

Supplementary Table S2

sn	CHR	SNP	Gene ID	C	A1	MAF	A1A1	A1A2
665	2	chr2:148672817	ACVR2A	T	G	0.005556	0	1
2899	12	chr12:43846296	ADAMTS20	T	G	0.005556	0	1
1154	4	chr4:87967279	AFF1	C	A	0.005556	0	1
1155	4	chr4:87967936	AFF1	T	C	0.005556	0	1
1912	7	chr7:91631234	AKAP9	C	A	0.005556	0	1
1915	7	chr7:91641671	AKAP9	TGC	CAA	0.005556	0	1
1919	7	chr7:91670064	AKAP9	C	T	0.005556	0	1
1921	7	chr7:91672096	AKAP9	G	T	0.005556	0	1
1923	7	chr7:91699372	AKAP9	A	-	0.005556	0	1
1927	7	chr7:91709156	AKAP9	G	T	0.005556	0	1
1929	7	chr7:91712728	AKAP9	A	C	0.005556	0	1
3951	19	chr19:40741244	AKT2	A	G	0.005556	0	1
486	1	chr1:243727211	AKT3	-	T	0.005556	0	1
520	2	chr2:29498305	ALK	-	A	0.005556	0	1
1299	5	chr5:112164622	APC	A	G	0.005556	0	1
1300	5	chr5:112164623	APC	-	T	0.005556	0	1
1303	5	chr5:112173971	APC	TA	GT	0.005556	0	1
1307	5	chr5:112175208	APC	-	A	0.005556	0	1
1316	5	chr5:112175611	APC	-	ACCACCTC	0.005556	0	1
4226	23	chrX:66943601	AR	-	A	0.088	4	0
62	1	chr1:27092820	ARID1A	-	A	0.005556	0	1
63	1	chr1:27092822	ARID1A	T	A	0.005556	0	1
64	1	chr1:27097699	ARID1A	A	T	0.02222	1	2
65	1	chr1:27099010	ARID1A	-	G	0.01111	1	0
70	1	chr1:27106343	ARID1A	T	C	0.005556	0	1
2915	12	chr12:46285667	ARID2	C	A	0.005556	0	1
312	1	chr1:150808978	ARNT	A	G	0.005556	0	1
2814	11	chr11:108117897	ATM	TTA	ATT	0.005556	0	1
2833	11	chr11:108175596	ATM	G	T	0.005556	0	1
2835	11	chr11:108201010	ATM	C	T	0.005556	0	1
979	3	chr3:142176618	ATR	-	T	0.005556	0	1
980	3	chr3:142176649	ATR	A	C	0.005556	0	1
982	3	chr3:142186845	ATR	-	T	0.005556	0	1
991	3	chr3:142269112	ATR	G	C	0.005556	0	1
994	3	chr3:142272647	ATR	A	T	0.01111	0	2
995	3	chr3:142274652	ATR	A	C	0.005556	0	1
4236	23	chrX:76849165	ATRX	T	C	0.008	0	1
4046	20	chr20:54959349	AURKA	T	-	0.005556	0	1
3586	17	chr17:8109871	AURKB	C	T	0.005556	0	1
3999	19	chr19:57744792	AURKC	T	C	0.005556	0	1
1601	6	chr6:69349192	BAI3	A	G	0.005556	0	1
1615	6	chr6:70071243	BAI3	G	A	0.005556	0	1
111	1	chr1:85733370	BCL10	C	A	0.005556	0	1
113	1	chr1:85736596	BCL10	T	G	0.005556	0	1
558	2	chr2:60773062	BCL11A	G	A	0.005556	0	1

1030	3	chr3:187447019	BCL6	A	G	0.005556 0	1
293	1	chr1:147090697	BCL9	T	C	0.005556 0	1
298	1	chr1:147094034	BCL9	T	A	0.005556 0	1
2793	11	chr11:102195293	BIRC3	C	A	0.005556 0	1
2795	11	chr11:102195716	BIRC3	T	G	0.005556 0	1
2796	11	chr11:102201890	BIRC3	C	T	0.005556 0	1
2797	11	chr11:102207645	BIRC3	A	C	0.01111 0	2
2798	11	chr11:102207653	BIRC3	C	A	0.005556 0	1
3719	17	chr17:76210389	BIRC5	A	G	0.005556 0	1
3722	17	chr17:76219645	BIRC5	T	C	0.02778 0	5
3291	15	chr15:91304145	BLM	T	A	0.01111 0	2
3299	15	chr15:91347493	BLM	A	C	0.005556 0	1
2657	10	chr10:97975168	BLNK	-	TA	0.03333 0	6
3691	17	chr17:59760648	BRIP1	C	T	0.005556 0	1
3697	17	chr17:59858190	BRIP1	T	G	0.005556 0	1
3698	17	chr17:59861596	BRIP1	A	T	0.005556 0	1
1855	7	chr7:2968269	CARD11	C	T	0.005556 0	1
3230	15	chr15:40913884	CASC5	T	G	0.005556 0	1
3244	15	chr15:40949531	CASC5	-	TTTT	0.005556 0	1
2849	11	chr11:119145464	CBL	-	TT	0.005556 0	1
391	1	chr1:193110968	CDC73	G	A	0.005556 0	1
393	1	chr1:193111251	CDC73	A	G	0.005556 0	1
3462	16	chr16:68844081	CDH1	T	C	0.005556 0	1
3448	16	chr16:65026991	CDH11	G	T	0.005556 0	1
3801	18	chr18:25589869	CDH2	A	G	0.005556 0	1
3804	18	chr18:25593716	CDH2	A	C	0.005556 0	1
3857	18	chr18:59221876	CDH20	A	G	0.02778 0	5
3617	17	chr17:37627782	CDK12	G	T	0.005556 0	1
2960	12	chr12:58143112	CDK4	-	AGG	0.005556 0	1
2403	9	chr9:21994158	CDKN2A	C	T	0.005556 0	1
3961	19	chr19:42791062	CIC	T	C	0.005556 0	1
3965	19	chr19:42798455	CIC	G	A	0.005556 0	1
3689	17	chr17:48277061	COL1A1	-	CCCCAGGC	0.01667 1	1
763	3	chr3:3194271	CRBN	C	A	0.005556 0	1
766	3	chr3:3197988	CRBN	G	C	0.005556 0	1
3360	16	chr16:3843610	CREBBP	G	T	0.005556 0	1
2291	8	chr8:113254080	CSMD3	-	CACACACG	0.01111 0	2
2296	8	chr8:113301795	CSMD3	TTA	ATT	0.005556 0	1
2302	8	chr8:113323397	CSMD3	G	T	0.005556 0	1
2311	8	chr8:113516216	CSMD3	G	A	0.01667 0	3
2313	8	chr8:113568949	CSMD3	G	T	0.005556 0	1
1340	5	chr5:138266523	CTNNA1	G	A	0.005556 0	1
1343	5	chr5:138269717	CTNNA1	-	AGA	0.005556 0	1
853	3	chr3:41267196	CTNNB1	A	C	0.005556 0	1
2651	10	chr10:96541627	CYP2C19	G	A	0.005556 0	1
4176	22	chr22:42524893	CYP2D6	T	C	0.005556 0	1
3830	18	chr18:50451642	DCC	G	T	0.005556 0	1

3831	18	chr18:50451662	DCC	C	G	0.005556 0	1
3844	18	chr18:50942526	DCC	T	G	0.005556 0	1
3845	18	chr18:50976845	DCC	C	A	0.005556 0	1
341	1	chr1:162737153	DDR2	T	A	0.01111 0	2
343	1	chr1:162740326	DDR2	CG	GT	0.01111 0	2
349	1	chr1:162748385	DDR2	T	G	0.005556 0	1
3153	14	chr14:95569893	DICER1	A	G	0.005556 0	1
499	2	chr2:25457148	DNMT3A	G	T	0.005556 0	1
506	2	chr2:25523013	DNMT3A	A	G	0.005556 0	1
119	1	chr1:97564040	DPYD	G	T	0.005556 0	1
128	1	chr1:98144767	DPYD	T	A	0.005556 0	1
133	1	chr1:98206046	DPYD	C	A	0.005556 0	1
135	1	chr1:98386487	DPYD	A	C	0.005556 0	1
1548	6	chr6:56341107	DST	A	T	0.08889 0	16
1549	6	chr6:56347533	DST	C	A	0.005556 0	1
1550	6	chr6:56350158	DST	C	A	0.005556 0	1
1562	6	chr6:56417148	DST	G	T	0.005556 0	1
1566	6	chr6:56417448	DST	C	A	0.005556 0	1
1588	6	chr6:56485091	DST	-	AAA	0.01111 1	0
1590	6	chr6:56485266	DST	C	G	0.005556 0	1
1593	6	chr6:56489467	DST	-	TTACTC	0.005556 0	1
4153	22	chr22:41542838	EP300	-	T	0.03333 3	0
4157	22	chr22:41550944	EP300	A	T	0.005556 0	1
2992	12	chr12:132466141	EP400	A	G	0.005556 0	1
2996	12	chr12:132490800	EP400	A	G	0.005556 0	1
2997	12	chr12:132497625	EP400	T	C	0.005556 0	1
3004	12	chr12:132529321	EP400	C	A	0.005556 0	1
3008	12	chr12:132535176	EP400	G	A	0.005556 0	1
3014	12	chr12:132562069	EP400	C	A	0.01111 1	0
942	3	chr3:89448462	EPHA3	C	T	0.005556 0	1
944	3	chr3:89462276	EPHA3	C	T	0.005556 0	1
945	3	chr3:89462294	EPHA3	C	A	0.005556 0	1
1626	6	chr6:93968004	EPHA7	C	T	0.05556 3	4
1627	6	chr6:93973530	EPHA7	G	T	0.005556 0	1
1634	6	chr6:94128960	EPHA7	C	T	0.005556 0	1
964	3	chr3:134885838	EPHB1	T	C	0.005556 0	1
3627	17	chr17:37868327	ERBB2	A	G	0.005556 0	1
3629	17	chr17:37868741	ERBB2	C	G	0.005556 0	1
3636	17	chr17:37883680	ERBB2	T	C	0.005556 0	1
2948	12	chr12:56479046	ERBB3	T	C	0.005556 0	1
700	2	chr2:212248634	ERBB4	T	G	0.005556 0	1
704	2	chr2:212495163	ERBB4	T	G	0.005556 0	1
709	2	chr2:212989451	ERBB4	T	G	0.005556 0	1
4068	21	chr21:39817470	ERG	C	T	0.01111 1	0
1878	7	chr7:13950941	ETV1	T	G	0.005556 0	1
3645	17	chr17:41610590	ETV4	G	C	0.005556 0	1
2329	8	chr8:118825146	EXT1	A	T	0.005556 0	1

2333	8	chr8:119122431	EXT1	A	G	0.005556 0	1
2746	11	chr11:44228576	EXT2	-	A	0.005556 0	1
2088	7	chr7:148523504	EZH2	A	T	0.01667 0	3
4218	23	chrX:63411640	FAM123B	ATAGAACT	-	0.008 0	1
3505	16	chr16:89857743	FANCA	C	G	0.005556 0	1
3516	16	chr16:89877320	FANCA	A	C	0.005556 0	1
780	3	chr3:10088295	FANCD2	G	A	0.005556 0	1
791	3	chr3:10132031	FANCD2	-	A	0.01111 0	2
3895	19	chr19:8146019	FBN3	G	T	0.01111 1	0
1196	4	chr4:153244077	FBXW7	A	C	0.005556 0	1
2165	8	chr8:38272357	FGFR1	A	T	0.04444 0	8
2688	10	chr10:123246886	FGFR2	C	T	0.005556 0	1
1065	4	chr4:1803326	FGFR3	-	C	0.005556 0	1
1073	4	chr4:1807545	FGFR3	-	C	0.01111 0	2
1377	5	chr5:176520463	FGFR4	A	G	0.005556 0	1
3021	13	chr13:28597449	FLT3	-	CT	0.02222 2	0
1403	5	chr5:180035995	FLT4	G	C	0.005556 0	1
712	2	chr2:216232553	FN1	G	A	0.005556 0	1
717	2	chr2:216237084	FN1	C	G	0.005556 0	1
737	2	chr2:216272993	FN1	A	C	0.005556 0	1
3051	13	chr13:41134840	FOXO1	C	A	0.005556 0	1
1642	6	chr6:108985258	FOXO3	G	A	0.005556 0	1
936	3	chr3:71179709	FOXP1	C	-	0.005556 0	1
1471	6	chr6:41559050	FOXP4	T	C	0.005556 0	1
3885	19	chr19:3531825	FZR1	G	C	0.005556 0	1
955	3	chr3:128202760	GATA2	C	G	0.03889 1	5
4052	20	chr20:57428437	GNAS	G	C	0.1222 0	22
2162	8	chr8:37691418	GPR124	A	C	0.005556 0	1
489	2	chr2:11751005	GREB1	T	G	0.01111 1	0
2803	11	chr11:106579288	GUCY1A2	A	G	0.005556 0	1
2189	8	chr8:42868456	HOOK3	-	TTTTTT	0.005556 0	1
3167	14	chr14:102548088	HSP90AA1	G	T	0.005556 0	1
3170	14	chr14:102548797	HSP90AA1	C	G	0.005556 0	1
3286	15	chr15:90628243	IDH2	A	C	0.005556 0	1
3305	15	chr15:99250742	IGF1R	C	A	0.005556 0	1
3313	15	chr15:99460151	IGF1R	T	G	0.005556 0	1
1809	6	chr6:160412166	IGF2R	T	A	0.01111 0	2
1819	6	chr6:160491086	IGF2R	G	A	0.005556 0	1
2184	8	chr8:42175297	IKBKB	C	T	0.005556 0	1
426	1	chr1:206647652	IKBKE	T	A	0.005556 0	1
1266	5	chr5:55237092	IL6ST	C	A	0.005556 0	1
1267	5	chr5:55237596	IL6ST	A	C	0.005556 0	1
1269	5	chr5:55247262	IL6ST	-	GAAA	0.005556 0	1
1273	5	chr5:55256341	IL6ST	T	C	0.005556 0	1
1277	5	chr5:55264283	IL6ST	G	T	0.005556 0	1
1422	6	chr6:397155	IRF4	T	C	0.005556 0	1
3073	13	chr13:110434840	IRS2	T	C	0.005556 0	1

279	1	chr1:145528319	ITGA10	T	G	0.005556 0	1
280	1	chr1:145528348	ITGA10	A	G	0.005556 0	1
282	1	chr1:145530939	ITGA10	T	C	0.02222 0	4
286	1	chr1:145533894	ITGA10	-	C	0.01667 0	3
838	3	chr3:37567515	ITGA9	C	A	0.005556 0	1
848	3	chr3:37791907	ITGA9	A	C	0.005556 0	1
4083	21	chr21:46327067	ITGB2	A	-	0.02222 2	0
3651	17	chr17:45360865	ITGB3	A	C	0.005556 0	1
3652	17	chr17:45361773	ITGB3	T	G	0.005556 0	1
3662	17	chr17:45377857	ITGB3	C	T	0.005556 0	1
3663	17	chr17:45377881	ITGB3	A	C	0.005556 0	1
2368	9	chr9:5081778	JAK2	TA	CT	0.01111 1	0
2370	9	chr9:5090443	JAK2	G	A	0.005556 0	1
2171	8	chr8:41791041	KAT6A	A	-	0.01111 1	0
2615	10	chr10:76735416	KAT6B	-	T	0.06667 1	10
2617	10	chr10:76736004	KAT6B	C	T	0.005556 0	1
2618	10	chr10:76744954	KAT6B	-	A	0.005556 0	1
2619	10	chr10:76744958	KAT6B	T	A	0.005556 0	1
2620	10	chr10:76744965	KAT6B	G	A	0.01111 0	2
4214	23	chrX:53245059	KDM5C	T	C	0 0	0
4205	23	chrX:44942869	KDM6A	C	T	0.008 0	1
1122	4	chr4:55953747	KDR	-	CG	0.03333 3	0
1126	4	chr4:55970908	KDR	G	T	0.005556 0	1
1130	4	chr4:55980293	KDR	A	C	0.005556 0	1
1131	4	chr4:55981509	KDR	T	-	0.005556 0	1
3901	19	chr19:10600522	KEAP1	A	G	0.005556 0	1
2561	10	chr10:3824270	KLF6	C	T	0.005556 0	1
2879	12	chr12:25398279	KRAS	CGC	-	0.005556 0	1
1249	5	chr5:38481879	LIFR	G	T	0.005556 0	1
1250	5	chr5:38482324	LIFR	T	G	0.005556 0	1
1252	5	chr5:38486091	LIFR	T	A	0.005556 0	1
1256	5	chr5:38499715	LIFR	A	G	0.005556 0	1
1258	5	chr5:38502822	LIFR	C	G	0.005556 0	1
1137	4	chr4:62599099	LPHN3	G	A	0.005556 0	1
1150	4	chr4:62897317	LPHN3	A	C	0.005556 0	1
597	2	chr2:141079482	LRP1B	G	T	0.005556 0	1
606	2	chr2:141202026	LRP1B	CA	AT	0.07778 7	0
607	2	chr2:141214069	LRP1B	G	C	0.005556 0	1
609	2	chr2:141232924	LRP1B	C	T	0.005556 0	1
624	2	chr2:141299350	LRP1B	T	C	0.005556 0	1
633	2	chr2:141598592	LRP1B	C	A	0.005556 0	1
637	2	chr2:141607906	LRP1B	T	A	0.005556 0	1
640	2	chr2:141680645	LRP1B	C	A	0.005556 0	1
652	2	chr2:141819743	LRP1B	T	C	0.005556 0	1
655	2	chr2:141986696	LRP1B	A	G	0.005556 0	1
656	2	chr2:142004935	LRP1B	C	A	0.005556 0	1
661	2	chr2:142888193	LRP1B	TA	GG	0.005556 0	1

881	3	chr3:46501310	LTF	A	C	0.005556 0	1
920	3	chr3:65376926	MAGI1	T	C	0.005556 0	1
2785	11	chr11:95724845	MAML2	C	T	0.005556 0	1
2790	11	chr11:95826226	MAML2	A	G	0.005556 0	1
2791	11	chr11:95826390	MAML2	A	G	0.005556 0	1
3270	15	chr15:66782073	MAP2K1	T	C	0.005556 0	1
441	1	chr1:220808683	MARK1	GC	TT	0.01111 0	2
3976	19	chr19:45805895	MARK4	A	T	0.005556 0	1
3807	18	chr18:47793930	MBD1	G	A	0.03333 0	6
3813	18	chr18:47801260	MBD1	C	A	0.01111 1	0
300	1	chr1:150550722	MCL1	G	A	0.005556 0	1
2755	11	chr11:64572073	MEN1	A	G	0.005556 0	1
2021	7	chr7:116339867	MET	G	T	0.005556 0	1
2025	7	chr7:116397717	MET	G	C	0.06111 0	11
929	3	chr3:69985829	MITF	C	T	0.005556 0	1
932	3	chr3:70000910	MITF	G	T	0.005556 0	1
833	3	chr3:37090047	MLH1	A	T	0.005556 0	1
2844	11	chr11:118376178	MLL	T	G	0.005556 0	1
2846	11	chr11:118390491	MLL	A	G	0.005556 0	1
2931	12	chr12:49433170	MLL2	C	-	0.01111 1	0
2096	7	chr7:151859655	MLL3	A	G	0.005556 0	1
2107	7	chr7:151879244	MLL3	-	T	0.04444 4	0
2112	7	chr7:151902163	MLL3	T	A	0.01111 1	0
2113	7	chr7:151902164	MLL3	T	A	0.005556 0	1
2114	7	chr7:151902167	MLL3	-	TT	0.005556 0	1
2117	7	chr7:151947941	MLL3	T	C	0.005556 0	1
2127	7	chr7:151971024	MLL3	A	G	0.005556 0	1
2567	10	chr10:21901248	MLLT10	T	-	0.01667 0	3
2568	10	chr10:21901253	MLLT10	T	G	0.01667 0	3
2572	10	chr10:22022026	MLLT10	T	A	0.005556 0	1
76	1	chr1:43803502	MPL	T	C	0.005556 0	1
82	1	chr1:43818486	MPL	T	C	0.005556 0	1
2781	11	chr11:94224026	MRE11A	G	T	0.005556 0	1
538	2	chr2:47639586	MSH2	T	A	0.005556 0	1
540	2	chr2:47641570	MSH2	G	A	0.005556 0	1
542	2	chr2:47643502	MSH2	C	A	0.02222 1	2
548	2	chr2:47705460	MSH2	-	ACTTCT	0.005556 0	1
35	1	chr1:11167502	MTOR	C	A	0.005556 0	1
457	1	chr1:236966821	MTR	TT	GG	0.02778 0	5
466	1	chr1:237016242	MTR	A	C	0.005556 0	1
469	1	chr1:237038012	MTR	T	A	0.005556 0	1
475	1	chr1:237058719	MTR	G	A	0.005556 0	1
322	1	chr1:155160052	MUC1	GAC	ACT	0.01111 1	0
325	1	chr1:155160768	MUC1	G	A	0.005556 0	1
92	1	chr1:45799181	MUTYH	T	G	0.01111 1	0
2338	8	chr8:128753001	MYC	TGA	-	0.01111 1	0
2340	8	chr8:128753260	MYC	T	G	0.005556 0	1

75	1	chr1:40363605	MYCL1	A	C	0.005556 0	1
490	2	chr2:16086048	MYCN	A	G	0.005556 0	1
3376	16	chr16:15808865	MYH11	G	A	0.005556 0	1
3391	16	chr16:15826573	MYH11	A	G	0.005556 0	1
4122	22	chr22:36690119	MYH9	CC	GT	0.005556 0	1
2225	8	chr8:71041018	NCOA2	A	C	0.005556 0	1
2226	8	chr8:71041202	NCOA2	C	T	0.005556 0	1
2231	8	chr8:71075661	NCOA2	G	A	0.005556 0	1
2232	8	chr8:71075779	NCOA2	C	G	0.01111 1	0
2234	8	chr8:71128917	NCOA2	G	A	0.005556 0	1
2593	10	chr10:51584910	NCOA4	A	G	0.01111 0	2
2595	10	chr10:51586458	NCOA4	ATAT	-	0.005556 0	1
3599	17	chr17:29527684	NF1	A	G	0.005556 0	1
3604	17	chr17:29563074	NF1	TTG	-	0.01111 0	2
3615	17	chr17:29684016	NF1	G	T	0.005556 0	1
670	2	chr2:178096253	NFE2L2	G	A	0.005556 0	1
1176	4	chr4:103533242	NFKB1	G	T	0.005556 0	1
1177	4	chr4:103533291	NFKB1	A	C	0.005556 0	1
1178	4	chr4:103533656	NFKB1	A	C	0.005556 0	1
1180	4	chr4:103537741	NFKB1	T	G	0.005556 0	1
2663	10	chr10:104156192	NFKB2	A	C	0.005556 0	1
3091	14	chr14:51221316	NIN	G	C	0.01111 1	0
3097	14	chr14:51225320	NIN	C	T	0.005556 0	1
3546	17	chr17:5487204	NLRP1	A	T	0.005556 0	1
147	1	chr1:120477935	NOTCH2	A	G	0.005556 0	1
159	1	chr1:120539655	NOTCH2	C	G	0.005556 0	1
1438	6	chr6:32164107	NOTCH4	A	G	0.005556 0	1
1442	6	chr6:32166734	NOTCH4	A	G	0.005556 0	1
1384	5	chr5:176637204	NSD1	C	T	0.01111 0	2
328	1	chr1:156811985	NTRK1	C	G	0.005556 0	1
329	1	chr1:156841496	NTRK1	A	G	0.005556 0	1
3280	15	chr15:88669573	NTRK3	A	G	0.005556 0	1
2506	9	chr9:134090676	NUP214	G	A	0.01111 1	0
2714	11	chr11:3794852	NUP98	A	T	0.005556 0	1
4245	23	chrX:110463549	PAK3	T	G	0 0	0
2430	9	chr9:37006542	PAX5	A	C	0.005556 0	1
57	1	chr1:19018422	PAX7	T	C	0.005556 0	1
901	3	chr3:52610602	PBRM1	C	A	0.005556 0	1
902	3	chr3:52610619	PBRM1	G	A	0.005556 0	1
161	1	chr1:144852315	PDE4DIP	T	C	0.04444 1	6
181	1	chr1:144859929	PDE4DIP	T	C	0.02778 0	5
182	1	chr1:144863360	PDE4DIP	C	T	0.02222 0	4
183	1	chr1:144863366	PDE4DIP	A	G	0.005556 0	1
184	1	chr1:144863384	PDE4DIP	A	C	0.005556 0	1
185	1	chr1:144863388	PDE4DIP	TT	GA	0.005556 0	1
192	1	chr1:144866660	PDE4DIP	T	G	0.005556 0	1
194	1	chr1:144866673	PDE4DIP	A	G	0.01111 0	2

208	1	chr1:144879054	PDE4DIP	C	T	0.02222 0	4
209	1	chr1:144879086	PDE4DIP	-	T	0.005556 0	1
216	1	chr1:144881463	PDE4DIP	T	C	0.02778 0	5
217	1	chr1:144881547	PDE4DIP	A	G	0.05 0	9
225	1	chr1:144886092	PDE4DIP	T	C	0.3667 0	66
227	1	chr1:144886267	PDE4DIP	T	G	0.02222 0	4
246	1	chr1:144923712	PDE4DIP	C	T	0.005556 0	1
247	1	chr1:144930571	PDE4DIP	A	C	0.4222 0	76
250	1	chr1:144930977	PDE4DIP	C	A	0.01111 0	2
255	1	chr1:144931423	PDE4DIP	C	T	0.005556 0	1
259	1	chr1:144994617	PDE4DIP	T	C	0.01667 0	3
261	1	chr1:144994670	PDE4DIP	A	C	0.03333 0	6
262	1	chr1:144994694	PDE4DIP	C	T	0.005556 0	1
1095	4	chr4:55129892	PDGFRA	C	T	0.01111 1	0
1096	4	chr4:55129894	PDGFRA	G	A	0.02222 2	0
1360	5	chr5:149499530	PDGFRB	T	A	0.1111 0	20
1366	5	chr5:149514424	PDGFRB	A	C	0.005556 0	1
3571	17	chr17:8045566	PER1	GC	AA	0.005556 0	1
418	1	chr1:204438894	PIK3C2B	G	A	0.005556 0	1
1012	3	chr3:178916986	PIK3CA	A	C	0.005556 0	1
1014	3	chr3:178922273	PIK3CA	AA	CC	0.005556 0	1
975	3	chr3:138461524	PIK3CB	G	A	0.005556 0	1
2019	7	chr7:106545513	PIK3CG	G	A	0.005556 0	1
1281	5	chr5:67522726	PIK3R1	T	G	0.005556 0	1
1286	5	chr5:67590496	PIK3R1	T	G	0.005556 0	1
1487	6	chr6:51524653	PKHD1	T	A	0.005556 0	1
1490	6	chr6:51613058	PKHD1	T	G	0.005556 0	1
1508	6	chr6:51889459	PKHD1	A	T	0.005556 0	1
1513	6	chr6:51890498	PKHD1	A	C	0.005556 0	1
1527	6	chr6:51921815	PKHD1	GCCTT	-	0.02222 2	0
1528	6	chr6:51923126	PKHD1	T	C	0.005556 0	1
677	2	chr2:190719333	PMS1	C	A	0.005556 0	1
678	2	chr2:190719788	PMS1	A	G	0.005556 0	1
1866	7	chr7:6027040	PMS2	C	A	0.005556 0	1
1867	7	chr7:6029511	PMS2	T	A	0.01111 0	2
1868	7	chr7:6035156	PMS2	G	T	0.005556 0	1
2033	7	chr7:124475481	POT1	G	T	0.005556 0	1
3704	17	chr17:66511530	PRKAR1A	G	C	0.01111 1	0
2190	8	chr8:48686929	PRKDC	C	T	0.005556 0	1
2199	8	chr8:48736499	PRKDC	G	C	0.005556 0	1
2205	8	chr8:48776046	PRKDC	G	A	0.005556 0	1
2212	8	chr8:48825021	PRKDC	C	G	0.005556 0	1
2213	8	chr8:48828031	PRKDC	C	A	0.005556 0	1
2453	9	chr9:98212211	PTCH1	T	G	0.005556 0	1
2467	9	chr9:98241253	PTCH1	C	T	0.005556 0	1
388	1	chr1:186646996	PTGS2	A	C	0.005556 0	1
389	1	chr1:186647541	PTGS2	C	A	0.005556 0	1

