

Table S1. Primer sequences for cloning C-terminal TRP32 constructs.

Construct (amino acids)	Forward (5'→3')	Reverse (5'→3')
C1 (138-162)	aaaagtcgacGGACAAGACCATGTTAGTTTAT	aaaagaattcAGACAAATAATTCATTGTACTAAAA
C2 (158-182)	aaaagtcgacATGAATTATTTGTCTGGTTAT	aaaagaattcATCAAATAATAATAAGGATTATAAC
C3 (178-198)	aaaagtcgacTATTATTATTTGATTATGTTACTC	aaaagaattcCTACTCTAAACTACTTTCACTA
C4 (158-177)	aaaagtcgacATGAATTATTTGTCTGGTTAT	aaaagaattcAGGATTATAACAACAATAATGATG
C5 (181-198)	aaaagtcgacTTGATTATGTTACTCCAGATTAT	aaaagaattcCTACTCTAAACTACTTTCACTA

Non-annealing sequences are shown in lowercase and contain restriction sites for Sall (gtcgac) and EcoRI (gaattc).

Table S2. Probe sequences used for EMSA.

Probe Name	Sequence (5'→3')
MEME Motif 1	CAGCACTTTGGGAGGCTGAGGCAGG
MEME Motif 2	GGGGTTTCACCATGTTGGCCAGGCTGGTC
MEME Motif3 (WT)	GCCGGGCGTGTTGGCGGGCACCTGTAATC
Mutant1 (Δ1)	AAAAAAAAAAGTGGCGGGCACCTGTAATC
Mutant 2(Δ2)	GCCGGGCGTAAAAAAAAAACCTGTAATC
Mutant 3(Δ3)	GCCGGGCGTGTTGGCGGGCAAAAAAAAAA

Table S3. QPCR primer sequences for TRP32 targets.

Gene	Name	Forward	Reverse	T <sub>m</sub>	Product Size
NM_001037171.1	ACOT9	CCCTCAGGAGCGGAACATTT	GGGCCACTCATGGAGTTGAA	60	384
NM_001101.3	ACTB	GATGATGATATCGCCGCGCTC	TCGTCGCCACATAGGAATC	61	167
NM_001272071	AP1S2	TGCAGCTTCCTTGAGTGCGA	ACGTGGGGTTTCAGCTTCTTTCG	64	318
NM_181720	ARHGAP30	GGGCACAGGTCTTGGGGGAT	GGTCTGGCTTCCGCTCTGAC	63.5	287
NM_001199456.1	BRD2	GCTCGTGGAGGGGAATACAG	TTTGGGATTGGACACCTCCG	60	201
NM_001300944	C11orf30	TTGGGTGAAAGACCAAGTTACAGT	CATTGGAGGCAGGACTGGCA	61.4	313
NM_001301837	C12orf57	ACGAGGCTCGGGATAACGCC	GCACAAGGGAGGGCCAACCTC	64	205
NM_001256373	C12orf79	GCTTTTGCCTTTTCATCACCTGC	TTGCCAGCCTCCTTCTGACAC	61.3	343

