

Table S1**List of primer combinations for TRα1 constructs with respective inserts cloned**

Primers^{a,b}	Insert/s	RE Sites^c	Source Vector^d
Pr-1, 2	A/B domain	Kpn I, Xba I	EG3
Pr-3, 4	DBD (1 amino acid less)	" "	"
Pr-5, 6	Hinge domain	" "	"
Pr-7, 8	LBD	" "	"
Pr-1, 4	A/B-DBD	" "	"
Pr-33, 34	DBD-Hinge	Hind III, Kpn I	"
Pr-37, 35	Hinge-LBD	" "	"
Pr-36, 34	A/B-DBD-Hinge	" "	"
Pr-33, 35	DBD-Hinge-LBD	" "	"
Pr-36, 46	A/B-LBD	" "	EG3-LBD
Pr-47, 48	A/B-Hinge-LBD	Xho I, Hind III	EG3-Hinge-LBD
Pr-37, 49	Hinge-LBDΔ408-410	Hind III, Kpn I	EG3
Pr-37, 50	Hinge-LBDΔ393-410	" "	"
Pr-37, 51	Hinge-LBDΔ268-410	" "	"
Pr-37, 52	Hinge-LBDΔ206-410	" "	"
Pr-57, 58	NESH12 -Hinge	Xho I, Hind III	EG3-Hinge
Pr-67, 68	NLS1	" "	EG3
Pr-77, 78	NESH12-F401A-Hinge	" "	EG3-Hinge
Pr-79, 80	NESH12-F397A,F401A-Hinge	" "	"
Pr-85, 86	NESH12-P398G-Hinge	" "	"
Pr-87, 88	NESH3H6-Hinge	" "	"
Pr 91, 92	NESH3-Hinge	" "	"
Pr-93, 94	NESH6-Hinge	" "	"
Pr-147,148	NESH12-NESH3-Hinge	Hind II Kpn I	EG3 NESH12-Hinge
Pr-149,150	NESH12-NESH6-Hinge	" "	"
Pr-153,154	NESH12-NESH12F401A-Hinge	" "	"
Pr-155,156	NESH12-NESH12P453T-Hinge	" "	"
Pr-95, 96	NESH12L400S-Hinge	" "	"
Pr-99, 100	NESH12L4A-Hinge	" "	"
Pr-101, 102	NESH12L400P-Hinge	" "	"
Pr-103, 104	NESH12P399T-Hinge	" "	"
Pr-107, 108	NESH12F401G-Hinge	" "	"
Pr-109, 110	NESH12F401P-Hinge	" "	"
Pr-111, 112	NESH12F401N-Hinge	" "	"
Pr-114, 115	NESH12F401P,F405P-Hinge	" "	"
Pr-116, 117	NESH12F401P,F405N-Hinge	" "	"
Pr-133, 134	2(NESH12)-Hinge	Hind III, Kpn I	EG3-NESH12-Hinge
Pr-135, 136	NESH12-WT+F401P-Hinge	" "	"
Pr-137, 138	NESH12-WT+F401P,F405N-Hinge	" "	"
Pr-135, 136	NESH12-F401P+F401P-Hinge	" "	EG3-NESH12-F401P-Hinge
Pr-137, 138	NESH12-F401P+ F401P,F405N -Hinge	" "	"
Pr-139, 140	hTRb1-A/BD	Kpn I, Xba I	EG3
Pr-141, 142	hTRb1-DBD	" "	"
NLS-2 Oligopeptide Mutations			
Pr-31, 32	NLS2-WT	Hind III, Kpn I	EG3
Pr-38, 39	NLS2-K29A	" "	"
Pr-40, 41	NLS2-P22L	" "	"
Pr-42, 43	NLS2-P22L-R26H	" "	"
Pr-44, 45	NLS2-5K/R	" "	"
Pr-167, 168	NLS2*-P22A	" "	"
Pr-169, 170	NLS2*-P22AG24A	" "	"
Pr-171, 172	NLS2* P22AD23A	" "	"
A/B Domain Mutagenesis Primers and Respective Mutations			
Pr-11, 12	R26H	None	EG3-A/B Domain

Pr-13, 14	K27A,R28A	“	“
Pr-15, 16	P22A	“	“
Pr-17, 18	K25A	“	“
Pr-23, 24	K25A, R26A	“	“
Pr-25, 26	R28A	“	“
Pr-163, 164	K29A	“	“
Pr-165, 166	P22—G24A	“	“
Pr-159, 160	vErbA A/B domain	Kpn I, Xba I	EG3
Pr-161, 162	cTRa1 A/B domain	“	“

TR α 1 and TR β 1 whole protein mutations

Pr-11, 12	TR α 1 R26H	None	GFP-TR α 1
Pr-174, 175	TR α 1 F401A	None	“
Pr-182, 183	TR β 1 F401A	“	GFP-TR β 1

^aSequence of individual primers or oligonucleotides mentioned in this table are presented in Table S2.

^bThe first primer in a pair is the forward primer and the second is the reverse primer.

^cRE sites, restriction endonuclease sites.

^dEG3, EGFPc1 based GFP-GST-GFP vector.

