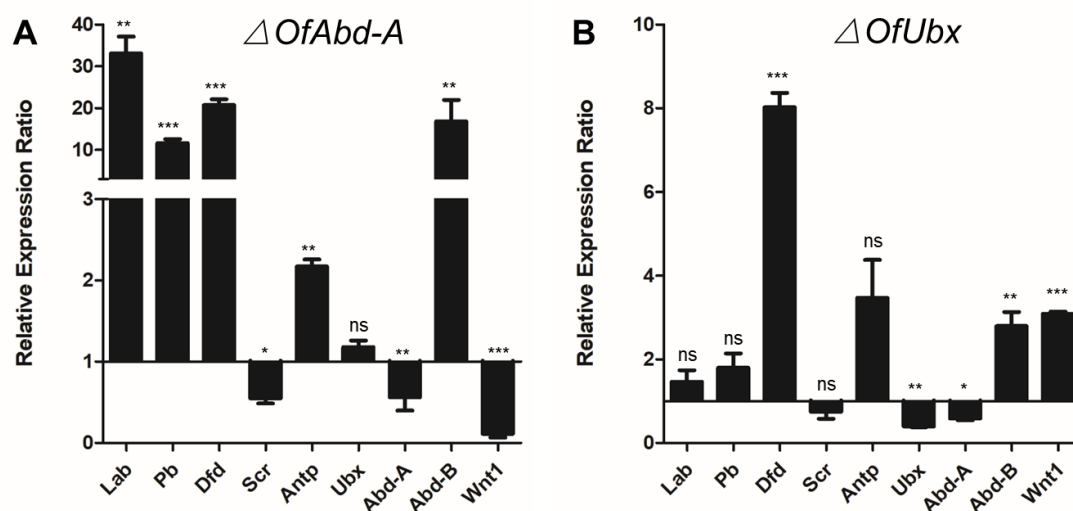


Table S1. Primers used in this study.

