Supplementary Information

Whole exome sequencing identifies a recurrent *NAB2-STAT6* fusion in solitary fibrous tumors

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Supplementary Methods

Tumor Collection

Material was collected under IRB-approved protocols at Memorial Sloan-Kettering Cancer Center (New York, NY) and Oregon Health and Science University Biolibrary (Portland OR). All patients provided informed consent. Cryomolds prepared from tumor specimens were macrodissected, when possible, to minimize contamination by normal and necrotic tissue prior to DNA preparation. Sample processing was carried out in accordance with IRB-approved protocols at the Broad Institute designed to secure samples and minimize identifying information.

Whole Exome Sequencing

100 ng of tumor and normal DNA was subjected to shearing, end repair, phosphorylation and ligation to barcoded sequencing adaptors. The ligated DNA was size-selected for fragments between 200-350 bp. These fragments underwent exonic hybrid capture with SureSelect v2 Exome bait (Agilent). The captured DNA was multiplexed and sequenced on multiple Illumina HiSeq flowcells to an average coverage of 98x per sample. Sequence data used for this analysis are available in dbGaP under accession number phs000568.v1.p1.

Mutation, Copy Number, and Fusion Analysis

Exome analysis was performed using Broad Institute pipelines.[1-3] The “Firehose” pipeline was used to manage input and output files and submit analyses for execution in GenePattern.[4] In brief, MuTect and MutSig algorithms were used to call somatic mutations and determine their statistical significance, respectively.[5,6] Small somatic insertions and deletions were detected using the Indelocator algorithm after local realignment of tumor and normal sequences. Copy number analysis was performed using the CapSeg for Capture algorithm (McKenna et al., in preparation).[7] The dRanger and BreakPointer algorithms were used to identify somatic fusions and their breakpoints.[3]

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Fusion Analysis and Validation

Genomic fusions were validated with primer sets designed for each unique breakpoint (**see Supplementary Table 5**). For cDNA validation, 50 ng of total RNA was reverse transcribed into cDNA using SuperScript III and random hexamer primers (Invitrogen) according to the manufacturer's instructions. The *NAB2-STAT6* fusion was amplified using 2 independent sets of M13 tagged breakpoint-spanning primers (**see Supplementary Table 5**). *GAPDH* was amplified using cDNA transcribed in the presence (+RT) and absence (-RT) of reverse transcriptase and exon-spanning primers (**see Supplementary Table 5**).

All PCR reactions were performed with HotStarTaq Master Mix (QIAGEN) and standard cycling conditions (95°C for 15m, 35 cycles of 94°C for 30s, 60°C for 30s, 72°C for 1m and final extension at 72°C for 10m). PCR product was confirmed by 1% agarose gel electrophoresis. Excess primers and dNTPS were removed using ExoSAP-IT Reagent (USB Corporation) according to the manufacturer's instructions prior to direct sequencing at GeneWiz.

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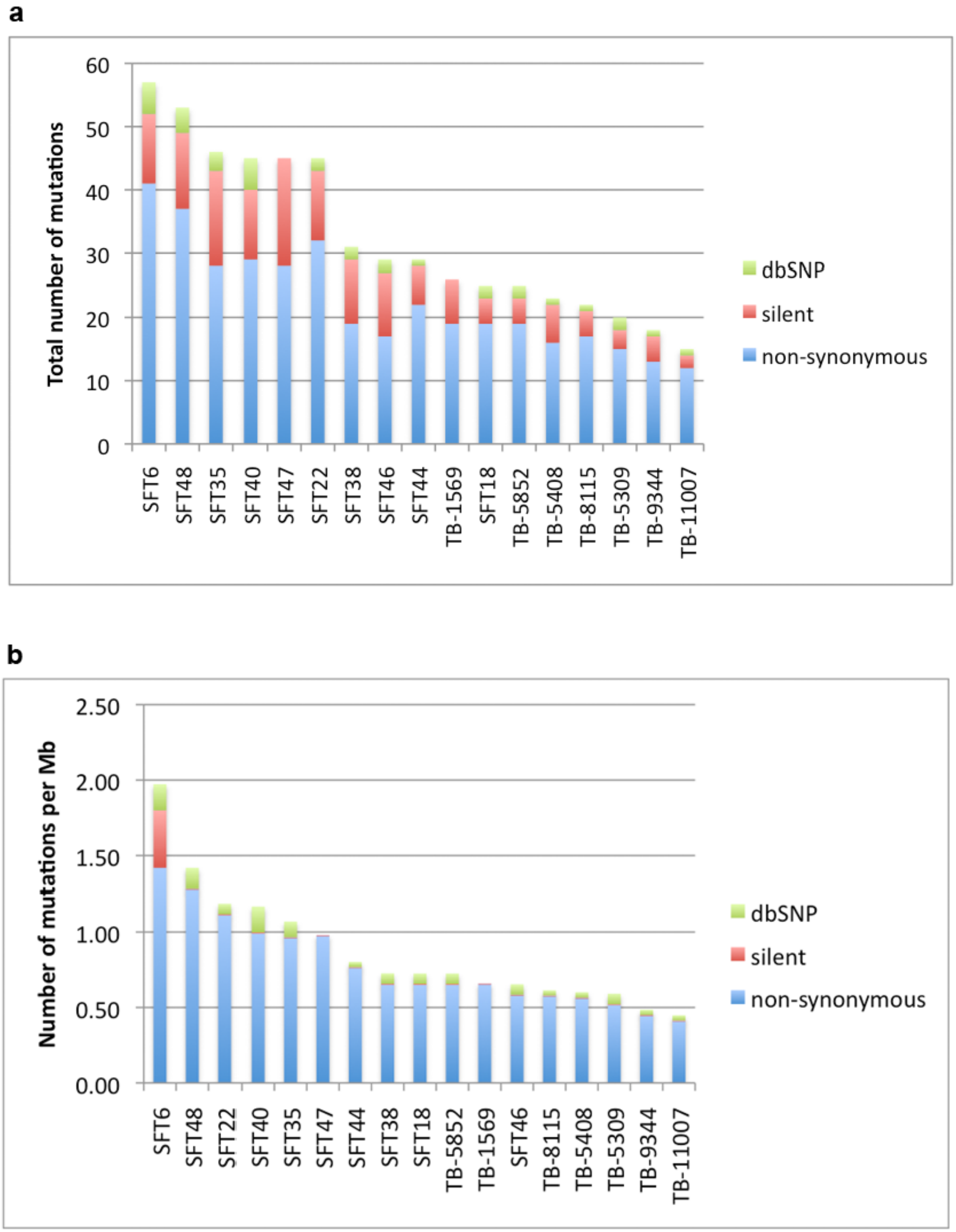
Supplementary Figure 1: Mutation rate in SFT. (**a**) Total number of mutations identified in each sample sorted by non-synonymous (missense), silent, and dbSNP, out of a median of 29 megabases covered by exome capture. (**b**) The mutation rate across all tumors graphed as mutations per megabase (Mb) of DNA.



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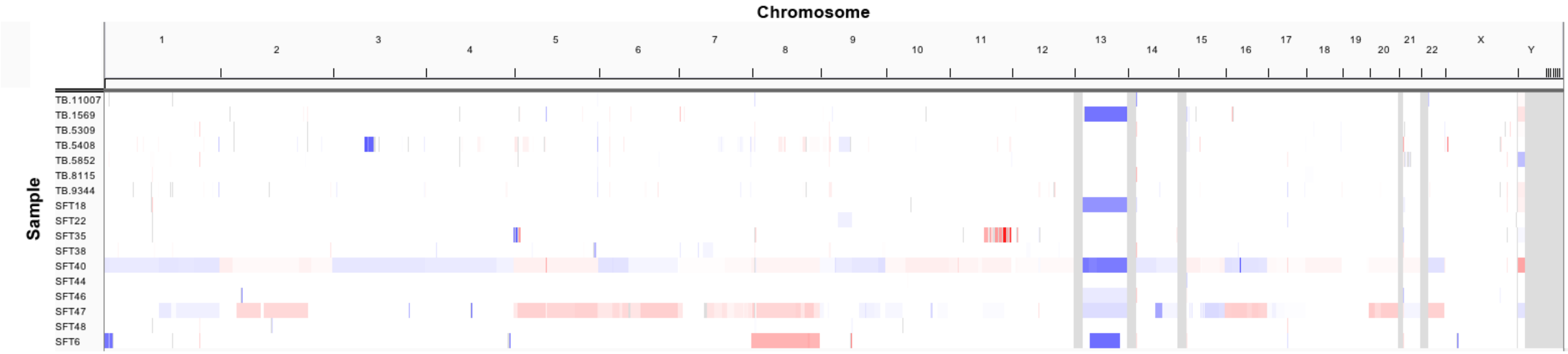
Supplementary Figure 2: Copy number profiles from whole exome sequencing. Read counts were converted into segmentation files for display in Integrated Genomics Viewer (IGV). Of note, broad loss of chromosome 13 is observed in 6 samples, and broad amplification of chromosome 8 is observed in 2 samples.



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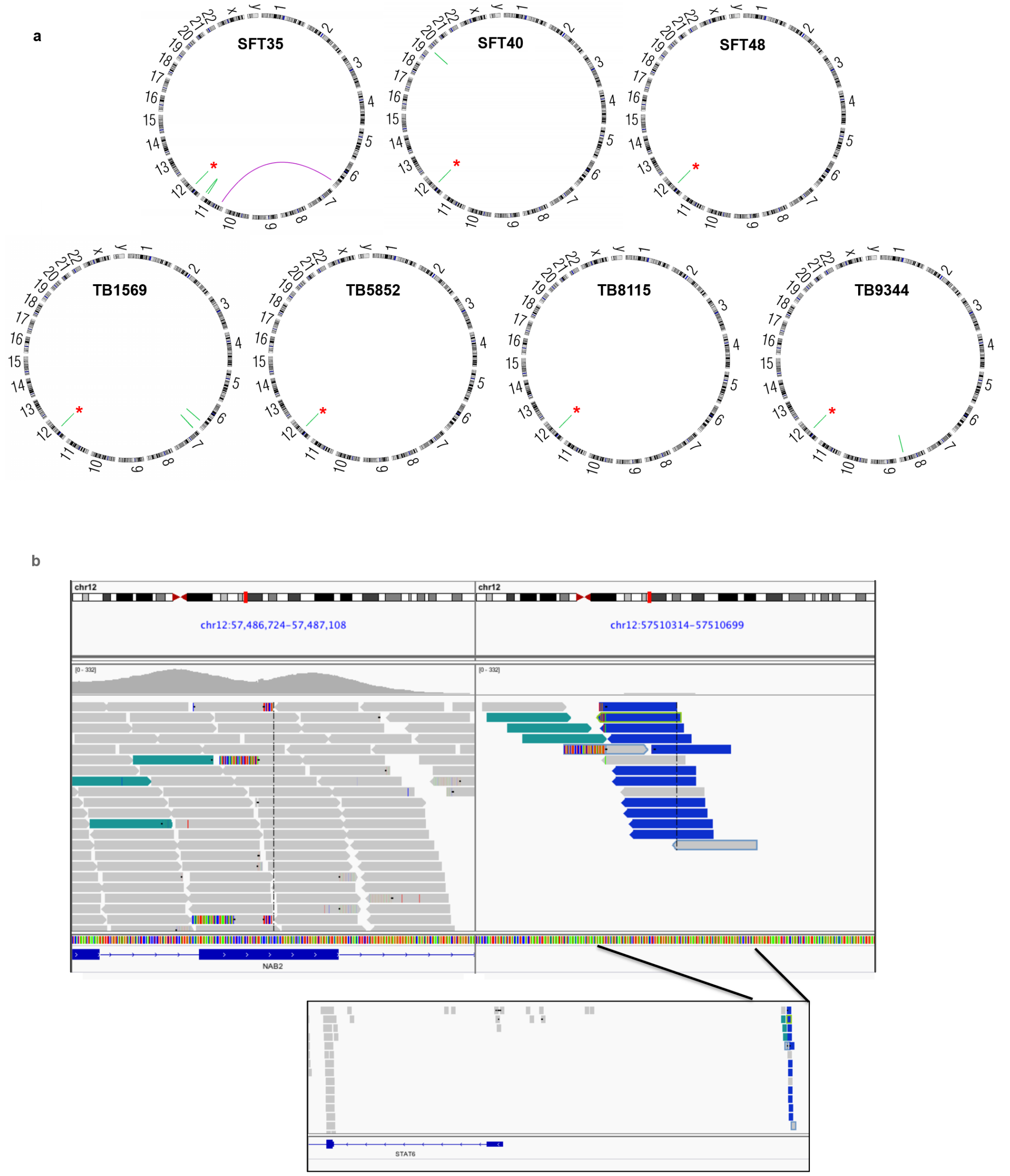
Supplementary Figure 3: Identification of the *NAB2-STAT6* fusion from whole exome sequencing. (**a**) Circos plots showing rearrangements identified from dRanger analysis of whole exome data. The *NAB2-STAT6* inversion is starred (*). (**b**) Split screen showing representative mate pairs mapping to different regions of the genome. For context, the bottom panel shows the location of the *STAT6* reads in relation to the transcription start site (blue exons). Dark blue and green sequences correspond to read pairs mapped in the reverse orientation compared to the reference. Gray bars correspond to sequences that align to the reference genome. Mismatched bases (in the case of reads spanning the breakpoint) are indicated by multi-color strips.



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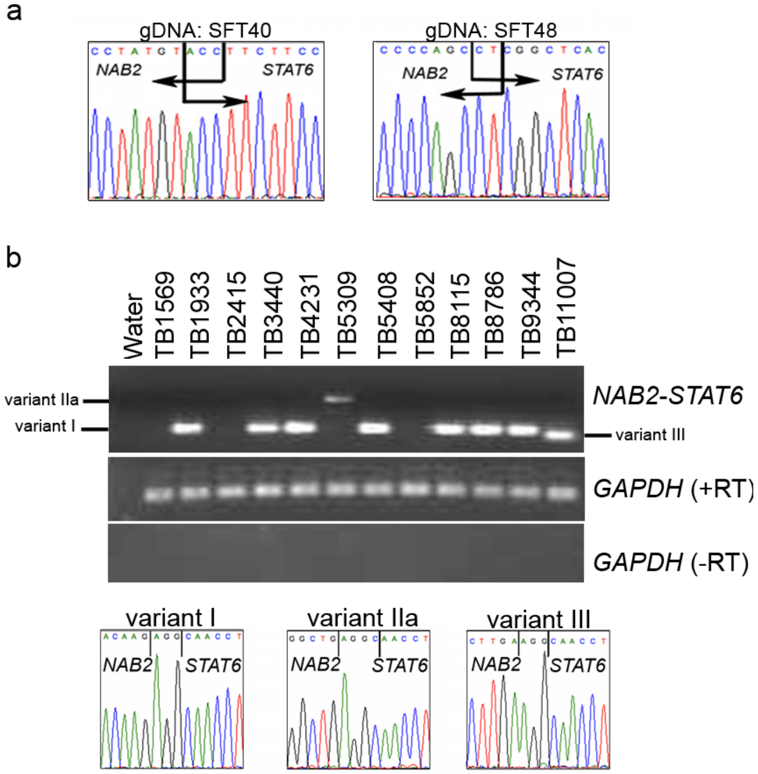
Supplementary Figure 4: Validation of the *NAB2-STAT6* fusion. (**a**) Chromatograms showing the genomic sequence of *NAB2-STAT6* in two representative tumors. (**b**) Representative RT-PCR products and sequencing chromatograms of three *NAB2-STAT6* fusion variants.