2971	12	chr12:112910806	PTPN11	A	-	0.005556 0	1
2382	9	chr9:8460647	PTPRD	-	A	0.01111 1	0
2390	9	chr9:8485904	PTPRD	T	A	0.005556 0	1
2391	9	chr9:8485984	PTPRD	T	C	0.005556 0	1
4030	20	chr20:40743814	PTPRT	G	T	0.01111 1	0
1330	5	chr5:131924445	RAD50	A	C	0.005556 0	1
804	3	chr3:12626400	RAF1	T	C	0.005556 0	1
805	3	chr3:12626737	RAF1	A	G	0.005556 0	1
808	3	chr3:12641349	RAF1	GG	AA	0.005556 0	1
2519	9	chr9:135981338	RALGDS	T	C	0.005556 0	1
3638	17	chr17:38504723	RARA	C	T	0.005556 0	1
2342	8	chr8:145737307	RECQL4	A	G	0.005556 0	1
563	2	chr2:61147771	REL	-	A	0.01111 0	2
564	2	chr2:61147775	REL	G	A	0.01111 0	2
362	1	chr1:185056670	RNF2	G	T	0.01111 0	2
363	1	chr1:185067185	RNF2	-	T	0.005556 0	1
3728	17	chr17:78262057	RNF213	T	A	0.005556 0	1
3730	17	chr17:78264358	RNF213	G	T	0.005556 0	1
3734	17	chr17:78268717	RNF213	T	A	0.005556 0	1
3754	17	chr17:78319102	RNF213	T	C	0.005556 0	1
3777	17	chr17:78351613	RNF213	T	A	0.01111 0	2
3782	17	chr17:78357518	RNF213	C	-	0.005556 0	1
1656	6	chr6:117710658	ROS1	G	T	0.005556 0	1
1838	6	chr6:166952128	RPS6KA2	T	C	0.005556 0	1
2246	8	chr8:92972668	RUNX1T1	C	G	0.01111 1	0
2248	8	chr8:93026955	RUNX1T1	A	G	0.005556 0	1
2249	8	chr8:93029480	RUNX1T1	A	C	0.005556 0	1
1209	5	chr5:233504	SDHA	C	T	0.01667 0	3
887	3	chr3:47155487	SETD2	A	G	0.005556 0	1
892	3	chr3:47163994	SETD2	G	A	0.005556 0	1
682	2	chr2:198262720	SF3B1	G	T	0.005556 0	1
1674	6	chr6:134498787	SGK1	T	C	0.005556 0	1
1675	6	chr6:134528524	SGK1	A	G	0.005556 0	1
3818	18	chr18:48575204	SMAD4	T	A	0.005556 0	1
3824	18	chr18:48593440	SMAD4	C	T	0.005556 0	1
3921	19	chr19:11170500	SMARCA4	T	C	0.005556 0	1
4101	22	chr22:24145672	SMARCB1	C	-	0.03333 3	0
4106	22	chr22:24167632	SMARCB1	C	T	0.03333 0	6
487	2	chr2:5833816	SOX11	T	-	0.01111 1	0
1021	3	chr3:181430876	SOX2	C	T	0.005556 0	1
4010	20	chr20:36031361	SRC	T	C	0.005556 0	1
4011	20	chr20:36031767	SRC	G	C	0.01111 0	2
746	2	chr2:219544800	STK36	T	C	0.005556 0	1
2675	10	chr10:104357022	SUFU	T	C	0.005556 0	1
2433	9	chr9:93606313	SYK	A	C	0.005556 0	1
1703	6	chr6:152457915	SYNE1	T	G	0.005556 0	1
1712	6	chr6:152470784	SYNE1	T	G	0.005556 0	1

1713	6	chr6:152472812	SYNE1	C	T	0.005556 0	1
1721	6	chr6:152529254	SYNE1	A	G	0.005556 0	1
1725	6	chr6:152542688	SYNE1	C	G	0.005556 0	1
1740	6	chr6:152631545	SYNE1	A	G	0.005556 0	1
1741	6	chr6:152631970	SYNE1	A	C	0.005556 0	1
1742	6	chr6:152639288	SYNE1	A	C	0.005556 0	1
1744	6	chr6:152644654	SYNE1	A	C	0.005556 0	1
1752	6	chr6:152652197	SYNE1	C	A	0.005556 0	1
1764	6	chr6:152674791	SYNE1	C	T	0.005556 0	1
1782	6	chr6:152712677	SYNE1	A	C	0.005556 0	1
1805	6	chr6:152823897	SYNE1	T	A	0.005556 0	1
4229	23	chrX:70597573	TAF1	C	G	0.008 0	1
4235	23	chrX:70683793	TAF1	T	C	0 0	0
2411	9	chr9:32631748	TAF1L	A	G	0.005556 0	1
4240	23	chrX:79279609	TBX22	C	G	0.008 0	1
3877	19	chr19:1646325	TCF3	CGAG	-	0.01111 0	2
573	2	chr2:85534779	TCF7L1	-	GAGG	0.005556 0	1
2680	10	chr10:114710518	TCF7L2	T	G	0.005556 0	1
2684	10	chr10:114911539	TCF7L2	T	C	0.005556 0	1
2599	10	chr10:70332342	TET1	G	A	0.005556 0	1
2609	10	chr10:70406386	TET1	A	C	0.01111 1	0
2614	10	chr10:70451510	TET1	A	T	0.005556 0	1
1187	4	chr4:106158026	TET2	T	A	0.005556 0	1
1191	4	chr4:106193885	TET2	-	T	0.005556 0	1
4213	23	chrX:48896874	TFE3	T	C	0.008 0	1
3203	15	chr15:39884882	THBS1	T	G	0.01111 0	2
3569	17	chr17:7579634	TP53	-	C	0.005556 0	1
370	1	chr1:186301473	TPR	T	A	0.005556 0	1
372	1	chr1:186304551	TPR	G	A	0.005556 0	1
374	1	chr1:186315243	TPR	T	-	0.01111 0	2
136	1	chr1:114940315	TRIM33	A	G	0.005556 0	1
141	1	chr1:114976234	TRIM33	T	C	0.005556 0	1
3132	14	chr14:92454746	TRIP11	T	-	0.005556 0	1
3135	14	chr14:92461911	TRIP11	T	A	0.01111 0	2
3141	14	chr14:92471880	TRIP11	T	C	0.005556 0	1
1971	7	chr7:98543325	TRRAP	G	A	0.005556 0	1
1973	7	chr7:98552756	TRRAP	C	A	0.005556 0	1
1974	7	chr7:98552760	TRRAP	T	C	0.005556 0	1
1975	7	chr7:98552779	TRRAP	T	C	0.005556 0	1
1982	7	chr7:98579357	TRRAP	T	C	0.005556 0	1
3336	16	chr16:2129453	TSC2	T	-	0.02222 2	0
3115	14	chr14:81554286	TSHR	C	T	0.005556 0	1
3116	14	chr14:81554303	TSHR	G	T	0.005556 0	1
3121	14	chr14:81606071	TSHR	A	G	0.005556 0	1
2255	8	chr8:103284936	UBR5	T	C	0.005556 0	1
2257	8	chr8:103289351	UBR5	C	T	0.005556 0	1
2261	8	chr8:103297404	UBR5	G	T	0.005556 0	1

2266	8	chr8:103307466	UBR5	C	T	0.005556 0	1
2280	8	chr8:103341456	UBR5	-	T	0.01111 0	2
2281	8	chr8:103354860	UBR5	C	G	0.005556 0	1
4197	23	chrX:41088723	USP9X	T	A	0.008 0	1
1083	4	chr4:1961342	WHSC1	T	C	0.005556 0	1
1084	4	chr4:1976481	WHSC1	G	T	0.04444 4	0
1085	4	chr4:1976483	WHSC1	G	C	0.03333 3	0
1086	4	chr4:1976485	WHSC1	GG	AC	0.005556 0	1
1087	4	chr4:1976486	WHSC1	G	C	0.005556 0	1
2140	8	chr8:30938754	WRN	-	T	0.005556 0	1
2145	8	chr8:30989869	WRN	C	A	0.005556 0	1
2152	8	chr8:31004834	WRN	A	T	0.005556 0	1
2157	8	chr8:31024684	WRN	T	G	0.005556 0	1
2870	12	chr12:6777111	ZNF384	-	C	0.06667 6	0
2873	12	chr12:6788242	ZNF384	C	T	0.005556 0	1

 Variants reported in ICGC

A2A2	O(HET)	E(HET)	P	Location	Allele	Consequen	IMPACT	SYMBOL
89	0.01111	0.01105	1	2:1486728	T	stop_gaine	HIGH	ACVR2A
89	0.01111	0.01105	1	12:438462	T	intron_vari	MODIFIER	ADAMTS20
89	0.01111	0.01105	1	4:8796727	C	intron_vari	MODIFIER	AFF1
89	0.01111	0.01105	1	4:8796793	T	synonymo	LOW	AFF1
89	0.01111	0.01105	1	7:9163123	C	missense_\	MODERATE	AKAP9
89	0.01111	0.01105	1	7:9164167	TGC	intron_vari	MODIFIER	AKAP9
89	0.01111	0.01105	1	7:9167006	C	missense_\	MODERATE	AKAP9
89	0.01111	0.01105	1	7:9167209	G	intron_vari	MODIFIER	AKAP9
89	0.01111	0.01105	1	7:9169937	A	frameshift_	HIGH	AKAP9
89	0.01111	0.01105	1	7:9170915	G	missense_\	MODERATE	AKAP9
89	0.01111	0.01105	1	7:9171272	A	missense_\	MODERATE	AKAP9
89	0.01111	0.01105	1	19:407412	A	missense_\	MODERATE	AKT2
89	0.01111	0.01105	1	1:2437272	-	intron_vari	MODIFIER	AKT3
89	0.01111	0.01105	1	2:2949830	-	frameshift_	HIGH	ALK
89	0.01111	0.01105	1	5:1121646	A	missense_\	MODERATE	APC
89	0.01111	0.01105	1	5:1121646	-	frameshift_	HIGH	APC
89	0.01111	0.01105	1	5:1121739	TA	stop_gaine	HIGH	APC
89	0.01111	0.01105	1	5:1121752	-	frameshift_	HIGH	APC
89	0.01111	0.01105	1	5:1121756	-	frameshift_	HIGH	APC
31	0	0.2024	5.546e-006	X:6694360	-	frameshift_	HIGH	AR
89	0.01111	0.01105	1	1:2709281	-	frameshift_	HIGH	ARID1A
89	0.01111	0.01105	1	1:2709282	T	missense_\	MODERATE	ARID1A
87	0.02222	0.04346	0.03342	1:2709769	A	stop_gaine	HIGH	ARID1A
89	0	0.02198	0.005587	1:2709900	-	frameshift_	HIGH	ARID1A
89	0.01111	0.01105	1	1:2710634	T	missense_\	MODERATE	ARID1A
89	0.01111	0.01105	1	12:462856	C	missense_\	MODERATE	ARID2
89	0.01111	0.01105	1	1:1508089	A	intron_vari	MODIFIER	ARNT
89	0.01111	0.01105	1	11:108117	TTA	intron_vari	MODIFIER	ATM
89	0.01111	0.01105	1	11:108175	G	intron_vari	MODIFIER	ATM
89	0.01111	0.01105	1	11:108201	C	synonymo	LOW	ATM
89	0.01111	0.01105	1	3:1421766	-	intron_vari	MODIFIER	ATR
89	0.01111	0.01105	1	3:1421766	A	intron_vari	MODIFIER	ATR
89	0.01111	0.01105	1	3:1421868	-	frameshift_	HIGH	ATR
89	0.01111	0.01105	1	3:1422691	G	missense_\	MODERATE	ATR
88	0.02222	0.02198	1	3:1422726	A	intron_vari	MODIFIER	ATR
89	0.01111	0.01105	1	3:1422746	A	intron_vari	MODIFIER	ATR
34	0.02857	0.02816	1	X:7684916	T	splice_don	HIGH	ATRX
89	0.01111	0.01105	1	20:549593	T	frameshift_	HIGH	AURKA
89	0.01111	0.01105	1	17:810987	C	synonymo	LOW	AURKB
89	0.01111	0.01105	1	19:577447	T	intron_vari	MODIFIER	AURKC
89	0.01111	0.01105	1	6:6934919	A	missense_\	MODERATE	BAI3
89	0.01111	0.01105	1	6:7007124	G	missense_\	MODERATE	BAI3
89	0.01111	0.01105	1	1:8573337	C	synonymo	LOW	BCL10
89	0.01111	0.01105	1	1:8573659	T	splice_regi	LOW	BCL10
89	0.01111	0.01105	1	2:6077306	G	intron_vari	MODIFIER	BCL11A

89	0.01111	0.01105	1	3:1874470	A	missense_\ MODERATE	BCL6
89	0.01111	0.01105	1	1:1470906	T	stop_gaine	HIGH BCL9
89	0.01111	0.01105	1	1:1470940	T	intron_vari	MODIFIER BCL9
89	0.01111	0.01105	1	11:102195	C	missense_\ MODERATE	BIRC3
89	0.01111	0.01105	1	11:102195	T	missense_\ MODERATE	BIRC3
89	0.01111	0.01105	1	11:102201	C	synonymo	LOW BIRC3
88	0.02222	0.02198	1	11:102207	A	missense_\ MODERATE	BIRC3
89	0.01111	0.01105	1	11:102207	C	missense_\ MODERATE	BIRC3
89	0.01111	0.01105	1	17:762103	A	5_prime_U	MODIFIER BIRC5
85	0.05556	0.05401	1	17:762196	T	3_prime_U	MODIFIER BIRC5
88	0.02222	0.02198	1	15:913041	T	missense_\ MODERATE	BLM
89	0.01111	0.01105	1	15:913474	A	missense_\ MODERATE	BLM
84	0.06667	0.06444	1	10:979751	-	intron_vari	MODIFIER BLNK
89	0.01111	0.01105	1	17:597606	C	3_prime_U	MODIFIER BRIP1
89	0.01111	0.01105	1	17:598581	T	intron_vari	MODIFIER BRIP1
89	0.01111	0.01105	1	17:598615	A	intron_vari	MODIFIER BRIP1
89	0.01111	0.01105	1	7:2968269	C	missense_\ MODERATE	CARD11
89	0.01111	0.01105	1	15:409138	T	missense_\ MODERATE	CASC5
89	0.01111	0.01105	1	15:409495	-	intron_vari	MODIFIER CASC5
89	0.01111	0.01105	1	11:119145	-	intron_vari	MODIFIER CBL
89	0.01111	0.01105	1	1:1931109	G	intron_vari	MODIFIER CDC73
89	0.01111	0.01105	1	1:1931112	A	intron_vari	MODIFIER CDC73
89	0.01111	0.01105	1	16:688440	T	intron_vari	MODIFIER CDH1
89	0.01111	0.01105	1	16:650269	G	intron_vari	MODIFIER CDH11
89	0.01111	0.01105	1	18:255898	A	intron_vari	MODIFIER CDH2
89	0.01111	0.01105	1	18:255937	A	missense_\ MODERATE	CDH2
85	0.05556	0.05401	1	18:592218	A	missense_\ MODERATE	CDH20
89	0.01111	0.01105	1	17:376277	G	missense_\ MODERATE	CDK12
89	0.01111	0.01105	1	12:581431	-	intron_vari	MODIFIER CDK4
89	0.01111	0.01105	1	9:2199415	C	intron_vari	MODIFIER RP11-145E
89	0.01111	0.01105	1	19:427910	T	synonymo	LOW CIC
89	0.01111	0.01105	1	19:427984	G	splice_regi	LOW CIC
88	0.01111	0.03278	0.01676	17:482770	-	intron_vari	MODIFIER COL1A1
89	0.01111	0.01105	1	3:3194271	C	missense_\ MODERATE	CRBN
89	0.01111	0.01105	1	3:3197988	G	intron_vari	MODIFIER CRBN
89	0.01111	0.01105	1	16:384361	G	synonymo	LOW CREBBP
88	0.02222	0.02198	1	8:1132540	-	intron_vari	MODIFIER CSMD3
89	0.01111	0.01105	1	8:1133017	TTA	intron_vari	MODIFIER CSMD3
89	0.01111	0.01105	1	8:1133233	G	splice_acce	HIGH CSMD3
87	0.03333	0.03278	1	8:1135162	G	intron_vari	MODIFIER CSMD3
89	0.01111	0.01105	1	8:1135689	G	intron_vari	MODIFIER CSMD3
89	0.01111	0.01105	1	5:1382665	G	missense_\ MODERATE	CTNNA1
89	0.01111	0.01105	1	5:1382697	-	inframe_de	MODERATE CTNNA1
89	0.01111	0.01105	1	3:4126719	A	missense_\ MODERATE	CTNNB1
89	0.01111	0.01105	1	10:965416	G	missense_\ MODERATE	CYP2C19
89	0.01111	0.01105	1	22:425248	T	missense_\ MODERATE	CYP2D6
89	0.01111	0.01105	1	18:504516	G	missense_\ MODERATE	DCC

89	0.01111	0.01105	1	18:504516	C	missense_\ MODERATE	DCC
89	0.01111	0.01105	1	18:509425	T	missense_\ MODERATE	DCC
89	0.01111	0.01105	1	18:509768	C	intron_vari	MODIFIER DCC
88	0.02222	0.02198	1	1:1627371	T	splice_regi	LOW DDR2
88	0.02222	0.02198	1	1:1627403	CG	intron_vari	MODIFIER DDR2
89	0.01111	0.01105	1	1:1627483	T	missense_\ MODERATE	DDR2
89	0.01111	0.01105	1	14:955698	A	synonymo	LOW DICER1
89	0.01111	0.01105	1	2:2545714	G	stop_lost	HIGH DNMT3A
89	0.01111	0.01105	1	2:2552301	A	missense_\ MODERATE	DNMT3A
89	0.01111	0.01105	1	1:9756404	G	splice_regi	LOW DPYD
89	0.01111	0.01105	1	1:9814476	T	intron_vari	MODIFIER DPYD
89	0.01111	0.01105	1	1:9820604	C	intron_vari	MODIFIER DPYD
89	0.01111	0.01105	1	1:9838648	A	5_prime_U	MODIFIER DPYD
74	0.1778	0.162	1	6:5634110	A	missense_\ MODERATE	DST
89	0.01111	0.01105	1	6:5634753	C	missense_\ MODERATE	DST
89	0.01111	0.01105	1	6:5635015	C	synonymo	LOW DST
89	0.01111	0.01105	1	6:5641714	G	missense_\ MODERATE	DST
89	0.01111	0.01105	1	6:5641744	C	missense_\ MODERATE	DST
89	0	0.02198	0.005587	6:5648509	-	intron_vari	MODIFIER DST
89	0.01111	0.01105	1	6:5648526	C	intron_vari	MODIFIER DST
89	0.01111	0.01105	1	6:5648946	-	intron_vari	MODIFIER DST
87	0	0.06444	2.705e-006	22:415428	-	intron_vari	MODIFIER EP300
89	0.01111	0.01105	1	22:415509	A	intron_vari	MODIFIER EP300
89	0.01111	0.01105	1	12:132466	A	missense_\ MODERATE	EP400
89	0.01111	0.01105	1	12:132490	A	missense_\ MODERATE	EP400
89	0.01111	0.01105	1	12:132497	T	synonymo	LOW EP400
89	0.01111	0.01105	1	12:132529	C	intron_vari	MODIFIER EP400
89	0.01111	0.01105	1	12:132535	G	missense_\ MODERATE	EP400
89	0	0.02198	0.005587	12:132562	C	missense_\ MODERATE	EP400
89	0.01111	0.01105	1	3:8944846	C	splice_regi	LOW EPHA3
89	0.01111	0.01105	1	3:8946227	C	intron_vari	MODIFIER EPHA3
89	0.01111	0.01105	1	3:8946229	C	missense_\ MODERATE	EPHA3
83	0.04444	0.1049	0.0005534	6:9396800	C	splice_acce	HIGH EPHA7
89	0.01111	0.01105	1	6:9397353	G	intron_vari	MODIFIER EPHA7
89	0.01111	0.01105	1	6:9412896	C	splice_regi	LOW EPHA7
89	0.01111	0.01105	1	3:1348858	T	synonymo	LOW EPHB1
89	0.01111	0.01105	1	17:378683	A	intron_vari	MODIFIER ERBB2
89	0.01111	0.01105	1	17:378687	C	intron_vari	MODIFIER ERBB2
89	0.01111	0.01105	1	17:378836	T	synonymo	LOW ERBB2
89	0.01111	0.01105	1	12:564790	T	intron_vari	MODIFIER ERBB3
89	0.01111	0.01105	1	2:2122486	T	synonymo	LOW ERBB4
89	0.01111	0.01105	1	2:2124951	T	intron_vari	MODIFIER ERBB4
89	0.01111	0.01105	1	2:2129894	T	intron_vari	MODIFIER ERBB4
89	0	0.02198	0.005587	21:398174	C	synonymo	LOW ERG
89	0.01111	0.01105	1	7:1395094	T	intron_vari	MODIFIER ETV1
89	0.01111	0.01105	1	17:416105	G	missense_\ MODERATE	ETV4
89	0.01111	0.01105	1	8:1188251	A	missense_\ MODERATE	EXT1

89	0.01111	0.01105	1	8:1191224:A	synonymou	LOW	EXT1
89	0.01111	0.01105	1	11:442285:-	intron_vari	MODIFIER	EXT2
87	0.03333	0.03278	1	7:1485235:A	intron_vari	MODIFIER	EZH2
34	0.02857	0.02816	1	X:6341163:ATAGAACT	frameshift_HIGH		AMER1
89	0.01111	0.01105	1	16:898577:C	intron_vari	MODIFIER	FANCA
89	0.01111	0.01105	1	16:898773:A	intron_vari	MODIFIER	FANCA
89	0.01111	0.01105	1	3:1008829:G	missense_	MODERATE	FANCD2
88	0.02222	0.02198	1	3:1013203:-	frameshift_HIGH		FANCD2
89	0	0.02198	0.005587	19:814601:G	intron_vari	MODIFIER	FBN3
89	0.01111	0.01105	1	4:1532440:A	stop_gaine	HIGH	FBXW7
82	0.08889	0.08494	1	8:3827235:A	synonymou	LOW	FGFR1
89	0.01111	0.01105	1	10:123246:C	missense_	MODERATE	FGFR2
89	0.01111	0.01105	1	4:1803325:-	intron_vari	MODIFIER	FGFR3
88	0.02222	0.02198	1	4:1807544:-	frameshift_HIGH		FGFR3
89	0.01111	0.01105	1	5:1765204:A	synonymou	LOW	FGFR4
88	0	0.04346	9.469e-005	13:285974:-	intron_vari	MODIFIER	FLT3
89	0.01111	0.01105	1	5:1800359:G	missense_	MODERATE	FLT4
89	0.01111	0.01105	1	2:2162325:G	intron_vari	MODIFIER	FN1
89	0.01111	0.01105	1	2:2162370:C	missense_	MODERATE	FN1
89	0.01111	0.01105	1	2:2162729:A	intron_vari	MODIFIER	FN1
89	0.01111	0.01105	1	13:411348:C	missense_	MODERATE	FOXO1
89	0.01111	0.01105	1	6:1089852:G	missense_	MODERATE	FOXO3
89	0.01111	0.01105	1	3:7117970:C	frameshift_HIGH		FOXP1
89	0.01111	0.01105	1	6:4155905:T	missense_	MODERATE	FOXP4
89	0.01111	0.01105	1	19:353182:G	intron_vari	MODIFIER	FZR1
84	0.05556	0.07475	0.114	3:1282027:C	synonymou	LOW	GATA2
68	0.2444	0.2146	0.3487	20:574284:G	synonymou	LOW	GNAS
89	0.01111	0.01105	1	8:3769141:A	intron_vari	MODIFIER	GPR124
89	0	0.02198	0.005587	2:1175100:T	missense_	MODERATE	GREB1
89	0.01111	0.01105	1	11:106579:A	synonymou	LOW	GUCY1A2
89	0.01111	0.01105	1	8:4286845:-	intron_vari	MODIFIER	HOOK3
89	0.01111	0.01105	1	14:102548:G	missense_	MODERATE	HSP90AA1
89	0.01111	0.01105	1	14:102548:C	intron_vari	MODIFIER	HSP90AA1
89	0.01111	0.01105	1	15:906282:A	missense_	MODERATE	IDH2
89	0.01111	0.01105	1	15:992507:C	intron_vari	MODIFIER	IGF1R
89	0.01111	0.01105	1	15:994601:T	intron_vari	MODIFIER	IGF1R
88	0.02222	0.02198	1	6:1604121:T	intron_vari	MODIFIER	IGF2R
89	0.01111	0.01105	1	6:1604910:G	missense_	MODERATE	IGF2R
89	0.01111	0.01105	1	8:4217529:C	splice_regio	LOW	IKBKB
89	0.01111	0.01105	1	1:2066476:T	intron_vari	MODIFIER	IKBKE
89	0.01111	0.01105	1	5:5523709:C	missense_	MODERATE	IL6ST
89	0.01111	0.01105	1	5:5523759:A	missense_	MODERATE	IL6ST
89	0.01111	0.01105	1	5:5524726:-	intron_vari	MODIFIER	IL6ST
89	0.01111	0.01105	1	5:5525634:T	missense_	MODERATE	IL6ST
89	0.01111	0.01105	1	5:5526428:G	intron_vari	MODIFIER	IL6ST
89	0.01111	0.01105	1	6:397155-3:T	synonymou	LOW	IRF4
89	0.01111	0.01105	1	13:110434:T	synonymou	LOW	IRS2

89	0.01111	0.01105	1	1:1455283	T	stop_gaine	HIGH	ITGA10
89	0.01111	0.01105	1	1:1455283	A	splice_regi	LOW	ITGA10
86	0.04444	0.04346	1	1:1455309	T	missense_\	MODERATE	ITGA10
87	0.03333	0.03278	1	1:1455338	-	frameshift_	HIGH	ITGA10
89	0.01111	0.01105	1	3:3756751	C	splice_acce	HIGH	ITGA9
89	0.01111	0.01105	1	3:3779190	A	intron_vari	MODIFIER	ITGA9
88	0	0.04346	9.469e-005	21:463270	A	intron_vari	MODIFIER	ITGB2
89	0.01111	0.01105	1	17:453608	A	missense_\	MODERATE	ITGB3
89	0.01111	0.01105	1	17:453617	T	intron_vari	MODIFIER	ITGB3
89	0.01111	0.01105	1	17:453778	C	missense_\	MODERATE	ITGB3
89	0.01111	0.01105	1	17:453778	A	missense_\	MODERATE	ITGB3
89	0	0.02198	0.005587	9:5081778	TA	stop_gaine	HIGH	JAK2
89	0.01111	0.01105	1	9:5090443	G	splice_regi	LOW	JAK2
89	0	0.02198	0.005587	8:4179104	A	frameshift_	HIGH	KAT6A
79	0.1111	0.1244	0.3243	10:767354	-	frameshift_	HIGH	KAT6B
89	0.01111	0.01105	1	10:767360	C	missense_\	MODERATE	KAT6B
89	0.01111	0.01105	1	10:767449	-	frameshift_	HIGH	KAT6B
89	0.01111	0.01105	1	10:767449	T	missense_\	MODERATE	KAT6B
88	0.02222	0.02198	1	10:767449	G	missense_\	MODERATE	KAT6B
35	0	0	1	X:5324505	T	missense_\	MODERATE	KDM5C
34	0.02857	0.02816	1	X:4494286	C	intron_vari	MODIFIER	KDM6A
87	0	0.06444	2.705e-006	4:5595374	-	intron_vari	MODIFIER	KDR
89	0.01111	0.01105	1	4:5597090	G	missense_\	MODERATE	KDR
89	0.01111	0.01105	1	4:5598029	A	missense_\	MODERATE	KDR
89	0.01111	0.01105	1	4:5598150	T	frameshift_	HIGH	KDR
89	0.01111	0.01105	1	19:106005	A	missense_\	MODERATE	KEAP1
89	0.01111	0.01105	1	10:382427	C	missense_\	MODERATE	KLF6
89	0.01111	0.01105	1	12:253982	CGC	inframe_in	MODERATE	KRAS
89	0.01111	0.01105	1	5:3848187	G	missense_\	MODERATE	LIFR
89	0.01111	0.01105	1	5:3848232	T	splice_regi	LOW	LIFR
89	0.01111	0.01105	1	5:3848609	T	intron_vari	MODIFIER	LIFR
89	0.01111	0.01105	1	5:3849971	A	intron_vari	MODIFIER	LIFR
89	0.01111	0.01105	1	5:3850282	C	missense_\	MODERATE	LIFR
89	0.01111	0.01105	1	4:6259909	G	missense_\	MODERATE	LPHN3
89	0.01111	0.01105	1	4:6289731	A	missense_\	MODERATE	LPHN3
89	0.01111	0.01105	1	2:1410794	G	intron_vari	MODIFIER	LRP1B
83	0	0.1435	2.919e-011	2:1412020	CA	splice_regi	LOW	LRP1B
89	0.01111	0.01105	1	2:1412140	G	synonymo	LOW	LRP1B
89	0.01111	0.01105	1	2:1412329	C	intron_vari	MODIFIER	LRP1B
89	0.01111	0.01105	1	2:1412993	T	missense_\	MODERATE	LRP1B
89	0.01111	0.01105	1	2:1415985	C	missense_\	MODERATE	LRP1B
89	0.01111	0.01105	1	2:1416079	T	splice_regi	LOW	LRP1B
89	0.01111	0.01105	1	2:1416806	C	missense_\	MODERATE	LRP1B
89	0.01111	0.01105	1	2:1418197	T	synonymo	LOW	LRP1B
89	0.01111	0.01105	1	2:1419866	A	intron_vari	MODIFIER	LRP1B
89	0.01111	0.01105	1	2:1420049	C	intron_vari	MODIFIER	LRP1B
89	0.01111	0.01105	1	2:1428881	TA	intron_vari	MODIFIER	LRP1B

