_001146208,NM_001145126
2.73E+02	8.09E+00	tripartite motif-c	tripartite motif-c	NM_001146208,	NM_001146208,NM_001145126
2.73E+02	8.09E+00	tripartite motif-c	tripartite motif-c	NM_001146208,	NM_001146208,NM_001145126
2.73E+02	8.09E+00	tripartite motif-c	tripartite motif-c	NM_001146208,	NM_001146208,NM_001145126
3.10E+02	8.27E+00	autoimmune reg	autoimmune reg	NM_000658	NM_000658
3.10E+02	8.27E+00	autoimmune reg	autoimmune reg	NM_000658	NM_000658
3.20E+02	8.32E+00	zinc finger and SC	zinc finger and SC	NM_182572	NM_182572
2.89E+02	8.17E+00	mahogunin, ring	mahogunin, ring	NM_015246,NM	NM_015246,NM_001142289,NM_
4.64E-03	-7.75E+00	membrane-spann	membrane-spann	NM_001098835,	NM_001098835,NM_152717
2.12E+02	7.73E+00	SRC kinase signal	SRC kinase signal	NM_025248	NM_025248
2.12E+02	7.73E+00	poly(A) binding p	protocadherin 18	NM_001114734	NM_001114734
4.48E-03	-7.80E+00	TBC1 (tre-2/USP6	TBC1 (tre-2/USP6	NM_015173	NM_015173
4.48E-03	-7.80E+00	pituitary tumor-t	pituitary tumor-t	NM_006607	NM_006607
2.28E+02	7.83E+00	SPARC related m	SPARC related m	NM_022138	NM_022138
2.06E+02	7.68E+00	RAN binding prot	zinc finger, DHHC	NM_002882	NM_002882
3.79E+02	8.57E+00	chromosome 14	chromosome 14	NM_001134875,	NM_001134875,NM_001134876
3.88E+02	8.60E+00	kallikrein-related	kallikrein-related	NM_007196,NM	NM_007196,NM_144507,NM_144
3.45E+02	8.43E+00	death-associated	death-associated	NM_001348	NM_001348
3.45E+02	8.43E+00	death-associated	death-associated	NM_001348	NM_001348
3.45E+02	8.43E+00	death-associated	death-associated	NM_001348	NM_001348
4.32E-03	-7.86E+00	suppression of tu	chromosome 11	NM_213618,NM	NM_213618,NM_139157,NM_005
2.39E+02	7.90E+00	zinc finger, FYVE	zinc finger, FYVE	NM_020972	NM_020972
3.00E+02	8.23E+00	CCAAT/enhancer	protein tyrosine	NM_005194	NM_005194
3.00E+02	8.23E+00	CCAAT/enhancer	protein tyrosine	NM_005194	NM_005194
3.00E+02	8.23E+00	CCAAT/enhancer	protein tyrosine	NM_005194	NM_005194
2.05E+02	7.68E+00	single-minded ho	single-minded ho	NM_005069,NM	NM_005069,NM_009586
2.67E+02	8.06E+00	resistance to inhi	resistance to inhi	NM_021932	NM_021932
3.33E+02	8.38E+00	chromosome 19	chromosome 19	NM_175063,NM	NM_175063,NM_206538
2.19E+02	7.78E+00	early B-cell facto	early B-cell facto	NM_001005463	NM_001005463
3.22E+02	8.33E+00	solute carrier fam	solute carrier fam	NM_020246	NM_020246
3.22E+02	8.33E+00	solute carrier fam	solute carrier fam	NM_020246	NM_020246

3.22E+02	8.33E+00	solute carrier fan	solute carrier fan	NM_020246	NM_020246
3.22E+02	8.33E+00	solute carrier fan	solute carrier fan	NM_020246	NM_020246
2.14E+02	7.74E+00	NADPH oxidase	AT rich interactiv	NM_015718	NM_015718
3.27E+02	8.35E+00	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
3.27E+02	8.35E+00	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
4.10E+02	8.68E+00	1-acylglycerol-3-	1-acylglycerol-3-	NM_020132	NM_020132
2.56E+02	8.00E+00	glutamate recept	glutamate recept	NM_138690	NM_138690
2.56E+02	8.00E+00	chromosome 19	chromosome 19	NM_001033026,	NM_001033026,NM_033420
2.56E+02	8.00E+00	chromosome 19	chromosome 19	NM_001033026,	NM_001033026,NM_033420
2.56E+02	8.00E+00	chromosome 19	chromosome 19	NM_001033026,	NM_001033026,NM_033420
2.56E+02	8.00E+00	chromosome 19	chromosome 19	NM_001033026,	NM_001033026,NM_033420
2.56E+02	8.00E+00	chromosome 19	chromosome 19	NM_001033026,	NM_001033026,NM_033420
4.71E+02	8.88E+00	FAT tumor suppr	melatonin recept	NM_001008781	NM_001008781
2.70E+02	8.08E+00	developmental p	developmental p	NM_138815	NM_138815
2.14E+02	7.74E+00	hypothetical LOC	zinc finger protei	NR_024497	NR_024497
2.38E+02	7.90E+00	proline rich 23A	proline rich 23A	NM_001134659	NM_001134659
2.38E+02	7.90E+00	proline rich 23A	proline rich 23A	NM_001134659	NM_001134659
2.59E+02	8.02E+00	family with sequ	golgin A6 family-	NM_001008226	NM_001008226
2.25E+02	7.81E+00	cyclin-dependent	cyclin-dependent	NM_002596,NM	NM_002596,NM_212503,NM_212
2.25E+02	7.81E+00	cyclin-dependent	cyclin-dependent	NM_002596,NM	NM_002596,NM_212503,NM_212
2.37E+02	7.89E+00	agrin	chromosome 1 o	NM_198576	NM_198576
5.20E-03	-7.59E+00	chromosome 10	chromosome 10	NM_032333	NM_032333
2.91E+02	8.19E+00	solute carrier fan	solute carrier fan	NM_001080431	NM_001080431
2.91E+02	8.19E+00	solute carrier fan	solute carrier fan	NM_001080431	NM_001080431
2.18E+02	7.77E+00	netrin 5	netrin 5	NM_145807	NM_145807
2.18E+02	7.77E+00	netrin 5	netrin 5	NM_145807	NM_145807
3.10E+02	8.28E+00	hypothetical LOC	calcium channel,	NR_024341	NR_024341
4.19E+02	8.71E+00	chorionic gonad	chorionic gonad	NM_033378	NM_033378
3.73E-03	-8.07E+00	membrane prote	chromosome 17	NM_005374	NM_005374
2.90E+02	8.18E+00	pannexin 2	TraB domain con	NM_052839	NM_052839
3.10E+02	8.27E+00	interferon stimul	aggrecan	NM_002201	NM_002201
3.10E+02	8.27E+00	interferon stimul	aggrecan	NM_002201	NM_002201
3.08E+02	8.27E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
4.24E-03	-7.88E+00	OTU domain con	OTU domain con	NM_130901	NM_130901
3.56E+02	8.48E+00	phosphatidylinos	phosphatidylinos	NM_012398	NM_012398
2.49E+02	7.96E+00	tektin 4	tektin 4	NM_144705	NM_144705
2.49E+02	7.96E+00	tektin 4	tektin 4	NM_144705	NM_144705
2.28E+02	7.83E+00	chromosome 12	chromosome 12	NM_153685	NM_153685
5.00E-03	-7.64E+00	zinc and ring fing	kelch repeat and	NR_003502	NR_003502
2.46E+02	7.94E+00	syntaxin binding	resistin	NM_006949,NM	NM_006949,NM_001127396
2.46E+02	7.94E+00	syntaxin binding	resistin	NM_006949,NM	NM_006949,NM_001127396
2.10E+02	7.72E+00	SRY (sex determi	hypothetical LOC	NM_014587	NM_014587
4.70E+02	8.88E+00	potassium inwar	cytohesin 2	NM_170720	NM_170720
4.47E-03	-7.81E+00	frequently rearra	frequently rearra	NM_005479	NM_005479
3.02E+02	8.24E+00	core-binding fact	core-binding fact	NM_175931,NM	NM_175931,NM_005187
3.36E-03	-8.22E+00	chromosome 1 o	chromosome 1 o	NM_182581	NM_182581
4.30E+02	8.75E+00	receptor-interact	receptor-interact	NM_020639	NM_020639
2.80E+02	8.13E+00	BCL6 corepresso	BCL6 corepresso	NM_001123383,	NM_001123383,NM_001123384,
2.10E+02	7.72E+00	interferon regula	interferon regula	NM_015649	NM_015649
2.29E+02	7.84E+00	SRY (sex determi	chromosome 13	NM_005986	NM_005986
2.29E+02	7.84E+00	SRY (sex determi	chromosome 13	NM_005986	NM_005986
2.32E+02	7.86E+00	zinc finger protei	zinc finger protei	NM_024836	NM_024836
3.93E-03	-7.99E+00	chromosome 7 o	hypothetical pro	NM_032120	NM_032120
3.93E-03	-7.99E+00	hypothetical pro	hypothetical pro	NR_026902	NR_026902
3.80E+02	8.57E+00	ankyrin repeat d	ankyrin repeat d	NR_027270	NR_027270
3.80E+02	8.57E+00	ankyrin repeat d	lipase, member	NR_027270	NR_027270
2.67E+02	8.06E+00	DEAD/H (Asp-Glu	ribosomal protei	NR_024005,NR_	NR_024005,NR_024004
2.70E+02	8.08E+00	calcineurin bindi	sushi domain co	NM_012295	NM_012295

2.31E+02	7.85E+00	cytochrome b-56	angiotensin I con	NM_001017917,	NM_001017917,NM_001017916,
5.08E+02	8.99E+00	WD repeat doma	WD repeat doma	NM_182552	NM_182552
3.52E+02	8.46E+00	TIMP metallopep	TIMP metallopep	NM_003255	NM_003255
3.52E+02	8.46E+00	TIMP metallopep	TIMP metallopep	NM_003255	NM_003255
3.41E+02	8.41E+00	golgin A8 family,	golgin A8 family,	NM_001023567,	NM_001023567,NR_027410
2.50E+02	7.96E+00	family with sequ	chromosome 22	NM_015381	NM_015381
3.31E+02	8.37E+00	tetra-peptide rep	tetra-peptide rep	NM_198479	NM_198479
3.86E-03	-8.02E+00	B double prime 1	methylcrotonoyl	NM_018429	NM_018429
3.86E-03	-8.02E+00	B double prime 1	methylcrotonoyl	NM_018429	NM_018429
3.74E-03	-8.06E+00	chromosome 6 o	sirtuin 5	NM_033069	NM_033069
2.66E+02	8.05E+00	TBC1 domain fan	TBC1 domain fan	NM_019020	NM_019020
2.75E+02	8.10E+00	E74-like factor 4	apoptosis-induci	NM_001127197,	NM_001127197,NM_001421
4.64E-03	-7.75E+00	Fc fragment of Ig	Fc fragment of Ig	NM_000569,NM	NM_000569,NM_001127592,NM_
2.34E+02	7.87E+00	---	nuclear factor I/(	NM_001145997	NM_001145997
2.39E+02	7.90E+00	mesoderm induc	mesoderm induc	NM_017550	NM_017550
2.39E+02	7.90E+00	mesoderm induc	mesoderm induc	NM_017550	NM_017550
4.68E-03	-7.74E+00	intracisternal A p	microtubule assc	NM_005897	NM_005897
4.70E-03	-7.73E+00	KIAA0101	thyroid hormone	NM_014736,NM	NM_014736,NM_001029989
3.84E-03	-8.03E+00	zinc finger protei	chromosome 21	NM_001098403,	NM_001098403,NM_001098402,
3.43E-03	-8.19E+00	ribonuclease, RN	methyltransferas	NM_002934	NM_002934
3.43E-03	-8.19E+00	ribonuclease, RN	methyltransferas	NM_002934	NM_002934
3.43E-03	-8.19E+00	ribonuclease, RN	methyltransferas	NM_002934	NM_002934
2.86E+02	8.16E+00	HOP homeobox	HOP homeobox	NM_139212,NM	NM_139212,NM_001145460,NM_
2.52E+02	7.98E+00	solute carrier fan	methyltransferas	NR_002594	NR_002594
4.37E-03	-7.84E+00	cathepsin L1	cathepsin L famil	NM_145918,NM	NM_145918,NM_001912
4.76E+02	8.90E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
4.76E+02	8.90E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
2.36E+02	7.88E+00	phosphodiestera	A kinase (PRKA) a	NM_173454,NM	NM_173454,NM_002605
4.83E-03	-7.69E+00	golgi-associated	nuclear undecap	NM_020399,NM	NM_020399,NM_001017408
4.83E-03	-7.69E+00	golgi-associated	nuclear undecap	NM_020399,NM	NM_020399,NM_001017408
2.68E+02	8.06E+00	gamma-aminobu	gamma-aminobu	NM_000815	NM_000815
2.68E+02	8.06E+00	gamma-aminobu	gamma-aminobu	NM_000815	NM_000815
2.68E+02	8.06E+00	gamma-aminobu	gamma-aminobu	NM_000815	NM_000815
3.05E+02	8.25E+00	chromosome 7 o	chromosome 7 o	NM_024067	NM_024067
3.05E+02	8.25E+00	chromosome 7 o	chromosome 7 o	NM_024067	NM_024067
3.05E+02	8.25E+00	chromosome 7 o	chromosome 7 o	NM_024067	NM_024067
2.29E+02	7.84E+00	dapper, antagoni	dapper, antagoni	NM_145056	NM_145056
3.04E+02	8.25E+00	dynein, axonema	dynein, axonema	NM_207437	NM_207437
2.54E+02	7.99E+00	potassium chann	potassium chann	NM_033310	NM_033310
2.54E+02	7.99E+00	potassium chann	potassium chann	NM_033310	NM_033310
2.20E+02	7.78E+00	metallothionein-	metallothionein-	NM_001039656	NM_001039656
2.32E+02	7.86E+00	5-oxoprolinase (A	5-oxoprolinase (A	NM_017570	NM_017570
3.45E+02	8.43E+00	peroxisomal prol	peroxisomal prol	NM_001037335,	NM_001037335,NM_033405
2.60E+02	8.02E+00	fibroblast growth	fibroblast growth	NM_022965,NM	NM_022965,NM_000142
2.94E+02	8.20E+00	immunity-related	immunity-related	NM_001007561	NM_001007561
3.66E-03	-8.10E+00	melanoregulin	peroxisomal tran	NM_018000	NM_018000
4.01E+02	8.65E+00	IQ motif and Sec	IQ motif and Sec	NM_015232	NM_015232
2.86E+02	8.16E+00	hypothetical LOC	1-acylglycerol-3-	NR_026961	NR_026961
2.30E+02	7.85E+00	KIAA0754	bone morphoger	NM_015038	NM_015038
2.30E+02	7.85E+00	bone morphoger	bone morphoger	NM_181809	NM_181809
2.46E+02	7.94E+00	transmembrane	transmembrane	NM_032326	NM_032326
2.46E+02	7.94E+00	transmembrane	transmembrane	NM_032326	NM_032326
2.93E+02	8.20E+00	potassium voltag	potassium voltag	NM_012283	NM_012283
5.02E-03	-7.64E+00	hypothetical LOC	hypothetical LOC	NR_027114	NR_027114
5.02E-03	-7.64E+00	hypothetical LOC	hypothetical LOC	NR_027114	NR_027114
2.39E+02	7.90E+00	chromosome 11	chromosome 11	NM_173573	NM_173573
3.81E-03	-8.04E+00	discs, large homo	3-hydroxybutyra	NM_004087,NM	NM_004087,NM_001098424
3.43E-03	-8.19E+00	centrosomal pro	quiescin Q6 sulfh	NM_014810	NM_014810

2.63E+02	8.04E+00	interleukin 11	transmembrane	NM_000641	NM_000641
2.38E+02	7.90E+00	nuclear transcrip	thioredoxin redu	NM_006166	NM_006166
3.91E+02	8.61E+00	suppressor of va	suppressor of va	NM_032701	NM_032701
3.91E+02	8.61E+00	suppressor of va	suppressor of va	NM_032701	NM_032701
3.91E+02	8.61E+00	suppressor of va	suppressor of va	NM_032701	NM_032701
2.20E+02	7.78E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
2.20E+02	7.78E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
2.38E+02	7.90E+00	hypothetical LOC	calcium channel,	NR_024341	NR_024341
3.69E+02	8.53E+00	potassium voltag	potassium voltag	NM_172109	NM_172109
2.37E+02	7.89E+00	Rho GTPase activ	Rho GTPase activ	NM_144967	NM_144967
2.84E+02	8.15E+00	stabilin 1	stabilin 1	NM_015136	NM_015136
2.13E+02	7.74E+00	chromosome 14	POM121 membr	NR_027006	NR_027006
4.33E-03	-7.85E+00	Zic family memb	Zic family memb	NM_032153	NM_032153
2.13E+02	7.74E+00	excision repair cr	excision repair cr	NM_001130867	NM_001130867
2.13E+02	7.74E+00	excision repair cr	excision repair cr	NM_001130867	NM_001130867
4.57E-03	-7.77E+00	Bardet-Biedl syn	transient recepto	NM_018190	NM_018190
3.26E+02	8.35E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
3.26E+02	8.35E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
3.79E-03	-8.04E+00	Wolf-Hirschhorn	Wolf-Hirschhorn	NM_133335,NM	NM_133335,NM_133330,NM_133
3.79E-03	-8.04E+00	Wolf-Hirschhorn	Wolf-Hirschhorn	NM_133334	NM_133334
2.33E+02	7.87E+00	ring finger protei	ring finger protei	NM_194439,NM	NM_194439,NM_001131034
3.76E-03	-8.05E+00	protocadherin 7	protocadherin 7	NM_032457,NM	NM_032457,NM_002589,NM_032
2.86E+02	8.16E+00	chromosome 6 o	hypothetical pro	NR_026780	NR_026780
2.56E+02	8.00E+00	glioma tumor su	glioma tumor su	NM_015711	NM_015711
3.98E-03	-7.97E+00	M-phase phosph	chromosome 12	NM_022782	NM_022782
3.98E-03	-7.97E+00	M-phase phosph	chromosome 12	NM_022782	NM_022782
3.91E-03	-8.00E+00	family with sequ	par-6 partitionin	NM_080829	NM_080829
3.10E+02	8.27E+00	COX19 cytochror	cytochrome P45	NM_001031617	NM_001031617
3.10E+02	8.27E+00	cytochrome P45	cytochrome P45	NM_017781	NM_017781
3.10E+02	8.27E+00	cytochrome P45	cytochrome P45	NM_017781	NM_017781
2.54E+02	7.99E+00	tubulin, alpha 3e	coiled-coil doma	NM_207312	NM_207312
2.59E+02	8.02E+00	potassium voltag	potassium voltag	NM_172106,NM	NM_172106,NM_172107,NM_172
3.31E+02	8.37E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.31E+02	8.37E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
2.71E+02	8.08E+00	family with sequ	family with sequ	NM_174901	NM_174901
2.41E+02	7.91E+00	coiled-coil doma	coiled-coil doma	NM_001080433	NM_001080433
2.41E+02	7.91E+00	BCL2/adenovirus	Janus kinase and	NM_004052	NM_004052
3.25E+02	8.34E+00	leucine rich repe	leucine rich repe	NM_022143	NM_022143
2.62E+02	8.03E+00	sema domain, im	sema domain, im	NM_020163	NM_020163
2.62E+02	8.03E+00	sema domain, im	sema domain, im	NM_020163	NM_020163
3.37E+02	8.40E+00	myomesin (M-pr	CUB and Sushi m	NM_003970	NM_003970
2.30E+02	7.84E+00	ArfGAP with GTP	ArfGAP with GTP	NM_031946,NM	NM_031946,NM_001042535
2.30E+02	7.84E+00	ArfGAP with GTP	ArfGAP with GTP	NM_031946,NM	NM_031946,NM_001042535
3.21E-03	-8.29E+00	TSPY-like 5	metadherin	NM_033512	NM_033512
3.55E+02	8.47E+00	fizzy/cell division	fizzy/cell division	NM_001136197,	NM_001136197,NM_001136198
3.55E+02	8.47E+00	fizzy/cell division	chromosome 19	NM_001136197,	NM_001136197,NM_001136198
2.29E+02	7.84E+00	ADP-ribosylation	protein kinase C	NM_001142293,	NM_001142293,NM_014570
2.24E+02	7.81E+00	glutathione pero	glutathione pero	NM_002085,NM	NM_002085,NM_001039847
3.71E-03	-8.07E+00	ethanolaminephi	chromosome 2 o	NM_033505	NM_033505
3.73E-03	-8.07E+00	tripartite motif fa	tripartite motif fa	NM_173553	NM_173553
2.26E+02	7.82E+00	family with sequ	family with sequ	NM_001039762	NM_001039762
2.26E+02	7.82E+00	family with sequ	neuropeptide S	NM_001039762	NM_001039762
2.71E+02	8.08E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,
2.71E+02	8.08E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,
2.51E+02	7.97E+00	transmembrane	aprataxin	NM_212558	NM_212558
2.51E+02	7.97E+00	transmembrane	aprataxin	NM_212558	NM_212558
2.75E+02	8.10E+00	t-complex 10 hoi	chromosome 6 o	NM_004610	NM_004610
2.75E+02	8.10E+00	t-complex 10 hoi	chromosome 6 o	NM_004610	NM_004610

3.50E+02	8.45E+00	lipoxygenase hor	lipoxygenase hor	NM_144612	NM_144612
2.24E+02	7.81E+00	hepatoma-derive	hepatoma-derive	NM_032631,NM	NM_032631,NM_001001520
2.93E+02	8.20E+00	solute carrier fan	ASMTL antisense	NM_001636	NM_001636
2.93E+02	8.20E+00	solute carrier fan	ASMTL antisense	NM_001636	NM_001636
2.93E+02	8.20E+00	solute carrier fan	ASMTL antisense	NM_001636	NM_001636
4.03E-03	-7.95E+00	neural precursor	regulatory factor	NM_198400,NM	NM_198400,NM_006154
2.87E+02	8.16E+00	oncostatin M	GATS protein-like	NM_020530	NM_020530
2.70E+02	8.07E+00	protein tyrosine	family with sequ	NM_015605,NM	NM_015605,NM_001042364,NM_
4.50E+02	8.81E+00	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
2.59E-03	-8.59E+00	chromosome 2 o	chromosome 2 o	NM_032266	NM_032266
2.91E+02	8.19E+00	zinc finger protei	zinc finger protei	NM_207395	NM_207395
2.65E+02	8.05E+00	ArfGAP with dua	ArfGAP with dua	NM_006869	NM_006869
2.65E+02	8.05E+00	ArfGAP with dua	ArfGAP with dua	NM_006869	NM_006869
4.94E-03	-7.66E+00	salt-inducible kin	chromosome 21	NM_173354	NM_173354
2.91E+02	8.19E+00	solute carrier fan	solute carrier fan	NM_001040661,	NM_001040661,NM_153247
2.91E+02	8.19E+00	solute carrier fan	solute carrier fan	NM_001040661,	NM_001040661,NM_153247
2.05E+02	7.68E+00	SR-related CTD-a	SR-related CTD-a	NM_021228	NM_021228
2.05E+02	7.68E+00	SR-related CTD-a	SR-related CTD-a	NM_021228	NM_021228
3.98E+02	8.64E+00	macrophage eryt	macrophage eryt	NM_005882,NM	NM_005882,NM_001017405
2.52E+02	7.98E+00	allantoicase	SRY (sex determi	NM_018436	NM_018436
3.22E+02	8.33E+00	alpha-1-B glycop	alpha-1-B glycop	NM_130786	NM_130786
3.22E+02	8.33E+00	A1BG antisense	A1BG antisense	NR_015380	NR_015380
3.00E+02	8.23E+00	platelet endothe	platelet endothe	NM_001080471	NM_001080471
3.00E+02	8.23E+00	platelet endothe	platelet endothe	NM_001080471	NM_001080471
4.13E-03	-7.92E+00	arginyl-tRNA syn	arginyl-tRNA syn	NM_020320	NM_020320
4.13E-03	-7.92E+00	arginyl-tRNA syn	arginyl-tRNA syn	NM_020320	NM_020320
2.10E+02	7.72E+00	chromosome 14	transmembrane	NM_001134875,	NM_001134875,NM_001134876
2.10E+02	7.72E+00	transmembrane	transmembrane	NM_025268	NM_025268
3.28E+02	8.36E+00	glioma tumor su	glioma tumor su	NM_015710	NM_015710
3.28E+02	8.36E+00	glioma tumor su	glioma tumor su	NM_015710	NM_015710
3.28E+02	8.36E+00	glioma tumor su	glioma tumor su	NM_015710	NM_015710
2.32E+02	7.86E+00	Prader-Willi regi	Prader-Willi regi	NR_026647	NR_026647
2.60E+02	8.02E+00	gap junction prot	gap junction prot	NM_006783,NM	NM_006783,NM_001110221,NM_
2.60E+02	8.02E+00	gap junction prot	crystallin, lambd	NM_006783,NM	NM_006783,NM_001110221,NM_
3.02E+02	8.24E+00	kinase suppresso	kinase suppresso	NM_173598	NM_173598
3.02E+02	8.24E+00	kinase suppresso	kinase suppresso	NM_173598	NM_173598
2.78E+02	8.12E+00	chromosome 21	non-protein codi	NM_058190	NM_058190
2.31E+02	7.85E+00	testis specific pr	RNA binding mot	NM_001077697	NM_001077697
2.31E+02	7.85E+00	testis specific pr	RNA binding mot	NM_001077697	NM_001077697
4.12E-03	-7.92E+00	DMRT-like family	DMRT-like family	NM_032110	NM_032110
2.16E+02	7.76E+00	placenta-specific	placenta-specific	NR_026740	NR_026740
1.73E+00	7.93E-01	pseudouridylate	E1A binding prot	NM_001002020,	NM_001002020,NM_025215,NM_
3.16E+02	8.30E+00	bromodomain c	bromodomain c	NM_058243	NM_058243
3.16E+02	8.30E+00	bromodomain c	bromodomain c	NM_058243	NM_058243
4.13E+02	8.69E+00	zeta-chain (TCR)	zeta-chain (TCR)	NM_207519	NM_207519
2.26E+02	7.82E+00	sema domain, tr	sema domain, tr	NM_030913	NM_030913
2.43E+02	7.92E+00	stannin	stannin	NM_003498	NM_003498
2.43E+02	7.92E+00	stannin	stannin	NM_003498	NM_003498
4.06E-03	-7.94E+00	AKT interacting	RPGRIP1-like	NM_001012398,	NM_001012398,NM_022476
4.06E-03	-7.94E+00	AKT interacting	RPGRIP1-like	NM_001012398,	NM_001012398,NM_022476
2.78E+02	8.12E+00	meteorin, glial c	meteorin, glial c	NM_001004431	NM_001004431
2.78E+02	8.12E+00	meteorin, glial c	meteorin, glial c	NM_001004431	NM_001004431
2.47E+02	7.95E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.57E+00	6.53E-01	CD7 molecule	secreted and tra	NM_006137	NM_006137
1.57E+00	6.53E-01	CD7 molecule	secreted and tra	NM_006137	NM_006137
1.57E+00	6.53E-01	CD7 molecule	secreted and tra	NM_006137	NM_006137
4.33E-03	-7.85E+00	synovial sarcom	synovial sarcom	NM_003147,NM	NM_003147,NM_175698
4.33E-03	-7.85E+00	synovial sarcom	synovial sarcom	NM_003147,NM	NM_003147,NM_175698

3.54E+02	8.47E+00	G protein-couple	jagged 2	NM_013345	NM_013345
4.12E-03	-7.92E+00	chromosome 2 o	chromosome 2 o	NM_001008215	NM_001008215
2.47E+02	7.95E+00	family with sequ	family with sequ	NR_027422	NR_027422
3.86E+02	8.59E+00	histocompatibilit	histocompatibilit	NM_012292	NM_012292
2.30E+02	7.85E+00	tyrosine kinase, r	succinate dehydr	NM_005781,NM	NM_005781,NM_001010938
3.10E+02	8.27E+00	NOP14 nucleolar	NOP14 nucleolar	NM_003703	NM_003703
3.10E+02	8.27E+00	NOP14 nucleolar	NOP14 nucleolar	NM_003703	NM_003703
3.10E+02	8.27E+00	NOP14 nucleolar	NOP14 nucleolar	NM_003703	NM_003703
4.32E+02	8.76E+00	v-erb-b2 erythrol	v-erb-b2 erythro	NM_004448	NM_004448
4.32E+02	8.76E+00	v-erb-b2 erythrol	v-erb-b2 erythro	NM_004448	NM_004448
4.32E+02	8.76E+00	v-erb-b2 erythro	v-erb-b2 erythro	NM_004448	NM_004448
2.30E+02	7.85E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.99E-03	-7.97E+00	tripartite motif-c	tripartite motif-c	NM_014818	NM_014818
3.18E+02	8.31E+00	mannose recepto	mannose recepto	NM_006039	NM_006039
2.45E+02	7.94E+00	fatty acid syntha	fatty acid syntha	NM_004104	NM_004104
2.88E+02	8.17E+00	SET domain cont	SET domain cont	NM_014712	NM_014712
2.88E+02	8.17E+00	SET domain cont	SET domain cont	NM_014712	NM_014712
4.01E-03	-7.96E+00	chromosome 21	chromosome 21	NR_026845	NR_026845
3.81E-03	-8.04E+00	apolipoprotein H	protein kinase C,	NM_000042	NM_000042
2.55E+02	8.00E+00	nicalin homolog	nicalin homolog	NM_020170	NM_020170
2.55E+02	8.00E+00	nicalin homolog	nicalin homolog	NM_020170	NM_020170
3.50E+02	8.45E+00	phytanoyl-CoA d	phytanoyl-CoA d	NM_001100877	NM_001100877
2.10E+02	7.72E+00	DEAD/H (Asp-Glu	killer cell lectin-li	NM_004400	NM_004400
2.67E+02	8.06E+00	zinc finger and B	zinc finger and B	NM_025224	NM_025224
2.67E+02	8.06E+00	zinc finger and B	zinc finger and B	NM_025224	NM_025224
3.73E-03	-8.07E+00	diacylglycerol kir	diacylglycerol kir	NM_201533	NM_201533
2.50E+02	7.97E+00	matrix metallope	matrix metallope	NR_002946	NR_002946
2.59E+02	8.02E+00	ankyrin repeat d	lipase, member I	NR_027270	NR_027270
3.19E+02	8.32E+00	WD repeat doma	WD repeat doma	NM_052821	NM_052821
3.14E+02	8.30E+00	glutamate-rich W	potassium inwar	NM_031485	NM_031485
2.18E+02	7.77E+00	discs, large (Dros	ceroid-lipofuscin	NM_004745	NM_004745
3.04E+02	8.25E+00	tweety homolog	dynein, axonema	NM_052869	NM_052869
2.62E+02	8.03E+00	solute carrier fan	TP53 target 3B	NR_003083	NR_003083
2.50E+02	7.96E+00	small nucleolar R	copine VII	NR_002450	NR_002450
2.50E+02	7.96E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
2.64E+02	8.04E+00	dihydrouridine sy	neurturin	NM_020175	NM_020175
2.64E+02	8.04E+00	dihydrouridine sy	neurturin	NM_020175	NM_020175
2.44E+02	7.93E+00	peptide deformy	peptide deformy	NM_022341,NM	NM_022341,NM_032382
2.25E+02	7.81E+00	potassium voltag	potassium voltag	NM_002237	NM_002237
4.10E+02	8.68E+00	hypothetical LOC	myocyte enhanc	NR_024383,NR_	NR_024383,NR_024384
4.10E+02	8.68E+00	hypothetical LOC	myocyte enhanc	NR_024383,NR_	NR_024383,NR_024384
4.10E+02	8.68E+00	hypothetical LOC	myocyte enhanc	NR_024383,NR_	NR_024383,NR_024384
2.49E+02	7.96E+00	collagen, type VI,	collagen, type VI,	NM_001848	NM_001848
2.49E+02	7.96E+00	collagen, type VI,	collagen, type VI,	NM_001848	NM_001848
2.49E+02	7.96E+00	collagen, type VI,	collagen, type VI,	NM_001848	NM_001848
2.83E+02	8.14E+00	H19, imprinted n	insulin-like growt	NR_002196	NR_002196
2.83E+02	8.14E+00	H19, imprinted n	insulin-like growt	NR_002196	NR_002196
2.64E+02	8.04E+00	amidohydrolase	amidohydrolase	NM_015944,NM	NM_015944,NM_001145815
2.66E+02	8.05E+00	ring finger protei	ring finger protei	NM_001109903,	NM_001109903,NM_032814
2.66E+02	8.05E+00	ring finger protei	ring finger protei	NM_001109903,	NM_001109903,NM_032814
2.66E+02	8.05E+00	ring finger protei	ring finger protei	NM_001109903,	NM_001109903,NM_032814
2.83E+02	8.14E+00	EGF-like-domain,	EGF-like-domain,	NM_016215	NM_016215
2.28E+02	7.83E+00	Rho GTPase activ	Rho GTPase activ	NM_020876	NM_020876
2.28E+02	7.83E+00	Rho GTPase activ	Rho GTPase activ	NM_020876	NM_020876
2.70E+02	8.08E+00	leucine-rich repe	chondroitin sulfa	NM_024652	NM_024652
2.70E+02	8.08E+00	leucine-rich repe	chondroitin sulfa	NM_024652	NM_024652
3.29E-03	-8.25E+00	HtrA serine pepti	deleted in maligr	NM_002775	NM_002775
3.16E+02	8.30E+00	mitochondrial rit	mitochondrial rit	NM_016034	NM_016034

3.63E-03	-8.10E+00	BTB and CNC hor	mitogen-activate	NM_021813	NM_021813
2.69E+02	8.07E+00	glutamic-oxaloac	NK2 transcriptio	NM_002079	NM_002079
2.69E+02	8.07E+00	glutamic-oxaloac	NK2 transcriptio	NM_002079	NM_002079
2.50E+02	7.97E+00	tau tubulin kinas	tau tubulin kinas	NM_032538	NM_032538
2.50E+02	7.97E+00	tau tubulin kinas	tau tubulin kinas	NM_032538	NM_032538
2.32E+02	7.86E+00	xylosyltransferas	polycystic kidney	NM_022166	NM_022166
2.32E+02	7.86E+00	xylosyltransferas	polycystic kidney	NM_022166	NM_022166
2.10E+02	7.71E+00	steroid-5-alpha-r	PAP associated d	NM_001047	NM_001047
3.15E+02	8.30E+00	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
3.15E+02	8.30E+00	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
3.67E+02	8.52E+00	v-akt murine thy	v-akt murine thy	NM_005163,NM	NM_005163,NM_001014432,NM_
2.21E+02	7.79E+00	tandem C2 doma	tandem C2 doma	NM_152332,NM	NM_152332,NM_001128595,NM_
2.21E+02	7.79E+00	tandem C2 doma	tandem C2 doma	NM_152332,NM	NM_152332,NM_001128595,NM_
3.09E+02	8.27E+00	calcyphosine	calcyphosine	NM_004058,NM	NM_004058,NM_080590
3.09E+02	8.27E+00	calcyphosine	calcyphosine	NM_004058,NM	NM_004058,NM_080590
2.30E+02	7.84E+00	four jointed box	four jointed box	NM_014344	NM_014344
2.30E+02	7.84E+00	four jointed box	four jointed box	NM_014344	NM_014344
4.09E-03	-7.93E+00	family with sequ	integrin, alpha 2	NM_198475	NM_198475
2.30E+02	7.84E+00	tubulin, beta pse	tubulin, beta pse	NR_027156	NR_027156
4.25E-03	-7.88E+00	bromodomain a	patatin-like phos	NM_015695	NM_015695
2.60E+02	8.02E+00	guanine nucleoti	guanine nucleoti	NM_002067	NM_002067
2.60E+02	8.02E+00	guanine nucleoti	guanine nucleoti	NM_002067	NM_002067
2.70E+02	8.08E+00	sialidase 4	sialidase 4	NM_080741	NM_080741
2.70E+02	8.08E+00	sialidase 4	sialidase 4	NM_080741	NM_080741
2.76E+02	8.11E+00	tubulin tyrosine l	tubulin tyrosine l	NM_001130045	NM_001130045
2.76E+02	8.11E+00	tubulin tyrosine l	tubulin tyrosine l	NM_001130045	NM_001130045
2.64E+02	8.04E+00	transmembrane	M-phase phosph	NM_130785,NM	NM_130785,NM_199254,NM_001
3.44E+02	8.43E+00	UNC homeobox	MICAL-like 2	NM_001080461	NM_001080461
3.44E+02	8.43E+00	UNC homeobox	MICAL-like 2	NM_001080461	NM_001080461
2.76E+02	8.11E+00	BTB (POZ) domai	transmembrane	NM_001011885,	NM_001011885,NM_025238
2.76E+02	8.11E+00	BTB (POZ) domai	transmembrane	NM_001011885,	NM_001011885,NM_025238
2.53E+02	7.98E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
2.53E+02	7.98E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
2.66E+02	8.05E+00	v-akt murine thy	zinc finger protei	NM_005465	NM_005465
3.19E+02	8.32E+00	sodium channel,	sodium channel,	NM_000334	NM_000334
3.13E-03	-8.32E+00	chromosome 18	chromosome 18	NM_001037331	NM_001037331
3.72E+02	8.54E+00	tumor necrosis f	chromosome 1 o	NM_003820	NM_003820
3.72E+02	8.54E+00	tumor necrosis f	chromosome 1 o	NM_003820	NM_003820
4.42E-03	-7.82E+00	chromosome 6 o	chromosome 6 o	NM_206921	NM_206921
4.42E-03	-7.82E+00	chromosome 6 o	chromosome 6 o	NM_206921	NM_206921
2.36E+02	7.88E+00	hyperpolarizatio	hyperpolarizatio	NM_001194	NM_001194
2.10E+02	7.72E+00	dipeptidase 3	dipeptidase 3	NM_022357,NM	NM_022357,NM_001129758
2.53E+02	7.98E+00	LAG1 homolog, c	LAG1 homolog, c	NM_021267,NM	NM_021267,NM_001492
2.53E+02	7.98E+00	LAG1 homolog, c	LAG1 homolog, c	NM_021267,NM	NM_021267,NM_001492
2.98E+02	8.22E+00	gem (nuclear org	NTPase, KAP fam	NM_024707,NM	NM_024707,NM_001007269
2.98E+02	8.22E+00	gem (nuclear org	NTPase, KAP fam	NM_024707,NM	NM_024707,NM_001007269
2.98E+02	8.22E+00	gem (nuclear org	NTPase, KAP fam	NM_024707,NM	NM_024707,NM_001007269
2.62E+02	8.03E+00	chromosome 22	bromodomain c	NR_026997	NR_026997
2.62E+02	8.03E+00	chromosome 22	bromodomain c	NR_026997	NR_026997
2.79E+02	8.12E+00	notch 1	EGF-like-domain,	NM_017617	NM_017617
4.08E-03	-7.94E+00	prominin 1	prominin 1	NM_001145848,	NM_001145848,NM_001145847,
4.08E-03	-7.94E+00	prominin 1	prominin 1	NM_001145848,	NM_001145848,NM_001145847,
2.61E+02	8.03E+00	GNAS complex l	GNAS complex l	NM_016592	NM_016592
2.70E+02	8.08E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
3.30E+02	8.37E+00	zinc finger protei	zinc finger protei	NM_153034	NM_153034
4.13E+02	8.69E+00	lamin B2	lamin B2	NM_032737	NM_032737
2.16E+02	7.76E+00	LIM domains co	LIM domains co	NM_014240	NM_014240
4.19E-03	-7.90E+00	zinc finger protei	FYVE, RhoGEF an	NM_001007101	NM_001007101

4.19E+02	8.71E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.60E+02	8.02E+00	NK6 homeobox	chromosome 10	NM_177400	NM_177400
3.06E+02	8.26E+00	glutamic-pyruvat	glutamic-pyruvat	NM_005309	NM_005309
4.96E-03	-7.66E+00	F-box and leucin	wingless-type MI	NM_152441	NM_152441
2.43E+02	7.92E+00	ryanodine recept	ryanodine recept	NM_000540,NM	NM_000540,NM_001042723
2.43E+02	7.92E+00	ryanodine recept	ryanodine recept	NM_000540,NM	NM_000540,NM_001042723
2.41E+02	7.91E+00	retinoic acid earl	UL16 binding pro	NM_130900	NM_130900
2.24E+02	7.81E+00	G protein-couple	SFT2 domain con	NM_005291	NM_005291
4.85E-03	-7.69E+00	docking protein	docking protein	NM_003974	NM_003974
3.38E+02	8.40E+00	wingless-type MI	wingless-type MI	NM_030775	NM_030775
3.38E+02	8.40E+00	wingless-type MI	wingless-type MI	NM_030775	NM_030775
2.98E+02	8.22E+00	synovial sarcom	synovial sarcom	NM_198935	NM_198935
2.98E+02	8.22E+00	synovial sarcom	synovial sarcom	NM_198935	NM_198935
2.77E+02	8.11E+00	reticulocalbin 2,	proline-serine-th	NM_002902	NM_002902
2.71E+02	8.08E+00	ring finger protei	ring finger protei	NM_194460	NM_194460
2.18E+02	7.77E+00	sequestosome 1	sequestosome 1	NM_001142299	NM_001142299
2.18E+02	7.77E+00	sequestosome 1	sequestosome 1	NM_001142299	NM_001142299
2.94E+02	8.20E+00	solute carrier fan	solute carrier fan	NM_152346	NM_152346
2.38E+02	7.90E+00	sialidase 4	programmed cell	NM_080741	NM_080741
3.37E-03	-8.21E+00	RAB6B, member	chromosome 3 o	NM_016577	NM_016577
3.74E+02	8.55E+00	signal-regulatory	signal-regulatory	NM_001040023	NM_001040023
3.97E-03	-7.98E+00	aquaporin 9	lipase, hepatic	NM_020980	NM_020980
3.97E-03	-7.98E+00	lipase, hepatic	lipase, hepatic	NM_000236	NM_000236
2.29E+02	7.84E+00	cadherin 15, type	cadherin 15, type	NM_004933	NM_004933
2.78E+02	8.12E+00	cathepsin D	synaptotagmin V	NM_001909	NM_001909
3.61E-03	-8.11E+00	inter-alpha (glob	inter-alpha (glob	NM_001001851	NM_001001851
3.61E-03	-8.11E+00	inter-alpha (glob	inter-alpha (glob	NM_001001851	NM_001001851
4.24E-03	-7.88E+00	BCL2-like 14 (apo	BCL2-like 14 (apo	NM_138723	NM_138723
4.24E-03	-7.88E+00	BCL2-like 14 (apo	BCL2-like 14 (apo	NM_138722,NM	NM_138722,NM_030766
1.98E+02	7.63E+00	RAB10, member	hydroxyacyl-CoA	NM_016131	NM_016131
2.62E+02	8.03E+00	transmembrane	transmembrane	NM_001008269	NM_001008269
2.97E+02	8.22E+00	lymphocyte antig	glycosylphosphat	NM_001135655,	NM_001135655,NM_002347
4.12E-03	-7.92E+00	colony stimulatir	interleukin 3 rec	NM_172247	NM_172247
2.13E+02	7.74E+00	zinc finger protei	zinc finger protei	NM_152600	NM_152600
2.13E+02	7.74E+00	zinc finger protei	zinc finger protei	NM_152600	NM_152600
2.61E+02	8.03E+00	beta-1,4-N-acety	beta-1,4-N-acety	NM_178537	NM_178537
2.61E+02	8.03E+00	beta-1,4-N-acety	beta-1,4-N-acety	NM_178537	NM_178537
2.61E+02	8.03E+00	beta-1,4-N-acety	beta-1,4-N-acety	NM_178537	NM_178537
2.61E+02	8.03E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
3.10E+02	8.27E+00	KIAA1875	KIAA1875	NR_024207	NR_024207
2.25E+02	7.81E+00	retinoic acid rece	retinoic acid rece	NM_002888	NM_002888
2.25E+02	7.81E+00	retinoic acid rece	major facilitator	NM_002888	NM_002888
3.05E+02	8.25E+00	nuclear factor I/	nuclear factor I/	NM_005597	NM_005597
3.05E+02	8.25E+00	nuclear factor I/	nuclear factor I/	NM_005597	NM_005597
3.02E+02	8.24E+00	chorionic gonad	chorionic gonad	NM_033378	NM_033378
3.57E+02	8.48E+00	sidekick homolog	sidekick homolog	NM_001079653	NM_001079653
3.02E+02	8.24E+00	chromosome 21	heat shock trans	NR_026863	NR_026863
3.02E+02	8.24E+00	chromosome 21	heat shock trans	NR_026863	NR_026863
2.27E+02	7.82E+00	cadherin 20, type	cadherin 20, type	NM_031891	NM_031891
2.96E+02	8.21E+00	programmed cell	chromosome 2 o	NM_005018	NM_005018
3.71E-03	-8.07E+00	synovial sarcom	lysophosphatidic	NM_014021	NM_014021
3.71E-03	-8.07E+00	synovial sarcom	lysophosphatidic	NM_014021	NM_014021
3.18E+02	8.31E+00	sialic acid binding	sialic acid binding	NM_001098612	NM_001098612
3.18E+02	8.31E+00	sialic acid binding	sialic acid binding	NM_001098612	NM_001098612
2.80E+02	8.13E+00	retinoic acid indu	retinoic acid indu	NM_001145520	NM_001145520
2.80E+02	8.13E+00	retinoic acid indu	retinoic acid indu	NM_001145520	NM_001145520
4.27E-03	-7.87E+00	zinc finger, DHH	zinc finger, DHH	NM_022494	NM_022494
4.27E-03	-7.87E+00	zinc finger, DHH	zinc finger, DHH	NM_022494	NM_022494

4.18E-03	-7.90E+00	zinc finger protei	family with sequ	NM_001001662	NM_001001662
4.18E-03	-7.90E+00	zinc finger protei	family with sequ	NM_001001662	NM_001001662
4.18E-03	-7.90E+00	zinc finger protei	family with sequ	NM_001001662	NM_001001662
2.39E+02	7.90E+00	chymotrypsin-lik	UDP-N-acetyl-alp	NM_001971	NM_001971
2.36E+02	7.88E+00	UNC homeobox	MICAL-like 2	NM_001080461	NM_001080461
2.87E+02	8.16E+00	secretin	secretin	NM_021920	NM_021920
2.87E+02	8.16E+00	secretin	dopamine recept	NM_021920	NM_021920
2.88E+02	8.17E+00	cadherin-related	cadherin-related	NM_021924,NM	NM_021924,NM_031264
2.88E+02	8.17E+00	cadherin-related	cadherin-related	NM_021924,NM	NM_021924,NM_031264
2.88E+02	8.17E+00	cadherin-related	cadherin-related	NM_021924,NM	NM_021924,NM_031264
3.33E+02	8.38E+00	strawberry notch	strawberry notch	NM_001100122,	NM_001100122,NM_014963
3.76E+02	8.56E+00	zinc finger protei	zinc finger protei	NR_003253,NM_	NR_003253,NM_003426
3.76E+02	8.56E+00	zinc finger protei	zinc finger protei	NR_003253,NM_	NR_003253,NM_003426
3.76E+02	8.56E+00	zinc finger protei	zinc finger protei	NR_003253,NM_	NR_003253,NM_003426
2.21E+02	7.79E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
2.21E+02	7.79E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
2.66E+02	8.06E+00	GNAS complex lc	GNAS complex lc	NM_001077490,	NM_001077490,NM_080425
2.66E+02	8.06E+00	GNAS complex lc	GNAS complex lc	NM_001077490,	NM_001077490,NM_080425
2.66E+02	8.06E+00	GNAS complex lc	GNAS complex lc	NM_001077490,	NM_001077490,NM_080425
4.47E+02	8.80E+00	cholinergic recep	potassium voltag	NM_000744	NM_000744
4.47E+02	8.80E+00	cholinergic recep	potassium voltag	NM_000744	NM_000744
4.47E+02	8.80E+00	cholinergic recep	potassium voltag	NM_000744	NM_000744
2.10E+02	7.72E+00	chromodomain h	chromodomain h	NM_015557	NM_015557
3.94E-03	-7.99E+00	CD22 molecule	free fatty acid re	NM_001771	NM_001771
2.34E+02	7.87E+00	5-hydroxytryptar	5-hydroxytryptar	NM_001040174	NM_001040174
2.27E+02	7.82E+00	TBC1 domain fan	TBC1 domain fan	NM_019020	NM_019020
2.27E+02	7.82E+00	TBC1 domain fan	TBC1 domain fan	NM_019020	NM_019020
3.67E-03	-8.09E+00	zinc finger protei	squalene epoxida	NM_152412	NM_152412
3.67E-03	-8.09E+00	zinc finger protei	squalene epoxida	NM_152412	NM_152412
2.29E+02	7.84E+00	methyltransferas	methyltransferas	NM_024086	NM_024086
2.29E+02	7.84E+00	methyltransferas	methyltransferas	NM_024086	NM_024086
2.70E+02	8.08E+00	GLI family zinc fir	zinc finger protei	NM_138465	NM_138465
2.70E+02	8.08E+00	GLI family zinc fir	zinc finger protei	NM_138465	NM_138465
3.14E+02	8.30E+00	amylase, alpha 1	amylase, alpha 1	NM_001008218,	NM_001008218,NM_001008219
4.05E-03	-7.95E+00	transcription fact	transcription fact	NM_005650,NM	NM_005650,NM_181492
4.05E-03	-7.95E+00	transcription fact	transcription fact	NM_005650,NM	NM_005650,NM_181492
2.35E+02	7.88E+00	ELAV (embryonic	ELAV (embryonic	NM_032281,NM	NM_032281,NM_001420
2.35E+02	7.88E+00	ELAV (embryonic	zinc finger protei	NM_032281,NM	NM_032281,NM_001420
2.31E+02	7.85E+00	KIAA0649	KIAA0649	NM_014811	NM_014811
4.11E-03	-7.93E+00	Ras association (	CD28 molecule	NM_203365	NM_203365
2.64E+02	8.04E+00	kelch domain coi	transmembrane	NM_014997	NM_014997
3.12E+02	8.29E+00	gametogenetin	gametogenetin	NM_152657	NM_152657
3.12E+02	8.29E+00	gametogenetin	gametogenetin	NM_152657	NM_152657
3.29E+02	8.36E+00	tenascin XB	tenascin XB	NM_019105,NM	NM_019105,NM_032470
2.29E+02	7.84E+00	cortexin 1	cortexin 1	NM_206833	NM_206833
2.30E+02	7.85E+00	zinc finger protei	zinc finger protei	NM_001080409	NM_001080409
2.23E+02	7.80E+00	5-methyltetrahyc	ryanodine recept	NM_000254	NM_000254
3.25E-03	-8.27E+00	Charcot-Leyden c	leucine twenty h	NM_001828	NM_001828
2.69E+02	8.07E+00	chromosome 4 o	protocadherin 1(	NM_001099783	NM_001099783
2.69E+02	8.07E+00	chromosome 4 o	protocadherin 1(	NM_001099783	NM_001099783
4.48E-03	-7.80E+00	proteasome (pro	phosphatidylinos	NM_174871	NM_174871
4.48E-03	-7.80E+00	proteasome (pro	phosphatidylinos	NM_174871	NM_174871
2.69E+02	8.07E+00	transmembrane	KIAA0125	NM_025268	NM_025268
2.48E+02	7.95E+00	chromosome 21	chromosome 21	NM_032261,NM	NM_032261,NM_001142854
2.48E+02	7.95E+00	chromosome 21	chromosome 21	NM_032261,NM	NM_032261,NM_001142854
2.98E+02	8.22E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.98E+02	8.22E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.56E+02	8.00E+00	CXXC finger 5	pleckstrin and Se	NM_016463	NM_016463

2.23E+02	7.80E+00	phospholamban	ASF1 anti-silencir	NM_002667	NM_002667
3.33E+02	8.38E+00	fibrillin 2	fibrillin 2	NM_001999	NM_001999
3.33E+02	8.38E+00	fibrillin 2	fibrillin 2	NM_001999	NM_001999
2.94E+02	8.20E+00	spleen tyrosine k	AU RNA binding	NR_024155	NR_024155
2.94E+02	8.20E+00	spleen tyrosine k	AU RNA binding	NR_024155	NR_024155
2.94E+02	8.20E+00	spleen tyrosine k	AU RNA binding	NR_024155	NR_024155
2.59E+02	8.02E+00	lectin, galactosid	lectin, galactosid	NM_001042507	NM_001042507
2.21E+02	7.79E+00	inscuteable hom	SRY (sex determi	NM_001042536	NM_001042536
2.06E+02	7.68E+00	zinc finger protei	zinc finger protei	NR_026569,NM_	NR_026569,NM_001143823,NM_
2.15E+02	7.75E+00	uridine-cytidine	Rap guanine nucl	NM_031432,NM	NM_031432,NM_001135954
2.15E+02	7.75E+00	uridine-cytidine	Rap guanine nucl	NM_031432,NM	NM_031432,NM_001135954
2.82E+02	8.14E+00	orthodenticle ho	exocyst complex	NM_172337,NM	NM_172337,NM_021728
2.43E+02	7.92E+00	coiled-coil domai	hypothetical pro	NM_152492	NM_152492
2.43E+02	7.92E+00	coiled-coil domai	hypothetical pro	NM_152492	NM_152492
2.58E+02	8.01E+00	nuclear factor I/	nuclear factor I/	NM_005597	NM_005597
3.18E+02	8.31E+00	mucin 6, oligome	mucin 6, oligome	NM_005961	NM_005961
3.18E+02	8.31E+00	mucin 6, oligome	mucin 6, oligome	NM_005961	NM_005961
3.18E+02	8.31E+00	mucin 6, oligome	mucin 6, oligome	NM_005961	NM_005961
3.12E+02	8.29E+00	REX1, RNA exonu	REX1, RNA exonu	NM_020695	NM_020695
3.12E+02	8.29E+00	REX1, RNA exonu	REX1, RNA exonu	NM_020695	NM_020695
3.80E-03	-8.04E+00	small nucleolar R	receptor (G prot	NR_002990	NR_002990
4.47E-03	-7.81E+00	olfactory recepto	olfactory recepto	NM_013937	NM_013937
4.47E-03	-7.81E+00	olfactory recepto	olfactory recepto	NM_013937	NM_013937
2.50E+02	7.97E+00	coiled-coil domai	coiled-coil domai	NM_032251	NM_032251
2.50E+02	7.97E+00	coiled-coil domai	coiled-coil domai	NM_032251	NM_032251
5.09E-03	-7.62E+00	MAD2L1 binding	MAD2L1 binding	NM_001003690	NM_001003690
2.30E+02	7.84E+00	KIAA1012	ring finger protei	NM_014939	NM_014939
3.79E+02	8.57E+00	homeodomain ir	homeodomain ir	NM_144685	NM_144685
3.79E+02	8.57E+00	homeodomain ir	homeodomain ir	NM_144685	NM_144685
3.79E+02	8.57E+00	homeodomain ir	homeodomain ir	NM_144685	NM_144685
3.34E+02	8.38E+00	neuromedin U	exocyst complex	NM_006681	NM_006681
3.34E+02	8.38E+00	neuromedin U	exocyst complex	NM_006681	NM_006681
4.21E-03	-7.89E+00	neurobeachin-lik	neurotrophin rec	NM_015175	NM_015175
2.96E+02	8.21E+00	chromobox hom	chromobox hom	NM_003655	NM_003655
2.48E+02	7.95E+00	DEAH (Asp-Glu-A	fibronectin type	NM_018180	NM_018180
2.54E+02	7.99E+00	LIM domain cont	tumor protein p6	NM_005578	NM_005578
3.44E-03	-8.18E+00	thyroid hormone	zinc finger protei	NM_016213	NM_016213
3.44E-03	-8.18E+00	zinc finger protei	zinc finger protei	NM_015042	NM_015042
3.44E-03	-8.18E+00	solute carrier fan	family with sequ	NM_012450	NM_012450
3.44E-03	-8.18E+00	solute carrier fan	family with sequ	NM_012450	NM_012450
4.92E-03	-7.67E+00	lymphocyte antig	chromosome 8 o	NM_001127213,	NM_001127213,NM_002346
2.23E+02	7.80E+00	protein tyrosine	protein tyrosine	NM_003660	NM_003660
3.70E-03	-8.08E+00	annexin A8-like 1	family with sequ	NM_001098845	NM_001098845
2.84E+02	8.15E+00	family with sequ	family with sequ	NM_138418	NM_138418
2.84E+02	8.15E+00	family with sequ	family with sequ	NM_138418	NM_138418
2.84E+02	8.15E+00	family with sequ	family with sequ	NM_138418	NM_138418
3.05E+02	8.25E+00	protein phosphat	protein phosphat	NM_001142502,	NM_001142502,NM_006663
3.05E+02	8.25E+00	protein phosphat	protein phosphat	NM_001142502,	NM_001142502,NM_006663
4.88E-03	-7.68E+00	NSA2 ribosome b	NSA2 ribosome b	NM_014886	NM_014886
4.35E-03	-7.84E+00	cell division cycle	cathelicidin antir	NM_201567,NM	NM_201567,NM_001789
4.35E-03	-7.84E+00	cell division cycle	cathelicidin antir	NM_201567,NM	NM_201567,NM_001789
4.33E-03	-7.85E+00	follistatin-like 1	NADH dehydroge	NM_007085	NM_007085
2.51E+02	7.97E+00	cleavage and pol	isoamyl acetate-	NM_016207	NM_016207
2.63E+02	8.04E+00	transformer 2 alp	CDC-like kinase 2	NM_013293	NM_013293
2.63E+02	8.04E+00	transformer 2 alp	CDC-like kinase 2	NM_013293	NM_013293
3.60E-03	-8.12E+00	GSG1-like	exportin 6	NM_144675,NM	NM_144675,NM_001109763
2.64E+02	8.04E+00	nuclear factor I/	TM2 domain con	NM_005595,NM	NM_005595,NM_001134673
2.64E+02	8.04E+00	nuclear factor I/	TM2 domain con	NM_005595,NM	NM_005595,NM_001134673

2.29E+02	7.84E+00	chromosome 19	coactivator-asso	NM_001136482	NM_001136482
2.99E+02	8.22E+00	zinc finger, FYVE	zinc finger, FYVE	NM_020972	NM_020972
2.99E+02	8.22E+00	zinc finger, FYVE	zinc finger, FYVE	NM_020972	NM_020972
2.12E+02	7.73E+00	neurexin 2	RAS guanyl relea	NM_138734,NM	NM_138734,NM_015080,NM_138
2.23E+02	7.80E+00	sema domain, im	sema domain, im	NM_017789	NM_017789
2.23E+02	7.80E+00	sema domain, im	sema domain, im	NM_017789	NM_017789
3.23E+02	8.33E+00	jumonji domain	WD repeat doma	NM_001005920	NM_001005920
2.56E+02	8.00E+00	calcium channel,	coiled-coil doma	NM_005183	NM_005183
2.80E-03	-8.48E+00	asteroid homolo	asteroid homolo	NM_014065	NM_014065
2.80E-03	-8.48E+00	asteroid homolo	asteroid homolo	NM_014065	NM_014065
3.94E-03	-7.99E+00	mitochondrial rib	mitochondrial rib	NM_015084	NM_015084
3.94E-03	-7.99E+00	mitochondrial rib	mitochondrial rib	NM_015084	NM_015084
3.94E-03	-7.99E+00	mitochondrial rib	mitochondrial rib	NM_015084	NM_015084
2.43E+02	7.92E+00	null	golgin A8 family,	null	null
2.51E+02	7.97E+00	zinc finger protei	zinc finger protei	NM_213605	NM_213605
2.89E+02	8.17E+00	golgi to ER traffic	golgi to ER traffic	NM_015949	NM_015949
4.55E-03	-7.78E+00	phosphatidyletha	retinoic acid indu	NM_148173,NM	NM_148173,NM_007169,NM_148
4.55E-03	-7.78E+00	phosphatidyletha	retinoic acid indu	NM_148173,NM	NM_148173,NM_007169,NM_148
2.35E+02	7.88E+00	BR serine/threon	BR serine/threon	NM_003957	NM_003957
2.15E+02	7.75E+00	potassium voltag	potassium voltag	NM_181798	NM_181798
2.45E+02	7.94E+00	basigin (Ok blood	basigin (Ok blood	NM_001728,NM	NM_001728,NM_198589
2.45E+02	7.94E+00	basigin (Ok blood	basigin (Ok blood	NM_001728,NM	NM_001728,NM_198589
4.42E-03	-7.82E+00	Jun dimerization	basic leucine zip	NM_001135049	NM_001135049
2.34E+02	7.87E+00	IWS1 homolog (S	myosin VIIB	NM_017969	NM_017969
2.34E+02	7.87E+00	myosin VIIB	myosin VIIB	NM_001080527	NM_001080527
3.34E+02	8.38E+00	furin (paired basi	furin (paired basi	NM_002569	NM_002569
4.00E+02	8.64E+00	guanidinoacetate	guanidinoacetate	NM_000156	NM_000156
3.18E+02	8.31E+00	F-box protein 24	F-box protein 24	NM_033506,NM	NM_033506,NM_012172
3.18E+02	8.31E+00	F-box protein 24	F-box protein 24	NM_033506,NM	NM_033506,NM_012172
2.26E+02	7.82E+00	DEAH (Asp-Glu-A	fibronectin type	NM_018180	NM_018180
2.23E+02	7.80E+00	arginine-fifty hor	rhomboid, veinle	NR_002222	NR_002222
4.08E-03	-7.94E+00	ArfGAP with GTP	family with sequ	NM_001077665	NM_001077665
2.80E+02	8.13E+00	chromosome 3 o	von Hippel-Linda	NM_018462	NM_018462
4.54E+02	8.83E+00	tetraspanin 4	tetraspanin 4	NM_001025237	NM_001025237
4.52E-03	-7.79E+00	zinc finger protei	hyaluronan bindi	NM_153695	NM_153695
2.89E+02	8.17E+00	chromosome 22	chromosome 22	NM_001009880,	NM_001009880,NM_015264
2.47E+02	7.95E+00	cancer/testis ant	cancer/testis ant	NM_001102658	NM_001102658
2.47E+02	7.95E+00	cancer/testis ant	thrombospondin	NM_001102658	NM_001102658
2.11E+02	7.72E+00	chromosome 8 o	chromosome 8 o	NM_001001795	NM_001001795
3.87E+02	8.59E+00	collagen, type IV,	collagen, type IV,	NM_001846	NM_001846
3.87E+02	8.59E+00	collagen, type IV,	collagen, type IV,	NM_001846	NM_001846
2.71E+02	8.08E+00	fibroblast growth	fibroblast growth	NM_003867	NM_003867
2.71E+02	8.08E+00	fibroblast growth	fibroblast growth	NM_003867	NM_003867
2.88E+02	8.17E+00	agrin	agrin	NM_198576	NM_198576
4.35E-03	-7.84E+00	latrophilin 1	CD97 molecule	NM_014921,NM	NM_014921,NM_001008701
4.35E-03	-7.84E+00	latrophilin 1	CD97 molecule	NM_014921,NM	NM_014921,NM_001008701
2.73E+02	8.09E+00	KIAA1486	KIAA1486	NM_020864	NM_020864
2.73E+02	8.09E+00	KIAA1486	KIAA1486	NM_020864	NM_020864
2.68E+02	8.06E+00	amiloride-sensiti	amiloride-sensiti	NM_020039,NM	NM_020039,NM_001095
2.68E+02	8.06E+00	amiloride-sensiti	amiloride-sensiti	NM_020039,NM	NM_020039,NM_001095
2.69E+02	8.07E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
2.69E+02	8.07E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
4.57E-03	-7.77E+00	tumor protein p5	hypothetical LOC	NM_001076787,	NM_001076787,NM_006034
2.15E+02	7.75E+00	killer cell lectin-li	C-type lectin don	NM_198508	NM_198508
4.92E-03	-7.67E+00	Rap guanine nucl	Rap guanine nucl	NM_007023	NM_007023
3.59E-03	-8.12E+00	chromosome 7 o	cullin 1	NM_145304	NM_145304
3.59E-03	-8.12E+00	chromosome 7 o	cullin 1	NM_145304	NM_145304
3.59E-03	-8.12E+00	chromosome 7 o	cullin 1	NM_145304	NM_145304

4.53E+02	8.82E+00	solute carrier fan	solute carrier fan	NM_001636	NM_001636
4.66E-03	-7.75E+00	CWC25 spliceosc	CWC25 spliceosc	NM_017748	NM_017748
2.36E+02	7.88E+00	azurocidin 1	proteinase 3	NM_001700	NM_001700
3.29E+02	8.36E+00	inverted formin,	adenylosuccinat	NM_032714	NM_032714
3.29E+02	8.36E+00	inverted formin,	adenylosuccinat	NM_032714	NM_032714
3.29E+02	8.36E+00	inverted formin,	adenylosuccinat	NM_032714	NM_032714
4.66E-03	-7.75E+00	transmembrane	transmembrane	NM_213601	NM_213601
2.26E+02	7.82E+00	JAZF zinc finger 1	JAZF zinc finger 1	NM_175061	NM_175061
2.35E+02	7.88E+00	similar to hCG17	similar to hCG17	NR_024014	NR_024014
2.35E+02	7.88E+00	similar to hCG17	similar to hCG17	NR_024014	NR_024014
3.80E-03	-8.04E+00	resistance to inhi	chromosome 12	NM_018157	NM_018157
2.85E+02	8.15E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
2.85E+02	8.15E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
2.95E+02	8.21E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
3.13E+02	8.29E+00	notch 1	notch 1	NM_017617	NM_017617
2.26E+02	7.82E+00	diacylglycerol lip	KDEL (Lys-Asp-Gl	NM_001142936,	NM_001142936,NM_139179
2.67E+02	8.06E+00	MAGE-like 2	MAGE-like 2	NM_019066	NM_019066
2.67E+02	8.06E+00	MAGE-like 2	MAGE-like 2	NM_019066	NM_019066
2.67E+02	8.06E+00	MAGE-like 2	necdin homolog	NM_019066	NM_019066
2.67E+02	8.06E+00	MAGE-like 2	necdin homolog	NM_019066	NM_019066
3.90E+02	8.61E+00	nucleus accumbe	nucleus accumbe	NM_052876	NM_052876
3.90E+02	8.61E+00	nucleus accumbe	nucleus accumbe	NM_052876	NM_052876
3.90E+02	8.61E+00	nucleus accumbe	nucleus accumbe	NM_052876	NM_052876
2.46E+02	7.94E+00	synaptotagmin V	troponin I type 2	NM_138567	NM_138567
2.46E+02	7.94E+00	synaptotagmin V	troponin I type 2	NM_138567	NM_138567
2.98E-03	-8.39E+00	hypothetical LOC	family with sequ	NR_021493	NR_021493
2.98E-03	-8.39E+00	hypothetical LOC	family with sequ	NR_021493	NR_021493
2.01E+02	7.65E+00	IQ motif containi	CREB regulated t	NM_003870	NM_003870
2.01E+02	7.65E+00	CREB regulated t	CREB regulated t	NM_022769,NM	NM_022769,NM_001042574
3.57E+02	8.48E+00	keratin 86	keratin 86	NM_002284	NM_002284
2.30E+02	7.85E+00	asparaginase hor	kinesin family me	NM_001080464	NM_001080464
2.54E+02	7.99E+00	tripartite motif-c	tripartite motif-c	NM_025058	NM_025058
3.64E+02	8.51E+00	BAH domain and	BAH domain and	NM_001080519	NM_001080519
3.64E+02	8.51E+00	BAH domain and	BAH domain and	NM_001080519	NM_001080519
3.64E+02	8.51E+00	BAH domain and	BAH domain and	NM_001080519	NM_001080519
3.79E-03	-8.04E+00	chymotrypsin-lik	chymotrypsin-lik	NM_007352	NM_007352
2.48E+02	7.95E+00	paraneoplastic a	paraneoplastic a	NM_032882	NM_032882
3.10E-03	-8.33E+00	T-box 2	T-box 2	NM_005994	NM_005994
4.24E-03	-7.88E+00	D-dopachrome t	D-dopachrome t	NM_001355,NM	NM_001355,NM_001084392
4.24E-03	-7.88E+00	D-dopachrome t	D-dopachrome t	NM_001355,NM	NM_001355,NM_001084392
4.24E-03	-7.88E+00	D-dopachrome t	D-dopachrome t	NM_001355,NM	NM_001355,NM_001084392
3.00E+02	8.23E+00	null	family with sequ	null	null
3.00E+02	8.23E+00	null	family with sequ	null	null
2.43E+02	7.92E+00	EF-hand domain	GRB10 interactin	NM_025202	NM_025202
1.97E+02	7.62E+00	tubulin tyrosine l	tubulin tyrosine l	NM_015140	NM_015140
4.25E-03	-7.88E+00	v-maf musculoap	hypothetical LOC	NM_032711,NM	NM_032711,NM_002359
3.74E-03	-8.06E+00	inhibitor of CDK,	inhibitor of CDK,	NM_213726	NM_213726
2.44E+02	7.93E+00	BR serine/threon	BR serine/threon	NM_003957	NM_003957
2.44E+02	7.93E+00	BR serine/threon	BR serine/threon	NM_003957	NM_003957
4.18E-03	-7.90E+00	fucosyltransferas	MAK16 homolog	NM_032664	NM_032664
2.16E+02	7.76E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
4.94E-03	-7.66E+00	peroxisomal biog	chromosome 19	NM_080662	NM_080662
4.94E-03	-7.66E+00	peroxisomal biog	chromosome 19	NM_080662	NM_080662
4.98E-03	-7.65E+00	ubiquinol-cytoch	MTERF domain c	NM_006294	NM_006294
1.50E+00	5.85E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.50E+00	5.85E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
3.40E-03	-8.20E+00	RNA (guanine-7-)	melanocortin 5 r	NM_003799	NM_003799
4.92E-03	-7.67E+00	chromosome 6 o	chromosome 6 o	NR_026780	NR_026780