Supplementary Table 1: Sample and patient characteristics

Sample	Platform	Age	Gender	Race	Histology	Tumor percent	Tumor type	Site	NAB2-STAT6 Fusion (Variant)
SFT6	WES/RT-PCR	70	Female	unknown	solitary fibrous tumor	100	N/A	pelvis	Y (variant I)
SFT18	WES	67	Female	unknown	solitary fibrous tumor	100	N/A	pelvis	N
SFT22	WES/RT-PCR	55	Male	unknown	solitary fibrous tumor	100	N/A	meningeal	N
SFT35	WES/RT-PCR	69	Female	unknown	solitary fibrous tumor	100	N/A	chest	Y (variant I)
SFT38	WES/RT-PCR	31	Male	unknown	solitary fibrous tumor	100	N/A	pelvis	N
SFT40-1*	WES/RT-PCR	70	Male	unknown	solitary fibrous tumor	100	N/A	chest	Y (variant I)
SFT40-2*	RT-PCR	70	Male	unknown	solitary fibrous tumor	N/A	N/A	chest	Y (variant I)
SFT40-3*	RT-PCR	70	Male	unknown	solitary fibrous tumor	N/A	N/A	chest	Y (variant I)
SFT40-4*	RT-PCR	70	Male	unknown	solitary fibrous tumor	N/A	N/A	chest	Y (variant I)
SFT44	WES/RT-PCR	29	Male	unknown	solitary fibrous tumor	100	N/A	meningeal	N
SFT46	WES	59	Female	unknown	solitary fibrous tumor	100	N/A	flank	N
SFT47	WES/RT-PCR	36	Male	unknown	solitary fibrous tumor	100	N/A	meningeal	N
SFT48-1*	WES/RT-PCR	81	Female	unknown	solitary fibrous tumor	100	N/A	chest	Y (variant I)
SFT48-2*	RT-PCR	81	Female	unknown	solitary fibrous tumor	N/A	N/A	chest	Y (variant I)
SFT8239	RT-PCR	80	Female	White	solitary fibrous tumor	N/A	primary	extremity	Y (variant I)
SFT8207	RT-PCR	78	Female	Black	solitary fibrous tumor	N/A	primary	chest	Y (variant I)
SFT2365	RT-PCR	79	Male	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT2242	RT-PCR	80	Female	White	solitary fibrous tumor	N/A	primary	pelvis	Y (variant I)
SFT4558	RT-PCR	59	Female	White	solitary fibrous tumor	N/A	primary	pelvis	N
SFT7096	RT-PCR	50	Female	White	solitary fibrous tumor	N/A	primary	pelvis	N
SFT4338	RT-PCR	58	Female	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT5183	RT-PCR	51	Male	Indian	solitary fibrous tumor	N/A	recurrent	chest	Y (variant I)
SFT0295	RT-PCR	35	Female	White	solitary fibrous tumor	N/A	primary	extremity	Y (variant IIb)

SFT2631	RT-PCR	57	Male	White	solitary fibrous tumor	N/A	primary	chest	Y (variant I)
SFT0191	RT-PCR	78	Female	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT0261	RT-PCR	88	Male	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT5776	RT-PCR	48	Female	White	solitary fibrous tumor	N/A	primary	abdomen	N
SFT9821	RT-PCR	50	Male	White	solitary fibrous tumor	N/A	primary	abdomen	N
SFT4566	RT-PCR	44	Male	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT0577-1*	RT-PCR	42	Male	White	solitary fibrous tumor	N/A	recurrent	abdomen	N
SFT0577-2*	RT-PCR	42	Male	White	solitary fibrous tumor	N/A	recurrent	abdomen	N
SFT8959	RT-PCR	73	Female	unknown	solitary fibrous tumor	N/A	primary	extremity	N
SFT2702	RT-PCR	12	Male	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT7187	RT-PCR	64	Male	White	solitary fibrous tumor	N/A	primary	extremity	N
SFT3612	RT-PCR	63	Male	White	solitary fibrous tumor	N/A	primary	chest	N
SFT8567	RT-PCR	48	Male	Black	solitary fibrous tumor	N/A	primary	chest	Y (variant I)
SFT1271	RT-PCR	57	Male	Black	solitary fibrous tumor	N/A	primary	abdomen	Y (variant I)
SFT9491	RT-PCR	59	Female	White	solitary fibrous tumor	N/A	primary	flank	N
SFT3144	RT-PCR	77	Male	White	solitary fibrous tumor	N/A	primary	chest	Y (variant I)
SFT7834	RT-PCR	31	Male	White	solitary fibrous tumor	N/A	primary	extremity	Y (variant IV)
SFT1000	RT-PCR	27	Male	White	solitary fibrous tumor	N/A	primary	pelvis	N
TB-1569	WES/RT-PCR	42	Male	White	solitary fibrous tumor	100	primary	Prostate, NOS	Y (variant VI; WES)
TB-1933	RT-PCR	46	Male	Hispanic	solitary fibrous tumor	95	primary	Lung, NOS	Y (variant I)
TB-2415	RT-PCR	52	Female	White	solitary fibrous tumor	90	primary	Soft tissue, NOS	N
TB-3440	RT-PCR	75	Male	White	solitary fibrous tumor	95	primary	Pleura	Y (variant I)
TB-4231	RT-PCR	77	Male	White	solitary fibrous tumor	100	primary	Lung, NOS	Y (variant I)
TB-5309	WES/RT-PCR	45	Female	White	solitary fibrous tumor	100	primary	Soft tissue, NOS	Y (variant IIa)
TB-5408	WES/RT-PCR	65	Male	White	solitary fibrous tumor	90	primary	Soft tissue, NOS	Y (variant I)

TB-5852	WES/RT-PCR	78	Male	Unknown	solitary fibrous tumor	100	primary	Peritoneum	Y (variant V; WES)
TB-8115	WES/RT-PCR	65	Female	White	solitary fibrous tumor	60	primary	Soft tissue, NOS	Y (variant I)
TB-8786	RT-PCR	65	Male	White	solitary fibrous tumor	70	primary	Lung, NOS	Y (variant I)
TB-9344	WES/RT-PCR	49	Female	White	solitary fibrous tumor	50	primary	Lung, NOS	Y (variant I)
TB-11007	WES/RT-PCR	54	Female	White	solitary fibrous tumor	90	primary	Soft tissue, NOS	Y (variant III)

NOS: not otherwise specified
WES: whole exome sequencing
RT-PCR: reverse-transcription polymerase chain reaction
N/A: not available
*Samples from the same patient

Supplemetary Table 2: List of mutated genes in SFT

rank	gene	description	Number of bases sequenced	number of non-synonmyous mutations	number of patients	number of mutation sites	q-value (False Discovery Rate: Benjamini-Hochberg procedure)
1	RBPJ	recombination signal binding protein for immunoglobulin kappa J region	26280	2	2	1	0.0011
2	NPEPPS	aminopeptidase puromycin sensitive	30597	2	2	1	0.111
3	OR10S1	olfactory receptor, family 10, subfamily S, member 1	16919	1	1	1	0.662
4	OR56A1	olfactory receptor, family 56, subfamily A, member 1	16337	1	1	1	0.662
5	OR6K6	olfactory receptor, family 6, subfamily K, member 6	17612	1	1	1	0.662
6	KLF1	Kruppel-like factor 1 (erythroid)	6813	1	1	1	0.662
7	ECD	ecdysoneless homolog (Drosophila)	33567	1	1	1	0.662
8	ZNF621	zinc finger protein 621	18906	1	1	1	0.662
9	OR4C16	olfactory receptor, family 4, subfamily C, member 16	15736	1	1	1	0.662
10	RAB2A	RAB2A, member RAS oncogene family	10556	1	1	1	0.662
11	CHRFAM7A	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) fusion	8730	1	1	1	0.662
12	MKRN3	makorin, ring finger protein, 3	25531	2	2	2	0.676
13	OR4D6	olfactory receptor, family 4, subfamily D, member 6	16114	1	1	1	0.756
14	SLAMF1	signaling lymphocytic activation molecule family member 1	17504	1	1	1	0.762
15	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	3655	1	1	1	0.762
16	CNPY4	canopy 4 homolog (zebrafish)	13090	1	1	1	0.762
17	COL1A1	collagen, type I, alpha 1	67078	2	2	2	0.762
18	H1FOO	H1 histone family, member O, oocyte-specific	8813	1	1	1	0.762
19	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	19787	1	1	1	0.762
20	MRGPRX1	MAS-related GPR, member X1	16509	1	1	1	0.762
21	OR4N4	olfactory receptor, family 4, subfamily N, member 4	16114	1	1	1	0.762
22	RGPD3	RANBP2-like and GRIP domain containing 3	53054	2	2	2	0.762
23	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	20650	1	1	1	0.762
24	ANGPT2	angiopoietin 2	25948	1	1	1	0.762
25	MS4A6E	membrane-spanning 4-domains, subfamily A, member 6E	7752	1	1	1	0.762
26	STOM	stomatin	14109	1	1	1	0.762
27	GLYAT	glycine-N-acyltransferase	15553	1	1	1	0.762
28	FGA	fibrinogen alpha chain	44381	1	1	1	0.762
29	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	10797	1	1	1	0.762
30	PRDM12	PR domain containing 12	12588	1	1	1	0.762
31	ULK3	unc-51-like kinase 3 (C. elegans)	12519	1	1	1	0.762
32	STX7	syntaxin 7	13962	1	1	1	0.762
33	MRPL52	mitochondrial ribosomal protein L52	6116	1	1	1	0.762
34	SHISA3	shisa homolog 3 (Xenopus laevis)	7927	1	1	1	0.762
35	TEX10	testis expressed 10	47600	1	1	1	0.762

36	KRT26	keratin 26	24034	1	1	1	0.765
37	HCFC2	host cell factor C2	40489	2	2	2	0.765
38	SH3D19	SH3 domain containing 19	41334	1	1	1	0.765
39	KCTD5	potassium channel tetramerisation domain containing 5	9464	1	1	1	0.765
40	OR10H3	olfactory receptor, family 10, subfamily H, member 3	16201	1	1	1	0.765
41	TAF1L	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	93235	2	2	2	0.765
42	ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	18969	1	1	1	0.775
43	ACSL3	acyl-CoA synthetase long-chain family member 3	37282	1	1	1	0.775
44	LTB	lymphotoxin beta (TNF superfamily, member 3)	9181	1	1	1	0.822
45	SIRPB2	signal-regulatory protein beta 2	17826	1	1	1	0.872
46	ZNF208	zinc finger protein 208	60397	2	2	2	0.872
47	ZNF878	zinc finger protein 878	26178	1	1	1	0.897
48	SYT14	synaptotagmin XIV	29040	1	1	1	0.897
49	PTH2R	parathyroid hormone 2 receptor	28820	1	1	1	0.897
50	PCDH11Y	protocadherin 11 Y-linked	29162	1	1	1	0.897
51	ZNF768	zinc finger protein 768	27531	1	1	1	0.897
52	ZNF727	zinc finger protein 727	8779	1	1	1	0.897
53	COX7B2	cytochrome c oxidase subunit VIIb2	4248	1	1	1	0.905
54	KIAA1486		28016	2	2	2	0.905
55	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	53728	1	1	1	0.905
56	PERP	PERP, TP53 apoptosis effector	10025	1	1	1	0.914
57	PJA2	praja 2, RING-H2 motif containing	36649	1	1	1	0.958
58	ATP7A	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	78033	1	1	1	0.958
59	SETD2	SET domain containing 2	106783	2	2	2	0.958
60	NANOS3	nanos homolog 3 (Drosophila)	8807	1	1	1	0.958
61	DHRS4	dehydrogenase/reductase (SDR family) member 4	12944	1	1	1	0.958
62	UNC13B	unc-13 homolog B (C. elegans)	82953	1	1	1	0.958
63	APBB3	amyloid beta (A4) precursor protein-binding, family B, member 3	25986	1	1	1	0.97
64	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	87265	1	1	1	0.97
65	BPIL2	bactericidal/permeability-increasing protein-like 2	26608	1	1	1	0.97
66	CD3G	CD3g molecule, gamma (CD3-TCR complex)	8773	1	1	1	0.97
67	ENC1	ectodermal-neural cortex (with BTB-like domain)	30158	1	1	1	0.97
68	SF3A2	splicing factor 3a, subunit 2, 66kDa	11397	1	1	1	0.97
69	KIAA1715	KIAA1715	22270	1	1	1	0.97
70	CPXM1	carboxypeptidase X (M14 family), member 1	32825	1	1	1	0.97
71	ANXA13	annexin A13	19074	1	1	1	0.97
72	EFCAB7	EF-hand calcium binding domain 7	32522	1	1	1	0.97
73	POTEH	POTE ankyrin domain family, member H	15404	1	1	1	0.97
74	CALCA	calcitonin-related polypeptide alpha	10234	1	1	1	0.97
75	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	41836	1	1	1	0.97
76	KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	11948	1	1	1	0.97

77	FRG1	FSHD region gene 1	13775	1	1	1	0.97
78	IL28B	interleukin 28B (interferon, lambda 3)	8746	1	1	1	0.97
79	LGI1	leucine-rich, glioma inactivated 1	28979	1	1	1	0.97
80	ITLN1	intelectin 1 (galactofuranose binding)	16490	1	1	1	0.97
81	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	43214	1	1	1	0.97
82	NKTR	natural killer-tumor recognition sequence	74865	1	1	1	0.985
83	KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1	20127	1	1	1	1
84	POTEG	POTE ankyrin domain family, member G	18487	1	1	1	1
85	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	13304	1	1	1	1
86	ULK4	unc-51-like kinase 4 (C. elegans)	66754	1	1	1	1
87	RFX6	regulatory factor X, 6	46979	1	1	1	1
88	ABR	active BCR-related gene	43143	1	1	1	1
89	MYH4	myosin, heavy chain 4, skeletal muscle	101448	1	1	1	1
90	ZBTB33	zinc finger and BTB domain containing 33	33994	1	1	1	1
91	SPPL2B	signal peptide peptidase like 2B	19603	1	1	1	1
92	NRBP1	nuclear receptor binding protein 1	28446	1	1	1	1
93	CWC25	CWC25 spliceosome-associated protein homolog (S. cerevisiae)	18256	1	1	1	1
94	NBPF9	neuroblastoma breakpoint family, member 9	43001	1	1	1	1
95	ST7L	suppression of tumorigenicity 7 like	29791	1	1	1	1
96	ARV1	ARV1 homolog (S. cerevisiae)	14083	1	1	1	1
97	SYNJ2BP	synaptojanin 2 binding protein	7718	1	1	1	1
98	CCNY	cyclin Y	16625	1	1	1	1
99	TBKBP1	TBK1 binding protein 1	15913	1	1	1	1
100	PRB2	proline-rich protein BstNI subfamily 2	21117	1	1	1	1
101	RBP1	retinol binding protein 1, cellular	7469	1	1	1	1
102	KIRREL	kin of IRRE like (Drosophila)	32866	1	1	1	1
103	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	14613	1	1	1	1
104	WNT5A	wingless-type MMTV integration site family, member 5A	14232	1	1	1	1
105	C12orf53	chromosome 12 open reading frame 53	9190	1	1	1	1
106	NMUR2	neuromedin U receptor 2	21486	1	1	1	1
107	WNT10B	wingless-type MMTV integration site family, member 10B	16632	1	1	1	1
108	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	22525	1	1	1	1
109	LPCAT2	lysophosphatidylcholine acyltransferase 2	26630	1	1	1	1
110	TSGA10IP	testis specific, 10 interacting protein	18369	1	1	1	1
111	NCL	nucleolin	36584	1	1	1	1
112	TH1L	TH1-like (Drosophila)	30426	1	1	1	1
113	C6	complement component 6	48766	1	1	1	1
114	SCGN	secretagogin, EF-hand calcium binding protein	14849	1	1	1	1
115	RNF182	ring finger protein 182	12716	1	1	1	1
116	GFM1	G elongation factor, mitochondrial 1	37908	1	1	1	1
117	FXR2	fragile X mental retardation, autosomal homolog 2	24030	1	1	1	1

