Hugo_Symbol	Entrez_Gen	Chromosom	Start_position	End_position	Variant_Cla	Reference_	Tumor_Seq	Tumor_Seq	Genome_Cl	Annotation	Transcript_	Transcript_	Transcript_	cDNA_Char	Codon_Cha	Protein_Ch	Other_Transcripts	Refseq_mRNA_Id
CTD-2192J16.20	0	19	12691164	12691164	3'UTR	C	C	T	g.chr19:12(	ENST00000 -	0	625					ZNF490_ENST00000311437.6_3'UTR	
AKR1A1	10327	1	46032770	46032770	3'UTR	C	C	T	g.chr1:460(	ENST00000 +	0	528					AKR1A1_ENST00000351829.4_Intron|AKR1A1_EN	
AKAP3	10566	12	4724854	4724854	3'UTR	G	G	A	g.chr12:472	ENST00000 -	0	3137					AKAP3_ENST000002288	NM_001278309.1
FCER1A	2205	1	159277781	159277781	3'UTR	C	C	A	g.chr1:159	ENST00000 +	0	932					FCER1A_ENST00000368	NM_002001.3
ABL1	25	9	133761129	133761129	3'UTR	G	G	A	g.chr9:133	ENST00000 +	0	3833						NM_005157.4
OR2L13	284521	1	248262672	248262672	5'UTR	G	G	C	g.chr1:248	ENST00000 +	0	332					OR2L13_ENST00000358	NM_175911.2
Unknown	0	5	62072618	62072618	IGR	G	G	A									IPO11 (148209 upstream) : None (None downstre	
KCNIP3	30818	2	95976299	95976299	Intron	T	T	G	g.chr2:959	ENST00000 +	2	316					KCNIP3_ENST00000360	NM_013434.4
CA8	767	8	61121269	61121269	Intron	T	T	C	g.chr8:611	ENST00000 -	8	1173						NM_004056.4
SUMF2	25870	7	56140772	56140772	Missense_M	G	G	A	g.chr7:561	ENST00000 +	3	395	c.364G>A	c.(364-366)	p.E122K		SUMF2_ENST00000437	NM_001042469.1|NM_(
NR3C2	0	4	149357871	149357871	Missense_M	C	C	T	g.chr4:149	ENST00000 -	2	504	c.142G>A	c.(142-144)	p.V48I		NR3C2_ENST00000511528.1_Missense_Mutation	
FRG1B	0	20	29628245	29628245	Missense_M	G	G	A	g.chr20:29	ENST00000 +	6	627	c.247G>A	c.(247-249)	p.A83T		FRG1B_ENST00000358464.4_Missense_Mutation	
RTP4	64108	3	187086270	187086270	Missense_M	A	A	G	g.chr3:187	ENST00000 +	1	151	c.41A>G	c.(40-42)gA	p.E14G			NM_022147.2
CSMD1	64478	8	4495039	4495039	Missense_M	T	T	C	g.chr8:449	ENST00000 -	2	682	c.127A>G	c.(127-129)	p.I43V		CSMD1_ENST00000400186.3_Missense_Mutatior	
CTNNA2	1496	2	80136918	80136918	Missense_M	A	A	C	g.chr2:801	ENST00000 +	11	1775	c.1051A>C	c.(1051-105	p.N351H		CTNNA2_ENST00000496558.1_Missense_Mutatic	
CUL9	23113	6	43164595	43164595	Missense_M	G	G	A	g.chr6:431	ENST00000 +	11	2882	c.2798G>A	c.(2797-279	p.R933H		CUL9_ENST0000037264	NM_015089.2
DYRK1B	9149	19	40318202	40318202	Missense_M	C	C	T	g.chr19:40	ENST00000 -	7	1370	c.902G>A	c.(901-903)	p.C301Y		DYRK1B_ENST00000348817.3_Missense_Mutatio	
OTOF	9381	2	26697530	26697530	Missense_M	A	A	C	g.chr2:266	ENST00000 -	26	3265	c.3139T>G	c.(3139-314	p.F1047V		OTOF_ENST0000033858	NM_194248.2
BNC1	646	15	83933158	83933158	Missense_M	C	C	T	g.chr15:83	ENST00000 -	4	930	c.845G>A	c.(844-846)	p.G282E		BNC1_ENST0000056970	NM_001717.3
SEZ6L2	26470	16	29883824	29883824	Missense_M	G	G	A	g.chr16:29	ENST00000 -	15	3039	c.2512C>T	c.(2512-251	p.R838W		SEZ6L2_ENST00000537	NM_001114099.2|NM_2
