

Supplementary Comparisons: relevant contrasts of immune priming treatments from the transcriptomic analysis. Treatment comparisons are titled on each page, and included are the differentially expressed genes, description, log2FoldChange, p-values, GO terms and names.

Comparison: DWV vs Naive

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100740347	LOC100740347	uncharacterized LOC100740347	3.047034272	0.0010109	NA	NA
					GO:0055114; GO:0035002; GO:0007424; GO:0035336; GO:0035149; GO:0006629	liquid clearance, open tracheal system; open tracheal system development; long-chain fatty-acyl-CoA metabolic process; lumen formation, open tracheal system; lipid metabolic process
LOC100741032	LOC100741032	fatty acyl-CoA reductase wat	3.423601649	0.04934464	GO:0006629	mitotic cell cycle; chromosome segregation; cortical actin cytoskeleton organization; protein dephosphorylation; dephosphorylation; cell projection assembly; response to wounding; peptidyl-tyrosine dephosphorylation; endocytic recycling; lipid metabolic process
					GO:0000278; GO:0007059; GO:0030866; GO:0006470; GO:0016311; GO:0030031; GO:0009611; GO:0035335; GO:0032456; GO:0006629	
LOC100741387	mtm	myotubularin	1.007622	0.02273079	GO:0006629	metabolic process
		nose resistant to fluoxetine protein 6	6.393281395	0.0489736	NA	NA
					GO:0055114; GO:0042593; GO:0022900; GO:0006090; GO:0006108	glucose homeostasis; electron transport chain; pyruvate metabolic process; malate metabolic process
LOC100743251	Men	Malic enzyme	1.28222367	0.03815688	GO:0006108	ecdysteroid metabolic process; instar larval or pupal development
		glucose dehydrogenase [FAD, quinone]	3.604196615	0.02195087	GO:0002165; GO:0055114	
		uncharacterized LOC100746302	1.772379693	0.0283907	NA	NA
						long-chain fatty acid biosynthetic process; fatty acid metabolic process; fatty acid biosynthetic process; very long-chain fatty acid biosynthetic process; fatty acid elongation, monounsaturated fatty acid; sphingolipid biosynthetic process; fatty acid elongation, saturated fatty acid; fatty acid elongation; fatty acid elongation, polyunsaturated fatty acid; lipid metabolic process
		elongation of very long chain fatty acids protein 6	2.656617835	0.01146448	GO:0042759; GO:0006631; GO:0006633; GO:0042761; GO:0034625; GO:0030148; GO:0019367; GO:0030497; GO:0034626; GO:0006629	
LOC100748215	LOC100748215					ubiquitin-dependent protein catabolic process; multicellular organism development
		uncharacterized LOC100748688	-3.129431663	0.04934464	GO:0006511; GO:0007275	
LOC100749524	LOC100749524	probable cytochrome b5 2	1.592263721	0.02195087	NA	NA
		uncharacterized LOC105681386	1.830584034	0.02195087	NA	NA
		uncharacterized LOC112213548	3.37283031	0.04934464	NA	NA
		uncharacterized LOC117152173	1.728358025	0.02609707	NA	NA

Comparison: DWV vs Sham

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100741694	LOC100741694	venom serine protease Bi-VSP- like	5.820558828	0.000258	GO:0006508	proteolysis
LOC100741871	LOC100741871	upstream stimulatory factor 2	-0.572686802	0.01798684	NA	NA
LOC105680709	LOC105680709	uncharacterized LOC105680709	-6.46499395	0.01784992	NA	NA
LOC105682028	Nplp3	Neuropeptide-like precursor 3	15.9649136	3.44E-06	NA	NA

[illegible]

Comparison: GFP vs Sham

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100741694	LOC100741694	venom serine protease Bi-VSP- like	4.934504234	0.0134944	GO:0006508	proteolysis
LOC105680709	LOC105680709	uncharacterized LOC105680709	-7.721999213	0.00030459	NA	NA
LOC105682028	Nplp3	Neuropeptide- like precursor 3	18.80268133	4.45E-10	NA	NA