118	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	12358	1	1	1	1
119	PCLO	piccolo (presynaptic cytomatrix protein)	244839	2	2	2	1
120	C20orf72	chromosome 20 open reading frame 72	17865	1	1	1	1
121	OR2T33	olfactory receptor, family 2, subfamily T, member 33	15636	1	1	1	1
122	HEPHL1	hephaestin-like 1	54664	1	1	1	1
123	MYO5C	myosin VC	90851	1	1	1	1
124	C10orf118	chromosome 10 open reading frame 118	45663	1	1	1	1
125	RELL2	RELT-like 2	15893	1	1	1	1
126	HOXB2	homeobox B2	16360	1	1	1	1
127	EPDR1	ependymin related protein 1 (zebrafish)	15122	1	1	1	1
128	GALT	galactose-1-phosphate uridylyltransferase	20126	1	1	1	1
129	TMEM181	transmembrane protein 181	24661	1	1	1	1
130	KLHL38	kelch-like 38 (Drosophila)	29880	1	1	1	1
131	RXFP1	relaxin/insulin-like family peptide receptor 1	39737	1	1	1	1
132	SOAT2	sterol O-acyltransferase 2	22157	1	1	1	1
133	PCM1	pericentriolar material 1	74140	1	1	1	1
134	IRS4	insulin receptor substrate 4	63212	2	2	2	1
135	SLC17A2	solute carrier family 17 (sodium phosphate), member 2	22964	1	1	1	1
136	ZNF845	zinc finger protein 845	48080	1	1	1	1
137	CAPN5	calpain 5	29887	1	1	1	1
138	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	10392	1	1	1	1
139	PRSS22	protease, serine, 22	13729	1	1	1	1
140	PADI3	peptidyl arginine deiminase, type III	33969	1	1	1	1
141	TXNDC6	thioredoxin domain containing 6	14039	1	1	1	1
142	ATP9A	ATPase, class II, type 9A	53527	1	1	1	1
143	QTRT1	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)	18722	1	1	1	1
144	SETX	senataxin	136141	1	1	1	1
145	VN1R2	vomeronasal 1 receptor 2	15771	1	1	1	1
146	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	32941	1	1	1	1
147	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	26081	1	1	1	1
148	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	29019	1	1	1	1
149	C12orf66	chromosome 12 open reading frame 66	22897	1	1	1	1
150	CLSPN	claspin homolog (Xenopus laevis)	68247	1	1	1	1
151	STX8	syntaxin 8	11458	1	1	1	1
152	CTSG	cathepsin G	13292	1	1	1	1
153	USP49	ubiquitin specific peptidase 49	30693	1	1	1	1
154	CDH5	cadherin 5, type 2, VE-cadherin (vascular epithelium)	38285	1	1	1	1
155	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	16822	1	1	1	1
156	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	19601	1	1	1	1
157	FES	feline sarcoma oncogene	38258	1	1	1	1
158	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	14741	1	1	1	1
159	ZNF831	zinc finger protein 831	75062	1	1	1	1

160	TPTE	transmembrane phosphatase with tensin homology	29567	1	1	1	1
161	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	38368	1	1	1	1
162	SFRP2	secreted frizzled-related protein 2	14515	1	1	1	1
163	LOC649330		15062	1	1	1	1
164	LASS4	LAG1 homolog, ceramide synthase 4	19269	1	1	1	1
165	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	16382	1	1	1	1
166	ZFP42	zinc finger protein 42 homolog (mouse)	15899	1	1	1	1
167	C2orf85		21891	1	1	1	1
168	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	40862	1	1	1	1
169	OR8D4	olfactory receptor, family 8, subfamily D, member 4	15977	1	1	1	1
170	DSG1	desmoglein 1	54563	1	1	1	1
171	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	11987	1	1	1	1
172	KCNH8	potassium voltage-gated channel, subfamily H (eag-related), member 8	57340	1	1	1	1
173	HIF1AN	hypoxia-inducible factor 1, alpha subunit inhibitor	16837	1	1	1	1
174	PARM1	prostate androgen-regulated mucin-like protein 1	15574	1	1	1	1
175	MTMR14	myotubularin related protein 14	31188	1	1	1	1
176	SLC45A2	solute carrier family 45, member 2	27433	1	1	1	1
177	CCKBR	cholecystokinin B receptor	22227	1	1	1	1
178	LYPD3	LY6/PLAUR domain containing 3	17360	1	1	1	1
179	RPUSD2	RNA pseudouridylate synthase domain containing 2	22797	1	1	1	1
180	ZNF814	zinc finger protein 814	27373	1	1	1	1
181	OXTR	oxytocin receptor	15308	1	1	1	1
182	PLIN5	perilipin 5	15064	1	1	1	1
183	VTN	vitronectin	21852	1	1	1	1
184	ZNF212	zinc finger protein 212	24216	1	1	1	1
185	SLC15A4	solute carrier family 15, member 4	20811	1	1	1	1
186	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	35332	1	1	1	1
187	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	15728	1	1	1	1
188	MLXIPL	MLX interacting protein-like	25649	1	1	1	1
189	PRAMEF11	PRAME family member 11	20523	1	1	1	1
190	ANKAR	ankyrin and armadillo repeat containing	71626	1	1	1	1
191	OR2L2	olfactory receptor, family 2, subfamily L, member 2	16031	2	1	2	1
192	BHLHB9	basic helix-loop-helix domain containing, class B, 9	27743	1	1	1	1
193	USP26	ubiquitin specific peptidase 26	45964	1	1	1	1
194	SEMG1	semenogelin I	23741	1	1	1	1
195	KRT72	keratin 72	22446	1	1	1	1
196	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	20420	1	1	1	1
197	CRY2	cryptochrome 2 (photolyase-like)	29104	1	1	1	1
198	KLF10	Kruppel-like factor 10	24803	1	1	1	1
199	MAN2B1	mannosidase, alpha, class 2B, member 1	46174	1	1	1	1
200	OR10H1	olfactory receptor, family 10, subfamily H, member 1	16047	1	1	1	1

201	ERC1	ELKS/RAB6-interacting/CAST family member 1	57964	1	1	1	1
202	BRSK1	BR serine/threonine kinase 1	31494	1	1	1	1
203	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	24439	1	1	1	1
204	CHD7	chromodomain helicase DNA binding protein 7	129479	2	2	2	1
205	ARMCX3	armadillo repeat containing, X-linked 3	19416	1	1	1	1
206	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	19367	1	1	1	1
207	GOT1L1	glutamic-oxaloacetic transaminase 1-like 1	16174	1	1	1	1
208	LPPR4		35520	1	1	1	1
209	AJAP1	adherens junctions associated protein 1	15898	1	1	1	1
210	UTY	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	26452	1	1	1	1
211	PDE3A	phosphodiesterase 3A, cGMP-inhibited	52620	1	1	1	1
212	SLC22A10	solute carrier family 22, member 10	28292	1	1	1	1
213	LRRK2	leucine-rich repeat kinase 2	130463	1	1	1	1
214	TTC30A	tetratricopeptide repeat domain 30A	30258	1	1	1	1
215	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	27351	1	1	1	1
216	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	49891	1	1	1	1
217	CCDC96	coiled-coil domain containing 96	23401	1	1	1	1
218	DMRT1	doublesex and mab-3 related transcription factor 1	14852	1	1	1	1
219	BLNK	B-cell linker	24371	1	1	1	1
220	ALPP	alkaline phosphatase, placental (Regan isozyme)	23705	1	1	1	1
221	MTPAP	mitochondrial poly(A) polymerase	29743	1	1	1	1
222	SHOC2	soc-2 suppressor of clear homolog (C. elegans)	29485	1	1	1	1
223	VARS2	valyl-tRNA synthetase 2, mitochondrial (putative)	50981	1	1	1	1
224	SCTR	secretin receptor	21943	1	1	1	1
225	PLD4	phospholipase D family, member 4	15204	1	1	1	1
226	SIRT7	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)	15949	1	1	1	1
227	SAGE1	sarcoma antigen 1	46815	1	1	1	1
228	CAPN12	calpain 12	28190	1	1	1	1
229	WAC	WW domain containing adaptor with coiled-coil	32579	1	1	1	1
230	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	44189	1	1	1	1
231	BDH1	3-hydroxybutyrate dehydrogenase, type 1	17951	1	1	1	1
232	CNTN5	contactin 5	52486	1	1	1	1
233	ARHGAP10	Rho GTPase activating protein 10	40955	1	1	1	1
234	ZFYVE1	zinc finger, FYVE domain containing 1	40398	1	1	1	1
235	DCLK3	doublecortin-like kinase 3	33367	1	1	1	1
236	KIAA1009	KIAA1009	50328	1	1	1	1

237	XIRP2	xin actin-binding repeat containing 2	206254	1	1	1	1
238	ZNF107	zinc finger protein 107	39980	1	1	1	1
239	ARSI	arylsulfatase family, member I	26421	1	1	1	1
240	GPR112	G protein-coupled receptor 112	157641	1	1	1	1
241	GOLGA2	golgi autoantigen, golgin subfamily a, 2	47807	1	1	1	1
242	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	19165	1	1	1	1
243	ALDOA	aldolase A, fructose-bisphosphate	19151	1	1	1	1
244	TTC7A	tetratricopeptide repeat domain 7A	41313	1	1	1	1
245	FXR1	fragile X mental retardation, autosomal homolog 1	32377	1	1	1	1
246	ERN1	endoplasmic reticulum to nucleus signaling 1	38983	1	1	1	1
247	HUNK	hormonally upregulated Neu-associated kinase	34942	1	1	1	1
248	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	54722	1	1	1	1
249	APLNR	apelin receptor	18410	1	1	1	1
250	WNT4	wingless-type MMTV integration site family, member 4	16634	1	1	1	1
251	LAMB3	laminin, beta 3	59579	1	1	1	1
252	CYFIP1	cytoplasmic FMR1 interacting protein 1	66370	1	1	1	1
253	SV2B	synaptic vesicle glycoprotein 2B	35689	1	1	1	1
254	ESYT2	extended synaptotagmin-like protein 2	39467	1	1	1	1
255	EFCAB5	EF-hand calcium binding domain 5	64021	1	1	1	1
256	ZNF609	zinc finger protein 609	72209	1	1	1	1
257	RBM15	RNA binding motif protein 15	49501	1	1	1	1
258	SHPK	sedoheptulokinase	23485	1	1	1	1
259	ZSWIM1	zinc finger, SWIM-type containing 1	24854	1	1	1	1
260	GDPD4	glycerophosphodiester phosphodiesterase domain containing 4	27372	1	1	1	1
261	ANLN	anillin, actin binding protein	58189	1	1	1	1
262	KIF2B	kinesin family member 2B	34442	1	1	1	1
263	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	25305	1	1	1	1
264	FAM83G	family with sequence similarity 83, member G	37568	1	1	1	1
265	CNNM1	cyclin M1	29404	1	1	1	1
266	ZNF2	zinc finger protein 2	22005	1	1	1	1
267	FAM155A	family with sequence similarity 155, member A	21867	1	1	1	1
268	MAPT	microtubule-associated protein tau	34436	1	1	1	1
269	ENGASE	endo-beta-N-acetylglucosaminidase	36250	1	1	1	1
270	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	30434	1	1	1	1
271	XIRP1	xin actin-binding repeat containing 1	93975	1	1	1	1
272	LILRA4	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	26024	1	1	1	1
273	HEXA	hexosaminidase A (alpha polypeptide)	27959	1	1	1	1
274	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	31694	1	1	1	1
275	ATL2	atlastin GTPase 2	29743	1	1	1	1
276	APBA1	amyloid beta (A4) precursor protein-binding, family A, member 1 (X11)	37610	1	1	1	1
277	KIAA1751	KIAA1751	38023	1	1	1	1
278	TBR1	T-box, brain, 1	26447	1	1	1	1

279	A1CF	APOBEC1 complementation factor	33216	1	1	1	1
280	DSG3	desmoglein 3 (pemphigus vulgaris antigen)	52039	1	1	1	1
281	RGNEF	Rho guanine nucleotide exchange factor (GEF) 28	59244	1	1	1	1
282	MUC17	mucin 17, cell surface associated	229998	2	2	2	1
283	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	37982	1	1	1	1
284	CLCA4	chloride channel, calcium activated, family member 4	47472	1	1	1	1
285	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	116359	1	1	1	1
286	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	207395	1	1	1	1
287	TRPV5	transient receptor potential cation channel, subfamily V, member 5	38156	1	1	1	1
288	UBE3C	ubiquitin protein ligase E3C	56077	1	1	1	1
289	NPHP3	nephronophthisis 3 (adolescent)	68225	1	1	1	1
290	DLG5	discs, large homolog 5 (Drosophila)	90419	1	1	1	1
291	HEATR7B2	HEAT repeat family member 7B2	68829	1	1	1	1
292	RP1	retinitis pigmentosa 1 (autosomal dominant)	109704	1	1	1	1
293	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	43608	1	1	1	1
294	AVIL	advillin	42847	1	1	1	1
295	ABI3BP	ABI gene family, member 3 (NESH) binding protein	44229	1	1	1	1
296	BRDT	bromodomain, testis-specific	49076	1	1	1	1
297	STK31	serine/threonine kinase 31	53606	1	1	1	1
298	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	119327	1	1	1	1
299	PTK2	PTK2 protein tyrosine kinase 2	54458	1	1	1	1
300	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	47203	1	1	1	1
301	USP16	ubiquitin specific peptidase 16	43048	1	1	1	1
302	ZFP28	zinc finger protein 28 homolog (mouse)	41344	1	1	1	1
303	TSC2	tuberous sclerosis 2	79832	1	1	1	1
304	GSN	gelsolin (amyloidosis, Finnish type)	34635	1	1	1	1
305	LRRC66	leucine rich repeat containing 66	44825	1	1	1	1
306	CDON	Cdon homolog (mouse)	65132	1	1	1	1
307	ITIH2	inter-alpha (globulin) inhibitor H2	49441	1	1	1	1
308	MMRN1	multimerin 1	62571	1	1	1	1
309	GLDC	glycine dehydrogenase (decarboxylating)	49715	1	1	1	1
310	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	46191	1	1	1	1
311	DTX3L	deltex 3-like (Drosophila)	37947	1	1	1	1
312	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	42919	1	1	1	1
313	AMPD1	adenosine monophosphate deaminase 1 (isoform M)	40660	1	1	1	1
314	KLHL14	kelch-like 14 (Drosophila)	31498	1	1	1	1
315	ZDBF2	zinc finger, DBF-type containing 2	110814	1	1	1	1
316	EEA1	early endosome antigen 1	70193	1	1	1	1
317	COL4A1	collagen, type IV, alpha 1	81953	1	1	1	1
318	TP63	tumor protein p63	38202	1	1	1	1
319	KIF24	kinesin family member 24	65421	1	1	1	1

