Supplementary Information:

Frequent mutations of chromatin remodeling genes in transitional cell carcinoma of the bladder

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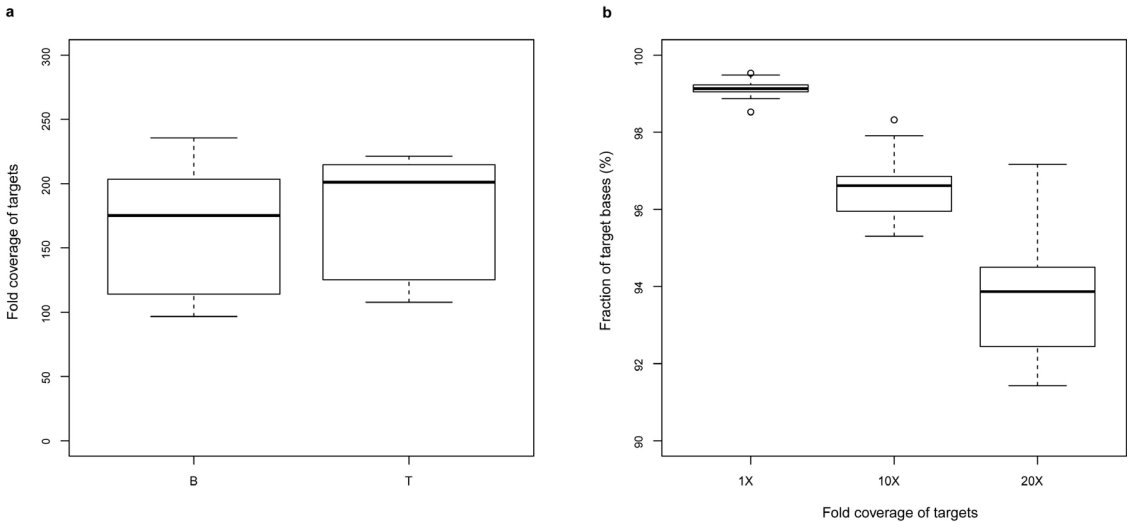

Supplementary Figure 1. Fold coverage of target regions for the peripheral blood and tumor samples sequenced in the Discovery Screen. a, The box plot depicts the distribution of mean coverage of all tumor and blood samples sequenced in the discovery stage. Lines in the two central boxes show the medians, and lines outside the two central boxes show the first and the third quartiles of the mean depths. B, peripheral blood; T, tumor samples. **b,** The box plot depicts the distribution of fraction of targeted bases covered by at least 1×, 10 × and 20 × across the 18 samples sequenced in the Discovery Screen. Lines in the inner three boxes show the medians, and lines outside the three boxes show the first and the third quartiles.

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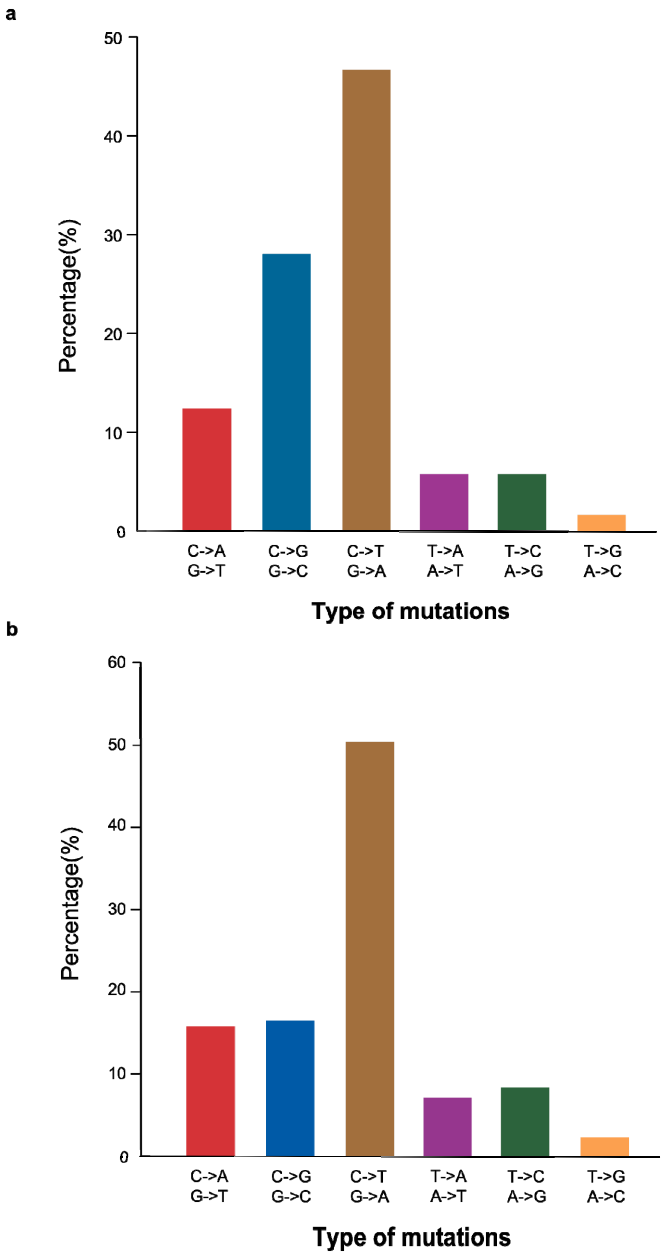

Supplementary Figure 2. Spectrum of somatic point mutations identified in the Discovery Screen (a) and the Prevalence Screen (b). The mutation spectrum for the single-base substitutions detected in the 97 TCCs was dominated by C:G->T:A transitions (*P* = 0.02, Wilcoxon test).

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Supplementary Table 1. Clinical characteristics of the TCC patients sequenced in the Discovery Screen and the Prevalence Screen.

Patient ID	Patient age (years)	Sex	Smoking status	Stage (TNM classification*)	Grade	Screen stage
B2	55	M	Smoker	T2N0M0	3	Discovery
B5	53	M	Never smoking	T4N0M0	2	Discovery
B8	55	M	NA	T3N0M0	3	Discovery
B9	81	M	Never smoking	T3N0M0	3	Discovery
B10	52	M	NA	T2N0M0	2	Discovery
B13	64	M	NA	T2N0M0	2	Discovery
B15	40	M	Never smoking	T4N0M0	2	Discovery
B17	61	M	NA	T2N0M0	2	Discovery
B20	66	M	Never smoking	T4N0M0	3	Discovery
B14	57	M	Never smoking	T2N0M0	2	Prevalence
B16	72	M	Never smoking	T1N0M0	3	Prevalence
B18	66	M	Never smoking	T1N0M0	2	Prevalence
B21	61	M	Never smoking	T4N0M0	1	Prevalence
B22	79	M	Never smoking	T4N0M0	2	Prevalence
B23	85	M	Never smoking	T1N0M0	3	Prevalence
B24	53	M	Smoker	T4N0M0	1	Prevalence
B25	65	M	Never smoking	T4N0M0	3	Prevalence
B34	66	M	Never smoking	T3N0M0	3	Prevalence
B35	80	M	Never smoking	T1N0M0	2	Prevalence
B36	65	M	Never smoking	T2N0M0	2	Prevalence
B37	71	M	Never smoking	T4N0M0	3	Prevalence
B41	69	M	Never smoking	T3N0M0	2	Prevalence
B43	43	M	Never smoking	T3N1M0	3	Prevalence
B45	82	M	Never smoking	T1N0M0	1	Prevalence
B47	84	M	Never smoking	T3N0M0	3	Prevalence
B50	73	M	Smoker	T2NXMX	2	Prevalence
B52	57	M	Never smoking	T3N0M0	1	Prevalence
B54	49	M	Never smoking	T4N0M0	2	Prevalence
B55	41	M	Never smoking	T3N0M0	2	Prevalence
B56	41	M	Never smoking	T1NxMx	2	Prevalence
B57	72	F	Never smoking	T2NxMx	1	Prevalence
B59	67	F	Never smoking	T3NxMx	2	Prevalence
B59-0	50	M	Never smoking	T2NxMx	2	Prevalence
B59-1	43	M	Never smoking	T1N0M0	1	Prevalence
B60	80	F	Never smoking	T4N0M0	3	Prevalence
B61	53	F	Never smoking	T3N0M0	3	Prevalence
B63	70	M	Smoker	T2N0M0	3	Prevalence
B64	66	M	Smoker	T1N0M0	1	Prevalence
B65	87	M	NA	T3N0M0	2	Prevalence
B66	54	M	Never smoking	T2N0M0	2	Prevalence
B66-0	50	F	Never smoking	TaN0M0	3	Prevalence
B68	85	M	Never smoking	T2N0M0	2	Prevalence
B69	87	M	Never smoking	T4N0M0	1	Prevalence
B70	65	M	Never smoking	T2N0M0	2	Prevalence
B71	65	M	Smoker	T2N0M0	3	Prevalence
B73	44	M	Never smoking	T1N0M0	1	Prevalence
B74	60	M	Never smoking	T3N0M0	3	Prevalence
B77	75	M	Smoker	T1N0M0	2	Prevalence
B78	80	M	Never smoking	TaN0M0	2	Prevalence
B79	63	M	Never smoking	T3N0M0	2	Prevalence

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Supplementary Table 1 continued. Clinical characteristics of the TCC patients sequenced in the Discovery Screen and the Prevalence Screen.

Patient ID	Patient age (years)	Sex	Smoking status	Stage (TNM classification*)	Grade	Screen stage
B80	76	M	Smoker	T4N0M0	3	Prevalence
B81	63	M	Never smoking	T2N0M0	3	Prevalence
B59-3	65	M	Smoker	T2N0M0	2	Prevalence
B62-0	58	M	Smoker	T1NoMo	1	Prevalence
B80-0	82	M	Never smoking	T1N0M0	2	Prevalence
B80-3	51	M	Smoker	T4N0M0	2	Prevalence
B80-4	54	M	Smoker	T1N0M0	1	Prevalence
B80-7	58	M	Smoker	T3N0M0	2	Prevalence
B80-8	63	F	Never Smoker	T2N0M0	3	Prevalence
B80-11	28	M	Smoker	T1N0M0	1	Prevalence
B80-13	63	M	Never smoking	T1N0M0	1	Prevalence
B81-1	62	M	Never smoking	T2N0M0	1	Prevalence
B82	56	M	Smoker	T3N0M0	2	Prevalence
B83	84	F	Never smoking	T3N0M0	1	Prevalence
B84	64	M	Never smoking	T1N0M0	1	Prevalence
B85-0	76	M	NA	TaN0M0	1	Prevalence
B85-2	74	M	Never smoking	TaN0M0	1	Prevalence
B86	48	M	Never smoking	T2N0M0	1	Prevalence
B87	57	M	Never smoking	T1N0M0	2	Prevalence
B88	56	M	Never smoking	T3N0M0	2	Prevalence
B89-1	65	M	Never smoking	T2N0M0	2	Prevalence
B89-3	65	M	Never smoking	T3N0M0	1	Prevalence
B89-4	71	M	Never smoking	T1N0M0	1	Prevalence
B89-5	50	M	Never smoking	T1N0M0	1	Prevalence
B89-10	65	M	Smoker	T1N0M0	1	Prevalence
B89-12	72	F	Never smoking	T2N0M0	3	Prevalence
B89-16	68	M	Never smoking	T1N0M0	1	Prevalence
B90	84	M	Never smoking	T1N0M0	1	Prevalence
B96	69	M	Smoker	T3N0M0	2	Prevalence
B98	63	M	Smoker	T3N0M0	3	Prevalence
B99	37	F	Never smoking	T1N0M0	1	Prevalence
B100	25	M	Smoker	T1N0M0	1	Prevalence
B101	69	F	Never smoking	T1N0M0	1	Prevalence
B102	45	M	Never smoking	T1N0M0	1	Prevalence
B103	54	M	Smoker	T1N0M0	1	Prevalence
B104	52	M	Never smoking	T2N0M0	1	Prevalence
B104-0	72	M	Smoker	T1N0M0	1	Prevalence
B105	62	M	Never smoking	T2NxMx	1	Prevalence
B105-0	60	M	Never smoking	T2NxMx	1	Prevalence
B105-1	64	M	Never smoking	T2NxMx	2	Prevalence
B106	56	M	Smoker	T2NxMx	1	Prevalence
B107	68	M	Never smoking	T2NxMx	3	Prevalence
B109	46	M	Never smoking	T1N0M0	1	Prevalence
B110	54	M	Smoker	T1N0M0	1	Prevalence
B111	45	M	Smoker	T1N0M0	1	Prevalence
B112	62	M	Smoker	T1N0M0	1	Prevalence
B114	73	M	Never smoking	T1N0M0	1	Prevalence

* The TNM cancer staging system was designed to gauge the extent of cancer in a patient's body. T describes the size of the tumor and whether it has invaded nearby tissue, N describes regional lymph nodes that are involved, and M describes distant metastasis (spread of cancer from one body part to another). NA，not available.

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Supplementary Table 2. Summary statistics of exome sequencing data obtained from the nine TCC patients in the Discovery Screen.

Case	Sample	Total reads	No. of uniquely mapping reads*	% of uniquely mapping reads*	No. of reads overlapping targets	% of reads overlapping targets	No. of non-duplicated reads	Mean fold coverage	% of targets covered by at least 1 ×	% of targets covered by at least 10 ×
B2	Blood	237,124,039	167,653,431	70.70	126,490,236	53.34	21,836,424	175.21	99.48	96.67
	Tumor	233,283,541	176,961,865	75.86	119,248,541	51.12	22,213,417	214.70	98.88	97.53
B5	Blood	84,087,752	74,966,971	89.15	44,514,793	52.94	19,056,226	96.62	99.04	95.95
	Tumor	96,829,842	87,478,265	90.34	50,772,926	52.44	21,276,835	107.72	99.28	96.44
B8	Blood	245,519,105	191,149,580	77.86	109,361,409	44.54	18,594,429	203.43	99.13	97.00
	Tumor	254,388,669	204,186,645	80.27	107,605,321	42.30	26,854,513	201.10	99.03	95.86
B9	Blood	252,596,951	200,042,184	79.19	105,024,854	41.58	17,912,219	193.38	98.53	95.30
	Tumor	234,044,094	192,369,656	82.19	101,280,384	43.27	20,767,778	188.17	99.06	96.42
B10	Blood	199,017,391	148,094,364	74.41	91,504,070	45.98	18,611,532	168.10	99.16	96.65
	Tumor	246,304,477	182,265,248	74.00	119,029,968	48.33	20,677,969	217.19	99.12	96.58
B13	Blood	79,582,529	71,719,028	90.12	46,337,260	58.23	22,227,413	100.78	99.14	95.73
	Tumor	101,716,803	92,657,746	91.09	59,554,240	58.55	26,707,803	125.22	99.15	96.39
B15	Blood	92,540,238	83,748,557	90.50	53,344,953	57.65	19,931,298	114.04	99.06	95.53
	Tumor	93,409,390	84,974,473	90.97	56,416,719	60.40	20,698,459	120.09	99.23	96.86
B17	Blood	197,778,961	139,308,995	70.44	110,341,211	55.79	20,445,729	204.77	99.10	96.78
	Tumor	231,796,676	177,964,858	76.78	114,766,954	49.51	23,496,509	207.26	99.53	97.91
B20	Blood	211,090,639	160,313,236	75.95	94,389,677	44.72	22,620,859	235.56	98.87	98.32
	Tumor	247,330,198	199,826,455	80.79	115,333,478	46.63	23,871,115	221.39	99.33	96.86

* based on the hg18 UCSC release of the human genome.

