Supplementary Information (1 PDF file)

Identification of Recurrent *NAB2-STAT6* Gene Fusions in Solitary Fibrous Tumor by Integrative Sequencing

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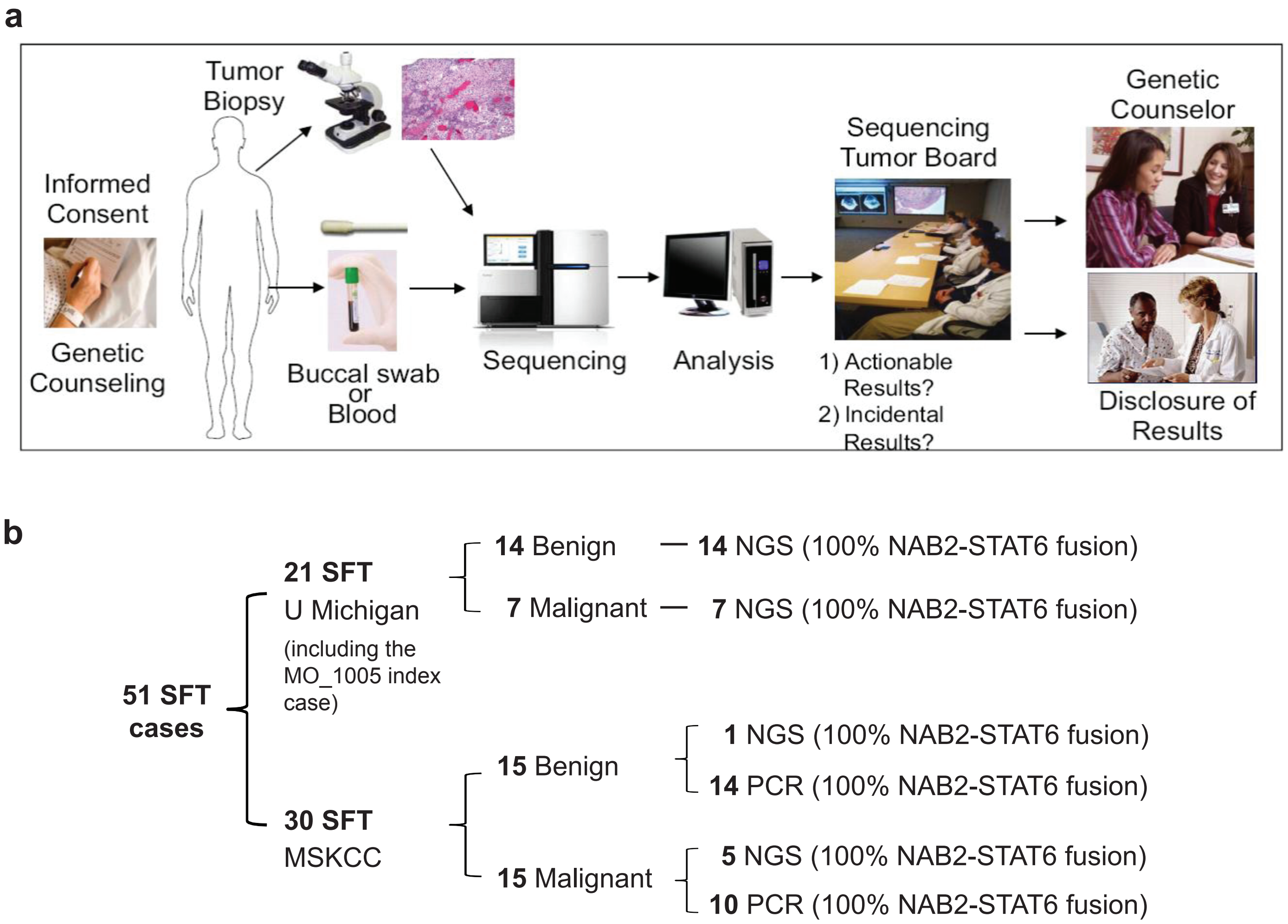
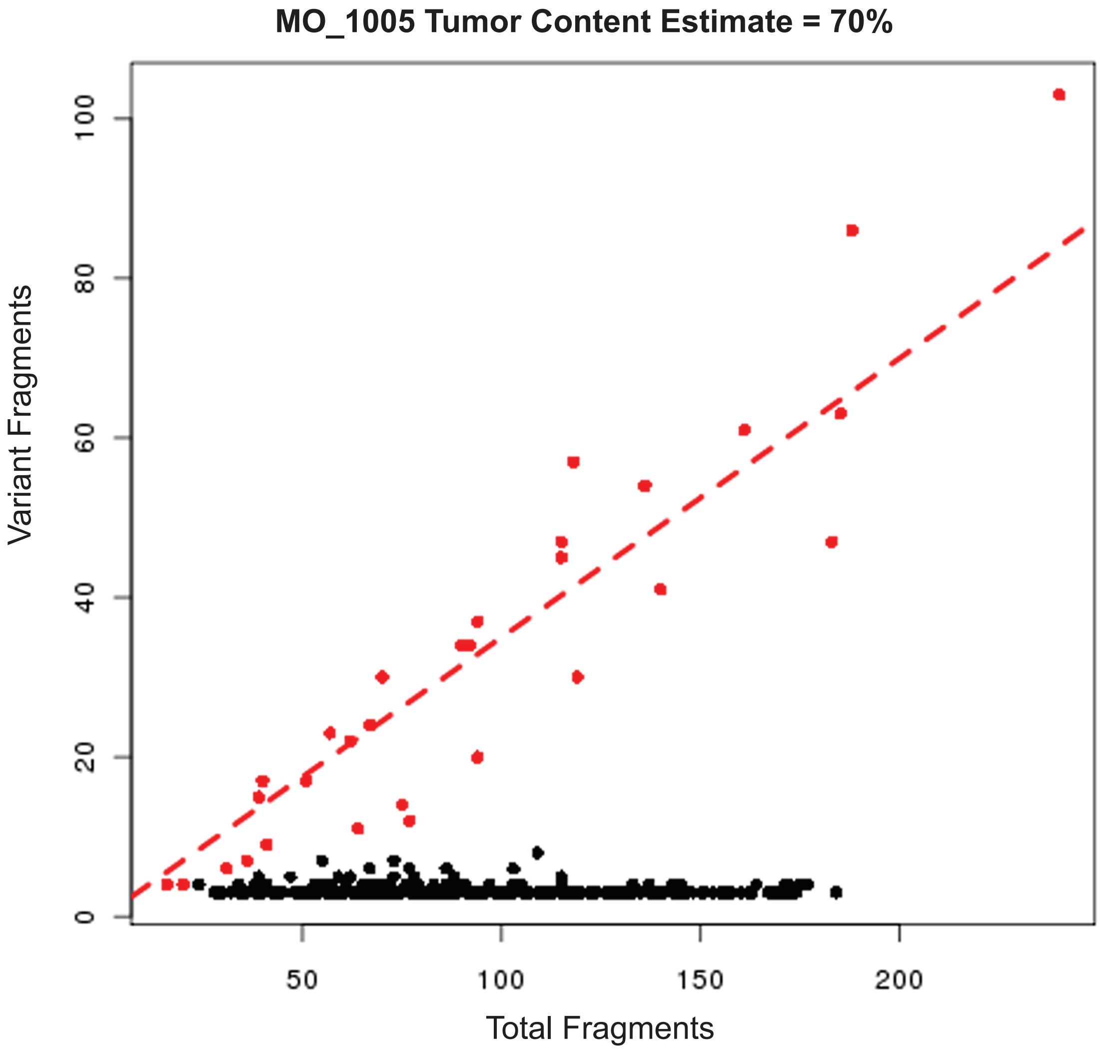
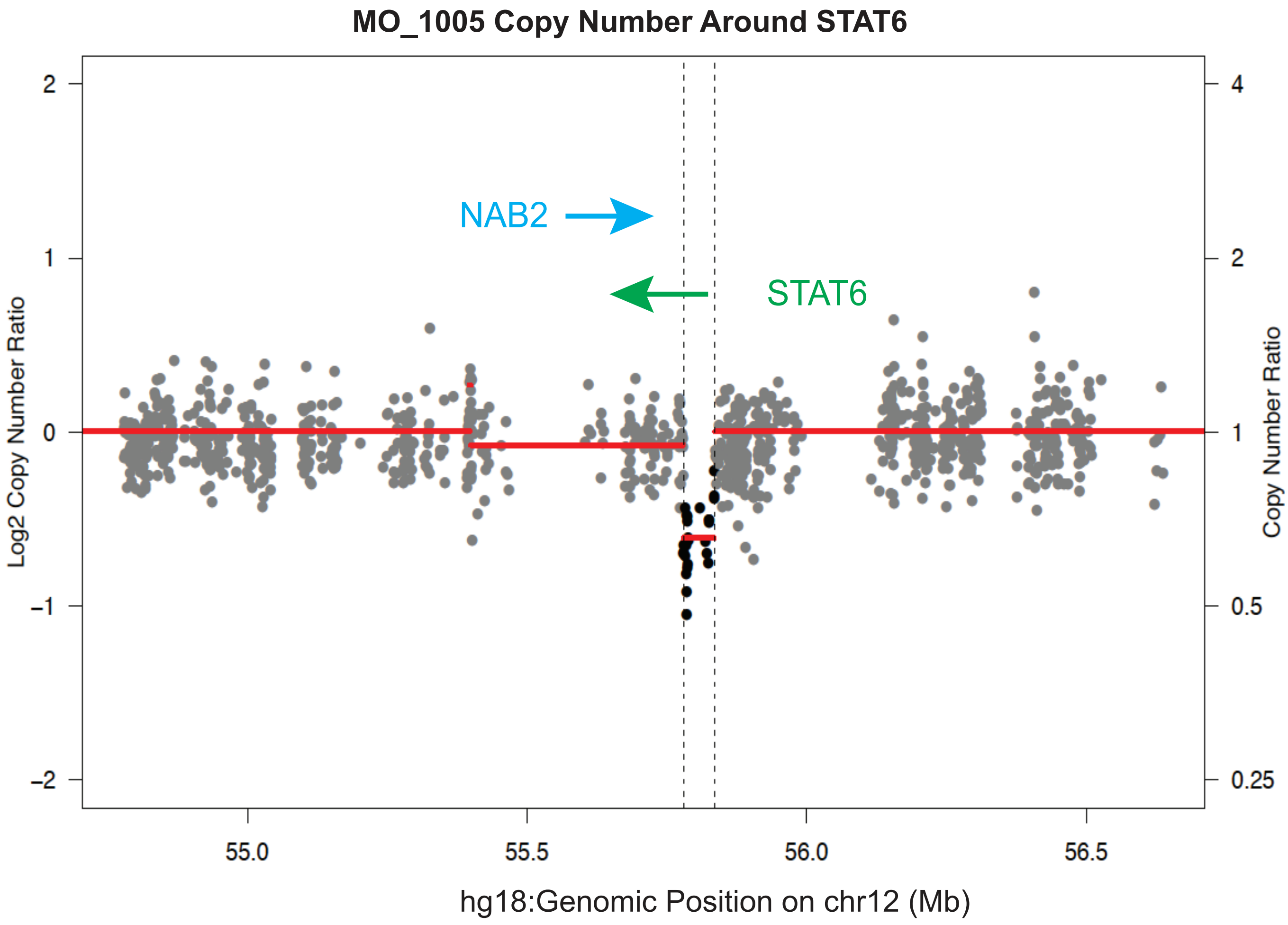
This file contains Supplementary Figures 1-10 with legends and Supplementary Tables 1-8.



Supplementary Figure 1. **a**. A schematic of the workflow for the clinical sequencing protocol (MI-ONCOSEQ) in which the index patient (MO_1005) was enrolled. Patients in this protocol meet with a genetic counselor and provide written informed consent. A sample of their normal tissue (i.e. blood or buccal swab) is obtained for germline studies. A CT-guided biopsy is employed to obtain tumor specimens. The samples are subjected to integrative sequencing and analyzed for mutations. Each patient is then presented at a multi-disciplinary Sequencing Tumor Board in which “actionable” and/or “informative” mutations are deliberated upon. This information can then be transmitted back to the patient and primary oncologist. **b**. Summary of the SFT cases analyzed in this study. In total, 51 SFT samples were analyzed, including 29 benign and 22 malignant. Among these samples, 27 underwent RNA sequencing and 24 were screened by RT-PCR for recurrent *NAB2-STAT6* fusions. MSKCC, Memorial Sloan-Kettering Cancer Center. NGS, next-generation sequencing (transcriptome sequencing). PCR, RT-PCR screening.