320	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	69854	1	1	1	1
321	ZEB1	zinc finger E-box binding homeobox 1	56304	1	1	1	1
322	ZC3H11A	zinc finger CCCH-type containing 11A	41666	1	1	1	1
323	FLG	filaggrin	197966	1	1	1	1
324	CHD2	chromodomain helicase DNA binding protein 2	95315	1	1	1	1
325	ITGAD	integrin, alpha D	59654	1	1	1	1
326	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	45078	1	1	1	1
327	AZI1	5-azacytidine induced 1	39902	1	1	1	1
328	NLRP11	NLR family, pyrin domain containing 11	53331	1	1	1	1
329	PDZRN4	PDZ domain containing RING finger 4	45578	1	1	1	1
330	BAI3	brain-specific angiogenesis inhibitor 3	79225	1	1	1	1
331	CLIP1	CAP-GLY domain containing linker protein 1	72221	1	1	1	1
332	TUBGCP3	tubulin, gamma complex associated protein 3	46114	1	1	1	1
333	PCDHAC2	protocadherin alpha subfamily C, 2	48634	1	1	1	1
334	SMC2	structural maintenance of chromosomes 2	61418	1	1	1	1
335	PTPRT	protein tyrosine phosphatase, receptor type, T	73658	1	1	1	1
336	CNTN2	contactin 2 (axonal)	53770	1	1	1	1
337	FRYL	FRY-like	155866	1	1	1	1
338	TNIK	TRAF2 and NCK interacting kinase	56319	1	1	1	1
339	CCDC135	coiled-coil domain containing 135	45238	1	1	1	1
340	BSN	bassoon (presynaptic cytomatrix protein)	183006	1	1	1	1
341	MUC4	mucin 4, cell surface associated	52611	1	1	1	1
342	C2orf71	chromosome 2 open reading frame 71	64051	1	1	1	1
343	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	40736	1	1	1	1
344	TPP2	tripeptidyl peptidase II	64636	1	1	1	1
345	DGKD	diacylglycerol kinase, delta 130kDa	61085	1	1	1	1
346	TRIP12	thyroid hormone receptor interactor 12	103887	1	1	1	1
347	DNMBP	dynamin binding protein	79694	1	1	1	1
348	DCHS2	dachsous 2 (Drosophila)	145982	1	1	1	1
349	BRCA2	breast cancer 2, early onset	171366	1	1	1	1
350	KIAA1462	KIAA1462	69335	1	1	1	1
351	MYO16	myosin XVI	85270	1	1	1	1
352	ATF7IP	activating transcription factor 7 interacting protein	65707	1	1	1	1
353	GPR158	G protein-coupled receptor 158	59245	1	1	1	1
354	DNAH17	dynein, axonemal, heavy chain 17	190115	1	1	1	1
355	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	69989	1	1	1	1
356	DOPEY1	dopey family member 1	126835	1	1	1	1
357	KIAA1432	KIAA1432	71442	1	1	1	1
358	KDM5C	lysine (K)-specific demethylase 5C	65353	1	1	1	1
359	ODZ1	odz, odd Oz/ten-m homolog 1(Drosophila)	140067	1	1	1	1
360	RUSC2	RUN and SH3 domain containing 2	72728	1	1	1	1

361	SCN4A	sodium channel, voltage-gated, type IV, alpha subunit	82440	1	1	1	1
362	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	79990	1	1	1	1
363	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	80092	1	1	1	1
364	USP34	ubiquitin specific peptidase 34	184844	1	1	1	1
365	ZCCHC6	zinc finger, CCHC domain containing 6	77694	1	1	1	1
366	KIAA1549	KIAA1549	77355	1	1	1	1
367	DSCAM	Down syndrome cell adhesion molecule	103994	1	1	1	1
368	ATM	ataxia telangiectasia mutated	158086	1	1	1	1
369	NIN	ninein (GSK3B interacting protein)	105623	1	1	1	1
370	MYO7A	myosin VIIA	70293	1	1	1	1
371	FRMPD1	FERM and PDZ domain containing 1	80557	1	1	1	1
372	DLC1	deleted in liver cancer 1	80280	1	1	1	1
373	FLG2	filaggrin family member 2	121915	1	1	1	1
374	DNAH1	dynein, axonemal, heavy chain 1	173852	1	1	1	1
375	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	117659	1	1	1	1
376	MDC1	mediator of DNA damage checkpoint 1	107450	1	1	1	1
377	PRIC285	helicase with zinc finger 2, transcriptional coactivator	69588	1	1	1	1
378	SPG11	spastic paraplegia 11 (autosomal recessive)	122178	1	1	1	1
379	ZFP106	zinc finger protein 106 homolog (mouse)	95426	1	1	1	1
380	MUC16	mucin 16, cell surface associated	731508	2	2	2	1
381	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	164018	1	1	1	1
382	ZNF462	zinc finger protein 462	128257	1	1	1	1
383	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	250804	1	1	1	1
384	WNK1	WNK lysine deficient protein kinase 1	139076	1	1	1	1
385	APOB	apolipoprotein B (including Ag(x) antigen)	231999	1	1	1	1
386	ZFHX3	zinc finger homeobox 3	187990	1	1	1	1
387	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	226799	1	1	1	1
388	TTN	titin	1803345	3	2	3	1
389	ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	37045	1	1	1	1
390	FAM47C	family with sequence similarity 47, member C	51987	1	1	1	1

Supplementary Table 3: All mutations identified from whole exome sequencing

Hugo_Symbol	Entrez_Gene_Id	NCBI_Build	Genome_Change	Strand	Exon	cDNA_Change	Protein Change	mutant allele fraction
EFCAB7	84455	37	g.chr1:64027506A>G	+	11	c.1475A>G	p.N492S	0.394737
CLCA4	22802	37	g.chr1:87040355G>C	+	10	c.1600G>C	p.D534H	0.353535
ECD	11319	37	g.chr10:74914127G>A	-	6	c.670C>T	p.R224C	0.069767
AVIL	10677	37	g.chr12:58207181G>C	-	3	c.167C>G	p.S56C	0.336735
NIN	51199	37	g.chr14:51224340T>A	-	18	c.3408A>T	p.E1136D	0.480392
TLE3	7090	37	g.chr15:70347550C>G	-	15	c.1425G>C	p.R475S	0.336066
DNAJA4	55466	37	g.chr15:78565494C>T	+	3	c.371C>T	p.T124M	0.026786
CACNG3	10368	37	g.chr16:24268200C>A	+	1	c.125C>A	p.T42N	0.434783
KRT33A	3883	37	g.chr17:39503421G>A	-	4	c.642C>T	p.D214D	0.466667
IL28B	282617	37	g.chr19:39735130T>A	-	2	c.185A>T	p.E62V	0.5
TTN	7273	37	g.chr2:179496965C>T	-	185	c.35952G>A	p.S11984S	0.409091
DSCAM	1826	37	g.chr21:41719750T>G	-	6	c.1057A>C	p.I353L	0.018519
BPIL2	254240	37	g.chr22:32833754T>C	-	7	c.740A>G	p.N247S	0.083333
FXR1	8087	37	g.chr3:180666171T>A	+	5	c.307T>A	p.Y103N	0.4
ARSI	340075	37	g.chr5:149677490G>C	-	2	c.997C>G	p.L333V	0.305085
FGFR4	2264	37	g.chr5:176517801G>A	+	4	c.411G>A	p.S137S	0.06383
PERP	64065	37	g.chr6:138428332C>T	-	1	c.146G>A	p.W49*	0.340206
FAM120B	84498	37	g.chr6:170697401G>A	+	7	c.2310G>A	p.V770V	0.459459
MUC17	140453	37	g.chr7:100677815G>T	+	3	c.3118G>T	p.G1040*	0.396522
PCM1	5108	37	g.chr8:17817906A>G	+	15	c.2275A>G	p.I759V	0.157895
OR1L6	392390	37	g.chr9:125512246G>A	+	1	c.228G>A	p.A76A	0.369369
KIAA1751	85452	37	g.chr1:1896472G>A	-	13	c.1430C>T	p.P477L	0.434783
STXBP3	6814	37	g.chr1:109315427A>G	+	7	c.579A>G	p.G193G	0.451613
FLG2	388698	37	g.chr1:152327287G>A	-	3	c.2975C>T	p.S992F	0.411609
SHOC2	8036	37	g.chr10:112764464A>G	+	5	c.1073A>G	p.Y358C	0.528302
OR56A1	120796	37	g.chr11:6048549C>T	-	1	c.386G>A	p.R129H	0.518519
MRGPRX1	259249	37	g.chr11:18955977C>T	-	1	c.355G>A	p.E119K	0.089552
NDUFS8	4728	37	g.chr11:67803835A>T	+	6	c.488A>T	p.D163V	0.090909
ATF7IP	55729	37	g.chr12:14613491C>A	+	9	c.2221C>A	p.P741T	0.419753
SYT10	341359	37	g.chr12:33560240A>G	-	3	c.561T>C	p.V187V	0.5
B4GALNT1	2583	37	g.chr12:58020596G>A	-	11	c.1533C>T	p.D511D	0.453333
ALDOA	226	37	g.chr16:30078965G>T	+	6	c.307G>T	p.G103C	0.415842
ITGAD	3681	37	g.chr16:31427573G>A	+	19	c.2323G>A	p.E775K	0.130435
MYH1	4619	37	g.chr17:10404916A>G	-	26	c.3343T>C	p.L1115L	0.272727
VTN	7448	37	g.chr17:26696624C>T	-	3	c.433G>A	p.G145R	0.432432
AZI1	22994	37	g.chr17:79171522G>C	-	13	c.1646C>G	p.S549C	0.633333
QTRT1	81890	37	g.chr19:10822873G>A	+	6	c.683G>A	p.G228E	0.153846
VN1R2	317701	37	g.chr19:53762302C>T	+	1	c.674C>T	p.A225V	0.368421
ZNF548	147694	37	g.chr19:57910567C>T	+	3	c.912C>T	p.T304T	0.064935
WDR35	57539	37	g.chr2:20113391G>A	-	28	c.3474C>T	p.C1158C	0.425676
ZNF2	7549	37	g.chr2:95847570C>G	+	6	c.994C>G	p.Q332E	0.414634
POTEE	445582	37	g.chr2:131976473G>T	+	1	c.498G>T	p.V166V	0.269841
TTN	7273	37	g.chr2:179415852A>G	-	285	c.83702T>C	p.V27901A	0.210526
TTN	7273	37	g.chr2:179456935T>G	-	251	c.51992A>C	p.K17331T	0.5
NAB1	4664	37	g.chr2:191524666T>A	+	4	c.764T>A	p.I255K	0.4
DNAJC13	23317	37	g.chr3:132247149G>A	+	54	c.6498G>A	p.M2166I	0.489362
RBP1	5947	37	g.chr3:139257681A>C	-	2	c.380T>G	p.F127C	0.576271
TIPARP	25976	37	g.chr3:156422578A>G	+	6	c.1632A>G	p.K544K	0.02381
COX7B2	170712	37	g.chr4:46737214G>C	-	3	c.-4C>G		0.533333
FGA	2243	37	g.chr4:155510705T>C	-	2	c.64A>G	p.S22G	0.408602
PCDHA13	56136	37	g.chr5:140263167G>A	+	1	c.1314G>A	p.T438T	0.505