2.54E+02	7.99E+00	chromobox hom	chromobox hom	NM_020649	NM_020649
3.16E+02	8.30E+00	transmembrane	transmembrane	NM_021259	NM_021259
3.86E-03	-8.02E+00	CD93 molecule	NTF2-like export	NM_012072	NM_012072
2.84E+02	8.15E+00	phospholipase A	phospholipase A	NM_003560,NM	NM_003560,NM_001004426
4.40E+02	8.78E+00	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
2.30E+02	7.85E+00	neuroblastoma b	lymphocyte-spec	NM_001102663	NM_001102663
2.30E+02	7.85E+00	neuroblastoma b	lymphocyte-spec	NM_001102663	NM_001102663
2.30E+02	7.85E+00	neuroblastoma b	lymphocyte-spec	NM_001102663	NM_001102663
4.01E+02	8.65E+00	speedy homolog	speedy homolog	NM_001008778	NM_001008778
2.91E+02	8.19E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
2.99E+02	8.22E+00	scleraxis homolo	heat shock trans	NM_001008271,	NM_001008271,NM_001080514
2.55E+02	8.00E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
2.55E+02	8.00E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
2.29E+02	7.84E+00	sterile alpha mot	sterile alpha mot	NM_015589	NM_015589
2.04E+02	7.67E+00	glucocorticoid m	stathmin-like 3	NM_012384	NM_012384
4.25E+02	8.73E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
4.25E+02	8.73E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
2.41E+02	7.91E+00	anoctamin 9	anoctamin 9	NM_001012302	NM_001012302
4.09E+02	8.67E+00	myosin binding p	myosin binding p	NM_000256	NM_000256
2.01E+02	7.65E+00	archaelysin famil	archaelysin famil	NM_133463	NM_133463
2.01E+02	7.65E+00	archaelysin famil	archaelysin famil	NM_133463	NM_133463
2.79E+02	8.12E+00	proline rich 23B	proline rich 23B	NM_001013650	NM_001013650
2.74E+02	8.10E+00	polymerase (RN	fibroblast growt	NM_005035	NM_005035
2.74E+02	8.10E+00	polymerase (RN	fibroblast growt	NM_005035	NM_005035
2.74E+02	8.10E+00	polymerase (RN	fibroblast growt	NM_005035	NM_005035
2.19E+02	7.78E+00	Wolf-Hirschhorn	Wolf-Hirschhorn	NM_005663	NM_005663
2.19E+02	7.78E+00	Wolf-Hirschhorn	Wolf-Hirschhorn	NM_005663	NM_005663
4.62E-03	-7.76E+00	CD72 molecule	CD72 molecule	NM_001782	NM_001782
2.48E+02	7.95E+00	ATP-binding cass	ATP-binding cass	NM_212533,NM	NM_212533,NM_001606
2.48E+02	7.95E+00	ATP-binding cass	ATP-binding cass	NM_212533,NM	NM_212533,NM_001606
4.72E-03	-7.73E+00	family with sequ	starch binding d	NM_001136570	NM_001136570
3.33E+02	8.38E+00	dipeptidase 1 (re	dipeptidase 1 (re	NM_004413	NM_004413
3.10E+02	8.28E+00	chromosome 2 o	ankyrin repeat d	NM_214461	NM_214461
4.13E-03	-7.92E+00	CUGBP, Elav-like	CUGBP, Elav-like	NM_006561	NM_006561
4.13E-03	-7.92E+00	CUGBP, Elav-like	CUGBP, Elav-like	NM_006561	NM_006561
2.91E+02	8.19E+00	Mps one binder	Mps one binder	NM_053005	NM_053005
2.36E+02	7.88E+00	sperm equatorial	non-protein codi	NM_145658	NM_145658
2.36E+02	7.88E+00	sperm equatorial	non-protein codi	NM_145658	NM_145658
2.99E+02	8.22E+00	thrombospondin	thrombospondin	NM_003247	NM_003247
2.99E+02	8.22E+00	thrombospondin	thrombospondin	NM_003247	NM_003247
2.95E+02	8.21E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
4.37E-03	-7.84E+00	ring finger protei	inhibitor of DNA	NM_182757	NM_182757
3.91E+02	8.61E+00	transcription fact	extracellular leu	NR_001288	NR_001288
2.56E+02	8.00E+00	olfactory recept	SPRY domain co	NM_001005496	NM_001005496
2.56E+02	8.00E+00	olfactory recept	SPRY domain co	NM_001005496	NM_001005496
3.18E+02	8.31E+00	KIAA0284	phospholipase D	NM_001112726,	NM_001112726,NM_015005
3.18E+02	8.31E+00	KIAA0284	phospholipase D	NM_001112726,	NM_001112726,NM_015005
3.04E+02	8.25E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
3.04E+02	8.25E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
3.01E+02	8.23E+00	zinc finger protei	zinc finger protei	NM_145806	NM_145806
3.31E+02	8.37E+00	GIPC PDZ domai	GIPC PDZ domai	NM_133261	NM_133261
3.31E+02	8.37E+00	GIPC PDZ domai	GIPC PDZ domai	NM_133261	NM_133261
2.08E+02	7.70E+00	nuclear factor of	nuclear factor of	NM_020529	NM_020529
2.25E+02	7.81E+00	chromosome 3 o	fragile histidine t	NM_198463	NM_198463
2.25E+02	7.81E+00	chromosome 3 o	fragile histidine t	NM_198463	NM_198463
3.06E+02	8.26E+00	collagen, type V,	collagen, type V,	NM_000093	NM_000093
3.36E+02	8.39E+00	chloride channel	chloride channel	NM_001287,NM	NM_001287,NM_001114331
2.82E+02	8.14E+00	hypothetical pro	hypothetical pro	NR_002942	NR_002942

3.05E+02	8.25E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.05E+02	8.25E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.78E+02	8.12E+00	transmembrane	transmembrane	NM_001145303,	NM_001145303,NM_144686
2.78E+02	8.12E+00	transmembrane	transmembrane	NM_001145303,	NM_001145303,NM_144686
2.45E+02	7.94E+00	topoisomerase (I	pre-B lymphocyt	NM_003935	NM_003935
2.45E+02	7.94E+00	topoisomerase (I	pre-B lymphocyt	NM_003935	NM_003935
2.68E+02	8.06E+00	pericentrin	pericentrin	NM_006031	NM_006031
3.90E+02	8.61E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
3.90E+02	8.61E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
3.90E+02	8.61E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
2.47E+02	7.95E+00	agrin	agrin	NM_198576	NM_198576
2.47E+02	7.95E+00	agrin	agrin	NM_198576	NM_198576
2.47E+02	7.95E+00	agrin	agrin	NM_198576	NM_198576
2.47E+02	7.95E+00	agrin	agrin	NM_198576	NM_198576
2.77E+02	8.11E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
3.08E+02	8.27E+00	lipocalin 10	lipocalin 6	NM_001001712	NM_001001712
3.08E+02	8.27E+00	lipocalin 6	lipocalin 6	NM_198946	NM_198946
2.74E+02	8.10E+00	ankyrin 1, erythr	ankyrin 1, erythr	NM_001142446,	NM_001142446,NM_001142445,
3.10E+02	8.28E+00	TGF-beta activat	mannosyl (beta-	NM_153497,NM	NM_153497,NM_006116
2.69E+02	8.07E+00	ATP-binding cass	ATP-binding cass	NM_001089	NM_001089
2.69E+02	8.07E+00	ATP-binding cass	ATP-binding cass	NM_001089	NM_001089
2.69E+02	8.07E+00	ATP-binding cass	ATP-binding cass	NM_001089	NM_001089
2.88E+02	8.17E+00	latent transformi	latent transformi	NM_001130144,	NM_001130144,NM_021070
3.69E-03	-8.08E+00	ER degradation e	glutamate recept	NM_014674	NM_014674
3.69E-03	-8.08E+00	ER degradation e	glutamate recept	NM_014674	NM_014674
3.41E-03	-8.20E+00	syntaxin 2	RAN, member R	NM_001980,NM	NM_001980,NM_194356
3.41E-03	-8.20E+00	syntaxin 2	RAN, member R	NM_001980,NM	NM_001980,NM_194356
2.30E+02	7.85E+00	syntaphilin	syntaphilin	NM_014723	NM_014723
2.91E+02	8.19E+00	rhomboid 5 hom	rhomboid 5 hom	NM_001005498,	NM_001005498,NM_024599
2.64E+02	8.04E+00	ribosomal RNA p	ribosomal RNA p	NR_002184	NR_002184
2.64E+02	8.04E+00	ribosomal RNA p	ribosomal RNA p	NR_002184	NR_002184
3.19E+02	8.32E+00	TBC1 domain fa	TBC1 domain fa	NM_020705	NM_020705
3.19E+02	8.32E+00	TBC1 domain fa	TBC1 domain fa	NM_020705	NM_020705
3.16E+02	8.30E+00	transmembrane	KIAA0125	NM_025268	NM_025268
3.16E+02	8.30E+00	transmembrane	KIAA0125	NM_025268	NM_025268
2.30E+02	7.85E+00	zinc finger, SWI	nanos homolog	NM_023072	NM_023072
3.05E+02	8.25E+00	chromosome 20	chromosome 20	NM_199181	NM_199181
2.77E+02	8.11E+00	dihydrouridine s	fatty acid syntha	NM_022156	NM_022156
2.55E+02	8.00E+00	protein kinase C	protein kinase C	NM_020804	NM_020804
2.61E+02	8.03E+00	myosin, heavy c	myosin, heavy c	NM_001145809,	NM_001145809,NM_024729,NM_
2.61E+02	8.03E+00	myosin, heavy c	myosin, heavy c	NM_001145809,	NM_001145809,NM_024729,NM_
2.48E+02	7.95E+00	tight junction pr	tight junction pr	NM_201629,NM	NM_201629,NM_004817
2.48E+02	7.95E+00	tight junction pr	tight junction pr	NM_201629,NM	NM_201629,NM_004817
4.52E-03	-7.79E+00	BMS1 homolog,	ret proto-oncog	NM_014753	NM_014753
2.62E+02	8.03E+00	mucin 6, oligom	mucin 6, oligom	NM_005961	NM_005961
2.62E+02	8.03E+00	mucin 6, oligom	mucin 6, oligom	NM_005961	NM_005961
2.99E+02	8.22E+00	opioid receptor,	ATPase, H+ trans	NM_000912	NM_000912
2.99E+02	8.22E+00	opioid receptor,	ATPase, H+ trans	NM_000912	NM_000912
3.35E+02	8.39E+00	alkB, alkylation r	alkB, alkylation r	NM_017621	NM_017621
3.35E+02	8.39E+00	alkB, alkylation r	alkB, alkylation r	NM_017621	NM_017621
3.65E+02	8.51E+00	protein tyrosine	protein tyrosine	NM_002840,NM	NM_002840,NM_130440
3.65E+02	8.51E+00	protein tyrosine	protein tyrosine	NM_002840,NM	NM_002840,NM_130440
3.37E+02	8.40E+00	family with sequ	hippocampus ab	NM_017561	NM_017561
3.37E+02	8.40E+00	family with sequ	hippocampus ab	NM_017561	NM_017561
2.93E+02	8.20E+00	unc-51-like kinas	pseudouridylate	NM_003565	NM_003565
2.93E+02	8.20E+00	unc-51-like kinas	pseudouridylate	NM_003565	NM_003565
3.00E+02	8.23E+00	chromosome 19	BTB (POZ) domai	NM_152771	NM_152771
3.00E+02	8.23E+00	chromosome 19	BTB (POZ) domai	NM_152771	NM_152771

3.00E+02	8.23E+00	chromosome 19	BTB (POZ) domai	NM_152771	NM_152771
2.44E+02	7.93E+00	defensin, beta 1	zinc finger protei	NM_001037804	NM_001037804
2.44E+02	7.93E+00	defensin, beta 1	zinc finger protei	NM_001037804	NM_001037804
2.69E+02	8.07E+00	kringle containin	kringle containin	NM_024507,NM	NM_024507,NM_172229
4.64E-03	-7.75E+00	non-protein codi	non-protein codi	NR_002811	NR_002811
4.35E-03	-7.84E+00	dolichyl-diphosp	kinesin family m	NM_005216	NM_005216
2.66E+02	8.05E+00	aprataxin	DnaJ (Hsp40) ho	NM_175069,NM	NM_175069,NM_175073,NM_17
3.02E+02	8.24E+00	C2 calcium-depe	C2 calcium-depe	NM_001136263	NM_001136263
4.01E+02	8.65E+00	cholinergic rece	cholinergic rece	NM_000742	NM_000742
4.81E-03	-7.70E+00	KIAA1267	leucine rich repe	NM_015443	NM_015443
2.10E+02	7.71E+00	DAB2 interacting	DAB2 interacting	NM_138709	NM_138709
2.83E+02	8.14E+00	chromosome 16	family with sequ	NM_001040165,	NM_001040165,NM_001040160,
3.53E-03	-8.14E+00	zinc finger protei	transmembrane	NM_015069	NM_015069
3.53E-03	-8.14E+00	zinc finger protei	transmembrane	NM_015069	NM_015069
2.32E+02	7.86E+00	MAP/microtubul	MAP/microtubul	NM_031417	NM_031417
1.99E+02	7.64E+00	age-related mac	HtrA serine pepti	NM_001099667	NM_001099667
2.86E+02	8.16E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
2.86E+02	8.16E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
5.52E-03	-7.50E+00	Src homology 2	Src homology 2	NM_001010846	NM_001010846
3.27E-03	-8.26E+00	olfactory recept	olfactory recept	NM_001001964	NM_001001964
3.27E-03	-8.26E+00	olfactory recept	olfactory recept	NM_001001964	NM_001001964
4.13E-03	-7.92E+00	ATPase, class I, t	solute carrier fa	NM_024837	NM_024837
2.61E+02	8.03E+00	GNAS complex l	GNAS complex l	NM_016592	NM_016592
2.83E+02	8.14E+00	SRY (sex determi	hypothetical LO	NM_014587	NM_014587
3.11E+02	8.28E+00	peptide YY, 2 (se	pancreatic polyp	NR_003064	NR_003064
2.60E+02	8.02E+00	amino-terminal	amino-terminal	NM_198970,NM	NM_198970,NM_001130,NM_19
4.54E+02	8.83E+00	PEG3 antisense	MER1 repeat co	NR_023847	NR_023847
4.54E+02	8.83E+00	PEG3 antisense	MER1 repeat co	NR_023847	NR_023847
2.64E+02	8.04E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
2.76E+02	8.11E+00	tubulin folding c	tubulin folding c	NM_005993	NM_005993
3.99E-03	-7.97E+00	sarcoglycan, bet	spermatogenesis	NM_000232	NM_000232
4.32E-03	-7.86E+00	small nucleolar	LIM and SH3 pro	NR_002576	NR_002576
4.32E-03	-7.86E+00	small nucleolar	LIM and SH3 pro	NR_002576	NR_002576
2.44E+02	7.93E+00	protein tyrosine	protein tyrosine	NM_007079,NM	NM_007079,NM_032611
2.90E+02	8.18E+00	zinc finger protei	zinc finger protei	NM_178167	NM_178167
2.90E+02	8.18E+00	zinc finger protei	zinc finger protei	NM_178167	NM_178167
3.62E+02	8.50E+00	natural killer-tu	zinc finger and B	NM_005385	NM_005385
2.94E+02	8.20E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.94E+02	8.20E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.59E+02	8.02E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.59E+02	8.02E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.59E+02	8.02E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
2.03E+02	7.66E+00	strawberry notc	strawberry notc	NM_001100122,	NM_001100122,NM_014963
3.86E-03	-8.02E+00	thyrotropin-rele	thyrotropin-rele	NM_013381	NM_013381
4.70E-03	-7.73E+00	ADAM metallop	non-protein codi	NR_002224	NR_002224
2.76E+02	8.11E+00	protease, serine,	family with sequ	NM_183375	NM_183375
4.01E+02	8.65E+00	protein tyrosine	protein tyrosine	NM_133178,NM	NM_133178,NM_133177,NM_00
4.01E+02	8.65E+00	protein tyrosine	protein tyrosine	NM_133178,NM	NM_133178,NM_133177,NM_00
2.90E+02	8.18E+00	discs, large (Dros	discs, large (Dros	NM_004745	NM_004745
2.90E+02	8.18E+00	discs, large (Dros	discs, large (Dros	NM_004745	NM_004745
2.23E+02	7.80E+00	kinesin family m	kinesin family m	NM_015656	NM_015656
2.23E+02	7.80E+00	kinesin family m	kinesin family m	NM_015656	NM_015656
4.25E-03	-7.88E+00	ribosomal protei	ribosomal protei	NM_002948	NM_002948
4.25E-03	-7.88E+00	ribosomal protei	ribosomal protei	NM_002948	NM_002948
3.46E+02	8.43E+00	tyrosine hydroxy	achaete-scute co	NM_199293,NM	NM_199293,NM_199292,NM_00
2.81E+02	8.13E+00	septin 7	endonuclease/e	NM_001788,NM	NM_001788,NM_001011553
2.81E+02	8.13E+00	septin 7	endonuclease/e	NM_001788,NM	NM_001788,NM_001011553
3.21E-03	-8.29E+00	germ cell associa	chromosome 17	NM_031965	NM_031965

2.15E+02	7.75E+00	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
2.15E+02	7.75E+00	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
3.82E+02	8.58E+00	solute carrier or	solute carrier or	NM_016354	NM_016354
3.69E-03	-8.08E+00	small nuclear rib	lin-7 homolog B (	NM_003089	NM_003089
2.89E+02	8.17E+00	cytochrome b-5	cytochrome b-5	NM_001017917,	NM_001017917,NM_001017916,
3.30E+02	8.36E+00	small nucleolar R	small nucleolar R	NR_000013	NR_000013
3.30E+02	8.36E+00	small nucleolar R	small nucleolar R	NR_000013	NR_000013
2.30E+02	7.84E+00	neuronal pentra	chromobox hom	NM_014293	NM_014293
2.26E+02	7.82E+00	Ets2 repressor fa	capicua homolog	NM_006494	NM_006494
2.33E+02	7.87E+00	zinc finger CCCH-	interleukin 17C	NM_144604	NM_144604
2.63E+02	8.04E+00	salt-inducible kin	salt-inducible kin	NM_173354	NM_173354
2.63E+02	8.04E+00	salt-inducible kin	salt-inducible kin	NM_173354	NM_173354
2.84E+02	8.15E+00	nuclear factor of	nuclear factor of	NM_001001716,	NM_001001716,NM_002503
2.84E+02	8.15E+00	nuclear factor of	nuclear factor of	NM_001001716,	NM_001001716,NM_002503
3.39E+02	8.41E+00	diacylglycerol ki	diacylglycerol ki	NM_001105540	NM_001105540
2.64E+02	8.04E+00	collagen, type IX,	collagen, type IX,	NM_001853	NM_001853
3.46E+02	8.43E+00	protein tyrosine	tyrosinase-relate	NM_002839,NM	NM_002839,NM_130391,NM_13
3.46E+02	8.43E+00	protein tyrosine	tyrosinase-relate	NM_002839,NM	NM_002839,NM_130391,NM_13
2.44E+02	7.93E+00	A kinase (PRKA)	widely interspace	NM_014371	NM_014371
4.09E-03	-7.93E+00	ZFAT antisense R	hypothetical LO	NR_002438	NR_002438
4.09E-03	-7.93E+00	ZFAT antisense R	hypothetical LO	NR_002438	NR_002438
2.84E+02	8.15E+00	PTK6 protein tyr	PTK6 protein tyr	NM_005975	NM_005975
3.77E-03	-8.05E+00	protocadherin 1	ring finger protei	NM_016580	NM_016580
3.77E-03	-8.05E+00	protocadherin 1	ring finger protei	NM_016580	NM_016580
3.07E+02	8.26E+00	leucine rich repe	leucine rich repe	NM_020862	NM_020862
2.36E+02	7.88E+00	protocadherin 9	kelch-like 1 (Dro	NM_020403,NM	NM_020403,NM_203487
2.36E+02	7.88E+00	protocadherin 9	kelch-like 1 (Dro	NM_020403,NM	NM_020403,NM_203487
1.98E+02	7.63E+00	midnolin	chromosome 19	NM_177401	NM_177401
2.93E+02	8.20E+00	solute carrier fan	solute carrier fan	NM_018484	NM_018484
3.66E+02	8.51E+00	small nucleolar R	small nucleolar R	NR_002326	NR_002326
2.72E+02	8.09E+00	EFR3 homolog B	EFR3 homolog B	NM_014971	NM_014971
2.72E+02	8.09E+00	EFR3 homolog B	EFR3 homolog B	NM_014971	NM_014971
3.07E+02	8.26E+00	CCCTC-binding f	phosphoenolpyr	NM_080618	NM_080618
3.07E+02	8.26E+00	CCCTC-binding f	phosphoenolpyr	NM_080618	NM_080618
3.07E+02	8.26E+00	CCCTC-binding f	phosphoenolpyr	NM_080618	NM_080618
3.07E+02	8.26E+00	CCCTC-binding f	phosphoenolpyr	NM_080618	NM_080618
3.07E+02	8.26E+00	CCCTC-binding f	phosphoenolpyr	NM_080618	NM_080618
2.34E+02	7.87E+00	ras homolog gen	RAB4A, member	NM_021205	NM_021205
2.76E+02	8.11E+00	integrin beta 1 bi	integrin beta 1 bi	NM_170678	NM_170678
3.52E-03	-8.15E+00	glutamine--fruct	NFU1 iron-sulfur	NM_002056	NM_002056
3.52E-03	-8.15E+00	glutamine--fruct	NFU1 iron-sulfur	NM_002056	NM_002056
4.22E-03	-7.89E+00	chromosome 12	pleckstrin homol	NM_001037671	NM_001037671
4.22E-03	-7.89E+00	pleckstrin homol	pleckstrin homol	NM_001004330	NM_001004330
2.78E+02	8.12E+00	chromosome 10	chromosome 10	NM_017609	NM_017609
2.15E+02	7.75E+00	uronyl-2-sulfotra	TGF-beta activat	NM_005715	NM_005715
2.50E+02	7.96E+00	cadherin 4, type	TAF4 RNA polym	NM_001794	NM_001794
2.19E+02	7.78E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.19E+02	7.78E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.38E+02	7.90E+00	Smith-Magenis s	Smith-Magenis s	NM_148886	NM_148886
3.94E-03	-7.99E+00	splA/ryanodine r	solute carrier fan	NM_025106	NM_025106
2.16E+02	7.76E+00	inositol-3-phosp	elongation facto	NM_016368	NM_016368
2.52E+02	7.98E+00	tubulin polymeri	zinc finger, DHH	NM_007030	NM_007030
4.52E-03	-7.79E+00	chromosome 21	neural cell adhes	NR_024090	NR_024090
4.52E-03	-7.79E+00	chromosome 21	neural cell adhes	NR_024090	NR_024090
2.63E+02	8.04E+00	NAD synthetase	keratin associate	NM_018161	NM_018161
5.11E-03	-7.61E+00	family with sequ	EPH receptor A2	NM_182623	NM_182623
2.30E+02	7.84E+00	chromosome 20	chromosome 20	NM_199181	NM_199181
2.30E+02	7.84E+00	chromosome 20	chromosome 20	NM_199181	NM_199181

2.15E+02	7.75E+00	DIRAS family, GT	DIRAS family, GT	NM_145173	NM_145173
2.15E+02	7.75E+00	DIRAS family, GT	DIRAS family, GT	NM_145173	NM_145173
4.05E-03	-7.95E+00	Bartter syndrom	proprotein conve	NM_057176	NM_057176
4.05E-03	-7.95E+00	Bartter syndrom	proprotein conve	NM_057176	NM_057176
2.69E+02	8.07E+00	complement con	STEAP family me	NM_182528	NM_182528
4.15E-03	-7.91E+00	protein tyrosine	signal transducin	NM_014241	NM_014241
2.34E+02	7.87E+00	sperm associate	phosphatidylinos	NM_012443,NM	NM_012443,NM_172242
2.10E+02	7.72E+00	p21 protein (Cdc	p21 protein (Cdc	NM_001014834,	NM_001014834,NM_001014832,N
2.68E+02	8.06E+00	abhydrolase dom	chromosome 3 o	NM_016006	NM_016006
2.68E+02	8.06E+00	abhydrolase dom	chromosome 3 o	NM_016006	NM_016006
2.84E+02	8.15E+00	ribosomal protei	connector enhan	NM_004586	NM_004586
2.37E+02	7.89E+00	E2F transcription	E2F transcription	NM_005225	NM_005225
3.07E+02	8.26E+00	hypothetical LOC	transmembrane	NR_024473	NR_024473
3.19E+02	8.32E+00	family with sequ	family with sequ	NM_198488	NM_198488
2.75E+02	8.10E+00	hypothetical LOC	splicing factor, ar	NR_026670	NR_026670
2.75E+02	8.10E+00	hypothetical LOC	splicing factor, ar	NR_026670	NR_026670
4.85E-03	-7.69E+00	von Willebrand f	CD9 molecule	NM_000552	NM_000552
2.64E+02	8.04E+00	phosphatidylinos	phosphatidylinos	NM_004910,NM	NM_004910,NM_001130848
2.64E+02	8.04E+00	phosphatidylinos	phosphatidylinos	NM_004910,NM	NM_004910,NM_001130848
2.64E+02	8.04E+00	phosphatidylinos	phosphatidylinos	NM_004910,NM	NM_004910,NM_001130848
4.88E-03	-7.68E+00	LIM domain bind	quinoid dihydrop	NM_001130834,	NM_001130834,NM_001290
3.81E-03	-8.04E+00	chromosome 9 o	carbonic anhydra	NM_032818	NM_032818
2.70E+02	8.08E+00	deleted in azoos	deleted in azoos	NM_001351	NM_001351
2.74E+02	8.10E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.00E+02	8.23E+00	nuclear prelamin	mesothelin	NM_022493	NM_022493
2.42E+02	7.92E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
4.47E-03	-7.81E+00	phosphopantoth	phosphopantoth	NM_001077447,	NM_001077447,NM_024664
3.47E+02	8.44E+00	GRAM domain co	GRAM domain co	NM_020895,NM	NM_020895,NM_001136199
3.47E+02	8.44E+00	GRAM domain co	GRAM domain co	NM_020895,NM	NM_020895,NM_001136199
2.04E+00	1.03E+00	null	POTE ankyrin doi	null	null
2.04E+00	1.03E+00	null	POTE ankyrin doi	null	null
2.27E+02	7.82E+00	glucokinase (hex	glucokinase (hex	NM_000162,NM	NM_000162,NM_033508,NM_033
2.30E+02	7.85E+00	methyltransferas	methyltransferas	NM_024086	NM_024086
2.58E+02	8.01E+00	family with sequ	family with sequ	NR_024019,NM_	NR_024019,NM_019057
2.83E+02	8.14E+00	H19, imprinted n	insulin-like growt	NR_002196	NR_002196
2.83E+02	8.14E+00	H19, imprinted n	insulin-like growt	NR_002196	NR_002196
3.93E-03	-7.99E+00	erythrocyte mem	chromosome 20	NM_012156	NM_012156
2.51E+02	7.97E+00	eukaryotic transl	eukaryotic transl	NM_001958	NM_001958
2.86E+02	8.16E+00	forkhead box F2	forkhead box C1	NM_001452	NM_001452
2.86E+02	8.16E+00	forkhead box F2	forkhead box C1	NM_001452	NM_001452
4.68E-03	-7.74E+00	TATA box bindin	adenosine deami	NM_139353,NM	NM_139353,NM_005679
4.68E-03	-7.74E+00	TATA box bindin	adenosine deami	NM_139353,NM	NM_139353,NM_005679
3.14E-03	-8.32E+00	zinc finger protei	zinc finger protei	NM_030613	NM_030613
3.14E-03	-8.32E+00	zinc finger protei	zinc finger protei	NM_030613	NM_030613
3.94E+02	8.62E+00	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
3.53E+02	8.46E+00	G protein-couple	hypothetical LOC	NM_198827	NM_198827
3.53E+02	8.46E+00	G protein-couple	hypothetical LOC	NM_198827	NM_198827
2.34E+02	7.87E+00	PR domain conta	PR domain conta	NM_021619	NM_021619
2.34E+02	7.87E+00	PR domain conta	PR domain conta	NM_021619	NM_021619
2.50E+02	7.96E+00	ankyrin repeat d	F-box protein, he	NM_001009942,	NM_001009942,NM_001009943,N
4.11E-03	-7.93E+00	caspase 10, apop	caspase 8, apopt	NM_001230,NM	NM_001230,NM_032977,NM_032
2.74E+02	8.10E+00	postmeiotic segr	GATS protein-like	NM_174930	NM_174930
3.54E+02	8.47E+00	apolipoprotein C	apolipoprotein C	NM_000483	NM_000483
2.60E+02	8.02E+00	myosin IG	myosin IG	NM_033054	NM_033054
3.18E+02	8.31E+00	vav 2 guanine nu	vav 2 guanine nu	NM_001134398,	NM_001134398,NM_003371
2.92E+02	8.19E+00	transmembrane	transmembrane	NM_020665	NM_020665
2.92E+02	8.19E+00	transmembrane	transmembrane	NM_020665	NM_020665
3.06E+02	8.26E+00	MAP kinase inter	MAP kinase inter	NM_017572,NM	NM_017572,NM_199054

2.42E+02	7.92E+00	ADAM metallope	ADAM metallope	NM_001109	NM_001109
2.42E+02	7.92E+00	ADAM metallope	ADAM metallope	NM_001109	NM_001109
2.23E+02	7.80E+00	zinc finger protei	zinc finger protei	NR_003952	NR_003952
4.30E-03	-7.86E+00	olfactory recepto	chromosome 1 o	NM_198074	NM_198074
4.30E-03	-7.86E+00	olfactory recepto	chromosome 1 o	NM_198074	NM_198074
3.71E-03	-8.07E+00	translocase of in	translocase of in	NM_005834	NM_005834
3.71E-03	-8.07E+00	translocase of in	translocase of in	NM_005834	NM_005834
2.32E+02	7.86E+00	lysophosphatidyl	lysophosphatidyl	NM_024830	NM_024830
2.32E+02	7.86E+00	lysophosphatidyl	lysophosphatidyl	NM_024830	NM_024830
2.41E+02	7.91E+00	protein phospha	protein phospha	NM_001145115	NM_001145115
2.41E+02	7.91E+00	protein phospha	protein phospha	NM_001145115	NM_001145115
2.66E+02	8.05E+00	family with sequ	family with sequ	NM_001130111,	NM_001130111,NM_031213
2.53E+02	7.98E+00	AHNAK nucleopr	AHNAK nucleopr	NM_024060	NM_024060
3.77E-03	-8.05E+00	RAB GTPase activ	calcyclin binding	NM_001035230	NM_001035230
3.77E-03	-8.05E+00	RAB GTPase activ	calcyclin binding	NM_001035230	NM_001035230
3.90E+02	8.61E+00	galactosamine (N	galactosamine (N	NM_000512	NM_000512
3.58E-03	-8.13E+00	small nucleolar R	lymphocyte trans	NR_003019	NR_003019
3.58E-03	-8.13E+00	lymphocyte trans	lymphocyte trans	NM_001136190,	NM_001136190,NM_017773
2.36E+02	7.88E+00	MAX dimerizatio	aspartic peptidas	NM_002357	NM_002357
2.36E+02	7.88E+00	MAX dimerizatio	aspartic peptidas	NM_002357	NM_002357
4.90E-03	-7.67E+00	Rho GTPase activ	secretogranin V (	NM_199357,NM	NM_199357,NM_014783
2.08E+02	7.70E+00	multiple C2 dom	multiple C2 dom	NM_024717,NM	NM_024717,NM_001002796
3.28E+02	8.36E+00	myocilin, trabecu	vesicle-associate	NM_000261	NM_000261
3.28E+02	8.36E+00	myocilin, trabecu	vesicle-associate	NM_000261	NM_000261
2.10E+02	7.71E+00	paired box 6	reticulocalbin 1,	NM_001604,NM	NM_001604,NM_000280,NM_001
2.36E+02	7.88E+00	vacuolar protein	vacuolar protein	NM_024667	NM_024667
3.68E-03	-8.09E+00	phosphoribosyl p	solute carrier fan	NM_002767	NM_002767
5.11E-03	-7.61E+00	small nucleolar R	zinc finger protei	NR_002962	NR_002962
2.52E+02	7.98E+00	tubulin, beta pol	FSHD region gen	NM_020040	NM_020040
3.26E+02	8.35E+00	AE binding prote	AE binding prote	NM_001129	NM_001129
3.26E+02	8.35E+00	AE binding prote	AE binding prote	NM_001129	NM_001129
2.60E+02	8.02E+00	family with sequ	family with sequ	NM_174951	NM_174951
4.33E-03	-7.85E+00	hydroxypyruvate	protein tyrosine	NM_031207	NM_031207
4.33E-03	-7.85E+00	hydroxypyruvate	protein tyrosine	NM_031207	NM_031207
2.54E+02	7.99E+00	golgin A8 family,	p21-activated kir	NR_027411	NR_027411
3.24E+02	8.34E+00	luteinizing horm	chorionic gonad	NM_000894	NM_000894
2.80E+02	8.13E+00	potassium voltag	potassium voltag	NM_003636,NM	NM_003636,NM_172130
2.80E+02	8.13E+00	potassium voltag	potassium voltag	NM_003636,NM	NM_003636,NM_172130
2.95E+02	8.21E+00	tumor necrosis f	tumor necrosis f	NM_003327	NM_003327
2.95E+02	8.21E+00	tumor necrosis f	tumor necrosis f	NM_003327	NM_003327
3.95E-03	-7.98E+00	high density lipo	septin 2	NM_203346,NM	NM_203346,NM_005336
4.06E+02	8.66E+00	chromosome 19	polypyrimidine t	NM_173481	NM_173481
4.81E-03	-7.70E+00	zinc finger protei	HFM1, ATP-depe	NM_016620,NM	NM_016620,NM_032186,NM_201
1.66E+00	7.29E-01	plexin B2	plexin B2	NM_012401	NM_012401
4.66E-03	-7.75E+00	signal recognitio	Bcl2 modifying fa	NM_003134	NM_003134
4.66E-03	-7.75E+00	signal recognitio	Bcl2 modifying fa	NM_003134	NM_003134
3.45E+02	8.43E+00	ADP-ribosylation	collagen, type XX	NM_018209,NM	NM_018209,NM_175609
3.45E+02	8.43E+00	ADP-ribosylation	collagen, type XX	NM_018209,NM	NM_018209,NM_175609
3.27E+02	8.35E+00	immunoglobulin	immunoglobulin	NM_201526	NM_201526
2.47E+02	7.95E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.31E-03	-8.24E+00	prune homolog 2	prune homolog 2	NM_015225	NM_015225
3.31E-03	-8.24E+00	prune homolog 2	prune homolog 2	NM_015225	NM_015225
2.79E+02	8.12E+00	asialoglycoprotei	asialoglycoprotei	NM_001671	NM_001671
2.68E+02	8.06E+00	KIAA1671	KIAA1671	NM_001145206	NM_001145206
2.68E+02	8.06E+00	KIAA1671	KIAA1671	NM_001145206	NM_001145206
2.11E+02	7.72E+00	tudor domain co	tropomodulin 1	NM_014290	NM_014290
2.42E+02	7.92E+00	small nucleolar R	RAS-like, family 1	NR_002575	NR_002575
3.30E+02	8.36E+00	collagen, type IV,	collagen, type IV,	NM_001846	NM_001846

2.90E+02	8.18E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
2.61E+02	8.03E+00	SET and MYND d	transcription fact	NM_022743	NM_022743
3.63E+02	8.50E+00	zinc finger protei	B-cell CLL/lymph	NM_001080417	NM_001080417
3.63E+02	8.50E+00	zinc finger protei	B-cell CLL/lymph	NM_001080417	NM_001080417
4.66E-03	-7.75E+00	melanocortin 3 r	chromosome 20	NM_019888	NM_019888
3.78E+02	8.56E+00	intraflagellar trar	intraflagellar trar	NM_014714	NM_014714
3.78E+02	8.56E+00	transmembrane	transmembrane	NM_024600	NM_024600
2.35E+02	7.88E+00	notch 1	notch 1	NM_017617	NM_017617
2.35E+02	7.88E+00	notch 1	notch 1	NM_017617	NM_017617
2.77E+02	8.11E+00	hypothetical LOC	hypothetical LOC	NR_027069	NR_027069
2.77E+02	8.11E+00	hypothetical LOC	orthodenticle ho	NR_027069	NR_027069
2.48E+02	7.95E+00	breast cancer est	mitogen-activate	NR_015445	NR_015445
2.43E+02	7.92E+00	glutamate recept	olfactory recepto	NR_027044	NR_027044
2.74E+02	8.10E+00	ferritin, heavy pc	inner centromere	NM_002032	NM_002032
3.43E-03	-8.19E+00	POM121 membr	transmembrane	NR_024592	NR_024592
3.40E-03	-8.20E+00	Rho guanine nuc	Rho guanine nuc	NM_003899	NM_003899
2.56E+02	8.00E+00	solute carrier fan	solute carrier fan	NM_001003841	NM_001003841
4.22E-03	-7.89E+00	lysine (K)-specific	actin pseudogene	NM_006618	NM_006618
2.92E+02	8.19E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
2.92E+02	8.19E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
3.27E+02	8.35E+00	HGF activator	docking protein	NM_001528	NM_001528
3.27E+02	8.35E+00	HGF activator	docking protein	NM_001528	NM_001528
3.80E+02	8.57E+00	heat shock 70kD	KIAA1598	NM_025015	NM_025015
4.74E-03	-7.72E+00	cancer/testis ant	thrombospondin	NM_001102658	NM_001102658
4.74E-03	-7.72E+00	cancer/testis ant	thrombospondin	NM_001102658	NM_001102658
2.37E+02	7.89E+00	sema domain, tra	sema domain, tra	NM_032108	NM_032108
3.98E-03	-7.97E+00	transcription elo	protein phospha	NM_174937	NM_174937
3.98E-03	-7.97E+00	transcription elo	protein phospha	NM_174937	NM_174937
2.34E+02	7.87E+00	antigen p97 (mel	antigen p97 (mel	NM_033316	NM_033316
3.57E+02	8.48E+00	macrophage eryt	macrophage eryt	NM_005882,NM	NM_005882,NM_001017405
3.40E+02	8.41E+00	cleavage and pol	cleavage and pol	NM_013291	NM_013291
4.40E-03	-7.83E+00	zinc finger protei	zinc finger protei	NM_014480	NM_014480
4.40E-03	-7.83E+00	zinc finger protei	zinc finger protei	NM_014480	NM_014480
4.62E-03	-7.76E+00	transmembrane	transmembrane	NM_032405	NM_032405
3.90E+02	8.61E+00	Rho GTPase activ	laminin, alpha 1	NM_030672,NM	NM_030672,NM_001010000
3.10E+02	8.28E+00	small nuclear ribo	small nuclear ribo	NM_003097,NM	NM_003097,NM_005678
2.78E+02	8.12E+00	NLR family, pyrin	NLR family, pyrin	NM_144687,NM	NM_144687,NM_033297
1.18E+00	2.40E-01	coxsackie virus a	POTE ankyrin dor	NR_024387	NR_024387
1.18E+00	2.40E-01	coxsackie virus a	POTE ankyrin dor	NR_024387	NR_024387
2.46E+02	7.94E+00	transmembrane	transmembrane	NM_001146336	NM_001146336
2.61E+02	8.03E+00	GDP-mannose 4,	GDP-mannose 4,	NM_001500	NM_001500
2.30E+02	7.85E+00	replication initiat	replication initiat	NM_014374	NM_014374
2.30E+02	7.85E+00	replication initiat	replication initiat	NM_014374	NM_014374
2.77E+02	8.11E+00	potassium voltag	potassium voltag	NM_002234	NM_002234
2.55E+02	8.00E+00	carbohydrate (N-	carbohydrate (N-	NM_022467	NM_022467
3.14E-03	-8.32E+00	piggyBac transpo	choline O-acetylt	NM_170753	NM_170753
2.57E+02	8.01E+00	protein tyrosine	SEH1-like (S. cere	NM_002828	NM_002828
3.33E+02	8.38E+00	small VCP/p97-ir	leucine zipper pr	NM_148893	NM_148893
4.33E-03	-7.85E+00	sphingosine-1-ph	sphingosine-1-ph	NM_005226	NM_005226
2.76E+02	8.11E+00	RAB40B, membe	RAB40B, membe	NM_006822	NM_006822
2.76E+02	8.11E+00	RAB40B, membe	RAB40B, membe	NM_006822	NM_006822
3.38E-03	-8.21E+00	spermatogenesis	chromosome 15	NM_024063	NM_024063
2.85E-03	-8.46E+00	RWD domain cor	ubiquitin specific	NM_016940	NM_016940
2.18E+02	7.77E+00	inhibitor of DNA	kinase D-interact	NM_002166	NM_002166
2.18E+02	7.77E+00	inhibitor of DNA	kinase D-interact	NM_002166	NM_002166
3.79E-03	-8.04E+00	ST8 alpha-N-acet	solute carrier org	NM_175052	NM_175052
3.84E-03	-8.03E+00	nudix (nucleoside	nudix (nucleoside	NR_002949	NR_002949
5.42E-03	-7.53E+00	solute carrier fan	SP110 nuclear bo	NM_152527	NM_152527

2.10E+02	7.71E+00	neuropilin (NRP)	neuropilin (NRP)	NM_018092	NM_018092
2.80E+02	8.13E+00	adenylosuccinate	SIVA1, apoptosis	NM_199165	NM_199165
2.80E+02	8.13E+00	adenylosuccinate	SIVA1, apoptosis	NM_199165	NM_199165
2.68E+02	8.06E+00	neuroligin 4, Y-lir	non-protein codi	NM_014893	NM_014893
2.45E+02	7.94E+00	UDP-GlcNAc:beta	meteorin, glial ce	NM_001009905	NM_001009905
2.45E+02	7.94E+00	UDP-GlcNAc:beta	meteorin, glial ce	NM_001009905	NM_001009905
3.11E-03	-8.33E+00	sex comb on mid	endothelin 2	NM_012236	NM_012236
4.53E-03	-7.78E+00	phenylalanyl-tRN	calreticulin	NM_004461	NM_004461
4.53E-03	-7.78E+00	phenylalanyl-tRN	calreticulin	NM_004461	NM_004461
3.56E-03	-8.14E+00	doublesex and m	doublesex and m	NM_021951	NM_021951
3.56E-03	-8.14E+00	doublesex and m	doublesex and m	NM_021951	NM_021951
2.60E+02	8.02E+00	strawberry notch	serine/threonine	NM_001100122,	NM_001100122,NM_014963
2.60E+02	8.02E+00	strawberry notch	serine/threonine	NM_001100122,	NM_001100122,NM_014963
2.58E+02	8.01E+00	Src-like-adaptor :	Src-like-adaptor :	NM_175077,NM	NM_175077,NM_032214
3.95E-03	-7.98E+00	GSG1-like	exportin 6	NM_144675,NM	NM_144675,NM_001109763
3.95E-03	-7.98E+00	GSG1-like	exportin 6	NM_144675,NM	NM_144675,NM_001109763
4.40E-03	-7.83E+00	6-phosphofructo	APEX nuclease (a	NM_002625	NM_002625
2.34E+02	7.87E+00	ADAM metallope	tubulin, gamma (	NM_001109	NM_001109
4.61E-03	-7.76E+00	immunoglobulin-	plakophilin 1 (ect	NM_178275	NM_178275
4.59E-03	-7.77E+00	chromosome 6 o	methylmalonyl C	NM_001013732	NM_001013732
4.59E-03	-7.77E+00	chromosome 6 o	methylmalonyl C	NM_001013732	NM_001013732
4.35E-03	-7.84E+00	RAS-like, family 1	general transcrip	NM_206827	NM_206827
2.22E+02	7.79E+00	olfactory recepto	hypothetical LOC	NM_001004698	NM_001004698
2.22E+02	7.79E+00	olfactory recepto	hypothetical LOC	NM_001004698	NM_001004698
3.13E+02	8.29E+00	aldehyde dehydr	aldehyde dehydr	NM_000694,NM	NM_000694,NM_001030010
2.48E+02	7.95E+00	polypyrimidine tr	polypyrimidine tr	NM_002819,NM	NM_002819,NM_031990,NM_031
2.48E+02	7.95E+00	polypyrimidine tr	polypyrimidine tr	NM_002819,NM	NM_002819,NM_031990,NM_031
4.02E-03	-7.96E+00	myogenic factor	myogenic factor	NM_002469	NM_002469
2.68E+02	8.06E+00	testis-specific tra	testis-specific tra	NR_001539	NR_001539
3.81E-03	-8.04E+00	enolase 1, (alpha	carbonic anhydra	NM_001428	NM_001428
3.81E-03	-8.04E+00	enolase 1, (alpha	carbonic anhydra	NM_001428	NM_001428
2.35E+02	7.88E+00	CXXC finger 5	pleckstrin and Se	NM_016463	NM_016463
2.60E+02	8.02E+00	mex-3 homolog I	mex-3 homolog I	NM_203304	NM_203304
4.29E-03	-7.87E+00	GRB2-related ada	GRB2-related ada	NM_006613	NM_006613
4.29E-03	-7.87E+00	GRB2-related ada	GRB2-related ada	NM_006613	NM_006613
3.09E+02	8.27E+00	non-protein codi	collagen, type XV	NR_027498,NM_	NR_027498,NM_199175
3.09E+02	8.27E+00	non-protein codi	collagen, type XV	NR_027498,NM_	NR_027498,NM_199175
3.09E+02	8.27E+00	non-protein codi	collagen, type XV	NR_027498,NM_	NR_027498,NM_199175
2.83E+02	8.14E+00	mitogen-activate	plexin B2	NM_002751	NM_002751
2.83E+02	8.14E+00	plexin B2	plexin B2	NM_012401	NM_012401
4.59E-03	-7.77E+00	tumor protein D5	DnaJ (Hsp40) hor	NM_199363,NM	NM_199363,NM_199362,NM_199
2.99E+02	8.22E+00	casein kinase 1, g	casein kinase 1, g	NM_001319	NM_001319
2.99E+02	8.22E+00	casein kinase 1, g	casein kinase 1, g	NM_001319	NM_001319
2.91E+02	8.19E+00	family with sequ	family with sequ	NM_205849	NM_205849
3.08E+02	8.27E+00	snail homolog 3 (	ring finger protei	NM_178310	NM_178310
3.06E+02	8.26E+00	bromodomain cc	bromodomain cc	NM_014577	NM_014577
4.16E-03	-7.91E+00	thyrotropin-relea	asparagine-linke	NM_007117	NM_007117
4.16E-03	-7.91E+00	asparagine-linke	asparagine-linke	NM_001136152	NM_001136152
2.88E+02	8.17E+00	solute carrier fan	solute carrier fan	NM_005629,NM	NM_005629,NM_001142805
3.05E+02	8.25E+00	mannosyl (alpha-	mannosyl (alpha-	NM_198955	NM_198955
3.05E+02	8.25E+00	mannosyl (alpha-	mannosyl (alpha-	NM_198955	NM_198955
3.18E+02	8.31E+00	myosin XVA	myosin XVA	NM_016239	NM_016239
3.18E+02	8.31E+00	myosin XVA	myosin XVA	NM_016239	NM_016239
2.15E+02	7.75E+00	zinc finger and B	zinc finger and B	NM_181842	NM_181842
2.15E+02	7.75E+00	zinc finger and B	zinc finger and B	NM_181842	NM_181842
2.65E+02	8.05E+00	zinc finger protei	zinc finger protei	NR_003952	NR_003952
2.07E+02	7.69E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
4.38E-03	-7.83E+00	zinc finger protei	glioma tumor su	NM_001101419	NM_001101419

3.46E-03	-8.17E+00	family with sequ	ankyrin repeat d	NR_027422	NR_027422
3.33E+02	8.38E+00	transmembrane	KIAA0125	NM_025268	NM_025268
3.64E-03	-8.10E+00	thiosulfate sulfur	upstream transcr	NM_001113205,	NM_001113205,NM_001113206,N
2.94E+02	8.20E+00	integrator compl	integrator compl	NR_027392	NR_027392
2.44E+02	7.93E+00	transmembrane	KIAA0125	NM_025268	NM_025268
2.44E+02	7.93E+00	transmembrane	KIAA0125	NM_025268	NM_025268
3.99E-03	-7.97E+00	adaptor-related	secretory carrier	NM_003664	NM_003664
3.99E-03	-7.97E+00	adaptor-related	secretory carrier	NM_003664	NM_003664
3.15E-03	-8.31E+00	solute carrier fan	centrosomal pro	NM_003038	NM_003038
3.15E-03	-8.31E+00	solute carrier fan	centrosomal pro	NM_003038	NM_003038
3.06E+02	8.26E+00	paired-like home	paired-like home	NM_153426,NM	NM_153426,NM_153427,NM_000
3.06E+02	8.26E+00	paired-like home	paired-like home	NM_153426,NM	NM_153426,NM_153427,NM_000
3.06E+02	8.26E+00	paired-like home	paired-like home	NM_153426,NM	NM_153426,NM_153427,NM_000
3.06E+02	8.26E+00	aquaporin 12B	aquaporin 12A	NM_001102467	NM_001102467
2.10E+02	7.72E+00	G protein-couple	G protein-couple	NM_001083909	NM_001083909
2.82E+02	8.14E+00	signal-induced pr	signal-induced pr	NM_153253	NM_153253
4.59E-03	-7.77E+00	N-acylsphingosin	N-acetyltransfera	NM_001127505,	NM_001127505,NM_004315,NM_
3.73E-03	-8.07E+00	LIM and senesce	LIM and senesce	NM_033514	NM_033514
4.01E+02	8.65E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
3.14E+02	8.30E+00	BTB (POZ) domai	BTB (POZ) domai	NM_032444	NM_032444
3.46E+02	8.43E+00	similar to hCG19	similar to hCG19	NR_026913	NR_026913
2.16E+02	7.76E+00	dihydrouridine sy	neurturin	NM_020175	NM_020175
2.98E+02	8.22E+00	glutamate recept	glutamate recept	NM_138690	NM_138690
2.91E+02	8.19E+00	hect domain and	makorin ring fing	NR_002824	NR_002824
2.50E+02	7.96E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
2.50E+02	7.96E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
5.00E-03	-7.64E+00	chromosome 13	SRY (sex determi	NM_152324	NM_152324
5.00E-03	-7.64E+00	chromosome 13	SRY (sex determi	NM_152324	NM_152324
2.22E+02	7.79E+00	fasciculation and	vitrin	NM_001042548,	NM_001042548,NM_005102
2.22E+02	7.79E+00	fasciculation and	vitrin	NM_001042548,	NM_001042548,NM_005102
4.07E+02	8.67E+00	null	POTE ankyrin do	null	null
2.15E+02	7.75E+00	lipid phosphate p	lipid phosphate p	NM_024888	NM_024888
2.61E+02	8.03E+00	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
2.96E+02	8.21E+00	transcription fac	transcription fac	NM_014972	NM_014972
3.28E+02	8.36E+00	ADAMTS-like 5	polo-like kinase 5	NM_213604	NM_213604
2.82E+02	8.14E+00	NK2 homeobox 1	NK2 homeobox 8	NM_003317,NM	NM_003317,NM_001079668
2.82E+02	8.14E+00	NK2 homeobox 1	NK2 homeobox 8	NM_003317,NM	NM_003317,NM_001079668
3.50E+02	8.45E+00	proprotein conve	proprotein conve	NM_017573	NM_017573
2.08E+02	7.70E+00	matrix metallope	matrix metallope	NM_147191	NM_147191
4.57E-03	-7.77E+00	pleckstrin homol	leucine rich repe	NM_014798	NM_014798
3.27E+02	8.35E+00	tetratricopeptide	tetratricopeptide	NM_016030	NM_016030
3.27E+02	8.35E+00	tetratricopeptide	tetratricopeptide	NM_016030	NM_016030
2.25E+02	7.81E+00	Zic family memb	propionyl CoA ca	NM_007129	NM_007129
2.72E+02	8.09E+00	olfactory recept	folate hydrolase	NM_001005512	NM_001005512
2.72E+02	8.09E+00	olfactory recept	folate hydrolase	NM_001005512	NM_001005512
4.30E-03	-7.86E+00	phospholipid tra	PDX1 C-terminal	NM_182676,NM	NM_182676,NM_006227
2.74E+02	8.10E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.40E-03	-8.20E+00	RUN and FYVE d	chemokine (C-X-	NM_198483	NM_198483
3.40E-03	-8.20E+00	chemokine (C-X-	chemokine (C-X-	NM_001557	NM_001557
3.25E-03	-8.27E+00	BCL6 corepresso	BCL6 corepresso	NM_001123383,	NM_001123383,NM_001123384,N
3.25E-03	-8.27E+00	BCL6 corepresso	BCL6 corepresso	NM_001123383,	NM_001123383,NM_001123384,N
5.15E-03	-7.60E+00	leucine-rich repe	leucine-rich repe	NM_015613	NM_015613
2.42E+02	7.92E+00	down-regulator	formin binding p	NM_001938	NM_001938
3.19E+02	8.32E+00	olfactory recept	olfactory recept	NM_001005484	NM_001005484
3.19E+02	8.32E+00	olfactory recept	olfactory recept	NM_001005484	NM_001005484
3.19E+02	8.32E+00	olfactory recept	olfactory recept	NM_001005484	NM_001005484
3.38E-03	-8.21E+00	neurotrimin	neurotrimin	NM_001048209	NM_001048209
3.38E-03	-8.21E+00	neurotrimin	neurotrimin	NM_001048209	NM_001048209

2.82E+02	8.14E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
2.82E+02	8.14E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
3.48E-03	-8.17E+00	proenkephalin	inositol monoph	NM_001135690,	NM_001135690,NM_006211
3.48E-03	-8.17E+00	proenkephalin	inositol monoph	NM_001135690,	NM_001135690,NM_006211
4.13E-03	-7.92E+00	N-myristoyltrans	N-myristoyltrans	NM_021079	NM_021079
2.46E+02	7.94E+00	Rho-related BTB	Rho-related BTB	NR_024555,NR_	NR_024555,NR_024554,NR_0245
2.99E+02	8.22E+00	uroplakin 1A	zinc finger and B	NM_007000	NM_007000
4.03E-03	-7.95E+00	hCG1645220	dynein, cytoplas	NM_001101330	NM_001101330
4.03E-03	-7.95E+00	hCG1645220	dynein, cytoplas	NM_001101330	NM_001101330
3.11E+02	8.28E+00	ventral anterior	potassium chann	NM_001112704	NM_001112704
3.43E+02	8.42E+00	CTD (carboxy-ter	potassium voltag	NM_048368,NM	NM_048368,NM_004715
3.86E-03	-8.02E+00	tripartite motif-c	tripartite motif-c	NM_172016	NM_172016
3.06E+02	8.26E+00	vesicle-associate	period homolog	NM_004781	NM_004781
3.20E+02	8.32E+00	transcription fac	transcription fac	NM_001136139,	NM_001136139,NM_003200
2.97E+02	8.22E+00	wingless-type MI	wingless-type MI	NM_003392	NM_003392
4.64E-03	-7.75E+00	zinc finger and B	heat shock 70kD	NM_001123329,	NM_001123329,NM_014950
3.23E+02	8.33E+00	egl nine homolog	egl nine homolog	NM_053046	NM_053046
2.88E+02	8.17E+00	drebrin 1	drebrin 1	NM_004395,NM	NM_004395,NM_080881
2.88E+02	8.17E+00	drebrin 1	drebrin 1	NM_004395,NM	NM_004395,NM_080881
2.59E+02	8.02E+00	patatin-like phos	patatin-like phos	NM_020376	NM_020376
2.59E+02	8.02E+00	patatin-like phos	patatin-like phos	NM_020376	NM_020376
2.39E+02	7.90E+00	potassium inwar	potassium inwar	NM_152868,NM	NM_152868,NM_004981
3.44E-03	-8.18E+00	macrophage exp	macrophage exp	NM_001039396	NM_001039396
2.60E+02	8.02E+00	transcription fac	transcription fac	NM_001136139,	NM_001136139,NM_003200
2.25E+02	7.81E+00	multimerin 2	multimerin 2	NM_024756	NM_024756
4.37E-03	-7.84E+00	KTEL (Lys-Tyr-Glu	chromosome 3 o	NR_024265,NM_	NR_024265,NM_152305
2.33E+02	7.87E+00	splA/ryanodine r	splA/ryanodine r	NM_080861	NM_080861
3.79E-03	-8.04E+00	heterogeneous n	annexin A8	NR_003277	NR_003277
3.26E+02	8.35E+00	vitrin	vitrin	NM_053276	NM_053276
2.87E+02	8.16E+00	lipase maturatio	lipase maturatio	NM_033200	NM_033200
2.62E+02	8.03E+00	complement con	EPH receptor B2	NM_000491	NM_000491
2.62E+02	8.03E+00	complement con	EPH receptor B2	NM_000491	NM_000491
2.62E+02	8.03E+00	complement con	EPH receptor B2	NM_000491	NM_000491
2.90E+02	8.18E+00	toll interacting p	toll interacting p	NM_019009	NM_019009
2.32E+02	7.86E+00	transmembrane	transmembrane	NM_017814	NM_017814
2.32E+02	7.86E+00	transmembrane	transmembrane	NM_017814	NM_017814
2.48E+02	7.95E+00	L antigen family,	ubiquitin-like 4A	NM_006014	NM_006014
3.67E+02	8.52E+00	tissue specific tra	tissue specific tra	NM_003313	NM_003313
2.58E+02	8.01E+00	inhibitor of CDK,	inhibitor of CDK,	NM_213726	NM_213726
2.47E+02	7.95E+00	heparan sulfate	placenta-specific	NM_004807	NM_004807
2.47E+02	7.95E+00	heparan sulfate	placenta-specific	NM_004807	NM_004807
2.56E+02	8.00E+00	ankyrin repeat d	ankyrin repeat d	NM_152345	NM_152345
2.82E+02	8.14E+00	ras-related C3 bo	cytohesin 4	NM_002872	NM_002872
2.82E+02	8.14E+00	ras-related C3 bo	cytohesin 4	NM_002872	NM_002872
3.73E+02	8.54E+00	solute carrier fan	ASMTL antisense	NM_001636	NM_001636
4.32E-03	-7.86E+00	gap junction pro	topoisomerase (	NM_152219	NM_152219
2.43E+02	7.92E+00	interferon induc	interferon induc	NM_001025295	NM_001025295
3.98E-03	-7.97E+00	---	surfactant protei	NM_006926	NM_006926
4.66E-03	-7.75E+00	defensin, beta 1	seven transmem	NM_001040448	NM_001040448
5.25E-03	-7.57E+00	mediator comple	mediator comple	NM_153450	NM_153450
2.38E+02	7.90E+00	protein tyrosine	protein tyrosine	NM_080392,NM	NM_080392,NM_080391
3.15E+02	8.30E+00	galactosamine (	galactosamine (	NM_000512	NM_000512
3.15E+02	8.30E+00	galactosamine (	galactosamine (	NM_000512	NM_000512
3.11E+02	8.28E+00	glutamate recep	glutamate recep	NM_138690	NM_138690
3.72E+02	8.54E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
3.72E+02	8.54E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
3.72E+02	8.54E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
3.72E+02	8.54E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636

2.66E+02	8.05E+00	Rho guanine nuc	Rho guanine nuc	NM_014629	NM_014629
2.54E+02	7.99E+00	chromosome 19	chromosome 19	NM_001033026,	NM_001033026,NM_033420
3.15E+02	8.30E+00	wntless homolog	wntless homolog	NM_024911	NM_024911
2.34E+02	7.87E+00	armadillo repeat	armadillo repeat	NM_024742,NM	NM_024742,NM_001105247
2.34E+02	7.87E+00	armadillo repeat	armadillo repeat	NM_024742,NM	NM_024742,NM_001105247
4.96E-03	-7.66E+00	defensin, beta 1	defensin, beta 1	NM_001040704,	NM_001040704,NM_152251
4.96E-03	-7.66E+00	defensin, beta 1	defensin, beta 1	NM_001040704,	NM_001040704,NM_152251
2.05E+02	7.68E+00	LON peptidase N	LON peptidase N	NM_152271	NM_152271
2.05E+02	7.68E+00	LON peptidase N	LON peptidase N	NM_152271	NM_152271
2.62E+02	8.03E+00	nuclear factor I/	nuclear factor I/	NM_005597	NM_005597
2.62E+02	8.03E+00	nuclear factor I/	nuclear factor I/	NM_005597	NM_005597
3.81E+02	8.57E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
4.52E-03	-7.79E+00	retinoschisin 1	protein phospha	NM_000330	NM_000330
4.52E-03	-7.79E+00	retinoschisin 1	protein phospha	NM_000330	NM_000330
2.13E+02	7.74E+00	eukaryotic transl	eukaryotic transl	NM_019843	NM_019843
1.49E+00	5.78E-01	solute carrier fan	solute carrier fan	NM_001110781	NM_001110781
1.49E+00	5.78E-01	solute carrier fan	solute carrier fan	NM_001110781	NM_001110781
2.85E+02	8.15E+00	LY6/PLAUR doma	LY6/PLAUR doma	NM_205545	NM_205545
4.11E+02	8.68E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
3.15E+02	8.30E+00	PDZ and LIM don	PDZ and LIM don	NM_176871,NM	NM_176871,NM_198042
2.40E+02	7.91E+00	programmed cell	mitochondrial ri	NR_003713	NR_003713
2.40E+02	7.91E+00	programmed cell	mitochondrial ri	NR_003713	NR_003713
2.55E+02	8.00E+00	chromosome 8 o	glutamate-rich 1	NM_175075	NM_175075
2.93E+02	8.20E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
2.93E+02	8.20E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.27E-03	-8.26E+00	chromosome 1 o	chromosome 1 o	NM_153035	NM_153035
3.27E-03	-8.26E+00	chromosome 1 o	chromosome 1 o	NM_153035	NM_153035
4.43E+02	8.79E+00	hypothetical LOC	hypothetical LOC	NR_024492	NR_024492
2.18E+02	7.77E+00	serpin peptidase	synaptosomal-as	NM_000185	NM_000185
5.13E-03	-7.61E+00	crystallin, gamm	crystallin, gamm	NM_005210	NM_005210
5.13E-03	-7.61E+00	crystallin, gamm	crystallin, gamm	NM_005210	NM_005210
3.66E-03	-8.10E+00	RAB37, member	solute carrier fan	NM_001006638	NM_001006638
3.31E-03	-8.24E+00	collagen, type IX,	collagen, type IX,	NM_001851,NM	NM_001851,NM_078485
3.09E+02	8.27E+00	paired-like home	H2A histone fam	NM_002653	NM_002653
2.23E+02	7.80E+00	coiled-coil domai	coiled-coil domai	NM_015603	NM_015603
3.40E+02	8.41E+00	Kruppel-like fact	Kruppel-like fact	NM_173484	NM_173484
2.84E+02	8.15E+00	DIO3 opposite st	deiodinase, iodo	NR_002770	NR_002770
2.84E+02	8.15E+00	DIO3 opposite st	deiodinase, iodo	NR_002770	NR_002770
2.68E+02	8.06E+00	---	---	NM_001080422	NM_001080422
3.27E+02	8.35E+00	glutamate recept	glutamate recept	NM_001145118	NM_001145118
3.27E+02	8.35E+00	glutamate recept	glutamate recept	NM_001145118	NM_001145118
2.93E+02	8.20E+00	PR domain conta	PR domain conta	NM_020226	NM_020226
2.93E+02	8.20E+00	PR domain conta	PR domain conta	NM_020226	NM_020226
2.93E+02	8.20E+00	PR domain conta	PR domain conta	NM_020226	NM_020226
2.78E+02	8.12E+00	dysbindin (dystro	growth arrest-sp	NM_024043,NM	NM_024043,NM_001042610
2.78E+02	8.12E+00	dysbindin (dystro	growth arrest-sp	NM_024043,NM	NM_024043,NM_001042610
3.30E+02	8.36E+00	exonuclease 3'-5	exonuclease 3'-5	NM_017820	NM_017820
3.30E+02	8.36E+00	exonuclease 3'-5	exonuclease 3'-5	NM_017820	NM_017820
3.38E+02	8.40E+00	odorant binding	ABO blood grou	NM_014581	NM_014581
3.97E-03	-7.98E+00	NADH dehydroge	NADH dehydroge	NM_004550	NM_004550
3.98E-03	-7.97E+00	cyclin-dependen	spindlin 1	NM_001039803,	NM_001039803,NM_178432,NM_
2.89E+02	8.17E+00	mucin 16, cell su	olfactory recepto	NM_024690	NM_024690
2.36E+02	7.88E+00	BR serine/threon	BR serine/threon	NM_003957	NM_003957
4.37E-03	-7.84E+00	cathepsin L1	cathepsin L famil	NM_145918,NM	NM_145918,NM_001912
3.79E+02	8.57E+00	immediate early	calcium channel,	NM_016545	NM_016545
3.33E-03	-8.23E+00	H2A histone fam	chromosome 5 o	NM_004893,NM	NM_004893,NM_001040158,NM_
4.11E-03	-7.93E+00	desmin	SPEG complex lo	NM_001927	NM_001927
2.67E+02	8.06E+00	histone deacetyl	phosphorylase ki	NM_018486	NM_018486

2.67E+02	8.06E+00	histone deacetyl	phosphorylase ki	NM_018486	NM_018486
2.85E+02	8.15E+00	slingshot homol	D-amino-acid oxi	NM_018984	NM_018984
2.85E+02	8.15E+00	D-amino-acid oxi	D-amino-acid oxi	NM_001917	NM_001917
2.13E+02	7.74E+00	mucin 4, cell surf	mucin 4, cell surf	NM_138297,NM	NM_138297,NM_004532,NM_01
2.13E+02	7.74E+00	mucin 4, cell surf	mucin 4, cell surf	NM_138297,NM	NM_138297,NM_004532,NM_01
2.51E+02	7.97E+00	small G protein s	small G protein s	NM_001098509	NM_001098509
2.97E+02	8.22E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.13E+02	8.29E+00	voltage-depende	solute carrier fan	NM_005662,NM	NM_005662,NM_001135694
2.44E+02	7.93E+00	Rho GTPase activ	Rho GTPase activ	NM_001159330,	NM_001159330,NM_199282
2.44E+02	7.93E+00	Rho GTPase activ	Rho GTPase activ	NM_001159330,	NM_001159330,NM_199282
2.63E+02	8.04E+00	family with sequ	ubiquitin-conjug	NM_001014980	NM_001014980
2.74E+02	8.10E+00	arginyl-tRNA syn	fibrillarin-like 1	NM_002887	NM_002887
3.71E-03	-8.07E+00	topoisomerase (I	chromosome 8 o	NM_052963	NM_052963
3.59E+02	8.49E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
2.68E+02	8.06E+00	CTD (carboxy-ter	potassium voltag	NM_048368,NM	NM_048368,NM_004715
2.68E+02	8.06E+00	CTD (carboxy-ter	potassium voltag	NM_048368,NM	NM_048368,NM_004715
2.90E+02	8.18E+00	jumonji domain	jumonji domain	NM_023007	NM_023007
2.90E+02	8.18E+00	jumonji domain	jumonji domain	NM_023007	NM_023007
2.28E+02	7.83E+00	hypothetical LOC	tetraspanin 31	NR_027032	NR_027032
2.28E+02	7.83E+00	hypothetical LOC	tetraspanin 31	NR_027032	NR_027032
4.30E-03	-7.86E+00	small nucleolar R	chromosome 8 o	NR_002581	NR_002581
3.29E-03	-8.25E+00	Meis homeobox	adenosine A2b r	NR_002211	NR_002211
3.49E+02	8.45E+00	hypothetical LOC	chromosome 9 o	NR_024369	NR_024369
5.37E-03	-7.54E+00	Down syndrome	chromosome 21	NM_001389	NM_001389
2.49E+02	7.96E+00	Rho GDP dissocia	Rho GDP dissocia	NM_001176	NM_001176
2.46E+02	7.94E+00	calcium homeost	calcium homeost	NM_006387	NM_006387
2.46E+02	7.94E+00	calcium homeost	calcium homeost	NM_006387	NM_006387
3.54E+02	8.47E+00	lysine (K)-specifi	lysine (K)-specifi	NM_001080424	NM_001080424
2.19E+02	7.78E+00	hect domain and	TP53 target 3B	NR_002827	NR_002827
2.19E+02	7.78E+00	hect domain and	TP53 target 3B	NR_002827	NR_002827
2.65E+02	8.05E+00	ELAV (embryonic	ELAV (embryonic	NM_032281,NM	NM_032281,NM_001420
2.65E+02	8.05E+00	ELAV (embryonic	ELAV (embryonic	NM_032281,NM	NM_032281,NM_001420
3.09E+02	8.27E+00	recombination si	recombination si	NM_014276	NM_014276
3.09E+02	8.27E+00	recombination si	recombination si	NM_014276	NM_014276
3.09E+02	8.27E+00	recombination si	recombination si	NM_014276	NM_014276
2.88E+02	8.17E+00	spleen focus forr	solute carrier fan	NM_001080547,	NM_001080547,NM_003120
2.88E+02	8.17E+00	spleen focus forr	solute carrier fan	NM_001080547,	NM_001080547,NM_003120
2.69E+02	8.07E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
2.69E+02	8.07E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
4.15E+02	8.70E+00	histone deacetyl	histone deacetyl	NM_032019,NM	NM_032019,NM_001159286
4.15E+02	8.70E+00	histone deacetyl	histone deacetyl	NM_032019,NM	NM_032019,NM_001159286
4.15E+02	8.70E+00	histone deacetyl	histone deacetyl	NM_032019,NM	NM_032019,NM_001159286
2.77E+02	8.11E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
2.46E+02	7.94E+00	ERBB receptor fe	solute carrier fan	NM_018948	NM_018948
2.39E+02	7.90E+00	zinc finger protei	zinc finger protei	NM_016423,NM	NM_016423,NM_001101672,NM_
2.39E+02	7.90E+00	zinc finger protei	zinc finger protei	NM_016423,NM	NM_016423,NM_001101672,NM_
2.39E+02	7.90E+00	zinc finger protei	zinc finger protei	NM_016423,NM	NM_016423,NM_001101672,NM_
3.57E+02	8.48E+00	autism susceptib	autism susceptib	NM_015570,NM	NM_015570,NM_001127232
3.57E+02	8.48E+00	autism susceptib	autism susceptib	NM_015570,NM	NM_015570,NM_001127232
2.76E+02	8.11E+00	sarcosine dehydr	sarcosine dehydr	NM_007101,NM	NM_007101,NM_001134707
3.26E+02	8.35E+00	HECT, C2 and W	coiled-coil doma	NM_020760	NM_020760
3.18E-03	-8.30E+00	angiopoietin 1	R-spondin 2 hom	NM_001146	NM_001146
4.40E-03	-7.83E+00	zinc finger protei	zinc finger protei	NM_001082480	NM_001082480
4.40E-03	-7.83E+00	zinc finger protei	zinc finger protei	NM_014789	NM_014789
3.21E-03	-8.29E+00	protein tyrosine	interferon, beta	NM_001010915	NM_001010915
3.22E+02	8.33E+00	chromosome 14	delta-like 1 hom	NR_024096	NR_024096
3.22E+02	8.33E+00	chromosome 14	delta-like 1 hom	NR_024096	NR_024096
4.52E-03	-7.79E+00	cholinergic recep	ADAM metallope	NM_000750	NM_000750

3.04E-03	-8.36E+00	glial cell derived	EGF-like, fibrone	NM_000514,NM	NM_000514,NM_199231,NM_19
3.04E-03	-8.36E+00	glial cell derived	EGF-like, fibrone	NM_000514,NM	NM_000514,NM_199231,NM_19
4.03E-03	-7.95E+00	calcineurin-like p	shisa homolog 9	NM_018340,NM	NM_018340,NM_001099455
2.42E+02	7.92E+00	protease, serine,	protease, serine,	NM_001135086	NM_001135086
2.42E+02	7.92E+00	protease, serine,	protease, serine,	NM_006799,NM	NM_006799,NM_144956,NM_144
2.56E+02	8.00E+00	jumonji, AT rich i	jumonji, AT rich i	NM_004973	NM_004973
3.76E-03	-8.05E+00	placenta-specific	family with sequ	NM_182832	NM_182832
3.79E-03	-8.04E+00	nucleoredoxin	translocase of in	NM_022463	NM_022463
3.42E+02	8.42E+00	phospholipase D	folliculin	NM_178836	NM_178836
3.35E+02	8.39E+00	coronin, actin bir	coronin, actin bir	NM_052820,NM	NM_052820,NM_003389
2.77E+02	8.11E+00	chromosome 20	chromosome 20	NM_178463	NM_178463
3.94E-03	-7.99E+00	serine peptidase	F-box and WD re	NM_001080525	NM_001080525
3.21E+02	8.33E+00	RER1 retention ir	RER1 retention ir	NM_007033	NM_007033
3.21E+02	8.33E+00	RER1 retention ir	RER1 retention ir	NM_007033	NM_007033
2.65E+02	8.05E+00	phosphohistidine	MAM domain co	NM_014172,NM	NM_014172,NM_001135861
2.75E+02	8.10E+00	potassium voltag	potassium voltag	NM_004700,NM	NM_004700,NM_172163
4.27E-03	-7.87E+00	splicing factor 3a	splicing factor 3a	NM_001005409,	NM_001005409,NM_005877
2.24E+02	7.81E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
2.24E+02	7.81E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
2.68E+02	8.06E+00	transmembrane	inverted formin,	NM_207379	NM_207379
2.68E+02	8.06E+00	transmembrane	inverted formin,	NM_207379	NM_207379
2.68E+02	8.06E+00	transmembrane	inverted formin,	NM_207379	NM_207379
4.21E-03	-7.89E+00	hypothetical LOC	methionine sulfo	NR_024281	NR_024281
2.18E+02	7.77E+00	cone-rod homeo	sulfotransferase	NM_000554	NM_000554
3.16E+02	8.30E+00	leucine rich repe	leucine rich repe	NM_144999	NM_144999
3.31E+02	8.37E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
4.59E-03	-7.77E+00	NADH dehydroge	asparagine-linke	NM_004549	NM_004549
3.80E+02	8.57E+00	agrin	agrin	NM_198576	NM_198576
3.34E+02	8.38E+00	retinitis pigment	chromosome 8 o	NM_178857	NM_178857
2.90E+02	8.18E+00	ATPase, Ca++ tra	ATPase, Ca++ tra	NM_173201,NM	NM_173201,NM_004320
2.90E+02	8.18E+00	ATPase, Ca++ tra	ATPase, Ca++ tra	NM_173201,NM	NM_173201,NM_004320
3.30E+02	8.36E+00	hypothetical LOC	adrenergic, alpha	NR_027110	NR_027110
2.39E+02	7.90E+00	v-erb-a erythrobl	IKAROS family zir	NM_005235,NM	NM_005235,NM_001042599
2.39E+02	7.90E+00	v-erb-a erythrobl	IKAROS family zir	NM_005235,NM	NM_005235,NM_001042599
3.32E-03	-8.23E+00	mitogen-activate	myocardin	NM_003010	NM_003010
2.41E+02	7.91E+00	pyridoxal (pyrido	pyridoxal (pyrido	NM_003681	NM_003681
2.41E+02	7.91E+00	pyridoxal (pyrido	pyridoxal (pyrido	NM_003681	NM_003681
2.83E+02	8.14E+00	FSHD region gen	zinc finger protei	NM_001124759	NM_001124759
2.83E+02	8.14E+00	FSHD region gen	zinc finger protei	NM_001124759	NM_001124759
2.83E+02	8.14E+00	FSHD region gen	zinc finger protei	NM_001124759	NM_001124759
4.53E-03	-7.78E+00	small Cajal body-	S-antigen	NR_003006	NR_003006
2.97E+02	8.22E+00	melanoma antige	melanoma antige	NM_001080790,	NM_001080790,NM_005365
3.45E-03	-8.18E+00	small nucleolar R	stonin 2	NR_003021	NR_003021
2.93E+02	8.20E+00	platelet-derived	ribosomal protei	NM_002608,NM	NM_002608,NM_033016
2.94E+02	8.20E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
2.94E+02	8.20E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
2.94E+02	8.20E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
4.19E+02	8.71E+00	carbohydrate kin	carbohydrate kin	NM_018210	NM_018210
2.29E+02	7.84E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
2.29E+02	7.84E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
2.67E+02	8.06E+00	aarF domain con	aarF domain con	NM_174922	NM_174922
2.67E+02	8.06E+00	aarF domain con	aarF domain con	NM_174922	NM_174922
2.34E+02	7.87E+00	zinc finger and B	zinc finger and B	NM_032792	NM_032792
2.34E+02	7.87E+00	zinc finger and B	zinc finger and B	NM_032792	NM_032792
4.47E-03	-7.81E+00	cytochrome P45	similar to hCG19	NM_000498	NM_000498
2.60E+02	8.02E+00	regulator of G-pr	regulator of G-pr	NM_006480	NM_006480
4.64E-03	-7.75E+00	Smad nuclear int	dynein, axonema	NM_024700	NM_024700
2.25E+02	7.81E+00	CDC42 binding pı	CDC42 binding pı	NM_017525	NM_017525