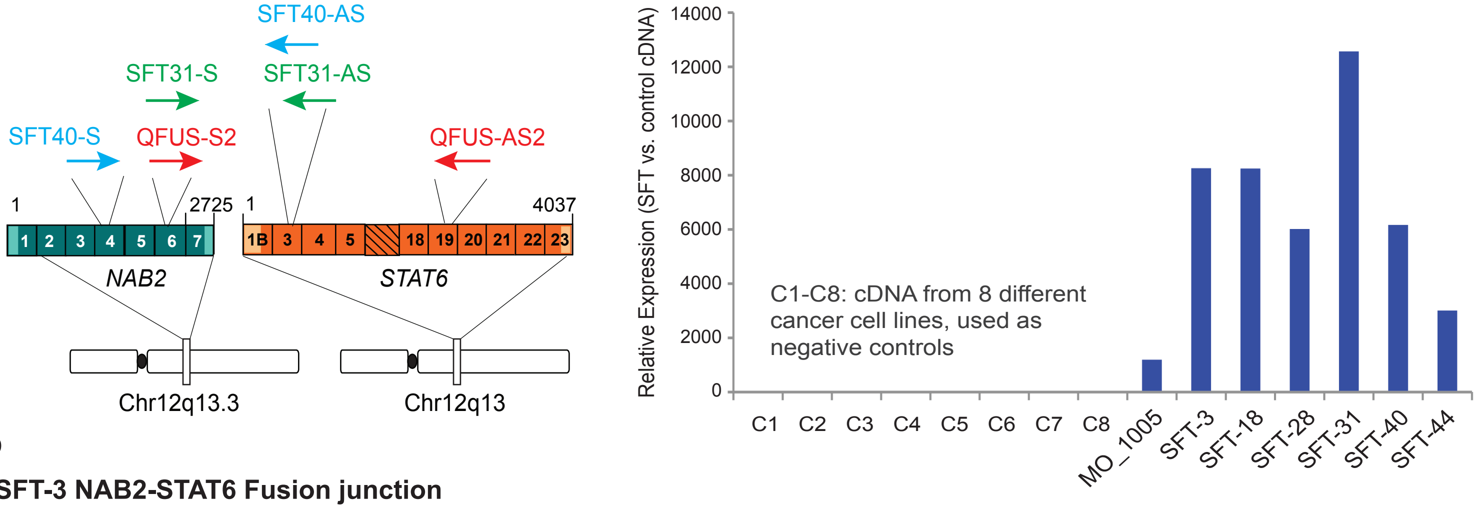


Supplementary Figure 2. Tumor content of index case MO_1005. Tumor content was estimated from the sequence data by fitting a binomial mixture model with two components to the set of most likely SNV candidates on 2-copy genomic regions. Details of data analysis were described in the Methods section.



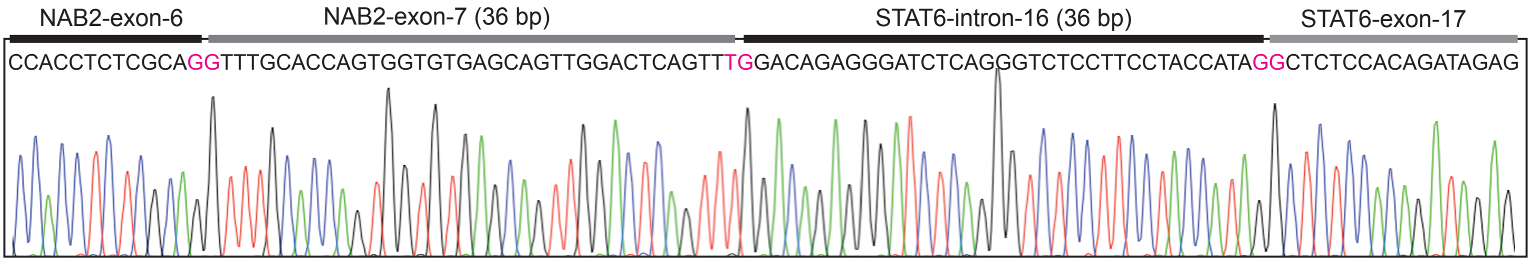
Supplementary Figure 3. Copy number changes around *STAT6* gene in MO_1005. Copy number aberrations were quantified and reported for each gene as the segmented normalized log2-transformed exon coverage ratios between each tumor sample and matched normal sample.

a

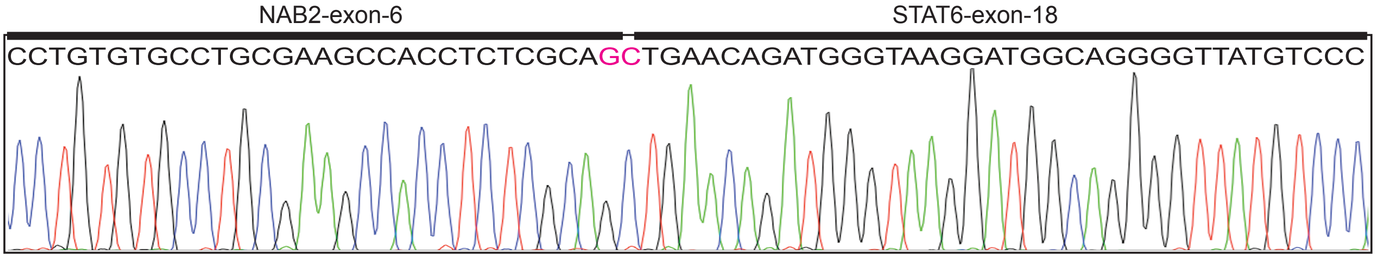


b

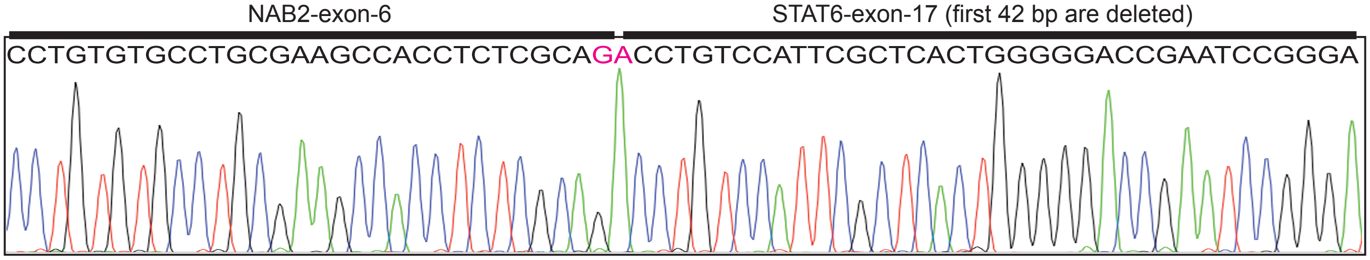
SFT-3 NAB2-STAT6 Fusion junction



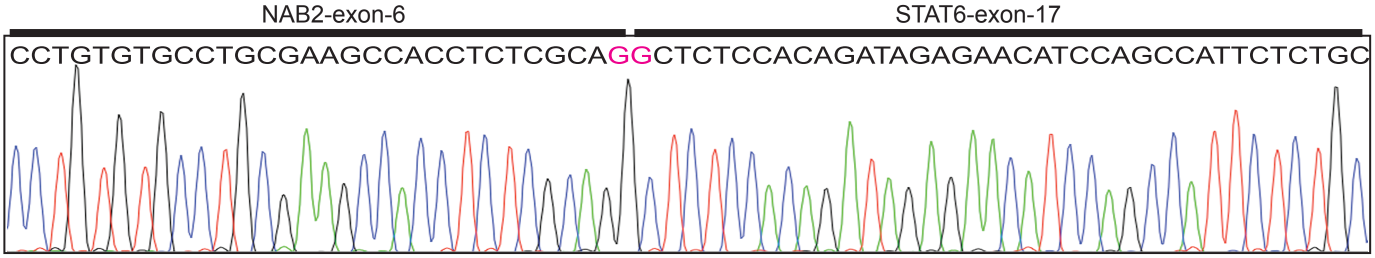
SFT-18 NAB2-STAT6 Fusion junction (same as in MO_1005)



SFT-28 NAB2-STAT6 Fusion junction

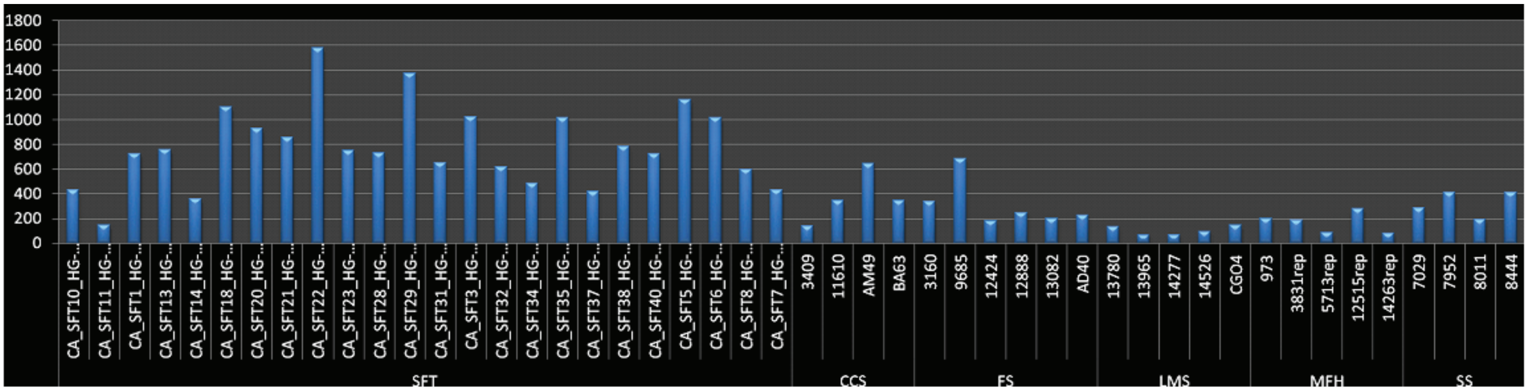


SFT-44 NAB2-STAT6 Fusion junction

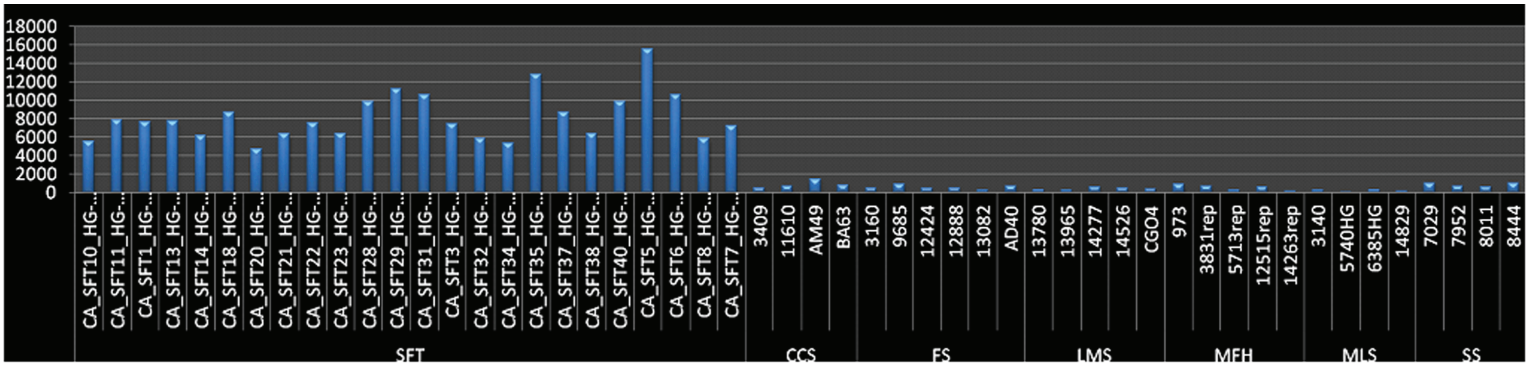


Supplementary Figure 4. a. Validation of *NAB2-STAT6* fusions in SFT samples by quantitative RT-PCR. **A.**The locations of PCR primer pairs are shown on the left. The relative expression levels of *NAB2-STAT6* fusions in SFT samples in comparison to control cDNAs are shown on the right. **b**. Sequences across *NAB2-STAT6* fusion junctions in SFT samples. PCR products generated by the same pairs of primers as in A (agarose gel image in Figure 2A) were sequenced and representative chromatograms of fusion junctions are shown.

