

Supplementary material for Diet-dependent gene expression in honey bees: honey vs. sucrose or high fructose corn syrup

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Table S1: Gene Ontology enrichment analyses for the honey vs. sucrose and honey vs. HFCS contrasts. Analyses were performed for genes significantly different between these two diet treatments (FDR<0.1), using honey bee orthologs to genes from *Drosophila melanogaster*.

Category	Term	Count	P-value
Upregulated by Honey relative to Sucrose			
GOTERM_BP_FAT	aromatic amino acid family metabolic process	7	5.56E-12
GOTERM_BP_FAT	L-phenylalanine metabolic process	3	3.65E-05
GOTERM_BP_FAT	biogenic amine biosynthetic process	3	0.0014
GOTERM_BP_FAT	oxidation reduction	6	0.0037
Upregulated by Sucrose relative to Honey			
GOTERM_BP_FAT	axonogenesis	7	6.31E-04
GOTERM_BP_FAT	cell projection organization	9	6.52E-04
GOTERM_BP_FAT	anion transport	4	0.0020
GOTERM_CC_FAT	intrinsic to membrane	14	0.0261
GOTERM_BP_FAT	post-embryonic organ development	6	0.0213
Upregulated by Honey relative to HFCS			
GOTERM_BP_FAT	aromatic amino acid family metabolic process	6	2.37E-11
UP_SEQ_FEATURE	metal ion-binding site:Iron	3	4.16E-05
GOTERM_BP_FAT	oxidation reduction	5	0.0017
Upregulated by HFCS relative to Honey			
GOTERM_CC_FAT	intrinsic to membrane	7	0.0027

Table S2. Gene Ontology terms enriched for genes that overlapped between honey-related contrasts and maturation-related microarray experiments. Number of genes within each term is shown in each column with *P* values in parentheses. Analyses were performed using honey bee orthologs to genes from *Drosophila melanogaster*.

	GO Term	Nurse vs. Forager	Control vs. vg RNAi	Pollen+Honey vs. Sucrose
Honey vs. Sucrose	aromatic amino acid family metabolic process	7 (1.47E-10)	7 (3.31E-08)	7 (2.50E-10)
	L-phenylalanine metabolic process	3 (9.58E-05)	3 (5.32E-04)	3 (1.13E-04)
	extracellular region	5 (0.002)	-	-
	metal ion-binding site:Iron	3 (4.94E-04)	-	3 (6.16E-04)
Honey vs. HFCS	aromatic amino acid family metabolic process	6 (1.06E-10)	6 (4.81E-09)	6 (3.32E-10)
	Tyrosine Metabolism	5 (8.51E-07)	-	5 (8.51E-07)
	metal ion-binding site:Iron	3 (8.31E-05)	3 (3.85E-04)	-

