

Table S4. Sets of putative binding sites of p53 family members in the genome predicted using our affinity data.

Protein ^a	DNA ^b	Cut-off above K_d				bp / bs *10⁴	Overlap with Hsp53		
		cut-off 0.5	1	1.5	2		cut-off 0.5 / 0.5+e _p	cut-off 1.0 / 1.0+e _p	cut-off 1.5 / 1.5+e _p
Dmp53	Dm	28	2642	23625	132104	6.8	---	---	---
	Hs	798	31735	264452	1377649	10	13 / 55	40 / 68	51 / 68
							15 / 81^c	68 / 95^c	86 / 99^c
Drp53	Dr	25	510	5531	47856	330	---	---	---
	Hs	138	1578	15291	110938	210	68 / 100	80 / 100	96 / 100
Hsp53	Hs	172	4346	74002	695373	76	---	---	---
Mmp53	Mm	577	7716	151408	---	34	---	---	---
	Hs	123	5861	144467	---	56	55 / 100	62 / 97	73 / 99
Xlp53	Xt	108	3057	46717	342778	56	---	---	---
	Hs	431	8461	97211	631454	39	97 / 100	87 / 98	76 / 96
p73CT	Hs	60	2135	21409	143797	150	52 / 97	58 / 98	75 / 98
ΔNp73β	Hs	164	2325	18248	91998	140	36 / 90	62 / 94	80 / 99
ΔNp63α	Hs	4389	191391	1463912	9415161	1.7	98 / 100	88 / 92	82 / 97
ΔNp63β	Hs	283	5593	60451	338048	59	70 / 99	62 / 93	51 / 95
ΔNp63γ	Hs	89	2829	38336	200551	120	72 / 98	64 / 98	69 / 98

^aFull-length proteins of p53 (Dm = *Drosophila melanogaster*, Dr = *Danio rerio*, Hs = *Homo sapiens*, Mm = *Mus musculus*, Xl = *Xenopus laevis*) and naturally occurring isoforms of human p63 and p73 were used. By contrast, p73CT is not naturally occurring and comprises p73 residues 104-383.

^bPrediction for specific genomes: Dm = *Drosophila melanogaster*, Dr = *Danio rerio*, Hs = *Homo sapiens*, Mm = *Mus musculus*, Xt = *Xenopus tropicalis*.

^cOverlap with ΔNp63α