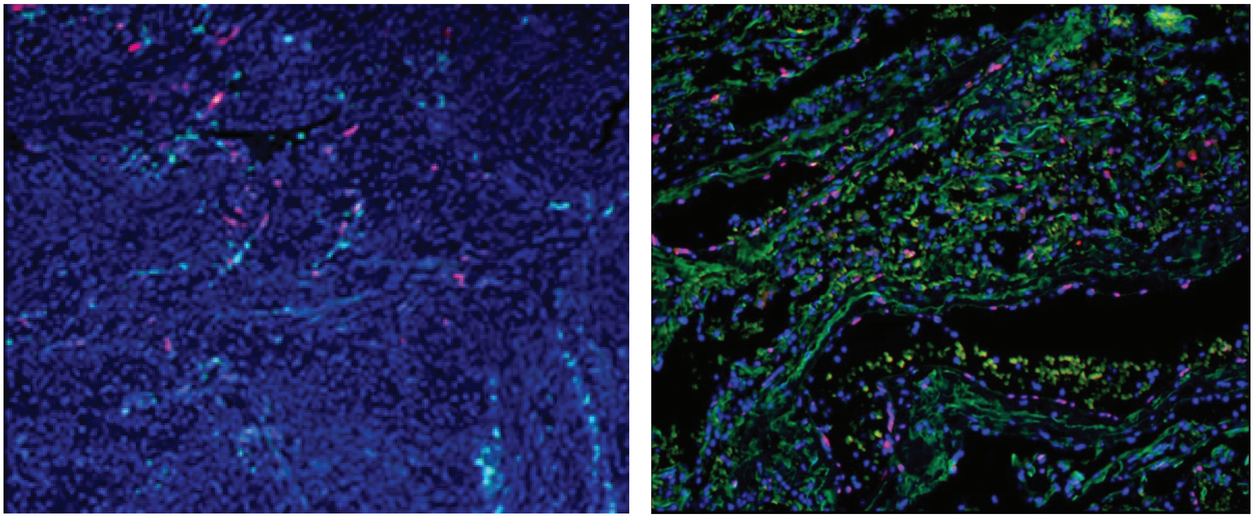
NAB2, 212803_s_at



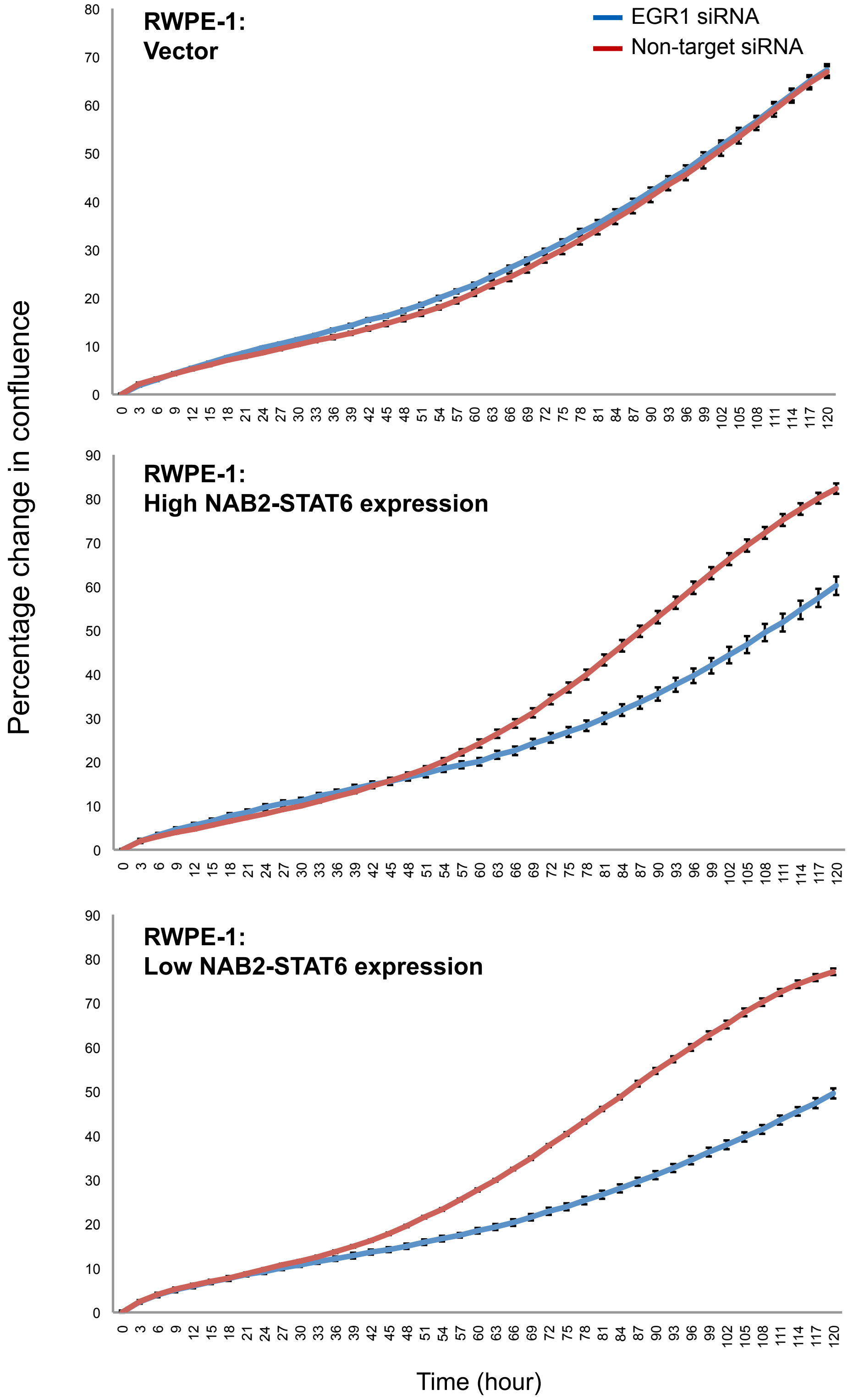
STAT6, 201331_s_at



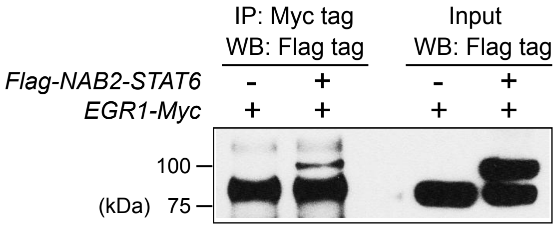
Supplementary Figure 5. Relative expression of *NAB2* and *STAT6* in SFT tumors as measured by Affymetrix U133A microarray analysis across a panel of soft tissue sarcomas. SFT, solitary fibrous tumor; CCS, clear cell sarcoma; FS, fibrosarcoma; LMS, leiomyosarcoma; MFH, malignant fibrous histiocytoma; MLS, myxoid liposarcoma; SS, synovial sarcoma.



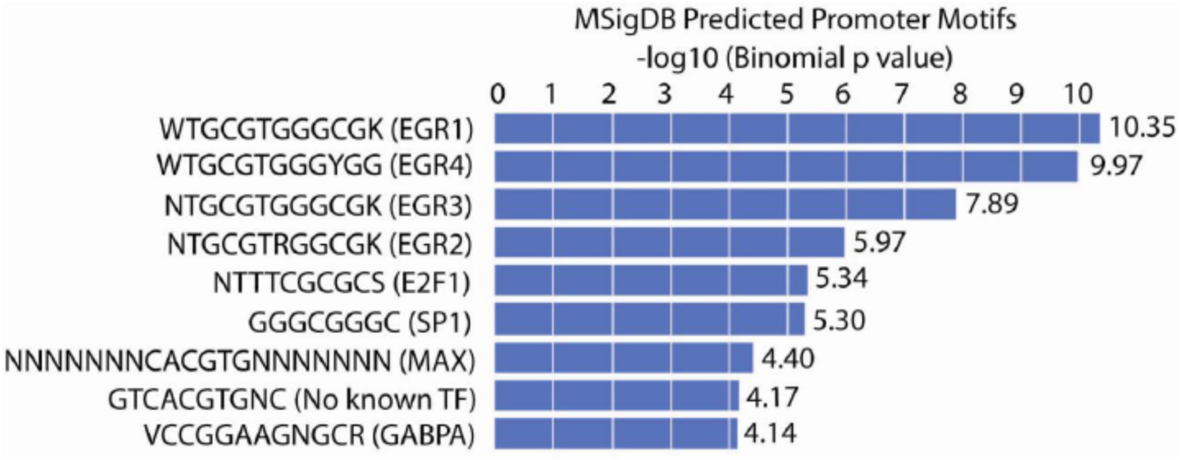
Supplementary Figure 6. Immunofluorescence staining of phophorylated STAT6. Immunostaining using antibodies against the phospho-STAT6 Y641 showed negative expression in the SFT tumors tested (a representative image of SFT-14 shown on the left; negative nuclei noted by the DAPI blue color), while nuclear expression of phosphorylated STAT6 was detected in the entrapped endothelial cells (left panel) or adjacent lung parenchyma (right panel; positive nuclei highlighted in pink).



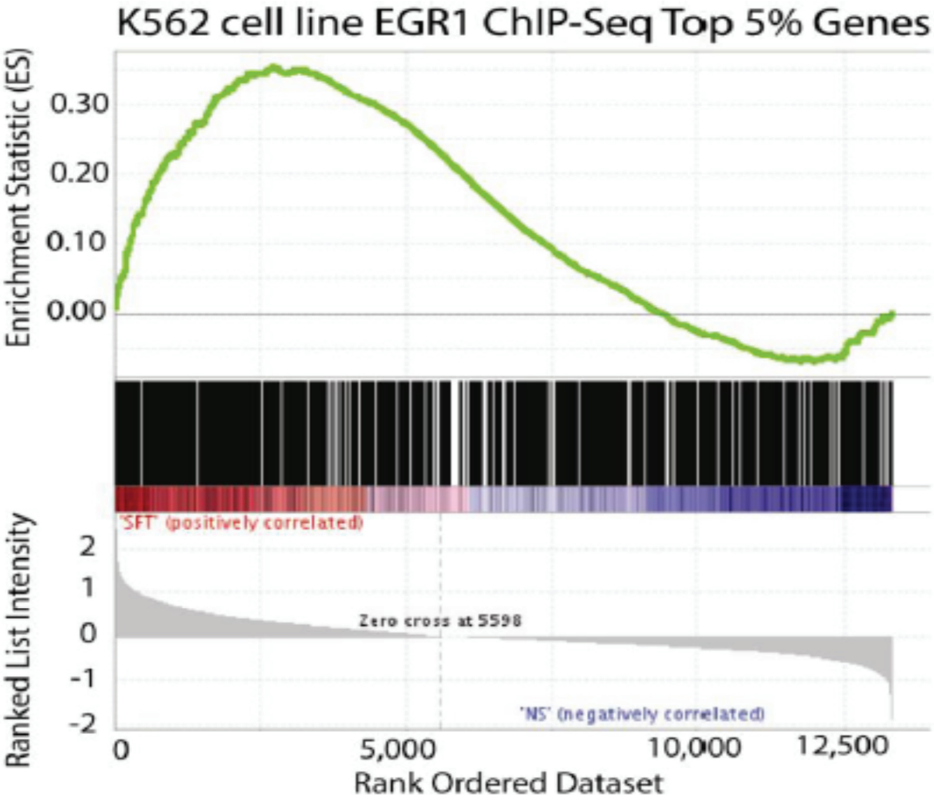
Supplementary Figure 7. SiRNA targeting *EGR1* effectively decreases cell proliferation of RWPE-1 cells stably expressing NAB2-STAT6 fusion proteins. RWPE-1 stables lines were transfected twice with siRNA targeting EGR1 or non-targeting siRNA. After 24 hrs, cells were plated at equal confluence in 24-well dishes and proliferation was analyzed using the live-cell imaging Incucyte Analyzer.



Supplementary Figure 8. Physical interaction of EGR1 and NAB2-STAT6 fusion proteins. 293T cells were transfected with myc-tagged EGR1 alone or co-transfected with myc-tagged EGR1 and Flag-tagged NAB2-STAT6. After 24 hrs, nuclear lystaes were immunoprecipitated with anti-myc tag antibody, followed by Western blotting with anti-Flag antibody. The size and expression level of the Flag-NAB2-STAT6 fusion protein in total nuclear lysate was shown on the right (1/10th the IP amount).



Supplementary Figure 9. K562 EGR1 ChIP-SEQ dataset (GSM803414) peak-to-gene mappings are highly enriched for EGR1 target genes. The bar plot shows the base 10 logarithm of binomial p-value of the enrichment of EGR1 promoter motifs within the DNA sequences comprising the top 5% of predicted EGR1 binding sites. The top four most highly enriched motifs are all of the early growth response family of transcription factors, with EGR1 being the topmost enriched.



Supplementary Figure 10. GSEA analysis of SFT gene expression profiles against EGR1 target genes derived from ChIP-SEQ data. In the upper panel, the Y axis shows the running enrichment score (ES) computed by the GSEA algorithm. The X axis shows genes rank-ordered by the degree of differential expression in SFT compared with non-SFT sarcoma samples. High ranking genes are over-expressed in SFT relative to non-SFT (red) and low ranking genes are over-expressed in non-SFT relative to SFT. The lower panel shows the intensity of the differential expression of each gene computed by the Signal2Noise algorithm.

