Identification of a novel strong and ubiquitous promoter/enhancer in the silkworm *Bombyx mori*

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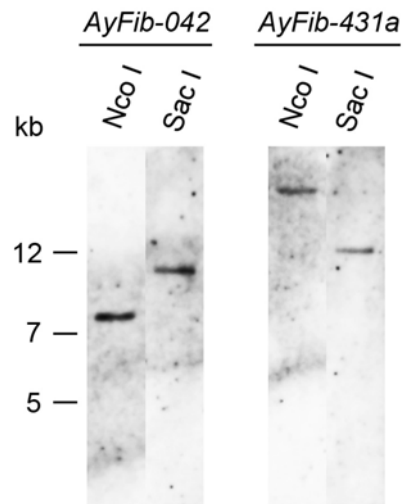   E-mail: hsezutsu@affrc.go.jp

Figure S1 Southern hybridyzation of *AyFib-042* and *AyFib-431a* genomic DNAs. A single band was detected in both strains. Note the difference in band potisions in *AyFib-042* and *AyFib-431a*.
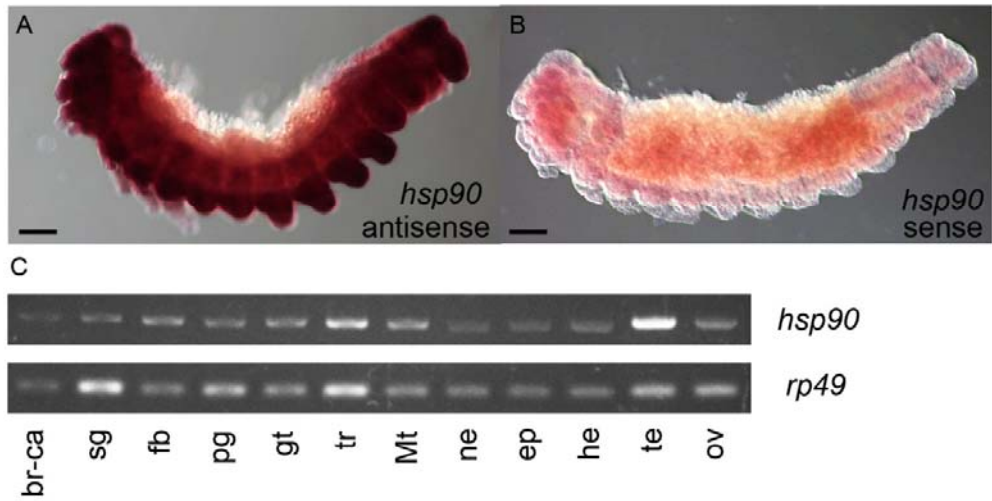
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Figure S2 Expression of *hsp90*. (A, B) *In situ* hybridyzation of *hsp90* in a stage 20 embryo. The embryo was stained with an *hsp90* antisense (A) or sense (B) probe. Bar represents 0.1 mm. (C) RT-PCR of *hsp90* (upper panel) or *rp49* (lower panel) in each tissue of a *w-c* spinning stage larva. Abbreviations are: br-ca, brain-corpora allata; sg, silk gland; fb, fat body; pg, prothoracic gland; gt, gut; tr, trachea; Mt, Malpighian tubule; ne, ventral nerves; ep, epidermis; he, hemocyte; te, testis; ov, ovary.
