

Figure S2 Alignment of the p53 functional REs and their flanks with the consensus sequences of Alu repeats

Alu subfamily consensus sequences assigned by CENSOR are used for alignment, which was made by NCBI Blast (bl2seq). The CNNG cores in the p53-binding motifs and their 'counterparts' in repeats are shown in boldface and underlined.

Thirteen REs in Alu repeats

Six REs associated with Boxes A/A' (plus AIFM2 RE1)

AIFM2 RE1, S = 8 (#85) & AIFM2 RE2, S = 10, AluJo (#10) Identities = 219/264 (82%)

AIFM2	236	GGG <u>CATG</u> CCAGGCACGGTGGCT <u>CATG</u> CCTACAGTCCCAGCACTTAGGGAGGCCAAGGCGGGAGGA	301
AluJo	1	GGCCGGGCGCGGTGGCT <u>CACG</u> CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGAGGA	60
		<-----RE2----->	
AIFM2	302	TCGTTTGAGCCCAGGAGTTGGAGA <u>CCAG</u> CCTGGGCAACATAG <u>CGAG</u> ACC-----	350
AluJo	61	TTGCTTGAGCCCAGGAGTTCGAGA <u>CCAG</u> CCTGGGCAACATAG <u>CGAG</u> ACCCGCTCTCTACA	120
		<-----RE1----->	
AIFM2	351	-----TACAAAAATTAGCCGGGCTTGTGGTGACACCTGTAGTCCCAGCTTCTCGGGAA	405
AluJo	121	AAAAATACAAAAATTAGCCGGGCGTGGTGGCGCGCGCCTGTAGTCCCAGCTACTCGGGAG	180
AIFM2	406	GCTGAGGTGGGAGGATTGCTTGAGCCCAGGAGTTTGAGGCTACAGTGAACCATGATCATT	465
AluJo	181	GCTGAGGCAGGAGGATCGCTTGAGCCCAGGAGTTCGAGGCTGCAGTGAGCTATGATCGCG	240
AIFM2	466	CCACTGCACTCCAGCCTAGGTGAC	489
AluJo	241	CCACTGCACTCCAGCCTGGGCGAC	264

BID, S = 0, AluSg (#148) Identities = 257/294 (87%)

BID	115	GTGGCTCAGCCTGTAATCCCAGCACTTTGAGAGGCTGAGGGGGGCGGATCGCAAGGTCA	174
AluSg	12	GTGGCTCAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCA	71

[illegible]

BID 235 TTAGCTGGG**CAT**GATGGTGC**CAT**GCCTATAGCCCCATCTGCTTGGGGGGCTGAAGCAGGAG 294
|
AluSg 132 TTAGCCGGG**CGT**GGTGCGCG**CGCG**CCTGTAAATCCCAGCTACTCGGGAGGCTGAGGCAGGAG 191

BID 295 AATCACTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCG 354
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| | ||||| |||||||

AluSg 192 AATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCA 251

BID	355	GCCTGGGTAACAGAGCGAGACTCCATCTCaaaaaaagaaaaaaaaaaaagaagaaa	408
AluSg	252	GCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	305

BNIP3L, S = 5, AluJo (#147) Identities = 178/225 (79%)

[illegible]

BNIP3L 182 GGAGTTTGAGCCCAGACTGGGCAACATGGTGAGACCCCATCTCTACAAAAGCTAAAA - - 239
 |||||
AluJo 74 GGAGTTCGAGACCAGCCTGGGCAACATAGCGAGA-CCCCGTCTCTACAAAAAATACAAAA 132

BNIP3L 240 ---AGCTAGTCTCAGTGCGGCATGCCTGTAGTCCCTGGTA--CAGGAGGCTGAGGCAGGA 294
AluJo 133 ATTAGCCGGGCGTGGTGCGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA 192

Detailed description: The diagram shows a sequence alignment between BNIP3L (top) and AluJo (bottom). The BNIP3L sequence is from position 240 to 294, and the AluJo sequence is from position 133 to 192. Both sequences are shown in all caps. Two specific regions are highlighted with boxes: 'AGCTAG' in BNIP3L and 'CCGG' in AluJo; and 'CATG' in BNIP3L and 'CGCG' in AluJo. Vertical bars connect corresponding positions in the two sequences, indicating matches or gaps. There are gaps at the beginning and end of both sequences relative to each other.