Supplementary Table 1. Nonsynonymous somatic mutations in MO_1005.

SAMPLE	GENE	LOC (hg19)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM	PolyPhen-2	SIFT	RPKPM
MO_1005	*EPRS*	chr1:220157596	C	G	12	77	0.16	p.L1014F	0	1.000	0	45.4
MO_1005	*RBM10*	chrX:47035963	A	G	30	119	0.25	p.N214S	1	0.997	0.80	21.9
MO_1005	*FCGR3A*	chr1:161518429	C	A	63	185	0.34	p.W70L,p.W69L,p.W34L	-2	1.000	0	12.6
MO_1005	*STX6*	chr1:180971785	C	A	61	161	0.38	p.S86I	-2	0.908	0	10.1
MO_1005	*ASCC3*	chr6:101076947	T	C	7	36	0.19	p.N1440S	1	0	0.33	7.8
MO_1005	*FRYL*	chr4:48559517	G	T	6	52	0.12	p.Q1360K	1	0.412	0.18	7.3
MO_1005	*ZNF711*	chrX:84525090	A	T	41	140	0.29	p.N349I	-3	0.021	0.02	6.2
MO_1005	*RNF103*	chr2:86847539	C	T	22	62	0.35	p.E94K	1	0.969	0.03	6.0
MO_1005	*ARHGEF5*	chr7:144060459	C	T	23	57	0.40	p.Q233*	-4	-	-	1.1
MO_1005	*GLIPR1L2*	chr12:75816819	G	C	6	60	0.10	p.K240N	0	0.396	0.40	0.4
MO_1005	*OR4K5*	chr14:20389481	C	T	86	188	0.46	p.T239M	-1	1.000	0	0.2
MO_1005	*SLFN14*	chr17:33884483	T	C	39	94	0.41	p.E200G	-2	0.999	0	0.1
MO_1005	*CLCA1*	chr1:86964441	G	A	34	92	0.37	p.S767N	1	0	0.37	0.0
MO_1005	*OR2G2*	chr1:247752034	C	T	103	240	0.43	p.R125C	-3	0.618	0.01	0.0

Supplementary Table 2. Gene Copy Number Gains in MO_1005.

Segment (hg19)	Genes in this region	Span	Number of exons	Copy Number Ratio
chr3:126260603-126260750	*CHST13*	148 bp	2	1.78
chr3:62358330-62358478	*FEZF2*	149 bp	2	1.71
chr16:72821707-72821891	*ZFHX3*	185 bp	2	1.64
chr7:114562539-114562682	*MDFIC*	144 bp	2	1.63
chr6:72892428-72892819	*RIMS1*	392 bp	3	1.59
chr7:149461819-149462177	*ZNF467*	359 bp	3	1.58
chr6:30888869-30908815	*VARS2, SFTA2, DPCR*	19,947 bp	3	1.45
chr19:39096074-39096826	*MAP4K1*	753 bp	4	1.41
chr6:159650958-159653511	*FNDC1*	2554 bp	6	1.33
chr7:142460789-142494836	*PRSS1, PRSS2*	34,048 bp	7	1.31

Supplementary Table 3. Gene Copy Number Losses in MO_1005.

Segment (hg19)	Genes in this region	Span	Number of exons	Copy Number Ratio
chr20:43726736-43726889	*KCNS1*	154 bp	2	0.49
chr20:61511187-61511461	*DIDO1*	275 bp	3	0.58
chr14:105617103-105617379	*JAG2*	277 bp	3	0.59
chr20:825648-825946	*FAM110A*	299 bp	3	0.61
chr12:22778235-22778399	*ETNK1*	165 bp	2	0.62
chr12:57493145-57548429	*STAT6, LRP1*	55,285 bp	26	0.66
chr13:49794585-49795038	*MLNR*	454 bp	3	0.68
chr4:53305141-53305907	*none*	767 bp	7	0.69
chr19:45656325-45656920	*NKPD1*	596 bp	5	0.70

Supplementary Table 4. Gene fusions identified in 27 SFT tumors. Recurrent *NAB2-STAT6* fusions are in bold.

SAMPLE	5' Gene	3' Gene	# Supporting Reads	Type	Note
MO_1005	***NAB2***	***STAT6***	1104	Intrachromosomal	
SFT-3	***NAB2***	***STAT6***	1271	Intrachromosomal	Reciprocal
SFT-3	*STAT6*	*NAB2*	127	Intrachromosomal	Reciprocal
SFT-3	*OXTR*	*ATXN10*	4	Interchromosomal	
SFT-18	***NAB2***	***STAT6***	1943	Intrachromosomal	Reciprocal
SFT-18	*STAT6*	*NAB2*	237	Intrachromosomal	Reciprocal
SFT-28	***NAB2***	***STAT6***	3131	Intrachromosomal	
SFT-28	*ACOX3*	*AX746755*	40	Read-Through	
SFT-28	*ZDHHC16*	*UBTD1*	5	Read-Through	
SFT-28	*NCOR2*	*OAF*	4	Interchromosomal	
SFT-31	***NAB2***	***STAT6***	3425	Intrachromosomal	
SFT-31	*ZNF337*	*C15ORF26*	12	Interchromosomal	
SFT-31	*PEPD*	*FXYD3*	14	Intrachromosomal	
SFT-40	***NAB2***	***STAT6***	1415	Intrachromosomal	
SFT-44	***NAB2***	***STAT6***	4483	Intrachromosomal	Reciprocal
SFT-44	***STAT6***	***NAB2***	119	Intrachromosomal	Reciprocal
SFT-44	*SLICK*	*CFH*	4	Intrachromosomal	
UM-SFT-1	***NAB2***	***STAT6***	885	Intrachromosomal	Reciprocal
UM-SFT-1	*STAT6*	*NAB2*	5	Intrachromosomal	Reciprocal
UM-SFT-2	***NAB2***	***STAT6***	25	Intrachromosomal	
UM-SFT-3	***NAB2***	***STAT6***	1768	Intrachromosomal	
UM-SFT-3	*ROC2*	*GRK7*	31	Read-Through	
UM-SFT-4	***NAB2***	***STAT6***	2185	Intrachromosomal	Reciprocal
UM-SFT-4	*STAT6*	*NAB2*	21	Intrachromosomal	Reciprocal
UM-SFT-4	*PSMD5*	*TRAF1*	9	Tandem duplication	
UM-SFT-4	*MYL3*	*TESSP5*	7	Read-Through	
UM-SFT-4	*DKFZP761E198*	*RNASEH2C*	4	Read-Through	
UM-SFT-5	***NAB2***	***STAT6***	717	Intrachromosomal	
UM-SFT-5	*BC035722*	*RAB28*	4	Read-Through	
UM-SFT-5	*AF268386*	*DDR2*	3	Tandem duplication	
UM-SFT-6	***NAB2***	***STAT6***	657	Intrachromosomal	Reciprocal
UM-SFT-6	*STAT6*	*NAB2*	44	Intrachromosomal	Reciprocal
UM-SFT-7	***NAB2***	***STAT6***	515	Intrachromosomal	Reciprocal
UM-SFT-7	*STAT6*	*NAB2*	24	Intrachromosomal	Reciprocal
UM-SFT-7	*ZMIZ1*	*LAYN*	10	Interchromosomal	
UM-SFT-7	*TGAT*	*CDH18*	10	Intrachromosomal	
UM-SFT-7	*NCOA2*	*MAL2*	6	Intrachromosomal	
UM-SFT-7	*ATXN1*	*GMPR*	6	Intrachromosomal	
UM-SFT-7	*ZFYVE1*	*SPRYD7*	5	Interchromosomal	
UM-SFT-7	*RASAL2*	*MAN1A2*	4	Intrachromosomal	
UM-SFT-8	***NAB2***	***STAT6***	1004	Intrachromosomal	Reciprocal
UM-SFT-8	*STAT6*	*NAB2*	127	Intrachromosomal	Reciprocal
UM-SFT-9	***NAB2***	***STAT6***	991	Intrachromosomal	Reciprocal
UM-SFT-9	*STAT6*	*NAB2*	40	Intrachromosomal	Reciprocal
UM-SFT-10	***NAB2***	***STAT6***	924	Intrachromosomal	
UM-SFT-11	***NAB2***	***STAT6***	1193	Intrachromosomal	Reciprocal
UM-SFT-11	*STAT6*	*NAB2*	26	Intrachromosomal	Reciprocal
UM-SFT-12	***NAB2***	***STAT6***	401	Intrachromosomal	
UM-SFT-13	***NAB2***	***STAT6***	470	Intrachromosomal	
UM-SFT-14	***NAB2***	***STAT6***	784	Intrachromosomal	Reciprocal
UM-SFT-14	*STAT6*	*NAB2*	24	Intrachromosomal	Reciprocal
UM-SFT-15	***NAB2***	***STAT6***	1313	Intrachromosomal	Reciprocal
UM-SFT-15	*STAT6*	*NAB2*	260	Intrachromosomal	Reciprocal
UM-SFT-16	***NAB2***	***STAT6***	571	Intrachromosomal	Reciprocal
UM-SFT-16	*STAT6*	*NAB2*	70	Intrachromosomal	Reciprocal
UM-SFT-16	*TMEM140*	*STRA8*	13	Read-Through	
UM-SFT-16	*AK097500*	*C17ORF78*	5	Read-Through	
UM-SFT-17	***NAB2***	***STAT6***	116	Intrachromosomal	
UM-SFT-18	***NAB2***	***STAT6***	472	Intrachromosomal	
UM-SFT-19	***NAB2***	***STAT6***	962	Intrachromosomal	
UM-SFT-20	***NAB2***	***STAT6***	609	Intrachromosomal	Reciprocal
UM-SFT-20	*STAT6*	*NAB2*	85	Intrachromosomal	Reciprocal

Supplementary Table 5. Recurrent Expression Outliers in SFT tumors (Part-1). Outliers are in bold.