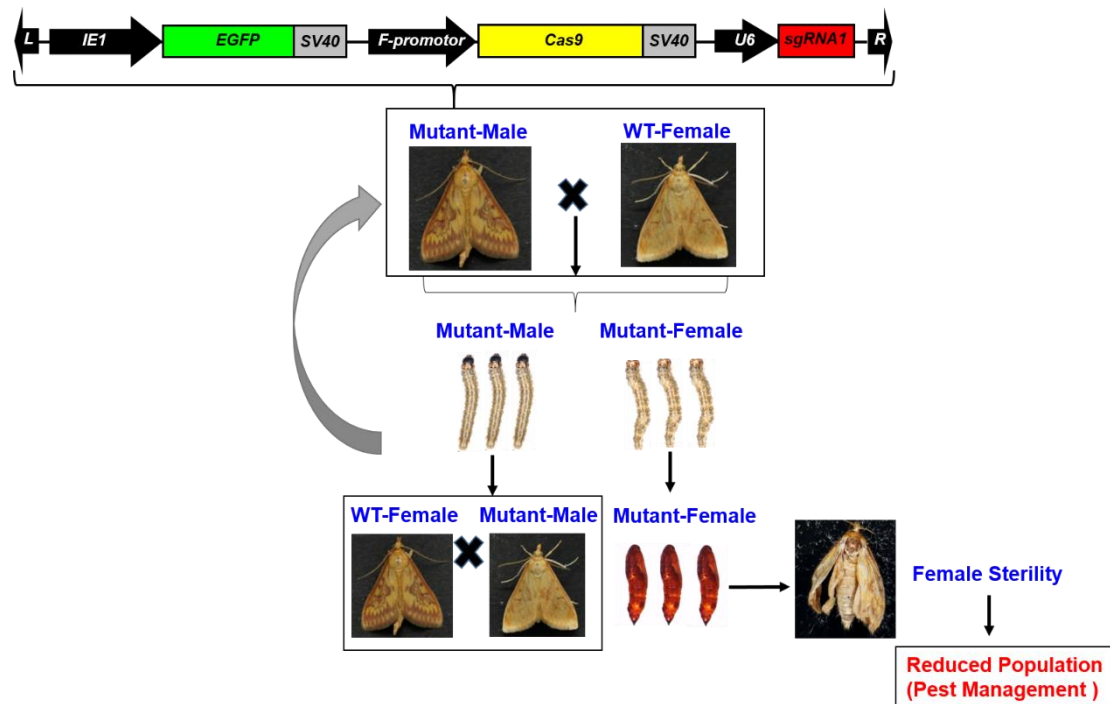
Primer name	Primer sequence(5'-3')	Primer purpose
Abd-A-sgF1	TAATACGACTCACTATAGGGGTCGGCAAACCTACACG	Preparation of sgRNA
	GTTTATAGAGCTAGAAATAGCAAGTTAAAATAAG	templates
Ubx-sgF1	TAATACGACTCACTATAGGTTATGGAGGGAAAGAATG	Preparation of sgRNA
	GTTTATAGAGCTAGAAATAGCAAGTTAAAATAAG	templates
Ubx-sgF2	TAATACGACTCACTATAGGGTAGAAGGTGTGGTTGGT	Preparation of sgRNA
	GTTTATAGAGCTAGAAATAGCAAGTTAAAATAAG	templates
GFP-sgF1	TAATACGACTCACTATAGGGCGAGGAGCTGTTCACCG	Preparation of sgRNA
	GTTTATAGAGCTAGAAATAGCAAGTTAAAATAAG	templates
GFP-sgF2	TAATACGACTCACTATAGGCCACAAGTTCAGCGTGTC	Preparation of sgRNA
	GTTTATAGAGCTAGAAATAGCAAGTTAAAATAAG	templates
sgRNA-R	AAAAGCACCGACTCGGTGCCACTTTTTCAAGTTGATAA	Preparation of sgRNA
	CGGACTAGCCTTATTTTAACTTGCTATTTCT	templates
Abd-A-F1	TTCTCGCTGTTGAACTGCTT	Identification of somatic mutations
Abd-A-R1	TTACGTGGGGACTTTGTTCA	Identification of somatic mutations
Ubx-F1	ATGAACTCCTACTTTGAGCAGGGTG	Identification of somatic mutations
Ubx-R1	CTTATTGGGCGCTCTCTTACAAGAC	Identification of somatic mutations
Abd-A-qF	CGGCAAACCTACACGAGGTT	RT-qPCR for <i>Abdominal A</i>
Abd-A-qR	TCCTGCTCCTCTCTCTCTCG	gene ( <i>Abd-A</i> )
Ubx -qF	CCACACCTTCTACCTTGGA	RT-qPCR for <i>Ultrabithorax</i>
Ubx -qR	TCATCCTCCGATTCTGGAAC	gene ( <i>Ubx</i> )
Lab-qF	CAACCAGCAGAACGGTTACA	RT-qPCR for <i>Labial</i> gene
Lab-qR	CCCCATAGTCCAGATTCGTG	( <i>Lab</i> )
Pb-qF	GGCTAAGCGGATCAAACAAG	RT-qPCR for <i>Proboscipedia</i>
Pb-qR	TGGGTAGTGACCGAGAGGAC	gene ( <i>Pb</i> )
Dfd-qF	ATTACCATCCGTTGCCTCAG	RT-qPCR for <i>Deformed</i> ( <i>Dfd</i> )
Dfd-qR	GGGCATGGAGTTTCTACCA	gene
Scr-qF	TGGAGCACAAAGCTAACGTG	RT-qPCR <i>Sex combs reduced</i>
Scr-qR	CATTCGCATTCACCGTACTC	( <i>Scr</i> ) gene
Antp-qF	AAGGATGCTCTGGACTCTGC	RT-qPCR for <i>Antennapedia</i>
Antp-qR	TATCTTCCGTCGCAGCTTCT	( <i>Antp</i> ) gene
Abd-B-qF	AGTGGTGGCGAGTACAAACC	RT-qPCR for <i>Abdominal B</i>
Abd-B-qR	CTGACTCGGGAGCGTAGTTT	( <i>Abd-B</i> ) gene
Wnt1-qF	ACGCCACACTGAGGAGAAAG	RT-qPCR for <i>Wingless</i>
Wnt1-qR	AACGCTGTCTCTCGACAACC	<i>Integrated family member 1</i>
		( <i>Wnt1</i> ) gene
Dll-Qf	TATCCAACTCGGCAAATTCC	RT-qPCR for <i>Distal-less</i> ( <i>Dll</i> )
Ddll-qR	GGAAGGGGTACCCTAACGAC	gene

