SUPPLEMENTARY TABLES

Supplementary Table S1: Forward and Reverse primer sequences used in Sanger sequencing for mutation identification in p53 gene (from exon 4 to exon 9)

Exon	Forward (5' to 3')	Reverse (5' to 3')
4	CGTCTTCCAGTTGCTTTATC	AAGAAGAAAACGGCATTTTG
5	TTTCAACTCTGTCTCCTTCC	AACCAGCCCCTGTCGTCTCTC
6	TGGTTGCCCAGGGTCCCCAG	GGAGGGCCACTGACAACCA
7	CTTGCCACAGGTCTCCCCAA	AGGGGTCAGAGGCAAGCAGA
8	AAAGGACAAG GGTGGTTGGG	CTGCACCCTTGGTCTCCTCC
9	CGGTGGAGGAGACCAAGGGT	AAGAAGAAAAAACGGCATTTTG

Supplementary Table S2: Phred Quality check of the sequencing data

Sample	Read Length	Total reads	Sequence with poor quality (Phred cut off 30)
TCT1	101	40085392	0
TCT2	101	38477800	0
TMU1	101	41984560	0
TMU2	101	40625508	0

TCT - Tumor Control (RNA isolated from tumor formed from pCMV10 Ctrl cells)

TMU - Tumor Mutant (RNA isolated from tumor formed from P152Lp53 expressing cells)

Supplementary Table S3: Alignment statistics of the sequencing data

Read statistics	**TCT1 for each pair 1 and pair 2 Alignment**	**TCT2 for each pair 1 and pair 2 Alignment**	**TMU1 for each pair 1 and pair 2 Alignment**	**TMU2 for each pair 1 and pair 2 Alignment**
Number of input reads(pair 1+pair 2)	20042686*2	19288900*2	20992485*2	20312754*2
Average input read length	202	202	202	202
UNIQUE READS:				
Uniquely mapped reads number	17204309*2	16169836*2	18084230*2	17226684*2
Uniquely mapped reads %	85.84%	83.83%	86.15%	84.81%
MULTI-MAPPING READS:				
Number of reads mapped to multiple loci	1497489*2	1400296*2	1530895*2	1450244*2
% of reads mapped to multiple loci	7.47%	7.26%	7.29%	7.14%
Number of reads mapped to too many loci	14148*2	11117*2	12565*2	14138*2
% of reads mapped to too many loci	0.07%	0.06%	0.06%	0.07%
UNMAPPED READS:				
% of reads unmapped: too many mismatches	0.00%	0.00%	0.00%	0.00%
% of reads unmapped: too short	6.51%	8.74%	6.40%	7.88%
% of reads unmapped: other	0.11%	0.11%	0.11%	0.10%

Supplementary Table S4: Forward and Reverse primer sequences for qPCR

Gene	**Forward (5’ to 3’)**	**Reverse (5’ to 3’)**
ITPR3	CCGCGTGAAGAACAAGACCG	CGCCCTCATTGCTGACAAGG
FOSB	CCTAGGAGACCCCGAGAGGA	GATCTTGCAGCCCGGTTTGT
TIAM1	TTGTGTGCACTGAAGGGGGC	CTTGCGGAGACGGCATCAGA
ARHGEF4	CGAGCGGAAGCGGAGACTT	CTGCTGGCTTTTGGCTTGAGG
PSAP	TCCTGGTGGAGGTGATGGAT	ATGGCGTTTGCAATGCTCGAC
CBLB	TCTTCTTCCTTCAGATCCCTTTGT	GTGGTTTAGGGGGTCTGGCT
BCL2	CAGTGCAATGGCTTCCATGAG	ATTCGTGGGTGGTCTTCGGC
PTCH1	TGATGCTGGCGGGATCTGAG	GCTGGAGACACCTCAGGATATGG
P4HA1	ATTTTGACTTTGCACGGAAAGATG	GGCTCCTCCTGCAGACACAT
COL4A5	GACCTCAAGGCTTACCAGGTCCA	GGACCATCCAAACCACGGGTA
IGF1R	CTCGGACGTCTGGTCCTTC	GCACATGCGCATCAGTTCAA
DUSP1	AGGCCATTGACTTCATAGACTCC	TGCTTCGCCTCTGCTTCACA
COL9A3	ACCAGGGTATTGCAGGTTCCG	CTCGACTGCCAGACTCTCCTTT
NPY1R	ACCACTCTCCTCTTGGTGCTG	TGGTTTCACTGGACCTGTACTT
FOXO4	ACTTTGAGCCAGATCCCTGAGT	TGTGTGTGACCAGACCCCAC
NR4A1	CTTGTCCTCATCACCGACCG	TGCCCAACAGACGTGACAGG
SPOCK3	CAGAGACAGCAAGACCCACCT	CACACCAGCACTGTCCAACAC
MMP1	AAGACAGATTCTACATGCGCACAA	CTGTCCCTGAACAGCCCAGT
COL11A1	CCCAGGGTCTGTTGGTTCAGT	CTTTCTCCTTTGGGACCGCCT

Supplementary Table S5: Representative data for the Allelic Discrimination assay to determine the zygosity of P152Lp53 (ID rs587782705 custom designed by Applied Biosystems). Table shows manual calls of SNP assays of patient tumor (66951) and control tumor (247221, 262411, 62265) samples where the alleles were called based upon their ΔRn and ΔCt values

SNP Assay Name (Lot No.)	**Sample**	**Allele1 ΔRn**	**Allele2 ΔRn**	**Allele 1 ΔCt**	**Allele2 ΔCt**	**Call**
1642570	**247221-T**	**1.784**	**0.166**	**23.194**	**26.547**	**Homozygous 1/1**
1642570	**262411-T**	**1.707**	**0.216**	**23.42**	**25.294**	**Homozygous 1/1**
1642570	**62265-T**	**1.923**	**0.270**	**21.216**	**23.923**	**Homozygous 1/1**
1642570	**66951-T**	**1.790**	**1.216**	**21.81**	**20.88**	**Heterozygous 1/2**
1642570	**66951-T**	**1.546**	**1.068**	**21.97**	**21.12**	**Heterozygous 1/2**
	NTC	**0.1039723**	**0.0217072**	**UD**	**UD**	**Negative Control (NC)**
	NTC	**0.1545828**	**0.0707385**	**UD**	**UD**	**Negative Control (NC)**

Supplementary Table S6: p53 Responsive-element consensus sequence -

Gene	**p53 promoter consensus sequence**
GADD45A	5’- TACAGAACATGTCTAAGCATGCTGGGGACT -3’ and 5’- AGTCCCCAGCATGCTTAGACATGTTCTGTA -3’
CDKN1A	5’- ATGAGGAACATGTCCCAACATGTTGAGCTC - 3’ and 5’ - GAGCTCAACATGTTGGGACATGTTCCTCAT- 3’
BAX	5’- TGGGCTCACAAGTTAGAGACAAGCCTGGGCG - 3’ and 5’- CGCCCAGGCTTGTCTCTAACTTGTGAGCCCA -3’
MDM2	5’- GGGCTGGTCAAGTTCAGACACGTCCGGCGT - 3’ and 5’- ACGCCGGACGTGTCTGAACTTGACCAGCCC - 3’