89	0.01111	0.01105	1	3:4650131(A	splice_acce	HIGH	LTF
89	0.01111	0.01105	1	3:6537692(T	synonymou	LOW	MAGI1
89	0.01111	0.01105	1	11:957248(C	missense_	\ MODERATE	MAML2
89	0.01111	0.01105	1	11:958262(A	synonymou	LOW	MAML2
89	0.01111	0.01105	1	11:958263(A	missense_	\ MODERATE	MAML2
89	0.01111	0.01105	1	15:667820(T	missense_	\ MODERATE	MAP2K1
88	0.02222	0.02198	1	1:2208086(GC	intron_vari	MODIFIER	MARK1
89	0.01111	0.01105	1	19:458058(A	missense_	\ MODERATE	MARK4
84	0.06667	0.06444	1	18:477939(G	upstream_	MODIFIER	CCDC11
89	0	0.02198	0.005587	18:478012(C	intron_vari	MODIFIER	MBD1
89	0.01111	0.01105	1	1:1505507(G	missense_	\ MODERATE	MCL1
89	0.01111	0.01105	1	11:645720(A	synonymou	LOW	MEN1
89	0.01111	0.01105	1	7:1163398(G	missense_	\ MODERATE	MET
79	0.1222	0.1148	1	7:1163977(G	missense_	\ MODERATE	MET
89	0.01111	0.01105	1	3:6998582(C	intron_vari	MODIFIER	MITF
89	0.01111	0.01105	1	3:7000091(G	intron_vari	MODIFIER	MITF
89	0.01111	0.01105	1	3:3709004(A	missense_	\ MODERATE	MLH1
89	0.01111	0.01105	1	11:118376(T	missense_	\ MODERATE	KMT2A
89	0.01111	0.01105	1	11:118390(A	missense_	\ MODERATE	KMT2A
89	0	0.02198	0.005587	12:494331(C	intron_vari	MODIFIER	KMT2D
89	0.01111	0.01105	1	7:1518596(A	synonymou	LOW	KMT2C
86	0	0.08494	1.095e-007	7:1518792(-	frameshift_	HIGH	KMT2C
89	0	0.02198	0.005587	7:1519021(T	intron_vari	MODIFIER	KMT2C
89	0.01111	0.01105	1	7:1519021(T	intron_vari	MODIFIER	KMT2C
89	0.01111	0.01105	1	7:1519021(-	intron_vari	MODIFIER	KMT2C
89	0.01111	0.01105	1	7:1519479(T	missense_	\ MODERATE	KMT2C
89	0.01111	0.01105	1	7:1519710(A	intron_vari	MODIFIER	KMT2C
87	0.03333	0.03278	1	10:219012(T	intron_vari	MODIFIER	MLLT10
87	0.03333	0.03278	1	10:219012(T	intron_vari	MODIFIER	MLLT10
89	0.01111	0.01105	1	10:220220(T	intron_vari	MODIFIER	MLLT10
89	0.01111	0.01105	1	1:4380350(T	5_prime_U	MODIFIER	MPL
89	0.01111	0.01105	1	1:4381848(T	downstream	MODIFIER	MPL
89	0.01111	0.01105	1	11:942240(G	missense_	\ MODERATE	MRE11A
89	0.01111	0.01105	1	2:4763958(T	stop_gaine	HIGH	MSH2
89	0.01111	0.01105	1	2:4764157(G	intron_vari	MODIFIER	MSH2
87	0.02222	0.04346	0.03342	2:4764350(C	missense_	\ MODERATE	MSH2
89	0.01111	0.01105	1	2:4770545(-	inframe_de	MODERATE	MSH2
89	0.01111	0.01105	1	1:1116750(C	3_prime_U	MODIFIER	MTOR
85	0.05556	0.05401	1	1:2369668(TT	missense_	\ MODERATE	MTR
89	0.01111	0.01105	1	1:2370162(A	splice_regi	LOW	MTR
89	0.01111	0.01105	1	1:2370380(T	intron_vari	MODIFIER	MTR
89	0.01111	0.01105	1	1:2370587(G	missense_	\ MODERATE	MTR
89	0	0.02198	0.005587	1:1551600(GAC	splice_acce	HIGH	MUC1
89	0.01111	0.01105	1	1:1551607(G	synonymou	LOW	MUC1
89	0	0.02198	0.005587	1:4579918(T	stop_gaine	HIGH	MUTYH
89	0	0.02198	0.005587	8:1287530(TGA	stop_gaine	HIGH	MYC
89	0.01111	0.01105	1	8:1287532(T	3_prime_U	MODIFIER	MYC

89	0.01111	0.01105	1	1:4036360!A	missense_\\ MODERATE MYCL	
89	0.01111	0.01105	1	2:1608604!A	synonymo\\ LOW	MYCN
89	0.01111	0.01105	1	16:158088!G	missense_\\ MODERATE MYH11	
89	0.01111	0.01105	1	16:158265!A	splice_regi\\ LOW	MYH11
89	0.01111	0.01105	1	22:366901!CC	intron_vari MODIFIER	MYH9
89	0.01111	0.01105	1	8:7104101!A	synonymo\\ LOW	NCOA2
89	0.01111	0.01105	1	8:7104120!C	missense_\\ MODERATE NCOA2	
89	0.01111	0.01105	1	8:7107566!G	intron_vari MODIFIER	NCOA2
89	0	0.02198	0.005587	8:7107577!C	missense_\\ MODERATE NCOA2	
89	0.01111	0.01105	1	8:7112891!G	missense_\\ MODERATE NCOA2	
88	0.02222	0.02198	1	10:515849!A	missense_\\ MODERATE NCOA4	
89	0.01111	0.01105	1	10:515864!ATAT	intron_vari MODIFIER	NCOA4
89	0.01111	0.01105	1	17:295276!A	intron_vari MODIFIER	NF1
88	0.02222	0.02198	1	17:295630!TTG	intron_vari MODIFIER	NF1
89	0.01111	0.01105	1	17:296840!G	missense_\\ MODERATE NF1	
89	0.01111	0.01105	1	2:1780962!G	missense_\\ MODERATE NFE2L2	
89	0.01111	0.01105	1	4:1035332!G	missense_\\ MODERATE NFKB1	
89	0.01111	0.01105	1	4:1035332!A	intron_vari MODIFIER	NFKB1
89	0.01111	0.01105	1	4:1035336!A	missense_\\ MODERATE NFKB1	
89	0.01111	0.01105	1	4:1035377!T	missense_\\ MODERATE NFKB1	
89	0.01111	0.01105	1	10:104156!A	intron_vari MODIFIER	NFKB2
89	0	0.02198	0.005587	14:512213!G	missense_\\ MODERATE NIN	
89	0.01111	0.01105	1	14:512253!C	missense_\\ MODERATE NIN	
89	0.01111	0.01105	1	17:548720!A	missense_\\ MODERATE NLRP1	
89	0.01111	0.01105	1	1:1204779!A	intron_vari MODIFIER	NOTCH2
89	0.01111	0.01105	1	1:1205396!C	missense_\\ MODERATE NOTCH2	
89	0.01111	0.01105	1	6:3216410!A	synonymo\\ LOW	NOTCH4
89	0.01111	0.01105	1	6:3216673!A	missense_\\ MODERATE NOTCH4	
88	0.02222	0.02198	1	5:1766372!C	missense_\\ MODERATE NSD1	
89	0.01111	0.01105	1	1:1568119!C	missense_\\ MODERATE INSRR	
89	0.01111	0.01105	1	1:1568414!A	missense_\\ MODERATE NTRK1	
89	0.01111	0.01105	1	15:886695!A	missense_\\ MODERATE NTRK3	
89	0	0.02198	0.005587	9:1340906!G	synonymo\\ LOW	NUP214
89	0.01111	0.01105	1	11:379485!A	intron_vari MODIFIER	NUP98
35	0	0	1	X:1104635!T	intron_vari MODIFIER	PAK3
89	0.01111	0.01105	1	9:3700654!A	splice_regi\\ LOW	PAX5
89	0.01111	0.01105	1	1:1901842!T	missense_\\ MODERATE PAX7	
89	0.01111	0.01105	1	3:5261060!C	missense_\\ MODERATE PBRM1	
89	0.01111	0.01105	1	3:5261061!G	missense_\\ MODERATE PBRM1	
83	0.06667	0.08494	0.1499	1:1448523!T	3_prime_U MODIFIER	PDE4DIP
85	0.05556	0.05401	1	1:1448599!T	missense_\\ MODERATE PDE4DIP	
86	0.04444	0.04346	1	1:1448633!C	missense_\\ MODERATE PDE4DIP	
89	0.01111	0.01105	1	1:1448633!A	synonymo\\ LOW	PDE4DIP
89	0.01111	0.01105	1	1:1448633!A	stop_gaine HIGH	PDE4DIP
89	0.01111	0.01105	1	1:1448633!TT	missense_\\ MODERATE PDE4DIP	
89	0.01111	0.01105	1	1:1448666!T	missense_\\ MODERATE PDE4DIP	
88	0.02222	0.02198	1	1:1448666!A	missense_\\ MODERATE PDE4DIP	

86	0.04444	0.04346	1	1:1448790	C	missense_	\ MODERATE	PDE4DIP
89	0.01111	0.01105	1	1:1448790	-	frameshift_	HIGH	PDE4DIP
85	0.05556	0.05401	1	1:1448814	T	missense_	\ MODERATE	PDE4DIP
81	0.1	0.095	1	1:1448815	A	missense_	\ MODERATE	PDE4DIP
24	0.7333	0.4644	2.399e-009	1:1448860	T	splice_regi	LOW	PDE4DIP
86	0.04444	0.04346	1	1:1448862	T	synonymo	LOW	PDE4DIP
89	0.01111	0.01105	1	1:1449237	C	missense_	\ MODERATE	PDE4DIP
14	0.8444	0.4879	8.431e-014	1:1449305	A	intron_vari	MODIFIER	PDE4DIP
88	0.02222	0.02198	1	1:1449309	C	intron_vari	MODIFIER	PDE4DIP
89	0.01111	0.01105	1	1:1449314	C	intron_vari	MODIFIER	PDE4DIP
87	0.03333	0.03278	1	1:1449946	T	missense_	\ MODERATE	PDE4DIP
84	0.06667	0.06444	1	1:1449946	A	missense_	\ MODERATE	PDE4DIP
89	0.01111	0.01105	1	1:1449946	C	missense_	\ MODERATE	PDE4DIP
89	0	0.02198	0.005587	4:5512989	C	synonymo	LOW	PDGFRA
88	0	0.04346	9.469e-005	4:5512989	G	missense_	\ MODERATE	PDGFRA
70	0.2222	0.1975	0.5916	5:1494995	T	intron_vari	MODIFIER	PDGFRB
89	0.01111	0.01105	1	5:1495144	A	missense_	\ MODERATE	PDGFRB
89	0.01111	0.01105	1	17:804556	GC	intron_vari	MODIFIER	PER1
89	0.01111	0.01105	1	1:2044388	G	missense_	\ MODERATE	PIK3C2B
89	0.01111	0.01105	1	3:1789169	A	intron_vari	MODIFIER	PIK3CA
89	0.01111	0.01105	1	3:1789222	AA	intron_vari	MODIFIER	PIK3CA
89	0.01111	0.01105	1	3:1384615	G	missense_	\ MODERATE	PIK3CB
89	0.01111	0.01105	1	7:1065455	G	intron_vari	MODIFIER	PIK3CG
89	0.01111	0.01105	1	5:6752272	T	stop_gaine	HIGH	PIK3R1
89	0.01111	0.01105	1	5:6759049	T	stop_gaine	HIGH	PIK3R1
89	0.01111	0.01105	1	6:5152465	T	missense_	\ MODERATE	PKHD1
89	0.01111	0.01105	1	6:5161305	T	missense_	\ MODERATE	PKHD1
89	0.01111	0.01105	1	6:5188945	A	stop_gaine	HIGH	PKHD1
89	0.01111	0.01105	1	6:5189049	A	missense_	\ MODERATE	PKHD1
88	0	0.04346	9.469e-005	6:5192181	GCCTT	intron_vari	MODIFIER	PKHD1
89	0.01111	0.01105	1	6:5192312	T	missense_	\ MODERATE	PKHD1
89	0.01111	0.01105	1	2:1907193	C	synonymo	LOW	PMS1
89	0.01111	0.01105	1	2:1907197	A	missense_	\ MODERATE	PMS1
89	0.01111	0.01105	1	7:6027040	C	synonymo	LOW	PMS2
88	0.02222	0.02198	1	7:6029511	T	stop_gaine	HIGH	PMS2
89	0.01111	0.01105	1	7:6035156	G	intron_vari	MODIFIER	PMS2
89	0.01111	0.01105	1	7:1244754	G	intron_vari	MODIFIER	POT1
89	0	0.02198	0.005587	17:665115	G	splice_regi	LOW	PRKAR1A
89	0.01111	0.01105	1	8:4868692	C	synonymo	LOW	PRKDC
89	0.01111	0.01105	1	8:4873649	G	missense_	\ MODERATE	PRKDC
89	0.01111	0.01105	1	8:4877604	G	synonymo	LOW	PRKDC
89	0.01111	0.01105	1	8:4882502	C	synonymo	LOW	PRKDC
89	0.01111	0.01105	1	8:4882803	C	intron_vari	MODIFIER	PRKDC
89	0.01111	0.01105	1	9:9821221	T	missense_	\ MODERATE	PTCH1
89	0.01111	0.01105	1	9:9824125	C	intron_vari	MODIFIER	PTCH1
89	0.01111	0.01105	1	1:1866469	A	intron_vari	MODIFIER	PTGS2
89	0.01111	0.01105	1	1:1866475	C	splice_regi	LOW	PTGS2

89	0.01111	0.01105	1	12:112910A	frameshift_HIGH	PTPN11
89	0	0.02198	0.005587	9:8460646-	intron_vari MODIFIER	PTPRD
89	0.01111	0.01105	1	9:8485904T	synonymo LOW	PTPRD
89	0.01111	0.01105	1	9:8485984T	missense_ \ MODERATE	PTPRD
89	0	0.02198	0.005587	20:407438G	intron_vari MODIFIER	PTPRT
89	0.01111	0.01105	1	5:1319244A	missense_ \ MODERATE	RAD50
89	0.01111	0.01105	1	3:1262640T	synonymo LOW	RAF1
89	0.01111	0.01105	1	3:1262673A	stop_gaine HIGH	RAF1
89	0.01111	0.01105	1	3:1264134GG	intron_vari MODIFIER	RAF1
89	0.01111	0.01105	1	9:1359813T	missense_ \ MODERATE	RALGDS
89	0.01111	0.01105	1	17:385047C	splice_regi LOW	RARA
89	0.01111	0.01105	1	8:1457373A	downstrea MODIFIER	GPT
88	0.02222	0.02198	1	2:6114777I-	frameshift_HIGH	REL
88	0.02222	0.02198	1	2:6114777G	missense_ \ MODERATE	REL
88	0.02222	0.02198	1	1:1850566G	intron_vari MODIFIER	RNF2
89	0.01111	0.01105	1	1:1850671I-	intron_vari MODIFIER	RNF2
89	0.01111	0.01105	1	17:782620T	missense_ \ MODERATE	RNF213
89	0.01111	0.01105	1	17:782643G	intron_vari MODIFIER	RNF213
89	0.01111	0.01105	1	17:782687T	missense_ \ MODERATE	RNF213
89	0.01111	0.01105	1	17:783191T	stop_gaine HIGH	RNF213
88	0.02222	0.02198	1	17:783516T	intron_vari MODIFIER	RNF213
89	0.01111	0.01105	1	17:783575C	frameshift_HIGH	RNF213
89	0.01111	0.01105	1	6:1177106G	missense_ \ MODERATE	ROS1
89	0.01111	0.01105	1	6:1669521T	intron_vari MODIFIER	RPS6KA2
89	0	0.02198	0.005587	8:9297266C	missense_ \ MODERATE	RUNX1T1
89	0.01111	0.01105	1	8:9302695A	missense_ \ MODERATE	RUNX1T1
89	0.01111	0.01105	1	8:9302948A	missense_ \ MODERATE	RUNX1T1
87	0.03333	0.03278	1	5:233504-2C	intron_vari MODIFIER	SDHA
89	0.01111	0.01105	1	3:4715548A	missense_ \ MODERATE	SETD2
89	0.01111	0.01105	1	3:4716399G	missense_ \ MODERATE	SETD2
89	0.01111	0.01105	1	2:1982627G	synonymo LOW	SF3B1
89	0.01111	0.01105	1	6:1344987T	intron_vari MODIFIER	SGK1
89	0.01111	0.01105	1	6:1345285A	missense_ \ MODERATE	SGK1
89	0.01111	0.01105	1	18:485752T	missense_ \ MODERATE	SMAD4
89	0.01111	0.01105	1	18:485934C	synonymo LOW	SMAD4
89	0.01111	0.01105	1	19:111705T	synonymo LOW	SMARCA4
87	0	0.06444	2.705e-006	22:241456C	intron_vari MODIFIER	SMARCB1
84	0.06667	0.06444	1	22:241676C	intron_vari MODIFIER	SMARCB1
89	0	0.02198	0.005587	2:5833815T	frameshift_HIGH	SOX11
89	0.01111	0.01105	1	3:1814308C	missense_ \ MODERATE	SOX2
89	0.01111	0.01105	1	20:360313T	intron_vari MODIFIER	SRC
88	0.02222	0.02198	1	20:360317G	synonymo LOW	SRC
89	0.01111	0.01105	1	2:2195448T	missense_ \ MODERATE	STK36
89	0.01111	0.01105	1	10:104357T	synonymo LOW	SUFU
89	0.01111	0.01105	1	9:9360631A	missense_ \ MODERATE	SYK
89	0.01111	0.01105	1	6:1524579T	synonymo LOW	SYNE1
89	0.01111	0.01105	1	6:1524707T	stop_gaine HIGH	SYNE1

89	0.01111	0.01105	1	6:1524728	C	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1525292	A	synonymous	LOW SYNE1
89	0.01111	0.01105	1	6:1525426	C	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1526315	A	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1526319	A	synonymous	LOW SYNE1
89	0.01111	0.01105	1	6:1526392	A	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1526446	A	synonymous	LOW SYNE1
89	0.01111	0.01105	1	6:1526521	C	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1526747	C	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1527126	A	missense_\ MODERATE	SYNE1
89	0.01111	0.01105	1	6:1528238	T	intron_variable	MODIFIER SYNE1
34	0.02857	0.02816	1	X:7059757	C	missense_\ MODERATE	TAF1
35	0	0	1	X:7068379	T	missense_\ MODERATE	TAF1
89	0.01111	0.01105	1	9:3263174	A	missense_\ MODERATE	TAF1L
34	0.02857	0.02816	1	X:7927960	C	missense_\ MODERATE	TBX22
88	0.02222	0.02198	1	19:164632	CGAG	intron_variable	MODIFIER TCF3
89	0.01111	0.01105	1	2:8553477	-	frameshift_	HIGH TCF7L1
89	0.01111	0.01105	1	10:114710	T	start_lost	HIGH TCF7L2
89	0.01111	0.01105	1	10:114911	T	missense_\ MODERATE	TCF7L2
89	0.01111	0.01105	1	10:703323	G	missense_\ MODERATE	TET1
89	0	0.02198	0.005587	10:704063	A	synonymous	LOW TET1
89	0.01111	0.01105	1	10:704515	A	missense_\ MODERATE	TET1
89	0.01111	0.01105	1	4:1061580	T	missense_\ MODERATE	TET2
89	0.01111	0.01105	1	4:1061938	-	frameshift_	HIGH TET2
34	0.02857	0.02816	1	X:4889687	T	missense_\ MODERATE	TFE3
88	0.02222	0.02198	1	15:398848	T	missense_\ MODERATE	THBS1
89	0.01111	0.01105	1	17:757963	-	intron_variable	MODIFIER TP53
89	0.01111	0.01105	1	1:1863014	T	missense_\ MODERATE	TPR
89	0.01111	0.01105	1	1:1863045	G	synonymous	LOW TPR
88	0.02222	0.02198	1	1:1863152	T	intron_variable	MODIFIER TPR
89	0.01111	0.01105	1	1:1149403	A	synonymous	LOW TRIM33
89	0.01111	0.01105	1	1:1149762	T	splice_region	LOW TRIM33
89	0.01111	0.01105	1	14:924547	T	intron_variable	MODIFIER TRIP11
88	0.02222	0.02198	1	14:924619	T	intron_variable	MODIFIER TRIP11
89	0.01111	0.01105	1	14:924718	T	missense_\ MODERATE	TRIP11
89	0.01111	0.01105	1	7:9854332	G	intron_variable	MODIFIER TRRAP
89	0.01111	0.01105	1	7:9855275	C	missense_\ MODERATE	TRRAP
89	0.01111	0.01105	1	7:9855276	T	stop_gained	HIGH TRRAP
89	0.01111	0.01105	1	7:9855277	T	missense_\ MODERATE	TRRAP
89	0.01111	0.01105	1	7:9857935	T	intron_variable	MODIFIER TRRAP
88	0	0.04346	9.469e-005	16:212945	T	intron_variable	MODIFIER TSC2
89	0.01111	0.01105	1	14:815542	C	intron_variable	MODIFIER TSHR
89	0.01111	0.01105	1	14:815543	G	missense_\ MODERATE	TSHR
89	0.01111	0.01105	1	14:816060	A	synonymous	LOW TSHR
89	0.01111	0.01105	1	8:1032849	T	missense_\ MODERATE	UBR5
89	0.01111	0.01105	1	8:1032893	C	missense_\ MODERATE	UBR5
89	0.01111	0.01105	1	8:1032974	G	synonymous	LOW UBR5

89	0.01111	0.01105	1	8:1033074	C	missense_ \ MODERATE	UBR5
88	0.02222	0.02198	1	8:1033414	-	intron_vari MODIFIER	UBR5
89	0.01111	0.01105	1	8:1033548	C	synonymo \ LOW	UBR5
34	0.02857	0.02816	1	X:4108872	T	intron_vari MODIFIER	USP9X
89	0.01111	0.01105	1	4:1961342	T	stop_gaine HIGH	WHSC1
86	0	0.08494	1.095e-007	4:1976481	G	intron_vari MODIFIER	WHSC1
87	0	0.06444	2.705e-006	4:1976483	G	intron_vari MODIFIER	WHSC1
89	0.01111	0.01105	1	4:1976485	GG	intron_vari MODIFIER	WHSC1
89	0.01111	0.01105	1	4:1976486	G	intron_vari MODIFIER	WHSC1
89	0.01111	0.01105	1	8:3093875	-	frameshift_ HIGH	WRN
89	0.01111	0.01105	1	8:3098986	C	intron_vari MODIFIER	WRN
89	0.01111	0.01105	1	8:3100483	A	intron_vari MODIFIER	WRN
89	0.01111	0.01105	1	8:3102468	T	missense_ \ MODERATE	WRN
84	0	0.1244	3.75e-010	12:677711	-	frameshift_ HIGH	ZNF384
89	0.01111	0.01105	1	12:678824	C	synonymo \ LOW	ZNF384

Gene	Feature_ty	Feature	BIOTYPE	EXON	INTRON	HGVSc	HGVSp	cDNA_posi
ENSG00000180137	Transcript	ENST00000263950	protein_coding	5/11	-	ENST00000263950	ENSP00000263950	1222
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	13/38	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	2/20	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	4/21	-	ENST00000263950	ENSP00000263950	524
ENSG00000180137	Transcript	ENST00000263950	protein_coding	8/50	-	ENST00000263950	ENSP00000263950	2236
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	8/49	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	18/50	-	ENST00000263950	ENSP00000263950	5002
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	20/49	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	27/50	-	ENST00000263950	ENSP00000263950	6591-6592
ENSG00000180137	Transcript	ENST00000263950	protein_coding	31/50	-	ENST00000263950	ENSP00000263950	7942
ENSG00000180137	Transcript	ENST00000263950	protein_coding	33/50	-	ENST00000263950	ENSP00000263950	8638
ENSG00000180137	Transcript	ENST00000263950	protein_coding	12/14	-	ENST00000263950	ENSP00000263950	1488
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	9/13	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	10/29	-	ENST00000263950	ENSP00000263950	2782
ENSG00000180137	Transcript	ENST00000263950	protein_coding	14/16	-	ENST00000263950	ENSP00000263950	2076
ENSG00000180137	Transcript	ENST00000263950	protein_coding	14/16	-	ENST00000263950	ENSP00000263950	2077
ENSG00000180137	Transcript	ENST00000263950	protein_coding	16/16	-	ENST00000263950	ENSP00000263950	3060-3061
ENSG00000180137	Transcript	ENST00000263950	protein_coding	16/16	-	ENST00000263950	ENSP00000263950	4297
ENSG00000180137	Transcript	ENST00000263950	protein_coding	16/16	-	ENST00000263950	ENSP00000263950	4700-4721
ENSG00000180137	Transcript	ENST00000263950	protein_coding	8/8	-	ENST00000263950	ENSP00000263950	3205
ENSG00000180137	Transcript	ENST00000263950	protein_coding	9/20	-	ENST00000263950	ENSP00000263950	3212
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ENSG00000180137	Transcript	ENST00000263950	protein_coding	13/20	-	ENST00000263950	ENSP00000263950	3797
ENSG00000180137	Transcript	ENST00000263950	protein_coding	20/20	-	ENST00000263950	ENSP00000263950	6325
ENSG00000180137	Transcript	ENST00000263950	protein_coding	17/21	-	ENST00000263950	ENSP00000263950	5199
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	6/21	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	8/62	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	37/62	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	50/63	-	ENST00000263950	ENSP00000263950	7762
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	44/46	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	44/46	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	39/47	-	ENST00000263950	ENSP00000263950	6740
ENSG00000180137	Transcript	ENST00000263950	protein_coding	14/47	-	ENST00000263950	ENSP00000263950	2960
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	11/46	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	10/46	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	26/34	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	6/11	-	ENST00000263950	ENSP00000263950	917-918
ENSG00000180137	Transcript	ENST00000263950	protein_coding	7/9	-	ENST00000263950	ENSP00000263950	718
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	4/6	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	3/32	-	ENST00000263950	ENSP00000263950	1446
ENSG00000180137	Transcript	ENST00000263950	protein_coding	29/32	-	ENST00000263950	ENSP00000263950	4899
ENSG00000180137	Transcript	ENST00000263950	protein_coding	3/3	-	ENST00000263950	ENSP00000263950	1380
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	1/2	ENST00000263950	-	-
ENSG00000180137	Transcript	ENST00000263950	protein_coding	-	2/3	ENST00000263950	-	-