	Number of Outlier Samples	**Gene Expression (RPKM). Bold = Outlier.**						
Gene		**MO_1005**	**SFT3**	**SFT18**	**SFT28**	**SFT31**	**SFT40**	**SFT44**
ABHD14A	4	**64.3**	**43.3**	20.1	**69.6**	13.7	5.5	**68.0**
ABI2	4	18.0	**26.1**	**26.0**	20.2	**36.5**	**36.0**	14.3
ACCN2	4	**70.4**	**90.9**	1.3	**36.1**	0.5	19.5	**25.4**
ADAMTSL5	4	9.9	**20.6**	**25.7**	**23.5**	12.6	8.2	**34.7**
AF136186	3	**526.8**	14.5	**892.2**	394.8	0.2	103.9	**893.2**
AFAP1L2	2	8.9	2.1	17.0	14.8	**51.2**	14.1	**53.6**
AHDC1	6	**41.8**	**38.9**	**59.9**	**38.6**	**58.2**	25.7	**34.1**
AK055602	3	4.3	76.0	**120.3**	30.3	**228.0**	45.1	**130.8**
AK074994	3	1.5	5.7	10.5	**149.6**	8.6	**29.3**	**25.5**
AK092048	4	**50.4**	**52.6**	**51.1**	**73.5**	0.1	20.2	11.3
AK092715	3	**36.2**	**41.3**	16.7	**61.3**	2.1	15.4	5.0
AK095458	3	**967.2**	**466.8**	218.2	74.5	**1494.8**	340.6	380.6
AK123035	2	37.4	23.2	**60.0**	12.3	10.2	20.1	**65.3**
AK308561:1	4	6.8	**34.2**	**31.5**	**135.7**	2.0	16.8	**57.3**
AK308561:2	4	5.4	**24.4**	**20.3**	**70.4**	1.0	12.6	**36.5**
AL831954	3	**23.4**	0.7	12.6	12.1	**53.2**	11.5	**41.6**
ALKBH5	3	79.1	**110.8**	**145.8**	77.9	76.0	**149.0**	94.5
ALX4	7	**155.6**	**142.8**	**101.3**	**97.7**	**98.9**	**79.7**	**122.8**
AQP5	3	**85.6**	**182.8**	3.9	39.7	0.1	5.3	**239.7**
AQP6	3	**34.1**	**46.6**	0.5	**20.6**	0.2	3.5	19.4
argBPIB	4	18.5	**26.9**	**25.1**	21.7	**32.6**	**35.3**	14.8
ARMCX2	2	**33.9**	**32.3**	21.3	11.6	17.8	12.0	8.1
ATP2B4	5	14.2	**152.7**	**162.4**	**225.4**	**223.5**	**115.6**	74.1
B4GALNT1	2	19.0	11.3	**57.4**	11.3	7.9	**38.2**	22.6
BAHCC1	5	**80.6**	**60.8**	**81.3**	**77.6**	31.2	0.7	**74.0**
BAI1	4	9.7	**24.5**	10.3	**41.3**	**27.4**	3.6	**29.5**
BC006113	2	1.2	0.5	2.1	**22.1**	0.6	3.8	**70.5**
BC010054	2	101.9	1278.0	**1982.5**	157.0	621.8	**2056.6**	755.0
BC034684	2	**1940.9**	944.6	484.0	201.8	**3241.9**	686.5	785.9
BC080605	5	18.2	**71.4**	**70.2**	**354.4**	3.4	**29.4**	**138.4**
BC110369	2	3.9	19.2	17.6	**75.7**	1.8	9.4	**31.9**
BCL2	3	6.2	**20.7**	**28.5**	0.5	14.8	**22.1**	12.5
BCOR	4	**68.6**	**50.2**	32.8	**119.8**	22.4	11.7	**64.6**
BGN	2	**2330.5**	155.6	110.7	**1581.6**	13.2	85.5	49.9
BHMT	2	**96.2**	**100.0**	2.3	0.2	0.3	1.3	10.4
BMP5	3	**44.2**	**45.5**	20.1	32.1	0.2	0.7	**44.2**
BOC	3	**56.3**	19.7	37.0	**107.4**	23.9	24.0	**71.7**
Borg4	3	**166.3**	75.1	118.2	**120.9**	**287.9**	42.6	107.2
C1orf92	3	16.5	**48.3**	**46.2**	**27.1**	12.4	17.7	8.8
C1QL1	5	**47.8**	**118.0**	**34.7**	**82.7**	1.5	12.3	**34.6**
C1QL4	3	0.3	2.2	**182.7**	4.2	0.6	**133.0**	**74.9**
C1QTNF4	2	0.7	9.3	12.1	11.3	14.2	**33.5**	**104.8**
C5orf46	2	**65.6**	0.7	0.1	**39.3**	0.0	0.8	0.2
C9orf41	3	12.9	**22.5**	**25.7**	6.4	**24.2**	6.5	12.6
CA11	7	**176.5**	**127.7**	**95.6**	**138.4**	**168.0**	**47.9**	**80.2**
CACNA2D1	3	**21.3**	**28.6**	**29.6**	12.9	0.1	13.7	6.5
CCDS43604	6	**37.0**	**31.9**	**40.1**	19.9	**24.9**	**65.6**	**24.1**
CCR10	3	**30.4**	17.6	**46.9**	9.2	7.5	15.0	**56.1**
CDC42EP4	2	**162.0**	72.9	115.0	113.9	**283.1**	41.7	103.8
CDH24	5	62.7	**209.7**	91.2	**416.6**	**151.3**	**137.5**	**202.7**
CDO1	2	33.1	**75.1**	15.8	12.2	33.7	16.6	**336.4**
CELSR2	2	**50.2**	0.9	0.5	**59.5**	21.7	0.1	12.3
CERCAM	7	**112.3**	**88.4**	**135.5**	**83.5**	**134.6**	**77.2**	**55.7**
CFH	5	**678.0**	**547.5**	**242.2**	**166.7**	87.7	2.6	**367.1**
CHAD	4	**854.5**	**108.5**	9.8	**165.8**	3.1	1.9	**571.9**
CHI3L1	3	**1660.9**	**849.7**	385.0	110.9	**3020.3**	568.5	668.9
CLEC4F	3	14.8	1.6	3.2	**58.0**	**76.1**	16.3	**48.0**
CLSTN3	2	21.7	20.8	**35.0**	13.7	**41.4**	24.9	12.4
CMKLR1	3	4.1	15.9	**32.9**	4.1	**36.9**	**74.4**	11.3
COL11A2:1	4	8.3	**36.6**	**29.5**	**22.2**	2.9	3.2	**25.1**
COL17A1	3	**372.1**	10.7	**649.6**	115.6	0.1	81.8	**530.3**

Supplementary Table 5. Recurrent Expression Outliers in SFT tumors (Part-2). Outliers are in bold.

	Number of Outlier Samples	Gene Expression (RPKM). Bold = Outlier.						
Gene		MO_1005	SFT3	SFT18	SFT28	SFT31	SFT40	SFT44
COL1A1	2	**1544.3**	392.2	732.4	840.2	9.6	**3766.5**	120.6
COL8A2	2	**55.1**	28.1	18.5	28.9	12.7	23.7	**110.5**
COMP	4	**251.8**	**340.4**	20.9	**268.3**	1.0	18.0	**323.4**
CPT1C	2	**20.5**	7.8	13.5	14.6	15.3	13.8	**23.7**
CPXM1	5	**79.7**	**617.2**	16.1	**150.1**	64.9	**119.2**	**223.2**
CPZ	5	30.7	**260.8**	**374.7**	**119.5**	1.0	**124.8**	**83.0**
CR594717	2	86.6	1083.1	**1683.8**	134.0	527.7	**1739.7**	635.2
CR596119	3	130.0	**1568.9**	**2528.7**	219.8	780.1	**2620.9**	949.1
CR597604	2	80.1	1021.8	**1558.4**	120.6	491.2	**1624.3**	601.0
CR598488	2	5.8	**37.6**	7.1	**33.8**	0.3	2.8	5.2
CR607033	2	93.7	1176.4	**1823.5**	144.3	571.9	**1892.7**	695.0
CR617227	2	30.6	4.5	23.4	10.2	**90.0**	**94.4**	5.9
CRTAC1	3	1.6	17.3	**58.2**	2.9	6.9	**143.5**	**28.8**
CTXN1	2	99.6	53.8	**128.5**	75.5	22.3	11.8	**197.2**
CXXC5	3	**70.1**	59.1	**95.9**	**87.1**	12.1	5.9	16.7
CYP11A1	4	**41.4**	**20.8**	18.3	**39.1**	3.0	18.9	**78.0**
D87946	6	**79.4**	**51.3**	**42.5**	**52.6**	**65.7**	19.7	**37.1**
D87947	6	**46.6**	**30.2**	**25.0**	**31.4**	**38.9**	11.6	**21.7**
DAGLA	4	5.3	9.3	**64.1**	9.4	**63.8**	**47.5**	**42.0**
DISP1	2	**21.8**	11.4	4.9	**43.1**	17.1	4.2	15.4
DKFZp434D2030	2	**26.8**	**35.6**	0.4	16.1	0.2	3.0	13.8
DKFZp434K2323	5	81.3	**263.8**	123.3	**680.6**	**179.4**	**172.0**	**274.1**
DKFZp686A1849	2	0.5	4.7	**21.0**	0.2	**34.2**	19.2	12.1
DKFZp761D0614	5	**21.0**	**48.6**	**23.4**	**82.8**	19.3	**31.7**	12.5
DKK1	2	**72.7**	9.6	10.2	16.7	12.6	0.5	**105.7**
DLX3	3	**89.4**	**69.1**	22.0	**80.3**	0.8	0.5	8.6
DLX4	4	**106.6**	**74.0**	**60.7**	**193.8**	1.4	0.9	13.1
DMXL2	2	8.5	15.5	6.3	19.8	**32.9**	**26.0**	15.3
DNALI1	2	32.2	21.3	29.2	**50.0**	32.6	8.7	**42.5**
DOK5	2	17.9	7.3	13.8	**20.7**	4.3	9.7	**44.5**
DPYS	2	**38.9**	**23.3**	1.9	0.1	10.7	0.4	1.8
DQ595431	6	**33.2**	**22.9**	**25.8**	19.4	**27.1**	**22.4**	**25.1**
DSE	2	14.5	21.4	**48.8**	8.6	**49.4**	11.7	6.3
ECEL1	2	**83.8**	41.9	10.9	24.7	**79.3**	1.3	0.1
EFNA2	4	**48.4**	**106.4**	1.5	**96.6**	0.1	0.1	**178.6**
EGFLAM	2	7.1	11.1	1.1	8.3	**31.9**	**31.1**	14.5
ELFN1	2	0.8	**20.7**	10.3	**37.6**	6.0	9.7	0.7
EMILIN2	2	9.8	23.4	**80.9**	17.4	40.4	36.4	**191.6**
ENC1	2	4.8	2.5	3.0	1.6	**239.7**	**89.6**	1.6
EPHB3	3	53.9	**65.1**	19.0	**62.9**	0.8	49.1	**82.1**
EPYC	2	0.1	0.4	**97.6**	**534.0**	6.5	3.9	7.6
ESM1	2	4.7	6.2	**25.5**	**20.2**	0.2	6.0	2.8
FAIM2	2	**31.5**	10.7	14.9	8.7	3.8	**44.8**	11.5
FAP	2	5.8	8.8	13.6	0.4	13.3	**40.4**	**25.8**
FBLN1	2	65.7	65.1	**1029.7**	52.0	**1055.5**	283.3	553.2
FEZF2	4	0.1	**98.9**	**25.4**	0.1	0.0	**37.8**	**34.3**
FGF2	2	13.9	**30.3**	**22.1**	7.9	8.1	9.3	11.3
FGFR1	6	47.1	**178.9**	**219.9**	**114.7**	**224.1**	**234.1**	**238.2**
FKSG40	6	**51.0**	**335.5**	**111.3**	**113.1**	**55.6**	18.3	**294.3**
FLJ00193	6	**83.0**	**149.7**	**151.6**	**143.6**	**66.9**	32.4	**68.2**
FLJ37078	2	17.5	16.1	**20.2**	8.2	11.6	**31.2**	13.7
FLJ37464	3	**28.6**	11.8	16.2	**27.4**	**26.5**	17.1	8.2
FOXP4	6	**169.0**	**190.3**	**144.9**	**158.0**	50.5	**127.8**	**182.3**
FRS2	2	8.4	8.5	**28.6**	18.5	14.5	**21.5**	13.8
FZD7	4	6.7	**181.7**	**76.9**	21.5	26.0	**85.4**	**104.6**
GFRAL	2	**23.3**	0.0	0.3	2.4	0.0	0.0	**33.1**
Gli2	4	13.4	16.4	**42.9**	15.5	**37.3**	**36.3**	**20.3**
GLI2	6	17.5	**24.3**	**52.4**	**25.1**	**36.8**	**42.8**	**30.9**
GLS	2	**39.5**	20.2	15.4	**43.4**	6.4	10.1	9.9
GP1BB	3	28.9	35.7	**52.8**	**60.3**	13.0	29.0	**122.0**
GPC4	3	**103.4**	**57.6**	5.8	0.2	14.7	9.0	**203.0**

Supplementary Table 5. Recurrent Expression Outliers in SFT tumors (Part-3). Outliers are in bold.