2.91E+02	8.19E+00	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
2.38E+02	7.90E+00	three prime repa	HAUS augmin-lik	NM_080701	NM_080701
3.07E+02	8.26E+00	hypothetical FLJ4	hypothetical FLJ4	NR_002314	NR_002314
2.53E+02	7.98E+00	notch 1	notch 1	NM_017617	NM_017617
3.71E-03	-8.07E+00	family with sequ	family with sequ	NM_015091	NM_015091
4.19E+02	8.71E+00	kelch-like 30 (Dr	kelch-like 30 (Dr	NM_198582	NM_198582
4.19E+02	8.71E+00	kelch-like 30 (Dr	kelch-like 30 (Dr	NM_198582	NM_198582
3.38E-03	-8.21E+00	taste receptor, t	taste receptor, t	NM_018980	NM_018980
2.79E+02	8.12E+00	dystrophia myot	dystrophia myot	NM_004943	NM_004943
3.09E+02	8.27E+00	family with sequ	family with sequ	NM_001142864	NM_001142864
3.09E+02	8.27E+00	family with sequ	family with sequ	NM_001142864	NM_001142864
3.09E+02	8.27E+00	family with sequ	chromatin licensi	NM_001142864	NM_001142864
3.12E+02	8.29E+00	gametogenetin	sprouty-related,	NM_152657	NM_152657
5.15E-03	-7.60E+00	nuclear receptor	translocation ass	NM_006540	NM_006540
2.91E+02	8.19E+00	solute carrier fan	solute carrier fan	NM_001080431	NM_001080431
2.00E+02	7.64E+00	GNAS complex lo	GNAS complex lo	NM_001077490,	NM_001077490,NM_080425
2.57E+02	8.01E+00	zinc finger, AN1-	zinc finger, AN1-	NM_021943	NM_021943
2.47E+02	7.95E+00	C1q and tumor n	poly (ADP-ribose	NM_178540	NM_178540
2.47E+02	7.95E+00	C1q and tumor n	poly (ADP-ribose	NM_178540	NM_178540
2.35E+02	7.88E+00	zinc finger protei	zinc finger protei	NM_014717	NM_014717
4.62E+02	8.85E+00	adherens junctio	adherens junctio	NM_001042478,	NM_001042478,NM_018836
4.62E+02	8.85E+00	adherens junctio	adherens junctio	NM_001042478,	NM_001042478,NM_018836
3.47E+02	8.44E+00	neugrin, neurite	zinc finger protei	NM_001033088,	NM_001033088,NM_016645
3.84E-03	-8.03E+00	heparan sulfate	chymotrypsin-lik	NM_005529	NM_005529
2.02E+02	7.66E+00	tripartite motif-c	tripartite motif-c	NM_030912	NM_030912
4.24E-03	-7.88E+00	glutathione S-tra	D-dopachrome t	NM_000854,NM	NM_000854,NM_001080843
4.24E-03	-7.88E+00	glutathione S-tra	D-dopachrome t	NM_000854,NM	NM_000854,NM_001080843
3.19E+02	8.32E+00	lipid phosphate	lipid phosphate	NM_022737	NM_022737
3.50E+02	8.45E+00	UBX domain pro	von Willebrand f	NM_152376	NM_152376
3.04E+02	8.25E+00	non-protein codi	ankyrin repeat d	NR_026795	NR_026795
3.02E+02	8.24E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.02E+02	8.24E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.93E-03	-7.99E+00	Bcl2 modifying f	budding uninhibi	NM_001003943,	NM_001003943,NM_001003942,
3.93E-03	-7.99E+00	Bcl2 modifying f	budding uninhibi	NM_001003943,	NM_001003943,NM_001003942,
2.69E+02	8.07E+00	zinc finger protei	family with sequ	NM_001001662	NM_001001662
2.69E+02	8.07E+00	zinc finger protei	family with sequ	NM_001001662	NM_001001662
2.07E+02	7.69E+00	forkhead box D4	forkhead box D4	NM_001126334	NM_001126334
3.54E+02	8.47E+00	zinc finger protei	zinc finger protei	NM_198526	NM_198526
3.54E+02	8.47E+00	zinc finger protei	zinc finger protei	NM_198526	NM_198526
2.34E+02	7.87E+00	family with sequ	transmembrane	NM_001002919	NM_001002919
2.34E+02	7.87E+00	family with sequ	transmembrane	NM_001002919	NM_001002919
2.74E+02	8.10E+00	ribosomal protei	prospero homeo	NM_012424,NM	NM_012424,NM_001136138
3.36E+02	8.39E+00	small nuclear rib	RER1 retention i	NR_024489	NR_024489
3.36E+02	8.39E+00	small nuclear rib	RER1 retention i	NR_024489	NR_024489
3.36E+02	8.39E+00	small nuclear rib	RER1 retention i	NR_024489	NR_024489
2.43E+02	7.92E+00	matrix metallope	matrix metallope	NM_006983	NM_006983
2.43E+02	7.92E+00	matrix metallope	matrix metallope	NM_006983	NM_006983
2.43E+02	7.92E+00	matrix metallope	matrix metallope	NR_002946	NR_002946
4.47E-03	-7.81E+00	CD79b molecule,	sodium channel,	NM_000626,NM	NM_000626,NM_021602,NM_001
2.25E+02	7.81E+00	chromosome 16	clusterin associa	NM_001080524	NM_001080524
2.72E+02	8.09E+00	abhydrolase dom	abhydrolase dom	NM_015407	NM_015407
2.72E+02	8.09E+00	abhydrolase dom	aminoacylase 1	NM_015407	NM_015407
2.19E+02	7.78E+00	TPTE and PTEN h	TPTE and PTEN h	NR_002821	NR_002821
2.77E+02	8.11E+00	keratinocyte gro	ankyrin repeat d	NR_003670	NR_003670
2.70E+02	8.07E+00	MDN1, midasin	caspase 8 associ	NM_014611	NM_014611
2.70E+02	8.07E+00	MDN1, midasin	caspase 8 associ	NM_014611	NM_014611
3.81E+02	8.57E+00	proline rich 22	proline rich 22	NM_153359,NM	NM_153359,NM_001134316
3.81E+02	8.57E+00	proline rich 22	proline rich 22	NM_153359,NM	NM_153359,NM_001134316

2.77E+02	8.11E+00	spermatid associ	spermatid associ	NM_152719	NM_152719
2.58E+02	8.01E+00	agrin	chromosome 1 o	NM_198576	NM_198576
2.58E+02	8.01E+00	agrin	chromosome 1 o	NM_198576	NM_198576
2.58E+02	8.01E+00	agrin	chromosome 1 o	NM_198576	NM_198576
3.66E-03	-8.10E+00	ring-box 1	E1A binding prot	NM_014248	NM_014248
3.44E-03	-8.18E+00	signal transducer	polymerase I anc	NM_213662,NM	NM_213662,NM_139276,NM_003
3.44E-03	-8.18E+00	signal transducer	polymerase I anc	NM_213662,NM	NM_213662,NM_139276,NM_003
3.89E-03	-8.01E+00	adenosine A3 rec	adenosine A3 rec	NM_000677	NM_000677
3.89E-03	-8.01E+00	adenosine A3 rec	RAP1A, member	NM_000677	NM_000677
4.62E-03	-7.76E+00	alpha-1-microglo	kinesin family me	NM_001633	NM_001633
3.99E-03	-7.97E+00	heat shock 27kD	chromosome 11	NM_001541	NM_001541
2.32E+02	7.86E+00	TEL2, telomere n	TEL2, telomere n	NM_016111	NM_016111
2.32E+02	7.86E+00	TEL2, telomere n	TEL2, telomere n	NM_016111	NM_016111
2.33E+02	7.87E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
2.33E+02	7.87E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
3.75E-03	-8.06E+00	thromboxane A s	thromboxane A s	NM_001130966	NM_001130966
2.98E+02	8.22E+00	chondroitin sulfa	histidine triad nu	NM_175856	NM_175856
2.98E+02	8.22E+00	chondroitin sulfa	histidine triad nu	NM_175856	NM_175856
2.98E+02	8.22E+00	chondroitin sulfa	histidine triad nu	NM_175856	NM_175856
2.82E+02	8.14E+00	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
4.24E-03	-7.88E+00	RNA binding mot	ets variant 2	NM_024321	NM_024321
3.01E+02	8.23E+00	wingless-type MI	wingless-type MI	NM_030761	NM_030761
2.73E+02	8.09E+00	null	phosphatidylinos	null	null
2.73E+02	8.09E+00	null	phosphatidylinos	null	null
2.73E+02	8.09E+00	null	phosphatidylinos	null	null
2.21E+02	7.79E+00	BCL6 corepresso	BCL6 corepresso	NM_001123383,	NM_001123383,NM_001123384,N
2.93E+02	8.20E+00	PQ loop repeat c	PQ loop repeat c	NM_001146343,	NM_001146343,NM_001146345,N
2.93E+02	8.20E+00	PQ loop repeat c	PQ loop repeat c	NM_001146343,	NM_001146343,NM_001146345,N
2.69E+02	8.07E+00	chromosome 10	UPF2 regulator o	NM_153256	NM_153256
2.69E+02	8.07E+00	chromosome 10	UPF2 regulator o	NM_153256	NM_153256
4.03E-03	-7.95E+00	olfactory recepto	olfactory recepto	NM_012363	NM_012363
3.53E+02	8.46E+00	RAB1B, member	RAB1B, member	NM_030981	NM_030981
2.68E+02	8.06E+00	tyrosine kinase 2	tyrosine kinase 2	NM_003331	NM_003331
3.12E+02	8.29E+00	poliovirus recept	poliovirus recept	NM_002855	NM_002855
3.12E+02	8.29E+00	poliovirus recept	poliovirus recept	NM_002855	NM_002855
2.64E+02	8.04E+00	LAG1 homolog, c	LAG1 homolog, c	NM_178842	NM_178842
3.97E-03	-7.98E+00	ATP-binding cass	claudin 10	NM_001105515	NM_001105515
3.97E-03	-7.98E+00	ATP-binding cass	claudin 10	NM_001105515	NM_001105515
3.28E+02	8.36E+00	zinc finger protei	zinc finger protei	NM_014643	NM_014643
2.42E+02	7.92E+00	nuclear factor of	nuclear factor of	NM_004554	NM_004554
2.51E+02	7.97E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
4.66E+02	8.86E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
4.66E+02	8.86E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.15E+02	8.30E+00	transmembrane	forkhead box D1	NM_153217	NM_153217
3.15E+02	8.30E+00	transmembrane	forkhead box D1	NM_153217	NM_153217
4.30E-03	-7.86E+00	VAMP (vesicle-as	adenomatosis pc	NM_194434,NM	NM_194434,NM_003574
4.30E-03	-7.86E+00	VAMP (vesicle-as	adenomatosis pc	NM_194434,NM	NM_194434,NM_003574
3.08E+02	8.27E+00	peptidase D	peptidase D	NM_000285	NM_000285
3.08E+02	8.27E+00	peptidase D	peptidase D	NM_000285	NM_000285
2.40E+02	7.91E+00	solute carrier fan	solute carrier fan	NM_001042422	NM_001042422
2.71E-03	-8.53E+00	hypothetical LOC	hypothetical LOC	NR_026979	NR_026979
2.76E+02	8.11E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
2.28E+02	7.83E+00	null	hypothetical LOC	null	null
2.28E+02	7.83E+00	null	hypothetical LOC	null	null
2.93E+02	8.20E+00	lon peptidase 1,	lon peptidase 1,	NM_004793	NM_004793
2.93E+02	8.20E+00	lon peptidase 1,	lon peptidase 1,	NM_004793	NM_004793
2.18E+02	7.77E+00	hypothetical LOC	hypothetical LOC	NR_027069	NR_027069
3.27E+02	8.35E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275

3.27E+02	8.35E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
2.42E+02	7.92E+00	chromosome 20	chromosome 20	NR_026959	NR_026959
3.33E-03	-8.23E+00	adrenergic, alpha	adrenergic, alpha	NM_000680	NM_000680
3.33E-03	-8.23E+00	adrenergic, alpha	adrenergic, alpha	NM_000680	NM_000680
2.48E+02	7.95E+00	inducible T-cell c	DNA (cytosine-5-	NM_015259	NM_015259
2.48E+02	7.95E+00	inducible T-cell c	DNA (cytosine-5-	NM_015259	NM_015259
2.53E+02	7.98E+00	collagen, type VI,	collagen, type VI,	NM_001849,NM	NM_001849,NM_058175,NM_05
2.53E+02	7.98E+00	collagen, type VI,	collagen, type VI,	NM_001849,NM	NM_001849,NM_058175,NM_05
2.84E+02	8.15E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
3.19E+02	8.32E+00	fibrosin-like 1	purinergic recept	NM_001142641	NM_001142641
3.30E+02	8.37E+00	collagen, type XV	collagen, type XV	NM_030582,NM	NM_030582,NM_130444
2.30E+02	7.84E+00	membrane meta	membrane meta	NM_033467	NM_033467
3.57E-03	-8.13E+00	HIG1 hypoxia ind	HIG1 hypoxia ind	NR_002780	NR_002780
2.70E+02	8.08E+00	CCAAT/enhancer	protein kinase, D	NM_005195	NM_005195
2.70E+02	8.08E+00	CCAAT/enhancer	protein kinase, D	NM_005195	NM_005195
3.60E-03	-8.12E+00	non-protein codi	RUN domain con	NR_026675	NR_026675
3.60E-03	-8.12E+00	RUN domain con	RUN domain con	NM_001012391	NM_001012391
4.43E-03	-7.82E+00	brain-enriched g	chromosome 14	NM_001159531,	NM_001159531,NM_020836
3.07E+02	8.26E+00	regulator of G-pr	HGF activator	NM_198227	NM_198227
3.02E+02	8.24E+00	protein kinase D2	protein kinase D2	NM_016457,NM	NM_016457,NM_001079880,NM_
4.02E-03	-7.96E+00	B-cell CLL/lymph	cardiotrophin 1	NM_004765	NM_004765
1.43E+00	5.11E-01	X antigen family,	X antigen family,	NM_020411,NM	NM_020411,NM_133430,NM_133
1.43E+00	5.11E-01	X antigen family,	X antigen family,	NM_020411,NM	NM_020411,NM_133430,NM_133
4.21E-03	-7.89E+00	ring finger protei	KIAA2022	NM_183353,NM	NM_183353,NM_016120
3.07E+02	8.26E+00	dihydropyrimidi	dihydropyrimidi	NM_006426	NM_006426
3.07E+02	8.26E+00	dihydropyrimidi	serine/threonine	NM_006426	NM_006426
3.24E+02	8.34E+00	phosphatidylinos	phosphatidylinos	NM_020820	NM_020820
3.24E+02	8.34E+00	phosphatidylinos	phosphatidylinos	NM_020820	NM_020820
3.24E+02	8.34E+00	spermatogenesis	C1q and tumor n	NM_153023	NM_153023
3.40E-03	-8.20E+00	sulfotransferase	sulfotransferase	NM_177528,NM	NM_177528,NM_001054
2.93E+02	8.20E+00	chromosome 19	chromosome 19	NM_138774	NM_138774
2.93E+02	8.20E+00	chromosome 19	chromosome 19	NM_138774	NM_138774
3.67E-03	-8.09E+00	amelotin	ameloblastin (en	NM_212557	NM_212557
3.67E-03	-8.09E+00	amelotin	ameloblastin (en	NM_212557	NM_212557
2.55E+02	8.00E+00	breakpoint cluste	zinc finger, DHHC	NM_004327,NM	NM_004327,NM_021574
2.48E+02	7.95E+00	placenta-specific	family with seque	NM_182832	NM_182832
2.48E+02	7.95E+00	placenta-specific	family with seque	NM_182832	NM_182832
2.59E+02	8.02E+00	tubulin tyrosine l	tubulin tyrosine l	NM_001080447	NM_001080447
2.52E+02	7.98E+00	somatostatin rec	somatostatin rec	NM_001051	NM_001051
2.88E+02	8.17E+00	transmembrane	forkhead box D1	NM_153217	NM_153217
3.50E+02	8.45E+00	solute carrier fa	solute carrier fa	NM_194255	NM_194255
3.50E+02	8.45E+00	solute carrier fa	solute carrier fa	NM_194255	NM_194255
2.71E+02	8.08E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
1.31E+00	3.90E-01	lipocalin 1 (tear	odorant binding	NM_002297	NM_002297
3.33E+02	8.38E+00	prostate tumor c	prostate tumor c	NM_017432	NM_017432
2.30E+02	7.85E+00	WNK lysine defic	WNK lysine defic	NM_006648	NM_006648
2.81E+02	8.13E+00	vestigial like 4 (D	chromosome 3 o	NM_001128221,	NM_001128221,NM_001128220,
3.62E-03	-8.11E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.62E-03	-8.11E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.85E-03	-8.02E+00	heart and neural	La ribonucleopro	NM_004821	NM_004821
2.42E+02	7.92E+00	zinc finger protei	zinc finger protei	NM_001146175	NM_001146175
2.42E+02	7.92E+00	zinc finger protei	zinc finger protei	NM_032370	NM_032370
2.77E+02	8.11E+00	Rho GTPase acti	FANCD2/FANCI-	NM_001039841	NM_001039841
2.77E+02	8.11E+00	Rho GTPase acti	FANCD2/FANCI-	NM_001039841	NM_001039841
2.78E+02	8.12E+00	arginine-glutami	arginine-glutami	NM_001042682,	NM_001042682,NM_012102,NM_
2.75E+02	8.10E+00	zinc finger protei	zinc finger protei	NM_152493	NM_152493
3.00E+02	8.23E+00	NLR family, pyrin	NLR family, pyrin	NM_017852	NM_017852
2.19E+02	7.78E+00	chromosome 4 o	protocadherin 1	NM_001099783	NM_001099783

2.19E+02	7.78E+00	chromosome 4 o	protocadherin 1	NM_001099783	NM_001099783
4.03E-03	-7.95E+00	mitogen-activate	hypothetical LOC	NR_026901	NR_026901
4.03E-03	-7.95E+00	mitogen-activate	hypothetical LOC	NR_026901	NR_026901
2.70E+02	8.08E+00	dysferlin interact	prolyl 4-hydroxyl	NM_001007533	NM_001007533
2.70E+02	8.08E+00	dysferlin interact	prolyl 4-hydroxyl	NM_001007533	NM_001007533
4.78E-03	-7.71E+00	chromosome 6 o	small ArfGAP 1	NM_145267	NM_145267
3.80E-03	-8.04E+00	gamma-glutamyl	transmembrane	NM_178311,NM	NM_178311,NM_178312
2.91E+02	8.19E+00	mucin 6, oligome	mucin 2, oligome	NM_005961	NM_005961
2.40E+02	7.91E+00	budding uninhibi	acyl-CoA oxidase	NM_004336	NM_004336
2.67E+02	8.06E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_002
2.67E+02	8.06E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_002
2.35E+02	7.88E+00	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
2.35E+02	7.88E+00	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
3.43E-03	-8.19E+00	small nucleolar R	small nucleolar R	NR_003324,NR_	NR_003324,NR_003318
4.74E-03	-7.72E+00	protein phospha	mannosidase, al	NM_020416,NM	NM_020416,NM_181876
4.74E-03	-7.72E+00	protein phospha	mannosidase, al	NM_020416,NM	NM_020416,NM_181876
2.66E+02	8.05E+00	unc-5 homolog A	unc-5 homolog A	NM_133369	NM_133369
2.66E+02	8.05E+00	unc-5 homolog A	unc-5 homolog A	NM_133369	NM_133369
2.34E+02	7.87E+00	glutathione S-tra	glutathione S-tra	NM_000848,NM	NM_000848,NM_001142368
2.34E+02	7.87E+00	glutathione S-tra	glutathione S-tra	NM_000561,NM	NM_000561,NM_146421
3.54E+02	8.47E+00	guanine nucleoti	guanine nucleoti	NM_001098722,	NM_001098722,NM_001098721,
3.29E+02	8.36E+00	chondroitin sulfa	chondroitin sulfa	NM_001897	NM_001897
3.01E+02	8.23E+00	hypothetical LOC	hypothetical LOC	NR_021490	NR_021490
3.26E+02	8.35E+00	AE binding prote	AE binding prote	NM_001129	NM_001129
3.26E+02	8.35E+00	AE binding prote	AE binding prote	NM_001129	NM_001129
3.03E+02	8.24E+00	T-cell, immune r	T-cell, immune r	NM_006019	NM_006019
3.51E+02	8.46E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
3.51E+02	8.46E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
2.88E+02	8.17E+00	splicing factor 3a	splicing factor 3a	NM_007165	NM_007165
2.30E+02	7.84E+00	TBC1 domain fa	TBC1 domain fa	NM_019020	NM_019020
2.83E+02	8.14E+00	thioesterase sup	thioesterase sup	NM_182578	NM_182578
2.83E+02	8.14E+00	thioesterase sup	thioesterase sup	NM_182578	NM_182578
4.63E+02	8.85E+00	DENN/MADD do	DENN/MADD do	NM_014856	NM_014856
4.33E-03	-7.85E+00	acylphosphatase	family with sequ	NM_001107,NM	NM_001107,NM_203488
4.33E-03	-7.85E+00	acylphosphatase	family with sequ	NM_001107,NM	NM_001107,NM_203488
2.84E+02	8.15E+00	neuroligin 4, Y-li	non-protein codi	NM_014893	NM_014893
2.76E+02	8.11E+00	protocadherin ga	protocadherin ga	NM_018922,NM	NM_018922,NM_032095
4.50E-03	-7.80E+00	molybdenum cof	molybdenum cof	NM_001075098,	NM_001075098,NM_138928,NM_
3.35E+02	8.39E+00	transformation/t	transformation/t	NM_003496	NM_003496
2.52E+02	7.98E+00	branched chain a	branched chain a	NM_001190	NM_001190
2.52E+02	7.98E+00	branched chain a	branched chain a	NM_001190	NM_001190
2.66E+02	8.05E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
2.66E+02	8.05E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.90E+02	8.61E+00	acetylserotonin	acetylserotonin	NM_004043	NM_004043
4.92E-03	-7.67E+00	RAS, dexametha	phosphatidyletha	NM_016084	NM_016084
2.70E+02	8.08E+00	Rho/Rac guanine	Rho/Rac guanine	NM_001130955	NM_001130955
2.70E+02	8.08E+00	Rho/Rac guanine	Rho/Rac guanine	NM_001130955	NM_001130955
3.14E+02	8.30E+00	v-rel reticuloend	v-rel reticuloend	NM_006509	NM_006509
3.11E+02	8.28E+00	topoisomerase (	topoisomerase (	NM_052963	NM_052963
2.52E+02	7.98E+00	zinc finger protei	integrator compl	NM_152626,NM	NM_152626,NM_007139
2.52E+02	7.98E+00	zinc finger protei	integrator compl	NM_152626,NM	NM_152626,NM_007139
2.57E+02	8.01E+00	adenine phosph	galactosamine (	NM_000485,NM	NM_000485,NM_001030018
2.57E+02	8.01E+00	inositol polyphos	inositol polyphos	NM_001135642,	NM_001135642,NM_016532,NM_
2.57E+02	8.01E+00	inositol polyphos	inositol polyphos	NM_001135642,	NM_001135642,NM_016532,NM_
3.54E+02	8.47E+00	notch 1	notch 1	NM_017617	NM_017617
3.39E-03	-8.20E+00	protease, serine,	GINS complex su	NM_001080492	NM_001080492
3.39E-03	-8.20E+00	protease, serine,	GINS complex su	NM_001080492	NM_001080492
2.85E+02	8.15E+00	family with sequ	family with sequ	NM_001039762	NM_001039762

2.85E+02	8.15E+00	family with sequ	family with sequ	NM_001039762	NM_001039762
2.85E+02	8.15E+00	family with sequ	family with sequ	NM_001039762	NM_001039762
2.92E+02	8.19E+00	RAS (RAD and GE	RAS (RAD and GE	NM_014012	NM_014012
2.83E+02	8.14E+00	transcription fact	extracellular leuc	NR_001288	NR_001288
2.83E+02	8.14E+00	extracellular leuc	extracellular leuc	NM_001128636	NM_001128636
2.09E+02	7.70E+00	adrenergic, alpha	adrenergic, alpha	NM_000683	NM_000683
2.99E+02	8.22E+00	microtubule-asso	microtubule-asso	NM_018174	NM_018174
2.99E+02	8.22E+00	microtubule-asso	microtubule-asso	NM_018174	NM_018174
2.99E+02	8.22E+00	microtubule-asso	microtubule-asso	NM_018174	NM_018174
4.45E-03	-7.81E+00	meteorin, glial ce	family with sequ	NM_024042	NM_024042
4.45E-03	-7.81E+00	meteorin, glial ce	family with sequ	NM_024042	NM_024042
3.08E+02	8.27E+00	RNA binding mot	RNA binding mot	NM_017495,NM	NM_017495,NM_183425
2.33E+02	7.87E+00	POTE ankyrin do	hypothetical LOC	NM_207355	NM_207355
2.33E+02	7.87E+00	POTE ankyrin do	hypothetical LOC	NM_207355	NM_207355
3.19E+02	8.32E+00	squamous cell ca	squamous cell ca	NM_005146	NM_005146
2.83E+02	8.14E+00	notch 1	EGF-like-domain,	NM_017617	NM_017617
2.80E+02	8.13E+00	chloride intracell	ATP-binding cass	NM_004669	NM_004669
2.49E+02	7.96E+00	tubulin folding co	tubulin folding co	NM_001281	NM_001281
2.49E+02	7.96E+00	tubulin folding co	tubulin folding co	NM_001281	NM_001281
2.10E+02	7.72E+00	kinesin family me	kinesin family me	NM_015656	NM_015656
2.10E+02	7.72E+00	kinesin family me	kinesin family me	NM_015656	NM_015656
4.59E-03	-7.77E+00	ATP5S-like	chromosome 19	NM_018035	NM_018035
2.08E+02	7.70E+00	zinc finger protei	zinc finger protei	NM_001033723	NM_001033723
2.08E+02	7.70E+00	zinc finger protei	zinc finger protei	NM_001033723	NM_001033723
3.86E-03	-8.02E+00	leucine rich repe	leucine rich repe	NM_201650,NM	NM_201650,NM_006992,NM_001
3.48E-03	-8.17E+00	ZFAT antisense R	hypothetical LOC	NR_002438	NR_002438
3.48E-03	-8.17E+00	ZFAT antisense R	hypothetical LOC	NR_002438	NR_002438
3.48E-03	-8.17E+00	ZFAT antisense R	hypothetical LOC	NR_002438	NR_002438
2.23E+02	7.80E+00	sorting nexin 8	eukaryotic transl	NM_013321	NM_013321
2.56E+02	8.00E+00	chromosome 3 o	enoyl-CoA, hydra	NM_001025266	NM_001025266
2.56E+02	8.00E+00	chromosome 3 o	enoyl-CoA, hydra	NM_001025266	NM_001025266
3.91E-03	-8.00E+00	complement con	complement con	NM_001017367	NM_001017367
4.40E-03	-7.83E+00	aspartate dehydr	aspartate dehydr	NM_001024656,	NM_001024656,NM_001114598
2.25E+02	7.81E+00	cornichon homol	glia maturation f	NM_005776	NM_005776
2.25E+02	7.81E+00	cornichon homol	glia maturation f	NM_005776	NM_005776
2.44E+02	7.93E+00	chromosome 4 o	chromosome 4 o	NM_001039717	NM_001039717
2.44E+02	7.93E+00	chromosome 4 o	chromosome 4 o	NM_001039717	NM_001039717
3.28E-03	-8.25E+00	regulatory factor	regulatory factor	NM_001145664	NM_001145664
3.28E-03	-8.25E+00	regulatory factor	mitogen-activate	NM_001145664	NM_001145664
2.21E+02	7.79E+00	interleukin 17 re	interleukin 17 re	NM_001001694	NM_001001694
4.21E-03	-7.89E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.65E+02	8.51E+00	coiled-coil domai	ADP-ribosylation	NM_199287	NM_199287
3.65E+02	8.51E+00	ADP-ribosylation	ADP-ribosylation	NM_001040025	NM_001040025
2.58E+02	8.01E+00	adaptor-related	adaptor-related	NM_012305	NM_012305
2.41E+02	7.91E+00	mucin 5B, oligom	mucin 5B, oligom	NM_002458	NM_002458
3.94E-03	-7.99E+00	zinc finger, matri	zinc finger, matri	NM_001003692,	NM_001003692,NM_019103
4.90E-03	-7.67E+00	Src homology 2 c	solute carrier fan	NM_138356	NM_138356
1.89E+00	9.16E-01	keratin associate	ubiquitin-conjuga	NM_198699	NM_198699
3.73E-03	-8.07E+00	G protein-couple	G protein-couple	NM_015234,NM	NM_015234,NM_001098518
2.80E+02	8.13E+00	phosphoglycerat	phosphoglycerat	NM_138575	NM_138575
3.02E+02	8.24E+00	odz, odd Oz/ten-	odz, odd Oz/ten-	NM_001098816	NM_001098816
3.02E+02	8.24E+00	odz, odd Oz/ten-	odz, odd Oz/ten-	NM_001098816	NM_001098816
2.92E+02	8.19E+00	actin, gamma 1	fascin homolog 2	NM_001614	NM_001614
3.14E+02	8.30E+00	mesothelin-like	RNA pseudouridy	NM_001025190	NM_001025190
2.96E-03	-8.40E+00	nucleotide-bindi	nucleotide-bindi	NM_022162	NM_022162
4.94E-03	-7.66E+00	ankyrin repeat d	transmembrane	NM_001146341	NM_001146341
2.46E+02	7.94E+00	hypothetical LOC	hypothetical LOC	NR_026882	NR_026882
3.81E+02	8.57E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_

3.81E+02	8.57E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.56E+02	8.48E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
3.66E+02	8.51E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.66E+02	8.51E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.66E+02	8.51E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.66E+02	8.51E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.94E-03	-7.99E+00	cholinergic recep	solute carrier fan	NM_000738	NM_000738
3.40E+02	8.41E+00	kalirin, RhoGEF k	kalirin, RhoGEF k	NM_001024660,	NM_001024660,NM_003947
3.00E+02	8.23E+00	protein tyrosine	protein tyrosine	NM_080588,NM	NM_080588,NM_002832
3.00E+02	8.23E+00	protein tyrosine	protein tyrosine	NR_002930	NR_002930
2.21E+02	7.79E+00	DNA (cytosine-5-	autoimmune reg	NM_013369,NM	NM_013369,NM_175867
2.56E+02	8.00E+00	ras responsive el	ras responsive el	NM_001003698,	NM_001003698,NM_001003699
4.50E-03	-7.80E+00	G patch domain	G patch domain	NM_018025	NM_018025
2.76E+02	8.11E+00	poly(A) polymera	poly(A) polymera	NM_020144	NM_020144
2.30E+02	7.84E+00	docking protein	docking protein	NM_173660	NM_173660
2.30E+02	7.84E+00	docking protein	docking protein	NM_173660	NM_173660
3.24E+02	8.34E+00	Janus kinase 2	Janus kinase 2	NM_004972	NM_004972
4.15E-03	-7.91E+00	ninein (GSK3B in	ninein (GSK3B in	NM_182944	NM_182944
4.15E-03	-7.91E+00	ninein (GSK3B in	ninein (GSK3B in	NM_182944	NM_182944
2.60E+02	8.02E+00	solute carrier fan	splA/ryanodine r	NM_018155,NM	NM_018155,NM_001104647
3.50E+02	8.45E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
2.71E+02	8.08E+00	FERM domain co	dapper, antagoni	NM_024919,NM	NM_024919,NM_001122841
4.85E-03	-7.69E+00	von Willebrand f	CD9 molecule	NM_000552	NM_000552
2.98E+02	8.22E+00	ectonucleoside t	ectonucleoside t	NM_001033113,	NM_001033113,NM_198585
3.55E-03	-8.14E+00	SPT2, Suppresso	transmembrane	NM_194285	NM_194285
2.37E+02	7.89E+00	H19, imprinted n	insulin-like grow	NR_002196	NR_002196
2.37E+02	7.89E+00	H19, imprinted n	insulin-like grow	NR_002196	NR_002196
2.39E+02	7.90E+00	otopetrin 1	otopetrin 1	NM_177998	NM_177998
3.93E-03	-7.99E+00	paired-like home	golgi brefeldin A	NM_005029	NM_005029
2.68E+02	8.06E+00	regulator of telo	regulator of telo	NM_032957,NM	NM_032957,NM_016434
2.68E+02	8.06E+00	regulator of telo	regulator of telo	NM_032957,NM	NM_032957,NM_016434
3.34E+02	8.38E+00	ATPase, H+ trans	ATPase, H+ trans	NM_001694	NM_001694
2.94E+02	8.20E+00	block of prolifera	block of prolifera	NM_015201	NM_015201
2.92E+02	8.19E+00	chromosome 10	chromosome 10	NM_001098483	NM_001098483
2.92E+02	8.19E+00	chromosome 10	chromosome 10	NM_001098483	NM_001098483
2.12E+02	7.73E+00	Kruppel-like fact	Kruppel-like fact	NM_138693	NM_138693
2.12E+02	7.73E+00	Kruppel-like fact	Kruppel-like fact	NM_138693	NM_138693
2.59E+02	8.02E+00	myosin, heavy ch	myosin, heavy ch	NM_020884	NM_020884
2.59E+02	8.02E+00	myosin, heavy ch	myosin, heavy ch	NM_020884	NM_020884
2.94E+02	8.20E+00	small nuclear rib	RER1 retention i	NR_024489	NR_024489
2.94E+02	8.20E+00	small nuclear rib	RER1 retention i	NR_024489	NR_024489
4.62E-03	-7.76E+00	serpin peptidase	serpin peptidase	NM_001085	NM_001085
2.15E+02	7.75E+00	acetylserotonin	acetylserotonin	NM_004043	NM_004043
2.15E+02	7.75E+00	acetylserotonin	acetylserotonin	NM_004043	NM_004043
3.63E+02	8.50E+00	kinocilin	MAP kinase inter	NM_001097611	NM_001097611
2.39E+02	7.90E+00	chromosome 2 o	chromosome 2 o	NM_207362	NM_207362
2.39E+02	7.90E+00	chromosome 2 o	chromosome 2 o	NM_207362	NM_207362
2.80E+02	8.13E+00	deoxyhypusine h	deoxyhypusine h	NM_031304,NM	NM_031304,NM_001145165
4.80E-03	-7.70E+00	apolipoprotein B	apolipoprotein B	NM_018690	NM_018690
2.81E+02	8.13E+00	coiled-coil doma	malic enzyme 3,	NM_001156474,	NM_001156474,NM_021827
2.81E+02	8.13E+00	coiled-coil doma	malic enzyme 3,	NM_001156474,	NM_001156474,NM_021827
3.20E+02	8.32E+00	NADH dehydrog	nudix (nucleosid	NM_007103	NM_007103
3.20E+02	8.32E+00	NADH dehydrog	nudix (nucleosid	NM_007103	NM_007103
3.20E+02	8.32E+00	NADH dehydrog	nudix (nucleosid	NM_007103	NM_007103
2.68E+02	8.06E+00	family with sequ	POU class 5 hom	NM_174911	NM_174911
2.68E+02	8.06E+00	POU class 5 hom	POU class 5 hom	NM_001159542,	NM_001159542,NR_002304
3.36E-03	-8.22E+00	solute carrier fan	solute carrier fan	NM_015482,NM	NM_015482,NM_021945
3.85E-03	-8.02E+00	acyl-CoA oxidase	BCL2-like 11 (apo	NM_001142808,	NM_001142808,NM_001105516,

2.46E+02	7.94E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
2.70E+02	8.07E+00	BCL6 corepresso	BCL6 corepresso	NM_001123383,	NM_001123383,NM_001123384,N
1.32E+00	4.03E-01	galactose-3-O-su	galactose-3-O-su	NM_004861	NM_004861
2.84E+02	8.15E+00	remodeling and s	remodeling and s	NM_016578	NM_016578
2.84E+02	8.15E+00	remodeling and s	remodeling and s	NM_016578	NM_016578
2.69E+02	8.07E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
2.69E+02	8.07E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
4.45E-03	-7.81E+00	HERPUD family n	septin 7	NM_022373	NM_022373
4.01E-03	-7.96E+00	follistatin-like 1	NADH dehydroge	NM_007085	NM_007085
2.43E-03	-8.69E+00	tripartite motif-c	histone cluster 1,	NM_006355	NM_006355
2.84E+02	8.15E+00	ubiquitin protein	DnaJ (Hsp40) hor	NM_014671	NM_014671
2.35E+02	7.88E+00	nuclear receptor	nuclear receptor	NM_004959	NM_004959
2.35E+02	7.88E+00	nuclear receptor	nuclear receptor	NM_004959	NM_004959
3.09E+02	8.27E+00	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
2.23E+02	7.80E+00	platelet-derived g	platelet-derived g	NM_002608,NM	NM_002608,NM_033016
2.23E+02	7.80E+00	platelet-derived g	platelet-derived g	NM_002608,NM	NM_002608,NM_033016
2.25E+02	7.81E+00	TNFAIP3 interact	SH3-domain binc	NM_024309	NM_024309
2.40E+02	7.91E+00	EPS8-like 3	colony stimulatir	NM_024526,NM	NM_024526,NM_133181,NM_139
2.40E+02	7.91E+00	EPS8-like 3	colony stimulatir	NM_024526,NM	NM_024526,NM_133181,NM_139
2.60E+02	8.02E+00	hypothetical LOC	calcium channel,	NR_024341	NR_024341
2.60E+02	8.02E+00	hypothetical LOC	calcium channel,	NR_024341	NR_024341
3.49E+02	8.45E+00	lipocalin 8	lipocalin 8	NM_178469	NM_178469
3.49E+02	8.45E+00	lipocalin 8	lipocalin 8	NM_178469	NM_178469
3.49E+02	8.45E+00	lipocalin 8	lipocalin 8	NM_178469	NM_178469
5.27E-03	-7.57E+00	par-6 partitioning	breast carcinoma	NM_032521	NM_032521
2.28E+02	7.83E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
2.28E+02	7.83E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
3.73E-03	-8.07E+00	poly(A)-specific r	MAS1 oncogene	NM_173516	NM_173516
3.73E-03	-8.07E+00	poly(A)-specific r	MAS1 oncogene	NM_173516	NM_173516
2.71E+02	8.08E+00	solute carrier fan	centrosomal pro	NM_004174	NM_004174
2.71E+02	8.08E+00	solute carrier fan	centrosomal pro	NM_004174	NM_004174
3.69E-03	-8.08E+00	serpin peptidase	serpin peptidase	NM_080474	NM_080474
2.90E+02	8.18E+00	extracellular leuc	MFNG O-fucosylt	NM_052906	NM_052906
2.90E+02	8.18E+00	extracellular leuc	MFNG O-fucosylt	NM_052906	NM_052906
2.81E-03	-8.48E+00	synaptic vesicle g	solute carrier org	NM_014848	NM_014848
3.15E+02	8.30E+00	myosin VIIB	myosin VIIB	NM_001080527	NM_001080527
3.15E+02	8.30E+00	myosin VIIB	myosin VIIB	NM_001080527	NM_001080527
2.54E+02	7.99E+00	YdjC homolog (ba	YdjC homolog (ba	NM_001017964	NM_001017964
2.37E+02	7.89E+00	SRSF protein kina	SRSF protein kina	NM_182692,NM	NM_182692,NM_182691
3.66E-03	-8.10E+00	ADAM metallope	RUN and FYVE dc	NM_021599	NM_021599
3.66E-03	-8.10E+00	ADAM metallope	RUN and FYVE dc	NM_021599	NM_021599
2.01E+02	7.65E+00	carbohydrate (N-	carbohydrate (N-	NM_004267	NM_004267
2.07E+02	7.69E+00	acetylserotonin (	acetylserotonin (	NM_004192	NM_004192
2.07E+02	7.69E+00	kinesin family me	kinesin family me	NM_015254	NM_015254
5.42E-03	-7.53E+00	cytokine recepto	colony stimulatir	NM_022148	NM_022148
4.19E-03	-7.90E+00	toll-like receptor	family with sequ	NM_006068	NM_006068
4.19E-03	-7.90E+00	toll-like receptor	family with sequ	NM_006068	NM_006068
3.48E-03	-8.17E+00	coiled-coil domai	coiled-coil domai	NM_001017437	NM_001017437
3.70E-03	-8.08E+00	UDP glucuronosy	UDP glucuronosy	NM_019075	NM_019075
2.48E+02	7.95E+00	protein phosphat	protein phosphat	NM_032902	NM_032902
2.48E+02	7.95E+00	protein phosphat	glutamic-pyruvat	NM_032902	NM_032902
3.57E-03	-8.13E+00	biorientation of c	cytoplasmic poly	NM_138369,NM	NM_138369,NM_001159651
3.57E-03	-8.13E+00	biorientation of c	cytoplasmic poly	NM_138369,NM	NM_138369,NM_001159651
2.81E+02	8.13E+00	ArfGAP with Rho	StAR-related lipic	NM_001135190,	NM_001135190,NM_015242,NM_
2.81E+02	8.13E+00	ArfGAP with Rho	StAR-related lipic	NM_001135190,	NM_001135190,NM_015242,NM_
3.07E-03	-8.35E+00	chromosome 17	chromosome 17	NM_001136483	NM_001136483
3.07E-03	-8.35E+00	chromosome 17	chromosome 17	NM_001136483	NM_001136483
3.58E-03	-8.13E+00	activating transcı	ATP synthase, H+	NM_001130059,	NM_001130059,NM_006856,NM_

2.38E+02	7.90E+00	leucine rich repe	leucine rich repe	NM_001080478	NM_001080478
3.07E+02	8.26E+00	quaking homolog	chromosome 6 o	NM_006775,NM	NM_006775,NM_206855,NM_20
3.07E+02	8.26E+00	quaking homolog	chromosome 6 o	NM_006775,NM	NM_006775,NM_206855,NM_20
3.01E-03	-8.38E+00	olfactory recepto	tubulin, gamma	NM_001080841	NM_001080841
3.37E+02	8.40E+00	sodium channel,	sodium channel,	NM_001037,NM	NM_001037,NM_199037
4.12E+02	8.69E+00	acetylserotonin (	acetylserotonin (	NM_004043	NM_004043
3.68E+02	8.52E+00	tryptase alpha/b	tryptase alpha/b	NM_003294	NM_003294
2.95E+02	8.21E+00	ADAM metallope	mortality factor	NM_014272	NM_014272
3.10E+02	8.27E+00	family with sequ	KIAA0182	NM_198491	NM_198491
4.19E-03	-7.90E+00	tripartite motif-c	V-set domain cor	NM_025188,NM	NM_025188,NM_001145635
4.19E-03	-7.90E+00	tripartite motif-c	V-set domain cor	NM_025188,NM	NM_025188,NM_001145635
3.15E+02	8.30E+00	nanos homolog	nanos homolog	NM_001029861	NM_001029861
2.49E+02	7.96E+00	Rho GTPase activ	Rho GTPase activ	NM_020876	NM_020876
2.90E+02	8.18E+00	mitogen-activate	mitogen-activate	NM_002969	NM_002969
3.24E+02	8.34E+00	inositol polyphos	inositol polyphos	NM_005539	NM_005539
2.27E+02	7.82E+00	SRSF protein kina	SRSF protein kina	NM_014370	NM_014370
4.05E-03	-7.95E+00	hexokinase 3 (wh	ubiquitin interact	NM_002115	NM_002115
4.70E-03	-7.73E+00	PQ loop repeat c	PQ loop repeat c	NM_001040125,	NM_001040125,NM_001040126,
2.93E+02	8.20E+00	splicing factor 3a	splicing factor 3a	NM_007165	NM_007165
3.09E+02	8.27E+00	solute carrier fan	poly(rC) binding	NM_194255	NM_194255
2.70E+02	8.08E+00	Rho guanine nuc	Rho guanine nuc	NM_153213	NM_153213
3.08E+02	8.27E+00	PDZ and LIM don	PDZ and LIM don	NM_001131027,	NM_001131027,NM_003687
3.08E+02	8.27E+00	PDZ and LIM don	PDZ and LIM don	NM_001131027,	NM_001131027,NM_003687
3.47E+02	8.44E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.47E+02	8.44E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
4.13E-03	-7.92E+00	zinc finger protei	zinc finger protei	NR_003936,NM_	NR_003936,NM_001105550,NM_
2.94E+02	8.20E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
2.94E+02	8.20E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
2.94E+02	8.20E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
4.13E-03	-7.92E+00	cartilage acidic p	chromosome 10	NM_018058	NM_018058
3.51E+02	8.46E+00	SRY (sex determi	protein interacti	NM_006941	NM_006941
3.51E+02	8.46E+00	SRY (sex determi	protein interacti	NM_006941	NM_006941
4.52E-03	-7.79E+00	Rap guanine nucl	Rap guanine nucl	NM_005312,NM	NM_005312,NM_198679
4.52E-03	-7.79E+00	Rap guanine nucl	Rap guanine nucl	NM_005312,NM	NM_005312,NM_198679
3.07E+02	8.26E+00	mitogen-activate	mitogen-activate	NM_016431	NM_016431
3.07E+02	8.26E+00	mitogen-activate	mitogen-activate	NM_016431	NM_016431
3.37E-03	-8.21E+00	retrotransposon	teratocarcinoma	NM_020769	NM_020769
3.37E-03	-8.21E+00	teratocarcinoma	teratocarcinoma	NR_002718	NR_002718
4.15E+02	8.70E+00	outer dense fibe	outer dense fibe	NM_182577	NM_182577
4.61E-03	-7.76E+00	T-cell activation	fibronectin type	NM_138810	NM_138810
3.23E+02	8.33E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
3.23E+02	8.33E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
3.23E+02	8.33E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
3.34E+02	8.38E+00	glutamic-oxaloac	NK2 transcriptio	NM_002079	NM_002079
3.34E+02	8.38E+00	glutamic-oxaloac	NK2 transcriptio	NM_002079	NM_002079
3.98E+02	8.64E+00	cell division cycle	granzyme M (lym	NM_004359	NM_004359
2.19E+02	7.78E+00	coiled-coil doma	coiled-coil doma	NM_001143980	NM_001143980
3.46E-03	-8.17E+00	X (inactive)-speci	X (inactive)-speci	NR_001564	NR_001564
3.96E+02	8.63E+00	lysine (K)-specific	lysine (K)-specific	NM_001005366,	NM_001005366,NM_032590
3.43E+02	8.42E+00	chromosome 11	peroxisomal biog	NM_001080446	NM_001080446
3.73E-03	-8.07E+00	G protein-couple	G protein-couple	NM_015234,NM	NM_015234,NM_001098518
3.73E-03	-8.07E+00	G protein-couple	G protein-couple	NM_015234,NM	NM_015234,NM_001098518
2.52E+02	7.98E+00	anaphase promo	anaphase promo	NM_013366	NM_013366
4.08E-03	-7.94E+00	topoisomerase (I	transferrin	NM_007027	NM_007027
4.08E-03	-7.94E+00	topoisomerase (I	transferrin	NM_007027	NM_007027
2.69E+02	8.07E+00	telomerase rever	telomerase rever	NM_198253,NM	NM_198253,NM_198255
4.37E-03	-7.84E+00	solute carrier fan	ARP3 actin-relate	NM_025181	NM_025181
2.65E+02	8.05E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020

2.65E+02	8.05E+00	ankyrin repeat d	G protein-couple	NR_027019,NR_	NR_027019,NR_027020
4.42E-03	-7.82E+00	transmembrane	ADAMTS-like 2	NM_001080483	NM_001080483
2.61E+02	8.03E+00	basigin (Ok bloo	hyperpolarizatio	NM_001728,NM	NM_001728,NM_198589
2.34E+02	7.87E+00	ADAM metallope	ADAM metallope	NM_005099	NM_005099
2.43E+02	7.92E+00	inositol polyphos	inositol polyphos	NR_003251,NM_	NR_003251,NM_014937
4.50E-03	-7.80E+00	zona pellucida gl	zona pellucida gl	NM_021186	NM_021186
4.50E-03	-7.80E+00	zona pellucida gl	zona pellucida gl	NM_021186	NM_021186
4.61E-03	-7.76E+00	NK6 homeobox 1	CDP-diacylglycer	NM_006168	NM_006168
4.66E-03	-7.75E+00	tribbles homolog	RanBP-type and	NM_021158	NM_021158
1.97E+02	7.62E+00	pim-3 oncogene	pim-3 oncogene	NM_001001852	NM_001001852
1.44E+00	5.22E-01	similar to cDNA s	similar to cDNA s	NM_001013729	NM_001013729
1.44E+00	5.22E-01	similar to cDNA s	chromosome 21	NM_001013729	NM_001013729
1.44E+00	5.22E-01	similar to cDNA s	chromosome 21	NM_001013729	NM_001013729
3.03E+02	8.24E+00	protocadherin ga	protocadherin ga	NM_018929,NM	NM_018929,NM_032407
2.07E+02	7.69E+00	chromodomain p	chromodomain p	NR_026590	NR_026590
2.07E+02	7.69E+00	chromodomain p	chromodomain p	NR_026590	NR_026590
3.20E+02	8.32E+00	olfactory recepto	olfactory recepto	NR_002158	NR_002158
4.94E-03	-7.66E+00	G protein-couple	DEAH (Asp-Glu-A	NM_018485	NM_018485
4.24E-03	-7.88E+00	neuroblastoma b	neuroblastoma b	NM_001143989	NM_001143989
3.88E+02	8.60E+00	SIX homeobox 2	S1 RNA binding d	NM_016932	NM_016932
3.88E+02	8.60E+00	SIX homeobox 2	S1 RNA binding d	NM_016932	NM_016932
3.49E-03	-8.16E+00	hypothetical LOC	peroxisome proli	NR_027033	NR_027033
3.74E+02	8.55E+00	coagulation facto	H2A histone fam	NM_001007524,	NM_001007524,NM_001007523
3.90E-03	-8.00E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
2.21E+02	7.79E+00	BCL2-associated	inositol polyphos	NM_004281	NM_004281
2.21E+02	7.79E+00	BCL2-associated	inositol polyphos	NM_004281	NM_004281
3.22E+02	8.33E+00	Rho guanine nuc	Rho guanine nuc	NM_001113513	NM_001113513
3.22E+02	8.33E+00	Rho guanine nuc	Rho guanine nuc	NM_001113513	NM_001113513
3.04E+02	8.25E+00	solute carrier fa	solute carrier fa	NM_015063	NM_015063
3.79E-03	-8.04E+00	5,10-methenylte	suppressor of tu	NM_006441	NM_006441
4.55E-03	-7.78E+00	MOB1, Mps One	methylenetetrah	NM_018221	NM_018221
2.78E+02	8.12E+00	EPS8-like 1	EPS8-like 1	NM_133180	NM_133180
3.77E-03	-8.05E+00	chromosome 6 o	D-aspartate oxid	NM_001123364	NM_001123364
2.76E+02	8.11E+00	diacylglycerol lip	diacylglycerol lip	NM_006133	NM_006133
2.64E+02	8.04E+00	deiodinase, iodo	non-protein codi	NM_001362	NM_001362
3.86E-03	-8.02E+00	zinc finger protei	zinc finger protei	NM_001099694	NM_001099694
3.86E-03	-8.02E+00	zinc finger protei	zinc finger protei	NM_001099694	NM_001099694
4.52E-03	-7.79E+00	keratin associate	keratin associate	NM_181605	NM_181605
4.52E-03	-7.79E+00	keratin associate	keratin associate	NM_181604	NM_181604
4.29E-03	-7.87E+00	RNA binding mot	receptor (G prot	NM_001080504	NM_001080504
3.90E-03	-8.00E+00	syntrophin, beta	vacuolar protein	NM_006750	NM_006750
2.30E+02	7.84E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
2.30E+02	7.84E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
3.20E+02	8.32E+00	wingless-type M	wingless-type M	NM_030761	NM_030761
2.60E+02	8.02E+00	zinc finger, CCHC	zinc finger, CCHC	NM_015144	NM_015144
2.60E+02	8.02E+00	zinc finger, CCHC	zinc finger, CCHC	NM_015144	NM_015144
2.49E+02	7.96E+00	ArfGAP with Rho	StAR-related lipi	NM_001135190,	NM_001135190,NM_015242,NM_
2.49E+02	7.96E+00	StAR-related lipi	StAR-related lipi	NM_006645	NM_006645
3.90E-03	-8.00E+00	synapsin III	synapsin III	NM_001135774,	NM_001135774,NM_003490,NM_
3.26E+02	8.35E+00	adenylosuccinate	adenylosuccinate	NM_152328	NM_152328
3.91E-03	-8.00E+00	zinc finger protei	zinc finger protei	NM_153257	NM_153257
2.89E+02	8.17E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
2.89E+02	8.17E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
2.89E+02	8.17E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
3.76E-03	-8.05E+00	ELAV (embryonic	DMRT-like family	NM_021952,NM	NM_021952,NM_001144774
3.76E-03	-8.05E+00	ELAV (embryonic	DMRT-like family	NM_021952,NM	NM_021952,NM_001144774
4.85E-03	-7.69E+00	RNA binding prot	ATP-binding cass	NM_006711,NM	NM_006711,NM_080594
4.85E-03	-7.69E+00	RNA binding prot	ATP-binding cass	NM_006711,NM	NM_006711,NM_080594

4.59E-03	-7.77E+00	inverted formin,	adenylosuccinate	NM_032714	NM_032714
4.15E-03	-7.91E+00	protein tyrosine	cripto, FRL-1, cry	NM_001142370,	NM_001142370,NM_014369
4.47E-03	-7.81E+00	purinergic recept	G protein-couple	NM_014879,NM	NM_014879,NM_001081455
3.53E+02	8.46E+00	H19, imprinted n	insulin-like growt	NR_002196	NR_002196
2.23E+02	7.80E+00	patched 1	chromosome 9 o	NM_001083602,	NM_001083602,NM_001083603,N
2.23E+02	7.80E+00	patched 1	chromosome 9 o	NM_001083602,	NM_001083602,NM_001083603,N
2.83E+02	8.14E+00	mucin 6, oligome	mucin 6, oligome	NM_005961	NM_005961
2.57E+02	8.01E+00	lipocalin 12	prostaglandin D2	NM_178536	NM_178536
2.57E+02	8.01E+00	lipocalin 12	prostaglandin D2	NM_178536	NM_178536
4.23E+02	8.72E+00	zinc finger RNA b	zinc finger RNA b	NM_015174	NM_015174
3.34E+02	8.38E+00	multiple endocri	multiple endocri	NM_130801,NM	NM_130801,NM_130800,NM_000
3.34E+02	8.38E+00	multiple endocri	multiple endocri	NM_130801,NM	NM_130801,NM_130800,NM_000
3.34E+02	8.38E+00	multiple endocri	multiple endocri	NM_130801,NM	NM_130801,NM_130800,NM_000
2.54E+02	7.99E+00	crystallin, beta A	myocardial infarc	NM_001886	NM_001886
2.12E+02	7.73E+00	guanine nucleoti	sphingosine-1-ph	NM_002068	NM_002068
2.12E+02	7.73E+00	sphingosine-1-ph	sphingosine-1-ph	NM_003775	NM_003775
2.85E+02	8.15E+00	retinol binding p	ubiquitination fa	NM_052960	NM_052960
2.16E+02	7.76E+00	hypothetical LOC	solute carrier fa	NR_027102	NR_027102
3.84E+02	8.58E+00	leprecan-like 2	leprecan-like 2	NM_014262	NM_014262
2.70E+02	8.08E+00	hypothetical LOC	hypothetical LOC	NR_027242	NR_027242
2.86E+02	8.16E+00	pecanex-like 2 (D	pecanex-like 2 (D	NM_014801	NM_014801
2.96E+02	8.21E+00	oculocutaneous	oculocutaneous	NM_000275	NM_000275
3.91E-03	-8.00E+00	lysophosphatidyl	lysophosphatidyl	NM_017839	NM_017839
3.91E-03	-8.00E+00	calpain, small su	calpain, small su	NM_032330	NM_032330
2.97E+02	8.22E+00	ephrin-A2	melanoma assoc	NM_001405	NM_001405
2.97E+02	8.22E+00	ephrin-A2	melanoma assoc	NM_001405	NM_001405
2.84E+02	8.15E+00	transmembrane	KIAA0125	NM_025268	NM_025268
2.84E+02	8.15E+00	transmembrane	KIAA0125	NM_025268	NM_025268
2.14E+02	7.74E+00	C2 calcium-depe	C2 calcium-depe	NM_001136263	NM_001136263
2.14E+02	7.74E+00	C2 calcium-depe	C2 calcium-depe	NM_001136263	NM_001136263
2.96E+02	8.21E+00	hypothetical LOC	hypothetical LOC	NR_027314	NR_027314
3.18E+02	8.31E+00	chromosome 6 o	chromosome 6 o	NM_173563	NM_173563
4.08E-03	-7.94E+00	SEC62 homolog (	G protein-couple	NM_003262	NM_003262
2.44E+02	7.93E+00	nucleoredoxin	nucleoredoxin	NM_022463	NM_022463
2.44E+02	7.93E+00	nucleoredoxin	nucleoredoxin	NM_022463	NM_022463
3.24E+02	8.34E+00	cyclic nucleotide	melanoma antige	NM_005140	NM_005140
3.24E+02	8.34E+00	cyclic nucleotide	melanoma antige	NM_005140	NM_005140
3.24E+02	8.34E+00	cyclic nucleotide	melanoma antige	NM_005140	NM_005140
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011548	NM_001011548
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011548	NM_001011548
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011548	NM_001011548
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011548	NM_001011548
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011548	NM_001011548
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011548	NM_001011548
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_002362	NM_002362
3.24E+02	8.34E+00	melanoma antige	melanoma antige	NM_001011550	NM_001011550
3.63E-03	-8.10E+00	prostaglandin D2	prostaglandin E r	NM_000953	NM_000953
3.31E+02	8.37E+00	glutamate recept	activating transc	NM_001134408	NM_001134408
3.18E+02	8.31E+00	solute carrier org	solute carrier org	NM_016354	NM_016354
3.18E+02	8.31E+00	solute carrier org	solute carrier org	NM_016354	NM_016354
2.91E+02	8.19E+00	similar to HGC6.	kinesin family me	NM_001129895	NM_001129895
2.91E+02	8.19E+00	similar to HGC6.	kinesin family me	NM_001129895	NM_001129895
2.91E+02	8.19E+00	similar to HGC6.	kinesin family me	NM_001129895	NM_001129895
2.91E+02	8.19E+00	similar to HGC6.	kinesin family me	NM_001129895	NM_001129895
2.68E+02	8.06E+00	chromosome 15	chromosome 15	NM_015492	NM_015492
2.68E+02	8.06E+00	chromosome 15	chromosome 15	NM_015492	NM_015492
3.19E+02	8.32E+00	zinc finger protei	hect domain and	NM_003414	NM_003414
3.80E+02	8.57E+00	MEF2 activating	Ras interacting p	NM_001130915,	NM_001130915,NM_182574

2.82E+02	8.14E+00	G protein-couple	G protein-couple	NM_019858,NM	NM_019858,NM_014449
2.82E+02	8.14E+00	G protein-couple	G protein-couple	NM_019858,NM	NM_019858,NM_014449
2.95E+02	8.21E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
4.76E-03	-7.72E+00	endoplasmic reti	calcineurin B hor	NM_033266	NM_033266
4.76E-03	-7.72E+00	endoplasmic reti	calcineurin B hor	NM_033266	NM_033266
3.32E+02	8.38E+00	solute carrier fan	solute carrier fan	NM_033102	NM_033102
2.08E+02	7.70E+00	limb region 1 hor	nucleolar proteir	NM_022458	NM_022458
2.08E+02	7.70E+00	limb region 1 hor	nucleolar proteir	NM_022458	NM_022458
4.61E-03	-7.76E+00	phosphodiestera	SEC22 vesicle tra	NM_001002810,	NM_001002810,NM_022359
4.61E-03	-7.76E+00	phosphodiestera	SEC22 vesicle tra	NM_001002810,	NM_001002810,NM_022359
2.18E+02	7.77E+00	notch 1	notch 1	NM_017617	NM_017617
3.58E+02	8.48E+00	slit homolog 1 (D	slit homolog 1 (D	NM_003061	NM_003061
3.58E+02	8.48E+00	slit homolog 1 (D	slit homolog 1 (D	NM_003061	NM_003061
3.58E+02	8.48E+00	slit homolog 1 (D	slit homolog 1 (D	NM_003061	NM_003061
4.94E+02	8.95E+00	solute carrier fan	solute carrier fan	NM_003562	NM_003562
2.20E+02	7.78E+00	5-azacytidine ind	5-azacytidine ind	NM_001009811,	NM_001009811,NM_014984
2.20E+02	7.78E+00	5-azacytidine ind	5-azacytidine ind	NM_001009811,	NM_001009811,NM_014984
2.93E+02	8.20E+00	mannose recepto	mannose recepto	NM_006039	NM_006039
2.67E+02	8.06E+00	insulin-like growt	family with sequ	NM_001007563	NM_001007563
2.67E+02	8.06E+00	insulin-like growt	family with sequ	NM_001007563	NM_001007563
3.74E+02	8.55E+00	mitogen-activate	mitogen-activate	NM_030662	NM_030662
3.44E-03	-8.18E+00	EPH receptor A6	ADP-ribosylation	NM_173655	NM_173655
2.67E+02	8.06E+00	B-cell CLL/lymph	B-cell CLL/lymph	NM_005178	NM_005178
2.67E+02	8.06E+00	B-cell CLL/lymph	B-cell CLL/lymph	NM_005178	NM_005178
3.20E-03	-8.29E+00	collectin sub-fam	allantoicase	NM_199235,NM	NM_199235,NM_024027
2.20E+02	7.78E+00	differentially exp	differentially exp	NM_207514	NM_207514
2.20E+02	7.78E+00	differentially exp	differentially exp	NM_207514	NM_207514
3.20E+02	8.32E+00	methyltransferas	methyltransferas	NM_024086	NM_024086
3.20E+02	8.32E+00	methyltransferas	methyltransferas	NM_024086	NM_024086
3.69E-03	-8.08E+00	hypothetical LOC	odz, odd Oz/ten-	NR_027107	NR_027107
4.70E-03	-7.73E+00	patatin-like phos	THAP domain co	NM_015723	NM_015723
3.98E-03	-7.97E+00	adaptor-related		laeverin	NM_001284	NM_001284
4.03E-03	-7.95E+00	aprataxin and PN	aprataxin and PN	NM_173545	NM_173545
2.15E+02	7.75E+00	isthmin 2 homolo	isthmin 2 homolo	NM_199296,NM	NM_199296,NM_199265,NM_182
2.15E+02	7.75E+00	isthmin 2 homolo	isthmin 2 homolo	NM_199296,NM	NM_199296,NM_199265,NM_182
4.38E-03	-7.83E+00	acyl-CoA synthet	visual system hor	NM_032501	NM_032501
3.26E+02	8.35E+00	dihydrouridine sy	dihydrouridine sy	NM_020175	NM_020175
3.26E+02	8.35E+00	dihydrouridine sy	dihydrouridine sy	NM_020175	NM_020175
4.45E-03	-7.81E+00	ubiquitin-like mo	Wilms tumor 1 ir	NM_005499	NM_005499
4.16E-03	-7.91E+00	teratocarcinoma	teratocarcinoma	NM_003212	NM_003212
3.86E-03	-8.02E+00	hypothetical LOC	family with sequ	NR_003291	NR_003291
2.39E+02	7.90E+00	zinc finger protei	zinc finger protei	NM_153813	NM_153813
2.39E+02	7.90E+00	zinc finger protei	zinc finger protei	NM_153813	NM_153813
2.70E+02	8.08E+00	plexin D1	transmembrane	NM_015103	NM_015103
2.47E+02	7.95E+00	scavenger recept	scavenger recept	NM_005505,NM	NM_005505,NM_001082959
2.47E+02	7.95E+00	scavenger recept	ubiquitin C	NM_005505,NM	NM_005505,NM_001082959
2.58E+02	8.01E+00	kelch-like 34 (Dro	kelch-like 34 (Dro	NM_153270	NM_153270
2.58E+02	8.01E+00	kelch-like 34 (Dro	kelch-like 34 (Dro	NM_153270	NM_153270
3.50E+02	8.45E+00	Sp3 transcription	Obg-like ATPase	NM_003111	NM_003111
3.50E+02	8.45E+00	Sp3 transcription	Obg-like ATPase	NM_003111	NM_003111
3.50E+02	8.45E+00	Sp3 transcription	Obg-like ATPase	NM_003111	NM_003111
4.85E-03	-7.69E+00	BEN domain con	PRP18 pre-mRNA	NM_001100912	NM_001100912
3.42E-03	-8.19E+00	Cas scaffolding p	Cas scaffolding p	NM_020356	NM_020356
2.40E+02	7.91E+00	phosphatidylinos	phosphatidylinos	NM_004910,NM	NM_004910,NM_001130848
2.40E+02	7.91E+00	LFNG O-fucosylp	LFNG O-fucosylp	NM_001040168,	NM_001040168,NM_001040167
2.40E+02	7.91E+00	LFNG O-fucosylp	LFNG O-fucosylp	NM_001040168,	NM_001040168,NM_001040167
3.76E+02	8.56E+00	t-complex 10 hor	chromosome 6 o	NM_004610	NM_004610
3.40E+02	8.41E+00	chromosome 9 o	chromosome 9 o	NM_207511	NM_207511

3.44E-03	-8.18E+00	UDP glucuronosy	UDP glucuronosy	NM_019093	NM_019093
1.36E+00	4.48E-01	nucleoporin 133	ATP-binding cass	NM_018230	NM_018230
2.76E+02	8.11E+00	phosphatidylinos	phosphodiestera	NM_001127178,	NM_001127178,NM_017733
2.76E+02	8.11E+00	phosphatidylinos	phosphodiestera	NM_001127178,	NM_001127178,NM_017733
4.68E-03	-7.74E+00	calsequestrin 1 (	calsequestrin 1 (	NM_001231	NM_001231
3.30E+02	8.37E+00	transmembrane	forkhead box D1	NM_153217	NM_153217
3.30E+02	8.37E+00	transmembrane	forkhead box D1	NM_153217	NM_153217
2.92E+02	8.19E+00	zinc finger protei	zinc finger protei	NM_033113	NM_033113
2.50E+02	7.97E+00	synaptosomal-as	synaptosomal-as	NM_053052	NM_053052
2.46E+02	7.94E+00	zinc finger, DHH	zinc finger, DHH	NM_024786	NM_024786
2.72E+02	8.09E+00	FLJ43860 protein	FLJ43860 protein	NM_207414	NM_207414
2.72E+02	8.09E+00	FLJ43860 protein	FLJ43860 protein	NM_207414	NM_207414
2.72E+02	8.09E+00	FLJ43860 protein	non-protein codi	NM_207414	NM_207414
2.99E+02	8.22E+00	hypothetical LO	hypothetical LO	NR_026664	NR_026664
2.99E+02	8.22E+00	hypothetical LO	hypothetical LO	NR_026664	NR_026664
4.12E-03	-7.92E+00	Rap guanine nuc	Rap guanine nuc	NM_005312,NM	NM_005312,NM_198679
3.21E+02	8.33E+00	UDP-N-acetyl-al	UDP-N-acetyl-al	NM_021808,NM	NM_021808,NM_001122636
3.21E+02	8.33E+00	UDP-N-acetyl-al	UDP-N-acetyl-al	NM_021808,NM	NM_021808,NM_001122636
2.98E+02	8.22E+00	transmembrane	transmembrane	NM_001097620	NM_001097620
2.98E+02	8.22E+00	transmembrane	transmembrane	NM_001097620	NM_001097620
2.98E+02	8.22E+00	transmembrane	transmembrane	NM_001097620	NM_001097620
5.22E+02	9.03E+00	adenosine deami	adenosine deami	NM_018702	NM_018702
3.48E-03	-8.17E+00	tripartite motif-c	tripartite motif-c	NM_033342	NM_033342
3.48E-03	-8.17E+00	tripartite motif-c	tripartite motif-c	NM_033342	NM_033342
3.34E-03	-8.22E+00	chromosome 14	chromosome 14	NM_001010860	NM_001010860
3.08E+02	8.27E+00	spermatogenesis	spermatogenesis	NM_001101677,	NM_001101677,NM_001012415
3.52E+02	8.46E+00	Zic family memb	propionyl CoA ca	NM_007129	NM_007129
3.51E-03	-8.15E+00	transmembrane	protein tyrosine	NM_001079809	NM_001079809
2.49E+02	7.96E+00	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
2.60E+02	8.02E+00	beta-1,4-N-acety	plakophilin 3	NM_178537	NM_178537
2.60E+02	8.02E+00	beta-1,4-N-acety	plakophilin 3	NM_178537	NM_178537
2.60E+02	8.02E+00	beta-1,4-N-acety	plakophilin 3	NM_178537	NM_178537
3.93E-03	-7.99E+00	UDP-galactose-4	3-hydroxymethyl	NM_001127621,	NM_001127621,NM_000403,NM_
3.93E-03	-7.99E+00	3-hydroxymethyl	3-hydroxymethyl	NM_000191	NM_000191
3.81E+02	8.57E+00	core-binding fact	core-binding fact	NM_175931,NM	NM_175931,NM_005187
3.81E+02	8.57E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
3.81E+02	8.57E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
2.98E+02	8.22E+00	PTK6 protein tyr	src-related kinas	NM_005975	NM_005975
2.75E+02	8.10E+00	interferon regula	similar to hCG16	NM_002163	NM_002163
2.75E+02	8.10E+00	interferon regula	similar to hCG16	NM_002163	NM_002163
2.99E+02	8.22E+00	chromosome 6 o	chromosome 6 o	NR_027005	NR_027005
2.99E+02	8.22E+00	chromosome 6 o	chromosome 6 o	NR_027005	NR_027005
2.90E+02	8.18E+00	XK, Kell blood gr	XK, Kell blood gr	NM_001011718	NM_001011718
2.90E+02	8.18E+00	XK, Kell blood gr	XK, Kell blood gr	NM_001011718	NM_001011718
3.97E-03	-7.98E+00	signal peptide, C	metallophospho	NM_173050	NM_173050
3.97E-03	-7.98E+00	signal peptide, C	metallophospho	NM_173050	NM_173050
2.30E+02	7.85E+00	hypothetical pro	forkhead box D4	NR_024443	NR_024443
2.30E+02	7.85E+00	hypothetical pro	forkhead box D4	NR_024443	NR_024443
2.30E+02	7.85E+00	hypothetical pro	forkhead box D4	NR_024443	NR_024443
3.05E+02	8.25E+00	sorting nexin 3	lactation elevate	NM_152827,NM	NM_152827,NM_003795
3.53E+02	8.46E+00	tetratricopeptide	tetratricopeptide	NM_017931	NM_017931
3.95E-03	-7.98E+00	leucine rich repe	fermitin family m	NM_152611	NM_152611
3.60E+02	8.49E+00	alkaline phospha	alkaline phospha	NM_031313	NM_031313
2.75E+02	8.10E+00	pregnancy specif	pregnancy specif	NM_002783	NM_002783
3.59E-03	-8.12E+00	transmembrane	transmembrane	NM_206832	NM_206832
3.59E-03	-8.12E+00	transmembrane	carboxypeptidas	NM_206832	NM_206832
3.71E+02	8.54E+00	cell division cycle	cell division cycle	NM_007065	NM_007065
3.71E+02	8.54E+00	cell division cycle	cell division cycle	NM_007065	NM_007065

