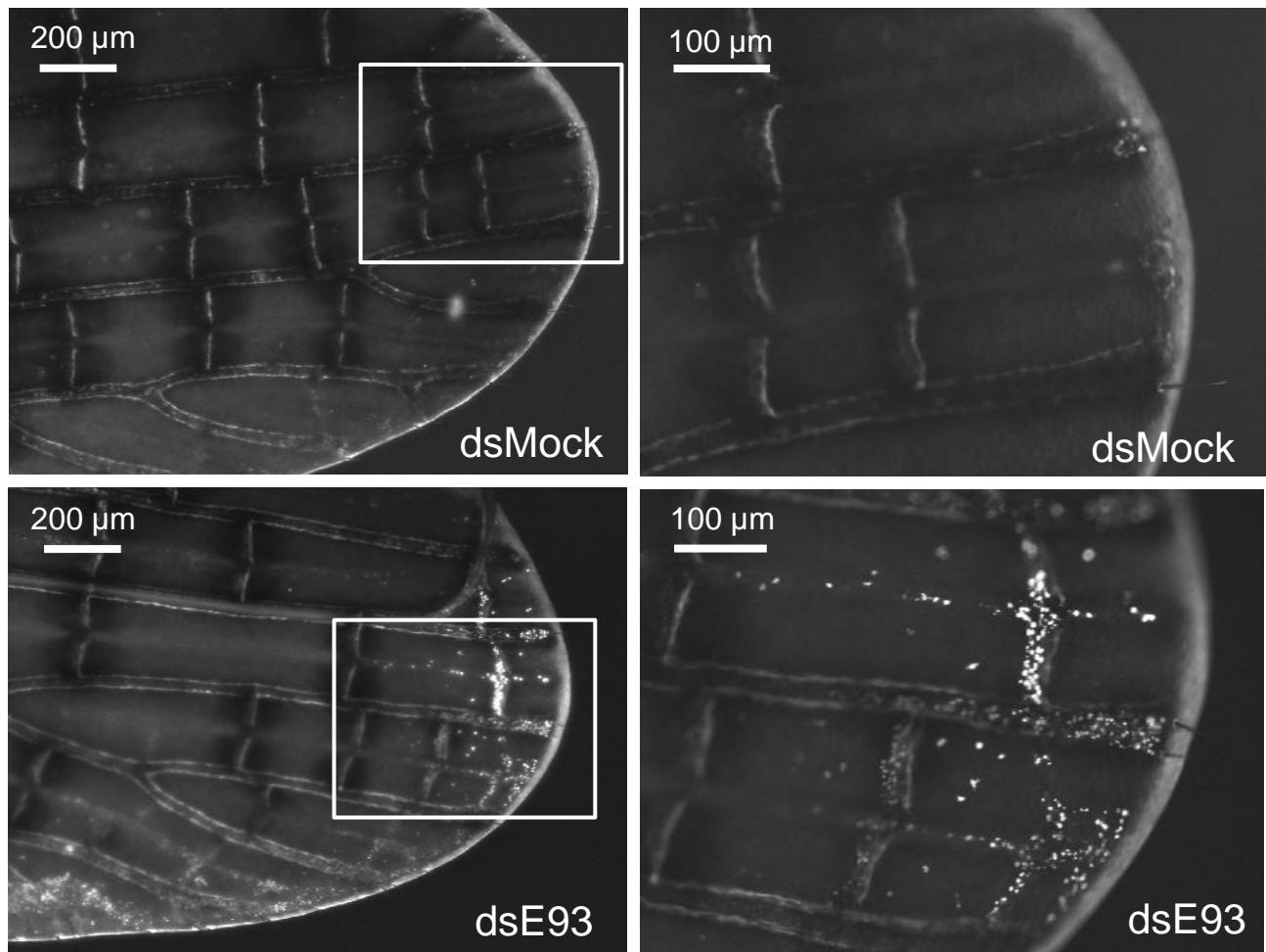
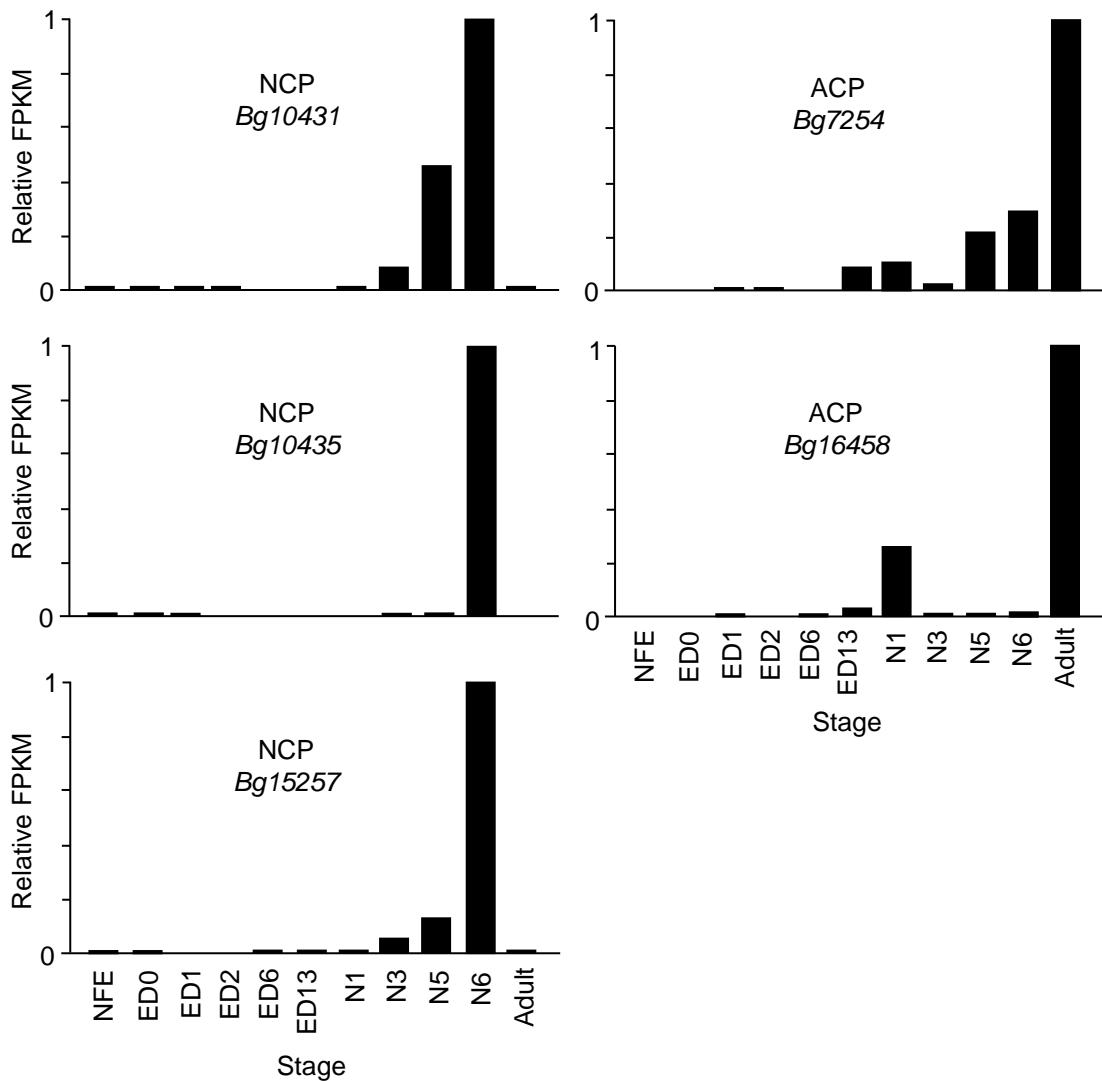


**Fig. S1. Cell proliferation in the prothoracic gland of *Blattella germanica*.**  
Double labeling EdU (discrete pink spots) and DAPI (background blue color) of prothoracic gland tissue in last instar control nymphs on day 0 (N6D0), day 1 (NsD1) and day 2 (N6D2), and E93-depleted adults in day 0 (AdD0), day 1 (NsD1) and day 2 (AdD2). Scale bars: 50  $\mu$ m.



