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Supplemental Information

Vibrio cholerae-Symbiont Interactions

Inhibit Intestinal Repair in *Drosophila*

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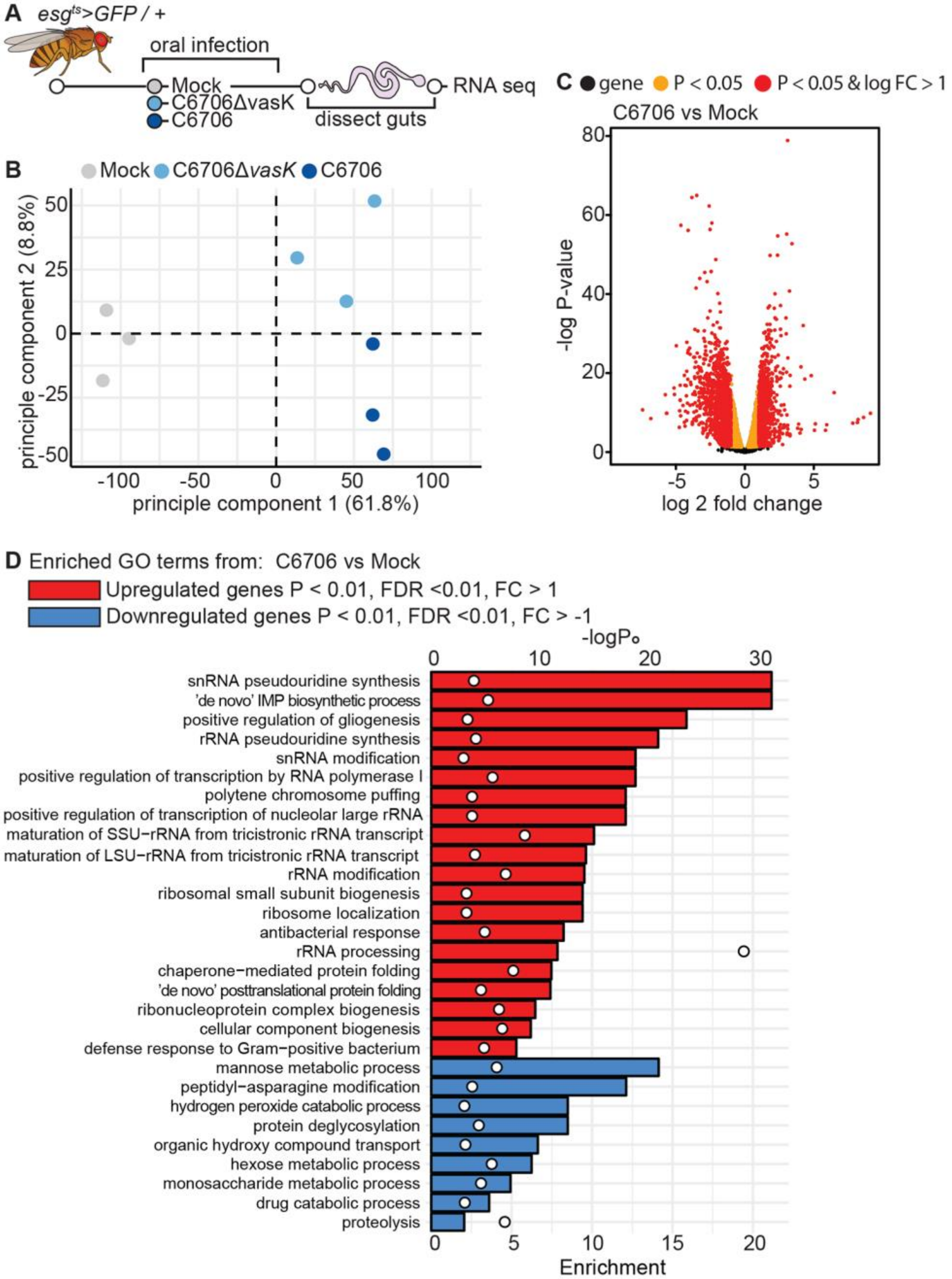
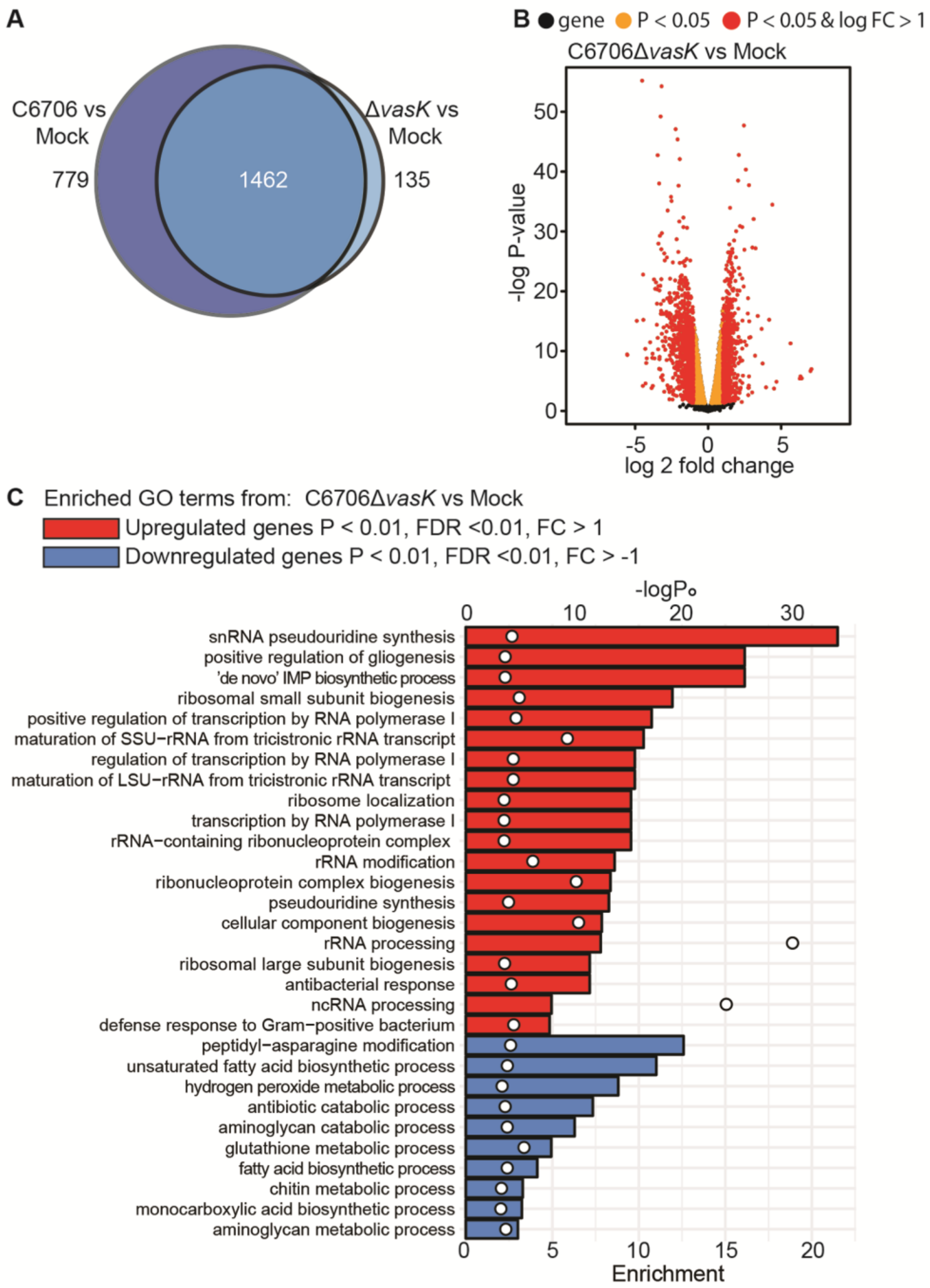
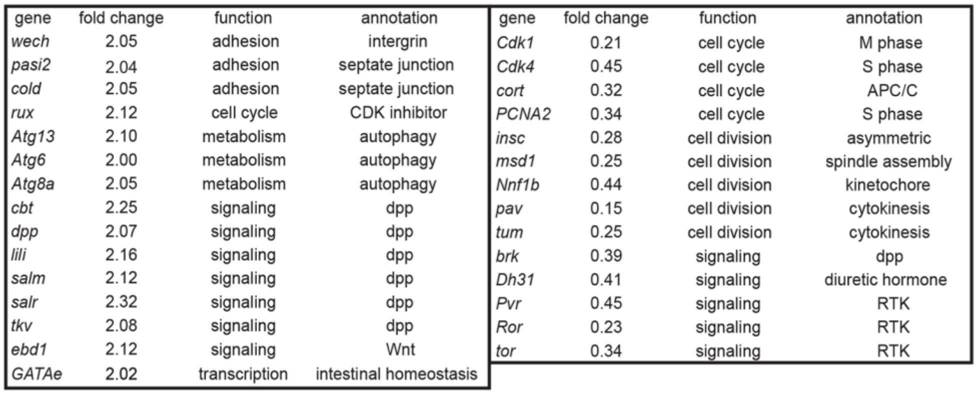
SUPPLEMENTAL INFORMATION