3.71E+02	8.54E+00	cell division cycle	cell division cycle	NM_007065	NM_007065
2.54E+02	7.99E+00	chromosome 16	chromosome 16	NM_182563	NM_182563
2.54E+02	7.99E+00	chromosome 16	chromosome 16	NM_182563	NM_182563
2.54E+02	7.99E+00	chromosome 16	chromosome 16	NM_182563	NM_182563
2.69E+02	8.07E+00	acetylserotonin	acetylserotonin	NM_004043	NM_004043
2.69E+02	8.07E+00	acetylserotonin	acetylserotonin	NM_004043	NM_004043
2.24E+02	7.81E+00	runt-related tran	runt-related tran	NM_004350,NM	NM_004350,NM_001031680
2.24E+02	7.81E+00	runt-related tran	runt-related tran	NM_004350,NM	NM_004350,NM_001031680
2.66E+02	8.05E+00	chromosome 10	placenta-specific	NM_025125	NM_025125
2.83E+02	8.14E+00	lysine (K)-specifi	lysine (K)-specifi	NM_015015	NM_015015
3.64E-03	-8.10E+00	leucine rich repe	leucine rich repe	NM_024750,NM	NM_024750,NM_024512
3.10E+02	8.27E+00	mitochondrial ri	solute carrier fa	NM_002949	NM_002949
2.73E+02	8.09E+00	notch 1	notch 1	NM_017617	NM_017617
2.73E+02	8.09E+00	notch 1	notch 1	NM_017617	NM_017617
2.74E+02	8.10E+00	chromobox hom	chromobox hom	NM_020649	NM_020649
4.13E-03	-7.92E+00	complement con	disabled homolo	NM_001737	NM_001737
3.18E+02	8.31E+00	NLR family mem	NLR family mem	NM_170722,NM	NM_170722,NM_024618
3.49E+02	8.45E+00	solute carrier fa	matrix metallope	NM_001110781	NM_001110781
3.49E+02	8.45E+00	matrix metallope	matrix metallope	NR_002946	NR_002946
3.15E-03	-8.31E+00	hypothetical LOC	LIM domain cont	NR_024413	NR_024413
2.12E+02	7.73E+00	docking protein	low density lipop	NM_173660	NM_173660
2.12E+02	7.73E+00	docking protein	low density lipop	NM_173660	NM_173660
2.51E+02	7.97E+00	tripartite motif-c	tripartite motif-c	NM_171982	NM_171982
4.38E+02	8.78E+00	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
4.09E-03	-7.93E+00	chromosome 1 o	TAR DNA binding	NM_173507	NM_173507
3.30E+02	8.37E+00	adenosine deami	adenosine deami	NM_001145407,	NM_001145407,NM_001033049,
3.30E+02	8.37E+00	adenosine deami	adenosine deami	NM_001145407,	NM_001145407,NM_001033049,
2.34E+02	7.87E+00	ring finger protei	family with sequ	NM_002938	NM_002938
2.43E+02	7.92E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
4.24E-03	-7.88E+00	chemokine (C-X-	RUN and FYVE d	NR_002712	NR_002712
4.24E-03	-7.88E+00	chemokine (C-X-	RUN and FYVE d	NR_002712	NR_002712
4.54E+02	8.83E+00	WD repeat dom	zinc finger, MYN	NM_138778	NM_138778
4.10E+02	8.68E+00	heparan sulfate	heparan sulfate	NM_005529	NM_005529
4.10E+02	8.68E+00	heparan sulfate	heparan sulfate	NM_005529	NM_005529
3.43E+02	8.42E+00	paternally expres	paternally expres	NM_015068,NM	NM_015068,NM_001040152
2.69E+02	8.07E+00	PR domain conta	PR domain conta	NM_020229	NM_020229
2.69E+02	8.07E+00	PR domain conta	PR domain conta	NM_020229	NM_020229
3.43E+02	8.42E+00	protein tyrosine	protein tyrosine	NM_080549,NM	NM_080549,NM_002831
1.68E+00	7.50E-01	asparagine-linke	transient recept	NR_024248	NR_024248
1.68E+00	7.50E-01	asparagine-linke	transient recept	NR_024248	NR_024248
2.26E+02	7.82E+00	ankyrin repeat a	ATP-binding cass	NM_080871,NM	NM_080871,NM_001142459,NM_
2.23E+02	7.80E+00	EGF-like-domain,	EGF-like-domain,	NM_016215	NM_016215
2.60E+02	8.02E+00	lectin, mannose-	regulator of G-pr	NM_006816	NM_006816
2.60E+02	8.02E+00	lectin, mannose-	regulator of G-pr	NM_006816	NM_006816
3.19E-03	-8.29E+00	Rho guanine nuc	Rho guanine nuc	NM_001128615,	NM_001128615,NM_019555,NM_
3.19E-03	-8.29E+00	Rho guanine nuc	Rho guanine nuc	NM_001128615,	NM_001128615,NM_019555,NM_
3.77E-03	-8.05E+00	transmembrane	telomeric repeat	NM_144676	NM_144676
2.81E+02	8.13E+00	chromosome 2 o	WD repeat dom	NM_001145054	NM_001145054
4.18E-03	-7.90E+00	keratin associate	keratin associate	NM_175858	NM_175858
3.48E+02	8.44E+00	hypothetical LOC	hypothetical LOC	NR_015434	NR_015434
3.74E+02	8.55E+00	glutamic-oxaloac	NK2 transcriptio	NM_002079	NM_002079
2.84E+02	8.15E+00	ArfGAP with SH3	ArfGAP with SH3	NM_017707,NM	NM_017707,NM_001143778
2.84E+02	8.15E+00	ArfGAP with SH3	ArfGAP with SH3	NM_017707,NM	NM_017707,NM_001143778
3.19E+02	8.32E+00	protein disulfide	protein disulfide	NM_006849	NM_006849
3.19E+02	8.32E+00	protein disulfide	protein disulfide	NM_006849	NM_006849
2.77E+02	8.11E+00	zinc finger protei	zinc finger protei	NR_003952	NR_003952
2.77E+02	8.11E+00	zinc finger protei	zinc finger protei	NR_003952	NR_003952
3.61E-03	-8.11E+00	dual specificity p	interferon regula	NM_020185	NM_020185

3.59E+02	8.49E+00	pentraxin 4, long	pentraxin 4, long	NM_001013658	NM_001013658
3.99E-03	-7.97E+00	scaffold attachm	scaffold attachm	NM_014649	NM_014649
2.43E+02	7.92E+00	glioma tumor su	glioma tumor su	NM_015711	NM_015711
2.43E+02	7.92E+00	glioma tumor su	glioma tumor su	NM_015711	NM_015711
2.90E+02	8.18E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
2.90E+02	8.18E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
3.41E+02	8.41E+00	kazrin	kazrin	NM_001018000	NM_001018000
3.41E+02	8.41E+00	kazrin	kazrin	NM_001018001	NM_001018001
4.59E-03	-7.77E+00	tandem C2 doma	fibulin 5	NM_152332,NM	NM_152332,NM_001128595,NM_
2.97E+02	8.22E+00	neuronal pentra	neuronal pentra	NM_002522	NM_002522
5.00E-03	-7.64E+00	T-cell leukemia/l	T-cell leukemia/l	NM_012468,NM	NM_012468,NM_020552,NM_014
3.52E+02	8.46E+00	pentatricopeptid	zinc finger protei	NM_024754	NM_024754
3.52E+02	8.46E+00	pentatricopeptid	zinc finger protei	NM_024754	NM_024754
3.52E+02	8.46E+00	pentatricopeptid	zinc finger protei	NM_024754	NM_024754
2.99E+02	8.22E+00	F-box and leucin	F-box and leucin	NM_024963	NM_024963
2.62E+02	8.03E+00	BAH domain and	BAH domain and	NM_001080519	NM_001080519
2.62E+02	8.03E+00	BAH domain and	BAH domain and	NM_001080519	NM_001080519
2.63E+02	8.04E+00	zinc finger protei	integrator compl	NM_152626,NM	NM_152626,NM_007139
2.63E+02	8.04E+00	zinc finger protei	integrator compl	NM_152626,NM	NM_152626,NM_007139
2.63E+02	8.04E+00	zinc finger protei	integrator compl	NM_152626,NM	NM_152626,NM_007139
2.64E+02	8.04E+00	Rho GTPase acti	Rho GTPase acti	NM_014882	NM_014882
2.73E+02	8.09E+00	latent transformi	latent transformi	NM_001042544	NM_001042544
2.73E+02	8.09E+00	latent transformi	latent transformi	NM_001042544	NM_001042544
3.57E-03	-8.13E+00	otoancorin	otoancorin	NM_144672	NM_144672
3.46E+02	8.43E+00	ATP-binding cass	ATP-binding cass	NM_019112	NM_019112
3.46E+02	8.43E+00	ATP-binding cass	ATP-binding cass	NM_019112	NM_019112
3.46E+02	8.43E+00	ATP-binding cass	ATP-binding cass	NM_019112	NM_019112
3.18E+02	8.31E+00	brain-specific an	brain-specific an	NM_001702	NM_001702
3.18E+02	8.31E+00	brain-specific an	brain-specific an	NM_001702	NM_001702
2.59E+02	8.02E+00	calcium homeost	calcium homeost	NM_006387	NM_006387
2.59E+02	8.02E+00	calcium homeost	calcium homeost	NM_006387	NM_006387
2.45E+02	7.94E+00	glutamate recep	high mobility gro	NM_000841	NM_000841
5.15E-03	-7.60E+00	DNA (cytosine-5-	dystrobrevin, be	NM_175630	NM_175630
2.59E+02	8.02E+00	BEN domain con	mannose-binding	NR_027512	NR_027512
2.56E+02	8.00E+00	bicaudal D homo	bicaudal D homo	NM_001003800,	NM_001003800,NM_015250
2.56E+02	8.00E+00	bicaudal D homo	bicaudal D homo	NM_001003800,	NM_001003800,NM_015250
3.59E+02	8.49E+00	SMAD family me	SMAD family me	NM_001145103	NM_001145103
2.53E+02	7.98E+00	chromatin licensi	chromatin licensi	NM_030928	NM_030928
2.53E+02	7.98E+00	chromatin licensi	chromatin licensi	NM_030928	NM_030928
2.72E+02	8.09E+00	G protein-couple	G protein-couple	NM_001508	NM_001508
5.20E-03	-7.59E+00	spastic paraplegi	cyclin A1	NM_015087,NM	NM_015087,NM_001142296,NM_
2.54E+02	7.99E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
2.54E+02	7.99E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
4.35E-03	-7.84E+00	troponin T type	mitochondrial rib	NM_001042781,	NM_001042781,NM_001042782,
2.31E+02	7.85E+00	t-SNARE domain	brain-specific an	NM_145003	NM_145003
4.32E-03	-7.86E+00	chromosome 9 o	chromosome 9 o	NM_032307	NM_032307
5.34E-03	-7.55E+00	adenosine deami	adenosine deami	NM_001012969,	NM_001012969,NM_001159280
3.66E+02	8.51E+00	zinc finger, DHH	zinc finger, DHH	NM_013373	NM_013373
3.66E+02	8.51E+00	zinc finger, DHH	zinc finger, DHH	NM_013373	NM_013373
3.66E+02	8.51E+00	zinc finger, DHH	zinc finger, DHH	NM_013373	NM_013373
5.06E-03	-7.63E+00	ATG4 autophagy	forkhead box D3	NM_178221,NM	NM_178221,NM_032852
2.31E+02	7.85E+00	nicalin homolog	nicalin homolog	NM_020170	NM_020170
3.12E+02	8.29E+00	zinc finger protei	zinc finger protei	NM_018555	NM_018555
2.68E+02	8.06E+00	forkhead box F2	forkhead box C1	NM_001452	NM_001452
2.68E+02	8.06E+00	forkhead box F2	forkhead box C1	NM_001452	NM_001452
4.25E-03	-7.88E+00	GRIP and coiled-	ADP-ribosylation	NM_024523	NM_024523
4.98E-03	-7.65E+00	transglutaminas	transglutaminas	NM_003245	NM_003245
3.84E+02	8.58E+00	CAP-GLY domain	CAP-GLY domain	NM_032421,NM	NM_032421,NM_003388

3.84E+02	8.58E+00	CAP-GLY domain	CAP-GLY domain	NM_032421,NM	NM_032421,NM_003388
4.11E-03	-7.93E+00	secretory carrier	secretory carrier	NM_052837	NM_052837
3.42E-03	-8.19E+00	tetraspanin 3	NKF3 kinase fam	NM_005724,NM	NM_005724,NM_198902
4.03E+02	8.65E+00	ADAMTS-like 4	ADAMTS-like 4	NM_025008,NM	NM_025008,NM_019032
4.03E+02	8.65E+00	ADAMTS-like 4	ADAMTS-like 4	NM_025008,NM	NM_025008,NM_019032
3.54E+02	8.47E+00	phospholipase C,	phospholipase C,	NM_014638	NM_014638
4.13E-03	-7.92E+00	protein kinase C,	Scm-like with fo	NM_006257	NM_006257
4.13E-03	-7.92E+00	protein kinase C,	Scm-like with fo	NM_006257	NM_006257
4.74E-03	-7.72E+00	chromosome 6 o	chromosome 6 o	NM_001085401	NM_001085401
3.57E+02	8.48E+00	chromosome 16	chromosome 16	NM_001080524	NM_001080524
3.57E+02	8.48E+00	chromosome 16	clusterin associat	NM_001080524	NM_001080524
4.47E-03	-7.81E+00	solute carrier fan	acyl-CoA dehydr	NM_152697	NM_152697
2.79E+02	8.12E+00	transforming gro	B9 protein doma	NM_000660	NM_000660
2.79E+02	8.12E+00	B9 protein doma	B9 protein doma	NM_030578	NM_030578
2.87E+02	8.16E+00	desmin	SPEG complex lo	NM_001927	NM_001927
2.64E+02	8.04E+00	tRNA methyltran	tRNA methyltran	NM_152307	NM_152307
2.64E+02	8.04E+00	tRNA methyltran	tRNA methyltran	NM_152307	NM_152307
2.63E+02	8.04E+00	histone deacetyl	histone deacetyl	NM_006037	NM_006037
3.62E-03	-8.11E+00	interleukin 17F	interleukin 17F	NM_052872	NM_052872
3.62E-03	-8.11E+00	interleukin 17F	interleukin 17F	NM_052872	NM_052872
2.72E+02	8.09E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
3.22E+02	8.33E+00	single stranded D	acyl-CoA thioest	NM_018070,NM	NM_018070,NM_145716,NM_001
3.79E-03	-8.04E+00	ubiquitin specific	UDP glucuronosy	NM_018218	NM_018218
3.79E-03	-8.04E+00	UDP glucuronosy	UDP glucuronosy	NM_019076	NM_019076
4.72E-03	-7.73E+00	coiled-coil and C	coiled-coil and C	NM_001080522,	NM_001080522,NR_024098
2.13E+02	7.74E+00	zinc finger, MYM	zinc finger, MYM	NM_001039650,	NM_001039650,NM_001039649
3.80E-03	-8.04E+00	leucine zipper, d	non-protein codi	NM_032287	NM_032287
3.80E-03	-8.04E+00	non-protein codi	non-protein codi	NM_001012986	NM_001012986
3.71E+02	8.54E+00	guanine nucleoti	guanine nucleoti	NM_002067	NM_002067
3.89E-03	-8.01E+00	ankyrin repeat d	Rho guanine nuc	NM_017664	NM_017664
2.67E+02	8.06E+00	transmembrane	KIAA0125	NM_025268	NM_025268
3.68E-03	-8.09E+00	dipeptidyl-peptic	dipeptidyl-peptic	NM_130797	NM_130797
3.68E-03	-8.09E+00	dipeptidyl-peptic	dipeptidyl-peptic	NM_130797	NM_130797
3.68E-03	-8.09E+00	dipeptidyl-peptic	dipeptidyl-peptic	NM_130797	NM_130797
3.03E+02	8.24E+00	zinc finger and B	zinc finger and B	NM_025224	NM_025224
2.70E+02	8.07E+00	myeloid/lymphoi	myeloid/lymphoi	NM_005934	NM_005934
2.70E+02	8.07E+00	myeloid/lymphoi	myeloid/lymphoi	NM_005934	NM_005934
3.85E-03	-8.02E+00	serine/threonine	solute carrier fan	NM_052902	NM_052902
2.72E+02	8.09E+00	chromosome 9 o	chromosome 9 o	NM_152833	NM_152833
2.72E+02	8.09E+00	chromosome 9 o	chromosome 9 o	NM_152833	NM_152833
4.25E-03	-7.88E+00	KIAA1529	KIAA1529	NM_020893	NM_020893
3.72E+02	8.54E+00	protamine 2	protamine 2	NM_002762	NM_002762
3.18E+02	8.31E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
3.18E+02	8.31E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
3.18E+02	8.31E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
2.61E+02	8.03E+00	mannosyl (alpha-	mannosyl (alpha-	NM_001114617,	NM_001114617,NM_001114618,
2.61E+02	8.03E+00	mannosyl (alpha-	mannosyl (alpha-	NM_001114617,	NM_001114617,NM_001114618,
4.42E-03	-7.82E+00	glycerol kinase 5	5'-3' exoribonucl	NM_001039547	NM_001039547
3.68E+02	8.52E+00	solute carrier fan	solute carrier fan	NM_001636	NM_001636
3.50E-03	-8.16E+00	transient recept	sedoheptulokina	NM_080706,NM	NM_080706,NM_080705,NM_01
3.04E+02	8.25E+00	ligase I, DNA, ATI	caspase recruitm	NM_000234	NM_000234
3.04E+02	8.25E+00	ligase I, DNA, ATI	caspase recruitm	NM_000234	NM_000234
3.14E-03	-8.32E+00	family with sequ	torsin family 3, m	NM_014864	NM_014864
3.05E+02	8.25E+00	hypothetical LOC	inhibitor of DNA	NR_015405	NR_015405
4.21E-03	-7.89E+00	cripto, FRL-1, cry	chromosome 2 o	NM_001079530	NM_001079530
4.21E-03	-7.89E+00	cripto, FRL-1, cry	chromosome 2 o	NM_001079530	NM_001079530
2.67E+02	8.06E+00	stimulated by ret	stimulated by ret	NM_001142620	NM_001142620
4.25E-03	-7.88E+00	cholesterol 25-hy	lipase A, lysosom	NM_003956	NM_003956

3.12E+02	8.29E+00	chromosome 4 o	chromosome 4 o	NM_152770	NM_152770
3.12E+02	8.29E+00	chromosome 4 o	chromosome 4 o	NM_152770	NM_152770
1.24E+00	3.06E-01	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
1.24E+00	3.06E-01	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.82E+02	8.14E+00	agrin	chromosome 1 o	NM_198576	NM_198576
2.82E+02	8.14E+00	agrin	chromosome 1 o	NM_198576	NM_198576
2.32E+02	7.86E+00	pleckstrin homol	pleckstrin homol	NM_001144759,	NM_001144759,NM_001144758
2.82E+02	8.14E+00	pleckstrin homol	pleckstrin homol	NM_052909	NM_052909
3.15E+02	8.30E+00	SVOP-like	SVOP-like	NM_001139456,	NM_001139456,NM_174959
4.85E-03	-7.69E+00	chromosome 14	olfactory recept	NM_001146683	NM_001146683
2.65E+02	8.05E+00	mucin 6, oligom	mucin 2, oligom	NM_005961	NM_005961
2.65E+02	8.05E+00	mucin 6, oligom	mucin 2, oligom	NM_005961	NM_005961
3.43E+02	8.42E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
3.43E+02	8.42E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
4.47E+02	8.80E+00	ST6 (alpha-N-ace	ST6 (alpha-N-ace	NM_175040,NM	NM_175040,NM_175039
4.47E+02	8.80E+00	ST6 (alpha-N-ace	ST6 (alpha-N-ace	NM_175040,NM	NM_175040,NM_175039
3.81E+02	8.57E+00	---	C-terminal bindi	NR_024569	NR_024569
3.69E-03	-8.08E+00	syntrophin, gam	thyroid peroxida	NM_018968	NM_018968
2.65E+02	8.05E+00	activin A recepto	activin A recepto	NM_001111031,	NM_001111031,NM_145259,NM_
3.61E+02	8.50E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
3.46E-03	-8.17E+00	paraoxonase 3	paraoxonase 2	NM_000940	NM_000940
3.86E+02	8.59E+00	histone deacetyl	ES cell expressed	NM_006044	NM_006044
3.86E+02	8.59E+00	histone deacetyl	ES cell expressed	NM_006044	NM_006044
4.90E-03	-7.67E+00	hypothetical LO	hypothetical LO	NR_024172,NR_	NR_024172,NR_024173
2.90E+02	8.18E+00	thromboxane A2	chromosome 19	NM_001060,NM	NM_001060,NM_201636
4.43E-03	-7.82E+00	chromosome 5 o	chromosome 5 o	NM_001001343	NM_001001343
4.43E-03	-7.82E+00	chromosome 5 o	chromosome 5 o	NM_001001343	NM_001001343
2.33E+02	7.87E+00	XPA binding prot	XPA binding prot	NM_020196	NM_020196
2.33E+02	7.87E+00	XPA binding prot	XPA binding prot	NM_020196	NM_020196
4.02E-03	-7.96E+00	neuronatin	catenin, beta lik	NM_005386,NM	NM_005386,NM_181689
4.02E-03	-7.96E+00	neuronatin	catenin, beta lik	NM_005386,NM	NM_005386,NM_181689
4.55E-03	-7.78E+00	vezatin, adheren	methionyl amino	NM_017599	NM_017599
3.51E+02	8.46E+00	sialic acid bindin	sialic acid bindin	NM_003830	NM_003830
3.41E-03	-8.20E+00	chromosome 10	chromosome 10	NM_001010896	NM_001010896
3.42E-03	-8.19E+00	origin recognitio	lipoma HMGIC f	NM_181747	NM_181747
3.42E-03	-8.19E+00	origin recognitio	lipoma HMGIC f	NM_181747	NM_181747
2.62E-03	-8.58E+00	eukaryotic transl	ribose 5-phosph	NM_004836	NM_004836
2.32E+02	7.86E+00	pleckstrin homol	pleckstrin homol	NM_001144759,	NM_001144759,NM_001144758
2.32E+02	7.86E+00	pleckstrin homol	pleckstrin homol	NM_001144759,	NM_001144759,NM_001144758
2.84E+02	8.15E+00	KIAA0467	KIAA0467	NM_015284	NM_015284
2.62E+02	8.03E+00	uridine-cytidine	uridine-cytidine	NM_017859	NM_017859
2.62E+02	8.03E+00	uridine-cytidine	uridine-cytidine	NM_017859	NM_017859
2.62E+02	8.03E+00	uridine-cytidine	uridine-cytidine	NM_017859	NM_017859
3.25E+02	8.34E+00	sal-like 3 (Droso	sal-like 3 (Droso	NM_171999	NM_171999
3.25E+02	8.34E+00	sal-like 3 (Droso	sal-like 3 (Droso	NM_171999	NM_171999
3.70E-03	-8.08E+00	hypothetical pro	hypothetical pro	NR_027073	NR_027073
3.86E-03	-8.02E+00	glutamate recep	chromosome 3 o	NM_001080423	NM_001080423
4.85E-03	-7.69E+00	ADP-ribosylation	protein kinase C	NM_001142293,	NM_001142293,NM_014570
3.40E+02	8.41E+00	phospholipase C,	chromosome 15	NM_004573	NM_004573
3.04E+02	8.25E+00	tryptase gamma	tryptase gamma	NM_012467	NM_012467
3.04E+02	8.25E+00	tryptase gamma	tryptase beta 2 (	NM_012467	NM_012467
3.08E+02	8.27E+00	zinc finger, DHH	hypothetical LO	NM_013373	NM_013373
3.08E+02	8.27E+00	zinc finger, DHH	hypothetical LO	NM_013373	NM_013373
3.35E+02	8.39E+00	PHD finger prote	cAMP responsiv	NM_001101802,	NM_001101802,NM_016621
1.44E+00	5.30E-01	solute carrier fa	solute carrier fa	NM_182838	NM_182838
1.44E+00	5.30E-01	solute carrier fa	solute carrier fa	NM_182838	NM_182838
1.44E+00	5.30E-01	solute carrier fa	solute carrier fa	NM_182838	NM_182838
2.70E+02	8.08E+00	arginine vasopre	arginine vasopre	NM_000707	NM_000707

3.97E+02	8.63E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
3.90E-03	-8.00E+00	dual specificity p	Fc receptor-like	NM_017823	NM_017823
2.52E+02	7.98E+00	LIM homeobox 2	NIMA (never in n	NM_004789	NM_004789
3.40E+02	8.41E+00	fibroblast growt	ring finger protei	NM_020637	NM_020637
2.62E+02	8.03E+00	copper metaboli	UDP-GlcNAc:bet	NM_152516	NM_152516
2.62E+02	8.03E+00	UDP-GlcNAc:bet	UDP-GlcNAc:bet	NM_006577	NM_006577
3.07E+02	8.26E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794
3.07E+02	8.26E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794
3.09E+02	8.27E+00	proline rich 25	lipase maturatio	NM_001013638	NM_001013638
3.79E-03	-8.04E+00	THUMP domain	solute carrier fa	NM_025264	NM_025264
2.97E+02	8.22E+00	differentially exp	differentially exp	NM_207514	NM_207514
2.93E+02	8.20E+00	proline/serine-ri	proline/serine-ri	NM_032636,NM	NM_032636,NM_001032291,NM_
2.93E+02	8.20E+00	proline/serine-ri	proline/serine-ri	NM_032636,NM	NM_032636,NM_001032291,NM_
2.95E+02	8.21E+00	Down syndrome	potassium inwar	NR_026840,NR_	NR_026840,NR_026839,NR_0268
4.72E-03	-7.73E+00	fragile histidine t	protein tyrosine	NM_002012	NM_002012
4.72E-03	-7.73E+00	fragile histidine t	protein tyrosine	NM_002012	NM_002012
3.58E+02	8.48E+00	abhydrolase do	abhydrolase do	NM_024527	NM_024527
3.41E+02	8.41E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
3.41E+02	8.41E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
2.69E+02	8.07E+00	ADAM metallop	ADAM metallop	NM_139055	NM_139055
2.69E+02	8.07E+00	ADAM metallop	ADAM metallop	NM_139055	NM_139055
2.45E+02	7.94E+00	tumor necrosis f	tumor necrosis f	NM_004195,NM	NM_004195,NM_148901,NM_14
2.85E+02	8.15E+00	doublesex and m	SWI/SNF related,	NM_181872,NM	NM_181872,NM_006557,NM_001
2.72E+02	8.09E+00	casein kinase 1,	casein kinase 1,	NM_139062,NM	NM_139062,NM_001893
2.72E+02	8.09E+00	casein kinase 1,	casein kinase 1,	NM_139062,NM	NM_139062,NM_001893
3.01E+02	8.23E+00	collagen, type VI	collagen, type VI	NM_001849,NM	NM_001849,NM_058175,NM_05
3.01E+02	8.23E+00	collagen, type VI	collagen, type VI	NM_001849,NM	NM_001849,NM_058175,NM_05
3.01E+02	8.23E+00	collagen, type VI	collagen, type VI	NM_001849,NM	NM_001849,NM_058175,NM_05
3.60E+02	8.49E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
3.84E-03	-8.03E+00	cytochrome P45	c-src tyrosine kin	NM_000761	NM_000761
3.84E-03	-8.03E+00	cytochrome P45	c-src tyrosine kin	NM_000761	NM_000761
2.83E+02	8.14E+00	galanin-like pept	galanin-like pept	NM_033106,NM	NM_033106,NM_001145546
3.23E-03	-8.27E+00	muscle RAS onco	extended synapt	NM_001085049	NM_001085049
2.38E+02	7.90E+00	tripartite motif-c	tripartite motif-c	NM_018207	NM_018207
2.38E+02	7.90E+00	tripartite motif-c	tripartite motif-c	NM_018207	NM_018207
3.29E+02	8.36E+00	coactivator-asso	coactivator-asso	NM_199141	NM_199141
2.30E+02	7.84E+00	IQ motif and Sec	IQ motif and Sec	NM_014869,NM	NM_014869,NM_001134382
2.25E+02	7.81E+00	chromosome 1 o	chromosome 1 o	NM_001110533,	NM_001110533,NM_152607
4.05E-03	-7.95E+00	fatty acid desatu	fatty acid desatu	NM_013402	NM_013402
4.66E-03	-7.75E+00	galactosylcerami	G protein-couple	NM_001037525	NM_001037525
2.73E+02	8.09E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
2.75E+02	8.10E+00	structural maint	structural maint	NM_148674	NM_148674
1.58E+00	6.63E-01	ribosomal RNA p	ribosomal RNA p	NM_015703	NM_015703
1.58E+00	6.63E-01	ribosomal RNA p	ribosomal RNA p	NM_015703	NM_015703
2.67E+02	8.06E+00	regulatory factor	regulatory factor	NM_000635,NM	NM_000635,NM_134433
2.42E+02	7.92E+00	meteorin, glial c	meteorin, glial c	NM_024042	NM_024042
2.66E+02	8.05E+00	G patch domain	MAGI family me	NM_015698	NM_015698
3.41E+02	8.41E+00	plexin A3	plexin A3	NM_017514	NM_017514
3.41E+02	8.41E+00	plexin A3	plexin A3	NM_017514	NM_017514
3.64E-03	-8.10E+00	choroideremia (	dachshund hom	NM_001145414	NM_001145414
2.09E+02	7.70E+00	zinc finger protei	zinc finger protei	NM_001127464	NM_001127464
2.09E+02	7.70E+00	zinc finger protei	zinc finger protei	NM_001127464	NM_001127464
1.47E+00	5.57E-01	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,
2.65E+02	8.05E+00	collagen, type X	collagen, type X	NM_030582,NM	NM_030582,NM_130444
2.43E+02	7.92E+00	chromobox hom	chromobox hom	NM_020649	NM_020649
3.80E-03	-8.04E+00	disrupted in rena	hypothetical LO	NM_032839	NM_032839
3.80E-03	-8.04E+00	disrupted in rena	hypothetical LO	NM_032839	NM_032839
3.33E+02	8.38E+00	dipeptidase 1 (re	dipeptidase 1 (re	NM_001128141	NM_001128141

3.30E+02	8.37E+00	chymotrypsinoge	chymotrypsinoge	NM_001025200	NM_001025200
3.30E+02	8.37E+00	chymotrypsinoge	chymotrypsinoge	NM_001025200	NM_001025200
2.90E+02	8.18E+00	peptidoglycan re	peptidoglycan re	NM_005091	NM_005091
3.34E-03	-8.22E+00	solute carrier fan	mediator comple	NM_173851	NM_173851
3.34E-03	-8.22E+00	solute carrier fan	mediator comple	NM_173851	NM_173851
2.68E+02	8.06E+00	SRY (sex determi	ATPase, class VI,	NM_003106	NM_003106
5.18E-03	-7.59E+00	chromosome X o	chromosome X o	NM_001031705	NM_001031705
5.18E-03	-7.59E+00	chromosome X o	chromosome X o	NM_001031705	NM_001031705
2.23E+02	7.80E+00	Fc fragment of Ig	Fc fragment of Ig	NM_003890	NM_003890
2.23E+02	7.80E+00	Fc fragment of Ig	Fc fragment of Ig	NM_003890	NM_003890
2.17E+02	7.76E+00	coiled-coil domai	chromosome 2 o	NM_138770	NM_138770
2.81E+02	8.13E+00	sushi, nidogen ar	sushi, nidogen ar	NM_001080437	NM_001080437
3.09E+02	8.27E+00	ubiquitin-like mo	ubiquitin-like mo	NM_003334	NM_003334
4.81E-03	-7.70E+00	adenylate kinase	ST6 (alpha-N-ace	NM_000476	NM_000476
3.21E-03	-8.28E+00	family with sequ	family with sequ	NM_153036	NM_153036
3.21E-03	-8.28E+00	family with sequ	family with sequ	NM_153036	NM_153036
3.21E+02	8.33E+00	isoprenylcysteine	hairy and enhanc	NM_012405	NM_012405
3.20E+02	8.32E+00	testis-specific tra	RNA binding mot	NR_001541	NR_001541
2.85E+02	8.15E+00	C1q and tumor n	C1q and tumor n	NM_198594,NM	NM_198594,NM_030968
2.85E+02	8.15E+00	C1q and tumor n	C1q and tumor n	NM_198594,NM	NM_198594,NM_030968
3.69E-03	-8.08E+00	protocadherin al	protocadherin al	NM_018909,NM	NM_018909,NM_031849,NM_031
3.69E-03	-8.08E+00	protocadherin al	protocadherin al	NM_018910,NM	NM_018910,NM_031852
3.59E-03	-8.12E+00	X (inactive)-speci	non-protein codi	NR_001564	NR_001564
3.59E-03	-8.12E+00	X (inactive)-speci	non-protein codi	NR_001564	NR_001564
2.46E+02	7.94E+00	family with sequ	family with sequ	NM_152704,NM	NM_152704,NM_199138
2.58E+02	8.01E+00	eukaryotic transl	pancreatic proge	NM_001958	NM_001958
2.58E+02	8.01E+00	eukaryotic transl	pancreatic proge	NM_001958	NM_001958
2.62E+02	8.03E+00	castor zinc finger	castor zinc finger	NM_017766	NM_017766
2.62E+02	8.03E+00	castor zinc finger	castor zinc finger	NM_017766	NM_017766
3.78E+02	8.56E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
3.60E+02	8.49E+00	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
3.60E+02	8.49E+00	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
2.80E+02	8.13E+00	mesoderm poste	mesoderm poste	NM_001039958	NM_001039958
3.05E+02	8.25E+00	zinc finger, SWIN	zinc finger, SWIN	NM_023072	NM_023072
3.05E+02	8.25E+00	zinc finger, SWIN	zinc finger, SWIN	NM_023072	NM_023072
4.53E-03	-7.78E+00	signal transducer	signal transducer	NM_003151	NM_003151
3.24E+02	8.34E+00	vav 1 guanine nu	vav 1 guanine nu	NM_005428	NM_005428
1.59E+00	6.70E-01	kinesin family me	chromosome 14	NM_015656	NM_015656
1.59E+00	6.70E-01	kinesin family me	chromosome 14	NM_015656	NM_015656
3.22E-03	-8.28E+00	small nucleolar R	cysteinyl-tRNA sy	NR_002982	NR_002982
4.09E-03	-7.93E+00	chromosome 12	transient recepto	NM_032829	NM_032829
2.67E+02	8.06E+00	NCK-associated p	NCK-associated p	NM_001037806	NM_001037806
2.67E+02	8.06E+00	NCK-associated p	NCK-associated p	NM_001037806	NM_001037806
3.30E+02	8.36E+00	ATPase, Ca++ tra	ATPase, Ca++ tra	NM_001001344,	NM_001001344,NM_021949
2.85E+02	8.15E+00	zinc activated lig	zinc activated lig	NM_180990	NM_180990
2.23E+02	7.80E+00	SH3-binding dom	SH3-binding dom	NM_030645	NM_030645
2.23E+02	7.80E+00	SH3-binding dom	SH3-binding dom	NM_030645	NM_030645
2.72E+02	8.09E+00	EGF-like-domain,	EGF-like-domain,	NM_016215	NM_016215
2.52E+02	7.98E+00	POU class 2 hom	death effector do	NM_002698	NM_002698
2.52E+02	7.98E+00	POU class 2 hom	death effector do	NM_002698	NM_002698
3.79E-03	-8.04E+00	---	surfactant protei	NM_006926	NM_006926
3.79E-03	-8.04E+00	---	surfactant protei	NM_006926	NM_006926
3.31E+02	8.37E+00	SH3-domain GRB	SH3-domain GRB	NM_003025	NM_003025
2.80E+02	8.13E+00	glutamic-pyruvat	major facilitator	NM_005309	NM_005309
3.86E-03	-8.02E+00	FAT tumor suppr	FAT tumor suppr	NM_001447	NM_001447
2.42E+02	7.92E+00	GLI family zinc fi	GLI family zinc fi	NM_000168	NM_000168
4.78E-03	-7.71E+00	nuclear receptor	spermatogenesis	NM_001145157	NM_001145157
4.78E-03	-7.71E+00	nuclear receptor	spermatogenesis	NM_001145157	NM_001145157

1.96E+02	7.62E+00	2,4-dienoyl CoA	2,4-dienoyl CoA	NM_020664	NM_020664
1.96E+02	7.62E+00	2,4-dienoyl CoA	2,4-dienoyl CoA	NM_020664	NM_020664
2.24E+02	7.81E+00	hypothetical LOC	RAB12, member	NR_024419	NR_024419
2.52E+02	7.98E+00	ciliary rootlet coi	ciliary rootlet coi	NR_026752	NR_026752
3.21E+02	8.33E+00	REST corepresso	TNF receptor-ass	NM_015156	NM_015156
3.14E+02	8.30E+00	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
3.14E+02	8.30E+00	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
3.95E-03	-7.98E+00	GATA binding pro	hypothetical pro	NM_032638,NM	NM_032638,NM_001145661,NM_
3.95E-03	-7.98E+00	hypothetical pro	hypothetical pro	NR_026954	NR_026954
2.36E+02	7.88E+00	chromosome 9 o	chromosome 9 o	NM_017995,NM	NM_017995,NM_024718
2.36E+02	7.88E+00	chromosome 9 o	chromosome 9 o	NM_017995,NM	NM_017995,NM_024718
2.36E+02	7.88E+00	chromosome 9 o	chromosome 9 o	NM_001080482	NM_001080482
4.98E-03	-7.65E+00	protease, serine,	protease, serine,	NM_002773	NM_002773
4.38E-03	-7.83E+00	peptidase D	carbohydrate (N-	NM_000285	NM_000285
4.38E-03	-7.83E+00	peptidase D	carbohydrate (N-	NM_000285	NM_000285
2.87E+02	8.16E+00	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
3.25E+02	8.34E+00	tuftelin interacti	tuftelin interacti	NM_001008697,	NM_001008697,NM_012143
3.80E-03	-8.04E+00	F-box and leucin	wingless-type MI	NM_152441	NM_152441
3.27E-03	-8.26E+00	calcium channel,	retinoblastoma b	NM_006539	NM_006539
3.06E+02	8.26E+00	protein phospha	glutamic-pyruvat	NM_032902	NM_032902
2.53E+02	7.98E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
2.53E+02	7.98E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
4.01E-03	-7.96E+00	chromosome 11	chromosome 11	NM_024650	NM_024650
2.62E+02	8.03E+00	angiopoietin-like	UbiA prenyltrans	NM_021146	NM_021146
2.62E+02	8.03E+00	angiopoietin-like	UbiA prenyltrans	NM_021146	NM_021146
2.65E+02	8.05E+00	glia maturation f	glia maturation f	NM_004877	NM_004877
2.65E+02	8.05E+00	glia maturation f	glia maturation f	NM_004877	NM_004877
3.06E+02	8.26E+00	archaelysin famil	archaelysin famil	NM_133463	NM_133463
1.47E+00	5.59E-01	adhesion regulat	adhesion regulat	NM_007002,NM	NM_007002,NM_175573
2.43E+02	7.92E+00	mitogen-activate	mitogen-activate	NM_002751	NM_002751
1.22E+00	2.89E-01	null	phosphatidylinos	null	null
1.22E+00	2.89E-01	null	phosphatidylinos	null	null
2.78E+02	8.12E+00	family with sequ	proteasome (pro	NM_032448	NM_032448
2.78E+02	8.12E+00	family with sequ	proteasome (pro	NM_032448	NM_032448
2.11E+00	1.08E+00	collagen, type X	collagen, type X	NM_030582,NM	NM_030582,NM_130444
2.20E+02	7.78E+00	chromosome 9 o	NOTCH-regulate	NM_017723	NM_017723
4.05E-03	-7.95E+00	chromosome X o	proline syntheta	NR_003671	NR_003671
4.22E-03	-7.89E+00	regulator of chro	Rho guanine nuc	NM_001136204,	NM_001136204,NM_018715
4.22E-03	-7.89E+00	regulator of chro	Rho guanine nuc	NM_001136204,	NM_001136204,NM_018715
1.16E+00	2.19E-01	growth factor in	growth factor in	NM_004188,NM	NM_004188,NM_001135031
1.16E+00	2.19E-01	growth factor in	growth factor in	NM_004188,NM	NM_004188,NM_001135031
3.34E-03	-8.22E+00	trafficking protei	trafficking protei	NM_001042646	NM_001042646
3.34E-03	-8.22E+00	trafficking protei	trafficking protei	NM_001042646	NM_001042646
2.70E+02	8.07E+00	nanos homolog	nanos homolog	NM_001098622	NM_001098622
2.30E+02	7.85E+00	wingless-type MI	wingless-type MI	NM_030753	NM_030753
2.30E+02	7.85E+00	wingless-type MI	wingless-type MI	NM_030753	NM_030753
2.30E+02	7.85E+00	chromosome 19	ephrin-A2	NM_017914	NM_017914
4.53E-03	-7.78E+00	family with sequ	coiled-coil doma	NR_026809	NR_026809
2.93E+02	8.20E+00	ADAMTS-like 2	ADAMTS-like 2	NM_014694	NM_014694
3.54E+02	8.47E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.54E+02	8.47E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.54E+02	8.47E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
2.28E+02	7.83E+00	pyruvate carbox	pyruvate carbox	NM_022172,NM	NM_022172,NM_001040716,NM_
2.80E+02	8.13E+00	fatty acid syntha	fatty acid syntha	NM_004104	NM_004104
2.80E+02	8.13E+00	fatty acid syntha	fatty acid syntha	NM_004104	NM_004104
2.62E+02	8.03E+00	lymphocyte anti	chromosome 8 o	NM_001127213,	NM_001127213,NM_002346
2.76E+02	8.11E+00	proteasome (pro	proteasome (pro	NM_001134340,	NM_001134340,NM_032302
4.13E-03	-7.92E+00	transmembrane	ArfGAP with FG r	NM_024795	NM_024795

3.12E+02	8.29E+00	twinfilin, actin-bi	protein phosphat	NM_007284	NM_007284
3.00E+02	8.23E+00	fascin homolog 1	fascin homolog 1	NM_003088	NM_003088
3.00E+02	8.23E+00	fascin homolog 1	fascin homolog 1	NM_003088	NM_003088
3.39E+02	8.41E+00	solute carrier fan	CCAAT/enhancer	NM_019849	NM_019849
3.39E+02	8.41E+00	solute carrier fan	CCAAT/enhancer	NM_019849	NM_019849
3.39E+02	8.41E+00	solute carrier fan	CCAAT/enhancer	NM_019849	NM_019849
2.94E+02	8.20E+00	elastase, neutrop	elastase, neutrop	NM_001972	NM_001972
3.25E+02	8.34E+00	G protein-couple	G protein-couple	NM_002929	NM_002929
2.65E+02	8.05E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
3.26E+02	8.35E+00	matrix metallope	matrix metallope	NR_002946	NR_002946
3.26E+02	8.35E+00	matrix metallope	matrix metallope	NR_002946	NR_002946
4.05E+02	8.66E+00	troponin I type 2	lymphocyte-spec	NM_001145841	NM_001145841
2.14E+02	7.74E+00	nucleolar comple	tubulin, alpha 3d	NR_002826	NR_002826
2.14E+02	7.74E+00	nucleolar comple	tubulin, alpha 3d	NR_002826	NR_002826
2.40E+02	7.91E+00	potassium chann	potassium chann	NM_016601	NM_016601
2.40E+02	7.91E+00	potassium chann	potassium chann	NM_016601	NM_016601
2.61E-03	-8.58E+00	mRNA turnover 4	mRNA turnover 4	NM_016183	NM_016183
4.04E+02	8.66E+00	tripartite motif-c	fumarylacetoace	NM_138800	NM_138800
3.29E-03	-8.25E+00	adenosine A3 rec	RAP1A, member	NM_000677	NM_000677
2.86E+02	8.16E+00	WD repeat doma	WD repeat doma	NM_024100	NM_024100
3.42E+02	8.42E+00	shisa homolog 6	shisa homolog 6	NM_207386	NM_207386
3.42E+02	8.42E+00	shisa homolog 6	shisa homolog 6	NM_207386	NM_207386
4.74E-03	-7.72E+00	chondroitin sulfa	outer dense fibe	NM_001897	NM_001897
3.37E+02	8.40E+00	protein phosphat	protein phosphat	NM_013239,NM	NM_013239,NM_199326
3.59E+02	8.49E+00	solute carrier fan	solute carrier fan	NM_006598	NM_006598
3.59E+02	8.49E+00	solute carrier fan	solute carrier fan	NM_001003841	NM_001003841
2.96E+02	8.21E+00	ubiquitin-conjuga	EF-hand calcium	NM_003350	NM_003350
4.35E-03	-7.84E+00	cyclin L1	ventricular zone	NM_020307	NM_020307
4.01E-03	-7.96E+00	poly(A) polymera	monocyte to ma	NM_020144	NM_020144
4.40E-03	-7.83E+00	egf-like module c	egf-like module c	NR_024075	NR_024075
3.76E-03	-8.05E+00	ornithine decarb	nucleolar protei	NM_002539	NM_002539
3.15E+02	8.30E+00	synaptosomal-as	protease, serine,	NM_053052	NM_053052
4.64E-03	-7.75E+00	capping protein (	chromosome 1 o	NM_004930	NM_004930
2.88E+02	8.17E+00	kinase non-catal	kinase non-catal	NM_152643	NM_152643
3.37E+02	8.40E+00	cysteine-rich pro	cysteine-rich pro	NM_001311	NM_001311
2.50E+02	7.96E+00	scinderin	scinderin	NM_001112706	NM_001112706
2.39E+02	7.90E+00	protease, serine,	zymogen granule	NM_006799,NM	NM_006799,NM_144956,NM_144
2.39E+02	7.90E+00	zymogen granule	zymogen granule	NM_145252	NM_145252
2.66E+02	8.05E+00	collagen, type VI	collagen, type VI	NM_001848	NM_001848
2.66E+02	8.05E+00	collagen, type VI	collagen, type VI	NM_001848	NM_001848
3.87E-03	-8.01E+00	tetraspanin 11	DEAD/H (Asp-Gl	NM_001080509	NM_001080509
4.83E-03	-7.69E+00	spectrin, beta, n	chromosome 11	NM_006946	NM_006946
2.85E+02	8.15E+00	PR domain conta	PR domain conta	NM_022115	NM_022115
3.95E-03	-7.98E+00	chromosome 10	SEC23 interactin	NM_024834	NM_024834
3.95E-03	-7.98E+00	chromosome 10	SEC23 interactin	NM_024834	NM_024834
2.42E+02	7.92E+00	notch 1	EGF-like-domain,	NM_017617	NM_017617
3.05E+02	8.25E+00	glutamine rich 2	glutamine rich 2	NM_032134	NM_032134
3.05E+02	8.25E+00	glutamine rich 2	glutamine rich 2	NM_032134	NM_032134
3.95E+02	8.63E+00	F-box and WD re	F-box and WD re	NM_018998	NM_018998
3.43E+02	8.42E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.43E+02	8.42E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.70E+02	8.53E+00	hypothetical LO	H19, imprinted n	NR_024471	NR_024471
3.70E+02	8.53E+00	hypothetical LO	H19, imprinted n	NR_024471	NR_024471
5.18E-03	-7.59E+00	angiopoietin-like	GTPase activatin	NM_012098	NM_012098
4.74E-03	-7.72E+00	leukocyte immur	leukocyte immur	NM_006669	NM_006669
2.52E+02	7.98E+00	plexin A1	plexin A1	NM_032242	NM_032242
2.52E+02	7.98E+00	plexin A1	plexin A1	NM_032242	NM_032242
2.51E+02	7.97E+00	solute carrier fan	solute carrier fan	NM_004785,NM	NM_004785,NM_001130012

2.96E+02	8.21E+00	early B-cell facto	early B-cell facto	NM_001005463	NM_001005463
2.53E+02	7.98E+00	anoctamin 9	anoctamin 9	NM_001012302	NM_001012302
2.53E+02	7.98E+00	anoctamin 9	anoctamin 9	NM_001012302	NM_001012302
3.54E+02	8.47E+00	mucin 5B, oligom	mucin 5B, oligom	NM_002458	NM_002458
3.54E+02	8.47E+00	mucin 5B, oligom	mucin 5B, oligom	NM_002458	NM_002458
3.54E+02	8.47E+00	mucin 5B, oligom	mucin 5B, oligom	NM_002458	NM_002458
1.83E+00	8.68E-01	ataxin 1	ataxin 1	NM_001128164,	NM_001128164,NM_000332
4.21E-03	-7.89E+00	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
4.21E-03	-7.89E+00	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
2.88E+02	8.17E+00	zinc finger protei	zinc finger protei	NM_032819	NM_032819
2.88E+02	8.17E+00	zinc finger protei	zinc finger protei	NM_032819	NM_032819
3.13E+02	8.29E+00	KH-type splicing	solute carrier fan	NM_003685	NM_003685
3.13E+02	8.29E+00	solute carrier fan	solute carrier fan	NM_173637	NM_173637
3.36E+02	8.39E+00	RASD family, mei	RASD family, mei	NM_014310	NM_014310
3.36E+02	8.39E+00	RASD family, mei	RASD family, mei	NM_014310	NM_014310
3.36E+02	8.39E+00	RASD family, mei	RASD family, mei	NM_014310	NM_014310
2.32E+02	7.86E+00	fms-related tyros	fms-related tyros	NM_002020	NM_002020
3.57E+02	8.48E+00	non-protein codi	phosphofructoki	NM_001098830	NM_001098830
3.09E+02	8.27E+00	transferrin recep	actin-like 6B	NM_003227	NM_003227
1.46E+00	5.44E-01	FSHD region gen	zinc finger protei	NM_001124759	NM_001124759
1.46E+00	5.44E-01	FSHD region gen	zinc finger protei	NM_001124759	NM_001124759
3.11E+02	8.28E+00	HHIP-like 2	HHIP-like 2	NM_024746	NM_024746
4.09E-03	-7.93E+00	tigger transposab	zinc finger protei	NM_033208	NM_033208
2.70E+02	8.08E+00	grainyhead-like 1	Kruppel-like fact	NM_198182	NM_198182
1.33E+00	4.11E-01	CTD (carboxy-ter	XRCC6 binding pi	NM_005730	NM_005730
1.33E+00	4.11E-01	CTD (carboxy-ter	XRCC6 binding pi	NM_005730	NM_005730
2.74E+02	8.10E+00	tumor protein p7	tumor protein p7	NM_001126240,	NM_001126240,NM_001126242,N
1.49E+00	5.73E-01	glycosyltransfera	glycosyltransfera	NM_024656	NM_024656
1.49E+00	5.73E-01	glycosyltransfera	glycosyltransfera	NM_024656	NM_024656
3.32E+02	8.38E+00	hypothetical LOC	CHRNA7 (choline	NR_026771	NR_026771
2.00E+00	1.00E+00	hypothetical LOC	hypothetical LOC	NR_027081	NR_027081
4.01E-03	-7.96E+00	B9 protein doma	B9 protein doma	NM_030578	NM_030578
4.01E-03	-7.96E+00	B9 protein doma	B9 protein doma	NM_030578	NM_030578
4.01E-03	-7.96E+00	B9 protein doma	B9 protein doma	NM_030578	NM_030578
4.19E-03	-7.90E+00	dickkopf homolo	dickkopf homolo	NM_014420	NM_014420
3.03E+02	8.24E+00	nuclear factor of	nuclear factor of	NM_172390,NM	NM_172390,NM_172388,NM_006
3.03E+02	8.24E+00	nuclear factor of	nuclear factor of	NM_172390,NM	NM_172390,NM_172388,NM_006
2.44E+02	7.93E+00	5-hydroxytryptar	5-hydroxytryptar	NM_000871	NM_000871
2.85E+02	8.15E+00	similar to cDNA s	chromosome 21	NM_001013729	NM_001013729
4.04E+02	8.66E+00	GTP binding prot	histamine recept	NM_015666	NM_015666
3.64E-03	-8.10E+00	potassium voltag	WAP four-disulfi	NM_172347	NM_172347
2.04E+02	7.67E+00	DCN1, defective	DCN1, defective	NM_001014283	NM_001014283
1.77E+00	8.20E-01	zinc finger protei	hepatopoietin PC	NM_014106	NM_014106
1.77E+00	8.20E-01	zinc finger protei	hepatopoietin PC	NM_014106	NM_014106
3.48E-03	-8.17E+00	AF4/FMR2 family	LON peptidase N	NM_001025108,	NM_001025108,NM_002285
4.83E-03	-7.69E+00	castor zinc finger	chromosome 1 o	NM_017766	NM_017766
4.83E-03	-7.69E+00	castor zinc finger	chromosome 1 o	NM_017766	NM_017766
3.13E+02	8.29E+00	GNAS complex lo	GNAS complex lo	NM_016592	NM_016592
4.01E-03	-7.96E+00	zinc finger protei	histone cluster 1,	NM_007149	NM_007149
4.01E-03	-7.96E+00	zinc finger protei	histone cluster 1,	NM_007149	NM_007149
3.51E-03	-8.15E+00	thrombospondin	histamine N-met	NM_001080427	NM_001080427
3.51E-03	-8.15E+00	thrombospondin	histamine N-met	NM_001080427	NM_001080427
3.99E-03	-7.97E+00	alpha 1,3-galacto	polyhomeotic ho	NM_001080438	NM_001080438
3.10E+02	8.27E+00	ankyrin repeat d	lipase, member I	NR_027270	NR_027270
3.10E+02	8.27E+00	ankyrin repeat d	lipase, member I	NR_027270	NR_027270
2.86E+02	8.16E+00	STEAP family me	STEAP family me	NM_018234,NM	NM_018234,NM_182915,NM_001
3.50E-03	-8.16E+00	programmed cell	mitochondrial rib	NR_003713	NR_003713
2.88E+02	8.17E+00	hypothetical pro	hypothetical pro	NR_002787	NR_002787

2.28E+02	7.83E+00	chromosome 1 o	chromosome 1 o	NM_152610	NM_152610
2.28E+02	7.83E+00	chromosome 1 o	chromosome 1 o	NM_152610	NM_152610
4.43E-03	-7.82E+00	chromosome 2 o	chromosome 2 o	NM_144736,NM	NM_144736,NM_001083946
2.70E+02	8.07E+00	diacylglycerol kir	diacylglycerol kir	NM_003647	NM_003647
2.67E+02	8.06E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
2.67E+02	8.06E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
2.67E+02	8.06E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
3.37E-03	-8.21E+00	neurogenin 1	chemokine (C-X-	NM_006161	NM_006161
3.37E-03	-8.21E+00	neurogenin 1	chemokine (C-X-	NM_006161	NM_006161
2.44E+02	7.93E+00	fibronectin leucir	fibronectin leucir	NM_013280	NM_013280
2.44E+02	7.93E+00	fibronectin leucir	fibronectin leucir	NM_013280	NM_013280
3.86E+02	8.59E+00	coiled-coil domai	ubiquitin specific	NM_001004306	NM_001004306
2.22E+02	7.79E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
2.22E+02	7.79E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
2.22E+02	7.79E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
3.68E+02	8.52E+00	Rho GTPase activ	Rho GTPase activ	NM_025251	NM_025251
3.31E-03	-8.24E+00	FYVE, RhoGEF an	FYVE, RhoGEF an	NM_001083536	NM_001083536
3.03E+02	8.24E+00	tubulin, alpha 3c	tubulin, alpha 3c	NM_006001	NM_006001
3.52E-03	-8.15E+00	WNT1 inducible	potassium chann	NM_003881	NM_003881
3.16E+02	8.30E+00	small nucleolar R	HLA-B associatec	NR_002971	NR_002971
3.16E+02	8.30E+00	small nucleolar R	HLA-B associatec	NR_002971	NR_002971
2.64E+02	8.04E+00	spindle and kinet	mitogen-activate	NM_001039535,	NM_001039535,NM_145060
2.64E+02	8.04E+00	mitogen-activate	mitogen-activate	NM_002747	NM_002747
3.30E-03	-8.25E+00	phosphatase and	phosphatase and	NM_080672	NM_080672
3.30E-03	-8.25E+00	phosphatase and	phosphatase and	NM_080672	NM_080672
2.32E+02	7.86E+00	insulin induced g	engrailed homeo	NM_005542,NM	NM_005542,NM_198337,NM_19
2.32E+02	7.86E+00	insulin induced g	engrailed homeo	NM_005542,NM	NM_005542,NM_198337,NM_19
2.93E+02	8.20E+00	heparan sulfate (	heparan sulfate (	NM_001009606	NM_001009606
3.10E-03	-8.34E+00	ethanolamine kir	renin	NM_018208	NM_018208
3.10E-03	-8.34E+00	ethanolamine kir	renin	NM_018208	NM_018208
2.62E+02	8.03E+00	maternally expre	maternally expre	NR_002766	NR_002766
2.62E+02	8.03E+00	maternally expre	maternally expre	NR_002766	NR_002766
2.62E+02	8.03E+00	maternally expre	maternally expre	NR_002766	NR_002766
2.62E+02	8.03E+00	maternally expre	maternally expre	NR_002766	NR_002766
2.97E+02	8.22E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
2.97E+02	8.22E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
3.00E+02	8.23E+00	G protein-couple	G protein-couple	NM_001004106,	NM_001004106,NM_002082,NM_
3.53E-03	-8.14E+00	antisense fragile	antisense fragile	NR_024503,NR_	NR_024503,NR_024502,NR_0245
3.53E-03	-8.14E+00	antisense fragile	antisense fragile	NR_024503,NR_	NR_024503,NR_024502,NR_0245
4.08E-03	-7.94E+00	protein tyrosine	centromere prot	NM_005401	NM_005401
2.10E+02	7.72E+00	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
3.63E-03	-8.10E+00	olfactomedin 1	KIAA0649	NM_006334	NM_006334
3.37E+02	8.40E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
3.37E+02	8.40E+00	crystallin, lambd	crystallin, lambd	NM_015974	NM_015974
3.37E+02	8.40E+00	crystallin, lambd	crystallin, lambd	NM_015974	NM_015974
2.92E+02	8.19E+00	ISL LIM homeob	ISL LIM homeob	NM_145805	NM_145805
2.92E+02	8.19E+00	ISL LIM homeob	ISL LIM homeob	NM_145805	NM_145805
5.00E-03	-7.64E+00	protease, serine,	myosin, light cha	NM_182702	NM_182702
4.68E-03	-7.74E+00	DENN/MADD do	chromosome 1 o	NM_144977	NM_144977
4.68E-03	-7.74E+00	DENN/MADD do	chromosome 1 o	NM_144977	NM_144977
3.51E-03	-8.15E+00	chromosome 6 o	chromosome 6 o	NR_026860	NR_026860
2.71E+02	8.08E+00	phosphatidylinos	phosphatidylinos	NM_012398	NM_012398
2.71E+02	8.08E+00	phosphatidylinos	phosphatidylinos	NM_012398	NM_012398
3.74E-03	-8.06E+00	keratin associate	keratin associate	NM_001123387	NM_001123387
1.17E+00	2.30E-01	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
1.17E+00	2.30E-01	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
2.73E+02	8.09E+00	PR domain conta	PR domain conta	NM_022115	NM_022115
3.05E+02	8.25E+00	paraneoplastic a	melanoma antig	NM_032882	NM_032882

2.50E+02	7.96E+00	methionine sulfo	methionine sulfo	NM_001135671	NM_001135671
2.50E+02	7.96E+00	methionine sulfo	methionine sulfo	NM_001135671	NM_001135671
3.49E+02	8.45E+00	NLR family, pyrin	zinc finger protei	NM_153447	NM_153447
2.47E+02	7.95E+00	docking protein	docking protein	NM_024872	NM_024872
4.88E-03	-7.68E+00	FYVE and coiled-	FYVE and coiled-	NM_024513	NM_024513
2.38E+02	7.90E+00	calcium homeost	calcium homeost	NM_001001412	NM_001001412
2.38E+02	7.90E+00	calcium homeost	calcium homeost	NM_001001412	NM_001001412
3.34E+02	8.38E+00	obscurin-like 1	obscurin-like 1	NM_015311	NM_015311
2.34E+02	7.87E+00	ATPase, Ca++ tra	zinc finger, ZZ-ty	NM_174953,NM	NM_174953,NM_174957,NM_174
2.43E+02	7.92E+00	kelch-like 26 (Dr	kelch-like 26 (Dr	NM_018316	NM_018316
2.43E+02	7.92E+00	kelch-like 26 (Dr	kelch-like 26 (Dr	NM_018316	NM_018316
3.08E+02	8.27E+00	transcription fact	extracellular leuc	NR_001288	NR_001288
3.08E+02	8.27E+00	transcription fact	extracellular leuc	NR_001288	NR_001288
2.75E+02	8.10E+00	G protein-couple	G protein-couple	NM_001145774	NM_001145774
3.17E-03	-8.30E+00	C2 calcium-depe	hypothetical pro	NM_001007595	NM_001007595
3.38E+02	8.40E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.38E+02	8.40E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.69E-03	-8.08E+00	small nucleolar R	small nucleolar R	NR_000005	NR_000005
2.55E+02	8.00E+00	RAB35, member	RAB35, member	NM_006861	NM_006861
1.49E+00	5.79E-01	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
1.49E+00	5.79E-01	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
1.49E+00	5.79E-01	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
3.01E+02	8.23E+00	TNF receptor-ass	complement con	NM_005658	NM_005658
4.02E-03	-7.96E+00	troponin T type	ladinin 1	NM_000364,NM	NM_000364,NM_001001432,NM_
3.25E+02	8.34E+00	epsin 1	NLR family, pyrin	NM_001130071	NM_001130071
3.15E-03	-8.31E+00	acyl-CoA thioest	spermidine/sper	NM_001037171,	NM_001037171,NM_001033583
3.15E-03	-8.31E+00	acyl-CoA thioest	spermidine/sper	NM_001037171,	NM_001037171,NM_001033583
1.50E+00	5.85E-01	ATPase, class II, t	ATPase, class II, t	NM_198531	NM_198531
1.50E+00	5.85E-01	ATPase, class II, t	ATPase, class II, t	NM_198531	NM_198531
1.50E+00	5.85E-01	ATPase, class II, t	ATPase, class II, t	NM_198531	NM_198531
2.56E+02	8.00E+00	core-binding fact	core-binding fact	NM_175931,NM	NM_175931,NM_005187
3.76E-03	-8.05E+00	WD repeat dom	stimulated by ret	NM_014149	NM_014149
3.62E+02	8.50E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
2.60E+02	8.02E+00	paraoxonase 3	paraoxonase 3	NM_000940	NM_000940
3.23E+02	8.33E+00	chromosome 2 o	ankyrin repeat d	NM_214461	NM_214461
2.14E+02	7.74E+00	claudin 9	claudin 9	NM_020982	NM_020982
2.54E+02	7.99E+00	major facilitator	major facilitator	NM_032219	NM_032219
2.54E+02	7.99E+00	major facilitator	major facilitator	NM_032219	NM_032219
2.71E+02	8.08E+00	chromosome 8 o	nicotinate phosp	NM_001100878	NM_001100878
2.71E+02	8.08E+00	nicotinate phosp	nicotinate phosp	NM_145201	NM_145201
4.01E-03	-7.96E+00	arginine vasopre	MARVEL domain	NM_021732	NM_021732
4.01E-03	-7.96E+00	arginine vasopre	MARVEL domain	NM_021732	NM_021732
3.85E-03	-8.02E+00	WD repeat and S	V-set and immu	NM_018639	NM_018639
2.90E+02	8.18E+00	heparan sulfate	placenta-specific	NM_004807	NM_004807
3.91E-03	-8.00E+00	dysbindin (dystr	growth arrest-sp	NM_024043,NM	NM_024043,NM_001042610
3.91E-03	-8.00E+00	dysbindin (dystr	growth arrest-sp	NM_024043,NM	NM_024043,NM_001042610
3.69E-03	-8.08E+00	protocadherin b	protocadherin b	NM_018930	NM_018930
3.62E+02	8.50E+00	transcription elo	ArfGAP with SH3	NM_003196	NM_003196
4.98E-03	-7.65E+00	chromosome 14	chromosome 14	NR_027004	NR_027004
3.00E+02	8.23E+00	mesoderm speci	mesoderm speci	NM_177524	NM_177524
2.48E+02	7.95E+00	zinc finger, FYVE	zinc finger, FYVE	NM_024071	NM_024071
2.73E+02	8.09E+00	MOB1, Mps One	MOB1, Mps One	NM_130807	NM_130807
2.90E+02	8.18E+00	splicing factor 3b	splicing factor 3b	NM_012426	NM_012426
4.29E-03	-7.87E+00	zinc finger protei	zinc finger protei	NM_152909	NM_152909
4.22E-03	-7.89E+00	protein kinase, A	UDP-N-acetyl-al	NM_016203,NM	NM_016203,NM_001040633,NM_
4.81E-03	-7.70E+00	serpin peptidase	ring finger and C	NM_000488	NM_000488
5.11E-03	-7.61E+00	KIAA0100	stromal cell-deri	NM_014680	NM_014680
2.64E+02	8.04E+00	GRB2-associated	GRB2-associated	NM_001037814	NM_001037814

2.64E+02	8.04E+00	GRB2-associated	GRB2-associated	NM_001037814	NM_001037814
3.98E-03	-7.97E+00	family with sequ	zinc finger protei	NM_145111	NM_145111
3.98E-03	-7.97E+00	family with sequ	zinc finger protei	NM_145111	NM_145111
3.25E+02	8.34E+00	oxidative stress i	oxidative stress i	NM_013370,NM	NM_013370,NM_182980
3.30E+02	8.36E+00	G protein-couple	G protein-couple	NM_178471	NM_178471
2.91E+02	8.19E+00	DEAD (Asp-Glu-A	homer homolog	NM_019070	NM_019070
1.43E+00	5.19E-01	---	---	NR_002820	NR_002820
2.43E+02	7.92E+00	apoptosis-associ	apoptosis-associ	NM_001080395	NM_001080395
3.80E-03	-8.04E+00	chromosome 16	chromosome 16	NM_153025	NM_153025
3.80E-03	-8.04E+00	jumping transloc	RAB13, member	NM_006694	NM_006694
3.80E-03	-8.04E+00	jumping transloc	RAB13, member	NM_006694	NM_006694
4.63E+02	8.85E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
2.88E+02	8.17E+00	adrenergic, beta,	adrenergic, beta,	NM_001619	NM_001619
4.33E-03	-7.85E+00	hypothetical LO	phospholipase C,	NR_002764	NR_002764
4.33E-03	-7.85E+00	hypothetical LO	phospholipase C,	NR_002764	NR_002764
2.68E+02	8.06E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
2.68E+02	8.06E+00	CREB regulated t	CREB regulated t	NM_001098482,	NM_001098482,NM_015321
2.78E+02	8.12E+00	melanoma antig	CSAG family, me	NM_153488	NM_153488
2.99E+02	8.22E+00	chromosome 17	chromosome 17	NM_001109760,	NM_001109760,NM_025161
3.17E+02	8.31E+00	chromosome 21	chromosome 21	NM_004928	NM_004928
3.17E+02	8.31E+00	chromosome 21	chromosome 21	NM_004928	NM_004928
3.01E+02	8.23E+00	IQ motif and Sec	nucleoporin 210	NM_014869,NM	NM_014869,NM_001134382
1.36E+00	4.46E-01	chromosome 10	chromosome 10	NM_017609	NM_017609
4.38E-03	-7.83E+00	hyaluronan and	EGF-like repeats	NM_001884	NM_001884
4.03E-03	-7.95E+00	guanine nucleoti	lysosomal traffic	NM_001098722,	NM_001098722,NM_001098721,
4.03E-03	-7.95E+00	guanine nucleoti	lysosomal traffic	NM_001098722,	NM_001098722,NM_001098721,
4.03E-03	-7.95E+00	guanine nucleoti	lysosomal traffic	NM_001098722,	NM_001098722,NM_001098721,
1.32E+00	4.04E-01	cytokine recepto	colony stimulati	NM_022148	NM_022148
1.32E+00	4.04E-01	colony stimulati	colony stimulati	NM_172249,NM	NM_172249,NM_172245,NM_00
4.66E-03	-7.75E+00	glutathione S-tra	similar to D-dop	NR_003081	NR_003081
2.99E+02	8.22E+00	solute carrier fa	solute carrier fa	NM_152346	NM_152346
2.99E+02	8.22E+00	solute carrier fa	solute carrier fa	NM_152346	NM_152346
3.41E-03	-8.20E+00	strawberry notc	serine/threonine	NM_001100122,	NM_001100122,NM_014963
3.79E-03	-8.04E+00	maternally expre	maternally expre	NR_024149	NR_024149
3.79E-03	-8.04E+00	maternally expre	maternally expre	NR_024149	NR_024149
2.98E+02	8.22E+00	SRY (sex determi	hypothetical LO	NM_014587	NM_014587
3.95E-03	-7.98E+00	CDC42 effector p	leukocyte-associ	NM_145057	NM_145057
2.99E+02	8.22E+00	ephrin-B1	ephrin-B1	NM_004429	NM_004429
1.35E+00	4.31E-01	transketolase-lik	transketolase-lik	NM_032136	NM_032136
1.35E+00	4.31E-01	transketolase-lik	transketolase-lik	NM_032136	NM_032136
1.35E+00	4.31E-01	transketolase-lik	chromosome 4 o	NM_032136	NM_032136
2.94E+02	8.20E+00	solute carrier fa	solute carrier fa	NM_207420	NM_207420
3.71E-03	-8.07E+00	family with sequ	family with sequ	NM_019054	NM_019054
3.71E-03	-8.07E+00	family with sequ	family with sequ	NM_019054	NM_019054
3.71E-03	-8.07E+00	family with sequ	family with sequ	NM_019054	NM_019054
4.02E+02	8.65E+00	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
4.02E+02	8.65E+00	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
4.02E+02	8.65E+00	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
2.28E+02	7.83E+00	killer cell immun	killer cell immun	NM_014511,NM	NM_014511,NM_015868
3.57E+02	8.48E+00	phosphofructoki	phosphofructoki	NM_002626	NM_002626
1.74E+00	8.02E-01	troponin T type	troponin T type	NM_001042781,	NM_001042781,NM_001042782,
2.62E+02	8.03E+00	vasoactive intest	vasoactive intest	NM_003382	NM_003382
2.62E+02	8.03E+00	vasoactive intest	vasoactive intest	NM_003382	NM_003382
1.59E+00	6.73E-01	zinc finger protei	zinc finger protei	NM_133444	NM_133444
2.28E+02	7.83E+00	active BCR-relat	active BCR-relat	NM_001159746	NM_001159746
2.28E+02	7.83E+00	active BCR-relat	active BCR-relat	NM_001159746	NM_001159746
3.60E+02	8.49E+00	COX19 cytochro	cytochrome P45	NM_001031617	NM_001031617
4.35E-03	-7.84E+00	chromosome 17	ArfGAP with dua	NM_024683	NM_024683

