

Table W1. Peptides Identified By MALDI-TOF.

Peptide	Band (kDa)		Position
	47	53	
1	TYQGSYGR	TYQGSYGR	102–110
2	KPLDGEYFTLQIR	KPLDGEYFTLQIR	321–333
3	KKPLDGEYFTLQIR	KKPLDGEYFTLQIR	320–333
4	TCPVQLWVDSTPPPGTR	TCPVQLWVDSTPPPGTR	140–156
5	ERFEMFR		336–342
6	QSQHMTEVVR		165–174
7	VEYLDDRNTFR		203–213
8	CSDSDGLAPPQHLIR		182–196

Table W2. Genes Induced following Adp53^{wt} Infection.

Probe Set(s)*	Gene Symbol [†]	Induced
218559_s_at	<i>MAFB</i>	5.8 [‡]
205249_at	<i>EGR2</i>	4.7
224646_x_at, 224997_x_at	<i>H19</i>	4.5
1554340_a_at	<i>C1orf187</i>	4.0 [§]
210609_s_at	<i>TP53I3</i>	3.9
211421_s_at	<i>RET</i>	3.8
225912_at	<i>TP53INP1</i>	3.8
205569_at	<i>LAMP3</i>	3.7
232165_at, 232164_s_at, 208156_x_at	<i>EPPK1</i>	3.5
212942_s_at	<i>KIAA1199</i>	3.1
210090_at	<i>ARC</i>	3.0
201235_s_at, 201236_s_at	<i>BTG2</i>	2.9
219583_s_at	<i>PATA7</i>	2.8
226913_s_at	<i>SOX8</i>	2.8
204859_s_at, 211554_s_at	<i>APAF1</i>	2.8
215785_s_at, 220999_s_at	<i>CYFIP2</i>	2.8
231115_at	<i>GTPBP2</i>	2.6
212070_at	<i>GPR56</i>	2.6
214890_s_at	<i>DKFZP564J102</i>	2.6
213268_at, 1555370_a_at	<i>CAMTA1</i>	2.5
242517_at	<i>GPR54</i>	2.5
232289_at	<i>FLJ14167</i>	2.5
204780_s_at, 215719_x_at, 216252_x_at, 204781_s_at	<i>TNFRSF6</i>	2.4
202181_at	<i>KIAA0247</i>	2.4
212907_at, 228181_at	<i>SLC30A1</i>	2.4
222546_s_at, 218180_s_at	<i>EPS8L2</i>	2.4
227306_at	<i>FLJ21245</i>	2.4
202284_s_at	<i>CDKN1A</i>	2.4
205286_at, 205287_s_at	<i>TFAP2C</i>	2.3
206153_at	<i>CYP4F11</i>	2.3
205493_s_at, 205492_s_at	<i>DPYSL4</i>	2.3
206832_s_at	<i>SEMA3F</i>	2.3
1557701_s_at	<i>POLH</i>	2.2
201578_at	<i>PODXL</i>	2.2
213469_at	<i>PGAP1</i>	2.2
206277_at	<i>P2RY2</i>	2.2
231928_at	<i>HES2</i>	2.2
204855_at	<i>SERPINB5</i>	2.2
203865_s_at	<i>ADARB1</i>	2.2
203045_at	<i>NINJ1</i>	2.1
235205_at	<i>LOC346887</i>	2.1
224724_at	<i>SULF2</i>	2.1
221577_x_at	<i>GDF15</i>	2.1
210367_s_at	<i>PTGES</i>	2.1
238542_at, 221291_at	<i>ULBP2</i>	2.0
228315_at	N/A	2.0
218346_s_at	<i>SESN1</i>	2.0
204379_s_at, 204380_s_at	<i>FGFR3</i>	2.0
230356_at	Transcribed locus	2.0
203722_at	<i>ALDH4A1</i>	2.0
202307_s_at	<i>TAP1</i>	1.9
219099_at	<i>C12orf5</i>	1.9
224793_s_at	<i>TGFBRI</i>	1.9
219936_s_at	<i>GPR87</i>	1.9
212496_s_at, 212492_s_at	<i>JMJD2B</i>	1.9

Table W2. (continued)