**Fig. S2. DAPI staining of *Blattella germanica* hindwing in control and E93-depleted adults.** The wings were plucked from 7-day-old adult females, and processed for DAPI staining for 1 h. The images show a general view of the apical part of representative wings, and a detail (white square) at higher magnification. The vein areas of wings from dsE93-treated insects show more intense DAPI staining than controls (dsMock-treated).



**Fig. S3. Transcriptomic expression of typical nymphal cuticular protein (NCP) genes: *Bg10431*, *Bg10435* and *Bg15257* and typical adult cuticular protein (ACP) genes: *Bg7254* and *Bg16458* in *Blattella germanica*.** Data were obtained from stage-specific transcriptomes that cover the life cycle (Ylla et al., 2018), as follows: non-fertilized egg (NFE); embryo 8, 24, 48, 144, and 312 h after oviposition (ED0, ED1, ED2, ED6, and ED13); first, third, fifth, and sixth (last) nymphal instar (N1, N3, N5, and N6); adult female. Data are expressed as FPKM, and is normalized against the maximum value (= 1) in each gene.

-4010 GGGCCTTCATTACAATAAATTGTTAGACAATTATTCAGTAATATTACATAAACAAATTGTGTCATCAGATAAGATTATGATACCA  
 -3920 ATGGCTTCAAAAACGTCACTAAAGTTGATTATTATTATTATCTATCTATTACAGGTAAACTATTAT  
 -3830 TTATATATTATTTATTGTGATATAGAGCT**AAGTCATGGAC**TTCTCTCCACTCTACCAGCTAACAAAATTACAAGATAAATTAC  
 -3790 ATTATTAATCAAGTAAAAGAAAATACAATAAAATTACAAGAAGTTAAATAAGTTATCATGAATAACTTTGTATTCATTGG  
 -3710 ATTTCAACTGTTGCTTGATTTTATTCATACACTCTGTGAGACAGAACATTAAACAGCATCATAAAATACAGACC  
 -3620 AGAATTACAATGAAGATAGTTAAAGATAGTTCAAAGGGATGAAACGAAAATTCCCCTACTGAAAAAAATTATTGTAGGGATCC  
 -3530 CTGTTCAAGTATTAAATTAAATCCAGTCAGTTCTGCTAGTTCTACTCTAGGTGTTACTTATGTTACGGAAGTTAGA  
 -3440 ATGATAAGTTGTAATAAAATAGCCTACTGCCTTAACTGTTATTAAATAAGAATAATGTAATCTCCATCAAATCCCTAAAAAAG  
 -3350 AGCTTCTGCTGAGATGAGACCGTAGTTCTGTAGAATAGTTATCAATAGCTACAGTTATACCTATATAAATAAATAAAAA  
 -3260 AACGCTTAAATCTCAATAAAGCTCATATCATGTGTTGAATTAAAAGTAGTTACTGATGCAGACAAACGGACAC  