3.77E-03	-8.05E+00	BEN domain con	PRP18 pre-mRN	NM_001100912	NM_001100912
3.77E-03	-8.05E+00	BEN domain con	PRP18 pre-mRN	NM_001100912	NM_001100912
3.55E+02	8.47E+00	low density lipop	low density lipop	NM_002337	NM_002337
1.60E+00	6.74E-01	tet oncogene fa	bolA homolog 3 (	NM_144993	NM_144993
4.13E+02	8.69E+00	dimethylarginine	dimethylarginine	NM_013974	NM_013974
3.84E-03	-8.03E+00	potassium volta	nitric oxide synt	NM_172056	NM_172056
4.16E+02	8.70E+00	pregnancy up-re	solute carrier fa	NM_001039582,	NM_001039582,NM_001135740
2.27E+02	7.82E+00	Rho GTPase acti	Rho GTPase acti	NM_001025598,	NM_001025598,NM_181720
2.73E+02	8.09E+00	LAG1 homolog, c	lines homolog 1 (	NM_178842	NM_178842
3.02E+02	8.24E+00	EPS8-like 2	EPS8-like 2	NM_022772	NM_022772
3.02E+02	8.24E+00	EPS8-like 2	EPS8-like 2	NM_022772	NM_022772
2.56E+02	8.00E+00	chromosome 6 o	hypothetical pro	NR_026780	NR_026780
2.91E+02	8.19E+00	ras responsive el	ras responsive el	NM_001003698,	NM_001003698,NM_001003699
2.45E+02	7.94E+00	retinitis pigment	retinitis pigment	NM_178857	NM_178857
2.36E+02	7.88E+00	sclerostin domai	ankyrin repeat a	NM_015464	NM_015464
2.36E+02	7.88E+00	sclerostin domai	ankyrin repeat a	NM_015464	NM_015464
4.50E-03	-7.80E+00	fatty acid bindin	chaperonin cont	NR_002935	NR_002935
3.50E+02	8.45E+00	G protein-couple	G protein-couple	NM_016235	NM_016235
3.36E-03	-8.22E+00	endothelin recep	POU class 4 hom	NM_003991,NM	NM_003991,NM_001122659,NM_
3.33E+02	8.38E+00	pitrilysin metallo	Kruppel-like fact	NM_014889	NM_014889
3.97E+02	8.63E+00	PQ loop repeat c	heat shock facto	NM_001146343,	NM_001146343,NM_001146345,
3.79E-03	-8.04E+00	craniofacial deve	transmembrane	NM_006324	NM_006324
4.52E-03	-7.79E+00	mannosidase, be	v-src sarcoma (S	NM_022077,NM	NM_022077,NM_001003897
2.52E+02	7.98E+00	SET domain cont	SET domain cont	NM_015048	NM_015048
2.52E+02	7.98E+00	SET domain cont	SET domain cont	NM_015048	NM_015048
4.18E-03	-7.90E+00	chromosome 12	chromosome 12	NM_001135864	NM_001135864
3.01E+02	8.23E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
3.60E+02	8.49E+00	chromosome 16	chromosome 16	NR_024347	NR_024347
3.28E+02	8.36E+00	calcium binding	calcium binding	NM_145200	NM_145200
4.09E-03	-7.93E+00	N-acetylglucosa	hydroxysteroid (	NM_000263	NM_000263
4.09E-03	-7.93E+00	N-acetylglucosa	hydroxysteroid (	NM_000263	NM_000263
4.90E-03	-7.67E+00	calmodulin regul	UBA domain con	NM_015447	NM_015447
3.19E+02	8.32E+00	laminin, alpha 5	laminin, alpha 5	NM_005560	NM_005560
3.19E+02	8.32E+00	laminin, alpha 5	laminin, alpha 5	NM_005560	NM_005560
2.48E+02	7.95E+00	CTD (carboxy-ter	CTD (carboxy-ter	NM_048368,NM	NM_048368,NM_004715
2.48E+02	7.95E+00	CTD (carboxy-ter	CTD (carboxy-ter	NM_048368,NM	NM_048368,NM_004715
2.34E+02	7.87E+00	chromosome 1 o	chromosome 1 o	NM_024676	NM_024676
2.34E+02	7.87E+00	chromosome 1 o	chromosome 1 o	NM_024676	NM_024676
2.34E+02	7.87E+00	family with sequ	family with sequ	NM_018166	NM_018166
3.25E+02	8.34E+00	chromosome 1 o	chromosome 1 o	NM_001114748	NM_001114748
3.25E+02	8.34E+00	chromosome 1 o	SSU72 RNA poly	NM_001114748	NM_001114748
2.84E+02	8.15E+00	notch 1	notch 1	NM_017617	NM_017617
2.84E+02	8.15E+00	notch 1	notch 1	NM_017617	NM_017617
3.76E-03	-8.05E+00	myotubularin rel	zinc finger RNA b	NM_001040446	NM_001040446
3.76E-03	-8.05E+00	myotubularin rel	zinc finger RNA b	NM_001040446	NM_001040446
3.13E+02	8.29E+00	solute carrier fa	solute carrier fa	NM_003052	NM_003052
2.83E+02	8.14E+00	paired box 8	paired box 8	NM_013952,NM	NM_013952,NM_013953,NM_013
3.45E+02	8.43E+00	family with sequ	family with sequ	NM_182614	NM_182614
2.14E+02	7.74E+00	sterile alpha mot	sterile alpha mot	NM_152486	NM_152486
2.14E+02	7.74E+00	sterile alpha mot	sterile alpha mot	NM_152486	NM_152486
3.58E-03	-8.13E+00	olfactory recept	olfactory recept	NM_001004195	NM_001004195
4.85E-03	-7.69E+00	family with sequ	fumarylacetoace	NM_016490	NM_016490
2.66E+02	8.05E+00	troponin T type	troponin T type	NM_001042781,	NM_001042781,NM_001042782,
1.83E+00	8.68E-01	ataxin 1	ataxin 1	NM_001128164,	NM_001128164,NM_000332
3.01E+02	8.23E+00	potassium chan	mitogen-activate	NM_005714,NM	NM_005714,NM_033347,NM_033
3.01E+02	8.23E+00	mitogen-activate	mitogen-activate	NM_002419	NM_002419
2.95E+02	8.21E+00	proline-rich tran	proline-rich tran	NM_145239	NM_145239
2.95E+02	8.21E+00	proline-rich tran	proline-rich tran	NM_145239	NM_145239

3.06E+02	8.26E+00	proprotein conve	proprotein conve	NM_138322	NM_138322
2.01E+02	7.65E+00	TBC1 domain fan	Meis homeobox	NM_178571	NM_178571
2.80E+02	8.13E+00	tumor necrosis fa	tumor necrosis fa	NM_001039664	NM_001039664
2.80E+02	8.13E+00	tumor necrosis fa	tumor necrosis fa	NM_001039664	NM_001039664
2.47E+02	7.95E+00	small nuclear ribo	RER1 retention in	NR_024489	NR_024489
3.54E+02	8.47E+00	solute carrier fan	solute carrier fan	NM_145282	NM_145282
2.87E-03	-8.45E+00	solute carrier fan	protein phosphat	NM_001135153	NM_001135153
2.43E+02	7.92E+00	chromosome 2 o	sushi, nidogen ar	NM_024861,NM	NM_024861,NM_001085437
2.43E+02	7.92E+00	chromosome 2 o	sushi, nidogen ar	NM_024861,NM	NM_024861,NM_001085437
2.70E+02	8.07E+00	chromosome 19	ephrin-A2	NM_017914	NM_017914
2.30E+02	7.84E+00	cholinergic recep	ADAM metallope	NM_000750	NM_000750
2.30E+02	7.84E+00	cholinergic recep	ADAM metallope	NM_000750	NM_000750
4.64E-03	-7.75E+00	potassium voltag	potassium voltag	NM_003471	NM_003471
4.64E-03	-7.75E+00	potassium voltag	potassium voltag	NM_003471	NM_003471
3.82E-03	-8.03E+00	growth regulatio	growth regulatio	NM_148903	NM_148903
4.66E-03	-7.75E+00	NLR family, pyrin	NLR family, pyrin	NM_001079821,	NM_001079821,NM_001127461
3.62E-03	-8.11E+00	TAF12 RNA polyr	RNA, U11 small r	NM_005644,NM	NM_005644,NM_001135218
3.28E-03	-8.25E+00	Bcl2 modifying fa	budding uninhibi	NM_001003943,	NM_001003943,NM_001003942,N
4.38E-03	-7.83E+00	potassium chann	spermatogenesis	NM_138318,NM	NM_138318,NM_138317,NM_021
2.63E+02	8.04E+00	aspartate dehydr	leucine rich repe	NM_001024656,	NM_001024656,NM_001114598
2.63E+02	8.04E+00	leucine rich repe	leucine rich repe	NM_001080457	NM_001080457
3.27E+02	8.35E+00	diacylglycerol lipa	diacylglycerol lipa	NM_006133	NM_006133
3.27E+02	8.35E+00	diacylglycerol lipa	diacylglycerol lipa	NM_006133	NM_006133
4.57E-03	-7.77E+00	fermitin family m	bone morphoger	NM_017671	NM_017671
3.50E-03	-8.16E+00	zinc finger protei	NLR family, pyrin	NM_032752	NM_032752
4.94E-03	-7.66E+00	chromosome 14	acyl-CoA thioeste	NM_024644	NM_024644
3.83E+02	8.58E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
3.83E+02	8.58E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
3.67E+02	8.52E+00	transcriptional re	transcriptional re	NM_033502	NM_033502
3.06E+02	8.26E+00	dystrophia myoto	dystrophia myoto	NM_004409,NM	NM_004409,NM_001081562,NM_
1.48E+00	5.62E-01	non-protein codi	phosphofructoki	NM_001098830	NM_001098830
1.48E+00	5.62E-01	non-protein codi	phosphofructoki	NM_001098830	NM_001098830
3.71E+02	8.54E+00	actin-like 8	actin-like 8	NM_030812	NM_030812
3.71E+02	8.54E+00	actin-like 8	actin-like 8	NM_030812	NM_030812
3.71E+02	8.54E+00	actin-like 8	actin-like 8	NM_030812	NM_030812
3.52E-03	-8.15E+00	tripartite motif-c	tripartite motif-c	NM_001105522	NM_001105522
2.69E+02	8.07E+00	carbohydrate (N-	carbohydrate (N-	NM_021615	NM_021615
2.69E+02	8.07E+00	carbohydrate (N-	carbohydrate (N-	NM_021615	NM_021615
5.11E-03	-7.61E+00	cut-like homeobo	cut-like homeobo	NM_015267	NM_015267
2.76E+02	8.11E+00	apolipoprotein B	ATPase family, A	NM_000384	NM_000384
2.08E+02	7.70E+00	cathepsin Z	cathepsin Z	NM_001336	NM_001336
1.25E+00	3.23E-01	serine incorporat	serine incorporat	NM_001033517	NM_001033517
1.25E+00	3.23E-01	serine incorporat	serine incorporat	NM_001033517	NM_001033517
3.30E+02	8.37E+00	TBC1 domain fan	TBC1 domain fan	NM_020705	NM_020705
2.12E+02	7.73E+00	lipase maturation	lipase maturation	NM_022773	NM_022773
2.12E+02	7.73E+00	lipase maturation	lipase maturation	NM_022773	NM_022773
4.38E-03	-7.83E+00	bleomycin hydro	transmembrane	NM_000386	NM_000386
2.22E+02	7.79E+00	zinc finger protei	zinc finger protei	NM_133374	NM_133374
2.22E+02	7.79E+00	zinc finger protei	zinc finger protei	NM_133374	NM_133374
2.22E+02	7.79E+00	Rho GDP dissocia	Rho GDP dissocia	NM_004309	NM_004309
3.59E-03	-8.12E+00	hypothetical LOC	hypothetical LOC	NR_015419	NR_015419
4.72E-03	-7.73E+00	sema domain, im	hepatocyte grow	NM_006379	NM_006379
4.88E+02	8.93E+00	NK6 homeobox 2	chromosome 10	NM_177400	NM_177400
3.87E-03	-8.01E+00	zinc finger protei	histone cluster 1,	NM_007149	NM_007149
2.77E+02	8.11E+00	tyrosine kinase, r	tyrosine kinase, r	NM_005781,NM	NM_005781,NM_001010938
3.76E+02	8.56E+00	ankyrin repeat do	ankyrin repeat do	NM_013275	NM_013275
3.76E+02	8.56E+00	ankyrin repeat do	ankyrin repeat do	NM_013275	NM_013275
3.76E+02	8.56E+00	ankyrin repeat do	ankyrin repeat do	NM_013275	NM_013275

2.42E+02	7.92E+00	profilin 2	TSC22 domain fa	NM_053024,NM	NM_053024,NM_002628
2.63E+02	8.04E+00	golgi to ER traffic	golgi to ER traffic	NM_015949	NM_015949
3.24E+02	8.34E+00	KIAA1644	leucine zipper, d	NM_001099294	NM_001099294
2.72E+02	8.09E+00	SRY (sex determi	SRY (sex determi	NM_006941	NM_006941
2.72E+02	8.09E+00	SRY (sex determi	SRY (sex determi	NM_006941	NM_006941
2.65E+02	8.05E+00	adenomatosis pc	adenomatosis pc	NM_005883	NM_005883
2.65E+02	8.05E+00	adenomatosis pc	adenomatosis pc	NM_005883	NM_005883
2.65E+02	8.05E+00	adenomatosis pc	adenomatosis pc	NM_005883	NM_005883
4.18E-03	-7.90E+00	RAB20, member	carbohydrate kin	NM_017817	NM_017817
3.81E-03	-8.04E+00	chromosome 1 o	TAR DNA binding	NM_173507	NM_173507
3.81E-03	-8.04E+00	chromosome 1 o	TAR DNA binding	NM_173507	NM_173507
3.57E+02	8.48E+00	AHNAK nucleopr	chromosome 14	NM_138420	NM_138420
3.57E+02	8.48E+00	AHNAK nucleopr	chromosome 14	NM_138420	NM_138420
2.37E+02	7.89E+00	plectin	plectin	NM_000445,NM	NM_000445,NM_201378,NM_201
2.42E+02	7.92E+00	phosphatidylseri	ribonuclease/ang	NM_030783	NM_030783
2.42E+02	7.92E+00	ribonuclease/ang	ribonuclease/ang	NM_002939,NM	NM_002939,NM_203383,NM_203
3.19E+02	8.32E+00	zinc finger, AN1-t	UNC homeobox	NM_182491	NM_182491
3.19E+02	8.32E+00	zinc finger, AN1-t	UNC homeobox	NM_182491	NM_182491
3.76E+02	8.56E+00	family with sequ	chromosome 22	NM_015381	NM_015381
3.76E+02	8.56E+00	family with sequ	chromosome 22	NM_015381	NM_015381
2.99E+02	8.22E+00	calcium homeost	calcium homeost	NM_001001412	NM_001001412
2.75E+02	8.10E+00	phosphofructoki	phosphofructoki	NM_002626	NM_002626
2.75E+02	8.10E+00	phosphofructoki	phosphofructoki	NM_002626	NM_002626
1.99E+00	9.94E-01	BR serine/threon	BR serine/threon	NM_003957	NM_003957
3.02E+02	8.24E+00	prosaposin-like 1	AFAP1 antisense	NM_001085382	NM_001085382
4.05E-03	-7.95E+00	ACN9 homolog (S	ACN9 homolog (S	NM_020186	NM_020186
4.53E-03	-7.78E+00	chromosome 17	zinc finger protei	NM_022344	NM_022344
7.43E-01	-4.29E-01	kaptin (actin binc	N-ethylmaleimid	NM_007059	NM_007059
7.43E-01	-4.29E-01	kaptin (actin binc	N-ethylmaleimid	NM_007059	NM_007059
2.93E+02	8.20E+00	cell adhesion mo	BUD13 homolog	NM_014333,NM	NM_014333,NM_001098517
4.37E-03	-7.84E+00	chromosome 6 o	chromosome 6 o	NM_018341	NM_018341
1.59E+00	6.69E-01	TAF4 RNA polym	TAF4 RNA polym	NM_003185	NM_003185
1.59E+00	6.69E-01	TAF4 RNA polym	TAF4 RNA polym	NM_003185	NM_003185
4.72E-03	-7.73E+00	hematopoietic ce	golgin B1	NM_005335	NM_005335
3.40E+02	8.41E+00	potassium voltag	potassium voltag	NM_172109	NM_172109
2.31E+02	7.85E+00	solute carrier fan	solute carrier fan	NM_213613,NM	NM_213613,NM_022042
3.75E-03	-8.06E+00	DPH5 homolog (S	sphingosine-1-ph	NM_001077394,	NM_001077394,NM_015958,NM_
2.38E+02	7.90E+00	mesoderm induc	mesoderm induc	NM_017550	NM_017550
3.47E+02	8.44E+00	ring finger protei	ring finger protei	NM_178841	NM_178841
3.47E+02	8.44E+00	ring finger protei	ring finger protei	NM_178841	NM_178841
3.76E+02	8.56E+00	platelet-derived	platelet-derived	NM_002609	NM_002609
3.76E+02	8.56E+00	platelet-derived	platelet-derived	NM_002609	NM_002609
4.37E+02	8.77E+00	laminin, beta 2 (l	laminin, beta 2 (l	NM_002292	NM_002292
4.76E-03	-7.72E+00	STEAP family me	STEAP family me	NM_024636	NM_024636
3.34E-03	-8.22E+00	kelch-like 33 (Dr	O-sialoglycoprot	NM_001109997	NM_001109997
1.76E+00	8.16E-01	keratin 28	keratin 28	NM_181535	NM_181535
1.76E+00	8.16E-01	keratin 28	keratin 28	NM_181535	NM_181535
1.42E+00	5.02E-01	integrin, alpha X	integrin, alpha X	NM_000887	NM_000887
1.42E+00	5.02E-01	integrin, alpha X	integrin, alpha X	NM_000887	NM_000887
4.16E+02	8.70E+00	actin, beta-like 2	actin, beta-like 2	NM_001017992	NM_001017992
4.16E+02	8.70E+00	actin, beta-like 2	actin, beta-like 2	NM_001017992	NM_001017992
3.95E-03	-7.98E+00	La ribonucleopro	GTP binding prot	NM_015155	NM_015155
3.52E+02	8.46E+00	laminin, beta 3	laminin, beta 3	NM_001017402,	NM_001017402,NM_001127641,N
3.25E+02	8.34E+00	dysferlin, limb gi	dysferlin, limb gi	NM_001130984,	NM_001130984,NM_001130982,N
3.25E+02	8.34E+00	dysferlin, limb gi	dysferlin, limb gi	NM_001130984,	NM_001130984,NM_001130982,N
3.80E-03	-8.04E+00	S100 calcium bin	trichohyalin-like	NM_005620	NM_005620
3.80E-03	-8.04E+00	S100 calcium bin	trichohyalin-like	NM_005620	NM_005620
5.49E-03	-7.51E+00	bromodomain, t	epoxide hydrolas	NM_001726	NM_001726

1.63E+00	7.04E-01	polymerase (RN	polymerase (RN	NM_005035	NM_005035
3.24E+02	8.34E+00	solute carrier fan	solute carrier fan	NM_194255	NM_194255
3.49E-03	-8.16E+00	cyclin I	cyclin G2	NM_006835	NM_006835
4.98E-03	-7.65E+00	mediator comple	mediator comple	NM_004275	NM_004275
2.62E+02	8.03E+00	fatty acid syntha	fatty acid syntha	NM_004104	NM_004104
2.62E+02	8.03E+00	fatty acid syntha	fatty acid syntha	NM_004104	NM_004104
3.75E-03	-8.06E+00	E74-like factor 5	ets homologous	NM_198381,NM	NM_198381,NM_001422
2.45E+02	7.94E+00	cyclin-dependen	mitogen-activate	NM_001009565	NM_001009565
2.45E+02	7.94E+00	cyclin-dependen	mitogen-activate	NM_001009565	NM_001009565
3.30E+02	8.36E+00	solute carrier fan	solute carrier fan	NM_006934,NM	NM_006934,NM_201649,NM_001
3.30E+02	8.36E+00	solute carrier fan	solute carrier fan	NM_006934,NM	NM_006934,NM_201649,NM_001
4.88E-03	-7.68E+00	phosphatidylino	phosphatidylino	NM_025163	NM_025163
4.88E-03	-7.68E+00	phosphatidylino	phosphatidylino	NM_025163	NM_025163
3.17E+02	8.31E+00	programmed cell	programmed cell	NM_005018	NM_005018
3.57E+02	8.48E+00	small nucleolar R	small nucleolar R	NR_003322,NR_	NR_003322,NR_003320
1.80E+00	8.46E-01	WD repeat dom	WD repeat dom	NM_017818	NM_017818
1.80E+00	8.46E-01	WD repeat dom	WD repeat dom	NM_017818	NM_017818
2.22E+02	7.79E+00	Rap guanine nucl	interleukin 6 (int	NM_012294	NM_012294
2.22E+02	7.79E+00	Rap guanine nucl	interleukin 6 (int	NM_012294	NM_012294
3.22E+02	8.33E+00	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
1.95E+00	9.66E-01	hypothetical LOC	coxsackie virus a	NR_026756	NR_026756
1.95E+00	9.66E-01	hypothetical LOC	coxsackie virus a	NR_026756	NR_026756
3.38E+02	8.40E+00	chloride channel	chloride channel	NM_001287,NM	NM_001287,NM_001114331
2.11E+02	7.72E+00	adenylate cyclas	adenylate cyclas	NM_183357	NM_183357
2.11E+02	7.72E+00	adenylate cyclas	adenylate cyclas	NM_183357	NM_183357
2.17E+02	7.76E+00	splicing factor, a	matrix metallope	NM_004592	NM_004592
3.21E-03	-8.28E+00	potassium voltag	follicle stimulati	NM_002233	NM_002233
3.82E-03	-8.03E+00	BEN domain con	shisa homolog 3	NM_001159547,	NM_001159547,NM_207406
4.43E-03	-7.82E+00	ASAP1 intronic tr	adenylate cyclas	NR_002765	NR_002765
4.43E-03	-7.82E+00	ASAP1 intronic tr	adenylate cyclas	NR_002765	NR_002765
3.45E-03	-8.18E+00	SP140 nuclear b	SP100 nuclear ar	NM_138402	NM_138402
3.45E-03	-8.18E+00	SP140 nuclear b	SP100 nuclear ar	NM_138402	NM_138402
3.94E+02	8.62E+00	trafficking protei	trafficking protei	NM_031466	NM_031466
3.79E-03	-8.04E+00	dystrophia myot	radial spoke hea	NM_004943	NM_004943
4.01E-03	-7.96E+00	StAR-related lipi	StAR-related lipi	NM_178007,NM	NM_178007,NM_052851,NM_17
4.01E-03	-7.96E+00	StAR-related lipi	replication facto	NM_178007,NM	NM_178007,NM_052851,NM_17
3.05E+02	8.25E+00	lipase, member	SUMO1/sentrin/	NM_139248	NM_139248
3.05E+02	8.25E+00	lipase, member	SUMO1/sentrin/	NM_139248	NM_139248
3.97E-03	-7.98E+00	stathmin 1	platelet-activatin	NM_203401,NM	NM_203401,NM_005563,NM_20
3.97E-03	-7.98E+00	stathmin 1	platelet-activatin	NM_203401,NM	NM_203401,NM_005563,NM_20
1.31E+00	3.95E-01	cancer/testis ant	cancer/testis ant	NM_001017436	NM_001017436
1.31E+00	3.95E-01	cancer/testis ant	cancer/testis ant	NM_001017436	NM_001017436
1.31E+00	3.95E-01	cancer/testis ant	cancer/testis ant	NM_001017436	NM_001017436
3.83E+02	8.58E+00	cysteine-rich pro	cysteine-rich pro	NM_001312	NM_001312
3.83E+02	8.58E+00	cysteine-rich pro	cysteine-rich pro	NM_001312	NM_001312
1.30E+00	3.83E-01	Ras association (	Ras association (	NM_014737	NM_014737
2.67E+02	8.06E+00	integrin, beta 4	integrin, beta 4	NM_001005619	NM_001005619
2.67E+02	8.06E+00	integrin, beta 4	integrin, beta 4	NM_001005619	NM_001005619
2.67E+02	8.06E+00	integrin, beta 4	integrin, beta 4	NM_001005619	NM_001005619
3.74E+02	8.55E+00	galactosamine (	galactosamine (	NM_000512	NM_000512
3.74E+02	8.55E+00	galactosamine (	galactosamine (	NM_000512	NM_000512
3.46E+02	8.43E+00	chromosome 2 o	chromosome 2 o	NM_001013662	NM_001013662
3.46E+02	8.43E+00	chromosome 2 o	chromosome 2 o	NM_001013662	NM_001013662
3.89E+02	8.60E+00	diacylglycerol ki	diacylglycerol ki	NM_152879	NM_152879
5.02E-03	-7.64E+00	renalase, FAD-de	lipase, family me	NM_001031709	NM_001031709
2.67E+02	8.06E+00	neuroligin 2	neuroligin 2	NM_020795	NM_020795
3.23E+02	8.33E+00	NK2 homeobox	paired box 9	NM_014360	NM_014360
3.23E+02	8.33E+00	NK2 homeobox	paired box 9	NM_014360	NM_014360

3.23E+02	8.33E+00	NK2 homeobox	paired box 9	NM_014360	NM_014360
2.18E+02	7.77E+00	wingless-type M	wingless-type M	NM_058238	NM_058238
2.18E+02	7.77E+00	wingless-type M	wingless-type M	NM_058238	NM_058238
2.46E+02	7.94E+00	zinc finger protei	zinc finger protei	NM_153813	NM_153813
2.45E+02	7.94E+00	CDC42 binding p	zinc finger protei	NM_014826,NM	NM_014826,NM_003607
2.45E+02	7.94E+00	CDC42 binding p	zinc finger protei	NM_014826,NM	NM_014826,NM_003607
2.97E+02	8.22E+00	fibroblast growt	fibroblast growt	NM_020637	NM_020637
2.97E+02	8.22E+00	fibroblast growt	fibroblast growt	NM_020637	NM_020637
3.22E-03	-8.28E+00	heart and neural	La ribonucleopro	NM_004821	NM_004821
3.22E-03	-8.28E+00	heart and neural	La ribonucleopro	NM_004821	NM_004821
5.04E-03	-7.63E+00	transmembrane	transmembrane	NM_020422	NM_020422
2.93E+02	8.20E+00	solute carrier fa	solute carrier fa	NM_031481	NM_031481
2.61E+02	8.03E+00	transmembrane	transmembrane	NM_021259	NM_021259
2.61E+02	8.03E+00	transmembrane	transmembrane	NM_021259	NM_021259
3.59E+02	8.49E+00	chromosome 9 o	chromosome 9 o	NM_017995,NM	NM_017995,NM_024718
3.59E+02	8.49E+00	chromosome 9 o	chromosome 9 o	NM_017995,NM	NM_017995,NM_024718
4.64E-03	-7.75E+00	BCL2-related pro	zinc finger, AN1-	NM_004049,NM	NM_004049,NM_001114735
4.78E-03	-7.71E+00	family with sequ	mitochondrial ri	NM_001135032,	NM_001135032,NM_032181
3.79E-03	-8.04E+00	aldehyde dehydr	family with sequ	NM_000695,NM	NM_000695,NM_001031615
3.79E-03	-8.04E+00	aldehyde dehydr	family with sequ	NM_000695,NM	NM_000695,NM_001031615
1.78E+00	8.28E-01	cytochrome P45	cytochrome P45	NM_000774	NM_000774
1.78E+00	8.28E-01	cytochrome P45	cytochrome P45	NM_000774	NM_000774
3.16E+02	8.30E+00	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
2.78E+02	8.12E+00	transcription fac	extracellular leu	NR_001288	NR_001288
2.78E+02	8.12E+00	transcription fac	extracellular leu	NR_001288	NR_001288
4.30E-03	-7.86E+00	SKI family transc	protein inhibitor	NM_001031807	NM_001031807
4.30E-03	-7.86E+00	SKI family transc	protein inhibitor	NM_001031807	NM_001031807
2.38E+02	7.90E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
4.61E-03	-7.76E+00	eukaryotic transl	eukaryotic transl	NM_017629	NM_017629
3.44E-03	-8.18E+00	transcription ter	chromosome 9 o	NM_007344	NM_007344
3.44E-03	-8.18E+00	transcription ter	chromosome 9 o	NM_007344	NM_007344
4.43E-03	-7.82E+00	ring finger protei	WD repeat doma	NM_145051	NM_145051
4.43E-03	-7.82E+00	ring finger protei	WD repeat doma	NM_145051	NM_145051
4.43E-03	-7.82E+00	ring finger protei	WD repeat doma	NM_145051	NM_145051
4.02E-03	-7.96E+00	glutathione redu	UBX domain pro	NM_000637	NM_000637
4.02E-03	-7.96E+00	glutathione redu	UBX domain pro	NM_000637	NM_000637
3.06E+02	8.26E+00	pleckstrin homol	solute carrier fa	NM_015164	NM_015164
1.42E+00	5.09E-01	matrix metallop	matrix metallop	NM_016155	NM_016155
1.36E+00	4.39E-01	cancer/testis ant	cancer/testis ant	NM_001017417	NM_001017417
1.36E+00	4.39E-01	cancer/testis ant	cancer/testis ant	NM_001017436,	NM_001017436,NM_152582
2.31E+02	7.85E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
2.31E+02	7.85E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
3.45E-03	-8.18E+00	CD47 molecule	intraflagellar tra	NM_001777,NM	NM_001777,NM_198793,NM_001
3.49E+02	8.45E+00	zinc finger protei	zinc finger protei	NM_001002836	NM_001002836
2.61E+02	8.03E+00	surfactant associ	NK2 homeobox 1	NM_001101341	NM_001101341
2.61E+02	8.03E+00	surfactant associ	NK2 homeobox 1	NM_001101341	NM_001101341
3.57E+02	8.48E+00	histamine recept	histamine recept	NM_001098212	NM_001098212
2.86E+02	8.16E+00	tetraspanin 14	SH2 domain cont	NM_030927,NM	NM_030927,NM_001128309
4.38E-03	-7.83E+00	mitochondrial fis	mitochondrial fis	NM_014637,NM	NM_014637,NM_001145839
3.55E+02	8.47E+00	BAI1-associated	BAI1-associated	NM_017450,NM	NM_017450,NM_006340,NM_017
3.55E+02	8.47E+00	BAI1-associated	BAI1-associated	NM_017450,NM	NM_017450,NM_006340,NM_017
4.21E-03	-7.89E+00	motilin	glutamate recept	NM_002418,NM	NM_002418,NM_001040109
3.00E+02	8.23E+00	zinc finger protei	zinc finger protei	NM_001127464	NM_001127464
3.00E+02	8.23E+00	zinc finger protei	zinc finger protei	NM_001127464	NM_001127464
3.57E-03	-8.13E+00	chromosome 7 o	monoacylglycero	NM_198571	NM_198571
2.98E+02	8.22E+00	protein tyrosine	paralemmin 2	NM_001145368,	NM_001145368,NM_002829,NM_
2.98E+02	8.22E+00	protein tyrosine	paralemmin 2	NM_001145368,	NM_001145368,NM_002829,NM_
4.68E-03	-7.74E+00	protease, serine,	protease, serine,	NM_001080492	NM_001080492

3.22E+02	8.33E+00	mannosyl (alpha	mannosyl (alpha	NM_014275,NM	NM_014275,NM_054013
3.90E-03	-8.00E+00	gamma-glutamyl	DiGeorge syndro	NR_003267	NR_003267
2.34E+02	7.87E+00	nuclear transcrip	nuclear transcrip	NM_002505,NM	NM_002505,NM_021705
1.65E+00	7.23E-01	parvin, gamma	parvin, gamma	NM_001137605,	NM_001137605,NR_024427
4.04E+02	8.66E+00	dead end homol	dead end homol	NM_194249	NM_194249
2.64E+02	8.04E+00	FKSG29	transmembrane	NR_024013	NR_024013
3.62E+02	8.50E+00	multiple EGF-like	multiple EGF-like	NM_001410	NM_001410
1.44E+00	5.22E-01	similar to cDNA s	similar to cDNA s	NM_001013729	NM_001013729
4.38E-03	-7.83E+00	arylsulfatase A	SH3 and multiple	NM_001085427,	NM_001085427,NM_001085428,
2.86E+02	8.16E+00	small nucleolar R	small nucleolar R	NR_002969	NR_002969
3.08E-03	-8.34E+00	KIAA1324	KIAA1324	NM_020775	NM_020775
1.91E+00	9.33E-01	potassium voltag	potassium voltag	NM_172056	NM_172056
1.91E+00	9.33E-01	potassium voltag	potassium voltag	NM_172056	NM_172056
3.08E+02	8.27E+00	ring finger protei	ring finger protei	NM_174903	NM_174903
2.58E+02	8.01E+00	zinc finger and B	zinc finger and B	NM_032792	NM_032792
1.45E+00	5.36E-01	pecanex-like 3 (	pecanex-like 3 (	NM_032223	NM_032223
1.45E+00	5.36E-01	pecanex-like 3 (	pecanex-like 3 (	NM_032223	NM_032223
3.68E-03	-8.09E+00	leucine rich repe	leucine rich repe	NM_024750,NM	NM_024750,NM_024512
3.68E-03	-8.09E+00	teratocarcinoma	teratocarcinoma	NM_003212	NM_003212
4.61E-03	-7.76E+00	olfactory recept	olfactory recept	NM_013936	NM_013936
3.81E+02	8.57E+00	pyrimidinergic re	pyrimidinergic re	NM_004154	NM_004154
3.95E-03	-7.98E+00	ankyrin repeat d	RANBP2-like and	NM_023016	NM_023016
3.70E+02	8.53E+00	non-metastatic c	non-metastatic c	NM_005009	NM_005009
3.23E-03	-8.27E+00	leucine-rich repe	leucine-rich repe	NM_021636	NM_021636
2.50E+02	7.96E+00	BAI1-associated	BAI1-associated	NM_017450,NM	NM_017450,NM_006340,NM_017
2.50E+02	7.96E+00	BAI1-associated	BAI1-associated	NM_017450,NM	NM_017450,NM_006340,NM_017
3.67E+02	8.52E+00	exosome compo	DDB1 and CUL4	NM_001002269,	NM_001002269,NM_016042
3.45E+02	8.43E+00	lysine (K)-specifi	lysine (K)-specifi	NM_015015	NM_015015
1.54E+00	6.20E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
1.54E+00	6.20E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
1.46E+00	5.51E-01	cancer/testis ant	cancer/testis ant	NM_001007551	NM_001007551
4.88E-03	-7.68E+00	anoctamin 6	anoctamin 6	NM_001142680	NM_001142680
4.88E-03	-7.68E+00	anoctamin 6	anoctamin 6	NM_001142680	NM_001142680
3.80E-03	-8.04E+00	CD177 molecule	testis expressed	NM_020406	NM_020406
3.80E-03	-8.04E+00	CD177 molecule	testis expressed	NM_020406	NM_020406
2.89E+02	8.17E+00	multiple EGF-like	multiple EGF-like	NM_001409	NM_001409
2.89E+02	8.17E+00	multiple EGF-like	multiple EGF-like	NM_001409	NM_001409
3.69E-03	-8.08E+00	solute carrier fa	solute carrier fa	NM_003058	NM_003058
3.26E+02	8.35E+00	polymerase (DN	polymerase (DN	NM_002691	NM_002691
3.26E+02	8.35E+00	polymerase (DN	polymerase (DN	NM_002691	NM_002691
2.03E+00	1.02E+00	coiled-coil domai	chromosome 2 o	NM_138770	NM_138770
2.03E+00	1.02E+00	coiled-coil domai	chromosome 2 o	NM_138770	NM_138770
3.22E-03	-8.28E+00	potassium chann	hypothetical LOC	NM_001142730,	NM_001142730,NM_001136205,
3.84E+02	8.58E+00	keratin 13	keratin 13	NM_153490,NM	NM_153490,NM_002274
2.67E+02	8.06E+00	proline-serine-th	proline-serine-th	NM_003978	NM_003978
2.67E+02	8.06E+00	proline-serine-th	proline-serine-th	NM_003978	NM_003978
3.53E+02	8.46E+00	kinesin family m	kinesin family m	NM_015656	NM_015656
3.39E-03	-8.20E+00	chromosome 22	bromodomain c	NR_026997	NR_026997
3.21E-03	-8.28E+00	potassium voltag	follicle stimulati	NM_002233	NM_002233
3.77E-03	-8.05E+00	HECT domain co	HEAT repeat con	NM_015382	NM_015382
3.77E-03	-8.05E+00	HECT domain co	HEAT repeat con	NM_015382	NM_015382
3.77E-03	-8.05E+00	nuclear RNA exp	thymosin beta 1	NM_017809,NM	NM_017809,NM_022053
4.83E-03	-7.69E+00	hypothetical LOC	ubiquitin specific	NR_024490	NR_024490
4.83E-03	-7.69E+00	hypothetical LOC	ubiquitin specific	NR_024490	NR_024490
3.61E-03	-8.11E+00	nuclear receptor	nuclear receptor	NM_003269	NM_003269
3.61E-03	-8.11E+00	nuclear receptor	nuclear receptor	NM_003269	NM_003269
1.33E+00	4.12E-01	protein arginine	protein arginine	NM_198318,NM	NM_198318,NM_198319,NM_001
1.33E+00	4.12E-01	protein arginine	protein arginine	NM_198318,NM	NM_198318,NM_198319,NM_001

1.33E+00	4.12E-01	chromosome 19	chromosome 19	NM_001101340	NM_001101340
1.85E+00	8.89E-01	transmembrane	transmembrane	NM_021259	NM_021259
1.85E+00	8.89E-01	transmembrane	transmembrane	NM_021259	NM_021259
2.86E+02	8.16E+00	tetraspanin 14	SH2 domain cont	NM_030927,NM	NM_030927,NM_001128309
1.84E+00	8.80E-01	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
3.46E+02	8.43E+00	solute carrier fan	solute carrier fan	NM_032034	NM_032034
4.01E+02	8.65E+00	neurexin 1	ankyrin repeat ar	NM_138735,NM	NM_138735,NM_004801,NM_001
3.90E-03	-8.00E+00	zinc finger and S	zinc finger protei	NM_024303	NM_024303
2.56E+02	8.00E+00	reticulon 4 recep	reticulon 4 recep	NM_023004	NM_023004
2.27E+00	1.18E+00	NK6 homeobox 2	chromosome 10	NM_177400	NM_177400
4.18E-03	-7.90E+00	Paf1, RNA polym	Paf1, RNA polym	NM_019088	NM_019088
4.18E-03	-7.90E+00	Paf1, RNA polym	Paf1, RNA polym	NM_019088	NM_019088
4.92E-03	-7.67E+00	protein kinase, A	UDP-N-acetyl-alp	NM_016203,NM	NM_016203,NM_001040633,NM_
3.49E+02	8.45E+00	nuclear respirato	ubiquitin-conjuga	NM_001040110	NM_001040110
2.83E+02	8.14E+00	family with sequ	platelet-derived	NM_020223	NM_020223
2.10E+02	7.72E+00	RNA binding mot	RNA binding mot	NM_001145346	NM_001145346
1.63E+00	7.04E-01	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
1.63E+00	7.04E-01	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
4.06E-03	-7.94E+00	transmembrane	aminocarboxymu	NM_030923	NM_030923
2.35E+02	7.88E+00	ankyrin repeat d	phosphoglucomu	NM_001012419,	NM_001012419,NM_032250
3.09E+02	8.27E+00	BTB (POZ) domai	BTB (POZ) domai	NM_017797	NM_017797
3.09E+02	8.27E+00	BTB (POZ) domai	BTB (POZ) domai	NM_017797	NM_017797
1.73E+00	7.92E-01	olfactory recepto	olfactory recepto	NM_001004695	NM_001004695
1.73E+00	7.92E-01	olfactory recepto	olfactory recepto	NM_001004692	NM_001004692
2.04E+02	7.67E+00	aldo-keto reduct	aldo-keto reduct	NM_020299	NM_020299
3.70E+02	8.53E+00	RAD54-like 2 (S.	testis expressed	NM_015106	NM_015106
2.76E+02	8.11E+00	mitogen-activate	mitogen-activate	NM_145109	NM_145109
3.21E-03	-8.29E+00	chromosome 6 o	chromosome 6 o	NR_026736,NR_	NR_026736,NR_026737,NM_0011
2.20E+02	7.78E+00	caspase recruitm	caspase recruitm	NM_052814,NM	NM_052814,NM_052813
2.20E+02	7.78E+00	caspase recruitm	caspase recruitm	NM_052814,NM	NM_052814,NM_052813
3.41E+02	8.41E+00	pyrroline-5-carb	pyrroline-5-carb	NM_006907	NM_006907
1.38E+00	4.64E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.38E+00	4.64E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.38E+00	4.64E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.38E+00	4.64E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
4.66E-03	-7.75E+00	natural cytotoxic	allograft inflamm	NM_001145467	NM_001145467
3.87E-03	-8.01E+00	calsequestrin 2 (	nescient helix loc	NM_001232	NM_001232
3.01E+02	8.23E+00	adrenergic, beta,	myosin XVIIIB	NM_005160	NM_005160
2.95E+02	8.21E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
2.98E+02	8.22E+00	C-type lectin don	C-type lectin don	NM_015226	NM_015226
2.98E+02	8.22E+00	C-type lectin don	C-type lectin don	NM_015226	NM_015226
2.87E+02	8.16E+00	glycosyltransfera	glycosyltransfera	NM_024656	NM_024656
2.37E+02	7.89E+00	NIMA (never in n	NIMA (never in n	NM_178170	NM_178170
3.60E-03	-8.12E+00	low density lipop	hypothetical FLJ	NM_017522,NM	NM_017522,NM_004631,NM_001
2.50E+02	7.97E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
3.09E-03	-8.34E+00	translocase of in	arginyl aminopep	NM_006335	NM_006335
3.09E-03	-8.34E+00	translocase of in	arginyl aminopep	NM_006335	NM_006335
2.74E+02	8.10E+00	tyrosine kinase w	tyrosine kinase w	NM_005424	NM_005424
2.74E+02	8.10E+00	tyrosine kinase w	tyrosine kinase w	NM_005424	NM_005424
4.11E-03	-7.93E+00	solute carrier fan	CD37 molecule	NM_014037	NM_014037
4.11E-03	-7.93E+00	solute carrier fan	CD37 molecule	NM_014037	NM_014037
3.64E+02	8.51E+00	acid phosphatase	acid phosphatase	NM_001111036,	NM_001111036,NM_001111035,
1.55E+00	6.36E-01	chromosome 10	G protein-couple	NM_173572	NM_173572
2.88E+02	8.17E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
2.88E+02	8.17E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
4.18E-03	-7.90E+00	olfactory recepto	olfactory recepto	NM_030901	NM_030901
4.67E+02	8.87E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794
4.67E+02	8.87E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794

2.76E+02	8.11E+00	mitogen-activate	mitogen-activate	NM_145109	NM_145109
1.54E+00	6.20E-01	sodium channel,	sodium channel,	NM_000334	NM_000334
3.51E+02	8.46E+00	ring finger protei	ring finger protei	NM_194460	NM_194460
2.59E+02	8.02E+00	WD repeat doma	hypothetical LOC	NM_018051	NM_018051
2.59E+02	8.02E+00	WD repeat doma	hypothetical LOC	NM_018051	NM_018051
3.57E-03	-8.13E+00	lysine-rich coiled	SET and MYND d	NM_016618	NM_016618
2.75E+02	8.10E+00	renal tumor anti	renal tumor anti	NM_014226	NM_014226
6.30E-01	-6.67E-01	cytochrome P45	echinoderm micr	NM_006668	NM_006668
1.27E+00	3.45E-01	X antigen family,	X antigen family,	NM_001079538	NM_001079538
1.27E+00	3.45E-01	X antigen family,	X antigen family,	NM_001079538	NM_001079538
1.45E+00	5.37E-01	ST3 beta-galacto	zinc finger and A	NM_173344,NM	NM_173344,NM_003033
1.45E+00	5.37E-01	ST3 beta-galacto	zinc finger and A	NM_173344,NM	NM_173344,NM_003033
1.45E+00	5.37E-01	ST3 beta-galacto	zinc finger and A	NM_173344,NM	NM_173344,NM_003033
1.45E+00	5.37E-01	ST3 beta-galacto	zinc finger and A	NM_173344,NM	NM_173344,NM_003033
1.45E+00	5.37E-01	ST3 beta-galacto	zinc finger and A	NM_173344,NM	NM_173344,NM_003033
1.45E+00	5.37E-01	ST3 beta-galacto	zinc finger and A	NM_173344,NM	NM_173344,NM_003033
2.38E+02	7.90E+00	RGD motif, leuci	RGD motif, leuci	NM_001013838	NM_001013838
1.69E+00	7.57E-01	sorting nexin 29	sorting nexin 29	NM_001080530	NM_001080530
1.69E+00	7.57E-01	sorting nexin 29	sorting nexin 29	NM_001080530	NM_001080530
3.68E-03	-8.09E+00	fibroblast growt	arginyltransferas	NM_001144913,	NM_001144913,NM_001144919
3.89E+02	8.60E+00	non-protein codi	non-protein codi	NR_024422	NR_024422
3.89E+02	8.60E+00	non-protein codi	non-protein codi	NR_024422	NR_024422
4.11E-03	-7.93E+00	adenylate cyclas	adenylate cyclas	NM_018417	NM_018417
4.11E-03	-7.93E+00	adenylate cyclas	adenylate cyclas	NM_018417	NM_018417
3.90E-03	-8.00E+00	neuritin 1	neuritin 1	NM_016588	NM_016588
2.18E+02	7.77E+00	family with sequ	scribbled homol	NM_198488	NM_198488
4.23E+02	8.72E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
1.58E+00	6.59E-01	hexaribonucleoti	hexaribonucleoti	NM_001082575	NM_001082575
1.58E+00	6.59E-01	hexaribonucleoti	hexaribonucleoti	NM_001082575	NM_001082575
2.75E+02	8.10E+00	strawberry notch	serine/threonine	NM_001100122,	NM_001100122,NM_014963
3.76E-03	-8.05E+00	solute carrier fan	platelet-derived	NM_001008539	NM_001008539
3.76E-03	-8.05E+00	solute carrier fan	platelet-derived	NM_001008539	NM_001008539
1.42E+00	5.05E-01	chromosome 21	heat shock trans	NR_026863	NR_026863
2.77E-03	-8.49E+00	Xg pseudogene,	Xg pseudogene,	NR_003254	NR_003254
1.18E+00	2.41E-01	steroid-5-alpha-r	mediator of cell	NM_000348	NM_000348
1.88E+00	9.09E-01	hypothetical LOC	hypothetical LOC	NR_024394	NR_024394
3.19E-03	-8.29E+00	Hermansky-Pudl	Hermansky-Pudl	NM_022081,NM	NM_022081,NM_152841
3.98E+02	8.64E+00	glutamate decarl	glutamate decarl	NM_013445,NM	NM_013445,NM_000817
3.98E+02	8.64E+00	glutamate decarl	glutamate decarl	NM_013445,NM	NM_013445,NM_000817
3.82E+02	8.58E+00	WD repeat doma	glutamate recept	NM_024100	NM_024100
2.97E+02	8.22E+00	tubulin tyrosine l	tubulin tyrosine l	NM_001139442	NM_001139442
2.97E+02	8.22E+00	tubulin tyrosine l	tubulin tyrosine l	NM_001139442	NM_001139442
2.81E-03	-8.47E+00	eukaryotic transl	eukaryotic transl	NM_001135652,	NM_001135652,NM_001135651,N
4.48E-03	-7.80E+00	histone cluster 1,	histone cluster 1,	NM_005320	NM_005320
3.65E+02	8.51E+00	ankyrin repeat d	ankyrin repeat d	NR_026556	NR_026556
1.56E+00	6.41E-01	family with sequ	hippocampus ab	NM_017561	NM_017561
3.75E-03	-8.06E+00	zinc finger protei	zinc finger protei	NM_001099284,	NM_001099284,NM_001099283,N
4.16E-03	-7.91E+00	ATG16 autophag	ATG16 autophag	NM_030803,NM	NM_030803,NM_017974
4.96E+02	8.96E+00	CD7 molecule	secreted and tra	NM_006137	NM_006137
1.51E+00	5.90E-01	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
1.85E+00	8.88E-01	growth hormone	ADP-ribosylhydr	NM_024719	NM_024719
1.85E+00	8.88E-01	growth hormone	ADP-ribosylhydr	NM_024719	NM_024719
2.81E-03	-8.48E+00	leucine rich repe	leucine rich repe	NM_001143757	NM_001143757
2.98E-03	-8.39E+00	laminin, alpha 4	ret finger protein	NM_001105209,	NM_001105209,NM_001105208
2.98E-03	-8.39E+00	laminin, alpha 4	ret finger protein	NM_001105209,	NM_001105209,NM_001105208
7.85E-01	-3.49E-01	NEDD4 binding p	ras homolog gen	NM_018177	NM_018177
1.52E+00	6.05E-01	ubiquitin-like wit	ubiquitin-like wit	NM_013282	NM_013282
4.88E-03	-7.68E+00	POU class 5 hom	psoriasis suscept	NM_002701,NM	NM_002701,NM_203289

1.58E+00	6.58E-01	olfactory recepto	olfactory recepto	NM_001004695	NM_001004695
1.69E+00	7.55E-01	similar to cDNA s	similar to cDNA s	NM_001013729	NM_001013729
1.50E+00	5.89E-01	ADAM metallope	non-protein codi	NR_002224	NR_002224
1.50E+00	5.89E-01	ADAM metallope	non-protein codi	NR_002224	NR_002224
2.90E+02	8.18E+00	THAP domain co	THAP domain co	NM_015963	NM_015963
4.08E-03	-7.94E+00	SIX homeobox 3	SIX homeobox 3	NM_005413	NM_005413
4.35E-03	-7.84E+00	coiled-coil domai	methyl-CpG bind	NM_145020	NM_145020
4.35E-03	-7.84E+00	coiled-coil domai	methyl-CpG bind	NM_145020	NM_145020
1.43E+00	5.11E-01	G protein-couple	jagged 2	NM_013345	NM_013345
4.19E-03	-7.90E+00	transmembrane	interleukin 10 re	NM_001077263	NM_001077263
4.19E-03	-7.90E+00	transmembrane	interleukin 10 re	NM_001077263	NM_001077263
5.08E+02	8.99E+00	WD repeat doma	WD repeat doma	NM_182552	NM_182552
4.06E-03	-7.94E+00	laminin, alpha 1	leucine rich repe	NM_005559	NM_005559
4.06E-03	-7.94E+00	laminin, alpha 1	leucine rich repe	NM_005559	NM_005559
3.01E-03	-8.38E+00	hexokinase 3 (wh	hexokinase 3 (wh	NM_002115	NM_002115
3.62E-03	-8.11E+00	mitogen-activate	peroxisomal biog	NM_005923	NM_005923
1.72E+00	7.79E-01	hexose-6-phosph	hexose-6-phosph	NM_004285	NM_004285
1.72E+00	7.79E-01	hexose-6-phosph	hexose-6-phosph	NM_004285	NM_004285
1.72E+00	7.79E-01	hexose-6-phosph	hexose-6-phosph	NM_004285	NM_004285
1.66E+00	7.27E-01	KIAA0182	KIAA0182	NM_014615	NM_014615
1.66E+00	7.27E-01	KIAA0182	KIAA0182	NM_014615	NM_014615
2.99E+02	8.22E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
3.16E+02	8.30E+00	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
3.31E-03	-8.24E+00	protocadherin ga	protocadherin ga	NM_018915,NM	NM_018915,NM_032009
3.31E-03	-8.24E+00	protocadherin ga	protocadherin ga	NM_018916,NM	NM_018916,NM_032011
3.11E+02	8.28E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
2.30E+02	7.84E+00	keratin 9	keratin 9	NM_000226	NM_000226
4.21E+02	8.72E+00	complement con	complement con	NM_001008223	NM_001008223
2.46E+02	7.94E+00	claudin 19	claudin 19	NM_001123395,	NM_001123395,NM_148960
2.25E+02	7.81E+00	ribosomal protei	ribosomal protei	NM_003942,NM	NM_003942,NM_001006944
1.38E+00	4.60E-01	POM121 membr	gamma-glutamyl	NR_024591	NR_024591
4.30E+02	8.75E+00	SH3 domain and	HtrA serine pepti	NM_018986	NM_018986
1.27E+00	3.46E-01	family with sequ	family with sequ	NM_201400,NM	NM_201400,NM_201598
1.27E+00	3.46E-01	family with sequ	family with sequ	NM_201400,NM	NM_201400,NM_201598
1.30E+00	3.79E-01	NAD(P)H dehydr	NIN1/RPN12 bin	NM_001025434,	NM_001025434,NM_001025433,N
1.30E+00	3.79E-01	NIN1/RPN12 bin	NIN1/RPN12 bin	NM_014062	NM_014062
1.30E+00	3.79E-01	NIN1/RPN12 bin	NIN1/RPN12 bin	NM_014062	NM_014062
1.42E+00	5.02E-01	cyclin-dependent	solute carrier fan	NM_033529,NM	NM_033529,NM_024011
1.50E+00	5.88E-01	olfactory recepto	olfactory recepto	NM_001005522	NM_001005522
3.34E+02	8.38E+00	arylsulfatase A	SH3 and multiple	NM_001085427,	NM_001085427,NM_001085428,N
3.34E+02	8.38E+00	arylsulfatase A	SH3 and multiple	NM_001085427,	NM_001085427,NM_001085428,N
4.16E+02	8.70E+00	collagen, type XV	collagen, type XV	NM_030582,NM	NM_030582,NM_130444
1.31E+00	3.85E-01	family with sequ	family with sequ	NM_182614	NM_182614
1.31E+00	3.85E-01	family with sequ	family with sequ	NM_182614	NM_182614
1.52E+00	6.00E-01	chromobox hom	TBC1 domain fan	NM_003655	NM_003655
1.52E+00	6.00E-01	chromobox hom	TBC1 domain fan	NM_003655	NM_003655
1.30E+00	3.74E-01	iroquois homeob	iroquois homeob	NM_016358	NM_016358
1.30E+00	3.74E-01	iroquois homeob	iroquois homeob	NM_016358	NM_016358
4.41E+02	8.79E+00	synaptotagmin II	synaptotagmin II	NM_032298	NM_032298
1.43E+00	5.11E-01	G protein-couple	jagged 2	NM_013345	NM_013345
1.43E+00	5.11E-01	G protein-couple	jagged 2	NM_013345	NM_013345
1.36E+00	4.43E-01	signal-regulatory	signal-regulatory	NM_001040023	NM_001040023
1.36E+00	4.43E-01	signal-regulatory	signal-regulatory	NM_001040023	NM_001040023
2.31E+02	7.85E+00	mindbomb homo	mindbomb homo	NM_080875	NM_080875
4.13E-03	-7.92E+00	cold shock doma	cold shock doma	NM_001007553,	NM_001007553,NM_001130523
4.13E-03	-7.92E+00	cold shock doma	cold shock doma	NM_001007553,	NM_001007553,NM_001130523
3.92E+02	8.61E+00	transmembrane	transmembrane	NM_024600	NM_024600
3.92E+02	8.61E+00	transmembrane	transmembrane	NM_024600	NM_024600

3.30E+02	8.36E+00	core-binding fact	core-binding fact	NM_175931,NM	NM_175931,NM_005187
7.25E-01	-4.63E-01	twelve-thirteen t	twelve-thirteen t	NR_024505	NR_024505
1.42E+00	5.10E-01	sushi-repeat-con	retinitis pigment	NM_006307	NM_006307
1.42E+00	5.10E-01	sushi-repeat-con	retinitis pigment	NM_006307	NM_006307
2.37E+02	7.89E+00	activity-regulate	activity-regulate	NM_015193	NM_015193
2.37E+02	7.89E+00	activity-regulate	activity-regulate	NM_015193	NM_015193
2.37E+02	7.89E+00	activity-regulate	activity-regulate	NM_015193	NM_015193
4.38E-03	-7.83E+00	CNKSR family me	RNA binding mot	NM_173515	NM_173515
7.76E-01	-3.66E-01	GRB2-related ad	GRB2-related ad	NM_006613	NM_006613
7.76E-01	-3.66E-01	GRB2-related ad	GRB2-related ad	NM_006613	NM_006613
1.50E+00	5.83E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
4.48E-03	-7.80E+00	ATP binding dom	chromosome 15	NM_001141972	NM_001141972
4.48E-03	-7.80E+00	ATP binding dom	chromosome 15	NM_001141972	NM_001141972
2.84E+02	8.15E+00	protein tyrosine	non-SMC conder	NM_130842,NM	NM_130842,NM_130843,NM_002
4.66E+02	8.86E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
2.50E+02	7.97E+00	cytochrome P45	chromosome 7 o	NM_017781	NM_017781
1.40E+00	4.90E-01	forkhead box I1	forkhead box I1	NM_144769,NM	NM_144769,NM_012188
1.40E+00	4.90E-01	forkhead box I1	forkhead box I1	NM_144769,NM	NM_144769,NM_012188
1.67E+00	7.37E-01	espin pseudogen	macrophage stir	NR_026567	NR_026567
3.60E+02	8.49E+00	meteorin, glial ce	meteorin, glial ce	NM_001004431	NM_001004431
1.42E+00	5.08E-01	ciliary rootlet coi	neuroblastoma b	NR_023386	NR_023386
1.42E+00	5.08E-01	ciliary rootlet coi	neuroblastoma b	NR_023386	NR_023386
8.23E-01	-2.81E-01	hypothetical LOC	potassium chann	NR_024492	NR_024492
8.23E-01	-2.81E-01	hypothetical LOC	potassium chann	NR_024492	NR_024492
1.12E+00	1.69E-01	GNAS complex lo	GNAS complex lo	NM_001077488	NM_001077488
1.12E+00	1.69E-01	GNAS complex lo	GNAS complex lo	NM_001077488	NM_001077488
4.34E+02	8.76E+00	mitochondrial rib	zinc finger, DHH	NM_024026	NM_024026
4.34E+02	8.76E+00	mitochondrial rib	zinc finger, DHH	NM_024026	NM_024026
1.30E+00	3.81E-01	telomerase rever	telomerase rever	NM_198253,NM	NM_198253,NM_198255
1.42E+00	5.11E-01	plasmalemma ve	plasmalemma ve	NM_031310	NM_031310
2.65E+02	8.05E+00	potassium voltag	secretion regulat	NM_004976,NM	NM_004976,NM_001112741
1.25E+00	3.25E-01	protein tyrosine	protein tyrosine	NM_015605,NM	NM_015605,NM_001042363,NM_
1.36E+00	4.41E-01	hypothetical LOC	hypothetical LOC	NR_026828	NR_026828
1.36E+00	4.41E-01	hypothetical LOC	hypothetical LOC	NR_026828	NR_026828
4.11E-03	-7.93E+00	electron-transfer	ISL LIM homeob	NM_001127716,	NM_001127716,NM_000126
4.40E-03	-7.83E+00	Sad1 and UNC84	Sad1 and UNC84	NM_025154,NM	NM_025154,NM_001130965
4.54E+02	8.83E+00	FAT tumor suppr	melatonin recept	NM_001008781	NM_001008781
1.32E+00	4.04E-01	alkaline phospha	alkaline phospha	NM_001632	NM_001632
3.28E+02	8.36E+00	family with sequ	annexin A8	NM_001137556,	NM_001137556,NM_001137549,
1.31E+00	3.88E-01	RAB11 family int	RAB11 family int	NM_001142272	NM_001142272
1.31E+00	3.88E-01	RAB11 family int	RAB11 family int	NM_001142272	NM_001142272
1.31E+00	3.88E-01	RAB11 family int	RAB11 family int	NM_001142272	NM_001142272
1.27E+00	3.42E-01	spectrin, beta, no	spectrin, beta, no	NM_006946	NM_006946
1.27E+00	3.42E-01	spectrin, beta, no	spectrin, beta, no	NM_006946	NM_006946
1.27E+00	3.42E-01	spectrin, beta, no	chromosome 11	NM_006946	NM_006946
1.78E+00	8.29E-01	glyoxylate reduct	glyoxylate reduct	NM_032569	NM_032569
1.48E+00	5.62E-01	non-protein codi	non-protein codi	NR_027457	NR_027457
1.28E+00	3.54E-01	rhomboid 5 hom	rhomboid 5 hom	NM_022450	NM_022450
1.28E+00	3.54E-01	rhomboid 5 hom	rhomboid 5 hom	NM_022450	NM_022450
1.28E+00	3.54E-01	rhomboid 5 hom	rhomboid 5 hom	NM_022450	NM_022450
1.57E+00	6.49E-01	kinesin family me	kinesin family me	NM_020816,NM	NM_020816,NM_001122819
4.05E-03	-7.95E+00	tetratricopeptide	tetratricopeptide	NM_031421	NM_031421
4.05E-03	-7.95E+00	tetratricopeptide	tetratricopeptide	NM_031421	NM_031421
1.44E+00	5.27E-01	ubiquitin-like wit	ubiquitin-like wit	NM_013282	NM_013282
1.44E+00	5.27E-01	ubiquitin-like wit	ubiquitin-like wit	NM_013282	NM_013282
3.85E+02	8.59E+00	multiple C2 dom	hypothetical prot	NM_001159644	NM_001159644
1.32E+00	4.02E-01	proline rich 20C	proline rich 20C	NM_001130405,	NM_001130405,NM_001130404,
4.05E+02	8.66E+00	patched domain	RAB18, member	NM_001034842	NM_001034842

4.24E+02	8.73E+00	transient recepto	transient recepto	NM_145068	NM_145068
1.43E+00	5.13E-01	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
1.43E+00	5.13E-01	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
1.43E+00	5.13E-01	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
1.34E+00	4.27E-01	regulator of G-pr	regulator of G-pr	NM_002924	NM_002924
1.49E+00	5.71E-01	neurexin 2	RAS guanyl relea	NM_138734,NM	NM_138734,NM_015080,NM_138
6.82E-01	-5.51E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
6.82E-01	-5.51E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
6.82E-01	-5.51E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
6.82E-01	-5.51E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
4.70E+02	8.88E+00	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
4.70E+02	8.88E+00	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.32E+00	3.95E-01	ATPase type 13A	ATPase type 13A	NM_020410	NM_020410
1.32E+00	3.95E-01	ATPase type 13A	ATPase type 13A	NM_020410	NM_020410
1.40E+00	4.86E-01	paired related ho	paired related ho	NM_016307	NM_016307
1.40E+00	4.86E-01	paired related ho	paired related ho	NM_016307	NM_016307
4.43E-03	-7.82E+00	septin 9	septin 9	NM_006640	NM_006640
1.48E+00	5.69E-01	protein phosphat	protein phosphat	NM_013239,NM	NM_013239,NM_199326
1.48E+00	5.69E-01	protein phosphat	protein phosphat	NM_013239,NM	NM_013239,NM_199326
1.57E+00	6.47E-01	hypothetical LOC	cytidine monoph	NR_026833	NR_026833
1.57E+00	6.47E-01	hypothetical LOC	cytidine monoph	NR_026833	NR_026833
4.18E-03	-7.90E+00	cytochrome c oxi	cytochrome c oxi	NM_001861	NM_001861
4.18E-03	-7.90E+00	cytochrome c oxi	cytochrome c oxi	NM_001861	NM_001861
4.51E+02	8.82E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
4.51E+02	8.82E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
1.82E+00	8.62E-01	THO complex 4	THO complex 4	NM_005782	NM_005782
1.89E+00	9.22E-01	cut-like homeob	cut-like homeob	NM_181552	NM_181552
1.52E+00	6.00E-01	SPEG complex lo	SPEG complex lo	NM_005876	NM_005876
4.53E-03	-7.78E+00	alanine-glyoxylat	collagen, type XX	NR_027475,NR_	NR_027475,NR_027474,NM_0312
1.38E+00	4.62E-01	synovial sarcoma	synovial sarcoma	NM_198935	NM_198935
1.38E+00	4.62E-01	synovial sarcoma	synovial sarcoma	NM_198935	NM_198935
4.24E+02	8.73E+00	family with sequ	chromosome 3 o	NM_153690	NM_153690
4.24E+02	8.73E+00	family with sequ	chromosome 3 o	NM_153690	NM_153690
1.42E+00	5.06E-01	YdjC homolog (b	coiled-coil doma	NM_001017964	NM_001017964
1.42E+00	5.06E-01	YdjC homolog (b	coiled-coil doma	NM_001017964	NM_001017964
8.64E-01	-2.11E-01	tetratricopeptide	tetratricopeptide	NM_001010854	NM_001010854
8.64E-01	-2.11E-01	tetratricopeptide	tetratricopeptide	NM_001010854	NM_001010854
3.91E+02	8.61E+00	ATPase, Ca++ tra	ATPase, Ca++ tra	NM_001683,NM	NM_001683,NM_001001331
3.91E+02	8.61E+00	ATPase, Ca++ tra	ATPase, Ca++ tra	NM_001683,NM	NM_001683,NM_001001331
1.40E+00	4.85E-01	zeta-chain (TCR)	zeta-chain (TCR)	NM_001079	NM_001079
1.71E+00	7.73E-01	protein phosphat	protein phosphat	NM_013239,NM	NM_013239,NM_199326
4.59E+02	8.84E+00	acetylserotonin O	acetylserotonin O	NM_004192	NM_004192
4.59E+02	8.84E+00	acetylserotonin O	acetylserotonin O	NM_004192	NM_004192
4.59E+02	8.84E+00	acetylserotonin O	acetylserotonin O	NM_004192	NM_004192
4.06E+02	8.66E+00	delta-like 4 (Dros	delta-like 4 (Dros	NM_019074	NM_019074
4.06E+02	8.66E+00	delta-like 4 (Dros	delta-like 4 (Dros	NM_019074	NM_019074
2.81E-03	-8.48E+00	leucine rich repe	leucine rich repe	NM_001143757	NM_001143757
1.90E+00	9.24E-01	ST8 alpha-N-acet	ST8 alpha-N-acet	NM_013305	NM_013305
4.38E+02	8.77E+00	PEG3 antisense R	MER1 repeat con	NR_023847	NR_023847
4.38E+02	8.77E+00	PEG3 antisense R	MER1 repeat con	NR_023847	NR_023847
1.68E+00	7.46E-01	exonuclease 3'-5	exonuclease 3'-5	NM_017820	NM_017820
1.68E+00	7.46E-01	exonuclease 3'-5	exonuclease 3'-5	NM_017820	NM_017820
4.30E-03	-7.86E+00	zinc finger protei	zinc finger protei	NM_001031721	NM_001031721
3.94E+02	8.62E+00	polymerase (RNA	polymerase (RNA	NM_005035	NM_005035
3.94E+02	8.62E+00	polymerase (RNA	polymerase (RNA	NM_005035	NM_005035
1.51E+00	5.92E-01	eukaryotic transl	eukaryotic transl	NM_001961	NM_001961
3.53E-03	-8.14E+00	GLIS family zinc f	transmembrane	NM_147193	NM_147193
3.53E-03	-8.14E+00	GLIS family zinc f	transmembrane	NM_147193	NM_147193

1.45E+00	5.41E-01	myosin light chai	Werner helicase	NM_001012418	NM_001012418
1.45E+00	5.41E-01	myosin light chai	Werner helicase	NM_001012418	NM_001012418
1.65E+00	7.26E-01	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
1.65E+00	7.26E-01	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
4.34E+02	8.76E+00	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
1.40E+00	4.84E-01	family with sequ	hypothetical FLJ	NM_203392	NM_203392
1.40E+00	4.84E-01	family with sequ	hypothetical FLJ	NM_203392	NM_203392
1.40E+00	4.84E-01	family with sequ	hypothetical FLJ	NM_203392	NM_203392
1.40E+00	4.84E-01	family with sequ	hypothetical FLJ	NM_203392	NM_203392
1.40E+00	4.84E-01	family with sequ	hypothetical FLJ	NM_203392	NM_203392
1.25E+00	3.27E-01	solute carrier fan	solute carrier fan	NM_182632	NM_182632
1.25E+00	3.27E-01	solute carrier fan	solute carrier fan	NM_182632	NM_182632
1.56E+00	6.37E-01	ATPase, H+/K+ tr	ring finger protei	NM_001676	NM_001676
1.56E+00	6.37E-01	ATPase, H+/K+ tr	ring finger protei	NM_001676	NM_001676
1.45E+00	5.33E-01	zinc finger protei	zinc finger protei	NM_001136509	NM_001136509
1.45E+00	5.33E-01	zinc finger protei	zinc finger protei	NM_001136509	NM_001136509
1.33E+00	4.06E-01	DOT1-like, histor	DOT1-like, histor	NM_032482	NM_032482
1.33E+00	4.06E-01	DOT1-like, histor	DOT1-like, histor	NM_032482	NM_032482
1.33E+00	4.06E-01	DOT1-like, histor	DOT1-like, histor	NM_032482	NM_032482
1.42E+00	5.09E-01	small nucleolar R	purinergic recept	NR_003688	NR_003688
1.42E+00	5.09E-01	small nucleolar R	purinergic recept	NR_003688	NR_003688
5.03E+02	8.97E+00	adenosine deami	adenosine deami	NM_018702	NM_018702
5.03E+02	8.97E+00	adenosine deami	adenosine deami	NM_018702	NM_018702
1.11E+00	1.50E-01	hypothetical LOC	calcium channel,	NR_024341	NR_024341
1.20E+00	2.62E-01	lysine (K)-specifi	lysine (K)-specifi	NM_015015	NM_015015
1.20E+00	2.62E-01	lysine (K)-specifi	lysine (K)-specifi	NM_015015	NM_015015
1.80E+00	8.46E-01	talin 2	tropomyosin 1 (a	NM_015059	NM_015059
1.35E+00	4.30E-01	chromosome 16	cadherin 15, type	NR_024347	NR_024347
1.35E+00	4.30E-01	chromosome 16	cadherin 15, type	NR_024347	NR_024347
4.08E+02	8.67E+00	jumonji domain (	jumonji domain (	NM_001005920	NM_001005920
4.03E-03	-7.95E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
1.26E+00	3.36E-01	transient recepto	sedoheptulokina	NM_080706,NM	NM_080706,NM_080705,NM_018
1.26E+00	3.36E-01	transient recepto	sedoheptulokina	NM_080706,NM	NM_080706,NM_080705,NM_018
1.26E+00	3.36E-01	transient recepto	sedoheptulokina	NM_080706,NM	NM_080706,NM_080705,NM_018
1.26E+00	3.36E-01	transient recepto	sedoheptulokina	NM_080706,NM	NM_080706,NM_080705,NM_018
1.26E+00	3.36E-01	transient recepto	sedoheptulokina	NM_080706,NM	NM_080706,NM_080705,NM_018
5.02E-03	-7.64E+00	transient recepto	potassium voltag	NM_007332	NM_007332
1.18E+00	2.43E-01	mediator comple	TBC1 domain fan	NM_005121	NM_005121
1.35E+00	4.34E-01	leucine rich repe	leucine-rich repe	NM_153353	NM_153353
1.54E+00	6.27E-01	Rho GTPase acti	Rho GTPase acti	NM_021226	NM_021226
1.54E+00	6.27E-01	Rho GTPase acti	Rho GTPase acti	NM_021226	NM_021226
1.27E+00	3.44E-01	solute carrier fan	dipeptidase 3	NM_001145963,	NM_001145963,NM_001145964,N
3.58E+02	8.48E+00	solute carrier fan	ret finger protei	NM_014227	NM_014227
1.43E+00	5.16E-01	netrin 5	fucosyltransfera	NM_145807	NM_145807
1.43E+00	5.16E-01	netrin 5	fucosyltransfera	NM_145807	NM_145807
1.43E+00	5.16E-01	netrin 5	fucosyltransfera	NM_145807	NM_145807
1.43E+00	5.16E-01	netrin 5	fucosyltransfera	NM_145807	NM_145807
4.03E+02	8.65E+00	nucleosome asse	nucleosome asse	NM_153757	NM_153757
4.03E+02	8.65E+00	nucleosome asse	nucleosome asse	NM_153757	NM_153757
4.03E+02	8.65E+00	nucleosome asse	nucleosome asse	NM_153757	NM_153757
1.37E+00	4.51E-01	lipocalin 1 (tear	odorant binding	NM_002297	NM_002297
1.37E+00	4.51E-01	lipocalin 1 (tear	odorant binding	NM_002297	NM_002297
4.42E+02	8.79E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
4.42E+02	8.79E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
4.47E-03	-7.81E+00	CD79b molecule,	sodium channel,	NM_000626,NM	NM_000626,NM_021602,NM_001
1.44E+00	5.27E-01	DENN/MADD do	solute carrier fan	NM_014957	NM_014957
1.44E+00	5.27E-01	DENN/MADD do	solute carrier fan	NM_014957	NM_014957
2.53E+02	7.98E+00	perilipin 5	perilipin 5	NM_001013706	NM_001013706

