**Species** Transposon Locus Туре Sequence GGGAAAGTCAATTTATTTATTGCAACTAG Flanking C.elegans CemaT1 F26H9 F26H9 Excised CGGAGCCTGGAGAAGTTTATAGAA Non-Excised F26H9 CCATAATTTTGACTCACCCTGTAGAA CemaT1 W04G5 Flanking GTTTGTCACTTTGTTATTCTGTTTTACGA W04G5 Excised CACCGGTTGTTTTTAAGATTATATACACA Non-Excised CTTACCATAATTTTGACTCACCCTGTATAC W04G5 CemaT1 Y51A2D Flanking GGTTACTGTAGGCTGGTGTTTGC Y51A2D Excised CTGTGTTTTAGTGTATAATTTTCCGTCAA Y51A2D Non-Excised TTACCATAATTTTGACTCACCCTGTAAT Tc1 T22F3 ATGACTACTGTAGCGCTTGTATCGA Flanking T22F3 Excised GATTATCAAAAATGGACAGCTATGTATATTCC T22F3 Non-Excised ATCTTTTTGGCCAGCACTGTATATT Tc1 Y94A7B Flanking TCCAAAAACATCACTTATGTACATGCAA Y94A7B Excised GGAATGGCTAAACGTGAATATGG Y94A7B Non-Excised GCCAGCACTGTACATGCAACA Tc1 ZK1251 Flanking CATCTCTAATTGTGCAGGTATGTATGC GCGTCTATTCTTATATTTTACTCTAATCAGTTG ZK1251 Excised ZK1251 Non-Excised TGGCCAGCACTGTATGCAAA C.briggsae CbmaT1<sup>e</sup> CBRG21D19 Flanking AAACTGATGTGTCAAAGTGGCCT CBRG21D19 Excised GCCATCAATGTTCATGATCTATGTATT CBRG21D19 Non-Excised TAATTTTGGCGGACCCTGTATT CbmaT1<sup>φ</sup> CCATGTTTTGGGTCATTTTTCA CB015K23 Flanking Excised CB015K23 GCTCTCGCTATCTCGCTACTACATAG CB015K23 Non-Excised TTTTGGCGGACCCTGTAGAT CbmaT1<sup>¢</sup> CGTGGTCGTTTAAGAAAGTACGC CB046A04 Flanking AATGGCCTATAGAACGTCCTTTATGT CB046A04 Excised CB046A04 Non-Excised TTGGCGGACCCTGTAAGC Tcb1 C009001188.Contig2 Flanking CCTCTAGAAGTCCGTTTGACACATATC C009001188.Contia2 Excised CCGCATCGCACACATATATGA C009001188.Contig2 Non-Excised CATTCTTTATGGCCAGTACTGTATGA C007801047.Contig1 CTTGACTTAACATTTGTAAGACCGAAATT Tcb1 Flanking C007801047.Contig1 Excised CAACGCGCATTGAACTTATAGATT C007801047.Contig1 Non-Excised GCATTCTTTATGGCCAGTACTGTAGAT Tcb1 C012001013.Contig3 Flanking AACAGTTGACAAATTTTCAGTATCACAAG C012001013.Contig3 Excised TTGGATATACCGTTTTTGAGATATACC C012001013.Contig3 Non-Excised GCATTCTTTATGGCCAGTACTGTACCT

 Table S1. Primers used to detect transposon excision frequencies for two transposable elements

 from three loci in both Caenorhabditis elegans and C. briggsae

<sup>•</sup>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.

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

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

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

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.

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

 Table S4. Effect sizes and standard errors for variables affecting TE excision

 frequency in *C. briggsae.*

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.

	Incidence rate of plates with unc-22 mutants		
	C. elegans	C. briggsae	
Intercept Hsp90-RNAi	0.08 <sup>***</sup> (0.06-0.12)	0.05 <sup>***</sup> (0.37-0.78)	
H202-Low	1.57 (0.89-2.77)	1.97 <sup>***</sup> (1.24-3.15)	
H2O2-High Heat-Low	4.31 <sup>***</sup> (2.66-7.16) 1 00 (0 57-1 76)	8.97 <sup>***</sup> (6.05-13.67) 1.31 (0.81-2.12)	
Heat-Serial	2.66 <sup>***</sup> (1.59-4.52)	2.78 <sup>***</sup> (1.81-4.39)	
Heat-High	5.08 <sup>***</sup> (3.16-8.38)	6.87 <sup>***</sup> (4.58-10.57)	
Strain-DH1300		1.38 <sup>***</sup> (1.20-1.59)	
Hsp90-RNAi x H202-Low	2.18 <sup>*</sup> (1.04-4.60)	2.95 <sup>***</sup> (1.57-5.58)	
Hsp90-RNAi x H202-High	4.56 <sup>***</sup> (2.33-8.90)	2.55 <sup>***</sup> (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 <sup>***</sup> (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	

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

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  $\pm$  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	$1.00 \pm 0.07$	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	$0.83 \pm 0.09$	0.86 ± 0.12



\*Transgenic C. briggsae strains were generated to express the Cel-sid-2 gene

**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).