CTSS	1520	1	150724429	150724429	Missense_M	A	A	G	g.chr1:150	ENST00000 -	5	715	c.455T>C	c.(454-456)	p.L152P		CTSS_ENST0000048076	NM_001199739.1|NM_(
CCDC181	57821	1	169391215	169391215	Missense_M	G	G	C	g.chr1:169	ENST00000 -	4	961	c.454C>G	c.(454-456)	p.L152V		CCDC181_ENST00000367806.3_Missense_Mutati	
NEB	4703	2	152500345	152500345	Missense_M	T	T	G	g.chr2:152	ENST00000 -	57	8145	c.7943A>C	c.(7942-794	p.D2648A		NEB_ENST00000604864	NM_001164507.1
PHLPP2	23035	16	71712830	71712830	Missense_M	T	T	C	g.chr16:71	ENST00000 -	7	1829	c.1096A>G	c.(1096-109	p.N366D		PHLPP2_ENST00000567016.1_Missense_Mutatio	
GABRG2	0	5	161580192	161580192	Missense_M	T	T	G	g.chr5:161	ENST00000 +	10	1706	c.1246T>G	c.(1246-124	p.C416G		GABRG2_ENST0000036	NM_000816.3|NM_1985
ATXN7L2	127002	1	110033878	110033878	Missense_M	G	G	A	g.chr1:110	ENST00000 +	10	1708	c.1693G>A	c.(1693-169	p.V565M		ATXN7L2_ENST0000045	NM_153340.4
OR4P4	81300	11	55406231	55406231	Missense_M	T	T	C	g.chr11:554	ENST00000 +	1	398	c.398T>C	c.(397-399)	p.I133T			NM_001004124.1
FRG1B	0	20	29628243	29628243	Missense_M	T	T	C	g.chr20:29	ENST00000 +	6	625	c.245T>C	c.(244-246)	p.L82S		FRG1B_ENST00000358464.4_Missense_Mutation	
CARM1	10498	19	11022906	11022906	Missense_M	C	C	T	g.chr19:11	ENST00000 +	5	795	c.605C>T	c.(604-606)	p.A202V		CARM1_ENST00000344	NM_199141.1
MSLNL	401827	16	824911	824911	Missense_M	C	C	T	g.chr16:824	ENST00000 -	7	1660	c.1661G>A	c.(1660-166	p.R554Q		MSLNL_ENST00000442466.1_Missense_Mutation	
DACH1	1602	13	72147042	72147042	Missense_M	G	G	A	g.chr13:721	ENST00000 -	4	1657	c.1235C>T	c.(1234-123	p.T412I		DACH1_ENST00000313	NM_080759.4
CDK5	1020	7	150754212	150754212	Missense_M	C	C	G	g.chr7:150	ENST00000 -	2	754	c.73G>C	c.(73-75)Ga	p.E25Q		CDK5_ENST0000029751	NM_004935.3
MAZ	4150	16	29819095	29819095	Missense_M	A	A	C	g.chr16:298	ENST00000 +	2	1095	c.989A>C	c.(988-990)	p.D330A		MAZ_ENST0000056340	NM_001042539.1
NOP14	8602	4	2954016	2954016	Missense_M	G	G	A	g.chr4:2954	ENST00000 -	6	921	c.856C>T	c.(856-858)	p.L286F		NOP14_ENST00000502735.1_Missense_Mutation	
PCDHGA4	0	5	140736478	140736478	Missense_M	G	G	A	g.chr5:140	ENST00000 +	1	1711	c.1711G>A	c.(1711-171	p.G571S		PCDHGA2_ENST000003	NM_018917.2
SLC25A11	8402	17	4843151	4843151	Missense_M	A	A	C	g.chr17:484	ENST00000 -	1	395	c.55T>G	c.(55-57)Tc	p.S19A		SLC25A11_ENST000005	NM_001165417.1|NM_(
SPHKAP	80309	2	228882624	228882624	Missense_M	C	C	A	g.chr2:228	ENST00000 -	7	2992	c.2946G>T	c.(2944-294	p.K982N		SPHKAP_ENST00000344	NM_001142644.1
ATRNL1	26033	10	117221456	117221456	Missense_M	C	C	A	g.chr10:117	ENST00000 +	22	3454	c.3328C>A	c.(3328-333	p.L1110I		ATRNL1_ENST00000423	NM_207303.2
DPY19L4	286148	8	95777417	95777417	Missense_M	G	G	C	g.chr8:957	ENST00000 +	9	976	c.877G>C	c.(877-879)	p.E293Q			NM_181787.2