Gene	Number of Outlier Samples	Gene Expression (RPKM). Bold = Outlier.						
		MO_1005	SFT3	SFT18	SFT28	SFT31	SFT40	SFT44
GPM6B	3	28.7	2.6	**212.1**	**168.9**	57.7	32.2	**170.3**
GPR162	2	10.5	6.3	9.6	**28.2**	14.8	7.5	**25.5**
GPR78	5	18.0	**150.3**	**217.7**	**70.6**	0.6	**71.7**	**48.0**
GPR88	7	**52.9**	**57.2**	**205.1**	**24.2**	**198.5**	**99.7**	**151.1**
GRIA2	4	10.7	**108.8**	**62.5**	0.1	**25.5**	**166.1**	0.1
GSN	3	712.6	**2319.7**	**2208.5**	200.3	722.5	1070.6	**1826.9**
HDAC9	2	**22.1**	11.6	17.4	**20.3**	7.2	0.4	16.1
HECTD2	3	15.1	**35.8**	17.2	**60.5**	14.7	**24.0**	9.2
hGli2	6	18.0	**25.0**	**53.0**	**26.3**	**36.4**	**43.4**	**32.0**
HOXB3	5	1.2	**98.7**	**54.0**	1.8	**54.9**	**34.3**	**31.0**
HOXB6	2	0.4	22.2	12.7	0.5	**45.7**	2.8	**31.2**
HOXB8	3	0.1	**41.7**	16.5	0.4	**26.2**	1.2	**43.0**
HOXC10	7	**99.1**	**155.5**	**98.7**	**417.7**	**137.4**	**72.4**	**228.0**
HOXC11	7	**63.8**	**96.8**	**77.0**	**70.3**	**63.7**	**44.7**	**117.8**
HOXC12	6	**30.7**	**40.9**	**41.7**	**27.3**	**26.2**	0.4	**94.5**
HOXC13	6	**40.2**	**24.6**	**42.7**	**33.5**	**22.7**	0.3	**70.1**
HOXC4	7	**90.3**	**52.0**	**46.5**	**109.5**	**46.8**	**55.3**	**63.8**
HOXC5	7	**32.1**	**26.9**	**20.9**	**48.9**	**23.3**	**23.0**	**22.6**
HOXC6	7	**128.1**	**90.2**	**57.4**	**165.0**	**57.7**	**60.7**	**86.4**
HOXC8	7	**44.9**	**43.2**	**33.5**	**157.8**	**22.2**	**28.6**	**32.8**
HOXC9	2	**95.8**	57.5	45.3	**98.0**	23.8	31.2	62.0
HSD11B1	5	**126.7**	**57.5**	**82.1**	11.3	4.7	**81.4**	**139.6**
IGF1	2	**43.0**	2.6	11.3	1.4	9.5	**160.8**	14.2
IGF2	7	**3169.1**	**4851.2**	**3275.5**	**11939.1**	**12992.3**	**4698.0**	**9851.7**
IGF2AS	7	**33.7**	**51.1**	**21.4**	**46.7**	**47.0**	**24.2**	**106.7**
IL11RA	6	**46.8**	**140.0**	**58.0**	**52.2**	**36.8**	28.0	**52.0**
INS-IGF2	7	**3687.9**	**5616.8**	**3804.4**	**14003.5**	**14716.8**	**5393.3**	**11495.2**
IQSEC3	4	12.2	**28.2**	**31.9**	8.5	**28.7**	**36.3**	14.0
ISLR	6	**980.0**	**1004.1**	**371.3**	**1250.7**	232.6	**277.6**	**1225.4**
ISYNA1	2	82.6	63.0	42.9	57.9	**134.1**	11.5	**108.9**
KAZALD1	6	**64.6**	**415.4**	**140.6**	**126.8**	**79.9**	27.2	**303.2**
KCNAB3	2	**20.9**	19.5	7.1	**37.6**	4.7	7.7	13.6
KCNC1	3	**20.2**	14.1	0.1	**80.6**	0.0	0.4	**31.8**
KCTD1	6	**116.0**	2.9	**62.3**	**52.7**	**248.2**	**49.0**	**187.2**
KERA	2	0.0	0.0	**151.9**	**267.8**	6.1	10.6	3.0
KHDRBS3	2	3.3	2.2	5.4	2.6	**62.3**	**52.9**	10.1
KIAA0182	7	**54.0**	**63.4**	**107.2**	**83.9**	**156.5**	**99.3**	**59.2**
KIAA0638	2	36.7	143.1	123.3	63.5	84.2	**211.0**	**149.1**
KIAA0709:1	5	**308.1**	**253.4**	**253.0**	161.9	187.9	**319.4**	**399.2**
KIAA0709:2	6	**270.8**	**232.4**	**235.0**	54.4	**207.0**	**324.7**	**274.4**
KIAA0827:2	2	13.1	**24.6**	20.5	**49.5**	11.2	11.8	11.9
KIAA0856	4	33.5	**44.1**	16.3	**64.2**	**53.4**	**62.4**	40.5
KIAA0897	2	**31.9**	8.8	**36.8**	17.6	11.6	16.1	4.3
KIAA0950	2	**37.4**	12.6	17.7	10.2	4.5	**53.4**	13.7
KIAA0957	2	**24.3**	**22.6**	5.6	12.1	3.4	6.6	11.2
KIAA1171	2	2.9	4.2	**27.1**	2.4	**28.2**	11.7	2.9
KIAA1308	2	**71.4**	63.5	49.5	**81.6**	17.6	8.8	67.7
KIAA1350	2	4.6	2.3	**80.6**	**87.3**	40.6	6.2	12.8
KIAA1444	2	**34.1**	1.1	6.0	**46.8**	0.4	11.1	10.7
KIAA1462	2	2.3	48.9	**99.6**	9.3	**266.2**	37.1	37.8
KIAA1482	4	**61.6**	24.9	**48.4**	**78.8**	6.2	36.7	**52.1**
KIAA1520	2	**25.1**	11.2	10.1	13.4	4.6	2.4	**24.3**
KIAA1547	5	**65.5**	**79.5**	**84.8**	**72.6**	24.9	24.2	**82.7**
LAG3	5	17.1	**81.8**	**135.9**	13.6	**34.7**	**44.9**	**283.9**
LHX2	2	5.0	**70.7**	0.7	0.2	0.0	11.1	**20.7**
LMO4	2	**364.5**	104.7	28.1	**300.8**	33.5	57.6	201.4
LOC126520	3	3.9	**52.0**	**31.4**	10.8	5.5	0.2	**49.2**
LOC284297	2	**180.3**	58.9	26.6	**292.7**	25.9	5.9	40.7
LOC404266	3	0.1	**57.9**	**32.3**	0.0	14.4	**20.5**	13.4
LOC91461	7	**316.5**	**303.0**	**147.9**	**505.4**	**280.7**	**258.6**	**322.2**
LPHN1	5	15.6	**33.5**	**27.1**	**35.5**	**32.7**	18.9	**42.0**

Supplementary Table 5. Recurrent Expression Outliers in SFT tumors (Part-4). Outliers are in bold.

Gene	Number of Outlier Samples	Gene Expression (RPKM). Bold = Outlier.						
		MO_1005	SFT3	SFT18	SFT28	SFT31	SFT40	SFT44
LRCH2	2	**20.3**	6.1	0.4	**49.0**	6.8	3.8	7.1
LRP3	4	61.9	**112.2**	**94.3**	50.0	**78.5**	55.0	**199.3**
LSP1	4	**250.9**	**255.6**	230.2	**369.4**	208.5	98.4	**517.5**
MAP3K12	2	37.1	30.6	25.3	**42.6**	**50.7**	27.4	16.4
MCOLN3	3	**62.9**	0.3	5.7	0.7	**197.5**	**49.9**	0.1
MPDZ	2	25.3	**32.4**	**63.9**	22.2	22.1	23.3	18.3
MPDZ_variant_protein	4	**31.7**	**37.3**	**71.7**	**31.4**	22.3	25.1	21.6
MRC2	6	**286.4**	**244.3**	**250.1**	114.7	**215.0**	**329.4**	**341.3**
MST123	6	67.7	**243.2**	**304.4**	**196.1**	**285.9**	**308.3**	**356.8**
MUM1	2	**34.5**	22.9	24.6	**32.0**	7.9	12.5	28.2
MXRA5	4	28.3	**405.9**	**276.5**	**83.0**	41.7	41.5	**88.7**
NAB1	7	**75.5**	**113.4**	**100.9**	**130.4**	**64.5**	**86.0**	**76.6**
NAB2	5	**92.2**	81.5	**89.1**	67.7	**136.7**	**91.4**	**117.8**
NCAM2	2	0.7	**28.2**	**32.9**	1.7	4.5	14.6	9.7
NEFL	2	0.2	0.0	14.9	0.0	**104.4**	**72.6**	0.0
NFIX	6	**408.1**	**436.6**	**437.1**	**451.6**	**387.4**	222.1	**617.4**
NPB:1	3	**25.7**	7.2	5.7	**157.6**	0.4	6.2	**122.8**
NPH4	2	**40.6**	0.6	1.8	9.8	**58.6**	4.6	0.8
NPW	7	**594.9**	**2341.1**	**588.3**	**1751.5**	**382.1**	**21.5**	**1178.0**
NR_002775	3	7.6	9.6	**41.6**	14.7	2.9	**23.1**	**21.6**
NR_002797	5	**198.7**	**271.2**	**215.7**	**362.0**	150.3	146.9	**538.5**
NR_003716	7	**124.5**	**116.8**	**119.2**	**194.9**	**140.0**	**42.0**	**174.1**
NR3C1	2	7.5	25.6	**68.7**	26.0	**43.0**	39.6	16.4
NRG2:3	2	5.9	9.3	5.2	**28.0**	19.6	1.8	**47.4**
NRGN	5	191.0	**480.4**	**279.3**	**579.4**	**699.3**	104.2	**2015.6**
NTRK1	4	**35.2**	**28.2**	**58.3**	**30.5**	0.0	14.0	0.8
NUMBL	4	37.3	**56.0**	**53.0**	34.5	43.6	**62.2**	**58.6**
NXPH4	2	**45.0**	0.7	2.0	10.8	**65.0**	5.0	0.9
OAF	2	164.2	192.9	25.0	**284.7**	97.7	7.3	**447.7**
OLFM2	5	6.1	**385.4**	**347.1**	**127.6**	9.1	**97.2**	**94.9**
PALM	3	**111.9**	98.5	**117.7**	89.8	59.8	72.7	**152.4**
PAM	2	**301.7**	**269.4**	29.8	166.6	100.8	29.3	33.8
PCDH10	2	1.3	**69.7**	**51.1**	9.3	0.2	0.2	23.6
PCOLCE	4	112.6	**1179.3**	**1089.3**	462.5	429.2	**710.2**	**1392.6**
PCSK1	3	**42.5**	6.8	3.7	3.3	**41.1**	**182.1**	9.4
PDGFD	3	**66.6**	38.3	**67.4**	5.6	12.5	**184.0**	19.9
PDZD4	2	**48.6**	1.6	9.9	**61.3**	0.5	15.2	20.2
PEAR1	6	**82.3**	**149.3**	**151.6**	**142.2**	**67.5**	32.1	**66.9**
PEG8/IGF2AS	7	**34.4**	**52.6**	**22.0**	**48.0**	**48.0**	**24.1**	**109.6**
PEPP1	3	**144.2**	54.5	**102.8**	62.7	50.6	77.3	**134.8**
PAM	2	**299.0**	**239.5**	23.8	107.1	93.8	23.0	23.3
PHYHIP	3	4.8	16.5	**154.8**	5.3	**68.0**	**49.2**	2.5
PLEKHA4	3	**134.3**	56.3	**109.3**	62.9	62.8	84.3	**118.0**
PLEKHG2	3	9.9	**29.2**	14.4	**31.4**	**32.8**	11.2	18.2
PLK5	3	2.7	**40.8**	**25.1**	8.0	4.6	0.1	**37.7**
PLSCR4	2	19.1	20.5	**68.9**	26.9	12.8	6.5	**65.0**
PNMAL1	2	**22.6**	13.9	13.9	6.3	**22.2**	17.2	15.5
PP14296	5	4.1	**81.2**	**111.1**	**54.9**	26.3	**150.7**	**261.8**
pp9974	7	**4580.0**	**6957.1**	**4723.8**	**17468.1**	**18147.8**	**6668.1**	**14211.7**
PPFIA4	2	**27.6**	7.5	**31.5**	14.5	11.4	13.6	3.7
PRCD	2	1.9	**43.2**	19.7	13.4	21.2	3.9	**31.7**
PRKACB	3	**131.1**	15.3	**113.3**	32.1	**173.6**	38.5	2.3
PROS1	2	**71.0**	15.2	7.2	**63.0**	8.2	7.1	12.9
PRRX2	5	57.9	**94.6**	**211.9**	**301.9**	**115.2**	52.2	**148.1**
PRTN3	2	1.1	**21.2**	1.9	2.9	11.9	0.9	**24.2**
PSD	2	16.7	18.9	**24.4**	8.1	9.2	16.3	**23.2**
PTCH2	4	10.6	**90.9**	**41.2**	**37.9**	2.4	5.9	**31.0**
PTGDS	2	526.8	616.5	4.1	**5060.5**	263.2	33.0	**6228.9**
PTPN13	2	4.7	17.8	**20.4**	1.4	**29.7**	18.2	10.9
PTPRV	2	**39.1**	0.9	7.9	0.3	4.8	**31.0**	0.1
RALGDS	2	**72.5**	66.2	51.4	**83.5**	18.3	9.1	70.9

Supplementary Table 5. Recurrent Expression Outliers in SFT tumors (Part-5). Outliers are in bold.

