



Figure S4: Transcript abundance from parental lines at stage 2 demonstrates differential maternal deposition of *M1BP*, *Dref* and *BEAF-32*. Counts for *D. simulans*/*D. mauritiana* and *D. simulans*/*D. sechellia* comparisons are averages across replicates from alignment to the *D. simulans* genome. Counts for *D. sechellia*/*D. mauritiana* comparison are averages across replicates from alignments to the *D. sechellia* genome. Error bars represent standard deviations. Count data for the same species and gene may differ across comparisons due to the genome used for alignment in each comparison and normalization of counts within a comparison.