Comparison: Heat-Killed vs Naïve

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100740362	LOC100740362	hymenoptaecin-like	-5.821036488	0.04579742	GO:0002376; GO:0042742; GO:0045087	immune system process; defense response to bacterium; innate immune response
LOC100741032	LOC100741032	fatty acyl-CoA reductase wat	3.203099981	0.03877048	GO:0055114; GO:0035002; GO:0007424; GO:0035336; GO:0035149; GO:0006629	liquid clearance, open tracheal system; open tracheal system development; long-chain fatty-acyl-CoA metabolic process; lumen formation, open tracheal system; lipid metabolic process
LOC100741387	mtm	myotubularin	0.874534348	0.03877048	GO:0000278; GO:0007059; GO:0030866; GO:0006470; GO:0016311; GO:0030031; GO:0009611; GO:0035335; GO:0032456; GO:0006629	mitotic cell cycle; chromosome segregation; cortical actin cytoskeleton organization; protein dephosphorylation; dephosphorylation; cell projection assembly; response to wounding; peptidyl-tyrosine dephosphorylation; endocytic recycling; lipid metabolic process
LOC100742963	LOC100742963	nose resistant to fluoxetine protein 6	5.988521901	0.03877048	NA	NA
LOC100743251	Men	Malic enzyme	1.155123387	0.03877048	GO:0055114; GO:0042593; GO:0022900; GO:0006090; GO:0006108	glucose homeostasis; electron transport chain; pyruvate metabolic process; malate metabolic process
LOC100743508	LOC100743508	elongation of very long chain fatty acids protein AAEL008004	2.066498155	0.03877048	GO:0006631; GO:0006633; GO:0042761; GO:0034625; GO:0030148; GO:0019367; GO:0030497; GO:0034626; GO:0006629	fatty acid metabolic process; fatty acid biosynthetic process; very long-chain fatty acid biosynthetic process; fatty acid elongation, monounsaturated fatty acid; sphingolipid biosynthetic process; fatty acid elongation, saturated fatty acid; fatty acid elongation; fatty acid elongation, polyunsaturated fatty acid; lipid metabolic process
LOC100744619	LOC100744619	very-long-chain 3- oxoacyl-CoA reductase	1.357750386	0.03877048	GO:0010884; GO:0031669; GO:0030308; GO:0032876; GO:0014067	positive regulation of lipid storage; cellular response to nutrient levels; negative regulation of cell growth; negative regulation of DNA endoreduplication; negative regulation of phosphatidylinositol 3- kinase signaling
LOC100744921	LOC100744921	glucose dehydrogenase [FAD, quinone]	3.458933144	0.0160758	GO:0045455; GO:0002165; GO:0055114	ecdysteroid metabolic process; instar larval or pupal development
LOC100745464	LOC100745464	apidaecins type 14	-5.274918916	0.0218934	NA	NA
LOC100748215	LOC100748215	elongation of very long chain fatty acids protein 6	2.469360926	0.0160758	GO:0042759; GO:0006631; GO:0006633; GO:0042761; GO:0034625; GO:0030148; GO:0019367; GO:0030497; GO:0034626; GO:0006629	long-chain fatty acid biosynthetic process; fatty acid metabolic process; fatty acid biosynthetic process; very long-chain fatty acid biosynthetic process; fatty acid elongation, monounsaturated fatty acid; sphingolipid biosynthetic process; fatty acid elongation, saturated fatty acid; fatty acid elongation; fatty acid elongation, polyunsaturated fatty acid; lipid metabolic process
LOC100749524	LOC100749524	probable cytochrome b5 2	1.449825051	0.03194105	NA	NA

Comparison: Heat-Killed vs Sham

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100741694	LOC100741694	venom serine protease Bi-VSP-like	6.477126894	1.32E-05	GO:0006508	proteolysis
						aromatic amino acid family metabolic process; regulation of circadian sleep/wake cycle, sleep; serotonin biosynthetic process; tracheal pit formation in open tracheal system; open tracheal system development; sleep
LOC100742465	Trhn	tryptophan hydroxylase	-2.895421408	0.00514625	GO:0030431	sleep
LOC100748947	LOC100748947	sugar transporter ERD6-like 5	15.72644368	9.87E-05	GO:0055085	transmembrane transport
LOC105680709	LOC105680709	uncharacterized LOC105680709	-7.726728361	0.00021409	NA	NA
LOC105681517	LOC105681517	uncharacterized LOC105681517	20.1288825	0.00514625	NA	NA
LOC105682028	Nplp3	Neuropeptide-like precursor 3	13.01846107	0.01049738	NA	NA
LOC112213713	LOC112213713	uncharacterized LOC112213713	-1.550636722	0.04115405	NA	NA