		Gene Expression (RPKM). Bold = Outlier.						
Gene	**Number of Outlier Samples**	**MO_1005**	**SFT3**	**SFT18**	**SFT28**	**SFT31**	**SFT40**	**SFT44**
RARA	5	**161.6**	**123.9**	**146.4**	**119.3**	79.0	74.6	**126.6**
RBM9	3	**48.0**	**80.9**	40.2	**47.0**	24.0	22.3	40.2
RCN3	6	**162.3**	**102.5**	**83.8**	**190.5**	79.1	**92.3**	**114.4**
ROM1	2	7.1	8.4	**26.2**	13.3	11.1	13.1	**30.2**
SALP	2	3.9	2.1	5.9	3.1	**61.7**	**53.6**	10.4
SCLIP	3	**113.2**	29.8	16.4	**89.3**	58.1	20.6	**146.7**
SCN4B	4	**51.0**	**559.4**	29.0	**41.8**	1.5	3.1	**837.6**
SEMA6C	5	**24.2**	**62.3**	**25.5**	**41.2**	9.1	15.4	**33.7**
SEMA7A	5	**222.4**	**204.7**	**141.9**	**69.3**	7.3	15.2	**181.2**
semaY	3	18.4	**49.5**	20.2	**30.0**	8.5	12.9	**21.9**
SEPT5	3	23.0	28.0	**38.0**	**44.5**	9.6	22.0	**85.4**
SERTAD2	3	**27.3**	**32.4**	**30.7**	16.0	22.6	20.7	22.0
SESN3	2	2.3	4.0	6.9	1.0	**24.7**	**26.9**	1.5
SEZ6L2	2	42.8	22.2	**83.4**	52.1	7.6	62.4	**86.3**
SH3PXD2A	4	29.5	**63.7**	**98.8**	36.9	23.6	**183.3**	**57.9**
SIPA1L1	2	15.6	5.7	6.4	13.2	**31.6**	6.8	**27.9**
SIX1	6	**61.0**	**43.6**	**21.0**	**68.7**	0.5	**38.4**	**75.2**
SLC38A10	3	**136.0**	**106.2**	79.8	72.0	39.6	28.0	**124.8**
SLIT2	2	**42.0**	0.3	1.9	3.3	7.1	**57.0**	14.2
SLITRK3	2	0.0	**33.5**	**26.8**	0.0	0.8	0.8	0.8
SMG6	2	26.3	39.0	**47.0**	29.9	31.1	24.3	**51.1**
SORCS2	4	**42.7**	5.3	**85.4**	0.5	**51.7**	**83.0**	1.1
SPHK1	2	27.0	**49.9**	22.4	38.2	1.6	4.8	**73.8**
STAT6	2	126.4	124.6	157.8	167.6	**301.6**	**203.4**	148.0
STIM2	4	**48.7**	21.1	**40.8**	**58.8**	5.4	31.4	**42.6**
STMN3	3	**117.8**	31.0	17.1	**93.0**	60.6	21.4	**152.9**
STRA6	5	3.7	**70.7**	**96.9**	**48.5**	23.5	**131.5**	**232.6**
SYNGAP1	5	**43.5**	26.4	**28.8**	**56.0**	**47.6**	**36.6**	8.1
SYT1	3	0.6	10.7	**23.4**	4.3	**24.4**	**30.0**	1.1
SYT7	6	**222.4**	**329.1**	**458.9**	**235.8**	123.3	**448.8**	**176.6**
TAL1	4	**40.7**	1.6	16.0	**44.8**	**58.3**	4.8	**46.7**
TBX15	3	0.3	9.6	1.9	**59.8**	**42.8**	25.3	**39.8**
TBX5	2	0.0	1.1	**56.3**	0.1	0.6	**50.6**	0.1
TCF-4B	4	14.9	**59.1**	**84.1**	**121.5**	33.7	42.1	**67.0**
TCF7L2	3	13.8	46.2	**71.7**	**71.4**	30.3	37.4	**56.6**
TCTN1	2	**26.9**	**32.5**	21.5	17.5	14.6	16.3	21.2
THBS4	2	61.9	**171.6**	4.9	2.6	1.0	**133.5**	14.2
TLE2	5	**231.2**	**218.3**	**225.0**	**316.5**	80.5	20.6	**342.8**
TLE3	5	**102.4**	**130.6**	**126.2**	**122.5**	30.3	34.1	**139.9**
TLX1	4	0.5	**68.8**	**34.6**	**90.3**	11.1	0.5	**92.6**
TMEM64	2	16.1	**24.5**	5.9	1.6	**38.2**	7.5	1.6
TNFAIP6	2	1.7	9.4	**37.2**	0.2	0.9	**48.0**	1.5
TNFRSF10C	2	11.5	7.0	**20.1**	2.2	15.8	4.3	**20.8**
TNNT3	6	31.4	**539.7**	**129.7**	**49.5**	**55.8**	**672.9**	**149.1**
TRIM17	3	**21.4**	**22.7**	19.4	**25.3**	18.6	14.9	6.8
TRIM67	3	**74.7**	0.0	0.0	**48.5**	0.0	0.0	**89.8**
TUBA8	2	2.8	15.9	5.0	2.6	**26.8**	3.4	**23.4**
TXNDC13	2	**66.8**	20.3	27.1	6.6	18.5	**64.4**	20.3
UACA	4	**49.1**	**76.9**	26.1	**170.8**	11.8	**52.1**	33.0
UBL7	2	87.0	51.5	61.6	**116.3**	12.9	15.9	**115.3**
UBTD2	2	11.6	22.2	**32.6**	10.2	25.4	**94.5**	9.4
UNC5B	2	19.8	3.7	19.8	3.4	**107.6**	**83.3**	2.7
UNQ440	5	**41.8**	16.8	**24.2**	**46.6**	**35.5**	**24.1**	11.3
UNQ440/PRO873	3	**27.1**	11.4	15.4	**25.8**	**25.2**	16.4	8.1
UNQ9369	2	**36.3**	**43.5**	29.3	23.3	19.7	22.0	28.1
USP53	2	3.6	1.8	**63.8**	**67.5**	31.8	4.9	10.0
VASN	3	**292.8**	**268.1**	158.1	156.6	112.3	66.5	**692.1**
VAX2	3	15.0	3.9	5.3	**38.4**	**43.4**	7.2	**80.9**
VCAM1	3	67.5	85.9	**194.1**	3.4	67.9	**202.3**	**114.2**
VWCE	2	**31.2**	8.1	13.4	7.7	11.0	2.2	**20.3**
WASF1	3	14.1	**37.0**	**30.8**	17.5	7.1	**25.7**	8.8

Supplementary Table 5. Recurrent Expression Outliers in SFT tumors (Part-6). Outliers are in bold.

Gene	Number of Outlier Samples	Gene Expression (RPKM). Bold = Outlier.						
		MO_1005	SFT3	SFT18	SFT28	SFT31	SFT40	SFT44
WDR19	2	**24.8**	18.2	15.9	**21.9**	12.8	18.9	13.5
WHSC1L1	3	12.1	17.8	**20.3**	**21.5**	**24.8**	15.1	19.7
WIPF3	2	0.6	0.5	**32.1**	0.1	**38.2**	3.2	9.7
Y19237	3	23.7	**36.5**	**33.2**	9.3	11.4	**49.3**	8.1
ZBTB7C	3	28.4	36.8	**68.0**	14.1	24.4	**75.1**	**50.9**
ZIC2	2	**108.4**	0.1	0.0	**122.0**	0.4	0.1	0.9
ZNF436	3	26.0	29.7	**54.6**	9.8	**30.0**	**47.6**	21.0
ZNF516	2	8.0	18.6	**22.1**	6.7	**31.7**	15.7	13.5

Supplementary Table 6. List of the Transcriptome-Sequencing Compendium (part-1).

Sample ID	Tissue_Type	Status
ADR11	Adrenal Gland	Cancer
ADR13	Adrenal Gland	Cancer
BL13B	Bladder	Cancer
BL14A	Bladder	Cancer
BL14C	Bladder	Cancer
BL16A	Bladder	Cancer
BL17B	Bladder	Cancer
BL18C	Bladder	Cancer
BL18P	Bladder	Cancer
BL18Z	Bladder	Cancer
BL19B	Bladder	Cancer
BL19E	Bladder	Cancer
BL1B	Bladder	Cancer
BL5B	Bladder	Cancer
BL7C	Bladder	Cancer
BL8B	Bladder	Cancer
BL8D	Bladder	Cancer
ARFGEF2-SULF2-T1	Breast	Cancer
ARFGEF2-SULF2-T2	Breast	Cancer
BrBe10001	Breast	Benign
BrBe10003	Breast	Benign
BrCa10001	Breast	Cancer
BrCa10002	Breast	Cancer
BrCa10003	Breast	Cancer
BrCa10004	Breast	Cancer
BrCa10005	Breast	Cancer
BrCa10006	Breast	Cancer
BrCa10007	Breast	Cancer
BrCa10008	Breast	Cancer
BrCa10009	Breast	Cancer
BrCa10010	Breast	Cancer
BrCa10011	Breast	Cancer
BrCa10012	Breast	Cancer
BrCa10013	Breast	Cancer
BrCa10014	Breast	Cancer
BrCa10015	Breast	Cancer
BrCa10016	Breast	Cancer
BrCa10017	Breast	Cancer
BrCa10018	Breast	Cancer
BrCa10020	Breast	Cancer
BrCa10021	Breast	Cancer
BrCa10022	Breast	Cancer
BrCa10023	Breast	Cancer
BrCa10024	Breast	Cancer
BrCa10025	Breast	Cancer
BrCa10026	Breast	Cancer
BrCa10027	Breast	Cancer
BrCa10028	Breast	Cancer
BrCa10029	Breast	Cancer
BrCa10030	Breast	Cancer
BrCa10031	Breast	Cancer
BrCa10032	Breast	Cancer
BrCa10033	Breast	Cancer
BrCa10034	Breast	Cancer
BrCa10035	Breast	Cancer
BrCa10036	Breast	Cancer
BrCa10037	Breast	Cancer
Brst104_LN	Breast	Cancer
Brst106_LN	Breast	Cancer
Brst33_LN	Breast	Cancer
Brst35_T	Breast	Cancer
Brst36_89_N	Breast	Benign
Brst37_T	Breast	Cancer
Brst38_T	Breast	Cancer
Brst39_T	Breast	Cancer
Brst40_T	Breast	Cancer
Brst42_N	Breast	Benign
Brst47_T	Breast	Cancer
Brst52_100_T	Breast	Cancer
Brst57_T	Breast	Cancer
Brst61_LN	Breast	Cancer
Brst62_T	Breast	Cancer
Brst63_T	Breast	Cancer
Brst66_T	Breast	Cancer
Brst72_T	Breast	Cancer
Brst74_LN	Breast	Cancer
Brst79_T	Breast	Cancer
Brst82_T	Breast	Cancer
Brst84_T	Breast	Cancer
Brst93_T	Breast	Cancer
Brst94_T	Breast	Cancer
Brst95_N	Breast	Benign
MCTP0484_T	Breast	Cancer
MCTP0485_T	Breast	Cancer
MCTP0486_T	Breast	Cancer
MCTP0487_T	Breast	Cancer
MCTP0488_T	Breast	Cancer
MCTP0490_T	Breast	Cancer
MCTP0491_T	Breast	Cancer
NO41B1	Colon	Benign
NO43B1	Colon	Benign
NO52B1	Colon	Benign
NO53B1	Colon	Benign
NO8B1	Colon	Benign
UCNP11B1	Colon	Benign
UCNP61B1	Colon	Benign
UCNP71B1	Colon	Benign
UCNP75B1	Colon	Benign
UCP6B2	Colon	Benign
UCP77B2	Colon	Benign
GCN-2000256	Gastric	Benign
GCN-2000521	Gastric	Benign
GCN-20020032	Gastric	Benign
GCN-970005	Gastric	Benign
GCN-980028	Gastric	Benign
GCT-2000256	Gastric	Cancer
GCT-2000521	Gastric	Cancer
GCT-20020032	Gastric	Cancer
GCT-200479	Gastric	Cancer
GCT-47149013	Gastric	Cancer

Supplementary Table 6. List of the Transcriptome-Sequencing Compendium (part-2).