PACSIN1	29993	37	g.chr6:34497291C>G	+	5	c.574C>G	p.Q192E	0.478261
ABP1	26	37	g.chr7:150554014C>T	+	3	c.456C>T	p.Y152Y	0.465753
KIAA1432	57589	37	g.chr9:5765734G>T	+	20	c.2836G>T	p.V946F	0.098901
PIGO	84720	37	g.chr9:35095515G>A	-	2	c.48C>T	p.L16L	0.3
FRMPD1	22844	37	g.chr9:37745019A>T	+	16	c.2990A>T	p.D997V	0.102804
GSN	2934	37	g.chr9:124073030G>C	+	4	c.573G>C	p.Q191H	0.418605
ABCA4	24	37	g.chr1:94510206G>C	-	20	c.3013C>G	p.L1005V	0.057692
BBOX1	8424	37	g.chr11:27114810C>T	+	5	c.430C>T	p.L144F	0.144737
CNTN5	53942	37	g.chr11:100211267G>A	+	22	c.2803G>A	p.V935I	0.360465
ERC1	23085	37	g.chr12:1225169G>C	+	7	c.1539G>C	p.K513N	0.078431
FGF23	8074	37	g.chr12:4479524G>A	-	3	c.741C>T	p.F247F	0.041958
DIP2B	57609	37	g.chr12:51084865G>A	+	13	c.1585G>A	p.V529I	0.041667
EP400	57634	37	g.chr12:132547141G>A	+	46	c.8229G>A	p.Q2743Q	0.068182
EDNRB	1910	37	g.chr13:78492690G>A	-	1	c.19C>T	p.L7L	0.571429
COL4A1	1282	37	g.chr13:110850913G>A	-	21	c.1186C>T	p.R396*	0.085714
OR6S1	341799	37	g.chr14:21109524G>A	-	1	c.327C>T	p.L109L	0.297872
CTSG	1511	37	g.chr14:25043946G>A	-	3	c.274C>T	p.R92C	0.46789
SYNJ2BP	55333	37	g.chr14:70842452C>T	-	3	c.238G>A	p.D80N	0.319527
ANGEL1	23357	37	g.chr14:77275802A>G	-	2	c.249T>C	p.D83D	0.322034
ISM2	145501	37	g.chr14:77951125G>A	-	2	c.279C>T	p.N93N	0.586207
NDUFV2	4729	37	g.chr18:9117858A>G	+	2	c.77A>G	p.H26R	0.508197
ZNF208	7757	37	g.chr19:22155114C>T	-	5	c.2422G>A	p.E808K	0.04878
ZNF578	147660	37	g.chr19:53014555A>G	+	6	c.921A>G	p.R307R	0.027273
NRBP1	29959	37	g.chr2:27663547G>C	+	14	c.1171G>C	p.D391H	0.146341
5-Mar	57574	37	g.chr2:217124215G>A	-	4	c.1053C>T	p.T351T	0.151515
INPP5D	3635	37	g.chr2:234106829C>T	+	24	c.2782C>T	p.H928Y	0.458333
DGKD	8527	37	g.chr2:234365940G>A	+	21	c.2546G>A	p.G849E	0.528455
ATP9A	10079	37	g.chr20:50217835G>C	-	28	c.3059C>G	p.T1020S	0.113208
USP16	10600	37	g.chr21:30411818G>A	+	9	c.880G>A	p.G294S	0.041096
MAGI1	9223	37	g.chr3:65349205T>C	-	21	c.3430A>G	p.N1144D	0.497409
FBXO40	51725	37	g.chr3:121345691T>C	+	4	c.2064T>C	p.R688R	0.168831
COL6A6	131873	37	g.chr3:130286027G>A	+	4	c.1764G>A	p.K588K	0.092784
BDH1	622	37	g.chr3:197239185G>A	-	8	c.613C>T	p.R205C	0.064516
UGT2B10	7365	37	g.chr4:69874742G>A	-	8	c.1029C>T	p.Y343Y	0.393443
SFRP2	6423	37	g.chr4:154702697C>T	-	3	c.794G>A	p.G265D	0.083333
ZFP42	132625	37	g.chr4:188924770C>T	+	3	c.809C>T	p.T270M	0.065217
C6	729	37	g.chr5:41199992C>T	-	4	c.323G>A	p.R108H	0.096154
PCDHB11	56125	37	g.chr5:140579656G>C	+	1	c.309G>C	p.V103V	0.147887
PCDHGA11	56105	37	g.chr5:140803155G>A	+	1	c.2361G>A	p.E787E	0.115385
SCGN	10590	37	g.chr6:25665223G>A	+	4	c.299G>A	p.R100Q	0.430233
MDC1	9656	37	g.chr6:30672779C>T	-	10	c.4181G>A	p.G1394E	0.477876
SUN3	256979	37	g.chr7:48046845G>A	-	6	c.409C>T	p.L137L	0.086207
ESYT2	57488	37	g.chr7:158590695C>T	-	3	c.589G>A	p.V197M	0.474576
SLC24A2	25769	37	g.chr9:19550157G>A	-	7	c.1457C>T	p.T486M	0.478632
ARID3C	138715	37	g.chr9:34623522G>A	-	4	c.765C>T	p.A255A	0.595238
IRS4	8471	37	g.chrX:107975971G>A	-	1	c.3604C>T	p.Q1202*	0.504274
TREX2	11219	37	g.chrX:152710673G>A	-	3	c.342C>T	p.A114A	0.5
ABCA4	24	37	g.chr1:94495088A>G	-	30	c.4452T>C	p.P1484P	0.340426
CELSR2	1952	37	g.chr1:109795590C>A	+	1	c.2889C>A	p.G963G	0.021505
TEDDM1	127670	37	g.chr1:182369318T>C	-	1	c.303A>G	p.K101K	0.016575
SPHAR	10638	37	g.chr1:229440926T>C	+	1	c.45T>C	p.F15F	0.4
KCNJ1	3758	37	g.chr11:128709968C>G	-	2	c.228G>C	p.K76N	0.030151
KRT86	3892	37	g.chr12:52698770C>T	+	5	c.694C>T	p.L232L	0.016461
RYR3	6263	37	g.chr15:34102757G>T	+	71	c.10104G>T	p.V3368V	0.347826
ZNF768	79724	37	g.chr16:30536074C>T	-	2	c.1387G>A	p.G463S	0.4

GAS8	2622	37	g.chr16:90102871G>A	+	6	c.633G>A	p.V211V	0.076923
MYH4	4622	37	g.chr17:10355460C>T	-	27	c.3536G>A	p.R1179H	0.269461
DNAH17	8632	37	g.chr17:76557907G>C	-	8	c.831C>G	p.I277M	0.263158
DSG3	1830	37	g.chr18:29041305G>A	+	8	c.929G>A	p.G310E	0.186047
MUC16	94025	37	g.chr19:9086870G>A	-	1	c.4945C>T	p.H1649Y	0.282051
USP34	9736	37	g.chr2:61577486C>T	-	12	c.1416G>A	p.W472*	0.283582
TRIP12	9320	37	g.chr2:230643633C>T	-	34	c.4943G>A	p.G1648D	0.049261
POTEH	23784	37	g.chr22:16287673C>G	-	1	c.213G>C	p.W71C	0.011521
TRIOBP	11078	37	g.chr22:38120282C>T	+	7	c.1719C>T	p.D573D	0.022346
OTUD4	54726	37	g.chr4:146059041A>G	-	21	c.2691T>C	p.H897H	0.016304
PRDM9	56979	37	g.chr5:23527609T>C	+	11	c.2412T>C	p.Y804Y	0.016
SLC45A2	51151	37	g.chr5:33951767C>T	-	5	c.1048G>A	p.D350N	0.042328
DDX4	54514	37	g.chr5:55063731T>A	+	7	c.357T>A	p.D119E	0.350877
MUC17	140453	37	g.chr7:100681244A>G	+	3	c.6547A>G	p.T2183A	0.01105
MLL3	58508	37	g.chr7:151877852T>C	-	36	c.7093A>G	p.T2365A	0.253333
GALT	2592	37	g.chr9:34650400A>G	+	11	c.1094A>G	p.H365R	0.316456
ZNF462	58499	37	g.chr9:109690558C>T	+	3	c.4365C>T	p.S1455S	0.277778
USP26	83844	37	g.chrX:132162055C>G	-	6	c.194G>C	p.R65T	0.538462
TSPAN2	10100	37	g.chr1:115603103A>T	-	4	c.327T>A	p.A109A	0.08
GPR158	57512	37	g.chr10:25886855G>A	+	11	c.2300G>A	p.R767Q	0.292683
CCNY	219771	37	g.chr10:35841999A>G	+	8	c.632A>G	p.N211S	0.172662
APLNR	187	37	g.chr11:57003773G>A	-	1	c.706C>T	p.R236C	0.430556
SLC22A10	387775	37	g.chr11:63069907C>T	+	7	c.1177C>T	p.R393*	0.260417
OR10S1	219873	37	g.chr11:123848223A>G	-	1	c.176T>C	p.L59P	0.3
IRAK3	11213	37	g.chr12:66638958C>T	+	11	c.1230C>T	p.C410C	0.574074
FLT1	2321	37	g.chr13:28964124C>T	-	13	c.1778G>A	p.R593Q	0.435897
MKRN3	7681	37	g.chr15:23812328G>A	+	1	c.1399G>A	p.V467M	0.470588
PLCB2	5330	37	g.chr15:40587177A>G	-	18	c.1866T>C	p.N622N	0.210145
HEXA	3073	37	g.chr15:72640429C>T	-	9	c.1033G>A	p.G345S	0.314815
FES	2242	37	g.chr15:91428301G>T	+	2	c.26G>T	p.S9I	0.187135
SV2B	9899	37	g.chr15:91835642G>A	+	12	c.1912G>A	p.A638T	0.449541
A2BP1	54715	37	g.chr16:7645598G>A	+	8	c.516G>A	p.A172A	0.630573
EEF2K	29904	37	g.chr16:22278158G>A	+	15	c.1725G>A	p.S575S	0.03125
COG4	25839	37	g.chr16:70515295G>A	-	18	c.2202C>T	p.L734L	0.020942
EFCAB5	374786	37	g.chr17:28407910A>T	+	17	c.3337A>T	p.M1113L	0.163934
KRTAP4-7	100132476	37	g.chr17:39240908T>C	+	1	c.450T>C	p.C150C	0.1875
KLHL14	57565	37	g.chr18:30350035C>T	-	2	c.520G>A	p.V174M	0.215385
DAZAP1	26528	37	g.chr19:1418703G>A	+	4	c.276G>A	p.P92P	0.022472
KIR2DS4	3809	37	g.chr19:55349057G>A	+	3	c.97G>A	p.A33T	0.503067
STK39	27347	37	g.chr2:169020276T>C	-	4	c.545A>G	p.Y182C	0.048387
GTF3C3	9330	37	g.chr2:197637807G>A	-	14	c.1902C>T	p.Y634Y	0.433962
ZDBF2	57683	37	g.chr2:207172481G>T	+	5	c.3229G>T	p.D1077Y	0.454545
SRMS	6725	37	g.chr20:62172255C>T	-	8	c.1383G>A	p.E461E	0.248677
PRIC285	85441	37	g.chr20:62195106G>A	-	9	c.5069C>T	p.A1690V	0.5
RTEL1	51750	37	g.chr20:62293950G>A	+	5	c.447G>A	p.E149E	0.431818
DGKG	1608	37	g.chr3:186015857G>A	-	4	c.306C>T	p.S102S	0.144444
TP63	8626	37	g.chr3:189526314C>T	+	4	c.578C>T	p.T193M	0.213333
SHISA3	152573	37	g.chr4:42400217C>G	+	1	c.144C>G	p.F48L	0.666667
ADH1C	126	37	g.chr4:100269004C>G	-	2	c.19_splice	p.V7_splice	0.380952
RGNEF	64283	37	g.chr5:73090232A>G	+	7	c.916A>G	p.K306E	0.25
KIAA0240	23506	37	g.chr6:42796293T>C	+	6	c.222T>C	p.D74D	0.320755
TMEM181	57583	37	g.chr6:158957795C>T	+	1	c.317C>T	p.P106L	0.347826
ZNF727	442319	37	g.chr7:63538806C>G	+	4	c.1379C>G	p.T460S	0.125
DNAJB6	10049	37	g.chr7:157177656T>C	+	7	c.574T>C	p.S192P	0.196429
PTPRN2	5799	37	g.chr7:157959907C>T	-	6	c.626G>A	p.R209Q	0.197531

DMRT1	1761	37	g.chr9:916850G>A	+	4	c.910G>A	p.V304M	0.240741
ITLN1	55600	37	g.chr1:160849139A>G	-	7	c.751T>C	p.C251R	0.066116
CNTN2	6900	37	g.chr1:205033545C>A	+	11	c.1336C>A	p.P446T	0.265537
OR2L2	26246	37	g.chr1:248201585C>G	+	1	c.16C>G	p.Q6E	0.323529
OR2L2	26246	37	g.chr1:248202383A>G	+	1	c.814A>G	p.I272V	0.348837
A1CF	29974	37	g.chr10:52587939A>T	-	7	c.721T>A	p.S241T	0.302326
LCOR	84458	37	g.chr10:98715043T>A	+	8	c.666T>A	p.P222P	0.380952
TEAD1	7003	37	g.chr11:12785877G>A	+	3	c.53G>A	p.G18E	0.381579
LRRK2	120892	37	g.chr12:40697802G>A	+	27	c.3643G>A	p.A1215T	0.490566
BRCA2	675	37	g.chr13:32913996A>G	+	11	c.5504A>G	p.N1835S	0.333333
DIS3	22894	37	g.chr13:73346364T>G	-	10	c.1436A>C	p.D479A	0.365854
TPP2	7174	37	g.chr13:103257200G>T	+	2	c.223G>T	p.D75Y	0.02521
SPG11	80208	37	g.chr15:44890837T>A	-	22	c.3884A>T	p.E1295V	0.407895
KCTD5	54442	37	g.chr16:2747985G>A	+	3	c.440G>A	p.S147N	0.09375
ZFHX3	463	37	g.chr16:72821615G>A	-	10	c.10560C>T	p.G3520G	0.192308
SCN4A	6329	37	g.chr17:62038591T>G	-	11	c.1807A>C	p.T603P	0.3
TTC7A	57217	37	g.chr2:47250580G>A	+	13	c.1544G>A	p.R515Q	0.461538
MYO1B	4430	37	g.chr2:192275800A>G	+	27	c.2775A>G	p.K925K	0.4
HUNK	30811	37	g.chr21:33297002G>A	+	2	c.484G>A	p.E162K	0.336735
UGT2B15	7366	37	g.chr4:69512918C>A	-	6	c.1497G>T	p.L499L	0.352
PARM1	25849	37	g.chr4:75937784G>T	+	2	c.193G>T	p.V65L	0.377049
NMUR2	56923	37	g.chr5:151784196C>T	-	1	c.479G>A	p.R160Q	0.422222
ABCB5	340273	37	g.chr7:20683156G>T	+	7	c.579G>T	p.S193S	0.285714
DNAJB9	4189	37	g.chr7:108213686G>A	+	3	c.561G>A	p.Q187Q	0.031579
VPS13B	157680	37	g.chr8:100789121G>A	+	41	c.7441G>A	p.V2481I	0.401274
UNC13B	10497	37	g.chr9:35376224T>C	+	14	c.1568T>C	p.L523P	0.04
VPS13A	23230	37	g.chr9:79959954G>C	+	52	c.7185G>C	p.L2395F	0.387931
SMC2	10592	37	g.chr9:106857730G>T	+	2	c.65G>T	p.G22V	0.373333
OR6K6	128371	37	g.chr1:158725536T>C	+	1	c.931T>C	p.F311L	0.032258
ENTPD7	57089	37	g.chr10:101455868T>C	+	9	c.999T>C	p.L333L	0.205479
OR51E1	143503	37	g.chr11:4674116C>T	+	2	c.360C>T	p.A120A	0.054054
HEPHL1	341208	37	g.chr11:93800809G>A	+	5	c.956G>A	p.R319Q	0.021552
ZNF384	171017	37	g.chr12:6781563G>A	-	8	c.1047C>T	p.Y349Y	0.0375
BCDIN3D	144233	37	g.chr12:50232265G>A	-	2	c.768C>T	p.D256D	0.376471
POTEG	404785	37	g.chr14:19553531G>A	+	1	c.115G>A	p.G39S	0.014205
ZFYVE1	53349	37	g.chr14:73441537G>A	-	10	c.1937C>T	p.A646V	0.136364
ANP32A	8125	37	g.chr15:69080211G>A	-	2	c.102C>T	p.L34L	0.151351
ULK3	25989	37	g.chr15:75134497C>A	-	3	c.283G>T	p.A95S	0.02439
MFSD6L	162387	37	g.chr17:8702136G>A	-	1	c.303C>T	p.D101D	0.319588
ZNF878	729747	37	g.chr19:12155673A>C	-	5	c.684T>G	p.S228R	0.017699
ZNF443	10224	37	g.chr19:12541141C>T	-	4	c.1845G>A	p.P615P	0.061224
ZNF208	7757	37	g.chr19:22155282T>C	-	5	c.2254A>G	p.K752E	0.05
CPXM1	56265	37	g.chr20:2775940G>A	-	12	c.1843C>T	p.L615F	0.053571
CHGB	1114	37	g.chr20:5903078C>T	+	4	c.288C>T	p.H96H	0.184211
POLR3H	171568	37	g.chr22:41928701A>G	-	4	c.257T>C	p.I86T	0.112
CNTN6	27255	37	g.chr3:1415346A>G	+	15	c.1845A>G	p.Q615Q	0.075
GFM1	85476	37	g.chr3:158366865T>C	+	5	c.608T>C	p.I203T	0.017647
DGKG	1608	37	g.chr3:185997721G>A	-	9	c.711C>T	p.D237D	0.019139
PJA2	9867	37	g.chr5:108714545G>C	-	4	c.643C>G	p.L215V	0.240385
B4GALT7	11285	37	g.chr5:177035977C>T	+	5	c.790C>T	p.R264W	0.029126
LTB	4050	37	g.chr6:31548695C>A	-	4	c.526G>T	p.E176*	0.285714
MLXIPL	51085	37	g.chr7:73012007C>T	-	9	c.1108G>A	p.A370T	0.384615
NR5A1	2516	37	g.chr9:127265482C>T	-	3	c.120G>A	p.T40T	0.6
BRDT	676	37	g.chr1:92445196A>G	+	8	c.1169A>G	p.K390R	0.328358
PSRC1	84722	37	g.chr1:109823835G>A	-	5	c.558C>T	p.S186S	0.222222