Probe Set(s)*	Gene Symbol [†]	Induced
203946_s_at	<i>ARG2</i>	1.9
39248_at	<i>AQP3</i>	1.9
205278_at	<i>GAD1</i>	1.8
207813_s_at	<i>FDXR</i>	1.8
203570_at	<i>LOXL1</i>	1.8
235230_at	<i>PLCXD2</i>	1.8
209050_s_at, 209051_s_at	<i>RALGDS</i>	1.8
219597_s_at	<i>DUOX1</i>	1.8
213568_at	<i>OSR2</i>	1.8
218032_at	<i>SNIN</i>	1.8
227964_at	<i>FKSG44</i>	1.8
209712_at, 209711_at	<i>SLC35D1</i>	1.7
225160_x_at, 229711_s_at	<i>MGC5370</i>	1.7
238335_at	<i>DNAJA5</i>	1.7
235467_s_at	<i>KCNC4</i>	1.7
215411_s_at	<i>TRAF3IP2</i>	1.7
203310_at	<i>STXBP3</i>	1.7
56256_at	<i>SIDT2</i>	1.7
228115_at	N/A	1.7
201032_at	<i>BLCAP</i>	1.7
208978_at	<i>CRIP2</i>	1.7
209693_at	<i>ASTN2</i>	1.7
227247_at	<i>PLEKHA8</i>	1.7
227295_at	<i>IKIP</i>	1.7
209790_s_at	<i>CASP6</i>	1.7
213716_s_at	<i>SECTM1</i>	1.7
210138_at	<i>RGS20</i>	1.7
205483_s_at	<i>G1P2</i>	1.7
31846_at, 209885_at	<i>RHOD</i>	1.6
201412_at	<i>LRP10</i>	1.6
227522_at	<i>LOC134147</i>	1.6
219322_s_at, 236381_s_at	<i>WDR8</i>	1.6
201963_at	<i>ACSL1</i>	1.6
235434_at	N/A	1.6
223754_at	<i>MGC13057</i>	1.6
1556194_a_at	N/A	1.6
241348_at, 219239_s_at	<i>ZNF654</i>	1.6
212510_at	<i>GPD1L</i>	1.6
336_at	<i>TBXA2R</i>	1.6
202627_s_at, 202628_s_at	<i>SERPINE1</i>	1.5
55081_at, 221779_at	<i>MICAL-L1</i>	1.5
212992_at	<i>C14orf78</i>	1.5
221215_s_at, 234730_s_at	<i>RIPK4</i>	1.5
233550_s_at, 223748_at	<i>SLC4A11</i>	1.5
219358_s_at	<i>CENTA2</i>	1.5
1555609_a_at	<i>WIG1</i>	1.5
227728_at, 231370_at, 203966_s_at	<i>PPM1A</i>	1.5
209295_at, 210405_x_at, 209294_x_at	<i>TNFRSF10B</i>	1.5
204061_at	<i>PRKX</i>	1.5
232946_s_at	<i>NADSYN1</i>	1.5
212800_at, 1552618_at, 212799_at	<i>STX6</i>	1.5
227420_at	<i>MGC17791</i>	1.5
1560228_at	<i>SNAI3</i>	1.5
202023_at	<i>EFNA1</i>	1.4
201834_at, 201835_s_at	<i>PRKAB1</i>	1.4
229616_s_at	<i>LOC196996</i>	1.4
203068_at	<i>KLHL21</i>	1.4
212812_at	N/A	1.4
227221_at	N/A	1.4
225864_at	<i>NSE2</i>	1.4
202587_s_at	<i>AK1</i>	1.4
226022_at	<i>SASH1</i>	1.4
212558_at	<i>SPRY1</i>	1.4
201302_at, 201301_s_at	<i>ANXA4</i>	1.4
208258_s_at, 209729_at, 31874_at	<i>GAS2L1</i>	1.4
218007_s_at, 238935_at, 222487_s_at	<i>RPS27L</i>	1.4
211833_s_at	<i>BAX</i>	1.4
231269_at	<i>ASCC3</i>	1.4
220161_s_at	<i>EPB41L4B</i>	1.4
222451_s_at	<i>ZDHHC9</i>	1.4
226604_at, 226600_at	<i>SMILE</i>	1.4
242705_x_at	<i>LRPAP1</i>	1.4
201117_s_at	<i>CPE</i>	1.4

Table W2. (continued)