 -3170 ATAGATAGGACAACCTGCAGTGAATTGCACTCCGACGTTAACACGGTCAAACATTAGTTACTTAATGTCACAACTCTA  
 -3080 ACTCTCAAGATAAGTTAACCTTAAAGACTAGCTCCGATATATCGACACTTCAAGAAGGTTAAAGGGTTAAAGATTAGGTATCTGCA  
 -2990 ATATATAATAACTATAACTACTGCCTGGTCAACAGCCCAGCTGTTAGCATTAGGGTCACACATGCTTAAATATGGAGGTGAACCA  
 -2900 TCATCCAACCTGTGAAGGGAAATATGTTAGCAGCTAGTCACAGAAAATTAGCTGTATCTGCAATCGCTACAGAAAGGACAG  
 -2810 AAGAGTTAACTAGACTGCTAAATAAAGTTAAAGCTTACGCAACTTCGCGTCCGCTAGCATAAATCTCTAATTATGATGTTCAAGACA  
 -2720 GATTAACCTCGTATTAAAAGTTAACACGGCTATAGCATAAGTTCTCATGCAGGTAGGCTATGGCATAGGAACAAAATTGTTGCC  
 -2630 AACAC**TCAAGGCAA**ATGTCGGAACTCTGTTGAATGCTCAACTTAAAGCAGATAAAAGTAGTACTGTTGGAATATTTCGAGAAAATT  
 -2540 GAGAACAAATATATCAGAATT**CCAAGGAA**GTTGGTAATAGATAATTAAAGGAATGATGCACTGTTGCTCTGAACAGAAATCT  
 -2450 AATAATGGTGTAGTTCAAAATTCTAGTTCTGCCCCATAAACCGCCATTACTGACATAACAAATAAAGGTAATTCTGAA  
 -2360 AACACACTAACTTATTAGTCAGCTGGTTGAACAAAACGTATTAGCCTATTATGCGATGTTTGTAAATCTATGATCACATTA  
 -2270 TTACCAACCACCTCTAACTTAATGTAATATGGATTATAATTACTCTGATAAAAATACCTTGTCAATAATAATAATAA  
 -2180 TAATAATAATAATAACCAGTGCCTTATGGCTAACGATCTCCTTGTCTTCAGAATTAAATTCTATAATT**TCAAGGATT**AGA  
 -2090 CTACACCTAGGTATATGCAACTCTTCGACTGTTAAATGTTGCTATTCAAAATATTGAAATTCGAGCCGGACTTCAGAAATTGGC  
 -2000 CGTTTATTTCATCAGATACATAATTACATATTACGTTAAAGATAATTAGTGGTAGCTGGTAAAAAATAATTACTAACAGCTGCTAA  
 -1910 GGAATTGGTGGCAGCTACAGATTGTCAGCATCATCCTAATTCTGTATCAGCAAAAGGAGCTTCATTAAAGCACCC  
 -1820 CTCGCACAAATGTACTATAATTAAAGACTTTGTTCTGTACTATGAATAACAGAACATAAAATAATATCAGATCAGAAGGGATGAA  
 -1730 CAATTATTATAATGCAATAATGAAATAACTAGATACTGAAACAAAGGTTGATGCTCATGAAAGTCACAATAAAAGCAATTATA  
 -1640 TCCATTAGCCTACATAGATAAAACAAATTACTAAATAATGAAAATGCCATCGAATGCAATGCCACGTGGTAACATGCTACGGCG  
 -1550 AGCAACAGCGGGATTGGGACCCCGCCCGTTAAAGAATGGCGCATCCGATCGATTGCGGCTCGGCCAACCTGCGGACAAGACG  
 -1460 CGAGGATTGCAACTCCCCCTCCCCCTCCCTCACCCCCCGGACTTTCTGTAGCGAGGAAAACCGAGGCTCTGCCAGAACGTT  
 -1370 CAAATTCTCCAGAAAATTCTCATTAAATTCTCATTTTTAATCTCTAAATTTGTGAATTTCATCATTCTTCC  
 -1280 GCATAACATTAAACTCTCGGCCATTAATTGGCGCAATAAAGGCGTGTATGATTAACTCTAAAGGCGTACAGTAGACTATATCA  
