Supplementary Table 1: Patient samples studied in this manuscript

Tissue	Sample	Clinical	Paired WES	SNP6.0	RNA-seq	IMPACT	H3K27me3 IHC
Frozen	2T	RT-associated	X	X	X	X	X
Frozen	4T	Sporadic	X	X	X	X	X
Frozen	5T	NF1-associated			X	X	X
Frozen	7T	RT-associated	X	X	X	X	X
Frozen	8T	Sporadic	X	X	X	X	X
Frozen	9T	NF1-associated	X	X	X	X	X
Frozen	10T	Sporadic	X	X	X	X	X
Frozen	11T	NF1-associated	X	X	X	X	X
Frozen	12T	NF1-associated	X	X	X	X	X
Frozen	13T	RT-associated	X	X	X	X	X
Frozen	14T	NF1-associated	X	X	X	X	X
Frozen	15T	NF1-associated	X	X		X	X
Frozen	16T	Sporadic	X	X	X	X	
Frozen	18T	RT-associated	X	X		X	X
Frozen	19T	NF1-associated	X	X	X	X	X
Frozen	20T	Epithelioid	X	X	X	X	X
Frozen	21T	Sporadic			X		X
Frozen	22T=46.3	NF1-associated			X		X
Paraffin	MPNST 01	Sporadic				X	X
Paraffin	MPNST 02.1	Sporadic				X	X
Paraffin	MPNST 02.2	Sporadic				X	X
Paraffin	MPNST 02.3	Sporadic				X	X
Paraffin	MPNST 03	NF1-associated				X	X
Paraffin	MPNST 04.1	NF1-associated				X	X
Paraffin	MPNST 04.2	NF1-associated				X	X
Paraffin	MPNST 05.1	NF1-associated				X	X
Paraffin	MPNST 05.2	Neurofibroma					X
Paraffin	MPNST 06.1	NF1-associated				X	X
Paraffin	MPNST 06.2	NF1-associated				X	X
Paraffin	MPNST 10	NF1-associated				X	X
Paraffin	MPNST 12.1	NF1-associated				X	X
Paraffin	MPNST 12.2	Neurofibroma				X	X
Paraffin	MPNST 13.1	NF1-associated				X	X
Paraffin	MPNST 13.2	Neurofibroma				X	X
Paraffin	MPNST 14	NF1-associated				X	X
Paraffin	MPNST 18	Sporadic				X	X
Paraffin	MPNST 19	NF1-associated				X	X
Paraffin	MPNST 21.1	NF1-associated				X	X
Paraffin	MPNST 21.2	Neurofibroma				X	X
Paraffin	MPNST 22	NF1-associated				X	X
Paraffin	MPNST 23	Sporadic				X	X
Paraffin	MPNST 24	RT-associated				X	X
Paraffin	MPNST 25	NF1-associated				X	X
Paraffin	MPNST 26	Epithelioid				X	X
Paraffin	MPNST 27	Sporadic				X	X
Paraffin	MPNST 28	NF1-associated				X	X
Paraffin	MPNST 29	Sporadic				X	X
Paraffin	MPNST 30	Sporadic					X
Paraffin	MPNST 32	NF1-associated					X
Paraffin	MPNST 33	NF1-associated					X

Paraffin	MPNST 34	Sporadic		X
Paraffin	MPNST 36	NF1-associated		X
Paraffin	MPNST 37.2	NF1-associated		X
Paraffin	MPNST 37.3	Neurofibroma		X
Paraffin	MPNST 38.1	Sporadic		X
Paraffin	MPNST 38.2	Sporadic		X
Paraffin	MPNST 39	RT-Associated		X
Paraffin	MPNST 40.1	NF1-associated		X
Paraffin	MPNST 40.2	NF1-associated		X
Paraffin	MPNST 40.3	NF1-associated		X
Paraffin	MPNST 43.1	NF1-associated	X	X
Paraffin	MPNST 43.2	Neurofibroma	X	X
Paraffin	MPNST 44	RT-Associated	X	X
Paraffin	MPNST 45	RT-Associated	X	X
Paraffin	MPNST 46.1	NF1-associated	X	X
Paraffin	MPNST 46.2	Neurofibroma	X	X
Paraffin	MPNST 46.3	NF1-associated	X	X
Paraffin	MPNST 47.1	NF1-associated	X	X
Paraffin	MPNST 47.2	Neurofibroma	X	X
Paraffin	MPNST 48	Sporadic	X	X
Paraffin	MPNST 50	Epithelioid	X	X
Paraffin	MPNST 51	NF1-associated	X	X
Paraffin	MPNST 52	RT-Associated	X	X
Paraffin	MPNST 53	RT-Associated	X	X
Paraffin	MPNST 54	RT-Associated		X
Paraffin	MPNST 55	RT-Associated		X

Supplementary Table 2: Whole exome sequencing metrics

Sample	Total Somatic Mutations	Non-synonymous Somatic Mutations	Num Reads (10^6)	Uniquely Aligned Reads (10^6)	% Uniquely Aligned Reads	On Target Bases (10^9)	% On or Near Bait	Mean Target Coverage	% Target Bases at 10x	% Target Bases at 20x
2N			258	254	98.3%	11.9	81.1%	169	99.2%	98.0%
2T	194	26	179	176	98.3%	8.3	81.8%	117	98.4%	95.4%
4N			253	247	97.8%	11.1	79.1%	158	99.1%	97.7%
4T	296	54	259	255	98.3%	11.2	77.5%	158	99.1%	97.7%
7N			196	193	98.5%	8.9	80.9%	126	98.4%	96.1%
7T	280	49	153	151	98.6%	6.9	80.5%	98	97.5%	92.3%
8N			207	204	98.5%	10.1	83.4%	143	98.3%	96.2%
8T	223	32	190	187	98.5%	9.1	82.4%	129	97.4%	94.0%
9N			273	270	99.0%	14.5	88.9%	206	98.9%	97.8%
9T	350	56	196	194	99.1%	10.5	89.3%	149	98.1%	95.5%
10N			98	97	98.7%	5.3	89.2%	75	96.4%	89.6%
10T	126	11	145	144	98.8%	7.9	89.6%	112	97.8%	94.1%
11N			158	156	98.5%	7.9	86.2%	112	97.6%	94.3%
11T	352	60	172	167	97.3%	6.9	69.3%	98	97.3%	92.6%
12N			246	242	98.6%	12.6	86.0%	178	98.4%	96.9%
12T	303	55	283	279	98.6%	14.3	86.5%	203	98.6%	97.2%
13N			155	151	97.2%	6.5	71.0%	91	97.8%	93.0%
13T	552	55	442	433	98.0%	19.9	75.1%	282	99.3%	98.6%
14N			193	188	97.7%	8.2	74.1%	116	98.1%	95.1%
14T	617	46	487	472	97.0%	16.4	59.9%	232	98.3%	96.9%
15N			140	137	97.9%	6.4	79.3%	91	97.5%	92.5%
15T	129	20	92	90	97.6%	4.0	73.7%	57	94.7%	83.6%
16N			467	458	98.0%	21.5	78.1%	305	99.1%	98.5%
16T	637	121	231	224	96.9%	9.2	69.0%	130	98.8%	96.6%
18N			238	236	99.4%	12.5	90.1%	285	61.7%	61.3%
18T	93	13	105	103	98.3%	4.8	77.8%	68	96.5%	88.2%
19N			201	198	98.3%	9.9	82.5%	140	98.7%	96.5%
19T	284	51	315	309	98.3%	15.2	81.5%	215	99.2%	98.2%
20N			132	130	98.0%	6.3	78.9%	89	97.0%	91.1%
20T	145	1	202	196	97.2%	7.6	67.2%	108	97.9%	94.7%

Supplementary Table 3: Mutations found in WES of MPNST Samples

Sample	Hugo Symbol	Entrez Gene Id	Genomic Location	Variant Classification	Variant Type	Reference Allele	Tumor Seq Allele	Codon Change	Protein Change
10T	C1orf222	85452	chr1:1871035-1871035	Nonsense_Mutation	SNP	T	A	Aag/Tag	K242*
10T	MUTYH	4595	chr1:45798142-45798142	Missense_Mutation	SNP	C	T	Ggc/Agc	G237S
10T	ESPN	83715	chr1:6500456-6500456	Missense_Mutation	SNP	C	T	Cac/Tac	H211Y
10T	KCNC2	3747	chr12:75444697-75444697	Missense_Mutation	SNP	C	T	cGc/cAc	R363H
10T	CEP76	79959	chr18:12702588-12702588	De_novo_Start_InFrame	SNP	G	T		
10T	TTN	7273	chr2:179456148-179456148	Missense_Mutation	SNP	T	C	Ata/Gta	I20102V
10T	OLIG1	116448	chr21:34442697-34442697	Missense_Mutation	SNP	A	T	Acc/Tcc	T49S
10T	CLIC6	54102	chr21:36042475-36042475	Missense_Mutation	SNP	G	A	gGg/gAg	G263E
10T	PRDM15	63977	chr21:43243719-43243719	Missense_Mutation	SNP	G	C	ttC/ttG	F938L
10T	CDC42EP1	11135	chr22:37964409-37964429	In_Frame_Del	DEL	CAGCGCCTGCTGCAAACCCCT	-	ccagcgcctgctgcaaacccctca/cca	PAPAANPS253P
10T	ATP8A1	10396	chr4:42588376-42588376	Missense_Mutation	SNP	C	G	Gat/Cat	D238H
11T	SPRR1B	6699	chr1:153005002-153005007	In_Frame_Del	DEL	GTTCCA	-	gttcca/-	VP61-
11T	DARS2	55157	chr1:173806106-173806106	Frame_Shift_Del	DEL	G	-	-	-231
11T	TRAF3IP3	80342	chr1:209950815-209950815	Missense_Mutation	SNP	A	C	gAt/gCt	D391A
11T	OSBPL9	114883	chr1:52253415-52253415	Missense_Mutation	SNP	T	C	gTt/gCt	V740A
11T	ERRFI1	54206	chr1:8074157-8074157	Missense_Mutation	SNP	C	T	Gac/Aac	D168N
11T	KLHL17	339451	chr1:897356-897356	Missense_Mutation	SNP	C	G	Cac/Gac	H214D
11T	PFKFB3	5209	chr10:6265961-6265961	Frame_Shift_Del	DEL	G	-	-	-432
11T	TM7SF2	7108	chr11:64881060-64881060	Frame_Shift_Del	DEL	C	-	-	-199
11T	EED	8726	chr11:85975217-85975217	Frame_Shift_Del	DEL	A	-	-	-213
11T	MTERFD3	80298	chr12:107371874-107371874	Frame_Shift_Del	DEL	C	-	-	-207
11T	SIRT4	23409	chr12:120741408-120741408	Missense_Mutation	SNP	G	A	cGt/cAt	R15H
11T	HNF1A	6927	chr12:121434510-121434510	Missense_Mutation	SNP	C	T	aCg/aTg	T425M
11T	WDR66	144406	chr12:122359379-122359381	In_Frame_Del	DEL	AAC	-	aaaacg/aag	KT56K
11T	WDR66	144406	chr12:122359385-122359385	Frame_Shift_Del	DEL	C	-	-	-58
11T	KRT1	3848	chr12:53069246-53069246	Missense_Mutation	SNP	C	G	Ggt/Cgt	G556R
11T	PDE1B	5153	chr12:54967267-54967267	Splice_Site	SNP	G	A		
11T	PDE1B	5153	chr12:54969796-54969796	Missense_Mutation	SNP	G	C	Gag/Cag	E430Q
11T	CARS2	79587	chr13:111358304-111358304	Missense_Mutation	SNP	G	A	aCg/aTg	T46M
11T	ARHGEF40	55701	chr14:21542562-21542562	Missense_Mutation	SNP	C	G	Cgg/Ggg	R225G
11T	GOLGA6L2	283685	chr15:23685085-23685085	Missense_Mutation	SNP	G	A	gCg/gTg	A846V
11T	JMJD7-PLA2G4B	8681	chr15:42127323-42127323	Frame_Shift_Del	DEL	T	-	-	-125
11T	JMJD7-PLA2G4B	8681	chr15:42127325-42127326	Frame_Shift_Del	DEL	CT	-	-	-126
11T	TUBGCP4	27229	chr15:43696699-43696706	Frame_Shift_Del	DEL	TACGACTA	-	-	-647
11T	ABCA3	21	chr16:2369671-2369671	Frame_Shift_Del	DEL	G	-	-	-262
11T	ASPHD1	253982	chr16:29912801-29912802	In_Frame_Ins	INS	-	GGG	cag/caGGGg	Q170QG
11T	CCL5	6352	chr17:34205532-34205534	In_Frame_Del	DEL	ACG	-	gtcgtc/gtc	VV62V
11T	UNC13D	201294	chr17:73832993-73832993	Nonsense_Mutation	SNP	C	T	tgG/tgA	W354*
11T	UBE2O	63893	chr17:74387193-74387193	Missense_Mutation	SNP	C	T	cGg/cAg	R1237Q
11T	ZNF233	353355	chr19:44778125-44778125	Missense_Mutation	SNP	A	T	Aat/Tat	N438Y
11T	MUC16	94025	chr19:9057522-9057522	Missense_Mutation	SNP	G	T	aCa/aAa	T9975K
11T	ZNF559	84527	chr19:9453744-9453745	Frame_Shift_Del	DEL	AA	-	-	-539
11T	TTN	7273	chr2:179399992-179399992	Missense_Mutation	SNP	C	T	Gaa/Aaa	E33784K
11T	FOSL2	2355	chr2:28616101-28616101	De_novo_Start_InFrame	SNP	A	T		
11T	HAAO	23498	chr2:42994744-42994744	Missense_Mutation	SNP	G	T	gCt/gAt	A258D
11T	SNPH	9751	chr20:1281256-1281256	Missense_Mutation	SNP	C	T	cCg/cTg	P114L
11T	CD96	10225	chr3:111356997-111356997	Missense_Mutation	SNP	A	G	Aat/Gat	N503D
11T	POLQ	10721	chr3:121195490-121195490	Missense_Mutation	SNP	C	T	aGt/aAt	S2101N
11T	GRM7	2917	chr3:7620292-7620292	Nonsense_Mutation	SNP	C	T	Cag/Tag	Q567*
11T	DSPP	1834	chr4:88536014-88536031	In_Frame_Del	DEL	AGCAGTGACAGCAGCAAC	-	agcagtgacagcagcaac/-	SSDSSN734-
11T	PJA2	9867	chr5:108714082-108714082	Missense_Mutation	SNP	C	A	gGa/gTa	G369V
11T	PJA2	9867	chr5:108714083-108714083	Nonsense_Mutation	SNP	C	A	Gga/Tga	G369*
11T	DNAH5	1767	chr5:13719087-13719087	Missense_Mutation	SNP	G	A	Cat/Tat	H4135Y
11T	DNAH5	1767	chr5:13721211-13721211	Missense_Mutation	SNP	G	C	atC/atG	I4059M
11T	PCDHB12	56124	chr5:140589497-140589497	Missense_Mutation	SNP	G	T	Gta/Tta	V340L
11T	CPEB4	80315	chr5:173380109-173380109	Missense_Mutation	SNP	T	A	aTa/aAa	I599K
11T	CDHR2	54825	chr5:175992356-175992356	Translation_Start_Site	SNP	G	A	atG/atA	M1I
11T	CDHR2	54825	chr5:175992357-175992357	Missense_Mutation	SNP	G	T	Gcc/Tcc	A2S
11T	GCNT6	NA	chr6:10634846-10634846	Frame_Shift_Del	DEL	C	-	-	-285
11T	ZBTB12	221527	chr6:31868632-31868655	In_Frame_Del	DEL	TGGTGGCGCTGATGCTGCTCACAA	-	cttgtgagcagcatcagcgccaccaag/cag	LVSSISATK143Q
11T	SKIV2L	6499	chr6:31935517-31935548	Frame_Shift_Del	DEL	TATTCACAACCCTGGTCTTGTGTGATAAGCCC	-	-	-870

11T	TMEM168	64418	chr7:112407431-112407431	Missense_Mutation	SNP	A	T	Tgg/Agg	W639R
11T	TAS2R3	50831	chr7:141464244-141464244	Missense_Mutation	SNP	A	T	Agc/Tgc	S96C
11T	AP5Z1	9907	chr7:4830340-4830340	Missense_Mutation	SNP	G	A	Gat/Aat	D659N
11T	PEX1	5189	chr7:92135583-92135584	Frame_Shift_Ins	INS	-	T	-/A	-626?
11T	SPAG1	6674	chr8:101253182-101253182	Missense_Mutation	SNP	T	A	Tcg/Acg	S905T
11T	SLC52A2	79581	chr8:145584258-145584259	Frame_Shift_Ins	INS	-	AA	-/AA	-337?
11T	NKAIN3	286183	chr8:63161649-63161649	Missense_Mutation	SNP	G	A	gGa/gAa	G6E
11T	ADHFE1	137872	chr8:67366364-67366364	Missense_Mutation	SNP	G	A	Ggc/Agc	G320S
11T	SPAG8	26206	chr9:35811497-35811498	In_Frame_Ins	INS	-	CCAGGA	ggc/gTCCTGGgc	G182VLG
11T	TGIF2LX	90316	chrX:89177445-89177445	Missense_Mutation	SNP	A	G	Atc/Gtc	I121V
12T	TRAF3IP3	80342	chr1:209950815-209950815	Missense_Mutation	SNP	A	C	gAt/gCt	D391A
12T	EFCAB2	84288	chr1:245133630-245133630	Missense_Mutation	SNP	G	C	aGg/aCg	R69T
12T	EFCAB2	84288	chr1:245133631-245133631	Missense_Mutation	SNP	G	T	agG/agT	R69S
12T	PTGFR	5737	chr1:78958666-78958666	Missense_Mutation	SNP	G	T	Ggc/Tgc	G80C
12T	ERRFI1	54206	chr1:8074157-8074157	Missense_Mutation	SNP	C	T	Gac/Aac	D168N
12T	KLHL17	339451	chr1:897356-897356	Missense_Mutation	SNP	C	G	Cac/Gac	H214D
12T	PFKFB3	5209	chr10:6265961-6265961	Frame_Shift_Del	DEL	G	-	-	-432
12T	AMBRA1	55626	chr11:46419062-46419062	Missense_Mutation	SNP	G	C	Ctg/Gtg	L1279V
12T	TM7SF2	7108	chr11:64881060-64881060	Frame_Shift_Del	DEL	C	-	-	-199
12T	EED	8726	chr11:85975217-85975217	Frame_Shift_Del	DEL	A	-	-	-213
12T	MTERFD3	80298	chr12:107371874-107371874	Frame_Shift_Del	DEL	C	-	-	-207
12T	HNF1A	6927	chr12:121434510-121434510	Missense_Mutation	SNP	C	T	aCg/aTg	T425M
12T	PDE1B	5153	chr12:54967267-54967267	Splice_Site	SNP	G	A		
12T	PDE1B	5153	chr12:54969796-54969796	Missense_Mutation	SNP	G	C	Gag/Cag	E430Q
12T	SARNP	84324	chr12:56154387-56154387	Missense_Mutation	SNP	C	T	cGa/cAa	R180Q
12T	GOLGA8I	283796	chr15:23261850-23261850	Missense_Mutation	SNP	C	A	gCg/gAg	A321E
12T	FSIP1	161835	chr15:40034005-40034005	Splice_Site	SNP	C	G		
12T	JMJD7-PLA2G4B	8681	chr15:42127323-42127323	Frame_Shift_Del	DEL	T	-	-	-125
12T	JMJD7-PLA2G4B	8681	chr15:42127325-42127326	Frame_Shift_Del	DEL	CT	-	-	-126
12T	TUBGCP4	27229	chr15:43696699-43696706	Frame_Shift_Del	DEL	TACGACTA	-	-	-647
12T	UNC13C	440279	chr15:54307066-54307066	Missense_Mutation	SNP	C	A	Cca/Aca	P656T
12T	ABCA3	21	chr16:2369671-2369671	Frame_Shift_Del	DEL	G	-	-	-262
12T	CENPBD1	92806	chr16:90038189-90038189	Missense_Mutation	SNP	C	G	Gat/Cat	D48H
12T	UBE2O	63893	chr17:74387193-74387193	Missense_Mutation	SNP	C	T	cGg/cAg	R1237Q
12T	MUC16	94025	chr19:9057522-9057522	Missense_Mutation	SNP	G	T	aCa/aAa	T9975K
12T	ZNF559	84527	chr19:9453744-9453745	Frame_Shift_Del	DEL	AA	-	-	-539
12T	TTN	7273	chr2:179399992-179399992	Missense_Mutation	SNP	C	T	Gaa/Aaa	E33784K
12T	FOSL2	2355	chr2:28616101-28616101	De_novo_Start_InFrame	SNP	A	T		
12T	HAAO	23498	chr2:42994744-42994744	Missense_Mutation	SNP	G	T	gCt/gAt	A258D
12T	ANKRD36C	100996862	chr2:96521367-96521367	Missense_Mutation	SNP	C	G	Gtg/Ctg	V1548L
12T	SNPH	9751	chr20:1281256-1281256	Missense_Mutation	SNP	C	T	cCg/cTg	P114L
12T	DSCAM	1826	chr21:41414529-41414529	Missense_Mutation	SNP	C	T	Gaa/Aaa	E1819K
12T	CDC42EP1	11135	chr22:37964409-37964429	In_Frame_Del	DEL	CAGCGCCTGCTGCAAACCCCT	-	ccagcgcctgctgcaaacccctca/cca	PAPAANPS253P
12T	CD96	10225	chr3:111356997-111356997	Missense_Mutation	SNP	A	G	Aat/Gat	N503D
12T	POLQ	10721	chr3:121195490-121195490	Missense_Mutation	SNP	C	T	aGt/aAt	S2101N
12T	PJA2	9867	chr5:108714082-108714082	Missense_Mutation	SNP	C	A	gGa/gTa	G369V
12T	PJA2	9867	chr5:108714083-108714083	Nonsense_Mutation	SNP	C	A	Gga/Tga	G369*
12T	DNAH5	1767	chr5:13719087-13719087	Missense_Mutation	SNP	G	A	Cat/Tat	H4135Y
12T	DNAH5	1767	chr5:13721211-13721211	Missense_Mutation	SNP	G	C	atC/atG	I4059M
12T	PCDHB12	56124	chr5:140589497-140589497	Missense_Mutation	SNP	G	T	Gta/Tta	V340L
12T	CPEB4	80315	chr5:173380109-173380109	Missense_Mutation	SNP	T	A	aTa/aAa	I599K
12T	CDHR2	54825	chr5:175992356-175992356	Translation_Start_Site	SNP	G	A	atG/atA	M1I
12T	CDHR2	54825	chr5:175992357-175992357	Missense_Mutation	SNP	G	T	Gcc/Tcc	A2S
12T	GCNT6	NA	chr6:10634846-10634846	Frame_Shift_Del	DEL	C	-	-	-285
12T	TBP	6908	chr6:170871022-170871023	In_Frame_Ins	INS	-	CAG	-/CAG	-67Q
12T	ZBTB12	221527	chr6:31868632-31868655	In_Frame_Del	DEL	TGGTGGCGCTGATGCTGCTCACAA	-	cttgtgagcagcatcagcgccaccaag/cag	LVSSISATK143Q
12T	SKIV2L	6499	chr6:31935517-31935548	Frame_Shift_Del	DEL	TATTCACAACCCTGGTCTTGTGTGATAAGCCC	-	-	-870
12T	TMEM168	64418	chr7:112407431-112407431	Missense_Mutation	SNP	A	T	Tgg/Agg	W639R
12T	PEX1	5189	chr7:92135583-92135584	Frame_Shift_Ins	INS	-	T	-/A	-626?
12T	SPAG1	6674	chr8:101253182-101253182	Missense_Mutation	SNP	T	A	Tcg/Acg	S905T
12T	TNFRSF11B	4982	chr8:119941069-119941069	Missense_Mutation	SNP	C	G	aGt/aCt	S167T
12T	SLC52A2	79581	chr8:145584258-145584259	Frame_Shift_Ins	INS	-	AA	-/AA	-337?
12T	NKAIN3	286183	chr8:63161649-63161649	Missense_Mutation	SNP	G	A	gGa/gAa	G6E
12T	ADHFE1	137872	chr8:67366364-67366364	Missense_Mutation	SNP	G	A	Ggc/Agc	G320S
12T	TGIF2LX	90316	chrX:89177445-89177445	Missense_Mutation	SNP	A	G	Atc/Gtc	I121V
13T	VAV3	10451	chr1:108226137-108226137	Missense_Mutation	SNP	G	C	Cga/Gga	R584G
13T	LMX1A	4009	chr1:165182890-165182890	Missense_Mutation	SNP	C	A	aaG/aaT	K219N

