

Supplementary Table 5 - Complete list of genetic variants for TP53 gene determined by targeted deep sequencing in the T-LBL samples.

IFT	PolyPhen2	IFT	MutationTaster	MutationAssessor	FATHMM	MetaVM	Occurrences	hgMD	PROVEAN	# locus	type	ref	length	genotype	posite	coverage	allele_coverage	maf	gene	transcript	location	function	codon	exon	protein	coding	utr	polyphen	grantham	normalisedA1	S000names	cosmic	dbpup	drugbank	gn	lmm	lfa	phabp				
S34								17_757407_3055_A_C	17_757407_A.C	1	A/C	A	1	A/C		1525	352,673	0.164	TP53	NM_000461.5	intronic														17_757407_P07710.P07820	1	1.48					
								17_757407_3056_G_A	17_757407_G.A	1	G/A	G	1	G/A		1535	371,662	0.164	TP53	NM_000461.5	intronic														17_757407_P07710.P07820	1	0.16					
								17_7579470_3448_CGG_CGC	17_7579470_CGG.CGC	1	CGG/CGC	GGG	1	CGG/CGC		583	296,287,050	0.39800	TP53	NM_000461.5	exonic	missense	CGC	4	p.Pro72Arg	C.215C>G			103.0	C			43787_18569_1268312_1268311_96366_45286-8 13077_44252_44466_138925_138926_46058-8	n1042522_n56275308			17_7579470_P07710.P07820	1	1.14, 6.68, 1.36			
S38								17_7579470_3458_CGG_CGC	17_7579470_CGG.CGC	1	CGG/CGC	GGG	1	CGG/CGC		583	11,790,050	0.39800	TP53	NM_000461.5	exonic	missense	CGC	4	p.Pro72Arg	C.215C>G			103.0	C			43787_18569_1268312_1268311_96366_45286-8 13077_44252_44466_138925_138926_46058-8	n1042522_n56275308			17_7579470_P07710.P07820	1	1.14, 6.68, 1.36			
S39								17_7579470_3457_G_T	17_7579470_G.T	1	G/T	G	1	G/T		1232	923,603	0.073	TP53	NM_000461.5	intronic														17_7579470_P07710.P07820	1	0.7					
S40								17_7579483_3458_CCCCAGCCCAAGT_C	17_7579483_CCCCAGCCCAAGT.C	12	CCCAGCCCAAGT/C	CCCAGCCCAAGT	16	CCCCAGCCCAAGT/C		2417	2007,41	0.153	TP53	NM_000461.5	intronic															17_7579483_P07710.P07820	1	2.36, 0.13, 0.39, 1.0, 1.96, 1.18, 0.8, 0.6, 46.3, 0.6, 0.7, 0.3, 0.8				
S42								17_7579446_3302_T_C	17_7579446_T.C	1	T/C	T	1	T/C		77	49,24	0.0	TP53	NM_000461.5	intronic															17_7579446_P07710.P07820	1	6.3				
								17_7579503_3308_C_A	17_7579503_C.A	1	G/A	G	1	G/A		140	137,50		TP53	NM_000461.5	exonic	missense	TTC	5	p.Val148Leu	C.427D>T	0.12	0.401	32.0	A			44904_46078_40958_220756_166439_220753-4 43787_220753_220754_46053_43878				17_7579503_P07710.P07820	1	1.45			
								17_7579470_3401_CGG_CGC	17_7579470_CGG.CGC	1	CGG/CGC	GGG	1	CGG/CGC		535,45	153	69,813,00	0.39800	TP53	NM_000461.5	exonic	missense	CGC	4	p.Pro72Arg	C.215C>G			103.0	C			43787_18569_1268312_1268311_96366_45286-8 13077_44252_44466_138925_138926_46058-8	n1042522_n56275308			17_7579470_P07710.P07820	1	1.14, 6.68, 1.36		

chr	start	end	strand	transcript	transcript_id	cds_start	cds_end	feature	score	name	source	score	name	source	score	name	source
17	938948	939128	-	CCGAGCCCCTCAGGT	CCGAGCCCCTCAGGT	17_938948_939128_-1	938948	939128	0.0	CGGC	CGGC	0.0	CGGC	CGGC	0.0	CGGC	CGGC

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chr	start	end	strand	transcript	transcript_id	cds_start	cds_end	feature	score	name	source	score	name	source	score	name	source
17	938948	939128	-	CCGAGCCCCTCAGGT	CCGAGCCCCTCAGGT	17_938948_939128_-1	938948	939128	0.0	CGGC	CGGC	0.0	CGGC	CGGC	0.0	CGGC	CGGC

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chr	start	end	strand	transcript	transcript_id	cds_start	cds_end	feature	score	name	source	score	name	source	score	name	source
17	938948	939128	-	CCGAGCCCCTCAGGT	CCGAGCCCCTCAGGT	17_938948_939128_-1	938948	939128	0.0	CGGC	CGGC	0.0	CGGC	CGGC	0.0	CGGC	CGGC

