Table S1. Primers used to detect transposon excision frequencies for two transposable elements from three loci in both *Caenorhabditis elegans* and *C. briggsae*

Species	Transposon	Locus	Type	Sequence
C.elegans	*CemaT1*	F26H9	Flanking	GGGAAAGTCAATTTATTTTATTGCAACTAG
		F26H9	Excised	CGGAGCCTGGAGAAGTTTATAGAA
		F26H9	Non-Excised	CCATAATTTTGACTCACCCTGTAGAA
	CemaT1	W04G5	Flanking	GTTTGTCACTTTGTTATTCTGTTTTACGA
		W04G5	Excised	CACCGGTTGTTTTTAAGATTATATACACA
		W04G5	Non-Excised	CTTACCATAATTTTGACTCACCCTGTATAC
	CemaT1	Y51A2D	Flanking	GGTTACTGTAGGCTGGTGTTTGC
		Y51A2D	Excised	CTGTGTTTTAGTGTATAATTTTCCGTCAA
		Y51A2D	Non-Excised	TTACCATAATTTTGACTCACCCTGTAAT
	Tc1	T22F3	Flanking	ATGACTACTGTAGCGCTTGTATCGA
		T22F3	Excised	GATTATCAAAAATGGACAGCTATGTATATTCC
		T22F3	Non-Excised	ATCTTTTTGGCCAGCACTGTATATT
	Tc1	Y94A7B	Flanking	TCCAAAAACATCACTTATGTACATGCAA
		Y94A7B	Excised	GGAATGGCTAAACGTGAATATGG
		Y94A7B	Non-Excised	GCCAGCACTGTACATGCAACA
	Tc1	ZK1251	Flanking	CATCTCTAATTGTGCAGGTATGTATGC
		ZK1251	Excised	GCGTCTATTCTTATATTTTACTCTAATCAGTTG
		ZK1251	Non-Excised	TGGCCAGCACTGTATGCAAA
C.briggsae	*CbmaT1*[φ]	CBRG21D19	Flanking	AAACTGATGTGTCAAAGTGGCCT
		CBRG21D19	Excised	GCCATCAATGTTCATGATCTATGTATT
		CBRG21D19	Non-Excised	TAATTTTGGCGGACCCTGTATT
	CbmaT1[φ]	CB015K23	Flanking	CCATGTTTTGGGTCATTTTTCA
		CB015K23	Excised	GCTCTCGCTATCTCGCTACTACATAG
		CB015K23	Non-Excised	TTTTGGCGGACCCTGTAGAT
	CbmaT1[φ]	CB046A04	Flanking	CGTGGTCGTTTAAGAAAGTACGC
		CB046A04	Excised	AATGGCCTATAGAACGTCCTTTATGT
		CB046A04	Non-Excised	TTGGCGGACCCTGTAAGC
	Tcb1	C009001188.Contig2	Flanking	CCTCTAGAAGTCCGTTTGACACATATC
		C009001188.Contig2	Excised	CCGCATCGCACACATATATGA
		C009001188.Contig2	Non-Excised	CATTCTTTATGGCCAGTACTGTATGA
	Tcb1	C007801047.Contig1	Flanking	CTTGACTTAACATTTGTAAGACCGAAATT
		C007801047.Contig1	Excised	CAACGCGCATTGAACTTATAGATT
		C007801047.Contig1	Non-Excised	GCATTCTTTATGGCCAGTACTGTAGAT
	Tcb1	C012001013.Contig3	Flanking	AACAGTTGACAAATTTTCAGTATCACAAG
		C012001013.Contig3	Excised	TTGGATATACCGTTTTTGAGATATACC
		C012001013.Contig3	Non-Excised	GCATTCTTTATGGCCAGTACTGTACCT

[φ]For *CbmaT1* loci CBRG21D19, CB015K23, and CB046A04, previously referred to as G2D19, CB015K23, and c004200728.Contig1, respectively (Brownlie et al. 2005). Nomenclature for *Tcb1* follows that described by Brownlie et al. 2005.