Table S2

List of sequences of primers used in the current study

Primer Name	Sequence
Pr-1	gggtaccatggaacagaagccaagca
Pr-2	gctctagactgctcgtctttgtccaggt
Pr-3	gggtacctgtgctgtgtgtggggac
Pr-4	gctctagatagaaccaggccatggcc
Pr-5	gggtaccgattcaaagcgggtggc
Pr-6	gctctagatcgctctgtttccaatg
Pr-7	gggtaccaaattcctgccgatgac
Pr-8	gctctagagactcctgatcctcaaacct
Pr-11	aggtcaccagatgaaagcataaaaggaagaacggccaat
Pr-12	attggccgttcttctttatgctttccatctggtgacct
Pr-13	ggtcaccagatgaaagcagcagcgaagaacggccaatgtcccc
Pr-14	ggggacattggccgttcttcgctgctcgtttccatctggtgacc
Pr-15	gaacagtgccaggcagcagatggaaagcga
Pr-16	tttcgctttccatctgctgacctggcactgttc
Pr-17	cagtgccaggtcaccagatggagcgcgaaaaggaagaa
Pr-18	ttcttcttttgcgctccatctggtgacctggcactg
Pr-23	gtgccaggtcaccagatggagcggcaaaaaggaagaacggccaat
Pr-24	attggccgttcttcttttgcgctccatctggtgacctggcac
Pr-25	accagatgaaagcgaagcgaagaacggccaatgtcc
Pr-26	ggacattggccgttcttcgcttttcgctttccatctggt
Pr-31	cccaagcttcgccagatggaaagcgaaaaaggaaggtacccc
Pr-32	gggtacccttcttttgcctttccatctggcgaagctggg
Pr-33	cccaagctcgtgtcgtgtgtgtggggac
Pr-34	gggtacctcgcctctgtttccaatgg
Pr-35	gggtaccgactcctgatcctcaaagacct
Pr-36	cccaagcttcgatggaacagaagccaagcaag
Pr-37	cccaagcttcgattcaaagcgggtggcc
Pr-38	cccaagcttcgccagatggaaagcgaaaaagggcgggtacccc
Pr-39	gggtaccgccttttgcctttccatctggcgaagctggg
Pr-40	cccaagcttcgctagatggaaagcgaaaaaggaaggtacccc
Pr-41	gggtacccttcttttgcctttccatctagcgaagctggg
Pr-42	cccaagcttcgctagatggaaagcacaagaaggaaggtaccc
Pr-43	gggtacccttcttttgcctttccatctagcgaagctggg
Pr-44	cccaagcttcgagcgaagcgaaaaaggaagggcgggtacccc
Pr-45	gggtaccgccttcttttgccttcgctgccaagctggg
Pr-46	gggtaccctgctcgtctttgtccaggt
Pr-47	ccgctcagctatggaacagaagccaagcaag
Pr-48	cccaagcttgctcgtctttgtccaggt
Pr-49	gggtaccatcctcaaagacctccaggaa
Pr-50	gggtaccgcactcgaacttcatgtgga
Pr-51	gggtaccgcatagcggacagctgcc

Pr-52 ggggtaccggcatggagacaataggtg
Pr-57 ccgctcgagctgtcgagtgccccaccgaactctccccactctctctggaggtctttgaggatcaagcttccc
Pr-58 gggaagctgatcctcaaagacctccaggaagagtggggggaagagttcgggtgggcactcgacagctcgagcgg
Pr-67 ccgctcgagctaagcgggtggccaaacgcaagctgattgagcagaaccgggagaggagcgaagcaagcttccc
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Pr-141 ggggtacctgtgtagtgtgtggtgacaaag
Pr-142 *gctctagaatccagcaccatctgttc*
Pr-147 cccaagcttcggtagaccttagaggcctcagcgagtttaccagatcatcaccocggccatcaccocggtggactttgccccaaaaa
ctgccatgggtacccc

Pr-148 ggggtaccatgggcagtttttggcaaagtcaccacgcgggtgatgocgggggatgatcttgtaaactcgctgaaggcctctag
Gtctaccgaagctggg

Pr-149 Cccaagcttcgcccatttctccagctgccttgaagaccagatcatcctcctgaagggctgctgcatggagatcatgtccctgagg
gcagctgtcggtagcccc

Pr-150 ggggtaccgacagctgcccgcaggacatgatctccatgcagcagccctcaggaggatgatctggtcttcaagaaggcagctcggagaa
catgggcgaagcttggg

Pr-153 cccaagcttcggtcgagtgccccaccgaactctccccactcgctctggaggctttgaggatggtacccc

Pr-154 ggggtaccatcctcaagacctccagagcgagtggggggaagagttcggtggggcactcgaccgaagcttggg

Pr-155 cccaagcttcggtcgagtgccccaccgaactctccccacactctcctggaggctttgaggatggtacccc

Pr-156 ggggtaccatcctcaagacctccaggaagagtggggaagagttcggtggggcactcgaccgaagcttggg

Pr-159 ggggtaccgagccagaggacactcgg

Pr-160 gctctagactgttcatctttgtccaggca

Pr-161 ggggtaccatggaacagaagcccagcac

Pr-162 gctctagactgttcatctttgtccaggta

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Pr-168 ggggtaccgcctccttttcgctttccatctgccgaagcttggg

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Pr-171 cccaagcttcggcagctggaaagcgaaaaaggaaggcgggtacccc

Pr-172 ggggtaccgcctccttttcgctttccagctgccgaagcttggg

Pr-174 cgaactctccccactcGCcctggaggtctttgaggatcag

Pr-175 ctgatcctcaagacctccagggcgagtggggggaagagttcg

Pr-182 cagaactctcccccttggccttgaaggttcgaggattag

Pr-183 ctaatcctcgaacactccaaggccaaggggggaagagttctg