13T	ILDR2	387597	chr1:166889959-166889959	Missense_Mutation	SNP	C	A	gaG/gaT	E623D
13T	IKBKE	9641	chr1:206651205-206651205	Splice_Site	SNP	G	A		
13T	CEP104	9731	chr1:3755571-3755571	Missense_Mutation	SNP	A	T	gTg/gAg	V283E
13T	LRP8	7804	chr1:53724087-53724087	Missense_Mutation	SNP	G	A	Ctt/Ttt	L705F
13T	C1orf173	127254	chr1:75038239-75038239	Missense_Mutation	SNP	T	A	aAg/aTg	K1052M
13T	AP000936.5	NA	chr11:116988859-116988860	Splice_Site	INS	-	TATA		
13T	NAV2	89797	chr11:19967974-19967974	Missense_Mutation	SNP	G	A	cGg/cAg	R748Q
13T	TNKS1BP1	85456	chr11:57077314-57077314	Nonsense_Mutation	SNP	C	T	tgG/tgA	W957*
13T	CUX2	23316	chr12:111746288-111746288	Missense_Mutation	SNP	C	A	Cag/Aag	Q406K
13T	MED13L	23389	chr12:116413375-116413375	Missense_Mutation	SNP	C	G	Gac/Cac	D1845H
13T	MUC19	283463	chr12:40830536-40830536	Missense_Mutation	SNP	G	A	Ggc/Agc	G716S
13T	KRT1	3848	chr12:53069223-53069243	In_Frame_Del	DEL	ACCTCCGGAGCCGTAGCTGCT	-	agcagctacggctccggaggt/-	SSYGSGG557-
13T	MBD6	114785	chr12:57921973-57921973	Missense_Mutation	SNP	G	T	aGc/aTc	S817I
13T	BRCA2	675	chr13:32911052-32911052	Missense_Mutation	SNP	A	G	Aac/Gac	N854D
13T	RB1	5925	chr13:48955572-48955572	Missense_Mutation	SNP	G	T	tGg/tTg	W563L
13T	VSX2	338917	chr14:74706391-74706391	Missense_Mutation	SNP	G	A	Gag/Aag	E43K
13T	TMEM63C	57156	chr14:77715209-77715209	Missense_Mutation	SNP	C	G	Cct/Gct	P622A
13T	UNC45A	55898	chr15:91491122-91491122	Splice_Site	SNP	T	G		
13T	SCNN1G	6340	chr16:23208725-23208725	Missense_Mutation	SNP	G	A	Gtc/Atc	V352I
13T	VPS35	55737	chr16:46694517-46694517	Missense_Mutation	SNP	T	C	gAc/gGc	D753G
13T	FTSJD1	55783	chr16:71319676-71319677	Frame_Shift_Ins	INS	-	GG	-/CC	-49?
13T	SDR42E1	93517	chr16:82033098-82033098	Missense_Mutation	SNP	C	T	cGg/cAg	R267Q
13T	KIAA0100	9703	chr17:26971087-26971087	Nonsense_Mutation	SNP	G	A	Cag/Tag	Q63*
13T	TP53	7157	chr17:7579334-7579335	Frame_Shift_Ins	INS	-	T	-/A	-118?
13T	REXO1	57455	chr19:1828298-1828298	Missense_Mutation	SNP	C	A	Ggc/Tgc	G164C
13T	SARS2	54938	chr19:39412083-39412083	Missense_Mutation	SNP	C	T	Gtc/Atc	V182I
13T	NMRK2	27231	chr19:3942194-3942194	Missense_Mutation	SNP	G	A	Gcc/Acc	A211T
13T	ZNF525	NA	chr19:53884865-53884865	Missense_Mutation	SNP	C	T	Cat/Tat	H345Y
13T	SLC9A2	6549	chr2:103318884-103318889	In_Frame_Del	DEL	ATAAGG	-	ataagg/-	IR590-
13T	SH3RF3	344558	chr2:110053581-110053581	Missense_Mutation	SNP	G	T	Gcc/Tcc	A603S
13T	TTN	7273	chr2:179427755-179427755	Nonsense_Mutation	SNP	G	A	Cga/Tga	R27702*
13T	NDRG3	57446	chr20:35335409-35335411	Frame_Shift_Del	DEL	TTC	-	-	-20
13T	NCOA3	8202	chr20:46279815-46279823	In_Frame_Del	DEL	GCAGCAGCA	-	atgcagcagcag/atg	MQQQ1247M
13T	DSCAM	1826	chr21:41550850-41550850	Splice_Site	SNP	G	A		
13T	SULT4A1	25830	chr22:44229566-44229566	Missense_Mutation	SNP	C	T	cGc/cAc	R186H
13T	HCLS1	3059	chr3:121350829-121350829	Missense_Mutation	SNP	T	A	gAg/gTg	E442V
13T	CPNE4	131034	chr3:131415460-131415460	Missense_Mutation	SNP	C	G	Gtg/Ctg	V163L
13T	SCN10A	6336	chr3:38793894-38793894	Missense_Mutation	SNP	C	T	gGa/gAa	G524E
13T	SPCS1	28972	chr3:52741747-52741749	In_Frame_Del	DEL	GTG	-	aagtgg/aag	KW143K
13T	ANK2	287	chr4:114276553-114276553	Missense_Mutation	SNP	A	T	gAa/gTa	E2260V
13T	GPR125	166647	chr4:22414845-22414845	Missense_Mutation	SNP	G	A	aCg/aTg	T731M
13T	RFC1	5981	chr4:39329172-39329172	Missense_Mutation	SNP	T	C	aAg/aGg	K179R
13T	KIF3A	11127	chr5:132034881-132034881	Missense_Mutation	SNP	C	T	aGg/aAg	R705K
13T	LARS	51520	chr5:145522585-145522585	Missense_Mutation	SNP	T	A	aAg/aTg	K647M
13T	ITK	3702	chr5:156670752-156670752	Missense_Mutation	SNP	C	T	Cgg/Tgg	R394W
13T	CDHR2	54825	chr5:176016159-176016159	Missense_Mutation	SNP	C	T	gCc/gTc	A995V
13T	LAMA4	3910	chr6:112451163-112451163	Missense_Mutation	SNP	C	T	Gaa/Aaa	E1350K
13T	TAGAP	117289	chr6:159457809-159457809	Missense_Mutation	SNP	C	T	Gag/Aag	E416K
13T	RXRB	6257	chr6:33165677-33165677	Missense_Mutation	SNP	A	T	Ttc/Atc	F228I
13T	SYNGAP1	8831	chr6:33405694-33405694	Missense_Mutation	SNP	G	T	Gac/Tac	D338Y
13T	RB1CC1	9821	chr8:53596248-53596248	Missense_Mutation	SNP	T	G	gAa/gCa	E77A
13T	SPTAN1	6709	chr9:131345428-131345428	Nonsense_Mutation	SNP	C	T	Cga/Tga	R627*
13T	PTCH1	5727	chr9:98209530-98209530	Missense_Mutation	SNP	C	A	agG/agT	R1336S
14T	FBXO44	93611	chr1:11718599-11718599	Missense_Mutation	SNP	C	G	Caa/Gaa	Q125E
14T	NBPF10	100132406	chr1:145323666-145323666	Missense_Mutation	SNP	A	G	gAc/gGc	D1168G
14T	ZNF687	57592	chr1:151259941-151259941	Missense_Mutation	SNP	G	A	Gat/Aat	D392N
14T	SLC27A3	11000	chr1:153750707-153750707	Missense_Mutation	SNP	G	A	cGt/cAt	R539H
14T	URB2	9816	chr1:229771660-229771660	Missense_Mutation	SNP	G	C	Gcg/Ccg	A434P
14T	RSPO1	284654	chr1:38077349-38077350	Splice_Site	INS	-	A		
14T	CDCA8	55143	chr1:38167456-38167456	Missense_Mutation	SNP	A	T	Act/Tct	T152S
14T	EED	8726	chr11:85977259-85977259	Splice_Site	SNP	G	A		
14T	PIK3C2G	5288	chr12:18544101-18544101	Missense_Mutation	SNP	G	A	Gaa/Aaa	E681K
14T	CAPRIN2	65981	chr12:30894022-30894022	Nonsense_Mutation	SNP	C	A	Gaa/Taa	E168*
14T	ZAR1L	646799	chr13:32885716-32885716	Missense_Mutation	SNP	G	A	tCc/tTc	S116F
14T	ABCC4	10257	chr13:95847154-95847154	Missense_Mutation	SNP	C	A	cGt/cTt	R400L
14T	ASB2	51676	chr14:94405822-94405822	Missense_Mutation	SNP	A	C	Ttc/Gtc	F417V
14T	OTUB2	78990	chr14:94511025-94511025	Nonsense_Mutation	SNP	C	T	Cag/Tag	Q133*
14T	FAM227B	196951	chr15:49627633-49627633	Missense_Mutation	SNP	G	T	aaC/aaA	N444K
14T	USP8	9101	chr15:50785016-50785016	Missense_Mutation	SNP	A	G	Act/Gct	T785A
14T	AGBL1	123624	chr15:86807802-86807802	Missense_Mutation	SNP	C	T	gCc/gTc	A421V
14T	MYH11	4629	chr16:15892547-15892547	Splice_Site	SNP	G	A		
14T	HS3ST4	9951	chr16:26147475-26147475	Missense_Mutation	SNP	A	T	cAc/cTc	H426L
14T	APOBR	55911	chr16:28508928-28508928	Missense_Mutation	SNP	G	T	Gat/Tat	D856Y
14T	KRTAP4-3	85290	chr17:39324305-39324319	In_Frame_Del	DEL	GCAGCAGGTGGTCCT	-	aggaccacctgctgc/-	RTTCC36-
14T	PLCD3	113026	chr17:43190893-43190893	Missense_Mutation	SNP	C	T	Gtc/Atc	V636I
14T	ZNF91	7644	chr19:23578250-23578250	De_novo_Start_InFrame	SNP	G	C		

14T	KIR2DL3	3804	chr19:55255377-55255377	Missense_Mutation	SNP	C	T	Cgt/Tgt	R169C
14T	AC007228.1	147670	chr19:57166477-57166477	Missense_Mutation	SNP	G	A	Gtg/Atg	V85M
14T	RALB	5899	chr2:121043586-121043586	Missense_Mutation	SNP	G	A	cGg/cAg	R106Q
14T	LCT	3938	chr2:136587221-136587221	Missense_Mutation	SNP	T	C	gAt/gGt	D249G
14T	UBR3	130507	chr2:170684520-170684520	Missense_Mutation	SNP	G	T	gGc/gTc	G168V
14T	JAG1	182	chr20:10639319-10639319	Missense_Mutation	SNP	C	G	aGc/aCc	S164T
14T	RSPH1	89765	chr21:43913174-43913174	Missense_Mutation	SNP	G	A	Cgg/Tgg	R24W
14T	CLTCL1	8218	chr22:19230425-19230425	Missense_Mutation	SNP	G	T	tCt/tAt	S185Y
14T	ABI3BP	25890	chr3:100712233-100712233	Missense_Mutation	SNP	C	T	tGc/tAc	C6Y
14T	FAM157A	728262	chr3:197880131-197880136	In_Frame_Del	DEL	GCAGCA	-	tggcagcag/tgg	WQQ70W
14T	LRRN1	57633	chr3:3886947-3886947	Missense_Mutation	SNP	G	T	Gat/Tat	D208Y
14T	ENAM	10117	chr4:71510053-71510053	Missense_Mutation	SNP	G	A	atG/atA	M970I
14T	MRPL1	65008	chr4:78784004-78784004	Translation_Start_Site	SNP	T	A	aTg/aAg	M1K
14T	FAT2	2196	chr5:150922691-150922691	Missense_Mutation	SNP	C	G	gGa/gCa	G2666A
14T	FLT4	2324	chr5:180055984-180055984	Missense_Mutation	SNP	C	A	aGc/aTc	S334I
14T	ADGB	79747	chr6:147073847-147073847	Missense_Mutation	SNP	C	A	Cag/Aag	Q1183K
14T	DHX16	8449	chr6:30633486-30633486	Missense_Mutation	SNP	G	A	Cgc/Tgc	R231C
14T	MOGAT3	346606	chr7:100839381-100839381	Missense_Mutation	SNP	A	C	Tgg/Ggg	W320G
14T	CUX1	1523	chr7:101842151-101842151	Splice_Site	SNP	T	C		
14T	DNAJC30	84277	chr7:73097188-73097188	Missense_Mutation	SNP	A	G	cTt/cCt	L189P
14T	KIAA0196	9897	chr8:126087247-126087247	Missense_Mutation	SNP	C	A	aGa/aTa	R324I
14T	ZNF618	114991	chr9:116811569-116811569	Missense_Mutation	SNP	G	A	Gag/Aag	E663K
14T	NXF3	56000	chrX:102334315-102334315	Missense_Mutation	SNP	G	A	tCc/tTc	S436F
15T	CCDC18	343099	chr1:93698065-93698069	Frame_Shift_Del	DEL	CTCTT	-	-	-791
15T	TRIM29	23650	chr11:119999163-119999163	Missense_Mutation	SNP	A	T	aTc/aAc	I282N
15T	EED	8726	chr11:85979502-85979503	Frame_Shift_Del	DEL	TT	-	-	-289
15T	CCNA1	8900	chr13:37013005-37013005	Splice_Site	SNP	G	A		
15T	OR4L1	122742	chr14:20529003-20529003	Missense_Mutation	SNP	G	C	aGc/aCc	S267T
15T	GOLGA6L2	283685	chr15:23685006-23685006	Missense_Mutation	SNP	A	T	gaT/gaA	D872E
15T	TNK1	8711	chr17:7287082-7287082	Frame_Shift_Del	DEL	G	-	-	-161
15T	CDC37	11140	chr19:10514115-10514115	Missense_Mutation	SNP	T	G	gAt/gCt	D14A
15T	AP2A1	160	chr19:50296320-50296320	Missense_Mutation	SNP	G	C	Gtc/Ctc	V226L
15T	ZNF606	80095	chr19:58490778-58490778	Nonsense_Mutation	SNP	C	A	Gga/Tga	G424*
15T	MORC1	27136	chr3:108677887-108677887	Missense_Mutation	SNP	G	T	aaC/aaA	N960K
15T	RAB7A	7879	chr3:128525287-128525287	Missense_Mutation	SNP	G	A	Gtt/Att	V85I
15T	XRN1	54464	chr3:142066097-142066097	Missense_Mutation	SNP	T	C	Aaa/Gaa	K1286E
15T	PIK3CA	5290	chr3:178947827-178947827	Missense_Mutation	SNP	G	T	tGt/tTt	C901F
15T	ULK4	54986	chr3:41996136-41996136	Missense_Mutation	SNP	T	C	aAa/aGa	K39R
15T	FAM184B	27146	chr4:17694987-17694987	Missense_Mutation	SNP	T	A	Ata/Tta	I476L
15T	GPRIN1	114787	chr5:176026123-176026123	Missense_Mutation	SNP	A	G	tTg/tCg	L238S
15T	FGF20	26281	chr8:16853160-16853160	Splice_Site	SNP	G	A		
15T	GPR112	139378	chrX:135430037-135430037	Missense_Mutation	SNP	C	T	cCc/cTc	P1391L
15T	TBX22	50945	chrX:79286075-79286075	Missense_Mutation	SNP	G	A	tGc/tAc	C343Y
16T	MTOR	2475	chr1:11269448-11269448	Missense_Mutation	SNP	T	C	cAa/cGa	Q1241R
16T	CD101	9398	chr1:117564257-117564257	Missense_Mutation	SNP	G	A	Gat/Aat	D694N
16T	FCRL5	83416	chr1:157512826-157512826	Missense_Mutation	SNP	G	A	Cgc/Tgc	R316C
16T	F5	2153	chr1:169512203-169512203	Missense_Mutation	SNP	T	C	Atg/Gtg	M714V
16T	ARPC5	10092	chr1:183599769-183599769	Missense_Mutation	SNP	G	A	Cgg/Tgg	R77W
16T	SLC26A9	115019	chr1:205902165-205902165	Missense_Mutation	SNP	A	G	gTg/gCg	V58A
16T	KCNH1	3756	chr1:211093003-211093003	Missense_Mutation	SNP	C	T	Gtg/Atg	V481M
16T	DISP1	84976	chr1:223116425-223116425	Missense_Mutation	SNP	A	G	tAc/tGc	Y87C
16T	SZT2	23334	chr1:43908604-43908604	Missense_Mutation	SNP	C	A	Cct/Act	P2699T
16T	PTCH2	8643	chr1:45288829-45288829	Missense_Mutation	SNP	G	A	gCg/gTg	A1090V
16T	SLC45A1	50651	chr1:8395635-8395635	Missense_Mutation	SNP	G	A	Gtc/Atc	V562I
16T	RBM20	282996	chr10:112572693-112572693	Missense_Mutation	SNP	G	A	atG/atA	M846I
16T	STOX1	219736	chr10:70644749-70644749	Missense_Mutation	SNP	G	A	atG/atA	M399I
16T	VDAC2	7417	chr10:76979060-76979060	Splice_Site	SNP	A	G		
16T	DYNC2H1	79659	chr11:103080620-103080620	Missense_Mutation	SNP	T	C	Ttc/Ctc	F2824L
16T	BTG4	54766	chr11:111369395-111369395	Missense_Mutation	SNP	G	A	aCg/aTg	T36M
16T	SLC6A5	9152	chr11:20652304-20652304	Missense_Mutation	SNP	G	A	Gtt/Att	V523I
16T	IMMP1L	196294	chr11:31455068-31455068	Missense_Mutation	SNP	G	A	aCa/aTa	T124I
16T	PDE2A	5138	chr11:72299859-72299859	Missense_Mutation	SNP	C	T	Gcc/Acc	A347T
16T	EED	8726	chr11:85977144-85977144	Frame_Shift_Del	DEL	A	-	-	-249
16T	CACNA1C	775	chr12:2702395-2702395	Missense_Mutation	SNP	G	T	gaG/gaT	E849D
16T	C12orf4	57102	chr12:4643351-4643351	Missense_Mutation	SNP	G	A	gCg/gTg	A99V
16T	RBMS2	5939	chr12:56975263-56975263	Missense_Mutation	SNP	G	A	Gga/Aga	G235R
16T	PTPN6	5777	chr12:7067215-7067215	Missense_Mutation	SNP	G	T	gGg/gTg	G447V
16T	ATP11A	23250	chr13:113459311-113459311	Missense_Mutation	SNP	A	G	cAa/cGa	Q68R
16T	EML1	2009	chr14:100259856-100259856	Missense_Mutation	SNP	T	C	Tcc/Ccc	S15P
16T	OR4N5	390437	chr14:20612258-20612258	Missense_Mutation	SNP	C	T	Cgc/Tgc	R122C
16T	OR4N5	390437	chr14:20612322-20612322	Missense_Mutation	SNP	C	G	gCa/gGa	A143G
16T	USP31	57478	chr16:23096231-23096231	Nonsense_Mutation	SNP	G	A	Caa/Taa	Q594*
16T	IL27	246778	chr16:28515276-28515276	Missense_Mutation	SNP	G	T	Ctg/Atg	L43M
16T	CCDC101	112869	chr16:28601455-28601455	Frame_Shift_Del	DEL	C	-	-	-110
16T	ATP2A1	487	chr16:28889744-28889744	De_novo_Start_InFrame	SNP	C	A		
16T	LINC00273	NA	chr16:33961363-33961363	Missense_Mutation	SNP	C	T	Gcc/Acc	A360T
16T	CPNE7	27132	chr16:89661771-89661771	Splice_Site	SNP	C	A		
16T	MYH13	8735	chr17:10219125-10219125	Missense_Mutation	SNP	T	C	gAg/gGg	E1290G
16T	SCARF1	8578	chr17:1548535-1548535	Splice_Site	SNP	T	C		
16T	NF1	4763	chr17:29562627-29562627	Splice_Site	SNP	A	C		