BNIP3L	295	GGATCACAGCCT - - GCCTGGAAGTCAAGGGTGCA GTGAGCTATG	337
AluJo	193	GGATC - - - GCTTGAGCCCAGGAGTT CGAGGCTGCAGT GAGCTATG	234

CASP10 RE1, S = 0, AluJo (#150) Identities = 232/278 (83%)

CASP10	107	GCCGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGTTGACGTGGGAGGATTGCTTGA	166
AluJo	9	GCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGAGGATTGCTTGA	68
CASP10	167	GCCCAGGAGCTCGAGATCAGGCTGGGCAATGAAGTGAGAGCCAGTTTCTACAAAAACATT	226
AluJo	69	GCCCAGGAGTTCGAGACCAGCCTGGGCAACATAGCGAGACCCCGTCTCTACAAAAA--A	125
CASP10	227	TTTAAAAATTTGCTGGG CATG GTGGG CATG CCTTTAGTTCCGGCTACTCTGGAGGTTGA	286
AluJo	126	TACAAAAATTAGCCGGG CGTG GTGGCG CGCG CCTGTAGTCCCAGCTACTCGGGAGGCTGA	185
CASP10	287	GGTGGGAGGATCACTTGAGCCCTGGAGGTTGAGGCTGCAGTGAAGTATGATCTTGCCACT	346
AluJo	186	GGCAGGAGGATCGCTTGAGCCAGGAGTTCGAGGCTGCAGTGAGCTATGATCGCGCCACT	245
CASP10	347	GCACTCCAGCCTGTGTGACAGAGCAAGACCCTGTCTCA	384
AluJo	246	GCACTCCAGCCTGGGCGACAGAGCGAGACCCTGTCTCA	283

CASP10 RE2, S = 0, AluSp (#150) Identities = 254/281 (90%)

CASP10	103	GGCTGGGCACGGTGGCTCACACCTGTCATCTCAGCACTTTGTGAGGCCGAGGTGGGTGAA	162
AluSp	1	GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGA	60
CASP10	163	TCACCTGAGGTCGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCCATCTCTACT	222
AluSp	61	TCACCTGAGGTCGGGAGTTTCGAGACCAGCCTGACCAACATGGAGAAACCCCGTCTCTACT	120
CASP10	223	AAAAATACAAAA - TTAGCCGGG <u>CATG</u> GTGGCA <u>CATG</u> CCTGTAATCCCAGATACTCAGGAG	281
AluSp	121	AAAAATACAAAAATTAGCCGGG <u>CGTG</u> GTGGCG <u>CATG</u> CCTGTAATCCCAGCTACTCGGGAG	180
CASP10	282	GCTGAGGCAGGAGAATCACTTGAACCCGAGAGGCAGAGGTTGCAGTGAGCCGAGATCATG	341
AluSp	181	GCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCG	240
CASP10	342	CCATTGCACTGCAGCCTGCATAACAAGAGCGAAACTCCATC	382
AluSp	241	CCATTGCACTCCAGCCTGGGCAACAAGAGCGAAACTCCGTC	281

TSC2 RE1, S = 0, AluSg (#148) Identities = 243/277 (87%)

TSC2	112	GGGTGCGGGGCTTATGCCTGTAATCCTAGGACTTTGGGAGGCCGAGGTGGGTGGATCAC	171
AluSg	5	GGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAC	64
TSC2	172	GAGGTCAGGAGTTCAAGACCACTCTGGCCAACATGGCGAAACCCGTCTGTACTAAAAG-	230
AluSg	65	GAGGTCAGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCCGTCTCTACTAAAAAT	124
TSC2	231	---ATGATGAGCCGGG <u>CATG</u> GTGGCA <u>CATG</u> CCTGTAATCCCAGCTACTTGGGAGGCTGAG	287
AluSg	125	ACAAAAATTAGCCGGG <u>CGTG</u> GTGGCG <u>CGCG</u> CCTGTAATCCCAGCTACTCGGGAGGCTGAG	184
TSC2	288	GCAGGAGAATCGCTTGAACCCGGGAGGCACAGGTTGCAGTGAGCCGAGATCGCCCCACTG	347
AluSg	185	GCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCACTG	244
TSC2	348	CACTCCAGTCTGGGTGACGGAGCAAGACTCTGTCTCa	384
AluSg	245	CACTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCA	281

