Figure S6

36bp mapped unique reads of ChIP and input samples in the non-*D. mel* species

UCSC LiftOver software

LiftOver sequence reads of non-D. *mel* species in reference to *D. mel* genome

Normalized CDP scores of non-*D. mel* species in reference to *D. mel* genome

QuEST software to generate Complied Density Profile scores

Normalization according to number of sequence reads and mappable genome size

ANOVA-like categorical linear model to CDP scores of each pair of *D. mel* and non-*D. mel* species at every single coordinate

ChIP enrichment estimates for *D. mel* and non-D. *mel* species

P value for the species /ChIP interaction term

D. mel specific binding non-D. mel specific binding Conserved binding

36bp mapped unique reads of ChIP and input samples in *D. mel*

Normalized CDP scores of *D. mel*