Table S2. Primers used to detect transposon insertion within the *unc*-22 gene in *Caenorhabditis elegans* and *C. briggsae*

Species	Name	Forward	Reverse
C. elegans	Ce-unc22-1	F1: ATGGGTCAAGACTTTGATTCGGA	R1: CAAGTACAGTAAGCTGAGCATGAGTT
	Ce-unc22-2	F2: AACCGCCGATGAAGTACAGTTTCCT	R2: TGAATTTTGGCTTAGCCAATT
	Ce-unc22-3	F3: TCCCGGCATGGTTGAAACACGAC	R3: CTTCCGTATTTGGTTCTCTTCTCAAT
	Ce-unc22-4	F4: ATGGGAACCAGCCATCACTGTTCCTGGCG	R4: ATTGGTAAGTCTGACCTGGTTTCAA
	Ce-unc22-5	F5: TCCGTGTCAAGGCTTTGAACAAGGCT	R5: AGCAGAGTTTTTGGTAATCTTTCCAA
	Ce-unc22-6	F6: GAGCTTACCTGGAATAGACCATTGAG	R6:CGCCATCCAGGTAATTGTACAATGGTTGCGG
	Ce-unc22-7	F7:AACCTGAATTCACAGTTGACAAACTCAGG	R7:TGTTCATCAACATCATATCCTCGCCTG
	Ce-unc22-8	F8: AGGAAAGATTGTACGTGGAAAAGGAACC	R8: TCCCTTATCATCTCCCTTTACTCGGTT
	Ce-unc22-9	F9:GAATACACAGTCCGTGCAAAGAA	R9: TTAGACAAGGAGAAGAGCTGCCGCA
C. briggsae	Cb-unc22-1	F1:ATGAACTACACGCCTGGATCGTA	R1:AGCAGAATCGGTTCCGTGTGCAT
	Cb-unc22-2	F2:GATGTGAAGCTGTTGGTCACATCTG	R2:ACAGCAATCTGGTTTGGTCTGG
	Cb-unc22-3	F3: GAATTGACAGACACGAAGGTTG	R3: TACTGGAACATCGAATTCCACAT
	Cb-unc22-4	F4: CGTGGAGAACCACCACCGAAGAAG	R4: GTTGGCTGTATCGTATTTTTCAATG
	Cb-unc22-5	F5: GGAAGATGGGTTCCAGCTGCTAAGG	R5: CTTGACGCGGAATTTGTATTCGT
	Cb-unc22-6	F6: GCAGTCAACCGTCAAGGAACATCTG	R6: CTTGATCCATCTTCCAGTCTTTGC
	Cb-unc22-7	F7: GTCAACACTTCACCAGTTCAAGG	F7: TGTGAGTCCAGTGACACGGTGTT
	Cb-unc22-8	F8: CCAAAGAAGACCTACGAGTTCAG	R8: AACAACATAGCTGGTGATCTTCGA
	Cb-unc22-9	F9: GAGAAAAGAGACTTATCAAAGG	R9: CGGCGAGAGTCCGGATAGAAGA
	Cb-unc22-10	F10: TTTGGAGGAGAGAACGATGATGAC	R10: TCATGCCTTAATGTCAAGCTTGAA

Table S3. Effect sizes and standard errors for variables affecting TE excision frequency in *C. elegans.*

	Excision Frequency (Log Units)	
	CemaT1	*Tc1*
Intercept	-5.04*** (0.09)	-5.05*** (0.07)
Hsp90-RNAi	0.68*** (0.12)	0.08 (0.08)
H202-Low	0.59*** (0.12)	0.83*** (0.08)
H2O2-High	1.42*** (0.12)	1.26*** (0.08)
Heat-Low	0.04 (0.12)	0.04 (0.08)
Heat-Serial	0.88*** (0.12)	0.91*** (0.08)
Heat-High	1.99*** (0.11)	1.85*** (0.08)
Locus-W04G5	0.96*** (0.06)	
Locus-Y51A2D	1.13*** (0.06)	
Locus-Y94A7		1.38*** (0.04)
Locus-K1251		1.42*** (0.04)
Strain-AB2		-0.23*** (0.03)
Hsp90-RNAi x H202-Low	0.71*** (0.17)	-0.08 (0.12)
Hsp90-RNAi x H202-High	0.67*** (0.17)	0.37*** (0.12)
Hsp90-RNAi x Heat-Low	0.01 (0.17)	-0.03 (0.12)
Hsp90-RNAi x Heat-Serial	2.03*** (0.17)	0.19 (0.12)
Hsp90-RNAi x Heat-High	1.05*** (0.16)	0.24** (0.12)
Observations	372	360
R^2	0.89	0.91
F Statistic	229.55*** (df = 13; 358)	247.01*** (df = 14; 345)

Estimated effects (and standard errors) are in log units relative to No Stress controls, in the absence of Hsp90-RNAi treatment, in the N2 strain, for F26H9 (*CemaT1*) or K1251 (*Tc1*) loci. Asterisks represent *P*-values, with $P < 0.1$ (*), $P < 0.05$ (**), and $P < 0.01$ (***). Only variables that were significant were included in each final model.