Probe Set(s)*	Gene Symbol [†]	Induced
242463_x_at	ZNF600	1.4
203695_s_at	DFNA5	1.4
205386_s_at	MDM2	1.4
203132_at	RB1	1.3
204060_s_at	PRKX, PRKY	1.3
210962_s_at	AKAP9	1.3
219938_s_at	PSTPIP2	1.3
223342_at	RRM2B	1.3
227134_at	SYTL1	1.3
205109_s_at	ARHGEF4	1.3
224690_at	C20orf108	1.3
213271_s_at	KIAA1117	1.3
221840_at	PTPRE	1.3
226782_at	SLC25A30	1.3
225049_at	BLOC1S2	1.3
224862_at	GNAQ	1.3
202071_at	SDC4	1.3
224901_at	SCD4	1.3
225734_at	FBXO22	1.3
226805_at	C20orf142	1.3
211675_s_at	MDFIC	1.3
220520_s_at	FLJ20130	1.3
204547_at	RAB40B	1.3
202409_at	LOC492304	1.3
203224_at, 203225_s_at	RFK	1.2
218168_s_at	CABC1	1.2
238480_at	C18orf17	1.2
227204_at	PARD6G	1.2
211272_s_at	DGKA	1.2
226302_at	ATP8B1	1.2
204160_s_at	ENPP4	1.2
224733_at	CKLFSF3	1.2
212099_at	RHOB	1.2
201565_s_at	ID2	1.2
228937_at	FLJ38725	1.2
221012_s_at, 223132_s_at	TRIM8	1.2
215646_s_at, 221731_x_at, 211571_s_at	CSPG2	1.2
218527_at	APTX	1.2
226483_at	FLJ32370	1.2
203115_at	FECH	1.2
202351_at	ITGAV	1.2
209075_s_at	NIFUN	1.2
222874_s_at	CLN8	1.2
222820_at	TNRC6C	1.2
225848_at	FLJ31413	1.2
209513_s_at	HSDL2	1.2
221640_s_at	LRDD	1.2
213038_at, 36564_at	IBRDC3	1.2
224618_at	N/A	1.2
244467_at	LOC440829	1.2
226580_at	BRMS1L	1.2
224461_s_at	AMID	1.2
212968_at	RFNG	1.2
202546_at	N/A	1.2
202392_s_at	PISD	1.2
209260_at	SFN	1.2
218373_at	FTS	1.2
218251_at	MID1IP1	1.2
202672_s_at	ATF3	1.2
217297_s_at	MYO9B	1.2
217889_s_at	CYBRD1	1.2
225223_at, 225219_at	SMAD5	1.1
212637_s_at, 212638_s_at	WWP1	1.1
218415_at	VPS33B	1.1
227776_at	N/A	1.1
221732_at	CANT1	1.1
226214_at	MIR16	1.1
225473_at	FLJ44670	1.1

Table W2. (continued)

Probe Set(s)*	Gene Symbol [†]	Induced
209286_at	CDC42EP3	1.1
210026_s_at	CARD10	1.1
209584_x_at	APOBEC3C	1.1
218627_at	FLJ11259	1.1
204493_at	BID	1.1
216080_s_at	FADS3	1.1
228347_at	SIX1	1.1
44040_at	FBXO41	1.1
235119_at	TAF3	1.1
209558_s_at	HIP1R	1.1
223195_s_at, 223196_s_at	SESN2	1.1
212124_at	RAI17	1.1
203216_s_at, 203215_s_at, 210480_s_at	MYO6	1.1
210260_s_at, 208296_x_at	TNFAIP8	1.1
220007_at	FLJ13984	1.1
230563_at	RASGEF1A	1.1
202794_at	INPP1	1.1
200704_at	LITAF	1.1
225334_at	C10orf32	1.1
34206_at	CENTD2	1.1
223474_at	C14orf4	1.1
228098_s_at	MYLIP	1.1
227013_at	LATS2	1.1
221843_s_at	KIAA1609	1.1
214434_at	HSPA12A	1.1
228220_at	FCHO2	1.1
36711_at	MAFF	1.1
213587_s_at	C7orf32	1.1
225604_s_at	C9orf19	1.1
203409_at	DDB2, LHX3	1.1
218066_at	SLC12A7	1.1
218764_at	PRKCH	1.1
203499_at	EPHA2	1.1
235252_at	KSR	1.1
201473_at	JUNB	1.1
214435_x_at, 224880_at	RALA	1.0
205442_at	N/A	1.0
222687_s_at	PHCA	1.0
224617_at	N/A	1.0
203537_at	PRPSAP2	1.0
203728_at	BAK1	1.0
212983_at	HRAS	1.0
225319_s_at	FLJ14775	1.0
203367_at	DUSP14	1.0
229746_x_at, 231819_at	CEBPZ	1.0
225347_at	ARL10B	1.0
218288_s_at	MDSO25	1.0
223385_at	CYP2S1	1.0
202755_s_at	GPC1	1.0
212966_at	HIC2	1.0
216041_x_at	GRN	1.0
235688_s_at	TRAF4	1.0
35160_at	LDB1	1.0
201494_at	PRCP	1.0
227357_at	TAB3	1.0
207076_s_at	ASS	1.0
202286_s_at	TACSTD2	1.0
209184_s_at	IRS2	1.0

*Probe sets used to identify features on the Affymetrix microarrays. Multiple probe sets are listed if individual genes were represented more than once on the array.