16T	SRCIN1	80725	chr17:36704789-36704789	Splice_Site	SNP	C	T		
16T	COPZ2	51226	chr17:46110636-46110636	Missense_Mutation	SNP	C	T	Gtc/Atc	V99I
16T	CACNA1G	8913	chr17:48653393-48653393	Frame_Shift_Del	DEL	G	-	-	-544
16T	GPRC5C	55890	chr17:72436622-72436622	Missense_Mutation	SNP	A	C	aAg/aCg	K281T
16T	EVPL	2125	chr17:74003944-74003944	Missense_Mutation	SNP	G	A	gCt/gTt	A1803V
16T	MEP1B	4225	chr18:29787340-29787340	Missense_Mutation	SNP	G	T	Gtc/Ttc	V225F
16T	RIT2	6014	chr18:40613781-40613781	Missense_Mutation	SNP	G	C	aCt/aGt	T52S
16T	CNDP2	55748	chr18:72183461-72183461	Splice_Site	SNP	A	G		
16T	EIF3G	8666	chr19:10226400-10226400	Missense_Mutation	SNP	C	T	cGc/cAc	R267H
16T	RGL3	57139	chr19:11529363-11529363	Missense_Mutation	SNP	C	T	gGc/gAc	G44D
16T	DAZAP1	26528	chr19:1434870-1434870	Nonsense_Mutation	SNP	C	T	Cag/Tag	Q395*
16T	CCDC105	126402	chr19:15132294-15132294	Missense_Mutation	SNP	C	T	tCg/tTg	S335L
16T	DMKN	93099	chr19:36002385-36002385	Missense_Mutation	SNP	A	T	agT/agA	S282R
16T	SIPA1L3	23094	chr19:38591749-38591749	Nonsense_Mutation	SNP	G	T	Gag/Tag	E638*
16T	CATSPERG	57828	chr19:38860676-38860678	In_Frame_Del	DEL	TTC	-	ttc/-	F1029-
16T	PSG3	5671	chr19:43237191-43237191	Missense_Mutation	SNP	A	G	Tcc/Ccc	S152P
16T	GLTSCR1	29998	chr19:48197625-48197625	Missense_Mutation	SNP	C	T	cCt/cTt	P846L
16T	TPRX1	284355	chr19:48305639-48305650	In_Frame_Del	DEL	GGGCCTGGGATC	-	ccgatcccaggccca/cca	PIPGP303P
16T	BCAT2	587	chr19:49299426-49299426	Missense_Mutation	SNP	G	A	cCt/cTt	P426L
16T	ZNF320	162967	chr19:53384422-53384422	Missense_Mutation	SNP	A	T	caT/caA	H319Q
16T	ZNF579	163033	chr19:56090567-56090567	Nonsense_Mutation	SNP	G	A	Cag/Tag	Q147*
16T	KHSRP	8570	chr19:6418768-6418768	Missense_Mutation	SNP	G	A	gCg/gTg	A242V
16T	HNRNPM	4670	chr19:8550966-8550966	Missense_Mutation	SNP	G	A	Gcc/Acc	A552T
16T	RAPGEF4	11069	chr2:173879194-173879194	Missense_Mutation	SNP	A	T	tAc/tTc	Y554F
16T	FSIP2	401024	chr2:186671449-186671449	Missense_Mutation	SNP	A	G	Aca/Gca	T5895A
16T	MAP2	4133	chr2:210558183-210558183	Missense_Mutation	SNP	G	T	gGa/gTa	G430V
16T	AC110619.2	NA	chr2:241390052-241390052	Missense_Mutation	SNP	C	T	Gcc/Acc	A119T
16T	WDR43	23160	chr2:29165206-29165206	Missense_Mutation	SNP	C	A	gCa/gAa	A588E
16T	SPAST	6683	chr2:32289070-32289070	Missense_Mutation	SNP	T	C	cTg/cCg	L57P
16T	ASTL	431705	chr2:96789857-96789857	Missense_Mutation	SNP	G	T	cCa/cAa	P343Q
16T	BMP7	655	chr20:55758870-55758870	Missense_Mutation	SNP	C	T	cGc/cAc	R289H
16T	ISX	91464	chr22:35462860-35462860	De_novo_Start_InFrame	SNP	C	T		
16T	SBF1	6305	chr22:50898519-50898519	Missense_Mutation	SNP	A	G	aTg/aCg	M1118T
16T	FANCD2	2177	chr3:10081508-10081508	Missense_Mutation	SNP	C	T	gCt/gTt	A225V
16T	NLGN1	22871	chr3:173997218-173997218	Missense_Mutation	SNP	A	G	cAc/cGc	H516R
16T	BDH1	622	chr3:197241218-197241218	Missense_Mutation	SNP	G	A	aCc/aTc	T160I
16T	KIAA0226	9711	chr3:197409490-197409490	Splice_Site	SNP	C	A		
16T	UBE2E1	7324	chr3:23930715-23930715	Missense_Mutation	SNP	T	C	cTt/cCt	L150P
16T	CCDC51	79714	chr3:48476470-48476470	Missense_Mutation	SNP	C	A	agG/agT	R23S
16T	ATRIP	84126	chr3:48506258-48506258	Missense_Mutation	SNP	A	G	cAc/cGc	H695R
16T	HYAL3	8372	chr3:50330790-50330790	Missense_Mutation	SNP	G	T	Ctg/Atg	L381M
16T	GLYCTK	132158	chr3:52324575-52324575	Missense_Mutation	SNP	C	T	Cgg/Tgg	R73W
16T	CRYBG3	131544	chr3:97593514-97593514	Missense_Mutation	SNP	G	A	gGg/gAg	G1159E
16T	CRELD1	78987	chr3:9985179-9985179	Missense_Mutation	SNP	G	C	tGt/tCt	C343S
16T	CENPE	1062	chr4:104102538-104102538	Frame_Shift_Del	DEL	T	-	-	-347
16T	TRIML2	205860	chr4:189020211-189020211	Missense_Mutation	SNP	T	C	gAa/gGa	E150G
16T	PPARGC1B	133522	chr5:149212429-149212429	Missense_Mutation	SNP	C	T	Cgg/Tgg	R265W
16T	NDST1	3340	chr5:149924960-149924960	Missense_Mutation	SNP	C	T	gCg/gTg	A686V
16T	DRD1	1812	chr5:174869930-174869930	Missense_Mutation	SNP	A	G	gTg/gCg	V58A
16T	ANKRD31	256006	chr5:74491653-74491653	Missense_Mutation	SNP	T	C	Aga/Gga	R274G
16T	GPR98	84059	chr5:89933605-89933605	Missense_Mutation	SNP	C	A	Ccc/Acc	P694T
16T	LAMA2	3908	chr6:129591892-129591892	Missense_Mutation	SNP	A	T	Aat/Tat	N816Y
16T	SCAF8	22828	chr6:155152176-155152176	Missense_Mutation	SNP	G	C	gGa/gCa	G820A
16T	PPP1R18	170954	chr6:30647150-30647150	Missense_Mutation	SNP	C	T	aGc/aAc	S543N
16T	ATP6V1G2	534	chr6:31513287-31513287	Missense_Mutation	SNP	C	A	caG/caT	Q125H
16T	BRPF3	27154	chr6:36179234-36179236	In_Frame_Del	DEL	CAA	-	ctcaac/ctc	LN793L
16T	ZAN	7455	chr7:100345262-100345262	Nonsense_Mutation	SNP	C	T	Cag/Tag	Q341*
16T	GPR37	2861	chr7:124404723-124404723	Missense_Mutation	SNP	T	C	gAg/gGg	E103G
16T	POT1	25913	chr7:124482942-124482942	Missense_Mutation	SNP	C	T	cGc/cAc	R361H
16T	IMPDH1	3614	chr7:128034378-128034378	Missense_Mutation	SNP	G	A	Cgg/Tgg	R578W
16T	TBXAS1	6916	chr7:139715576-139715576	Missense_Mutation	SNP	C	A	gCa/gAa	A474E
16T	MGAM	8972	chr7:141726933-141726933	Missense_Mutation	SNP	C	T	gCg/gTg	A334V
16T	AC006372.1	NA	chr7:157318655-157318655	Missense_Mutation	SNP	G	A	Gct/Act	A37T
16T	PTPRN2	5799	chr7:157903567-157903567	Missense_Mutation	SNP	C	T	Gtc/Atc	V556I
16T	MYO1G	64005	chr7:45018494-45018494	Nonsense_Mutation	SNP	C	A	Gag/Tag	E23*
16T	HGF	3082	chr7:81358929-81358929	Missense_Mutation	SNP	G	C	ttC/ttG	F344L
16T	PCLO	27445	chr7:82785454-82785454	Missense_Mutation	SNP	G	C	tCt/tGt	S168C
16T	LRP12	29967	chr8:105509315-105509315	Missense_Mutation	SNP	C	T	Gtg/Atg	V489M
16T	PKHD1L1	93035	chr8:110460538-110460538	Missense_Mutation	SNP	G	A	atG/atA	M1981I
16T	SLC30A8	169026	chr8:118147628-118147628	Missense_Mutation	SNP	C	A	aCa/aAa	T21K
16T	PUF60	22827	chr8:144903843-144903843	Missense_Mutation	SNP	G	A	gCc/gTc	A74V
16T	NRBP2	340371	chr8:144919466-144919466	Missense_Mutation	SNP	G	A	tCg/tTg	S361L
16T	SLC39A4	55630	chr8:145639262-145639262	Missense_Mutation	SNP	G	T	Ctg/Atg	L431M
16T	PTK2B	2185	chr8:27294635-27294635	Splice_Site	SNP	A	G		
16T	FBXO25	26260	chr8:400045-400045	Missense_Mutation	SNP	A	G	aAg/aGg	K146R
16T	PTDSS1	9791	chr8:97312034-97312034	Frame_Shift_Del	DEL	G	-	-	-238
16T	RPL35	11224	chr9:127620286-127620286	Missense_Mutation	SNP	G	C	Ctc/Gtc	L95V
16T	B4GALT1	2683	chr9:33120546-33120546	Missense_Mutation	SNP	A	G	tTg/tCg	L236S
16T	NFX1	4799	chr9:33294754-33294755	Frame_Shift_Del	DEL	CA	-	-	-121
16T	DAPK1	1612	chr9:90311928-90311928	Missense_Mutation	SNP	G	A	gGc/gAc	G807D

16T	TREX2	11219	chrX:152710665-152710665	Missense_Mutation	SNP	C	T	aGc/aAc	S118N
16T	TREX2	11219	chrX:152719970-152719973	Splice_Site	DEL	GGGA	-		
16T	PNCK	139728	chrX:152938488-152938488	Missense_Mutation	SNP	T	A	tAc/tTc	Y98F
16T	FOXP3	50943	chrX:49111938-49111938	Missense_Mutation	SNP	C	T	atG/atA	M221I
18T	LCE4A	199834	chr1:152681679-152681679	Missense_Mutation	SNP	C	G	tCc/tGc	S43C
18T	OR2AK2	391191	chr1:248129277-248129277	Missense_Mutation	SNP	T	A	cTc/cAc	L215H
18T	KLHL1	57626	chr13:70535460-70535460	Missense_Mutation	SNP	A	T	cTt/cAt	L266H
18T	CEP152	22995	chr15:49083444-49083444	Missense_Mutation	SNP	T	C	aAt/aGt	N321S
18T	LCTL	197021	chr15:66844145-66844145	Missense_Mutation	SNP	T	A	aAg/aTg	K460M
18T	STRA6	64220	chr15:74476323-74476323	Missense_Mutation	SNP	G	A	Ctt/Ttt	L431F
18T	ERN1	2081	chr17:62125288-62125288	Missense_Mutation	SNP	C	T	cGc/cAc	R820H
18T	OR7C2	26658	chr19:15052676-15052676	Missense_Mutation	SNP	A	G	Atc/Gtc	I126V
18T	FCGBP	8857	chr19:40433964-40433964	Missense_Mutation	SNP	T	C	aAg/aGg	K102R
18T	CBLC	23624	chr19:45293295-45293295	Missense_Mutation	SNP	G	A	Gac/Aac	D318N
18T	PCDP1	200373	chr2:120369269-120369269	Missense_Mutation	SNP	G	A	cGa/cAa	R421Q
18T	FAM117B	150864	chr2:203630405-203630405	Missense_Mutation	SNP	G	A	cGa/cAa	R563Q
18T	SSTR4	6754	chr20:23017231-23017231	Missense_Mutation	SNP	C	A	Ctg/Atg	L371M
19T	FLG	2312	chr1:152281706-152281706	Missense_Mutation	SNP	G	A	Cat/Tat	H1886Y
19T	CHRNB2	1141	chr1:154543865-154543865	Missense_Mutation	SNP	G	A	aGt/aAt	S189N
19T	RGSL1	353299	chr1:182458236-182458236	Missense_Mutation	SNP	T	A	aTg/aAg	M539K
19T	ADORA1	134	chr1:203098228-203098228	Missense_Mutation	SNP	G	C	Gtc/Ctc	V87L
19T	C1orf65	164127	chr1:223567068-223567068	Missense_Mutation	SNP	G	T	aGc/aTc	S84I
19T	RYR2	6262	chr1:237777404-237777404	Missense_Mutation	SNP	G	T	cGg/cTg	R1657L
19T	TRIT1	54802	chr1:40349132-40349132	Missense_Mutation	SNP	G	T	cCc/cAc	P11H
19T	SLC5A9	200010	chr1:48694788-48694788	Missense_Mutation	SNP	G	T	aGg/aTg	R118M
19T	SPSB1	80176	chr1:9416134-9416134	Missense_Mutation	SNP	T	G	Tcg/Gcg	S62A
19T	SAA2	6289	chr11:18267478-18267478	Missense_Mutation	SNP	G	A	gCc/gTc	A70V
19T	TBX5	6910	chr12:114841695-114841695	Missense_Mutation	SNP	G	C	gaC/gaG	D3E
19T	KRT1	3848	chr12:53069223-53069243	In_Frame_Del	DEL	ACCTCCGGAGCCGTAGCTGCT	-	agcagctacggctccggaggt/-	SSYGSGG557-
19T	SMARCC2	6601	chr12:56572631-56572631	Missense_Mutation	SNP	T	A	gAt/gTt	D381V
19T	KCTD12	115207	chr13:77459685-77459685	Nonsense_Mutation	SNP	G	T	tCg/tAg	S200*
19T	RBM23	55147	chr14:23374840-23374840	Missense_Mutation	SNP	G	T	Cat/Aat	H144N
19T	AKAP6	9472	chr14:33291948-33291948	Missense_Mutation	SNP	G	C	caG/caC	Q1643H
19T	GOLGA8F	NA	chr15:28632820-28632820	Missense_Mutation	SNP	T	C	cTg/cCg	L463P
19T	APBA2	321	chr15:29393810-29393810	Missense_Mutation	SNP	G	A	atG/atA	M449I
19T	CASC5	57082	chr15:40913900-40913900	Missense_Mutation	SNP	G	A	Gga/Aga	G506R
19T	TMEM87A	25963	chr15:42525452-42525452	Missense_Mutation	SNP	G	C	Ctt/Gtt	L341V
19T	SH3GL3	6457	chr15:84241340-84241340	Nonsense_Mutation	SNP	G	T	Gaa/Taa	E127*
19T	C19orf55	148137	chr19:36250830-36250830	Missense_Mutation	SNP	G	C	gaG/gaC	E83D
19T	IL18RAP	8807	chr2:103068343-103068343	Missense_Mutation	SNP	C	A	gCc/gAc	A501D
19T	SLC9A4	389015	chr2:103142751-103142751	Missense_Mutation	SNP	C	A	Ccc/Acc	P662T
19T	CCDC141	285025	chr2:179701849-179701849	Missense_Mutation	SNP	G	C	tCt/tGt	S1366C
19T	INPP5D	3635	chr2:233986946-233986946	Missense_Mutation	SNP	G	C	Gac/Cac	D110H
19T	PLB1	151056	chr2:28748168-28748168	Missense_Mutation	SNP	A	C	cAa/cCa	Q93P
19T	LTBP1	4052	chr2:33482545-33482545	Missense_Mutation	SNP	C	T	Cgg/Tgg	R788W
19T	SNRNP200	23020	chr2:96943407-96943407	Missense_Mutation	SNP	C	A	gGg/gTg	G1934V
19T	CNGA3	1261	chr2:99012801-99012801	Missense_Mutation	SNP	C	G	Ctg/Gtg	L394V
19T	BCL2L1	598	chr20:30309541-30309541	Missense_Mutation	SNP	C	G	Gta/Cta	V161L
19T	PEX26	55670	chr22:18566327-18566327	Missense_Mutation	SNP	C	T	Cgg/Tgg	R166W
19T	ITGA9	3680	chr3:37560813-37560813	Missense_Mutation	SNP	G	C	Gat/Cat	D402H
19T	PDLIM3	27295	chr4:186423546-186423546	Missense_Mutation	SNP	A	C	Ttc/Gtc	F333V
19T	ANAPC4	29945	chr4:25379100-25379108	In_Frame_Del	DEL	GCAGCTCCC	-	aagcagctcccg/aag	KQLP17K
19T	SEL1L3	23231	chr4:25823715-25823715	Missense_Mutation	SNP	C	A	gGg/gTg	G398V
19T	FRYL	285527	chr4:48592787-48592787	Missense_Mutation	SNP	C	T	Ggt/Agt	G466S
19T	LRRC66	339977	chr4:52861026-52861026	Missense_Mutation	SNP	G	A	gCa/gTa	A721V
19T	LRRC66	339977	chr4:52861027-52861027	Missense_Mutation	SNP	C	A	Gca/Tca	A721S
19T	DSPP	1834	chr4:88536014-88536031	In_Frame_Del	DEL	AGCAGTGACAGCAGCAAC	-	agcagtgacagcagcaac/-	SSDSSN734-
19T	PCDHGA2	56113	chr5:140719886-140719886	Missense_Mutation	SNP	C	T	Ccc/Tcc	P450S
19T	STK10	6793	chr5:171520444-171520444	Missense_Mutation	SNP	T	C	aAc/aGc	N509S
19T	DAXX	1616	chr6:33289330-33289330	Missense_Mutation	SNP	A	C	tgT/tgG	C74W
19T	ZBTB9	221504	chr6:33424262-33424262	Missense_Mutation	SNP	G	C	gGc/gCc	G462A
19T	RP11-1220K2.2	NA	chr7:141864822-141864830	Frame_Shift_Del	DEL	AGGTAAGAG	-	-	-884
19T	ADCYAP1R1	117	chr7:31104510-31104510	Missense_Mutation	SNP	C	A	Cag/Aag	Q39K
19T	IKZF1	10320	chr7:50444492-50444492	Splice_Site	SNP	G	C		
19T	PCMTD1	115294	chr8:52746113-52746113	Missense_Mutation	SNP	C	T	Gtt/Att	V183I
19T	WWP1	11059	chr8:87474055-87474055	Missense_Mutation	SNP	G	C	tgG/tgC	W883C
19T	SLC46A2	57864	chr9:115652983-115652983	De_novo_Start_InFrame	SNP	G	A		
19T	RBMXL3	139804	chrX:114426781-114426781	Missense_Mutation	SNP	G	C	gGg/gCg	G926A
20T	ATG12	9140	chr5:115177381-115177381	Missense_Mutation	SNP	G	A	Cgg/Tgg	R4W
2T	WDR11	55717	chr10:122633387-122633387	Missense_Mutation	SNP	C	A	aCc/aAc	T503N
2T	CAMK2G	818	chr10:75576829-75576829	Missense_Mutation	SNP	C	A	Ggt/Tgt	G496C
2T	ELMOD1	55531	chr11:107535762-107535762	Missense_Mutation	SNP	C	T	Cat/Tat	H282Y
2T	UBQLN3	50613	chr11:5529414-5529414	Missense_Mutation	SNP	G	C	Ccc/Gcc	P459A
2T	NIPA1	123606	chr15:23060881-23060881	Missense_Mutation	SNP	A	G	tTc/tCc	F84S
2T	VPS18	57617	chr15:41192635-41192635	Missense_Mutation	SNP	G	A	cGg/cAg	R540Q