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chr	start	end	strand	transcript	transcript_id	cds_start	cds_end	feature	score	name	source	score	name	source	score	name	source
17	938948	939128	-	CCGAGCCCCTCAGGT	CCGAGCCCCTCAGGT	17_938948_939128_-1	938948	939128	0.0	CGGC	CGGC	0.0	CGGC	CGGC	0.0	CGGC	CGGC

SFT	PolyPhen2	IFT	MutationFactor	MutationAssessor	FATHMM	MetaSVM	Occurrences	hgmd	PROVEAN	# locus	type	ref	length	amtype	pscore	coverage	allele coverage	maf	gene	transcript	location	function	codon	exon	protein	coding	ift	polyphen	grantham	normalizedat	S000xomes	cosmic	dbnp	drugbank	ip	chem	ifam	phospho
							12	17_7579643_3356_CCCCAGCCCTCCAGT_C	17_7579643_CCCCAGCCCTCCAGT_C	17_7579643	indel	ECCCAGCCCTCCAGG	16	CCCCAGCCCTCCAGT/C	1.00E+10	530	345,185	0.153	TP93	NM_005463	intronic													AMAF=0.3385:EMAF=0.2049:MAF=0.2511	r5979882:n1787832:n15020764:n14653483:178930088:n81712732:n6651936:n18866738	1-(p-ethyl-9H-carbazol-3-yl)-N-methylmethanamine	GO:000515:GO:0030308:GO:0003700:GO:0044212:GO:0009303:GO:0007912:GO:0009792:GO:0001170:PF08561:PF07710:PF00870	2.36,0.11,0.88,0.2,0.15,0.39,1.0,1.96,1.18,0.06,0.06,0.46,4.6,38,0.47,0.46,0.38

SFT	PolyPhen2	IFT	MutationFactor	MutationAssessor	FATHMM	MetaSVM	Occurrences	hgmd	PROVEAN	# locus	type	ref	length	amtype	pscore	coverage	allele coverage	maf	gene	transcript	location	function	codon	exon	protein	coding	ift	polyphen	grantham	normalizedat	S000xomes	cosmic	dbnp	drugbank	ip	chem	ifam	phospho
							12	17_7579643_3376_CCCCAGCCCTCCAGT_C	17_7579643_CCCCAGCCCTCCAGT_C	17_7579643	indel	ECCCAGCCCTCCAGG	16	CCCCAGCCCTCCAGT/C	1.00E+10	2536	1831,705	0.153	TP93	NM_005463	intronic													AMAF=0.3385:EMAF=0.2049:MAF=0.2511	r5979882:n1787832:n15020764:n14653483:178930088:n81712732:n6651936:n18866738	1-(p-ethyl-9H-carbazol-3-yl)-N-methylmethanamine	GO:000515:GO:0030308:GO:0003700:GO:0044212:GO:0009303:GO:0007912:GO:0009792:GO:0001170:PF08561:PF07710:PF00870	2.36,0.11,0.88,0.2,0.15,0.39,1.0,1.96,1.18,0.06,0.06,0.46,4.6,38,0.47,0.46,0.38

SFT	PolyPhen2	IFT	MutationFactor	MutationAssessor	FATHMM	MetaSVM	Occurrences	hgmd	PROVEAN	# locus	type	ref	length	amtype	pscore	coverage	allele coverage	maf	gene	transcript	location	function	codon	exon	protein	coding	ift	polyphen	grantham	normalizedat	S000xomes	cosmic	dbnp	drugbank	ip	chem	ifam	phospho
							0	17_7579643_3388_A_G	17_7579643_A_G	17_7579643	snv	A	1	CG/C	4.073803E-317	453	201,249,0,1,0	0.3985,0	TP93	NM_005463	intronic												43787:18869:1268332:1268331:96580:45288:43807:44256:44466:1186925:138626:46058:4808	r5042522:n56275308	1-(p-ethyl-9H-carbazol-3-yl)-N-methylmethanamine	GO:000515:GO:0030308:GO:0003700:GO:0044212:GO:0009303:GO:0007912:GO:0009792:GO:0001170:PF08561:PF07710:PF00870	1.14,0.69,1.38	
							0	17_7579643_3344_CGG_CGC	17_7579643_CGG_CGC	17_7579643	snv	CGG	1	CGG/CGC	4.073803E-317	453	201,249,0,1,0	0.3985,0	TP93	NM_005463	intronic													43787:18869:1268332:1268331:96580:45288:43807:44256:44466:1186925:138626:46058:4808	r5042522:n56275308	1-(p-ethyl-9H-carbazol-3-yl)-N-methylmethanamine	GO:000515:GO:0030308:GO:0003700:GO:0044212:GO:0009303:GO:0007912:GO:0009792:GO:0001170:PF08561:PF07710:PF00870	1.14,0.69,1.38