Table S4. Effect sizes and standard errors for variables affecting TE excision frequency in *C. briggsae.*

	Excision Frequency (Log Units)	
	CbmaT1	*Tcb1*
Intercept	-2.75*** (0.08)	-1.31*** (0.09)
Hsp90-RNAi	0.10 (0.09)	0.09 (0.11)
H202-Low	0.49*** (0.09)	0.55*** (0.11)
H2O2-High	1.27*** (0.09)	1.11*** (0.11)
Heat-Low	-0.09 (0.09)	-0.08 (0.11)
Heat-Serial	0.99*** (0.09)	0.56*** (0.11)
Heat-High	1.72*** (0.09)	1.17*** (0.11)
Locus-CB015K23	0.16** (0.07)	
Locus-CB046A04	-1.55*** (0.07)	
Locus-C007801047		-0.81*** (0.08)
Locus-C012001013		-2.29*** (0.08)
Strain-DH1300	0.94*** (0.07)	0.06 (0.08)
Hsp90-RNAi x H202-Low	0.24* (0.13)	-0.02 (0.16)
Hsp90-RNAi x H202-High	0.59*** (0.13)	0.33** (0.16)
Hsp90-RNAi x Heat-Low	-0.08 (0.13)	-0.01 (0.16)
Hsp90-RNAi x Heat-Serial	0.15 (0.13)	0.22 (0.16)
Hsp90-RNAi x Heat-High	0.35*** (0.13)	0.38** (0.16)
CB015K23 x DH1300	-2.00*** (0.09)	
CB046A04 x DH1300	0.001 (0.09)	
C007801047 x DH1300		0.46*** (0.11)
C012001013 x DH1300		-0.46*** (0.11)
Observations	289	288
R^2	0.93	0.91
F Statistic	210.26*** (df = 16; 272)	180.64*** (df = 16; 271)

Estimated effects (and standard errors) are in log units relative to No Stress controls, in the absence of Hsp90-RNAi treatment, in the AF16 strain, for CBRG21D19 (*CbmaT1*) or C009001188 (*Tc1*) loci. Asterisks represent *P*-values, with $P < 0.1$ (*), $P < 0.05$ (**), and $P < 0.01$ (***).Only variables that were significant were included in each final model.

Table S5. Incidence rates and standard errors for variables affecting *unc-22* mutation frequency.

	Incidence rate of plates with *unc-22* mutants	
	C. elegans	*C. briggsae*
Intercept	0.08*** (0.06-0.12)	0.05*** (0.37-0.78)
Hsp90-RNAi	1.16 (0.67-2.00)	0.90 (0.54-1.53)
H202-Low	1.57 (0.89-2.77)	1.97*** (1.24-3.15)
H2O2-High	4.31*** (2.66-7.16)	8.97*** (6.05-13.67)
Heat-Low	1.00 (0.57-1.76)	1.31 (0.81-2.12)
Heat-Serial	2.66*** (1.59-4.52)	2.78*** (1.81-4.39)
Heat-High	5.08*** (3.16-8.38)	6.87*** (4.58-10.57)
Strain-DH1300		1.38*** (1.20-1.59)
Hsp90-RNAi x H202-Low	2.18* (1.04-4.60)	2.95*** (1.57-5.58)
Hsp90-RNAi x H202-High	4.56*** (2.33-8.90)	2.55*** (1.41-4.61)
Hsp90-RNAi x Heat-Low	1.00 (0.46-2.16)	1.26 (0.64-2.49)
Hsp90-RNAi x Heat-Serial	3.15*** (1.58-6.30)	3.64*** (1.98-6.72)
Hsp90-RNAi x Heat-High	3.24*** (1.66-6.34)	3.69*** (2.03-6.72)
Observations	36	72

Incidence rate is provided as exponentiated output of general linear regression with quasibinomial family, and values are for all loci relative to No Stress controls, in the absence of Hsp90-RNAi treatment. For *C. briggsae* values are relative to AF16 strain, whereas only one strain was examined in *C. elegans*. Only variables that were significant were included in each final model.