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Supplementary Table 3. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type	Validation status
ABCA4	B8	g.chr1:94351206C>T	c.71G>A	CGC=>CAC	Arg=>His	p.R24H	missense	genotyping
ABT1	B2	g.chr6:26706810C>G	c.777C>G	CCC=>CCG	Pro=>Pro	p.P259P	synonymous	NV
ACAD10	B5	g.chr12:110643907G>C	c.1042G>C	GAT=>CAT	Asp=>His	p.D348H	missense	NV
ACO1	B5	g.chr9:32440052C>T	c.2613C>T	CTC=>CTT	Leu=>Leu	p.L871L	synonymous	NV
ADAMTSL3	B5	g.chr15:82491167C>G	c.4733C>G	TCC=>TGC	Ser=>Cys	p.S1578C	missense	genotyping
ADCY2	B5	g.chr5:7762361G>A	c.1439G>A	CGC=>CAC	Arg=>His	p.R480H	missense	genotyping
ALDH1B1	B15	g.chr9:38386397G>T	c.652G>T	GCC=>TCC	Ala=>Ser	p.A218S	missense	genotyping
ALDH3A1	B8	g.chr17:19587243G>A	c.288C>T	GAC=>GAT	Asp=>Asp	p.D96D	synonymous	NV
ALOX12	B13	g.chr17:6842847A>C	c.509A>C	AAG=>ACG	Lys=>Thr	p.K170T	missense	genotyping
ALS2CR11	B5	g.chr2:202144928C>T	c.814G>A	GAA=>AAA	Glu=>Lys	p.E272K	missense	genotyping
AMAC1L2	B15	g.chr8:11226628G>A	c.603G>A	CTG=>CTA	Leu=>Leu	p.L201L	synonymous	NV
AMAC1L2	B15	g.chr8:11226629G>T	c.604G>T	GCG=>TCG	Ala=>Ser	p.A202S	missense	NV
ANK2	B10	g.chr4:114494501G>A	c.5278G>A	GAA=>AAA	Glu=>Lys	p.E1760K	missense	genotyping
ANK3	B10	g.chr10:61544007G>A	c.2930C>T	TCA=>TTA	Ser=>Leu	p.S977L	missense	genotyping
ANKLE1	B20	g.chr19:17255674G>A	c.1101G>A	CTG=>CTA	Leu=>Leu	p.L367L	synonymous	NV
ANKMY2	B20	g.chr7:16610882C>G	c.1000G>C	GTT=>CTT	Val=>Leu	p.V334L	missense	NV
ANO5	B5	g.chr11:22248513G>A	c.1978G>A	GAC=>AAC	Asp=>Asn	p.D660N	missense	genotyping
ANO7	B15	g.chr2:241779331C>A	c.320C>A	CCC=>CAC	Pro=>His	p.P107H	missense	genotyping
ANO7	B15	g.chr2:241779332C>A	c.321C>A	CCC=>CCA	Pro=>Pro	p.P107P	synonymous	NV
ANPEP	B15	g.chr15:88145685C>T	c.1727G>A	CGC=>CAC	Arg=>His	p.R576H	missense	genotyping
AOAH	B8	g.chr7:36546519C>T	c.1237G>A	GTT=>ATT	Val=>Ile	p.V413I	missense	genotyping
AP2B1	B5	g.chr17:31001755G>C	c.1630G>C	GAG=>CAG	Glu=>Gln	p.E544Q	missense	genotyping
ARHGAP28	B10	g.chr18:6866166G>T	c.772G>T	GAA=>TAA	Glu=>Stop	p.E258*	nonsense	genotyping
ARHGEF18	B10	g.chr19:7415121G>C	c.354G>C	CGG=>CGC	Arg=>Arg	p.R118R	synonymous	NV
ARID1A	B13	g.chr1:26966872_26966872delC	c.2994_2994delC	-	-	-	Frame shift indel	Sanger sequencing
ARID1A	B5	g.chr1:26971940C>G	c.3590C>G	TCC=>TGC	Ser=>Cys	p.S1197C	missense	genotyping
ARID1A	B5	g.chr1:26972451C>A	c.3743C>A	TCA=>TAA	Ser=>Stop	p.S1248*	nonsense	genotyping
ARID1A	B13	g.chr1:26978951C>G	c.5975C>G	TCA=>TGA	Ser=>Stop	p.S1992*	nonsense	genotyping
ARID1A	B13	g.chr1:26979357C>G	c.6381C>G	ATC=>ATG	Ile=>Met	p.I2127M	missense	genotyping
ARID1A	B13	g.chr1:26979782C>T	c.6806C>T	TCA=>TTA	Ser=>Leu	p.S2269L	missense	genotyping
ARMC4	B10	g.chr10:28316466G>C	c.237C>G	GTC=>GTG	Val=>Val	p.V79V	synonymous	NV
ASB15	B13	g.chr7:123056623G>C	c.1339G>C	GAC=>CAC	Asp=>His	p.D447H	missense	genotyping
ASRGL1	B9	g.chr11:61880445C>G	c.263C>G	TCT=>TGT	Ser=>Cys	p.S88C	missense	NV
ATG2B	B5	g.chr14:95839211C>T	c.4977G>A	ATG=>ATA	Met=>Ile	p.M1659I	missense	genotyping
ATN1	B13	g.chr12:6915836C>G	c.1145C>G	TCT=>TGT	Ser=>Cys	p.S382C	missense	NV
ATP4B	B10	g.chr13:113355326C>T	c.418G>A	GAG=>AAG	Glu=>Lys	p.E140K	missense	NV
ATP5C1	B10	g.chr10:7881856G>A	c.544G>A	GAA=>AAA	Glu=>Lys	p.E182K	missense	genotyping
ATP6AP1L	B5	g.chr5:81649710C>T	c.510C>T	CTC=>CTT	Leu=>Leu	p.L170L	synonymous	NV
ATP8A1	B10	g.chr4:42312812G>A	c.404C>T	ACG=>ATG	Thr=>Met	p.T135M	missense	genotyping
ATXN2L	B15	g.chr16:28754797C>T	c.2938C>T	CCT=>TCT	Pro=>Ser	p.P980S	missense	NV
AVL9	B10	g.chr7:32565266G>A	c.880G>A	GAG=>AAG	Glu=>Lys	p.E294K	missense	genotyping
BAI3	B15	g.chr6:70155325G>A	c.4390G>A	GCA=>ACA	Ala=>Thr	p.A1464T	missense	genotyping
BCL9L	B5	g.chr11:118284280G>C	c.321C>G	CTC=>CTG	Leu=>Leu	p.L107L	synonymous	NV
BPTF	B10	g.chr17:63370923A>C	c.7051A>C	ACC=>CCC	Thr=>Pro	p.T2351P	missense	NV
BRIP1	B8	g.chr17:57231267C>T	c.1316G>A	CGA=>CAA	Arg=>Gln	p.R439Q	missense	genotyping
BRPF1	B10	g.chr3:9761820G>A	c.3049G>A	GCT=>ACT	Ala=>Thr	p.A1017T	missense	genotyping
BRPF3	B20	g.chr6:36280519C>G	c.1555C>G	CTT=>GTT	Leu=>Val	p.L519V	missense	NV
BTAF1	B5	g.chr10:93706392G>A	c.829G>A	GAG=>AAG	Glu=>Lys	p.E277K	missense	NV
BTAF1	B10	g.chr10:93768659C>G	c.4850C>G	TCA=>TGA	Ser=>Stop	p.S1617*	nonsense	genotyping
BTBD16	B13	g.chr10:124079042C>G	c.969C>G	CTC=>CTG	Leu=>Leu	p.L323L	synonymous	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
C10orf137	B5	g.chr10:127414386A>T	c.1579A>T	AGC=>TGC	Ser=>Cys	p.S527C	missense	genotyping
C14orf101	B15	g.chr14:56155131G>A	c.1123G>A	GTT=>ATT	Val=>Ile	p.V375I	missense	genotyping
C15orf55	B17	g.chr15:32428089G>A	c.644G>A	CGT=>CAT	Arg=>His	p.R215H	missense	NV
C17orf80	B15	g.chr17:68743656C>G	c.440C>G	TCT=>TGT	Ser=>Cys	p.S147C	missense	genotyping
C19orf15	B10	g.chr19:43542984G>A	c.544G>A	GAG=>AAG	Glu=>Lys	p.E182K	missense	genotyping
C1orf101	B5	g.chr1:242821652G>C	c.2185G>C	GAA=>CAA	Glu=>Gln	p.E729Q	missense	genotyping
C1orf106	B10	g.chr1:199143599G>T	c.790G>T	GAT=>TAT	Asp=>Tyr	p.D264Y	missense	NV
C1orf54	B20	g.chr1:148513119G>C	c.52G>C	GAA=>CAA	Glu=>Gln	p.E18Q	missense	NV
C20orf27	B5	g.chr20:3687245C>A	c.175G>T	GAG=>TAG	Glu=>Stop	p.E59*	nonsense	NV
C20orf46	B5	g.chr20:1109857G>A	c.406C>T	CTG=>TTG	Leu=>Leu	p.L136L	synonymous	NV
C20orf72	B2	g.chr20:17918682T>G	c.965T>G	CTT=>CGT	Leu=>Arg	p.L322R	missense	NV
C4orf17	B9	g.chr4:100662853C>G	c.301C>G	CCA=>GCA	Pro=>Ala	p.P101A	missense	genotyping
C4orf21	B2	g.chr4:113758535T>C	c.2112A>G	CTA=>CTG	Leu=>Leu	p.L704L	synonymous	NV
C8orf55	B2	g.chr8:143813851G>A	c.619G>A	GAC=>AAC	Asp=>Asn	p.D207N	missense	NV
C8orf76	B20	g.chr8:124322731C>T	c.37G>A	GAG=>AAG	Glu=>Lys	p.E13K	missense	NV
C9orf102	B15	g.chr9:97717875G>A	c.926G>A	GGC=>GAC	Gly=>Asp	p.G309D	missense	genotyping
CA9	B20	g.chr9:35664191_35664208delGGAGAGGAGGATCTACCT	c.236_253delGGAGAGGAGGATCTACCT	-	-	-	indel	NV
CANX	B8	g.chr5:179082462G>C	c.1234G>C	GAA=>CAA	Glu=>Gln	p.E412Q	missense	genotyping
CCDC111	B5	g.chr4:185843642A>T	c.1182A>T	AAA=>AAT	Lys=>Asn	p.K394N	missense	genotyping
CD163L1	B10	g.chr12:7418513C>T	c.3201G>A	CTG=>CTA	Leu=>Leu	p.L1067L	synonymous	NV
CD163L1	B8	g.chr12:7419397G>A	c.2748C>T	AAC=>AAT	Asn=>Asn	p.N916N	synonymous	NV
CD1C	B8	g.chr1:156529060C>G	c.661C>G	CTG=>GTG	Leu=>Val	p.L221V	missense	genotyping
CD86	B10	g.chr3:123321057G>A	c.976G>A	GAT=>AAT	Asp=>Asn	p.D326N	missense	genotyping
CDH5	B8	g.chr16:64978229G>C	c.227G>C	AGT=>ACT	Ser=>Thr	p.S76T	missense	genotyping
CDKN1A	B2	g.chr6:36759900_36759916delGCAAGGCCTGCCGCCGC	c.45_61delGCAAGGCCTGCCGCCGC	-	-	-	Frame shift indel	NV
CDKN1A	B15	g.chr6:36760002G>A	c.146G>A	TGG=>TAG	Trp=>Stop	p.W49*	nonsense	genotyping
CDKN1A	B13	g.chr6:36760042insT	c.186insT	-	-	-	Frame shift indel	Sanger sequencing
CEP135	B9	g.chr4:56541102G>C	c.1510G>C	GAA=>CAA	Glu=>Gln	p.E504Q	missense	genotyping
CEP192	B15	g.chr18:13089550G>A	c.4845G>A	TTG=>TTA	Leu=>Leu	p.L1615L	synonymous	NV
CHD6	B20	g.chr20:39595594G>T	c.63C>A	TCC=>TCA	Ser=>Ser	p.S21S	synonymous	NV
CHRD	B13	g.chr3:185583853G>A	c.1273G>A	GGC=>AGC	Gly=>Ser	p.G425S	missense	genotyping
CLSPN	B15	g.chr1:35986760C>G	c.2305G>C	GAG=>CAG	Glu=>Gln	p.E769Q	missense	genotyping
CNTN4	B20	g.chr3:3072855C>T	c.3032C>T	TCA=>TTA	Ser=>Leu	p.S1011L	missense	NV
CNTNAP2	B8	g.chr7:146460373C>T	c.1187C>T	TCA=>TTA	Ser=>Leu	p.S396L	missense	genotyping
COBL	B9	g.chr7:51064103G>A	c.2184C>T	ACC=>ACT	Thr=>Thr	p.T728T	synonymous	NV
COL3A1	B10	g.chr2:189583277G>T	c.3952G>T	GAT=>TAT	Asp=>Tyr	p.D1318Y	missense	genotyping
COL3A1	B10	g.chr2:189583646G>A	c.4039G>A	GAA=>AAA	Glu=>Lys	p.E1347K	missense	genotyping
COL7A1	B8	g.chr3:48606028G>C	c.372C>G	CTC=>CTG	Leu=>Leu	p.L124L	synonymous	NV
CPA4	B8	g.chr7:129737984C>T	c.915C>T	ATC=>ATT	Ile=>Ile	p.I305I	synonymous	NV
CREB3L2	B20	g.chr7:137217876G>A	c.1309C>T	CCC=>TCC	Pro=>Ser	p.P437S	missense	NV
CREBBP	B13	g.chr16:3735319G>A	c.3874C>T	CAG=>TAG	Gln=>Stop	p.Q1292*	nonsense	genotyping
CREBBP	B5	g.chr16:3783541G>A	c.1063C>T	CAG=>TAG	Gln=>Stop	p.Q355*	nonsense	genotyping
CRNKL1	B10	g.chr20:19968414C>G	c.1867G>C	GAC=>CAC	Asp=>His	p.D623H	missense	genotyping
CRYBA4	B2	g.chr22:25356390G>A	c.530G>A	CGG=>CAG	Arg=>Gln	p.R177Q	missense	NV
CST1	B10	g.chr20:23679392C>T	c.112G>A	GAC=>AAC	Asp=>Asn	p.D38N	missense	NV
CUBN	B8	g.chr10:16997052C>T	c.7336G>A	GAA=>AAA	Glu=>Lys	p.E2446K	missense	genotyping
CUX1	B15	g.chr7:101631942G>T	c.2645G>T	TGG=>TTG	Trp=>Leu	p.W882L	missense	NV
CUX1	B15	g.chr7:101631943G>T	c.2646G>T	TGG=>TGT	Trp=>Cys	p.W882C	missense	NV
CYP1A1	B10	g.chr15:72802398G>C	c.94C>G	CAG=>GAG	Gln=>Glu	p.Q32E	missense	genotyping
CYTSB	B5	g.chr17:20049276A>T	c.1322A>T	GAG=>GTG	Glu=>Val	p.E441V	missense	genotyping

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
DCHS2	B10	g.chr4:155375824A>G	c.8065T>C	TGC=>CGC	Cys=>Arg	p.C2689R	missense	NV
DCST1	B20	g.chr1:153280691G>C	c.726G>C	CTG=>CTC	Leu=>Leu	p.L242L	synonymous	NV
DDRGK1	B5	g.chr20:3131972C>A	c.182G>T	GGA=>GTA	Gly=>Val	p.G61V	missense	genotyping
DGKH	B13	g.chr13:41687733C>G	c.3143C>G	ACT=>AGT	Thr=>Ser	p.T1048S	missense	genotyping
DIP2C	B15	g.chr10:400450C>A	c.2341G>T	GTG=>TTG	Val=>Leu	p.V781L	missense	genotyping
DISP1	B10	g.chr1:221243646G>C	c.2284G>C	GAG=>CAG	Glu=>Gln	p.E762Q	missense	genotyping
DMD	B15	g.chrX:31657672G>A	c.277C>T	CGA=>TGA	Arg=>Stop	p.R93*	nonsense	genotyping
DNAH17	B10	g.chr17:74077150C>T	c.205G>A	GAG=>AAG	Glu=>Lys	p.E69K	missense	genotyping
DNAJC27	B2	g.chr2:25024110T>C	c.701A>G	AAT=>AGT	Asn=>Ser	p.N234S	missense	NV
DNMT1	B2	g.chr19:10135020C>T	c.860G>A	AGA=>AAA	Arg=>Lys	p.R287K	missense	NV
DOCK8	B5	g.chr9:423939A>T	c.4646A>T	CAG=>CTG	Gln=>Leu	p.Q1549L	missense	genotyping
EGLN1	B15	g.chr1:229623649G>A	c.609C>T	AAC=>AAT	Asn=>Asn	p.N203N	synonymous	NV
EIF2C4	B17	g.chr1:36072243G>A	c.1445G>A	TGT=>TAT	Cys=>Tyr	p.C482Y	missense	NV
EMILIN2	B15	g.chr18:2882023G>C	c.1898G>C	AGA=>ACA	Arg=>Thr	p.R633T	missense	NV
ENO2	B10	g.chr12:6899092T>C	c.769T>C	TAT=>CAT	Tyr=>His	p.Y257H	missense	genotyping
EP300	B10	g.chr22:39875951C>T	c.2620C>T	CAG=>TAG	Gln=>Stop	p.Q874*	nonsense	genotyping
EPDR1	B13	g.chr7:37926788_37926800delAGGCAGTGGCAGC	c.83_95delAGGCAGTGGCAGC	-	-	-	Frame shift indel	NV
ERBB3	B9	g.chr12:54765214C>T	c.403C>T	CGC=>TGC	Arg=>Cys	p.R135C	missense	genotyping
ERBB3	B5	g.chr12:54768804G>A	c.994G>A	GAG=>AAG	Glu=>Lys	p.E332K	missense	genotyping
ERBB3	B8	g.chr12:54774492G>T	c.1744G>T	GGG=>TGG	Gly=>Trp	p.G582W	missense	genotyping
ERN2	B5	g.chr16:23629351T>C	c.364A>G	ATG=>GTG	Met=>Val	p.M122V	missense	NV
ESPL1	B8	g.chr12:51949441C>G	c.448C>G	CTG=>GTG	Leu=>Val	p.L150V	missense	genotyping
ESPNP	B13	g.chr1:16907043_16907050delGCGCGCGT	c.313_320delGCGCGCGT	-	-	-	Frame shift indel	NV
EXOSC9	B2	g.chr4:122953975C>T	c.964C>T	CCT=>TCT	Pro=>Ser	p.P322S	missense	NV
FAH	B5	g.chr15:78254484G>A	c.909G>A	CTG=>CTA	Leu=>Leu	p.L303L	synonymous	NV
FARP2	B8	g.chr2:242051542G>A	c.1797G>A	CAG=>CAA	Gln=>Gln	p.Q599Q	synonymous	NV
FASTKD5	B8	g.chr20:3076441G>A	c.1276C>T	CGA=>TGA	Arg=>Stop	p.R426*	nonsense	NV
FBXL3	B17	g.chr13:76487661G>A	c.527C>T	TCG=>TTG	Ser=>Leu	p.S176L	missense	NV
FFAR2	B5	g.chr19:40633118T>A	c.662T>A	GTG=>GAG	Val=>Glu	p.V221E	missense	NV
FLNB	B5	g.chr3:58039558G>A	c.616G>A	GAT=>AAT	Asp=>Asn	p.D206N	missense	genotyping
FMNL1	B17	g.chr17:40674756G>C	c.1557G>C	CCG=>CCC	Pro=>Pro	p.P519P	synonymous	NV
FRMPD1	B17	g.chr9:37736463insATGG	c.303insATGG	-	-	-	Frame shift indel	NV
FURIN	B2	g.chr15:89225914C>T	c.2187C>T	TTC=>TTT	Phe=>Phe	p.F729F	synonymous	NV
GALM	B5	g.chr2:38746996A>T	c.189A>T	GAA=>GAT	Glu=>Asp	p.E63D	missense	genotyping
GALNT13	B9	g.chr2:154806836T>C	c.359T>C	GTC=>GCC	Val=>Ala	p.V120A	missense	genotyping
GART	B15	g.chr21:33816453C>G	c.1305G>C	TTG=>TTC	Leu=>Phe	p.L435F	missense	genotyping
GATC	B15	g.chr12:119379305G>A	c.298G>A	GCT=>ACT	Ala=>Thr	p.A100T	missense	genotyping
GATC	B15	g.chr12:119379306C>T	c.299C>T	GCT=>GTT	Ala=>Val	p.A100V	missense	genotyping
GCLM	B8	g.chr1:94127238C>A	c.721G>T	GAG=>TAG	Glu=>Stop	p.E241*	nonsense	genotyping
GCNT3	B17	g.chr15:57697812_57697818delAACTTTC	c.84_90delAACTTTC	-	-	-	Frame shift indel	NV
GHRHR	B9	g.chr7:30982594C>G	c.1000C>G	CTG=>GTG	Leu=>Val	p.L334V	missense	genotyping
GKN2	B15	g.chr2:69027849G>C	c.249C>G	ATC=>ATG	Ile=>Met	p.I83M	missense	genotyping
GLDC	B10	g.chr9:6592171G>C	c.1093C>G	CTT=>GTT	Leu=>Val	p.L365V	missense	genotyping
GLRA3	B15	g.chr4:175801538C>G	c.1324G>C	GAG=>CAG	Glu=>Gln	p.E442Q	missense	genotyping
GNA13	B10	g.chr17:60441372C>T	c.599G>A	AGA=>AAA	Arg=>Lys	p.R200K	missense	genotyping
GNA14	B9	g.chr9:79236161G>A	c.489C>T	ATC=>ATT	Ile=>Ile	p.I163I	synonymous	NV
GNL2	B9	g.chr1:37807229C>G	c.1678G>C	GAG=>CAG	Glu=>Gln	p.E560Q	missense	NV
GON4L	B5	g.chr1:154052272G>A	c.1109C>T	TCA=>TTA	Ser=>Leu	p.S370L	missense	genotyping
GPR114	B2	g.chr16:56153869C>T	c.137C>T	TCT=>TTT	Ser=>Phe	p.S46F	missense	NV
GPR158	B15	g.chr10:25901606C>T	c.1537C>T	CGA=>TGA	Arg=>Stop	p.R513*	nonsense	NV
GPR182	B10	g.chr12:55675448T>C	c.188T>C	ATG=>ACG	Met=>Thr	p.M63T	missense	genotyping
GPR32	B10	g.chr19:55966290A>T	c.621A>T	GAA=>GAT	Glu=>Asp	p.E207D	missense	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
GPR34	B2	g.chrX:41440309T>C	c.479T>C	ATA=>ACA	Ile=>Thr	p.I160T	missense	NV
GPR64	B17	g.chrX:18934281T>G	c.1647A>C	GTA=>GTC	Val=>Val	p.V549V	synonymous	NV
GRIA4	B2	g.chr11:105355574G>C	c.2607G>C	GAG=>GAC	Glu=>Asp	p.E869D	missense	NV
GRIN2B	B15	g.chr12:13797804C>T	c.724G>A	GAA=>AAA	Glu=>Lys	p.E242K	missense	genotyping
GRK4	B10	g.chr4:2993973C>T	c.967C>T	CGT=>TGT	Arg=>Cys	p.R323C	missense	genotyping
GRM5	B5	g.chr11:88420278G>A	c.411C>T	TTC=>TTT	Phe=>Phe	p.F137F	synonymous	NV
GRM8	B8	g.chr7:126331895A>T	c.806T>A	CTG=>CAG	Leu=>Gln	p.L269Q	missense	genotyping
GRXCR2	B5	g.chr5:145232654G>A	c.71C>T	TCC=>TTC	Ser=>Phe	p.S24F	missense	genotyping
GSG1	B15	g.chr12:13135015T>C	c.14A>G	GAG=>GGG	Glu=>Gly	p.E5G	missense	genotyping
GSR	B8	g.chr8:30673482G>C	c.752C>G	TCA=>TGA	Ser=>Stop	p.S251*	nonsense	genotyping
HDAC4	B9	g.chr2:239750456G>A	c.591C>T	AGC=>AGT	Ser=>Ser	p.S197S	synonymous	NV
HDC	B13	g.chr15:48333721C>T	c.618G>A	GTG=>GTA	Val=>Val	p.V206V	synonymous	NV
HEATR3	B9	g.chr16:48670257G>A	c.610G>A	GAA=>AAA	Glu=>Lys	p.E204K	missense	NV
HEXA	B9	g.chr15:70433127C>G	c.418G>C	GAG=>CAG	Glu=>Gln	p.E140Q	missense	genotyping
HMCN1	B13	g.chr1:184158191C>T	c.958C>T	CGA=>TGA	Arg=>Stop	p.R320*	nonsense	genotyping
HMGXB4	B15	g.chr22:33991035G>A	c.654G>A	GCG=>GCA	Ala=>Ala	p.A218A	synonymous	NV
HOXB8	B15	g.chr17:44046973_44046981delGTCCTGGGC	c.94_102delGTCCTGGGC	-	-	-	indel	NV
HOXC5	B8	g.chr12:52714459T>C	c.585T>C	AAT=>AAC	Asn=>Asn	p.N195N	synonymous	NV
HRAS	B15	g.chr11:524288C>T	c.35G>A	GGC=>GAC	Gly=>Asp	p.G12D	missense	NV
HS3ST3A1	B8	g.chr17:13340848G>T	c.612C>A	CCC=>CCA	Pro=>Pro	p.P204P	synonymous	NV
HSD17B4	B20	g.chr5:118842597C>G	c.604C>G	CAG=>GAG	Gln=>Glu	p.Q202E	missense	NV
HSD17B6	B5	g.chr12:55464914C>T	c.583C>T	CAA=>TAA	Gln=>Stop	p.Q195*	nonsense	genotyping
HSPA4L	B20	g.chr4:128967952G>C	c.2089G>C	GAG=>CAG	Glu=>Gln	p.E697Q	missense	NV
HSPG2	B17	g.chr1:22058700T>G	c.5239A>C	ACC=>CCC	Thr=>Pro	p.T1747P	missense	genotyping
HSPH1	B8	g.chr13:30609517G>C	c.2515C>G	CCA=>GCA	Pro=>Ala	p.P839A	missense	NV
IFT57	B10	g.chr3:109364126C>G	c.1178G>C	AGA=>ACA	Arg=>Thr	p.R393T	missense	genotyping
IFT57	B13	g.chr3:109423788C>A	c.72G>T	GGG=>GGT	Gly=>Gly	p.G24G	synonymous	NV
IGSF6	B5	g.chr16:21566053G>A	c.329C>T	TCA=>TTA	Ser=>Leu	p.S110L	missense	NV
IL18RAP	B15	g.chr2:102406237C>A	c.68C>A	TCA=>TAA	Ser=>Stop	p.S23*	nonsense	genotyping
IL32	B2	g.chr16:3059298insG	c.59insG	-	-	-	Frame shift indel	NV
INTU	B9	g.chr4:128828353C>T	c.1330C>T	CAG=>TAG	Gln=>Stop	p.Q444*	nonsense	NV
IQGAP1	B5	g.chr15:88797091G>A	c.1243G>A	GAA=>AAA	Glu=>Lys	p.E415K	missense	genotyping
IQSEC3	B5	g.chr12:117874G>A	c.175G>A	GAG=>AAG	Glu=>Lys	p.E59K	missense	genotyping
IREB2	B10	g.chr15:76570091G>A	c.2257G>A	GAT=>AAT	Asp=>Asn	p.D753N	missense	genotyping
IRF1	B13	g.chr5:131848006G>A	c.800C>T	TCT=>TTT	Ser=>Phe	p.S267F	missense	genotyping
IRF2	B10	g.chr4:185587176C>G	c.37G>C	GAG=>CAG	Glu=>Gln	p.E13Q	missense	genotyping
IRF8	B13	g.chr16:84512318C>T	c.1210C>T	CGG=>TGG	Arg=>Trp	p.R404W	missense	NV
KANK2	B10	g.chr19:11148353G>A	c.1661C>T	GCG=>GTG	Ala=>Val	p.A554V	missense	NV
KANK3	B2	g.chr19:8295374G>C	c.2341C>G	CTG=>GTG	Leu=>Val	p.L781V	missense	NV
KATNAL1	B2	g.chr13:29755844G>A	c.71C>T	TCA=>TTA	Ser=>Leu	p.S24L	missense	NV
KBTBD4	B10	g.chr11:47555894C>T	c.234G>A	CTG=>CTA	Leu=>Leu	p.L78L	synonymous	NV
KBTBD4	B10	g.chr11:47556004C>A	c.124G>T	GAG=>TAG	Glu=>Stop	p.E42*	nonsense	genotyping
KCNMA1	B9	g.chr10:78681000G>A	c.561C>T	CTC=>CTT	Leu=>Leu	p.L187L	synonymous	NV
KCTD7	B15	g.chr7:65741631G>C	c.847G>C	GAG=>CAG	Glu=>Gln	p.E283Q	missense	genotyping
KIAA0141	B13	g.chr5:141294310A>G	c.1124A>G	TAT=>TGT	Tyr=>Cys	p.Y375C	missense	genotyping
KIAA0556	B9	g.chr16:27668406_27668410delAAGAC	c.2235_2239delAAGAC	-	-	-	Frame shift indel	Sanger sequencing
KIAA1199	B5	g.chr15:79017240C>A	c.3272C>A	TCC=>TAC	Ser=>Tyr	p.S1091Y	missense	genotyping
KIAA1199	B5	g.chr15:79017311C>T	c.3343C>T	CAG=>TAG	Gln=>Stop	p.Q1115*	nonsense	genotyping
KIAA1377	B10	g.chr11:101338015G>A	c.1039G>A	GAA=>AAA	Glu=>Lys	p.E347K	missense	NV
KIAA1529	B8	g.chr9:99120611G>A	c.1554G>A	ACG=>ACA	Thr=>Thr	p.T518T	synonymous	NV
KIF15	B5	g.chr3:44810900A>G	c.827A>G	CAT=>CGT	His=>Arg	p.H276R	missense	genotyping
KIFAP3	B8	g.chr1:168274082C>G	c.490G>C	GAT=>CAT	Asp=>His	p.D164H	missense	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
KLC2	B5	g.chr11:65786019C>T	c.459C>T	AAC=>AAT	Asn=>Asn	p.N153N	synonymous	NV
KLC4	B15	g.chr6:43148598G>A	c.1601G>A	AGA=>AAA	Arg=>Lys	p.R534K	missense	genotyping
KLC4	B15	g.chr6:43148639G>C	c.1642G>C	GAG=>CAG	Glu=>Gln	p.E548Q	missense	genotyping
KLC4	B15	g.chr6:43148643G>A	c.1646G>A	GGA=>GAA	Gly=>Glu	p.G549E	missense	genotyping
KRAS	B5	g.chr12:25271543T>A	c.182A>T	CAA=>CTA	Gln=>Leu	p.Q61L	missense	NV
KRAS	B13	g.chr12:25271544G>T	c.181C>A	CAA=>AAA	Gln=>Lys	p.Q61K	missense	genotyping
KRAS	B13	g.chr12:25271545A>T	c.180T>A	GGT=>GGA	Gly=>Gly	p.G60G	synonymous	NV
KRT33A	B5	g.chr17:36759142G>A	c.413C>T	TCA=>TTA	Ser=>Leu	p.S138L	missense	genotyping
KRTAP5-5	B20	g.chr11:1608190_1608219delTACTGCTGCCAGTCCAGCTGCTGTAAGCCC	c.171_200delTACTGCTGCCAGTCCAGCTGCTGTAAGCCC	-	-	-	indel	NV
LAMA2	B9	g.chr6:129461023G>A	c.409G>A	GCG=>ACG	Ala=>Thr	p.A137T	missense	NV
LAMA4	B8	g.chr6:112619550C>A	c.699G>T	AGG=>AGT	Arg=>Ser	p.R233S	missense	genotyping
LAMP2	B8	g.chrX:119466885G>A	c.524C>T	GCT=>GTT	Ala=>Val	p.A175V	missense	genotyping
LARP5	B10	g.chr10:880956C>A	c.470G>T	CGA=>CTA	Arg=>Leu	p.R157L	missense	genotyping
LEPRE1	B2	g.chr1:42990832G>C	c.1436C>G	TCT=>TGT	Ser=>Cys	p.S479C	missense	NV
LGSN	B10	g.chr6:64053587G>T	c.194C>A	ACC=>AAC	Thr=>Asn	p.T65N	missense	genotyping
LMBRD2	B8	g.chr5:36144470C>G	c.1820G>C	AGA=>ACA	Arg=>Thr	p.R607T	missense	NV
LNX1	B10	g.chr4:54037836A>G	c.1445T>C	TTG=>TCG	Leu=>Ser	p.L482S	missense	genotyping
LNX1	B15	g.chr4:54039588C>T	c.1276G>A	GTC=>ATC	Val=>Ile	p.V426I	missense	genotyping
LOXL2	B10	g.chr8:23273640C>T	c.439G>A	GAC=>AAC	Asp=>Asn	p.D147N	missense	genotyping
LRP2	B10	g.chr2:169842550C>T	c.1723G>A	GAC=>AAC	Asp=>Asn	p.D575N	missense	genotyping
LZTS1	B2	g.chr8:20154753C>G	c.969G>C	AAG=>AAC	Lys=>Asn	p.K323N	missense	NV
MADD	B13	g.chr11:47261041G>A	c.1807G>A	GAG=>AAG	Glu=>Lys	p.E603K	missense	NV
MAGEB18	B13	g.chrX:26067379insTG	c.356insTG	-	-	-	Frame shift indel	NV
MAP3K5	B10	g.chr6:137013859C>T	c.1744G>A	GAG=>AAG	Glu=>Lys	p.E582K	missense	genotyping
MCM3	B8	g.chr6:52251543C>T	c.835G>A	GAG=>AAG	Glu=>Lys	p.E279K	missense	genotyping
MED1	B9	g.chr17:34819982G>A	c.2018C>T	TCC=>TTC	Ser=>Phe	p.S673F	missense	genotyping
MED7	B2	g.chr5:156498561G>A	c.460C>T	CAA=>TAA	Gln=>Stop	p.Q154*	nonsense	NV
MERTK	B10	g.chr2:112482440C>G	c.1877C>G	TCT=>TGT	Ser=>Cys	p.S626C	missense	genotyping
METTL10	B10	g.chr10:126467636A>G	c.257T>C	ATT=>ACT	Ile=>Thr	p.I86T	missense	genotyping
MITF	B9	g.chr3:70071016T>A	c.339T>A	TGT=>TGA	Cys=>Stop	p.C113*	nonsense	genotyping
MLH1	B15	g.chr3:37042462G>C	c.1369G>C	GAA=>CAA	Glu=>Gln	p.E457Q	missense	genotyping
MLL	B9	g.chr11:117864643C>A	c.4437C>A	TGC=>TGA	Cys=>Stop	p.C1479*	nonsense	NV
MLL2	B15	g.chr12:47712976G>A	c.11779C>T	CAG=>TAG	Gln=>Stop	p.Q3927*	nonsense	NV
MLL3	B5	g.chr7:151510591G>A	c.5287C>T	CAG=>TAG	Gln=>Stop	p.Q1763*	nonsense	genotyping
MLL3	B5	g.chr7:151531025_151531025delC	c.4020_4020delC	-	-	-	Frame shift indel	Sanger sequencing
MLL3	B20	g.chr7:151557958A>G	c.2959T>C	TAC=>CAC	Tyr=>His	p.Y987H	missense	NV
MMAB	B10	g.chr12:108491010C>T	c.238G>A	GAC=>AAC	Asp=>Asn	p.D80N	missense	genotyping
MOBKL2C	B5	g.chr1:46847931C>G	c.790G>C	GAG=>CAG	Glu=>Gln	p.E264Q	missense	NV
MOSPD2	B20	g.chrX:14839445C>G	c.868C>G	CTT=>GTT	Leu=>Val	p.L290V	missense	NV
MPO	B5	g.chr17:53713001G>C	c.118C>G	CTG=>GTG	Leu=>Val	p.L40V	missense	genotyping
MS4A14	B5	g.chr11:59939537C>A	c.520C>A	CCA=>ACA	Pro=>Thr	p.P174T	missense	genotyping
MSN	B20	g.chrX:64873800G>C	c.1126G>C	GAG=>CAG	Glu=>Gln	p.E376Q	missense	NV
MTBP	B10	g.chr8:121599376C>T	c.2351C>T	TCC=>TTC	Ser=>Phe	p.S784F	missense	genotyping
MTNR1B	B10	g.chr11:92354331C>T	c.294C>T	CTC=>CTT	Leu=>Leu	p.L98L	synonymous	NV
MUTYH	B20	g.chr1:45570919G>T	c.595C>A	CCA=>ACA	Pro=>Thr	p.P199T	missense	NV
MYEOV	B10	g.chr11:68819667C>T	c.174C>T	CTC=>CTT	Leu=>Leu	p.L58L	synonymous	NV
MYH6	B8	g.chr14:22937864G>A	c.1804C>T	CTC=>TTC	Leu=>Phe	p.L602F	missense	NV
MYST1	B15	g.chr16:31039293G>A	c.419G>A	CGC=>CAC	Arg=>His	p.R140H	missense	genotyping
NCCRP1	B5	g.chr19:44381687G>C	c.490G>C	GAG=>CAG	Glu=>Gln	p.E164Q	missense	NV
NCOA4	B2	g.chr10:51252248G>C	c.540G>C	GAG=>GAC	Glu=>Asp	p.E180D	missense	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
NCOA7	B2	g.chr6:126252650G>C	c.1757G>C	GGA=>GCA	Gly=>Ala	p.G586A	missense	NV
NCOR1	B9	g.chr17:16009188C>T	c.448G>A	GGA=>AGA	Gly=>Arg	p.G150R	missense	NV
NEO1	B2	g.chr15:71382013G>T	c.4309G>T	GAA=>TAA	Glu=>Stop	p.E1437*	nonsense	NV
NF1	B5	g.chr17:26711630G>T	-	-	-	-	spliceSite	genotyping
NFE2L3	B13	g.chr7:26190733C>G	c.890C>G	TCT=>TGT	Ser=>Cys	p.S297C	missense	genotyping
NFE2L3	B13	g.chr7:26190885C>G	c.1042C>G	CAT=>GAT	His=>Asp	p.H348D	missense	genotyping
NFE2L3	B13	g.chr7:26191117C>G	c.1274C>G	TCA=>TGA	Ser=>Stop	p.S425*	nonsense	genotyping
NFE2L3	B13	g.chr7:26191508C>A	c.1665C>A	GTC=>GTA	Val=>Val	p.V555V	synonymous	NV
NGFRAP1	B20	g.chrX:102519301G>A	c.226G>A	GAA=>AAA	Glu=>Lys	p.E76K	missense	NV
NKD1	B15	g.chr16:49224615G>A	c.835G>A	GTG=>ATG	Val=>Met	p.V279M	missense	genotyping
NLRP13	B10	g.chr19:61105215C>T	c.2787G>A	CTG=>CTA	Leu=>Leu	p.L929L	synonymous	NV
NLRP14	B10	g.chr11:7020837G>A	c.1004G>A	AGA=>AAA	Arg=>Lys	p.R335K	missense	genotyping
NLRP9	B20	g.chr19:60927249G>A	c.2068C>T	CTG=>TTG	Leu=>Leu	p.L690L	synonymous	NV
NPR2	B15	g.chr9:35799413G>C	c.3115G>C	GAG=>CAG	Glu=>Gln	p.E1039Q	missense	genotyping
NR1D2	B5	g.chr3:23976187C>T	c.394C>T	CAA=>TAA	Gln=>Stop	p.Q132*	nonsense	genotyping
NT5C3L	B9	g.chr17:37242235G>C	c.225C>G	CAC=>CAG	His=>Gln	p.H75Q	missense	NV
NUP210	B15	g.chr3:13370078G>C	c.2604C>G	CTC=>CTG	Leu=>Leu	p.L868L	synonymous	NV
NUP62	B10	g.chr19:55103337C>T	c.1540G>A	GAG=>AAG	Glu=>Lys	p.E514K	missense	genotyping
NUPL1	B5	g.chr13:24803637C>T	c.1340C>T	CCA=>CTA	Pro=>Leu	p.P447L	missense	NV
OGDH	B15	g.chr7:44630570C>A	c.103C>A	CAA=>AAA	Gln=>Lys	p.Q35K	missense	genotyping
OIP5	B10	g.chr15:39411455G>C	c.339C>G	GTC=>GTG	Val=>Val	p.V113V	synonymous	NV
OPCML	B10	g.chr11:132032309G>A	c.283C>T	CCA=>TCA	Pro=>Ser	p.P95S	missense	genotyping
OR10A4	B10	g.chr11:6854722G>A	c.268G>A	GAC=>AAC	Asp=>Asn	p.D90N	missense	genotyping
OR2B2	B5	g.chr6:27987022G>C	c.1055C>G	CCT=>CGT	Pro=>Arg	p.P352R	missense	genotyping
OR4F6	B10	g.chr15:100163966_100163969delTAGA	c.419_422delTAGA	-	-	-	Frame shift indel	NV
OR4S2	B2	g.chr11:55175650G>A	c.695G>A	CGC=>CAC	Arg=>His	p.R232H	missense	NV
OR52N2	B5	g.chr11:5798759C>G	c.618C>G	CTC=>CTG	Leu=>Leu	p.L206L	synonymous	NV
OR5B17	B2	g.chr11:57882559C>A	c.560G>T	TGC=>TTC	Cys=>Phe	p.C187F	missense	NV
OR5D13	B2	g.chr11:55298025T>A	c.536T>A	TTT=>TAT	Phe=>Tyr	p.F179Y	missense	NV
OR5I1	B9	g.chr11:55460135insA	c.318insA	-	-	-	Frame shift indel	NV
OR5M9	B10	g.chr11:55987241G>C	c.213C>G	TTC=>TTG	Phe=>Leu	p.F71L	missense	genotyping
OR8K3	B13	g.chr11:55842436A>G	c.78A>G	CCA=>CCG	Pro=>Pro	p.P26P	synonymous	NV
OR9Q1	B5	g.chr11:57704009G>C	c.517G>C	GAG=>CAG	Glu=>Gln	p.E173Q	missense	genotyping
OSGIN2	B8	g.chr8:91006157C>T	c.740C>T	TCT=>TTT	Ser=>Phe	p.S247F	missense	genotyping
PADI4	B13	g.chr1:17562797G>C	c.1952G>C	AGA=>ACA	Arg=>Thr	p.R651T	missense	genotyping
PAK3	B9	g.chrX:110326372C>T	c.1255C>T	CGA=>TGA	Arg=>Stop	p.R419*	nonsense	genotyping
PANX1	B15	g.chr11:93502303G>A	c.177G>A	TCG=>TCA	Ser=>Ser	p.S59S	synonymous	NV
PAOX	B2	g.chr10:135047602C>T	c.1017C>T	ATC=>ATT	Ile=>Ile	p.I339I	synonymous	NV
PARD6B	B8	g.chr20:48799813A>T	c.500A>T	AAA=>ATA	Lys=>Ile	p.K167I	missense	genotyping
PCDHA13	B15	g.chr5:140244290G>A	c.2253G>A	TCG=>TCA	Ser=>Ser	p.S751S	synonymous	NV
PCDHB3	B2	g.chr5:140462767G>A	c.2350G>A	GAG=>AAG	Glu=>Lys	p.E784K	missense	NV
PCDHGA2	B13	g.chr5:140699217C>T	c.495C>T	AAC=>AAT	Asn=>Asn	p.N165N	synonymous	NV
PCIF1	B13	g.chr20:44007787G>A	c.1199G>A	CGC=>CAC	Arg=>His	p.R400H	missense	genotyping
PCK1	B2	g.chr20:55571272C>T	c.521C>T	ACG=>ATG	Thr=>Met	p.T174M	missense	NV
PCP2	B10	g.chr19:7604334G>A	c.10C>T	CAG=>TAG	Gln=>Stop	p.Q4*	nonsense	NV
PDXDC1	B5	g.chr16:15003163T>A	c.191T>A	TTA=>TAA	Leu=>Stop	p.L64*	nonsense	NV
PFKL	B10	g.chr21:44556440C>T	c.403C>T	CGC=>TGC	Arg=>Cys	p.R135C	missense	genotyping
PGLYRP2	B8	g.chr19:15448180C>T	c.301G>A	GAC=>AAC	Asp=>Asn	p.D101N	missense	NV
PIP5K3	B5	g.chr2:208898942C>G	c.3162C>G	CTC=>CTG	Leu=>Leu	p.L1054L	synonymous	NV
PIPOX	B5	g.chr17:24396034A>T	c.146A>T	CAT=>CTT	His=>Leu	p.H49L	missense	genotyping
PLA2G3	B10	g.chr22:29866050G>A	c.291C>T	ATC=>ATT	Ile=>Ile	p.I97I	synonymous	NV
PLCB1	B10	g.chr20:8669032C>G	c.2350C>G	CTG=>GTG	Leu=>Val	p.L784V	missense	genotyping
PLXNB1	B15	g.chr3:48423472G>A	c.6118C>T	CGG=>TGG	Arg=>Trp	p.R2040W	missense	genotyping

