

eAPPENDIX. List of Mutated Genes and Specific Mutations With Respective Frequency in the Study Population (N = 35)

Gene	Mutation	Mutation, No. (%)
TERT promoter	c.-146C>T	18 (51)
	c.-124C>T	8 (23)
	139_-138CC>TT	1 (3)
	Total	27 (77)
CDKN2A/B	Loss both	2 (6)
	Copy number loss both	2 (6)
	p.P81L missense LOF 35.7%	1 (3)
	P16INK4a splice site 151-1_151GG>AA and p14ARF splice site 194-1_194GG>AA subclonal	1 (3)
	p16INK4a P70fs*36 and p14ARF Q85fs*62	1 (3)
	p16INK4a F90L and p14ARF P105T	1 (3)
	CDKN2A p.V51I splice region variant LOF 76.3%	1 (3)
	p16INK4a R80* and p14ARF P94L, p16INK4a P81L	1 (3)
	CDKN2A p.A57fs frameshift LOF 33.2%	1 (3)
	CDKN2A p.W110* stop gain LOF 8.7%	1 (3)
	Loss unspecified	1 (3)
	CDKN2A loss	1 (3)
	p16INK4a splice site 151-25_188del63 and p14ARF splice site 194-25_231del63	1 (3)
	Total	15 (43)
BRAF	V600E	7 (20)
	V600K	6 (17)
	Total	13 (37)
NF1	Loss exons 1-7	1 (3)
	p.R1241 stop gain LOF 60.2%	1 (3)
	p.Q1815* stop gain LOF 32.8%	1 (3)
	1527+1_1527+2GT>TC splice site	1 (3)
	p.Q1822* stop gain LOF 49.8%	1 (3)
	Q1395*, Q519* splice site 6007-1G>A	1 (3)
	Q1617*, rearrangement intron 1	1 (3)
	R1204W, W1685*	1 (3)
	p.Q589* stop gain LOF 65.6%	1 (3)
	p.Q1255* stop gain LOF 14.5% p.R2450* stop gain LOF 11.7%	1 (3)
	Q519*, Y2192*	1 (3)
	Total	11 (31)
TP53	p.IR195 stop gain LOF 40.5%	1 (3)
	p.P27L missense LOF 14.9%	1 (3)
	c.559+1G>T splice region variant LOF 38.4%	1 (3)
	p.R110fs frameshift LOF 51.7%	1 (3)
	R213*	1 (3)
	R282W	1 (3)
	p.G187S splice region variant LOF 65.6%	1 (3)
	p.P177S	1 (3)
	Loss unspecified	1 (3)
	Total	9 (26)
NRAS	Q61R	2 (6)
	p.Q61K missense (exon 3) GOF 21.9%	1 (3)
	p.Q61K missense (exon 3) GOF 16.6%	1 (3)
	Q61H	1 (3)
	p.Q61R missense (exon 3) GOF 51.9%	1 (3)
	p.G13D missense (exon 2) GOF 38.2%	1 (3)
	Q61K	1 (3)
	Total	8 (23)
PTEN	V166fs*14	1 (3)
	R130G-subclonal, H196fs*6, G251D	1 (3)
	Loss exons 4-9	1 (3)
	p.V166fs frameshift LOF 8.3%; p.D252G missense LOF 6.1%	1 (3)
	A137fs*42	1 (3)
	Total	5 (14)

SETD2	Q1638* Splice site 88-1G>A R620* R1492* Deletion exons 2-3 Total	1 (3) 1 (3) 1 (3) 1 (3) 1 (3) 5 (14)
ARID2	p.R274*stop gain LOF 7.4% p.R542* stop gain LOF 32.9% p.G1658*stop gain LOF 16.3%; c.1581-1G>A splice region variant LOF 8.8% Total	1 (3) 1 (3) 1 (3) 3 (9)
CBL	Y371N R420Q P417S Total	1 (3) 1 (3) 1 (3) 3 (9)
IDH1	R132C p.R132G missense GOF 15.8% Total	2 (6) 1 (3) 3 (9)
MTAP	Loss unspecified Copy number loss Total	1 (3) 2 (6) 3 (9)
RAC1	P29S unspecified P29S subclonal p.P29S missense GOF 11.5% Total	1 (3) 1 (3) 1 (3) 3 (9)
APC	P1609L Loss exon 16 Total	1 (3) 1 (3) 2 (6)
ATM	P1382fs*6 K468fs*18 Total	1 (3) 1 (3) 2 (6)
CCND1	Amplification Amplification-equivocal Total	1 (3) 1 (3) 2 (6)
DNMT3A	Q696* p.Q656* stop gain LOF 35.8% Total	1 (3) 1 (3) 2 (6)
ERBB4	p.E452K missense GOF 37.7% E452K unspecified Total	1 (3) 1 (3) 2 (6)
FBXW7	L594F S426L, S582L Total	1 (3) 1 (3) 2 (6)
FGF12	E149K Total	1 (3) 1 (3)
FGFR2	R210Q N549K Total	1 (3) 1 (3) 2 (6)
FLT1	R281Q E72K Total	1 (3) 1 (3) 2 (6)
MEN1	R465* p.R98* stop gain LOF 12.8% Total	1 (3) 1 (3) 2 (6)
MSH6	p.F451fs frameshift LOF 49.9% F1104fs*1 Total	1 (3) 1 (3) 2 (6)
MUTYH	G382D p.Y179C missense LOF 48.7% Total	1 (3) 1 (3) 2 (6)