Table S6. Hsp90 (*daf-21*) mRNA transcript levels for two strains of *Caenorhabditis elegans* and two strains of *C. briggsae* following experimental exposure to environmental stress. Values presented are mean ± standard error for five biological replicates for each strain and treatment and are derived from qRT-PCR. All treatments resulted in higher ($P < 0.05$) Hsp90 mRNA levels relative to 'No Stress' control animals.

	C. elegans		*C. briggsae*	
Treatment:	N2	AB2	AF16	DH1300
No Stress	1.00 ± 0.06	1.00 ± 0.05	1.00 ± 0.07	1.00 ± 0.08
Heat - Low	2.21 ± 0.09	2.16 ± 0.11	2.18 ± 0.12	2.04 ± 0.13
Heat - Serial	2.15 ± 0.11	2.23 ± 0.16	1.99 ± 0.15	2.19 ± 0.12
Heat - High	2.22 ± 0.07	2.21 ± 0.07	2.22 ± 0.16	2.15 ± 0.14
H2O2 -Low	1.97 ± 0.11	2.18 ± 0.17	2.22 ± 0.13	1.98 ± 0.09
H2O2 - High	2.18 ± 0.12	1.94 ± 0.08	1.99 ± 0.14	2.21 ± 0.08

Table S7. Hsp90 (*daf-21*) mRNA transcript knockdown for two strains of *Caenorhabditis elegans* and two strains of *C. briggsae* following daf-21-dsRNA exposure through bacterial feeding, and subsequent exposure to environmental stress. Transcript knockdown levels for all treatments are relative to 'No dsRNA' control animals (zero knockdown), which were fed with bacteria that lacked the daf-21 hairpin expression cassette. All treatments analyzed resulted in significant ($P < 0.05$) knockdown of Hsp90 mRNA levels. A value of 1.00 reflects complete knockdown; all values represent three independent replicate experiments of pools of 20 worms.

	C. elegans		*C. briggsae*	
Treatment:	N2	AB2	AF16	DH1300
No Stress	0.90 ± 0.08	0.89 ± 0.07	0.87 ± 0.05	0.90 ± 0.05
Heat - Low	0.91 ± 0.04	0.88 ± 0.13	0.86 ± 0.10	0.90 ± 0.07
Heat - High	0.84 ± 0.13	0.79 ± 0.14	0.74 ± 0.12	0.82 ± 0.17
H2O2 - High	0.76 ± 0.13	0.80 ± 0.15	0.83 ± 0.09	0.86 ± 0.12

