

Figure S1. No compensation of expression of NL genes upon *emerin* or *baf* loss. Read counts from RNA-seq data of NL genes including *emerin*, *emerin2*, *dman1* and *baf* from wild type (CS, *yw*, *nos*), *emerin* mutant (G/PK, G/PI) and *baf* GLKD ovaries.

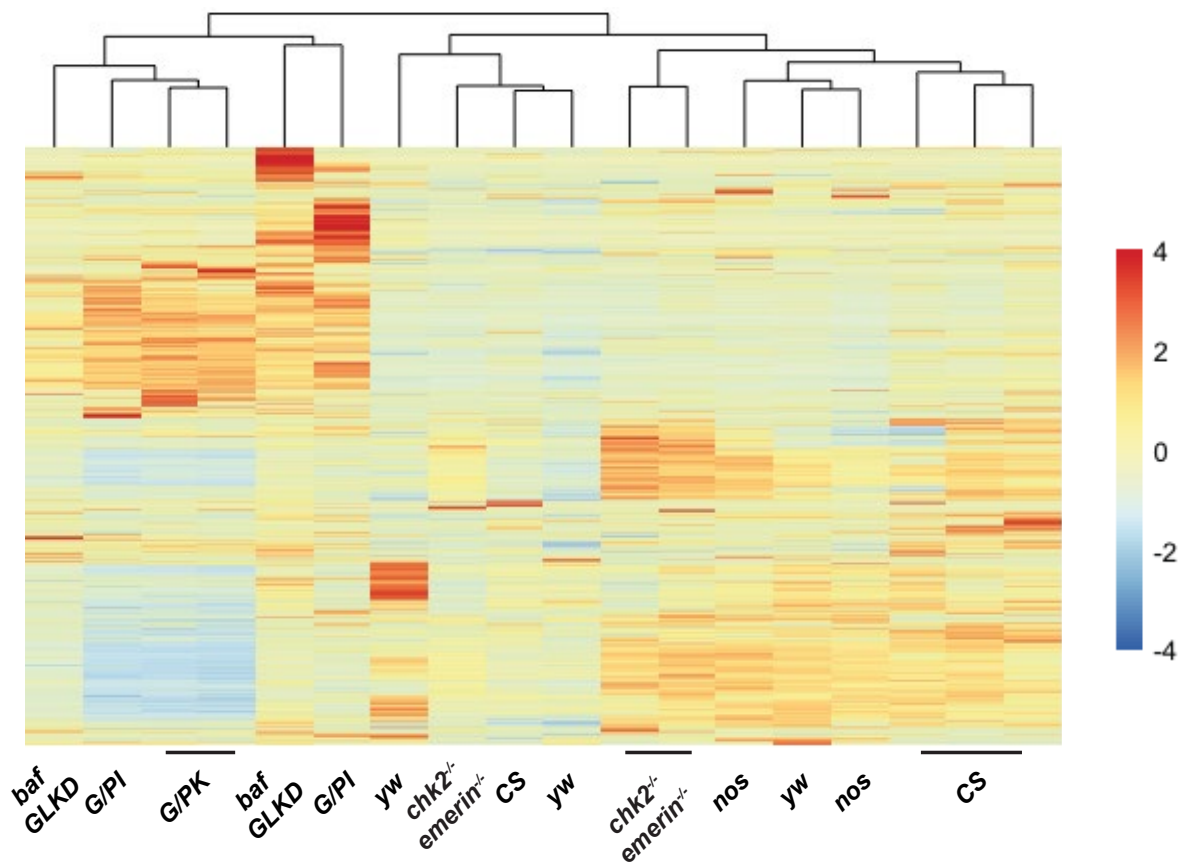


Figure S2. Unsupervised clustering aligns gene expression of *chk2*, *emerin* double mutants with *wild type* reference strains. Shown is a heat map of read counts from RNA-seq data of *emerin* mutant (*G/PK*, *G/PI*), *baf GLKD*, *chk2*, *emerin* double mutants, and *wild type* references (*CS*, *yw*, *nos*), represented with single z-score scaling.

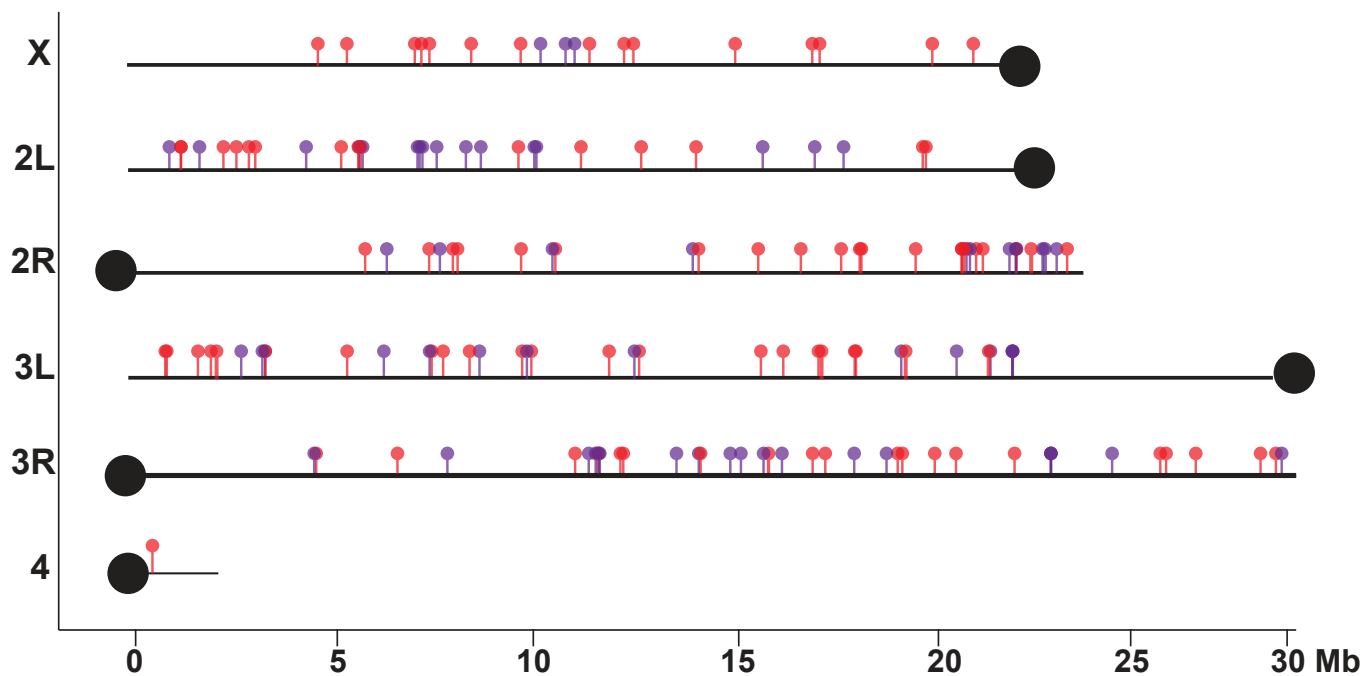


Figure S3. Genome-wide distribution of up-regulated EDGs. Shown is the genome-wide distribution of the 157 upregulated EDGs, displayed as those shared with BAF (purple) or those that are emerin-only (red). Gene positions are indicated on the six major chromosome arms as raised dots. Chromosome length is indicated in megabase pairs (Mb).