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
PNPLA2	B13	g.chr11:811806A>C	c.366A>C	TCA=>TCC	Ser=>Ser	p.S122S	synonymous	NV
POLD1	B5	g.chr19:55601316C>G	c.1308C>G	TTC=>TTG	Phe=>Leu	p.F436L	missense	genotyping
POLG	B15	g.chr15:87672974C>T	c.1116G>A	GAG=>GAA	Glu=>Glu	p.E372E	synonymous	NV
POLR3B	B2	g.chr12:105375054C>T	c.2302C>T	CGT=>TGT	Arg=>Cys	p.R768C	missense	NV
PORCN	B8	g.chrX:48254673C>G	c.183C>G	TTC=>TTG	Phe=>Leu	p.F61L	missense	genotyping
PPIG	B13	g.chr2:170201745A>G	c.1731A>G	TCA=>TCG	Ser=>Ser	p.S577S	synonymous	NV
PPM1G	B10	g.chr2:27460445C>T	c.844G>A	GAT=>AAT	Asp=>Asn	p.D282N	missense	genotyping
PPP1R9A	B5	g.chr7:94378002C>T	c.641C>T	TCT=>TTT	Ser=>Phe	p.S214F	missense	genotyping
PRDM10	B5	g.chr11:129333003G>C	c.82C>G	CCG=>GCG	Pro=>Ala	p.P28A	missense	genotyping
PREP	B17	g.chr6:105832909G>A	c.1936C>T	CCG=>TCG	Pro=>Ser	p.P646S	missense	NV
PRMT5	B9	g.chr14:22463743G>C	c.955C>G	CTG=>GTG	Leu=>Val	p.L319V	missense	genotyping
PRMT7	B10	g.chr16:66948514C>G	c.1965C>G	GCC=>GCG	Ala=>Ala	p.A655A	synonymous	NV
PROKR1	B9	g.chr2:68726877C>G	c.420C>G	GTC=>GTG	Val=>Val	p.V140V	synonymous	NV
PRPSAP2	B5	g.chr17:18721817G>C	c.321G>C	GTG=>GTC	Val=>Val	p.V107V	synonymous	NV
PTPRC	B5	g.chr1:196969980A>C	c.1686A>C	GCA=>GCC	Ala=>Ala	p.A562A	synonymous	NV
PTPRH	B10	g.chr19:60389707_60389720delCCGGGACCAGTCAT	c.769_782delCCGGGACCAGTCAT	-	-	-	Frame shift indel	NV
PWP2	B13	g.chr21:44358157G>A	-	-	-	-	spliceSite	genotyping
RBM46	B9	g.chr4:155939445G>A	c.681G>A	GTG=>GTA	Val=>Val	p.V227V	synonymous	NV
RBM6	B17	g.chr3:50070421_50070421delC	c.1423_1423delC	-	-	-	Frame shift indel	NV
RBMS2	B5	g.chr12:55261248G>C	c.556G>C	GAG=>CAG	Glu=>Gln	p.E186Q	missense	NV
RFC1	B5	g.chr4:38968006G>C	c.3217C>G	CCA=>GCA	Pro=>Ala	p.P1073A	missense	genotyping
RHOT1	B5	g.chr17:27558138G>C	c.1513G>C	GAA=>CAA	Glu=>Gln	p.E505Q	missense	NV
RHPN2	B17	g.chr19:38174669C>A	c.1544G>T	CGA=>CTA	Arg=>Leu	p.R515L	missense	NV
RPS11	B5	g.chr19:54692595G>C	c.154G>C	GAG=>CAG	Glu=>Gln	p.E52Q	missense	genotyping
RPS2	B17	g.chr16:1952795G>A	c.492C>T	CCC=>CCT	Pro=>Pro	p.P164P	synonymous	NV
RSHL1	B2	g.chr19:50990978insCTCCTCGCCCTCCTCCTC	c.11insCTCCTCGCCCTCCTCCTC	-	-	-	indel	NV
RSL1D1	B8	g.chr16:11839366insT	c.221insT	-	-	-	Frame shift indel	NV
S1PR1	B15	g.chr1:101478121C>T	c.993C>T	TGC=>TGT	Cys=>Cys	p.C331C	synonymous	NV
SACS	B2	g.chr13:22810400C>A	c.5174G>T	TGC=>TTC	Cys=>Phe	p.C1725F	missense	NV
SAMD9L	B5	g.chr7:92601013G>A	c.2208C>T	ATC=>ATT	Ile=>Ile	p.I736I	synonymous	NV
SAMD9L	B5	g.chr7:92601459G>A	c.1762C>T	CAA=>TAA	Gln=>Stop	p.Q588*	nonsense	genotyping
SAR1B	B2	g.chr5:133973176G>C	c.332C>G	TCA=>TGA	Ser=>Stop	p.S111*	nonsense	NV
SASH1	B10	g.chr6:148803043C>T	c.316C>T	CAG=>TAG	Gln=>Stop	p.Q106*	nonsense	genotyping
SCRN3	B5	g.chr2:175000827_175000839delTCAAATTTATCAG	c.43_55delTCAAATTTATCAG	-	-	-	Frame shift indel	NV
SDK1	B5	g.chr7:4180413C>T	c.295C>T	CAG=>TAG	Gln=>Stop	p.Q99*	nonsense	genotyping
SEMA4F	B9	g.chr2:74755209C>G	c.899C>G	CCT=>CGT	Pro=>Arg	p.P300R	missense	genotyping
SEMA4F	B9	g.chr2:74755302C>T	c.992C>T	TCT=>TTT	Ser=>Phe	p.S331F	missense	genotyping
SEMA6C	B15	g.chr1:149378753C>A	c.282G>T	GGG=>GGT	Gly=>Gly	p.G94G	synonymous	NV
SEMA6D	B13	g.chr15:45843717C>G	c.1020C>G	TTC=>TTG	Phe=>Leu	p.F340L	missense	genotyping
SERPING1	B10	g.chr11:57124026C>T	c.150C>T	ATC=>ATT	Ile=>Ile	p.I50I	synonymous	NV
SESN2	B13	g.chr1:28458962_28458962delC	c.18_18delC	-	-	-	Frame shift indel	Sanger sequencing
SF3B2	B2	g.chr11:65582189C>G	c.866C>G	TCT=>TGT	Ser=>Cys	p.S289C	missense	NV
SF4	B10	g.chr19:19288323G>A	c.114C>T	CTC=>CTT	Leu=>Leu	p.L38L	synonymous	NV
SH3RF1	B17	g.chr4:170279847C>T	c.1325G>A	CGG=>CAG	Arg=>Gln	p.R442Q	missense	NV
SHPK	B13	g.chr17:3474111G>A	c.474C>T	ATC=>ATT	Ile=>Ile	p.I158I	synonymous	NV
SIL1	B13	g.chr5:138310948G>T	c.1143C>A	ATC=>ATA	Ile=>Ile	p.I381I	synonymous	NV
SLAMF9	B5	g.chr1:158188132G>C	c.813C>G	CTC=>CTG	Leu=>Leu	p.L271L	synonymous	NV
SLC14A2	B9	g.chr18:41512974insC	c.214insC	-	-	-	Frame shift indel	NV
SLC15A1	B8	g.chr13:98137859C>T	c.1804G>A	GGA=>AGA	Gly=>Arg	p.G602R	missense	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
SLC22A17	B8	g.chr14:22886185G>A	c.1293C>T	ACC=>ACT	Thr=>Thr	p.T431T	synonymous	NV
SLC25A25	B10	g.chr9:129900756G>A	c.90G>A	CTG=>CTA	Leu=>Leu	p.L30L	synonymous	NV
SLC25A44	B2	g.chr1:154446706G>A	c.805G>A	GAA=>AAA	Glu=>Lys	p.E269K	missense	NV
SLC26A4	B9	g.chr7:107140268G>C	c.2284G>C	GAG=>CAG	Glu=>Gln	p.E762Q	missense	genotyping
SLC41A3	B17	g.chr3:127258016G>C	c.70C>G	CTT=>GTT	Leu=>Val	p.L24V	missense	NV
SLC44A3	B2	g.chr1:95083576G>A	c.896G>A	TGG=>TAG	Trp=>Stop	p.W299*	nonsense	NV
SLC45A1	B10	g.chr1:8313160G>A	c.1020G>A	CCG=>CCA	Pro=>Pro	p.P340P	synonymous	NV
SLC5A8	B9	g.chr12:100084554C>T	c.1375G>A	GGA=>AGA	Gly=>Arg	p.G459R	missense	NV
SLCO4C1	B10	g.chr5:101655119G>C	c.446C>G	TCA=>TGA	Ser=>Stop	p.S149*	nonsense	NV
SMPD4	B8	g.chr2:130650631G>A	c.122C>T	GCG=>GTG	Ala=>Val	p.A41V	missense	NV
SNPH	B20	g.chr20:1233951A>T	c.738A>T	GCA=>GCT	Ala=>Ala	p.A246A	synonymous	NV
SP110	B5	g.chr2:230782913G>C	c.806C>G	TCC=>TGC	Ser=>Cys	p.S269C	missense	genotyping
SPAG1	B5	g.chr8:101306582C>G	c.1694C>G	TCA=>TGA	Ser=>Stop	p.S565*	nonsense	genotyping
SPAG1	B5	g.chr8:101306654C>T	c.1766C>T	TCT=>TTT	Ser=>Phe	p.S589F	missense	genotyping
SPARC	B2	g.chr5:151035889G>C	c.54C>G	GCC=>GCG	Ala=>Ala	p.A18A	synonymous	NV
SPTB	B8	g.chr14:64306151A>G	c.5847T>C	AAT=>AAC	Asn=>Asn	p.N1949N	synonymous	NV
SRCAP	B2	g.chr16:30643506C>T	c.5260C>T	CTG=>TTG	Leu=>Leu	p.L1754L	synonymous	NV
SRRM2	B5	g.chr16:2756097C>T	c.5567C>T	ACA=>ATA	Thr=>Ile	p.T1856I	missense	genotyping
ST6GAL2	B9	g.chr2:106816941G>A	c.1037C>T	TCG=>TTG	Ser=>Leu	p.S346L	missense	NV
STAG2	B10	g.chrX:123048197C>A	c.3173C>A	TCA=>TAA	Ser=>Stop	p.S1058*	nonsense	genotyping
STRN4	B5	g.chr19:51928261G>T	c.612C>A	GGC=>GGA	Gly=>Gly	p.G204G	synonymous	NV
SUPT16H	B10	g.chr14:20895268T>A	c.2588A>T	GAC=>GTC	Asp=>Val	p.D863V	missense	genotyping
SUPT16H	B10	g.chr14:20895269C>G	c.2587G>C	GAC=>CAC	Asp=>His	p.D863H	missense	genotyping
SYNE1	B10	g.chr6:152587376G>T	c.21255C>A	TTC=>TTA	Phe=>Leu	p.F7085L	missense	genotyping
SYNE1	B10	g.chr6:152587406G>C	c.21225C>G	CTC=>CTG	Leu=>Leu	p.L7075L	synonymous	NV
TAF1	B8	g.chrX:70504672C>T	c.339C>T	ATC=>ATT	Ile=>Ile	p.I113I	synonymous	NV
TAOK3	B8	g.chr12:117084201C>G	c.1914G>C	AAG=>AAC	Lys=>Asn	p.K638N	missense	genotyping
TAOK3	B5	g.chr12:117094743G>A	c.1801C>T	CTC=>TTC	Leu=>Phe	p.L601F	missense	genotyping
TAS2R9	B10	g.chr12:10853615G>A	c.327C>T	CTC=>CTT	Leu=>Leu	p.L109L	synonymous	NV
TDRD1	B15	g.chr10:115963268G>C	c.2005G>C	GAT=>CAT	Asp=>His	p.D669H	missense	genotyping
TET1	B5	g.chr10:70097011C>T	c.4665C>T	CTC=>CTT	Leu=>Leu	p.L1555L	synonymous	NV
TEX14	B13	g.chr17:54031771G>T	c.1934C>A	TCT=>TAT	Ser=>Tyr	p.S645Y	missense	genotyping
TG	B15	g.chr8:134053254C>A	c.6009C>A	GAC=>GAA	Asp=>Glu	p.D2003E	missense	genotyping
TGFB2	B8	g.chr1:216586988A>G	c.322A>G	ATG=>GTG	Met=>Val	p.M108V	missense	NV
TIA1	B15	g.chr2:70297071T>C	c.648A>G	GTA=>GTG	Val=>Val	p.V216V	synonymous	NV
TICAM1	B2	g.chr19:4768010G>A	c.1380C>T	TTC=>TTT	Phe=>Phe	p.F460F	synonymous	NV
TLL1	B8	g.chr4:167155062C>G	c.942C>G	CTC=>CTG	Leu=>Leu	p.L314L	synonymous	NV
TMCC2	B17	g.chr1:203464441_203464442delCT	c.127_128delCT	-	-	-	Frame shift indel	NV
TMEM35	B20	g.chrX:100236409C>T	c.312C>T	TTC=>TTT	Phe=>Phe	p.F104F	synonymous	NV
TMEM42	B8	g.chr3:44881655C>G	c.459C>G	CCC=>CCG	Pro=>Pro	p.P153P	synonymous	NV
TMEM44	B5	g.chr3:195790562C>T	c.1305G>A	CTG=>CTA	Leu=>Leu	p.L435L	synonymous	NV
TMEM56	B20	g.chr1:95429775C>G	c.555C>G	TTC=>TTG	Phe=>Leu	p.F185L	missense	NV
TMEM63A	B2	g.chr1:224116614C>T	c.1012G>A	GAA=>AAA	Glu=>Lys	p.E338K	missense	NV
TMPRSS13	B5	g.chr11:117294523_117294537delGGGCTGGAGATGCCT	c.263_277delGGGCTGGAGATGCCT	-	-	-	indel	NV
TMPRSS2	B9	g.chr21:41761628insCT	c.109insCT	-	-	-	Frame shift indel	Sanger sequencing
TNFAIP8L3	B15	g.chr15:49137513G>T	c.736C>A	CAC=>AAC	His=>Asn	p.H246N	missense	genotyping
TNFAIP8L3	B15	g.chr15:49137514G>T	c.735C>A	ACC=>ACA	Thr=>Thr	p.T245T	synonymous	NV
TP53	B8	g.chr17:7519167T>C	c.488A>G	TAC=>TGC	Tyr=>Cys	p.Y163C	missense	genotyping
TP53	B9	g.chr17:7519238_7519251delCTTGGCCAGTTGGC	c.418_431delCTTGGCCAGTTGGC	-	-	-	Frame shift indel	Sanger sequencing
TP53BP1	B2	g.chr15:41535394C>A	c.2689G>T	GAA=>TAA	Glu=>Stop	p.E897*	nonsense	NV
TPCN1	B8	g.chr12:112195425C>T	c.789C>T	TTC=>TTT	Phe=>Phe	p.F263F	synonymous	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
TRIM23	B15	g.chr5:64942586G>A	c.686C>T	TCA=>TTA	Ser=>Leu	p.S229L	missense	genotyping
TRIM62	B17	g.chr1:33419341G>T	c.280C>A	CAG=>AAG	Gln=>Lys	p.Q94K	missense	NV
TRPM2	B20	g.chr21:44613600C>T	c.717C>T	ATC=>ATT	Ile=>Ile	p.I239I	synonymous	NV
TRPM5	B5	g.chr11:2383864C>G	c.3285G>C	CTG=>CTC	Leu=>Leu	p.L1095L	synonymous	NV
TRPM6	B10	g.chr9:76593377G>A	c.2640C>T	TTC=>TTT	Phe=>Phe	p.F880F	synonymous	NV
TRPV5	B15	g.chr7:142315962G>T	c.2030C>A	GCC=>GAC	Ala=>Asp	p.A677D	missense	genotyping
TSR1	B5	g.chr17:2174797C>G	c.2097G>C	CTG=>CTC	Leu=>Leu	p.L699L	synonymous	NV
TTC3	B5	g.chr21:37486323C>T	c.5156C>T	TCT=>TTT	Ser=>Phe	p.S1719F	missense	NV
TTC3	B5	g.chr21:37486341C>G	c.5174C>G	TCT=>TGT	Ser=>Cys	p.S1725C	missense	NV
TULP3	B9	g.chr12:2909750C>T	c.470C>T	TCT=>TTT	Ser=>Phe	p.S157F	missense	NV
TYR	B13	g.chr11:88551006G>A	c.237G>A	TCG=>TCA	Ser=>Ser	p.S79S	synonymous	NV
UBC	B8	g.chr12:123964210C>T	c.61G>A	GAC=>AAC	Asp=>Asn	p.D21N	missense	genotyping
UBR4	B5	g.chr1:19349822A>T	c.7266T>A	ATT=>ATA	Ile=>Ile	p.I2422I	synonymous	NV
UGCGL2	B10	g.chr13:95304647G>A	c.4092C>T	CGC=>CGT	Arg=>Arg	p.R1364R	synonymous	NV
UPB1	B5	g.chr22:23236778A>G	c.426A>G	GCA=>GCG	Ala=>Ala	p.A142A	synonymous	NV
UPF1	B13	g.chr19:18832188C>T	c.2241C>T	TTC=>TTT	Phe=>Phe	p.F747F	synonymous	NV
USP26	B17	g.chrX:131988074_131988084delTGGCCTTTTTT	c.902_912delTGGCCTTTTTT	-	-	-	Frame shift indel	Sanger sequencing
USP48	B10	g.chr1:21928841T>C	c.1243A>G	ATG=>GTG	Met=>Val	p.M415V	missense	genotyping
USP5	B17	g.chr12:6843489C>T	c.2113C>T	CTC=>TTC	Leu=>Phe	p.L705F	missense	NV
USP5	B20	g.chr12:6844609A>G	c.2419A>G	ATT=>GTT	Ile=>Val	p.I807V	missense	NV
UTX	B8	g.chrX:44827705C>A	c.3341C>A	TCA=>TAA	Ser=>Stop	p.S1114*	nonsense	NV
UVRAG	B9	g.chr11:75529941G>C	c.1936G>C	GGT=>CGT	Gly=>Arg	p.G646R	missense	genotyping
VCPIP1	B10	g.chr8:67741283G>A	c.465C>T	GGC=>GGT	Gly=>Gly	p.G155G	synonymous	NV
VN1R4	B17	g.chr19:58462070G>T	c.661C>A	CTC=>ATC	Leu=>Ile	p.L221I	missense	NV
VPS13B	B15	g.chr8:100238142C>T	c.2203C>T	CTT=>TTT	Leu=>Phe	p.L735F	missense	NV
VPS13D	B20	g.chr1:12253676G>T	c.2011G>T	GAA=>TAA	Glu=>Stop	p.E671*	nonsense	NV
WDR34	B15	g.chr9:130435934C>A	c.1521G>T	GTG=>GTT	Val=>Val	p.V507V	synonymous	NV
WDR52	B9	g.chr3:114598207G>C	c.1627C>G	CTT=>GTT	Leu=>Val	p.L543V	missense	NV
XAF1	B8	g.chr17:6602265C>A	c.166C>A	CAG=>AAG	Gln=>Lys	p.Q56K	missense	NV
YAP1	B10	g.chr11:101490268G>A	c.505G>A	GAT=>AAT	Asp=>Asn	p.D169N	missense	genotyping
ZDHHC23	B10	g.chr3:115155509G>C	c.434G>C	GGA=>GCA	Gly=>Ala	p.G145A	missense	genotyping
ZFHX3	B15	g.chr16:71379700C>T	c.9976G>A	GCC=>ACC	Ala=>Thr	p.A3326T	missense	NV
ZFP37	B20	g.chr9:114845466G>A	c.1253C>T	TCA=>TTA	Ser=>Leu	p.S418L	missense	NV
ZHX3	B2	g.chr20:39265653T>C	c.1318A>G	AGT=>GGT	Ser=>Gly	p.S440G	missense	NV
ZIK1	B5	g.chr19:62793764A>T	c.773A>T	CAG=>CTG	Gln=>Leu	p.Q258L	missense	genotyping
ZKSCAN4	B9	g.chr6:28321104T>A	c.1407A>T	GAA=>GAT	Glu=>Asp	p.E469D	missense	NV
ZMYND10	B5	g.chr3:50357582C>G	c.178G>C	GAG=>CAG	Glu=>Gln	p.E60Q	missense	genotyping
ZMYND8	B2	g.chr20:45308303C>G	c.2140G>C	GAT=>CAT	Asp=>His	p.D714H	missense	NV
ZMYND8	B2	g.chr20:45308369C>G	c.2074G>C	GAG=>CAG	Glu=>Gln	p.E692Q	missense	NV
ZMYND8	B2	g.chr20:45308415C>T	c.2028G>A	GAG=>GAA	Glu=>Glu	p.E676E	synonymous	NV
ZNF124	B5	g.chr1:245389669G>A	c.100C>T	CAG=>TAG	Gln=>Stop	p.Q34*	nonsense	NV
ZNF174	B13	g.chr16:3398555A>T	c.859A>T	AGC=>TGC	Ser=>Cys	p.S287C	missense	genotyping
ZNF295	B2	g.chr21:42286840T>A	c.434A>T	CAA=>CTA	Gln=>Leu	p.Q145L	missense	NV
ZNF295	B5	g.chr21:42287117C>T	c.157G>A	GAA=>AAA	Glu=>Lys	p.E53K	missense	genotyping
ZNF32	B9	g.chr10:43459613A>T	c.713T>A	ATC=>AAC	Ile=>Asn	p.I238N	missense	NV
ZNF329	B9	g.chr19:63331075C>T	c.1608G>A	GAG=>GAA	Glu=>Glu	p.E536E	synonymous	NV
ZNF432	B20	g.chr19:57228798C>G	c.1946G>C	GGA=>GCA	Gly=>Ala	p.G649A	missense	NV
ZNF471	B15	g.chr19:61719525C>G	c.103C>G	CAG=>GAG	Gln=>Glu	p.Q35E	missense	genotyping
ZNF502	B10	g.chr3:44738353G>C	c.1040G>C	GGA=>GCA	Gly=>Ala	p.G347A	missense	genotyping
ZNF536	B15	g.chr19:35717711C>T	c.2288C>T	TCC=>TTC	Ser=>Phe	p.S763F	missense	genotyping
ZNF552	B5	g.chr19:63011821C>T	c.623G>A	GGA=>GAA	Gly=>Glu	p.G208E	missense	NV
ZNF559	B15	g.chr19:9313381insT	c.254insT	-	-	-	Frame shift indel	NV
ZNF592	B20	g.chr15:83127154G>C	c.244G>C	GAG=>CAG	Glu=>Gln	p.E82Q	missense	NV