2T	C15orf43	145645	chr15:45258410-45258410	Missense_Mutation	SNP	G	T	Gca/Tca	A135S
2T	RAI1	10743	chr17:17698358-17698358	Missense_Mutation	SNP	C	G	cCc/cGc	P699R
2T	ABCA10	10349	chr17:67215766-67215766	Frame_Shift_Del	DEL	A	-	-	-150
2T	KCTD11	147040	chr17:7256362-7256362	Missense_Mutation	SNP	G	T	cGg/cTg	R34L
2T	TPRX1	284355	chr19:48305639-48305650	In_Frame_Del	DEL	GGGCCTGGGATC	-	ccgatcccaggccca/cca	PIPGP303P
2T	KDM4B	23030	chr19:5077407-5077407	Missense_Mutation	SNP	G	T	Gac/Tac	D236Y
2T	C2orf40	84417	chr2:106682293-106682293	Missense_Mutation	SNP	G	T	Ggc/Tgc	G25C
2T	G6PC2	57818	chr2:169764223-169764223	Missense_Mutation	SNP	G	T	tgG/tgT	W234C
2T	BIRC6	57448	chr2:32617143-32617144	Frame_Shift_Ins	INS	-	TT	-/TT	-293?
2T	YWHAQ	10971	chr2:9770554-9770563	Frame_Shift_Del	DEL	CCTTCTGGAT	-	-	-7
2T	YWHAQ	10971	chr2:9770608-9770608	De_novo_Start_InFrame	SNP	G	C		
2T	RGS19	10287	chr20:62705343-62705343	Missense_Mutation	SNP	A	T	Tcc/Acc	S173T
2T	CDC42EP1	11135	chr22:37964409-37964429	In_Frame_Del	DEL	CAGCGCCTGCTGCAAACCCCT	-	ccagcgcctgctgcaaacccctca/cca	PAPAANPS253P
2T	MYH15	22989	chr3:108183545-108183545	Missense_Mutation	SNP	C	G	aaG/aaC	K577N
2T	OR2V2	285659	chr5:180582378-180582378	Missense_Mutation	SNP	A	G	Act/Gct	T146A
2T	ZKSCAN4	387032	chr6:28213204-28213204	Missense_Mutation	SNP	C	T	cGg/cAg	R443Q
2T	EPHA1	2041	chr7:143095090-143095090	Missense_Mutation	SNP	A	T	aTc/aAc	I513N
2T	SYBU	55638	chr8:110587382-110587382	Missense_Mutation	SNP	C	G	tGc/tCc	C587S
2T	C8orf42	157695	chr8:442614-442614	Missense_Mutation	SNP	C	T	Gct/Act	A115T
2T	KIAA2026	158358	chr9:5922247-5922247	Missense_Mutation	SNP	C	T	aGt/aAt	S1250N
4T	KCND3	3752	chr1:112525311-112525311	Missense_Mutation	SNP	C	T	cGg/cAg	R13Q
4T	KCNN3	3782	chr1:154842242-154842244	In_Frame_Del	DEL	GAA	-	cttcag/cag	LQ66Q
4T	PTGS2	5743	chr1:186646890-186646890	Missense_Mutation	SNP	G	A	cCc/cTc	P177L
4T	PTGS2	5743	chr1:186646891-186646891	Missense_Mutation	SNP	G	T	Ccc/Acc	P177T
4T	CC2D1B	200014	chr1:52825017-52825017	Missense_Mutation	SNP	T	C	cAg/cGg	Q344R
4T	TRIM8	81603	chr10:104417052-104417052	Missense_Mutation	SNP	C	T	Cac/Tac	H533Y
4T	DOCK1	1793	chr10:129201389-129201389	Missense_Mutation	SNP	A	G	gAg/gGg	E1312G
4T	TYSND1	219743	chr10:71905927-71905927	Missense_Mutation	SNP	C	G	aGc/aCc	S139T
4T	DYNC2H1	79659	chr11:103048349-103048349	Missense_Mutation	SNP	C	T	cCa/cTa	P1980L
4T	NLRX1	79671	chr11:119044391-119044391	Missense_Mutation	SNP	G	A	Gcc/Acc	A145T
4T	CCDC88B	283234	chr11:64120593-64120593	Missense_Mutation	SNP	C	T	Cgg/Tgg	R1190W
4T	TIGD3	220359	chr11:65124586-65124586	Missense_Mutation	SNP	G	A	cGg/cAg	R436Q
4T	LTBP3	4054	chr11:65311010-65311010	Missense_Mutation	SNP	C	G	gaG/gaC	E788D
4T	KRTAP5-8	57830	chr11:71249530-71249532	In_Frame_Del	DEL	TTC	-	tgttcc/tgc	CS143C
4T	USP30	84749	chr12:109495799-109495799	Missense_Mutation	SNP	G	A	Gcc/Acc	A88T
4T	B3GNT9	84752	chr16:67183815-67183815	Missense_Mutation	SNP	T	A	Atc/Ttc	I192F
4T	PLCG2	5336	chr16:81934315-81934315	Missense_Mutation	SNP	C	T	aCg/aTg	T431M
4T	KRTAP9-4	85280	chr17:39406416-39406416	Nonsense_Mutation	SNP	C	A	tgC/tgA	C148*
4T	DHX8	1659	chr17:41566815-41566815	Splice_Site	SNP	A	G		
4T	NEURL4	84461	chr17:7224979-7224979	Missense_Mutation	SNP	T	C	gAg/gGg	E1000G
4T	NEURL4	84461	chr17:7224980-7224980	Nonsense_Mutation	SNP	C	A	Gag/Tag	E1000*
4T	EMR1	2015	chr19:6897182-6897182	Missense_Mutation	SNP	C	G	agC/agG	S87R
4T	CFD	1675	chr19:861914-861914	Missense_Mutation	SNP	G	C	gaG/gaC	E198D
4T	MUC16	94025	chr19:9000455-9000455	Missense_Mutation	SNP	A	G	gTc/gCc	V13510A
4T	ALS2CR8	79800	chr2:203820452-203820452	Missense_Mutation	SNP	A	T	Ata/Tta	I205L
4T	KIF1A	547	chr2:241696843-241696843	Missense_Mutation	SNP	C	A	gaG/gaT	E917D
4T	SLC3A1	6519	chr2:44508578-44508578	Missense_Mutation	SNP	T	G	atT/atG	I221M
4T	EFCAB8	388795	chr20:31455508-31455508	Missense_Mutation	SNP	G	A	Gcc/Acc	A55T
4T	TSHZ2	128553	chr20:51872635-51872635	Missense_Mutation	SNP	C	A	Caa/Aaa	Q880K
4T	DIDO1	11083	chr20:61512569-61512569	Missense_Mutation	SNP	C	G	aGg/aCg	R1580T
4T	NEFH	4744	chr22:29885599-29885604	In_Frame_Del	DEL	AGGAAG	-	aaggaagag/aag	KEE657K
4T	CELSR1	9620	chr22:46760610-46760610	Missense_Mutation	SNP	G	A	Ccg/Tcg	P2860S
4T	PPP6R2	9701	chr22:50874867-50874867	Missense_Mutation	SNP	A	G	Aac/Gac	N530D
4T	IQSEC1	9922	chr3:12942511-12942511	Missense_Mutation	SNP	T	C	cAa/cGa	Q1106R
4T	COL6A6	131873	chr3:130380542-130380542	Missense_Mutation	SNP	G	A	atG/atA	M1964I
4T	DAG1	1605	chr3:49568395-49568395	Missense_Mutation	SNP	G	T	Gtg/Ttg	V151L
4T	RBM5	10181	chr3:50155888-50155889	Frame_Shift_Del	DEL	GA	-	-	-816
4T	CACNA2D2	9254	chr3:50402317-50402317	Splice_Site	SNP	A	T		
4T	UGT2A1	10941	chr4:70505048-70505048	Missense_Mutation	SNP	A	C	aTt/aGt	I305S
4T	USO1	8615	chr4:76727667-76727667	Missense_Mutation	SNP	A	G	gAa/gGa	E782G
4T	KIAA0947	23379	chr5:5463498-5463498	Missense_Mutation	SNP	G	A	Gat/Aat	D1351N
4T	FAM184A	79632	chr6:119345509-119345509	Missense_Mutation	SNP	G	A	gCc/gTc	A210V
4T	ATXN1	6310	chr6:16327907-16327909	In_Frame_Del	DEL	TGA	-	catcag/cag	HQ211Q
4T	PPIL1	51645	chr6:36842496-36842496	Missense_Mutation	SNP	G	T	aCc/aAc	T18N
4T	SPAM1	6677	chr7:123593880-123593880	Missense_Mutation	SNP	C	A	Caa/Aaa	Q86K
4T	PCLO	27445	chr7:82579970-82579970	Missense_Mutation	SNP	T	A	Att/Ttt	I3312F
4T	ODF1	4956	chr8:103573029-103573037	In_Frame_Del	DEL	TGCAACCCG	-	tgcaacccg/-	CNP224-
4T	DLGAP2	9228	chr8:1626529-1626529	Missense_Mutation	SNP	C	G	aCc/aGc	T733S
4T	KIF13B	23303	chr8:29043894-29043894	Frame_Shift_Del	DEL	C	-	-	-138
4T	PRKDC	5591	chr8:48694949-48694949	Missense_Mutation	SNP	T	C	Atg/Gtg	M3795V
4T	MFHAS1	9258	chr8:8750162-8750162	Missense_Mutation	SNP	T	C	gAg/gGg	E136G
4T	NHS	4810	chrX:17744069-17744069	Missense_Mutation	SNP	G	A	Gtc/Atc	V594I
4T	XK	7504	chrX:37587361-37587361	Missense_Mutation	SNP	G	C	gaG/gaC	E327D
4T	PFKFB1	5207	chrX:54964076-54964076	Missense_Mutation	SNP	G	T	Cag/Aag	Q394K
7T	CACNA1E	777	chr1:181721295-181721295	Missense_Mutation	SNP	G	C	Gac/Cac	D1250H

7T	DNAH14	127602	chr1:225519194-225519196	In_Frame_Del	DEL	AAC	-	aaacaa/aaa	KQ3167K
7T	LRRC53	NA	chr1:74946467-74946467	Nonsense_Mutation	SNP	G	A	Caa/Taa	Q92*
7T	SUFU	51684	chr10:104268923-104268923	Splice_Site	SNP	C	A		
7T	CDH23	64072	chr10:73544679-73544679	Missense_Mutation	SNP	A	G	aAc/aGc	N1848S
7T	ANO3	63982	chr11:26669256-26669256	Missense_Mutation	SNP	G	C	gGt/gCt	G810A
7T	KLHL1	57626	chr13:70535460-70535460	Missense_Mutation	SNP	A	T	cTt/cAt	L266H
7T	CEP152	22995	chr15:49083444-49083444	Missense_Mutation	SNP	T	C	aAt/aGt	N321S
7T	PLEKHO2	80301	chr15:65157813-65157813	Missense_Mutation	SNP	G	A	cGg/cAg	R400Q
7T	STRA6	64220	chr15:74476323-74476323	Missense_Mutation	SNP	G	A	Ctt/Ttt	L431F
7T	LINC00273	NA	chr16:33961602-33961602	Missense_Mutation	SNP	G	A	gCg/gTg	A280V
7T	NF1	4763	chr17:29490210-29490210	Nonsense_Mutation	SNP	A	T	Aag/Tag	K99*
7T	GP1BA	2811	chr17:4836942-4836942	Missense_Mutation	SNP	C	A	tCc/tAc	S348Y
7T	ERN1	2081	chr17:62125288-62125288	Missense_Mutation	SNP	C	T	cGc/cAc	R820H
7T	RAC3	5881	chr17:79990294-79990294	Missense_Mutation	SNP	T	C	Tac/Cac	Y23H
7T	GALR1	2587	chr18:74962598-74962598	Nonsense_Mutation	SNP	G	T	Gag/Tag	E32*
7T	OR7C2	26658	chr19:15052676-15052676	Missense_Mutation	SNP	A	G	Atc/Gtc	I126V
7T	FCGBP	8857	chr19:40433964-40433964	Missense_Mutation	SNP	T	C	aAg/aGg	K102R
7T	CBLC	23624	chr19:45293295-45293295	Missense_Mutation	SNP	G	A	Gac/Aac	D318N
7T	CCDC155	147872	chr19:49920665-49920666	In_Frame_Ins	INS	-	CTGCTG	-/CTGCTG	-530LL
7T	KIR2DL4	3805	chr19:55325444-55325444	Missense_Mutation	SNP	C	G	Ccc/Gcc	P358A
7T	PCDP1	200373	chr2:120369269-120369269	Missense_Mutation	SNP	G	A	cGa/cAa	R421Q
7T	LRP1B	53353	chr2:141232707-141232707	Missense_Mutation	SNP	C	A	Gtc/Ttc	V3209F
7T	FAM117B	150864	chr2:203630405-203630405	Missense_Mutation	SNP	G	A	cGa/cAa	R563Q
7T	PTH2R	5746	chr2:209309528-209309528	Nonsense_Mutation	SNP	G	T	Gaa/Taa	E257*
7T	GIGYF2	26058	chr2:233712210-233712230	In_Frame_Del	DEL	CAGCAGCAGCAGCTGCCACAG	-	cagcagcagcagctgccacag/-	QQQQLPQ1227-
7T	SSTR4	6754	chr20:23017231-23017231	Missense_Mutation	SNP	C	A	Ctg/Atg	L371M
7T	FAM182B	548321	chr20:25755509-25755510	Frame_Shift_Ins	INS	-	CGGC	-/GCCG	-149A?
7T	ARHGEF38	54848	chr4:106588717-106588717	Missense_Mutation	SNP	G	C	Gtg/Ctg	V669L
7T	NDST4	64579	chr4:115997325-115997325	Missense_Mutation	SNP	A	T	Ttc/Atc	F290I
7T	C4orf50	389197	chr4:5990708-5990709	Frame_Shift_Del	DEL	TC	-	-	-264
7T	SLCO6A1	133482	chr5:101813478-101813478	Missense_Mutation	SNP	C	G	gGg/gCg	G235A
7T	HSD17B4	3295	chr5:118865659-118865659	Missense_Mutation	SNP	C	T	gCt/gTt	A638V
7T	MCCC2	64087	chr5:70952658-70952658	Missense_Mutation	SNP	A	C	Aag/Cag	K555Q
7T	VTA1	51534	chr6:142491539-142491539	Missense_Mutation	SNP	T	G	tTt/tGt	F131C
7T	NOX3	50508	chr6:155743975-155743990	Frame_Shift_Del	DEL	CCCGTCCACTGCCAGC	-	-	-382
7T	PGC	5225	chr6:41708310-41708310	Missense_Mutation	SNP	C	A	gGt/gTt	G229V
7T	AGAP3	116988	chr7:150840917-150840917	Missense_Mutation	SNP	A	G	Atc/Gtc	I875V
7T	AGMO	392636	chr7:15425188-15425188	Splice_Site	SNP	C	A		
7T	COL28A1	340267	chr7:7459558-7459558	Frame_Shift_Del	DEL	T	-	-	-675
7T	COL1A2	1278	chr7:94057062-94057068	Frame_Shift_Del	DEL	AAGGACT	-	-	-1131
7T	BAALC	79870	chr8:104225228-104225228	Missense_Mutation	SNP	C	T	aCg/aTg	T116M
7T	MTMR7	9108	chr8:17157708-17157708	Missense_Mutation	SNP	T	A	cAg/cTg	Q549L
7T	UBXN2B	137886	chr8:59329469-59329469	Missense_Mutation	SNP	C	G	Cct/Gct	P49A
7T	BHLHE22	27319	chr8:65494017-65494018	In_Frame_Ins	INS	-	GCA	ggc/gGCAgc	G224GS
7T	C9orf174	100499483	chr9:100090424-100090424	Missense_Mutation	SNP	A	G	gAa/gGa	E639G
7T	CACNA1B	774	chr9:140772670-140772672	Frame_Shift_Del	DEL	ATA	-	-	-95
7T	GLIS3	169792	chr9:4286157-4286157	Missense_Mutation	SNP	A	C	aTg/aGg	M90R
7T	CNKSR2	22866	chrX:21627515-21627515	Nonsense_Mutation	SNP	C	A	taC/taA	Y824*
8T	FCRL3	115352	chr1:157650551-157650551	Missense_Mutation	SNP	C	G	gGa/gCa	G656A
8T	APOBEC4	403314	chr1:183616968-183616968	Missense_Mutation	SNP	C	G	Gta/Cta	V317L
8T	TAS1R2	80834	chr1:19166845-19166845	Missense_Mutation	SNP	G	A	Cac/Tac	H590Y
8T	EPS15	2060	chr1:51871581-51871581	Missense_Mutation	SNP	G	C	tCt/tGt	S558C
8T	MKI67	4288	chr10:129910700-129910700	Nonsense_Mutation	SNP	G	A	Caa/Taa	Q556*
8T	CCDC81	60494	chr11:86111834-86111834	Frame_Shift_Del	DEL	C	-	-	-291
8T	RECQL	5965	chr12:21636469-21636469	Missense_Mutation	SNP	T	G	Aac/Cac	N181H
8T	PCNX	22990	chr14:71476358-71476358	Missense_Mutation	SNP	C	G	ttC/ttG	F879L
8T	RSL24D1	51187	chr15:55475536-55475536	Missense_Mutation	SNP	T	G	cAt/cCt	H132P
8T	NF1	4763	chr17:29496946-29496946	Missense_Mutation	SNP	G	T	Gat/Tat	D173Y
8T	CD300LF	146722	chr17:72700807-72700807	Missense_Mutation	SNP	G	C	atC/atG	I64M
8T	TP53	7157	chr17:7577121-7577121	Missense_Mutation	SNP	G	A	Cgt/Tgt	R273C
8T	DNM2	1785	chr19:10909174-10909174	Missense_Mutation	SNP	C	G	Ccc/Gcc	P450A
8T	CYP4F12	66002	chr19:15807274-15807274	Missense_Mutation	SNP	G	T	aGc/aTc	S450I
8T	RHPN2	85415	chr19:33490564-33490564	Missense_Mutation	SNP	G	T	Ctc/Atc	L385I
8T	KCNJ14	3770	chr19:48968002-48968002	Missense_Mutation	SNP	A	C	Aca/Cca	T427P
8T	C3	718	chr19:6713444-6713444	Missense_Mutation	SNP	G	T	Ctg/Atg	L284M
8T	KDM3A	55818	chr2:86693730-86693730	Nonsense_Mutation	SNP	A	T	Aag/Tag	K415*
8T	LPIN3	64900	chr20:39986529-39986529	Missense_Mutation	SNP	T	C	Tac/Cac	Y683H
8T	DZIP3	9666	chr3:108353817-108353817	Missense_Mutation	SNP	C	A	Cag/Aag	Q306K
8T	CAND2	23066	chr3:12858844-12858844	Missense_Mutation	SNP	G	A	Gcc/Acc	A805T
8T	C3orf58	205428	chr3:143691671-143691671	Missense_Mutation	SNP	A	G	gAc/gGc	D166G
8T	CLGN	1047	chr4:141320022-141320022	Frame_Shift_Del	DEL	G	-	-	-289
8T	FREM3	166752	chr4:144498982-144498982	Missense_Mutation	SNP	T	C	Agc/Ggc	S2068G
8T	TMEM156	80008	chr4:38990491-38990491	Missense_Mutation	SNP	C	T	aGa/aAa	R240K
8T	TBP	6908	chr6:170871038-170871040	In_Frame_Del	DEL	CAA	-	caa/-	Q72-
8T	EHMT2	10919	chr6:31857080-31857080	Nonsense_Mutation	SNP	G	A	Cga/Tga	R404*
8T	FTSJD2	23070	chr6:37429368-37429368	Missense_Mutation	SNP	G	A	aGc/aAc	S380N
8T	MUC12	10071	chr7:100636426-100636426	Missense_Mutation	SNP	C	T	aCg/aTg	T1004M
8T	PTPRZ1	5803	chr7:121652183-121652183	Missense_Mutation	SNP	C	A	aCa/aAa	T1028K

8T	GTPBP10	85865	chr7:90014334-90014334	Missense_Mutation	SNP	G	A	Gat/Aat	D344N
8T	RP1L1	94137	chr8:10467581-10467581	Missense_Mutation	SNP	C	T	Gaa/Aaa	E1343K
9T	FMO5	2330	chr1:146684093-146684093	Missense_Mutation	SNP	C	A	aaG/aaT	K166N
9T	FLG	2312	chr1:152281706-152281706	Missense_Mutation	SNP	G	A	Cat/Tat	H1886Y
9T	MR1	3140	chr1:181018451-181018451	Splice_Site	SNP	G	A		
9T	RGSL1	353299	chr1:182458236-182458236	Missense_Mutation	SNP	T	A	aTg/aAg	M539K
9T	C1orf65	164127	chr1:223567068-223567068	Missense_Mutation	SNP	G	T	aGc/aTc	S84I
9T	TRIT1	54802	chr1:40349132-40349132	Missense_Mutation	SNP	G	T	cCc/cAc	P11H
9T	SLC5A9	200010	chr1:48694788-48694788	Missense_Mutation	SNP	G	T	aGg/aTg	R118M
9T	SLC1A7	6512	chr1:53558269-53558269	Missense_Mutation	SNP	C	A	Ggc/Tgc	G330C
9T	SPSB1	80176	chr1:9416134-9416134	Missense_Mutation	SNP	T	G	Tcg/Gcg	S62A
9T	CCDC172	374355	chr10:118101703-118101703	Missense_Mutation	SNP	G	T	atG/atT	M146I
9T	SORL1	6653	chr11:121458806-121458806	Missense_Mutation	SNP	G	A	Gga/Aga	G1298R
9T	PITPNM1	9600	chr11:67266224-67266224	Missense_Mutation	SNP	G	A	Cct/Tct	P443S
9T	RBM23	55147	chr14:23374840-23374840	Missense_Mutation	SNP	G	T	Cat/Aat	H144N
9T	AKAP6	9472	chr14:33291948-33291948	Missense_Mutation	SNP	G	C	caG/caC	Q1643H
9T	APBA2	321	chr15:29393810-29393810	Missense_Mutation	SNP	G	A	atG/atA	M449I
9T	CASC5	57082	chr15:40913900-40913900	Missense_Mutation	SNP	G	A	Gga/Aga	G506R
9T	TMEM87A	25963	chr15:42525452-42525452	Missense_Mutation	SNP	G	C	Ctt/Gtt	L341V
9T	SH3GL3	6457	chr15:84241340-84241340	Nonsense_Mutation	SNP	G	T	Gaa/Taa	E127*
9T	TCF25	22980	chr16:89971406-89971406	Missense_Mutation	SNP	G	T	tgG/tgT	W510C
9T	NCOR1	9611	chr17:15960951-15960951	Missense_Mutation	SNP	G	C	tCt/tGt	S2090C
9T	OR4D1	26689	chr17:56232770-56232770	Missense_Mutation	SNP	C	T	Ctc/Ttc	L86F
9T	ZNF536	9745	chr19:30934477-30934477	Missense_Mutation	SNP	A	G	gAa/gGa	E3G
9T	IL18RAP	8807	chr2:103068343-103068343	Missense_Mutation	SNP	C	A	gCc/gAc	A501D
9T	RPRM	56475	chr2:154334920-154334920	Missense_Mutation	SNP	T	G	Atg/Ctg	M54L
9T	CCDC141	285025	chr2:179701849-179701849	Missense_Mutation	SNP	G	C	tCt/tGt	S1366C
9T	INPP5D	3635	chr2:233986946-233986946	Missense_Mutation	SNP	G	C	Gac/Cac	D110H
9T	SNRNP200	23020	chr2:96943407-96943407	Missense_Mutation	SNP	C	A	gGg/gTg	G1934V
9T	CNGA3	1261	chr2:99012801-99012801	Missense_Mutation	SNP	C	G	Ctg/Gtg	L394V
9T	BCL2L1	598	chr20:30309541-30309541	Missense_Mutation	SNP	C	G	Gta/Cta	V161L
9T	PEX26	55670	chr22:18566327-18566327	Missense_Mutation	SNP	C	T	Cgg/Tgg	R166W
9T	ITGA9	3680	chr3:37560813-37560813	Missense_Mutation	SNP	G	C	Gat/Cat	D402H
9T	TLR2	7097	chr4:154623916-154623916	De_novo_Start_InFrame	SNP	G	T		
9T	PDLIM3	27295	chr4:186423546-186423546	Missense_Mutation	SNP	A	C	Ttc/Gtc	F333V
9T	ANAPC4	29945	chr4:25379100-25379108	In_Frame_Del	DEL	GCAGCTCCC	-	aagcagctcccg/aag	KQLP17K
9T	FRYL	285527	chr4:48592787-48592787	Missense_Mutation	SNP	C	T	Ggt/Agt	G466S
9T	LRRC66	339977	chr4:52861026-52861026	Missense_Mutation	SNP	G	A	gCa/gTa	A721V
9T	LRRC66	339977	chr4:52861027-52861027	Missense_Mutation	SNP	C	A	Gca/Tca	A721S
9T	UGT2B15	7366	chr4:69536038-69536038	Missense_Mutation	SNP	C	A	gGt/gTt	G100V
9T	PCDHGA2	56113	chr5:140719886-140719886	Missense_Mutation	SNP	C	T	Ccc/Tcc	P450S
9T	PCDHGB3	56102	chr5:140751268-140751268	Missense_Mutation	SNP	A	C	aAg/aCg	K436T
9T	STK10	6793	chr5:171520444-171520444	Missense_Mutation	SNP	T	C	aAc/aGc	N509S
9T	AMACR	23600	chr5:34005972-34005972	Missense_Mutation	SNP	T	C	Att/Gtt	I94V
9T	DAXX	1616	chr6:33289330-33289330	Missense_Mutation	SNP	A	C	tgT/tgG	C74W
9T	ZBTB9	221504	chr6:33424262-33424262	Missense_Mutation	SNP	G	C	gGc/gCc	G462A
9T	RP11-1220K2.2	NA	chr7:141864822-141864830	Frame_Shift_Del	DEL	AGGTAAGAG	-	-	-884
9T	NT5C3	51251	chr7:33054364-33054364	Missense_Mutation	SNP	G	C	tCt/tGt	S330C
9T	DPYS	1807	chr8:105441854-105441854	Missense_Mutation	SNP	T	C	cAc/cGc	H290R
9T	ARHGAP39	80728	chr8:145770939-145770939	Missense_Mutation	SNP	C	T	Gtg/Atg	V739M
9T	PCMTD1	115294	chr8:52746113-52746113	Missense_Mutation	SNP	C	T	Gtt/Att	V183I
9T	TGS1	96764	chr8:56699449-56699449	Missense_Mutation	SNP	T	G	gTa/gGa	V331G
9T	SGK223	157285	chr8:8175848-8175848	Missense_Mutation	SNP	G	T	aCg/aAg	T1346K
9T	WWP1	11059	chr8:87474055-87474055	Missense_Mutation	SNP	G	C	tgG/tgC	W883C
9T	SLC46A2	57864	chr9:115652983-115652983	De_novo_Start_InFrame	SNP	G	A		
9T	CEL	1056	chr9:135945963-135945963	Missense_Mutation	SNP	G	C	Gcc/Ccc	A471P
9T	RBMXL3	139804	chrX:114426781-114426781	Missense_Mutation	SNP	G	C	gGg/gCg	G926A
9T	GPR64	10149	chrX:19017284-19017284	Missense_Mutation	SNP	A	T	aTt/aAt	I815N

