Neighborhood <sup>a</sup>	Collinear Blocks <sup>b</sup>	Species Where Disrupted <sup>c</sup>
CG15446-CG1494	553, 554, 555	wil, pse
CG4767-CG17329	892, 893, 894, 895, 897, 898, 899	ana, pse, wil, vir, moj, gri
CG13330-CG13440	1208, 1209, 1210, 1211, 1212	ere, yak, pse, wil, vir, moj, gri
CG14225-CG33931	527, 528, 529, 530, 531, 532	yak, ana, pse, wil, vir, moj, gri

Table S1. Phylogenetic organization of four gene neighborhoods of *D. melanogaster* in other *Drosophila* species according to recent reconstructions of their gene order

Based on comparative data from [1].

<sup>a</sup> Empirically disrupted in *D. melanogaster* [2].

<sup>b</sup> Numerical code of those collinear blocks in which the genes of the neighborhood are located. Collinear blocks were delineated based on conservation of gene order, but not necessarily on conservation of gene orientation (GO definition), across nine *Drosophila* species; gene transpositions in and out were allowed [1].

<sup>c</sup> ere, D. erecta; yak, D. yakuba; ana, D. ananassae; pse, D. pseudoobscura; wil, D. willistoni; vir, D. virilis; moj, D. mojavensis; gri, D. grimshawi.

## **Supporting References**

- von Grotthuss M, Ashburner M, Ranz JM (2010) Fragile regions and not functional constraints predominate in shaping gene organization in the genus Drosophila. Genome Res 20: 1084-1096.
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