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Supplementary Table 3 continued. Details of predicted somatic mutations detected in the Discovery Screen.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type	Validation status
ZNF623	B5	g.chr8:144804284A>T	c.1099A>T	AGA=>TGA	Arg=>Stop	p.R367*	nonsense	genotyping
ZNF80	B9	g.chr3:115437890C>G	c.722G>C	GGA=>GCA	Gly=>Ala	p.G241A	missense	genotyping
ZP4	B8	g.chr1:236115394C>A	c.1080G>T	CTG=>CTT	Leu=>Leu	p.L360L	synonymous	NV
ZSCAN12	B5	g.chr6:28474071C>A	c.91G>T	GAT=>TAT	Asp=>Tyr	p.D31Y	missense	NV
ZSCAN22	B20	g.chr19:63541504A>T	c.476A>T	AAT=>ATT	Asn=>Ile	p.N159I	missense	NV

#Genomic positions are coordinates in the hg18 UCSC release of the human genome. g., genomic sequence; c., cDNA sequence; p., protein sequence. $ Mutated positions indicate the sites in the protein-coding region of the cDNA sequence. § Frame shift indel, frameshift insertions and deletions; indel, in frame insertions and deletions which still change more than one single codon. * Stop codon. NV, not validated.

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Supplementary Table 4. Summary statistics of targeted exon sequencing in the Prevalence Screen.

Samples	Mean fold coverage	% of targets covered by at least 1 ×	% of targets covered by at least 10 ×
B100-Blood	70.04	98.60	90.40
B100-Tumor	80.57	98.90	92.00
B101-Blood	62.80	98.50	89.70
B101-Tumor	73.66	98.70	91.20
B102-Blood	63.09	98.20	89.00
B102-Tumor	61.85	98.50	89.80
B103-Blood	69.19	98.50	89.90
B103-Tumor	66.91	98.60	90.20
B104-0-Blood	79.26	98.80	91.90
B104-0-Tumor	68.69	98.50	89.70
B104-Blood	76.45	98.60	91.00
B104-Tumor	63.40	98.40	89.30
B105-0-Blood	68.18	98.60	90.60
B105-0-Tumor	64.98	98.50	89.70
B105-1-Blood	53.37	98.40	87.80
B105-1-Tumor	52.70	98.30	87.00
B105-Blood	55.89	98.40	88.20
B105-Tumor	51.61	98.40	87.40
B106-Blood	90.08	99.00	93.00
B106-Tumor	68.26	98.60	90.70
B107-Blood	103.13	98.90	93.10
B107-Tumor	77.70	98.50	90.50
B109-Blood	71.35	98.70	90.80
B109-Tumor	89.32	98.90	92.50
B110-Blood	73.66	98.80	91.20
B110-Tumor	68.96	98.70	90.90
B111-Blood	89.79	98.80	92.50
B111-Tumor	80.75	98.70	91.40
B112-Blood	73.74	98.60	90.70
B112-Tumor	80.97	98.80	91.80
B114-Blood	70.71	98.60	90.40
B114-Tumor	85.67	98.70	91.50
B14-Blood	80.89	98.60	90.50
B14-Tumor	66.83	98.30	89.10
B16-Blood	70.63	98.60	90.20
B16-Tumor	88.44	98.80	91.80
B18-Blood	161.04	99.20	95.10
B18-Tumor	70.14	98.70	90.40
B21-Blood	77.68	98.80	91.80
B21-Tumor	89.99	98.40	90.70
B22-Blood	73.22	98.20	89.00
B22-Tumor	73.54	98.20	88.80
B23-Blood	100.74	98.60	91.60
B23-Tumor	69.46	98.20	88.50
B24-Blood	87.45	98.50	91.10
B24-Tumor	71.99	98.20	88.80
B25-Blood	88.98	98.40	90.60
B25-Tumor	81.81	98.40	90.70
B34-Blood	100.52	98.70	91.70
B34-Tumor	87.82	98.70	91.40
B35-Blood	71.39	98.50	89.90

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Supplementary Table 4 continued. Summary statistics of targeted exon sequencing in the Prevalence Screen.

Samples	Mean fold coverage	% of targets covered by at least 1 ×	% of targets covered by at least 10 ×
B35-Tumor	87.56	98.60	91.40
B36-Blood	66.82	98.40	89.50
B36-Tumor	66.73	98.10	87.80
B37-Blood	95.04	98.80	92.10
B37-Tumor	73.89	98.60	90.20
B41-Blood	74.22	98.40	89.40
B41-Tumor	68.93	98.50	89.70
B43-Blood	78.58	98.10	89.40
B43-Tumor	67.29	98.30	88.90
B45-Blood	92.79	98.40	91.60
B45-Tumor	71.77	98.50	90.10
B47-Blood	73.72	98.00	88.90
B47-Tumor	69.51	97.90	88.20
B50-Blood	71.37	98.00	88.30
B50-Tumor	63.27	97.70	86.60
B52-Blood	114.46	98.60	92.50
B52-Tumor	74.48	98.10	88.80
B54-Blood	119.73	98.80	93.30
B54-Tumor	74.94	98.60	90.10
B55-Blood	72.54	98.00	88.50
B55-Tumor	66.30	98.00	88.50
B56-Blood	67.23	98.20	90.20
B56-Tumor	69.97	98.40	90.20
B57-Blood	77.74	98.10	89.30
B57-Tumor	102.86	98.70	92.40
B59-0-Blood	161.32	99.10	95.60
B59-0-Tumor	62.39	98.60	90.60
B59-1-Blood	152.60	99.10	95.00
B59-1-Tumor	59.31	98.20	88.50
B59-3-Blood	73.21	98.60	90.80
B59-3-Tumor	113.12	99.00	93.60
B59-Blood	157.01	98.70	94.00
B59-Tumor	74.29	98.30	89.80
B60-Blood	112.02	98.70	92.80
B60-Tumor	64.50	98.10	88.30
B61-Blood	66.60	97.70	86.80
B61-Tumor	144.84	98.80	94.20
B62-0-Blood	68.56	98.30	90.00
B62-0-Tumor	64.13	98.40	89.80
B63-Blood	70.31	98.30	89.00
B63-Tumor	88.81	98.30	90.50
B64-Blood	68.27	98.10	88.00
B64-Tumor	80.44	98.40	89.80
B65-Blood	65.12	98.30	88.70
B65-Tumor	70.31	98.30	88.90
B66-0-Blood	85.78	98.50	91.20
B66-0-Tumor	64.81	98.00	88.30
B66-Blood	80.51	98.30	89.50
B66-Tumor	68.33	98.20	88.80
B68-Blood	73.17	98.40	90.30
B68-Tumor	77.53	98.30	89.60
B69-Blood	65.11	98.30	88.90
B69-Tumor	134.84	99.00	94.00
B70-Blood	63.22	98.60	89.80
B70-Tumor	140.89	99.00	94.60

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Supplementary Table 4 continued. Summary statistics of targeted exon sequencing in the Prevalence Screen.