Six REs associated with Box B (AIFM2 RE1 is shown above, together with AIFM2 RE2)

BCL2L14, S = 0, AluJr (#87) Identities = 260/310 (83%)

(NOTE: Alu is in the reverse orientation)

BCL2L14	39	tttttttttttctttatttttGTTTCTTAAGAGAGTGTCTCCCTCTGCCACCCAGGCTGG	98
AluJr	310	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAGACAGGGTCTCGCTCTGTCGCCCAGGCTGG	251
BCL2L14	99	AGTGCACTGGCGCGATCATAGCTCACTGCAGCCTCCAACTCCCAGGCTCAAGCGATTCTC	158
AluJr	250	AGTGCACTGGCGCGATCATAGCTCACTGCAGCCTCGAACTCCTGGGCTCAAGCGATCCTC	191
BCL2L14	159	CCCCCTCAGCCTCCCAAGTGGCTGGGACTGCAGGTGCACACCACCACGCCCAGCTAAttt	218
AluJr	190	CCGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCGGCCACCACGCCCGGCTAATTT	131
BCL2L14	219	ttttcattttttGTAGAGACGG-----AGC CAAG GCTGGT CTTG AACTCCTG	265
AluJr	130	TTAT-ATTTTTTGTAGAGACGGGGTCTCGCTATGTTGC CCAG GCTGGT CTCG AACTCCTG	72
BCL2L14	266	GGCTTAAGCGATCCTGCTCCCTGGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCAC	325
AluJr	71	GCCTCAAGCGATCCTCCGCCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCAC	12
BCL2L14	326	TGGGTCCGGC	335
AluJr	11	CGCGCCCGGC	2

CASP6, S = 4, AluJr (#80) Identities = 253/304 (83%)

CASP6	172	GGCCAGGTGTGGTGGTTCATGCTGGTAATCCCAGCACTTTGGGAAGCCAAGGTGGGAGGA	231
AluJr	1	GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGAGGA	60
CASP6	232	TCACTTAAGG <u>CAAG</u> GAGTTTGAGAC <u>CAAG</u> TCTGGGCAACAGAGTGAGACCTGGTCTCTACa	291
AluJr	61	TCGCTTGAGG <u>CCAG</u> GAGTTCGAGAC <u>CCAG</u> CCTGGGCAACATAGCGAGACCCCGTCTCTACA	120
CASP6	292	aaaaataaaaaTCAATTAGCTGGGCATGGTGGCG-----GTAGTCCCAGCTACTCTGG	344
AluJr	121	AAAAATATAAA--AATTAGCCGGGCGTGGTGGCGCGCGCCTGTAGTCCCAGCTACTCGGG	178
CASP6	345	AGGCTGAAGGGGGAGGATTGCTTGATCCCAGGAGTTCAAGGCTGCACGGAGCTGTGATCA	404
AluJr	179	AGGCTGAGGCGGGAGGATCGCTTGAGCCCAGGAGTTCGAGGCTGCAGTGAGCTATGATCG	238
CASP6	405	TGCCACTGCACTCCAGGCTGGGCAACAGAGTGAGACCTTGCTCtaaaaataaaaaataaa	464
AluJr	239	CGCCACTGCACTCCAGCCTGGGCGACAGAGCGAGACCCTGTCTCAAAAAAAAAAAAAAAAAA	298
CASP6	465	ataa	468
AluJr	299	AAAA	302

EphA2, S = 3, AluSz (#93) Identities = 246/285 (86%)

EphA2	163	GGGCAGGGTGGCTCAGGCCTGTAATTCCAGCACTTTGGGAGGCCGAGGCAGGCAGATCAT	222
AluSz	5	GGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAC	64
EphA2	223	TTGAGGTCAGGAGCTCCAGAC <u>CATGC</u> CCTGGCCAAC <u>CATGG</u> TGAAACCCCGTCTCTACTAAAA	282
AluSz	65	TTGAGGTCAGGAGTTTCAGAC <u>CCAGC</u> CCTGGCCAAC <u>CATGG</u> TGAAACCCCGTCTCTACTAAAA	124
EphA2	283	ATACaaaaaaTTAGCTGGGCGTGGTGCCACTCACCTGTAATCCCATCTACTAAGGAGGC	342
AluSz	125	ATAC--AAAAATTAGCCGGGCGTGGTGCGCGCGCCTGTAATCCCAGCTACTCGGGAGGC	182
EphA2	343	TAAGGCAGGAGAATCACTTGAACCCCAGAGGCAGAGATTGCAGTGAGCCGAGATTGCGCC	402
AluSz	183	TGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGC-	241
EphA2	403	ACTCACTGCACTCCAGCCTGGGC---CAGCAAGACTCTGTCTCa	443
AluSz	242	---CACTGCACTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCA	283