 -1190 ATTAGAATCAATAGCGCATATTGCTACCTCTGTAGTATCTGATTGAGTTGAAACAAATACTCTGGTGTACAGTGTGGCTCGCA  
 -1100 AACTATAGACGTCACTTAAATATTCTTCAGGACAACAGTGGGAATCGTGGCCTCTCCATTATGAGTGACGACACACGC  
 -1010 GAGTTGATAGTGCACGGGTGATCGCAGGCCAGTGAATGTAATTCTATTACGAAGAAGCGTGTATGTTGCACTCAAGCTCTTG  
 -920 TTTCTTCTAGGAGGATAACGCTAAGGAGTCTACTACTCGCACGTGAGTCTAACCTCTGAGGACGCCGCAAGACACGTGACTCGGATCAA  
 -830 TACGCCCGTCCGCGCCGAGACGCTTGTCTATTGATCGACGCCGCGACGCTGCCGCCGGGATCGATTCCGGACGTCGGAGACG  
 -740 AGGCCCGCGTGTGCGCCGCTGTGCGCCGAGGCCGAGCGCCGGAGCTCGAACCCGGGGCGGAGCTCCCGAACAAAACAGGT  
 -650 TTGGCGTGGCGAAGGCAGCGGGCGGGAGAAAGAGTCAGGGTCAGTTGCAAGCAAATGGCGAGTGCTCTATGCTCGTGTGTT  
 -560 ACGAGCAGCGAGCGATCAAAAAGAGCTCAAGATGGACCAAGAACATGGTCAGTAGTAGTTGCAAAGTGTGTCTAGT  
 -470 GCTCCGAGGCTGTGGCTCGGCCAGCTGGCTAACCTGCAAAAGTCAGGTTGCAAGGTTCCGGGTCCCCCTGGTGCAT  
 -380 CACCCCGCGTTCTGGCGCCCCCTGGGCTCTGGGCCCTACCGCGGGTGCAGCTCCGCAGTCTCCGCAAGAAACCCGCTCTGGCC  
 -290 GCCCCCGTCAACATTCTCAAATTGGGGCGCATTTCTTCAGGCTACCAAACATCAGCTGGTGGGGGGTGCCTCGAGCCTG  
 -200 GAACAGCGGGGCAAGAACGTAACAGCCATGCCATGCCAACCGCAATACCGAGGTAATACCGGAAAATGGAAAAGTAGGTGAAAATG  
 -110 TGACGTGTCGAGCAGCGCGAGCAAGCAGCGGTCGAGTGTCTGGGCCGAAATCCGATCAGCTGGTGGGGGGTGCCTCGAGCCTG  
 -20 AGCGCGTGGCTGAGGAGTT**ATG**GGCCGCAAGATGGAAACAGTATCAGGACTCAGTGCTCAGATCTCGCTCAGAGTGGACGCTGGAGC

**Fig. S4. The nucleotide sequence of the promoter region of the *E93* gene of *Blattella germanica*.** The ATG translation initiation codon is indicated in bold blue, a canonical EcRE (Cherbas et al., 1991; Kayukawa et al., 2017) is indicated in bold green, and a sequence (TCAAGGCAA) compatible with a FiRE (Lavogna et al., 1991; Ohno et al., 1994; de Mendonca et al., 2002) is indicated in bold yellow and underlined, except a mismatched nucleotide. Three other potential FiREs are indicated in yellow and underlined, except the mismatched nucleotides.

**Table S1.** Primers used to measure gene expression levels with qRT-PCR and to prepare dsRNAs for RNAi experiments (highlighted in yellow).