Samples	Mean fold coverage	% of targets covered by at least 1 ×	% of targets covered by at least 10 ×
B71-Blood	76.27	98.30	89.00
B71-Tumor	134.06	98.70	93.20
B73-Blood	81.58	98.60	90.80
B73-Tumor	63.59	98.30	88.70
B74-Blood	70.81	98.30	89.00
B74-Tumor	65.80	98.20	88.30
B77-Blood	54.31	97.70	85.50
B77-Tumor	50.83	97.70	84.70
B78-Blood	66.40	98.40	89.20
B78-Tumor	86.10	98.60	90.80
B79-Blood	71.95	98.60	90.20
B79-Tumor	99.20	98.70	92.00
B80-0-Blood	71.49	98.80	90.90
B80-0-Tumor	79.25	98.70	90.80
B80-11-Blood	83.84	98.80	91.60
B80-11-Tumor	67.23	98.70	90.10
B80-13-Blood	68.54	98.50	89.50
B80-13-Tumor	65.88	98.60	89.80
B80-3-Blood	80.81	98.60	90.80
B80-3-Tumor	76.28	98.60	90.80
B80-4-Blood	111.78	98.90	93.30
B80-4-Tumor	68.52	98.50	89.60
B80-7-Blood	66.39	98.50	89.70
B80-7-Tumor	66.72	98.50	89.70
B80-8-Blood	67.69	98.50	89.70
B80-8-Tumor	93.87	98.70	91.70
B80-Blood	92.71	98.70	91.50
B80-Tumor	68.44	98.50	89.30
B81-1-Blood	88.55	98.60	91.50
B81-1-Tumor	66.59	98.40	89.10
B81-Blood	66.10	98.00	87.50
B81-Tumor	83.15	98.70	91.10
B82-Blood	67.85	98.30	89.10
B82-Tumor	86.58	98.80	91.60
B83-Blood	64.05	97.90	87.70
B83-Tumor	70.15	98.20	89.20
B84-Blood	77.13	98.80	91.60
B84-Tumor	64.66	98.60	89.90
B85-0-Blood	64.76	98.50	89.70
B85-0-Tumor	100.75	99.00	93.20
B85-2-Blood	65.94	98.50	89.40
B85-2-Tumor	116.63	99.00	93.60
B86-Blood	80.69	98.30	89.20
B86-Tumor	69.05	98.20	87.80
B87-Blood	69.96	98.20	88.90
B87-Tumor	84.81	98.70	91.60
B88-Blood	65.53	98.40	89.50
B88-Tumor	76.85	98.60	90.90
B89-10-Blood	67.87	98.30	89.00
B89-10-Tumor	87.55	98.70	92.10
B89-12-Blood	67.10	98.40	89.70
B89-12-Tumor	68.78	98.20	89.00
B89-16-Blood	51.20	97.30	85.00
B89-16-Tumor	52.35	97.50	85.10
B89-1-Blood	66.91	98.20	89.70

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Supplementary Table 4 continued. Summary statistics of targeted exon sequencing in the Prevalence Screen.

Samples	Mean fold coverage	% of targets covered by at least 1 ×	% of targets covered by at least 10 ×
B89-1-Tumor	75.94	98.50	90.60
B89-3-Blood	70.57	98.60	90.40
B89-3-Tumor	99.29	98.80	92.30
B89-4-Blood	96.90	98.60	91.80
B89-4-Tumor	69.27	98.40	89.70
B89-5-Blood	64.85	97.90	87.60
B89-5-Tumor	75.06	98.20	89.10
B90-Blood	66.74	98.40	89.40
B90-Tumor	101.38	98.80	92.70
B96-Blood	116.87	99.10	94.10
B96-Tumor	76.11	98.70	90.90
B98-Blood	80.45	98.70	91.30
B98-Tumor	69.43	98.50	90.20
B99-Blood	83.78	98.50	91.70
B99-Tumor	216.59	99.20	95.80

Reads were aligned to the hg18 UCSC release of the human genome.

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Supplementary Table 5. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein) §	Mutation Type
ABCA4	B8	g.chr1:94351206C>T	c.71G>A	CGC=>CAC	Arg=>His	p.R24H	missense
ACAD10	B69	g.chr12:110652016C>T	c.1267C>T	CGA=>TGA	Arg=>Stop	p.R423*	nonsense
ACAD10	B81-1	g.chr12:110624480A>T	c.319A>T	AGA=>TGA	Arg=>Stop	p.R107*	nonsense
ADAMTSL3	B5	g.chr15:82491167C>G	c.4733C>G	TCC=>TGC	Ser=>Cys	p.S1578C	missense
ADAMTSL3	B79	g.chr15:82442799C>T	c.3415C>T	CGG=>TGG	Arg=>Trp	p.R1139W	missense
ADAMTSL3	B83	g.chr15:82383690A>G	c.2018A>G	CAT=>CGT	His=>Arg	p.H673R	missense
ADCY2	B106	g.chr5:7842879C>G	c.2594C>G	GCT=>GGT	Ala=>Gly	p.A865G	missense
ADCY2	B36	g.chr5:7879853G>A	c.3145G>A	GTC=>ATC	Val=>Ile	p.V1049I	missense
ADCY2	B5	g.chr5:7762361G>A	c.1439G>A	CGC=>CAC	Arg=>His	p.R480H	missense
ADCY2	B69	g.chr5:7855442C>T	c.2740C>T	CGG=>TGG	Arg=>Trp	p.R914W	missense
ALDH1B1	B15	g.chr9:38386397G>T	c.652G>T	GCC=>TCC	Ala=>Ser	p.A218S	missense
ALOX12	B13	g.chr17:6842847A>C	c.509A>C	AAG=>ACG	Lys=>Thr	p.K170T	missense
ALS2CR11	B35	g.chr2:202155089G>A	c.613C>T	CAG=>TAG	Gln=>Stop	p.Q205*	nonsense
ALS2CR11	B5	g.chr2:202144928C>T	c.814G>A	GAA=>AAA	Glu=>Lys	p.E272K	missense
ALS2CR11	B59-3	g.chr2:202109244C>G	c.1251G>C	TTG=>TTC	Leu=>Phe	p.L417F	missense
ANK2	B10	g.chr4:114494501G>A	c.5278G>A	GAA=>AAA	Glu=>Lys	p.E1760K	missense
ANK2	B65	g.chr4:114497630G>A	c.8407G>A	GAA=>AAA	Glu=>Lys	p.E2803K	missense
ANK2	B69	g.chr4:114508384T>C	c.11246T>C	GTT=>GCT	Val=>Ala	p.V3749A	missense
ANK2	B70	g.chr4:114494287G>C	c.5064G>C	CAG=>CAC	Gln=>His	p.Q1688H	missense
ANK2	B83	g.chr4:114494249G>A	c.5026G>A	GAA=>AAA	Glu=>Lys	p.E1676K	missense
ANK2	B85-0	g.chr4:114382734C>T	c.811C>T	CAT=>TAT	His=>Tyr	p.H271Y	missense
ANK2	B89-4	g.chr4:114494679C>T	c.5456C>T	GCG=>GTG	Ala=>Val	p.A1819V	missense
ANK3	B10	g.chr10:61544007G>A	c.2930C>T	TCA=>TTA	Ser=>Leu	p.S977L	missense
ANK3	B65	g.chr10:61503559C>G	c.7086G>C	CAG=>CAC	Gln=>His	p.Q2362H	missense
ANK3	B71	g.chr10:61504958G>C	c.5687C>G	TCT=>TGT	Ser=>Cys	p.S1896C	missense
ANK3	B85-0	g.chr10:61516453A>G	c.3736T>C	TGT=>CGT	Cys=>Arg	p.C1246R	missense
ANK3	B89-4	g.chr10:61709388T>A	c.130A>T	AGT=>TGT	Ser=>Cys	p.S44C	missense
ANO5	B5	g.chr11:22248513G>A	c.1978G>A	GAC=>AAC	Asp=>Asn	p.D660N	missense
ANO7	B15	g.chr2:241779331C>A	c.320C>A	CCC=>CAC	Pro=>His	p.P107H	missense
ANPEP	B15	g.chr15:88145685C>T	c.1727G>A	CGC=>CAC	Arg=>His	p.R576H	missense
AOAH	B8	g.chr7:36546519C>T	c.1237G>A	GTT=>ATT	Val=>Ile	p.V413I	missense
AP2B1	B5	g.chr17:31001755G>C	c.1630G>C	GAG=>CAG	Glu=>Gln	p.E544Q	missense
ARHGAP28	B10	g.chr18:6866166G>T	c.772G>T	GAA=>TAA	Glu=>Stop	p.E258*	nonsense
ARID1A	B13	g.chr1:26966872_26966872delC	c.2994_2994delC	-	-	-	Frame shift indel
ARID1A	B13	g.chr1:26978951C>G	c.5975C>G	TCA=>TGA	Ser=>Stop	p.S1992*	nonsense
ARID1A	B13	g.chr1:26979357C>G	c.6381C>G	ATC=>ATG	Ile=>Met	p.I2127M	missense
ARID1A	B13	g.chr1:26979782C>T	c.6806C>T	TCA=>TTA	Ser=>Leu	p.S2269L	missense
ARID1A	B24	g.chr1:26962263C>T	c.2632C>T	CAG=>TAG	Gln=>Stop	p.Q878*	nonsense
ARID1A	B35	g.chr1:26971984C>T	c.3634C>T	CAG=>TAG	Gln=>Stop	p.Q1212*	nonsense
ARID1A	B37	g.chr1:26978314G>T	c.5338G>T	GAA=>TAA	Glu=>Stop	p.E1780*	nonsense
ARID1A	B37	g.chr1:26978674G>A	c.5698G>A	GAT=>AAT	Asp=>Asn	p.D1900N	missense
ARID1A	B47	g.chr1:26978197C>T	c.5221C>T	CAG=>TAG	Gln=>Stop	p.Q1741*	nonsense
ARID1A	B5	g.chr1:26971940C>G	c.3590C>G	TCC=>TGC	Ser=>Cys	p.S1197C	missense
ARID1A	B5	g.chr1:26972451C>A	c.3743C>A	TCA=>TAA	Ser=>Stop	p.S1248*	nonsense
ARID1A	B52	g.chr1:26978192_26978225delCAGGACAGAGAACGCTACTGGATCCTGGGAGGTT	c.1643_1676delCAGGACAGAGAACGCTACTGGATCCTGGGAGGTT	-	-	-	Frame shift indel
ARID1A	B60	g.chr1:26974055C>T	c.4750C>T	CAG=>TAG	Gln=>Stop	p.Q1584*	nonsense
ARID1A	B71	g.chr1:26931800C>G	c.1850C>G	TCA=>TGA	Ser=>Stop	p.S617*	nonsense
ARID1A	B79	g.chr1:26974670G>A	c.5009G>A	TGG=>TAG	Trp=>Stop	p.W1670*	nonsense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
ARID1A	B85-0	g.chr1:26978582_26978582delG	c.1253_1253delG	-	-	-	Frame shift indel
ARID1A	B85-2	g.chr1:26973782C>T	c.4477C>T	CAG=>TAG	Gln=>Stop	p.Q1493*	nonsense
ARID1A	B90	g.chr1:26931847C>T	c.1897C>T	CAG=>TAG	Gln=>Stop	p.Q633*	nonsense
ASB15	B13	g.chr7:123056623G>C	c.1339G>C	GAC=>CAC	Asp=>His	p.D447H	missense
ATG2B	B5	g.chr14:95839211C>T	c.4977G>A	ATG=>ATA	Met=>Ile	p.M1659I	missense
ATG2B	B65	g.chr14:95839158G>A	c.5030C>T	TCC=>TTC	Ser=>Phe	p.S1677F	missense
ATG2B	B69	g.chr14:95821862G>A	c.6220C>T	CGC=>TGC	Arg=>Cys	p.R2074C	missense
ATG2B	B69	g.chr14:95826624G>A	c.5758C>T	CGC=>TGC	Arg=>Cys	p.R1920C	missense
ATG2B	B89-16	g.chr14:95828189C>G	-	-	-	-	spliceSite
ATP5C1	B10	g.chr10:7881856G>A	c.544G>A	GAA=>AAA	Glu=>Lys	p.E182K	missense
ATP8A1	B10	g.chr4:42312812G>A	c.404C>T	ACG=>ATG	Thr=>Met	p.T135M	missense
ATP8A1	B74	g.chr4:42276655A>G	c.932T>C	GTC=>GCC	Val=>Ala	p.V311A	missense
ATP8A1	B89-12	g.chr4:42152142T>C	c.2746A>G	AGA=>GGA	Arg=>Gly	p.R916G	missense
AVL9	B10	g.chr7:32565266G>A	c.880G>A	GAG=>AAG	Glu=>Lys	p.E294K	missense
AVL9	B35	g.chr7:32576277G>A	c.1336G>A	GAT=>AAT	Asp=>Asn	p.D446N	missense
BAI3	B15	g.chr6:70155325G>A	c.4390G>A	GCA=>ACA	Ala=>Thr	p.A1464T	missense
BAI3	B69	g.chr6:70127703G>C	c.3817G>C	GAA=>CAA	Glu=>Gln	p.E1273Q	missense
BAI3	B98	g.chr6:70122468G>A	c.3590G>A	CGA=>CAA	Arg=>Gln	p.R1197Q	missense
BRIP1	B36	g.chr17:57281349C>T	c.430G>A	GCA=>ACA	Ala=>Thr	p.A144T	missense
BRIP1	B54	g.chr17:57212541A>G	c.1798T>C	TTT=>CTT	Phe=>Leu	p.F600L	missense
BRIP1	B8	g.chr17:57231267C>T	c.1316G>A	CGA=>CAA	Arg=>Gln	p.R439Q	missense
BRPF1	B10	g.chr3:9761820G>A	c.3049G>A	GCT=>ACT	Ala=>Thr	p.A1017T	missense
BRPF1	B89-10	g.chr3:9763006G>A	c.3347G>A	CGA=>CAA	Arg=>Gln	p.R1116Q	missense
BTAF1	B10	g.chr10:93768659C>G	c.4850C>G	TCA=>TGA	Ser=>Stop	p.S1617*	nonsense
BTAF1	B106	g.chr10:93733969C>G	c.2255C>G	CCG=>CGG	Pro=>Arg	p.P752R	missense
BTAF1	B22	g.chr10:93713895C>T	c.1486C>T	CTC=>TTC	Leu=>Phe	p.L496F	missense
C10orf137	B5	g.chr10:127414386A>T	c.1579A>T	AGC=>TGC	Ser=>Cys	p.S527C	missense
C10orf137	B65	g.chr10:127403965A>G	c.599A>G	TAT=>TGT	Tyr=>Cys	p.Y200C	missense
C10orf137	B71	g.chr10:127424303G>A	c.2526G>A	TGG=>TGA	Trp=>Stop	p.W842*	nonsense
C14orf101	B15	g.chr14:56155131G>A	c.1123G>A	GTT=>ATT	Val=>Ile	p.V375I	missense
C15orf55	B106	g.chr15:32427855C>A	c.410C>A	TCT=>TAT	Ser=>Tyr	p.S137Y	missense
C15orf55	B65	g.chr15:32435866G>A	c.2281G>A	GGA=>AGA	Gly=>Arg	p.G761R	missense
C17orf80	B15	g.chr17:68743656C>G	c.440C>G	TCT=>TGT	Ser=>Cys	p.S147C	missense
C17orf80	B86	g.chr17:68743901C>T	c.685C>T	CAT=>TAT	His=>Tyr	p.H229Y	missense
C19orf15	B10	g.chr19:43542984G>A	c.544G>A	GAG=>AAG	Glu=>Lys	p.E182K	missense
C19orf15	B77	g.chr19:43539321A>T	c.215A>T	CAG=>CTG	Gln=>Leu	p.Q72L	missense
C1orf101	B5	g.chr1:242821652G>C	c.2185G>C	GAA=>CAA	Glu=>Gln	p.E729Q	missense
C1orf101	B69	g.chr1:242790806G>A	c.1243G>A	GTC=>ATC	Val=>Ile	p.V415I	missense
C1orf101	B86	g.chr1:242818457A>T	c.2136A>T	AAA=>AAT	Lys=>Asn	p.K712N	missense
C1orf106	B63	g.chr1:199144480G>A	-	-	-	-	spliceSite
C20orf72	B50	g.chr20:17916910C>A	c.833C>A	GCC=>GAC	Ala=>Asp	p.A278D	missense
C4orf17	B105-0	g.chr4:100670007G>A	c.415G>A	GCC=>ACC	Ala=>Thr	p.A139T	missense
C4orf17	B9	g.chr4:100662853C>G	c.301C>G	CCA=>GCA	Pro=>Ala	p.P101A	missense
C8orf76	B35	g.chr8:124313088T>C	c.448A>G	ATT=>GTT	Ile=>Val	p.I150V	missense
C8orf76	B69	g.chr8:124308018G>A	c.851C>T	TCG=>TTG	Ser=>Leu	p.S284L	missense
C9orf102	B15	g.chr9:97717875G>A	c.926G>A	GGC=>GAC	Gly=>Asp	p.G309D	missense
CANX	B14	g.chr5:179082463A>G	c.1235A>G	GAA=>GGA	Glu=>Gly	p.E412G	missense
CANX	B8	g.chr5:179082462G>C	c.1234G>C	GAA=>CAA	Glu=>Gln	p.E412Q	missense
CCDC111	B5	g.chr4:185843642A>T	c.1182A>T	AAA=>AAT	Lys=>Asn	p.K394N	missense
CCDC111	B65	g.chr4:185836533G>A	c.998G>A	AGC=>AAC	Ser=>Asn	p.S333N	missense
CD1C	B8	g.chr1:156529060C>G	c.661C>G	CTG=>GTG	Leu=>Val	p.L221V	missense
CD86	B10	g.chr3:123321057G>A	c.976G>A	GAT=>AAT	Asp=>Asn	p.D326N	missense
CD86	B96	g.chr3:123305118C>T	c.134C>T	TCT=>TTT	Ser=>Phe	p.S45F	missense
CDH5	B22	g.chr16:64970913G>A	c.172G>A	GAA=>AAA	Glu=>Lys	p.E58K	missense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
CDH5	B8	g.chr16:64978229G>C	c.227G>C	AGT=>ACT	Ser=>Thr	p.S76T	missense
CDKN1A	B13	g.chr6:36760042insT	c.186insT	-	-	-	Frame shift indel
CDKN1A	B15	g.chr6:36760002G>A	c.146G>A	TGG=>TAG	Trp=>Stop	p.W49*	nonsense
CEP135	B22	g.chr4:56532274C>T	c.1192C>T	CAG=>TAG	Gln=>Stop	p.Q398*	nonsense
CEP135	B9	g.chr4:56541102G>C	c.1510G>C	GAA=>CAA	Glu=>Gln	p.E504Q	missense
CHD6	B35	g.chr20:39488150C>A	c.4126G>T	GCA=>TCA	Ala=>Ser	p.A1376S	missense
CHD6	B36	g.chr20:39550622C>T	c.1717G>A	GTC=>ATC	Val=>Ile	p.V573I	missense
CHD6	B55	g.chr20:39478647G>T	c.6481C>A	CAC=>AAC	His=>Asn	p.H2161N	missense
CHD6	B59-3	g.chr20:39474294C>G	c.7155G>C	CAG=>CAC	Gln=>His	p.Q2385H	missense
CHD6	B65	g.chr20:39549856T>A	c.1864A>T	AAA=>TAA	Lys=>Stop	p.K622*	nonsense
CHD6	B69	g.chr20:39513999C>T	c.3404G>A	CGT=>CAT	Arg=>His	p.R1135H	missense
CHD6	B89-4	g.chr20:39595593G>A	c.64C>T	CCA=>TCA	Pro=>Ser	p.P22S	missense
CHRD	B13	g.chr3:185583853G>A	c.1273G>A	GGC=>AGC	Gly=>Ser	p.G425S	missense
CLSPN	B15	g.chr1:35986760C>G	c.2305G>C	GAG=>CAG	Glu=>Gln	p.E769Q	missense
CLSPN	B79	g.chr1:35975175T>A	c.3836A>T	AAT=>ATT	Asn=>Ile	p.N1279I	missense
CLSPN	B89-4	g.chr1:36002674T>A	c.362A>T	CAG=>CTG	Gln=>Leu	p.Q121L	missense
CNTNAP2	B8	g.chr7:146460373C>T	c.1187C>T	TCA=>TTA	Ser=>Leu	p.S396L	missense
COL3A1	B10	g.chr2:189583277G>T	c.3952G>T	GAT=>TAT	Asp=>Tyr	p.D1318Y	missense
COL3A1	B10	g.chr2:189583646G>A	c.4039G>A	GAA=>AAA	Glu=>Lys	p.E1347K	missense
COL3A1	B59-3	g.chr2:189557778G>C	c.127G>C	GAT=>CAT	Asp=>His	p.D43H	missense
CREB3L2	B106	g.chr7:137217719A>G	c.1466T>C	CTT=>CCT	Leu=>Pro	p.L489P	missense
CREBBP	B105	g.chr16:3747903G>A	c.3517C>T	CGA=>TGA	Arg=>Stop	p.R1173*	nonsense
CREBBP	B109	g.chr16:3728619G>C	c.4336C>G	CGC=>GGC	Arg=>Gly	p.R1446G	missense
CREBBP	B110	g.chr16:3840811G>A	c.286C>T	CAG=>TAG	Gln=>Stop	p.Q96*	nonsense
CREBBP	B13	g.chr16:3735319G>A	c.3874C>T	CAG=>TAG	Gln=>Stop	p.Q1292*	nonsense
CREBBP	B37	g.chr16:3840787G>A	c.310C>T	CAA=>TAA	Gln=>Stop	p.Q104*	nonsense
CREBBP	B5	g.chr16:3783541G>A	c.1063C>T	CAG=>TAG	Gln=>Stop	p.Q355*	nonsense
CREBBP	B59	g.chr16:3757755G>A	c.3217C>T	CAG=>TAG	Gln=>Stop	p.Q1073*	nonsense
CREBBP	B62-0	g.chr16:3748902G>T	c.3323C>A	TCA=>TAA	Ser=>Stop	p.S1108*	nonsense
CREBBP	B63	g.chr16:3726706C>A	c.4506G>T	TGG=>TGT	Trp=>Cys	p.W1502C	missense
CREBBP	B66	g.chr16:3718066G>A	c.6983C>T	TCG=>TTG	Ser=>Leu	p.S2328L	missense
CREBBP	B66	g.chr16:3747299T>C	c.3689A>G	TAT=>TGT	Tyr=>Cys	p.Y1230C	missense
CREBBP	B80-13	g.chr16:3760937G>A	c.2515C>T	CAG=>TAG	Gln=>Stop	p.Q839*	nonsense
CREBBP	B89-1	g.chr16:3768750_3768753delGGCT	c.1894_1897delGGCT	-	-	-	Frame shift indel
CREBBP	B89-4	g.chr16:3741727C>A	-	-	-	-	spliceSite
CREBBP	B89-4	g.chr16:3782055T>A	c.1258A>T	AAG=>TAG	Lys=>Stop	p.K420*	nonsense
CRNKL1	B10	g.chr20:19968414C>G	c.1867G>C	GAC=>CAC	Asp=>His	p.D623H	missense
CRNKL1	B109	g.chr20:19976490C>G	c.1024G>C	GAG=>CAG	Glu=>Gln	p.E342Q	missense
CRNKL1	B80-8	g.chr20:19966137C>T	c.2209G>A	GAA=>AAA	Glu=>Lys	p.E737K	missense
CUBN	B36	g.chr10:17193029C>T	c.910G>A	GAA=>AAA	Glu=>Lys	p.E304K	missense
CUBN	B8	g.chr10:16997052C>T	c.7336G>A	GAA=>AAA	Glu=>Lys	p.E2446K	missense
CUBN	B90	g.chr10:17186430G>A	c.1411C>T	CAG=>TAG	Gln=>Stop	p.Q471*	nonsense
CUX1	B36	g.chr7:101631404G>A	c.2107G>A	GAT=>AAT	Asp=>Asn	p.D703N	missense
CYP1A1	B10	g.chr15:72802398G>C	c.94C>G	CAG=>GAG	Gln=>Glu	p.Q32E	missense
CYTSB	B5	g.chr17:20049276A>T	c.1322A>T	GAG=>GTG	Glu=>Val	p.E441V	missense
CYTSB	B80	g.chr17:20048706A>T	c.752A>T	AAG=>ATG	Lys=>Met	p.K251M	missense
DDRGK1	B5	g.chr20:3131972C>A	c.182G>T	GGA=>GTA	Gly=>Val	p.G61V	missense
DGKH	B13	g.chr13:41687733C>G	c.3143C>G	ACT=>AGT	Thr=>Ser	p.T1048S	missense
DIP2C	B15	g.chr10:400450C>A	c.2341G>T	GTG=>TTG	Val=>Leu	p.V781L	missense
DIP2C	B21	g.chr10:423696C>T	c.1651G>A	GGC=>AGC	Gly=>Ser	p.G551S	missense
DIP2C	B34	g.chr10:449960G>T	c.950C>A	CCG=>CAG	Pro=>Gln	p.P317Q	missense
DISP1	B10	g.chr1:221243646G>C	c.2284G>C	GAG=>CAG	Glu=>Gln	p.E762Q	missense
DISP1	B22	g.chr1:221244930G>C	c.3568G>C	GAG=>CAG	Glu=>Gln	p.E1190Q	missense