Sca-qF	AGTACGTCCACGGATTGGA	RT-qPCR for <i>Scabrous (Sca)</i>
Sca-qR	CTTGAAGCCACTCACGTTCA	gene
Transcript-qF	TTTATTGGCGATCCTGAACC	RT-qPCR for <i>Transcript</i> gene
Transcript-qR	GAATCCTCTCTGCCCAACTG	
Larp-qF	GCCTCTCCGGTTCTACTCC	RT-qPCR for <i>La-related</i>
Larp-qR	ACTTGTCGAGACACGCCTTT	<i>protein (Larp)</i> gene
Centrosomin-qF	GCTTAGCACTTCCGGTAGGA	RT-qPCR for <i>Centrosomin</i>
Centrosomin-qR	ACATCTGCTTGTGGGAAAGG	gene
Dpp-qF	ACGGCTACGACGCCTACTAC	RT-qPCR for <i>decapentaplegic</i>
Dpp-qR	GCACCACATTGTTCACTTCG	( <i>Dpp</i> ) gene
Connectin-qF	CCTTTTGAAGGTGTTTCGAG	RT-qPCR for <i>Connectin</i> gene
Connectin-qR	TCGCTTTTCGATTCTGTTTCT	
Wnt4-qF	GCGTAGGCAGTTTCGGTAAG	RT-qPCR for <i>Wingless</i>
Wnt4-qR	CGTGACATTTGCACACTTCC	<i>Integrated family member 4</i>
		( <i>Wnt4</i> ) gene
B-tubulin-qF	GCTGGTGGAGAACACAGACA	RT-qPCR for <i>Beta-tubulin</i>
B-tubulin -qR	ATGTTGACTGCGAGCTTCTCT	gene
Spalt-qF	CACACCAAGGAACGACCTTT	RT-qPCR for <i>Spalt</i> gene
Spalt-qR	GTCAGCATGTGCTGCTTCAT	
Knot-qF	TTACACGGGGGACGATACAT	RT-qPCR for <i>Knot</i> gene
Knot-qR	TAGCCCAGACATCAGACATGA	
Actin-qF	CCGTCCTCTGACCGAGGCTC	RT-qPCR for <i>Actin</i> gene
Actin-qR	GGTGTGGGAGACACCATCTCCG	



**Figure S1.** Relative transcript levels of downstream genes in *OfAbd-A* and *OfUbx* mutants. Transcript levels of indicated mRNAs in *OfAbd-A* (A) and *OfUbx* (B) mutants relative to wild-type levels. Three individual biological replicates of real-time PCR were performed. Asterisks (\*, \*\* or \*\*\*) indicate significant differences ( $P < 0.05$ ,  $P < 0.01$ ,  $P < 0.001$ ).

0.01 or  $P < 0.001$ , respectively) compared with wild type adults using a two-tailed t-test. ns represents no significant difference.



**Figure S2.** Prospective CRISPR/Cas9 mediated female specific transgenic pest control schematic.