

Description Of Additional Supplementary Information

Supplementary Data 1. Summary of all Micro-C sequencing libraries used in this study.

Supplementary Data 2. Sequencing depth and mapping summary for Micro-C libraries used in this study.

Supplementary Data 3. Differential tissue-specific expression in *E. scolopes* across gene pair categories.

Supplementary Data 4. Tissue specificity of gene expression (τ) across interaction categories and chromosomal origin.

Supplementary Data 5. Intervening gene density across gene pairs in *E. scolopes* and *O. bimaculoides*, grouped by interaction status.

Supplementary Data 6. Differential tissue-specific expression in *E. scolopes* across gene pair categories and *P. maximus* chromosomal origin.

Supplementary Data 7. Median genomic distances and statistical comparisons between gene pairs across interaction statuses, grouped by *P. maximus* chromosomal origin and genomic distance categories for the three focal coleoid species.

Supplementary Data 8. Enriched known DNA motifs in loop anchor-associated sequences in *E. scolopes*.

Supplementary Data 9. Enriched known DNA motifs in loop anchor-associated sequences in *S. officinalis*.

Supplementary Data 10. Enriched known DNA motifs in loop anchor-associated sequences in *O. bimaculoides*.

Supplementary Data 11. Enriched known DNA motifs in the CRISPR-cas9 knockout region in *E. berryi*.

Supplementary Data 12. CRISPR–Cas9 guide RNAs used for targeted knockout of the intronic region of Quaking B in *E. berryi*.