ENSG0000(Transcript	ENST0000C protein_co 5/10	-	ENST0000C ENSP0000C 1541
ENSG0000(Transcript	ENST0000C protein_co 8/10	-	ENST0000C ENSP0000C 1476
ENSG0000(Transcript	ENST0000C protein_co -	8/9	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 2/9	-	ENST0000C ENSP0000C 2803
ENSG0000(Transcript	ENST0000C protein_co 2/9	-	ENST0000C ENSP0000C 3226
ENSG0000(Transcript	ENST0000C protein_co 6/9	-	ENST0000C ENSP0000C 3992
ENSG0000(Transcript	ENST0000C protein_co 9/9	-	ENST0000C ENSP0000C 4377
ENSG0000(Transcript	ENST0000C protein_co 9/9	-	ENST0000C ENSP0000C 4385
ENSG0000(Transcript	ENST0000C protein_co 1/5	-	ENST0000C - 123
ENSG0000(Transcript	ENST0000C protein_co 5/5	-	ENST0000C - 639
ENSG0000(Transcript	ENST0000C protein_co 7/22	-	ENST0000C ENSP0000C 1660
ENSG0000(Transcript	ENST0000C protein_co 19/22	-	ENST0000C ENSP0000C 3773
ENSG0000(Transcript	ENST0000C protein_co -	16-Jul	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 20/20	-	ENST0000C - 4027
ENSG0000(Transcript	ENST0000C protein_co -	12/19	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	11/19	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 13/25	-	ENST0000C ENSP0000C 2121
ENSG0000(Transcript	ENST0000C protein_co 11/27	-	ENST0000C ENSP0000C 1890
ENSG0000(Transcript	ENST0000C protein_co -	24/26	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	15-Apr	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	6/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	7/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	5/15	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	4/12	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	4/15	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 3/16	-	ENST0000C ENSP0000C 754
ENSG0000(Transcript	ENST0000C protein_co 12/12	-	ENST0000C ENSP0000C 2752
ENSG0000(Transcript	ENST0000C protein_co 2/14	-	ENST0000C ENSP0000C 1730
ENSG0000(Transcript	ENST0000C protein_co -	6/7	ENST0000C - -
ENSG0000(Transcript	ENST0000C nonsense_	4/5	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 2/20	-	ENST0000C ENSP0000C 247
ENSG0000(Transcript	ENST0000C protein_co 18/20	-	ENST0000C ENSP0000C 4366
ENSG0000(Transcript	ENST0000C protein_co -	Feb-50	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 10/11	-	ENST0000C ENSP0000C 1040
ENSG0000(Transcript	ENST0000C protein_co -	5/10	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 4/31	-	ENST0000C ENSP0000C 1803
ENSG0000(Transcript	ENST0000C protein_co -	65/70	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	56/70	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	49/70	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	29/70	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	25/70	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 16/18	-	ENST0000C ENSP0000C 2287
ENSG0000(Transcript	ENST0000C protein_co 18/18	-	ENST0000C ENSP0000C 2750-2752
ENSG0000(Transcript	ENST0000C protein_co 6/15	-	ENST0000C ENSP0000C 1060
ENSG0000(Transcript	ENST0000C protein_co 5/9	-	ENST0000C ENSP0000C 774
ENSG0000(Transcript	ENST0000C protein_co 4/9	-	ENST0000C ENSP0000C 674
ENSG0000(Transcript	ENST0000C protein_co 5/29	-	ENST0000C ENSP0000C 1503

ENSG0000(Transcript	ENST0000C protein_co 5/29	-	ENST0000C ENSP0000C 1523
ENSG0000(Transcript	ENST0000C protein_co 21/29	-	ENST0000C ENSP0000C 3779
ENSG0000(Transcript	ENST0000C protein_co -	22/28	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	12/18	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	13/18	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 18/19	-	ENST0000C ENSP0000C 2737
ENSG0000(Transcript	ENST0000C protein_co 23/29	-	ENST0000C ENSP0000C 4132
ENSG0000(Transcript	ENST0000C protein_co 23/23	-	ENST0000C ENSP0000C 3077
ENSG0000(Transcript	ENST0000C protein_co 3/23	-	ENST0000C ENSP0000C 510
ENSG0000(Transcript	ENST0000C protein_co -	21/22	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	7/22	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	3/22	ENST0000C - -
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ENSG0000(Transcript	ENST0000C protein_co 73/84	-	ENST0000C ENSP0000C 14043
ENSG0000(Transcript	ENST0000C protein_co 70/84	-	ENST0000C ENSP0000C 13689
ENSG0000(Transcript	ENST0000C protein_co 69/84	-	ENST0000C ENSP0000C 13498
ENSG0000(Transcript	ENST0000C protein_co 42/84	-	ENST0000C ENSP0000C 8781
ENSG0000(Transcript	ENST0000C protein_co 42/84	-	ENST0000C ENSP0000C 8481
ENSG0000(Transcript	ENST0000C protein_co -	22/83	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	22/83	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	21/83	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	11/30	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	16/30	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 4/53	-	ENST0000C ENSP0000C 1652
ENSG0000(Transcript	ENST0000C protein_co 14/53	-	ENST0000C ENSP0000C 3188
ENSG0000(Transcript	ENST0000C protein_co 17/53	-	ENST0000C ENSP0000C 3622
ENSG0000(Transcript	ENST0000C protein_co -	36/52	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 41/53	-	ENST0000C ENSP0000C 7479
ENSG0000(Transcript	ENST0000C protein_co 53/53	-	ENST0000C ENSP0000C 9332
ENSG0000(Transcript	ENST0000C protein_co -	6/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	9/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 10/17	-	ENST0000C ENSP0000C 1991
ENSG0000(Transcript	ENST0000C protein_co -	10/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	9/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	1/16	ENST0000C - -
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ENSG0000(Transcript	ENST0000C protein_co -	8/26	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	9/26	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 26/27	-	ENST0000C ENSP0000C 3451
ENSG0000(Transcript	ENST0000C protein_co -	3/27	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 28/28	-	ENST0000C ENSP0000C 3944
ENSG0000(Transcript	ENST0000C protein_co -	17/27	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	2/27	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 4/12	-	ENST0000C ENSP0000C 300
ENSG0000(Transcript	ENST0000C protein_co -	9/13	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 7/13	-	ENST0000C ENSP0000C 809
ENSG0000(Transcript	ENST0000C protein_co 8/11	-	ENST0000C ENSP0000C 2494

ENSG000001	Transcript	ENST000001	protein_co 1/11	-	ENST000001	ENSP000001	1662
ENSG000001	Transcript	ENST000001	protein_co -	10/13	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	8/19	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 2/2	-	ENST000001	ENSP000001	1800-1801
ENSG000001	Transcript	ENST000001	protein_co -	14/42	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	4/42	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 15/43	-	ENST000001	ENSP000001	1259
ENSG000001	Transcript	ENST000001	protein_co 37/43	-	ENST000001	ENSP000001	3832
ENSG000001	Transcript	ENST000001	protein_co -	58/63	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 12/12	-	ENST000001	ENSP000001	3310
ENSG000001	Transcript	ENST000001	protein_co 15/19	-	ENST000001	ENSP000001	2333
ENSG000001	Transcript	ENST000001	protein_co 15/18	-	ENST000001	ENSP000001	2634
ENSG000001	Transcript	ENST000001	protein_co -	5/17	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 13/18	-	ENST000001	ENSP000001	1976
ENSG000001	Transcript	ENST000001	protein_co 10/18	-	ENST000001	ENSP000001	1553
ENSG000001	Transcript	ENST000001	protein_co -	19/23	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 29/30	-	ENST000001	ENSP000001	3945
ENSG000001	Transcript	ENST000001	protein_co -	42/45	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 40/46	-	ENST000001	ENSP000001	6632
ENSG000001	Transcript	ENST000001	protein_co -	16/45	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 2/3	-	ENST000001	ENSP000001	1173
ENSG000001	Transcript	ENST000001	protein_co 2/3	-	ENST000001	ENSP000001	1565
ENSG000001	Transcript	ENST000001	protein_co 16-Jan	-	ENST000001	ENSP000001	280-281
ENSG000001	Transcript	ENST000001	protein_co 13/17	-	ENST000001	ENSP000001	1984
ENSG000001	Transcript	ENST000001	protein_co -	8/12	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 4/6	-	ENST000001	ENSP000001	1292
ENSG000001	Transcript	ENST000001	protein_co 1/13	-	ENST000001	ENSP000001	669
ENSG000001	Transcript	ENST000001	protein_co -	10/18	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 18/33	-	ENST000001	ENSP000001	3158
ENSG000001	Transcript	ENST000001	protein_co 8/9	-	ENST000001	ENSP000001	2424
ENSG000001	Transcript	ENST000001	protein_co -	20/21	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 12/12	-	ENST000001	ENSP000001	2808
ENSG000001	Transcript	ENST000001	protein_co -	10/11	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 9/11	-	ENST000001	ENSP000001	1282
ENSG000001	Transcript	ENST000001	protein_co -	1/20	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	10/20	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	1/47	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 31/48	-	ENST000001	ENSP000001	4587
ENSG000001	Transcript	ENST000001	protein_co -	12/21	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	3/21	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 17/17	-	ENST000001	ENSP000001	2888
ENSG000001	Transcript	ENST000001	protein_co 17/17	-	ENST000001	ENSP000001	2384
ENSG000001	Transcript	ENST000001	protein_co -	14/16	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 8/17	-	ENST000001	ENSP000001	1175
ENSG000001	Transcript	ENST000001	protein_co -	4/16	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 5/9	-	ENST000001	ENSP000001	666
ENSG000001	Transcript	ENST000001	protein_co 1/2	-	ENST000001	ENSP000001	4076

ENSG0000(Transcript	ENST0000C protein_co 4/30	-	ENST0000C ENSP0000C 515
ENSG0000(Transcript	ENST0000C protein_co -	4/29	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 7/30	-	ENST0000C ENSP0000C 846
ENSG0000(Transcript	ENST0000C protein_co 13/30	-	ENST0000C ENSP0000C 1715
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ENSG0000(Transcript	ENST0000C protein_co -	22/27	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	4/16	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 3/15	-	ENST0000C ENSP0000C 327
ENSG0000(Transcript	ENST0000C protein_co -	3/14	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 12/15	-	ENST0000C ENSP0000C 1943
ENSG0000(Transcript	ENST0000C protein_co 12/15	-	ENST0000C ENSP0000C 1967
ENSG0000(Transcript	ENST0000C protein_co 19/25	-	ENST0000C ENSP0000C 2982-2983
ENSG0000(Transcript	ENST0000C protein_co -	20/24	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 18/18	-	ENST0000C ENSP0000C 5241-5242
ENSG0000(Transcript	ENST0000C protein_co 18-Aug	-	ENST0000C ENSP0000C 1810
ENSG0000(Transcript	ENST0000C protein_co 8/18	-	ENST0000C ENSP0000C 2398
ENSG0000(Transcript	ENST0000C protein_co 12/18	-	ENST0000C ENSP0000C 2979
ENSG0000(Transcript	ENST0000C protein_co 12/18	-	ENST0000C ENSP0000C 2983
ENSG0000(Transcript	ENST0000C protein_co 12/18	-	ENST0000C ENSP0000C 2990
ENSG0000(Transcript	ENST0000C protein_co 7/26	-	ENST0000C ENSP0000C 1414
ENSG0000(Transcript	ENST0000C protein_co -	23/28	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	27/29	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 13/30	-	ENST0000C ENSP0000C 2185
ENSG0000(Transcript	ENST0000C protein_co 6/30	-	ENST0000C ENSP0000C 1094
ENSG0000(Transcript	ENST0000C protein_co 4/30	-	ENST0000C ENSP0000C 724-725
ENSG0000(Transcript	ENST0000C protein_co 4/6	-	ENST0000C ENSP0000C 1881
ENSG0000(Transcript	ENST0000C protein_co 2/4	-	ENST0000C ENSP0000C 500
ENSG0000(Transcript	ENST0000C protein_co 2/6	-	ENST0000C ENSP0000C 104-105
ENSG0000(Transcript	ENST0000C protein_co 20/20	-	ENST0000C ENSP0000C 3275
ENSG0000(Transcript	ENST0000C protein_co -	19/19	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	16/19	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	11/19	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 11/20	-	ENST0000C ENSP0000C 1680
ENSG0000(Transcript	ENST0000C protein_co 7/25	-	ENST0000C ENSP0000C 1351
ENSG0000(Transcript	ENST0000C protein_co 22/25	-	ENST0000C ENSP0000C 3705
ENSG0000(Transcript	ENST0000C protein_co -	82/90	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	64/90	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 62/91	-	ENST0000C ENSP0000C 10890
ENSG0000(Transcript	ENST0000C protein_co -	59/90	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 44/91	-	ENST0000C ENSP0000C 8357
ENSG0000(Transcript	ENST0000C protein_co 30/91	-	ENST0000C ENSP0000C 5981
ENSG0000(Transcript	ENST0000C protein_co -	28/90	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co 21/91	-	ENST0000C ENSP0000C 4180
ENSG0000(Transcript	ENST0000C protein_co 8/91	-	ENST0000C ENSP0000C 2085
ENSG0000(Transcript	ENST0000C protein_co -	6/90	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	4/90	ENST0000C - -
ENSG0000(Transcript	ENST0000C protein_co -	1/90	ENST0000C - -

ENSG0000(Transcript	ENST0000C protein_co -	1/16	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 14/23	-	ENST0000C ENSP0000C 2307	
ENSG0000(Transcript	ENST0000C protein_co 3/5	-	ENST0000C ENSP0000C 3467	
ENSG0000(Transcript	ENST0000C protein_co 2/5	-	ENST0000C ENSP0000C 2254	
ENSG0000(Transcript	ENST0000C protein_co 2/5	-	ENST0000C ENSP0000C 2090	
ENSG0000(Transcript	ENST0000C protein_co 10/11	-	ENST0000C ENSP0000C 1571	
ENSG0000(Transcript	ENST0000C protein_co -	11/17	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 17/17	-	ENST0000C ENSP0000C 2517	
ENSG0000(Transcript	ENST0000C protein_co -	-	-	-
ENSG0000(Transcript	ENST0000C protein_co -	10/15	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 2/3	-	ENST0000C ENSP0000C 994	
ENSG0000(Transcript	ENST0000C protein_co 10/10	-	ENST0000C ENSP0000C 2085	
ENSG0000(Transcript	ENST0000C protein_co 2/21	-	ENST0000C ENSP0000C 916	
ENSG0000(Transcript	ENST0000C protein_co 8/21	-	ENST0000C ENSP0000C 2178	
ENSG0000(Transcript	ENST0000C protein_co -	2/9	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	6/9	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 17/19	-	ENST0000C ENSP0000C 2152	
ENSG0000(Transcript	ENST0000C protein_co 27/36	-	ENST0000C ENSP0000C 9594	
ENSG0000(Transcript	ENST0000C protein_co 32/36	-	ENST0000C ENSP0000C 11328	
ENSG0000(Transcript	ENST0000C protein_co -	32/53	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 43/59	-	ENST0000C ENSP0000C 11226	
ENSG0000(Transcript	ENST0000C protein_co 36/59	-	ENST0000C ENSP0000C 5920	
ENSG0000(Transcript	ENST0000C protein_co -	25/58	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	25/58	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	25/58	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 12/59	-	ENST0000C ENSP0000C 1951	
ENSG0000(Transcript	ENST0000C protein_co -	6/58	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	22-May	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	5/22	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	18/22	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 1/12	-	ENST0000C -	25
ENSG0000(Transcript	ENST0000C protein_co -	-	-	-
ENSG0000(Transcript	ENST0000C protein_co 3/20	-	ENST0000C ENSP0000C 349	
ENSG0000(Transcript	ENST0000C protein_co 4/16	-	ENST0000C ENSP0000C 902	
ENSG0000(Transcript	ENST0000C protein_co -	5/15	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 6/16	-	ENST0000C ENSP0000C 1233	
ENSG0000(Transcript	ENST0000C protein_co 14/16	-	ENST0000C ENSP0000C 2483-2488	
ENSG0000(Transcript	ENST0000C protein_co 58/58	-	ENST0000C -	7767
ENSG0000(Transcript	ENST0000C protein_co 2/33	-	ENST0000C ENSP0000C 522-523	
ENSG0000(Transcript	ENST0000C protein_co -	17/32	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co -	23/32	ENST0000C -	-
ENSG0000(Transcript	ENST0000C protein_co 31/33	-	ENST0000C ENSP0000C 3861	
ENSG0000(Transcript	ENST0000C protein_co 6/8	5/7	ENST0000C -	?-1154
ENSG0000(Transcript	ENST0000C protein_co 3/8	-	ENST0000C ENSP0000C 831	
ENSG0000(Transcript	ENST0000C protein_co 3/16	-	ENST0000C ENSP0000C 377	
ENSG0000(Transcript	ENST0000C protein_co 3/3	-	ENST0000C ENSP0000C 1671-1672	
ENSG0000(Transcript	ENST0000C protein_co 3/3	-	ENST0000C -	1931

ENSG000001 Transcript	ENST000001 protein_co 3/3	-	ENST000001 ENSP000001 749
ENSG000001 Transcript	ENST000001 protein_co 3/3	-	ENST000001 ENSP000001 1521
ENSG000001 Transcript	ENST000001 protein_co 41/42	-	ENST000001 ENSP000001 5796
ENSG000001 Transcript	ENST000001 protein_co -	27/41	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co -	28/40	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 17/23	-	ENST000001 ENSP000001 3704
ENSG000001 Transcript	ENST000001 protein_co 17/23	-	ENST000001 ENSP000001 3520
ENSG000001 Transcript	ENST000001 protein_co -	8/22	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 8/23	-	ENST000001 ENSP000001 935
ENSG000001 Transcript	ENST000001 protein_co 3/23	-	ENST000001 ENSP000001 246
ENSG000001 Transcript	ENST000001 protein_co 9/12	-	ENST000001 ENSP000001 1309
ENSG000001 Transcript	ENST000001 protein_co -	10/11	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co -	9/57	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co -	29/57	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 53/58	-	ENST000001 ENSP000001 8160
ENSG000001 Transcript	ENST000001 protein_co 5/5	-	ENST000001 ENSP000001 1633
ENSG000001 Transcript	ENST000001 protein_co 21/24	-	ENST000001 ENSP000001 2861
ENSG000001 Transcript	ENST000001 protein_co -	21/23	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 22/24	-	ENST000001 ENSP000001 2952
ENSG000001 Transcript	ENST000001 protein_co 24/24	-	ENST000001 ENSP000001 3367
ENSG000001 Transcript	ENST000001 protein_co -	3/22	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 20/30	-	ENST000001 ENSP000001 4890
ENSG000001 Transcript	ENST000001 protein_co 18/30	-	ENST000001 ENSP000001 2619
ENSG000001 Transcript	ENST000001 protein_co 1/17	-	ENST000001 ENSP000001 74
ENSG000001 Transcript	ENST000001 protein_co -	22/33	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 4/34	-	ENST000001 ENSP000001 936
ENSG000001 Transcript	ENST000001 protein_co 29/30	-	ENST000001 ENSP000001 5431
ENSG000001 Transcript	ENST000001 protein_co 24/30	-	ENST000001 ENSP000001 4643
ENSG000001 Transcript	ENST000001 protein_co 5/23	-	ENST000001 ENSP000001 1849
ENSG000001 Transcript	ENST000001 protein_co 19/22	-	ENST000001 ENSP000001 3713
ENSG000001 Transcript	ENST000001 protein_co 7/17	-	ENST000001 ENSP000001 840
ENSG000001 Transcript	ENST000001 protein_co 12/19	-	ENST000001 ENSP000001 1487
ENSG000001 Transcript	ENST000001 protein_co 31/36	-	ENST000001 ENSP000001 5814
ENSG000001 Transcript	ENST000001 protein_co -	6/32	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co -	15/15	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co -	3/9	ENST000001 - -
ENSG000001 Transcript	ENST000001 protein_co 5/8	-	ENST000001 ENSP000001 1359
ENSG000001 Transcript	ENST000001 protein_co 23/30	-	ENST000001 ENSP000001 3671
ENSG000001 Transcript	ENST000001 protein_co 23/30	-	ENST000001 ENSP000001 3654
ENSG000001 Transcript	ENST000001 protein_co 44/44	-	ENST000001 - 7419
ENSG000001 Transcript	ENST000001 protein_co 38/44	-	ENST000001 ENSP000001 6446
ENSG000001 Transcript	ENST000001 protein_co 37/44	-	ENST000001 ENSP000001 6334
ENSG000001 Transcript	ENST000001 protein_co 37/44	-	ENST000001 ENSP000001 6328
ENSG000001 Transcript	ENST000001 protein_co 37/44	-	ENST000001 ENSP000001 6310
ENSG000001 Transcript	ENST000001 protein_co 37/44	-	ENST000001 ENSP000001 6305-6306
ENSG000001 Transcript	ENST000001 protein_co 34/44	-	ENST000001 ENSP000001 5873
ENSG000001 Transcript	ENST000001 protein_co 34/44	-	ENST000001 ENSP000001 5860

ENSG000001	Transcript	ENST000001	protein_co	27/44	-	ENST000001	ENSP000001	4687
ENSG000001	Transcript	ENST000001	protein_co	27/44	-	ENST000001	ENSP000001	4655
ENSG000001	Transcript	ENST000001	protein_co	25/44	-	ENST000001	ENSP000001	4024
ENSG000001	Transcript	ENST000001	protein_co	25/44	-	ENST000001	ENSP000001	3940
ENSG000001	Transcript	ENST000001	protein_co	-	23/43	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	23/44	-	ENST000001	ENSP000001	3258
ENSG000001	Transcript	ENST000001	protein_co	6/44	-	ENST000001	ENSP000001	1037
ENSG000001	Transcript	ENST000001	protein_co	-	5/43	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	5/43	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	5/43	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	1/44	-	ENST000001	ENSP000001	406
ENSG000001	Transcript	ENST000001	protein_co	1/44	-	ENST000001	ENSP000001	353
ENSG000001	Transcript	ENST000001	protein_co	1/44	-	ENST000001	ENSP000001	329
ENSG000001	Transcript	ENST000001	protein_co	4/23	-	ENST000001	ENSP000001	757
ENSG000001	Transcript	ENST000001	protein_co	4/23	-	ENST000001	ENSP000001	759
ENSG000001	Transcript	ENST000001	protein_co	-	19/22	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	4/23	-	ENST000001	ENSP000001	990
ENSG000001	Transcript	ENST000001	protein_co	-	21/22	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	3/34	-	ENST000001	ENSP000001	594
ENSG000001	Transcript	ENST000001	protein_co	-	2/20	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	5/20	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	4/23	-	ENST000001	ENSP000001	571
ENSG000001	Transcript	ENST000001	protein_co	-	10/10	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	2/16	-	ENST000001	ENSP000001	839
ENSG000001	Transcript	ENST000001	protein_co	12/16	-	ENST000001	ENSP000001	2174
ENSG000001	Transcript	ENST000001	protein_co	61/67	-	ENST000001	ENSP000001	10547
ENSG000001	Transcript	ENST000001	protein_co	58/67	-	ENST000001	ENSP000001	9632
ENSG000001	Transcript	ENST000001	protein_co	32/67	-	ENST000001	ENSP000001	5425
ENSG000001	Transcript	ENST000001	protein_co	32/67	-	ENST000001	ENSP000001	4386
ENSG000001	Transcript	ENST000001	protein_co	-	16/66	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	16/67	-	ENST000001	ENSP000001	1783
ENSG000001	Transcript	ENST000001	protein_co	9/13	-	ENST000001	ENSP000001	1568
ENSG000001	Transcript	ENST000001	protein_co	9/13	-	ENST000001	ENSP000001	2023
ENSG000001	Transcript	ENST000001	protein_co	11/15	-	ENST000001	ENSP000001	1462
ENSG000001	Transcript	ENST000001	protein_co	10/15	-	ENST000001	ENSP000001	1170
ENSG000001	Transcript	ENST000001	protein_co	-	8/14	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	14/18	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	1/10	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	87/87	-	ENST000001	ENSP000001	12246
ENSG000001	Transcript	ENST000001	protein_co	65/87	-	ENST000001	ENSP000001	8896
ENSG000001	Transcript	ENST000001	protein_co	43/87	-	ENST000001	ENSP000001	5718
ENSG000001	Transcript	ENST000001	protein_co	25/87	-	ENST000001	ENSP000001	2940
ENSG000001	Transcript	ENST000001	protein_co	-	22/86	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	21/24	-	ENST000001	ENSP000001	3761
ENSG000001	Transcript	ENST000001	protein_co	-	8/23	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	4/9	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	3/9	ENST000001	-	-

ENSG000001	Transcript	ENST000001	protein_co 7/16	-	ENST000001	ENSP000001	1012-1013
ENSG000001	Transcript	ENST000001	protein_co -	29/42	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 25/43	-	ENST000001	ENSP000001	3457
ENSG000001	Transcript	ENST000001	protein_co 25/43	-	ENST000001	ENSP000001	3377
ENSG000001	Transcript	ENST000001	protein_co -	22/30	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 8/25	-	ENST000001	ENSP000001	1505
ENSG000001	Transcript	ENST000001	protein_co 16/17	-	ENST000001	ENSP000001	2189
ENSG000001	Transcript	ENST000001	protein_co 15/17	-	ENST000001	ENSP000001	1992
ENSG000001	Transcript	ENST000001	protein_co -	9/16	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 9/18	-	ENST000001	ENSP000001	1605
ENSG000001	Transcript	ENST000001	protein_co -	3/8	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	-	-	-	-
ENSG000001	Transcript	ENST000001	protein_co 10/11	-	ENST000001	ENSP000001	1401
ENSG000001	Transcript	ENST000001	protein_co 10/11	-	ENST000001	ENSP000001	1405
ENSG000001	Transcript	ENST000001	protein_co -	1/6	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	4/6	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 4/68	-	ENST000001	ENSP000001	848
ENSG000001	Transcript	ENST000001	protein_co -	6/67	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 9/68	-	ENST000001	ENSP000001	1813
ENSG000001	Transcript	ENST000001	protein_co 29/68	-	ENST000001	ENSP000001	7110
ENSG000001	Transcript	ENST000001	protein_co -	54/67	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 59/68	-	ENST000001	ENSP000001	14254-14257
ENSG000001	Transcript	ENST000001	protein_co 12/43	-	ENST000001	ENSP000001	1813
ENSG000001	Transcript	ENST000001	protein_co -	3/21	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 11/11	-	ENST000001	ENSP000001	1661
ENSG000001	Transcript	ENST000001	protein_co 3/11	-	ENST000001	ENSP000001	364
ENSG000001	Transcript	ENST000001	protein_co 2/11	-	ENST000001	ENSP000001	244
ENSG000001	Transcript	ENST000001	protein_co -	7/14	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 5/21	-	ENST000001	ENSP000001	4637
ENSG000001	Transcript	ENST000001	protein_co 3/21	-	ENST000001	ENSP000001	2175
ENSG000001	Transcript	ENST000001	protein_co 22/25	-	ENST000001	ENSP000001	3347
ENSG000001	Transcript	ENST000001	protein_co -	3/13	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 3/14	-	ENST000001	ENSP000001	929
ENSG000001	Transcript	ENST000001	protein_co 3/12	-	ENST000001	ENSP000001	936
ENSG000001	Transcript	ENST000001	protein_co 10/12	-	ENST000001	ENSP000001	1729
ENSG000001	Transcript	ENST000001	protein_co 34/36	-	ENST000001	ENSP000001	4988
ENSG000001	Transcript	ENST000001	protein_co -	5/8	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	7/8	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 1/1	-	ENST000001	ENSP000001	1017-1018
ENSG000001	Transcript	ENST000001	protein_co 1/1	-	ENST000001	ENSP000001	1155
ENSG000001	Transcript	ENST000001	protein_co -	13/13	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 14/14	-	ENST000001	ENSP000001	1945
ENSG000001	Transcript	ENST000001	protein_co 9/27	-	ENST000001	ENSP000001	1412
ENSG000001	Transcript	ENST000001	protein_co 7/12	-	ENST000001	ENSP000001	1048
ENSG000001	Transcript	ENST000001	protein_co 2/14	-	ENST000001	ENSP000001	281
ENSG000001	Transcript	ENST000001	protein_co 141/146	-	ENST000001	ENSP000001	26099
ENSG000001	Transcript	ENST000001	protein_co 136/146	-	ENST000001	ENSP000001	25072