NM_001105530	CAP1	GGAGAGCGGCTGATCGCAGT	ACAGGACCAGCAAGCAGCGA	64.6	200
NM_007276	CBX3	GCTGAAAGTGGTCCCAAAGGGGTA	CGACAAATTCTTCAGGCTCTGCCTC	64.3	361
NM_001300964	CDK19	CCTCGCCTCCCAGTCACTG	AGATCTTGGAAGTGCATGGGC	64	289
NM_138363.1	CEP95	GGCTCGGATGCTGAGTGGGT	CTGCAAGTAGTCCAAGGCCAGTG	64	228
NM_182523	CMC1	ACCCCGCAGACCAGCATCTC	TGCTTGTGGAAGCTTCTGTAGCC	64	306
NM_001297733	COX18	ATCCTGGCCAAGCTAGGTGGAAAAT	GTCGGGTGCAGTGAGGTCAGG	64.6	349
NM_001012967	DDX60L	AGGCAAAGGTGTTGTCAGTGC	TCCGGGAGTTCGGCAAGGAT	62.5	400
NM_017925	DENND4c	TTGCCCCAGGAAGAAGCCGT	TGGAGAGCTGATGGAGTGGCTT	63.8	286
NM_019030	DHX29	CCCCCTCCAGGAGTCAGGAAG	AAGCCATCTCTGACCCGCC	63.9	212
NM_024963	FBXL18	GCCAACGCCAGTTCTTCCAG	ACCACCACAGGTTCCGGCGG	64.6	352
NM_031904	FRMD8	GTGCCCTGGCTGTGGAGAAC	CACGTCATCGTCTGGGGCACT	65.1	225
NM_017769	G2E3	GGACCAGAAAATACCCAGCCAA	AGGGTGTGTGGACTCTCTGAA	60.5	235
NM_138801.2	GALM	GGCTTCGCCGAGTTGGAAGG	CGCCATTTGACAGCACCCGA	64	208
NM_001256488	GOLGB1	TCCGTCCCAACTGCTAGTGGC	AGCCAGGCGCTCCTGAACAT	64.4	327
NM_021639	GPBP1L1	CGCTGCCCGTTGGTGTCTCA	CACGAACAGCAGCTTTCAAGGCA	64.9	399
NM_005684	GPR52	AGCGTCACTCCTGCCCACTT	ACTCGTGGACACCTGTGGAGT	63.4	264
NM_021958	HLX	CCCCCTCCAGCAAAGACCTCA	GCGCGACCATGAACGCTTCC	64.4	338
NM_001130689	HMGB2	CTTGGCACGATATGCAGCAA	CAGCCAAAGATAAACAACCATATGA		
NM_194247	HNRNPA3	TTGGAAGAGGCGAGTCCGGT	ACACGCCATCAACCTTGTGT	63.1	337
NM_022465	IKZF4	ATGACGGCGGTTCCCCTCACTT	AAGAGTGCTGGCTGTTGGGGG	65.6	354
NM_001267728	ING1	ACGATTGGTCGCTGAGGCGG	CGCGTTCTCACGGTTCTCGT	64.2	397
NM_001297655	KIF2C	CCTTGCTGACTCTCCGAATGGC	CCTGAGCCGTGATGCGAAGC	63.8	393
NM_182931	KMT2E	GGGGTTCGGGTGTCTCGTGT	GCTCATGACGTTGCCTCTGG	63.9	227
NM_014708	KNTC1	CGCAGACCATCGAATCCTGCT	CCCGATCGCCGGTACTGGAT	63.4	229
NM_002298	LCP1	TGATTTTTGGTGGGGCGGGGA	GGCAAAGGCAAGCAAGCAGCC	65.2	371
NM_001282460	LRRC63	GTGCCAAGCCCTCCACCTATGA	GGCCAGGTTGGTCATGGCTGTT	64.9	348
NM_005911	MAT2A	GCCCGCTGCTTCGTTCCG	TCCTGCTGAAGGTGGGCATCAA	63	278
NM_001130079	MOV10	G TTCAGAGGGCCCCAAGCGGTA	CGAGTCTGAAGAACCTGACCCGA	65.2	369
NM_014046	MRPS18B	CGCCACACGGGTATCATCT	TCCGCTGGTGTCTAGGGGG	62.7	351
NM_001099286	MTFR2	TTCCTAACGCCCTCCGCTTGA	CAGAGTTCAAGAGCGGGATCAACT	63.2	303
NM_001123226.1	MTO1	AGTGATTCAGCCAGGCTACG	CACTGGTGCCAGAGTAGTG	60	386
NM_002475	MYL6B	GGCCAAGAACCAGGCCAAG	TGGCTGGAACGTGCTTTCGC	64	287
NM_001144030	NAT10	GGTCCCTTCTCGCTCGCCATC	GCAGCACACACATGCCGAAGG	65	393