FLG	2312	37	g.chr1:152279722G>A	-	3	c.7640C>T	p.S2547L	0.220532
WAC	51322	37	g.chr10:28822958T>G	+	2	c.73T>G	p.Y25D	0.180556
DLG5	9231	37	g.chr10:79601670G>A	-	7	c.1406C>T	p.A469V	0.040541
DNMBP	23268	37	g.chr10:101646272T>C	-	13	c.3403A>G	p.T1135A	0.261905
HIF1AN	55662	37	g.chr10:102306957A>G	+	7	c.955A>G	p.M319V	0.451613
CCKBR	887	37	g.chr11:6291944T>C	+	4	c.722T>C	p.I241T	0.384615
UCP2	7351	37	g.chr11:73686556C>T	-	7	c.795G>A	p.G265G	0.134146
KCNA5	3741	37	g.chr12:5154819C>T	+	1	c.1506C>T	p.I502I	0.202128
ANO4	121601	37	g.chr12:101336184A>G	+	5	c.327A>G	p.G109G	0.268657
TEP1	7011	37	g.chr14:20840981C>T	-	49	c.6987G>A	p.S2329S	0.0375
MRPL52	122704	37	g.chr14:23303430G>A	+	5	c.272G>A	p.W91*	0.22449
DHRS4	10901	37	g.chr14:24424420C>T	+	2	c.305C>T	p.T102M	0.1875
BAZ1A	11177	37	g.chr14:35245621T>C	-	18	c.2337A>G	p.K779K	0.318182
RPUSD2	27079	37	g.chr15:40866379T>G	+	3	c.1557T>G	p.H519Q	0.056604
ARNT2	9915	37	g.chr15:80886021T>C	+	19	c.2136T>C	p.F712F	0.272727
OR4F6	390648	37	g.chr15:102346447T>C	+	1	c.525T>C	p.D175D	0.294118
SPIRE2	84501	37	g.chr16:89929977T>C	+	11	c.1669T>C	p.L557L	0.214286
NLK	51701	37	g.chr17:26449755T>C	+	2	c.585T>C	p.D195D	0.217391
FOXJ1	2302	37	g.chr17:74134121G>T	-	2	c.579C>A	p.G193G	0.103448
ENGASE	64772	37	g.chr17:77082094C>T	+	14	c.1895C>T	p.S632F	0.339623
RGPD3	653489	37	g.chr2:107041215A>G	-	20	c.3208T>C	p.F1070L	0.197826
C2orf85	285093	37	g.chr2:242815069C>G	+	2	c.1362C>G	p.D454E	0.185185
FAM65C	140876	37	g.chr20:49218957A>G	-	13	c.1299T>C	p.G433G	0.218182
NUP50	10762	37	g.chr22:45580377T>C	+	8	c.1248T>C	p.C416C	0.038961
SETD2	29072	37	g.chr3:47155478T>A	-	5	c.4603A>T	p.N1535Y	0.431034
WNT5A	7474	37	g.chr3:55504230C>G	-	5	c.1033G>C	p.D345H	0.36
ATG3	64422	37	g.chr3:112255428C>T	-	10	c.688G>A	p.E230K	0.191489
ENC1	8507	37	g.chr5:73932105C>T	-	2	c.206G>A	p.R69H	0.236364
VARS2	57176	37	g.chr6:30893656G>A	+	28	c.2962_splice	p.G988_splice	0.165217
KIAA1009	22832	37	g.chr6:84862443G>A	-	23	c.3450C>T	p.F1150F	0.333333
EPDR1	54749	37	g.chr7:37960536A>G	+	1	c.355A>G	p.T119A	0.1875
ZNF107	51427	37	g.chr7:64166810A>C	+	7	c.128A>C	p.Q43P	0.16
CNPY4	245812	37	g.chr7:99720495A>G	+	4	c.431A>G	p.E144G	0.121212
ZNF212	7988	37	g.chr7:148947387G>T	+	2	c.162G>T	p.K54N	0.127273
EXT1	2131	37	g.chr8:119122863G>A	-	1	c.423C>T	p.S141S	0.056818
PTK2	5747	37	g.chr8:141675072A>C	-	31	c.2890T>G	p.L964V	0.2
KIF24	347240	37	g.chr9:34306329A>G	-	3	c.734T>C	p.I245T	0.234568
SETX	23064	37	g.chr9:135205342T>C	-	10	c.1643A>G	p.Q548R	0.2
FAM69B	138311	37	g.chr9:139617935G>A	+	5	c.1005G>A	p.E335E	0.285714
FAM47C	442444	37	g.chrX:37027200A>C	+	1	c.717A>C	p.P239P	0.071429
PRAMEF11	440560	37	g.chr1:12887612T>C	-	3	c.245A>G	p.H82R	0.011765
LOC649330	649330	37	g.chr1:12907683G>A	-	1	c.460C>T	p.R154*	0.477778
WNT4	54361	37	g.chr1:22456168C>T	-	2	c.254G>A	p.R85Q	0.26
IL12RB2	3595	37	g.chr1:67861538C>T	+	16	c.2355C>T	p.P785P	0.440945
ITIH2	3698	37	g.chr10:7774376G>A	+	14	c.1723G>A	p.A575T	0.086957
ZEB1	6935	37	g.chr10:31809668G>A	+	7	c.1405G>A	p.G469R	0.46
GLYAT	10249	37	g.chr11:58477426G>A	-	6	c.704C>T	p.P235L	0.097561
SHANK2	22941	37	g.chr11:70332483C>T	-	21	c.3915G>A	p.T1305T	0.025
CDON	50937	37	g.chr11:125880478C>T	-	8	c.1310G>A	p.R437H	0.037736
WNK1	65125	37	g.chr12:970329C>G	+	7	c.1771C>G	p.Q591E	0.377049
C12orf53	196500	37	g.chr12:6804798G>A	-	5	c.625C>T	p.R209*	0.491228
PDZRN4	29951	37	g.chr12:41966407G>T	+	10	c.1229G>T	p.G410V	0.05
CLIP1	6249	37	g.chr12:122812709C>T	-	16	c.3034G>A	p.E1012K	0.066667
SLC15A4	121260	37	g.chr12:129283812G>A	-	7	c.1565C>T	p.T522I	0.422222
ACSM2B	348158	37	g.chr16:20554459G>A	-	12	c.1407C>T	p.S469S	0.031746

CCDC135	84229	37	g.chr16:57732895G>A	+	3	c.337G>A	p.V113M	0.026718
FAM83G	644815	37	g.chr17:18880989C>T	-	5	c.1990G>A	p.G664S	0.44
COL1A1	1277	37	g.chr17:48268189G>A	-	33	c.2332C>T	p.P778S	0.442308
KIF2B	84643	37	g.chr17:51902295T>C	+	1	c.1901T>C	p.I634T	0.042254
OR10H1	26539	37	g.chr19:15918805C>T	-	1	c.43G>A	p.V15I	0.206349
OSCAR	126014	37	g.chr19:54600278G>A	-	4	c.319C>T	p.L107L	0.034483
LILRA4	23547	37	g.chr19:54849455C>G	-	4	c.407G>C	p.G136A	0.04
NLRP11	204801	37	g.chr19:56329269C>T	-	4	c.271_splice	p.R91_splice	0.037736
ZFP28	140612	37	g.chr19:57066116C>G	+	8	c.1962C>G	p.F654L	0.06
APOB	338	37	g.chr2:21250699C>G	-	14	c.2067_splice	p.E689_splice	0.422222
ATL2	64225	37	g.chr2:38527425A>C	-	10	c.1117T>G	p.S373A	0.053763
RGPD3	653489	37	g.chr2:107041110C>A	-	20	c.3313G>T	p.V1105L	0.023392
SCTR	6344	37	g.chr2:120223390C>T	-	5	c.478G>A	p.A160T	0.164706
TTC30A	92104	37	g.chr2:178482772G>A	-	1	c.658C>T	p.R220C	0.06
OXTR	5021	37	g.chr3:8794796C>A	-	4	c.1037G>T	p.C346F	0.056604
SLC22A14	9389	37	g.chr3:38347529G>A	+	2	c.12G>A	p.E4E	0.032
MUC4	4585	37	g.chr3:195505836G>C	-	3	c.12231C>G	p.H4077Q	0.375
ZNF732	654254	37	g.chr4:266220C>T	-	3	c.423G>A	p.Q141Q	0.625
DCHS2	54798	37	g.chr4:155287395C>T	-	5	c.661G>A	p.V221M	0.392157
CTNND2	1501	37	g.chr5:11022928G>A	-	17	c.2952C>T	p.A984A	0.287879
RNF182	221687	37	g.chr6:13977813C>T	+	3	c.463C>T	p.P155S	0.027972
PCLO	27445	37	g.chr7:82584741C>T	-	5	c.5528G>A	p.R1843H	0.044693
PNOC	5368	37	g.chr8:28186731C>T	+	2	c.57C>T	p.S19S	0.473214
TAF1L	138474	37	g.chr9:32634312C>A	-	1	c.1266G>T	p.L422L	0.10177
RUSC2	9853	37	g.chr9:35547771C>G	+	2	c.1253C>G	p.T418S	0.015385
ZNF462	58499	37	g.chr9:109773231C>G	+	13	c.7441C>G	p.L2481V	0.119403
KIF12	113220	37	g.chr9:116856721C>T	-	9	c.720G>A	p.K240K	0.531915
FAM47C	442444	37	g.chrX:37027156C>G	+	1	c.673C>G	p.Q225E	0.034091
FAM47C	442444	37	g.chrX:37027980C>T	+	1	c.1497C>T	p.C499C	0.377551
GPR173	54328	37	g.chrX:53106646A>G	+	2	c.843A>G	p.E281E	0.222222
KDM5C	8242	37	g.chrX:53239989C>A	-	11	c.1452G>T	p.Q484H	0.270833
IRS4	8471	37	g.chrX:107977308G>A	-	1	c.2267C>T	p.P756L	0.043103
ST6GALNAC5	81849	37	g.chr1:77510088G>A	+	3	c.461G>A	p.R154H	0.438596
MOV10	4343	37	g.chr1:113240682T>G	+	15	c.2265T>G	p.A755A	0.401961
AMPD1	270	37	g.chr1:115229470A>C	-	4	c.277T>G	p.S93A	0.375
SELL	6402	37	g.chr1:169679608G>A	-	2	c.54C>T	p.F18F	0.777778
ZC3H11A	9877	37	g.chr1:203816359A>G	+	15	c.1090A>G	p.I364V	0.447368
SYT14	255928	37	g.chr1:210194441C>T	+	4	c.284C>T	p.A95V	0.552239
MYO7A	4647	37	g.chr11:76868324G>T	+	8	c.736_splice	p.A246_splice	0.5
GDPD4	220032	37	g.chr11:76980056C>A	-	8	c.537G>T	p.M179I	0.541667
OR8D4	338662	37	g.chr11:123777260G>T	+	1	c.122G>T	p.G41V	0.521127
KRT72	140807	37	g.chr12:52984637C>T	-	6	c.1072G>A	p.G358R	0.345238
SFRS8	6433	37	g.chr12:132199476G>A	+	3	c.498G>A	p.E166E	0.029703
MYO16	23026	37	g.chr13:109535506G>A	+	13	c.1459G>A	p.E487K	0.064935
TUBGCP3	10426	37	g.chr13:113143953A>C	-	21	c.2507T>G	p.F836C	0.533333
PLD4	122618	37	g.chr14:105396438C>T	+	6	c.713C>T	p.T238M	0.454545
ZFP106	64397	37	g.chr15:42717038G>T	-	13	c.5115C>A	p.C1705*	0.333333
ZFHX3	463	37	g.chr16:72829959G>T	-	9	c.6622C>A	p.P2208T	0.319672
SHPK	23729	37	g.chr17:3539425G>C	-	1	c.89C>G	p.S30C	0.478261
SIRT7	51547	37	g.chr17:79870399C>A	-	10	c.1096G>T	p.E366*	0.5
NFIX	4784	37	g.chr19:13192541A>G	+	8	c.1150A>G	p.I384V	0.37037
TBC1D8	11138	37	g.chr2:101654956G>A	-	7	c.1197C>T	p.P399P	0.405556
TBR1	10716	37	g.chr2:162273318G>T	+	1	c.397G>T	p.A133S	0.467033
TTN	7273	37	g.chr2:179621299G>A	-	44	c.10391C>T	p.T3464I	0.048387
KIAA1486	57624	37	g.chr2:226447052G>A	+	4	c.919G>A	p.A307T	0.373134