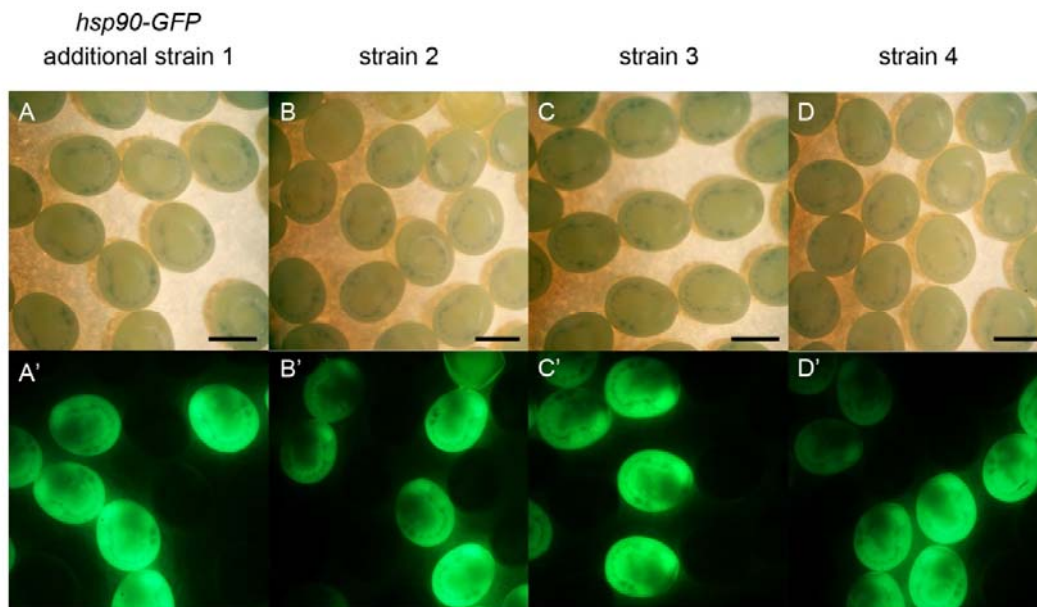
Figure S3 Embryonic GFP expression in four additional *hsp90-GFP* transgenic strains. (A, A') Strain 1. (B, B') Strain 2. (C, C') Strain 3. (D, D') Strain 4. (A, B, C, D) Bright-field images. (A', B', C', D') GFP images. Bar represents 1 mm.

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   1  CCATGGCTCAGTTCGCTTTAAATATCGATAGTCTTTAAAAAAAAAATTATGATGTGAAATCTGAAAAGGTTTGCGCACTATGCGCTCATGC   90
  91  AATTTCAACTTTAATCAATAGCCCTAAAGCAGTGCTGCCAACAAATAAAAAAATATTTATTGTAAGTGAGATAACTAAATTTGTCAGAAT   180
 181  TCATCGCTTCTTTGCTATTTTTTATTATGGTTTGTGTTTAATTATATTTTAAACGTGTTGATGAAATAGTAAGATAATTAGCATTAAATT   270
 271  TACACCACTTTCGTGAAGGTTTTCTGGCTAATCGTTTCAGTTTGTGTGGCATAAAACTATGGGCTATAACTATTGCTGGTGAGACTTTAA   360
 361  CAGCTTCATAAGGACGGGTGGATTAACTCAAAAACACAGCTTGGAGGGAAAGAGTTTGCTAATAGCCGCCAGAGTGCCTCCAAAAGGGGT   450
 451  TTAATAGTACTAGGACAGTTACTTTACGAGTGCATCTACTCCGTGTCGAGAAGCTTAGAGCTCAGTATCACATACAAATCGTCGACGAGT   540
 541  TAGCTGAACCATGCTTTTATTGCTCTTGGCGTTAAAATTAGTAGTGATAATGAGAACGTATCAGGTGGATCTTGCATTATTTGAAAGATG   630
 631  AGACTAAAGATCTGTAGGTTGTGCGAGAGAATGTCGCGAGGCAAAAATAGTTTCCTCTACCTGTAGATAACGAGAACACAAATTTTATAC   720
 721  AGGGTGTATAGGAGAAGACGAGGAACAATTATTTTAATGATTTCTGACATCTAAATGAACAATAAGATTTTACTTTTGATGAACAAAACA   810
 811  AGTAACTCACATCTTAAACTGAACGTTACTACGTTCTGGTTTGCTATTGTAATTTTAATCAATGTTTTCTCCAATCTGCATTATGATACA   900
 901  ATAAAAGCTCATTAT*TCGCGTTTCCTTCACTCGCGTTTTCACTATTCGCAGATTAAAATGTGTCCCAATTCCTATTTTCGCAATTAAAGA*   990
 991  *TCTCTTTATTCGCGGATCTAATCGATACATAGACATTGATAAAAAGAAATCCAATATTAAGTATTCAACTGAATATCCTTTATAATCGCG*  1080
1081  *CTATAATCACGGTTTATCTATAAAGCCTTGTTCGGACTAGGCGAGTATTTTAGTCGAGTACCGAGTAATTTAGTAGCTAAATGTGTCCGA*  1170
1171  *GCACCAAAAGTTTAGTCGAGTAGGTTAGTAAATAATTTAGTAAAGCCAATCCATTTTGTTCTATTTTATCGGGCGAGTAGCGCCTCCCAC*  1260
1261  *CACGCGTCCTAGCTCACTGGCTCACTGACTAAACAAGTCCGAACCTGTTGATTAGTCGAGTTCATTAGTGGCGCTTCTCAAATGGAACTT*  1350
1351  *TCGGACATTCTTAAACTATCGAAGTATTCTTTGGGATCTCTTCCAATGCTAATTCTTTCAGAAGACATTTATCTCTTCAATCGATCCATT*  1440
1441  *TTCGTACCTATAACTTATTTTTCATAATCACAGAAATTTGCTCGTCCACCTTTTCTAAAATAGCCATTACGATTAGCTTAATCAGTTTAT*  1530