Supplementary Table 4: Genes sequenced in IMPACT assay

HUGO Symbol	Approved name	Location
ABL1	c-abl oncogene 1, non-receptor tyrosine kinase	9q34.1
ACIN1	apoptotic chromatin condensation inducer 1	14q11.2
AEBP2	AE binding protein 2	12p12.3
AKT1	v-akt murine thymoma viral oncogene homolog 1	14q32.32-q32.33
AKT2	v-akt murine thymoma viral oncogene homolog 2	19q13.1-q13.2
AKT3	v-akt murine thymoma viral oncogene homolog 3	1q44
ALK	anaplastic lymphoma receptor tyrosine kinase	2p23
ALOX12B	arachidonate 12-lipoxygenase, 12R type	17p13.1
APC	adenomatous polyposis coli	5q21-q22
AR	androgen receptor	Xq12
ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	Xp11.3-p11.23
ARID1A	AT rich interactive domain 1A (SWI-like)	1p36.1-p35
ARID1B	AT rich interactive domain 1B (SWI1-like)	6q25.3
ARID2	AT rich interactive domain 2 (ARID, RFX-like)	12q13.11
ARID5B	AT rich interactive domain 5B (MRF1-like)	10q11.22
ASXL1	additional sex combs like 1 (Drosophila)	20q11
ASXL2	additional sex combs like 2 (Drosophila)	2p24.1
ATM	ataxia telangiectasia mutated	11q22-q23
ATR	ataxia telangiectasia and Rad3 related	3q23
ATRX	alpha thalassemia/mental retardation syndrome X-linked	Xq21.1
AURKA	aurora kinase A	20q13
AURKB	aurora kinase B	17p13.1
AXIN1	axin 1	16p13.3
AXIN2	axin 2	17q23-q24
AXL	AXL receptor tyrosine kinase	19q13.1
B2M	beta-2-microglobulin	15q21-q22.2
BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	3p21.31-p21.2
BARD1	BRCA1 associated RING domain 1	2q34-q35
BBC3	BCL2 binding component 3	19q13.3-q13.4
BCL2	B-cell CLL/lymphoma 2	18q21.3
BCL2L1	BCL2-like 1	20q11.21
BCL2L11	BCL2-like 11 (apoptosis facilitator)	2q13
BCL6	B-cell CLL/lymphoma 6	3q27
BCOR	BCL6 corepressor	Xp11.4
BIRC6	baculoviral IAP repeat containing 6	2p22.3
BLM	Bloom syndrome, RecQ helicase-like	15q26.1
BMPR1A	bone morphogenetic protein receptor, type IA	10q22.3
BRAF	v-raf murine sarcoma viral oncogene homolog B	7q34
BRCA1	breast cancer 1, early onset	17q21.31
BRCA2	breast cancer 2, early onset	13q12-q13
BRD4	bromodomain containing 4	19p13.12
BRIP1	BRCA1 interacting protein C-terminal helicase 1	17q22.2
BTK	Bruton agammaglobulinemia tyrosine kinase	Xq21.33-q22
CARD11	caspase recruitment domain family, member 11	7p22
CARF	calcium responsive transcription factor	2q33.3
CASP8	caspase 8, apoptosis-related cysteine peptidase	2q33-q34
CBFB	core-binding factor, beta subunit	16q22.1
CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	11q23.3
CCND1	cyclin D1	11q13
CCND2	cyclin D2	12p13
CCND3	cyclin D3	6p21
CCNE1	cyclin E1	19q12
CD274	CD274 molecule	9p24.1
CD276	CD276 molecule	15q23-q24
CD79B	CD79b molecule, immunoglobulin-associated beta	17q23
CDC73	cell division cycle 73	1q25

CDH1	cadherin 1, type 1, E-cadherin (epithelial)	16q22.1
CDHR2	cadherin-related family member 2	5q35.2
CDK12	cyclin-dependent kinase 12	17q12
CDK4	cyclin-dependent kinase 4	12q13
CDK6	cyclin-dependent kinase 6	7q21-q22
CDK8	cyclin-dependent kinase 8	13q12
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	6p21.1
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	12p13.1-p12
CDKN2A	cyclin-dependent kinase inhibitor 2A	9p21
CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	9p21
CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1p32.3
CHEK1	checkpoint kinase 1	11q24.2
CHEK2	checkpoint kinase 2	22q12.1
CIC	capicua transcriptional repressor	19q13.2
CREBBP	CREB binding protein	16p13.3
CRKL	v-crk avian sarcoma virus CT10 oncogene homolog-like	22q11.21
CRLF2	cytokine receptor-like factor 2	Xp22.3 and Yp11.
CSF1R	colony stimulating factor 1 receptor	5q32
CTCF	CCCTC-binding factor (zinc finger protein)	16q21-q22.3
CTLA4	cytotoxic T-lymphocyte-associated protein 4	2q33
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	3p21
CUL3	cullin 3	2q36.2
DAXX	death-domain associated protein	6p21.3
DCLRE1C	DNA cross-link repair 1C	10p13
DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1	3q26.3
DDR2	discoidin domain receptor tyrosine kinase 2	1q12-q23
DICER1	dicer 1, ribonuclease type III	14q32.13
DIS3	DIS3 exosome endoribonuclease and 3'-5' exoribonuclease	13q21.32
DNMT1	DNA (cytosine-5-)-methyltransferase 1	19p13.2
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	2p23
DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	20q11.2
DOT1L	DOT1-like histone H3K79 methyltransferase	19p13.3
E2F3	E2F transcription factor 3	6p22
EED	embryonic ectoderm development	11q14.2-q22.3
EGFL7	EGF-like-domain, multiple 7	9q34.3
EGFR	epidermal growth factor receptor	7p12
EIF1AX	eukaryotic translation initiation factor 1A, X-linked	Xp22.13
EP300	E1A binding protein p300	22q13.2
EPCAM	epithelial cell adhesion molecule	2p21
EPHA3	EPH receptor A3	3p11.2
EPHA5	EPH receptor A5	4q13.1
EPHB1	EPH receptor B1	3q21-q23
ERBB2	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2	17q11.2-q12
ERBB3	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	12q13
ERBB4	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 4	2q33.3-q34
ERCC2	excision repair cross-complementation group 2	19q13.3
ERCC3	excision repair cross-complementation group 3	2q21
ERCC4	excision repair cross-complementation group 4	16p13.3
ERCC5	excision repair cross-complementation group 5	13q22-q34
ERCC6	excision repair cross-complementation group 6	10q11
ERG	v-ets avian erythroblastosis virus E26 oncogene homolog	21q22.3
ESR1	estrogen receptor 1	6q24-q27
ETV1	ets variant 1	7p22
ETV6	ets variant 6	12p13
EZH1	enhancer of zeste homolog 1 (Drosophila)	17q21.1-q21.3
EZH2	enhancer of zeste homolog 2 (Drosophila)	7q35-q36
FAM123B	APC membrane recruitment protein 1	Xq11.1
FAM175A	family with sequence similarity 175, member A	4q21.23
FAM46C	family with sequence similarity 46, member C	1p12

FANCA	Fanconi anemia, complementation group A	16q24.3
FANCB	Fanconi anemia, complementation group B	Xp22.2
FANCC	Fanconi anemia, complementation group C	9q22.3
FANCD2	Fanconi anemia, complementation group D2	3p25.3
FANCE	Fanconi anemia, complementation group E	6p22-p21
FANCF	Fanconi anemia, complementation group F	11p15
FANCG	Fanconi anemia, complementation group G	9p13
FAT1	FAT atypical cadherin 1	4q35.2
FBXW7	F-box and WD repeat domain containing 7, E3 ubiquitin protein ligase	4q31.23
FGF19	fibroblast growth factor 19	11q13.1
FGF3	fibroblast growth factor 3	11q13
FGF4	fibroblast growth factor 4	11q13.3
FGFR1	fibroblast growth factor receptor 1	8p11.23-p11.22
FGFR2	fibroblast growth factor receptor 2	10q25.3-q26
FGFR3	fibroblast growth factor receptor 3	4p16.3
FGFR4	fibroblast growth factor receptor 4	5q35.2
FH	fumarate hydratase	1q42.1
FLCN	folliculin	17p11.2
FLT1	fms-related tyrosine kinase 1	13q12
FLT3	fms-related tyrosine kinase 3	13q12
FLT4	fms-related tyrosine kinase 4	5q34-q35
FOXA1	forkhead box A1	14q12-q13
FOXL2	forkhead box L2	3q23
FOXP1	forkhead box P1	3p14.1
FUBP1	far upstream element (FUSE) binding protein 1	1p31.1
GATA1	GATA binding protein 1 (globin transcription factor 1)	Xp11.23
GATA2	GATA binding protein 2	3q21
GATA3	GATA binding protein 3	10p15
GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	19p13.3
GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	9q21
GNAS	GNAS complex locus	20q13.2-q13.3
GREM1	gremlin 1, DAN family BMP antagonist	15q13.3
GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	16p13.2
GSK3B	glycogen synthase kinase 3 beta	3q13.3
H3F3A	H3 histone, family 3A	1q42.12
H3F3B	H3 histone, family 3B (H3.3B)	17q25.1
H3F3C	H3 histone, family 3C	12p11.21
HAAO	3-hydroxyanthranilate 3,4-dioxygenase	2p
HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	7q21.1
HIST1H1C	histone cluster 1, H1c	6p21.3
HIST1H2BD	histone cluster 1, H2bd	6p22.1
HIST1H3B	histone cluster 1, H3b	6p22.1
HNF1A	HNF1 homeobox A	12q24.31
HRAS	Harvey rat sarcoma viral oncogene homolog	11p15.5
ICOSLG	inducible T-cell co-stimulator ligand	21q22.3
IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	2q34
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	15q26.1
IFNGR1	interferon gamma receptor 1	6q23-q24
IGF1	insulin-like growth factor 1 (somatomedin C)	12q23.2
IGF1R	insulin-like growth factor 1 receptor	15q26.3
IGF2	insulin-like growth factor 2 (somatomedin A)	11p15.5
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	1q31
IKZF1	IKAROS family zinc finger 1 (Ikaros)	7p12.2
IL10	interleukin 10	1q31-q32
IL7R	interleukin 7 receptor	5p13
INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	2q11.2
INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	4q31.1
INSR	insulin receptor	19p13.3-p13.2
IRF4	interferon regulatory factor 4	6p25-p23

IRS1	insulin receptor substrate 1	2q36
IRS2	insulin receptor substrate 2	13q34
JAG1	jagged 1	20p12.1-p11.23
JAK1	Janus kinase 1	1p32.3-p31.3
JAK2	Janus kinase 2	9p24
JAK3	Janus kinase 3	19p13-p12
JARID2	jumonji, AT rich interactive domain 2	6p24-p23
JUN	jun proto-oncogene	1p32-p31
KAT5	K(lysine) acetyltransferase 5	11q13
KDM5A	lysine (K)-specific demethylase 5A	12p13.33
KDM5C	lysine (K)-specific demethylase 5C	Xp11.22-p11.21
KDM6A	lysine (K)-specific demethylase 6A	Xp11.2
KDM6B	lysine (K)-specific demethylase 6B	17p13.1
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	4q11-q12
KEAP1	kelch-like ECH-associated protein 1	19p13.2
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	4q12
KLF4	Kruppel-like factor 4 (gut)	9q31
KRAS	Kirsten rat sarcoma viral oncogene homolog	12p12.1
LATS1	large tumor suppressor kinase 1	6q25.1
LATS2	large tumor suppressor kinase 2	13q11-q12
LIG4	ligase IV, DNA, ATP-dependent	13q33-q34
LMO1	LIM domain only 1 (rhombotin 1)	11p15
MAP2K1	mitogen-activated protein kinase kinase 1	15q22.1-q22.33
MAP2K2	mitogen-activated protein kinase kinase 2	19p13.3
MAP2K4	mitogen-activated protein kinase kinase 4	17p12
MAP3K1	mitogen-activated protein kinase kinase kinase 1, E3 ubiquitin protein ligase	5q11.2
MAP3K13	mitogen-activated protein kinase kinase kinase 13	3q27
MAPK1	mitogen-activated protein kinase 1	22q11.2
MAX	MYC associated factor X	14q23
MCL1	myeloid cell leukemia 1	1q21
MCPH1	microcephalin 1	8p23.1
MDC1	mediator of DNA-damage checkpoint 1	6p21.3
MDM2	MDM2 oncogene, E3 ubiquitin protein ligase	12q13-q14
MDM4	MDM4, p53 regulator	1q32
MED12	mediator complex subunit 12	Xq13
MEF2B	myocyte enhancer factor 2B	19p13.11
MEN1	multiple endocrine neoplasia I	11q13
MET	met proto-oncogene	7q31
MITF	microphthalmia-associated transcription factor	3p14.1-p12.3
MLH1	mutL homolog 1	3p22.3
MLL	lysine (K)-specific methyltransferase 2A	11q23
MLL2	lysine (K)-specific methyltransferase 2D	12q13.12
MLL3	lysine (K)-specific methyltransferase 2C	7q36
MPL	myeloproliferative leukemia virus oncogene	1p34
MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	11q21
MSH2	mutS homolog 2	2p21
MSH6	mutS homolog 6	2p16
MTF2	metal response element binding transcription factor 2	1p22.1
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	1p36
MUTYH	mutY homolog	1p34.1
MYC	v-myc avian myelocytomatosis viral oncogene homolog	8q24
MYCL1	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	1p34.3
MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	2p24.3
MYD88	myeloid differentiation primary response 88	3p22
MYOD1	myogenic differentiation 1	11p15
NBN	nibrin	8q21-q24
NCOR1	nuclear receptor corepressor 1	17p11.2
NF1	neurofibromin 1	17q11.2
NF2	neurofibromin 2 (merlin)	22q12.2

NFE2L2	nuclear factor, erythroid 2-like 2	2q31
NKX2-1	NK2 homeobox 1	14q13.3
NKX3-1	NK3 homeobox 1	8p21.2
NOTCH1	notch 1	9q34.3
NOTCH2	notch 2	1p13-p11
NOTCH3	notch 3	19p13.2-p13.1
NOTCH4	notch 4	6p21.3
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	5q35.1
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	1p13.2
NSD1	nuclear receptor binding SET domain protein 1	5q35
NTRK1	neurotrophic tyrosine kinase, receptor, type 1	1q21-q22
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	9q22.1
NTRK3	neurotrophic tyrosine kinase, receptor, type 3	15q24-q25
PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	11q13-q14
PAK7	p21 protein (Cdc42/Rac)-activated kinase 7	20p12
PALB2	partner and localizer of BRCA2	16p12.1
PARK2	parkin RBR E3 ubiquitin protein ligase	6q25.2-q27
PARP1	poly (ADP-ribose) polymerase 1	1q41-q42
PAX5	paired box 5	9p13.2
PBRM1	polybromo 1	3p21
PDCD1	programmed cell death 1	2q37.3
PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	4q12
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	5q33.1
PDPK1	3-phosphoinositide dependent protein kinase 1	16p13.3
PHF1	PHD finger protein 1	6p21.3
PHF19	PHD finger protein 19	9q34.11
PHOX2B	paired-like homeobox 2b	4p13
PIK3C2G	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	12p12
PIK3C3	phosphatidylinositol 3-kinase, catalytic subunit type 3	18q12.3
PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	3q26.3
PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta	3q22.3
PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta	1p36.2
PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma	7q22
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	5q13.1
PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	19p13.11
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	1p34.1
PIM1	pim-1 oncogene	6p21
PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	19q13.2
PLK2	polo-like kinase 2	5q12.1-q13.2
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	18q21.32
PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	2q31-q33
PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	7p22.1
PNRC1	proline-rich nuclear receptor coactivator 1	6q16.1
POLE	polymerase (DNA directed), epsilon, catalytic subunit	12q24.3
POLQ	polymerase (DNA directed), theta	3q13.3
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	19q13
PRDM1	PR domain containing 1, with ZNF domain	6q21
PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	17q24.2
PRKDC	protein kinase, DNA-activated, catalytic polypeptide	8q11
PTCH1	patched 1	9q22.1-q31
PTEN	phosphatase and tensin homolog	10q23
PTPN11	protein tyrosine phosphatase, non-receptor type 11	12q24.1
PTPRD	protein tyrosine phosphatase, receptor type, D	9p24.1-p23
PTPRS	protein tyrosine phosphatase, receptor type, S	19p13.3
RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	7p22
RAD50	RAD50 homolog (S. cerevisiae)	5q23-q31
RAD51	RAD51 recombinase	15q15.1
RAD51B	RAD51 paralog B	14q23-q24.2
RAD51C	RAD51 paralog C	17q25.1

RAD51D	RAD51 paralog D	17q11
RAD52	RAD52 homolog (S. cerevisiae)	12p13-p12.2
RAD54L	RAD54-like (S. cerevisiae)	1p32
RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	3p25
RARA	retinoic acid receptor, alpha	17q21.1
RASA1	RAS p21 protein activator (GTPase activating protein) 1	5q13
RB1	retinoblastoma 1	13q14.2
RBM10	RNA binding motif protein 10	Xp11.3
RECQL4	RecQ protein-like 4	8q24.3
REL	v-rel avian reticuloendotheliosis viral oncogene homolog	2p13-p12
RET	ret proto-oncogene	10q11.2
REV3L	REV3-like, polymerase (DNA directed), zeta, catalytic subunit	6q22
RFWD2	ring finger and WD repeat domain 2, E3 ubiquitin protein ligase	1q25.1-q25.2
RHOA	ras homolog family member A	3p21.3
RICTOR	RPTOR independent companion of MTOR, complex 2	5p13.1
RIT1	Ras-like without CAAX 1	1q21.2
RNF43	ring finger protein 43	17q23.2
ROS1	c-ros oncogene 1 , receptor tyrosine kinase	6q21-q22
RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	11q11-q13
RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	11q13.1
RPTOR	regulatory associated protein of MTOR, complex 1	17q25.3
RUNX1	runt-related transcription factor 1	21q22.3
RYBP	RING1 and YY1 binding protein	3p14.2
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	5p15
SDHAF2	succinate dehydrogenase complex assembly factor 2	11q12.2
SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	1p36.1-p35
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	1q23.3
SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein	11q23
SETD2	SET domain containing 2	3p21.31
SF3B1	splicing factor 3b, subunit 1, 155kDa	2q33.1
SH2D1A	SH2 domain containing 1A	Xq25
SHQ1	SHQ1, H/ACA ribonucleoprotein assembly factor	3p13
SLX4	SLX4 structure-specific endonuclease subunit	16p13.3
SMAD2	SMAD family member 2	18q21
SMAD3	SMAD family member 3	15q21-q22
SMAD4	SMAD family member 4	18q21.1
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	19p13.3
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b,	22q11.23
SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d,	12q13-q14
SMO	smoothened, frizzled class receptor	7q32.1
SOCS1	suppressor of cytokine signaling 1	16p13.13
SOX17	SRY (sex determining region Y)-box 17	8q11.23
SOX2	SRY (sex determining region Y)-box 2	3q26.3-q27
SOX9	SRY (sex determining region Y)-box 9	17q24.3
SPEN	spen family transcriptional repressor	1p36
SPOP	speckle-type POZ protein	17q21.33
SRC	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog	20q12-q13
STAG2	stromal antigen 2	Xq25
STK11	serine/threonine kinase 11	19p13.3
STK40	serine/threonine kinase 40	1p34.3
SUFU	suppressor of fused homolog (Drosophila)	10q24.32
SUZ12	SUZ12 polycomb repressive complex 2 subunit	17q21
SYK	spleen tyrosine kinase	9q22
TBX3	T-box 3	12q24.21
TERT	telomerase reverse transcriptase	5p15.33
TET1	tet methylcytosine dioxygenase 1	10q21
TET2	tet methylcytosine dioxygenase 2	4q24
TGFBR1	transforming growth factor, beta receptor 1	9q22
TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	3p22

TMEM127	transmembrane protein 127	2q11.2
TMPRSS2	transmembrane protease, serine 2	21q22.3
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	6q23-q25
TNFRSF14	tumor necrosis factor receptor superfamily, member 14	1p36.32
TOP1	topoisomerase (DNA) I	20q12-q13.1
TP53	tumor protein p53	17p13.1
TP63	tumor protein p63	3q27-q29
TRAF7	TNF receptor-associated factor 7, E3 ubiquitin protein ligase	16p13.3
TSC1	tuberous sclerosis 1	9q34
TSC2	tuberous sclerosis 2	16p13.3
TSHR	thyroid stimulating hormone receptor	14q24-q31
U2AF1	U2 small nuclear RNA auxiliary factor 1	21q22.3
VHL	von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase	3p25.3
VTCN1	V-set domain containing T cell activation inhibitor 1	1p12
WRN	Werner syndrome, RecQ helicase-like	8p12
WT1	Wilms tumor 1	11p13
XIAP	X-linked inhibitor of apoptosis	Xq25
XPO1	exportin 1	2p15
XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	19q13.2
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	7q36
XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	5q14.2
XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-br	2q35
XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	22q13.2
YAP1	Yes-associated protein 1	11q13
YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	18p11.31-p11.21

Supplementary Table 5: Expression of genes differientially expressed between PRC2 intact and PRC2 loss