1.57E+00	6.52E-01	BARX homeobox	transmembrane	NM_003658	NM_003658
1.57E+00	6.52E-01	BARX homeobox	transmembrane	NM_003658	NM_003658
1.54E+00	6.25E-01	intercellular adhe	intercellular adhe	NM_000201	NM_000201
1.54E+00	6.25E-01	intercellular adhe	intercellular adhe	NM_000201	NM_000201
1.33E+00	4.09E-01	chemokine-like f	CKLF-like MARVE	NM_016326,NM	NM_016326,NM_181641,NM_181
1.33E+00	4.09E-01	CKLF-like MARVE	CKLF-like MARVE	NM_052999,NM	NM_052999,NM_181268
1.86E+00	8.98E-01	pregnancy specif	pregnancy specif	NM_002782	NM_002782
1.86E+00	8.98E-01	pregnancy specif	pregnancy specif	NM_002782	NM_002782
6.40E-01	-6.44E-01	RWD domain co	ubiquitin specific	NM_016940	NM_016940
1.40E+00	4.89E-01	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
3.02E-03	-8.37E+00	calcium channel,	calcium channel,	NM_201571,NM	NM_201571,NM_201572
1.81E+00	8.59E-01	thyroid peroxida	thyroid peroxida	NM_000547,NM	NM_000547,NM_175719,NM_17
1.81E+00	8.59E-01	thyroid peroxida	thyroid peroxida	NM_000547,NM	NM_000547,NM_175719,NM_17
1.42E+00	5.03E-01	adaptor-related	adaptor-related	NM_012305	NM_012305
4.04E+02	8.66E+00	carbohydrate kin	carbohydrate kin	NM_018210	NM_018210
4.04E+02	8.66E+00	carbohydrate kin	carbohydrate kin	NM_018210	NM_018210
1.70E+00	7.67E-01	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
1.70E+00	7.67E-01	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
1.32E+00	3.99E-01	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
1.32E+00	3.99E-01	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
1.65E+00	7.25E-01	casein kinase 1,	CD7 molecule	NM_139062,NM	NM_139062,NM_001893
1.65E+00	7.25E-01	casein kinase 1,	CD7 molecule	NM_139062,NM	NM_139062,NM_001893
1.65E+00	7.25E-01	casein kinase 1,	CD7 molecule	NM_139062,NM	NM_139062,NM_001893
1.25E+00	3.27E-01	rabphilin 3A-like	rabphilin 3A-like	NM_006987	NM_006987
1.25E+00	3.27E-01	rabphilin 3A-like	rabphilin 3A-like	NM_006987	NM_006987
1.68E+00	7.48E-01	melanoma assoc	melanoma assoc	NR_024247	NR_024247
1.68E+00	7.48E-01	melanoma assoc	melanoma assoc	NR_024247	NR_024247
4.37E+02	8.77E+00	SPARC related m	thrombospondin	NM_022138	NM_022138
4.37E+02	8.77E+00	SPARC related m	thrombospondin	NM_022138	NM_022138
3.59E+02	8.49E+00	family with sequ	KIAA0182	NM_198491	NM_198491
1.72E+00	7.84E-01	NADH dehydroge	ribosomal protei	NM_004548	NM_004548
1.72E+00	7.84E-01	small nucleolar R	small nucleolar R	NR_002327	NR_002327
1.87E+00	9.06E-01	zinc finger protei	zinc finger protei	NM_001007248	NM_001007248
1.87E+00	9.06E-01	zinc finger protei	zinc finger protei	NM_001007248	NM_001007248
1.88E+00	9.14E-01	zinc finger protei	zinc finger protei	NM_173480	NM_173480
1.88E+00	9.14E-01	zinc finger protei	zinc finger protei	NM_173480	NM_173480
1.32E+00	4.00E-01	ATPase family, A	ATPase family, A	NM_031921	NM_031921
1.32E+00	4.00E-01	ATPase family, A	ATPase family, A	NM_031921	NM_031921
1.36E+00	4.46E-01	null	hypothetical LOC	null	null
3.95E+02	8.63E+00	plexin B2	plexin B2	NM_012401	NM_012401
4.61E-03	-7.76E+00	Kruppel-like fact	hypothetical LOC	NM_001300	NM_001300
3.72E+02	8.54E+00	collagen, type IV	collagen, type IV	NM_001846	NM_001846
1.72E+00	7.85E-01	hypothetical pro	hypothetical pro	NR_002787	NR_002787
1.72E+00	7.85E-01	hypothetical pro	hypothetical pro	NR_002787	NR_002787
4.17E+02	8.70E+00	fibronectin type	fibronectin type	NM_032532	NM_032532
4.17E+02	8.70E+00	fibronectin type	fibronectin type	NM_032532	NM_032532
3.61E+02	8.50E+00	null	hypothetical LOC	null	null
1.63E+00	7.06E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.61E+02	8.50E+00	deleted in azoos	phospholipase C	NM_001351	NM_001351
1.37E+00	4.56E-01	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
1.59E+00	6.66E-01	purinergic recept	purinergic recept	NM_002558	NM_002558
3.28E-03	-8.25E+00	GNAS complex l	TH1-like (Drosop	NM_001077488	NM_001077488
1.76E+00	8.12E-01	phosphatidylinos	phosphatidylinos	NM_001127178,	NM_001127178,NM_017733
3.83E+02	8.58E+00	cell division cycl	granzyme M (ly	NM_004359	NM_004359
3.83E+02	8.58E+00	granzyme M (ly	granzyme M (ly	NM_005317	NM_005317
1.36E+00	4.46E-01	smoothelin-like	smoothelin-like	NM_001114974	NM_001114974
3.75E+02	8.55E+00	nuclear factor of	nuclear factor of	NM_001001716,	NM_001001716,NM_002503
3.75E+02	8.55E+00	nuclear factor of	nuclear factor of	NM_001001716,	NM_001001716,NM_002503

3.56E+02	8.48E+00	H19, imprinted n	H19, imprinted n	NR_002196	NR_002196
3.52E+02	8.46E+00	chromosome 12	chromosome 12	NM_152638	NM_152638
1.37E+00	4.51E-01	growth arrest-sp	growth arrest-sp	NM_001143945	NM_001143945
1.37E+00	4.51E-01	growth arrest-sp	growth arrest-sp	NM_001143945	NM_001143945
1.37E+00	4.51E-01	growth arrest-sp	growth arrest-sp	NM_001143945	NM_001143945
1.37E+00	4.51E-01	growth arrest-sp	growth arrest-sp	NM_001143945	NM_001143945
1.37E+00	4.51E-01	growth arrest-sp	growth arrest-sp	NM_001143945	NM_001143945
1.55E+00	6.32E-01	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
1.55E+00	6.32E-01	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
1.78E+00	8.36E-01	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
1.25E+00	3.18E-01	solute carrier fan	solute carrier fan	NM_001099646,	NM_001099646,NM_152908
1.17E+00	2.26E-01	S-antigen	diacylglycerol kir	NM_000541	NM_000541
1.17E+00	2.26E-01	S-antigen	diacylglycerol kir	NM_000541	NM_000541
1.17E+00	2.26E-01	S-antigen	diacylglycerol kir	NM_000541	NM_000541
1.17E+00	2.26E-01	S-antigen	diacylglycerol kir	NM_000541	NM_000541
1.50E+00	5.87E-01	protein tyrosine	protein tyrosine	NM_005401	NM_005401
1.50E+00	5.87E-01	protein tyrosine	protein tyrosine	NM_005401	NM_005401
1.25E+00	3.21E-01	claudin 5	hypothetical LOC	NM_001130861,	NM_001130861,NM_003277
1.25E+00	3.21E-01	hypothetical LOC	hypothetical LOC	NR_024381	NR_024381
1.61E+00	6.87E-01	SET domain cont	SET domain cont	NM_015048	NM_015048
4.50E+02	8.82E+00	paired-like home	paired-like home	NM_153426,NM	NM_153426,NM_153427,NM_000
4.26E+02	8.73E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
1.82E+00	8.61E-01	telomerase rever	telomerase rever	NM_198253,NM	NM_198253,NM_198255
3.91E+02	8.61E+00	chromosome 19	polypyrimidine tı	NM_173481	NM_173481
4.42E+02	8.79E+00	heparan sulfate	heparan sulfate	NM_005529	NM_005529
1.29E+00	3.65E-01	pitrilysin metallo	Kruppel-like fact	NM_014889	NM_014889
1.29E+00	3.65E-01	pitrilysin metallo	Kruppel-like fact	NM_014889	NM_014889
1.70E+00	7.67E-01	cat eye syndrom	cat eye syndrom	NR_015352	NR_015352
4.79E+02	8.90E+00	peroxisomal prol	glucocorticoid m	NM_001037335,	NM_001037335,NM_033405
4.79E+02	8.90E+00	peroxisomal prol	glucocorticoid m	NM_001037335,	NM_001037335,NM_033405
1.31E+00	3.90E-01	malonyl-CoA dec	oxidative stress i	NM_012213	NM_012213
4.08E+02	8.67E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
4.55E+02	8.83E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
4.55E+02	8.83E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.83E+02	8.58E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
3.83E+02	8.58E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
3.82E+02	8.58E+00	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
3.82E+02	8.58E+00	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
3.92E+02	8.62E+00	family with sequ	family with sequ	NM_001136233	NM_001136233
1.39E+00	4.74E-01	cancer/testis ant	cancer/testis ant	NM_001017436,	NM_001017436,NM_152582
1.39E+00	4.74E-01	cancer/testis ant	cancer/testis ant	NM_001017436,	NM_001017436,NM_152582
1.39E+00	4.74E-01	cancer/testis ant	cancer/testis ant	NM_001017435	NM_001017435
3.50E+02	8.45E+00	proprotein conve	proprotein conve	NM_017573	NM_017573
3.50E+02	8.45E+00	proprotein conve	proprotein conve	NM_017573	NM_017573
3.95E-03	-7.98E+00	exonuclease 3'-5	UDP-N-acetyl-alp	NM_018199	NM_018199
3.95E-03	-7.98E+00	exonuclease 3'-5	UDP-N-acetyl-alp	NM_018199	NM_018199
1.23E+00	2.93E-01	retina and anteri	retina and anteri	NM_013435	NM_013435
4.28E+02	8.74E+00	neuroblastoma b	lymphocyte-spec	NM_001102663	NM_001102663
1.29E+00	3.70E-01	chromosome 6 o	regulating synap	NR_026807	NR_026807
1.29E+00	3.70E-01	chromosome 6 o	regulating synap	NR_026807	NR_026807
4.17E+02	8.71E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
1.32E+00	3.96E-01	PHD finger prote	PHD finger prote	NM_001135862,	NM_001135862,NM_138415
1.32E+00	3.96E-01	PHD finger prote	PHD finger prote	NM_001135862,	NM_001135862,NM_138415
1.45E+00	5.40E-01	family with sequ	family with sequ	NM_001010924	NM_001010924
1.45E+00	5.40E-01	family with sequ	family with sequ	NM_001010924	NM_001010924
1.26E+00	3.31E-01	casein kinase 1,	casein kinase 1,	NM_139062,NM	NM_139062,NM_001893
3.87E+02	8.60E+00	TEA domain fami	TEA domain fami	NM_003214	NM_003214
3.87E+02	8.60E+00	TEA domain fami	TEA domain fami	NM_003214	NM_003214

4.31E+02	8.75E+00	anoctamin 1, cal	anoctamin 1, cal	NM_018043	NM_018043
1.23E+00	2.99E-01	neuropeptides B,	neuropeptides B,	NM_005286	NM_005286
4.04E+02	8.66E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
4.04E+02	8.66E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
1.64E+00	7.15E-01	tripartite motif-c	tripartite motif-c	NM_015271	NM_015271
1.64E+00	7.15E-01	tripartite motif-c	tripartite motif-c	NM_015271	NM_015271
4.49E+02	8.81E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.48E+00	5.63E-01	POU class 6 hom	DAZ associated p	NM_002702,NR_	NM_002702,NR_026893
1.48E+00	5.63E-01	POU class 6 hom	DAZ associated p	NM_002702,NR_	NM_002702,NR_026893
1.84E+00	8.82E-01	nuclear factor (e	nuclear factor (e	NM_003204	NM_003204
3.55E+02	8.47E+00	5'-nucleotidase,	5'-nucleotidase,	NM_033253,NM	NM_033253,NM_001002006
3.55E+02	8.47E+00	5'-nucleotidase,	5'-nucleotidase,	NM_033253,NM	NM_033253,NM_001002006
4.10E+02	8.68E+00	UDP-N-acetyl-alp	hypothetical LOC	NM_021808,NM	NM_021808,NM_001122636
1.13E+00	1.78E-01	ankyrin repeat d	POTE ankyrin do	NR_026916	NR_026916
1.13E+00	1.78E-01	ankyrin repeat d	POTE ankyrin do	NR_026916	NR_026916
1.13E+00	1.78E-01	ankyrin repeat d	POTE ankyrin do	NR_026916	NR_026916
4.15E+02	8.70E+00	receptor-interact	receptor-interact	NM_020639	NM_020639
4.15E+02	8.70E+00	receptor-interact	receptor-interact	NM_020639	NM_020639
4.15E+02	8.70E+00	receptor-interact	receptor-interact	NM_020639	NM_020639
1.51E+00	5.92E-01	glucuronidase, b	family with sequ	NR_027503	NR_027503
1.51E+00	5.92E-01	glucuronidase, b	family with sequ	NR_027503	NR_027503
1.51E+00	5.92E-01	glucuronidase, b	family with sequ	NR_027503	NR_027503
1.62E+00	6.95E-01	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
1.62E+00	6.95E-01	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
2.18E+00	1.12E+00	keratin associate	ubiquitin-conjug	NM_198699	NM_198699
4.29E+02	8.75E+00	interleukin 3 rec	solute carrier fan	NM_002183	NM_002183
4.29E+02	8.75E+00	solute carrier fan	solute carrier fan	NM_001636	NM_001636
3.63E+02	8.51E+00	lipase maturatio	SRY (sex determi	NM_022773	NM_022773
4.21E+02	8.72E+00	nuclear factor (e	nuclear factor (e	NM_003204	NM_003204
2.11E+00	1.08E+00	olfactomedin-lik	olfactomedin-lik	NM_015441	NM_015441
2.11E+00	1.08E+00	olfactomedin-lik	olfactomedin-lik	NM_015441	NM_015441
4.21E+02	8.72E+00	chromosome 18	chromosome 18	NM_181481,NM	NM_181481,NM_181482
4.21E+02	8.72E+00	chromosome 18	chromosome 18	NM_181481,NM	NM_181481,NM_181482
4.21E+02	8.72E+00	chromosome 18	chromosome 18	NM_181481,NM	NM_181481,NM_181482
4.52E+02	8.82E+00	phytanoyl-CoA 2	phytanoyl-CoA 2	NM_014759,NM	NM_014759,NM_001099335
4.52E+02	8.82E+00	phytanoyl-CoA 2	phytanoyl-CoA 2	NM_014759,NM	NM_014759,NM_001099335
1.40E+00	4.84E-01	ATP-binding cass	ATP-binding cass	NM_022436	NM_022436
1.57E+00	6.53E-01	connector enhan	connector enhan	NR_023345	NR_023345
1.21E+00	2.77E-01	nuclear receptor	nuclear receptor	NM_003269	NM_003269
1.21E+00	2.77E-01	nuclear receptor	nuclear receptor	NM_003269	NM_003269
3.68E+02	8.52E+00	coronin, actin bi	coronin, actin bi	NM_020441,NM	NM_020441,NM_001018070
4.13E+02	8.69E+00	low density lipop	low density lipop	NM_000527	NM_000527
4.13E+02	8.69E+00	low density lipop	low density lipop	NM_000527	NM_000527
1.60E+00	6.74E-01	family with sequ	KIAA0182	NM_198491	NM_198491
3.60E+02	8.49E+00	collagen, type V,	collagen, type V,	NM_000093	NM_000093
3.60E+02	8.49E+00	collagen, type V,	collagen, type V,	NM_000093	NM_000093
1.47E+00	5.52E-01	solute carrier fan	solute carrier fan	NM_198580	NM_198580
1.47E+00	5.52E-01	solute carrier fan	solute carrier fan	NM_198580	NM_198580
2.33E+00	1.22E+00	trinucleotide rep	trinucleotide rep	NM_001080495	NM_001080495
4.47E+02	8.80E+00	hypothetical pro	tumor suppressi	NR_024468	NR_024468
4.47E+02	8.80E+00	hypothetical pro	tumor suppressi	NR_024468	NR_024468
1.38E+00	4.70E-01	UDP-GlcNAc:bet	meteorin, glial c	NM_001009905	NM_001009905
1.38E+00	4.70E-01	UDP-GlcNAc:bet	meteorin, glial c	NM_001009905	NM_001009905
1.61E+00	6.86E-01	TBC1 domain fan	family with sequ	NM_014346	NM_014346
1.61E+00	6.86E-01	TBC1 domain fan	family with sequ	NM_014346	NM_014346
1.44E+00	5.27E-01	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
1.42E+00	5.04E-01	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
1.42E+00	5.04E-01	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212

1.68E+00	7.48E-01	prohibitin 2	prohibitin 2	NM_007273,NM	NM_007273,NM_001144831
3.50E+02	8.45E+00	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
3.50E+02	8.45E+00	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
3.44E+02	8.43E+00	signal sequence	cancer antigen 1	NM_003144	NM_003144
3.44E+02	8.43E+00	signal sequence	cancer antigen 1	NM_003144	NM_003144
1.33E+00	4.10E-01	odorant binding	progestagen-ass	NM_014582	NM_014582
1.33E+00	4.10E-01	progestagen-ass	progestagen-ass	NM_001018049,	NM_001018049,NM_002571
1.43E+00	5.19E-01	potassium chann	potassium chann	NM_018992	NM_018992
1.43E+00	5.19E-01	potassium chann	potassium chann	NM_018992	NM_018992
2.62E-03	-8.58E+00	eukaryotic transl	ribose 5-phosph	NM_004836	NM_004836
1.75E+00	8.07E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
1.75E+00	8.07E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
3.70E+02	8.53E+00	DNA (cytosine-5-	DNA (cytosine-5-	NM_013369,NM	NM_013369,NM_175867
3.83E+02	8.58E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794
3.83E+02	8.58E+00	cadherin 4, type	cadherin 4, type	NM_001794	NM_001794
1.35E+00	4.34E-01	ATP-binding cass	trefoil factor 3 (i	NM_207174	NM_207174
1.35E+00	4.34E-01	ATP-binding cass	trefoil factor 3 (i	NM_207174	NM_207174
4.53E+02	8.82E+00	potassium inwar	cytohesin 2	NM_170720	NM_170720
4.53E+02	8.82E+00	potassium inwar	cytohesin 2	NM_170720	NM_170720
1.25E+00	3.26E-01	zinc finger protei	zinc finger protei	NM_006352	NM_006352
1.25E+00	3.26E-01	zinc finger protei	zinc finger protei	NM_006352	NM_006352
3.90E+02	8.61E+00	major vault prot	major vault prot	NM_017458	NM_017458
3.90E+02	8.61E+00	major vault prot	major vault prot	NM_017458	NM_017458
1.37E+00	4.58E-01	CTF18, chromos	CTF18, chromos	NM_022092	NM_022092
1.37E+00	4.58E-01	CTF18, chromos	CTF18, chromos	NM_022092	NM_022092
1.28E+00	3.55E-01	elongation facto	elongation facto	NM_006532	NM_006532
1.28E+00	3.55E-01	elongation facto	elongation facto	NM_006532	NM_006532
1.57E+00	6.51E-01	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
1.57E+00	6.51E-01	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
1.32E+00	4.04E-01	fibrinogen gamm	lecithin retinol a	NM_021870	NM_021870
1.44E+00	5.24E-01	cullin 4A	cullin 4A	NM_001008895	NM_001008895
1.44E+00	5.24E-01	cullin 4A	cullin 4A	NM_001008895	NM_001008895
4.54E+02	8.83E+00	tetraspanin 4	tetraspanin 4	NM_001025237	NM_001025237
1.70E+00	7.62E-01	null	transmembrane	null	null
1.70E+00	7.62E-01	null	transmembrane	null	null
1.73E+00	7.87E-01	iroquois homeo	hypothetical LO	NM_024337	NM_024337
1.73E+00	7.87E-01	iroquois homeo	hypothetical LO	NM_024337	NM_024337
1.20E+00	2.59E-01	SH3-binding do	SH3-binding do	NM_001101401	NM_001101401
3.95E+02	8.63E+00	plexin B2	plexin B2	NM_012401	NM_012401
3.95E+02	8.63E+00	plexin B2	plexin B2	NM_012401	NM_012401
3.95E+02	8.63E+00	plexin B2	plexin B2	NM_012401	NM_012401
1.40E+00	4.85E-01	kinesin family m	kinesin family m	NM_004522	NM_004522
1.40E+00	4.85E-01	kinesin family m	kinesin family m	NM_004522	NM_004522
3.80E+02	8.57E+00	discs, large (Dros	discs, large (Dros	NM_014902	NM_014902
1.34E+00	4.22E-01	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
1.34E+00	4.22E-01	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
1.34E+00	4.22E-01	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
3.33E+02	8.38E+00	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
3.33E+02	8.38E+00	kelch-like 17 (Dr	kelch-like 17 (Dr	NM_198317	NM_198317
3.33E+02	8.38E+00	kelch-like 17 (Dr	pleckstrin homol	NM_198317	NM_198317
1.58E+00	6.64E-01	iroquois homeo	iroquois homeo	NM_016358	NM_016358
1.58E+00	6.64E-01	iroquois homeo	iroquois homeo	NM_016358	NM_016358
1.52E+00	6.00E-01	phosphatidylglyc	phosphatidylglyc	NM_024419	NM_024419
1.52E+00	6.00E-01	phosphatidylglyc	phosphatidylglyc	NM_024419	NM_024419
3.81E+02	8.57E+00	solute carrier fa	solute carrier fa	NM_003044	NM_003044
1.48E+00	5.69E-01	patatin-like phos	patatin-like phos	NM_152286,NM	NM_152286,NM_001098537
1.37E+00	4.53E-01	UDP-N-acetyl-al	UDP-N-acetyl-al	NM_004481	NM_004481
1.37E+00	4.53E-01	UDP-N-acetyl-al	UDP-N-acetyl-al	NM_004481	NM_004481

1.13E+00	1.72E-01	X-ray repair com	X-ray repair com	NM_001100118,	NM_001100118,NM_005432,NM_
4.67E+02	8.87E+00	ring finger protei	ring finger protei	NM_020914	NM_020914
1.53E+00	6.14E-01	PML-RARA regul	PML-RARA regul	NM_032152	NM_032152
1.39E+00	4.71E-01	tubulin, alpha 3e	tubulin, alpha 3e	NM_207312	NM_207312
1.39E+00	4.71E-01	tubulin, alpha 3e	tubulin, alpha 3e	NM_207312	NM_207312
1.42E+00	5.07E-01	chromosome 4 o	protocadherin 1	NM_001099783	NM_001099783
1.42E+00	5.07E-01	chromosome 4 o	protocadherin 1	NM_001099783	NM_001099783
3.47E-03	-8.17E+00	spermatogenesis	chromosome 15	NM_024063	NM_024063
3.52E+02	8.46E+00	H19, imprinted n	H19, imprinted n	NR_002196	NR_002196
1.77E+00	8.27E-01	pericentrin	pericentrin	NM_006031	NM_006031
3.51E+02	8.46E+00	PDZ domain con	PDZ domain con	NM_024895	NM_024895
3.51E+02	8.46E+00	PDZ domain con	PDZ domain con	NM_024895	NM_024895
1.19E+00	2.50E-01	non-protein codi	non-protein codi	NR_024367	NR_024367
1.19E+00	2.50E-01	non-protein codi	non-protein codi	NR_024367	NR_024367
1.56E+00	6.46E-01	protease, serine-	protease, serine-	NM_214710	NM_214710
1.56E+00	6.46E-01	protease, serine-	protease, serine-	NM_214710	NM_214710
1.56E+00	6.46E-01	protease, serine-	protease, serine-	NM_214710	NM_214710
3.39E+02	8.41E+00	ubiquitin specific	ubiquitin specific	NM_025090	NM_025090
3.39E+02	8.41E+00	ubiquitin specific	ubiquitin specific	NM_025090	NM_025090
1.59E+00	6.69E-01	psoriasis suscept	HLA complex gro	NR_026816	NR_026816
3.73E+02	8.54E+00	CUGBP, Elav-like	CUGBP, Elav-like	NM_001025087,	NM_001025087,NM_020180,NM_
1.70E+00	7.64E-01	BEN domain con	BEN domain con	NM_001100912	NM_001100912
1.70E+00	7.64E-01	BEN domain con	BEN domain con	NM_001100912	NM_001100912
1.70E+00	7.64E-01	BEN domain con	BEN domain con	NM_001100912	NM_001100912
3.40E+02	8.41E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
3.40E+02	8.41E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
3.51E+02	8.46E+00	pseudouridylate	E1A binding prot	NM_001002020,	NM_001002020,NM_025215,NM_
3.85E+02	8.59E+00	guanidinoacetat	guanidinoacetat	NM_138924	NM_138924
3.85E+02	8.59E+00	guanidinoacetat	guanidinoacetat	NM_138924	NM_138924
3.30E+02	8.37E+00	protease, serine-	paralemmin	NM_214710	NM_214710
3.30E+02	8.37E+00	protease, serine-	paralemmin	NM_214710	NM_214710
4.72E+02	8.88E+00	acetylserotonin	acetylserotonin	NM_004192	NM_004192
4.24E+02	8.73E+00	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
4.24E+02	8.73E+00	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
3.82E+02	8.58E+00	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
1.49E+00	5.73E-01	outer dense fibe	mucosal vascula	NM_182577	NM_182577
1.49E+00	5.73E-01	outer dense fibe	mucosal vascula	NM_182577	NM_182577
4.52E+02	8.82E+00	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
2.00E+00	1.00E+00	eukaryotic transl	eukaryotic transl	NM_003755	NM_003755
2.00E+00	1.00E+00	eukaryotic transl	eukaryotic transl	NM_003755	NM_003755
4.34E+02	8.76E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_00
4.72E+02	8.88E+00	chromosome 10	La ribonucleopro	NR_027152,NR_	NR_027152,NR_027151
3.64E+02	8.51E+00	tektin 5	tektin 5	NM_144674	NM_144674
1.72E+00	7.80E-01	zinc finger protei	zinc finger protei	NM_001080417	NM_001080417
1.91E+00	9.31E-01	tubulin, alpha 3c	tubulin, alpha 3c	NM_006001	NM_006001
4.17E+02	8.71E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.30E+02	8.37E+00	transmembrane	EPS8-like 2	NM_001042463,	NM_001042463,NM_174940
2.01E+00	1.01E+00	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
2.01E+00	1.01E+00	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
3.28E+02	8.36E+00	aarF domain con	aarF domain con	NM_174922	NM_174922
3.28E+02	8.36E+00	cleavage and pol	cleavage and pol	NM_013291	NM_013291
3.28E+02	8.36E+00	cleavage and pol	cleavage and pol	NM_013291	NM_013291
1.50E+00	5.85E-01	mesoderm induc	mesoderm induc	NM_017550	NM_017550
1.50E+00	5.85E-01	mesoderm induc	mesoderm induc	NM_017550	NM_017550
3.47E-03	-8.17E+00	archaelysin famil	archaelysin famil	NM_001033569,	NM_001033569,NM_001033570,
3.47E-03	-8.17E+00	archaelysin famil	arylsulfatase G	NM_001033569,	NM_001033569,NM_001033570,
1.57E+00	6.47E-01	transmembrane	poly(A) binding p	NR_026730	NR_026730
3.07E+02	8.26E+00	WD repeat doma	WD repeat doma	NM_052821	NM_052821

1.49E+00	5.78E-01	RAS p21 protein	cell division cycle	NM_007368	NM_007368
1.49E+00	5.78E-01	RAS p21 protein	cell division cycle	NM_007368	NM_007368
3.63E+02	8.51E+00	opioid growth fa	opioid growth fa	NM_007346	NM_007346
1.47E+00	5.54E-01	jumonji domain	jumonji domain	NM_001005920	NM_001005920
1.45E+00	5.39E-01	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
1.45E+00	5.39E-01	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.11E-03	-8.33E+00	sex comb on mid	endothelin 2	NM_012236	NM_012236
4.07E+02	8.67E+00	CUB and Sushi m	CUB and Sushi m	NM_052896	NM_052896
4.07E+02	8.67E+00	CUB and Sushi m	CUB and Sushi m	NM_052896	NM_052896
3.62E+02	8.50E+00	family with sequ	family with sequ	NM_001002034	NM_001002034
3.86E+02	8.59E+00	solute carrier fan	solute carrier fan	NM_001126335,	NM_001126335,NM_014270
2.32E+00	1.22E+00	synaptotagmin II	synaptotagmin II	NM_032298	NM_032298
3.39E+02	8.41E+00	growth arrest an	guanine nucleoti	NM_015675	NM_015675
3.39E+02	8.41E+00	guanine nucleoti	guanine nucleoti	NM_052847	NM_052847
3.53E+02	8.46E+00	galactose-3-O-su	galactose-3-O-su	NM_022134	NM_022134
1.57E+00	6.55E-01	hypothetical LOC	hypothetical LOC	NR_015441	NR_015441
1.57E+00	6.55E-01	hypothetical LOC	hypothetical LOC	NR_015441	NR_015441
2.18E+00	1.13E+00	fibronectin type	fibronectin type	NM_032532	NM_032532
4.52E+02	8.82E+00	KIAA1751	KIAA1751	NM_001080484	NM_001080484
3.63E+02	8.51E+00	opioid growth fa	opioid growth fa	NM_007346	NM_007346
1.36E+00	4.42E-01	hypothetical LOC	hypothetical pro	NR_024101	NR_024101
3.68E+02	8.52E+00	solute carrier org	solute carrier org	NM_016354	NM_016354
3.68E+02	8.52E+00	solute carrier org	solute carrier org	NM_016354	NM_016354
3.51E+02	8.46E+00	protein tyrosine	protein tyrosine	NM_002840,NM	NM_002840,NM_130440
4.65E+02	8.86E+00	RNA pseudourid	RNA pseudourid	NM_058192	NM_058192
1.56E+00	6.45E-01	zinc finger protei	zinc finger protei	NM_001159279	NM_001159279
1.56E+00	6.45E-01	zinc finger protei	zinc finger protei	NM_001159279	NM_001159279
3.38E+02	8.40E+00	chromosome 19	proprotein conve	NM_152482	NM_152482
3.38E+02	8.40E+00	proprotein conve	proprotein conve	NM_017573	NM_017573
4.17E+02	8.70E+00	glycerophosphoc	glycerophosphoc	NM_024307	NM_024307
3.94E+02	8.62E+00	zinc finger protei	zinc finger protei	NM_133444	NM_133444
1.44E+00	5.23E-01	ATPase family, A	ATPase family, A	NM_018188	NM_018188
1.13E+00	1.70E-01	ribosomal protei	ubiquitin-conjug	NM_001021	NM_001021
1.34E+00	4.21E-01	zinc finger protei	hect domain and	NM_003414	NM_003414
1.34E+00	4.21E-01	zinc finger protei	hect domain and	NM_003414	NM_003414
1.34E+00	4.21E-01	zinc finger protei	hect domain and	NM_003414	NM_003414
3.12E+02	8.29E+00	chromosome 6 o	chromosome 6 o	NM_145028	NM_145028
3.40E+02	8.41E+00	fucosyltransferas	fucosyltransferas	NM_004479	NM_004479
3.40E+02	8.41E+00	fucosyltransferas	fucosyltransferas	NM_004479	NM_004479
3.58E+02	8.48E+00	acetylserotonin (	acetylserotonin (	NM_004192	NM_004192
3.83E+02	8.58E+00	family with sequ	family with sequ	NM_020223	NM_020223
3.83E+02	8.58E+00	family with sequ	family with sequ	NM_020223	NM_020223
3.83E+02	8.58E+00	family with sequ	family with sequ	NM_020223	NM_020223
3.08E-03	-8.34E+00	olfactory recepto	tubulin, gamma (	NM_001080841	NM_001080841
3.76E+02	8.56E+00	iroquois homeob	iroquois homeob	NM_005853	NM_005853
3.70E+02	8.53E+00	CAP-GLY domain	CAP-GLY domain	NM_032421,NM	NM_032421,NM_003388
3.67E+02	8.52E+00	hypothetical LOC	hypothetical LOC	NR_015454	NR_015454
1.25E+00	3.24E-01	tetra-peptide rep	tetra-peptide rep	NM_198479	NM_198479
1.25E+00	3.24E-01	tetra-peptide rep	cone-rod homeo	NM_198479	NM_198479
1.34E+00	4.22E-01	deleted in maligr	deleted in maligr	NM_004406,NM	NM_004406,NM_017579,NM_007
1.34E+00	4.22E-01	deleted in maligr	deleted in maligr	NM_004406,NM	NM_004406,NM_017579,NM_007
3.25E-03	-8.26E+00	mitogen-activate	tetraspanin 33	NR_002144	NR_002144
3.37E+02	8.40E+00	tumor necrosis fa	mitochondrial int	NM_018647	NM_018647
3.37E+02	8.40E+00	tumor necrosis fa	mitochondrial int	NM_018647	NM_018647
1.64E+00	7.18E-01	zinc finger and S(	zinc finger and S(	NM_032805	NM_032805
1.26E+00	3.31E-01	butyrophilin-like	olfactory recepto	NM_152547	NM_152547
1.26E+00	3.31E-01	butyrophilin-like	olfactory recepto	NM_152547	NM_152547
4.08E+02	8.67E+00	dynein, light chai	microtubule-asso	NM_014183	NM_014183

1.55E+00	6.34E-01	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
1.55E+00	6.34E-01	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
1.62E+00	6.94E-01	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
1.62E+00	6.94E-01	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
1.93E+00	9.46E-01	ADAM metallope	non-protein codi	NR_002224	NR_002224
1.38E+00	4.63E-01	small nucleolar R	small nucleolar R	NR_004381	NR_004381
1.39E+00	4.77E-01	WW domain bin	WW domain bin	NM_012478	NM_012478
1.39E+00	4.77E-01	WW domain bin	WW domain bin	NM_012478	NM_012478
1.56E+00	6.40E-01	nicalin homolog	nicalin homolog	NM_020170	NM_020170
1.56E+00	6.40E-01	nicalin homolog	nicalin homolog	NM_020170	NM_020170
1.42E+00	5.03E-01	gamma-glutamyl	gamma-glutamyl	NM_178311,NM	NM_178311,NM_178312
3.56E+02	8.48E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
3.88E+02	8.60E+00	---	zinc finger protei	NR_027050	NR_027050
3.77E+02	8.56E+00	BRI3 binding pro	BRI3 binding pro	NM_080626	NM_080626
3.77E+02	8.56E+00	BRI3 binding pro	BRI3 binding pro	NM_080626	NM_080626
1.22E+00	2.82E-01	family with sequ	family with sequ	NR_026714	NR_026714
1.22E+00	2.82E-01	family with sequ	family with sequ	NR_026714	NR_026714
1.34E+00	4.25E-01	hornerin	hornerin	NM_001009931	NM_001009931
1.34E+00	4.25E-01	hornerin	hornerin	NM_001009931	NM_001009931
3.75E+02	8.55E+00	notch 3	notch 3	NM_000435	NM_000435
3.75E+02	8.55E+00	notch 3	notch 3	NM_000435	NM_000435
4.10E+02	8.68E+00	microtubule assc	microtubule assc	NM_015241	NM_015241
4.02E+02	8.65E+00	spire homolog 2	spire homolog 2	NM_032451	NM_032451
1.26E+00	3.32E-01	complement con	cytochrome P45	NM_001002029,	NM_001002029,NM_007293
1.26E+00	3.32E-01	cytochrome P45	cytochrome P45	NM_001128590,	NM_001128590,NM_000500
3.27E+02	8.35E+00	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
3.27E+02	8.35E+00	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
1.42E+00	5.01E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
2.53E-03	-8.63E+00	RNA binding mot	RNA binding mot	NM_006047,NM	NM_006047,NM_152838
1.79E+00	8.43E-01	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
1.52E+00	6.04E-01	kazrin	kazrin	NM_001017999	NM_001017999
1.52E+00	6.04E-01	kazrin	kazrin	NM_001017999	NM_001017999
3.24E+02	8.34E+00	lymphocyte-spec	troponin T type	NM_001013255	NM_001013255
3.59E+02	8.49E+00	tet oncogene fan	bolA homolog 3	NM_144993	NM_144993
1.57E+00	6.50E-01	kelch-like 21 (Dr	kelch-like 21 (Dr	NM_014851	NM_014851
1.57E+00	6.50E-01	kelch-like 21 (Dr	kelch-like 21 (Dr	NM_014851	NM_014851
2.05E+00	1.04E+00	BR serine/threon	BR serine/threon	NM_003957	NM_003957
1.41E+00	5.01E-01	protein kinase C,	protein kinase C,	NM_002744	NM_002744
1.76E+00	8.13E-01	calsyntenin 1	calsyntenin 1	NM_001009566,	NM_001009566,NM_014944
1.76E+00	8.13E-01	calsyntenin 1	calsyntenin 1	NM_001009566,	NM_001009566,NM_014944
4.08E+02	8.67E+00	anterior pharynx	carbonic anhydra	NM_001145646,	NM_001145646,NM_031301
4.08E+02	8.67E+00	anterior pharynx	carbonic anhydra	NM_001145646,	NM_001145646,NM_031301
1.45E+00	5.31E-01	SEC16 homolog	SEC16 homolog	NM_014866	NM_014866
4.06E+02	8.66E+00	chromosome 19	polypyrimidine t	NM_173481	NM_173481
3.47E+02	8.44E+00	golgi to ER traffic	golgi to ER traffic	NM_015949	NM_015949
3.47E+02	8.44E+00	golgi to ER traffic	golgi to ER traffic	NM_015949	NM_015949
3.22E+02	8.33E+00	tryptase delta 1	tryptase delta 1	NM_012217	NM_012217
1.63E+00	7.07E-01	phosphodiestera	phosphodiestera	NM_000921	NM_000921
1.63E+00	7.07E-01	phosphodiestera	phosphodiestera	NM_000921	NM_000921
1.63E+00	7.07E-01	phosphodiestera	phosphodiestera	NM_000921	NM_000921
3.58E+02	8.48E+00	ankyrin repeat a	ankyrin repeat a	NM_016150	NM_016150
3.60E+02	8.49E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
8.34E-01	-2.62E-01	interleukin 28B (	interleukin 28A (	NM_172139	NM_172139
4.28E+02	8.74E+00	heparan sulfate	heparan sulfate	NM_005529	NM_005529
4.28E+02	8.74E+00	heparan sulfate	heparan sulfate	NM_005529	NM_005529
3.87E-03	-8.01E+00	forkhead box O3	tripartite motif-c	NR_026718	NR_026718
3.72E+02	8.54E+00	acetylserotonin	acetylserotonin	NM_004192	NM_004192
5.00E+02	8.97E+00	hypothetical LOC	coxsackie virus a	NR_026756	NR_026756

3.45E-03	-8.18E+00	small nuclear rib	gamma-glutamyl	NM_004175	NM_004175
3.58E+02	8.48E+00	purinergic recept	ATPase, Ca++ tra	NM_002558	NM_002558
3.05E+02	8.25E+00	zinc finger and B	zinc finger and B	NM_001128833,	NM_001128833,NM_020899
3.05E+02	8.25E+00	zinc finger and B	zinc finger and B	NM_001128833,	NM_001128833,NM_020899
4.69E+02	8.87E+00	polycystic kidney	xylosyltransferas	NM_178541	NM_178541
3.23E+02	8.34E+00	alkB, alkylation r	alkB, alkylation r	NM_017621	NM_017621
1.82E+00	8.66E-01	PDZ domain cont	PDZ domain cont	NM_015009	NM_015009
1.82E+00	8.66E-01	PDZ domain cont	PDZ domain cont	NM_015009	NM_015009
3.52E+02	8.46E+00	cystathionine-be	cystathionine-be	NM_000071	NM_000071
3.52E+02	8.46E+00	cystathionine-be	cystathionine-be	NM_000071	NM_000071
3.72E+02	8.54E+00	Y box binding pr	Y box binding pr	NM_015982	NM_015982
3.72E+02	8.54E+00	Y box binding pr	Y box binding pr	NM_015982	NM_015982
3.28E+02	8.36E+00	family with sequ	scribbled homolo	NM_198488	NM_198488
4.37E+02	8.77E+00	nuclear factor (e	nuclear factor (e	NM_003204	NM_003204
3.61E+02	8.50E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.18E-03	-8.30E+00	T-box 2	T-box 2	NM_005994	NM_005994
3.18E-03	-8.30E+00	T-box 2	T-box 2	NM_005994	NM_005994
2.35E+00	1.23E+00	ring finger protei	ring finger protei	NM_020914	NM_020914
1.46E+00	5.45E-01	protein kinase, c	protein kinase, c	NM_002732	NM_002732
1.46E+00	5.45E-01	protein kinase, c	protein kinase, c	NM_002732	NM_002732
3.67E+02	8.52E+00	ciliary rootlet coi	ciliary rootlet coi	NM_014675	NM_014675
3.67E+02	8.52E+00	ciliary rootlet coi	ciliary rootlet coi	NM_014675	NM_014675
4.16E+02	8.70E+00	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
3.76E+02	8.56E+00	galactosamine (N	galactosamine (N	NM_000512	NM_000512
3.76E+02	8.56E+00	galactosamine (N	galactosamine (N	NM_000512	NM_000512
3.90E+02	8.61E+00	olfactory recepto	olfactory recepto	NM_001004471	NM_001004471
3.90E+02	8.61E+00	olfactory recepto	olfactory recepto	NM_001004471	NM_001004471
3.72E+02	8.54E+00	chromobox hom	TBC1 domain fan	NM_003655	NM_003655
3.40E-03	-8.20E+00	zinc finger protei	transmembrane	NM_015069	NM_015069
3.22E+02	8.33E+00	G protein-couple	G protein-couple	NM_001004106,	NM_001004106,NM_002082,NM_
3.22E+02	8.33E+00	G protein-couple	G protein-couple	NM_001004106,	NM_001004106,NM_002082,NM_
1.90E+00	9.27E-01	ubiquitin specific	ubiquitin specific	NM_032172	NM_032172
1.90E+00	9.27E-01	ubiquitin specific	ubiquitin specific	NM_032172	NM_032172
3.32E-03	-8.23E+00	mitogen-activate	myocardin	NM_003010	NM_003010
3.90E+02	8.61E+00	polycystic kidney	NODAL modulato	NM_178541	NM_178541
1.28E+00	3.56E-01	calcium channel,	calcium channel,	NM_198397,NM	NM_198397,NM_198378,NM_19
4.28E+02	8.74E+00	hypothetical LOC	hypothetical LOC	NR_026052	NR_026052
4.28E+02	8.74E+00	hypothetical LOC	hypothetical LOC	NR_026052	NR_026052
4.28E+02	8.74E+00	hypothetical LOC	hypothetical LOC	NR_026052	NR_026052
3.67E+02	8.52E+00	zinc finger and B	zinc finger and B	NM_003443	NM_003443
1.31E+00	3.93E-01	lymphocyte-spec	lymphocyte-spec	NM_001013253	NM_001013253
1.31E+00	3.93E-01	lymphocyte-spec	lymphocyte-spec	NM_001013253	NM_001013253
3.57E+02	8.48E+00	protein phospha	protein phospha	NM_015316	NM_015316
4.08E+02	8.67E+00	tectorin alpha	tectorin alpha	NM_005422	NM_005422
2.85E+02	8.16E+00	oculocutaneous	oculocutaneous	NM_000275	NM_000275
1.72E+00	7.84E-01	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165
3.10E+02	8.28E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
3.10E+02	8.28E+00	core-binding fact	acyl-CoA synthet	NM_175931,NM	NM_175931,NM_005187
4.04E+02	8.66E+00	tenascin XB	tenascin XB	NM_019105,NM	NM_019105,NM_032470
3.77E+02	8.56E+00	adhesion regulat	adhesion regulat	NM_007002,NM	NM_007002,NM_175573
3.82E+02	8.58E+00	coronin, actin bi	coronin, actin bi	NM_020441,NM	NM_020441,NM_001018070
3.80E+02	8.57E+00	pleckstrin homol	pleckstrin homol	NM_001143821	NM_001143821
4.10E+02	8.68E+00	aldehyde dehydr	aldehyde dehydr	NM_170726,NM	NM_170726,NM_003748
4.10E+02	8.68E+00	aldehyde dehydr	aldehyde dehydr	NM_170726,NM	NM_170726,NM_003748
2.16E+00	1.11E+00	hypothetical pro	tumor suppressi	NR_024468	NR_024468
1.99E+00	9.94E-01	heparan sulfate	heparan sulfate	NM_005529	NM_005529
1.41E+00	4.95E-01	solute carrier fa	solute carrier fa	NM_003046	NM_003046
1.41E+00	4.95E-01	solute carrier fa	solute carrier fa	NM_001008539	NM_001008539

1.22E+00	2.84E-01	cytochrome c oxi	cytochrome c oxi	NM_001864	NM_001864
3.98E+02	8.64E+00	gamma-aminobu	gamma-aminobu	NM_000814,NM	NM_000814,NM_021912
3.98E+02	8.64E+00	gamma-aminobu	gamma-aminobu	NM_000814,NM	NM_000814,NM_021912
3.45E+02	8.43E+00	abhydrolase dom	abhydrolase dom	NM_024527	NM_024527
3.36E+02	8.39E+00	prostate transme	prostate transme	NM_199171,NM	NM_199171,NM_199170,NM_19
3.36E+02	8.39E+00	prostate transme	prostate transme	NM_199171,NM	NM_199171,NM_199170,NM_19
1.33E+00	4.17E-01	unc-5 homolog A	unc-5 homolog A	NM_133369	NM_133369
1.57E+00	6.52E-01	paraoxonase 1	paraoxonase 1	NM_000446	NM_000446
1.30E+00	3.80E-01	tyrosine hydroxy	achaete-scute co	NM_199293,NM	NM_199293,NM_199292,NM_00
2.95E+02	8.21E+00	goosecoid home	dicer 1, ribonucle	NM_173849	NM_173849
4.00E+02	8.64E+00	solute carrier fan	family with sequ	NM_001142600,	NM_001142600,NM_052934,NM_
1.46E+00	5.47E-01	SMAD family me	SMAD family me	NM_005904	NM_005904
1.46E+00	5.47E-01	SMAD family me	SMAD family me	NM_005904	NM_005904
1.19E+00	2.47E-01	DAZ associated p	DAZ associated p	NM_018959,NM	NM_018959,NM_170711
1.19E+00	2.47E-01	DAZ associated p	DAZ associated p	NM_018959,NM	NM_018959,NM_170711
1.19E+00	2.47E-01	DAZ associated p	DAZ associated p	NM_018959,NM	NM_018959,NM_170711
3.62E+02	8.50E+00	t-complex 10 ho	chromosome 6 o	NM_004610	NM_004610
3.62E+02	8.50E+00	t-complex 10 ho	chromosome 6 o	NM_004610	NM_004610
1.51E+00	5.96E-01	hypothetical pro	zinc finger, BED-	NR_026993	NR_026993
3.67E+02	8.52E+00	dihydrouridine s	dihydrouridine s	NM_020175	NM_020175
1.34E+00	4.19E-01	acetylserotonin	acetylserotonin	NM_004043	NM_004043
4.17E+02	8.71E+00	cytochrome P45	transcription fac	NR_002570	NR_002570
1.38E+00	4.60E-01	basic helix-loop-	highly accelerate	NM_080606	NM_080606
1.38E+00	4.60E-01	basic helix-loop-	highly accelerate	NM_080606	NM_080606
2.98E-03	-8.39E+00	protocadherin 1	protocadherin 1	NM_020766,NM	NM_020766,NM_001105243
3.92E+02	8.61E+00	tubulin, beta pol	tubulin, beta pol	NM_020040	NM_020040
3.92E+02	8.61E+00	tubulin, beta pol	tubulin, beta pol	NM_020040	NM_020040
1.57E+00	6.49E-01	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
1.57E+00	6.49E-01	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
1.47E+00	5.54E-01	G protein-couple	G protein-couple	NM_001098201	NM_001098201
1.47E+00	5.54E-01	G protein-couple	G protein-couple	NM_001098201	NM_001098201
1.47E+00	5.54E-01	G protein-couple	G protein-couple	NM_001098201	NM_001098201
3.39E-03	-8.20E+00	sex hormone-bin	sex hormone-bin	NR_027462	NR_027462
4.37E+02	8.77E+00	solute carrier fan	solute carrier fan	NM_001636	NM_001636
3.06E+02	8.26E+00	ectonucleoside t	ectonucleoside t	NM_001033113,	NM_001033113,NM_198585
3.06E+02	8.26E+00	ectonucleoside t	ectonucleoside t	NM_001033113,	NM_001033113,NM_198585
1.40E+00	4.82E-01	KIAA1751	KIAA1751	NM_001080484	NM_001080484
1.40E+00	4.82E-01	KIAA1751	KIAA1751	NM_001080484	NM_001080484
3.98E+02	8.64E+00	paternally expres	paternally expres	NM_015068,NM	NM_015068,NM_001040152
3.98E+02	8.64E+00	paternally expres	paternally expres	NM_015068,NM	NM_015068,NM_001040152
3.98E+02	8.64E+00	paternally expres	paternally expres	NM_015068,NM	NM_015068,NM_001040152
4.45E+02	8.80E+00	WD repeat doma	WD repeat doma	NM_018051	NM_018051
4.45E+02	8.80E+00	WD repeat doma	WD repeat doma	NM_018051	NM_018051
4.29E+02	8.74E+00	SAM pointed do	SAM pointed do	NM_012391	NM_012391
3.82E+02	8.58E+00	parvin, gamma	parvin, gamma	NM_022141,NR_	NM_022141,NR_024426
3.82E+02	8.58E+00	parvin, gamma	parvin, gamma	NM_001137606	NM_001137606
1.45E+00	5.35E-01	EP300 interactin	EP300 interactin	NM_001008394	NM_001008394
3.04E-03	-8.36E+00	cat eye syndrom	cat eye syndrom	NM_017424	NM_017424
3.04E-03	-8.36E+00	cat eye syndrom	cat eye syndrom	NM_017424	NM_017424
3.90E+02	8.61E+00	Rho GTPase acti	laminin, alpha 1	NM_030672,NM	NM_030672,NM_001010000
3.90E+02	8.61E+00	Rho GTPase acti	laminin, alpha 1	NM_030672,NM	NM_030672,NM_001010000
1.64E+00	7.13E-01	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
1.64E+00	7.13E-01	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.93E+02	8.62E+00	G protein pathwa	G protein pathwa	NM_004127,NM	NM_004127,NM_212492
3.39E+02	8.40E+00	tubulin, beta 3	tubulin, beta 3	NM_006086	NM_006086
3.39E+02	8.40E+00	tubulin, beta 3	tubulin, beta 3	NM_006086	NM_006086
3.39E+02	8.40E+00	zinc finger protei	zinc finger protei	NM_138447	NM_138447
1.37E+00	4.58E-01	polycystic kidney	xylosyltransferas	NM_178541	NM_178541

1.37E+00	4.58E-01	polycystic kidney	xylosyltransferas	NM_178541	NM_178541
1.37E+00	4.58E-01	polycystic kidney	xylosyltransferas	NM_178541	NM_178541
1.37E+00	4.58E-01	polycystic kidney	xylosyltransferas	NM_178541	NM_178541
3.92E+02	8.61E+00	RAS p21 protein	cell division cycle	NM_007368	NM_007368
3.92E+02	8.61E+00	RAS p21 protein	cell division cycle	NM_007368	NM_007368
2.19E+00	1.13E+00	inositol monoph	chromosome 8 o	NM_017813	NM_017813
2.19E+00	1.13E+00	inositol monoph	chromosome 8 o	NM_017813	NM_017813
3.53E+02	8.46E+00	D-2-hydroxyglut	galactose-3-O-su	NM_152783	NM_152783
3.53E+02	8.46E+00	D-2-hydroxyglut	galactose-3-O-su	NM_152783	NM_152783
3.53E+02	8.46E+00	D-2-hydroxyglut	galactose-3-O-su	NM_152783	NM_152783
1.52E+00	6.04E-01	SMAD family me	SMAD family me	NM_001145103	NM_001145103
1.55E+00	6.32E-01	peroxisome proli	peroxisome proli	NM_005036,NM	NM_005036,NM_001001928
1.55E+00	6.32E-01	peroxisome proli	peroxisome proli	NM_005036,NM	NM_005036,NM_001001928
1.32E+00	3.95E-01	melanophilin	prolactin releasir	NM_001042467,	NM_001042467,NM_024101
1.32E+00	3.95E-01	melanophilin	prolactin releasir	NM_001042467,	NM_001042467,NM_024101
2.96E+02	8.21E+00	peptidase D	peptidase D	NM_000285	NM_000285
3.60E+02	8.49E+00	solute carrier fan	ASMTL antisense	NM_001636	NM_001636
3.27E+02	8.35E+00	diacylglycerol kir	diacylglycerol kir	NM_001105540	NM_001105540
3.90E+02	8.61E+00	ArfGAP with GTP	ArfGAP with GTP	NM_014914,NM	NM_014914,NM_001037131
3.90E+02	8.61E+00	ArfGAP with GTP	ArfGAP with GTP	NM_014914,NM	NM_014914,NM_001037131
3.68E+02	8.52E+00	troponin T type	troponin T type	NM_001042781,	NM_001042781,NM_001042782,
3.14E+02	8.29E+00	notch 1	notch 1	NM_017617	NM_017617
3.14E+02	8.29E+00	notch 1	notch 1	NM_017617	NM_017617
3.99E+02	8.64E+00	hypothetical LOC	hypothetical LOC	NR_024488	NR_024488
3.67E+02	8.52E+00	mitogen-activate	mitogen-activate	NM_005456	NM_005456
3.67E+02	8.52E+00	mitogen-activate	mitogen-activate	NM_005456	NM_005456
4.00E+02	8.64E+00	UV radiation resi	wingless-type MI	NM_003369	NM_003369
1.30E+00	3.73E-01	hypothetical LOC	hypothetical LOC	NR_027426	NR_027426
1.30E+00	3.73E-01	hypothetical LOC	hypothetical LOC	NR_027426	NR_027426
3.66E-03	-8.09E+00	acetylcholinester	mucin 17, cell su	NM_015831,NM	NM_015831,NM_000665
4.28E+02	8.74E+00	connector enhan	connector enhan	NR_023345	NR_023345
3.57E+02	8.48E+00	growth arrest-sp	growth arrest-sp	NM_001143946	NM_001143946
3.44E+02	8.43E+00	VENT homeobox	VENT homeobox	NR_001559	NR_001559
2.82E+02	8.14E+00	family with sequ	family with sequ	NM_001142864	NM_001142864
4.04E+02	8.66E+00	RAB35, member	RAB35, member	NM_006861	NM_006861
4.04E+02	8.66E+00	RAB35, member	RAB35, member	NM_006861	NM_006861
1.40E+00	4.90E-01	growth hormone	ADP-ribosylhydro	NM_024719	NM_024719
1.40E+00	4.90E-01	growth hormone	ADP-ribosylhydro	NM_024719	NM_024719
3.22E+02	8.33E+00	HGF activator	HGF activator	NM_001528	NM_001528
2.80E-03	-8.48E+00	asteroid homolo	asteroid homolo	NM_014065	NM_014065
4.01E+02	8.65E+00	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
1.30E+00	3.79E-01	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
1.30E+00	3.79E-01	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
3.92E+02	8.61E+00	coagulation fact	melatonin recept	NM_000128	NM_000128
3.92E+02	8.61E+00	coagulation fact	melatonin recept	NM_000128	NM_000128
3.89E+02	8.60E+00	GTP binding prot	histamine recept	NM_015666	NM_015666
3.89E+02	8.60E+00	GTP binding prot	histamine recept	NM_015666	NM_015666
3.71E+02	8.54E+00	cleavage and pol	cleavage and pol	NM_013291	NM_013291
3.71E+02	8.54E+00	cleavage and pol	cleavage and pol	NM_013291	NM_013291
3.73E+02	8.54E+00	hypothetical LOC	hypothetical LOC	NR_026828	NR_026828
3.28E+02	8.36E+00	solute carrier fan	Kruppel-like fact	NM_006934,NM	NM_006934,NM_201649,NM_001
3.98E+02	8.64E+00	lipid phosphate p	lipid phosphate p	NM_024888	NM_024888
3.98E+02	8.64E+00	lipid phosphate p	lipid phosphate p	NM_024888	NM_024888
3.98E+02	8.64E+00	lipid phosphate p	lipid phosphate p	NM_024888	NM_024888
1.45E+00	5.35E-01	5'-nucleotidase c	5'-nucleotidase c	NM_022908,NM	NM_022908,NM_001134231
1.45E+00	5.35E-01	5'-nucleotidase c	5'-nucleotidase c	NM_022908,NM	NM_022908,NM_001134231
2.95E+02	8.21E+00	metastasis assoc	metastasis assoc	NM_004689	NM_004689
2.95E+02	8.21E+00	metastasis assoc	metastasis assoc	NM_004689	NM_004689

2.64E+00	1.40E+00	Rho GDP dissocia	THO complex 4	NM_004309	NM_004309
4.24E+02	8.73E+00	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
1.53E+00	6.10E-01	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,
3.56E+02	8.48E+00	fibrosin-like 1	fibrosin-like 1	NM_001142641	NM_001142641
3.56E+02	8.48E+00	fibrosin-like 1	fibrosin-like 1	NM_001142641	NM_001142641
3.99E+02	8.64E+00	ubiquitin-like wit	ubiquitin-like wit	NM_013282	NM_013282
3.99E+02	8.64E+00	ubiquitin-like wit	ubiquitin-like wit	NM_013282	NM_013282
1.37E+00	4.57E-01	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
1.37E+00	4.57E-01	DnaJ (Hsp40) ho	protein tyrosine	NM_058246	NM_058246
3.29E-03	-8.25E+00	TSPY-like 5	metadherin	NM_033512	NM_033512
3.89E+02	8.60E+00	tripartite motif-c	fumarylacetoace	NM_138800	NM_138800
3.89E+02	8.60E+00	tripartite motif-c	fumarylacetoace	NM_138800	NM_138800
3.34E+02	8.38E+00	cat eye syndrom	cat eye syndrom	NM_017829,NM	NM_017829,NM_033070
3.34E+02	8.38E+00	cat eye syndrom	cat eye syndrom	NM_017829,NM	NM_017829,NM_033070
3.82E+02	8.58E+00	ras responsive el	signal sequence	NM_001003698,	NM_001003698,NM_001003699
1.29E+00	3.70E-01	chorionic somat	chorionic somat	NM_022644	NM_022644
1.29E+00	3.70E-01	chorionic somat	chorionic somat	NM_022644	NM_022644
1.29E+00	3.70E-01	chorionic somat	growth hormone	NM_022644	NM_022644
1.92E+00	9.44E-01	programmed cell	mitochondrial ri	NR_003713	NR_003713
1.92E+00	9.44E-01	programmed cell	mitochondrial ri	NR_003713	NR_003713
3.28E+02	8.36E+00	zinc and ring fing	zinc and ring fing	NM_032173	NM_032173
4.66E+02	8.86E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
4.66E+02	8.86E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
4.66E+02	8.86E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
3.98E+02	8.64E+00	dimethylarginine	dimethylarginine	NM_013974	NM_013974
3.98E+02	8.64E+00	dimethylarginine	dimethylarginine	NM_013974	NM_013974
2.68E+02	8.07E+00	zinc finger protei	zinc finger protei	NM_001127464	NM_001127464
2.68E+02	8.07E+00	zinc finger protei	zinc finger protei	NM_001127464	NM_001127464
3.26E+02	8.35E+00	solute carrier fa	solute carrier fa	NM_006598	NM_006598
1.41E+00	5.01E-01	protein kinase C,	protein kinase C,	NM_002744	NM_002744
1.41E+00	5.01E-01	protein kinase C,	protein kinase C,	NM_002744	NM_002744
3.37E+02	8.40E+00	hypothetical LO	calcium channel,	NR_024341	NR_024341
3.37E+02	8.40E+00	hypothetical LO	calcium channel,	NR_024341	NR_024341
3.37E+02	8.40E+00	hypothetical LO	calcium channel,	NR_024341	NR_024341
3.57E+02	8.48E+00	glycophorin C (	bridging integra	NM_002101,NM	NM_002101,NM_016815
3.57E+02	8.48E+00	glycophorin C (	bridging integra	NM_002101,NM	NM_002101,NM_016815
3.37E+02	8.40E+00	zinc finger protei	zinc finger protei	NM_001002836	NM_001002836
3.37E+02	8.40E+00	zinc finger protei	zinc finger protei	NM_001002836	NM_001002836
3.68E+02	8.52E+00	coronin, actin bi	coronin, actin bi	NM_020441,NM	NM_020441,NM_001018070
3.68E+02	8.52E+00	coronin, actin bi	coronin, actin bi	NM_020441,NM	NM_020441,NM_001018070
1.55E+00	6.37E-01	Rhox homeobox	Rhox homeobox	NM_032498	NM_032498
3.02E+02	8.24E+00	notch 1	notch 1	NM_017617	NM_017617
3.65E+02	8.51E+00	chromosome 14	chromosome 14	NM_018228	NM_018228
3.36E+02	8.39E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
3.65E+02	8.51E+00	NFAT activating	NFAT activating	NM_145912	NM_145912
3.19E+02	8.32E+00	ArfGAP with Rho	ArfGAP with Rho	NM_001135190,	NM_001135190,NM_015242,NM_
3.19E+02	8.32E+00	ArfGAP with Rho	ArfGAP with Rho	NM_001135190,	NM_001135190,NM_015242,NM_
1.14E+00	1.90E-01	exosome compo	exosome compo	NM_019037	NM_019037
1.14E+00	1.90E-01	exosome compo	exosome compo	NM_019037	NM_019037
1.27E+00	3.45E-01	X antigen family,	X antigen family,	NM_001097603,	NM_001097603,NM_001097602,
3.32E+02	8.38E+00	patatin-like phos	patatin-like phos	NM_152286,NM	NM_152286,NM_001098537
1.56E+00	6.40E-01	cytochrome P45	transcription fac	NR_002570	NR_002570
1.56E+00	6.40E-01	cytochrome P45	transcription fac	NR_002570	NR_002570
3.32E+02	8.38E+00	---	zinc finger protei	NR_027050	NR_027050
3.32E+02	8.38E+00	---	zinc finger protei	NR_027050	NR_027050
3.71E+02	8.53E+00	SET binding fact	SET binding fact	NM_002972	NM_002972
3.01E+02	8.23E+00	melanoma antig	melanoma antig	NM_001011544,	NM_001011544,NM_005366
1.53E+00	6.12E-01	zinc finger protei	zinc finger protei	NM_152625	NM_152625

1.53E+00	6.12E-01	zinc finger protei	zinc finger protei	NM_152625	NM_152625
1.53E+00	6.12E-01	zinc finger protei	zinc finger protei	NM_152625	NM_152625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
3.52E+02	8.46E+00	H19, imprinted n	H19, imprinted n	NR_002196	NR_002196
3.54E+02	8.47E+00	lysine (K)-specifi	lysine (K)-specifi	NM_001080424	NM_001080424
2.03E+00	1.02E+00	hypothetical pro	growth arrest-sp	NR_024609	NR_024609
2.03E+00	1.02E+00	hypothetical pro	growth arrest-sp	NR_024609	NR_024609
3.70E+02	8.53E+00	FERM and PDZ d	RNA (guanine-9-)	NM_014907	NM_014907
1.34E+00	4.22E-01	BEN domain con	BEN domain con	NR_027512	NR_027512
1.34E+00	4.22E-01	BEN domain con	BEN domain con	NR_027512	NR_027512
3.06E+02	8.26E+00	cathepsin D	cathepsin D	NM_001909	NM_001909
3.06E+02	8.26E+00	cathepsin D	cathepsin D	NM_001909	NM_001909
7.55E-01	-4.06E-01	jerky homolog (n	prostate stem ce	NM_003724,NM	NM_003724,NM_001077527
3.39E+02	8.41E+00	chromosome 16	chromosome 16	NM_175900	NM_175900
3.39E+02	8.41E+00	chromosome 16	chromosome 16	NM_175900	NM_175900
1.74E+00	8.00E-01	zinc finger protei	zinc finger protei	NM_001099638,	NM_001099638,NM_007145,NM_
1.74E+00	8.00E-01	zinc finger protei	zinc finger protei	NM_001099638,	NM_001099638,NM_007145,NM_
1.35E+00	4.32E-01	similar to HGC6.3	kinesin family me	NM_001129895	NM_001129895
3.23E+02	8.34E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
3.23E+02	8.34E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
3.25E+02	8.34E+00	PQ loop repeat c	PQ loop repeat c	NM_001146343,	NM_001146343,NM_001146345,N
3.25E+02	8.34E+00	PQ loop repeat c	PQ loop repeat c	NM_001146343,	NM_001146343,NM_001146345,N
3.72E-03	-8.07E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.19E+02	8.32E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
3.19E+02	8.32E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
1.58E+00	6.64E-01	testis expressed	olfactory recepto	NM_144582	NM_144582
1.58E+00	6.64E-01	olfactory recepto	olfactory recepto	NR_002185	NR_002185
1.84E+00	8.79E-01	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
3.07E+02	8.26E+00	TBC1 domain fan	TBC1 domain fan	NM_020705	NM_020705
4.68E+02	8.87E+00	fibroblast growth	ring finger protei	NM_021923	NM_021923
1.39E+00	4.79E-01	chromosome 14	POM121 membr	NR_027006	NR_027006
3.12E+02	8.29E+00	DEAD (Asp-Glu-A	DEAD (Asp-Glu-A	NM_175066	NM_175066
3.12E+02	8.29E+00	DEAD (Asp-Glu-A	DEAD (Asp-Glu-A	NM_175066	NM_175066
3.12E+02	8.29E+00	DEAD (Asp-Glu-A	DEAD (Asp-Glu-A	NM_175066	NM_175066
1.29E+00	3.66E-01	t-SNARE domain	t-SNARE domain	NM_145003	NM_145003
1.29E+00	3.66E-01	t-SNARE domain	t-SNARE domain	NM_145003	NM_145003
3.40E+02	8.41E+00	tetratricopeptide	tetratricopeptide	NM_017931	NM_017931
3.40E+02	8.41E+00	tetratricopeptide	tetratricopeptide	NM_017931	NM_017931
3.39E+02	8.41E+00	zinc finger, CCHC	zinc finger, CCHC	NM_015144	NM_015144
3.39E+02	8.41E+00	zinc finger, CCHC	zinc finger, CCHC	NM_015144	NM_015144
3.39E+02	8.41E+00	zinc finger, CCHC	zinc finger, CCHC	NM_015144	NM_015144
3.39E+02	8.41E+00	zinc finger, CCHC	zinc finger, CCHC	NM_015144	NM_015144
3.81E+02	8.57E+00	F-box and WD re	F-box and WD re	NM_018998	NM_018998
3.81E+02	8.57E+00	F-box and WD re	F-box and WD re	NM_018998	NM_018998
1.49E+00	5.77E-01	SEC16 homolog	SEC16 homolog	NM_014866	NM_014866
1.49E+00	5.77E-01	SEC16 homolog	SEC16 homolog	NM_014866	NM_014866
1.49E+00	5.77E-01	SEC16 homolog	SEC16 homolog	NM_014866	NM_014866
3.12E+02	8.29E+00	melanoma antige	melanoma antige	NM_002362	NM_002362
3.12E+02	8.29E+00	melanoma antige	melanoma antige	NM_001011549	NM_001011549
3.12E+02	8.29E+00	melanoma antige	melanoma antige	NM_001011549	NM_001011549
3.56E+02	8.48E+00	rhomboid, veinle	STIP1 homology	NM_003961	NM_003961
2.69E+02	8.07E+00	cytospin A	adenosine A2a re	NM_015330,NM	NM_015330,NM_001145468
3.84E+02	8.59E+00	Ras and Rab inte	Ras and Rab inte	NM_024832	NM_024832
3.84E+02	8.59E+00	Ras and Rab inte	Ras and Rab inte	NM_024832	NM_024832
1.54E+00	6.27E-01	chromosome 10	La ribonucleopro	NR_027152,NR_	NR_027152,NR_027151
1.54E+00	6.27E-01	chromosome 10	La ribonucleopro	NR_027152,NR_	NR_027152,NR_027151
2.94E+02	8.20E+00	polymerase (RNA	piwi-like 2 (Dros	NM_001722	NM_001722

