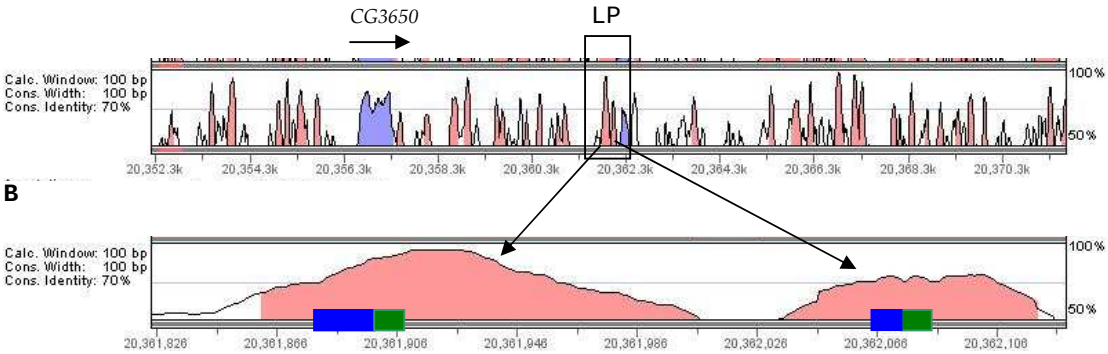
A

```
>D. melanogaster (CAF1) chr2R:20361824-20362128 (+)
>D. pseudoobscura (CAF1) chr3:10768778-10769063 (-)
```



C

Proximal peak, Putative Pangolin (TCF) binding sites at 20,361,878-900 and putative Brinker site at 20,361,901:

```
020361849  TCCCGCAGCGAATGGCATATGCGTGCGATTTTGATT  020361883
>>>>>>>>>  ||| || | |   |||||||||||||||||| ||||  <<<<<<<<<
010769072  TCCTGCGGTG--CGGCATATGCGTGCGATTTGGATT  010769022

020361884  TTTATTTGATTTGATTGCGGCGTCAACTTAATTAAGCGACCAACTACCAACAATGGCCAG  020361943
>>>>>>>>>  || ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||   <<<<<<<<<
010769021  TTGATTTGATTTGATTGCGGCGTCAACTTAATTAAGCGACCAACTACCAACAATGGGCAA  010768962

020361944  CAAATTGAAACAGCAGTCGGGCATTTGAAGTTCA  020362003
>>>>>>>>>  |||||||||||||||||||||||||||||||||||  <<<<<<<<<
010768961  CAAATTGAAACAGCAGTCGGGCATTTGAAGTTCA  010768917
```

```
MA0237.1 pan 8.684 0.944949725027386 29 36 1 TTTTGATT
MA0237.1 pan 6.362 0.86001167505196 35 42 1 TTTTTATT
MA0237.1 pan 7.867 0.915064114850847 40 47 1 ATTTGATT
MA0237.1 pan 7.867 0.915064114850847 45 52 1 ATTTGATT
MA0213.1 brk 7.734 0.887305509235301 53 60 1 GCGGCGTC
MA0237.1 pan 6.582 0.868059207780036 119 126 1 ATTTGAAG
```

Distal peak, putative Pangolin (TCF) site at 20,362,063 and putative Brinker site at 20,362,075:

```
020362050  CATTTGTAATTCCTTTTATTCCGCTGCCGCCAAAAGTCATTGAAACGTGTAATCTGCAGC  020362109
>>>>>>>>>  |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||  <<<<<<<<<
010768867  CATTTGTAATTCCTTTTATTTCGCTGCCGCCAAAAGTCATTGAAACGTGTAATCTGCAGC  010768808

020362110  ACGTGCGCAG
>>>>>>>>>  ||||||||||
010768807  ACGTGCGCAG
```

```
MA0237.1 pan 6.645 0.870363728515804 13 20 1 CTTTTATT
MA0213.1 brk 7.036 0.861705558327069 24 31 1 CTGCCGCC
```

Figure S4. A) Vista plot comparing the genomic region downstream of the Dll transcript between *D. melanogaster* and *D. pseudobscura* using Release 2006 coordinates (compare with fig. 8). B) 305bp fragment containing Vista peaks in LP enhancer region. Putative Pangolin and Brinker-Mad binding sites indicated in blue and green respectively. Pangolin (the Drosophila TCF homologue) is the transcriptional effector of the Wnt signaling pathway, and Brinker and Mad are the transcriptional effectors of the Dpp (the Drosophila BMP homologue) signaling pathway. C) Putative binding site sequences and coordinates indicated in blue and green, as revealed by searching the JASPAR database (http://jaspar.cgb.ki.se/).