Sample	Mean PRC2 Loss	Mean PRC2 Intact	Fold Change (Log 2)	FDR
PITX1	855	2	8.20	2.91E-86
EYA1	3064	10	7.82	6.22E-63
NXPH2	181	0	7.61	3.23E-27
HMX1	278	1	7.39	8.59E-41
CACNG7	1229	3	7.34	1.65E-31
OTX2	734	2	7.00	5.97E-26
OLFM3	1281	6	6.96	2.93E-32
LGR5	2905	14	6.95	4.90E-36
TNMD	12037	37	6.74	1.10E-23
DLK1	93096	193	6.72	1.00E-20
DPY19L2P1	408	3	6.67	6.35E-32
BPIFB4	4796	10	6.64	1.05E-19
PAPPA2	2448	16	6.60	2.53E-40
PAX7	700	4	6.35	1.69E-22
NPY5R	115	0	6.11	5.77E-16
KCTD8	159	1	6.10	5.41E-27
RP11-1102P16.1	157	2	6.09	5.30E-26
FEZF1	222	1	6.05	3.50E-20
FOXN4	84	1	6.03	1.45E-19
HOXD11	180	1	6.02	1.79E-17
SALL3	329	2	5.99	7.87E-17
LIN28B	231	1	5.97	2.46E-17
UNC13C	178	2	5.93	5.37E-26
PROK2	255	3	5.92	2.05E-25
CXCL6	626	4	5.90	1.44E-17
TMEM179	99	1	5.89	6.65E-21
EPHA7	1113	10	5.86	3.39E-25
RP11-849I19.1	199	1	5.82	1.97E-14
C1QL4	1864	25	5.80	2.39E-33
GAS2	5955	98	5.79	8.36E-61
RP6-24A23.7	208	1	5.79	1.41E-14
RP1-170O19.14	40	0	5.74	2.09E-18
FOXE1	202	2	5.71	1.51E-16
ALDH1A2	7847	65	5.71	8.44E-19
LMX1A	225	2	5.65	5.45E-14
CLVS2	68	0	5.65	2.42E-16
RP1-170O19.17	51	0	5.63	5.52E-14
RP11-966I7.1	37	0	5.56	4.22E-17
SELV	45	0	5.55	3.40E-19
RP11-366M4.3	710	6	5.49	2.05E-14
SYT13	597	7	5.47	8.26E-16

RP11-160A10.2	63	0	5.42	3.79E-14
ZNF804B	138	2	5.39	1.33E-13
ALX4	1249	14	5.39	2.97E-16
EMX1	188	3	5.38	3.61E-15
ALX3	40	0	5.34	2.18E-10
ANKRD18B	139	2	5.25	1.11E-16
AC026150.5	22	0	5.23	2.08E-10
RORB	245	6	5.23	4.59E-26
NPW	1058	19	5.22	2.13E-21
RP11-99H20.1	33	0	5.17	1.30E-09
HOXA13	1300	29	5.11	7.63E-21
EMX2	288	7	5.06	7.33E-21
BTBD17	58	0	5.06	8.48E-11
GPC5	64	1	5.06	3.26E-15
FAM123A	38	2	5.01	6.47E-14
EVX1-AS	24	0	4.99	6.08E-10
LHX9	674	13	4.99	1.02E-16
UGT3A2	199	4	4.99	4.01E-13
RP11-510C10.4	43	0	4.99	6.26E-10
ZIC2	421	5	4.98	8.49E-13
ZFHX4-AS1	1399	26	4.98	1.27E-15
TBR1	452	4	4.97	2.81E-10
GPR64	1717	43	4.97	8.83E-32
AC116614.1	95	2	4.97	1.65E-11
RP5-1121E10.2	13	0	4.94	8.47E-09
JPH4	1480	30	4.94	8.37E-20
CNNM1	270	6	4.92	1.95E-15
MRPL9P1	36	0	4.90	5.91E-09
CA10	634	6	4.89	2.11E-09
WIF1	6516	110	4.88	1.03E-11
GABRA5	144	2	4.88	8.02E-10
SCAND3	389	11	4.86	5.01E-22
NPY1R	1146	35	4.83	8.08E-17
KRT25	31	0	4.81	2.11E-08
SLC16A9	1689	41	4.80	7.89E-17
CYP26A1	1027	24	4.79	7.58E-17
MUM1L1	594	16	4.79	8.44E-19
DBX2	72	2	4.78	6.79E-12
RP11-343B18.2	42	0	4.77	1.16E-08
ADCY2	947	19	4.75	3.76E-13
CRYGD	125	1	4.73	2.56E-08
SLC15A1	40	1	4.73	2.03E-12
LYPD6B	186	6	4.71	9.26E-25
GLT1D1	213	8	4.68	9.45E-24
PLEKHG4B	1540	33	4.68	2.32E-13
DDIT4L	2093	55	4.67	1.77E-17
EMX2OS	98	2	4.65	1.60E-16

SLC9A2	277	8	4.63	2.26E-13
FADS6	21	1	4.62	3.34E-10
ZIC5	33	2	4.61	3.75E-11
GPR50	31	1	4.61	2.57E-09
SH3GL2	109	4	4.58	9.44E-19
SNX18P7	13	0	4.58	1.77E-07
STMN2	1756	33	4.56	1.11E-09
RP11-255A11.21	33	1	4.51	7.59E-08
CDX2	199	4	4.50	1.09E-08
RBM24	728	18	4.49	4.05E-11
CNPY1	205	5	4.49	1.77E-08
HOTTIP	64	3	4.49	1.47E-10
POU4F1	259	7	4.47	1.14E-10
ESX1	14	0	4.47	6.78E-07
BTBD11	1062	41	4.47	1.10E-16
MAGEL2	25	0	4.44	4.71E-07
CDH8	415	12	4.43	3.52E-14
ARHGEF4	2198	61	4.43	1.05E-12
RP5-1024C24.1	46	3	4.42	2.40E-13
PNMT	121	4	4.41	3.12E-10
DSC3	293	6	4.39	1.65E-09
PNMA3	675	25	4.39	1.34E-20
HS3ST3A1	401	14	4.39	1.54E-16
SLC8A2	325	11	4.38	1.64E-11
HMX2	38	1	4.37	6.37E-11
LIX1	159	3	4.37	2.83E-09
NTRK2	3006	87	4.36	3.76E-12
ATP1A2	3075	77	4.36	1.14E-10
MYOD1	615	8	4.36	3.97E-07
CCK	91	2	4.34	1.44E-07
IRS4	49	1	4.32	7.59E-08
COL11A2	12250	450	4.30	2.07E-09
COL2A1	8863	177	4.28	9.85E-08
AC010729.1	23	1	4.28	2.76E-10
DPY19L2P4	195	10	4.24	3.92E-08
RP11-326E22.1	15	0	4.24	7.44E-08
CDH10	277	5	4.24	1.46E-07
WNK2	725	23	4.23	7.93E-11
AC091878.1	39	2	4.23	3.58E-11
CHRNA7	71	2	4.23	7.42E-18
FAM19A4	91	2	4.22	1.76E-07
DBC1	785	10	4.21	1.54E-06
RP11-35O15.1	32	1	4.20	3.12E-10
CTD-2231H16.1	81	4	4.20	6.72E-12
ANKRD18A	327	10	4.19	2.76E-09
PCDHA1	50	2	4.18	1.29E-08
JPH1	1668	70	4.17	1.83E-17

CXCL5	353	8	4.13	5.21E-07
FEZF1-AS1	352	8	4.12	2.55E-07
RP11-260M19.2	30	1	4.12	6.32E-09
RIMS4	604	14	4.11	2.39E-07
PRRT4	571	21	4.11	1.57E-11
CTD-2195M15.1	24	1	4.10	3.96E-10
C14orf144	61	3	4.10	8.44E-09
KCNH2	889	33	4.09	3.31E-10
CRYM	1037	32	4.09	5.52E-09
RASL11B	3416	153	4.08	1.46E-15
C1QTNF3	7542	347	4.08	1.59E-17
GPR88	170	8	4.07	1.96E-14
SIX2	2713	82	4.06	4.20E-08
HOXA11-AS	433	21	4.06	6.07E-21
FAM150B	387	14	4.05	2.64E-09
NEFM	2353	80	4.05	1.71E-08
RIMBP2	434	21	4.04	9.32E-12
DLX3	678	21	4.03	3.15E-08
NHLH2	190	5	4.03	7.89E-07
FAM189A1	183	7	4.02	2.76E-09
RP11-495K9.3	46	2	4.00	1.98E-06
SCXA	13	1	3.99	2.33E-08
USH1G	68	4	3.99	2.95E-08
ESRRG	248	9	3.99	2.56E-08
TLX1	280	6	3.98	4.62E-06
MSGN1	8	0	3.98	2.34E-05
FAM163B	51	1	3.98	8.93E-08
GAS1	5357	255	3.96	4.45E-15
GNAT1	9	0	3.96	3.52E-05
LHX8	530	20	3.96	2.55E-08
PAX2	347	10	3.96	9.64E-07
HIF3A	6179	180	3.96	2.85E-07
NUDT10	428	18	3.95	4.39E-10
ANKRD62P1-PARP4	10	1	3.95	2.74E-06
SIAH3	94	4	3.94	3.40E-08
ASIC2	393	11	3.94	1.35E-06
CACNA1G-AS1	191	7	3.94	3.47E-08
AP001626.2	50	2	3.93	3.24E-07
ADRB2	2008	91	3.93	2.46E-11
TPTEP1	1718	87	3.92	6.94E-12
IGF2	112231	2668	3.90	4.20E-06
SIM1	706	21	3.90	6.67E-07
CACNA1G	4217	139	3.90	1.56E-07
PRR18	85	4	3.89	5.67E-08
ENTPD8	135	8	3.88	8.38E-09
FBN3	1188	46	3.88	3.52E-08
USH1C	681	21	3.88	9.15E-06

SH3GL3	227	12	3.88	2.33E-08
CNTN2	243	10	3.87	1.65E-07
NCAN	74	3	3.87	1.33E-08
GPR27	623	26	3.87	6.09E-09
YBX2	318	17	3.87	4.72E-10
XXbac-BPG308K3.5	6	0	3.87	5.39E-05
RP4-755D9.1	225	10	3.87	7.22E-10
GRM4	409	12	3.86	4.31E-06
LEMD1	149	7	3.86	5.94E-09
RP11-247C2.2	233	11	3.86	1.99E-11
GREB1L	246	11	3.86	1.16E-08
MFAP4	29792	1141	3.84	7.88E-08
BEGAIN	988	45	3.82	1.66E-09
GALNT14	880	57	3.82	4.60E-14
RP11-964E11.2	35	1	3.81	3.31E-05
KIAA2022	116	5	3.81	3.24E-08
RP11-944C7.1	10	0	3.81	6.19E-05
VGLL2	203	6	3.81	1.51E-06
AC008063.2	27	2	3.80	8.13E-06
WNT3A	144	7	3.80	5.01E-08
FAM65C	1648	72	3.80	7.96E-09
CTD-2124B20.3	9	0	3.80	1.01E-04
KCNMB2	305	18	3.79	1.74E-10
CNTNAP3	343	12	3.79	1.09E-06
LRFN2	43	2	3.79	7.70E-07
C14orf23	51	3	3.78	3.25E-07
MYL3	199	9	3.78	2.03E-09
CPAMD8	1751	72	3.77	6.64E-08
EFNA2	461	20	3.76	2.67E-07
PART1	123	8	3.75	6.47E-08
LINC00626	53	3	3.75	5.27E-07
CHODL	1532	58	3.75	6.58E-07
MST4	3098	218	3.74	2.47E-17
AC140481.7	11	0	3.74	7.97E-05
SLC1A6	139	6	3.74	3.98E-06
SCUBE1	413	18	3.72	3.41E-07
HS6ST2	771	36	3.71	3.31E-07
TCF24	64	4	3.71	3.46E-11
ZNF423	1909	100	3.71	4.94E-11
COL13A1	4588	295	3.70	9.93E-09
PTPRD	4140	197	3.70	2.06E-08
RP1-177G6.2	336	14	3.70	1.24E-06
SLC7A10	564	25	3.69	4.34E-07
DLX4	1245	57	3.68	4.79E-08
MSX1	2299	129	3.68	5.03E-12
CDH22	72	5	3.68	3.15E-07
FAHD2P1	10	0	3.67	9.72E-05

NOL4	24	1	3.67	1.60E-06
GS1-421I3.2	9	1	3.66	3.74E-05
RP11-384O8.1	46	2	3.66	2.43E-08
FGF12	438	27	3.65	2.46E-12
TMEM196	110	7	3.65	3.34E-06
RP11-495K9.6	13	0	3.65	1.57E-04
ACTN2	620	41	3.64	1.54E-13
AC008060.8	22	1	3.63	7.84E-06
IQSEC3	1100	45	3.62	3.52E-06
RP11-354A14.1	6	0	3.62	4.30E-05
SNAP91	130	6	3.61	4.94E-06
GAL3ST3	76	4	3.61	1.41E-06
RP11-171A24.3	6	0	3.61	3.22E-05
EVX1	39	4	3.60	2.49E-06
PPP2R2C	218	11	3.59	1.42E-06
MAPK4	188	10	3.59	7.47E-07
RP11-359N11.2	14	1	3.59	2.16E-05
GPR20	129	5	3.57	2.24E-06
ACAN	5023	206	3.56	6.12E-06
PROKR2	44	2	3.56	6.43E-05
AC018730.3	7	1	3.56	9.72E-05
CENPVP3	5	0	3.55	3.86E-04
EN1	624	30	3.55	9.89E-07
RP11-538I12.3	9	1	3.54	1.18E-04
HMGCLL1	556	31	3.54	2.62E-05
PTH1R	2647	154	3.53	9.45E-09
HS3ST6	27	1	3.53	9.72E-05
MPPED2	1103	77	3.52	5.78E-14
RP11-527L4.2	7	0	3.52	9.53E-05
HOXC-AS5	79	4	3.52	5.35E-09
GPR143	274	12	3.51	6.74E-06
SLC25A48	150	8	3.50	3.52E-06
CA12	2547	158	3.50	3.48E-08
AC009236.2	7	0	3.50	2.67E-05
DUSP9	340	19	3.49	2.75E-06
ASTN1	1129	46	3.49	2.45E-05
OXGR1	45	4	3.48	1.57E-08
PLAG1	2952	206	3.47	3.67E-10
RP11-649A16.1	52	3	3.47	3.88E-06
AC025627.7	23	2	3.47	3.25E-07
AC068057.1	7	0	3.47	7.06E-04
CLPSL2	16	1	3.47	2.14E-04
MTNR1A	8	0	3.47	3.87E-05
RP6-24A23.3	34	2	3.47	6.91E-07
MCF2	144	8	3.47	1.40E-06
CTA-150C2.13	53	2	3.47	3.49E-05
RP1-104O17.3	5	0	3.46	5.79E-04

CACNG8	435	24	3.45	1.04E-06
IGLON5	630	35	3.45	1.24E-06
CTD-2330J20.2	5	0	3.45	6.25E-04
MSX2	682	31	3.42	2.34E-05
ZIC1	4587	332	3.42	3.18E-09
RP11-966I7.2	32	3	3.42	4.60E-06
MSX2P1	19	1	3.42	2.55E-04
BCL11A	543	46	3.42	2.49E-12
HOXB-AS5	217	9	3.42	2.97E-04
BPIFB3	15	2	3.41	6.94E-05
SNTG2	60	5	3.41	1.04E-07
UNC93B2	6	0	3.41	9.20E-04
CAMKV	86	7	3.41	2.46E-13
RP11-364B14.3	31	1	3.41	2.71E-04
GDA	119	9	3.40	6.99E-06
C7orf62	5	0	3.40	8.84E-04
RP11-844P9.2	81	9	3.40	1.34E-07
GDF7	145	11	3.40	4.61E-08
PWRN1	62	2	3.39	3.55E-04
SLC6A11	53	4	3.38	2.67E-05
HS6ST3	6	0	3.38	9.84E-04
DSG2	1547	91	3.38	2.58E-06
AP001092.4	27	2	3.37	1.05E-05
LANCL3	129	10	3.37	1.03E-11
IRX4	155	8	3.37	6.28E-05
CYTL1	9736	590	3.37	4.76E-06
MAB21L1	1601	101	3.37	1.54E-06
RP11-429J17.5	8	0	3.36	5.10E-04
HOXB13	2989	164	3.36	1.26E-05
SLC38A4	125	9	3.36	1.30E-05
AC005077.7	7	0	3.36	9.90E-05
PLXNA4	1565	115	3.36	2.18E-10
DACT2	292	20	3.35	6.18E-08
CTD-3064M3.3	404	27	3.35	3.18E-07
AC133680.1	10	0	3.35	2.66E-04
PRSS50	231	12	3.35	9.07E-05
HTR2A	287	15	3.34	1.40E-05
FOXO1B	5	0	3.34	1.15E-03
RP11-186F10.2	9	0	3.34	1.55E-04
RP11-38H17.1	97	4	3.33	2.07E-04
GPM6A	385	33	3.33	4.16E-06
NRTN	82	8	3.33	5.73E-10
PAK7	20	2	3.33	1.45E-04
HOXA11	624	40	3.33	7.53E-07
RP11-168E14.1	23	1	3.33	4.58E-06
KCND2	177	11	3.32	1.92E-06
ELFN1	1291	102	3.31	1.73E-13

MAPK15	1006	70	3.31	4.00E-06
LRRC3B	90	7	3.31	6.99E-06
KCNJ3	59	3	3.31	5.10E-05
GLB1L3	240	17	3.31	1.40E-06
ANKRD62P1	4	0	3.31	1.30E-03
CRABP1	7413	213	3.31	6.74E-04
GPR144	30	3	3.31	7.64E-05
DIO3	888	36	3.30	2.28E-04
DIRAS2	83	6	3.30	6.21E-06
EBF3	3638	295	3.30	1.05E-09
GBX1	20	2	3.29	9.65E-07
RP11-1134I14.4	7	0	3.29	2.77E-04
DMBX1	72	8	3.29	9.16E-09
OGDHL	285	22	3.29	2.54E-06
IGDCC4	3453	251	3.29	1.38E-08
CHRM2	98	8	3.28	3.33E-05
KRTAP21-2	6	0	3.28	5.75E-04
UROC1	33	2	3.28	1.22E-04
SNX18P3	26	1	3.28	8.27E-05
AC004540.4	99	8	3.27	7.84E-06
LHX5	22	2	3.27	6.72E-05
ASS1	3684	296	3.27	1.38E-08
RP11-561C5.6	134	11	3.27	4.33E-06
RP11-91P17.1	5	0	3.26	1.81E-03
CPA6	182	12	3.26	2.97E-05
CTC-478M6.1	6	0	3.26	1.98E-03
AC018730.1	50	3	3.26	2.57E-05
CGB7	31	3	3.25	3.48E-08
CILP2	6044	328	3.25	5.77E-05
RP11-748L13.1	9	0	3.24	1.02E-03
NOTUM	225	17	3.24	3.53E-07
RYR1	1804	119	3.24	3.14E-06
GPER	884	72	3.24	1.66E-10
RP11-360I20.2	27	2	3.24	3.31E-04
NKD1	322	25	3.23	1.97E-08
NKAIN1P1	17	1	3.22	6.04E-04
DGCR5	203	18	3.22	1.38E-10
NXPH4	2467	162	3.21	8.38E-06
MSI1	328	27	3.21	4.85E-08
SAMD11	1366	114	3.21	2.12E-07
RP11-422P22.1	11	1	3.20	1.12E-03
NKD2	3045	282	3.20	7.12E-10
ROBO2	1423	81	3.20	1.03E-04
CTA-392E5.1	20	1	3.19	1.23E-03
CYP2W1	54	6	3.18	5.96E-07
AP000662.4	162	15	3.18	5.19E-09
C1orf145	238	20	3.18	8.89E-09

ZFHX4	10617	885	3.18	2.33E-08
FAM19A3	460	36	3.18	2.61E-06
ASXL3	280	20	3.18	2.69E-06
CTC-276P9.1	7	1	3.17	9.69E-04
TCEAL2	421	26	3.17	6.46E-04
NRG1	170	16	3.17	5.11E-07
PTX3	1804	123	3.17	1.30E-05
RP11-763B22.7	9	1	3.16	5.45E-04
TIMM8AP1	53	6	3.16	7.25E-06
C21orf88	14	1	3.16	5.31E-05
CTXN3	7	0	3.16	1.93E-03
IGSF9	370	29	3.15	3.88E-06
CTD-3064M3.1	6	1	3.15	9.12E-04
TTLL2	8	1	3.15	1.98E-04
CLDN19	112	6	3.15	1.26E-03
ADD2	840	81	3.14	3.84E-16
HMGA2	6265	487	3.14	2.85E-06
IGDCC3	548	36	3.13	5.17E-05
PROKR1	53	4	3.13	1.32E-04
EVX2	94	5	3.13	7.79E-04
RP1-104O17.1	5	0	3.12	1.36E-03
GRIK1	602	48	3.12	1.87E-06
SGCZ	52	3	3.12	1.30E-03
AC108025.2	8	0	3.12	1.55E-03
MIR199A2	14	1	3.12	1.20E-04
CECR2	235	19	3.12	1.51E-06
CTD-2062F14.3	16	1	3.12	1.03E-04
AC073316.1	13	2	3.11	4.13E-05
TLL2	646	52	3.11	2.71E-04
GABRG1	18	1	3.11	2.41E-04
AC140481.1	173	13	3.11	7.18E-05
CNTNAP4	111	5	3.11	9.41E-04
FAM108A7P	22	1	3.11	2.58E-05
TRIM72	34	3	3.10	5.39E-05
C20orf166-AS1	75	6	3.10	5.18E-06
SYN2	296	27	3.10	5.32E-09
FOXQ1	159	11	3.10	2.99E-05
LRRC4B	1370	116	3.09	1.14E-07
FGFR3	1142	103	3.09	4.04E-07
BMP4	1375	134	3.08	4.68E-12
ZNF556	18	1	3.08	8.37E-06
GOLGA8IP	35	3	3.08	2.83E-05
AHRR	417	35	3.08	1.23E-06
NPPC	598	28	3.08	1.03E-03
RP11-143E21.7	253	26	3.08	2.05E-05
TAS1R1	67	5	3.08	1.48E-05
RP1-170O19.20	9	0	3.08	9.22E-04