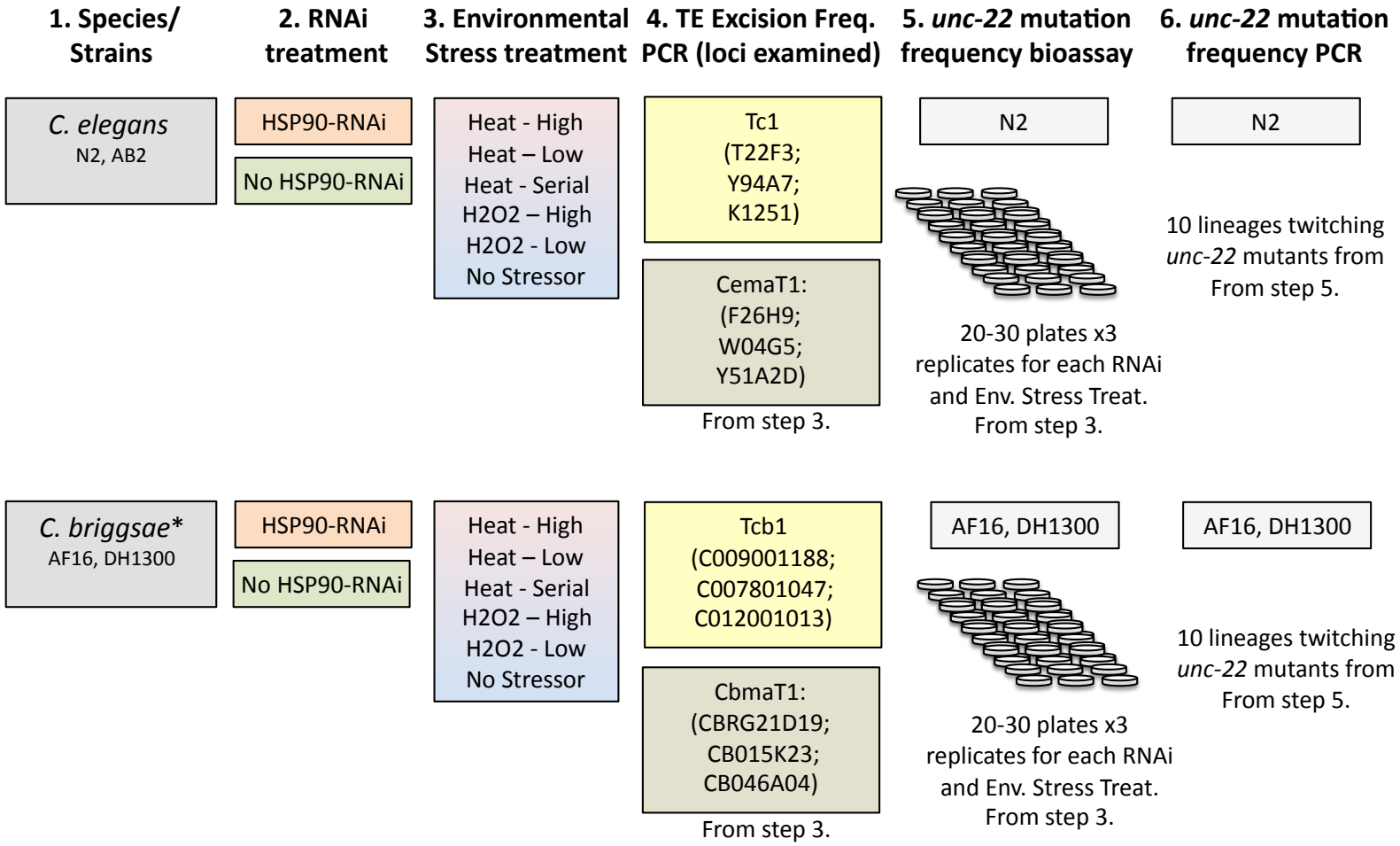

Figure S1. Experimental design for testing stress-induced transposon excision, insertion, and phenotypic effects in two species of nematode (*Caenorhabditis elegans* and *C. briggsae*)(step 1). Two strains of both species were exposed to double-stranded RNA which either silences the Hsp90 (*daf-21*) gene, or acts as a control (step 2). All worms were then exposed (step 3) to different environmental stressors, and TE excision frequency was then measured for three loci each (step 4). Mutation frequency was measured by both bioassay (step 5) or reporter (*unc-22*) gene frequency as measured by PCR (step 6)