Gene	Forward primer	Reverse primer	Accession code
<i>Actin 5C (Act5C)</i>	AGCTTCCCTGATGGTCAGGTGA	TGTCGGCAATTCCAGGGTACATGGT	AJ862721
<i>Bg7254</i>	TTTGTACGGCTACAGCATCG	ACTGACCCAAAGCGTCTTGT	Scaffold293:1224685-1234782*
<i>Bg10431</i>	CTCATGCCGCTCCAGTACTAT	CACGGTAAGACACGACAGGA	Scaffold1062:264085-266425*
<i>Bg10435</i>	CTCTGGTGATGGGCATTTCT	GATTTCAGAGGAGCAGAGG	Scaffold1062:351421-355992*
<i>Bg15257</i>	AGATCCCTCATGCACCAATC	GCGTGATGTTCAACCTCCTT	Scaffold1678:100341-119028*
<i>Bg16458</i>	GATGGGAGAACCTACCAGCA	CTGGATCTGCGCTAACACA	Scaffold550:516136-531892*
<i>blistered (bs)</i>	GACGGAGCTCACGTACAACA	CCAGCGGTCTTACTTTCTGC	HF912428.1
<i>Broad-complex (br)</i>	CGGGTCGAAGGGAAAGACA	CTTGGCGCCGAATGCTGCGAT	FN651774
<i>caspase-1 (casp-1)</i>	AAGCGGAAGGATTCTACCA	GATGACTGCCTGCCTCTTC	LN812812.1
<i>disembodied (dib)</i>	GCAACAGACAATGGACCTCA	AGATCCAATGCAACCTCCTC	Scaffold1245:376847-417309*
<i>E75A</i>	GTGCTATTGAGTGTCGACATGAT	TCATGATCCCTGGAGTGGTAGAT	AM238653.1
<i>E93</i>	TCCAATGTTGATCTGCAA	TTTGGGATGCAAAGAAATCC	HF536494.1
<i>Ecdysone receptor (EcR)</i>	GACAAACTCCTCAGAGAAGATAAA	CTCCCAATCCTGCCAGACTA	AM039690.1
<i>fushi tarazu factor1 (ftz-f1)</i>	TTGTCACATCGACAAGACGCA	GTACATCGGGCCGAATTGTTCT	CAQ57670.1
<i>HR3A</i>	GATGAGCTGCTCTAAAGGCAT	AGGTGACCGAACTCCACATCTC	AM259128.1
<i>inhibitor of apoptosis-1 (iap1)</i>	TCCACCTGTGCATCATCATC	GCGTGCATCGTCTAAACCT	FN668727.1
<i>Krüppel homolog 1 (Kr-h1)</i>	GCGAGTATTGCAAGCAAATCA	GGGACGTTCTCGTATGGA	HE575250.1
<i>neverland (nvd)</i>	CTGGGGCCAGTCACAATACT	GCAGGGGCTTGTCAATGTAT	Scaffold2003:130463-150129*
<i>Notch (N)</i>	GCTAAGAGGCTTGGATGC	TGCCAGTGGTCTGAGAG	HF969255.1
<i>nubbin (nub)</i>	CGTCACCAAGAAACACAGA	CGAGATTGGTCTGTGAGAAA	LT216433
<i>phantom (phm)</i>	CTAGGCACCAGAGCACCTTC	GCAAGCACTGTGTCTTCAA	Scaffold1282:295424-296920*
<i>Retinoid X receptor (RXR)</i>	ATAATTGACAAGAGGCAGAGGAA	TGAACAGCCTCCCTTTCAT	AJ854489.1
<i>scalloped (sd)</i>	GCCCACAGAGTGTCTTC	CCCCTGCCATCTTGAATA	HF969263.1
<i>shadow (sad)</i>	ATGAGGAGGTTCAAGGTGTG	CTGGCCAGAAGTCATTGGT	Scaffold189:1562047-1594901*
<i>Ultrabithorax (Ubx)</i>	AAGAGGTGCCAGACGTACA	TTGGAACCAAATTTGATCTGTC	LT216435
<i>vestigial (vg)</i>	AACTGTGTTCACTCACT	AAGGAGGAAAGTTGCGAGC	LN901335
<i>dsE93</i>	AAAGAGTTGCGGAGCAGA	CCACTGCTAGAACCCACTCC	HF536494.1
<i>dsFTZ-F1</i>	GAATAGTTCAAGGCCTTTGAAGCT	GGGACGCATGTAGACCTTCTTG	CAQ57670.1
<i>dsMock</i>	ATCCTTCTGGACCCGGCA	ATGAAGGCTCGACGATCCTA	K01149.1

\*Genes manually annotated in *Blattella germanica* genome, available as BioProject PRJNA203136.