

A

Dmel ACTTTTGAAATGATCACATGTGCTCCGATTTCTGTCAGTCTGAATTAGCATA
GACCGGAAGGCTCTGACAAAATCAGTCTA
 Dsim ACTTTTGAAACGATCACATGTGCTCCGATTTCTGTCAGTATAGAATT
ATTATACGACCGGACGGCTCTGACAAAATCAGTCTA
 Dsec ACTTTTAAACGATCACATGTGCTCCGATTTCTGTCAGTCTGAATTAGCATA
GACCGGAAGGCTCTGACAAAATCAGTCTA
 Dyak ACTTTTTAAATCATCACATGTGCCACGATTTCTGTCAGTTGCAATT
GGCATACGACCTGAAGGCTCTGATGAAATCAGTCTA
 Dere ACTTTTAAATGATCACATGTGCTACGATTTCTGTCAGCTTCAATTAGCATA
CGATCCGAGGGCTCCAATGAAATCAGTCTA



Dmel GCTGGAGCCTTGTACCGTTACCACTTTCTGGAAATATTCATCTAAATT
CCAGTGCCTTCC-AAAATTTTCAA
 Dsim GCTGGAGCCCTGTAACCGTTCAAGACCAGTTCTTTCTGGAAATATTCAT
CTAAATTCCAGTGCCTTCC-AAAATTTTCAA
 Dsec GCTGGAGCCTTGTACCGTTCAAGACCAGTTCTTTCTGGAAATATTCAT
CTAAATTCCAGTGCCTTCC-AAAAATTTTCAA
 Dyak GCTGGAGCCTTGTACCGTTGGACCAGATTCTTTCTGGAAATATTCAT
CTAAATTCCAGTGCCTTCC-AAAATTTTCAA
 Dere GCTGGGTCTTGTACCGTTCAAGACCAGTTCTTTCTGGAAATATTCAT
CTAAATTCCAGTGCCTTCC-AAAATTTTCAA



B

Dmel TGAAGGCCTTGAAGCTTGTAACTGCCCCCTGGCAAT TTATAATACA
ACAAAAAA-TTAGTAAATACATGGCTA CATATCGATT
 Dsim TGAAGGCCTTAAAGCCTTAACTGCCCCCTGGCAAT TTATAATACA
ACAAAAAA--TAAGTAAATACATGGCTA CATATCGATT
 Dsec TGAAGGCCTTAAAGCTTGTAACTGCCCCCTGGCAAT TTATAATACA
ACAAAAAAATATGTAATACATGGCTA CATATCGATT
 Dyak TGAAGGCCTTAAAGCTTGTAAATTTC-
AA-TGCCCCCTGGCAAT ATATTATATAACAA-AGTAAATACATGGCTA
AATATC-ATTC
 Dere TGAATGCCTTAAAGCTTGTAAATTTC
AAAGCTGCCCCCTGGCAAT TTCTTATATAACAA-AGTAAATACATGGCTA
AATATC-ATTC



Figure S1. (A) Alignment of the *ocn* 5' flanking and 5' UTR sequences of *D. melanogaster*, *D. simulans*, *D. sechellia*, *D. yakuba*, and *D. erecta*. The arrowheads indicate the boundaries of the *ocn* promoter sequence included in our expression constructs. The transcriptional start site is indicated by an arrow. (B) Alignment of the *ocn* 3' UTR sequences of *D. melanogaster*, *D. simulans*, *D. sechellia*, *D. yakuba*, and *D. erecta*. The two conserved regions are shaded. The arrowheads indicate the boundaries of the 3' UTR sequence included in our expression construct.