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Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
DISP1	B69	g.chr1:221244607C>T	c.3245C>T	GCG=>GTG	Ala=>Val	p.A1082V	missense
DMD	B15	g.chrX:31657672G>A	c.277C>T	CGA=>TGA	Arg=>Stop	p.R93*	nonsense
DNAH17	B10	g.chr17:74077150C>T	c.205G>A	GAG=>AAG	Glu=>Lys	p.E69K	missense
DOCK8	B5	g.chr9:423939A>T	c.4646A>T	CAG=>CTG	Gln=>Leu	p.Q1549L	missense
DOCK8	B85-0	g.chr9:418491G>A	c.4264G>A	GCC=>ACC	Ala=>Thr	p.A1422T	missense
EIF2C4	B55	g.chr1:36063883C>T	c.505C>T	CGT=>TGT	Arg=>Cys	p.R169C	missense
EIF2C4	B85-0	g.chr1:36070325G>T	c.1197G>T	GAG=>GAT	Glu=>Asp	p.E399D	missense
EMILIN2	B89-4	g.chr18:2881074T>A	c.949T>A	TAT=>AAT	Tyr=>Asn	p.Y317N	missense
ENO2	B10	g.chr12:6899092T>C	c.769T>C	TAT=>CAT	Tyr=>His	p.Y257H	missense
EP300	B10	g.chr22:39875951C>T	c.2620C>T	CAG=>TAG	Gln=>Stop	p.Q874*	nonsense
EP300	B106	g.chr22:39898450A>T	c.4454A>T	GAT=>GTT	Asp=>Val	p.D1485V	missense
EP300	B66	g.chr22:39896441_39896446delCCCAAG	c.2874_2879delCCCAAG	-	-	-	indel
EP300	B78	g.chr22:39875801C>T	c.2470C>T	CAA=>TAA	Gln=>Stop	p.Q824*	nonsense
EP300	B80-13	g.chr22:39899617G>C	c.4662G>C	AAG=>AAC	Lys=>Asn	p.K1554N	missense
EP300	B80-4	g.chr22:39904544C>A	c.6883C>A	CAA=>AAA	Gln=>Lys	p.Q2295K	missense
EP300	B80-8	g.chr22:39843235C>T	c.193C>T	CAG=>TAG	Gln=>Stop	p.Q65*	nonsense
EP300	B86	g.chr22:39902296C>T	c.4879C>T	CGG=>TGG	Arg=>Trp	p.R1627W	missense
EP300	B87	g.chr22:39895519insT	c.3006insT	-	-	-	Frame shift indel
EP300	B89-10	g.chr22:39896446_39896457delGCCCAAGCGACT	c.2869_2880delGCCCAAGCGACT	-	-	-	p.AQAT957_960del
EP300	B89-4	g.chr22:39896421A>T	c.4352A>T	CAT=>CTT	His=>Leu	p.H1451L	missense
EP300	B90	g.chr22:39898557G>C	c.4561G>C	GAA=>CAA	Glu=>Gln	p.E1521Q	missense
EP300	B96	g.chr22:39843686_39843696delCTGGCAACTTA	c.645_655delCTGGCAACTTA	-	-	-	Frame shift indel
ERBB3	B110	g.chr12:54775827G>C	c.2025G>C	AGG=>AGC	Arg=>Ser	p.R675S	missense
ERBB3	B22	g.chr12:54766608G>A	c.448G>A	GAG=>AAG	Glu=>Lys	p.E150K	missense
ERBB3	B36	g.chr12:54781711C>T	c.3634C>T	CCT=>TCT	Pro=>Ser	p.P1212S	missense
ERBB3	B5	g.chr12:54768804G>A	c.994G>A	GAG=>AAG	Glu=>Lys	p.E332K	missense
ERBB3	B50	g.chr12:54763898T>A	c.179T>A	ATG=>AAG	Met=>Lys	p.M60K	missense
ERBB3	B50	g.chr12:54768165C>T	c.826C>T	CCC=>TCC	Pro=>Ser	p.P276S	missense
ERBB3	B52	g.chr12:54768804G>A	c.994G>A	GAG=>AAG	Glu=>Lys	p.E332K	missense
ERBB3	B8	g.chr12:54774492G>T	c.1744G>T	GGG=>TGG	Gly=>Trp	p.G582W	missense
ERBB3	B9	g.chr12:54765214C>T	c.403C>T	CGC=>TGC	Arg=>Cys	p.R135C	missense
ESPL1	B104-0	g.chr12:51966106G>C	c.3319G>C	GAG=>CAG	Glu=>Gln	p.E1107Q	missense
ESPL1	B52	g.chr12:51966032G>C	c.3245G>C	GGG=>GCG	Gly=>Ala	p.G1082A	missense
ESPL1	B59	g.chr12:51964158G>A	c.3127G>A	GAC=>AAC	Asp=>Asn	p.D1043N	missense
ESPL1	B66	g.chr12:51963435G>T	c.2923G>T	GAA=>TAA	Glu=>Stop	p.E975*	nonsense
ESPL1	B8	g.chr12:51949441C>G	c.448C>G	CTG=>GTG	Leu=>Val	p.L150V	missense
ESPL1	B96	g.chr12:51956839G>C	c.1869G>C	TGG=>TGC	Trp=>Cys	p.W623C	missense
FGFR3	B103	g.chr4:1773362C>T	c.742C>T	CGC=>TGC	Arg=>Cys	p.R248C	missense
FGFR3	B104	g.chr4:1775897A>G	c.1118A>G	TAT=>TGT	Tyr=>Cys	p.Y373C	missense
FGFR3	B106	g.chr4:1775887G>T	c.1108G>T	GGC=>TGC	Gly=>Cys	p.G370C	missense
FGFR3	B110	g.chr4:1773362C>T	c.742C>T	CGC=>TGC	Arg=>Cys	p.R248C	missense
FGFR3	B114	g.chr4:1775897A>G	c.1118A>G	TAT=>TGT	Tyr=>Cys	p.Y373C	missense
FGFR3	B18	g.chr4:1775897A>G	c.1118A>G	TAT=>TGT	Tyr=>Cys	p.Y373C	missense
FGFR3	B56	g.chr4:1773467C>T	c.847C>T	CCC=>TCC	Pro=>Ser	p.P283S	missense
FGFR3	B89-4	g.chr4:1775897A>G	c.1118A>G	TAT=>TGT	Tyr=>Cys	p.Y373C	missense
FGFR3	B90	g.chr4:1775897A>G	c.1118A>G	TAT=>TGT	Tyr=>Cys	p.Y373C	missense
FLNB	B24	g.chr3:58096914G>T	c.4840G>T	GCC=>TCC	Ala=>Ser	p.A1614S	missense
FLNB	B37	g.chr3:58070032C>G	c.2142C>G	ATC=>ATG	Ile=>Met	p.I714M	missense
FLNB	B5	g.chr3:58039558G>A	c.616G>A	GAT=>AAT	Asp=>Asn	p.D206N	missense
FRMPD1	B80-8	g.chr9:37734574C>G	c.2545C>G	CAG=>GAG	Gln=>Glu	p.Q849E	missense
GALM	B5	g.chr2:38746996A>T	c.189A>T	GAA=>GAT	Glu=>Asp	p.E63D	missense
GALNT13	B9	g.chr2:154806836T>C	c.359T>C	GTC=>GCC	Val=>Ala	p.V120A	missense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
GART	B15	g.chr21:33816453C>G	c.1305G>C	TTG=>TTC	Leu=>Phe	p.L435F	missense
GATC	B15	g.chr12:119379305G>A	c.298G>A	GCT=>ACT	Ala=>Thr	p.A100T	missense
GATC	B15	g.chr12:119379306C>T	c.299C>T	GCT=>GTT	Ala=>Val	p.A100V	missense
GCLM	B8	g.chr1:94127238C>A	c.721G>T	GAG=>TAG	Glu=>Stop	p.E241*	nonsense
GHRHR	B9	g.chr7:30982594C>G	c.1000C>G	CTG=>GTG	Leu=>Val	p.L334V	missense
GKN2	B15	g.chr2:69027849G>C	c.249C>G	ATC=>ATG	Ile=>Met	p.I83M	missense
GLDC	B10	g.chr9:6592171G>C	c.1093C>G	CTT=>GTT	Leu=>Val	p.L365V	missense
GLRA3	B15	g.chr4:175801538C>G	c.1324G>C	GAG=>CAG	Glu=>Gln	p.E442Q	missense
GNA13	B10	g.chr17:60441372C>T	c.599G>A	AGA=>AAA	Arg=>Lys	p.R200K	missense
GON4L	B5	g.chr1:154052272G>A	c.1109C>T	TCA=>TTA	Ser=>Leu	p.S370L	missense
GPR158	B71	g.chr10:25927085G>A	c.2524G>A	GAG=>AAG	Glu=>Lys	p.E842K	missense
GPR182	B10	g.chr12:55675448T>C	c.188T>C	ATG=>ACG	Met=>Thr	p.M63T	missense
GPR182	B89-4	g.chr12:55675511G>A	c.251G>A	CGG=>CAG	Arg=>Gln	p.R84Q	missense
GRIA4	B80	g.chr11:105294798G>T	c.1420G>T	GCA=>TCA	Ala=>Ser	p.A474S	missense
GRIN2B	B15	g.chr12:13797804C>T	c.724G>A	GAA=>AAA	Glu=>Lys	p.E242K	missense
GRK4	B10	g.chr4:2993973C>T	c.967C>T	CGT=>TGT	Arg=>Cys	p.R323C	missense
GRM8	B37	g.chr7:125873466C>G	c.2627G>C	AGA=>ACA	Arg=>Thr	p.R876T	missense
GRM8	B8	g.chr7:126331895A>T	c.806T>A	CTG=>CAG	Leu=>Gln	p.L269Q	missense
GRXCR2	B5	g.chr5:145232654G>A	c.71C>T	TCC=>TTC	Ser=>Phe	p.S24F	missense
GSG1	B15	g.chr12:13135015T>C	c.14A>G	GAG=>GGG	Glu=>Gly	p.E5G	missense
GSR	B8	g.chr8:30673482G>C	c.752C>G	TCA=>TGA	Ser=>Stop	p.S251*	nonsense
HEXA	B59	g.chr15:70424856C>A	c.1511G>T	CGC=>CTC	Arg=>Leu	p.R504L	missense
HEXA	B9	g.chr15:70433127C>G	c.418G>C	GAG=>CAG	Glu=>Gln	p.E140Q	missense
HMCN1	B104-0	g.chr1:184239532G>C	c.4408G>C	GAC=>CAC	Asp=>His	p.D1470H	missense
HMCN1	B111	g.chr1:184198370G>T	c.1926G>T	AAG=>AAT	Lys=>Asn	p.K642N	missense
HMCN1	B13	g.chr1:184158191C>T	c.958C>T	CGA=>TGA	Arg=>Stop	p.R320*	nonsense
HMCN1	B60	g.chr1:184239532G>A	c.4408G>A	GAC=>AAC	Asp=>Asn	p.D1470N	missense
HMCN1	B69	g.chr1:184276882C>T	c.6295C>T	CGA=>TGA	Arg=>Stop	p.R2099*	nonsense
HMCN1	B69	g.chr1:184373396C>T	c.13726C>T	CGA=>TGA	Arg=>Stop	p.R4576*	nonsense
HMCN1	B80	g.chr1:184381266G>T	c.14375G>T	GGG=>GTG	Gly=>Val	p.G4792V	missense
HMCN1	B86	g.chr1:184237416C>A	c.4268C>A	CCA=>CAA	Pro=>Gln	p.P1423Q	missense
HMCN1	B89-12	g.chr1:184100291G>T	c.406G>T	GGT=>TGT	Gly=>Cys	p.G136C	missense
HMCN1	B89-12	g.chr1:184323322G>C	c.9285G>C	AAG=>AAC	Lys=>Asn	p.K3095N	missense
HOXB8	B57	g.chr17:44046699C>T	c.367G>A	GAG=>AAG	Glu=>Lys	p.E123K	missense
HRAS	B105-0	g.chr11:524286C>G	c.37G>C	GGT=>CGT	Gly=>Arg	p.G13R	missense
HRAS	B52	g.chr11:523552C>G	c.351G>C	AAG=>AAC	Lys=>Asn	p.K117N	missense
HRAS	B54	g.chr11:524286C>G	c.37G>C	GGT=>CGT	Gly=>Arg	p.G13R	missense
HRAS	B62-0	g.chr11:523874T>C	c.182A>G	CAG=>CGG	Gln=>Arg	p.Q61R	missense
HRAS	B70	g.chr11:524286C>G	c.37G>C	GGT=>CGT	Gly=>Arg	p.G13R	missense
HRAS	B80-11	g.chr11:523874T>C	c.182A>G	CAG=>CGG	Gln=>Arg	p.Q61R	missense
HRAS	B80-4	g.chr11:523874T>C	c.182A>G	CAG=>CGG	Gln=>Arg	p.Q61R	missense
HRAS	B80-7	g.chr11:523874T>C	c.182A>G	CAG=>CGG	Gln=>Arg	p.Q61R	missense
HRAS	B85-0	g.chr11:523874T>C	c.182A>G	CAG=>CGG	Gln=>Arg	p.Q61R	missense
HRAS	B99	g.chr11:524288C>T	c.35G>A	GGC=>GAC	Gly=>Asp	p.G12D	missense
HSD17B6	B5	g.chr12:55464914C>T	c.583C>T	CAA=>TAA	Gln=>Stop	p.Q195*	nonsense
HSPA4L	B74	g.chr4:128945696T>C	c.1004T>C	ATT=>ACT	Ile=>Thr	p.I335T	missense
HSPG2	B17	g.chr1:22058700T>G	c.5239A>C	ACC=>CCC	Thr=>Pro	p.T1747P	missense
HSPG2	B69	g.chr1:22074773C>T	c.3238G>A	GCA=>ACA	Ala=>Thr	p.A1080T	missense
HSPG2	B69	g.chr1:22075397G>A	c.2915C>T	ACG=>ATG	Thr=>Met	p.T972M	missense
IFT57	B10	g.chr3:109364126C>G	c.1178G>C	AGA=>ACA	Arg=>Thr	p.R393T	missense
IL18RAP	B15	g.chr2:102406237C>A	c.68C>A	TCA=>TAA	Ser=>Stop	p.S23*	nonsense
IL18RAP	B98	g.chr2:102430091C>T	c.1202C>T	ACG=>ATG	Thr=>Met	p.T401M	missense
INTU	B96	g.chr4:128854631G>A	c.2650G>A	GAA=>AAA	Glu=>Lys	p.E884K	missense
IQGAP1	B5	g.chr15:88797091G>A	c.1243G>A	GAA=>AAA	Glu=>Lys	p.E415K	missense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
IQSEC3	B5	g.chr12:117874G>A	c.175G>A	GAG=>AAG	Glu=>Lys	p.E59K	missense
IREB2	B10	g.chr15:76570091G>A	c.2257G>A	GAT=>AAT	Asp=>Asn	p.D753N	missense
IREB2	B79	g.chr15:76570097A>G	c.2263A>G	ATA=>GTA	Ile=>Val	p.I755V	missense
IRF1	B13	g.chr5:131848006G>A	c.800C>T	TCT=>TTT	Ser=>Phe	p.S267F	missense
IRF2	B10	g.chr4:185587176C>G	c.37G>C	GAG=>CAG	Glu=>Gln	p.E13Q	missense
IRF2	B69	g.chr4:185576808G>A	c.236C>T	GCG=>GTG	Ala=>Val	p.A79V	missense
KATNAL1	B86	g.chr13:29682508C>A	c.1219G>T	GAT=>TAT	Asp=>Tyr	p.D407Y	missense
KATNAL1	B86	g.chr13:29682523C>A	c.1204G>T	GAT=>TAT	Asp=>Tyr	p.D402Y	missense
KBTBD4	B10	g.chr11:47556004C>A	c.124G>T	GAG=>TAG	Glu=>Stop	p.E42*	nonsense
KBTBD4	B65	g.chr11:47551211C>G	c.1404G>C	AAG=>AAC	Lys=>Asn	p.K468N	missense
KBTBD4	B74	g.chr11:47551747C>T	c.868G>A	GTG=>ATG	Val=>Met	p.V290M	missense
KCTD7	B15	g.chr7:65741631G>C	c.847G>C	GAG=>CAG	Glu=>Gln	p.E283Q	missense
KIAA0141	B104-0	g.chr5:141294077C>T	c.986C>T	TCT=>TTT	Ser=>Phe	p.S329F	missense
KIAA0141	B13	g.chr5:141294310A>G	c.1124A>G	TAT=>TGT	Tyr=>Cys	p.Y375C	missense
KIAA0141	B70	g.chr5:141288021C>T	c.386C>T	TCA=>TTA	Ser=>Leu	p.S129L	missense
KIAA0556	B9	g.chr16:27668406_27668410delAAGAC	c.2235_2239delAAGAC	-	-	-	Frame shift indel
KIAA1199	B5	g.chr15:79017240C>A	c.3272C>A	TCC=>TAC	Ser=>Tyr	p.S1091Y	missense
KIAA1199	B5	g.chr15:79017311C>T	c.3343C>T	CAG=>TAG	Gln=>Stop	p.Q1115*	nonsense
KIF15	B23	g.chr3:44816918A>T	c.1207A>T	AGC=>TGC	Ser=>Cys	p.S403C	missense
KIF15	B5	g.chr3:44810900A>G	c.827A>G	CAT=>CGT	His=>Arg	p.H276R	missense
KIF15	B60	g.chr3:44859672G>C	c.3637G>C	GAG=>CAG	Glu=>Gln	p.E1213Q	missense
KLC4	B15	g.chr6:43148598G>A	c.1601G>A	AGA=>AAA	Arg=>Lys	p.R534K	missense
KLC4	B15	g.chr6:43148639G>C	c.1642G>C	GAG=>CAG	Glu=>Gln	p.E548Q	missense
KLC4	B15	g.chr6:43148643G>A	c.1646G>A	GGA=>GAA	Gly=>Glu	p.G549E	missense
KLC4	B89-5	g.chr6:43142028G>A	c.632G>A	CGT=>CAT	Arg=>His	p.R211H	missense
KRAS	B13	g.chr12:25271544G>T	c.181C>A	CAA=>AAA	Gln=>Lys	p.Q61K	missense
KRAS	B25	g.chr12:25289552C>A	c.34G>T	GGT=>TGT	Gly=>Cys	p.G12C	missense
KRAS	B35	g.chr12:25289552C>A	c.34G>T	GGT=>TGT	Gly=>Cys	p.G12C	missense
KRAS	B45	g.chr12:25289551C>A	c.35G>T	GGT=>GTT	Gly=>Val	p.G12V	missense
KRAS	B81-1	g.chr12:25289551C>G	c.35G>C	GGT=>GCT	Gly=>Ala	p.G12A	missense
KRAS	B89-1	g.chr12:25289552C>G	c.34G>C	GGT=>CGT	Gly=>Arg	p.G12R	missense
KRT33A	B5	g.chr17:36759142G>A	c.413C>T	TCA=>TTA	Ser=>Leu	p.S138L	missense
KRT33A	B69	g.chr17:36756280C>T	c.1043G>A	CGG=>CAG	Arg=>Gln	p.R348Q	missense
LAMA4	B36	g.chr6:112537368C>G	c.5416G>C	GGC=>CGC	Gly=>Arg	p.G1806R	missense
LAMA4	B36	g.chr6:112572718T>C	c.2443A>G	ATT=>GTT	Ile=>Val	p.I815V	missense
LAMA4	B63	g.chr6:112564143A>T	c.3268T>A	TTT=>ATT	Phe=>Ile	p.F1090I	missense
LAMA4	B66-0	g.chr6:112600558C>T	c.1478G>A	AGG=>AAG	Arg=>Lys	p.R493K	missense
LAMA4	B79	g.chr6:112603267C>T	c.1277G>A	CGT=>CAT	Arg=>His	p.R426H	missense
LAMA4	B8	g.chr6:112619550C>A	c.699G>T	AGG=>AGT	Arg=>Ser	p.R233S	missense
LAMA4	B83	g.chr6:112681969G>A	c.77C>T	TCC=>TTC	Ser=>Phe	p.S26F	missense
LAMA4	B89-4	g.chr6:112681967C>A	c.79G>T	GGG=>TGG	Gly=>Trp	p.G27W	missense
LAMP2	B8	g.chrX:119466885G>A	c.524C>T	GCT=>GTT	Ala=>Val	p.A175V	missense
LARP5	B10	g.chr10:880956C>A	c.470G>T	CGA=>CTA	Arg=>Leu	p.R157L	missense
LARP5	B82	g.chr10:920416G>A	c.112C>T	CAG=>TAG	Gln=>Stop	p.Q38*	nonsense
LEPRE1	B36	g.chr1:42985267G>A	c.2318C>T	ACT=>ATT	Thr=>Ile	p.T773I	missense
LGSN	B10	g.chr6:64053587G>T	c.194C>A	ACC=>AAC	Thr=>Asn	p.T65N	missense
LNX1	B10	g.chr4:54037836A>G	c.1445T>C	TTG=>TCG	Leu=>Ser	p.L482S	missense
LNX1	B15	g.chr4:54039588C>T	c.1276G>A	GTC=>ATC	Val=>Ile	p.V426I	missense
LNX1	B69	g.chr4:54068391G>A	c.337C>T	CGG=>TGG	Arg=>Trp	p.R113W	missense
LNX1	B88	g.chr4:54057301G>C	c.708C>G	ATC=>ATG	Ile=>Met	p.I236M	missense
LOXL2	B10	g.chr8:23273640C>T	c.439G>A	GAC=>AAC	Asp=>Asn	p.D147N	missense
LRP2	B10	g.chr2:169842550C>T	c.1723G>A	GAC=>AAC	Asp=>Asn	p.D575N	missense
LRP2	B35	g.chr2:169781170C>T	c.5665G>A	GAC=>AAC	Asp=>Asn	p.D1889N	missense
LRP2	B36	g.chr2:169858960G>A	c.596C>T	GCT=>GTT	Ala=>Val	p.A199V	missense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
LRP2	B65	g.chr2:169808183C>G	c.3526G>C	GAT=>CAT	Asp=>His	p.D1176H	missense
LRP2	B66	g.chr2:169710650C>G	c.12841G>C	GAA=>CAA	Glu=>Gln	p.E4281Q	missense
LRP2	B68	g.chr2:169770858T>C	c.7477A>G	ATG=>GTG	Met=>Val	p.M2493V	missense
LRP2	B69	g.chr2:169774310G>A	c.6368C>T	GCG=>GTG	Ala=>Val	p.A2123V	missense
LRP2	B80	g.chr2:169767606G>C	c.8115C>G	TTC=>TTG	Phe=>Leu	p.F2705L	missense
LRP2	B84	g.chr2:169721033C>A	c.12148G>T	GAG=>TAG	Glu=>Stop	p.E4050*	nonsense
MADD	B69	g.chr11:47257129A>T	c.1213A>T	ATT=>TTT	Ile=>Phe	p.I405F	missense
MAGEB18	B80-0	g.chrX:26067394C>T	c.371C>T	ACG=>ATG	Thr=>Met	p.T124M	missense
MAP3K5	B10	g.chr6:137013859C>T	c.1744G>A	GAG=>AAG	Glu=>Lys	p.E582K	missense
MCM3	B8	g.chr6:52251543C>T	c.835G>A	GAG=>AAG	Glu=>Lys	p.E279K	missense
MED1	B9	g.chr17:34819982G>A	c.2018C>T	TCC=>TTC	Ser=>Phe	p.S673F	missense
MERTK	B10	g.chr2:112482440C>G	c.1877C>G	TCT=>TGT	Ser=>Cys	p.S626C	missense
MERTK	B37	g.chr2:112477205C>T	c.1756C>T	CTT=>TTT	Leu=>Phe	p.L586F	missense
MERTK	B89-16	g.chr2:112421468G>A	c.610G>A	GAG=>AAG	Glu=>Lys	p.E204K	missense
METTL10	B10	g.chr10:126467636A>G	c.257T>C	ATT=>ACT	Ile=>Thr	p.I86T	missense
MITF	B52	g.chr3:70096892G>A	c.1063G>A	GGA=>AGA	Gly=>Arg	p.G355R	missense
MITF	B9	g.chr3:70071016T>A	c.339T>A	TGT=>TGA	Cys=>Stop	p.C113*	nonsense
MLH1	B15	g.chr3:37042462G>C	c.1369G>C	GAA=>CAA	Glu=>Gln	p.E457Q	missense
MLL	B103	g.chr11:117864574C>A	c.4368C>A	CAC=>CAA	His=>Gln	p.H1456Q	missense
MLL	B112	g.chr11:117864643C>G	c.4437C>G	TGC=>TGG	Cys=>Trp	p.C1479W	missense
MLL	B35	g.chr11:117895917C>G	c.11348C>G	TCT=>TGT	Ser=>Cys	p.S3783C	missense
MLL	B66	g.chr11:117875247_117875266delTTGAAGTTTTCAGAAGAGTG	c.5939_5958delTTGAAGTTTTCAGAAGAGTG	-	-	-	Frame shift indel
MLL	B69	g.chr11:117852746C>G	c.3173C>G	TCA=>TGA	Ser=>Stop	p.S1058*	nonsense
MLL	B69	g.chr11:117864633_117864635delGTC	c.4428_4430delGTC	-	-	-	indel
MLL	B71	g.chr11:117880473C>G	c.8647C>G	CTT=>GTT	Leu=>Val	p.L2883V	missense
MLL	B73	g.chr11:117879382C>T	c.7556C>T	ACA=>ATA	Thr=>Ile	p.T2519I	missense
MLL3	B5	g.chr7:151510591G>A	c.5287C>T	CAG=>TAG	Gln=>Stop	p.Q1763*	nonsense
MLL3	B5	g.chr7:151531025_151531025delC	c.4020_4020delC	-	-	-	Frame shift indel
MLL3	B60	g.chr7:151639897G>A	c.658C>T	CAA=>TAA	Gln=>Stop	p.Q220*	nonsense
MLL3	B70	g.chr7:151504437G>A	c.9034C>T	CAA=>TAA	Gln=>Stop	p.Q3012*	nonsense
MLL3	B89-12	g.chr7:151476545T>A	c.13400A>T	AAG=>ATG	Lys=>Met	p.K4467M	missense
MLL3	B89-4	g.chr7:151482083C>A	c.12221G>T	GGT=>GTT	Gly=>Val	p.G4074V	missense
MMAB	B10	g.chr12:108491010C>T	c.238G>A	GAC=>AAC	Asp=>Asn	p.D80N	missense
MPO	B5	g.chr17:53713001G>C	c.118C>G	CTG=>GTG	Leu=>Val	p.L40V	missense
MPO	B86	g.chr17:53710482G>C	c.909C>G	ATC=>ATG	Ile=>Met	p.I303M	missense
MS4A14	B5	g.chr11:59939537C>A	c.520C>A	CCA=>ACA	Pro=>Thr	p.P174T	missense
MTBP	B10	g.chr8:121599376C>T	c.2351C>T	TCC=>TTC	Ser=>Phe	p.S784F	missense
MTBP	B86	g.chr8:121532430C>T	c.206C>T	TCA=>TTA	Ser=>Leu	p.S69L	missense
MYH6	B69	g.chr14:22939832C>T	c.1336G>A	GCC=>ACC	Ala=>Thr	p.A446T	missense
MYST1	B15	g.chr16:31039293G>A	c.419G>A	CGC=>CAC	Arg=>His	p.R140H	missense
NCOA7	B66	g.chr6:126252215C>G	c.1322C>G	TCT=>TGT	Ser=>Cys	p.S441C	missense
NCOR1	B107	g.chr17:15914252G>C	c.4465C>G	CAA=>GAA	Gln=>Glu	p.Q1489E	missense
NCOR1	B45	g.chr17:15935901C>A	-	-	-	-	spliceSite
NCOR1	B66	g.chr17:15981413C>G	c.1446G>C	AAG=>AAC	Lys=>Asn	p.K482N	missense
NCOR1	B69	g.chr17:15924760G>A	c.3184C>T	CCA=>TCA	Pro=>Ser	p.P1062S	missense
NCOR1	B69	g.chr17:15997435C>G	-	-	-	-	spliceSite
NCOR1	B74	g.chr17:16030638C>T	c.197G>A	CGA=>CAA	Arg=>Gln	p.R66Q	missense
NCOR1	B96	g.chr17:15914368G>A	c.4349C>T	TCA=>TTA	Ser=>Leu	p.S1450L	missense
NF1	B101	g.chr17:26689262G>C	c.6798G>C	CAG=>CAC	Gln=>His	p.Q2266H	missense
NF1	B104-0	g.chr17:26584256G>C	c.3607G>C	GAT=>CAT	Asp=>His	p.D1203H	missense
NF1	B36	g.chr17:26578434A>C	c.2324A>C	GAG=>GCG	Glu=>Ala	p.E775A	missense
NF1	B5	g.chr17:26711630G>T	-	-	-	-	spliceSite