2.83E+02	8.14E+00	unc-51-like kinas	pseudouridylate	NM_003565	NM_003565
1.29E+00	3.65E-01	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
3.59E+02	8.49E+00	ribosomal protei	ubiquitin-conjuga	NM_000991,NM	NM_000991,NM_001136134,NM_
3.59E+02	8.49E+00	ubiquitin-conjuga	ubiquitin-conjuga	NM_014501	NM_014501
1.99E+00	9.94E-01	exocyst complex	exocyst complex	NM_018303	NM_018303
1.99E+00	9.94E-01	exocyst complex	exocyst complex	NM_018303	NM_018303
2.72E+02	8.09E+00	nuclear receptor	nuclear receptor	NM_016346,NM	NM_016346,NM_014249
2.72E+02	8.09E+00	nuclear receptor	nuclear receptor	NM_016346,NM	NM_016346,NM_014249
3.73E+02	8.54E+00	CUGBP, Elav-like	CUGBP, Elav-like	NM_001025087,	NM_001025087,NM_020180,NM_
3.00E+02	8.23E+00	N-sulfoglucosam	N-sulfoglucosam	NM_000199	NM_000199
3.34E-03	-8.22E+00	family with sequ	zyxin	NM_001031690,	NM_001031690,NM_014690
3.86E+02	8.59E+00	cholinergic recep	cholinergic recep	NM_000742	NM_000742
3.90E+02	8.61E+00	regulatory factor	regulatory factor	NM_000635,NM	NM_000635,NM_134433
1.32E+00	4.02E-01	calmodulin bindi	calmodulin bindi	NM_015215	NM_015215
4.34E+02	8.76E+00	C-type lectin don	C-type lectin don	NM_015226	NM_015226
1.27E+00	3.47E-01	apolipoprotein B	ATPase family, A	NM_000384	NM_000384
1.27E+00	3.47E-01	apolipoprotein B	ATPase family, A	NM_000384	NM_000384
4.06E+02	8.66E+00	chromosome 9 o	spermatid perinu	NR_026677	NR_026677
4.16E+02	8.70E+00	chorionic gonado	neurotrophin 4	NM_033142	NM_033142
4.35E+02	8.76E+00	adaptor-related	adaptor-related	NM_003938	NM_003938
1.35E+00	4.29E-01	aquaporin 12B	aquaporin 12A	NM_001102467	NM_001102467
1.35E+00	4.29E-01	aquaporin 12B	aquaporin 12A	NM_001102467	NM_001102467
1.24E+00	3.13E-01	fms-related tyros	fms-related tyros	NM_002020	NM_002020
3.41E+02	8.41E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.41E+02	8.41E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.02E+02	8.24E+00	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
3.02E+02	8.24E+00	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
3.50E+02	8.45E+00	kinocilin	kinocilin	NM_001097611	NM_001097611
3.50E+02	8.45E+00	kinocilin	kinocilin	NM_001097611	NM_001097611
3.18E+02	8.31E+00	chitinase domain	chitinase domain	NM_023947,NM	NM_023947,NM_001142674,NM_
1.19E+00	2.48E-01	dynein, axonema	dynein, axonema	NM_020877	NM_020877
1.19E+00	2.48E-01	dynein, axonema	dynein, axonema	NM_020877	NM_020877
1.19E+00	2.48E-01	ribosomal protei	ribosomal protei	NR_002778	NR_002778
1.67E+00	7.42E-01	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
1.67E+00	7.42E-01	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
1.67E+00	7.42E-01	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
2.01E+00	1.01E+00	early growth res	early growth res	NM_001964	NM_001964
2.01E+00	1.01E+00	early growth res	early growth res	NM_001964	NM_001964
2.27E+00	1.18E+00	NK6 homeobox 2	chromosome 10	NM_177400	NM_177400
2.27E+00	1.18E+00	acetylserotonin	acetylserotonin	NM_004192	NM_004192
2.27E+00	1.18E+00	acetylserotonin	acetylserotonin	NM_004192	NM_004192
3.18E+02	8.31E+00	hypothetical LOC	lymphocyte-spec	NR_015424	NR_015424
3.18E+02	8.31E+00	hypothetical LOC	lymphocyte-spec	NR_015424	NR_015424
3.99E+02	8.64E+00	triosephosphate	mitogen-activate	NR_002187	NR_002187
3.47E+02	8.44E+00	inositol polyphos	inositol polyphos	NM_019892	NM_019892
2.94E+02	8.20E+00	SH3-domain binc	SH3-domain binc	NM_001122681	NM_001122681
2.91E+02	8.18E+00	C2 calcium-depe	C2 calcium-depe	NM_001136263	NM_001136263
1.34E+00	4.24E-01	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
1.34E+00	4.24E-01	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
2.99E+02	8.22E+00	small nuclear rib	small nuclear rib	NM_003097,NM	NM_003097,NM_005678
2.03E+00	1.02E+00	tetraspanin 4	tetraspanin 4	NM_001025237	NM_001025237
1.77E+00	8.24E-01	forkhead box P4	forkhead box P4	NM_138457,NM	NM_138457,NM_001012426,NM_
1.77E+00	8.24E-01	forkhead box P4	forkhead box P4	NM_138457,NM	NM_138457,NM_001012426,NM_
2.04E+00	1.03E+00	chromosome 10	La ribonucleopro	NR_027152,NR_	NR_027152,NR_027151
3.41E+02	8.41E+00	zinc finger protei	zinc finger protei	NM_198526	NM_198526
3.41E+02	8.41E+00	zinc finger protei	zinc finger protei	NM_198526	NM_198526
3.06E+02	8.26E+00	leukemia inhibitc	leukemia inhibitc	NM_002309	NM_002309
3.53E+02	8.46E+00	heparan sulfate	placenta-specific	NM_004807	NM_004807

3.53E+02	8.46E+00	heparan sulfate	placenta-specific	NM_004807	NM_004807
1.50E+00	5.85E-01	KIAA1211	KIAA1211	NM_020722	NM_020722
1.50E+00	5.85E-01	KIAA1211	KIAA1211	NM_020722	NM_020722
1.66E+00	7.33E-01	WD repeat doma	zinc finger, MYN	NM_138778	NM_138778
1.66E+00	7.33E-01	WD repeat doma	zinc finger, MYN	NM_138778	NM_138778
3.16E+02	8.30E+00	tubulin polymeri	tubulin polymeri	NM_007030	NM_007030
3.16E+02	8.30E+00	tubulin polymeri	tubulin polymeri	NM_007030	NM_007030
2.89E+02	8.17E+00	fibroblast growt	ring finger protei	NM_021923	NM_021923
2.89E+02	8.17E+00	fibroblast growt	ring finger protei	NM_021923	NM_021923
2.15E+00	1.11E+00	glycerophospho	mitogen-activate	NM_024307	NM_024307
1.56E+00	6.40E-01	BEN domain con	BEN domain con	NM_001080450	NM_001080450
4.63E+02	8.86E+00	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_025219	NM_025219
4.63E+02	8.86E+00	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_025219	NM_025219
4.63E+02	8.86E+00	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_025219	NM_025219
3.44E+02	8.43E+00	chromosome 16	chromosome 16	NM_001080524	NM_001080524
3.82E+02	8.58E+00	carboxypeptidas	carboxypeptidas	NM_001080513	NM_001080513
3.82E+02	8.58E+00	carboxypeptidas	leucine rich repe	NM_001080513	NM_001080513
3.82E+02	8.58E+00	carboxypeptidas	leucine rich repe	NM_001080513	NM_001080513
2.87E-03	-8.44E+00	cation channel, s	cation channel, s	NR_002318	NR_002318
1.20E+00	2.59E-01	polymerase (RN	fibroblast growt	NM_005035	NM_005035
1.20E+00	2.59E-01	polymerase (RN	fibroblast growt	NM_005035	NM_005035
2.76E+02	8.11E+00	solute carrier fan	dipeptidase 3	NM_001145963,	NM_001145963,NM_001145964,
1.32E+00	4.01E-01	C1q and tumor n	calcium channel,	NM_207419	NM_207419
1.32E+00	4.01E-01	C1q and tumor n	calcium channel,	NM_207419	NM_207419
4.06E+02	8.66E+00	chromosome 20	cadherin 4, type	NM_173644	NM_173644
4.06E+02	8.66E+00	chromosome 20	cadherin 4, type	NM_173644	NM_173644
2.83E+02	8.15E+00	hypothetical pro	delta-like 1 (Dros	NR_002787	NR_002787
2.83E+02	8.15E+00	hypothetical pro	delta-like 1 (Dros	NR_002787	NR_002787
3.61E+02	8.49E+00	testis expressed	testis expressed	NM_031451	NM_031451
3.61E+02	8.49E+00	testis expressed	testis expressed	NM_031451	NM_031451
3.61E+02	8.49E+00	testis expressed	testis expressed	NM_031451	NM_031451
3.08E+02	8.27E+00	lamin A/C	lamin A/C	NM_005572,NM	NM_005572,NM_170707,NM_17
1.67E+00	7.36E-01	MGC44478	deltex homolog	NR_003262	NR_003262
1.67E+00	7.36E-01	MGC44478	deltex homolog	NR_003262	NR_003262
1.66E+00	7.33E-01	adaptor-related	adaptor-related	NM_130787,NM	NM_130787,NM_014203
1.66E+00	7.33E-01	adaptor-related	adaptor-related	NM_130787,NM	NM_130787,NM_014203
3.70E-03	-8.08E+00	AN1, ubiquitin-li	family with sequ	NM_174890,NM	NM_174890,NM_001128324
3.17E+02	8.31E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
3.17E+02	8.31E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
3.17E+02	8.31E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
3.08E+02	8.27E+00	cancer/testis ant	cancer/testis ant	NM_001017438	NM_001017438
3.98E-03	-7.97E+00	hypothetical LO	grainyhead-like	NR_027087	NR_027087
4.67E+02	8.87E+00	zinc finger and B	zinc finger and B	NM_001145338,	NM_001145338,NM_005453
4.67E+02	8.87E+00	zinc finger and B	zinc finger and B	NM_001145338,	NM_001145338,NM_005453
4.67E+02	8.87E+00	zinc finger and B	zinc finger and B	NM_001145338,	NM_001145338,NM_005453
4.67E+02	8.87E+00	zinc finger and B	zinc finger and B	NM_001145338,	NM_001145338,NM_005453
3.28E+02	8.36E+00	immunoglobulin	immunoglobulin	NM_020962	NM_020962
3.28E+02	8.36E+00	immunoglobulin	immunoglobulin	NM_020962	NM_020962
1.45E+00	5.35E-01	membrane-asso	acidic (leucine-ri	NM_017923	NM_017923
3.87E-03	-8.01E+00	solute carrier fan	hypoxia up-regul	NM_001467	NM_001467
3.25E+02	8.34E+00	acyl-CoA thioest	acyl-CoA thioest	NM_181866,NM	NM_181866,NM_181865,NM_181
1.96E+00	9.69E-01	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
3.25E+02	8.34E+00	protein phospha	short stature hor	NM_013239,NM	NM_013239,NM_199326
3.16E+02	8.30E+00	ADAMTS-like 5	polo-like kinase	NM_213604	NM_213604
7.79E-01	-3.60E-01	golgi-associated,	golgi-associated,	NM_014001,NM	NM_014001,NM_138619
7.79E-01	-3.60E-01	golgi-associated,	golgi-associated,	NM_014001,NM	NM_014001,NM_138619
3.50E+02	8.45E+00	bromodomain c	bromodomain c	NM_007371	NM_007371
1.40E+00	4.87E-01	protocadherin g	protocadherin g	NM_003735,NM	NM_003735,NM_032094

1.40E+00	4.87E-01	protocadherin ga	protocadherin ga	NM_003735,NM	NM_003735,NM_032094
1.40E+00	4.87E-01	protocadherin ga	protocadherin ga	NM_003735,NM	NM_003735,NM_032094
3.16E+02	8.30E+00	myocilin, trabecu	vesicle-associate	NM_000261	NM_000261
3.60E+02	8.49E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
2.79E+02	8.12E+00	solute carrier fam	microtubule asso	NM_181785,NM	NM_181785,NM_001135919
7.49E-01	-4.16E-01	phosducin-like 2	phosducin-like 2	NM_152401	NM_152401
7.49E-01	-4.16E-01	phosducin-like 2	phosducin-like 2	NM_152401	NM_152401
1.25E+00	3.24E-01	lymphocyte antig	HLA-B associated	NM_025262	NM_025262
1.40E+00	4.85E-01	RNA polymerase	RUN domain con	NR_003369	NR_003369
1.28E+00	3.57E-01	acyl-CoA oxidase	acyl-CoA oxidase	NM_003501,NM	NM_003501,NM_001101667
1.28E+00	3.57E-01	acyl-CoA oxidase	acyl-CoA oxidase	NM_003501,NM	NM_003501,NM_001101667
3.61E+02	8.50E+00	similar to HGC6.3	kinesin family me	NM_001129895	NM_001129895
3.79E+02	8.57E+00	transmembrane	LIM domain bind	NM_153365	NM_153365
3.79E+02	8.57E+00	transmembrane	LIM domain bind	NM_153365	NM_153365
3.06E+02	8.26E+00	aspartate beta-hy	aspartate beta-hy	NM_181718	NM_181718
3.06E+02	8.26E+00	aspartate beta-hy	aspartate beta-hy	NM_181718	NM_181718
1.68E+00	7.52E-01	baculoviral IAP re	zinc finger protei	NM_033341	NM_033341
3.86E+02	8.59E+00	nischarin	nischarin	NM_007184	NM_007184
1.64E+00	7.13E-01	ubiquitin-like wit	ubiquitin-like wit	NM_013282	NM_013282
2.96E+02	8.21E+00	lipocalin 6	lipocalin 6	NM_198946	NM_198946
2.96E+02	8.21E+00	lipocalin 6	lipocalin 6	NM_198946	NM_198946
2.95E+02	8.21E+00	hypothetical LOC	transmembrane	NR_024473	NR_024473
4.49E+02	8.81E+00	kinase non-cataly	kinase non-cataly	NM_152643	NM_152643
1.23E+00	3.00E-01	cell wall biogene	DCN1, defective	NM_025087	NM_025087
3.26E+02	8.35E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
3.24E+02	8.34E+00	chloride channel	chloride channel	NM_001287,NM	NM_001287,NM_001114331
3.21E+02	8.33E+00	dipeptidase 1 (re	dipeptidase 1 (re	NM_001128141	NM_001128141
2.94E-03	-8.41E+00	solute carrier fam	protein phosphat	NM_001135153	NM_001135153
1.25E+00	3.25E-01	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
1.25E+00	3.25E-01	testis-specific tra	testis-specific tra	NR_003593,NR_	NR_003593,NR_001540
3.08E+02	8.27E+00	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
3.08E+02	8.27E+00	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
1.99E+00	9.93E-01	discs, large (Dros	discs, large (Dros	NM_014902	NM_014902
1.82E+00	8.66E-01	netrin 3	netrin 3	NM_006181	NM_006181
2.96E+02	8.21E+00	FAT tumor suppr	zinc finger protei	NM_005245	NM_005245
2.96E+02	8.21E+00	FAT tumor suppr	zinc finger protei	NM_005245	NM_005245
2.79E+02	8.12E+00	zinc finger protei	integrator compl	NM_015852	NM_015852
2.79E+02	8.12E+00	zinc finger protei	integrator compl	NM_015852	NM_015852
1.28E+00	3.59E-01	carbonic anhydra	kinesin family me	NM_020178,NM	NM_020178,NM_001082533,NM_
1.28E+00	3.59E-01	kinesin family me	kinesin family me	NM_032559	NM_032559
4.04E+02	8.66E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,N
4.04E+02	8.66E+00	G protein-couple	G protein-couple	NM_138445	NM_138445
4.04E+02	8.66E+00	G protein-couple	G protein-couple	NM_138445	NM_138445
1.88E+00	9.13E-01	telomerase rever	telomerase rever	NM_198253,NM	NM_198253,NM_198255
2.94E+02	8.20E+00	fizzy/cell division	fizzy/cell division	NM_001136197,	NM_001136197,NM_001136198
3.38E-03	-8.21E+00	MOCO sulphuras	MOCO sulphuras	NM_017898	NM_017898
3.40E-03	-8.20E+00	collagen, type IX,	collagen, type IX,	NM_001851,NM	NM_001851,NM_078485
3.31E+02	8.37E+00	alveolar soft part	alveolar soft part	NM_024083	NM_024083
3.32E+02	8.38E+00	fibroblast growth	fibroblast growth	NM_019113	NM_019113
3.15E+02	8.30E+00	wntless homolog	wntless homolog	NM_024911	NM_024911
1.41E+00	4.99E-01	guanine nucleoti	calmodulin-like 6	NM_002074	NM_002074
3.21E+02	8.33E+00	chromosome 19	chromosome 19	NM_175063,NM	NM_175063,NM_206538
3.86E+02	8.59E+00	protein phosphat	protein phosphat	NM_013239,NM	NM_013239,NM_199326
3.86E+02	8.59E+00	protein phosphat	protein phosphat	NM_013239,NM	NM_013239,NM_199326
4.01E+02	8.65E+00	integrator compl	integrator compl	NM_001080453	NM_001080453
4.01E+02	8.65E+00	integrator compl	integrator compl	NM_001080453	NM_001080453
2.74E+02	8.10E+00	ADAM metallope	ADAM metallope	NM_014244	NM_014244
2.74E+02	8.10E+00	ADAM metallope	ADAM metallope	NM_014244	NM_014244

4.04E+02	8.66E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,N
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.46E+00	5.51E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.85E+00	8.85E-01	zinc finger protei	zinc finger protei	NM_001159279	NM_001159279
1.85E+00	8.85E-01	zinc finger protei	zinc finger protei	NM_001159279	NM_001159279
1.19E+00	2.55E-01	glutamine-fructo	CCR4-NOT transc	NM_005110	NM_005110
1.19E+00	2.55E-01	glutamine-fructo	CCR4-NOT transc	NM_005110	NM_005110
3.97E+02	8.63E+00	family with sequ	family with sequ	NM_015381	NM_015381
3.97E+02	8.63E+00	family with sequ	family with sequ	NM_015381	NM_015381
3.38E+02	8.40E+00	transcription fact	transcription fact	NM_001042425,	NM_001042425,NM_003220,NM_
3.29E+02	8.36E+00	inositol polyphos	inositol polyphos	NM_019892	NM_019892
3.29E+02	8.36E+00	inositol polyphos	inositol polyphos	NM_019892	NM_019892
3.61E+02	8.49E+00	glutamate recept	chromosome 3 o	NM_001080423	NM_001080423
1.26E+00	3.31E-01	hypothetical LOC	hypothetical LOC	NR_015454	NR_015454
1.26E+00	3.31E-01	hypothetical LOC	hypothetical LOC	NR_015454	NR_015454
3.49E+02	8.45E+00	N-acetylglucosan	N-acetylglucosan	NM_032520	NM_032520
3.49E+02	8.45E+00	N-acetylglucosan	N-acetylglucosan	NM_032520	NM_032520
2.81E+02	8.13E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
2.81E+02	8.13E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.82E-03	-8.03E+00	chromosome 1 o	nuclear factor I/	NM_152377	NM_152377
3.10E+02	8.28E+00	chromosome 14	delta-like 1 hom	NR_024096	NR_024096
3.34E+02	8.38E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.06E+02	8.26E+00	ATP-binding cass	ATP-binding cass	NM_019112	NM_019112
3.06E+02	8.26E+00	ATP-binding cass	ATP-binding cass	NM_019112	NM_019112
3.05E+02	8.25E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.05E+02	8.25E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.04E+02	8.25E+00	solute carrier fan	hypothetical pro	NM_001080431	NM_001080431
1.42E+00	5.04E-01	transcription fact	transcription fact	NM_014553	NM_014553
1.42E+00	5.04E-01	transcription fact	transcription fact	NM_014553	NM_014553
3.04E+02	8.25E+00	dynein, axonema	dynein, axonema	NM_207437	NM_207437
1.44E+00	5.24E-01	cytochrome b-56	angiotensin I con	NM_001017917,	NM_001017917,NM_001017916,N
1.27E+00	3.48E-01	leucine rich repe	leucine rich repe	NM_020710	NM_020710
3.17E+02	8.31E+00	tubulin tyrosine l	megalencephalic	NM_001080447	NM_001080447
3.12E+02	8.29E+00	mex-3 homolog /	mex-3 homolog /	NM_001093725	NM_001093725
3.12E+02	8.29E+00	mex-3 homolog /	mex-3 homolog /	NM_001093725	NM_001093725
3.12E+02	8.29E+00	mex-3 homolog /	mex-3 homolog /	NM_001093725	NM_001093725
3.83E+02	8.58E+00	CHRNA7 (choline	CHRNA7 (choline	NM_148911,NM	NM_148911,NM_139320
3.33E-03	-8.23E+00	proteasome (pro	proteasome (pro	NM_002813	NM_002813
3.33E-03	-8.23E+00	proteasome (pro	proteasome (pro	NM_002813	NM_002813
4.29E+02	8.75E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
4.29E+02	8.75E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
2.11E+00	1.08E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
1.49E+00	5.73E-01	X antigen family,	synovial sarcoma	NM_020411,NM	NM_020411,NM_133430,NM_133
1.49E+00	5.73E-01	X antigen family,	synovial sarcoma	NM_020411,NM	NM_020411,NM_133430,NM_133
1.44E+00	5.24E-01	cytochrome b-56	angiotensin I con	NM_001017917,	NM_001017917,NM_001017916,N
2.86E+02	8.16E+00	src-related kinas	chromosome 20	NM_080823	NM_080823
1.27E+00	3.50E-01	BEN domain con	BEN domain con	NR_027512	NR_027512
1.27E+00	3.50E-01	BEN domain con	BEN domain con	NR_027512	NR_027512
3.43E+02	8.42E+00	ret finger protei	ret finger protei	NM_001159545,	NM_001159545,NM_001098527,N
3.01E+02	8.23E+00	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
3.01E+02	8.23E+00	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
3.85E+02	8.59E+00	glutamate recept	glutamate recept	NM_000843	NM_000843

3.85E+02	8.59E+00	glutamate recept	glutamate recept	NM_000843	NM_000843
1.39E+00	4.76E-01	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
1.39E+00	4.76E-01	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.40E+02	8.41E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.19E+02	8.32E+00	actinin, alpha 4	actinin, alpha 4	NM_004924	NM_004924
3.19E+02	8.32E+00	actinin, alpha 4	actinin, alpha 4	NM_004924	NM_004924
2.83E+02	8.14E+00	ADAMTS-like 2	ADAMTS-like 2	NM_014694	NM_014694
5.06E+02	8.98E+00	glyoxylate reduct	glyoxylate reduct	NM_032569	NM_032569
3.44E+02	8.43E+00	small nucleolar R	DIO3 opposite st	NR_003224	NR_003224
4.06E+02	8.66E+00	fucosyltransferas	fucosyltransferas	NM_001097638,	NM_001097638,NM_000511
4.06E+02	8.66E+00	fucosyltransferas	fucosyltransferas	NM_001097638,	NM_001097638,NM_000511
3.10E+02	8.28E+00	lysophosphatidyl	lysophosphatidyl	NM_024830	NM_024830
3.10E+02	8.28E+00	lysophosphatidyl	lysophosphatidyl	NM_024830	NM_024830
3.84E+02	8.59E+00	CASK interacting	CASK interacting	NM_020764	NM_020764
3.84E+02	8.59E+00	CASK interacting	CASK interacting	NM_020764	NM_020764
1.59E+00	6.70E-01	calmodulin regul	UBA domain con	NM_015447	NM_015447
1.59E+00	6.70E-01	calmodulin regul	UBA domain con	NM_015447	NM_015447
3.90E-03	-8.00E+00	tachykinin recept	tetraspanin 15	NM_001057	NM_001057
2.93E+02	8.19E+00	junctophilin 3	junctophilin 3	NM_020655	NM_020655
4.21E+02	8.72E+00	ATP-binding cass	ATP-binding cass	NM_212533,NM	NM_212533,NM_001606
4.21E+02	8.72E+00	ATP-binding cass	ATP-binding cass	NM_212533,NM	NM_212533,NM_001606
1.56E+00	6.44E-01	phosphatase and	protease, serine,	NR_023917	NR_023917
3.00E+02	8.23E+00	lipid phosphate p	azurocidin 1	NM_024888	NM_024888
3.00E+02	8.23E+00	azurocidin 1	azurocidin 1	NM_001700	NM_001700
2.80E+02	8.13E+00	alkaline phospha	alkaline phospha	NM_001632	NM_001632
3.38E+02	8.40E+00	leucine rich repe	leucine rich repe	NM_001080457	NM_001080457
3.38E+02	8.40E+00	leucine rich repe	leucine rich repe	NM_001080457	NM_001080457
3.22E-03	-8.28E+00	piggyBac transpc	choline O-acetylt	NM_170753	NM_170753
3.24E+02	8.34E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_002
3.24E+02	8.34E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_002
3.95E+02	8.63E+00	chromosome 10	G protein-couple	NM_173572	NM_173572
4.89E+02	8.93E+00	GRAM domain cc	GRAM domain cc	NM_015124	NM_015124
3.87E+02	8.60E+00	septin 9	septin 9	NM_001113494	NM_001113494
2.79E+02	8.12E+00	lymphocyte antig	glycosylphosphat	NM_001135655,	NM_001135655,NM_002347
1.40E+00	4.86E-01	PR domain conta	PR domain conta	NM_022115	NM_022115
2.91E+02	8.18E+00	TP53 target 3	solute carrier fan	NM_016212	NM_016212
2.91E+02	8.18E+00	TP53 target 3	solute carrier fan	NM_016212	NM_016212
1.82E+00	8.66E-01	netrin 3	netrin 3	NM_006181	NM_006181
3.68E+02	8.52E+00	hypothetical LOC	hypothetical LOC	NR_026943	NR_026943
4.12E+02	8.69E+00	acetylserotonin (	acetylserotonin (	NM_004043	NM_004043
1.61E+00	6.83E-01	zinc finger protei	zinc finger protei	NM_001100598,	NM_001100598,NM_173831,NM_
1.61E+00	6.83E-01	zinc finger protei	zinc finger protei	NM_001100598,	NM_001100598,NM_173831,NM_
3.56E+02	8.48E+00	serine/threonine	solute carrier fan	NM_003576,NM	NM_003576,NM_001032296
3.39E+02	8.40E+00	chromosome 11	chromosome 11	NM_173573	NM_173573
2.61E+02	8.03E+00	dysferlin interact	prolyl 4-hydroxyl	NM_001007533	NM_001007533
2.98E+02	8.22E+00	SRY (sex determi	hypothetical LOC	NM_014587	NM_014587
2.98E+02	8.22E+00	SRY (sex determi	hypothetical LOC	NM_014587	NM_014587
3.67E+02	8.52E+00	chromosome 3 o	chromosome 3 o	NM_001145030	NM_001145030
1.31E+00	3.93E-01	lymphocyte-spec	lymphocyte-spec	NM_001013253	NM_001013253
2.72E+02	8.09E+00	chromosome 19	chromosome 19	NM_152771	NM_152771
2.94E+02	8.20E+00	bromodomain cc	bromodomain cc	NM_014577	NM_014577
3.67E+02	8.52E+00	non-protein codi	collagen, type XV	NR_027498,NM_	NR_027498,NM_199175
2.85E+02	8.16E+00	immediate early	chromosome 9 o	NM_203434	NM_203434
3.16E+02	8.30E+00	reticulon 1	chromosome 14	NM_206852,NM	NM_206852,NM_206857,NM_021
3.16E+02	8.30E+00	reticulon 1	chromosome 14	NM_206852,NM	NM_206852,NM_206857,NM_021
2.93E+02	8.20E+00	platelet-derived	ribosomal protei	NM_002608,NM	NM_002608,NM_033016
2.98E+02	8.22E+00	mitochondrial rit	mitochondrial rit	NM_002949	NM_002949
2.69E+02	8.07E+00	scavenger recept	scavenger recept	NR_002934	NR_002934

2.69E+02	8.07E+00	scavenger recept	scavenger recept	NR_002934	NR_002934
1.38E+00	4.67E-01	zinc finger protei	coiled-coil domai	NM_020787	NM_020787
1.38E+00	4.67E-01	coiled-coil domai	coiled-coil domai	NM_014695	NM_014695
4.62E+02	8.85E+00	filamin C, gamm	filamin C, gamm	NM_001127487,	NM_001127487,NM_001458
4.62E+02	8.85E+00	filamin C, gamm	filamin C, gamm	NM_001127487,	NM_001127487,NM_001458
2.69E+02	8.07E+00	fizzy/cell division	fizzy/cell division	NM_001136197,	NM_001136197,NM_001136198
2.86E+02	8.16E+00	lymphocyte anti	glycosylphospha	NM_001135655,	NM_001135655,NM_002347
2.86E+02	8.16E+00	lymphocyte anti	glycosylphospha	NM_001135655,	NM_001135655,NM_002347
3.46E+02	8.43E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
2.61E+02	8.03E+00	pre-B lymphocyt	BMS1 homolog,	NM_007128	NM_007128
2.97E+02	8.22E+00	G protein-couple	G protein-couple	NM_005301	NM_005301
3.91E+02	8.61E+00	family with sequ	ubiquitin-conjug	NM_001014980	NM_001014980
3.91E+02	8.61E+00	ubiquitin-conjug	ubiquitin-conjug	NM_194458,NM	NM_194458,NM_058167,NM_194
3.91E+02	8.61E+00	ubiquitin-conjug	ubiquitin-conjug	NM_194458,NM	NM_194458,NM_058167,NM_194
3.89E+02	8.60E+00	family with sequ	forkhead box I1	NM_001129891	NM_001129891
3.89E+02	8.60E+00	family with sequ	forkhead box I1	NM_001129891	NM_001129891
4.10E+02	8.68E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
1.26E+00	3.33E-01	sonic hedgehog	non-protein codi	NM_000193	NM_000193
1.26E+00	3.33E-01	sonic hedgehog	non-protein codi	NM_000193	NM_000193
3.85E+02	8.59E+00	transcription elo	transcription elo	NM_016427	NM_016427
1.36E+00	4.38E-01	glutamic-oxaloac	cadherin 8, type	NM_002080	NM_002080
1.36E+00	4.38E-01	glutamic-oxaloac	cadherin 8, type	NM_002080	NM_002080
3.77E+02	8.56E+00	transcription fac	extracellular leuc	NR_001288	NR_001288
3.77E+02	8.56E+00	transcription fac	extracellular leuc	NR_001288	NR_001288
1.76E+00	8.15E-01	troponin T type	troponin T type	NM_001042781,	NM_001042781,NM_001042782,
1.75E+00	8.10E-01	anoctamin 1, cal	anoctamin 1, cal	NM_018043	NM_018043
1.75E+00	8.10E-01	anoctamin 1, cal	anoctamin 1, cal	NM_018043	NM_018043
3.70E+02	8.53E+00	serine/threonine	serine/threonine	NM_173575	NM_173575
1.15E+00	2.07E-01	NADH dehydrog	NADH dehydrog	NM_015965	NM_015965
1.15E+00	2.07E-01	NADH dehydrog	NADH dehydrog	NM_015965	NM_015965
3.10E+02	8.28E+00	chromosome 19	chromosome 19	NM_174983	NM_174983
3.42E+02	8.42E+00	chromosome 11	chromosome 11	NM_013265	NM_013265
2.60E+02	8.02E+00	proline rich 23C	proline rich 23C	NM_001134657	NM_001134657
3.06E+02	8.26E+00	SH3 domain and	SH3 domain and	NM_018986	NM_018986
3.06E+02	8.26E+00	SH3 domain and	SH3 domain and	NM_018986	NM_018986
1.29E+00	3.68E-01	transcription fac	transcription fac	NM_001136139,	NM_001136139,NM_003200
1.29E+00	3.68E-01	transcription fac	transcription fac	NM_001136139,	NM_001136139,NM_003200
1.69E+00	7.57E-01	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
1.69E+00	7.57E-01	FERM domain co	FERM domain co	NM_024919,NM	NM_024919,NM_001122841
3.65E+02	8.51E+00	FSHD region gen	zinc finger protei	NM_001124759	NM_001124759
4.10E+02	8.68E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
3.40E+02	8.41E+00	cholinergic rece	cholinergic rece	NM_000744	NM_000744
3.93E+02	8.62E+00	phosphatidylino	phosphatidylino	NM_058004,NM	NM_058004,NM_002650
3.94E+02	8.62E+00	zinc finger protei	zinc finger protei	NM_133444	NM_133444
1.50E+00	5.80E-01	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
1.50E+00	5.80E-01	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
3.55E+02	8.47E+00	potassium volta	potassium volta	NM_172109	NM_172109
3.55E+02	8.47E+00	potassium volta	potassium volta	NM_172109	NM_172109
2.66E+02	8.06E+00	E2F transcription	peroxisomal me	NM_005225	NM_005225
3.28E+02	8.36E+00	guanine nucleot	proline rich 25	NM_016541	NM_016541
1.31E+00	3.87E-01	TBC1 domain fa	TBC1 domain fa	NM_020773	NM_020773
1.31E+00	3.87E-01	TBC1 domain fa	TBC1 domain fa	NM_020773	NM_020773
1.31E+00	3.87E-01	TBC1 domain fa	TBC1 domain fa	NM_020773	NM_020773
1.17E+00	2.32E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.17E+00	2.32E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.17E+00	2.32E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.23E+00	2.95E-01	family with sequ	family with sequ	NM_032448	NM_032448
4.72E+02	8.88E+00	growth hormone	ADP-ribosylhydr	NM_024719	NM_024719

4.72E+02	8.88E+00	growth hormone	ADP-ribosylhydr	NM_024719	NM_024719
3.07E+02	8.26E+00	nucleoporin 133	ATP-binding cass	NM_018230	NM_018230
2.68E+02	8.06E+00	WD repeat dom	WD repeat dom	NM_173479	NM_173479
3.53E+02	8.46E+00	bromodomain c	bromodomain c	NM_007371	NM_007371
2.98E+02	8.22E+00	C2 calcium-depe	zinc finger protei	NM_015500,NM	NM_015500,NM_199050
2.98E+02	8.22E+00	C2 calcium-depe	zinc finger protei	NM_015500,NM	NM_015500,NM_199050
1.78E+00	8.33E-01	pericentrin	pericentrin	NM_006031	NM_006031
1.14E+00	1.85E-01	ankyrin 1, erythr	ankyrin 1, erythr	NM_001142446,	NM_001142446,NM_001142445,
1.14E+00	1.85E-01	ankyrin 1, erythr	ankyrin 1, erythr	NM_001142446,	NM_001142446,NM_001142445,
4.28E+02	8.74E+00	SIX homeobox 2	S1 RNA binding	NM_016932	NM_016932
3.37E+02	8.40E+00	lipoxygenase hor	lipoxygenase hor	NM_144612	NM_144612
1.45E+00	5.36E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.45E+00	5.36E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
1.45E+00	5.36E-01	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.12E+02	8.29E+00	solute carrier fa	solute carrier fa	NM_194255	NM_194255
3.41E+02	8.41E+00	guanine nucleoti	guanine nucleoti	NM_001098722,	NM_001098722,NM_001098721,
3.41E+02	8.41E+00	guanine nucleoti	guanine nucleoti	NM_001098722,	NM_001098722,NM_001098721,
1.35E+00	4.30E-01	sirtuin 7	sirtuin 7	NM_016538	NM_016538
2.96E+02	8.21E+00	copine family m	copine family m	NM_153635	NM_153635
1.36E+00	4.41E-01	BTB (POZ) domai	phosphofurin aci	NM_033271	NM_033271
3.17E+02	8.31E+00	scavenger recep	scavenger recep	NM_153334,NM	NM_153334,NM_182895
2.81E+02	8.13E+00	coiled-coil domai	malic enzyme 3,	NM_001156474,	NM_001156474,NM_021827
2.98E+02	8.22E+00	cat eye syndrom	cat eye syndrom	NM_017829,NM	NM_017829,NM_033070
2.98E+02	8.22E+00	cat eye syndrom	cat eye syndrom	NM_017829,NM	NM_017829,NM_033070
4.59E+02	8.84E+00	polycomb group	polycomb group	NM_006315	NM_006315
4.59E+02	8.84E+00	polycomb group	polycomb group	NM_006315	NM_006315
4.59E+02	8.84E+00	polycomb group	polycomb group	NM_006315	NM_006315
2.09E+00	1.06E+00	heparan sulfate	heparan sulfate	NM_005529	NM_005529
3.76E+02	8.56E+00	POTE ankyrin do	similar to cDNA	NM_174981	NM_174981
3.76E+02	8.56E+00	POTE ankyrin do	similar to cDNA	NM_174981	NM_174981
3.44E+02	8.43E+00	small nucleolar R	DIO3 opposite st	NR_003224	NR_003224
3.60E+02	8.49E+00	hypothetical pro	neurotensin rece	NR_024470	NR_024470
1.81E+00	8.58E-01	chromosome 7 o	core 1 synthase,	NM_198097	NM_198097
1.81E+00	8.58E-01	chromosome 7 o	core 1 synthase,	NM_198097	NM_198097
2.87E+02	8.17E+00	glutamate recep	glutamate recep	NM_138690	NM_138690
4.41E+02	8.79E+00	chromosome 21	chromosome 21	NR_027243	NR_027243
2.97E+02	8.22E+00	latent transformi	latent transformi	NM_000428	NM_000428
2.97E+02	8.22E+00	latent transformi	latent transformi	NM_000428	NM_000428
1.14E+00	1.92E-01	protein phospha	protein phospha	NM_014678	NM_014678
1.14E+00	1.92E-01	protein phospha	protein phospha	NM_014678	NM_014678
4.17E+02	8.70E+00	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
4.17E+02	8.70E+00	DIP2 disco-inter	DIP2 disco-inter	NM_014974	NM_014974
2.62E+02	8.03E+00	MORN repeat co	transmembrane	NM_173855	NM_173855
1.34E+00	4.18E-01	methyl-CpG bind	CXXC finger 1 (P	NM_015845,NM	NM_015845,NM_015846,NM_00
1.39E+00	4.80E-01	hypothetical LOC	NADH dehydrog	NR_026664	NR_026664
4.21E+02	8.72E+00	complement con	complement con	NM_001008223	NM_001008223
4.21E+02	8.72E+00	complement con	complement con	NM_001008223	NM_001008223
3.64E-03	-8.10E+00	paired box 4	staphylococcal n	NM_006193	NM_006193
3.30E+02	8.37E+00	netrin 1	netrin 1	NM_004822	NM_004822
3.30E+02	8.37E+00	netrin 1	netrin 1	NM_004822	NM_004822
2.70E+02	8.08E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
4.38E+02	8.77E+00	H19, imprinted n	insulin-like grow	NR_002196	NR_002196
3.09E+02	8.27E+00	lymphocyte anti	lymphocyte anti	NM_003695	NM_003695
3.09E+02	8.27E+00	lymphocyte anti	lymphocyte anti	NM_003695	NM_003695
2.93E+02	8.19E+00	KIAA0415	KIAA0415	NM_014855	NM_014855
2.93E+02	8.19E+00	KIAA0415	KIAA0415	NM_014855	NM_014855
3.13E+02	8.29E+00	v-ski sarcoma vir	v-ski sarcoma vir	NM_003036	NM_003036
3.49E-03	-8.16E+00	sulfotransferase	sulfotransferase	NM_177528,NM	NM_177528,NM_001054

2.94E+02	8.20E+00	keratin 2	keratin 2	NM_000423	NM_000423
2.83E+02	8.14E+00	integrator compl	integrator compl	NM_001080453	NM_001080453
3.74E+02	8.55E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,
3.74E+02	8.55E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,
2.74E+02	8.10E+00	LY6/PLAUR dom	LY6/PLAUR dom	NM_205545	NM_205545
3.67E+02	8.52E+00	casein kinase 1,	casein kinase 1,	NR_027320	NR_027320
3.67E+02	8.52E+00	casein kinase 1,	hypothetical LO	NR_027320	NR_027320
2.74E+02	8.10E+00	zinc finger protei	zinc finger protei	NM_017652	NM_017652
2.74E+02	8.10E+00	zinc finger protei	zinc finger protei	NM_017652	NM_017652
1.26E+00	3.28E-01	transmembrane	transmembrane	NM_001136218,	NM_001136218,NM_018022
2.65E+02	8.05E+00	inositol(myo)-1(	cell death-induci	NM_014214	NM_014214
3.06E+02	8.26E+00	dystrophia myot	dystrophia myot	NM_004409,NM	NM_004409,NM_001081562,NM_
1.54E+00	6.24E-01	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
1.54E+00	6.24E-01	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
1.54E+00	6.24E-01	nuclear factor of	CTD (carboxy-ter	NM_172387,NM	NM_172387,NM_172389
1.87E+00	9.01E-01	phospholysine p	family with sequ	NM_022126	NM_022126
1.87E+00	9.01E-01	phospholysine p	family with sequ	NM_022126	NM_022126
1.53E+00	6.10E-01	non-protein codi	collagen, type X	NR_027498,NM_	NR_027498,NM_199175
2.99E+02	8.22E+00	BAI1-associated	BAI1-associated	NM_003933	NM_003933
2.99E+02	8.22E+00	BAI1-associated	BAI1-associated	NM_003933	NM_003933
1.39E+00	4.78E-01	potassium voltag	potassium voltag	NM_004519	NM_004519
1.39E+00	4.78E-01	potassium voltag	potassium voltag	NM_004519	NM_004519
3.77E+02	8.56E+00	5-oxoprolinase (	5-oxoprolinase (	NM_017570	NM_017570
3.77E+02	8.56E+00	5-oxoprolinase (	5-oxoprolinase (	NM_017570	NM_017570
3.75E+02	8.55E+00	acetylserotonin	acetylserotonin	NM_004043	NM_004043
3.27E+02	8.35E+00	kinesin family m	kinesin family m	NM_001130099,	NM_001130099,NM_005550,NM_
3.27E+02	8.35E+00	kinesin family m	kinesin family m	NM_001130099,	NM_001130099,NM_005550,NM_
3.65E+02	8.51E+00	chromosome 14	chromosome 14	NM_001134875,	NM_001134875,NM_001134876
3.65E+02	8.51E+00	chromosome 14	chromosome 14	NM_001134875,	NM_001134875,NM_001134876
1.85E+00	8.87E-01	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
1.85E+00	8.87E-01	chromosome X o	chromosome X o	NM_001145140,	NM_001145140,NM_001145139
1.51E+00	5.95E-01	intraflagellar tra	rhodopsin	NM_052990,NM	NM_052990,NM_052989,NM_05
3.03E+02	8.24E+00	myosin VA (heav	cAMP-regulated	NM_000259,NM	NM_000259,NM_001142495
3.21E+02	8.33E+00	small VCP/p97-i	leucine zipper pr	NM_148893	NM_148893
3.21E+02	8.33E+00	small VCP/p97-i	leucine zipper pr	NM_148893	NM_148893
3.06E+02	8.26E+00	vav 2 guanine nu	vav 2 guanine nu	NM_001134398,	NM_001134398,NM_003371
3.73E-03	-8.07E+00	synaptotagmin X	asparagine-linke	NM_198992	NM_198992
3.64E+02	8.51E+00	chromosome 17	serpin peptidase	NM_032895,NM	NM_032895,NM_001001870
3.64E+02	8.51E+00	chromosome 17	serpin peptidase	NM_032895,NM	NM_032895,NM_001001870
2.75E+02	8.10E+00	Ras association (	Ras association (	NM_003475,NM	NM_003475,NM_001143994
2.75E+02	8.10E+00	Ras association (	Ras association (	NM_003475,NM	NM_003475,NM_001143994
2.04E+00	1.03E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.67E+02	8.52E+00	peroxidasin hom	peroxidasin hom	NM_012293	NM_012293
3.15E+02	8.30E+00	retinoid X recept	retinoid X recept	NM_002957	NM_002957
2.99E+02	8.22E+00	chromosome 2 o	ankyrin repeat d	NM_214461	NM_214461
2.99E+02	8.22E+00	chromosome 2 o	ankyrin repeat d	NM_214461	NM_214461
2.99E+02	8.22E+00	chromosome 2 o	ankyrin repeat d	NM_214461	NM_214461
1.39E+00	4.74E-01	platelet-derived	protein kinase, c	NM_002607,NM	NM_002607,NM_033023
1.39E+00	4.74E-01	platelet-derived	protein kinase, c	NM_002607,NM	NM_002607,NM_033023
3.59E+02	8.49E+00	chromosome 16	chromosome 16	NM_001001410	NM_001001410
3.59E+02	8.49E+00	chromosome 16	chromosome 16	NM_001001410	NM_001001410
7.29E-01	-4.57E-01	antigen p97 (mel	discs, large hom	NM_033316	NM_033316
5.88E-01	-7.67E-01	interleukin 28B (	interleukin 28A (	NM_172139	NM_172139
1.36E+00	4.42E-01	KIAA1267	leucine rich repe	NM_015443	NM_015443
1.36E+00	4.42E-01	KIAA1267	leucine rich repe	NM_015443	NM_015443
1.36E+00	4.42E-01	leucine rich repe	leucine rich repe	NM_014834	NM_014834
2.78E+02	8.12E+00	GEM interacting	ATPase type 13A	NM_016573	NM_016573
3.56E+02	8.48E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249

3.56E+02	8.48E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.56E+02	8.48E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.01E+02	8.23E+00	sprouty-related,	sprouty-related,	NM_001042522,	NM_001042522,NM_001039616
3.90E+02	8.61E+00	GRB10 interactin	GRB10 interactin	NM_022574	NM_022574
3.90E+02	8.61E+00	GRB10 interactin	GRB10 interactin	NM_022574	NM_022574
7.74E-01	-3.69E-01	glutamate recept	zinc finger CCCH	NM_000831	NM_000831
3.76E+02	8.56E+00	chromosome 3 o	chromosome 3 o	NM_007354	NM_007354
3.76E+02	8.56E+00	chromosome 3 o	chromosome 3 o	NM_007354	NM_007354
3.99E+02	8.64E+00	ArfGAP with GTP	ArfGAP with GTP	NM_014914,NM	NM_014914,NM_001037131
3.33E+02	8.38E+00	carboxypeptidas	carboxypeptidas	NM_001868	NM_001868
1.31E+00	3.87E-01	glioma tumor su	glioma tumor su	NM_015710	NM_015710
4.20E+02	8.71E+00	chloride channel	natriuretic pepti	NM_021735,NM	NM_021735,NM_021737,NM_021
3.69E+02	8.53E+00	G-protein signali	G-protein signali	NM_001145638,	NM_001145638,NM_015597
3.69E+02	8.53E+00	G-protein signali	G-protein signali	NM_001145639	NM_001145639
3.18E+02	8.31E+00	zinc finger protei	zinc finger protei	NM_153034	NM_153034
3.18E+02	8.31E+00	zinc finger protei	zinc finger protei	NM_153034	NM_153034
2.83E+02	8.15E+00	SIN3 homolog B,	SIN3 homolog B,	NM_015260	NM_015260
2.83E+02	8.15E+00	SIN3 homolog B,	SIN3 homolog B,	NM_015260	NM_015260
3.64E+02	8.51E+00	non-protein codi	non-protein codi	NR_027457	NR_027457
3.76E+02	8.56E+00	neurofascin	neurofascin	NM_015090	NM_015090
3.72E+02	8.54E+00	hypothetical prot	tumor necrosis f	NR_026927	NR_026927
3.37E+02	8.40E+00	solute carrier fan	hypothetical prot	NM_001080431	NM_001080431
3.17E+02	8.31E+00	hypothetical LOC	collagen, type XV	NR_026943	NR_026943
3.17E+02	8.31E+00	hypothetical LOC	collagen, type XV	NR_026943	NR_026943
3.17E+02	8.31E+00	hypothetical LOC	collagen, type XV	NR_026943	NR_026943
3.88E+02	8.60E+00	chromosome 9 o	chromosome 9 o	NM_001004353	NM_001004353
3.88E+02	8.60E+00	chromosome 9 o	cofactor of BRCA	NM_001004353	NM_001004353
3.83E+02	8.58E+00	Janus kinase and	Janus kinase and	NM_001105521	NM_001105521
2.86E+02	8.16E+00	potassium chann	potassium chann	NM_020822	NM_020822
2.86E+02	8.16E+00	potassium chann	potassium chann	NM_020822	NM_020822
1.41E+00	4.96E-01	acetylserotonin	acetylserotonin	NM_004043	NM_004043
1.41E+00	4.96E-01	acetylserotonin	acetylserotonin	NM_004043	NM_004043
4.28E+02	8.74E+00	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
3.39E+02	8.41E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.58E+02	8.01E+00	sequestosome 1	sequestosome 1	NM_001142299	NM_001142299
3.53E+02	8.46E+00	hepsin	hepsin	NM_002151,NM	NM_002151,NM_182983
1.18E+00	2.43E-01	myosin IE	myosin IE	NM_004998	NM_004998
1.18E+00	2.43E-01	lactate dehydrog	lactate dehydrog	NM_033195	NM_033195
3.72E+02	8.54E+00	jumonji domain	jumonji domain	NM_001114632,	NM_001114632,NM_005090,NR_
3.72E+02	8.54E+00	jumonji domain	jumonji domain	NM_001114632,	NM_001114632,NM_005090,NR_
3.72E+02	8.54E+00	jumonji domain	jumonji domain	NM_001114632,	NM_001114632,NM_005090,NR_
1.71E+00	7.71E-01	UDP-N-acetyl-al	hypothetical LOC	NM_021808,NM	NM_021808,NM_001122636
1.40E+00	4.83E-01	postmeiotic segr	postmeiotic segr	NR_023383	NR_023383
1.40E+00	4.83E-01	postmeiotic segr	postmeiotic segr	NR_023383	NR_023383
1.40E+00	4.83E-01	postmeiotic segr	postmeiotic segr	NR_023383	NR_023383
1.98E+00	9.87E-01	DDB1 and CUL4	DDB1 and CUL4	NM_138353	NM_138353
1.98E+00	9.87E-01	DDB1 and CUL4	DDB1 and CUL4	NM_138353	NM_138353
1.98E+00	9.87E-01	DDB1 and CUL4	DDB1 and CUL4	NM_138353	NM_138353
3.95E+02	8.63E+00	ribosomal RNA p	ribosomal RNA p	NM_015056	NM_015056
3.95E+02	8.63E+00	ribosomal RNA p	ribosomal RNA p	NM_015056	NM_015056
1.77E+00	8.21E-01	protein kinase C,	protein kinase C,	NM_145040	NM_145040
8.00E-01	-3.22E-01	F-box and WD re	F-box and WD re	NM_031456	NM_031456
8.00E-01	-3.22E-01	F-box and WD re	F-box and WD re	NM_031456	NM_031456
8.53E-01	-2.30E-01	ADP-ribosylhydr	ADP-ribosylhydr	NM_138430	NM_138430
8.53E-01	-2.30E-01	ADP-ribosylhydr	ADP-ribosylhydr	NM_138430	NM_138430
1.59E+00	6.73E-01	suppressor of cy	cerebellin 2 prec	NM_004232	NM_004232
3.01E+02	8.23E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
3.01E+02	8.23E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332

3.13E+02	8.29E+00	spectrin, beta, er	spectrin, beta, er	NM_000347	NM_000347
3.13E+02	8.29E+00	spectrin, beta, er	spectrin, beta, er	NM_000347	NM_000347
2.63E+02	8.04E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
2.63E+02	8.04E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
4.90E+02	8.94E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
4.90E+02	8.94E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
4.90E+02	8.94E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
2.57E+02	8.00E+00	protein tyrosine	protein tyrosine	NM_130853,NM	NM_130853,NM_130854,NM_002
2.86E+02	8.16E+00	paralemmin	chromosome 19	NM_001040134,	NM_001040134,NM_002579
3.86E-03	-8.02E+00	kelch-like 38 (Dr	annexin A13	NM_001081675	NM_001081675
3.08E-03	-8.34E+00	hexokinase 3 (w	ubiquitin interac	NM_002115	NM_002115
1.73E+00	7.92E-01	brain-specific an	activity-regulate	NM_001702	NM_001702
1.73E+00	7.92E-01	brain-specific an	activity-regulate	NM_001702	NM_001702
3.31E+02	8.37E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
3.31E+02	8.37E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
3.30E+02	8.37E+00	acidic repeat con	acidic repeat con	NM_052957	NM_052957
2.61E+02	8.03E+00	hypothetical LOC	hypothetical LOC	NR_027242	NR_027242
2.61E+02	8.03E+00	hypothetical LOC	hypothetical LOC	NR_027242	NR_027242
3.65E+02	8.51E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
1.33E+00	4.11E-01	CTD (carboxy-ter	potassium voltag	NM_048368,NM	NM_048368,NM_004715
1.33E+00	4.11E-01	CTD (carboxy-ter	potassium voltag	NM_048368,NM	NM_048368,NM_004715
3.78E+02	8.56E+00	formin homolog	formin homolog	NM_025135	NM_025135
1.32E+00	3.96E-01	cytochrome b-5	angiotensin I con	NM_001017917,	NM_001017917,NM_001017916,
1.32E+00	3.96E-01	cytochrome b-5	angiotensin I con	NM_001017917,	NM_001017917,NM_001017916,
2.97E+02	8.22E+00	paired-like home	H2A histone fam	NM_002653	NM_002653
2.97E+02	8.22E+00	paired-like home	H2A histone fam	NM_002653	NM_002653
2.80E+02	8.13E+00	solute carrier fan	solute carrier fan	NM_207348	NM_207348
2.61E+02	8.03E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
2.61E+02	8.03E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
2.82E+02	8.14E+00	chromosome 10	enoyl CoA hydra	NM_001098483	NM_001098483
2.82E+02	8.14E+00	chromosome 10	enoyl CoA hydra	NM_001098483	NM_001098483
4.76E+02	8.90E+00	solute carrier fan	solute carrier fan	NM_003562	NM_003562
3.85E-03	-8.02E+00	v-akt murine thy	chromosome 19	NM_001626	NM_001626
3.85E-03	-8.02E+00	v-akt murine thy	chromosome 19	NM_001626	NM_001626
3.09E+02	8.27E+00	human immuno	guanylate cyclas	NM_024503,NM	NM_024503,NM_001127714
3.09E+02	8.27E+00	human immuno	guanylate cyclas	NM_024503,NM	NM_024503,NM_001127714
3.89E+02	8.60E+00	polynucleotide k	polynucleotide k	NM_007254	NM_007254
3.25E+02	8.34E+00	sodium channel,	sodium channel,	NM_001037,NM	NM_001037,NM_199037
3.72E-03	-8.07E+00	KIAA0087	chromosome 7 o	NR_022006	NR_022006
1.32E+00	4.02E-01	aquaporin 7 pse	family with sequ	NR_002823	NR_002823
1.32E+00	4.02E-01	aquaporin 7 pse	family with sequ	NR_002823	NR_002823
3.96E+02	8.63E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
3.96E+02	8.63E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
1.78E+00	8.33E-01	heat shock 70kD	KIAA1598	NM_025015	NM_025015
3.78E+02	8.56E+00	mucin 20, cell su	mucin 20, cell su	NM_152673	NM_152673
3.03E+02	8.24E+00	KIAA0664	KIAA0664	NM_015229	NM_015229
3.22E-03	-8.28E+00	polymerase (DN	polymerase (DN	NM_017443,NR_	NM_017443,NR_027261
2.98E+02	8.22E+00	spectrin, beta, n	spectrin, beta, n	NM_006946	NM_006946
2.98E+02	8.22E+00	spectrin, beta, n	spectrin, beta, n	NM_006946	NM_006946
3.40E+02	8.41E+00	cholinergic recep	cholinergic recep	NM_000744	NM_000744
3.78E+02	8.56E+00	mucin 6, oligom	mucin 6, oligom	NM_005961	NM_005961
3.78E+02	8.56E+00	mucin 6, oligom	mucin 6, oligom	NM_005961	NM_005961
2.08E+00	1.06E+00	C-type lectin don	C-type lectin don	NM_015226	NM_015226
2.76E+02	8.11E+00	pantothenate ki	pantothenate ki	NM_018216	NM_018216
2.76E+02	8.11E+00	pantothenate ki	pantothenate ki	NM_018216	NM_018216
3.32E+02	8.38E+00	unc-93 homolog	unc-93 homolog	NM_030930	NM_030930
3.32E+02	8.38E+00	unc-93 homolog	unc-93 homolog	NM_030930	NM_030930
3.27E+02	8.35E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,

3.27E+02	8.35E+00	chromosome 7 o	chromosome 7 o	NM_001134395,	NM_001134395,NM_001134396,N
3.03E+02	8.24E+00	BTB (POZ) domai	BTB (POZ) domai	NM_032444	NM_032444
3.03E+02	8.24E+00	BTB (POZ) domai	BTB (POZ) domai	NM_032444	NM_032444
1.19E+00	2.50E-01	grainyhead-like 1	Kruppel-like fact	NM_198182	NM_198182
1.19E+00	2.50E-01	grainyhead-like 1	Kruppel-like fact	NM_198182	NM_198182
2.76E+02	8.11E+00	protein phospha	protein phospha	NM_014678	NM_014678
2.76E+02	8.11E+00	protein phospha	protein phospha	NM_014678	NM_014678
1.85E+00	8.85E-01	tectorin alpha	tectorin alpha	NM_005422	NM_005422
1.85E+00	8.85E-01	tectorin alpha	tectorin alpha	NM_005422	NM_005422
3.53E+02	8.46E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
3.53E+02	8.46E+00	regulatory associ	regulatory associ	NM_020761	NM_020761
3.84E+02	8.59E+00	protein arginine	protein arginine	NM_198318,NM	NM_198318,NM_198319,NM_001
1.99E+00	9.89E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
1.99E+00	9.89E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
1.99E+00	9.89E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
3.23E+02	8.34E+00	PHD finger prote	cAMP responsive	NM_001101802,	NM_001101802,NM_016621
2.63E+02	8.04E+00	mitochondrial ri	hypothetical LOC	NM_021134	NM_021134
3.23E+02	8.34E+00	family with sequ	protein phospha	NM_001001794	NM_001001794
2.73E+02	8.09E+00	transmembrane	KIAA0125	NM_025268	NM_025268
4.03E+02	8.65E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
4.03E+02	8.65E+00	SHC (Src homolo	SHC (Src homolo	NM_012435	NM_012435
4.07E+02	8.67E+00	Enah/Vasp-like	Enah/Vasp-like	NM_016337	NM_016337
2.58E-03	-8.60E+00	leucine-rich repe	leucine-rich repe	NM_020678	NM_020678
2.58E-03	-8.60E+00	leucine-rich repe	leucine-rich repe	NM_020678	NM_020678
1.93E+00	9.52E-01	nucleolar comple	tubulin, alpha 3d	NR_002826	NR_002826
1.93E+00	9.52E-01	nucleolar comple	tubulin, alpha 3d	NR_002826	NR_002826
1.93E+00	9.52E-01	tubulin, alpha 3d	tubulin, alpha 3d	NM_080386	NM_080386
2.58E+02	8.01E+00	frizzled homolog	piwi-like 1 (Dros	NM_007197	NM_007197
2.58E+02	8.01E+00	frizzled homolog	piwi-like 1 (Dros	NM_007197	NM_007197
3.05E+02	8.25E+00	strawberry notc	serine/threonine	NM_001100122,	NM_001100122,NM_014963
1.69E+00	7.61E-01	TBC1 domain fam	family with sequ	NM_014346	NM_014346
1.98E+00	9.87E-01	RAB35, member	RAB35, member	NM_006861	NM_006861
4.30E-03	-7.86E+00	IKAROS family zi	zona pellucida bi	NM_183231,NM	NM_183231,NM_183232,NM_012
4.30E-03	-7.86E+00	IKAROS family zi	zona pellucida bi	NM_183231,NM	NM_183231,NM_183232,NM_012
3.99E+02	8.64E+00	nuclear factor of	nuclear factor of	NM_172387,NM	NM_172387,NM_172389
2.70E-03	-8.53E+00	cytospin B	cytospin B	NM_152904,NM	NM_152904,NM_001033553
2.70E-03	-8.53E+00	cytospin B	cytospin B	NM_152904,NM	NM_152904,NM_001033553
8.55E-01	-2.26E-01	hypothetical LOC	zinc finger protei	NR_015417	NR_015417
8.55E-01	-2.26E-01	hypothetical LOC	zinc finger protei	NR_015417	NR_015417
2.88E+02	8.17E+00	solute carrier fam	solute carrier fam	NM_031947	NM_031947
2.88E+02	8.17E+00	solute carrier fam	solute carrier fam	NM_031947	NM_031947
3.21E+02	8.33E+00	prostate tumor o	prostate tumor o	NM_017432	NM_017432
3.41E+02	8.41E+00	solute carrier fam	DnaJ (Hsp40) ho	NM_003459	NM_003459
3.41E+02	8.41E+00	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_173650	NM_173650
1.70E+00	7.62E-01	asparagine-linke	transient recept	NR_024248	NR_024248
1.83E+00	8.68E-01	kelch-like 30 (Dr	kelch-like 30 (Dr	NM_198582	NM_198582
2.93E+02	8.19E+00	chondroitin sulfa	chondroitin sulfa	NR_001554,NR_	NR_001554,NR_002194
2.93E+02	8.19E+00	chondroitin sulfa	golgin A2 pseudo	NR_001554,NR_	NR_001554,NR_002194
2.93E+02	8.19E+00	chondroitin sulfa	golgin A2 pseudo	NR_001554,NR_	NR_001554,NR_002194
3.11E+02	8.28E+00	WD repeat doma	WD repeat doma	NM_032259	NM_032259
1.77E+00	8.26E-01	Rho-related BTB	Rho-related BTB	NM_015178	NM_015178
1.77E+00	8.26E-01	Rho-related BTB	Rho-related BTB	NM_015178	NM_015178
3.91E-03	-8.00E+00	inositol 1,4,5-tri	synaptotagmin X	NM_001034841	NM_001034841
3.91E-03	-8.00E+00	inositol 1,4,5-tri	synaptotagmin X	NM_001034841	NM_001034841
3.96E+02	8.63E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
3.96E+02	8.63E+00	hypothetical LOC	fibrosin-like 1	NR_024563	NR_024563
1.18E+00	2.35E-01	cysteinyl-tRNA s	cysteinyl-tRNA s	NM_024537	NM_024537
1.18E+00	2.35E-01	cysteinyl-tRNA s	cysteinyl-tRNA s	NM_024537	NM_024537

1.18E+00	2.35E-01	cysteinyl-tRNA sy	cysteinyl-tRNA sy	NM_024537	NM_024537
2.51E+02	7.97E+00	SET and MYND d	transcription fact	NM_022743	NM_022743
2.61E+02	8.03E+00	GLI family zinc fir	zinc finger protei	NM_138465	NM_138465
3.40E+02	8.41E+00	potassium voltag	potassium voltag	NM_172109	NM_172109
3.40E+02	8.41E+00	potassium voltag	potassium voltag	NM_172109	NM_172109
2.11E+00	1.08E+00	DENN/MADD do	DENN/MADD do	NM_014856	NM_014856
3.01E+02	8.23E+00	gametogenetin	gametogenetin	NM_152657	NM_152657
4.08E+02	8.67E+00	carbohydrate (ke	carbohydrate (ke	NM_003654	NM_003654
4.08E+02	8.67E+00	carbohydrate (ke	carbohydrate (ke	NM_003654	NM_003654
4.08E+02	8.67E+00	carbohydrate (ke	carbohydrate (ke	NM_003654	NM_003654
4.08E+02	8.67E+00	carbohydrate (ke	carbohydrate (ke	NM_003654	NM_003654
1.34E+00	4.25E-01	suppressor of zes	leucine rich repe	NM_015355	NM_015355
1.34E+00	4.25E-01	suppressor of zes	leucine rich repe	NM_015355	NM_015355
1.34E+00	4.25E-01	leucine rich repe	leucine rich repe	NM_052888	NM_052888
2.50E+02	7.96E+00	solute carrier fan	divergent-paired	NR_002938	NR_002938
3.70E+02	8.53E+00	chromosome 17	chromosome 17	NM_001145536	NM_001145536
1.44E+00	5.28E-01	rhomboid, veinle	rhomboid, veinle	NM_003961	NM_003961
3.28E+02	8.36E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
3.28E+02	8.36E+00	copine VII	copine VII	NM_014427,NM	NM_014427,NM_153636
4.24E-03	-7.88E+00	complement con	disabled homolo	NM_001737	NM_001737
2.19E+00	1.13E+00	fibroblast growth	ring finger protei	NM_021923	NM_021923
3.75E+02	8.55E+00	cytochrome P45(	cytochrome P45(	NM_000106,NM	NM_000106,NM_001025161
3.75E+02	8.55E+00	cytochrome P45(	cytochrome P45(	NM_000106,NM	NM_000106,NM_001025161
3.75E+02	8.55E+00	cytochrome P45(	cytochrome P45(	NM_000106,NM	NM_000106,NM_001025161
3.94E+02	8.62E+00	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
3.94E+02	8.62E+00	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
3.94E+02	8.62E+00	tuberous sclerosi	tuberous sclerosi	NM_000548,NM	NM_000548,NM_001077183,NM_
1.55E+00	6.33E-01	BTG3 associated	BTG3 associated	NM_017869,NM	NM_017869,NM_079837
3.87E+02	8.59E+00	glutamate-rich 1	discs, large (Dros	NM_207332	NM_207332
4.08E+02	8.67E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
2.09E+00	1.06E+00	tenascin XB	tenascin XB	NM_019105,NM	NM_019105,NM_032470
4.35E-03	-7.85E+00	neuroblastoma b	neuroblastoma b	NM_001143987,	NM_001143987,NM_001143988
1.27E+00	3.43E-01	sialidase 2 (cytos	inositol polyphos	NM_005383	NM_005383
3.93E+02	8.62E+00	keratin 17	eukaryotic transl	NM_000422	NM_000422
1.20E+00	2.67E-01	stress-induced-pl	fermitin family m	NM_006819	NM_006819
1.20E+00	2.67E-01	stress-induced-pl	fermitin family m	NM_006819	NM_006819
2.92E+02	8.19E+00	microtubule assc	microtubule assc	NM_001033602	NM_001033602
2.53E+02	7.98E+00	transforming gro	transforming gro	NM_015927	NM_015927
2.53E+02	7.98E+00	transforming gro	transforming gro	NM_015927	NM_015927
2.28E+00	1.19E+00	PHD and ring fing	PHD and ring fing	NM_020901	NM_020901
2.28E+00	1.19E+00	PHD and ring fing	PHD and ring fing	NM_020901	NM_020901
1.19E+00	2.57E-01	coiled-coil domai	coiled-coil domai	NM_182568	NM_182568
1.19E+00	2.57E-01	coiled-coil domai	coiled-coil domai	NM_182568	NM_182568
3.14E+02	8.30E+00	mesothelin-like	mesothelin-like	NM_001025190	NM_001025190
2.74E+02	8.10E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
2.74E+02	8.10E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
3.33E+02	8.38E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
1.20E+00	2.62E-01	WD repeat doma	WD repeat doma	NM_145294	NM_145294
1.20E+00	2.62E-01	WD repeat doma	WD repeat doma	NM_145294	NM_145294
2.43E+02	7.93E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
2.43E+02	7.93E+00	MAD1 mitotic ar	MAD1 mitotic ar	NM_003550,NM	NM_003550,NM_001013837,NM_
3.99E+02	8.64E+00	interferon regula	interferon regula	NM_001571	NM_001571
3.99E+02	8.64E+00	interferon regula	interferon regula	NM_001571	NM_001571
3.60E-03	-8.12E+00	chromosome 16	chromosome 16	NM_001012991	NM_001012991
1.15E+00	1.99E-01	family with sequ	KIAA0182	NM_198491	NM_198491
3.95E+02	8.63E+00	ephrin-B2	ephrin-B2	NM_004093	NM_004093
3.95E+02	8.63E+00	ephrin-B2	ephrin-B2	NM_004093	NM_004093
2.50E+02	7.97E+00	bol, boule-like (D	phospholipase C-	NM_033030,NM	NM_033030,NM_197970

3.13E+02	8.29E+00	dysferlin, limb gi	dysferlin, limb gi	NM_001130984,	NM_001130984,NM_001130982,N
1.91E+00	9.36E-01	kinesin family me	kinesin family me	NM_020816,NM	NM_020816,NM_001122819
3.82E+02	8.58E+00	lysine (K)-specific	lysine (K)-specific	NM_001005366,	NM_001005366,NM_032590
3.82E+02	8.58E+00	lysine (K)-specific	lysine (K)-specific	NM_001005366,	NM_001005366,NM_032590
3.08E+02	8.27E+00	wingless-type MI	wingless-type MI	NM_030761	NM_030761
3.08E+02	8.27E+00	wingless-type MI	wingless-type MI	NM_030761	NM_030761
3.12E+02	8.29E+00	Janus kinase 2	Janus kinase 2	NM_004972	NM_004972
3.83E+02	8.58E+00	claudin 15	claudin 15	NM_014343	NM_014343
1.52E+00	6.01E-01	hypothetical pro	tumor necrosis fa	NR_026927	NR_026927
1.64E+00	7.17E-01	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
2.50E+02	7.96E+00	major histocomp	major histocomp	NR_003937	NR_003937
2.50E+02	7.96E+00	major histocomp	major histocomp	NR_003937	NR_003937
1.96E+00	9.68E-01	zinc finger RNA b	zinc finger RNA b	NM_015174	NM_015174
1.96E+00	9.68E-01	zinc finger RNA b	zinc finger RNA b	NM_015174	NM_015174
3.41E+02	8.41E+00	notch 1	notch 1	NM_017617	NM_017617
1.22E+00	2.88E-01	cyclin N-terminal	cyclin N-terminal	NM_173478	NM_173478
3.96E+02	8.63E+00	RAB11 family int	RAB11 family int	NM_014700	NM_014700
3.96E+02	8.63E+00	RAB11 family int	RAB11 family int	NM_014700	NM_014700
3.96E+02	8.63E+00	RAB11 family int	RAB11 family int	NM_001142272	NM_001142272
3.63E+02	8.51E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
3.63E+02	8.51E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
3.63E+02	8.51E+00	protein kinase, c	protein kinase, c	NM_002735	NM_002735
2.53E+02	7.98E+00	chromosome 2 o	hypothetical LOC	NM_173821	NM_173821
3.70E+02	8.53E+00	chromosome 21	heat shock trans	NR_026863	NR_026863
4.00E+02	8.64E+00	SET binding facto	SET binding facto	NM_002972	NM_002972
4.00E+02	8.64E+00	SET binding facto	SET binding facto	NM_002972	NM_002972
1.47E+00	5.56E-01	thrombospondin	thrombospondin	NM_003247	NM_003247
1.95E+00	9.61E-01	UV radiation resi	wingless-type MI	NM_003369	NM_003369
1.95E+00	9.61E-01	UV radiation resi	wingless-type MI	NM_003369	NM_003369
2.38E+00	1.25E+00	filamin C, gamma	filamin C, gamma	NM_001127487,	NM_001127487,NM_001458
3.15E+02	8.30E+00	vasoactive intest	vasoactive intest	NM_003382	NM_003382
3.15E+02	8.30E+00	vasoactive intest	vasoactive intest	NM_003382	NM_003382
1.35E+00	4.34E-01	proline rich 20C	proline rich 20A	NM_001130405,	NM_001130405,NM_001130404,N
1.35E+00	4.34E-01	proline rich 20C	proline rich 20A	NM_001130405,	NM_001130405,NM_001130404,N
1.35E+00	4.34E-01	proline rich 20C	proline rich 20A	NM_001130405,	NM_001130405,NM_001130404,N
1.35E+00	4.34E-01	proline rich 20A	proline rich 20A	NM_198441,NM	NM_198441,NM_001130404,NM_
3.08E+02	8.27E+00	keratin 34	keratin 31	NM_021013	NM_021013
2.63E+02	8.04E+00	PR domain conta	PR domain conta	NM_022115	NM_022115
1.78E+00	8.34E-01	chromosome 19	polypyrimidine t	NM_173481	NM_173481
2.66E+02	8.06E+00	nuclear factor I/	nuclear factor I/	NM_002501	NM_002501
1.36E+00	4.41E-01	chymotrypsinoge	chymotrypsinoge	NM_001025200	NM_001025200
1.36E+00	4.41E-01	chymotrypsinoge	chymotrypsinoge	NM_001025200	NM_001025200
3.09E+02	8.27E+00	phosphatidylinos	phosphatidylinos	NM_012398	NM_012398
3.09E+02	8.27E+00	phosphatidylinos	phosphatidylinos	NM_012398	NM_012398
3.58E+02	8.48E+00	guanine nucleoti	guanine nucleoti	NM_002067	NM_002067
3.58E+02	8.48E+00	guanine nucleoti	guanine nucleoti	NM_002067	NM_002067
3.87E+02	8.60E+00	GRB2-associated	cat eye syndrom	NM_001037814	NM_001037814
1.19E+00	2.53E-01	v-maf musculoap	v-maf musculoap	NM_032711,NM	NM_032711,NM_002359
3.19E+02	8.32E+00	SH3-domain GRB	SH3-domain GRB	NM_003025	NM_003025
1.32E+00	4.02E-01	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
1.32E+00	4.02E-01	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
3.44E+02	8.43E+00	keratin 86	keratin 86	NM_002284	NM_002284
2.63E+02	8.04E+00	collectin sub-fam	collectin sub-fam	NM_199235,NM	NM_199235,NM_024027
4.73E+02	8.89E+00	caveolin 3	caveolin 3	NM_001234,NM	NM_001234,NM_033337
4.30E-03	-7.86E+00	proteasome (pro	proteasome (pro	NM_176863,NM	NM_176863,NM_005789
4.15E+02	8.70E+00	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
4.15E+02	8.70E+00	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
1.46E+00	5.47E-01	nuclear factor of	cysteine/histidin	NM_013432	NM_013432