ENSG000001	Transcript	ENST000001	protein_co 135/146	-	ENST000001	ENSP000001	24928
ENSG000001	Transcript	ENST000001	protein_co 125/146	-	ENST000001	ENSP000001	23279
ENSG000001	Transcript	ENST000001	protein_co 118/146	-	ENST000001	ENSP000001	22131
ENSG000001	Transcript	ENST000001	protein_co 89/146	-	ENST000001	ENSP000001	17607
ENSG000001	Transcript	ENST000001	protein_co 88/146	-	ENST000001	ENSP000001	17351
ENSG000001	Transcript	ENST000001	protein_co 86/146	-	ENST000001	ENSP000001	17102
ENSG000001	Transcript	ENST000001	protein_co 82/146	-	ENST000001	ENSP000001	16478
ENSG000001	Transcript	ENST000001	protein_co 78/146	-	ENST000001	ENSP000001	14225
ENSG000001	Transcript	ENST000001	protein_co 68/146	-	ENST000001	ENSP000001	11617
ENSG000001	Transcript	ENST000001	protein_co 52/146	-	ENST000001	ENSP000001	8341
ENSG000001	Transcript	ENST000001	protein_co -	9/145	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 6/38	-	ENST000001	ENSP000001	905
ENSG000001	Transcript	ENST000001	protein_co 38/38	-	ENST000001	ENSP000001	5589
ENSG000001	Transcript	ENST000001	protein_co 1/1	-	ENST000001	ENSP000001	3920
ENSG000001	Transcript	ENST000001	protein_co 3/8	-	ENST000001	ENSP000001	432
ENSG000001	Transcript	ENST000001	protein_co -	3/18	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 11/12	-	ENST000001	ENSP000001	1547-1550
ENSG000001	Transcript	ENST000001	protein_co 1/14	-	ENST000001	ENSP000001	510
ENSG000001	Transcript	ENST000001	protein_co 10/14	-	ENST000001	ENSP000001	1564
ENSG000001	Transcript	ENST000001	protein_co 2/12	-	ENST000001	ENSP000001	456
ENSG000001	Transcript	ENST000001	protein_co 4/12	-	ENST000001	ENSP000001	4109
ENSG000001	Transcript	ENST000001	protein_co 12/12	-	ENST000001	ENSP000001	6559
ENSG000001	Transcript	ENST000001	protein_co 3/11	-	ENST000001	ENSP000001	3787
ENSG000001	Transcript	ENST000001	protein_co 10/11	-	ENST000001	ENSP000001	5207
ENSG000001	Transcript	ENST000001	protein_co 3/10	-	ENST000001	ENSP000001	552
ENSG000001	Transcript	ENST000001	protein_co 17/22	-	ENST000001	ENSP000001	2811
ENSG000001	Transcript	ENST000001	protein_co -	10-Mar	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 38/51	-	ENST000001	ENSP000001	5755
ENSG000001	Transcript	ENST000001	protein_co 34/51	-	ENST000001	ENSP000001	5127
ENSG000001	Transcript	ENST000001	protein_co -	23/50	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 20/20	-	ENST000001	ENSP000001	3423
ENSG000001	Transcript	ENST000001	protein_co -	5/19	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	15/20	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	13/20	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 11/21	-	ENST000001	ENSP000001	2814
ENSG000001	Transcript	ENST000001	protein_co -	31/71	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 40/72	-	ENST000001	ENSP000001	5954
ENSG000001	Transcript	ENST000001	protein_co 40/72	-	ENST000001	ENSP000001	5958
ENSG000001	Transcript	ENST000001	protein_co 40/72	-	ENST000001	ENSP000001	5977
ENSG000001	Transcript	ENST000001	protein_co -	57/71	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	28/41	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co -	4/10	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co 5/11	-	ENST000001	ENSP000001	645
ENSG000001	Transcript	ENST000001	protein_co 10/11	-	ENST000001	ENSP000001	1063
ENSG000001	Transcript	ENST000001	protein_co 48/59	-	ENST000001	ENSP000001	7401
ENSG000001	Transcript	ENST000001	protein_co 45/59	-	ENST000001	ENSP000001	6965
ENSG000001	Transcript	ENST000001	protein_co 40/59	-	ENST000001	ENSP000001	6254

ENSG000001	Transcript	ENST000001	protein_co	31/59	-	ENST000001	ENSP000001	4631
ENSG000001	Transcript	ENST000001	protein_co	-	10/58	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	9/59	-	ENST000001	ENSP000001	1546
ENSG000001	Transcript	ENST000001	protein_co	-	42/44	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	19/24	-	ENST000001	ENSP000001	3561
ENSG000001	Transcript	ENST000001	protein_co	-	20/23	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	20/23	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	20/23	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	20/23	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	9/35	-	ENST000001	ENSP000001	1460
ENSG000001	Transcript	ENST000001	protein_co	-	23/34	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	-	29/34	ENST000001	-	-
ENSG000001	Transcript	ENST000001	protein_co	34/35	-	ENST000001	ENSP000001	4378
ENSG000001	Transcript	ENST000001	protein_co	11/11	-	ENST000001	ENSP000001	1711
ENSG000001	Transcript	ENST000001	protein_co	4/11	-	ENST000001	ENSP000001	382

1174	392	P/S	Cca/Tca	-	-	-1	-	HGNC
736	246	Q/*	Cag/Tag	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
53	18	N/T	aAc/aCc	-	-	1	-	HGNC
476	159	R/I	aGa/aTa	-	-	1	-	HGNC
1242	414	N	aaT/aaC	-	-	1	-	HGNC
1627	543	P/T	Cca/Aca	-	-	1	-	HGNC
1635	545	E/D	gaA/gaC	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1542	514	K/N	aaA/aaT	-	-	1	-	HGNC
3655	1219	L/I	Ctt/Att	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1717	573	I/V	Atc/Gtc	-	-	-1	-	HGNC
1500	500	E/D	gaG/gaT	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
330	110	E/D	gaG/gaT	-	-	-1	-	HGNC
2354	785	R/Q	cGg/cAg	-	-	1	-	HGNC
1697	566	L/R	cTg/cGg	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	Clone_base
207	69	N	aaC/aaT	-	-	1	-	HGNC
4326	1442	T	acA/acG	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1017	339	S/R	agT/agG	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
993	331	S	tcA/tcC	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
2197	733	K/E	Aaa/Gaa	-	-	1	-	HGNC
2660-2662	887-888	QK/Q	cAGAag/ca	-	-	1	-	HGNC
780	260	H/Q	caC/caA	-	-	1	-	HGNC
692	231	N/S	aAc/aGc	-	-	1	-	HGNC
559	187	A/T	Gcc/Acc	-	-	-1	-	HGNC
887	296	L/R	cTt/cGt	-	-	1	-	HGNC

907	303	D/H	Gat/Cat	-	-	1	-	HGNC
3163	1055	G/C	Ggt/Tgt	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
2299	767	A/S	Gca/Tca	-	-	1	-	HGNC
3840	1280	S	agC/agT	-	-	-1	-	HGNC
2739	913	*/Y	taA/taC	-	-	-1	-	HGNC
172	58	P/S	Ccc/Tcc	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
13835	4612	Q/L	cAg/cTg	-	-	-1	-	HGNC
13481	4494	V/G	gTg/gGg	-	-	-1	-	HGNC
13290	4430	P	ccT/ccG	-	-	-1	-	HGNC
8573	2858	Q/P	cAa/cCa	-	-	-1	-	HGNC
8273	2758	L/R	cTt/cGt	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1543	515	G/R	Gga/Aga	-	-	1	-	HGNC
3079	1027	V/M	Gtg/Atg	-	-	1	-	HGNC
3513	1171	A	gcC/gcT	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
7370	2457	K/R	aAg/aGg	-	-	1	-	HGNC
9223	3075	T/P	Acc/Ccc	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1766	589	K/T	aAa/aCa	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1749	583	S	agC/agT	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
3292	1098	L	Ctg/Ttg	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
3633	1211	T	acC/acA	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
114	38	T	acA/acG	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
510	170	Q/H	caG/caC	-	-	-1	-	HGNC
1687	563	S/C	Agc/Tgc	-	-	-1	-	HGNC

855	285	H	caC/caT	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1527-1528	509-510	-/MSSX	-/ATGAGTT	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1166	389	Y/C	tAt/tGt	-	-	1	-	HGNC
3739	1247	K/X	Aaa/aa	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
2080	694	E/*	Gaa/Taa	-	-	-1	-	HGNC
2010	670	I	atA/atT	-	-	-1	-	HGNC
2042	681	Y/C	tAc/tGc	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1720	574	P/X	Ccc/cc	-	-	1	-	HGNC
1308	436	V	gtG/gtA	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
3866	1289	S/T	aGc/aCc	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
6262	2088	L/V	Ctg/Gtg	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
788	263	F/C	tTt/tGt	-	-	-1	-	HGNC
1222	408	M/V	Atg/Gtg	-	-	1	-	HGNC
126-127	42-43	-/X	-/G	-	-		-1	HGNC
1526	509	A/V	gCc/gTc	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
960	320	G	ggC/ggG	-	-	-1	-	HGNC
117	39	P	ccC/ccG	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
2858	953	R/L	cGg/cTg	-	-	1	-	HGNC
2034	678	F	ttC/ttT	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
2526	842	E/D	gaA/gaC	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1168	390	D/Y	Gac/Tac	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
4439	1480	Q/R	cAa/cGa	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
2575	859	S/A	Tcc/Gcc	-	-	-1	-	HGNC
2071	691	V/L	Gta/Tta	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
862	288	D/N	Gac/Aac	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
540	180	D	gaC/gaT	-	-	1	-	HGNC
3561	1187	E	gaG/gaA	-	-	-1	-	HGNC

624	208	R/S	agG/agT	-	-	-1	-	HGNC
1224	408	V	gtG/gtA	-	-	1	-	HGNC
5708	1903	I/T	aTc/aCc	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
3522	1174	P	ccG/ccT	-	-	-1	-	HGNC
3338	1113	D/G	gAt/gGt	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
753	251	C/W	tgC/tgG	-	-	-1	-	HGNC
64	22	C/R	Tgt/Cgt	-	-	-1	-	HGNC
1057	353	V/M	Gtg/Atg	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-		1 -	HGNC
7777	2593	L/V	Tta/Gta	-	-	1	-	HGNC
1078	360	S/P	Tca/Cca	-	-	-1	-	HGNC
2394	798	F/L	ttT/ttG	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
2485	829	P/T	Cca/Aca	-	-	1	-	HGNC
2900	967	G/V	gGc/gTc	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
4699	1567	A/P	Gca/Cca	-	-	-1	-	HGNC
2428	810	R/G	Aga/Gga	-	-	-1	-	HGNC
74	25	Q/L	cAg/cTg	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
716	239	T/S	aCt/aGt	-	-	-1	-	HGNC
5292	1764	D	gaC/gaT	-	-	-1	-	HGNC
4504	1502	P/S	Ccc/Tcc	-	-	-1	-	HGNC
1804	602	C/R	Tgt/Cgt	-	-	1	-	HGNC
3316	1106	L/V	Ctt/Gtt	-	-	-1	-	HGNC
799	267	A/T	Gca/Aca	-	-	1	-	HGNC
1325	442	A/V	gCc/gTc	-	-	-1	-	HGNC
5670	1890	G	ggA/ggG	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
761	254	T/I	aCc/aTc	-	-	1	-	HGNC
3571	1191	F/V	Ttt/Gtt	-	-	-1	-	HGNC
3554	1185	F/S	tTc/tCc	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
6155	2052	R/Q	cGa/cAa	-	-	-1	-	HGNC
6043	2015	I/V	Atc/Gtc	-	-	-1	-	HGNC
6037	2013	L	Cta/Tta	-	-	-1	-	HGNC
6019	2007	E/*	Gag/Tag	-	-	-1	-	HGNC
6014-6015	2005	L/Q	cTC/cAA	-	-	-1	-	HGNC
5582	1861	S/Y	tCc/tAc	-	-	-1	-	HGNC
5569	1857	R/C	Cgc/Tgc	-	-	-1	-	HGNC

814-815	272	E/EX	gaa/gAaa	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
2913	971	L	ctT/ctA	-	-	-1	-	HGNC
2833	945	A/T	Gca/Aca	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1118	373	S/Y	tCt/tAt	-	-	1	-	HGNC
1749	583	R	agG/agA	-	-	-1	-	HGNC
1552	518	R/*	Cga/Tga	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1583	528	S/N	aGc/aAc	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	4753	1	-	HGNC
1081	361	K/X	Aaa/aa	-	-	1	-	HGNC
1085	362	K/R	aAa/aGa	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
705	235	E/D	gaA/gaT	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1670	557	E/V	gAg/gTg	-	-	1	-	HGNC
6967	2323	Q/*	Cag/Tag	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
14111-141	4704	S/SX	agc/agCc	-	-	1	-	HGNC
1614	538	E/D	gaA/gaC	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1650	550	C/W	tgC/tgG	-	-	-1	-	HGNC
353	118	S/F	tCc/tTc	-	-	-1	-	HGNC
233	78	R/I	aGa/aTa	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
4594	1532	R/W	Cgg/Tgg	-	-	-1	-	HGNC
2132	711	V/A	gTc/gCc	-	-	-1	-	HGNC
3255	1085	A	gcA/gcC	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
331	111	P/S	Cca/Tca	-	-	-1	-	HGNC
398	133	Y/F	tAc/tTc	-	-	1	-	HGNC
1191	397	V	gtT/gtC	-	-	1	-	HGNC
4707	1569	D	gaC/gaT	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
962-963	321	Q/HX	cag/caTg	-	-	1	-	HGNC
728	243	V/A	gTg/gCg	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1596	532	P	ccC/ccG	-	-	1	-	HGNC
1133	378	P/L	cCt/cTt	-	-	1	-	HGNC
882	294	G	ggC/ggT	-	-	1	-	HGNC
133	45	R/S	Cgc/Agc	-	-	1	-	HGNC
25497	8499	I	atC/atA	-	-	-1	-	HGNC
24470	8157	S/*	tCa/tAa	-	-	-1	-	HGNC

24326	8109	Q/R	cAg/cGg	-	-	-1	-	HGNC
22677	7559	D	gaC/gaT	-	-	-1	-	HGNC
21529	7177	Q/E	Caa/Gaa	-	-	-1	-	HGNC
17005	5669	L/F	Ctc/Ttc	-	-	-1	-	HGNC
16749	5583	L	ctG/ctT	-	-	-1	-	HGNC
16500	5500	K/N	aaG/aaT	-	-	-1	-	HGNC
15876	5292	P	ccG/ccT	-	-	-1	-	HGNC
13623	4541	S/R	agT/agG	-	-	-1	-	HGNC
11015	3672	N/S	aAc/aGc	-	-	-1	-	HGNC
7739	2580	R/I	aGa/aTa	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
895	299	V/L	Gtg/Ctg	-	-	1	-	HGNC
5579	1860	S/F	tCt/tTt	-	-	1	-	HGNC
3830	1277	P/L	cCt/cTt	-	-	-1	-	HGNC
404	135	G/A	gGg/gCg	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
1272-1275	424-425	KR/X	aaGAGG/a	-	-	1	-	HGNC
3	1	M/I	atG/atT	-	-	1	-	HGNC
1057	353	P/S	Cct/Tct	-	-	1	-	HGNC
247	83	N/D	Aat/Gat	-	-	1	-	HGNC
3900	1300	T	acC/acA	-	-	1	-	HGNC
6350	2117	V/D	gTt/gAt	-	-	1	-	HGNC
2927	976	Q/L	cAg/cTg	-	-	1	-	HGNC
4347	1449	S/X	tcT/tc	-	-	1	-	HGNC
292	98	A/T	Gca/Aca	-	-	-1	-	HGNC
2646	882	Q/H	caG/caT	-	-	1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
5458	1820	S/T	Tcg/Acg	-	-	-1	-	HGNC
4830	1610	I	atT/atC	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
3339	1113	R	cgC/cgT	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
2440	814	E/K	Gaa/Aaa	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
5745	1915	E/D	gaA/gaC	-	-	1	-	HGNC
5749	1917	R/*	Cga/Tga	-	-	1	-	HGNC
5768	1923	A/V	gCg/gTg	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
323	108	I/S	aTt/aGt	-	-	1	-	HGNC
741	247	E	gaG/gaA	-	-	1	-	HGNC
6794	2265	R/Q	cGa/cAa	-	-	-1	-	HGNC
6358	2120	K/E	Aaa/Gaa	-	-	-1	-	HGNC
5647	1883	R	Agg/Cgg	-	-	-1	-	HGNC

4024	1342	M/V	Atg/Gtg	-	-	-1	-	HGNC
-	-	-	-	-	-	-1	-	HGNC
939	313	S	tcC/tcG	-	-	-1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
3130	1044	Q/*	Cag/Tag	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
1211	404	I/X	aTt/at	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
-	-	-	-	-	-	1	-	HGNC
4129	1377	G/C	Ggt/Tgt	-	-	1	-	HGNC
1503	501	Q/X	caG/ca	-	-	-1	-	HGNC
174	58	S	tcA/tcG	-	-	-1	-	HGNC

HGNC_ID	CANONICA	MANE	TSL	APPRIS	CCDS	ENSP	SWISSPROT	TREMBL
173	YES	-	-	-	CCDS33301	ENSP0000C P27037	B4DWQ2	
17178	YES	-	-	-	CCDS31778	ENSP0000C P59510	-	
7135	YES	-	-	-	CCDS54775	ENSP0000C P51825	Q712L1,F5I	
7135	YES	-	-	-	CCDS54775	ENSP0000C P51825	Q712L1,F5I	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
379	YES	-	-	-	CCDS5622.	ENSP0000C Q99996	Q8IW64	
392	YES	-	-	-	CCDS12552	ENSP0000C P31751	Q05BV0,M	
393	YES	-	-	-	CCDS31077	ENSP0000C Q9Y243	F8VS91	
427	YES	-	-	-	CCDS33172	ENSP0000C Q9UM73	Q580I3	
583	YES	-	-	-	CCDS4107.	ENSP0000C P25054	Q9UM98,Q	
583	YES	-	-	-	CCDS4107.	ENSP0000C P25054	Q9UM98,Q	
583	YES	-	-	-	CCDS4107.	ENSP0000C P25054	Q9UM98,Q	
583	YES	-	-	-	CCDS4107.	ENSP0000C P25054	Q9UM98,Q	
583	YES	-	-	-	CCDS4107.	ENSP0000C P25054	Q9UM98,Q	
644	YES	-	-	-	CCDS14387	ENSP0000C -	Q9NUA2,Q	
11110	YES	-	-	-	CCDS285.1	ENSP0000C O14497	Q96T01,Q9	
11110	YES	-	-	-	CCDS285.1	ENSP0000C O14497	Q96T01,Q9	
11110	YES	-	-	-	CCDS285.1	ENSP0000C O14497	Q96T01,Q9	
11110	YES	-	-	-	CCDS285.1	ENSP0000C O14497	Q96T01,Q9	
11110	YES	-	-	-	CCDS285.1	ENSP0000C O14497	Q96T01,Q9	
18037	YES	-	-	-	CCDS31783	ENSP0000C Q68CP9	Q96SQ4,F8	
700	YES	-	-	-	CCDS970.1	ENSP0000C P27540	-	
795	YES	-	-	-	CCDS31665	ENSP0000C Q13315	M0QXY8,E9	
795	YES	-	-	-	CCDS31665	ENSP0000C Q13315	M0QXY8,E9	
795	YES	-	-	-	CCDS31665	ENSP0000C Q13315	M0QXY8,E9	
882	YES	-	-	-	CCDS3124.	ENSP0000C Q13535	-	
882	YES	-	-	-	CCDS3124.	ENSP0000C Q13535	-	
882	YES	-	-	-	CCDS3124.	ENSP0000C Q13535	-	
882	YES	-	-	-	CCDS3124.	ENSP0000C Q13535	-	
882	YES	-	-	-	CCDS3124.	ENSP0000C Q13535	-	
882	YES	-	-	-	CCDS3124.	ENSP0000C Q13535	-	
886	YES	-	-	-	CCDS14434	ENSP0000C P46100	B4DLE1	
11393	YES	-	-	-	CCDS13451	ENSP0000C O14965	Q5QPD4,Q	
11390	YES	-	-	-	CCDS11134	ENSP0000C Q96GD4	J3QR41,J3K	
11391	YES	-	-	-	CCDS33128	ENSP0000C Q9UQB9	-	
945	YES	-	-	-	CCDS4968.	ENSP0000C O60242	S4R3D0,B7	
945	YES	-	-	-	CCDS4968.	ENSP0000C O60242	S4R3D0,B7	
989	YES	-	-	-	CCDS704.1	ENSP0000C O95999	-	
989	YES	-	-	-	CCDS704.1	ENSP0000C O95999	-	
13221	YES	-	-	-	CCDS1862.	ENSP0000C Q9H165	D6W5D9,Q	

1001	YES	-	-	-	CCDS3289. ENSP0000C P41182	C9JL16,C9J
1008	YES	-	-	-	CCDS3083. ENSP0000C O00512	-
1008	YES	-	-	-	CCDS3083. ENSP0000C O00512	-
591	YES	-	-	-	CCDS8315. ENSP0000C Q13489	-
591	YES	-	-	-	CCDS8315. ENSP0000C Q13489	-
591	YES	-	-	-	CCDS8315. ENSP0000C Q13489	-
591	YES	-	-	-	CCDS8315. ENSP0000C Q13489	-
591	YES	-	-	-	CCDS8315. ENSP0000C Q13489	-
593	YES	-	-	-	CCDS3275. ENSP0000C -	H3BLT4
593	YES	-	-	-	CCDS3275. ENSP0000C -	H3BLT4
1058	YES	-	-	-	CCDS1036. ENSP0000C P54132	-
1058	YES	-	-	-	CCDS1036. ENSP0000C P54132	-
14211	YES	-	-	-	CCDS7446. ENSP0000C Q8WV28	Q2MD56
20473	YES	-	-	-	CCDS11631. ENSP0000C Q9BX63	J3KS24
20473	YES	-	-	-	CCDS11631. ENSP0000C Q9BX63	J3KS24
20473	YES	-	-	-	CCDS11631. ENSP0000C Q9BX63	J3KS24
16393	YES	-	-	-	CCDS5336. ENSP0000C Q9BXL7	Q8TES3,E2
24054	YES	-	-	-	CCDS4202. ENSP0000C Q8NG31	-
24054	YES	-	-	-	CCDS4202. ENSP0000C Q8NG31	-
1541	YES	-	-	-	CCDS8418. ENSP0000C P22681	-
16783	YES	-	-	-	CCDS1382. ENSP0000C Q6P1J9	-
16783	YES	-	-	-	CCDS1382. ENSP0000C Q6P1J9	-
1748	YES	-	-	-	CCDS1086. ENSP0000C P12830	B3GN61
1750	YES	-	-	-	CCDS1080. ENSP0000C P55287	H3BUU9,H
1759	YES	-	-	-	CCDS11891. ENSP0000C P19022	C9JMH2,C9
1759	YES	-	-	-	CCDS11891. ENSP0000C P19022	C9JMH2,C9
1760	YES	-	-	-	CCDS11977. ENSP0000C Q9HBT6	Q8N9J3,K7
24224	YES	-	-	-	CCDS11337. ENSP0000C Q9NYV4	-
1773	YES	-	-	-	CCDS8953. ENSP0000C P11802	Q6LC83,F8
-	YES	-	-	-	- ENSP0000C -	F2Z2F3
14214	YES	-	-	-	CCDS12601. ENSP0000C Q96RK0	-
14214	YES	-	-	-	CCDS12601. ENSP0000C Q96RK0	-
2197	YES	-	-	-	CCDS11561. ENSP0000C P02452	Q9UMA6,C
30185	YES	-	-	-	CCDS2562. ENSP0000C Q96SW2	-
30185	YES	-	-	-	CCDS2562. ENSP0000C Q96SW2	-
2348	YES	-	-	-	CCDS1050. ENSP0000C Q92793	Q75MY6,I3
19291	YES	-	-	-	CCDS6315. ENSP0000C Q7Z407	-
19291	YES	-	-	-	CCDS6315. ENSP0000C Q7Z407	-
19291	YES	-	-	-	CCDS6315. ENSP0000C Q7Z407	-
19291	YES	-	-	-	CCDS6315. ENSP0000C Q7Z407	-
19291	YES	-	-	-	CCDS6315. ENSP0000C Q7Z407	-
2509	YES	-	-	-	CCDS3424. ENSP0000C P35221	F8W845,E5
2509	YES	-	-	-	CCDS3424. ENSP0000C P35221	F8W845,E5
2514	YES	-	-	-	CCDS2694. ENSP0000C P35222	G9GAG7,E5
2621	YES	-	-	-	CCDS7436. ENSP0000C P33261	-
2625	YES	-	-	-	CCDS46721. ENSP0000C -	Q6NWU0,C
2701	YES	-	-	-	CCDS11952. ENSP0000C P43146	J3QQJ6

2701	YES	-	-	-	CCDS11952 ENSP0000C P43146	J3QQJ6
2701	YES	-	-	-	CCDS11952 ENSP0000C P43146	J3QQJ6
2701	YES	-	-	-	CCDS11952 ENSP0000C P43146	J3QQJ6
2731	YES	-	-	-	CCDS1241. ENSP0000C Q16832	Q5T245,Q5
2731	YES	-	-	-	CCDS1241. ENSP0000C Q16832	Q5T245,Q5
2731	YES	-	-	-	CCDS1241. ENSP0000C Q16832	Q5T245,Q5
17098	YES	-	-	-	CCDS9931. ENSP0000C Q9UPY3	Q5D0K5,B3
2978	YES	-	-	-	CCDS33157 ENSP0000C Q9Y6K1	Q8WVA9,C
2978	YES	-	-	-	CCDS33157 ENSP0000C Q9Y6K1	Q8WVA9,C
3012	YES	-	-	-	CCDS30777 ENSP0000C Q12882	-
3012	YES	-	-	-	CCDS30777 ENSP0000C Q12882	-
3012	YES	-	-	-	CCDS30777 ENSP0000C Q12882	-
3012	YES	-	-	-	CCDS30777 ENSP0000C Q12882	-
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
1090	YES	-	-	-	CCDS47443 ENSP0000C Q03001	Q86T18
3373	YES	-	-	-	CCDS1401C ENSP0000C Q09472	B5A250
3373	YES	-	-	-	CCDS1401C ENSP0000C Q09472	B5A250
11958	YES	-	-	-	CCDS31925 ENSP0000C Q96L91	-
11958	YES	-	-	-	CCDS31925 ENSP0000C Q96L91	-
11958	YES	-	-	-	CCDS31925 ENSP0000C Q96L91	-
11958	YES	-	-	-	CCDS31925 ENSP0000C Q96L91	-
11958	YES	-	-	-	CCDS31925 ENSP0000C Q96L91	-
11958	YES	-	-	-	CCDS31925 ENSP0000C Q96L91	-
3387	YES	-	-	-	CCDS2922. ENSP0000C P29320	-
3387	YES	-	-	-	CCDS2922. ENSP0000C P29320	-
3387	YES	-	-	-	CCDS2922. ENSP0000C P29320	-
3390	YES	-	-	-	CCDS5031. ENSP0000C Q15375	-
3390	YES	-	-	-	CCDS5031. ENSP0000C Q15375	-
3390	YES	-	-	-	CCDS5031. ENSP0000C Q15375	-
3392	YES	-	-	-	CCDS46921 ENSP0000C P54762	C9K090,C9J.
3430	YES	-	-	-	CCDS32642 ENSP0000C P04626	Q9NP09,J3
3430	YES	-	-	-	CCDS32642 ENSP0000C P04626	Q9NP09,J3
3430	YES	-	-	-	CCDS32642 ENSP0000C P04626	Q9NP09,J3
3431	YES	-	-	-	CCDS31833 ENSP0000C P21860	Q9NNX2,F8
3432	YES	-	-	-	CCDS2394. ENSP0000C Q15303	Q580Q7,Q5
3432	YES	-	-	-	CCDS2394. ENSP0000C Q15303	Q580Q7,Q5
3432	YES	-	-	-	CCDS2394. ENSP0000C Q15303	Q580Q7,Q5
3446	YES	-	-	-	CCDS46648 ENSP0000C P11308	Q16031,B4
3490	YES	-	-	-	CCDS55088 ENSP0000C P50549	C9J9L1,C9J.
3493	YES	-	-	-	CCDS11465 ENSP0000C P43268	K7EMW0
3512	YES	-	-	-	CCDS6324. ENSP0000C Q16394	T2FFJ4,S5Y

