

1 **Additional files**

2 **Table A1.** The sequences of primers used for PCR and sequencing analysis of *TP53* exons.

Region	Sequences of primers	
	Forward	Reverse
Polymerase chain reaction		
Exons 2-3	5'-atccccacttttctcttgc-3'	5'-gaaaagagcagtcagaggac-3'
Exon 4	5'-cctctgactgctcttttacc-3'	5'-tcatggaagccagcccctcag-3'
Exon 5	5'-ttccacacccccgcccggca-3'	5'-acctgggcaaccagccctg-3'
Exon 6	5'-acagggctggttcccagg-3'	5'-agtgcaaaccagacctcag-3'
Exon 7	5'-actggcctcatcttggcct-3'	5'-gtcagaggcaagcagaggct-3'
Exon 8	5'-taaatgggacaggtaggacc-3'	5'-tccaccgcttctgtcctgc-3'
cDNA exons 4-8	5'-gagccgagtcagatcctag-3'	5'-gcagtgctcgcttagtgctc-3'
Sequencing analysis		
Exons 2-3	5'-tcttgagcagccagact-3'	5'-agagcagtcagaggaccag-3'
Exon 4	5'-ccatctacagtcccccttgc-3'	5'-caacttgggacaggagtcag-3'
Exon 5	5'-caagcagtcacagcacatga-3'	5'-aaccagccctgtcgtctct-3'
Exon 6	5'-caggcctctgattcctact-3'	5'-agacctcaggggctcatag-3'
Exon 7	5'-atctcctaggttgctctga-3'	5'-tggcaagtggctcctgacct-3'
Exon 8	5'-ctctttcctatcctgagta-3'	5'-ctgcttcttaccctgctta-3'
cDNA exons 4-8	5'-ccctctgagtcaggaaacat-3'	5'-cccttcttgcggagattct-3'

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4 **Table A2.** The primer sequences used for *TP53* intron 3 sequencing.

Region	PCR Primer	Sequencing Primer
Intron 3	FV 5'-atccccacttttctcttgc-3' REV 5'-tcatggaagccagcccctcag-3'	FV 5'-tcttgagcagccagact-3' REV 5'-caacttgggacaggagtcag-3'

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6 **Table A3.** Sequences of primers used during PIN3 and codon 72 bacterial subcloning
7 procedure.

Type of reaction	Sequences of primers	
Cloning	BamHI restriction enzyme	5'-gcaagatccatgggactgactttctgctc-3'
	HindIII restriction enzyme	5'-cctggaagcttttctgggaaggacagaaga-3'
Polymerase chain reaction	Forward	5'-taaacgacggccagtgaat-3'
	Reverse	5'-caggaaacagctatgacctga-3'
Sequencing analysis	Forward	5'-gactgactttctgcttctgt-3'
	Reverse	5'-gctatgacctgattacgcc-3'

8 **Table A4.** Results from dual luciferase reporter assays.