1.46E+00	5.47E-01	cysteine/histidin	cysteine/histidin	NM_138496	NM_138496
3.52E+02	8.46E+00	WD repeat doma	WD repeat doma	NM_017491,NM	NM_017491,NM_005112
3.52E+02	8.46E+00	WD repeat doma	WD repeat doma	NM_017491,NM	NM_017491,NM_005112
3.86E+02	8.59E+00	active BCR-relate	active BCR-relate	NM_001159746	NM_001159746
2.80E+02	8.13E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
1.10E+00	1.35E-01	O-linked N-acety	acidic repeat con	NM_181673,NM	NM_181673,NM_181672
3.61E-03	-8.11E+00	WNT1 inducible	potassium chann	NM_003881	NM_003881
3.61E-03	-8.11E+00	WNT1 inducible	potassium chann	NM_003881	NM_003881
3.10E+02	8.27E+00	family with sequ	KIAA0182	NM_198491	NM_198491
3.10E+02	8.27E+00	family with sequ	KIAA0182	NM_198491	NM_198491
3.79E-03	-8.05E+00	hypothetical LOC	odz, odd Oz/ten-	NR_027107	NR_027107
3.44E+02	8.43E+00	macrophage eryt	macrophage eryt	NM_005882,NM	NM_005882,NM_001017405
2.00E+00	1.00E+00	stonin 1	general transcrip	NM_006873	NM_006873
2.00E+00	1.00E+00	stonin 1	general transcrip	NM_006873	NM_006873
2.00E+00	1.00E+00	general transcrip	general transcrip	NM_006872,NM	NM_006872,NM_172196
1.35E+00	4.30E-01	pleckstrin homol	pleckstrin homol	NM_052909	NM_052909
1.35E+00	4.30E-01	pleckstrin homol	pleckstrin homol	NM_052909	NM_052909
2.94E+02	8.20E+00	glutamic-pyruvat	glutamic-pyruvat	NM_005309	NM_005309
1.66E+00	7.30E-01	calcitonin-relate	calcitonin-relate	NM_001741,NM	NM_001741,NM_001033952
1.66E+00	7.30E-01	calcitonin-relate	calcitonin-relate	NM_001741,NM	NM_001741,NM_001033952
4.86E+02	8.93E+00	family with sequ	family with sequ	NM_033387	NM_033387
4.86E+02	8.93E+00	family with sequ	family with sequ	NM_033387	NM_033387
1.83E+00	8.72E-01	1-acylglycerol-3-	1-acylglycerol-3-	NM_020132	NM_020132
1.83E+00	8.72E-01	1-acylglycerol-3-	1-acylglycerol-3-	NM_020132	NM_020132
2.85E+02	8.16E+00	matrix metallope	matrix metallope	NM_016155	NM_016155
2.85E+02	8.16E+00	matrix metallope	matrix metallope	NM_016155	NM_016155
1.95E+00	9.66E-01	solute carrier fan	family with sequ	NM_001142600,	NM_001142600,NM_052934,NM_
2.99E+02	8.22E+00	coiled-coil domai	coiled-coil domai	NM_001114938	NM_001114938
2.99E+02	8.22E+00	coiled-coil domai	coiled-coil domai	NM_001114938	NM_001114938
3.10E+02	8.28E+00	hypothetical LOC	calcium channel,	NR_024341	NR_024341
3.85E+02	8.59E+00	ST8 alpha-N-acet	ST8 alpha-N-acet	NM_013305	NM_013305
3.61E+02	8.50E+00	potassium chann	potassium chann	NM_020822	NM_020822
3.61E+02	8.50E+00	potassium chann	potassium chann	NM_020822	NM_020822
1.14E+00	1.90E-01	GNAS complex l	GNAS complex l	NM_001077488	NM_001077488
3.97E+02	8.63E+00	hypothetical LOC	hypothetical pro	NR_024101	NR_024101
2.67E+02	8.06E+00	DDB1 and CUL4 a	ubiquitin associa	NM_015397	NM_015397
2.67E+02	8.06E+00	DDB1 and CUL4 a	ubiquitin associa	NM_015397	NM_015397
3.25E+02	8.34E+00	malonyl-CoA dec	oxidative stress i	NM_012213	NM_012213
1.58E+00	6.56E-01	spire homolog 2	spire homolog 2	NM_032451	NM_032451
1.58E+00	6.56E-01	spire homolog 2	spire homolog 2	NM_032451	NM_032451
1.25E+00	3.18E-01	eukaryotic transl	pancreatic proge	NM_001958	NM_001958
1.25E+00	3.18E-01	eukaryotic transl	pancreatic proge	NM_001958	NM_001958
3.84E+02	8.59E+00	chromosome 19	chromosome 19	NM_001101340	NM_001101340
2.84E+02	8.15E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
2.84E+02	8.15E+00	TP53 target 3	ubiquitin-conjug	NM_016212	NM_016212
2.66E+02	8.06E+00	zinc finger, DHH	zinc finger, DHH	NM_024786	NM_024786
4.19E+02	8.71E+00	cold inducible R	chromosome 19	NM_001280,NR_	NM_001280,NR_023312,NR_0233
3.37E-03	-8.21E+00	N-terminal aspar	RRN3 RNA polym	NM_173474	NM_173474
3.37E-03	-8.21E+00	N-terminal aspar	RRN3 RNA polym	NM_173474	NM_173474
1.84E+00	8.77E-01	transmembrane	M-phase phosph	NM_130785,NM	NM_130785,NM_199254,NM_001
1.84E+00	8.77E-01	transmembrane	M-phase phosph	NM_130785,NM	NM_130785,NM_199254,NM_001
1.53E+00	6.15E-01	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_025219	NM_025219
1.53E+00	6.15E-01	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_025219	NM_025219
1.29E+00	3.65E-01	kinase non-catal	kinase non-catal	NM_152643	NM_152643
1.29E+00	3.65E-01	kinase non-catal	kinase non-catal	NM_152643	NM_152643
3.12E-03	-8.33E+00	deafness, autoso	oxysterol binding	NM_001127454,	NM_001127454,NM_004403,NM_
3.48E+02	8.44E+00	ATPase family, A	ATPase family, A	NM_001039211	NM_001039211
3.48E+02	8.44E+00	ATPase family, A	ATPase family, A	NM_001039211	NM_001039211

3.70E+02	8.53E+00	perilipin 3	perilipin 3	NM_005817	NM_005817
3.70E+02	8.53E+00	perilipin 3	perilipin 3	NM_005817	NM_005817
3.91E+02	8.61E+00	lysophosphatidyl	lysophosphatidyl	NM_024830	NM_024830
3.91E+02	8.61E+00	lysophosphatidyl	lysophosphatidyl	NM_024830	NM_024830
1.33E+00	4.15E-01	zinc finger and B	heat shock 70kD	NM_001123329,	NM_001123329,NM_014950
1.84E+00	8.83E-01	keratin associate	keratin associate	NM_031964	NM_031964
3.29E+02	8.36E+00	gamma-glutamyl	gamma-glutamyl	NM_199127	NM_199127
4.03E+02	8.65E+00	forkhead box D2	Skint-like (pseud	NM_004474	NM_004474
4.03E+02	8.65E+00	forkhead box D2	Skint-like (pseud	NM_004474	NM_004474
2.78E+02	8.12E+00	testis-specific tra	testis specific pr	NR_003593,NR_	NR_003593,NR_001540
2.78E+02	8.12E+00	testis-specific tra	testis specific pr	NR_003593,NR_	NR_003593,NR_001540
1.34E+00	4.23E-01	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
1.34E+00	4.23E-01	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
2.58E+02	8.01E+00	pericentrin	pericentrin	NM_006031	NM_006031
1.17E+00	2.26E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
1.17E+00	2.26E-01	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
3.49E+02	8.45E+00	phosphoinositid	netrin 1	NM_014308,NM	NM_014308,NM_001142633
1.81E+00	8.59E-01	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
1.81E+00	8.59E-01	signal peptide pe	signal peptide pe	NM_152988,NM	NM_152988,NM_001077238
3.41E+02	8.41E+00	tubulin polymeri	zinc finger, DHH	NM_007030	NM_007030
3.41E+02	8.41E+00	tubulin polymeri	zinc finger, DHH	NM_007030	NM_007030
3.44E+02	8.43E+00	sialidase 4	sialidase 4	NM_080741	NM_080741
3.44E+02	8.43E+00	sialidase 4	sialidase 4	NM_080741	NM_080741
2.53E+02	7.98E+00	zinc finger CCCH	zinc finger CCCH	NM_015117	NM_015117
2.53E+02	7.98E+00	zinc finger CCCH	zinc finger CCCH	NM_015117	NM_015117
2.83E+02	8.14E+00	lymphocyte anti	glycosylphospha	NM_003695	NM_003695
2.92E+02	8.19E+00	E4F transcription	E4F transcription	NM_004424	NM_004424
1.25E+00	3.21E-01	XPA binding prot	XPA binding prot	NM_020196	NM_020196
1.25E+00	3.21E-01	XPA binding prot	XPA binding prot	NM_020196	NM_020196
1.74E+00	8.02E-01	myosin binding p	myosin binding p	NM_000256	NM_000256
1.74E+00	8.02E-01	myosin binding p	myosin binding p	NM_000256	NM_000256
1.71E+00	7.71E-01	potassium intern	LY6/PLAUR dom	NM_002250	NM_002250
3.02E-03	-8.37E+00	fragile site, folic	leucine-rich, glio	NM_145246	NM_145246
3.02E-03	-8.37E+00	fragile site, folic	leucine-rich, glio	NM_145246	NM_145246
3.10E+02	8.28E+00	acyl-CoA thioest	acyl-CoA thioest	NM_147161,NM	NM_147161,NM_015547
2.83E+02	8.15E+00	immunity-relate	immunity-relate	NM_001007561	NM_001007561
2.83E+02	8.15E+00	immunity-relate	immunity-relate	NM_001007561	NM_001007561
3.52E+02	8.46E+00	transmembrane	transmembrane	NM_001136103	NM_001136103
2.82E+02	8.14E+00	hypothetical pro	hypothetical pro	NR_002942	NR_002942
3.77E-03	-8.05E+00	lymphocyte anti	glycosylphospha	NM_003695	NM_003695
4.43E+02	8.79E+00	patatin-like phos	patatin-like phos	NM_152286,NM	NM_152286,NM_001098537
4.43E+02	8.79E+00	patatin-like phos	patatin-like phos	NM_152286,NM	NM_152286,NM_001098537
3.17E+02	8.31E+00	chondroitin sulfa	chondroitin sulfa	NM_001897	NM_001897
3.17E+02	8.31E+00	chondroitin sulfa	chondroitin sulfa	NM_001897	NM_001897
3.76E+02	8.56E+00	shroom family m	shroom family m	NM_001649	NM_001649
3.76E+02	8.56E+00	shroom family m	shroom family m	NM_001649	NM_001649
3.37E+02	8.40E+00	ankyrin repeat a	ankyrin repeat a	NM_080871,NM	NM_080871,NM_001142459,NM_
3.51E+02	8.46E+00	ADP-ribosylation	ADP-ribosylation	NM_001040025	NM_001040025
1.75E+00	8.05E-01	biphenyl hydrola	biphenyl hydrola	NR_026650,NR_	NR_026650,NR_026649,NR_0266
1.75E+00	8.05E-01	biphenyl hydrola	biphenyl hydrola	NR_026650,NR_	NR_026650,NR_026649,NR_0266
3.28E+02	8.36E+00	GTP binding prot	protein phospha	NM_012227	NM_012227
1.39E+00	4.70E-01	meteorin, glial c	meteorin, glial c	NM_001004431	NM_001004431
1.39E+00	4.70E-01	meteorin, glial c	meteorin, glial c	NM_001004431	NM_001004431
2.88E+02	8.17E+00	chromosome 17	chromosome 17	NM_001109760,	NM_001109760,NM_025161
3.01E+02	8.23E+00	tripartite motif-c	tripartite motif-c	NM_033278,NM	NM_033278,NM_006458
3.95E+02	8.63E+00	mucin 4, cell surf	tyrosine kinase,	NM_138297,NM	NM_138297,NM_004532,NM_01
3.66E+02	8.52E+00	p21 protein (Cdc	p21 protein (Cdc	NM_001014834,	NM_001014834,NM_001014832,
1.83E+00	8.68E-01	ataxin 1	ataxin 1	NM_001128164,	NM_001128164,NM_000332

1.83E+00	8.68E-01	ataxin 1	ataxin 1	NM_001128164,	NM_001128164,NM_000332
2.94E+02	8.20E+00	lymphocyte antig	glycosylphosphat	NM_003695	NM_003695
1.83E+00	8.68E-01	ataxin 1	ataxin 1	NM_001128164,	NM_001128164,NM_000332
2.77E+02	8.11E+00	calcium channel,	calcium channel,	NM_021098,NM	NM_021098,NM_001005407
3.10E+02	8.28E+00	mucin 2, oligome	mucin 5AC, oligo	NM_002457	NM_002457
3.10E+02	8.28E+00	mucin 2, oligome	mucin 5AC, oligo	NM_002457	NM_002457
2.73E+02	8.09E+00	deltex homolog 3	deltex homolog 3	NM_178502	NM_178502
2.73E+02	8.09E+00	deltex homolog 3	deltex homolog 3	NM_178502	NM_178502
1.10E+00	1.41E-01	leukocyte-associa	tweety homolog	NM_002287,NM	NM_002287,NM_021706
4.14E-03	-7.92E+00	pepsinogen 4, gr	pepsinogen 5, gr	NM_001079808	NM_001079808
4.14E-03	-7.92E+00	pepsinogen 5, gr	pepsinogen 5, gr	NM_014224	NM_014224
3.41E+02	8.41E+00	DnaJ (Hsp40) hor	protein tyrosine	NM_058246	NM_058246
3.41E+02	8.41E+00	DnaJ (Hsp40) hor	protein tyrosine	NM_058246	NM_058246
2.83E+02	8.15E+00	elastase, neutrop	elastase, neutrop	NM_001972	NM_001972
2.80E+02	8.13E+00	neuroligin 3	neuroligin 3	NM_018977	NM_018977
2.80E+02	8.13E+00	neuroligin 3	neuroligin 3	NM_018977	NM_018977
3.69E+02	8.53E+00	YdjC homolog (ba	coiled-coil domai	NM_001017964	NM_001017964
3.61E+02	8.49E+00	shroom family m	shroom family m	NM_001649	NM_001649
3.61E+02	8.49E+00	shroom family m	shroom family m	NM_001649	NM_001649
3.61E+02	8.49E+00	shroom family m	shroom family m	NM_001649	NM_001649
2.91E+02	8.18E+00	thimet oligopept	thimet oligopept	NM_003249	NM_003249
3.61E+02	8.49E+00	mitogen-activate	mitogen-activate	NM_030662	NM_030662
2.72E+02	8.09E+00	peroxisomal biog	phospholipase C,	NM_002617,NM	NM_002617,NM_153818
3.06E+02	8.26E+00	collagen, type V,	collagen, type V,	NM_000093	NM_000093
1.74E+00	7.95E-01	deformed epider	deformed epider	NM_021008	NM_021008
1.74E+00	7.95E-01	deformed epider	deformed epider	NM_021008	NM_021008
3.74E+02	8.55E+00	CTF18, chromoso	CTF18, chromoso	NM_022092	NM_022092
3.74E+02	8.55E+00	CTF18, chromoso	CTF18, chromoso	NM_022092	NM_022092
3.88E-03	-8.01E+00	THUMP domain	solute carrier fan	NM_025264	NM_025264
1.66E+00	7.31E-01	ribosomal protei	ribosomal protei	NR_003572	NR_003572
1.66E+00	7.31E-01	ribosomal protei	ribosomal protei	NR_003572	NR_003572
3.43E+02	8.42E+00	phosphatidylinos	phosphatidylinos	NM_012398	NM_012398
2.82E+02	8.14E+00	C1q and tumor n	calcium channel,	NM_207419	NM_207419
2.69E+02	8.07E+00	glucokinase (hex	YKT6 v-SNARE hc	NM_000162,NM	NM_000162,NM_033508,NM_033
1.82E+00	8.65E-01	zinc finger protei	zinc finger protei	NM_001134655	NM_001134655
1.82E+00	8.65E-01	zinc finger protei	zinc finger protei	NM_001134655	NM_001134655
2.52E+02	7.98E+00	peptidase inhibit	peptidase inhibit	NM_153370	NM_153370
2.52E+02	7.98E+00	peptidase inhibit	peptidase inhibit	NM_153370	NM_153370
1.34E+00	4.19E-01	zinc finger protei	zinc finger protei	NM_153813	NM_153813
3.54E+02	8.47E+00	chromosome 13	SRY (sex determi	NM_152324	NM_152324
3.61E+02	8.49E+00	ankyrin repeat d	phosphoglucomu	NM_001012419,	NM_001012419,NM_032250
3.57E+02	8.48E+00	hypothetical LOC	Rh family, C glyc	NR_015411	NR_015411
3.09E+02	8.27E+00	isoprenylcysteine	hairy and enhanc	NM_012405	NM_012405
3.09E+02	8.27E+00	isoprenylcysteine	hairy and enhanc	NM_012405	NM_012405
3.09E+02	8.27E+00	UDP-N-acetyl-alp	UDP-N-acetyl-alp	NM_021808,NM	NM_021808,NM_001122636
1.13E+00	1.79E-01	wingless-type MI	wingless-type MI	NM_003395	NM_003395
3.65E-03	-8.10E+00	PRP38 pre-mRNA	PRP38 pre-mRNA	NM_032864	NM_032864
3.65E-03	-8.10E+00	PRP38 pre-mRNA	PRP38 pre-mRNA	NM_032864	NM_032864
1.72E+00	7.82E-01	glycerophosphoc	glycerophosphoc	NM_024307	NM_024307
3.50E+02	8.45E+00	netrin 3	netrin 3	NM_006181	NM_006181
1.74E+00	8.02E-01	DIP2 disco-intera	DIP2 disco-intera	NM_014974	NM_014974
3.17E+02	8.31E+00	chromosome 8 o	chromosome 8 o	NR_026785	NR_026785
2.82E+02	8.14E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
2.82E+02	8.14E+00	protein tyrosine	protein tyrosine	NM_130842,NM	NM_130842,NM_130843,NM_002
3.79E+02	8.57E+00	cell division cycle	heat shock prote	NM_001134420	NM_001134420
3.79E+02	8.57E+00	cell division cycle	heat shock prote	NM_001134420	NM_001134420
3.70E+02	8.53E+00	Rho GTPase activ	Rho GTPase activ	NM_021226	NM_021226
2.88E+02	8.17E+00	uroplakin 1A	zinc finger and BT	NM_007000	NM_007000

2.88E+02	8.17E+00	uroplakin 1A	zinc finger and B	NM_007000	NM_007000
2.86E+02	8.16E+00	lymphocyte-spec	lymphocyte-spec	NR_027238	NR_027238
1.33E+00	4.16E-01	DnaJ (Hsp40) ho	DnaJ (Hsp40) ho	NM_001001394	NM_001001394
3.69E+02	8.53E+00	chromosome 19	BTB (POZ) domai	NM_152771	NM_152771
3.69E+02	8.53E+00	chromosome 19	BTB (POZ) domai	NM_152771	NM_152771
2.09E+00	1.06E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
2.94E+02	8.20E+00	chromosome 20	chromosome 20	NM_199181	NM_199181
3.61E+02	8.49E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
3.61E+02	8.49E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
3.61E+02	8.49E+00	ankyrin repeat d	ankyrin repeat d	NM_013275	NM_013275
1.41E+00	4.98E-01	null	rabphilin 3A-like	null	null
1.41E+00	4.98E-01	null	rabphilin 3A-like	null	null
1.33E+00	4.15E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.33E+00	4.15E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
1.33E+00	4.15E-01	POTE ankyrin do	POTE ankyrin do	NM_001005356,	NM_001005356,NR_027480
3.32E+02	8.38E+00	peroxisomal prol	peroxisomal prol	NM_001037335,	NM_001037335,NM_033405
3.32E+02	8.38E+00	peroxisomal prol	peroxisomal prol	NM_001037335,	NM_001037335,NM_033405
1.90E+00	9.27E-01	transmembrane	KIAA1671	NM_001001663	NM_001001663
1.38E+00	4.67E-01	castor zinc finger	castor zinc finger	NM_017766	NM_017766
3.21E+02	8.33E+00	calmodulin regul	calmodulin regul	NM_015447	NM_015447
3.21E+02	8.33E+00	calmodulin regul	calmodulin regul	NM_015447	NM_015447
3.40E+02	8.41E+00	notch 1	notch 1	NM_017617	NM_017617
3.40E+02	8.41E+00	notch 1	notch 1	NM_017617	NM_017617
3.40E+02	8.41E+00	notch 1	notch 1	NM_017617	NM_017617
2.75E+02	8.10E+00	protein inhibitor	protein inhibitor	NM_015897	NM_015897
2.75E+02	8.10E+00	protein inhibitor	protein inhibitor	NM_015897	NM_015897
2.75E+02	8.10E+00	protein inhibitor	protein inhibitor	NM_015897	NM_015897
2.75E+02	8.10E+00	protein inhibitor	zinc finger and B	NM_015897	NM_015897
1.15E+00	1.98E-01	X antigen family,	X antigen family,	NM_133179	NM_133179
1.15E+00	1.98E-01	X antigen family,	X antigen family,	NM_133179	NM_133179
1.15E+00	1.98E-01	X antigen family,	family with sequ	NM_133179	NM_133179
3.32E+02	8.38E+00	peroxisomal prol	peroxisomal prol	NM_001037335,	NM_001037335,NM_033405
1.60E+00	6.82E-01	family with sequ	hypothetical LOC	NM_015667	NM_015667
1.60E+00	6.82E-01	family with sequ	hypothetical LOC	NM_015667	NM_015667
3.88E+02	8.60E+00	TBC1 domain fa	TBC1 domain fa	NM_019020	NM_019020
3.88E+02	8.60E+00	TBC1 domain fa	TBC1 domain fa	NM_019020	NM_019020
4.08E-03	-7.94E+00	---	surfactant protei	NM_006926	NM_006926
1.79E+00	8.44E-01	mucin 6, oligome	mucin 2, oligome	NM_005961	NM_005961
1.79E+00	8.44E-01	mucin 6, oligome	mucin 2, oligome	NM_005961	NM_005961
1.95E+00	9.60E-01	transmembrane	transmembrane	NM_021259	NM_021259
1.16E+00	2.13E-01	otospiralin	glypican 1	NM_148961	NM_148961
3.83E+02	8.58E+00	protein phospha	protein phospha	NM_013239,NM	NM_013239,NM_199326
2.74E+02	8.10E+00	CD164 sialomuci	G protein-couple	NM_207397	NM_207397
2.77E+02	8.11E+00	agrin	agrin	NM_198576	NM_198576
3.74E-03	-8.06E+00	zinc finger protei	zinc finger protei	NM_144684	NM_144684
3.74E-03	-8.06E+00	zinc finger protei	zinc finger protei	NM_173530	NM_173530
4.37E+02	8.77E+00	anoctamin 8	anoctamin 8	NM_020959	NM_020959
1.91E+00	9.35E-01	adaptor-related	adaptor-related	NM_003938	NM_003938
4.28E+02	8.74E+00	zinc finger protei	zinc finger protei	NM_001079906	NM_001079906
3.64E+02	8.51E+00	obscurin, cytosk	obscurin, cytosk	NM_052843,NM	NM_052843,NM_001098623
2.73E+02	8.09E+00	poliovirus recept	poliovirus recept	NM_001135768,	NM_001135768,NM_001135769,N
1.88E+00	9.07E-01	connector enhan	connector enhan	NR_023345	NR_023345
2.70E+02	8.08E+00	UDP-Gal:betaGal	family with sequ	NM_080605	NM_080605
2.70E+02	8.08E+00	family with sequ	family with sequ	NM_001014980	NM_001014980
1.52E+00	6.08E-01	gap junction pro	gap junction pro	NM_001097642	NM_001097642
3.82E-03	-8.03E+00	Ras association (	aryl hydrocarbo	NM_001080521	NM_001080521
3.82E-03	-8.03E+00	Ras association (	aryl hydrocarbo	NM_001080521	NM_001080521
1.70E+00	7.69E-01	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165

1.70E+00	7.69E-01	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165
3.11E+02	8.28E+00	protein kinase D	protein kinase D	NM_016457,NM	NM_016457,NM_001079880,NM_
3.11E+02	8.28E+00	protein kinase D	protein kinase D	NM_016457,NM	NM_016457,NM_001079880,NM_
3.45E-03	-8.18E+00	chromosome 1 o	chromosome 1 o	NM_182581	NM_182581
3.45E-03	-8.18E+00	chromosome 1 o	chromosome 1 o	NM_182581	NM_182581
3.17E+02	8.31E+00	calcium activate	calcium activate	NM_138793	NM_138793
3.17E+02	8.31E+00	calcium activate	calcium activate	NM_138793	NM_138793
3.97E+02	8.63E+00	hypothetical LO	fibrosin-like 1	NR_024563	NR_024563
3.97E+02	8.63E+00	hypothetical LO	fibrosin-like 1	NR_024563	NR_024563
2.88E+02	8.17E+00	F-box and leucin	F-box and leucin	NM_024963	NM_024963
2.86E+02	8.16E+00	eukaryotic transl	eukaryotic transl	NM_001130053,	NM_001130053,NM_032378,NM_
1.43E+00	5.18E-01	BARX homeobox	BARX homeobox	NM_003658	NM_003658
1.43E+00	5.18E-01	BARX homeobox	BARX homeobox	NM_003658	NM_003658
3.30E+02	8.37E+00	intercellular adh	intercellular adh	NM_003259	NM_003259
1.29E+00	3.69E-01	chromosome 13	non-protein codi	NM_153218	NM_153218
4.09E-03	-7.93E+00	zinc finger protei	zinc finger family	NM_012256	NM_012256
1.40E+00	4.87E-01	coiled-coil domai	beta-1,4-N-acety	NM_032358,NM	NM_032358,NM_001130146
2.90E+02	8.18E+00	polypyrimidine t	polypyrimidine t	NM_002819,NM	NM_002819,NM_031990,NM_031
2.90E+02	8.18E+00	polypyrimidine t	polypyrimidine t	NM_002819,NM	NM_002819,NM_031990,NM_031
2.43E+02	7.93E+00	hypothetical LO	splicing factor, a	NR_026670	NR_026670
1.98E+00	9.83E-01	chromosome 21	non-protein codi	NM_058190	NM_058190
1.98E+00	9.83E-01	chromosome 21	non-protein codi	NM_058190	NM_058190
1.36E+00	4.45E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.36E+00	4.45E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.36E+00	4.45E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.36E+00	4.45E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.36E+00	4.45E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.36E+00	4.45E-01	chromosome 1 o	Fc fragment of Ig	NM_001013625	NM_001013625
1.69E+00	7.59E-01	chromosome 21	chromosome 21	NM_144991	NM_144991
1.29E+00	3.62E-01	Zic family memb	Zic family memb	NM_032153	NM_032153
3.46E-03	-8.18E+00	UDP glucuronos	UDP glucuronos	NM_019077	NM_019077
3.72E+02	8.54E+00	hypothetical pro	peripheral myeli	NR_026880	NR_026880
3.72E+02	8.54E+00	hypothetical pro	peripheral myeli	NR_026880	NR_026880
3.91E+02	8.61E+00	WDR45-like	RAB40B, membe	NM_019613	NM_019613
2.61E+02	8.03E+00	BAI1-associated	BAI1-associated	NM_003933	NM_003933
2.61E+02	8.03E+00	BAI1-associated	BAI1-associated	NM_003933	NM_003933
1.65E+00	7.27E-01	fibrinogen C dom	fibrinogen C dom	NM_001145106,	NM_001145106,NM_032843
1.65E+00	7.27E-01	fibrinogen C dom	fibrinogen C dom	NM_001145106,	NM_001145106,NM_032843
1.40E+00	4.85E-01	neuroligin 4, Y-li	non-protein codi	NM_014893	NM_014893
1.40E+00	4.85E-01	neuroligin 4, Y-li	non-protein codi	NM_014893	NM_014893
1.40E+00	4.85E-01	neuroligin 4, Y-li	non-protein codi	NM_014893	NM_014893
1.23E+00	3.03E-01	family with sequ	fumarylacetoace	NM_016490	NM_016490
3.33E+02	8.38E+00	calmodulin regul	calmodulin regul	NM_015447	NM_015447
2.75E+02	8.10E+00	transmembrane	proteasome (pro	NM_001097620	NM_001097620
2.75E+02	8.10E+00	transmembrane	proteasome (pro	NM_001097620	NM_001097620
4.48E+02	8.81E+00	DIRAS family, GT	DIRAS family, GT	NM_145173	NM_145173
4.48E+02	8.81E+00	DIRAS family, GT	DIRAS family, GT	NM_145173	NM_145173
3.83E+02	8.58E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.83E+02	8.58E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
3.83E+02	8.58E+00	lipase maturatio	lipase maturatio	NM_022773	NM_022773
1.78E+00	8.29E-01	active BCR-relat	active BCR-relat	NM_001159746	NM_001159746
4.07E-03	-7.94E+00	family with sequ	transmembrane	NM_001002919	NM_001002919
2.86E+02	8.16E+00	paralemmin	chromosome 19	NM_001040134,	NM_001040134,NM_002579
1.64E+00	7.14E-01	G protein pathw	G protein pathw	NM_004127,NM	NM_004127,NM_212492
1.69E+00	7.53E-01	---	zinc finger protei	NR_027050	NR_027050
1.69E+00	7.53E-01	---	zinc finger protei	NR_027050	NR_027050
2.55E+02	7.99E+00	mucin 6, oligom	mucin 2, oligom	NM_005961	NM_005961
2.55E+02	7.99E+00	mucin 2, oligom	mucin 2, oligom	NM_002457	NM_002457

1.42E+00	5.02E-01	carbohydrate (N-	carbohydrate (N-	NM_024533	NM_024533
2.51E+02	7.97E+00	GDP-mannose 4,	GDP-mannose 4,	NM_001500	NM_001500
1.78E+00	8.33E-01	heat shock 70kD	KIAA1598	NM_025015	NM_025015
1.78E+00	8.33E-01	heat shock 70kD	KIAA1598	NM_025015	NM_025015
4.38E-03	-7.83E+00	carcinoembryoni	carcinoembryoni	NM_020219,NM	NM_020219,NM_001127893
4.30E-03	-7.86E+00	small nucleolar R	chromosome 8 o	NR_002581	NR_002581
3.44E+02	8.43E+00	smoothelin-like	smoothelin-like	NM_001114974	NM_001114974
1.25E+00	3.19E-01	Fc fragment of Ig	Fc fragment of Ig	NM_003890	NM_003890
1.25E+00	3.19E-01	Fc fragment of Ig	Fc fragment of Ig	NM_003890	NM_003890
3.44E-03	-8.18E+00	signal transducer	polymerase I and	NM_213662,NM	NM_213662,NM_139276,NM_003
2.97E+02	8.22E+00	non-protein codi	collagen, type XV	NR_027498,NM_	NR_027498,NM_199175
3.70E+02	8.53E+00	zinc finger protei	zinc finger protei	NM_144631	NM_144631
3.70E+02	8.53E+00	zinc finger protei	zinc finger protei	NM_144631	NM_144631
3.09E+02	8.27E+00	MOB1, Mps One	MOB1, Mps One	NM_130807	NM_130807
3.28E+02	8.36E+00	telomerase rever	telomerase rever	NM_198253,NM	NM_198253,NM_198255
3.58E+02	8.48E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
3.58E+02	8.48E+00	GTP binding prot	GTP binding prot	NM_012227	NM_012227
3.61E+02	8.49E+00	mitogen-activate	mitogen-activate	NM_030662	NM_030662
1.71E+00	7.72E-01	solute carrier fan	solute carrier fan	NM_001636	NM_001636
1.58E+00	6.62E-01	prostaglandin I2	guanine nucleoti	NM_000960	NM_000960
3.50E+02	8.45E+00	alkaline phospha	alkaline phospha	NM_001631	NM_001631
3.12E+02	8.29E+00	vacuolar protein	vacuolar protein	NM_015378,NM	NM_015378,NM_018156
3.12E+02	8.29E+00	vacuolar protein	vacuolar protein	NM_015378,NM	NM_015378,NM_018156
3.74E+02	8.55E+00	adenomatosis pc	adenomatosis pc	NM_153360	NM_153360
1.30E+00	3.76E-01	thrombospondin	thrombospondin	NM_003247	NM_003247
3.84E+02	8.59E+00	G protein-couple	G protein-couple	NM_001083909	NM_001083909
3.01E+02	8.23E+00	twinfilin, actin-bi	protein phospha	NM_007284	NM_007284
3.89E+02	8.60E+00	obscurin-like 1	obscurin-like 1	NM_015311	NM_015311
3.11E+02	8.28E+00	lemur tyrosine ki	lemur tyrosine ki	NM_001080434	NM_001080434
3.11E+02	8.28E+00	lemur tyrosine ki	lemur tyrosine ki	NM_001080434	NM_001080434
1.87E+00	9.06E-01	adaptor-related	adaptor-related	NM_003938	NM_003938
1.87E+00	9.06E-01	adaptor-related	adaptor-related	NM_003938	NM_003938
3.54E+02	8.47E+00	protein kinase C	protein kinase C	NM_016223	NM_016223
2.35E+02	7.88E+00	arylsulfatase D	arylsulfatase D	NM_001669	NM_001669
2.35E+02	7.88E+00	arylsulfatase D	arylsulfatase D	NM_001669	NM_001669
4.18E-03	-7.90E+00	fucosyltransferas	MAK16 homolog	NM_032664	NM_032664
4.18E-03	-7.90E+00	fucosyltransferas	MAK16 homolog	NM_032664	NM_032664
2.69E+02	8.07E+00	cytospin A	adenosine A2a re	NM_015330,NM	NM_015330,NM_001145468
1.38E+00	4.62E-01	ArfGAP with SH3	ArfGAP with SH3	NM_001135191,	NM_001135191,NM_003887
1.38E+00	4.62E-01	ArfGAP with SH3	ArfGAP with SH3	NM_001135191,	NM_001135191,NM_003887
1.76E+00	8.20E-01	odz, odd Oz/ten-	odz, odd Oz/ten-	NM_001098816	NM_001098816
1.76E+00	8.20E-01	odz, odd Oz/ten-	odz, odd Oz/ten-	NM_001098816	NM_001098816
1.76E+00	8.13E-01	interleukin 3 rec	solute carrier fan	NM_002183	NM_002183
1.76E+00	8.13E-01	solute carrier fan	solute carrier fan	NM_001636	NM_001636
3.59E-03	-8.12E+00	Rho GTPase acti	ATP-binding cass	NM_004815	NM_004815
2.74E+02	8.10E+00	insulin-like grow	insulin-like grow	NM_004970,NM	NM_004970,NM_001146006,NR_
3.12E+02	8.29E+00	pim-3 oncogene	pim-3 oncogene	NM_001001852	NM_001001852
4.00E+02	8.64E+00	obscurin-like 1	obscurin-like 1	NM_015311	NM_015311
4.00E+02	8.64E+00	obscurin-like 1	obscurin-like 1	NM_015311	NM_015311
4.18E+02	8.71E+00	calmodulin bindi	calmodulin bindi	NM_015215	NM_015215
4.18E+02	8.71E+00	calmodulin bindi	calmodulin bindi	NM_015215	NM_015215
4.00E+02	8.64E+00	zinc finger protei	non-protein codi	NM_003408	NM_003408
3.22E+02	8.33E+00	ATPase, class VI,	ATPase, class VI,	NM_032189,NM	NM_032189,NM_015205
1.66E+00	7.27E-01	non-protein codi	hydroxysteroid (	NR_024129	NR_024129
1.66E+00	7.27E-01	non-protein codi	hydroxysteroid (	NR_024129	NR_024129
3.01E+02	8.23E+00	aquaporin 9	lipase, hepatic	NM_020980	NM_020980
2.70E+02	8.08E+00	BCL6 corepresso	BCL6 corepresso	NM_001123383,	NM_001123383,NM_001123384,
3.73E+02	8.54E+00	low density lipop	adrenergic, alpha	NM_002337	NM_002337

3.73E+02	8.54E+00	low density lipop	adrenergic, alpha	NM_002337	NM_002337
3.33E+02	8.38E+00	similar to hCG19	similar to hCG19	NR_026913	NR_026913
3.33E+02	8.38E+00	similar to hCG19	similar to hCG19	NR_026913	NR_026913
3.86E-03	-8.02E+00	placenta-specific	family with sequ	NM_182832	NM_182832
3.59E-03	-8.12E+00	chromosome 5 o	F-box protein 4	NM_175921	NM_175921
3.16E-03	-8.31E+00	angel homolog 1	chromosome 14	NM_015305	NM_015305
1.41E+00	5.01E-01	chorionic gonado	chorionic gonado	NM_033183	NM_033183
1.41E+00	5.01E-01	chorionic gonado	chorionic gonado	NM_033183	NM_033183
2.94E+02	8.20E+00	vesicle-associate	period homolog	NM_004781	NM_004781
2.94E+02	8.20E+00	period homolog	period homolog	NM_016831	NM_016831
2.93E+02	8.19E+00	ribosomal protei	ribosomal protei	NM_001006932,	NM_001006932,NM_021135
2.93E+02	8.19E+00	ribosomal protei	ribosomal protei	NM_001006932,	NM_001006932,NM_021135
4.08E+02	8.67E+00	STIP1 homology	STIP1 homology	NM_005861	NM_005861
4.08E+02	8.67E+00	STIP1 homology	STIP1 homology	NM_005861	NM_005861
3.32E+02	8.38E+00	rabphilin 3A-like	rabphilin 3A-like	NM_006987	NM_006987
3.32E+02	8.38E+00	rabphilin 3A-like	rabphilin 3A-like	NM_006987	NM_006987
3.08E+02	8.27E+00	zinc finger protei	zinc finger protei	NM_016535	NM_016535
3.08E+02	8.27E+00	zinc finger protei	zinc finger protei	NM_016535	NM_016535
3.08E+02	8.27E+00	zinc finger protei	zinc finger protei	NM_016535	NM_016535
2.88E+02	8.17E+00	scleraxis homolo	heat shock trans	NM_001008271,	NM_001008271,NM_001080514
3.51E-03	-8.15E+00	histocompatibilit	histocompatibilit	NM_021182	NM_021182
2.45E+02	7.94E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
2.45E+02	7.94E+00	galanin receptor	sal-like 3 (Drosop	NM_001480	NM_001480
3.00E+02	8.23E+00	glutamate recept	glutamate recept	NM_138690	NM_138690
3.00E+02	8.23E+00	glutamate recept	glutamate recept	NM_138690	NM_138690
1.84E+00	8.80E-01	ras responsive el	signal sequence	NM_001003698,	NM_001003698,NM_001003699
3.80E-03	-8.04E+00	RMI1, RecQ med	solute carrier fan	NM_024945	NM_024945
3.13E+02	8.29E+00	ATPase, H+/K+ e	G protein-couple	NM_000705	NM_000705
3.55E-03	-8.14E+00	paired box 4	staphylococcal n	NM_006193	NM_006193
3.29E+02	8.36E+00	POM121 membr	gamma-glutamyl	NR_024591	NR_024591
2.72E+02	8.09E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
2.72E+02	8.09E+00	lysine (K)-specific	lysine (K)-specific	NM_015015	NM_015015
3.42E+02	8.42E+00	small nuclear RN	small nuclear RN	NM_003086	NM_003086
3.40E+02	8.41E+00	G protein-couple	hypothetical LOC	NM_198827	NM_198827
3.40E+02	8.41E+00	G protein-couple	hypothetical LOC	NM_198827	NM_198827
1.70E+00	7.63E-01	NCK adaptor pro	NCK adaptor pro	NM_001004720	NM_001004720
1.70E+00	7.63E-01	NCK adaptor pro	NCK adaptor pro	NM_001004720	NM_001004720
4.14E-03	-7.92E+00	olfactory recepto	olfactory recepto	NM_012363	NM_012363
3.74E-03	-8.06E+00	upstream transcr	upstream transcr	NM_207005,NM	NM_207005,NM_007122
1.39E+00	4.78E-01	PR domain conta	PR domain conta	NM_022115	NM_022115
1.39E+00	4.78E-01	PR domain conta	PR domain conta	NM_022115	NM_022115
3.75E+02	8.55E+00	melanophilin	prolactin releasir	NM_001042467,	NM_001042467,NM_024101
3.93E+02	8.62E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
3.93E+02	8.62E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
3.93E+02	8.62E+00	EH-domain conta	EH-domain conta	NM_014601	NM_014601
2.66E+02	8.06E+00	GRAM domain co	GRAM domain co	NM_015124	NM_015124
2.66E+02	8.06E+00	GRAM domain co	GRAM domain co	NM_015124	NM_015124
1.60E+00	6.76E-01	nuclear receptor	nuclear receptor	NM_006312,NM	NM_006312,NM_001077261
2.78E+02	8.12E+00	family with sequ	family with sequ	NM_198549	NM_198549
2.78E+02	8.12E+00	family with sequ	family with sequ	NM_198549	NM_198549
3.79E+02	8.57E+00	adenosine deami	adenosine deami	NM_018702	NM_018702
2.63E+02	8.04E+00	EGF-like-domain,	EGF-like-domain,	NM_030652	NM_030652
2.63E+02	8.04E+00	EGF-like-domain,	EGF-like-domain,	NM_030652	NM_030652
3.16E+02	8.30E+00	zinc finger protei	zinc finger protei	NM_014643	NM_014643
3.16E+02	8.30E+00	zinc finger protei	zinc finger protei	NM_014643	NM_014643
4.14E+02	8.69E+00	null	transmembrane	null	null
2.74E+02	8.10E+00	insulin-like growt	insulin-like growt	NM_004970,NM	NM_004970,NM_001146006,NR_
4.06E-03	-7.94E+00	Janus kinase 1	adenylate kinase	NM_002227	NM_002227

1.33E+00	4.16E-01	transcription elo	transcription elo	NM_001100817,	NM_001100817,NM_145653
1.33E+00	4.16E-01	transcription elo	transcription elo	NM_001100817,	NM_001100817,NM_145653
1.33E+00	4.16E-01	transcription elo	transcription elo	NM_001100817,	NM_001100817,NM_145653
1.33E+00	4.16E-01	transcription elo	transcription elo	NM_001100817,	NM_001100817,NM_145653
1.33E+00	4.16E-01	transcription elo	transcription elo	NM_001100817,	NM_001100817,NM_145653
4.26E+02	8.73E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
4.26E+02	8.73E+00	cadherin, EGF LA	cadherin, EGF LA	NM_014246	NM_014246
2.01E+00	1.01E+00	zinc finger protei	zinc finger protei	NM_018197,NM	NM_018197,NM_199426,NM_022
2.01E+00	1.01E+00	zinc finger protei	zinc finger protei	NM_018197,NM	NM_018197,NM_199426,NM_022
1.66E+00	7.35E-01	CD7 molecule	secreted and tra	NM_006137	NM_006137
1.32E+00	4.06E-01	forkhead box L1	F-box protein 31	NM_005250	NM_005250
5.27E+02	9.04E+00	insulin-like grow	insulin-like grow	NM_000875	NM_000875
3.26E+02	8.35E+00	core-binding fact	core-binding fact	NM_175931,NM	NM_175931,NM_005187
3.26E+02	8.35E+00	core-binding fact	core-binding fact	NM_175931,NM	NM_175931,NM_005187
3.34E+02	8.38E+00	protein phospha	dynein, cytoplasn	NM_178588,NM	NM_178588,NM_178587,NM_002
1.21E+00	2.71E-01	prosaposin-like 1	AFAP1 antisense	NM_001085382	NM_001085382
1.21E+00	2.71E-01	prosaposin-like 1	AFAP1 antisense	NM_001085382	NM_001085382
1.45E+00	5.39E-01	RAB12, member	KIAA0802	NM_001025300	NM_001025300
1.45E+00	5.39E-01	RAB12, member	KIAA0802	NM_001025300	NM_001025300
2.90E+02	8.18E+00	null	phosphatidylinos	null	null
2.90E+02	8.18E+00	null	phosphatidylinos	null	null
1.39E+00	4.70E-01	TYRO protein tyr	TYRO protein tyr	NM_198125,NM	NM_198125,NM_003332
1.39E+00	4.70E-01	TYRO protein tyr	TYRO protein tyr	NM_198125,NM	NM_198125,NM_003332
1.77E+00	8.25E-01	zeta-chain (TCR)	zeta-chain (TCR)	NM_207519	NM_207519
1.82E+00	8.67E-01	NADH dehydroge	NADH dehydroge	NM_024407	NM_024407
1.82E+00	8.67E-01	NADH dehydroge	NADH dehydroge	NM_024407	NM_024407
1.82E+00	8.67E-01	NADH dehydroge	NADH dehydroge	NM_024407	NM_024407
2.93E+02	8.19E+00	solute carrier fan	hypothetical pro	NM_001080431	NM_001080431
3.26E-03	-8.26E+00	angiopoietin 1	R-spondin 2 hom	NM_001146	NM_001146
1.53E+00	6.17E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
1.53E+00	6.17E-01	BTG3 associated	zinc finger protei	NM_017869,NM	NM_017869,NM_079837
3.23E+02	8.33E+00	NK2 homeobox 8	paired box 9	NM_014360	NM_014360
2.78E+02	8.12E+00	mucin 5B, oligon	mucin 5B, oligon	NM_002458	NM_002458
2.78E+02	8.12E+00	mucin 5B, oligon	mucin 5B, oligon	NM_002458	NM_002458
1.24E+00	3.08E-01	regulatory factor	relaxin 3	NM_002918	NM_002918
1.24E+00	3.08E-01	regulatory factor	relaxin 3	NM_002918	NM_002918
2.72E+02	8.09E+00	peroxisomal biog	phospholipase C,	NM_002617,NM	NM_002617,NM_153818
2.61E+02	8.03E+00	ATPase, aminoph	ATPase, aminoph	NM_138813	NM_138813
2.61E+02	8.03E+00	ATPase, aminoph	ATPase, aminoph	NM_138813	NM_138813
1.88E+00	9.11E-01	ubiquitin-conjug	ubiquitin-conjug	NM_014501	NM_014501
2.65E+02	8.05E+00	zinc finger protei	zinc finger protei	NM_152493	NM_152493
3.64E-03	-8.10E+00	natriuretic pepti	natriuretic pepti	NM_006172	NM_006172
3.39E+02	8.40E+00	sialic acid binding	sialic acid binding	NM_003830	NM_003830
3.39E+02	8.40E+00	sialic acid binding	sialic acid binding	NM_003830	NM_003830
2.94E+02	8.20E+00	caspase 8 associ	gap junction prot	NM_001137668,	NM_001137668,NM_001137667,N
1.18E+00	2.37E-01	immunoglobulin	immunoglobulin	NM_201526	NM_201526
4.61E+02	8.85E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
2.50E+02	7.96E+00	5-hydroxytryptar	interleukin-1 rec	NM_000863	NM_000863
2.81E+02	8.13E+00	hect domain and	makorin ring fing	NR_002824	NR_002824
2.81E+02	8.13E+00	hect domain and	makorin ring fing	NR_002824	NR_002824
2.64E+02	8.05E+00	AT rich interactiv	AT rich interactiv	NM_005224	NM_005224
3.78E+02	8.56E+00	iroquois homeob	iroquois homeob	NM_016358	NM_016358
3.78E+02	8.56E+00	iroquois homeob	iroquois homeob	NM_016358	NM_016358
3.22E+02	8.33E+00	regulatory factor	regulatory factor	NM_000635,NM	NM_000635,NM_134433
2.94E+02	8.20E+00	1-acylglycerol-3-	family with sequ	NM_001012727,	NM_001012727,NM_006412
2.94E+02	8.20E+00	1-acylglycerol-3-	family with sequ	NM_001012727,	NM_001012727,NM_006412
2.91E+02	8.18E+00	prolactin releasir	prolactin releasir	NM_015893	NM_015893
2.91E+02	8.18E+00	prolactin releasir	prolactin releasir	NM_015893	NM_015893

3.28E+02	8.36E+00	solute carrier fan	solute carrier fan	NM_001003841	NM_001003841
3.25E+02	8.34E+00	scavenger recept	scavenger recept	NM_005505,NM	NM_005505,NM_001082959
3.82E-03	-8.03E+00	G protein-couple	G protein-couple	NM_015234,NM	NM_015234,NM_001098518
3.06E+02	8.26E+00	fascin homolog 1	fascin homolog 1	NM_003088	NM_003088
3.06E+02	8.26E+00	fascin homolog 1	fascin homolog 1	NM_003088	NM_003088
2.90E+02	8.18E+00	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165
2.90E+02	8.18E+00	forkhead box K1	forkhead box K1	NM_001037165	NM_001037165
3.06E+02	8.26E+00	plexin B2	plexin B2	NM_012401	NM_012401
1.10E+00	1.41E-01	potassium voltag	potassium voltag	NM_030779,NM	NM_030779,NM_173092
1.10E+00	1.41E-01	potassium voltag	potassium voltag	NM_030779,NM	NM_030779,NM_173092
3.53E+02	8.46E+00	phosphodiestera	phosphodiestera	NM_001145292	NM_001145292
3.53E+02	8.46E+00	phosphodiestera	phosphodiestera	NM_001145292	NM_001145292
3.48E+02	8.44E+00	adenosine mono	adenosine mono	NM_004037	NM_004037
3.48E+02	8.44E+00	adenosine mono	adenosine mono	NM_004037	NM_004037
3.25E+02	8.34E+00	G protein-couple	zinc finger, AN1-	NM_001098201	NM_001098201
3.05E+02	8.25E+00	v-ski sarcoma vir	v-ski sarcoma vir	NM_003036	NM_003036
3.05E+02	8.25E+00	v-ski sarcoma vir	v-ski sarcoma vir	NM_003036	NM_003036
1.60E+00	6.80E-01	tet oncogene fan	bolA homolog 3	NM_144993	NM_144993
8.52E-01	-2.31E-01	ubiquitin specific	5-hydroxytryptar	NM_020886	NM_020886
3.12E+02	8.29E+00	family with sequ	family with sequ	NM_015381	NM_015381
3.43E+02	8.42E+00	paralemmin	paralemmin	NM_001040134,	NM_001040134,NM_002579
4.23E+02	8.72E+00	mucin 5AC, oligo	mucin 5AC, oligo	NM_017511	NM_017511
8.37E-01	-2.57E-01	LIM and senesce	LIM and senesce	NM_033514,NR_	NM_033514,NR_027144,NR_0271
4.46E+02	8.80E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
4.46E+02	8.80E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
3.04E+02	8.25E+00	procollagen-lysin	procollagen-lysin	NM_001084	NM_001084
3.39E+02	8.41E+00	laminin, beta 3	laminin, beta 3	NM_001017402,	NM_001017402,NM_001127641,
3.41E+02	8.41E+00	golgin A8 family,	golgin A8 family,	NM_001023567,	NM_001023567,NR_027410
8.88E-01	-1.71E-01	RAS-like, family 1	adaptor-related	NM_006477,NM	NM_006477,NM_001007279
8.88E-01	-1.71E-01	RAS-like, family 1	adaptor-related	NM_006477,NM	NM_006477,NM_001007279
3.49E+02	8.45E+00	HEAT repeat con	scleraxis homolo	NM_032450,NM	NM_032450,NM_001099281,NM_
3.49E+02	8.45E+00	HEAT repeat con	scleraxis homolo	NM_032450,NM	NM_032450,NM_001099281,NM_
2.99E-03	-8.39E+00	cyclin Y	gap junction prot	NM_145012	NM_145012
2.99E-03	-8.39E+00	cyclin Y	gap junction prot	NM_145012	NM_145012
2.99E-03	-8.39E+00	gap junction prot	gap junction prot	NM_153368	NM_153368
1.60E+00	6.76E-01	chromosome 3 o	caveolin 3	NM_015931	NM_015931
1.60E+00	6.76E-01	caveolin 3	caveolin 3	NM_001234,NM	NM_001234,NM_033337
3.21E+02	8.33E+00	transmembrane	KIAA0125	NM_025268	NM_025268
3.21E+02	8.33E+00	transmembrane	KIAA0125	NM_025268	NM_025268
1.66E+00	7.29E-01	plexin B2	plexin B2	NM_012401	NM_012401
2.59E+02	8.02E+00	telomerase rever	telomerase rever	NM_198253,NM	NM_198253,NM_198255
3.06E+02	8.26E+00	apoptosis-associ	apoptosis-associ	NM_001080395	NM_001080395
2.61E+02	8.03E+00	phosphatidylinos	phosphatidylinos	NM_018390	NM_018390
2.61E+02	8.03E+00	phosphatidylinos	phosphatidylinos	NM_018390	NM_018390
1.80E+00	8.50E-01	v-src sarcoma (S	v-src sarcoma (S	NM_198291	NM_198291
1.80E+00	8.50E-01	v-src sarcoma (S	v-src sarcoma (S	NM_198291	NM_198291
1.90E+00	9.23E-01	zinc finger protei	zinc finger protei	NM_001007248	NM_001007248
1.90E+00	9.23E-01	zinc finger protei	zinc finger protei	NM_001007248	NM_001007248
4.71E-03	-7.73E+00	MFNG O-fucosyl	caspase recruitm	NM_002405	NM_002405
3.83E+02	8.58E+00	hexaribonucleoti	hexaribonucleoti	NM_001082575	NM_001082575
2.89E+02	8.17E+00	G protein-couple	G protein-couple	NM_001004106,	NM_001004106,NM_002082,NM_
2.89E+02	8.17E+00	G protein-couple	G protein-couple	NM_001004106,	NM_001004106,NM_002082,NM_
2.39E+02	7.90E+00	Rho GDP dissocia	Rho GDP dissocia	NM_001176	NM_001176
1.33E+00	4.11E-01	family with sequ	family with sequ	NM_031453	NM_031453
1.33E+00	4.11E-01	family with sequ	family with sequ	NM_031453	NM_031453
1.33E+00	4.11E-01	family with sequ	cerebral dopami	NM_031453	NM_031453
3.22E+02	8.33E+00	RAB11B, membe	RAB11B, membe	NM_004218	NM_004218
3.22E+02	8.33E+00	RAB11B, membe	RAB11B, membe	NM_004218	NM_004218

3.14E+02	8.29E+00	vitrin	vitrin	NM_053276	NM_053276
3.14E+02	8.29E+00	vitrin	vitrin	NM_053276	NM_053276
3.50E+02	8.45E+00	PR domain conta	PR domain conta	NM_199454,NM	NM_199454,NM_022114
3.80E+02	8.57E+00	myelin associate	myelin associate	NM_080600,NM	NM_080600,NM_002361
3.80E+02	8.57E+00	myelin associate	myelin associate	NM_080600,NM	NM_080600,NM_002361
3.80E+02	8.57E+00	myelin associate	myelin associate	NM_080600,NM	NM_080600,NM_002361
4.05E+02	8.66E+00	---	---	NR_024569	NR_024569
4.05E+02	8.66E+00	---	C-terminal bindi	NR_024569	NR_024569
3.46E+02	8.43E+00	pentraxin 4, long	pentraxin 4, long	NM_001013658	NM_001013658
1.86E+00	8.95E-01	zinc finger protei	zinc finger protei	NM_015069	NM_015069
3.26E+02	8.35E+00	activin A recepto	activin A recepto	NM_001077401	NM_001077401
3.26E+02	8.35E+00	activin A recepto	activin A recepto	NM_001077401	NM_001077401
2.65E+02	8.05E+00	interferon regula	similar to hCG16	NM_002163	NM_002163
3.03E+02	8.24E+00	UDP-N-acetyl-alp	myeloid/lymphoi	NM_022087	NM_022087
3.33E+02	8.38E+00	dynein, axonema	dynein, axonema	NM_020877	NM_020877
3.33E+02	8.38E+00	dynein, axonema	dynein, axonema	NM_020877	NM_020877
3.33E+02	8.38E+00	dynein, axonema	dynein, axonema	NM_020877	NM_020877
3.28E+02	8.36E+00	sorting nexin 8	sorting nexin 8	NM_013321	NM_013321
3.59E+02	8.49E+00	tumor necrosis f	chromosome 1 o	NM_003820	NM_003820
3.38E+02	8.40E+00	transcription fac	transcription fac	NM_001042425,	NM_001042425,NM_003220,NM_
1.45E+00	5.33E-01	WD repeat doma	F-box and leucin	NM_032259	NM_032259
1.45E+00	5.33E-01	WD repeat doma	F-box and leucin	NM_032259	NM_032259
3.67E-03	-8.09E+00	zinc finger protei	zinc finger protei	NR_003952	NR_003952
3.26E+02	8.35E+00	adenylosuccinate	adenylosuccinate	NM_152328	NM_152328
3.22E-03	-8.28E+00	nephronophthisi	potassium voltag	NM_015102	NM_015102
1.39E+00	4.74E-01	obscurin, cytosk	obscurin, cytosk	NM_052843,NM	NM_052843,NM_001098623
2.49E+02	7.96E+00	transducin (beta)	transducin (beta)	NM_006453	NM_006453
1.51E+00	5.94E-01	protamine 2	protamine 2	NM_002762	NM_002762
2.56E+02	8.00E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
2.56E+02	8.00E+00	polycystic kidney	polycystic kidney	NM_000296,NM	NM_000296,NM_001009944
4.47E+02	8.80E+00	keratin associate	keratin associate	NM_033191	NM_033191
1.88E+00	9.09E-01	hypothetical LOC	hypothetical LOC	NR_024394	NR_024394
3.39E+02	8.40E+00	lymphocyte-spec	lymphocyte-spec	NM_002339	NM_002339
3.53E-03	-8.15E+00	leucine rich repe	leucine rich repe	NM_032270	NM_032270
3.53E-03	-8.15E+00	leucine rich repe	leucine rich repe	NM_032270	NM_032270
2.88E+02	8.17E+00	SPANX family, m	SPANX family, m	NM_145665,NM	NM_145665,NM_032417
4.30E-03	-7.86E+00	damage-specific	damage-specific	NM_001923	NM_001923
1.18E+00	2.38E-01	tubulin, beta 3	tubulin, beta 3	NM_006086	NM_006086
1.18E+00	2.38E-01	tubulin, beta 3	tubulin, beta 3	NM_006086	NM_006086
1.18E+00	2.38E-01	tubulin, beta 3	tubulin, beta 3	NM_006086	NM_006086
4.49E-03	-7.80E+00	RIMS binding pro	hypermethylate	NM_001128635	NM_001128635
1.18E+00	2.36E-01	GTF2I repeat do	NOP2/Sun doma	NR_002164	NR_002164
1.18E+00	2.36E-01	GTF2I repeat do	NOP2/Sun doma	NR_002164	NR_002164
1.18E+00	2.36E-01	GTF2I repeat do	NOP2/Sun doma	NR_002164	NR_002164
3.11E+02	8.28E+00	egl nine homolo	egl nine homolo	NM_053046	NM_053046
1.43E+00	5.17E-01	zinc finger protei	zinc finger protei	NM_153813	NM_153813
1.43E+00	5.17E-01	zinc finger protei	zinc finger protei	NM_153813	NM_153813
2.33E+00	1.22E+00	kinase non-cataly	undifferentiated	NM_152643	NM_152643
1.23E+00	3.02E-01	macrophage stim	ciliary rootlet co	NR_002729	NR_002729
1.23E+00	3.02E-01	macrophage stim	ciliary rootlet co	NR_002729	NR_002729
1.23E+00	3.02E-01	macrophage stim	ciliary rootlet co	NR_002729	NR_002729
2.68E+02	8.07E+00	keratin 8	keratin 8	NM_002273	NM_002273
3.88E+02	8.60E+00	histone deacetyl	histone deacetyl	NM_006037	NM_006037
3.32E+02	8.38E+00	solute carrier fan	solute carrier fan	NM_033102	NM_033102
3.32E+02	8.38E+00	solute carrier fan	solute carrier fan	NM_033102	NM_033102
3.38E+02	8.40E+00	RGM domain fan	RGM domain fan	NM_020211	NM_020211
3.38E+02	8.40E+00	RGM domain fan	RGM domain fan	NM_020211	NM_020211
3.22E+02	8.33E+00	furin (paired basi	furin (paired basi	NM_002569	NM_002569

3.22E+02	8.33E+00	furin (paired basi	furin (paired basi	NM_002569	NM_002569
2.94E+02	8.20E+00	piwi-like 2 (Drosc	piwi-like 2 (Drosc	NM_018068	NM_018068
2.94E+02	8.20E+00	piwi-like 2 (Drosc	piwi-like 2 (Drosc	NM_001135721	NM_001135721
2.97E+02	8.22E+00	solute carrier fan	solute carrier fan	NM_004174	NM_004174
3.39E+02	8.40E+00	GDNF family rece	GDNF family rece	NM_001495	NM_001495
3.39E+02	8.40E+00	GDNF family rece	GDNF family rece	NM_001495	NM_001495
3.39E+02	8.40E+00	GDNF family rece	GDNF family rece	NM_001495	NM_001495
1.64E+00	7.18E-01	N-deacetylase/N	translocation ass	NM_022569	NM_022569
1.64E+00	7.18E-01	N-deacetylase/N	translocation ass	NM_022569	NM_022569
2.56E+02	8.00E+00	TBC1 domain fan	TBC1 domain fan	NM_019020	NM_019020
1.70E+00	7.66E-01	pericentrin	pericentrin	NM_006031	NM_006031
1.70E+00	7.66E-01	pericentrin	pericentrin	NM_006031	NM_006031
3.56E+02	8.48E+00	non-metastatic c	non-metastatic c	NM_005009	NM_005009
3.56E+02	8.48E+00	non-metastatic c	non-metastatic c	NM_005009	NM_005009
3.56E+02	8.48E+00	non-metastatic c	non-metastatic c	NM_005009	NM_005009
2.46E+02	7.94E+00	MAP kinase inter	MAP kinase inter	NM_017572,NM	NM_017572,NM_199054
2.46E+02	7.94E+00	MAP kinase inter	MAP kinase inter	NM_017572,NM	NM_017572,NM_199054
1.20E+00	2.67E-01	GRB10 interactin	GRB10 interactin	NM_022574	NM_022574
1.20E+00	2.67E-01	GRB10 interactin	GRB10 interactin	NM_022574	NM_022574
2.54E+02	7.99E+00	protamine 1	chromosome 16	NM_002761	NM_002761
3.51E-03	-8.15E+00	tetraspanin 3	NKF3 kinase fam	NM_005724,NM	NM_005724,NM_198902
3.51E-03	-8.15E+00	tetraspanin 3	NKF3 kinase fam	NM_005724,NM	NM_005724,NM_198902
1.99E+00	9.90E-01	SIX homeobox 2	S1 RNA binding d	NM_016932	NM_016932
1.99E+00	9.90E-01	SIX homeobox 2	S1 RNA binding d	NM_016932	NM_016932
4.41E+02	8.79E+00	mediator comple	mediator comple	NM_001003891,	NM_001003891,NM_015889
2.64E+02	8.04E+00	transmembrane	M-phase phosph	NM_130785,NM	NM_130785,NM_199254,NM_001
2.64E+02	8.04E+00	transmembrane	M-phase phosph	NM_130785,NM	NM_130785,NM_199254,NM_001
3.80E-03	-8.04E+00	tachykinin recept	tachykinin recept	NM_001057	NM_001057
1.58E+00	6.58E-01	microtubule-assc	microtubule-assc	NM_181509	NM_181509
2.91E+02	8.18E+00	chromosome 20	chromosome 20	NM_080825	NM_080825
3.26E+02	8.35E+00	PAP associated d	PAP associated d	NM_006999	NM_006999
3.26E+02	8.35E+00	PAP associated d	PAP associated d	NM_006999	NM_006999
3.09E+02	8.27E+00	iroquois homeot	iroquois homeot	NM_016358	NM_016358
3.99E+02	8.64E+00	ArfGAP with dua	ArfGAP with dua	NM_006869	NM_006869
1.89E+00	9.21E-01	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
1.89E+00	9.21E-01	RAS p21 protein	RAS p21 protein	NM_007368	NM_007368
3.40E+02	8.41E+00	ARP3 actin-relate	dipeptidyl-peptic	NM_005721	NM_005721
3.40E+02	8.41E+00	ARP3 actin-relate	dipeptidyl-peptic	NM_005721	NM_005721
3.40E+02	8.41E+00	ARP3 actin-relate	dipeptidyl-peptic	NM_005721	NM_005721
1.74E+00	8.00E-01	SET binding facto	SET binding facto	NM_002972	NM_002972
2.80E+02	8.13E+00	iroquois homeot	iroquois homeot	NM_016358	NM_016358
2.80E+02	8.13E+00	iroquois homeot	iroquois homeot	NM_016358	NM_016358
2.44E+02	7.93E+00	unc-5 homolog A	unc-5 homolog A	NM_133369	NM_133369
3.36E+02	8.39E+00	sidekick homolog	sidekick homolog	NM_152744	NM_152744
3.36E+02	8.39E+00	sidekick homolog	sidekick homolog	NM_152744	NM_152744
3.36E+02	8.39E+00	sidekick homolog	sidekick homolog	NM_152744	NM_152744
4.23E-03	-7.89E+00	SRY (sex determi	SRY (sex determi	NM_031439	NM_031439
3.27E+02	8.35E+00	histone deacetyl	histone deacetyl	NM_006037	NM_006037
3.51E+02	8.46E+00	ankyrin repeat do	lipase, member I	NR_027270	NR_027270
3.51E+02	8.46E+00	ankyrin repeat do	lipase, member I	NR_027270	NR_027270
4.53E-03	-7.79E+00	glycerol kinase 5	5'-3' exoribonucl	NM_001039547	NM_001039547
3.49E+02	8.45E+00	N-acetylglucosan	N-acetylglucosan	NM_032520	NM_032520
2.61E+02	8.03E+00	GNAS complex lo	GNAS complex lo	NM_016592	NM_016592
1.36E+00	4.43E-01	phospholipid scra	Zic family memb	NM_001085420	NM_001085420
3.07E+02	8.26E+00	naked cuticle hor	naked cuticle hor	NM_033120	NM_033120
3.07E+02	8.26E+00	naked cuticle hor	naked cuticle hor	NM_033120	NM_033120
3.07E+02	8.26E+00	naked cuticle hor	naked cuticle hor	NM_033120	NM_033120
3.23E+02	8.34E+00	pleckstrin homol	pleckstrin homol	NM_198850	NM_198850

3.23E+02	8.34E+00	pleckstrin homol	pleckstrin homol	NM_198850	NM_198850
2.96E+02	8.21E+00	FGFR1 oncogene	chemokine (C-C	NM_007045,NM	NM_007045,NM_194429
2.96E+02	8.21E+00	FGFR1 oncogene	chemokine (C-C	NM_007045,NM	NM_007045,NM_194429
1.77E+00	8.25E-01	gamma-glutamyl	gamma-glutamyl	NM_178026	NM_178026
1.77E+00	8.25E-01	gamma-glutamyl	gamma-glutamyl	NM_178026	NM_178026
3.87E+02	8.60E+00	dynamin 1 pseud	dynamin 1 pseud	NR_003260	NR_003260
3.44E+02	8.43E+00	mohawk homeo	mohawk homeo	NM_173576	NM_173576
3.44E+02	8.43E+00	mohawk homeo	mohawk homeo	NM_173576	NM_173576
2.51E+02	7.97E+00	MCF.2 cell line d	MCF.2 cell line d	NM_024979	NM_024979
2.49E+02	7.96E+00	DOT1-like, histor	DOT1-like, histor	NM_032482	NM_032482
2.49E+02	7.96E+00	DOT1-like, histor	DOT1-like, histor	NM_032482	NM_032482
1.79E+00	8.36E-01	programmed cell	mitochondrial ri	NR_003713	NR_003713
2.92E+02	8.19E+00	solute carrier fa	ectonucleoside t	NM_031212	NM_031212
3.35E+02	8.39E+00	amyloid beta (A4	amyloid beta (A4	NM_001130414,	NM_001130414,NM_005503
3.35E+02	8.39E+00	amyloid beta (A4	amyloid beta (A4	NM_001130414,	NM_001130414,NM_005503
3.78E+02	8.56E+00	mucin 6, oligom	mucin 6, oligom	NM_005961	NM_005961
3.00E+02	8.23E+00	coiled-coil doma	proline rich 24	NM_015603	NM_015603
3.35E+02	8.39E+00	PHD finger prote	tubulin, alpha 3c	NR_002801	NR_002801
3.01E+02	8.23E+00	coiled-coil doma	beta-1,4-N-acety	NM_032358,NM	NM_032358,NM_001130146
3.38E+02	8.40E+00	phytanoyl-CoA d	phytanoyl-CoA d	NM_001100876,	NM_001100876,NM_174933
3.38E+02	8.40E+00	phytanoyl-CoA d	phytanoyl-CoA d	NM_001100876,	NM_001100876,NM_174933
3.00E+02	8.23E+00	von Willebrand f	von Willebrand f	NM_000552	NM_000552
4.02E+02	8.65E+00	similar to cDNA s	chromosome 21	NM_001013729	NM_001013729
3.16E+02	8.30E+00	psoriasis suscept	psoriasis suscept	NM_014069	NM_014069
2.56E+02	8.00E+00	nicalin homolog	nicalin homolog	NM_020170	NM_020170
2.56E+02	8.00E+00	nicalin homolog	nicalin homolog	NM_020170	NM_020170
2.83E+02	8.15E+00	solute carrier fa	solute carrier fa	NM_152346	NM_152346
2.83E+02	8.15E+00	solute carrier fa	solute carrier fa	NM_152346	NM_152346
2.56E+02	8.00E+00	troponin T type	troponin T type	NM_001042781,	NM_001042781,NM_001042782,
4.28E+02	8.74E+00	melanoma antig	melanoma antig	NM_001098800	NM_001098800
3.28E+02	8.36E+00	phosphatidylseri	phosphatidylseri	NM_030783	NM_030783
3.28E+02	8.36E+00	phosphatidylseri	phosphatidylseri	NM_030783	NM_030783
4.06E+02	8.67E+00	zinc finger protei	zinc finger protei	NM_001130031,	NM_001130031,NM_001130032,
3.19E+02	8.32E+00	pentraxin 4, long	TEL2, telomere n	NM_001013658	NM_001013658
2.94E+02	8.20E+00	archaelysin famil	archaelysin famil	NM_133463	NM_133463
3.19E+02	8.32E+00	family with sequ	family with sequ	NM_178468	NM_178468
2.48E+02	7.95E+00	Janus kinase 2	Janus kinase 2	NM_004972	NM_004972
2.48E+02	7.95E+00	Janus kinase 2	Janus kinase 2	NM_004972	NM_004972
8.73E-01	-1.97E-01	arachidonate 12-	arachidonate 12-	NR_002710	NR_002710
1.23E+00	2.97E-01	chromosome 21	chromosome 21	NM_058190	NM_058190
1.23E+00	2.97E-01	chromosome 21	chromosome 21	NM_058190	NM_058190
3.72E-03	-8.07E+00	TAF12 RNA polyr	RNA, U11 small r	NM_005644,NM	NM_005644,NM_001135218
3.01E+02	8.23E+00	REX1, RNA exon	REX1, RNA exon	NM_020695	NM_020695
2.28E+00	1.19E+00	solute carrier fa	solute carrier fa	NM_003562	NM_003562
1.34E+00	4.21E-01	Ras association (	Ras association (	NM_170714,NM	NM_170714,NM_007182,NM_17
3.87E-03	-8.01E+00	brain expressed,	nuclear RNA exp	NM_001012978,	NM_001012978,NM_001159560
3.87E-03	-8.01E+00	nuclear RNA exp	nuclear RNA exp	NM_001099686,	NM_001099686,NM_017809
3.43E-03	-8.19E+00	cystatin 11	cystatin 11	NM_130794,NM	NM_130794,NM_080830
3.43E-03	-8.19E+00	cystatin 11	cystatin 11	NM_130794,NM	NM_130794,NM_080830
2.69E+02	8.07E+00	WNT inhibitory f	LEM domain con	NM_007191	NM_007191
2.69E+02	8.07E+00	WNT inhibitory f	LEM domain con	NM_007191	NM_007191
1.48E+00	5.61E-01	SAM pointed do	chromosome 6 o	NM_012391	NM_012391
1.48E+00	5.61E-01	SAM pointed do	chromosome 6 o	NM_012391	NM_012391
3.46E+02	8.43E+00	hexamthylene bi	hexamthylene bi	NM_144608	NM_144608
3.46E+02	8.43E+00	hexamthylene bi	hexamthylene bi	NM_144608	NM_144608
3.14E+02	8.29E+00	chromosome 9 o	chromosome 9 o	NM_032823	NM_032823
3.14E+02	8.29E+00	chromosome 9 o	chromosome 9 o	NM_032823	NM_032823
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