NM_173638.4	NBPF15	TGGGTCTCAATTTTTACTGTGCCT	ACCCACCAAAACCAATCAGCA	61	207
NM_004289	NFE2L3	CGGATGTGCGAGCGAGGAGA	CTCCCAATGAGATGCCCTCCAGT	64.2	296
NM_207308	NUP210L	CTTGCGTCTACACCGCCTCC	TGAGGCGTATCGGTTGCGTAGA	63.5	260
NM_016081	PALLD	GCTGAGAGGGAAACGAACGG	AGACTTTGTATTCTGATTAGCTGT	59.5	397
NM_017851	PARP16	TCGCCCTTGCCCTAACCCAG	AATCCAGCTCACCAGGTCCCA	63.8	320
NM_001048183	PHACTR4	CTCCCTTTTTCCCCCTCCCCG	TCTGTAGTGGGCTGGTCTGCT	63.7	200
NM_017934	PHIP	GCTGGTGTAGCCAGTAGGCA	GCCATCACTGTGCCATGCTCT	62.6	342
NM_178136.2	POLDIP3	GGGGTAGCGGAGGTGGTGTT	TCAGGGTCCACTTCGGCAGG	64	245
NM_007215	POLG2	TGGGGACCTAGACCGAGGCA	ACCAGGCCACACAGAAATCCCA	64.3	232
NM_020366	RPGRIP1	CCCTTGAGCAGGATGAACCG	GGCCCCCTCTTGGGTTTCTC	61.6	386
NM_001253382	RPL15	AGATAGGTCTCCCTCCTGTGCGGC	ACAGTGGCGTCCAGCTCGCTC	67.4	373
NM_000986	RPL24	CGTGGAGCTGTGCGCCATGAA	TTTACTGCTCGGCGGGTTC	63.2	246
NM_001030009	RPS15A	CTTCCGCGCCGCCACAAT	ACTGGCGGGATGGAAGCAGA	64.1	312
NM_001025	RPS23	TTGTGGCTCCTTCTGCGGT	TGCGACCAAATCCAGCAACCAG	64.1	379
NM_025158	RUFY1	TGAGATCGTGGACCGAAGCCAG	AGCCGACTGGAGCAACACCTT	64.3	286
NM_012240.2	SIRT4	AGTGTCCGTAGAGCTGTGAGAGAA	AGTGTGCAGGGTTAGGCTGGT	63	399
NM_020846	SLAIN2	CCATCCTCAACCCCAGTGCGA	GAACCAGAACTGCGCCGAGA	63.6	269
NM_003049	SLC10A1	ATGCCCTCACGGCCTTTGT	AGCGCATGTATTGTGGCCGTT	64.1	343
NM_001145250	SP9	ATCCGCCAGCGCCATA	TCAATGTGCTTCTGGGAATCC		
NM_003971	SPAG9	TCAGCCGACTTTTCAGCTCCT	TCCAGCCAAAAGCCTGCACT	62	279
NM_172209	TAPBP	TCTGCTCCTCGCTGTGGCTT	GGGACCCGGAGCCAGAGATG	64.1	322
NM_001205201	TEX28	AGCCCCGTGTGATTGTTGAGGA	AGGGACCGCATGAAGGCAC	64.6	234
NM_144632	TMEM182	ATGCTCCTGGGGTAGTTGCT	GAAGGGGTGAAATCCAGGCAGT	62.9	224
NM_018247	TMEM30A	GCGAAGACTCGGAGACCGGA	AGGGACTGGAAGGCTCTGTTCC	63.7	205
NM_021109.3	TMSB4X	GTGCGCCTCGCTTCGCTTTT	CGCGGCCTTCGTTGTCAGTAG	64	329
NM_000550	TYRP1	AGGATGTGCTCAGTGCTTGGA	TCTGTGTTGGTGACTGGGGGC	64.3	361
NM_001039590	USP9X	AGTCAAACCTCAGCGAAGTCCCA	GCCTGAGGAGCACATAGCCAC	63.5	269
NM_007146	VEZF1	AAAGACCCTTCAAATGCCAAACGTG	AGGTTTGGCACAGGTTAGCAGC	63.6	390
NM_022553	VPS52	AAGGTTCCGGGGCTAGTTTGT	CCCCAAGTTGCAGTGGTTCCTG	62.8	345
NM_032786	ZC3H10	GGGTAGGCGGCTCTTTGTCTG	AACGCTTGCTCGCTTGAC	64	351