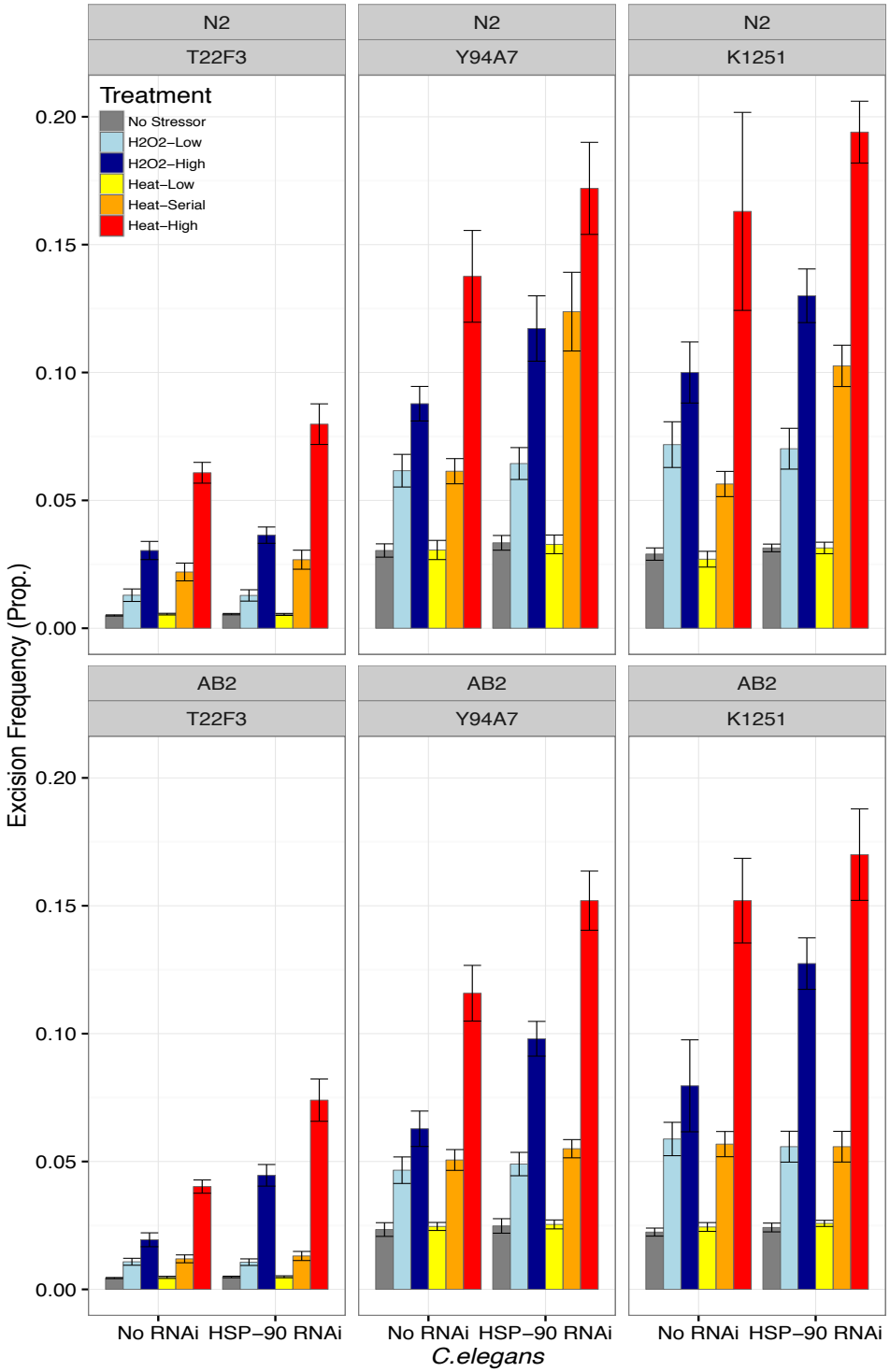

Figure S2. Excision frequency for *Tc1* transposons at three loci (K1251, T22F3, Y94A7) for two strains of *C. elegans* (N2, AB2) in response to five different conditions of environmental stress, plus no stress controls. Excision frequency given as the proportion of excision footprints to the number of non-excised transposons at a given locus. Oxidative stress treatments are shown in light (Low-H2O2) and dark (High-H2O2) blue, while heat stress is indicated by yellow (Low; 35°C for 1 h), orange (Serial; five serial exposures of 35°C for 1 h, 30 min at 20°C) and red (High; 39°C for 2 h). Gray indicates controls with no stress treatment.