CTA-714B7.5	12	1	3.07	4.04E-04
LY6H	391	46	3.07	8.43E-06
SDR9C7	22	1	3.07	9.27E-04
FEZF2	9	0	3.07	1.53E-03
C16orf11	26	2	3.07	9.07E-05
NELL2	1074	104	3.07	3.28E-08
FGF10	1053	70	3.07	1.38E-04
LINC00533	3	0	3.07	4.43E-03
RPL29P19	90	9	3.06	6.09E-05
HOXD13	1670	126	3.06	1.30E-04
OBSCN	7036	568	3.06	2.49E-06
MOS	2	0	3.06	4.28E-03
RP11-117L5.4	4	0	3.06	4.49E-03
CHRNB4	41	2	3.06	1.41E-04
PDE9A	942	100	3.06	7.48E-12
COX6B2	96	7	3.06	2.99E-05
RP11-588P8.1	5	0	3.06	4.84E-03
PRHOXNB	3	0	3.05	4.73E-03
AC010984.3	5	0	3.05	2.33E-03
AC012065.7	289	35	3.04	2.70E-13
GABRE	5631	432	3.04	1.96E-05
RP11-116O18.1	30	4	3.04	2.89E-04
CDH3	1226	111	3.04	5.29E-07
FAM69C	434	32	3.04	1.35E-04
RP11-166A12.1	4	0	3.04	4.82E-03
KCNK4	3	0	3.04	2.92E-03
NOG	127	10	3.03	3.48E-05
BZRAP1	2222	193	3.03	6.78E-06
ELAVL4	282	27	3.03	4.53E-05
DMRTA2	444	27	3.02	7.95E-04
RGS2	15776	1568	3.02	8.93E-08
MIR4297	7	1	3.02	7.18E-04
KCNN1	243	22	3.01	8.08E-07
CTD-2319I12.1	240	23	3.00	1.18E-05
FOXG1	1186	74	3.00	7.22E-04
ARHGAP28	2856	265	3.00	4.49E-06
GADL1	21	2	3.00	2.13E-06
RP11-432J24.3	10	1	3.00	1.85E-04
FAM83F	2	25	-3.01	1.56E-04
TRBV5-1	1	13	-3.02	1.16E-06
RPL39P29	0	7	-3.02	6.64E-03
RP11-737O24.1	0	7	-3.05	5.13E-03
RP11-4G2.1	1	16	-3.06	4.32E-04
LINC00346	20	195	-3.09	4.98E-09
RP11-79E3.3	0	5	-3.12	3.75E-03
CTD-2374C24.1	0	6	-3.13	2.45E-03
RP11-173C20.2	40	424	-3.17	2.16E-09

RP11-279O17.2	0	3	-3.19	3.65E-03
OR2M4	0	5	-3.19	3.88E-03
RP11-11N5.1	0	9	-3.25	5.86E-04
AC011899.9	13	184	-3.32	1.33E-06
RP1-102K2.6	1	12	-3.39	6.28E-05
RP11-348J24.2	1	11	-3.47	3.97E-05
PANX3	1	24	-3.47	1.73E-05
NFYAP1	0	10	-3.50	3.38E-04
RP11-575F12.2	3	75	-3.58	2.36E-05
MAGEA2B	0	11	-3.66	2.52E-04
OR8Q1P	0	10	-3.77	1.25E-04
BMP8B	152	3175	-4.17	7.81E-24
RP11-521D12.1	0	14	-4.24	8.56E-07
OR8A1	0	19	-4.47	7.03E-07
RP11-6N13.1	0	15	-4.61	2.47E-07

Supplementary Table 6: Gene Ontology Analysis of Genes upregulated 8-fold, FDR<0.05 in PRC2 Lost Samples

Category	Term	Gene Count	% of list	Fold Enrichment	PValue	Benjamini FDR
UP_SEQ_FEATURE	DNA-binding region:Homeobox	33	9.65	10.25	7.12E-23	7.64E-20
SP_PIR_KEYWORDS	Homeobox	35	10.23	8.59	1.07E-21	3.12E-19
INTERPRO	IPR017970:Homeobox, conserved site	35	10.23	8.38	1.84E-21	9.61E-19
INTERPRO	IPR001356:Homeobox	34	9.94	8.03	2.88E-20	7.50E-18
SP_PIR_KEYWORDS	developmental protein	55	16.08	4.19	3.78E-19	5.50E-17
INTERPRO	IPR012287:Homeodomain-related	33	9.65	7.70	4.16E-19	7.23E-17
SMART	SM00389:HOX	34	9.94	6.88	1.14E-18	1.31E-16
GOTERM_BP_FAT	GO:0030182~neuron differentiation	37	10.82	4.68	1.64E-14	2.58E-11
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	43	12.57	3.85	6.37E-14	2.62E-11
GOTERM_MF_FAT	GO:0003700~transcription factor activity	50	14.62	2.79	6.01E-11	1.24E-08
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	64	18.71	2.30	1.77E-10	2.43E-08
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	26	7.60	4.70	2.74E-10	1.43E-07
GOTERM_BP_FAT	GO:0060173~limb development	16	4.68	8.61	4.26E-10	1.67E-07
GOTERM_BP_FAT	GO:0048736~appendage development	16	4.68	8.61	4.26E-10	1.67E-07
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	16	4.68	8.96	2.39E-10	1.88E-07
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	16	4.68	8.96	2.39E-10	1.88E-07
GOTERM_BP_FAT	GO:0001501~skeletal system development	26	7.60	4.52	6.09E-10	1.91E-07
GOTERM_BP_FAT	GO:0048666~neuron development	26	7.60	4.25	2.17E-09	4.85E-07
GOTERM_BP_FAT	GO:0030900~forebrain development	18	5.26	6.57	1.91E-09	5.00E-07
GOTERM_BP_FAT	GO:0051216~cartilage development	13	3.80	9.74	7.05E-09	1.38E-06
SP_PIR_KEYWORDS	glycoprotein	117	34.21	1.61	2.08E-08	2.02E-06
GOTERM_BP_FAT	GO:0007389~pattern specification process	22	6.43	4.57	1.46E-08	2.54E-06
GOTERM_BP_FAT	GO:0042471~ear morphogenesis	12	3.51	10.08	2.25E-08	3.53E-06
SP_PIR_KEYWORDS	cell membrane	71	20.76	1.92	7.70E-08	5.60E-06
SP_PIR_KEYWORDS	dna-binding	63	18.42	2.00	1.29E-07	7.53E-06
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	15	4.39	6.25	1.15E-07	1.64E-05
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	113	33.04	1.61	3.57E-08	1.92E-05
GOTERM_BP_FAT	GO:0007423~sensory organ development	19	5.56	4.60	1.64E-07	2.14E-05
SP_PIR_KEYWORDS	signal	91	26.61	1.66	4.70E-07	2.28E-05
GOTERM_BP_FAT	GO:0045165~cell fate commitment	15	4.39	5.98	2.00E-07	2.41E-05
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	12	3.51	7.65	4.22E-07	4.72E-05
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	12	3.51	7.65	4.22E-07	4.72E-05
GOTERM_BP_FAT	GO:0048568~embryonic organ development	16	4.68	5.16	4.83E-07	5.05E-05
GOTERM_BP_FAT	GO:0003002~regionalization	17	4.97	4.78	5.25E-07	5.15E-05
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	61	17.84	1.91	6.07E-07	5.60E-05
GOTERM_BP_FAT	GO:0031175~neuron projection development	19	5.56	4.11	8.57E-07	7.46E-05
GOTERM_BP_FAT	GO:0043583~ear development	12	3.51	7.00	1.04E-06	8.55E-05
UP_SEQ_FEATURE	compositionally biased region:Poly-Ala	24	7.02	3.60	2.66E-07	9.52E-05
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	61	17.84	1.87	1.29E-06	1.01E-04
GOTERM_BP_FAT	GO:0007409~axonogenesis	16	4.68	4.60	2.09E-06	1.56E-04
UP_SEQ_FEATURE	signal peptide	91	26.61	1.65	6.24E-07	1.67E-04
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	29	8.48	2.68	3.60E-06	2.56E-04
GOTERM_BP_FAT	GO:0045449~regulation of transcription	77	22.51	1.64	4.12E-06	2.69E-04
GOTERM_BP_FAT	GO:0007610~behavior	25	7.31	2.96	3.99E-06	2.72E-04
GOTERM_BP_FAT	GO:0001655~urogenital system development	12	3.51	6.05	4.47E-06	2.80E-04
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	12	3.51	5.94	5.33E-06	3.21E-04
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	16	4.68	4.24	5.58E-06	3.24E-04
GOTERM_CC_FAT	GO:0030425~dendrite	14	4.09	4.99	4.50E-06	3.42E-04
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	10	2.92	7.49	6.72E-06	3.63E-04
GOTERM_BP_FAT	GO:0042472~inner ear morphogenesis	9	2.63	8.91	6.52E-06	3.65E-04
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	16	4.68	4.16	6.99E-06	3.65E-04
GOTERM_CC_FAT	GO:0044459~plasma membrane part	66	19.30	1.74	3.28E-06	3.74E-04
GOTERM_CC_FAT	GO:0043005~neuron projection	20	5.85	3.40	6.70E-06	3.82E-04
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	17	4.97	3.86	8.54E-06	4.32E-04
GOTERM_CC_FAT	GO:0005886~plasma membrane	98	28.65	1.51	2.23E-06	5.08E-04
GOTERM_CC_FAT	GO:0045202~synapse	20	5.85	3.27	1.14E-05	5.20E-04
GOTERM_BP_FAT	GO:0009953~dorsal/ventral pattern formation	9	2.63	8.32	1.10E-05	5.41E-04
GOTERM_BP_FAT	GO:0001656~metanephros development	8	2.34	10.08	1.20E-05	5.72E-04
GOTERM_BP_FAT	GO:0007411~axon guidance	11	3.22	5.70	2.22E-05	9.95E-04
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	14	4.09	4.31	2.22E-05	0.00102288
GOTERM_BP_FAT	GO:0048732~gland development	12	3.51	4.93	3.16E-05	0.00137594
GOTERM_BP_FAT	GO:0001657~ureteric bud development	7	2.05	11.09	3.31E-05	0.00140273

GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	19	5.56	3.15	3.42E-05	0.00140928
GOTERM_BP_FAT	GO:0030030~cell projection organization	20	5.85	3.01	3.71E-05	0.00145383
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	16	4.68	3.62	3.68E-05	0.00147735
GOTERM_MF_FAT	GO:0042165~neurotransmitter binding	11	3.22	5.80	1.88E-05	0.00193749
GOTERM_CC_FAT	GO:0034702~ion channel complex	14	4.09	3.97	5.22E-05	0.0019833
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	16	4.68	3.47	6.11E-05	0.00233333
UP_SEQ_FEATURE	compositionally biased region:Ala-rich	13	3.80	5.01	1.16E-05	0.00249501
GOTERM_BP_FAT	GO:0048706~embryonic skeletal system development	9	2.63	6.48	6.98E-05	0.00260391
GOTERM_BP_FAT	GO:0048839~inner ear development	9	2.63	6.32	8.40E-05	0.00305699
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	11	3.22	4.80	9.67E-05	0.00343911
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	18	5.26	3.02	1.03E-04	0.00357131
INTERPRO	IPR003961:Fibronectin, type III	14	4.09	4.09	4.03E-05	0.00418596
SP_PIR_KEYWORDS	differentiation	21	6.14	2.71	1.10E-04	0.0045474
GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	10	2.92	5.72	6.00E-05	0.00493265
GOTERM_BP_FAT	GO:0044057~regulation of system process	17	4.97	3.05	1.49E-04	0.00506195
INTERPRO	IPR013098:Immunoglobulin I-set	12	3.51	4.83	3.95E-05	0.00513575
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	8	2.34	6.82	1.59E-04	0.0052817
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	20	5.85	2.68	1.75E-04	0.00558951
GOTERM_BP_FAT	GO:0035295~tube development	14	4.09	3.53	1.74E-04	0.0056594
UP_SEQ_FEATURE	topological domain:Cytoplasmic	87	25.44	1.52	3.36E-05	0.00599681
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	39	11.40	1.86	1.86E-04	0.00604027
SP_PIR_KEYWORDS	neurogenesis	11	3.22	4.47	1.83E-04	0.00663865
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	38	11.11	1.86	2.49E-04	0.00706707
SP_PIR_KEYWORDS	synapse	13	3.80	3.62	2.69E-04	0.00780144
GOTERM_MF_FAT	GO:0003677~DNA binding	67	19.59	1.56	1.15E-04	0.00786028
GOTERM_BP_FAT	GO:0002062~chondrocyte differentiation	5	1.46	15.40	2.55E-04	0.00796272
SP_PIR_KEYWORDS	disulfide bond	74	21.64	1.50	2.52E-04	0.00810702
SP_PIR_KEYWORDS	ionic channel	16	4.68	2.99	3.36E-04	0.00885792
GOTERM_BP_FAT	GO:0035115~embryonic forelimb morphogenesis	5	1.46	14.59	3.18E-04	0.0097412
SMART	SM00060:FN3	14	4.09	3.50	1.71E-04	0.00977239
SP_PIR_KEYWORDS	membrane	135	39.47	1.28	4.07E-04	0.00982282
GOTERM_BP_FAT	GO:0001822~kidney development	9	2.63	5.20	3.29E-04	0.00985965
GOTERM_MF_FAT	GO:0022836~gated channel activity	17	4.97	2.98	1.93E-04	0.01131749
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	11	3.22	4.95	7.84E-05	0.01194749
UP_SEQ_FEATURE	topological domain:Extracellular	72	21.05	1.56	9.71E-05	0.01294374
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	9	2.63	4.94	4.64E-04	0.01362919
GOTERM_BP_FAT	GO:0048704~embryonic skeletal system morphogenesis	7	2.05	6.81	5.33E-04	0.01535295
SP_PIR_KEYWORDS	Secreted	47	13.74	1.65	7.49E-04	0.01546103
SP_PIR_KEYWORDS	cleavage on pair of basic residues	14	4.09	3.07	7.05E-04	0.01566289
GOTERM_BP_FAT	GO:0060675~ureteric bud morphogenesis	5	1.46	12.60	5.76E-04	0.01628855
GOTERM_BP_FAT	GO:0001658~branching involved in ureteric bud morphogenesis	5	1.46	12.60	5.76E-04	0.01628855
GOTERM_BP_FAT	GO:0035136~forelimb morphogenesis	5	1.46	12.60	5.76E-04	0.01628855
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	53	15.50	1.58	6.22E-04	0.01725733
GOTERM_BP_FAT	GO:0030902~hindbrain development	7	2.05	6.47	7.03E-04	0.01915297
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	17	4.97	2.65	7.15E-04	0.01915563
GOTERM_BP_FAT	GO:0030850~prostate gland development	4	1.17	20.16	8.49E-04	0.02231996
SP_PIR_KEYWORDS	cell junction	17	4.97	2.53	0.00123834	0.02375208
GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	10	2.92	3.96	9.55E-04	0.02388171
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	36	10.53	1.78	9.25E-04	0.02390333
GOTERM_BP_FAT	GO:0042733~embryonic digit morphogenesis	5	1.46	11.09	9.55E-04	0.0242527
GOTERM_BP_FAT	GO:0021537~telencephalon development	7	2.05	5.97	0.00107624	0.02644482
GOTERM_CC_FAT	GO:0005576~extracellular region	53	15.50	1.53	0.00118348	0.02663802
SP_PIR_KEYWORDS	deafness	8	2.34	4.75	0.00148835	0.02672596
KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	13	3.80	3.31	4.02E-04	0.02697881
GOTERM_CC_FAT	GO:0044456~synapse part	13	3.80	3.07	0.00109957	0.02748634
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	7	2.05	5.79	0.00126218	0.03046914
SP_PIR_KEYWORDS	ion transport	21	6.14	2.16	0.00192353	0.03064749
SP_PIR_KEYWORDS	egf-like domain	12	3.51	3.10	0.00182526	0.03078871
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	24	7.02	2.07	0.00133633	0.03174331
GOTERM_BP_FAT	GO:0021915~neural tube development	7	2.05	5.71	0.00136389	0.03190484
GOTERM_BP_FAT	GO:0006811~ion transport	27	7.89	1.95	0.00140087	0.03227509
GOTERM_BP_FAT	GO:0007631~feeding behavior	7	2.05	5.62	0.00147174	0.03245304
GOTERM_BP_FAT	GO:0001759~induction of an organ	4	1.17	17.06	0.00143297	0.03252557
GOTERM_BP_FAT	GO:0042474~middle ear morphogenesis	4	1.17	17.06	0.00143297	0.03252557
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	14	4.09	2.81	0.00146415	0.03274854
GOTERM_MF_FAT	GO:0004983~neuropeptide Y receptor activity	4	1.17	21.73	6.64E-04	0.03361149

GOTERM_MF_FAT	GO:0005216~ion channel activity	18	5.26	2.53	7.69E-04	0.03462465
INTERPRO	IPR006209:EGF	10	2.92	4.37	4.78E-04	0.03493408
GOTERM_BP_FAT	GO:0060348~bone development	9	2.63	4.06	0.00168746	0.03611196
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	16	4.68	2.53	0.00167725	0.03639358
GOTERM_CC_FAT	GO:0034703~cation channel complex	9	2.63	3.96	0.00195418	0.03648358
INTERPRO	IPR000611:Neuropeptide Y receptor	4	1.17	24.68	4.44E-04	0.03780991
GOTERM_BP_FAT	GO:0006937~regulation of muscle contraction	7	2.05	5.39	0.00183454	0.03867333
GOTERM_BP_FAT	GO:0021978~telencephalon regionalization	3	0.88	41.58	0.00188264	0.03914245
GOTERM_CC_FAT	GO:0042995~cell projection	24	7.02	2.00	0.00195354	0.03972072
SP_PIR_KEYWORDS	neurotransmitter receptor	6	1.75	6.25	0.00265356	0.03987844
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	23	6.73	2.04	0.00198556	0.04070129
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	10	2.92	4.54	3.70E-04	0.04315423
GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	18	5.26	2.46	0.00108101	0.04358334
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	17	4.97	2.37	0.00221844	0.04478692
GOTERM_CC_FAT	GO:0014701~junctional sarcoplasmic reticulum membrane	3	0.88	34.86	0.00282439	0.04839532
GOTERM_BP_FAT	GO:0060021~palate development	5	1.46	8.66	0.00245972	0.04891371
SP_PIR_KEYWORDS	transcription regulation	51	14.91	1.49	0.00346557	0.04925718
UP_SEQ_FEATURE	disulfide bond	71	20.76	1.49	4.89E-04	0.0511736
GOTERM_BP_FAT	GO:0001654~eye development	9	2.63	3.78	0.00262999	0.05156241
GOTERM_BP_FAT	GO:0060350~endochondral bone morphogenesis	4	1.17	13.86	0.0026963	0.05217813
GOTERM_MF_FAT	GO:0005261~cation channel activity	14	4.09	2.77	0.00170126	0.05253262
GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	18	5.26	2.37	0.00160425	0.05363157
GOTERM_BP_FAT	GO:0007268~synaptic transmission	14	4.09	2.60	0.00288661	0.05508413
GOTERM_CC_FAT	GO:0030054~cell junction	19	5.56	2.13	0.00351139	0.05567621
GOTERM_BP_FAT	GO:0050801~ion homeostasis	17	4.97	2.30	0.00299593	0.05642781
GOTERM_MF_FAT	GO:0015267~channel activity	18	5.26	2.37	0.00156246	0.05688481
GOTERM_BP_FAT	GO:0019229~regulation of vasoconstriction	5	1.46	8.15	0.00308455	0.05736272
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	16	4.68	2.37	0.0031637	0.05810549
GOTERM_BP_FAT	GO:0050877~neurological system process	36	10.53	1.65	0.00326328	0.05919017
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	16	4.68	2.33	0.00366642	0.06551436
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	9	2.63	4.38	0.00104237	0.06566426
GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	9	2.63	3.85	0.00233835	0.0665751
GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	9	2.63	3.85	0.00233835	0.0665751
INTERPRO	IPR003598:Immunoglobulin subtype 2	12	3.51	3.25	0.00122456	0.06847464
SP_PIR_KEYWORDS	DNA binding	14	4.09	2.44	0.00519551	0.069639
GOTERM_BP_FAT	GO:0060284~regulation of cell development	11	3.22	2.97	0.00397142	0.06998383
GOTERM_BP_FAT	GO:0030001~metal ion transport	18	5.26	2.15	0.0043742	0.07596848
GOTERM_BP_FAT	GO:0045168~cell-cell signaling involved in cell fate specification	4	1.17	11.67	0.00448393	0.07695307
GOTERM_BP_FAT	GO:0031128~developmental induction	4	1.17	11.67	0.00448393	0.07695307
GOTERM_BP_FAT	GO:0006940~regulation of smooth muscle contraction	5	1.46	7.30	0.00464251	0.07787193
GOTERM_BP_FAT	GO:0060351~cartilage development involved in endochondral bone morphogenesis	3	0.88	27.72	0.00459584	0.07795019
GOTERM_BP_FAT	GO:0048589~developmental growth	7	2.05	4.46	0.00474809	0.07873557
GOTERM_BP_FAT	GO:0007517~muscle organ development	11	3.22	2.89	0.00486158	0.0797044
SP_PIR_KEYWORDS	growth factor	8	2.34	3.63	0.00669538	0.08148399
SP_PIR_KEYWORDS	osteogenesis	4	1.17	10.32	0.00647663	0.08235695
GOTERM_BP_FAT	GO:0042462~eye photoreceptor cell development	4	1.17	11.09	0.00520598	0.08424204
GOTERM_BP_FAT	GO:0060349~bone morphogenesis	4	1.17	11.09	0.00520598	0.08424204
SP_PIR_KEYWORDS	ectodermal dysplasia	4	1.17	9.89	0.00731102	0.08512858
GOTERM_BP_FAT	GO:0051480~cytosolic calcium ion homeostasis	8	2.34	3.76	0.00539638	0.0854379
GOTERM_BP_FAT	GO:0006928~cell motion	18	5.26	2.10	0.00539402	0.0862702
GOTERM_BP_FAT	GO:0007507~heart development	11	3.22	2.84	0.00553757	0.08670683
GOTERM_CC_FAT	GO:0030424~axon	9	2.63	3.29	0.00608178	0.0885561
GOTERM_BP_FAT	GO:0040007~growth	10	2.92	3.03	0.00584798	0.09045402
GOTERM_BP_FAT	GO:0021532~neural tube patterning	4	1.17	10.56	0.005994	0.09171086
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	4	1.17	10.56	0.005994	0.09171086
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	23	6.73	1.86	0.00605639	0.09173135
GOTERM_BP_FAT	GO:0010941~regulation of cell death	26	7.60	1.77	0.00622776	0.09331177
SP_PIR_KEYWORDS	transmembrane	104	30.41	1.24	0.00840779	0.09360533
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	20	5.85	1.97	0.00639977	0.09486765
GOTERM_BP_FAT	GO:0007218~neuropeptide signaling pathway	7	2.05	4.17	0.00655969	0.09622181
SMART	SM00353:HLH	9	2.63	3.75	0.0026381	0.09630275

Supplementary Table 7: Gene Set Enrichment Analysis of the MPNST Expression Profile between PRC2 loss and intact samples with FDR <0.001