[†]Official gene symbols were determined using the Entrez Gene database (<http://www.ncbi.nlm.nih.gov/sites/entrez>).

[‡]Log₂ (fold increase in expression) resulting from infection with adenoviruses expressing the indicated variant of p53.

[§]The values highlighted in yellow were increased in response to one or more variants of p53 and details are provided in Table W3.

Table W3. Genes Induced in Response to Infection with Ad-p53^{QS1} and/or Ad-p53^{QS2}.

Gene Symbol	Variant of p53			
	WT	QS1	QS2	QS1/QS2
QS1 and QS2				
<i>C1orf187*</i>	15.5 [†]	4.6	9.2	0.6 [‡]
<i>TP53I3§</i>	14.4	4.0	2.5	1.1
<i>RET</i>	13.9	8.6	8.3	4.9
<i>TP53INP1</i>	13.9	2.6	2.9	1.3
<i>EPPK1</i>	11.4	4.1	4.8	1.6
<i>BTG2</i>	7.5	5.1	4.1	1.9
<i>GPR56</i>	6.1	3.1	2.7	1.1
<i>FAS</i>	5.3	3.4	3.2	1.9
<i>KIAA0247</i>	5.3	2.5	2.3	1.1
<i>EPS8L2</i>	5.1	3.1	2.9	1.4
<i>PODXL</i>	4.6	2.6	2.5	1.2
<i>PGAP1</i>	4.6	2.5	2.5	1.3
<i>SERPINB5</i>	4.4	2.5	2.0	1.1
<i>NINJ1</i>	4.3	2.3	2.5	1.3
<i>TAP1</i>	3.7	2.3	2.5	1.3
<i>C12orf5</i>	3.6	2.3	2.0	1.5
<i>DNAJA5</i>	3.2	3.1	3.0	2.4
<i>PTPRE</i>	2.4	2.1	2.4	1.2
QS1 not QS2				
<i>CAMTA1</i>	5.8	2.6	2.7	2.3
<i>FLJ21245</i>	5.1	3.0	2.2	1.1
<i>CDKN1A</i>	5.1	2.1	1.7	0.6
<i>ULBP2</i>	4.1	2.0	1.6	1.3
Transcribed locus	3.9	2.1	2.5	1.3
<i>TGFBR1</i>	3.6	2.0	1.8	1.5
<i>KCNC4</i>	3.2	2.7	0.9	3.5
<i>LRP10</i>	3.0	2.0	1.8	1.1
<i>BAX</i>	2.5	2.3	1.8	1.1
<i>ASCC3</i>	2.5	2.1	1.5	1.5
QS2 not QS1				
<i>LAMP3</i>	13.0	2.3	3.5	1.2
<i>SLC30A1</i>	5.2	2.5	2.3	1.2
<i>CYP4F11</i>	4.9	3.6	3.5	2.5
<i>LOC346887</i>	4.3	2.0	2.1	1.1
<i>SLC25A30</i>	2.4	1.9	2.1	2.0

Genes induced by one or both variants of p53 are grouped together.

*Official gene symbols were determined using the Entrez Gene database (<http://www.ncbi.nlm.nih.gov/sites/entrez>).

[†]Fold increase in expression following infection with adenoviruses expressing the indicated variant of p53. values are ordered by decreasing fold change in expression following Adp53^{wt} infection.

[‡]The values highlighted in yellow were not considered to be induced because they did not meet statistical criteria described in the Materials and Methods.

[§]The fold induction of the gene highlighted in green in response to Adp53^{QS1} and Adp53^{QS2} infection was reduced more than two-fold compared to the level induced in response to Adp53^{wt} infection.

Table W4. Correlation between Microarray and RT-PCR Results.

Transcript	Variant of p53									
	WT		QS1		QS2		QS1/QS2			
	M*	RT	M	RT	M	RT	M	RT	M	RT
<i>TP53IP3</i>	+++ [†]	+++	+	+	+	+	+	+	—	—
<i>MAFB</i>	+++	+++	—	—	—	—	—	—	—	—
<i>APAF1</i>	++	++	—	+	—	+	—	—	—	—
<i>CDKN1A</i>	++	++	+	+/-	—	+/-	—	—	—	—
<i>SERPINB5</i>	++	++	+	+	+	+	+	+	—	—
<i>MDM2</i>	+	+	—	—	—	—	—	—	—	—
<i>DDB2</i>	+	+	—	—	—	—	—	—	—	—
<i>TNFRSF6</i>	++	++	++	++	++	++	—	—	—	—
<i>BTG2</i>	+	+	+	+	+	+	—	—	—	—
<i>TNFRSF10B</i>	+	+	+/-	+	+/-	+	—	—	—	—
<i>BAK1</i>	+	+	—	+	—	+	—	—	—	—
<i>CASP6</i>	+	+	—	+/-	—	+/-	—	—	—	—

*M and RT denote microarray and RT-PCR expression data, respectively.