Supplemental Figure 1. The T6SS modifies whole gut transcriptional responses to *V. cholerae*. Related to figures 2 and 3. **(A)** Schematic representation of the RNA-sequencing of *V. cholerae* infected guts, n=10 guts per replicate. **(B)** Principle component analysis from the counts per million obtained from RNA-sequencing of guts dissected from mock infected flies or flies infected with C6706 or C6706Δ*vasK*. **(C)** Volcano plots of differentially expressed genes from comparison of C6706 to Mock. Each dot represents a single gene. Yellow indicates a P<0.05 and red indicates P<0.05 and log2 fold change >1 or <-1. **(D)** Gene Ontology (GO) analysis from the top 500 up or down regulated differently expressed genes (P<0.01, false discovery rate (FDR) <0.01, and log2 fold change >1 or < -1) from comparisons of C6706 to Mock. Bars (bottom X-axis) represent enrichment scores and circles (top X-axis) represent -logP values for each enriched GO term.



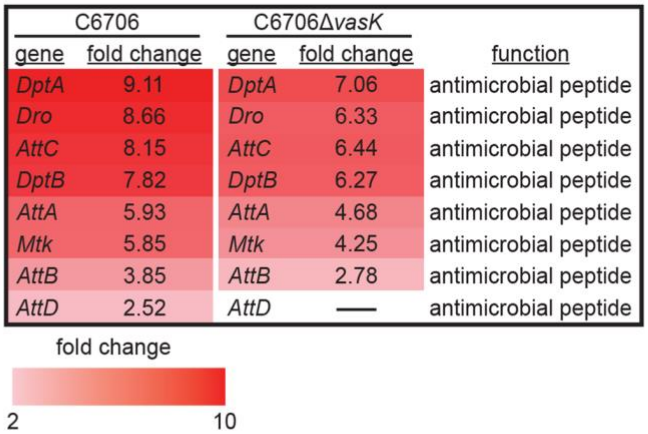
Supplemental Figure 2. The gut transcriptional responses to C6706Δ*vasK*. Related to figures 2 and 3. **(A)** Venn diagram of differentially expressed genes (P<0.01, FDR< 0.01, and log2 fold change >1 or < -1) from comparisons of C6706 to Mock and C6706Δ*vasK* to Mock. **(B)** Volcano plot of differentially expressed genes from comparison of C6706Δ*vasK* to Mock. Each dot represents a gene. Yellow indicates a P < 0.05 and red indicates P<0.05 and log2 fold change >1 or <-1. **(C)** Gene Ontology (GO) analysis from the top 500 up or down regulated differently expressed genes (P<0.01, FDR < 0.01, and log2 fold change >1 or < -1) from comparisons of C6706Δ*vasK* to Mock. Bars (bottom X-axis) represent enrichment scores and circles (top X-axis) represent -logP values for each enriched GO term.



gene	fold change	function	annotation
wech	2.05	adhesion	intergrin
pasi2	2.04	adhesion	septate junction
cold	2.05	adhesion	septate junction
rux	2.12	cell cycle	CDK inhibitor
Atg13	2.10	metabolism	autophagy
Atg6	2.00	metabolism	autophagy
Atg8a	2.05	metabolism	autophagy
cbt	2.25	signaling	dpp
dpp	2.07	signaling	dpp
lili	2.16	signaling	dpp
salm	2.12	signaling	dpp
salr	2.32	signaling	dpp
tkv	2.08	signaling	dpp
ebd1	2.12	signaling	Wnt
GATAe	2.02	transcription	intestinal homeostasis

gene	fold change	function	annotation
Cdk1	0.21	cell cycle	M phase
Cdk4	0.45	cell cycle	S phase
cort	0.32	cell cycle	APC/C
PCNA2	0.34	cell cycle	S phase
insc	0.28	cell division	asymmetric
msd1	0.25	cell division	spindle assembly
Nnf1b	0.44	cell division	kinetochore
pav	0.15	cell division	cytokinesis
tum	0.25	cell division	cytokinesis
brk	0.39	signaling	dpp
Dh31	0.41	signaling	diuretic hormone
Pvr	0.45	signaling	RTK
Ror	0.23	signaling	RTK
tor	0.34	signaling	RTK

Supplemental Figure 3. The T6SS promotes a unique transcriptional response from the intestine. Related to figures 2 and 3. Representative genes involved in intestinal homeostasis, growth, and stress responses differentially regulated in response to C6706 relative to C6706Δ*vasK* from RNA-seq of *Drosophila* whole guts.



C6706		C6706Δ*vasK*		
gene	fold change	gene	fold change	function
DptA	9.11	*DptA*	7.06	antimicrobial peptide
Dro	8.66	*Dro*	6.33	antimicrobial peptide
AttC	8.15	*AttC*	6.44	antimicrobial peptide
DptB	7.82	*DptB*	6.27	antimicrobial peptide
AttA	5.93	*AttA*	4.68	antimicrobial peptide
Mtk	5.85	*Mtk*	4.25	antimicrobial peptide
AttB	3.85	*AttB*	2.78	antimicrobial peptide
AttD	2.52	*AttD*	—	antimicrobial peptide

Supplemental Figure 4. Infection with *V. cholerae* promotes the transcription of antimicrobial peptides. Related to figures 3 and supplemental figures 1 and 2. Antimicrobial peptide expressed from RNA-seq of *Drosophila* whole guts *infected* with C6706 or C6706Δ*vasK*. Fold change was obtained from comparisons of C6706 to mock and C6706Δ*vask* to mock respectively.