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
MEISSNER_BRAIN_HCP_WITH_H3K27ME3	266	0.70	3.34	0	0
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	428	0.65	3.26	0	0
ORKIN_PRC_MODULE	432	0.64	3.24	0	0
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	337	0.65	3.22	0	0
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	127	0.73	3.18	0	0
DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN	179	0.69	3.17	0	0
NIKOLSKY_BREAST_CANCER_8Q23_Q24_AMPLICON	153	0.71	3.13	0	0
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN	74	0.80	3.12	0	0
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3	343	0.64	3.12	0	0
RICKMAN_HEAD_AND_NECK_CANCER_A	96	0.71	2.93	0	0
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	139	0.66	2.91	0	0
MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	141	0.65	2.86	0	0
KONG_E2F3_TARGETS	97	0.67	2.78	0	0
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP	87	0.67	2.78	0	0
MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	209	0.60	2.77	0	0
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	148	0.63	2.76	0	0
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP	321	0.57	2.75	0	0
CROONQUIST_NRAS_SIGNALING_DN	72	0.71	2.75	0	0
CROONQUIST_IL6_DEPRIVATION_DN	98	0.67	2.74	0	0
CUI_TCF21_TARGETS_2_UP	420	0.55	2.74	0	0
MEISSNER_NPC_HCP_WITH_H3K4ME2	487	0.54	2.73	0	0
CORRE_MULTIPLE_MYELOMA_DN	60	0.72	2.73	0	0
MEISSNER_NPC_HCP_WITH_H3K27ME3	79	0.67	2.70	0	0
ISHIDA_E2F_TARGETS	52	0.73	2.69	0	0
LEE_EARLY_T_LYMPHOCYTE_UP	104	0.64	2.68	0	0
WHITEFORD_PEDIATRIC_CANCER_MARKERS	116	0.63	2.67	0	0
LI_WILMS_TUMOR	27	0.84	2.66	0	0
MARKEY_RB1_ACUTE_LOF_DN	227	0.58	2.66	0	0
AMUNDSON_GAMMA_RADIATION_RESPONSE	40	0.76	2.65	0	0
KUNINGER_IGF1_VS_PDGFB_TARGETS_UP	82	0.66	2.64	0	0
CHANG_CYCLING_GENES	146	0.59	2.59	0	0
JAEGER_METASTASIS_DN	255	0.54	2.58	0	0
KANG_DOXORUBICIN_RESISTANCE_UP	54	0.70	2.58	0	0
MIKKELSEN_IPS_WITH_HCP_H3K27ME3	101	0.62	2.58	0	0
DURAND_STROMA_MAX_UP	294	0.53	2.58	0	0
MISSIAGLIA_REGULATED_BY_METHYLATION_DN	119	0.60	2.55	0	0
REACTOME_NCAM1_INTERACTIONS	39	0.73	2.53	0	0
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	83	0.62	2.52	0	0
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	87	0.62	2.52	0	0
WHITFIELD_CELL_CYCLE_LITERATURE	44	0.69	2.52	0	0
PLASARI_TGFB1_TARGETS_10HR_DN	243	0.53	2.51	0	0
SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN	423	0.50	2.50	0	0
WANG_MLL_TARGETS	285	0.52	2.50	0	0
FARMER_BREAST_CANCER_CLUSTER_2	33	0.74	2.50	0	0
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	125	0.58	2.49	0	0
FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	50	0.68	2.48	0	0

CATION_CHANNEL_ACTIVITY	118	0.58	2.47	0	0
HOELZEL_NF1_TARGETS_DN	108	0.59	2.47	0	0
CAHOY_NEURONAL	99	0.59	2.46	0	0
SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER	86	0.61	2.46	0	0
NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP	20	0.85	2.46	0	0
BLUM_RESPONSE_TO_SALIRASIB_DN	341	0.50	2.45	0	0
NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP	19	0.83	2.45	0	0
SKELETAL_DEVELOPMENT	102	0.58	2.44	0	0
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	172	0.54	2.42	0	0
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP	180	0.54	2.42	0	0
REACTOME_COLLAGEN_FORMATION	58	0.64	2.42	0	0
SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_IN_CANCER	27	0.76	2.42	0	0
RB_P107_DN.V1_UP	139	0.55	2.41	0	0
VERNELL_RETINOBLASTOMA_PATHWAY_UP	70	0.62	2.41	0	0
MEL18_DN.V1_DN	144	0.55	2.39	0	0
HATADA_METHYLATED_IN_LUNG_CANCER_UP	384	0.48	2.38	0	0
WONG_ENDMETRIUM_CANCER_DN	81	0.59	2.38	0	0
LY_AGING_MIDDLE_DN	16	0.85	2.36	0	0
PID_WNT_SIGNALING_PATHWAY	28	0.74	2.36	0	0
MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	84	0.59	2.36	0	0
ZHANG_TLX_TARGETS_60HR_DN	275	0.50	2.36	0	0
GSE19825_NAIVE_VS_DAY3_EFF_CD8_TCELL_UP	197	0.52	2.35	0	0
LE_EGR2_TARGETS_UP	108	0.55	2.35	0	0
ZHAN_MULTIPLE_MYELOMA_PR_UP	44	0.65	2.35	0	0
KOBAYASHI_EGFR_SIGNALING_24HR_DN	247	0.50	2.34	0	0
NERVOUS_SYSTEM_DEVELOPMENT	381	0.47	2.34	0	0
REACTOME_STRIATED_MUSCLE_CONTRACTION	27	0.74	2.34	0	0
CAIRO_LIVER_DEVELOPMENT_UP	164	0.52	2.32	0	1.42E-05
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	271	0.49	2.33	0	1.44E-05
MEISSNER_BRAIN_HCP_WITH_H3K4ME2_AND_H3K27ME3	57	0.63	2.33	0	1.46E-05
STAEGE_EWING_FAMILY_TUMOR	33	0.69	2.28	0	2.49E-05
JAATINEN_HEMATOPOIETIC_STEM_CELL_UP	305	0.47	2.28	0	2.52E-05
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN	162	0.51	2.29	0	2.55E-05
WONG_EMBRYONIC_STEM_CELL_CORE	334	0.47	2.30	0	2.58E-05
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	184	0.51	2.30	0	2.61E-05
SHEPARD_BMYB_MORPHOLINO_DN	197	0.50	2.30	0	2.64E-05
DAWSON_METHYLATED_IN_LYMPHOMA_TCL1	59	0.61	2.30	0	2.67E-05
BOQUEST_STEM_CELL_UP	260	0.48	2.30	0	2.71E-05
GATED_CHANNEL_ACTIVITY	121	0.54	2.30	0	2.74E-05
PRC2_EZH2_UP.V1_UP	187	0.51	2.31	0	2.78E-05
LY_AGING_PREMATURE_DN	30	0.72	2.31	0	2.81E-05
GSE13485_DAY7_VS_DAY21_YF17D_VACCINE_PBMC_DN	160	0.52	2.31	0	2.85E-05
WU_APOPTOSIS_BY_CDKN1A_VIA_TP53	55	0.61	2.27	0	5.74E-05
DELYS_THYROID_CANCER_DN	230	0.48	2.27	0	5.80E-05
BURTON_ADIPOGENESIS_3	101	0.55	2.27	0	5.86E-05
EGUCHI_CELL_CYCLE_RB1_TARGETS	23	0.74	2.27	0	5.92E-05
SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	39	0.65	2.27	0	5.99E-05
GSE15750_DAY6_VS_DAY10_EFF_CD8_TCELL_UP	198	0.49	2.27	0	6.06E-05
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	26	0.73	2.27	0	6.12E-05

CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN	99	0.55	2.25	0	6.62E-05
NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_DN	18	0.78	2.26	0	6.69E-05
RHODES_UNDIFFERENTIATED_CANCER	69	0.58	2.26	0	6.76E-05
MORI_IMMATURE_B_LYMPHOCYTE_DN	90	0.55	2.27	0	6.83E-05
REACTOME_NEURONAL_SYSTEM	276	0.47	2.24	0	7.36E-05
ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN	301	0.46	2.24	0	7.43E-05
BURTON_ADIPOGENESIS_PEAK_AT_24HR	43	0.64	2.25	0	7.51E-05
CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN	164	0.50	2.25	0	7.58E-05
METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	145	0.51	2.25	0	7.66E-05
REN_ALVEOLAR_RHABDOMYOSARCOMA_UP	98	0.53	2.24	0	8.12E-05
SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN	56	0.60	2.24	0	8.20E-05
RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP	233	0.48	2.24	0	8.27E-05
LE_NEURONAL_DIFFERENTIATION_DN	19	0.77	2.24	0	8.35E-05
KONDO_PROSTATE_CANCER_HCP_WITH_H3K27ME3	95	0.54	2.23	0	8.96E-05
TANG_SENESCENCE_TP53_TARGETS_DN	57	0.59	2.23	0	9.04E-05
SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_2	47	0.62	2.22	0	9.70E-05
E2F3_UP.V1_UP	182	0.49	2.23	0	9.79E-05
VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	66	0.58	2.23	0	9.88E-05
WNT_SIGNALING	89	0.54	2.22	0	1.06E-04
GSE19825_NAIVE_VS_IL2RALOW_DAY3_EFF_CD8_TCELL_UP	196	0.48	2.21	0	1.24E-04
SHEPARD_CRUSH_AND_BURN_MUTANT_DN	180	0.49	2.21	0	1.42E-04
ION_CHANNEL_ACTIVITY	147	0.50	2.20	0	1.57E-04
GSE30962_PRIMARY_VS_SECONDARY_ACUTE_LCMV_INF_CD8_TCELL_UP	197	0.48	2.20	0	1.59E-04
HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_UP	77	0.55	2.20	0	1.67E-04
BMI1_DN_MEL18_DN.V1_DN	143	0.50	2.20	0	1.68E-04
VECCHI_GASTRIC_CANCER_EARLY_UP	415	0.44	2.20	0	1.70E-04
YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN	257	0.46	2.20	0	1.71E-04
RPS14_DN.V1_DN	183	0.48	2.20	0	1.73E-04
KANG_AR_TARGETS_UP	17	0.78	2.20	0	1.74E-04
OXFORD_RALA_OR_RALB_TARGETS_UP	48	0.61	2.20	0	1.80E-04
DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN	68	0.56	2.20	0	1.82E-04
KEGG_CARDIAC_MUSCLE_CONTRACTION	73	0.55	2.20	0	1.83E-04
SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY	154	0.49	2.19	0	1.96E-04
MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN	56	0.59	2.19	0	2.02E-04
GSE15750_DAY6_VS_DAY10_TRAF6KO_EFF_CD8_TCELL_UP	196	0.48	2.19	0	2.08E-04
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	64	0.57	2.19	0	2.09E-04
AMINE_RECEPTOR_ACTIVITY	34	0.65	2.19	0	2.22E-04
POTASSIUM_CHANNEL_ACTIVITY	50	0.59	2.18	0	2.54E-04
KRAS.600.LUNG.BREAST_UP.V1_DN	282	0.45	2.18	0	2.58E-04
LIU_PROSTATE_CANCER_DN	469	0.43	2.18	0	2.60E-04
LEE_TARGETS_OF_PTCH1_AND_SUFU_DN	83	0.54	2.18	0	2.60E-04
PETROVA_PROX1_TARGETS_UP	28	0.68	2.18	0	2.62E-04
BRIDEAU_IMPRINTED_GENES	62	0.57	2.18	0	2.64E-04

HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN	47	0.61	2.17	0	2.65E-04
ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN	45	0.62	2.17	0	2.67E-04
ESC_V6.5_UP_LATE.V1_UP	188	0.48	2.17	0	2.68E-04
WANG_LSD1_TARGETS_UP	24	0.72	2.17	0	2.70E-04
HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP	163	0.48	2.17	0	2.72E-04
GSE15750_WT_VS_TRAF6KO_DAY10_EFF_CD8_TCELL_DN	197	0.47	2.17	0	2.72E-04
KATSANOU_ELAVL1_TARGETS_DN	147	0.49	2.17	0	2.74E-04
ZHANG_TLX_TARGETS_UP	89	0.54	2.17	0	2.74E-04
KRAS.KIDNEY_UP.V1_UP	141	0.49	2.16	0	2.76E-04
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	135	0.50	2.17	0	2.76E-04
NIELSEN_SYNOVIAL_SARCOMA_UP	18	0.75	2.16	0	2.77E-04
REN_BOUND_BY_E2F	61	0.57	2.17	0	2.78E-04
POTASSIUM_ION_TRANSPORT	57	0.59	2.17	0	2.78E-04
MIKKELSEN_ES_ICP_WITH_H3K27ME3	41	0.62	2.16	0	2.79E-04
PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP	56	0.59	2.16	0	2.81E-04
JACKSON_DNMT1_TARGETS_DN	25	0.68	2.16	0	2.81E-04
SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN	22	0.72	2.16	0	2.83E-04
VOLTAGE_GATED_POTASSIUM_CHANNEL_COMPLEX	40	0.63	2.16	0	2.93E-04
BMI1_DN.V1_DN	140	0.49	2.16	0	2.94E-04
PLASARI_NFIC_TARGETS_BASAL_UP	27	0.67	2.16	0	2.96E-04
SMITH_LIVER_CANCER	45	0.61	2.16	0	2.98E-04
LEE_NEURAL_CREST_STEM_CELL_DN	117	0.50	2.15	0	2.99E-04
CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP	141	0.49	2.15	0	3.04E-04
VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	18	0.75	2.15	0.002227	3.22E-04
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	15	0.79	2.15	0	3.32E-04
GSE8515_IL1_VS_IL6_4H_STIM_)MAC_DN	193	0.47	2.15	0	3.34E-04
KAMMINGA_EZH2_TARGETS	41	0.63	2.15	0	3.36E-04
RIZ_ERYTHROID_DIFFERENTIATION	77	0.54	2.14	0	3.37E-04
BEIER_GLIOMA_STEM_CELL_UP	35	0.64	2.14	0	3.39E-04
GSE13485_CTRL_VS_DAY21_YF17D_VACCINE_PBMC_DN	162	0.48	2.14	0	3.41E-04
VOLTAGE_GATED_CHANNEL_ACTIVITY	73	0.55	2.14	0	3.48E-04
SONG_TARGETS_OF_IE86_CMV_PROTEIN	60	0.57	2.13	0	3.69E-04
MARKEY_RB1_CHRONIC_LOF_UP	114	0.51	2.13	0	3.71E-04
LY_AGING_OLD_DN	56	0.57	2.13	0	3.74E-04
ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CHROMATIN_ARCHITECTURE	77	0.53	2.13	0	3.76E-04
PEREZ_TP63_TARGETS	341	0.44	2.13	0	3.78E-04
TSENG_ADIPOGENIC_POTENTIAL_DN	46	0.60	2.13	0	3.86E-04
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	18	0.75	2.13	0	3.96E-04
WALLACE_JAK2_TARGETS_UP	25	0.68	2.13	0	4.06E-04
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	86	0.52	2.13	0	4.20E-04
RUIZ_TNC_TARGETS_DN	139	0.49	2.13	0	4.22E-04
GHANDHI_DIRECT_IRRADIATION_DN	33	0.64	2.13	0	4.27E-04
RIZ_ERYTHROID_DIFFERENTIATION_CCNE1	40	0.61	2.13	0	4.29E-04
GSE10325_MYELOID_VS_LUPUS_MYELOID_UP	194	0.46	2.12	0	4.81E-04
KEGG_CALCIUM_SIGNALING_PATHWAY	176	0.48	2.12	0	4.84E-04
SHEPARD_BMYB_TARGETS	71	0.54	2.11	0	5.44E-04

VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN	137	0.49	2.11	0	5.47E-04
RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN	28	0.66	2.11	0	5.50E-04
FUJII_YBX1_TARGETS_DN	197	0.47	2.11	0	5.82E-04
MODY_HIPPOCAMPUS_PRENATAL	42	0.60	2.10	0	6.27E-04
REICHERT_MITOSIS_LIN9_TARGETS	28	0.65	2.10	0	6.30E-04
HEART_DEVELOPMENT	37	0.62	2.10	0	6.33E-04
KEGG_BASAL_CELL_CARCINOMA	55	0.57	2.10	0	6.35E-04
MEISSNER_BRAIN_HCP_WITH_H3K4ME2	16	0.74	2.10	0	6.36E-04
ZHAN_MULTIPLE_MYELOMA_MS_UP	47	0.58	2.10	0	6.37E-04
RIZ_ERYTHROID_DIFFERENTIATION_12HR	43	0.59	2.10	0	6.37E-04
ASTON_MAJOR_DEPRESSIVE_DISORDER_UP	48	0.57	2.10	0	6.37E-04
EXTRACELLULAR_MATRIX	99	0.50	2.10	0	6.38E-04
METAL_ION_TRANSPORT	116	0.49	2.10	0	6.39E-04
TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_UP	20	0.72	2.10	0	6.41E-04
CALCIUM_CHANNEL_ACTIVITY	33	0.63	2.09	0	6.61E-04
SANSOM_APC_TARGETS_UP	123	0.49	2.09	0	6.79E-04
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	22	0.70	2.09	0	6.87E-04
SENESE_HDAC1_TARGETS_DN	243	0.44	2.09	0	6.89E-04
THEODOROU_MAMMARY_TUMORIGENESIS	31	0.64	2.09	0	7.00E-04
CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	211	0.46	2.09	0	7.02E-04
PTEN_DN.V2_DN	141	0.48	2.09	0	7.04E-04
AUXILIARY_TRANSPORT_PROTEIN_ACTIVITY	25	0.67	2.08	0	7.66E-04
PEREZ_TP53_AND_TP63_TARGETS	199	0.45	2.08	0	8.04E-04
BIOCARTA_ALK_PATHWAY	37	0.60	2.07	0	8.08E-04
BRAIN_DEVELOPMENT	51	0.57	2.08	0	8.11E-04
SYNAPTIC_TRANSMISSION	172	0.46	2.07	0	8.12E-04
LIM_MAMMARY_LUMINAL_MATURE_DN	98	0.49	2.07	0	8.20E-04
BONCI_TARGETS_OF_MIR15A_AND_MIR16_1	91	0.51	2.07	0	8.31E-04
VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	15	0.76	2.07	0	8.43E-04
RIZ_ERYTHROID_DIFFERENTIATION_6HR	40	0.60	2.07	0	8.49E-04
RIZ_ERYTHROID_DIFFERENTIATION_HBZ	41	0.59	2.07	0	8.65E-04
KEGG_AXON_GUIDANCE	128	0.48	2.07	0	8.71E-04
PID_FOXM1PATHWAY	40	0.59	2.06	0	9.37E-04
KAUFFMANN_MELANOMA_RELAPSE_UP	61	0.54	2.06	0	9.38E-04
MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3	135	0.47	2.06	0	9.49E-04
TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	43	0.57	2.06	0	9.54E-04
PROTEINACEOUS_EXTRACELLULAR_MATRIX	98	0.50	2.05	0	9.99E-04
REGULATION_OF_NEUROTRANSMITTER_LEVELS	24	0.67	2.05	0	1.00E-03
AMINE_BINDING	23	0.68	2.05	0	0.001

Supplementary Table 8: Primer sequences for human RT-PCR and ChIP

RT-PCR Primer	**Sequence**
CDX2 F	CGGCAGCCAAGTGAAAACC
CDX2 R	CTCCGGATGGTGATGTAGCG
IGF2 F	TCGCCGAACCAAAGTGGATT
IGF2 R	GGGGCAGAGATAGTGGGAGA
TLX1 F	AGGCGCTCAAAATGACCGAT
TLX1 R	ACAAGCCGTTACCTCCACTT
PAX2 F	CAGGAATGGTGCCTGGGAG
PAX2 R	TTAGTAAGGCGGGGTTGCTG
ESX1 F	AACTTACCGTGACCTCGCTG
ESX1 R	TCCGTGCCAACGTTGTTTTC
POU4F1 F	CGGTAGGACTTGGCTGTGAG
POU4F1 R	TGTTTTCGCCCAACATGCAG
HMX2 F	CAGCCTGTCCGTGTCCTC
HMX2 R	CTTGGGGGTACCCAGGCA
FOXN4 F	CGTACAGCTGTCTGATCGCC
FOXN4 R	GGAGCCGCTCATCTTGTTCT
BCL11Av1E2 F	ATGATGAACCAGACCACGGC
BCL11Av1E2 R	CGATTGGTGAAGGGGAAGGT
WIF1 F	CCAGCCGTCTAAACGGGAA
WIF1 R	CTGCCGGGAAAACTCCTCG
DSC3 F	GCTGGTGAAGCCTGCAAAAA
DSC3 R	TCTGCAGACCTGAAGCACTC
CDH8 F	CCGAGAGGCATGAACGGAAT
CDH8 R	AAATTTCTCTTGTGGGGCCCTG
RPL27 F	CATGGGCAAGAAGAAGATCG
RPL27 R	TCCAAGGGGATATCCACAGA

ChIP Primer	**Sequence**
IGF2 ChIP F	GGGGCAGAGATAGTGGGAGA
IGF2 ChIP R	TCTGTTTCTCTCCGTGCTGT
TLX1 ChIP F	GACCAGATCCTCAACAGCCC
TLX1 ChIP R	TATTCTCCGTCCTGGAGGC
PAX2 ChIP F	GGCTTGCAGAACAAATGCCA
PAX2 ChIP R	TCTGGAGTTCTCCCTCCCTG
ESX1 ChIP F	CTTCCGTGCCAACGTTGTTT
ESX1 ChIP R	TTACCGTGACCTCGCTGATG
HMX2 ChIP F	CACCTTCCACCCAGATCACC
HMX2 ChIP R	CCTTGCCCGCATCTTCTTTG
FOXN4 ChIP F	TCAGAAATGCCACAAGCCCT
FOXN4 ChIP R	CAGTGTTTGTGTGTTGCGGG
WIF1 ChIP F	AGAGGAGGACATAGGCAGGG
WIF1 ChIP R	GATGCTCACCAGGCAAGAGT
CDH8 ChIP F	GCCTGCCTGCCAAATGTAAC
CDH8 ChIP R	CCAATGAGATCCGTCAGGGG
GAPDH ChIP F	TACTAGCGGTTTTACGGGCG
GAPDH ChIP R	TCGAACAGGAGGAGCAGAGAGCGA

Supplementary Note

Biospecimens were collected during surgical resection from patients with pathologic diagnosis of malignant peripheral nerve sheath tumors or neurofibromas. Material was collected under IRB-approved protocols (IRB#06-107) at Memorial Sloan-Kettering Cancer Center (New York, NY). All patients provided informed consent. Pathologic diagnosis was confirmed by at least two pathologists using diagnostic formalin-fixed and paraffin-embedded (FFPE) sections to select cases with estimated tumor content of >70%. The majority of the tumors are collected from different patients. In some cases, more than one tumor was selected from the same patient and these tumors were resected from distinct anatomical locations in different surgeries.