NOTCH1	p.FQ474 stop gain LOF 33.1%	1 (3)
	E455K	1 (3)
	Total	2 (6)
NPM1	583-2A>G splice site	1 (3)
	Loss unspecified	1 (3)
	Total	2 (6)
PIK3CA	R38H	1 (3)
	E542K	1 (3)
	Total	2 (6)
RAD21	Deletion exons 3-4	1 (3)
	Amplification	1 (3)
	Total	2 (6)
RAF1	S257L	1 (3)
	Amplification	1 (3)
	Total	2 (6)
ROS1	P1440S	1 (3)
	E402K subclonal	1 (3)
	Total	2 (6)
SF3B1	G742D	1 (3)
	E902K	1 (3)
	Total	2 (6)
SPEN	S268fs*98	1 (3)
	Q1757*	1 (3)
	Total	2 (6)
ABL1	ABL1-BCR non-canonical fusion	1 (3)
ARID1A	Q1519fs*13	1 (3)
ATRX	Deletion exons 9-10	1 (3)
BAP1	L633fs*4	1 (3)
BRCA2	S2670L	1 (3)
CARD11	D632N	1 (3)
CD70	R163*	1 (3)
CDK6	Amplification-equivocal	1 (3)
CDKN1B	p.Q141* stop gain LOF 11.0%	1 (3)
CHEK2	I157T	1 (3)
CIC	p.Q979 stop gain LOF 38.4%	1 (3)
CREBBP	Q1773*	1 (3)
CRKL	Amplification-equivocal	1 (3)
CTNNB1	S45F	1 (3)
DIS3	p.R780K missense GOF 35.8%	1 (3)
DDR1	R296C	1 (3)
EBF1	p.NQ195 stop gain LOF 17.5%	1 (3)
EGFR	S720F	1 (3)
ERCC3	p.K688K splice region variant LOF 31.5%	1 (3)
FAM46C	p.Q106 stop gain LOF 20.8%	1 (3)
FANCG	Rearrangement intron 13	1 (3)
FGF12	E149K	1 (3)

FGFR1	R445W	1 (3)
FLT3	M664I	1 (3)
GABRA6	W188*	1 (3)
GNA11	Q209L	1 (3)
GNAQ	Q209P	1 (3)
GRIN2A	p.W843* stop gain LOF 18.4%	1 (3)
HGF	E174K	1 (3)
IKZF1	p.Q149* stop gain LOF 29.5%	1 (3)
JAK2	V617F	1 (3)
KDM5C	Q706*	1 (3)
KDR	G494E	1 (3)
KMT2C (MLL3)	p.R2403 stop gain LOF 22.1%	1 (3)
KMT2D (MLL2)	R2734*	1 (3)
KRAS	V14I	1 (3)
LRP1B	c.8663-2A>C splice region LOF 45.9%	1 (3)
MAP2K1 (MEK1)	P124L	1 (3)
MITF	Amplification	1 (3)
MYC	Amplification	1 (3)
PARK2	G354R	1 (3)
PBRM1	p.E967 stop gain LOF 21.9%	1 (3)
PIK3C2G	E425K	1 (3)
PIK3R1	P194fs*12	1 (3)
PMS2	p.Q781 stop gain LOF 20.7%	1 (3)
PPP6C	p.P223S missense LOF 15.2%; p.R301C missense LOF 10.0%	1 (3)
PRKN	p.K427* stop gain LOF 25.2%	1 (3)
PTCH1	Splice site 3306_3306+1GG>AA	1 (3)
PTPRT	c.2370-1G>A splice region variant LOF 28.7%	1 (3)
RAD51D	W268*	1 (3)
RAD54L	E469*	1 (3)
RB1	Splice site 1128-2A>T, C553*	1 (3)
RICTOR	Amplification	1 (3)
RUNX1	c.97+1G>A splice region LOF 13.7%	1 (3)
SLIT2	p.C1385* stop gain LOF 26.4%	1 (3)
SNCAIP	W574*	1 (3)
STK11	L282fs*3	1 (3)
SUZ12	p.K341fs frameshift LOF 11.6%	1 (3)
TBX3	P646S	1 (3)
WT1	M1I	1 (3)

Abbreviations: del, deletion; GOF, gain of function; LOF, loss of function.