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
NF1	B59	g.chr17:26686074C>T	c.5905C>T	CAA=>TAA	Gln=>Stop	p.Q1969*	nonsense
NF1	B60	g.chr17:26533672G>C	c.751G>C	GAC=>CAC	Asp=>His	p.D251H	missense
NF1	B78	g.chr17:26600183G>A	c.4030G>A	GAA=>AAA	Glu=>Lys	p.E1344K	missense
NFE2L3	B103	g.chr7:26191453G>A	c.1610G>A	CGT=>CAT	Arg=>His	p.R537H	missense
NFE2L3	B111	g.chr7:26190712G>C	c.869G>C	AGT=>ACT	Ser=>Thr	p.S290T	missense
NFE2L3	B13	g.chr7:26190733C>G	c.890C>G	TCT=>TGT	Ser=>Cys	p.S297C	missense
NFE2L3	B13	g.chr7:26190885C>G	c.1042C>G	CAT=>GAT	His=>Asp	p.H348D	missense
NFE2L3	B13	g.chr7:26191117C>G	c.1274C>G	TCA=>TGA	Ser=>Stop	p.S425*	nonsense
NFE2L3	B83	g.chr7:26191329C>T	c.1486C>T	CAT=>TAT	His=>Tyr	p.H496Y	missense
NKD1	B15	g.chr16:49224615G>A	c.835G>A	GTG=>ATG	Val=>Met	p.V279M	missense
NKD1	B69	g.chr16:49224717G>A	c.937G>A	GTG=>ATG	Val=>Met	p.V313M	missense
NLRP14	B10	g.chr11:7020837G>A	c.1004G>A	AGA=>AAA	Arg=>Lys	p.R335K	missense
NLRP14	B69	g.chr11:7016568G>A	c.175G>A	GCC=>ACC	Ala=>Thr	p.A59T	missense
NLRP14	B98	g.chr11:7020534C>G	c.701C>G	TCA=>TGA	Ser=>Stop	p.S234*	nonsense
NPR2	B105-0	g.chr9:35792269G>A	c.1699G>A	GAA=>AAA	Glu=>Lys	p.E567K	missense
NPR2	B15	g.chr9:35799413G>C	c.3115G>C	GAG=>CAG	Glu=>Gln	p.E1039Q	missense
NPR2	B69	g.chr9:35792578G>A	c.1789G>A	GAA=>AAA	Glu=>Lys	p.E597K	missense
NR1D2	B5	g.chr3:23976187C>T	c.394C>T	CAA=>TAA	Gln=>Stop	p.Q132*	nonsense
NUP62	B10	g.chr19:55103337C>T	c.1540G>A	GAG=>AAG	Glu=>Lys	p.E514K	missense
NUP62	B45	g.chr19:55103321A>T	c.1556T>A	ATC=>AAC	Ile=>Asn	p.I519N	missense
OGDH	B15	g.chr7:44630570C>A	c.103C>A	CAA=>AAA	Gln=>Lys	p.Q35K	missense
OPCML	B10	g.chr11:132032309G>A	c.283C>T	CCA=>TCA	Pro=>Ser	p.P95S	missense
OPCML	B89-4	g.chr11:132032242A>G	c.350T>C	GTG=>GCG	Val=>Ala	p.V117A	missense
OPCML	B96	g.chr11:132032228G>A	c.364C>T	CAT=>TAT	His=>Tyr	p.H122Y	missense
OR10A4	B10	g.chr11:6854722G>A	c.268G>A	GAC=>AAC	Asp=>Asn	p.D90N	missense
OR2B2	B5	g.chr6:27987022G>C	c.1055C>G	CCT=>CGT	Pro=>Arg	p.P352R	missense
OR4F6	B36	g.chr15:100163866T>G	c.421T>G	TGC=>GGC	Cys=>Gly	p.C141G	missense
OR5M9	B10	g.chr11:55987241G>C	c.213C>G	TTC=>TTG	Phe=>Leu	p.F71L	missense
OR9Q1	B5	g.chr11:57704009G>C	c.517G>C	GAG=>CAG	Glu=>Gln	p.E173Q	missense
OSGIN2	B8	g.chr8:91006157C>T	c.740C>T	TCT=>TTT	Ser=>Phe	p.S247F	missense
PADI4	B13	g.chr1:17562797G>C	c.1952G>C	AGA=>ACA	Arg=>Thr	p.R651T	missense
PADI4	B23	g.chr1:17547097A>T	c.1122A>T	AGA=>AGT	Arg=>Ser	p.R374S	missense
PAK3	B9	g.chrX:110326372C>T	c.1255C>T	CGA=>TGA	Arg=>Stop	p.R419*	nonsense
PARD6B	B8	g.chr20:48799813A>T	c.500A>T	AAA=>ATA	Lys=>Ile	p.K167I	missense
PCIF1	B13	g.chr20:44007787G>A	c.1199G>A	CGC=>CAC	Arg=>His	p.R400H	missense
PCK1	B23	g.chr20:55573934C>T	c.1537C>T	CAT=>TAT	His=>Tyr	p.H513Y	missense
PFKL	B10	g.chr21:44556440C>T	c.403C>T	CGC=>TGC	Arg=>Cys	p.R135C	missense
PFKL	B96	g.chr21:44550152C>A	c.132C>A	TTC=>TTA	Phe=>Leu	p.F44L	missense
PIPOX	B5	g.chr17:24396034A>T	c.146A>T	CAT=>CTT	His=>Leu	p.H49L	missense
PLCB1	B10	g.chr20:8669032C>G	c.2350C>G	CTG=>GTG	Leu=>Val	p.L784V	missense
PLCB1	B106	g.chr20:8657699A>C	c.1766A>C	TAT=>TCT	Tyr=>Ser	p.Y589S	missense
PLCB1	B37	g.chr20:8657750C>A	c.1817C>A	TCA=>TAA	Ser=>Stop	p.S606*	nonsense
PLXNB1	B15	g.chr3:48423472G>A	c.6118C>T	CGG=>TGG	Arg=>Trp	p.R2040W	missense
PLXNB1	B69	g.chr3:48429574C>T	c.4544G>A	AGC=>AAC	Ser=>Asn	p.S1515N	missense
POLD1	B5	g.chr19:55601316C>G	c.1308C>G	TTC=>TTG	Phe=>Leu	p.F436L	missense
POLD1	B69	g.chr19:55601302C>T	c.1294C>T	CGG=>TGG	Arg=>Trp	p.R432W	missense
PORCN	B8	g.chrX:48254673C>G	c.183C>G	TTC=>TTG	Phe=>Leu	p.F61L	missense
PPM1G	B10	g.chr2:27460445C>T	c.844G>A	GAT=>AAT	Asp=>Asn	p.D282N	missense
PPP1R9A	B5	g.chr7:94378002C>T	c.641C>T	TCT=>TTT	Ser=>Phe	p.S214F	missense
PPP1R9A	B63	g.chr7:94378011C>T	c.650C>T	GCC=>GTC	Ala=>Val	p.A217V	missense
PRDM10	B5	g.chr11:129333003G>C	c.82C>G	CCG=>GCG	Pro=>Ala	p.P28A	missense
PRDM10	B64	g.chr11:129322343C>T	c.169G>A	GAC=>AAC	Asp=>Asn	p.D57N	missense
PRMT5	B9	g.chr14:22463743G>C	c.955C>G	CTG=>GTG	Leu=>Val	p.L319V	missense
PWP2	B13	g.chr21:44358157G>A	-	-	-	-	spliceSite

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
RB1	B105-1	g.chr13:47832153G>A	-	-	-	-	spliceSite
RB1	B109	g.chr13:47832195C>T	c.649C>T	CAG=>TAG	Gln=>Stop	p.Q217*	nonsense
RB1	B23	g.chr13:47937216A>T	c.2293A>T	AAA=>TAA	Lys=>Stop	p.K765*	nonsense
RB1	B34	g.chr13:47937506G>C	-	-	-	-	spliceSite
RB1	B37	g.chr13:47839721C>T	c.1030C>T	CAG=>TAG	Gln=>Stop	p.Q344*	nonsense
RB1	B47	g.chr13:47935932T>A	c.2171T>A	ATT=>AAT	Ile=>Asn	p.I724N	missense
RB1	B74	g.chr13:47845630G>A	-	-	-	-	spliceSite
RB1	B80-0	g.chr13:47849157G>A	c.1318G>A	GAA=>AAA	Glu=>Lys	p.E440K	missense
RB1	B83	g.chr13:47928427C>G	c.1901C>G	TCA=>TGA	Ser=>Stop	p.S634*	nonsense
RB1	B85-0	g.chr13:47852343C>T	c.1463C>T	GCG=>GTG	Ala=>Val	p.A488V	missense
RB1	B86	g.chr13:47853581G>T	-	-	-	-	spliceSite
RFC1	B36	g.chr4:39029412T>A	c.83A>T	AAG=>ATG	Lys=>Met	p.K28M	missense
RFC1	B5	g.chr4:38968006G>C	c.3217C>G	CCA=>GCA	Pro=>Ala	p.P1073A	missense
RPS11	B5	g.chr19:54692595G>C	c.154G>C	GAG=>CAG	Glu=>Gln	p.E52Q	missense
SACS	B77	g.chr13:22808100T>A	c.7474A>T	ATT=>TTT	Ile=>Phe	p.I2492F	missense
SACS	B90	g.chr13:22809606G>C	c.5968C>G	CAG=>GAG	Gln=>Glu	p.Q1990E	missense
SAMD9L	B105-1	g.chr7:92601129A>G	c.2092T>C	TTC=>CTC	Phe=>Leu	p.F698L	missense
SAMD9L	B5	g.chr7:92601459G>A	c.1762C>T	CAA=>TAA	Gln=>Stop	p.Q588*	nonsense
SAMD9L	B83	g.chr7:92599488C>T	c.3733G>A	GAA=>AAA	Glu=>Lys	p.E1245K	missense
SASH1	B10	g.chr6:148803043C>T	c.316C>T	CAG=>TAG	Gln=>Stop	p.Q106*	nonsense
SCRN3	B86	g.chr2:174995966C>T	c.862C>T	CAA=>TAA	Gln=>Stop	p.Q288*	nonsense
SCRN3	B89-12	g.chr2:174997470A>G	c.939A>G	ATA=>ATG	Ile=>Met	p.I313M	missense
SDK1	B5	g.chr7:4180413C>T	c.295C>T	CAG=>TAG	Gln=>Stop	p.Q99*	nonsense
SDK1	B86	g.chr7:4085723G>A	c.3305G>A	AGG=>AAG	Arg=>Lys	p.R1102K	missense
SEMA4F	B9	g.chr2:74755209C>G	c.899C>G	CCT=>CGT	Pro=>Arg	p.P300R	missense
SEMA4F	B9	g.chr2:74755302C>T	c.992C>T	TCT=>TTT	Ser=>Phe	p.S331F	missense
SEMA6D	B105-1	g.chr15:45841199G>A	c.497G>A	TGC=>TAC	Cys=>Tyr	p.C166Y	missense
SEMA6D	B110	g.chr15:45840888A>G	c.415A>G	AAT=>GAT	Asn=>Asp	p.N139D	missense
SEMA6D	B13	g.chr15:45843717C>G	c.1020C>G	TTC=>TTG	Phe=>Leu	p.F340L	missense
SEMA6D	B71	g.chr15:45844508G>A	c.1390G>A	GTA=>ATA	Val=>Ile	p.V464I	missense
SESN2	B13	g.chr1:28458962_28458962delC	c.18_18delC	-	-	-	Frame shift indel
SESN2	B36	g.chr1:28470874C>T	c.259C>T	CCT=>TCT	Pro=>Ser	p.P87S	missense
SH3RF1	B34	g.chr4:170254280C>A	c.2632G>T	GGC=>TGC	Gly=>Cys	p.G878C	missense
SH3RF1	B69	g.chr4:170254295G>A	c.2617C>T	CGT=>TGT	Arg=>Cys	p.R873C	missense
SH3RF1	B89-4	g.chr4:170426861C>G	c.78G>C	TTG=>TTC	Leu=>Phe	p.L26F	missense
SLC26A4	B9	g.chr7:107140268G>C	c.2284G>C	GAG=>CAG	Glu=>Gln	p.E762Q	missense
SLCO4C1	B69	g.chr5:101634275C>T	c.754G>A	GCC=>ACC	Ala=>Thr	p.A252T	missense
SMPD4	B89-12	g.chr2:130627432C>T	c.2072G>A	GGA=>GAA	Gly=>Glu	p.G691E	missense
SP110	B5	g.chr2:230782913G>C	c.806C>G	TCC=>TGC	Ser=>Cys	p.S269C	missense
SPAG1	B23	g.chr8:101259313C>G	c.394C>G	CGT=>GGT	Arg=>Gly	p.R132G	missense
SPAG1	B5	g.chr8:101306582C>G	c.1694C>G	TCA=>TGA	Ser=>Stop	p.S565*	nonsense
SPAG1	B5	g.chr8:101306654C>T	c.1766C>T	TCT=>TTT	Ser=>Phe	p.S589F	missense
SRRM2	B22	g.chr16:2753220C>T	c.2690C>T	CCT=>CTT	Pro=>Leu	p.P897L	missense
SRRM2	B5	g.chr16:2756097C>T	c.5567C>T	ACA=>ATA	Thr=>Ile	p.T1856I	missense
SRRM2	B80	g.chr16:2754950T>G	c.4420T>G	TCT=>GCT	Ser=>Ala	p.S1474A	missense
SRRM2	B80	g.chr16:2756589C>T	c.6059C>T	TCC=>TTC	Ser=>Phe	p.S2020F	missense
STAG2	B10	g.chrX:123048197C>A	c.3173C>A	TCA=>TAA	Ser=>Stop	p.S1058*	nonsense
STAG2	B109	g.chrX:123037893T>C	c.2564T>C	ATT=>ACT	Ile=>Thr	p.I855T	missense
STAG2	B89-4	g.chrX:123011737G>T	c.914G>T	CGA=>CTA	Arg=>Leu	p.R305L	missense
SUPT16H	B10	g.chr14:20895268T>A	c.2588A>T	GAC=>GTC	Asp=>Val	p.D863V	missense
SUPT16H	B10	g.chr14:20895269C>G	c.2587G>C	GAC=>CAC	Asp=>His	p.D863H	missense
SYNE1	B10	g.chr6:152587376G>T	c.21255C>A	TTC=>TTA	Phe=>Leu	p.F7085L	missense
SYNE1	B104	g.chr6:152788249C>T	c.5248G>A	GAT=>AAT	Asp=>Asn	p.D1750N	missense
SYNE1	B21	g.chr6:152681023G>C	c.16245C>G	TTC=>TTG	Phe=>Leu	p.F5415L	missense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
SYNE1	B80-3	g.chr6:152779553C>G	c.5733G>C	TTG=>TTC	Leu=>Phe	p.L1911F	missense
SYNE1	B83	g.chr6:152776237C>T	c.6194G>A	AGG=>AAG	Arg=>Lys	p.R2065K	missense
SYNE1	B86	g.chr6:152804947C>T	c.3985G>A	GAT=>AAT	Asp=>Asn	p.D1329N	missense
SYNE1	B96	g.chr6:152499480C>T	c.2180G>A	CGG=>CAG	Arg=>Gln	p.R727Q	missense
TAOK3	B47	g.chr12:117123638C>T	c.833G>A	CGA=>CAA	Arg=>Gln	p.R278Q	missense
TAOK3	B5	g.chr12:117094743G>A	c.1801C>T	CTC=>TTC	Leu=>Phe	p.L601F	missense
TAOK3	B8	g.chr12:117084201C>G	c.1914G>C	AAG=>AAC	Lys=>Asn	p.K638N	missense
TDRD1	B15	g.chr10:115963268G>C	c.2005G>C	GAT=>CAT	Asp=>His	p.D669H	missense
TDRD1	B45	g.chr10:115971127G>A	c.2792G>A	TGG=>TAG	Trp=>Stop	p.W931*	nonsense
TDRD1	B89-4	g.chr10:115971201T>C	c.2866T>C	TAT=>CAT	Tyr=>His	p.Y956H	missense
TEX14	B114	g.chr17:54034912T>G	c.1375A>C	AAA=>CAA	Lys=>Gln	p.K459Q	missense
TEX14	B13	g.chr17:54031771G>T	c.1934C>A	TCT=>TAT	Ser=>Tyr	p.S645Y	missense
TG	B101	g.chr8:133963297G>A	c.646G>A	GAT=>AAT	Asp=>Asn	p.D216N	missense
TG	B15	g.chr8:134053254C>A	c.6009C>A	GAC=>GAA	Asp=>Glu	p.D2003E	missense
TG	B60	g.chr8:134099264C>T	c.6622C>T	CGG=>TGG	Arg=>Trp	p.R2208W	missense
TG	B77	g.chr8:133994551G>A	c.4237G>A	GAC=>AAC	Asp=>Asn	p.D1413N	missense
TG	B78	g.chr8:133968926G>C	c.2127G>C	GAG=>GAC	Glu=>Asp	p.E709D	missense
TG	B80-0	g.chr8:133988174G>C	c.3694G>C	GAG=>CAG	Glu=>Gln	p.E1232Q	missense
TMPRSS2	B9	g.chr21:41761628insCT	c.109insCT	-	-	-	Frame shift indel
TNFAIP8L3	B15	g.chr15:49137513G>T	c.736C>A	CAC=>AAC	His=>Asn	p.H246N	missense
TP53	B101	g.chr17:7517824C>G	c.839G>C	AGA=>ACA	Arg=>Thr	p.R280T	missense
TP53	B104-0	g.chr17:7517852C>T	c.811G>A	GAG=>AAG	Glu=>Lys	p.E271K	missense
TP53	B14	g.chr17:7517824C>T	c.839G>A	AGA=>AAA	Arg=>Lys	p.R280K	missense
TP53	B16	g.chr17:7517881C>T	-	-	-	-	spliceSite
TP53	B23	g.chr17:7517653T>A	-	-	-	-	spliceSite
TP53	B36	g.chr17:7517824C>G	c.839G>C	AGA=>ACA	Arg=>Thr	p.R280T	missense
TP53	B37	g.chr17:7518305T>C	c.701A>G	TAC=>TGC	Tyr=>Cys	p.Y234C	missense
TP53	B59-3	g.chr17:7520258G>A	c.154C>T	CAA=>TAA	Gln=>Stop	p.Q52*	nonsense
TP53	B60	g.chr17:7517810C>A	c.853G>T	GAG=>TAG	Glu=>Stop	p.E285*	nonsense
TP53	B61	g.chr17:7517810C>A	c.853G>T	GAG=>TAG	Glu=>Stop	p.E285*	nonsense
TP53	B63	g.chr17:7518936C>A	c.638G>T	CGA=>CTA	Arg=>Leu	p.R213L	missense
TP53	B66	g.chr17:7520038G>A	c.374C>T	ACG=>ATG	Thr=>Met	p.T125M	missense
TP53	B71	g.chr17:7519095C>G	-	-	-	-	spliceSite
TP53	B74	g.chr17:7517822C>T	c.841G>A	GAC=>AAC	Asp=>Asn	p.D281N	missense
TP53	B74	g.chr17:7517824C>T	c.839G>A	AGA=>AAA	Arg=>Lys	p.R280K	missense
TP53	B77	g.chr17:7517810C>T	c.853G>A	GAG=>AAG	Glu=>Lys	p.E285K	missense
TP53	B8	g.chr17:7519167T>C	c.488A>G	TAC=>TGC	Tyr=>Cys	p.Y163C	missense
TP53	B81	g.chr17:7518993A>C	c.581T>G	CTT=>CGT	Leu=>Arg	p.L194R	missense
TP53	B84	g.chr17:7517866C>T	c.797G>A	GGA=>GAA	Gly=>Glu	p.G266E	missense
TP53	B89-12	g.chr17:7518982C>A	c.592G>T	GAA=>TAA	Glu=>Stop	p.E198*	nonsense
TP53	B9	g.chr17:7519238_7519251delCTTGGCCAGTTGGC	c.418_431delCTTGGCCAGTTGGC	-	-	-	Frame shift indel
TRIM23	B101	g.chr5:64943386C>T	c.445G>A	GAG=>AAG	Glu=>Lys	p.E149K	missense
TRIM23	B15	g.chr5:64942586G>A	c.686C>T	TCA=>TTA	Ser=>Leu	p.S229L	missense
TRPV5	B15	g.chr7:142315962G>T	c.2030C>A	GCC=>GAC	Ala=>Asp	p.A677D	missense
UBC	B8	g.chr12:123964210C>T	c.61G>A	GAC=>AAC	Asp=>Asn	p.D21N	missense
USP26	B17	g.chrX:131988074_131988084delTGGCCTTTTTT	c.902_912delTGGCCTTTTTT	-	-	-	Frame shift indel
USP26	B82	g.chrX:131987256C>T	c.2659G>A	GAG=>AAG	Glu=>Lys	p.E887K	missense
USP48	B10	g.chr1:21928841T>C	c.1243A>G	ATG=>GTG	Met=>Val	p.M415V	missense
UTX	B101	g.chrX:44807883_44807892delAAGTGGAAGT	c.1801_1810delAAGTGGAAGT	-	-	-	Frame shift indel
UTX	B101	g.chrX:44813956_44813965delTACCTCAGGT	c.2095_2104delTACCTCAGGT	-	-	-	Frame shift indel
UTX	B104-0	g.chrX:44764915T>G	c.560T>G	TTA=>TGA	Leu=>Stop	p.L187*	nonsense