DTNB	1838	2	25861940	25861940	Nonsense_I	G	G	A	g.chr2:258	ENST00000 -	3	340	c.91C>T	c.(91-93)Cg	p.R31*		DTNB_ENST0000040718	NM_001256303.1|NM_(
ARHGAP26	23092	5	142283200	142283200	Nonsense_I	C	C	A	g.chr5:142	ENST00000 +	8	1153	c.798C>A	c.(796-798)	p.Y266*		ARHGAP26_ENST00000	NM_001135608.1
RP11-707M1.1	0	11	49831701	49831701	RNA	G	G	T	g.chr11:498	ENST00000 +	0	1926						
HPCAL1	3241	2	10560207	10560207	Silent	C	C	T	g.chr2:105	ENST00000 +	4	850	c.324C>T	c.(322-324)	p.Y108Y		HPCAL1_ENST00000307	NM_134421.2
MAGEA12	4111	X	151900285	151900285	Silent	G	G	A	g.chrX:151	ENST00000 -	3	869	c.516C>T	c.(514-516)	p.I172I		MAGEA12_ENST000003	NM_001166386.1
ARHGAP15	55843	2	144525663	144525663	Silent	C	C	A	g.chr2:144	ENST00000 +	14	1517	c.1350C>A	c.(1348-135	p.I450I		CTD-2252P21.1_ENST00	NM_018460.3
LY9	4063	1	160784539	160784539	Silent	C	C	T	g.chr1:160	ENST00000 +	4	1090	c.1060C>T	c.(1060-106	p.L354L		LY9_ENST00000368035.	NM_001261456.1|NM_(
DPP9	91039	19	4689663	4689663	Silent	G	G	A	g.chr19:468	ENST00000 -	15	1945	c.1668C>T	c.(1666-166	p.L556L		DPP9_ENST0000059467	NM_139159.4
RAP1GAP	5909	1	21930202	21930202	Silent	C	C	T	g.chr1:219	ENST00000 -	16	1640	c.1632G>A	c.(1630-163	p.A544A		RAP1GAP_ENST00000374761.2_Intron|RAP1GAP_	
ENOX2	10495	X	129837113	129837113	Silent	G	G	A	g.chrX:129	ENST00000 -	5	582	c.165C>T	c.(163-165)	p.A55A		ENOX2_ENST00000492	NM_182314.1
IGSF3	3321	1	117122123	117122123	Silent	T	T	A	g.chr1:1171	ENST00000 -	10	3990	c.3225A>T	c.(3223-322	p.T1075T		IGSF3_ENST0000036948	NM_001007237.1
FAM160B2	64760	8	21959775	21959775	Silent	G	G	A	g.chr8:219	ENST00000 +	15	1987	c.1941G>A	c.(1939-194	p.P647P			NM_022749.5
BAZ2A	11176	12	56993811	56993811	Silent	C	C	T	g.chr12:569	ENST00000 -	26	5071	c.4872G>A	c.(4870-487	p.Q1624Q		BAZ2A_ENST00000549884.1_Silent_p.Q1654Q|BA	
TRPV5	56302	7	142626649	142626649	Silent	G	G	A	g.chr7:142	ENST00000 -	4	709	c.361C>T	c.(361-363)	p.L121L		TRPV5_ENST000004426	NM_019841.4
WSCD1	23302	17	5993659	5993659	Silent	C	C	T	g.chr17:599	ENST00000 +	4	951	c.561C>T	c.(559-561)	p.G187G		WSCD1_ENST00000317744.5_Silent_p.G187G|WS	
ENG	2022	9	130587621	130587621	Silent	C	C	T	g.chr9:130	ENST00000 -	6	985	c.705G>A	c.(703-705)	p.T235T		ENG_ENST00000373203.4_Silent_p.T235T	
HADHB	3032	2	26502095	26502095	Silent	G	G	A	g.chr2:265	ENST00000 +	9	827	c.723G>A	c.(721-723)	p.Q241Q		HADHB_ENST00000494	NM_000183.2
RIC3	79608	11	8161580	8161580	Silent	C	C	A	g.chr11:816	ENST00000 -	2	350	c.285G>T	c.(283-285)	p.L95L		RIC3_ENST00000419822	NM_001206671.2|NM_(
DEGS1	8560	1	224377421	224377421	Silent	G	G	A	g.chr1:224	ENST00000 +	2	391	c.225G>A	c.(223-225)	p.A75A		DEGS1_ENST000004658	NM_003676.3
APLNR	187	11	57004263	57004263	Silent	C	C	A	g.chr11:57	ENST00000 -	1	412	c.216G>T	c.(214-216)	p.A72A			NM_005161.4
STEAP3	55240	2	120003285	120003285	Silent	G	G	A	g.chr2:120	ENST00000 +	3	717	c.213G>A	c.(211-213)	p.A71A		STEAP3_ENST00000425	NM_182915.2