Sample ID	Tissue_Type	Status
GCT-980025	Gastric	Cancer
GCT-980028	Gastric	Cancer
GCT-76629543	Gastric	Cancer
GCT-970005	Gastric	Cancer
GCT-980211	Gastric	Cancer
GCT-980269	Gastric	Cancer
GCT-990071	Gastric	Cancer
Ambion_normal_lung	Lung	Benign
Clontech_normal_lung	Lung	Benign
L26	Lung	Cancer
L33	Lung	Cancer
L36	Lung	Cancer
L39	Lung	Cancer
C41-2	Lymphoma	Cancer
C60	Lymphoma	Cancer
D50	Lymphoma	Cancer
E58-1	Lymphoma	Cancer
F78	Lymphoma	Cancer
G17	Lymphoma	Cancer
MeBe10001	Melanocyte	Benign
MEL13	Melanoma	Cancer
MEL41	Melanoma	Cancer
MEL52	Melanoma	Cancer
MEL56	Melanoma	Cancer
MEL58	Melanoma	Cancer
MEL74	Melanoma	Cancer
MEL83	Melanoma	Cancer
MeBe10002	Melanoma	Benign
MCC-1	Merkel	Cancer
MCC-2	Merkel	Cancer
MCC-3	Merkel	Cancer
DS13_T	Pancreas	Cancer
DS15_T	Pancreas	Cancer
DS18_T	Pancreas	Cancer
DS416_T_xeno	Pancreas	Cancer
DS420_N	Pancreas	Benign
DS459_T	Pancreas	Cancer
DS577_T_xeno	Pancreas	Cancer
DS597_T_xeno	Pancreas	Cancer
DS825_T	Pancreas	Cancer
DS844_T	Pancreas	Cancer
DS848_N	Pancreas	Benign
DSF82_T_xeno	Pancreas	Cancer
Pen-10A_T	Pancreas	Cancer
Pen-9A_T	Pancreas	Cancer
Pen4	Pancreas	Cancer
MCTP-0529	Prostate	Cancer
MCTP-0534	Prostate	Cancer
MDA-PCa-153-7	Prostate	Cancer
MDA-PCa-183-A	Prostate	Cancer
PrBe10002	Prostate	Benign
PrBe10003	Prostate	Benign
PrBe10013	Prostate	Benign
PrBe10014	Prostate	Benign
PrBe10015	Prostate	Benign
PrBe10016	Prostate	Benign
PrBe10017	Prostate	Benign
PrBe10018	Prostate	Benign
PrCa10001	Prostate	Cancer
PrCa10002	Prostate	Cancer
PrCa10003	Prostate	Cancer
PrCa10004	Prostate	Cancer
PrCa10006	Prostate	Cancer
PrCa10007	Prostate	Cancer
PrCa10013	Prostate	Cancer
PrCa10014	Prostate	Cancer
PrCa10015	Prostate	Cancer
PrCa10016	Prostate	Cancer
PrCa10017	Prostate	Cancer
PrCa10018	Prostate	Cancer
PrCa10019	Prostate	Cancer
PrCa10021	Prostate	Cancer
PrCa10023	Prostate	Cancer
PrCa10024	Prostate	Cancer
PrCa10025	Prostate	Cancer
PrCa10026	Prostate	Cancer
PrCa10027	Prostate	Cancer
PrCa10028	Prostate	Cancer
PrCa10029	Prostate	Cancer
PrCa10030	Prostate	Cancer
PrCa10031	Prostate	Cancer
PrCa10032	Prostate	Cancer
PrCa10033	Prostate	Cancer
PrCa10034	Prostate	Cancer
PrCa10035	Prostate	Cancer
PrCa10036	Prostate	Cancer
PrCa10037	Prostate	Cancer
PrCa10038	Prostate	Cancer
PrMe10009	Prostate	Cancer
PrMe10010	Prostate	Cancer
PrMe10011	Prostate	Cancer
PrMe10012	Prostate	Cancer
TMP-aM23	Prostate	Cancer
ULM2927	Prostate	Cancer
ULM4340	Prostate	Cancer
ULM792	Prostate	Cancer
ULMB11239-97	Prostate	Cancer
ULMB2440-97	Prostate	Cancer
aM15	Prostate	Cancer
aM16	Prostate	Cancer
aM17	Prostate	Cancer
aM20	Prostate	Cancer
aM21	Prostate	Cancer
aM22	Prostate	Cancer
aM23	Prostate	Cancer
aM26	Prostate	Cancer
aM28	Prostate	Cancer
aM29	Prostate	Cancer
aM31	Prostate	Cancer
aM33	Prostate	Cancer

Supplementary Table 6. List of the Transcriptome-Sequencing Compendium (part-3).

Sample ID	Tissue_Type	Status
aM36	Prostate	Cancer
aM37	Prostate	Cancer
aM38	Prostate	Cancer
aM39	Prostate	Cancer
aM40	Prostate	Cancer
aM41	Prostate	Cancer
aM44	Prostate	Cancer
aM59	Prostate	Cancer
aM6	Prostate	Cancer
aM7	Prostate	Cancer
aN10_6	Prostate	Benign
aN11_1	Prostate	Benign
aN13_2	Prostate	Benign
aN14_4	Prostate	Benign
aN15_3	Prostate	Benign
aN23	Prostate	Benign
aN25	Prostate	Benign
aN27	Prostate	Benign
aN29	Prostate	Benign
aN31	Prostate	Benign
aN32	Prostate	Benign
aN33	Prostate	Benign
aT12_4	Prostate	Cancer
aT1_3	Prostate	Cancer
aT20	Prostate	Cancer
aT38	Prostate	Cancer
aT42	Prostate	Cancer
aT45	Prostate	Cancer
aT47	Prostate	Cancer
aT49	Prostate	Cancer
aT52	Prostate	Cancer
aT53	Prostate	Cancer
aT54	Prostate	Cancer
aT56	Prostate	Cancer
aT57	Prostate	Cancer
aT58	Prostate	Cancer
aT5_5	Prostate	Cancer
aT61	Prostate	Cancer
aT62	Prostate	Cancer
aT64	Prostate	Cancer
aT65	Prostate	Cancer
aT66	Prostate	Cancer
aT67	Prostate	Cancer
aT6_1	Prostate	Cancer
aT76	Prostate	Cancer
aT8_2	Prostate	Cancer
K11T	Renal	Cancer
K13T	Renal	Cancer
K14T	Renal	Cancer
K16T	Renal	Cancer
K18T	Renal	Cancer
K19T	Renal	Cancer
K20T	Renal	Cancer
K2T	Renal	Cancer
K3T	Renal	Cancer
K5T	Renal	Cancer
K7T	Renal	Cancer
K8T	Renal	Cancer
AC1-T	Salivary Gland	Cancer
AC3-T	Salivary Gland	Cancer
ME2-T	Salivary Gland	Cancer
ME3-T	Salivary Gland	Cancer

Supplementary Table 7. Sequencing statistics for SFT tumors analyzed.

Sample	Library Type	Yield (Mbases)	% Reads Pass Filter	# Reads PF	% of >= Q30 Bases (PF)	Mean Quality Score (PF)	Error Rate PhiX
MO_1005 Normal	Genomic	19,266	93.7	192,658,962	89.6	34.1	0.32
MO_1005 Tumor	Genomic	14,501	95.4	145,006,666	91.8	35.0	0.28
MO_1005 Normal	Exome (Roche EZ Exome v2)	15,884	95.7	158,838,386	91.3	34.9	0.34
MO_1005 Tumor	Exome (Roche EZ Exome v2)	18,913	94.7	189,130,200	90.8	34.6	0.38
MO_1005 Tumor	Transcriptome	17,331	94.5	173,308,880	89.2	34.1	0.14
STF-3 (MSKCC)	Transcriptome	21,056	91.0	210,562,550	90.8	33.6	0.36
STF-18 (MSKCC)	Transcriptome	20,641	91.2	206,405,522	90.5	34.0	0.43
STF-28 (MSKCC)	Transcriptome	19,035	92.7	190,346,700	91.7	34.2	0.37
STF-31 (MSKCC)	Transcriptome	21,614	91.5	216,140,296	90.9	33.8	0.39
STF-40 (MSKCC)	Transcriptome	18,473	92.7	184,732,802	90.8	34.4	0.41
STF-44 (MSKCC)	Transcriptome	11,147	91.6	111,466,992	88.2	33.5	0.63
UM-SFT-1	Transcriptome	8,724	92.8	87,235,760	85.0	32.2	0.80
UM-SFT-2	Transcriptome	11,491	92.8	114,909,272	85.0	32.6	0.80
UM-SFT-3	Transcriptome	10,194	92.8	101,936,248	85.0	32.0	0.80
UM-SFT-4	Transcriptome	10,403	92.8	104,025,054	85.0	31.9	0.80
UM-SFT-5	Transcriptome	10,053	92.0	100,532,460	84.2	32.3	0.85
UM-SFT-6	Transcriptome	12,087	92.0	120,872,254	84.2	32.1	0.85
UM-SFT-7	Transcriptome	10,597	92.0	105,970,756	84.2	31.5	0.85
UM-SFT-8	Transcriptome	12,941	90.9	129,409,894	88.2	32.9	0.69
UM-SFT-9	Transcriptome	12,746	90.9	151,738,538	89.2	34.3	0.83
UM-SFT-10	Transcriptome	10,682	92.1	127,161,984	89.4	34.1	1.18
UM-SFT-11	Transcriptome	12,335	93.0	146,841,784	89.5	34.1	1.29
UM-SFT-12	Transcriptome	12,532	93.0	149,187,386	89.5	34.2	1.29
UM-SFT-13	Transcriptome	11,326	93.0	134,828,390	89.5	34.3	1.29
UM-SFT-14	Transcriptome	11,656	89.6	138,764,520	89.0	33.9	1.02
UM-SFT-15	Transcriptome	10,437	89.6	124,254,778	89.0	33.5	1.02
UM-SFT-16	Transcriptome	11,002	92.5	130,973,398	89.0	33.9	1.14
UM-SFT-17	Transcriptome	11,484	92.5	136,711,022	89.0	33.9	1.14
UM-SFT-18	Transcriptome	14,416	91.1	144,164,630	88.6	33.5	0.65
UM-SFT-19	Transcriptome	12,905	91.1	129,047,456	88.6	33.2	0.65
UM-SFT-20	Transcriptome	15,174	90.9	151,738,538	88.2	33.5	0.69

Supplementary Table 8. Primer sequences.

Cloning of MO_1005 NAB2-STAT6 fusion allele	
NAB2 FL-S1	CAACGGTCCGACCATGCACAGAGCGCCTTCC
NAB2_STAT6 JUNC-AS	CCTTACCCATCTGTTCAGCTGCGAGAGGTGGCTTCGCAGG
NAB2_STAT6 JUNC-S	AAGCCACCTCTCGCAGCTGAACAGATGGGTAAGGATGGCA
STAT6 FL-AS	CAACGGACCGCAAGTGTCCAGAGCAGGTCTG
NAB2-RT1	CCTCAGCCTCCACTTTCACG
STAT6-RT1	CAGGGGAATGATAGAAAGGAA
Sequencing primers	
NAB2-P1	GTACGCATGGTGGTGGAAAGTGTG
NAB2-P2	GGGATGCTGGGGAGGTCACATC
Quantitative RT-PCR primers	
NAB2STAT6 QFUS-S2	GCTATGGAGCCGACACATCCTG
NAB2STAT6 QFUS-AS2	GGAAGTGGTTGGTCCCTTTCCA
NAB2STAT6 SFT31-S	TGCAGCAGACACTGATGGACGAG
NAB2STAT6 SFT31-AS	TCTCCAGCCAGTCACCCAGAAGA
NAB2STAT6 SFT40-S	CCCTCCACTGAAGAAGCTGAAACAA
NAB2STAT6 SFT40-AS	CACTAGCCAAGTTGCAGCAGAAGG
IGF2 QPCR_S1	ACCTGGCCCTCCTGGAGACG
IGF2 QPCR_AS1	GGGGAAGTTGTCCGGAAGCACG
RRAD QPCR_S1	GCGGCGGCGGAAACCCTAAA
RRAD QPCR_AS1	CGGGACCGTCCACTCGCACA
H19 QPCR_S1	GTAGGCGCCCAGGCATCGTG
H19 QPCR_AS1	TCCAACCAGCTGCCACGTCC
NAB2ex5 Forward	CCTGTCTGGGGAGAGTCTGGATG
STAT6ex20 Reverse	GGGGGGATGGAGTGAGAGTGTG
STAT6 Ex13F	GCCTTCCAGCACCGTTCTGTGTC
NAB2 Ex7R	GAGAGCGTGGGGGTCTGTGTG
STAT6 Ex1F	TGGTGGTGGTGGTGGAAGG
NAB2 Ex7R	GAGAGCGTGGGGGTCTGTGTG
Long-range genomic PCR primers	
NAB2STAT6 GEN-S1	TGTGGGGTCATGTCCAAGGCT
NAB2STAT6 GEN-AS1	CGGTCATCTTGATGGTAGCTGGG
ChIP PCR primers	
NAB1-ChIP-F7	GTGGGCGGGAAGAAGCG
NAB1-ChIP-R7	GGACTGCTCAGCCCCAAC
NAB2-ChIP-F2	TTCCGGACTAGGGGAAACCT
NAB2-ChIP-R2	GAGCCTACGACGTGACTTCC
NAB2-ChIP-1S	TCGCTCCCTGTGCGTCCTG
NAB2-ChIP-1AS	CTGTCCCTCCCTCCACGTCTTC
TGFB1-ChIP-F3	AAAGCGGGTGATCCAGATGC
TGFB1-ChIP-R3	TTCCCAGCCTGACTCTCCTT
CEBPA-ChIP-F5	GCCCACGTGGTCGGTAG
CEBPA-ChIP-R5	CTCAAGACCAAGACTCGCCC
CASP9-ChIP-F1	GTCAGTCTTCGCTCCCCAC
CASP9-ChIP-R1	ACGCAGTGGTGGATTCTGG
CASP9-ChIP-F7	AGGGAAACCATGAGTGGAGC
CASP9-ChIP-R7	GTAAGGTGGGCTTGGTTGGA
STAT6 pGL4 reporter primers	
STAT6 pGL4-S	AGTATTTCAGAGAAAACACTTCATGGAAGACACTTCCAGAGAAGACATTTCCTAGAAAACACGG
STAT6 pGL4-AS	TGTTTTCTAGGAAATGTCTTCTCTGGAAGTGTCTTCCATGAAGTGTTTTCTCTGAAATACTGTT