PTPRT	11122	37	g.chr20:40710653C>T	-	30	c.4141G>A	p.G1381R	0.454545
ZSWIM1	90204	37	g.chr20:44512200A>T	+	2	c.969A>T	p.E323D	0.056338
CCR4	1233	37	g.chr3:32995658G>A	+	2	c.744G>A	p.V248V	0.382353
DCLK3	85443	37	g.chr3:36759633C>T	-	4	c.1621G>A	p.V541M	0.37234
GSTCD	79807	37	g.chr4:106647804G>A	+	4	c.963G>A	p.R321R	0.62069
EMB	133418	37	g.chr5:49706766A>G	-	4	c.417T>C	p.S139S	0.37037
PCDHAC2	56134	37	g.chr5:140347141G>A	+	1	c.790G>A	p.V264I	0.41
RELL2	285613	37	g.chr5:141019200G>A	+	5	c.487G>A	p.V163M	0.583333
MTHFD1L	25902	37	g.chr6:151293167_151293168AA>GT	+	20	c.2098_2099AA>GT	p.K700V	0.48
ELN	2006	37	g.chr7:73474271T>C	+	23	c.1488T>C	p.G496G	0.104167
ELN	2006	37	g.chr7:73474290T>G	+	23	c.1507T>G	p.L503V	0.266667
ELN	2006	37	g.chr7:73474307C>T	+	23	c.1524C>T	p.G508G	0.078947
RELN	5649	37	g.chr7:103207091C>T	-	32	c.4704G>A	p.A1568A	0.473684
KIAA1549	57670	37	g.chr7:138604123T>A	-	2	c.249A>T	p.K83N	0.44898
UBE3C	9690	37	g.chr7:157046771C>T	+	20	c.2818C>T	p.R940C	0.5
DLC1	10395	37	g.chr8:12957624C>G	-	9	c.2222G>C	p.S741T	0.04
CHD7	55636	37	g.chr8:61707573G>A	+	4	c.2125G>A	p.A709T	0.325
UQCRB	7381	37	g.chr8:97244053C>A	-	3	c.207G>T	p.L69L	0.346154
GLDC	2731	37	g.chr9:6644632T>C	-	2	c.316A>G	p.K106E	0.510204
TAF1L	138474	37	g.chr9:32631455G>A	-	1	c.4123C>T	p.R1375W	0.439153
ZCCHC6	79670	37	g.chr9:88967826G>A	-	2	c.289C>T	p.Q97*	0.38172
IKBKAP	8518	37	g.chr9:111665931A>T	-	15	c.1662T>A	p.D554E	0.444444
PNPLA4	8228	37	g.chrX:7894143T>C	-	2	c.18A>G	p.L6L	0.428571
ODZ1	10178	37	g.chrX:123518248C>T	-	29	c.6512G>A	p.R2171H	0.457627
LAMB3	3914	37	g.chr1:209797286G>A	-	14	c.2036C>T	p.P679L	0.054348
C10orf118	55088	37	g.chr10:115917313C>A	-	3	c.759G>T	p.Q253H	0.140351
OR4C16	219428	37	g.chr11:55339962G>A	+	1	c.359G>A	p.R120H	0.1875
MS4A6E	245802	37	g.chr11:60107369G>T	+	3	c.385G>T	p.V129L	0.2249
SLC12A3	6559	37	g.chr16:56926039G>A	+	20	c.2413G>A	p.A805T	0.051724
XIRP2	129446	37	g.chr2:168103772C>T	+	8	c.5870C>T	p.S1957L	0.125
KCNH8	131096	37	g.chr3:19491797G>T	+	9	c.1575G>T	p.E525D	0.121739
ZNF621	285268	37	g.chr3:40574124A>G	+	5	c.863A>G	p.E288G	0.061538
SH3TC2	79628	37	g.chr5:148392171G>A	-	13	c.3180C>T	p.D1060D	0.12
PCLO	27445	37	g.chr7:82764498T>C	-	3	c.2368A>G	p.K790E	0.064286
ACOT9	23597	37	g.chrX:23724801G>A	-	10	c.759C>T	p.P253P	0.101449
ZBTB33	10009	37	g.chrX:119388643G>T	+	2	c.1373G>T	p.R458I	0.064815
GPR112	139378	37	g.chrX:135431708A>G	+	6	c.5843A>G	p.N1948S	0.25
SOAT2	8435	37	g.chr12:53515086G>A	+	12	c.1138_splice	p.D380_splice	0.105263
NAB2	4665	37	g.chr12:57486733G>A	+	4	c.1125G>A	p.L375L	0.471831
STAT6	6778	37	g.chr12:57492604G>A	-	18	c.2037C>T	p.S679S	0.373626
CIT	11113	37	g.chr12:120166348G>A	-	27	c.3424C>T	p.L1142L	0.45122
OR4N4	283694	37	g.chr15:22332432C>T	+	3	c.-742C>T		0.053435
CYFIP1	23191	37	g.chr15:22928467T>G	+	5	c.344T>G	p.L115R	0.078212
CDH1	999	37	g.chr16:68842648A>G	+	5	c.584A>G	p.Q195R	0.101695
CWC25	54883	37	g.chr17:36971223A>T	-	3	c.319T>A	p.C107S	0.5
ERN1	2081	37	g.chr17:62141429G>A	-	10	c.1004C>T	p.T335M	0.518519
CD7	924	37	g.chr17:80274571G>A	-	2	c.369C>T	p.Y123Y	0.086093
TRMT1	55621	37	g.chr19:13221056G>A	-	7	c.935C>T	p.P312L	0.512821
C19orf51	352909	37	g.chr19:55670703G>A	-	12	c.1353C>T	p.F451F	0.157895
DPP4	1803	37	g.chr2:162895527G>C	-	7	c.424C>G	p.L142V	0.04717
KIAA1486	57624	37	g.chr2:226447451G>A	+	4	c.1318G>A	p.V440I	0.535714
SIRPB2	284759	37	g.chr20:1456924G>A	-	5	c.917C>T	p.A306V	0.11236
TH1L	51497	37	g.chr20:57568133A>C	+	11	c.1337A>C	p.D446A	0.472727
ADAMTS1	9510	37	g.chr21:28213340G>A	-	4	c.1355C>T	p.T452I	0.468966
DNAH1	25981	37	g.chr3:52422507G>A	+	58	c.9245G>A	p.R3082H	0.444444

FAT4	79633	37	g.chr4:126372524T>C	+	9	c.10353T>C	p.G3451G	0.056962
RP1	6101	37	g.chr8:55538622G>T	+	4	c.2180G>T	p.C727F	0.490909
NDRG1	10397	37	g.chr8:134262769G>A	-	10	c.612C>T	p.N204N	0.522727
SAGE1	55511	37	g.chrX:134990686C>T	+	12	c.1351C>T	p.R451*	0.057971
TSSK3	81629	37	g.chr1:32828341C>A	+	1	c.39C>A	p.G13G	0.396552
BLNK	29760	37	g.chr10:97956683C>G	-	16	c.1232G>C	p.R411T	0.04902
HCFC2	29915	37	g.chr12:104476357A>T	+	6	c.847A>T	p.T283S	0.247191
CDH5	1003	37	g.chr16:66434745G>A	+	11	c.1663G>A	p.V555M	0.284211
MAPT	4137	37	g.chr17:44091637T>G	+	12	c.1895T>G	p.L632R	0.12
ST8SIA5	29906	37	g.chr18:44260231C>T	-	7	c.905G>A	p.G302D	0.115942
LASS4	79603	37	g.chr19:8316126T>G	+	3	c.166T>G	p.F56V	0.290323
MUC16	94025	37	g.chr19:9085136G>T	-	1	c.6679C>A	p.P2227T	0.318182
MAN2B1	4125	37	g.chr19:12757478G>A	-	24	c.2992C>T	p.R998C	0.380952
CAPN12	147968	37	g.chr19:39225474G>C	-	15	c.1723C>G	p.L575V	0.269231
ASB3	51130	37	g.chr2:53927482T>C	-	8	c.1164A>G	p.Q388Q	0.354839
SEMG1	6406	37	g.chr20:43836680C>A	+	2	c.742C>A	p.H248N	0.37594
ZNF831	128611	37	g.chr20:57769093G>A	+	1	c.3019G>A	p.D1007N	0.088235
NT5DC2	64943	37	g.chr3:52562087G>A	-	7	c.663C>T	p.D221D	0.5
TNIK	23043	37	g.chr3:170784371_170784372AC>TG	-	31	c.3852_3853GT>CA	p.S1285T	0.077922
SH3D19	152503	37	g.chr4:152095866G>A	-	7	c.650C>T	p.S217L	0.33526
RXFP1	59350	37	g.chr4:159520558T>C	+	4	c.367T>C	p.S123P	0.333333
STK31	56164	37	g.chr7:23794080C>A	+	10	c.1280C>A	p.T427N	0.279279
PTPRZ1	5803	37	g.chr7:121651157C>T	+	12	c.2057C>T	p.S686F	0.080645
PADI3	51702	37	g.chr1:17603108G>A	+	12	c.1402G>A	p.V468M	0.293103
RBM15	64783	37	g.chr1:110882560G>A	+	1	c.533G>A	p.G178E	0.333333
ARV1	64801	37	g.chr1:231114994A>G	+	1	c.143A>G	p.Y48C	0.5
CALCA	796	37	g.chr11:14991524T>C	-	3	c.184A>G	p.K62E	0.427083
CRY2	1408	37	g.chr11:45882512T>C	+	4	c.644T>C	p.M215T	0.487179
OR4C13	283092	37	g.chr11:49974700C>T	+	1	c.726C>T	p.I242I	0.468927
ATM	472	37	g.chr11:108196072T>C	+	46	c.6608T>C	p.I2203T	0.507143
C12orf66	144577	37	g.chr12:64609516T>C	-	2	c.463A>G	p.I155V	0.6
SERPINA6	866	37	g.chr14:94770776C>T	-	5	c.1197G>A	p.A399A	0.072464
CHRFAM7A	89832	37	g.chr15:30659622C>T	-	9	c.719G>A	p.W240*	0.363636
MEGF11	84465	37	g.chr15:66190299A>G	-	23	c.3108T>C	p.N1036N	0.535714
TSC2	7249	37	g.chr16:2114352C>T	+	15	c.1523C>T	p.A508V	0.076087
ABR	29	37	g.chr17:959326C>A	-	14	c.1510G>T	p.G504C	0.380952
IGF2BP1	10642	37	g.chr17:47119680G>A	+	9	c.1018G>A	p.E340K	0.469697
ZNF845	91664	37	g.chr19:53854397G>C	+	4	c.469G>C	p.E157Q	0.045455
BRSK1	84446	37	g.chr19:55805719G>A	+	7	c.632G>A	p.R211Q	0.166667
OGG1	4968	37	g.chr3:9793620G>A	+	3	c.552G>A	p.L184L	0.068182
XIRP1	165904	37	g.chr3:39228976C>G	-	2	c.1961G>C	p.G654A	0.4375
BSN	8927	37	g.chr3:49692992C>G	+	5	c.6003C>G	p.I2001M	0.436364
C3orf17	25871	37	g.chr3:112738432C>T	-	1	c.63G>A	p.G21G	0.410256
PRPS1L1	221823	37	g.chr7:18066671A>G	-	1	c.735T>C	p.Y245Y	0.443182
TAF1L	138474	37	g.chr9:32631979C>T	-	1	c.3599G>A	p.R1200H	0.03937
LPPR4	9890	37	g.chr1:99771502A>G	+	7	c.1228A>G	p.M410V	0.101449
OR2T33	391195	37	g.chr1:248436810G>C	-	1	c.307C>G	p.P103A	0.10084
MTPAP	55149	37	g.chr10:30611436C>A	-	6	c.1103G>T	p.S368I	0.269841
FAM160A2	84067	37	g.chr11:6239142T>C	-	9	c.1674A>G	p.A558A	0.189474
CBL	867	37	g.chr11:119148891T>C	+	8	c.1111T>C	p.Y371H	0.204082
SLCO1B3	28234	37	g.chr12:21028173T>A	+	8	c.732T>A	p.T244T	0.044983
WNT10B	7480	37	g.chr12:49359949G>A	-	5	c.1099C>T	p.R367C	0.133333
EEA1	8411	37	g.chr12:93221741T>G	-	12	c.1351A>C	p.K451Q	0.189189
MKRN3	7681	37	g.chr15:23812196C>T	+	1	c.1267C>T	p.P423S	0.138462
PTH2R	5746	37	g.chr2:209358098C>T	+	13	c.1367C>T	p.T456M	0.25

C20orf72	92667	37	g.chr20:17968878C>A	+	4	c.801C>A	p.D267E	0.123077
ABI3BP	25890	37	g.chr3:100527069C>G	-	19	c.1608G>C	p.Q536H	0.078947
NPHP3	27031	37	g.chr3:132432003A>G	-	6	c.1085T>C	p.L362S	0.152174
ARHGAP10	79658	37	g.chr4:148786004T>C	+	6	c.494T>C	p.I165T	0.119048
HEATR7B2	133558	37	g.chr5:40998203G>A	-	42	c.4709C>T	p.A1570V	0.074419
ZNF366	167465	37	g.chr5:71756259G>A	-	2	c.1065C>T	p.H355H	0.071429
KCNN2	3781	37	g.chr5:113740315G>T	+	3	c.763G>T	p.D255Y	0.210526
APBB3	10307	37	g.chr5:139941715C>T	-	6	c.596G>A	p.R199H	0.09434
PCDHA5	56143	37	g.chr5:140203019C>T	+	1	c.1659C>T	p.F553F	0.19708
BAI3	577	37	g.chr6:70048813T>G	+	25	c.3194T>G	p.M1065R	0.063205
DOPEY1	23033	37	g.chr6:83818692G>T	+	5	c.384G>T	p.L128F	0.109677
TEX10	54881	37	g.chr9:103092392A>G	-	6	c.1310T>C	p.L437P	0.171642
PCDH11Y	83259	37	g.chrY:5605924C>T	+	5	c.3964C>T	p.R1322C	0.078947
ST7L	54879	37	g.chr1:113161707G>A	-	1	c.29C>T	p.A10V	0.090909
KIRREL	55243	37	g.chr1:158045965G>A	+	2	c.115G>A	p.V39M	0.048544
KIAA1614	57710	37	g.chr1:180907749C>T	+	6	c.2820C>T	p.I940I	0.1
LGI1	9211	37	g.chr10:95557306C>T	+	8	c.1420C>T	p.R474*	0.076923
OR4A47	403253	37	g.chr11:48510470C>T	+	1	c.126C>T	p.L42L	0.060606
OR4D6	219983	37	g.chr11:59225211C>T	+	1	c.778C>T	p.R260W	0.453901
TSGA10IP	254187	37	g.chr11:65721135C>A	+	7	c.1249C>A	p.H417N	0.4
CAPN5	726	37	g.chr11:76795988_76795989AC>TG	+	2	c.56_57AC>TG	p.D19V	0.238095
KRT80	144501	37	g.chr12:52566110G>A	-	7	c.1050C>T	p.A350A	0.123894
SUPT16H	11198	37	g.chr14:21826502C>G	-	20	c.2386G>C	p.E796Q	0.381579
DSG1	1828	37	g.chr18:28923517G>A	+	12	c.1792G>A	p.A598T	0.078261
SPPL2B	56928	37	g.chr19:2353079C>G	+	16	c.1651C>G	p.P551A	0.366667
ZNF814	730051	37	g.chr19:58385546G>T	-	3	c.1212C>A	p.D404E	0.25
POTEF	728378	37	g.chr2:130832810C>T	-	17	c.2235G>A	p.G745G	0.09322
KIAA1715	80856	37	g.chr2:176802120G>A	-	12	c.1006C>T	p.P336S	0.058824
ANKAR	150709	37	g.chr2:190541613C>T	+	1	c.184C>T	p.Q62*	0.122951
NCL	4691	37	g.chr2:232320315T>C	-	13	c.1853A>G	p.N618S	0.431373
USP49	25862	37	g.chr6:41771694G>C	-	5	c.1411C>G	p.L471V	0.122449
TMEM195	392636	37	g.chr7:15425185G>C	-	10	c.960C>G	p.V320V	0.08547
ATP7A	538	37	g.chrX:77254160C>T	+	5	c.1522C>T	p.R508W	0.4
CLSPN	63967	37	g.chr1:36203608C>T	-	22	c.3649G>A	p.A1217T	0.403509
NBPF9	400818	37	g.chr1:144815953A>G	+	12	c.1324A>G	p.N442D	0.056911
KRTAP5-4	387267	37	g.chr11:1643228G>A	-	1	c.54C>T	p.G18G	0.109375
MYO5C	55930	37	g.chr15:52504010G>A	-	35	c.4213C>T	p.R1405C	0.142857
QPRT	23475	37	g.chr16:29706106G>A	+	2	c.135G>A	p.A45A	0.065217
NFATC3	4775	37	g.chr16:68225638C>T	+	9	c.3066C>T	p.N1022N	0.057803
KRT26	353288	37	g.chr17:38928008C>T	-	1	c.358G>A	p.E120K	0.083333
BZRAP1	9256	37	g.chr17:56386538C>T	-	22	c.4095G>A	p.L1365L	0.369863
KLF1	10661	37	g.chr19:12997882C>T	-	1	c.73G>A	p.D25N	0.153846
OR10H3	26532	37	g.chr19:15852438C>G	+	1	c.236C>G	p.T79S	0.244776
ZFP42	132625	37	g.chr4:188924186C>T	+	3	c.225C>T	p.C75C	0.433962
RFX6	222546	37	g.chr6:117198968T>A	+	2	c.233T>A	p.L78*	0.351852
STX7	8417	37	g.chr6:132791751C>G	-	6	c.402G>C	p.E134D	0.096
AKAP12	9590	37	g.chr6:151671760A>G	+	4	c.2234A>G	p.E745G	0.367347
RAB2A	5862	37	g.chr8:61496786G>A	+	4	c.206G>A	p.R69H	0.447368
STOM	2040	37	g.chr9:124111399T>A	-	5	c.524A>T	p.Q175L	0.2
SF3A2	8175	37	g.chr19:2248458delC	+	9	c.1308delC	p.H436fs	0.33
SLC20A1	6574	37	g.chr2:113416607_113416608delAG	+	7	c.984_985delAG	p.P328fs	0.12
SETD2	29072	37	g.chr3:47164513delC	-	3	c.1613delG	p.G538fs	0.18
ANLN	54443	37	g.chr7:36455435delA	+	8	c.1464delA	p.V488fs	0.34
PRSS22	64063	37	g.chr16:2908034_2908036delCAG	-	1	c.70_72delCTG	p.L24del	0.33
NPEPPS	9520	37	g.chr17:45669428_45669429insA	+	11	c.1365_splice	p.K455_splice	0.32