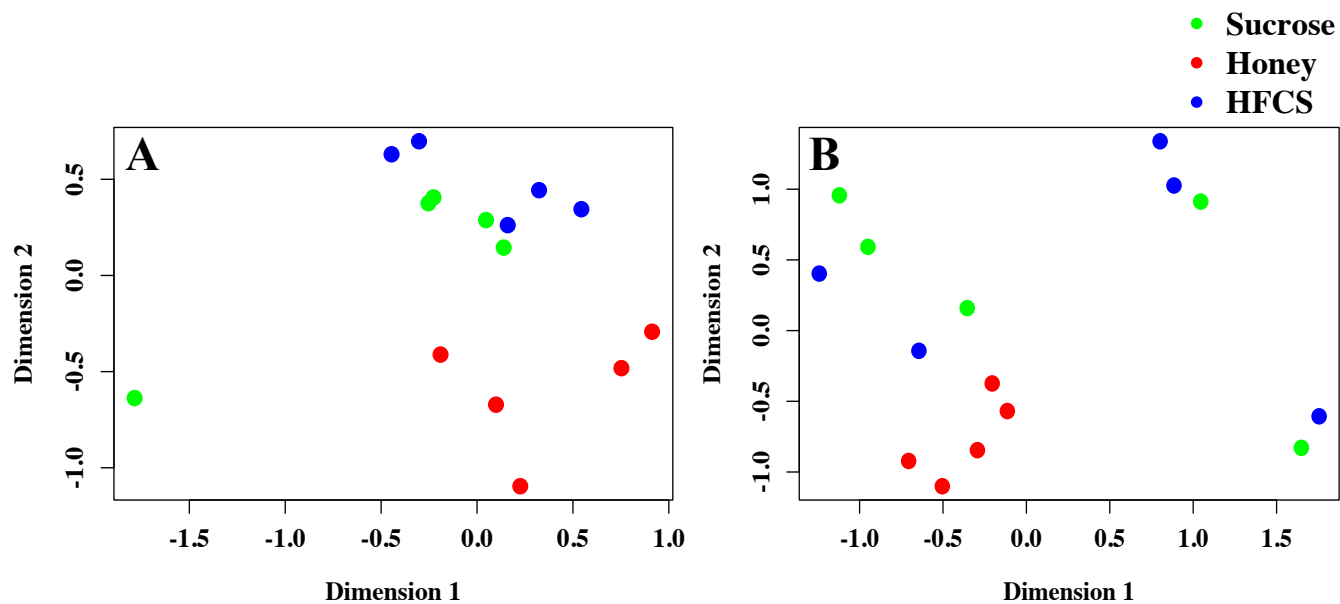


Figure S1: Multidimensional scaling (MDS) plots generated separately for each colony. (A) MDS plot for the colony heavily infected with deformed wing virus (Colony A). (B) MDS plot for the colony with lower levels of viral infection (Colony B). Green = sucrose fed bees; blue = bees fed high fructose corn syrup; red = bees fed honey. Plots were generated using plotMDS function in edgeR, using normalized counts and log fold changes of the top 100 genes.

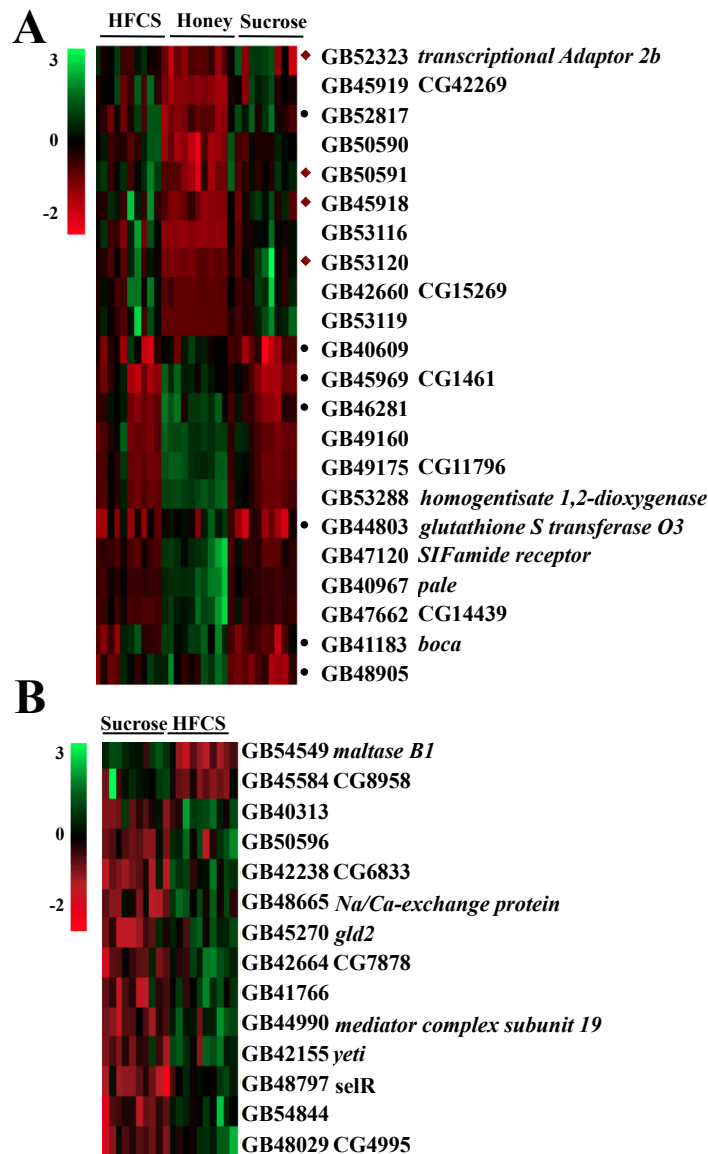


Figure S2: Heat map depicting log fold changes (median-centered values) for top predictor genes of diet treatments. Columns represent samples for each specified diet treatment and rows represent genes. Honey bee accession numbers are shown for each gene as well as the gene name for the corresponding *Drosophila melanogaster* ortholog, if present. (A) shows a joint list of top predictor genes for Honey vs. Sucrose and Honey vs. HFCS contrast. (•) denotes top predictors for the Honey vs. Sucrose contrast only. (♦) are for top predictors specific to the Honey vs. HFCS contrast. (B) show top predictors for the HFCS and sucrose comparison.