

Antennapedia
D.mel -LYPWMR--RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKE-
A.mel -LYPWMR--RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKE-
T.cas -LYPWMR--RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKE-
A.pis -LYPWMR--RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKE-
D.pul -LYPWMR--RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKE-

Sex combs reduced
D.mel -IYPWMK--TKRQRTSYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKEH-
A.mel -IYPWMK--TKRQRTSYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKEH-
T.cas -IYPWMK--TKRQRTSYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKEH-
A.pis -IYPWMK--TKRQRTSYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKEH-
D.pul -IYPWMK--TKRQRTSYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKEH-

Ultrabithorax
D.mel -FYPWMA--RRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALCLTERQIKIWFQNRMMKWKKEI-
A.mel -FYPWMA--RRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALCLTERQIKIWFQNRMMKWKKEI-
T.cas -FYPWMA--RRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALCLTERQIKIWFQNRMMKWKKEI-
A.pis -FYPWMA--RRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALCLTERQIKIWFQNRMMKWKKEI-
D.pul --FYPWMA--RRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALCLTERQIKIWFQNRMMKWKKEI-

Fig. S2. Conservation of YPWM motif and homeodomain in other Hox proteins. The residues flanking the YPWM motif and homeodomain sequences of Antennapedia, Sex combs reduced, and Ultrabithorax are highly conserved. Sequences were obtained from the genomes of *Drosophila melanogaster* (*D.mel*), *Apis mellifera* (*A.mel*), *Tribolium castaneum* (*T.cas*), *Acyrtosiphon pisum* (*A.pis*), and *Daphnia pulex* (*D.pul*). Only nonsynonymous amino acid substitutions are highlighted.

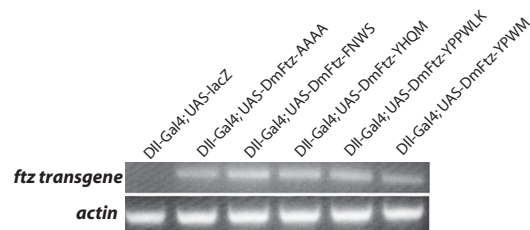


Fig. S3. Expression levels of “degen-YPWM” transgenes are similar. A *Dll-Gal4* driver was used to express degen-YPWM transgenes in developing imaginal discs during *Drosophila* development. L1 larvae were collected, and cDNA was made from 1 µg of RNA. RT-PCR confirmed a *ftz* transgene product was detected in all degen-YPWM lines, but was absent in the control line (*lacZ*). Actin levels in all samples were similar. For each transgene, only one antennal-to-leg phenotype was seen; there was no variation.

Table S1. The *ftz* genes generally contain small introns and encode short linker regions between the YPWM motif and homeodomain

Species	Intron size (bp)	# Residues in linker
<i>D. mel</i>	150	11
<i>A. gam</i>	59	11
<i>A. aeg</i>	60	?
<i>B. mor</i>	89	10
<i>A. mel</i>	1657	13
<i>N. vit</i>	157	14
<i>T. cas</i>	50	9
<i>D. mac</i>	60	9
<i>A. pis</i>	224	?
<i>S. gre</i>	>679*	11
<i>F. aur</i>	335	5
<i>P. sal</i>	141	8
<i>S. car</i>	150	10
<i>D. pul</i>	?	8

*Complete intron sequence not published.