1531  *TCACTCTATTGCGTTGCAGTCTGTTCATCCTGCAAAACACCACTCACTTGTGTACTCTACTGGACCGTAATGCGAACGATTTCTGTGCAG*  1620
1621  *TAGCGAGTAGTTTAGCCACTAAATTACTCGGTACTCGACTAAAATACTCGCCTAGTCCGAACAAGGCTTTAGCGACATATTTACGTAACG*  1710
1711  *TATACACCCCGATAAAGAGATTTACTGTCCAAAAAAAAACGTCAAAAAATGGAACAAATTATGTGCTTTTTATTTATTGGTATTACTAATT*  1800
1801  *TCGTTAAGAATTTCATCGGAAGCAGCCAGCGCCGAATGCGGTGAATAGTAAAACTATAAGAAGGAAGCGGTTGGAATGATCTGGGTAAAA*  1890
1891  *TGTTATTTCTTACGAATTACGATGATTCTTTGATTAAATTTGGAAAAGTTTTGTGGTCAAATTATTTAACATTCATCTTGTATCATTTAT*  1980
1981  *TGACTCTAATTTCAACTAAGTTATTTCTGTAATGTTAAAATTTCGATGCTT*[TTCTAGAATATTCA]G[GAATGTTCCAGA]*TATTCTTGTGTG*  2070
                                                          HSE-3            HSE-2
2071  *TAGATCGTATTGCCACCTTGTGCCAAATAGCGGCACTAAAATAATTCGGCAGAGCTATACAACATTGGTAATTTTATTTATTTTGCTAT*  2160
2161  *TTTCCCCAGTTTTTTAAATTACTGTGTTTTTAACTAGCAATTACATTTAATTGGATGCAATTTACACTGCCTTAATAATTTTTTTTTAGT*  2250
2251  *TGTAATTTGGTTTCTTACGTTTATGCTGTATATTTTTAGTGATCTGCAAAATGCGAAACACTGAACAGCTTAGGAAAATTAAAATGTGA*  2340
2341  *GATGTTTCTTTTACTTAAATAAATACTTAAAATATAACAGAGAAAAAACATTTTTAACTAGTCTGGCATATTTTAGTGAATCTATTGATG*  2430
2431  *AAAATGAACGAAATATGTAATTACCTTTATAATTTCTTGAATTATTTTAAGGAAATATATTTTTCCTAACACTTTAAACTTCAAAGCGGG*  2520
2521  *TGATGCAATAATAACTAACACAAAAAGAAACTTGCAGTGTTAAGTAAATGATTTTTCTCTTCGTTTTATGGCCTCCCAAAATGAAATAAT*  2610
2611  *TGCCAATTAATTTGAAATGATTAATTATTTTTATTTAATATTGTTTCGGTTTGTATTGATGGTAAAATGTTGATGCTCTCTGACGGAAAT*  2700
2701  *AGCGTCAGAA*[TCGAGAAACTTC]*TACTGATTCATAGATGTCGCTTGCTAGAGGAAAGTATAAAAACGAATTACACACCGCGCCCggcgtt*  2790
                      HSE-1
2791  *atttgaactaagagaagtacggagactaacgtttgatactttgcgctttgaaacacgtgtgttaaaaaccctctagtcattttgtgtgaa*  2880
2881  *ttaa*                                                                                           2884
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Figure S4 Sequence of *Bombyx* hsp90$^{P2.9k}$ fragment. The boxed region shows three putative HSE elements. The transcribed region of *hsp90* is written in lower case. The hsp90$^{P2.0k}$ sequence is shown in the italic character. The underlined region shows the genomic fragment used for *hsp90-GAL4* transgenic strain in Uchino *et al.* (2006).