ALPP	250	37	g.chr2:233243529_233243531delTGC	+	1	c.17_19delTGC	p.L13del	0.11
CCDC96	257236	37	g.chr4:7044507_7044509delCTC	-	1	c.157_159delGAG	p.E53del	0.5
TRPV5	56302	37	g.chr7:142625819delG	-	6	c.729delC	p.P243fs	0.24
APBA1	320	37	g.chr9:72082865delG	-	5	c.1356delC	p.P452fs	0.41
GRIN1	2902	37	g.chr9:140056884_140056886delGAG	+	13	c.1780_1782delGAG	p.E598del	0.08
BHLHB9	80823	37	g.chrX:102004419_102004421delGAG	+	4	c.496_498delGAG	p.E171del	0.07
UTY	7404	37	g.chrY:15448217_15448218insA	-	16	c.1771_splice	p.G591_splice	0.57
CD3G	917	37	g.chr11:118220583delA	+	3	c.205delA	p.K69fs	0.05
SLC24A1	9187	37	g.chr15:65918177_65918179delCTG	+	2	c.1759_1761delCTG	p.L591del	0.06
NANOS3	342977	37	g.chr19:13988575_13988577delAGC	+	1	c.513_515delAGC	p.A172del	0.33
RBPJ	3516	37	g.chr4:26417145_26417146insA	+	5	c.243_244insA	p.K81fs	0.07
SLC17A2	10246	37	g.chr6:25921520delT	-	3	c.361delA	p.M121fs	0.06
PRB2	653247	37	g.chr12:11546732_11546733insAGA	-	3	c.279_280insTCT	p.93_94insS	0.02
CHD2	1106	37	g.chr15:93540315_93540316insA	+	29	c.3724_3725insA	p.E1242fs	0.1
FXR2	9513	37	g.chr17:7517826delC	-	1	c.25delG	p.D9fs	0.33
TBKBP1	9755	37	g.chr17:45786123_45786124insC	+	8	c.1024_1025insC	p.S342fs	0.33
GOLGA2	2801	37	g.chr9:131019390delA	-	26	c.2965delT	p.Y989fs	0.04
CNNM1	26507	37	g.chr10:101089768delC	+	1	c.624delC	p.R208fs	0.33
HOXB2	3212	37	g.chr17:46622130_46622132delAGG	-	1	c.142_144delCCT	p.P48del	0.06
LYPD3	27076	37	g.chr19:43969653_43969655delAGC	-	1	c.69_71delGCT	p.23_24LL>L	0.03
MMRN1	22915	37	g.chr4:90844391_90844393delAGC	+	4	c.923_925delAGC	p.Q313del	0.02
G3BP1	10146	37	g.chr5:151173719delG	+	5	c.352_splice	p.G118_splice	0.37
KLF10	7071	37	g.chr8:103664245_103664246delTT	-	3	c.314_315delAA	p.Q105fs	0.51
GABBR2	9568	37	g.chr9:101151274delG	-	10	c.1391delC	p.P464fs	0.2
TIE1	7075	37	g.chr1:43782873_43782875delGAG	+	15	c.2413_2415delGAG	p.E806del	0.3
SLAMF1	6504	37	g.chr1:160589600_160589601insT	-	5	c.829_830insA	p.S277fs	0.05
PDE3A	5139	37	g.chr12:20803536_20803537insA	+	14	c.2925_splice	p.Q975_splice	0.11
PPP1R1C	151242	37	g.chr2:182981975_182981977delGAA	+	5	c.283_285delGAA	p.E98del	0.33
FRYL	285527	37	g.chr4:48544039_48544042delCTTA	-	45	c.5687_splice	p.Q1896_splice	0.2
ANXA13	312	37	g.chr8:124707762delT	-	6	c.451delA	p.I151fs	0.04
ZNF609	23060	37	g.chr15:64972995_64972997delCAC	+	7	c.4096_4098delCAC	p.H1371del	0.03
LPCAT2	54947	37	g.chr16:55566753delG	+	6	c.721delG	p.V241fs	0.19
KLHL38	340359	37	g.chr8:124659179delC	-	2	c.1426delG	p.V476fs	0.12
KIAA1462	57608	37	g.chr10:30316501_30316503delCTG	-	2	c.2574_2576delCAG	p.858_859SS>S	0.09
PLIN5	440503	37	g.chr19:4523962delC	-	8	c.970delG	p.D324fs	0.33
C2orf71	388939	37	g.chr2:29295647_29295649delTCC	-	1	c.1479_1481delGGA	p.493_494EE>E	0.04
TXNDC6	347736	37	g.chr3:138033173delC	-	6	c.460_splice	p.V154_splice	0.37
LRRC66	339977	37	g.chr4:52883766delT	-	1	c.14delA	p.Y5fs	0.35
ARMCX3	51566	37	g.chrX:100880152_100880154delTGA	+	5	c.183_185delTGA	p.D66del	0.02
AJAP1	55966	37	g.chr1:4772583_4772585delCCA	+	2	c.653_655delCCA	p.T225del	0.33
HCFC2	29915	37	g.chr12:104481762delA	+	9	c.1232_splice	p.G411_splice	0.46
SACS	26278	37	g.chr13:23910010_23910025delCTCTAAACATGCGTCC	-	10	c.7990_8005delGGACGCATGTTTAGAG	p.G2664fs	0.4
FAM155A	728215	37	g.chr13:108518338delC	-	1	c.607delG	p.D203fs	0.03
STX8	9482	37	g.chr17:9408350_9408359delAGTACCTTGG	-	5	c.448_splice	p.E150_splice	0.16
NPEPPS	9520	37	g.chr17:45669428_45669429insA	+	11	c.1365_splice	p.K455_splice	0.24
PSMA7	5688	37	g.chr20:60715953delC	-	2	c.144delG	p.K48fs	0.41
DTX3L	151636	37	g.chr3:122283372_122283383delTAAGTCCTCGGG	+	1	c.99_110delTAAGTCCTCGGG	p.KSSG34del	0.16
VEPH1	79674	37	g.chr3:157081226_157081227insT	-	9	c.1661_1662insA	p.N554fs	0.04
GOT1L1	137362	37	g.chr8:37791833_37791834insT	-	9	c.1243_1244insA	p.T415fs	0.09
ACSL3	2181	37	g.chr2:223781198_223781199insA	+	5	c.540_541insA	p.F180fs	0.11
ULK4	54986	37	g.chr3:41860984_41860985insT	-	19	c.1778_1779insA	p.K593fs	0.09
TPTE	7179	37	g.chr21:10944697delA	-	11	c.537delT	p.F179fs	0.02
MTMR14	64419	37	g.chr3:9739546_9739549delTGTC	+	18	c.1765_1768delTGTC	p.C589fs	0.18
FRG1	2483	37	g.chr4:190873437_190873439delAAG	+	3	c.254_256delAAG	p.E86del	0.03
KIAA1009	22832	37	g.chr6:84896233delA	-	12	c.1218delT	p.F406fs	0.03

COL1A1	1277	37	g.chr17:48270191_48270192insC	-	27	c.1841_1842insG	p.G614fs	0.27
ADH1B	125	37	g.chr4:100237419delT	-	4	c.300delA	p.K100fs	0.4
NKTR	4820	37	g.chr3:42679035_42679036insC	+	13	c.1839_1840insC	p.S613fs	0.02
ANGPT2	285	37	g.chr8:6378797_6378798insT	-	4	c.700_701insA	p.I234fs	0.05
RBPJ	3516	37	g.chr4:26417145_26417146insA	+	5	c.243_244insA	p.K81fs	0.03
PRDM12	59335	37	g.chr9:133543701_133543702delGT	+	3	c.570_splice	p.E190_splice	0.12
H1FOO	132243	37	g.chr3:129268110_129268111insA	+	3	c.645_646insA	p.R215fs	0.33
CHD7	55636	37	g.chr8:61769038_61769040delGGA	+	34	c.7199_7201delGGA	p.2400_2401RR>R	0.21

Supplementary Table 4: dRanger fusion results

individual	chr of first partner	strand (partner 1)	chr coordinates of first partner	chr of second partner	strand (partner 2)	chr coordinates of second partner	class	span (nts)	# reads in tumor	# reads in normal	gene 1	site 1	gene 2	site 2	predicted fusion	BPresult
SFT35	12	0	57486880	12	0	57509206	inversion	22332	6	0	*NAB2*	Exon 5 of NAB2(+)	*STAT6*	4.0 kb from *STAT6*(-) transcription start site	-	1*
	6	1	151358108	11	1	18892699	inter_chr	NaN	5	0	*MTHFD1L*	Exon 26 of MTHFD1L(+)	*MRGPRX1*	IGR: 63Kb before MRGPRX1(-)	-	0
	11	1	117167586	11	0	131750892	long_range	14583310	5	0	*BACE1*	Intron of BACE1(-): 3bp after exon 2	*NTM*	Intron of NTM(+): 31Kb before exon 2	Antisense fusion	1
SFT38	17	1	39619088	17	0	39633854	tandem_dup	14766	5	0	*KRT32*	Exon 6 of KRT32(-)	*KRT35*	Exon 6 of KRT35(-)	Protein fusion: mid-	0
SFT40	12	1	57486902	12	1	57510439	inversion	23538	11	0	*NAB2*	Exon 5 of NAB2(+)	*STAT6*	5.2 kb from *STAT6*(-) transcription start site	-	1*
	20	0	1559360	20	0	1895757	inversion	336397	6	0	*SIRPB1*	Intron of SIRPB1(-): 20bp before exon 2	*SIRPA*	Exon 3 of SIRPA(+)	Protein fusion: mid-	0
	12	0	57486907	12	0	57510439	inversion	23577	4	0	*NAB2*	Exon 5 of NAB2(+)	*STAT6*	5.2 kb from *STAT6*(-) transcription start site	-	1*
SFT46	7	1	142124497	7	0	142162351	tandem_dup	37854	4	0	*TRYX3*	IGR: 173Kb before TRYX3(-)	*TRYX3*	IGR: 210Kb before TRYX3(-)	-	0
SFT48	12	1	57486924	12	1	57507668	inversion	20744	8	0	*NAB2*	Exon 5 of NAB2(+)	*STAT6*	2.5 kb from *STAT6*(-) transcription start site	Protein fusion: mid-	1*
	12	0	57486925	12	0	57507666	inversion	20721	6	0	*NAB2*	Exon 5 of NAB2(+)	*STAT6*	2.5 kb from *STAT6*(-) transcription start site	Protein fusion: mid-	1*
TB-1569	12	0	57487019	12	0	57493334	inversion	6320	11	0	*NAB2*	Intron of NAB2(+): 40bp after exon 5	*STAT6*	Intron of *STAT6*(-): 115bp before exon 16	Protein fusion: in	1*
TB-5309	19	1	54783495	19	1	55175600	inversion	392105	7	0	*LILRB2*	Exon 5 of LILRB2(-)	*LILRB4*	Intron of LILRB4(+): 37bp before exon 4	Protein fusion: mid-	0
TB-5852	12	0	57486740	12	0	57501443	inversion	14701	7	0	*NAB2*	Exon 4 of NAB2(+)	*STAT6*	Exon 3 of *STAT6*(-)	Protein fusion: mid-	1*
TB-8115	12	1	57486777	12	1	57506957	inversion	20184	13	0	*NAB2*	Intron of NAB2(+): 18bp after exon 4	*STAT6*	1.8 kb from *STAT6*(-) transcription start site	Transcript fusion	1*
	12	0	57486775	12	0	57506958	inversion	20197	13	0	*NAB2*	Intron of NAB2(+): 16bp after exon 4	*STAT6*	1.8 kb from *STAT6*(-) transcription start site	Transcript fusion (NAB2	1*
TB-9344	12	0	57486867	12	0	57510088	inversion	23217	5	0	*NAB2*	Exon 5 of NAB2(+)	*STAT6*	4.9 kb from *STAT6*(-) transcription start site	-	1*
	8	0	117655583	8	1	117782526	deletion	126953	4	0	*EIF3H*	IGR: 1Kb before EIF3H(-)	*UTP23*	Exon 2 of UTP23(+)	-	1

BP: Breakpointer algorithm. 1=positive (read identified that crosses the breakpoint); 0=negative
*NAB2-STAT6 fusion

Supplementary Table 5: Primer Sequences

Primer_name	Primer_sequence
SFT40_NAB2F	**TGTAAAACGACGGCCAGT**AAGAACTGGGAGGCCCTCCA
SFT_40_STAT6R	**CAGGAAACAGCTATGAC**ATCTCCACCCTCCTGCTCTG
SFT_48_NAB2F	**TGTAAAACGACGGCCAGT**TGCATATAGGGGCACTGGGC
SFT_48_STAT6R	**CAGGAAACAGCTATGAC**ACTGTATCACCCTCCCCTGG
NAB2F1	**TGTAAAACGACGGCCAGT**GCACGAGCTCACCATCAACG
STAT6R1	**CAGGAAACAGCTATGAC**AAGATGCCGCAGGTGTTGGG
NAB2F2	**TGTAAAACGACGGCCAG**TGCCCGAGAGAGCACCTACTT
STAT6R1	**CAGGAAACAGCTATGAC**ACATAGAGCCGCTGCACTTT
GAPDH_F	GAGTCAACGGATTTGGTCGT
GAPDH_R	TTGATTTTGGAGGGATCTCG

M13 tags are boldfaced

Supplementary Information

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