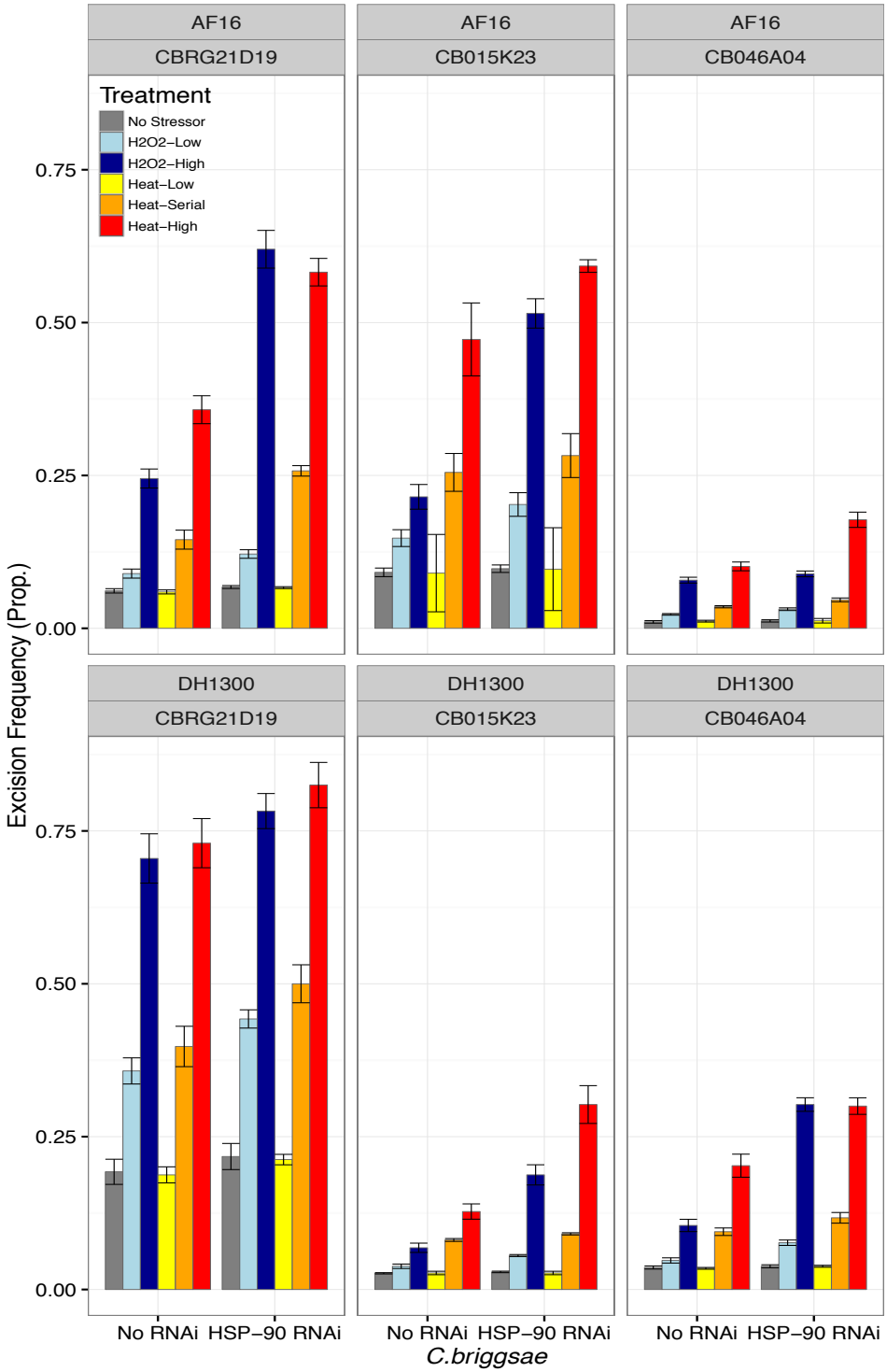

Figure S3. Excision frequency for *CbmaT1* transposons at three loci (CBRG21D19, CB015K23, CB046A04) for two strains of *C. briggsae* (AF16, DH1300) in response to five different conditions of environmental stress, plus no stress controls. Excision frequency given as the proportion of excision footprints to the number of non-excised transposons at a given locus. Oxidative stress treatments are shown in light (Low-H2O2) and dark (High-H2O2) blue, while heat stress is indicated by yellow (Low; 35°C for 1 h), orange (Serial; five serial exposures of 35°C for 1 h, 30 min at 20°C) and red (High; 39°C for 2 h). Gray indicates controls with no stress treatment. CBRG21D19, CB015K23, and CB046A04 previously referred to as G2D19, CB015K23, and c004200728.Contig1, respectively (Brownlie et al. 2005).