3512	YES	-	-	-	CCDS6324. ENSP0000C Q16394	T2FFJ4,S5Y
3513	YES	-	-	-	CCDS53618 ENSP0000C Q93063	E9PNL9,E9I
3527	YES	-	-	-	CCDS5891. ENSP0000C Q15910	Q75MQ0,C
26837	YES	-	-	-	CCDS14377 ENSP0000C Q5JTC6	-
3582	YES	-	-	-	CCDS32515 ENSP0000C O15360	H3BT53
3582	YES	-	-	-	CCDS32515 ENSP0000C O15360	H3BT53
3585	YES	-	-	-	CCDS2595. ENSP0000C Q9BXW9	-
3585	YES	-	-	-	CCDS2595. ENSP0000C Q9BXW9	-
18794	YES	-	-	-	CCDS12196 ENSP0000C Q75N90	-
16712	YES	-	-	-	CCDS3777. ENSP0000C Q969H0	S4R3N3,H9
3688	YES	-	-	-	CCDS55223 ENSP0000C P11362	E9PN14,D3
3689	YES	-	-	-	CCDS7620. ENSP0000C P21802	Q9UMB0,C
3690	YES	-	-	-	CCDS54706 ENSP0000C P22607	Q8NI16
3690	YES	-	-	-	CCDS54706 ENSP0000C P22607	Q8NI16
3691	YES	-	-	-	CCDS4410. ENSP0000C P22455	G3JVM2,E7
3765	YES	-	-	-	CCDS31953 ENSP0000C P36888	-
3767	YES	-	-	-	CCDS4457. ENSP0000C P35916	D6RFF2
3778	YES	-	-	-	CCDS42814 ENSP0000C P02751	Q9H382,Q7
3778	YES	-	-	-	CCDS42814 ENSP0000C P02751	Q9H382,Q7
3778	YES	-	-	-	CCDS42814 ENSP0000C P02751	Q9H382,Q7
3819	YES	-	-	-	CCDS9371. ENSP0000C Q12778	-
3821	YES	-	-	-	CCDS5068. ENSP0000C O43524	B4DVZ6
3823	YES	-	-	-	CCDS58837 ENSP0000C -	Q8IXF4,E9F
20842	YES	-	-	-	CCDS34447 ENSP0000C Q8IVH2	Q8N4A5,QI
24824	YES	-	-	-	CCDS45916 ENSP0000C Q9UM11	-
4171	YES	-	-	-	CCDS3049. ENSP0000C P23769	C9J965
4392	YES	-	-	-	CCDS46622 ENSP0000C Q5JWF2	S4R3W4,S4
17849	YES	-	-	-	CCDS6097. ENSP0000C Q96PE1	-
24885	YES	-	-	-	CCDS42655 ENSP0000C Q4ZG55	-
4684	YES	-	-	-	CCDS5817C ENSP0000C P33402	-
23576	YES	-	-	-	CCDS6139. ENSP0000C Q86VS8	-
5253	YES	-	-	-	CCDS3216C ENSP0000C P07900	Q96HX7,Q8
5253	YES	-	-	-	CCDS3216C ENSP0000C P07900	Q96HX7,Q8
5383	YES	-	-	-	CCDS10355 ENSP0000C P48735	HOYLL5,B4I
5465	YES	-	-	-	CCDS10378 ENSP0000C P08069	HOYNR0,HC
5465	YES	-	-	-	CCDS10378 ENSP0000C P08069	HOYNR0,HC
5467	YES	-	-	-	CCDS5273. ENSP0000C P11717	A0N9R7,AC
5467	YES	-	-	-	CCDS5273. ENSP0000C P11717	A0N9R7,AC
5960	YES	-	-	-	CCDS6128. ENSP0000C O14920	E5RGW5
14552	YES	-	-	-	CCDS30996 ENSP0000C Q14164	-
6021	YES	-	-	-	CCDS3971. ENSP0000C P40189	-
6021	YES	-	-	-	CCDS3971. ENSP0000C P40189	-
6021	YES	-	-	-	CCDS3971. ENSP0000C P40189	-
6021	YES	-	-	-	CCDS3971. ENSP0000C P40189	-
6021	YES	-	-	-	CCDS3971. ENSP0000C P40189	-
6119	YES	-	-	-	CCDS4469. ENSP0000C Q15306	-
6126	YES	-	-	-	CCDS9510. ENSP0000C Q9Y4H2	Q9UP29,Q8

[illegible]

6720	YES	-	-	-	CCDS33747 ENSP0000C P02788	C9J0S5,A8k
946	YES	-	-	-	CCDS3378C ENSP0000C Q96QZ7	-
16259	YES	-	-	-	CCDS44714 ENSP0000C Q8IZL2	-
16259	YES	-	-	-	CCDS44714 ENSP0000C Q8IZL2	-
16259	YES	-	-	-	CCDS44714 ENSP0000C Q8IZL2	-
6840	YES	-	-	-	CCDS10216 ENSP0000C Q02750	A4QPA9
6896	YES	-	-	-	CCDS31025 ENSP0000C Q9P0L2	B4DIB3
13538	YES	-	-	-	CCDS56097 ENSP0000C Q96L34	Q96GZ3,K7
26530	YES	-	-	-	CCDS1194C ENSP0000C Q96M91	-
6916	YES	-	-	-	CCDS5932C ENSP0000C -	K7ESN0
6943	YES	-	-	-	CCDS957.1 ENSP0000C Q07820	B4DG83
7010	YES	-	-	-	CCDS8083. ENSP0000C O00255	Q9GZQ5
7029	YES	-	-	-	CCDS47685 ENSP0000C P08581	Q9UEJ3,B4
7029	YES	-	-	-	CCDS47685 ENSP0000C P08581	Q9UEJ3,B4
7105	YES	-	-	-	CCDS43106 ENSP0000C O75030	C9K0S7
7105	YES	-	-	-	CCDS43106 ENSP0000C O75030	C9K0S7
7127	YES	-	-	-	CCDS2663. ENSP0000C P40692	Q5GJ64,F2:
7132	YES	-	-	-	CCDS55791 ENSP0000C Q03164	Q9UPD0,Q:
7132	YES	-	-	-	CCDS55791 ENSP0000C Q03164	Q9UPD0,Q:
7133	YES	-	-	-	CCDS44873 ENSP0000C O14686	Q6PIA1,Q5
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
13726	YES	-	-	-	CCDS5931. ENSP0000C Q8NEZ4	Q6N019,Q:
16063	YES	-	-	-	CCDS55708 ENSP0000C P55197	Q71UR7,B4
16063	YES	-	-	-	CCDS55708 ENSP0000C P55197	Q71UR7,B4
16063	YES	-	-	-	CCDS55708 ENSP0000C P55197	Q71UR7,B4
7217	YES	-	-	-	CCDS483.1 ENSP0000C P40238	-
7217	YES	-	-	-	CCDS483.1 ENSP0000C P40238	-
7230	YES	-	-	-	CCDS8299. ENSP0000C P49959	Q9BS79,F5
7325	YES	-	-	-	CCDS1834. ENSP0000C P43246	Q53RU4,C9
7325	YES	-	-	-	CCDS1834. ENSP0000C P43246	Q53RU4,C9
7325	YES	-	-	-	CCDS1834. ENSP0000C P43246	Q53RU4,C9
7325	YES	-	-	-	CCDS1834. ENSP0000C P43246	Q53RU4,C9
3942	YES	-	-	-	CCDS127.1 ENSP0000C P42345	Q96QW8,B
7468	YES	-	-	-	CCDS1614. ENSP0000C Q99707	-
7468	YES	-	-	-	CCDS1614. ENSP0000C Q99707	-
7468	YES	-	-	-	CCDS1614. ENSP0000C Q99707	-
7468	YES	-	-	-	CCDS1614. ENSP0000C Q99707	-
7508	YES	-	-	-	CCDS5564C ENSP0000C -	Q9UMI8,Q:
7508	YES	-	-	-	CCDS5564C ENSP0000C -	Q9UMI8,Q:
7527	YES	-	-	-	CCDS520.1 ENSP0000C Q9UIF7	E5KP26,Q8
7553	YES	-	-	-	CCDS6359. ENSP0000C P01106	Q6LBK7,B4
7553	YES	-	-	-	CCDS6359. ENSP0000C P01106	Q6LBK7,B4

[illegible]

15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
15580	YES	-	-	-	CCDS55627 ENSP0000C Q5VU43	I1VE15
8803	YES	-	-	-	CCDS3495. ENSP0000C P16234	D6RIG5,D6
8803	YES	-	-	-	CCDS3495. ENSP0000C P16234	D6RIG5,D6
8804	YES	-	-	-	CCDS4303. ENSP0000C P09619	E5RJ14,E5F
8804	YES	-	-	-	CCDS4303. ENSP0000C P09619	E5RJ14,E5F
8845	YES	-	-	-	CCDS11131 ENSP0000C O15534	J3QLQ5,A2
8972	YES	-	-	-	CCDS1446. ENSP0000C O00750	Q5SW98,Q
8975	YES	-	-	-	CCDS43171 ENSP0000C P42336	Q4LE51,C9.
8975	YES	-	-	-	CCDS43171 ENSP0000C P42336	Q4LE51,C9.
8976	YES	-	-	-	CCDS3104. ENSP0000C P42338	Q9BTS4,Q6
8978	YES	-	-	-	CCDS5739. ENSP0000C P48736	Q24M88,E9
8979	YES	-	-	-	CCDS3993. ENSP0000C P27986	J7GXU7,J7C
8979	YES	-	-	-	CCDS3993. ENSP0000C P27986	J7GXU7,J7C
9016	YES	-	-	-	CCDS4935. ENSP0000C P08F94	-
9016	YES	-	-	-	CCDS4935. ENSP0000C P08F94	-
9016	YES	-	-	-	CCDS4935. ENSP0000C P08F94	-
9016	YES	-	-	-	CCDS4935. ENSP0000C P08F94	-
9016	YES	-	-	-	CCDS4935. ENSP0000C P08F94	-
9016	YES	-	-	-	CCDS4935. ENSP0000C P08F94	-
9121	YES	-	-	-	CCDS2302. ENSP0000C P54277	Q5FBZ2,C9.
9121	YES	-	-	-	CCDS2302. ENSP0000C P54277	Q5FBZ2,C9.
9122	YES	-	-	-	CCDS5343. ENSP0000C P54278	-
9122	YES	-	-	-	CCDS5343. ENSP0000C P54278	-
9122	YES	-	-	-	CCDS5343. ENSP0000C P54278	-
17284	YES	-	-	-	CCDS5793. ENSP0000C Q9NUX5	C9JPG9,A8I
9388	YES	-	-	-	CCDS11678 ENSP0000C P10644	Q96P62,K7
9413	YES	-	-	-	- ENSP0000C P78527	F5GX40
9413	YES	-	-	-	- ENSP0000C P78527	F5GX40
9413	YES	-	-	-	- ENSP0000C P78527	F5GX40
9413	YES	-	-	-	- ENSP0000C P78527	F5GX40
9413	YES	-	-	-	- ENSP0000C P78527	F5GX40
9585	YES	-	-	-	CCDS6714. ENSP0000C Q13635	Q6TKQ0,F8
9585	YES	-	-	-	CCDS6714. ENSP0000C Q13635	Q6TKQ0,F8
9605	YES	-	-	-	CCDS1371. ENSP0000C P35354	D9MWI3
9605	YES	-	-	-	CCDS1371. ENSP0000C P35354	D9MWI3

9644	YES	-	-	-	CCDS9163. ENSP0000C Q06124	B3GUD4,B3
9668	YES	-	-	-	CCDS4378C ENSP0000C P23468	C9J6E4,B4C
9668	YES	-	-	-	CCDS4378C ENSP0000C P23468	C9J6E4,B4C
9668	YES	-	-	-	CCDS4378C ENSP0000C P23468	C9J6E4,B4C
9682	YES	-	-	-	CCDS4287C ENSP0000C O14522	-
9816	YES	-	-	-	CCDS3423C ENSP0000C Q92878	C9JNH8,A8
9829	YES	-	-	-	CCDS2612. ENSP0000C P04049	L7RRS6
9829	YES	-	-	-	CCDS2612. ENSP0000C P04049	L7RRS6
9829	YES	-	-	-	CCDS2612. ENSP0000C P04049	L7RRS6
9842	YES	-	-	-	CCDS6959. ENSP0000C Q12967	Q9HAY0,Q9
9864	YES	-	-	-	CCDS1136C ENSP0000C P10276	Q6I9R7,J3C
4552	YES	-	-	-	CCDS6430. ENSP0000C P24298	-
9954	YES	-	-	-	CCDS1864. ENSP0000C Q04864	-
9954	YES	-	-	-	CCDS1864. ENSP0000C Q04864	-
10061	YES	-	-	-	CCDS1365. ENSP0000C Q99496	-
10061	YES	-	-	-	CCDS1365. ENSP0000C Q99496	-
14539	YES	-	-	-	CCDS5860C ENSP0000C Q63HN8	H3BLU6
14539	YES	-	-	-	CCDS5860C ENSP0000C Q63HN8	H3BLU6
14539	YES	-	-	-	CCDS5860C ENSP0000C Q63HN8	H3BLU6
14539	YES	-	-	-	CCDS5860C ENSP0000C Q63HN8	H3BLU6
14539	YES	-	-	-	CCDS5860C ENSP0000C Q63HN8	H3BLU6
14539	YES	-	-	-	CCDS5860C ENSP0000C Q63HN8	H3BLU6
10261	YES	-	-	-	CCDS5116. ENSP0000C P08922	-
10431	YES	-	-	-	CCDS3457C ENSP0000C Q15349	D6RHW7,D
1535	YES	-	-	-	CCDS5654C ENSP0000C Q06455	Q9HBV9,E5
1535	YES	-	-	-	CCDS5654C ENSP0000C Q06455	Q9HBV9,E5
1535	YES	-	-	-	CCDS5654C ENSP0000C Q06455	Q9HBV9,E5
10680	YES	-	-	-	CCDS3853. ENSP0000C P31040	Q0QF12,B3
18420	YES	-	-	-	CCDS2749. ENSP0000C Q9BYW2	C9JG86
18420	YES	-	-	-	CCDS2749. ENSP0000C Q9BYW2	C9JG86
10768	YES	-	-	-	CCDS3335C ENSP0000C O75533	Q9NTB4,F8
10810	YES	-	-	-	CCDS4747C ENSP0000C O00141	E9PP33,E9I
10810	YES	-	-	-	CCDS4747C ENSP0000C O00141	E9PP33,E9I
6770	YES	-	-	-	CCDS1195C ENSP0000C Q13485	Q9BYG6,K7
6770	YES	-	-	-	CCDS1195C ENSP0000C Q13485	Q9BYG6,K7
11100	YES	-	-	-	CCDS1225C ENSP0000C P51532	B4DSI8,A7E
11103	YES	-	-	-	CCDS13817 ENSP0000C Q12824	-
11103	YES	-	-	-	CCDS13817 ENSP0000C Q12824	-
11191	YES	-	-	-	CCDS1654. ENSP0000C P35716	Q05CHO
11195	YES	-	-	-	CCDS3239. ENSP0000C P48431	-
11283	YES	-	-	-	CCDS1329C ENSP0000C P12931	Q9H7V3,Q9
11283	YES	-	-	-	CCDS1329C ENSP0000C P12931	Q9H7V3,Q9
17209	YES	-	-	-	CCDS2421. ENSP0000C Q9NRP7	C9JDA4,C9.
16466	YES	-	-	-	CCDS7537. ENSP0000C Q9UMX1	-
11491	YES	-	-	-	CCDS6688. ENSP0000C P43405	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-

17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
17089	YES	-	-	-	CCDS5236. ENSP0000C Q8NF91	-
11535	YES	-	-	-	CCDS14412 ENSP0000C P21675	-
11535	YES	-	-	-	CCDS14412 ENSP0000C P21675	-
18056	YES	-	-	-	CCDS35003 ENSP0000C Q8IZX4	-
11600	YES	-	-	-	CCDS14445 ENSP0000C Q9Y458	C3TX51
11633	YES	-	-	-	CCDS12074 ENSP0000C P15923	Q6PJU3,K7
11640	YES	-	-	-	CCDS1971. ENSP0000C Q9HCS4	Q53T87,C9
11641	YES	-	-	-	CCDS53577 ENSP0000C Q9NQBO	E2GH26,C6
11641	YES	-	-	-	CCDS53577 ENSP0000C Q9NQBO	E2GH26,C6
29484	YES	-	-	-	CCDS7281. ENSP0000C Q8NFU7	-
29484	YES	-	-	-	CCDS7281. ENSP0000C Q8NFU7	-
29484	YES	-	-	-	CCDS7281. ENSP0000C Q8NFU7	-
25941	YES	-	-	-	CCDS4712C ENSP0000C Q6N021	E7EPB1,D6
25941	YES	-	-	-	CCDS4712C ENSP0000C Q6N021	E7EPB1,D6
11752	YES	-	-	-	CCDS14315 ENSP0000C P19532	B4DIA5
11785	YES	-	-	-	CCDS32194 ENSP0000C P07996	Q7KYY3,A8
11998	YES	-	-	-	CCDS11118 ENSP0000C P04637	S5LQU8,Q7
12017	YES	-	-	-	CCDS41446 ENSP0000C P12270	Q9UE33
12017	YES	-	-	-	CCDS41446 ENSP0000C P12270	Q9UE33
12017	YES	-	-	-	CCDS41446 ENSP0000C P12270	Q9UE33
16290	YES	-	-	-	CCDS872.1 ENSP0000C Q9UPN9	-
16290	YES	-	-	-	CCDS872.1 ENSP0000C Q9UPN9	-
12305	YES	-	-	-	CCDS9899. ENSP0000C Q15643	G3V4R7
12305	YES	-	-	-	CCDS9899. ENSP0000C Q15643	G3V4R7
12305	YES	-	-	-	CCDS9899. ENSP0000C Q15643	G3V4R7
12347	YES	-	-	-	CCDS59066 ENSP0000C Q9Y4A5	C9K0N1
12347	YES	-	-	-	CCDS59066 ENSP0000C Q9Y4A5	C9K0N1
12347	YES	-	-	-	CCDS59066 ENSP0000C Q9Y4A5	C9K0N1
12347	YES	-	-	-	CCDS59066 ENSP0000C Q9Y4A5	C9K0N1
12347	YES	-	-	-	CCDS59066 ENSP0000C Q9Y4A5	C9K0N1
12363	YES	-	-	-	CCDS10458 ENSP0000C P49815	-
12373	YES	-	-	-	CCDS9872. ENSP0000C -	Q0VAP8,F5
12373	YES	-	-	-	CCDS9872. ENSP0000C -	Q0VAP8,F5
12373	YES	-	-	-	CCDS9872. ENSP0000C -	Q0VAP8,F5
16806	YES	-	-	-	CCDS34933 ENSP0000C O95071	Q49A65,E5
16806	YES	-	-	-	CCDS34933 ENSP0000C O95071	Q49A65,E5
16806	YES	-	-	-	CCDS34933 ENSP0000C O95071	Q49A65,E5

16806	YES	-	-	-	CCDS34933 ENSP0000C O95071	Q49A65,E5
16806	YES	-	-	-	CCDS34933 ENSP0000C O95071	Q49A65,E5
16806	YES	-	-	-	CCDS34933 ENSP0000C O95071	Q49A65,E5
12632	YES	-	-	-	CCDS4393C ENSP0000C Q93008	-
12766	YES	-	-	-	CCDS3394C ENSP0000C O96028	D6RIS1,D6f
12766	YES	-	-	-	CCDS3394C ENSP0000C O96028	D6RIS1,D6f
12766	YES	-	-	-	CCDS3394C ENSP0000C O96028	D6RIS1,D6f
12766	YES	-	-	-	CCDS3394C ENSP0000C O96028	D6RIS1,D6f
12766	YES	-	-	-	CCDS3394C ENSP0000C O96028	D6RIS1,D6f
12791	YES	-	-	-	CCDS6082. ENSP0000C Q14191	-
12791	YES	-	-	-	CCDS6082. ENSP0000C Q14191	-
12791	YES	-	-	-	CCDS6082. ENSP0000C Q14191	-
12791	YES	-	-	-	CCDS6082. ENSP0000C Q14191	-
11955	YES	-	-	-	CCDS44817 ENSP0000C Q8TF68	F5H3Z9,F5f
11955	YES	-	-	-	CCDS44817 ENSP0000C Q8TF68	F5H3Z9,F5f

UNIPARC	SIFT	PolyPhen	DOMAINS	HGVS_OFF! AF	AFR_AF	AMR_AF	EAS_AF
UPI000012	-	-	Superfamil	-			
UPI000045	-	-	-	-			
UPI000013	-	-	-	-			
UPI000013	-	-	Pfam_dom	-			
UPI000002	deleterious possibly_d	-	Coiled-coils	-			
UPI000002	-	-	-	-			
UPI000002	deleterious possibly_d	-	Coiled-coils	-			
UPI000002	-	-	-	-			
UPI000002	-	-	Coiled-coils	6			
UPI000002	deleterious possibly_d	-	hmmpanth	-			
UPI000002	tolerated(C benign(0.0	-	hmmpanth	-			
UPI000004	tolerated(C benign(0.0	-	Gene3D:1.	-			
UPI000003	-	-	-	-			
UPI000016	-	-	Pfam_dom	-			
UPI000013	tolerated(C benign(0.0	-	hmmpanth	-			
UPI000013	-	-	hmmpanth	1			
UPI000013	-	-	hmmpanth	-			
UPI000013	-	-	hmmpanth	2			
UPI000013	-	-	Low_comp	4			
UPI000016	-	-	Gene3D:1.	2			
UPI000016	-	-	hmmpanth	-			
UPI000016	deleterious probably_c	-	hmmpanth	-			
UPI000016	-	-	Gene3D:1.	-			
UPI000016	-	-	hmmpanth	3			
UPI000016	deleterious probably_c	-	Pfam_dom	-			
UPI00001D	tolerated(1 benign(0.0	-	hmmpanth	-			
UPI000003	-	-	-	-			
UPI0000DE	-	-	-	-			
UPI0000DE	-	-	-	-			
UPI0000DE	-	-	Superfamil	-			
UPI000003	-	-	-	-			
UPI000003	-	-	-	-			
UPI000003	-	-	hmmpanth	-			
UPI000003	tolerated(C benign(0)	-	hmmpanth	-			
UPI000003	-	-	-	-			
UPI000003	-	-	-	-			
UPI000016	-	-	-	-			
UPI000013	-	-	hmmpanth	-			
UPI000013	-	-	Gene3D:1.	-			
UPI000013	-	-	-	-			
UPI00001A	tolerated(C benign(0.1	-	-	-			
UPI00001A	tolerated(C benign(0.0	-	-	-			
UPI000012	-	-	-	-			
UPI000012	-	-	-	-			
UPI000013	-	-	-	-			

UPI000012 tolerated(C benign(0) hmmpanth -
UPI000013 - - hmmpanth -
UPI000013 - - - -
UPI000000 tolerated(C benign(0.0) Gene3D:1.-
UPI000000 tolerated(C benign(0) Gene3D:1.-
UPI000000 - - Coiled-coil:-
UPI000000 tolerated(C benign(0.2) hmmpanth -
UPI000000 deleterious probably_d hmmpanth -
UPI000013 - - - -
UPI000013 - - - -
UPI000012 tolerated(C benign(0.0) - -
UPI000012 deleterious benign(0.1) PROSITE_p -
UPI000006 - - - -
UPI000013 - - - -
UPI000013 - - - -
UPI000013 - - - -
UPI00003F tolerated(C benign(0.1) hmmpanth -
UPI0000E5 tolerated(C benign(0.1) hmmpanth -
UPI0000E5 - - - 4
UPI000013 - - - 10
UPI000002 - - - -
UPI000002 - - - -
UPI000003 - - - -
UPI000013 - - - -
UPI000013 - - - -

UPI000013 tolerated(C benign(0) hmmpanth -
UPI000013 tolerated(C benign(0.0) Gene3D:4.-
UPI000013 tolerated_l benign(0.1) Low_comp -
UPI000011 - - - -
UPI000045 - - - -
UPI000013 - - hmmpanth -
UPI000013 - - hmmpanth -
UPI000013 - - - -1
UPI000006 deleterious benign(0.0) hmmpanth -
UPI000006 - - - -
UPI000000 - - hmmpanth -
UPI00001E - - - -
UPI00001E - - - -
UPI00001E - - - -
UPI00001E - - - -
UPI00001E - - - -
UPI000012 tolerated(C benign(0.0) hmmpanth -
UPI000012 - - hmmpanth 5
UPI000012 deleterious probably_d Gene3D:1.-
UPI000013 tolerated(C benign(0.0) Gene3D:1.-
UPI000015 tolerated(C benign(0.0) hmmpanth -
UPI00001A tolerated(C benign(0.0) Low_comp -

UPI00001A deleterious possibly_d:PROSITE_p -
 UPI00001A deleterious possibly_d:hmmpanth -
 UPI00001A - - - -
 UPI000013 - - - -
 UPI000013 - - - -
 UPI000013 deleterious benign(0.3)Gene3D:1.1 -
 UPI000016 - - hmmpanth -
 UPI000000 - - - -
 UPI000000 tolerated_l probably_d hmmpanth -
 UPI000045 - - - -
 UPI000045 - - - -
 UPI000045 - - - -
 UPI000045 - - - -
 UPI00001C deleterious possibly_d:Gene3D:1.1 -
 UPI00001C deleterious probably_d Gene3D:1.1 -
 UPI00001C - - Gene3D:1.1 -
 UPI00001C deleterious benign(0.0)Gene3D:1.1 -
 UPI00001C deleterious probably_d hmmpanth -
 UPI00001C - - - -
 UPI00001C - - - -
 UPI00001C - - - -
 UPI00001A - - - 6
 UPI00001A - - - -
 UPI000045 deleterious probably_d hmmpanth -
 UPI000045 tolerated(C benign(0.0)hmmpanth -
 UPI000045 - - PROSITE_p -
 UPI000045 - - - -
 UPI000045 deleterious probably_d hmmpanth -
 UPI000045 tolerated_l benign(0.0)hmmpanth -
 UPI000016 - - - -
 UPI000016 - - - -
 UPI000016 tolerated(C benign(0.2)hmmpanth -
 UPI000004 - - - -
 UPI000004 - - - -
 UPI000004 - - - -
 UPI000012 - - hmmpanth -
 UPI000003 - - - -
 UPI000003 - - - -
 UPI000003 - - PIRSF_dom -
 UPI000012 - - - -
 UPI000004 - - PIRSF_dom -
 UPI000004 - - - -
 UPI000004 - - - -
 UPI000018 - - hmmpanth -
 UPI000012 - - - -
 UPI000000 tolerated(C benign(0.0)Pfam_dom -
 UPI000012 deleterious probably_d Superfamil -

