

## **Supplemental Figure S1**

The UCSC Genome Browser alignment of the *D. melaogaster* *Ugt36Bc* WRE region with several other *Drosophila* species. Several species with particularly poor conservation have been omitted. The TCF binding sites identified by DNA footprinting in *D. melanogaster* (Figure 4A,B) are over-scored with the AGAWAW sequences shown in bold. DNA sequence conservation breaks down fairly uniformly across the WRE with increasing evolutionary distance. No particularly well-conserved DNA sequences, including the footprinted TCF sites, are obvious in any species.

## Supplemental Data

**Table S1** Primers for dsRNA, *in situ* probes, real-time PCR, and ChIP analysis

<b>Primers for real-time PCR measurement of gene expression</b>	
<i>naked cuticle</i>	TAAAATTCTCGCGGGCTACAA / CGCACCTGGTGGTACATCAG (#272-273)
<i>CG6234</i>	AGGCGTTGAGGACCCATCTAC / CTGGTTGTCGTCGTGCTCTTC (#157-158)
<i>Ugt36Bc</i>	CCGAATGTGCCTGGAGTAATC / TCCGTGCTTGCCCTTCTC (#161-162)
<i>Tiggrin</i>	AATGGCGGTTATGTGGTGG / GGAGGCCTTGGTAGACAC (#329-330)
<i>Peroxidasin</i>	CTTTCGATGTGGGTGACAA / GTTGCTCCGCTTGGTAGG (#327-328)
<i>Ugt58Fa</i>	CGGTGATGCCACTCTGGT / CTCTGGCGAGGAAGTGGT (#331-332)
$\beta$ - <i>Tubulin56D</i>	AGACCTACTGCATGACAAAC / GACAAGATGGTCAGGTAC (#274-275)
<i>luciferase</i>	GCCCTCCGCATAGAACTG / TGATGAAACATTCCAAAACCGTGAT (#384-385)
<b>Primers for real-time PCR measurement of ChIP signals</b>	
<i>Ugt36Bc</i> WRE	CCGGAAAGCATGAGTTGCAC / TCGCCCCTATCTACCCACAAA (#308-309)
Cloned <i>Ugt36Bc</i> WRE	ATTGACCTCGTTGCAGGACAGGATGTGGT / ATTGCGGCCGCACATGTTCCAGATGCTGCTCG (#648-649)
<b>Primers used to generate dsRNA</b>	
All primers in this section also have the T7 binding sequence (GCGTTAACGACTCACTATAAGGGAGA) appended to the 5' end.	
<i>Ctrl(1) (bla)</i>	CCGTGTCGCCCTTATTCCCTT / GACCCACGCTCACCGGCTC (#133-143)
<i>Ctrl(2) (GFP)</i>	AGCTGTTCACCGGGGTGGT / GGTACCGAACTCCAGCAGG (#804-805)
<i>TCF(1)</i>	GAAGATGACTACGATGATGATAAACTAGGCAGGA / AATAGGGTTTCGGGATGTGTTGGCA (Fang et al, 2006)
<i>TCF(2)</i>	TACTGATGAAAGATTTT / TGCTTCAGGTTCCCTTGGAT (#743-744)
<i>Arm(1) 3'UTR</i>	CCGAGCTAACGGTAAGG / GCAAACATTGTTAACCTTCC (#57-86)
<i>Arm(2) ORF</i>	GGTCACCTGTGCCGCCGT / AGAGAACAGCGGCCGCGTAT (#184-185)
<i>Axin(1)</i>	ATTCTTGCGCAAGAGTCAGC / CCAGGAGGTGGATTTCAG
<i>Axin(2)</i>	GAGACGCCGAAATGCTCTAGAGG / GATCCTGGCGCAGTCCTGACGGC (#404-405)
<i>CtBP ORF</i>	ATGCACAAAGCACCTCGAAATACACGA / GCACCAGGTGCGATCTGTTAACGTGAAT (Fang et al, 2006)
<i>Brinker</i>	TCCAGGCCAGCGCTGCAGGT / CATCATCATCATCACCATCACC (#380-381)
<i>Snail</i>	CCGCTCTATACTCGATCCCG / TGGGATGTCATTCGCACTG (#665-666)
<i>Reptin</i>	AAGGAGGTGGTGCACACTGT / AACATGTAGTCATCCTGGTACT (#796-797)
<b>Primers used to generate cRNA <i>In Situ</i> probes</b>	
<i>Peroxidasin</i>	ATTTAGGTGACACTATAGAAGTGTGAGCTCACAGAGAAACTG / TTAATACGACTCACTATAGGGAGAGTTGCACCTGGTGCAGACGT (#831-832)
<i>Tiggrin</i>	ATTTAGGTGACACTATABAAGTGTGAGGGCTCTGGCGGGAT / TTAATACGACTCACTATAGGGAGATCCGCTCAAGTCCACGGGTT (#652-653)
<i>Ugt36Bc #1</i>	ATTTAGGTGACACTATABAAGTGTGAGCACAAACCGGAGCAC / TTAATACGACTCACTATAGGGAGATGTATTGTGATTCAAGGAAG (#650-651)
<i>Ugt36Bc #2</i>	ATTTAGGTGACACTATABAAGTGTGAGCTTGCAGGC / TTAATACGACTCACTATAGGGAGACTACTGCTTCCACCTTCTT (#866-867)