Table SI. Somatic mutations detected by next-generation sequencing.

Gene	c.HGVS	p.HGVS	Allele Frequency (%)
HRAS	c.37G>A	p.G13S	12.9
GAB2	c.1240C>T	p.R414C	12.7
JAK3	c.349C>T	p.R117C	12.3
ALK	c.979G>A	p.A327T	12.0
ALK	c.2081A>G	p.H694R	11.4
EGFR	c.2006G>A	p.R669Q	11.1
NTRK3	c.1990G>A	p.A664T	10.5
PTCH2	c.359G>A	p.R120H	10.3
NOTCH4	c.2155A>G	p.T719A	9.9
FGFR3	c.742C>T	p.R248C	9.7
ATM	c.748C>T	p.R250*	9.4
RHOA	c.56C>T	p.T19I	9.1
RHOA	c.139G>A	p.E47K	9.0
NOTCH3	c.4822G>A	p.A1608T	8.6
SRC	c.100G>A	p.A34T	4.4
MSH6	c.2195G>A	p.R732Q	4.0
APC	c.4150T[3>4]	p.S1385*	4.0
NOTCH4	c.4415G>A	p.R1472Q	3.9
AKT1	c.226C>T	p.R76C	3.9
SMARCB1	c.641C>T	p.T214M	3.7
APC	c.646C>T	p.R216*	3.7
CTNNB1	c.1693C>T	p.R565C	3.5
TERT	c.-58-u4351C>T	-	2.9
ERG	c.881G>A	p.R294H	2.9
SMARCA4	c.4772G>A	p.R1591Q	2.4
PIK3CA	c.1849C>T	p.R617W	2.0
NRAS	c.34G>T	p.G12C	1.9
PDGFRB	c.3074T>C	p.L1025P	1.6
NOTCH1	c.4672G>A	p.G1558R	1.4
CSF1R	c.431G>A	p.R144H	1.3
IRS2	c.974A>G	p.H325R	1.2
IRS2	c.3809C>A	p.P1270Q	1.0
TERT	c.-58-u2855C>T	-	0.9
ATR	c.7792C>T	p.R2598*	0.8
NOTCH1	c.2474C>T	p.T825M	0.8
ERG	c.475C>A	p.L159I	0.8
MED12	c.4820A>G	p.E1607G	0.8
MTOR	c.3901C>T	p.R1301C	0.7
IL7R	c.616C>T	p.R206*	0.7
CDK13	c.895G>A	p.A299T	0.7
TSC1	c.1700C>T	p.A567V	0.5
MLL	c.2521C>T	p.P841S	0.5
CDK12	c.3721C>T	p.P1241S	0.5

-, c.-58-u4351C>T and c.-58-u2855C>T occur on the promoter region of the telomerase reverse transcriptase gene, and the amino acid change cannot be predicted; *, stop codon in a nonsense variant.