UPI000012	-	Pfam_dom	-
UPI0000EE	-	-	5
UPI000006	-	-	-
UPI0000ED	-	Pfam_dom	-
UPI000052	-	-	-
UPI000052	-	-	-
UPI000006 deleterious probably_d	hmmpanth	-	
UPI000006	-	hmmpanth	6
UPI000013	-	-	-
UPI000007	-	SMART_do	-
UPI0001CE	-	PROSITE_p	-
UPI000002 deleterious probably_d	PROSITE_p	-	
UPI000002	-	-	2
UPI000002	-	Gene3D:1.1	4
UPI000012	-	Low_comp	-
UPI00001F	-	-	-1
UPI000014 tolerated(C benign(0.0)	-	-	-
UPI0000E5	-	-	-
UPI0000E5 tolerated(C possibly_d	hmmpanth	-	
UPI0000E5	-	-	-
UPI000013 tolerated(C probably_d	Low_comp	-	
UPI000012 tolerated(C benign(0.0)	hmmpanth	-	
UPI000020	-	-	-
UPI000007 deleterious probably_d	Superfamil	-	
UPI00001D	-	-	-
UPI000007	-	PROSITE_p	-
UPI0000E4	-	Low_comp	-
UPI00004A	-	-	-
UPI000016 deleterious probably_d	hmmpanth	-	
UPI000002	-	Gene3D:3.1	-
UPI000006	-	-	8
UPI000040 tolerated_l benign(0.2)	hmmpanth	-	
UPI000040	-	-	-
UPI000012 deleterious possibly_d	hmmpanth	-	
UPI000012	-	-	-
UPI000012	-	-	-
UPI000007	-	-	-
UPI000007 tolerated(C benign(0.0)	hmmpanth	-	
UPI000003	-	-	-
UPI000003	-	-	-
UPI000013 tolerated(C benign(0.0)	-	-	
UPI000013 tolerated(C possibly_d	hmmpanth	-	
UPI000013	-	-	-5
UPI000013 tolerated(C benign(0.2)	PROSITE_p	-	
UPI000013	-	-	-
UPI000012	-	hmmpanth	-
UPI000006	-	hmmpanth	-

UPI000013 - - Gene3D:3n -
 UPI000013 - - - -
 UPI000013 deleterious probably_c Pfam_dom -
 UPI000013 - - Gene3D:3n 3
 UPI00001A - - - -
 UPI00001A - - - -
 UPI000016 - - - -
 UPI000013 tolerated(C possibly_d: hmmpanth -
 UPI000013 - - - -
 UPI000013 deleterious probably_c hmmpanth -
 UPI000013 tolerated(C benign(0.3: hmmpanth -
 UPI000012 - - PIRSF_dom -
 UPI000012 - - - -
 UPI000013 - - hmmpanth -
 UPI000013 - - hmmpanth
 UPI000013 tolerated(C benign(0.3: hmmpanth -
 UPI000013 - - hmmpanth 5
 UPI000013 deleterious probably_c hmmpanth -
 UPI000013 tolerated(C probably_c hmmpanth -
 UPI000013 tolerated(C benign(0.0: hmmpanth -
 UPI000013 - - - -
 UPI000003 - - - -
 UPI000003 tolerated(C benign(0.0: PROSITE_p -
 UPI000003 tolerated(C probably_c PROSITE_p -
 UPI000003 - - hmmpanth -
 UPI000007 deleterious probably_c hmmpanth -
 UPI000000 tolerated(C benign(0.0: hmmpanth -
 UPI000013 - - Gene3D:3.4 -
 UPI000004 tolerated(C benign(0.0: hmmpanth -
 UPI000004 - - - -
 UPI000004 - - - -
 UPI000004 - - - -
 UPI000004 tolerated(C benign(0.0: Superfamil -
 UPI000162 deleterious probably_c PROSITE_p -
 UPI000162 deleterious probably_c PROSITE_p -
 UPI00001B - - - -
 UPI00001B - - - -
 UPI00001B - - Pfam_dom -
 UPI00001B - - - -
 UPI00001B tolerated(C benign(0) hmmpanth -
 UPI00001B tolerated(C possibly_d: PROSITE_p -
 UPI00001B - - - -
 UPI00001B tolerated(C probably_c PROSITE_p -
 UPI00001B - - PROSITE_p -
 UPI00001B - - - -
 UPI00001B - - - -
 UPI00001B - - - -
 UPI00001B - - - -

UPI000016 -	-	-	-
UPI000045 -	-	hmmpanth -	
UPI00001B tolerated(C benign(0)		hmmpanth -	
UPI00001B -	-	hmmpanth -	
UPI00001B deleterious probably_d		hmmpanth -	
UPI000013 tolerated(C benign(0.0		Gene3D:1.-	
UPI000004 -	-	-	-
UPI000004 deleterious benign(0.0		PROSITE_p -	
UPI000014 -	-	-	-
UPI0001F9 -	-	-	-
UPI000006 deleterious probably_d		PROSITE_p -	
UPI000024 -	-	hmmpanth -	
UPI000014 deleterious possibly_d		PROSITE_p -	
UPI000014 deleterious probably_d		hmmpanth -	
UPI000002 -	-	-	-
UPI000002 -	-	-	-
UPI000000 deleterious probably_d		hmmpanth -	
UPI0001E5 deleterious benign(0.3		PIRSF_dom -	
UPI0001E5 tolerated(C probably_d		PIRSF_dom -	
UPI0000EE -	-	-	-
UPI000014 -	-	hmmpanth -	
UPI000014 -	-	hmmpanth -	
UPI000014 -	-	-	-
UPI000014 -	-	-	-
UPI000014 -	-	-	-
UPI000014 tolerated_l benign(0.0		-	
UPI000014 -	-	-	-
UPI00001F -	-	-	
UPI00001F -	-	-	-
UPI00001F -	-	-	-
UPI000002 -	-	-	-
UPI000002 -	-	-	-
UPI000012 deleterious probably_d		hmmpanth -	
UPI000004 -	-	Gene3D:3.-	
UPI000004 -	-	-	-
UPI000004 deleterious benign(0.3		Gene3D:1.-	
UPI000004 -	-	Gene3D:3.2	
UPI000012 -	-	-	-
UPI000003 tolerated(C benign(0.2		Gene3D:3.-	
UPI000003 -	-	-	-
UPI000003 -	-	-	-
UPI000003 deleterious probably_d		Gene3D:2c -	
UPI000003 -	-	-	-
UPI000003 -	-	hmmpanth -	
UPI000006 -	-	hmmpanth -	
UPI0000D6 -	-	Coiled-coils -	
UPI0000D6 -	-	-	-

UPI000047 deleterious possibly_d:hmmpanth -

UPI000012 - - Gene3D:4.-

UPI00005B tolerated(C benign(0.1: Coiled-coils -

UPI00005B - - -

UPI000012 - - -

UPI000012 - - hmmpanth -

UPI000012 deleterious possibly_d:hmmpanth -

UPI000012 - - -

UPI000012 deleterious probably_d:hmmpanth -

UPI000012 tolerated(C possibly_d:hmmpanth -

UPI000193 tolerated(C probably_d:hmmpanth -

UPI000193 - - - 1

UPI000012 - - -

UPI000012 - - -

UPI000012 tolerated_l probably_d:hmmpanth -

UPI000012 deleterious probably_d:hmmpanth -

UPI000019 tolerated(C benign(0.0: hmmpanth -

UPI000019 - - -

UPI000019 tolerated(C benign(0.0: hmmpanth -

UPI000019 deleterious possibly_d: - -

UPI000016 - - -

UPI0000DE deleterious benign(0.3: Gene3D:1.-

UPI0000DE deleterious probably_d Coiled-coils -

UPI000003 tolerated(C benign(0.0: Gene3D:1.-

UPI000013 - - -

UPI000013 tolerated(C benign(0.3: Gene3D:2g -

UPI000013 - - PROSITE_p -

UPI000013 tolerated(C benign(0.0: hmmpanth -

UPI000006 tolerated_l benign(0) hmmpanth -

UPI000012 deleterious possibly_d: PROSITE_p -

UPI000013 deleterious possibly_d: PROSITE_p -

UPI000006 tolerated(C benign(0.3: hmmpanth -

UPI00001B - - Low_comp -

UPI000013 - - -

UPI0000D6 - - -

UPI000013 - - -

UPI000004 tolerated(C benign(0.4: PROSITE_p -

UPI000013 deleterious probably_d Pfam_dom -

UPI000013 deleterious probably_d Pfam_dom -

UPI000045 - - -

UPI000045 tolerated(C probably_d:hmmpanth -

UPI000045 tolerated(1 benign(0.0: Coiled-coils -

UPI000045 - - Coiled-coils -

UPI000045 - - Coiled-coils -

UPI000045 deleterious probably_d Coiled-coils -

UPI000045 deleterious probably_d Coiled-coils -

UPI000045 deleterious probably_d Coiled-coils -

UPI000045 deleterious possibly_d:hmmpanth -
 UPI000045 - - hmmpanth -
 UPI000045 deleterious probably_d:hmmpanth -
 UPI000045 tolerated(C probably_d Coiled-coils -
 UPI000045 - - - -
 UPI000045 - - hmmpanth -
 UPI000045 deleterious benign(0.2: Coiled-coils -
 UPI000045 - - - -
 UPI000045 - - - -
 UPI000045 - - - -
 UPI000045 tolerated(C benign(0.3: Pfam_dom -
 UPI000045 deleterious probably_d Pfam_dom -
 UPI000045 deleterious probably_d Pfam_dom -
 UPI000013 - - Gene3D:2.1 -
 UPI000013 tolerated(C benign(0) Gene3D:2.1 -
 UPI000013 - - - -
 UPI000013 tolerated(C benign(0.0: Gene3D:2.1 -
 UPI000013 - - - -
 UPI000020 tolerated_l possibly_d:hmmpanth -
 UPI000013 - - - -
 UPI000013 - - - -
 UPI000004 tolerated(C benign(0.2: Gene3D:3.1 -
 UPI000007 - - - -
 UPI000013 - - Gene3D:2.1 -
 UPI000013 - - Coiled-coils -
 UPI000013 tolerated(C benign(0) hmmpanth -
 UPI000013 deleterious probably_d Gene3D:2.1 -
 UPI000013 - - hmmpanth -
 UPI000013 tolerated(C benign(0) - -
 UPI000013 - - - -
 UPI000013 tolerated(1 benign(0) - -
 UPI000004 - - hmmpanth -
 UPI000004 tolerated(C benign(0.1: Gene3D:1.1 -
 UPI000013 - - hmmpanth -
 UPI000013 - - Superfamil -
 UPI000013 - - - -
 UPI000007 - - - -
 UPI000000 - - - -
 UPI000045 - - PROSITE_p -
 UPI000045 deleterious possibly_d: PROSITE_p -
 UPI000045 - - Pfam_dom -
 UPI000045 - - Gene3D:1.1 -
 UPI000045 - - - -
 UPI00001A tolerated(C probably_d Superfamil -
 UPI00001A - - - -
 UPI000000 - - - -
 UPI000000 - - - -

UPI000013	-	Gene3D:3.1.4
UPI000013	-	-
UPI000013	-	Superfamily
UPI000013	tolerated(C benign(0.0)	Superfamily
UPI000024	-	-
UPI000006	deleterious possibly_d	hmmpanth
UPI000004	-	Superfamily
UPI000004	-	Superfamily
UPI000004	-	-
UPI000012	deleterious probably_c	Superfamily
UPI000013	-	-
UPI000000	-	-
UPI000013	-	hmmpanth 5
UPI000013	deleterious probably_c	hmmpanth
UPI000007	-	-
UPI000007	-	5
UPI0001D3	tolerated(C benign(0)	hmmpanth
UPI0001D3	-	-
UPI0001D3	tolerated(C benign(0.0)	hmmpanth
UPI0001D3	-	hmmpanth
UPI0001D3	-	-
UPI0001D3	-	hmmpanth 2
UPI000013	tolerated(C probably_c	hmmpanth
UPI000020	-	-
UPI0001D5	deleterious probably_c	Pfam_dom
UPI0001D5	deleterious possibly_d	hmmpanth
UPI0001D5	deleterious probably_c	hmmpanth
UPI000000	-	-
UPI00017E	deleterious probably_c	PROSITE_p
UPI00017E	tolerated_l benign(0)	hmmpanth
UPI000013	-	Gene3D:1.1-
UPI000013	-	-
UPI000013	tolerated(C benign(0.0)	hmmpanth
UPI000005	deleterious probably_c	Superfamily
UPI000005	-	Gene3D:2.1-
UPI000006	-	Superfamily
UPI000000	-	3
UPI000000	-	-
UPI000013	-	hmmpanth
UPI000003	tolerated(C benign(0.0)	hmmpanth
UPI000000	-	-
UPI000000	-	hmmpanth
UPI000003	tolerated(C benign(0.0)	hmmpanth
UPI000007	-	Pfam_dom
UPI000012	deleterious probably_c	PROSITE_p
UPI000204	-	Gene3D:1.1-
UPI000204	-	Gene3D:1.1-

UPI000204 -	probably_d	hmmpanth -
UPI000204 -	-	hmmpanth -
UPI000204 -	possibly_d	Gene3D:1.1 -
UPI000204 -	probably_d	hmmpanth -
UPI000204 -	-	Coiled-coils -
UPI000204 -	benign(0.1)	hmmpanth -
UPI000204 -	-	hmmpanth -
UPI000204 -	benign(0.1)	Gene3D:1.1 -
UPI000204 -	benign(0)	hmmpanth -
UPI000204 -	benign(0.0)	Gene3D:1.1 -
UPI000204 -	-	- -
UPI000013 tolerated(C	benign(0)	Low_comp -
UPI000013 tolerated_I	benign(0.1)	PIRSF_dom -
UPI000007 tolerated(C	benign(0.0)	Low_comp -
UPI000013 tolerated(C	benign(0.0)	Gene3D:1h -
UPI000013 -	-	- -
UPI000013 -	-	Gene3D:1.1 -
UPI000002 deleterious	possibly_d	Gene3D:4.1 -
UPI000002 deleterious	probably_d	PROSITE_p -
UPI000013 deleterious	benign(0.0)	hmmpanth -
UPI000013 -	-	hmmpanth -
UPI000013 deleterious	possibly_d	hmmpanth -
UPI00001D tolerated(C	benign(0.0)	hmmpanth -
UPI00001D -	-	hmmpanth 3
UPI000011 tolerated(C	benign(0.0)	hmmpanth -
UPI00001F deleterious	probably_d	Superfamil -
UPI000002 -	-	- -
UPI000046 deleterious	benign(0.2)	hmmpanth -
UPI000046 -	-	Coiled-coils -
UPI000046 -	-	- -
UPI000013 -	-	- -
UPI000013 -	-	- -
UPI000013 -	-	- -
UPI000013 -	-	- -
UPI000013 deleterious	possibly_d	Coiled-coils -
UPI000045 -	-	- -
UPI000045 tolerated(C	benign(0.0)	hmmpanth -
UPI000045 -	-	hmmpanth -
UPI000045 deleterious	probably_d	hmmpanth -
UPI000045 -	-	- -
UPI000013 -	-	- -
UPI000013 -	-	- -
UPI000013 deleterious	probably_d	Prints_dorr -
UPI000013 -	-	Superfamil -
UPI000012 deleterious	possibly_d	hmmpanth -
UPI000012 tolerated(C	benign(0.0)	Coiled-coils -
UPI000012 -	-	hmmpanth -

UPI000012 deleterious benign(0.2)	hmmpanth	-
UPI000012	-	-
UPI000012	-	hmmpanth
UPI00001A	-	-
UPI000007	-	PROSITE_p
UPI000007	-	-
UPI000007	-	-
UPI000007	-	-
UPI000007	-	-
UPI000013	-	Low_comp 3
UPI000013	-	-
UPI000013	-	-
UPI000013 deleterious benign(0.2)	-	-
UPI00001A	-	Coiled-coils
UPI00001A	-	hmmpanth

EUR_AF SAS_AF AA_AF EA_AF gnomAD_A gnomAD_A gnomAD_A gnomAD_A gnomAD_E









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LoFtool	miRNA	BLOSUM62	CADD_PHR	CADD_RAW	Condel	GTEX_V6p	GTEX_V6p	Interpro_d
0.0781	-	-	39	7.406226	-	-	-	Activin_typ
0.85	-	-	3.862	0.075802	-	-	-	-
0.657	-	-	1.954	-0.048597	-	-	-	-
0.657	-	-	0.115	-0.462847	-	-	-	-
0.933	-	-2	25.8	3.677638	deleterious	-	-	ELK_domai
0.933	-	-	-	-	-	-	-	-
0.933	-	-1	24.7	3.394578	deleterious	-	-	-
0.933	-	-	9.341	0.495403	-	-	-	-
0.933	-	-	-	-	-	-	-	-
0.933	-	-2	22.8	2.605057	deleterious	-	-	-
0.933	-	-1	9.977	0.566458	neutral(0.2	-	-	-
0.324	-	-1	22.8	2.627499	neutral(0.0	-	-	Protein_Kir
0.341	-	-	-	-	-	-	-	-
0.202	-	-	-	-	-	-	-	-
0.00386	-	3	22.9	2.629020	neutral(0.0	-	-	Armadillo-I
0.00386	-	-	-	-	-	-	-	-
0.00386	-	-	-	-	-	-	-	-
0.00386	-	-	-	-	-	-	-	-
0.00386	-	-	-	-	-	-	-	-
0.0125	-	-	-	-	-	-	-	-
0.0215	-	-	-	-	-	-	-	-
0.0215	-	3	27.3	3.924020	deleterious	-	-	-
0.0215	-	-	35	6.027999	-	-	-	ARID_DNA
0.0215	-	-	-	-	-	-	-	-
0.0215	-	-2	32	4.243295	deleterious	-	-	Armadillo-I
0.259	-	-1	19.88	2.064992	neutral(0.0	-	-	-
0.54	-	-	14.16	1.148492	-	-	-	-
0.782	-	-	-	-	-	-	-	-
0.782	-	-	7.001	0.283820	-	-	-	-
0.782	-	-	15.00	1.317277	-	-	-	-
0.718	-	-	-	-	-	-	-	-
0.718	-	-	0.402	-0.285761	-	-	-	-
0.718	-	-	-	-	-	-	-	-
0.718	-	1	19.01	1.979767	neutral(0.0	-	-	Armadillo-I
0.718	-	-	9.228	0.483378	-	-	-	-
0.718	-	-	1.225	-0.119947	-	-	-	-
0.00517	-	-	34	4.525380	-	-	-	-
0.674	-	-	-	-	-	-	-	-
0.635	-	-	10.85	0.669733	-	-	-	-
0.907	-	-	10.43	0.619176	-	-	-	-
0.364	-	1	22.8	2.583007	neutral(0.0	-	-	-
0.364	-	1	22.0	2.306643	neutral(0.2	-	-	-
0.289	-	-	16.72	1.688332	-	-	-	-
0.289	-	-	16.05	1.553495	-	-	-	-
0.0194	-	-	18.87	1.965485	-	-	-	-

0.155	-	-1	19.94	2.070122	neutral(0.0-	-	-
0.25	-	-	37	7.053725	-	-	-
0.25	-	-	14.67	1.247520	-	-	-
0.509	-	0	7.528	0.324729	neutral(0.0-	-	-
0.509	-	-3	0.945	-0.158338	neutral(0.0-	-	-
0.509	-	-	4.924	0.140265	-	-	-
0.509	-	-1	17.75	1.838520	neutral(0.3-	-	Zinc_finger
0.509	-	2	25.5	3.612242	deleterious-	-	Zinc_finger
0.889	-	-	10.03	0.571227	-	-	-
0.889	-	-	8.399	0.400995	-	-	-
0.959	-	0	10.94	0.681812	neutral(0.2-	-	Bloom_syn
0.959	-	2	24.7	3.401847	neutral(0.4-	-	HRDC_dom
TA	0.0565	AGAMMAC-		1.243	-0.11783	-	-
0.64	-	-	12.78	0.925681	-	-	-
0.64	-	-	1.466	-0.093081	-	-	-
0.64	-	-	8.957	0.455416	-	-	-
0.251	-	3	19.79	2.056444	neutral(0.2-	-	-
0.729	-	2	14.03	1.124374	neutral(0.0-	-	-
0.729	-	-	-	-	-	-	-
TT	0.302	Noonan_sy-		3.427	0.049922	-	-
0.112	-	-	16.98	1.731263	-	-	-
0.112	-	-	0.729	-0.196982	-	-	-
0.329	-	-	13.80	1.084741	-	-	-
-	-	-	9.404	0.502186	-	-	-
0.499	-	-	6.275	0.230097	-	-	-
0.499	-	2	15.67	1.468705	neutral(0.0-	-	Cadherin_p
0.23	-	1	23.4	2.901114	neutral(0.0-	-	Cadherin,_
0.134	-	-2	22.1	2.339211	neutral(0.3-	-	-
0.303	-	-	-	-	-	-	-
-	-	-	21.0	2.162886	-	-	-
0.0161	-	-	10.93	0.679899	-	-	-
0.0161	-	-	23.0	2.699524	-	-	-
CCCCAGgcc	0.00406	-	-	-	-	-	-
0.219	-	-1	22.3	2.405989	neutral(0.3-	-	CULT_dom
0.219	-	-	9.094	0.469422	-	-	-
0.0011	-	-	10.84	0.668680	-	-	-
0.585	-	-	-	-	-	-	-
0.585	-	-	-	-	-	-	-
0.585	-	-	33	4.504386	-	-	-
0.585	-	-	3.665	0.064129	-	-	-
0.585	-	-	1.349	-0.105685	-	-	-
0.34	-	1	23.6	2.975696	neutral(0.3-	-	-
0.34	-	-	-	-	-	-	-
0.208	-	0	24.0	3.162167	deleterious-	-	Armadillo-I
0.923	-	1	6.551	0.249920	neutral(0.2-	-	-
-	-	0	15.68	1.469832	neutral(0.3-	-	-
0.313	-	-2	22.2	2.375680	neutral(0.0-	-	Immunogl

0.313	-	-1	27.5	3.943797	deleterious-	-	Immunogl
0.313	-	-3	34	4.734982	deleterious-	-	-
0.313	-	-	6.121	0.219197	-	-	-
0.0426	-	-	22.0	2.313914	-	-	-
0.0426	-	-	-	-	-	-	-
0.0426	-	1	24.3	3.257354	deleterious-	-	Protein_kir
0.233	-	-	11.03	0.692801	-	-	-
0.15	-	-	14.93	1.302455	-	-	S-adenosyl
0.15	-	-1	23.8	3.068783	neutral(0.4-	-	-
0.11	-	-	13.73	1.071748	-	-	-
0.11	-	-	0.251	-0.353513	-	-	-
0.11	-	-	11.05	0.694998	-	-	-
0.11	-	-	13.64	1.057698	-	-	-
0.554	-	-2	27.6	3.956325	deleterious-	-	-
0.554	-	-3	32	4.273851	deleterious-	-	-
0.554	-	-	10.37	0.612156	-	-	-
T		0.554 NEUROPAT-		22.3	2.384179	-	-
0.554	-	-2	32	4.246285	deleterious-	-	-
0.554	-	-	-	-	-	-	-
0.554	-	-	18.00	1.869520	-	-	-
0.554	-	-	-	-	-	-	-
0.000482	-	-	-	-	-	-	-
0.000482	-	-	1.602	-0.079592	-	-	-
0.00889	-	-2	34	4.772741	deleterious-	-	-
0.00889	-	1	17.89	1.856615	neutral(0.2-	-	-
0.00889	-	-	5.977	0.209217	-	-	-
0.00889	-	-	7.223	0.300684	-	-	-
0.00889	-	2	28.5	4.047229	deleterious-	-	-
0.00889	-	-1	20.6	2.122317	neutral(0.2-	-	-
0.291	-	-	13.78	1.080875	-	-	-
0.291	-	-	6.802	0.268680	-	-	-
0.291	-	-1	22.3	2.394410	neutral(0.0-	-	Ephrin_rec
0.223	-	-	34	4.705756	-	-	-
0.223	-	-	10.77	0.660535	-	-	-
0.223	-	-	22.7	2.536341	-	-	-
0.19	-	-	12.51	0.887231	-	-	-
0.149	-	-	5.346	0.167281	-	-	-
0.149	-	-	10.12	0.582008	-	-	-
0.149	-	-	22.1	2.335405	-	-	-
0.31	-	-	0.728	-0.197352	-	-	-
0.147	-	-	6.256	0.228688	-	-	-
0.147	-	-	2.108	-0.036405	-	-	-
0.147	-	-	11.08	0.698708	-	-	-
0.0739	-	-	10.84	0.668915	-	-	-
-	-	-	8.688	0.428553	-	-	-
0.868	-	0	15.91	1.522045	neutral(0.0-	-	PEA3-type_
0.00765	-	-1	29.7	4.156915	deleterious-	-	Exostosin_

0.00765	-	-	18.70	1.947023	-	-	-	-
0.0377	-	-	-	-	-	-	-	-
0.0135	-	-	5.465	0.174987	-	-	-	-
-	-	-	-	-	-	-	-	-
0.0821	-	-	0.638	-0.217210	-	-	-	-
0.0821	-	-	0.215	-0.375976	-	-	-	-
0.989	-	-2	27.1	3.902580	deleterious-	-	-	-
0.989	-	-	-	-	-	-	-	-
0.0141	-	-	1.818	-0.059955	-	-	-	-
0.0563	-	-	38	7.225216	-	-	-	WD40-repe
0.00524	-	-	8.608	0.420816	-	-	-	-
0.00179	-	-2	32	4.342552	deleterious-	-	-	Protein_kir
0.0225	-	-	-	-	-	-	-	-
0.0225	-	-	-	-	-	-	-	-
0.0501	-	-	3.467	0.052311	-	-	-	-
0.218	-	-	-	-	-	-	-	-
0.0227	-	1	12.18	0.842662	neutral(0.0-	-	-	-
0.719	-	-	7.440	0.317651	-	-	-	-
0.719	-	1	24.8	3.403721	deleterious-	-	-	Fibronectin
0.719	-	-	12.69	0.913562	-	-	-	-
-	-	-2	25.6	3.640798	deleterious-	-	-	-
-	-	1	14.60	1.233916	neutral(0.0-	-	-	Fork_head_
-	0.0611	Mental_ret-	-	-	-	-	-	-
0.0749	-	0	32	4.301314	deleterious-	-	-	Fork_head_
0.0431	-	-	0.660	-0.212137	-	-	-	-
-	-	-	12.45	0.879744	-	-	-	-
0.00834	-	-	21.7	2.256372	-	-	-	-
0.682	-	-	0.983	-0.152403	-	-	-	-
0.471	-	-2	29.8	4.168297	deleterious-	-	-	-
0.0879	-	-	4.803	0.132698	-	-	-	-
0.17	-	-	-	-	-	-	-	-
0.567	-	2	22.8	2.627633	neutral(0.3-	-	-	-
0.567	-	-	0.889	-0.167359	-	-	-	-
0.307	-	-3	25.9	3.709981	deleterious-	-	-	Isopropylm
0.107	-	-	4.558	0.117619	-	-	-	-
0.107	-	-	4.557	0.117545	-	-	-	-
0.339	-	-	7.126	0.293305	-	-	-	-
0.339	-	1	17.05	1.743266	neutral(0.0-	-	-	Mannose-6
0.698	-	-	11.91	0.805703	-	-	-	-
0.68	-	-	9.461	0.508429	-	-	-	-
0.442	-	1	15.27	1.376163	neutral(0.0-	-	-	-
0.442	-	1	23.5	2.963806	deleterious-	-	-	-
0.442	-	-	-	-	-	-	-	-
0.442	-	1	22.9	2.652036	neutral(0.0-	-	-	Fibronectin
0.442	-	-	1.310	-0.110062	-	-	-	-
0.136	-	-	8.649	0.424760	-	-	-	-
-	-	-	12.05	0.825487	-	-	-	-