[†]The number of + symbols indicates the relative increase in transcript level, — indicates that the transcript was not increased by the variant, and +/- indicates that the transcript is marginally increased.

A

	subdomain 1	subdomain 2
Primate		
P04637 Human	MEEPQSDPSVEPPLSQETFSDLWKLLEPENNVLSPPLSQAMDDMLSPDDIEQWFTEDPGPDEAPRMPEAAPPV	
P13481 Green	MEEPQSDPSIEPPLSQETFSDLWKLLEPENNVLSPPLSQAVDDMLSPDDLAQWLTEDPGPDEAPRMSEAAPHM	
P56424 Rhesus	MEEPQSDPSIEPPLSQETFSDLWKLLEPENNVLSPPLSQAVDDMLSPDDLAQWLTEDPGPDEAPRMSEAAPPV	
	*****: *****: *****: *****: *****: *****: *****: *: *****: . **** :	
	box 1	

B

	subdomain 1	subdomain 2
Rodent		
P02340 Mouse	MTAMEESQSDISLELPLSQETFSGLWKLLEPFPEDILP-----SPHCMDLQLPQDVEEFFE---GPSEALRVSGAPAAQ	
P10361 Rat	---MEDSQSDMSIELPLSQETFSCLWKLLEPFPDDILPTTATGSPNSMEDLFQDVAEELLE---GPEEALQWS-APAAQ	
O09185 Ch. Hamster	---MEEPQSDLSIELPLSQETFSDLWKLLEPPNNVLSTLP--SSDSIEELFLSENVIGWULEDGGALQGVAAAAASTAE	
	: . ***: *: **: *****: : *.	*....: *: *: * : * . : .. : * . : *:
	box 1	

C

	subdomain 1	subdomain 2
Combined alignment		
P04637 Human	---MEEPQSDPSVEPPLSQETFSDLWKLLEPENNVLSPPL--SQAMDDMLSPDDIEQWFTEDPGPDEAPRMPEAAPPV	
P13481 Green	---MEEPQSDPSIEPPLSQETFSDLWKLLEPENNVLSPPL--SQAVDDMLSPDDLAQWLTEDPGPDEAPRMSEAAPHM	
P56424 Rhesus	---MEEPQSDPSIEPPLSQETFSDLWKLLEPENNVLSPPL--SQAVDDMLSPDDLAQWLTEDPGPDEAPRMSEAAPPV	
P02340 Mouse	MTAMEESQSDISLELPLSQETFSGLWKLLEPFPEDILP-----SPHCMDLQLPQDVEEFFE---GPSEALRVSGAPAAQ	
P10361 Rat	---MEDSQSDMSIELPLSQETFSCLWKLLEPFPDDILPTTATGSPNSMEDLFQDVAEELLE---GPEEALQWS-APAAQ	
O09185 Ch. Hamster	---MEEPQSDLSIELPLSQETFSDLWKLLEPPNNVLSTLP--SSDSIEELFLSENVIGWULEDGGALQGVAAAAASTAE	
	: . ***: *: **: *****: : *.	* : : : : : : * . : .. : * . : *..
	box 1	

** denotes sequence identity.

': denotes conservative substitutions.

' denotes semiconservative substitutions.

= marks residues mutated in the human QS variants of p53.

Figure W1. Amino acid sequence alignments of the N-terminal transactivation domains of p53 of rodent and primate origin. Sequence of the first 72 amino acids of p53 from representative primate and rodent species was performed using CLUSTAL W software (Thompson JD, Higgins DG, and Gibson TJ (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res 22, 4673–4680.) hosted on <http://scbr.bii.a-star.edu.sg> and accessed through <http://p53.bii.a-star.edu.sg>. (A) Sequence comparisons were performed for (A) human (*Homo sapiens*), African green monkey (*Chlorocebus sabaeus*) and rhesus monkey (*Macaca mulatta*) p53, (B) mouse (*Mus musculus*), rat (*Rattus norvegicus*), and Chinese hamster (*Cricetulus griseus*) p53, and (C) all six species listed in A and B. Legends for A, B, and C are inset in the lower left corner of panel C.