



Figure 1 shows unique model organism gene matches in a single Drosophila species. Figure 2 unique MOD gene matches for a given taxonomic grouping. About 90% of MOD genes are matched in all Drosophila, about 9% match in some subset, and about 1% match in a single Drosophila species. The Dsim assembly used (2005 wu-mosaic) has some yeast genome contamination accounting for its higher yeast gene count, and possibly the extra human gene count. The Dyak assembly used here has removed yeast genome contamination.