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Supplementary Table 5 continued. A list of all confirmed somatic mutations detected in the 97 TCCs.

Gene Symbol	Tumor ID	Nucleotide (genomic)#	Nucleotide (cDNA)$	Codon change	Amino acid change	Amino acid (protein)§	Mutation Type
UTX	B105	g.chrX:44803468A>G	c.1007A>G	GAT=>GGT	Asp=>Gly	p.D336G	missense
UTX	B111	g.chrX:44830137T>A	c.3517T>A	TAC=>AAC	Tyr=>Asn	p.Y1173N	missense
UTX	B114	g.chrX:44834051G>A	c.3668G>A	GGC=>GAC	Gly=>Asp	p.G1223D	missense
UTX	B16	g.chrX:44823540_44823543delAGTA	c.857_857delA	-	-	-	Frame shift indel
UTX	B57	g.chrX:44823355A>T	c.2959A>T	AAA=>TAA	Lys=>Stop	p.K987*	nonsense
UTX	B57	g.chrX:44827761C>T	c.3397C>T	CAA=>TAA	Gln=>Stop	p.Q1133*	nonsense
UTX	B66	g.chrX:44827705C>T	c.3341C>T	TCA=>TTA	Ser=>Leu	p.S1114L	missense
UTX	B69	g.chrX:44827715_44827717delTCT	c.856_858delTCT	-	-	-	p.S286_286del
UTX	B77	g.chrX:44807610G>C	-	-	-	-	spliceSite
UTX	B79	g.chrX:44854391C>T	c.4129C>T	CAG=>TAG	Gln=>Stop	p.Q1377*	nonsense
UTX	B82	g.chrX:44813948insA	c.2102insA	-	-	-	Frame shift indel
UTX	B83	g.chrX:44822653C>G	c.2897C>G	CCT=>CGT	Pro=>Arg	p.P966R	missense
UTX	B85-0	g.chrX:44814168C>G	c.2324C>G	TCA=>TGA	Ser=>Stop	p.S775*	nonsense
UTX	B85-2	g.chrX:44833965G>A	c.3582G>A	TGG=>TGA	Trp=>Stop	p.W1194*	nonsense
UTX	B89-16	g.chrX:44718869C>T	c.349C>T	CAG=>TAG	Gln=>Stop	p.Q117*	nonsense
UTX	B89-4	g.chrX:44823391G>T	c.2995G>T	GAA=>TAA	Glu=>Stop	p.E999*	nonsense
UTX	B89-5	g.chrX:44718898C>G	c.378C>G	TAC=>TAG	Tyr=>Stop	p.Y126*	nonsense
UTX	B90	g.chrX:44803566C>T	c.1105C>T	CAG=>TAG	Gln=>Stop	p.Q369*	nonsense
UTX	B96	g.chrX:44807746C>T	c.1663C>T	CAG=>TAG	Gln=>Stop	p.Q555*	nonsense
UVRAG	B69	g.chr11:75504653G>A	c.1343G>A	CGG=>CAG	Arg=>Gln	p.R448Q	missense
UVRAG	B9	g.chr11:75529941G>C	c.1936G>C	GGT=>CGT	Gly=>Arg	p.G646R	missense
VPS13B	B112	g.chr8:100274384A>T	c.2438A>T	CAA=>CTA	Gln=>Leu	p.Q813L	missense
VPS13B	B64	g.chr8:100095244A>G	c.52A>G	ATC=>GTC	Ile=>Val	p.I18V	missense
VPS13B	B69	g.chr8:100589248G>A	c.4232G>A	CGC=>CAC	Arg=>His	p.R1411H	missense
VPS13B	B71	g.chr8:100588596G>C	c.4213G>C	GAA=>CAA	Glu=>Gln	p.E1405Q	missense
VPS13B	B80-0	g.chr8:100658896G>C	c.5079G>C	GAG=>GAC	Glu=>Asp	p.E1693D	missense
YAP1	B10	g.chr11:101490268G>A	c.505G>A	GAT=>AAT	Asp=>Asn	p.D169N	missense
ZDHHC23	B10	g.chr3:115155509G>C	c.434G>C	GGA=>GCA	Gly=>Ala	p.G145A	missense
ZFHX3	B36	g.chr16:71551124G>A	c.422C>T	GCG=>GTG	Ala=>Val	p.A141V	missense
ZFHX3	B60	g.chr16:71550398G>A	c.1148C>T	TCC=>TTC	Ser=>Phe	p.S383F	missense
ZFHX3	B69	g.chr16:71385957C>A	c.8125G>T	GCC=>TCC	Ala=>Ser	p.A2709S	missense
ZFHX3	B80	g.chr16:71549289T>C	c.2257A>G	AAC=>GAC	Asn=>Asp	p.N753D	missense
ZFHX3	B80-0	g.chr16:71384976G>A	c.9106C>T	CGG=>TGG	Arg=>Trp	p.R3036W	missense
ZIK1	B5	g.chr19:62793764A>T	c.773A>T	CAG=>CTG	Gln=>Leu	p.Q258L	missense
ZMYND10	B5	g.chr3:50357582C>G	c.178G>C	GAG=>CAG	Glu=>Gln	p.E60Q	missense
ZMYND8	B21	g.chr20:45338770T>G	c.1175A>C	AAC=>ACC	Asn=>Thr	p.N392T	missense
ZMYND8	B66	g.chr20:45311519G>A	c.1693C>T	CTC=>TTC	Leu=>Phe	p.L565F	missense
ZMYND8	B89-3	g.chr20:45356915C>G	c.469G>C	GAA=>CAA	Glu=>Gln	p.E157Q	missense
ZNF174	B13	g.chr16:3398555A>T	c.859A>T	AGC=>TGC	Ser=>Cys	p.S287C	missense
ZNF174	B65	g.chr16:3398475C>T	c.779C>T	TCA=>TTA	Ser=>Leu	p.S260L	missense
ZNF295	B5	g.chr21:42287117C>T	c.157G>A	GAA=>AAA	Glu=>Lys	p.E53K	missense
ZNF471	B15	g.chr19:61719525C>G	c.103C>G	CAG=>GAG	Gln=>Glu	p.Q35E	missense
ZNF502	B10	g.chr3:44738353G>C	c.1040G>C	GGA=>GCA	Gly=>Ala	p.G347A	missense
ZNF536	B15	g.chr19:35717711C>T	c.2288C>T	TCC=>TTC	Ser=>Phe	p.S763F	missense
ZNF623	B106	g.chr8:144804645A>G	c.1460A>G	TAT=>TGT	Tyr=>Cys	p.Y487C	missense
ZNF623	B5	g.chr8:144804284A>T	c.1099A>T	AGA=>TGA	Arg=>Stop	p.R367*	nonsense
ZNF80	B106	g.chr3:115438210C>G	c.402G>C	GAG=>GAC	Glu=>Asp	p.E134D	missense
ZNF80	B9	g.chr3:115437890C>G	c.722G>C	GGA=>GCA	Gly=>Ala	p.G241A	missense

#Genomic positions are coordinates in the hg18 UCSC release of the human genome. g., genomic sequence; c., cDNA sequence; p., protein sequence. $Mutated positions indicate the sites in the protein-coding region of the cDNA sequence. § Frame shift indel, frameshift insertions and deletions; indel, in frame insertions and deletions which still change more than one single codon. * Stop codon.

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Supplementary Table 6. The background mutation rates of different mutation types estimated from the Discovery Screen.

Mutation type	No. of mutations	Background mutation rate (per Mb)
A>C	4	0.06
A>G	12	0.18
A>T	17	0.25
C>A at CpG	5	0.81
C>A at non CpG	24	0.41
C>G at CpG	1	0.16
C>G at non CpG	59	1.00
C>T at CpG	25	4.06
C>T at non CpG	69	1.17
G>A at CpG	36	5.86
G>A at non CpG	73	1.26
G>C at CpG	4	0.65
G>C at non CpG	58	1.00
G>T at CpG	2	0.33
G>T at non CpG	23	0.40
T>A	8	0.12
T>C	13	0.19
T>G	3	0.04
indel	29	0.11

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Supplementary Table 7. A list of the genes which showed significantly higher mutation rates than the background.

Gene Symbol	Missense mutations	Nonsense mutations	Indels	Splice site changes	Silent mutations	Total mutations	N:S ratio	*P* value (N:S)	Patients harboring non-silent mutations	Nucleotides sufficiently covered (Mb)	Gene size (Kb)	*P* value (passenger probability)
UTX	5	11	5	1	1	23	22:1	1.54×10^{-5}	20	0.40	4.21	2.22×10^{-37}
TP53	13	4	1	3	1	22	21:1	2.72×10^{-5}	20	0.11	1.18	1.01×10^{-49}
ARID1A	4	11	3	0	0	18	-	1.61×10^{-5}	13	0.58	10.98	1.99×10^{-32}
CREBBP	4	9	1	1	2	17	15:2	3.35×10^{-3}	13	0.61	7.33	3.42×10^{-26}
EP300	6	3	4	0	0	13	-	3.46×10^{-4}	13	0.76	7.25	6.58×10^{-15}
RB1	3	4	0	4	1	12	11:1	7.12×10^{-3}	11	0.26	2.79	1.00×10^{-11}
HRAS	10	0	0	0	0	10	-	2.17×10^{-3}	10	0.05	1.08	7.89×10^{-7}
FGFR3	9	0	0	0	0	9	-	4.01×10^{-3}	9	0.14	4.51	1.69×10^{-18}
LRP2	8	1	0	0	0	9	-	4.01×10^{-3}	9	1.47	13.97	4.47×10^{-10}
ERBB3	9	0	0	0	2	11	9:2	5.85×10^{-2}	8	0.42	4.03	3.28×10^{-18}
LAMA4	8	0	0	0	1	9	8:1	3.46×10^{-2}	7	0.58	11.29	4.77×10^{-9}
CHD6	6	1	0	0	2	9	7:2	1.38×10^{-1}	7	0.85	8.15	6.00×10^{-9}
NF1	5	1	0	1	1	8	7:1	5.76×10^{-2}	7	0.86	16.98	8.76×10^{-10}
MLL	5	1	2	0	1	9	8:1	3.46×10^{-2}	7	1.20	11.91	2.00×10^{-11}
ANK2	7	0	0	0	1	8	7:1	5.76×10^{-2}	7	1.23	17.49	3.07×10^{-8}
NCOR1	5	0	0	2	0	7	-	1.37×10^{-2}	6	0.72	7.32	3.21×10^{-6}
KRAS	6	0	0	0	1	7	6:1	9.47×10^{-2}	6	0.07	1.14	3.29×10^{-26}
ESPL1	5	1	0	0	1	7	6:1	9.47×10^{-2}	6	0.63	6.36	2.76×10^{-11}
MLL3	2	3	1	0	1	7	6:1	9.47×10^{-2}	5	1.52	26.81	1.58×10^{-6}
ANK3	5	0	0	0	1	6	5:1	1.54×10^{-1}	5	1.41	16.14	9.10×10^{-4}
ZFHX3	5	0	0	0	0	5	-	1.54×10^{-1}	5	1.04	11.11	5.52×10^{-3}
LNX1	4	0	0	0	1	5	4:1	2.44×10^{-1}	4	0.20	1.90	4.26×10^{-4}
SEMA6D	4	0	0	0	0	4	-	8.61×10^{-2}	4	0.34	15.53	7.10×10^{-4}
ADCY2	4	0	0	0	0	4	-	8.61×10^{-2}	4	0.34	3.28	1.74×10^{-3}
ATG2B	4	0	0	1	0	5	-	4.66×10^{-2}	4	0.63	6.24	2.42×10^{-3}
NFE2L3	5	1	0	0	1	7	6:1	9.47×10^{-2}	4	0.16	2.09	1.33×10^{-17}
NLRP14	2	1	0	0	0	3	-	1.59×10^{-1}	3	0.35	3.28	1.45×10^{-5}
ALS2CR11	2	1	0	0	0	3	-	1.59×10^{-1}	3	0.18	1.87	4.69×10^{-5}
SRRM2	4	0	0	0	1	5	4:1	2.44×10^{-1}	3	0.79	8.26	9.26×10^{-5}
OPCML	3	0	0	0	1	4	3:1	3.78×10^{-1}	3	0.12	2.06	1.13×10^{-4}
KIAA0141	3	0	0	0	0	3	-	1.59×10^{-1}	3	0.16	1.55	3.73×10^{-4}
NPR2	3	0	0	0	0	3	-	1.59×10^{-1}	3	0.32	6.13	3.91×10^{-4}
DISP1	3	0	0	0	1	4	3:1	3.78×10^{-1}	3	0.48	4.58	7.65×10^{-4}
PLCB1	2	1	0	0	0	3	-	1.59×10^{-1}	3	0.40	7.17	8.41×10^{-4}
MERTK	3	0	0	0	1	4	3:1	3.78×10^{-1}	3	0.31	3.00	1.06×10^{-3}
SH3RF1	3	0	0	0	0	3	-	1.59×10^{-1}	3	0.27	2.67	1.23×10^{-3}
TAOK3	3	0	0	0	0	3	-	1.59×10^{-1}	3	0.28	2.70	1.89×10^{-3}
ZMYND8	3	0	0	0	1	4	3:1	3.78×10^{-1}	3	0.36	7.05	3.80×10^{-3}
C1orf101	3	0	0	0	1	4	3:1	3.78×10^{-1}	3	0.25	2.50	8.89×10^{-3}
FLNB	3	0	0	0	1	4	3:1	3.78×10^{-1}	3	0.81	7.81	9.88×10^{-3}
CLSPN	3	0	0	0	0	3	-	1.59×10^{-1}	3	0.41	4.02	1.06×10^{-2}
KLC4	4	0	0	0	0	4	-	8.61×10^{-2}	2	0.17	3.77	2.65×10^{-6}
ZNF80	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.08	0.82	2.95×10^{-4}
COL3A1	3	0	0	0	0	3	-	1.59×10^{-1}	2	0.38	4.40	4.14×10^{-4}
C4orf17	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.11	1.08	1.10×10^{-3}
HEXA	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.15	1.59	2.22×10^{-3}
AVL9	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.20	1.95	3.05×10^{-3}
MTBP	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.28	2.72	4.40×10^{-3}
CD86	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.10	1.96	4.76×10^{-3}

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Supplementary Table 7 continued. A list of the genes which showed significantly higher mutation rates than the background.

Gene Symbol	Missense mutations	Nonsense mutations	Indels	Splice site changes	Silent mutations	Total mutations	N:S ratio	*P* value (N:S)	Patients harboring non-silent mutations	Nucleotides sufficiently covered (Mb)	Gene size (Kb)	*P* value (passenger probability)
PPP1R9A	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.35	3.30	8.99×10^{-3}
SPAG1	2	1	0	0	0	3	-	1.59×10^{-1}	2	0.24	2.78	9.74×10^{-3}
IL18RAP	1	1	0	0	0	2	-	2.93×10^{-1}	2	0.18	1.80	1.04×10^{-2}
C15orf55	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.35	3.40	1.58×10^{-2}
TRIM23	2	0	0	0	0	2	-	2.93×10^{-1}	2	0.18	5.08	1.74×10^{-2}

N:S, non-silent : silent mutation.

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Supplementary Table 8. Permutation analysis of concurrence and mutual exclusion of mutations in the frequently mutated genes.

Gene1	Gene2	No. of samples with mutations in Gene1	No. of samples with mutations in Gene2	No. of samples with mutations in both genes	No. of samples with mutations in only one gene	Expected No. of samples with mutations in both genes by permutation	Expected No. of samples with mutations in only one gene by permutation	*P* value of mutations concurrence	*P* value of mutual exclusion among mutations
ANK2	*ANK3*	7	5	4	4	0.61349	10.77303	0.0004309	0.999995
ANK2	*CHD6*	7	7	3	8	0.85372	12.29255	0.0328197	0.997301
CHD6	*LRP2*	7	9	4	8	1.08983	13.82033	0.0084993	0.999474
LRP2	*MLL*	9	7	3	10	1.08964	13.82072	0.0683443	0.991557
LRP2	*ZFHX3*	9	5	3	8	0.78313	12.43375	0.0237094	0.998556
HRAS	*TP53*	10	20	0	30	3.29707	23.40586	1	0.0125049
HRAS	*UTX*	10	21	1	29	3.44959	24.10081	0.990274	0.0440656
KRAS	*UTX*	6	21	0	27	2.09287	22.81426	1	0.0468466
TP53	*ANK2*	20	7	0	27	2.32794	22.34412	1	0.0494707
TP53	*FGFR3*	20	9	0	29	2.97538	23.04924	1	0.0200616
TP53	*KRAS*	20	6	0	26	2.00085	21.9983	1	0.0774966

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