GDF15, S = 0, FLAM_C (#92) Identities = 106/127 (83%)

(NOTE: FLAM_C is in the reverse orientation)

GDF15	214	TTCtttttttttAGAGATGAGGTATTGCCAT CTTG CCCAGAC CTTG TCTCGAACTCCTGGGC	273
FLAM_C	128	TTTTTTTTTTTAGAGACGGGTCTCGCTAT GTTG CCCAGG CTGG TCTCGAACTCCTGGGC	69
GDF15	274	TCAAACAATCCACCCACCTCGGCCTCCCAAAGTGCTGAGATTACTGACATAAGCCACCAT	333
FLAM_C	68	TCAAGCGATCCTCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGC	9
GDF15	334	GCCTGGC	340
FLAM_C	8	GCCCGGC	2

HTT(HD), S = 3, AluSq2 (#93) Identities = 266/299 (88%)

(NOTE: Alu is in the reverse orientation)

HTT	43	tttattttattttattttttttGAGACAGAGTCTCACTCTTGTACCCAGGCTGGAGTGCA	102
AluSq2	304	TTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTTTCGCTCTTGTGCGCCAGGCTGGAGTGCA	245
HTT	103	ATGGCATGATCTTGGCTCACTGCAACCTCCACCTCCCAGGTTCAAGCAATTCT---GCCT	159
AluSq2	244	ATGGCGCGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCT	185
HTT	160	CAGCCTCCGGAATAGCTGGGACTACAGGCATGCACCACTACACCCGGCTAATTTTTGTAT	219
AluSq2	184	CAGCCTCCCGAGTAGCTGGGATTACAGGCGCCCGCCACCACGCCCGGCTAATTTTTGTAT	125
HTT	220	TTTTAGTAGAGACAGGGTTTCGCC <u>CATG</u> TTGGCCAGG <u>CTGG</u> TCTCGAACTCCTGACCTCTG	279
AluSq2	124	TTTTAGTAGAGACGGGGTTTCAC <u>CATG</u> TTGGCCAGG <u>CTGG</u> TCTCGAACTCCTGACCTCAG	65
HTT	280	GTGATCTGCCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCACC	338
AluSq2	64	GTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCC	6

TSC2 RE2, S = 13, AluJb (#75) Identities = 234/282 (82%)

(NOTE: Alu is in the reverse orientation)

TSC2	44	GAGACAAGGTCTCACTCTGTCACCCAGGCCGGGGTGCAGTGTACAATCATGGCTCACTA	103
AluJb	282	GAGACAGGGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCACGGCTCACTG	223
TSC2	104	CAGCCTCAACCTGCCAGGCTCACGTGATCCTCCTACTTTAGCCTCTCAAGTAGCTGGGAC	163
AluJb	222	CAGCCTCGACCTCCCGGGCTCAAGCGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAC	163
TSC2	164	TACAGGCATGCAGCACCCACGCCTGGCTAAGTTTTGTATTTTTTGTCTGTGACAGGGTCTCA	223
AluJb	162	TACAGGCGCGCGCCACCACGCCCGGCTAATTTTTGTATTTTTTGTAGAGACGGGGTTTCA	103
TSC2	224	CTGTGTTGCCCAGGCTAGTCTGAAACTCCTGGGCTGACGTGACCCTCTCCCCTCTGCCAC	283
AluJb	102	CCATGTTGCCCAGGCTGGTCTCGAACTCCTGGGCTCAAGTGATCCTCCCGCCTCGGCCTC	43
TSC2	284	CCGAAGTGCTGAGATTACAGGTGTGAGCCACCGCACTTGGCC	325
AluJb	42	CCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCC	1