Comparison: IAPV vs GFP

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100740347	LOC100740347	uncharacterized LOC100740347	-2.4609251	0.03954134	NA	NA
LOC100744287	LOC100744287	esterase FE4-like	7.14902816	0.00036229	NA	NA
LOC100746168	LOC100746168	sodium-dependent nutrient amino acid transporter 1-like	-1.1451536	0.01601858	GO:0006836; GO:1902475; GO:0003333	neurotransmitter transport; L-alpha-amino acid transmembrane transport; amino acid transmembrane transport
LOC100747731	Obp1	odorant binding protein 1	7.72915514	1.74E-05	GO:0007608; GO:0007619; GO:0007606; GO:0019236; GO:0042048	sensory perception of smell; courtship behavior; sensory perception of chemical stimulus; response to pheromone; olfactory behavior
LOC105680855	LOC105680855	uncharacterized LOC105680855	-3.0766149	0.03954134	NA	NA

Comparison: IAPV vs Naïve

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100744287	LOC100744287	esterase FE4-like	6.371142586	0.00397911	NA	NA
						sensory perception of smell; courtship behavior; sensory perception of chemical stimulus; response to pheromone; olfactory behavior
LOC100747731	Obp1	odorant binding protein 1	7.56649022	4.36E-05	GO:0007608; GO:0007619; GO:0007606; GO:0019236; GO:0042048	ubiquitin-dependent protein catabolic process; multicellular organism development
LOC100748688	LOC100748688	uncharacterized LOC100748688	-3.570811017	0.01304206	GO:0006511; GO:0007275	transmembrane transport; glucose import
LOC100749069	LOC100749069	uncharacterized LOC100749069	-18.2666006	0.00087079	GO:0055085; GO:0046323	
LOC100749853	LOC100749853	protein C19orf12 homolog	-3.294764557	0.01304206	NA	NA
LOC105680206	LOC105680206	uncharacterized LOC105680206	6.63887177	0.02860822	NA	NA
LOC105680855	LOC105680855	uncharacterized LOC105680855	-3.001649595	0.04993823	NA	NA

Comparison: IAPV vs Sham

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100741694	LOC100741694	venom serine protease Bi-VSP- like	5.43862094	0.00122409	GO:0006508	proteolysis
LOC100747731	Obp1	odorant binding protein 1	6.415632066	0.00113962	GO:0007608; GO:0007619; GO:0007606; GO:0019236; GO:0042048	sensory perception of smell; courtship behavior; sensory perception of chemical stimulus; response to pheromone; olfactory behavior
LOC105680206	LOC105680206	uncharacterized LOC105680206	6.688479027	0.03463138	NA	NA
LOC105682028	Nplp3	Neuropeptide-like precursor 3	18.86460252	3.67E-10	NA	NA

Comparison: Low
vs Sham

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100748947	LOC100748947	sugar transporter ERD6-like 5	13.45683717	0.01133654	GO:0055085	transmembrane transport
LOC105680709	LOC105680709	uncharacterized LOC105680709	-6.203943268	0.041098129	NA	NA
LOC105682028	Nplp3	Neuropeptide-like precursor 3	15.18111166	3.43E-05	NA	NA

Comparison: Sham vs Naïve

gene	gene_name	gene_description	log2FoldChange	padj	GO_terms	GO_names
LOC100740407	LOC100740407	venom dipeptidyl peptidase 4	-1.374050405	0.01809294	GO:0006508; GO:0046718; GO:0050919	proteolysis; viral entry into host cell; negative chemotaxis ubiquitin-dependent protein catabolic process; multicellular organism
LOC100748688	LOC100748688	uncharacterized LOC100748688 sugar transporter	-3.329693673	0.03714986	GO:0006511; GO:0007275	development transmembrane transport
LOC100748947	LOC100748947	ERD6-like 5	-15.84717914	7.54E-05	GO:0055085	
LOC100749853	LOC100749853	protein C19orf12 homolog	-3.246171266	0.0189343	NA	NA
LOC105680709	LOC105680709	uncharacterized LOC105680709	6.2283913	0.0227896	NA	NA
LOC105681517	LOC105681517	uncharacterized LOC105681517	-18.53193629	0.0227896	NA	NA
LOC105682028	Nplp3	Neuropeptide-like precursor 3	-16.77809627	2.66E-07	NA	NA