KIF16B	55614	20	16352331	16352331	Silent	A	A	G	g.chr20:163	ENST00000 -	21	3583	c.3426T>C	c.(3424-342	p.S1142S		KIF16B_ENST00000408	NM_001199865.1|NM_(
GRM8	0	7	126882950	126882950	Silent	G	G	T	g.chr7:126	ENST00000 -	2	1117	c.309C>A	c.(307-309)	p.L103L		GRM8_ENST00000444921.2_Silent_p.L103L|GRM	
GJA10	84694	6	90605555	90605555	Silent	C	C	T	g.chr6:906	ENST00000 +	1	1368	c.1368C>T	c.(1366-136	p.S456S			NM_032602.1
CADPS	8618	3	62518716	62518716	Silent	G	G	T	g.chr3:625	ENST00000 -	13	2470	c.2121C>A	c.(2119-212	p.G707G		CADPS_ENST0000037579	NM_003716.3
ATL1	51062	14	51087375	51087375	Silent	C	C	G	g.chr14:51	ENST00000 +	10	1402	c.921C>G	c.(919-921)	p.P307P		ATL1_ENST0000035703	NM_001127713.1
NF2	4771	22	30000101	30000101	Splice_Site	G	G	C	g.chr22:30	ENST00000 +	1	555	c.114_splic	c.e1+1	p.E38_splic		NF2_ENST00000413209	NM_000268.3|NM_0164

Refseq_prot_Id	SwissProt_acc_Id	SwissProt_entry_Id	Description	UniProt_AApos
NST00000372070.3_Intron	P14550	AK1A1_HUMAN	aldo-keto reductase family 1, member A1 (aldehyde reductase)	
NP_001265238.1	O75969	AKAP3_HUMAN	A kinase (PRKA) anchor protein 3	
NP_001992.1	P12319	FCERA_HUMAN	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	
NP_005148.2	P00519	ABL1_HUMAN	c-abl oncogene 1, non-receptor tyrosine kinase	
NP_787107.1	Q8N349	OR2LD_HUMAN	olfactory receptor, family 2, subfamily L, member 13	
am)				
NP_038462.1	Q9Y2W7	CSEN_HUMAN	Kv channel interacting protein 3, calsenilin	
NP_004047.3	P35219	CAH8_HUMAN	carbonic anhydrase VIII	
NP_001035934.2|NP_05622(	Q8NBJ7	SUMF2_HUMAN	sulfatase modifying factor 2	103
_p.V48I|NR3C2_ENST000005	P08235	MCR_HUMAN	nuclear receptor subfamily 3, group C, member 2	48
_p.A83T|FRG1B_ENST00000439954.2_Missense_Mutation_p.A88T				
NP_071430.2	Q96DX8	RTP4_HUMAN	receptor (chemosensory) transporter protein 4	14
n_p.I43V|CSMD1_ENST00000(	Q96PZ7	CSMD1_HUMAN	CUB and Sushi multiple domains 1	43
on_p.N351H|CTNNA2_ENST0(	P26232	CTNA2_HUMAN	catenin (cadherin-associated protein), alpha 2	351
NP_055904.1	Q8IWT3	CUL9_HUMAN	cullin 9	933
n_p.C301Y|DYRK1B_ENST000	Q9Y463	DYR1B_HUMAN	dual-specificity tyrosine-(Y)-phosphorylation regulated kinas	301
NP_919224.1	Q9HC10	OTOF_HUMAN	otoferlin	1047
NP_001708.3	Q01954	BNC1_HUMAN	basonuclin 1	282
NP_001107571.1|NP_96386(	Q6UXD5	SE6L2_HUMAN	seizure related 6 homolog (mouse)-like 2	838
NP_001186668.1|NP_00407(	P25774	CATS_HUMAN	cathepsin S	152
ion_p.L152V|CCDC181_ENST00000491570.1_5'UTR|CCDC181_ENST00000367805			coiled-coil domain containing 181	
NP_001157979.1	P20929	NEBU_HUMAN	nebulin	2648
n_p.N401D|PHLPP2_ENST000	Q6ZVD8	PHLP2_HUMAN	PH domain and leucine rich repeat protein phosphatase 2	366
NP_000807.2|NP_944494.1	P18507	GBRG2_HUMAN	gamma-aminobutyric acid (GABA) A receptor, gamma 2	408
