Table S4: Enriched motifs found upstream of maternally deposited genes

Motif	Predicted Binding Proteins	Enriched in upstream regions of *D. sechellia* genes that are conserved in expression (E-value)	Enriched in upstream regions of *D. sechellia* genes that are changing in expression (E-value)	Enriched in upstream regions of *D. simulans* genes that are conserved in expression (E-value)	Enriched in upstream regions of *D. simulans* genes that are changing in expression (E-value)
	Dref, BEAF-32	(*sec* x *mau*) x *sec* (1.7e-009) (*sim* x *sec*) x *sim* (9.6e-011)	(*mau* x *sec*) x *mau* (2.2e-023) (*sec* x *mau*) x *sec* (3.5e-024) (*sim* x *sec*) x *sim* (2.7e-011)	(*sim* x *sec*) x *sim* (1.7e-006)	(*mau* x *sim*) x *mau* (2.5e-010) (*sim* x *mau*) x *sim* (2.8e-032) (*sim* x *sec*) x *sim* (2.2e-032)
	M1BP	(*mau* x *sec*) x *mau* (2.8e-006) (*sec* x *mau*) x *sec* (3.0e-009) (*sim* x *sec*) x *sim* (1.1e-006)	(*mau* x *sec*) x *mau* (7.7e-008) (*sec* x *mau*) x *sec* (5.5e-028) (*sim* x *sec*) x *sim* (1.8e-015)		(*sim* x *mau*) x *sim* (2.3e-008)
	crp, salivary gland-expressed bHLH, similar to Deadpan, E-box, nau (only in *sec* x *mau* and *sim* x *sec* comparison in *D. sechellia* upstream regions)	(*mau* x *sec*) x *mau* (6.6e-007) (*sec* x *mau*) x *sec* (6.6e-003) (*sim* x *sec*) x *sim* (7.5e-004)			

Table S4: Enriched motifs found upstream of maternally deposited genes. Sequences 500bp upstream were extracted for genes in *D. simulans* and *D. sechellia* that change in regulation or that are conserved in each pairwise comparison. Motifs that were significantly enriched in analysis using MEME and HOMER are listed in the table and predicted binding proteins discovered using Tomtom and Homer are also described. E-values generated by MEME indicating the enrichment of each motif compared to background in each cross are also listed. The position weight matrix represented is a representative example of the discovered motifs.