Normalized Firefly luciferase activity			
Cell line	Construct	Normalized luciferase activity	Mean value
AD293	C	0.265; 0.370; 0.517; 0.294; 0.288; 0.311; 0.260; 0.232; 0.254; 0.128; 0.195	0.283
	A1	0.481; 0.467; 0.669; 0.350; 0.432; 0.405; 0.306; 0.315; 0.285; 0.150; 0.267	0.375
	A2	0.544; 0.561; 0.773; 0.385; 0.476; 0.446; 0.344; 0.332; 0.317; 0.189; 0.365	0.430
SW962	C	0.023; 0.036; 0.036; 0.044; 0.037; 0.045; 0.044; 0.037	0.038
	A1	0.022; 0.047; 0.035; 0.040; 0.042; 0.036; 0.034; 0.038	0.037
	A2	0.038; 0.082; 0.056; 0.053; 0.077; 0.054; 0.048; 0.060	0.059
Normalized luciferase activity in reference to control sample			
Cell line	Ratio	Ratio value	Mean value
AD293	A1/C	1.82; 1.26; 1.29; 1.19; 1.50; 1.30; 1.18; 1.36; 1.12; 1.17; 1.37	1.32
	A2/C	2.05; 1.52; 1.50; 1.31; 1.65; 1.43; 1.32; 1.43; 1.25; 1.48; 1.87	1.53
	A2/A1	1.13; 1.20; 1.16; 1.10; 1.10; 1.10; 1.12; 1.05; 1.11; 1.26; 1.37	1.16
SW962	A1/C	0.96; 1.31; 0.97; 0.91; 1.14; 0.80; 0.77; 1.03	0.98
	A2/C	1.65; 2.28; 1.56; 1.20; 2.08; 1.20; 1.09; 1.62	1.59
	A2/A1	1.73; 1.74; 1.60; 1.33; 1.83; 1.50; 1.41; 1.58	1.59
Results of statistical analysis			
Cell line	Ratio	p value	
AD293	A1 vs. C	0.05566	
	A2 vs. C	0.00833	
	A1 vs. A2	0.33164	
	A1/C vs. A2/C	0.01923	
SW962	A1 vs. C	0.64538	
	A2 vs. C	0.00109	
	A1 vs. A2	0.00109	
	A1/C vs. A2/C	0.00186	
Total	A1/C vs. A2/C	0.00019	

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11 **Table A5.** Intron 3 sequence from *TP53* gene, potentially capable of forming G-quadruplex
 12 structure [9].

<i>TP53</i> intron 3 (A1)	GTAAGGACAAGGGTTGGGCTGGGGACCTGGAGGGCTGGGG GGCTGGGGGGCTGAGGACCTGGTCCTCTGACTGCTCTTTTC ACCCATCTACAG
<i>TP53</i> intron 3 (A2)	GTAAGGACAAGGGTTGGGCTGGGGACCTGGAGGGCTGGGG ACCTGGAGGGCTGGGGGGCTGGGGGGCTGAGGACCTGGTC CTCTGACTGCTCTTTTCACCCATCTACAG

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14 **Table A6.** Summary results of *TP53* sequencing analysis from 307 samples with the distinction
 15 for the diagnosis[2,3,19,20].

Diagnosis	Samples with <i>TP53</i> mutation	Samples without <i>TP53</i> mutation	Total number of samples	% of mutated samples
glioma	25	72	97	25.8%
soft tissue sarcoma	9	85	94	9.6%
colorectal cancer	19	12	31	61,3%
prostate cancer	1	19	20	5%
leukemia (AML)	2	21	23	8.7%
invasive breast duct carcinoma	8	34	42	19.0%

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23 **Table A7.** The results of RNAfold prediction.

	Canonical structure prediction mode		G-quadruplex prediction mode	
	A1	A2	A1	A2
Minimum free energy kcal/mol	-9.60	-11.90	-23.16	-25.36
	<p>GTAAGGACAAGGTTGGGCTGGGACCTGGAGGCTGGGGGCTGGGGGCTGAGGACCTGGTCCTCTGACTGCTCTTTTCACCCATCTACAG</p> <p>.....(((.....))).....(((.....))).....(((.....))).....(((.....))).....(((.....))).....</p>	<p>GTAAGGACAAGGTTGGGCTGGGACCTGGAGGCTGGGGACCTGGAGGCTGGGGGCTGGGGGCTGAGGACCTGGTCCTCTGACTGCTCTTTTCACCCATCTA</p> <p>CAG</p> <p>.....(((.....))).....(((.....))).....(((.....))).....(((.....))).....(((.....))).....(((.....))).....</p> <p>.....</p>	<p>GTAAGGACAAGGTTGGGCTGGGACCTGGAGGCTGGGGGCTGGGGGCTGAGGACCTGGTCCTCTGACTGCTCTTTTCACCCATCTACAG</p> <p>.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....</p>	<p>GTAAGGACAAGGTTGGGCTGGGACCTGGAGGCTGGGGACCTGGAGGCTGGGGGCTGGGGGCTGAGGACCTGGTCCTCTGACTGCTCTTTTCACCCATCTA</p> <p>CAG</p> <p>.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....+++.....</p> <p>.....</p>