NP_699171.3	Q5T6C5	AT7L2_HUMAN	ataxin 7-like 2	565
NP_001004124.1	Q8NGL7	OR4P4_HUMAN	olfactory receptor, family 4, subfamily P, member 4	133
_p.L82S|FRG1B_ENST00000439954.2_Missense_Mutation_p.L87S				
NP_954592.1	Q86X55	CARM1_HUMAN	coactivator-associated arginine methyltransferase 1	202
_p.R203Q	Q96KJ4	MSLNL_HUMAN	mesothelin-like	203
NP_542937.2	Q9UI36	DACH1_HUMAN	dachshund homolog 1 (Drosophila)	462
NP_004926.1	Q00535	CDK5_HUMAN	cyclin-dependent kinase 5	25
NP_001036004.1	P56270	MAZ_HUMAN	MYC-associated zinc finger protein (purine-binding transcript	330
_p.L286F|NOP14-AS1_ENST0	P78316	NOP14_HUMAN	NOP14 nucleolar protein	286
NP_061740.1				
NP_001158889.1|NP_00355(	Q02978	M2OM_HUMAN	solute carrier family 25 (mitochondrial carrier; oxoglutarate	19
NP_001136116.1	Q2M3C7	SPKAP_HUMAN	SPHK1 interactor, AKAP domain containing	982
NP_997186.1	Q5VV63	ATRN1_HUMAN	attractin-like 1	1110
NP_861452.2	Q7Z388	D19L4_HUMAN	dpy-19-like 4 (C. elegans)	293
NP_001243232.1|NP_06870(	O60941	DTNB_HUMAN	dystrobrevin, beta	31
NP_001129080.1	Q9UNA1	RHG26_HUMAN	Rho GTPase activating protein 26	266
NP_602293.1	P37235	HPCL1_HUMAN	hippocalcin-like 1	108
NP_001159858.1	P43365	MAGAC_HUMAN	melanoma antigen family A, 12	172
NP_060930.3	Q53QZ3	RHG15_HUMAN	Rho GTPase activating protein 15	450
NP_001248385.1|NP_00233(	Q9HBG7	LY9_HUMAN	lymphocyte antigen 9	354
NP_631898.3	Q86TI2	DPP9_HUMAN	dipeptidyl-peptidase 9	527
_ENST00000374765.4_Intron	P47736	RPGP1_HUMAN	RAP1 GTPase activating protein	460
NP_872114.1	Q16206	ENOX2_HUMAN	ecto-NOX disulfide-thiol exchanger 2	55
NP_001007238.1	O75054	IGSF3_HUMAN	immunoglobulin superfamily, member 3	1075
NP_073586.5	Q86V87	F16B2_HUMAN	family with sequence similarity 160, member B2	647
AZ2A_ENST00000379441.3_Si	Q9UIF9	BAZ2A_HUMAN	bromodomain adjacent to zinc finger domain, 2A	1656
NP_062815.2	Q9NQA5	TRPV5_HUMAN	transient receptor potential cation channel, subfamily V, me	121
SCD1_ENST00000573634.1_Si	Q658N2	WSCD1_HUMAN	WSC domain containing 1	187
	P17813	EGLN_HUMAN	endoglin	235
NP_000174.1	P55084	ECHB_HUMAN	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/en	241
NP_001193600.1|NP_07883(	Q7Z5B4	RIC3_HUMAN	RIC3 acetylcholine receptor chaperone	95
NP_003667.1	O15121	DEGS1_HUMAN	delta(4)-desaturase, sphingolipid 1	75
NP_005152.1	P35414	APJ_HUMAN	apelin receptor	72
NP_878919.2	Q658P3	STEA3_HUMAN	STEAP family member 3, metalloreductase	71
NP_001186794.1|NP_07898(	Q96L93	KI16B_HUMAN	kinesin family member 16B	1142
18_ENST00000405249.1_Silen	O00222	GRM8_HUMAN	glutamate receptor, metabotropic 8	103
NP_115991.1	Q969M2	CXA10_HUMAN	gap junction protein, alpha 10, 62kDa	456
NP_003707.2	Q9ULU8	CAPS1_HUMAN	Ca++-dependent secretion activator	707
NP_001121185.1	Q8WXF7	ATLA1_HUMAN	atlastin GTPase 1	307
NP_000259.1|NP_057502.2|	P35240	MERL_HUMAN	neurofibromin 2 (merlin)	38