

Figure S1 Alignment of p53 functional REs with the consensus sequences of human repeats (see Table 1)

The CNNG cores in the p53 binding motifs and their ‘counterparts’ in repeats are shown in boldface and highlighted in yellow, except for the CG dinucleotides that are highlighted in magenta. Locations of the Boxes A/A’ and B in Alu repeats are shown in Figure 1. If a p53 RE is aligned with Alu repeat, its ‘div’ value is shown, which is defined as the ratio between the number of substitutions and the length of matching region.

Thirteen REs in Alu repeats

Six REs associated with Boxes A/A' (positions 10 and 150)

AIFM2 RE2 (S = 10) div = 3/24

```
AIFM2 RE2      GGGCATGGCCAGGCACGGTGGCTCATGCCT
                  ||||| ||| ||||| ||||| |||||
AluJo           GGGCGGGCGCGGTGGCTCACGCCT
```

BID (S = 0) div = 5/20

```
BID             GGGCATGATGGTGATGCCT
                  ||||| ||| ||||| |||||
AluSg            GGGCGTGTGGCGCGCCCT
```

BNIP3L (S = 5) div = 9/25

```
BNIP3L          AAGCTAGTCTCAGTGGCGCATGCCT
                  ||||| ||| ||||| |||||
AluJo/Jr         TAGCGGGCGTGGTGGCGCGCCCT
```

CASP10 RE1 (S = 0) div = 5/20

```
CASP10 RE1      GGGCATG GTGGGAATGCCT
                  ||||| ||||| ||||| |||||
AluJo/Jr         GGGCGTGTGGCGCGCCCT
```

CASP10 RE2 (S = 0) div = 2/20

```
CASP10 RE2      GGGCATG GTGGCAATGCCT
                  ||||| ||||| ||||| |||||
AluSp            GGGCGTGTGGCGCATGCCT
```

TSC2 RE1 (S = 0) div = 4/20

```
TSC2 RE1        GGGCATG GTGGCAATGCCT
                  ||||| ||||| ||||| |||||
AluSg            GGGCGTGTGGCGCGCCCT
```

Seven REs associated with Box B (position 85)

AIFM2 RE1 (S = 8) div = 0/28

AIFM2 RE1	AGA CCAG CCTGGGCAACATAG CGAG ACC
AluJo	AGA CCAG CCTGGGCAACATAG CGAG ACC

BCL2L14 (S = 0) div = 3/20

BCL2L14	AGC CAAG GCTGGT CTTG AAC
AluJr/Jo	TGC CCAG GCTGGT CTCG AAC

CASP6 (S = 4) div = 4/24

CASP6	AGG CAAG GAGTTTGAGA CAAG TCT
AluJr	AGG CCAG GAGTTCGAGA CCAG CCT

EPHA2 (S = 3) div = 2/23

EPHA2	AGA CATG CCTGGCCAA CATG GTG
AluSz	AGA CCAG CCTGGCCAA CATG GTG

GDF15 (S = 0) div = 4/20

GDF15	CAT CTTG CCCAGA CTTG TCT
FLAM_C	TAT GTTG CCCAGG CTGG TCT

HTT/HD (S = 3) div = 1/23

HTT	CGC CATG TTGGCCAGG CTGG TCT
AluSq2	CAC CATG TTGGCCAGG CTGG TCT

TSC2 RE2 (S = 13) div = 6/33

TSC2 RE2	AGG CTAG TCTGAACTCCTGGGCTGA CGTG ACC
AluJb	AGG CTGG TCTCGAACTCCTGGGCTCA AGTG ATC

Eleven REs in non-Alu repeats

CASP10 RE3 (S = 5)

CASP10 BS3	ATCCAAA CTTG CTGG-TTTAAAT CTTG GCT
MIR	AGCCAGA CTGC CTGGGTTCGAAT CCCG GCT

CCNK (S = 2)

CCNK	AAA CTAG CTTGCAGAC CATG CTG
MIRb	TAC CTAC CTCGCAG

COL18A1 (S = 0)

COL18A1	TGA CATG TGTAAG CATG TAT
(TG) _n	TG- TGTG TGTGTG TGTG TGT

CRYZ (S = 3)

CRYZ	CTG CAAG TCCATTAAA CCTG TTT
THE1B	CTG TGAG TCCATTAAA CCTC TTT

CTSD (S = 0)

CTSD	AAC CTT-G GTTTGC AAGA GGC
MER4D	TAT TTT G GTTTACA

MMP2 (S = 0)

MMP2	AGA CAAG CCTGAA CTTG TCT
LTR88b	AGA CATG CCCAGA CATG TCT

PLK2 (S = 3)

PLK2	GGT CATG ATTTCCTTAA CTTGCCT
MER34C	GGT CACC TCCCCATAA CTGGCCT

SCARA3 (S = 0)

SCARA3	GGG CAAG CCCAGA CAAG TTG
MER81	GGG CAAA CCAGGA CGAG TTG

SCN3B (S = 0)

SCN3B	TGA CTT-G CTCTGCC CTT-GCCT
THE1B	TGM CTT G CTCCTC CTT G CCT

TP53INP1 (S = 0)

TP53INP1	GAA CTTG GGGGAA CAT ----- G TTT
MER21B	GAA CTCA GGGAAACACTTTACTTACGTTT

TRIM22 (S = 0)

TRIM22	TGA CATG TCTAGG CATG TAG
LTR10D	TGG CGTG CCTGGG CATC TAA