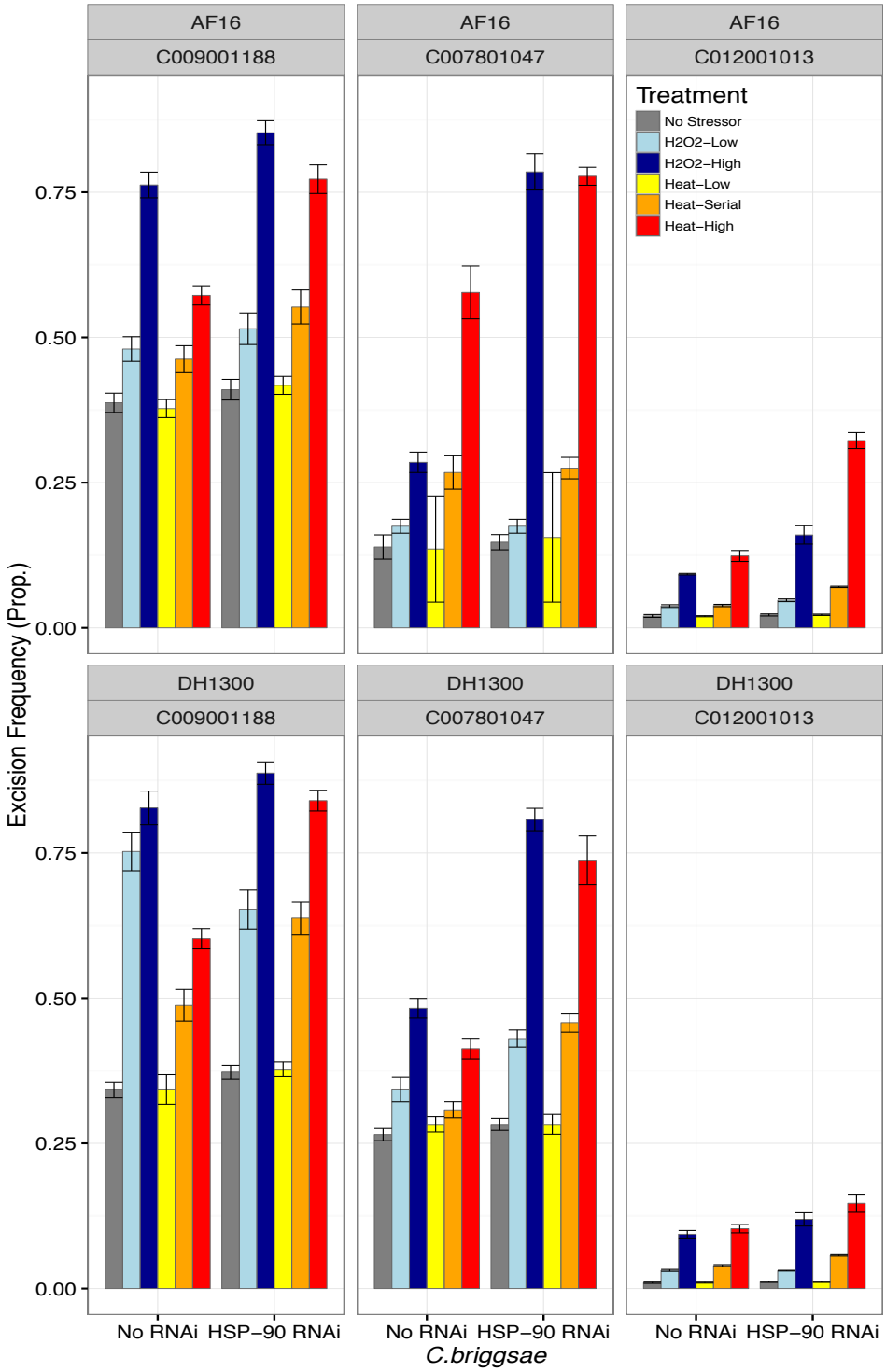

Figure S4. Excision frequency for *Tcb1* transposons at three loci (C009001188, C007801047, C012001013) for two strains of *C. briggsae* (AF16, DH1300) in response to five different conditions of environmental stress, plus no stress controls. Excision frequency given as the proportion of excision footprints to the number of non-excised transposons at a given locus. Oxidative stress treatments are shown in light (Low-H2O2) and dark (High-H2O2) blue, while heat stress is indicated by yellow (Low; 35°C for 1 h), orange (Serial; five serial exposures of 35°C for 1 h, 30 min at 20°C) and red (High; 39°C for 2 h). Gray indicates controls with no stress treatment. The complete names for C009001188, C007801047, and C012001013 are C009001188.Contig2, C007801047.Contig1, and c012001013.Contig3 (Brownlie et al. 2005).