0.788	-	-	34	4.792552	-	-	-	-
0.788	-	-	17.26	1.774085	-	-	-	-
0.788	-	-1	25.8	3.683552	deleterious-	-	-	von_Willeb
0.788	-	-	-	-	-	-	-	-
0.555	-	-	34	4.735569	-	-	-	-
0.555	-	-	3.487	0.053510	-	-	-	-
0.0333	-	-	-	-	-	-	-	-
0.127	-	-2	23.9	3.119135	deleterious-	-	-	Integrin_be
0.127	-	-	5.928	0.205845	-	-	-	-
0.127	-	-3	29.1	4.107675	deleterious-	-	-	Integrin_be
0.127	-	2	9.285	0.489452	neutral(0.3-	-	-	Integrin_be
0.189	-	-	-	-	-	-	-	-
0.189	-	-	18.02	1.871992	-	-	-	-
-	-	-	-	-	-	-	-	-
T	-	blepharopt-	-	-	-	-	-	-
-	-	2	22.9	2.658825	neutral(0.1-	-	-	-
-	-	-	-	-	-	-	-	-
-	-	-2	25.6	3.628204	deleterious-	-	-	Acyl-CoA_M
-	-	-2	24.6	3.353220	deleterious-	-	-	Acyl-CoA_M
0.0636	-	1	21.2	2.185731	neutral(0.0-	-	-	-
0.187	-	-	9.465	0.508878	-	-	-	-
0.196	-	-	-	-	-	-	-	-
0.196	-	-1	22.1	2.320052	neutral(0.3-	-	-	Immunoglc
0.196	-	0	26.0	3.714263	deleterious-	-	-	Immunoglc
0.196	-	-	-	-	-	-	-	-
0.303	-	-1	27.8	3.983225	deleterious-	-	-	Kelch-type_
-	-	2	16.12	1.570001	neutral(0.0-	-	-	-
0.19	-	-	-	-	-	-	-	-
0.794	-	1	14.37	1.187971	neutral(0.2-	-	-	-
0.794	-	-	13.44	1.025156	-	-	-	-
0.794	-	-	9.779	0.543742	-	-	-	-
0.794	-	-	6.080	0.216398	-	-	-	-
0.794	-	1	16.18	1.581649	neutral(0.0-	-	-	Fibronectin
0.1	-	-2	27.8	3.982775	deleterious-	-	-	Olfactomec
0.1	-	2	29.4	4.131108	deleterious-	-	-	GPCR,_fam
0.00916	-	-	3.691	0.065654	-	-	-	-
0.00916	-	-	-	-	-	-	-	-
0.00916	-	-	7.501	0.322523	-	-	-	-
0.00916	-	-	6.327	0.233782	-	-	-	-
0.00916	-	1	21.4	2.214939	neutral(0.0-	-	-	Six-bladed_
0.00916	-	-2	19.89	2.066164	neutral(0.2-	-	-	Six-bladed_
0.00916	-	-	14.54	1.222358	-	-	-	-
0.00916	-	1	22.2	2.353637	deleterious-	-	-	Low-densit
0.00916	-	-	9.974	0.566107	-	-	-	-
0.00916	-	-	0.546	-0.240307	-	-	-	-
0.00916	-	-	17.08	1.746742	-	-	-	-
0.00916	-	-	-	-	-	-	-	-

0.943	-	-	26.4	3.792239	-	-	-	-
0.519	-	-	7.918	0.357593	-	-	-	-
-	-	0	20.4	2.101275	neutral(0.0-	-	-	-
-	-	-	10.03	0.571590	-	-	-	-
-	-	-1	26.5	3.808703	deleterious-	-	-	-
0.0532	-	0	23.5	2.955567	neutral(0.0-	-	-	Protein_kir
0.503	-	-	-	-	-	-	-	-
0.0914	-	3	24.2	3.211385	neutral(0.3-	-	-	KA1_doma
0.881	-	-	5.554	0.180810	-	-	-	-
0.0163	-	-	9.155	0.475720	-	-	-	-
-	-	-3	28.5	4.051832	deleterious-	-	-	Apoptosis_
-	-	-	7.137	0.294141	-	-	-	-
0.442	-	2	22.6	2.535191	deleterious-	-	-	Sema_dom
0.442	-	-2	24.2	3.210616	deleterious-	-	-	IPT_domain
0.203	-	-	14.72	1.258585	-	-	-	-
0.203	-	-	3.594	0.059874	-	-	-	-
0.00165	-	-2	31	4.201806	deleterious-	-	-	DNA_mism
-	-	-1	23.6	2.979099	deleterious-	-	-	-
-	-	0	27.9	3.991116	deleterious-	-	-	-
-	-	-	-	-	-	-	-	-
-	-	-	0.079	-0.513979	-	-	-	-
-	-	-	-	-	-	-	-	-
-	-	-	9.015	0.461254	-	-	-	-
-	-	-	3.939	0.080365	-	-	-	-
TT	-	Intellectual-	-	-	-	-	-	-
-	-	1	22.7	2.566067	neutral(0.3-	-	-	-
-	-	-	3.826	0.073684	-	-	-	-
-	-	0.336 Precursor_	-	-	-	-	-	-
0.336	-	-	3.475	0.052780	-	-	-	-
0.336	-	-	10.91	0.678125	-	-	-	-
0.343	-	-	16.85	1.710423	-	-	-	-
0.343	-	-	6.987	0.282799	-	-	-	-
0.21	-	2	23.8	3.088828	deleterious-	-	-	Calcineurin
0.00971	-	-	36	6.503360	-	-	-	DNA_mism
0.00971	-	-	0.191	-0.392294	-	-	-	-
0.00971	-	-1	24.5	3.325596	neutral(0.4-	-	-	DNA_mism
0.00971	-	-	-	-	-	-	-	-
0.246	-	-	7.909	0.356795	-	-	-	-
0.507	-	-2	-	-	neutral(0.3-	-	-	-
0.507	-	-	9.003	0.460082	-	-	-	-
0.507	-	-	0.074	-0.522855	-	-	-	-
0.507	-	-2	29.5	4.137936	deleterious-	-	-	Vitamin_B1
-	-	-	-	-	-	-	-	-
-	-	-	7.305	0.307075	-	-	-	-
0.0243	-	-	35	5.707665	-	-	-	-
-	-	-	-	-	-	-	-	-
-	-	-	6.258	0.228872	-	-	-	-

-	-	-1	23.0	2.704582	deleterious-	-	Transcripti
0.0238	-	-	19.97	2.073351	-	-	-
0.00613	-	-1	22.5	2.450798	neutral(0.0-	-	Myosin_tai
0.00613	-	-	5.592	0.183322	-	-	-
0.00606	-	-	-	-	-	-	-
-	-	-	0.782	-0.186567	-	-	-
-	-	-1	29.5	4.135182	deleterious-	-	Nuclear_re
-	-	-	0.947	-0.158037	-	-	-
-	-	-2	22.7	2.554222	deleterious-	-	-
-	-	-3	23.8	3.076697	deleterious-	-	-
0.729	-	1	22.9	2.641645	deleterious-	-	-
0.729	-	-	-	-	-	-	-
0.116	-	-	0.502	-0.252733	-	-	-
-	0.116	Familial_sp-	-	-	-	-	-
0.116	-	1	23.7	3.049200	neutral(0.4-	-	Armadillo-l
0.199	-	-1	27.6	3.960079	deleterious-	-	-
0.307	-	0	14.81	1.276887	neutral(0.0-	-	Ankyrin_re
0.307	-	-	5.720	0.191786	-	-	-
0.307	-	-1	21.7	2.251376	neutral(0.0-	-	Ankyrin_re
0.307	-	-3	24.8	3.421374	deleterious-	-	Ankyrin_re
0.18	-	-	12.28	0.856663	-	-	-
0.943	-	-1	22.7	2.538545	deleterious-	-	-
0.943	-	-2	29.5	4.134348	deleterious-	-	-
0.926	-	-2	13.34	1.008306	neutral(0.0-	-	DAPIN_dor
0.0156	-	-	2.212	-0.028634	-	-	-
0.0156	-	1	21.6	2.232939	neutral(0.3-	-	EGF-like_ca
0.138	-	-	22.0	2.311136	-	-	-
0.138	-	-1	22.7	2.565874	neutral(0.3-	-	-
0.00186	-	-3	7.774	0.345199	neutral(0.0-	-	PWWP_dor
0.239	-	1	24.8	3.423621	deleterious-	-	Protein_kir
0.0395	-	0	25.6	3.637826	deleterious-	-	Immunoglc
0.0394	-	0	23.5	2.950345	neutral(0.1-	-	-
0.247	-	-	18.92	1.971145	-	-	-
0.00393	-	-	14.17	1.150139	-	-	-
0.173	-	-	8.905	0.450156	-	-	-
0.0277	-	-	3.724	0.067609	-	-	-
0.00758	-	-1	22.7	2.542591	neutral(0.1-	-	Homeobox
0.0745	-	-1	29.0	4.094349	deleterious-	-	Bromo_adj
0.0745	-	-2	32	4.266889	deleterious-	-	Bromo_adj
0.984	-	-	11.21	0.714842	-	-	-
0.984	-	1	19.91	2.068006	deleterious-	-	-
0.984	-	3	18.90	1.968324	neutral(0.0-	-	-
0.984	-	-	17.73	1.836965	-	-	-
0.984	-	-	35	6.029872	-	-	-
0.984	-	-2	-	-	deleterious-	-	-
0.984	-	-2	29.3	4.121785	deleterious-	-	-
0.984	-	-3	26.7	3.841075	deleterious-	-	-

0.984	-	-2	23.6	2.999948	deleterious-	-	-
0.984	-	-	-	-	-	-	-
0.984	-	0	25.1	3.509040	deleterious-	-	-
0.984	-	-3	27.4	3.931768	deleterious-	-	-
0.984	-	-	16.46	1.639154	-	-	-
0.984	-	-	0.283	-0.336353	-	-	-
0.984	-	1	24.0	3.145100	neutral(0.4-	-	-
0.984	-	-	11.73	0.782126	-	-	-
0.984	-	-	13.89	1.100022	-	-	-
0.984	-	-	22.1	2.339766	-	-	-
0.984	-	0	24.2	3.225818	neutral(0.3-	-	Centrosom
0.984	-	-2	33	4.348391	deleterious-	-	Centrosom
0.984	-	1	26.1	3.743393	deleterious-	-	Centrosom
0.125	-	-	3.624	0.061688	-	-	-
0.125	-	-1	15.96	1.533929	neutral(0.0-	-	Immunoglc
0.123	-	-	7.155	0.295555	-	-	-
0.123	-	-3	21.8	2.262483	neutral(0.2-	-	Immunoglc
0.55	-	-	-	-	-	-	-
0.455	-	-1	23.5	2.921353	neutral(0.2-	-	-
0.268	-	-	13.34	1.009527	-	-	-
0.268	-	-	-	-	-	-	-
0.313	-	-2	22.5	2.453366	neutral(0.0-	-	Ubiquitin-r
0.49	-	-	2.599	-0.001577	-	-	-
0.295	-	-	40	7.633873	-	-	Phosphatid
0.295	-	-	39	7.558851	-	-	PI3K_p85_?
0.00772	-	-3	2.935	0.019984	neutral(0.0-	-	-
0.00772	-	-2	24.5	3.313009	deleterious-	-	Pectin_lyas
0.00772	-	-	35	5.402483	-	-	-
0.00772	-	0	1.813	-0.060414	neutral(0.0-	-	-
0.00772	-	-	-	-	-	-	-
0.00772	-	3	14.48	1.209674	neutral(0.0-	-	-
0.0827	-	-	2.237	-0.026767	-	-	-
0.0827	-	1	16.18	1.582987	neutral(0.0-	-	High_mobi
0.382	-	-	0.258	-0.349763	-	-	-
0.382	-	-	41	7.841557	-	-	DNA_mism
0.382	-	-	5.678	0.189001	-	-	-
0.832	-	-	0.131	-0.444509	-	-	-
0.0537	-	-	0.516	-0.248736	-	-	-
-	-	-	5.377	0.169296	-	-	-
-	-	-2	28.2	4.021655	deleterious-	-	PIK-related
-	-	-	9.229	0.483530	-	-	-
-	-	-	6.896	0.275833	-	-	-
-	-	-	5.897	0.203741	-	-	-
0.000344	-	-2	25.7	3.648875	deleterious-	-	-
0.000344	-	-	3.141	0.032690	-	-	-
-	-	-	1.575	-0.082245	-	-	-
-	-	-	23.5	2.931204	-	-	-

0.0482	-	-	-	-	-	-	-	-
0.0868	-	-	-	-	-	-	-	-
0.0868	-	-	9.257	0.486494	-	-	-	-
0.0868	-	0	22.7	2.565591	neutral(0.2-	-	-	Fibronectin
0.0898	-	-	3.980	0.082794	-	-	-	-
0.987	-	-2	26.8	3.853747	deleterious-	-	-	-
0.184	-	-	21.1	2.177613	-	-	-	-
0.184	-	-	47	8.606048	-	-	-	Protein_kir
0.184	-	-	-	-	-	-	-	-
0.515	-	1	24.4	3.278076	deleterious-	-	-	Ras_guanir
0.0723	-	-	5.141	0.154077	-	-	-	-
0.43	-	-	3.057	0.027540	-	-	-	-
0.286	-	-	-	-	-	-	-	-
0.286	-	2	29.1	4.105709	deleterious-	-	-	-
0.223	-	-	5.507	0.177746	-	-	-	-
0.223	-	-	-	-	-	-	-	-
0.208	-	2	0.379	-0.294293	neutral(0.0-	-	-	-
0.208	-	-	3.854	0.075321	-	-	-	-
0.208	-	-2	5.790	0.196477	neutral(0.3-	-	-	-
0.208	-	-	35	5.110141	-	-	-	-
0.208	-	-	5.113	0.152244	-	-	-	-
0.208	-	-	-	-	-	-	-	-
0.134	-	2	23.0	2.701035	deleterious-	-	-	-
-	-	-	3.880	0.076908	-	-	-	-
0.31	-	-2	32	4.286540	deleterious-	-	-	Zinc_finger
0.31	-	-2	28.6	4.059482	deleterious-	-	-	-
0.31	-	-3	28.5	4.047912	deleterious-	-	-	-
0.432	-	-	6.616	0.254695	-	-	-	-
0.0294	-	-3	29.7	4.151683	deleterious-	-	-	AWS_doma
0.0294	-	0	15.81	1.500287	neutral(0.2-	-	-	-
-	-	-	12.16	0.840407	-	-	-	-
0.43	-	-	8.602	0.420246	-	-	-	-
0.43	-	-1	21.4	2.210603	neutral(0.2-	-	-	Phox_homi
0.116	-	3	26.2	3.759026	deleterious-	-	-	MAD_homi
0.116	-	-	11.75	0.785729	-	-	-	-
0.000689	-	-	10.16	0.586993	-	-	-	-
-	-	-	-	-	-	-	-	-
-	-	-	7.265	0.303968	-	-	-	-
-	-	-	-	-	-	-	-	-
-	-	0	23.5	2.944635	neutral(0.0-	-	-	-
0.0217	-	-	4.082	0.088868	-	-	-	-
0.0217	-	-	6.038	0.213436	-	-	-	-
0.886	-	-3	13.15	0.980109	neutral(0.3-	-	-	Armadillo-l
-	-	-	12.47	0.881866	-	-	-	-
0.00792	-	-1	26.0	3.719458	deleterious-	-	-	SH2_doma
0.881	-	-	8.632	0.423201	-	-	-	-
0.881	-	-	57	9.847167	-	-	-	-

0.881	-	1	26.3	3.770044	-	-	-	-
0.881	-	-	7.620	0.332311	-	-	-	-
0.881	-	2	23.9	3.118009	-	-	-	-
0.881	-	0	26.9	3.874711	-	-	-	-
0.881	-	-	2.362	-0.017757	-	-	-	-
0.881	-	0	21.6	2.230064	-	-	-	-
0.881	-	-	0.143	-0.433131	-	-	-	-
0.881	-	-1	16.65	1.676785	-	-	-	-
0.881	-	1	16.22	1.591346	-	-	-	-
0.881	-	-3	22.8	2.589760	-	-	-	-
0.881	-	-	8.548	0.415087	-	-	-	-
0.152	-	1	12.57	0.895578	neutral(0.0-	-	-	-
0.152	-	-2	21.3	2.193336	neutral(0.0-	-	-	-
0.582	-	-3	17.63	1.823622	neutral(0.3-	-	-	Bromodom
0.0586	-	0	5.445	0.173697	neutral(0.0-	-	-	p53-like_tr
0.497	-	-	-	-	-	-	-	-
0.118	-	-	-	-	-	-	-	-
0.0268	-	1	23.6	3.002021	deleterious-	-	-	CTNNB1_bi
0.0268	-	-1	26.5	3.818797	deleterious-	-	-	CTNNB1_bi
0.247	-	1	22.8	2.590147	neutral(0.4-	-	-	-
0.247	-	-	6.859	0.273003	-	-	-	-
0.247	-	-3	26.6	3.820431	deleterious-	-	-	-
0.998	-	-2	13.74	1.074132	neutral(0.3-	-	-	-
0.998	-	-	-	-	-	-	-	-
0.192	-	0	18.56	1.932384	neutral(0.0-	-	-	-
0.104	-	0	23.4	2.882177	deleterious-	-	-	-
C	0.000965	ADRENOCC-	-	-	-	-	-	-
0.361	-	1	23.4	2.897938	neutral(0.3-	-	-	-
0.361	-	-	11.81	0.793127	-	-	-	-
0.361	-	-	-	-	-	-	-	-
0.028	-	-	16.25	1.598130	-	-	-	-
0.028	-	-	16.32	1.612783	-	-	-	-
0.9	-	-	-	-	-	-	-	-
0.9	-	-	4.369	0.106133	-	-	-	-
0.9	-	1	23.6	2.970558	deleterious-	-	-	-
0.0406	-	-	17.56	1.814685	-	-	-	-
0.0406	-	2	18.37	1.911581	neutral(0.0-	-	-	Armadillo-l
0.0406	-	-	43	8.183281	-	-	-	Armadillo-l
0.0406	-	0	28.8	4.075952	deleterious-	-	-	Armadillo-l
0.0406	-	-	0.790	-0.184942	-	-	-	-
0.000276	-	-	-	-	-	-	-	-
0.272	-	-	4.415	0.108894	-	-	-	-
0.272	-	-2	26.7	3.841200	deleterious-	-	-	Leucine-ric
0.272	-	-	16.87	1.713805	-	-	-	-
0.0612	-	1	32	4.240419	deleterious-	-	-	HECT_dom
0.0612	-	1	21.7	2.248015	neutral(0.0-	-	-	-
0.0612	-	-	12.38	0.870098	-	-	-	-

0.0612	-	1	23.6	3.002175	neutral(0.4-	-	-
0.0612	-	-	-	-	-	-	-
0.0612	-	-	10.76	0.658659	-	-	-
-	-	-	12.56	0.895252	-	-	-
0.00276	-	-	38	7.200462	-	-	AWS_domæ
0.00276	-	-	12.54	0.891654	-	-	-
0.00276	-	-	13.54	1.041425	-	-	-
0.00276	-	-	-	-	-	-	-
0.00276	-	-	12.68	0.911763	-	-	-
0.988	-	-	-	-	-	-	-
0.988	-	-	0.333	-0.312875	-	-	-
0.988	-	-	8.520	0.412391	-	-	-
0.988	-	-3	8.988	0.458480	neutral(0.4-	-	-
0.197	-	-	-	-	-	-	-
0.197	-	-	9.900	0.557496	-	-	-

-	-	-	-	0	-	G	0.1769168	NR
-	-	-	-	0	-	C	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	0	MALT_lym	A	0.2731034	NR
-	-	-	-	0	-	G	0.4682574	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	0	-	C	0.6778984	NR
-	-	-	-	2	-	A	0.6207210	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	2	-	A	0.1092634	NR
-	-	-	-	0	-	C	0.4957713	NR
-	-	-	-	-	-	-	-	NR
-	-	-	-	-	FANCONI_	T	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	0	-	T	0.5194465	NR
-	-	-	-	2	-	G	0.0745868	NR
-	-	-	-	-	-	TTTT	-	NR
-	-	-	-	-	-	-	-	NR
-	-	-	-	-	HYPERPAR	A	-	NR
-	-	-	-	-	-	g	-	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	2	-	C	0.2701084	NR
-	-	-	-	0	-	G	0.3653853	NR
-	-	-	-	0	-	T	1.2840433	NR
-	-	-	-	-	MELANOM	AGG	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	CAPICUA_	C	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	-	-	-	NR
-	-	-	-	2	-	A	0.0989413	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	-----Cg	-	NR
-	-	-	-	-	-	ATT	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	0	-	A	1.3629024	NR
-	-	-	-	-	Butterfly-sl	AGA	-	NR
-	-	-	-	2	-	C	2.2137141	NR
-	-	-	-	0	-	A	0.0059104	NR
-	-	-	-	0	-	C	0.1638847	NR
-	-	-	-	0	-	T	0.2893329	NR

-	-	-	-	0	-	G	0.7372215	NR
-	-	-	-	0	-	G	0.7217725	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	SPONDYLO	GC	-	NR
-	-	-	-	0	-	G	0.9148740	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	2	Overgrowth	T	-	NR
-	-	-	-	0	-	G	0.9638527	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	0	-	T	1.3485295	NR
-	-	-	-	0	-	A	1.5162887	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	-	0 neutral(0.4	-1	0.167898	NR
-	-	-	-	0	-	A	0.6866158	NR
-	-	-	-	-	-	AAA	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	TTACTC	-	NR
-	-	-	-	-	RUBINSTEI	T	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	0	-	G	0.1804570	NR
-	-	-	-	0	-	G	0.4499171	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	-	-	A	-	NR
-	-	-	-	0	-	A	0.3657255	NR
-	-	-	-	0	-	A	1.5168048	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	0	-	A	0.2473641	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	T	-	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	-	-	C	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	-	-	t	-	NR
-	-	-	-	-	-	G	-	NR
-	-	-	-	2	-	C	0.3247939	NR
-	-	-	-	0	-	T	1.1959237	NR

-	-	-	-	-	G	-	NR
-	-	-	-	-	Exostoses_A	-	NR
-	-	-	-	-	T	-	NR
-	-	-	-	-	OSTEOPATI-	-	NR
-	-	-	-	-	G	-	NR
-	-	-	-	-	C	-	NR
-	-	-	-	0	a	0.5695223	NR
-	-	-	-	-	FANCONI_A	-	NR
-	-	-	-	-	T	-	NR
-	-	-	-	0	C	-	NR
-	-	-	-	-	EncephalocT	-	NR
-	-	-	-	0	T	1.9310558	NR
-	-	-	-	-	ACHONDROC	-	NR
-	-	-	-	-	c	-	NR
-	-	-	-	-	G	-	NR
-	-	-	-	-	CT	-	NR
-	-	-	-	0	C	0.1145077	NR
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-	-	-	-	2	G	0.9135416	NR
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-	-	-	-	0	C	1.1614020	NR
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-	-	-	-	0	-	C	0.7427756	NR
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-	-	-	-	0	-	G	0.8365473	NR
-	-	-	-	0	-	G	0.5017323	NR
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-	-	-	-	2	T	0.0255764	NR
-	-	-	-	-	C	-	NR
-	-	-	-	2	Colorectal_	2.0327957	NR
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-	-	-	-	-	C	-	NR
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-	-	-	-	-	LYMPHAN(-	-	NR
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-	-	-	-	0	-	T	1.1360345'	NR
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-	-	-	-	0	-	WERNER_Sg	0.1420064'	NR
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NR	none	NR	NR	none	chr18:50832036
NR	none	NR	NR	none	chr19:11123688

NR	none	NR	NR	none	chr19:1207176
NR	none	NR	NR	none	chr19:1221293
NR	none	NR	NR	none	chr19:45860637
NR	none	NR	NR	none	chr2:141092084
NR	none	NR	NR	none	chr2:141116447
NR	none	NR	NR	none	chr2:141201978
NR	none	NR	NR	none	chr2:141232800
NR	none	NR	NR	none	chr2:141245207
NR	none	NR	NR	none	chr2:141274576
NR	none	NR	NR	none	chr2:141625410
NR	none	NR	NR	none	chr2:141773397
NR	none	NR	NR	none	chr2:142567910
NR	none	NR	NR	none	chr2:209108317
NR	none	NR	NR	none	chr2:209113192
NR	none	NR	NR	none	chr2:219545345
NR	none	NR	NR	none	chr2:29416481
NR	none	NR	NR	none	chr2:29940529
NR	none	NR	NR	none	chr2:47637507
NR	none	NR	NR	none	chr2:47698108
NR	none	NR	NR	none	chr2:60773146
NR	none	NR	NR	none	chr2:61717816
NR	none	NR	NR	none	chr20:39788754
NR	none	NR	NR	none	chr20:39792063
NR	none	NR	NR	none	chr20:57474021
NR	none	NR	NR	none	chr20:57485812
NR	none	NR	NR	none	chr22:36684816
NR	none	NR	NR	none	chr22:41513774
NR	none	NR	NR	none	chr22:41547910
NR	none	NR	NR	none	chr22:41574892
NR	none	NR	NR	none	chr3:12626080
NR	none	NR	NR	none	chr3:142242985
NR	none	NR	NR	none	chr3:142281353
NR	none	NR	NR	none	chr3:178916917
NR	none	NR	NR	none	chr3:187440264
NR	none	NR	NR	none	chr3:187440364
NR	none	NR	NR	none	chr3:187443314
NR	none	NR	NR	none	chr3:188327409
NR	none	NR	NR	none	chr3:195594858
NR	none	NR	NR	none	chr3:37090407
NR	none	NR	NR	none	chr3:41275179
NR	none	NR	NR	none	chr3:47059214
NR	none	NR	NR	none	chr3:47162886
NR	none	NR	NR	none	chr3:52440855
NR	none	NR	NR	none	chr3:52613209
NR	none	NR	NR	none	chr3:89390150
NR	none	NR	NR	none	chr3:89391112
NR	none	NR	NR	none	chr3:89521664

NR	none	NR	NR	none	chr4:106155199
NR	none	NR	NR	none	chr4:106156187
NR	none	NR	NR	none	chr4:106157698
NR	none	NR	NR	none	chr4:106164916
NR	none	NR	NR	none	chr4:106196829
NR	none	NR	NR	none	chr4:55593481
NR	none	NR	NR	none	chr4:55602724
NR	none	NR	NR	none	chr4:55960993
NR	none	NR	NR	none	chr4:87968524
NR	none	NR	NR	none	chr5:131927610
NR	none	NR	NR	none	chr5:180043918
NR	none	NR	NR	none	chr5:38489330
NR	none	NR	NR	none	chr5:67575548
NR	none	NR	NR	none	chr5:67588148
NR	none	NR	NR	none	chr5:7889295
NR	none	NR	NR	none	chr6:106547325
NR	none	NR	NR	none	chr6:106547372
NR	none	NR	NR	none	chr6:117724379
NR	none	NR	NR	none	chr6:135518349
NR	none	NR	NR	none	chr6:138196066
NR	none	NR	NR	none	chr6:152527386
NR	none	NR	NR	none	chr6:152712428
NR	none	NR	NR	none	chr6:152712559
NR	none	NR	NR	none	chr6:152841662
NR	none	NR	NR	none	chr6:160493913
NR	none	NR	NR	none	chr6:395895
NR	none	NR	NR	none	chr6:51497503
NR	none	NR	NR	none	chr6:51609303
NR	none	NR	NR	none	chr6:51889474
NR	none	NR	NR	none	chr6:51907698
NR	none	NR	NR	none	chr6:51907900
NR	none	NR	NR	none	chr7:100411556
NR	none	NR	NR	none	chr7:100417397
NR	none	NR	NR	none	chr7:106508539
NR	none	NR	NR	none	chr7:106508919
NR	none	NR	NR	none	chr7:106509331
NR	none	NR	NR	none	chr7:116340262
NR	none	NR	NR	none	chr7:126173716
NR	none	NR	NR	none	chr7:2959172
NR	none	NR	NR	none	chr7:2979559
NR	none	NR	NR	none	chr7:55249063
NR	none	NR	NR	none	chr7:55270249
NR	none	NR	NR	none	chr8:103266602
NR	none	NR	NR	none	chr8:103326128
NR	none	NR	NR	none	chr8:113364696
NR	none	NR	NR	none	chr8:113841946
NR	none	NR	NR	none	chr8:114111084

[illegible]

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