Supplemental information

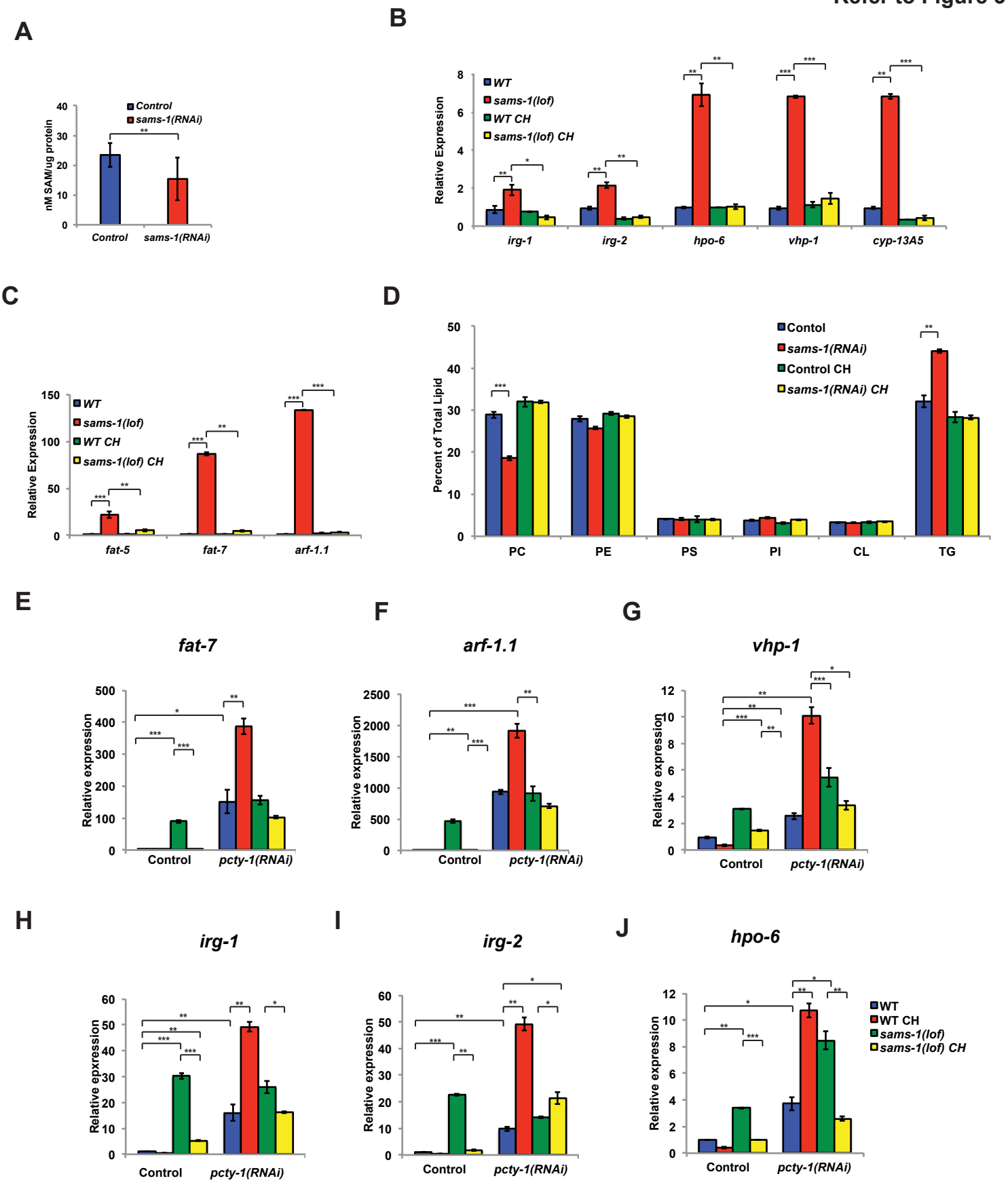
1. **Table S1**. List of genes and human orthologs. Refers to Figure 1.
2. **Table S2** (Microsoft Excel file). **Co-regulation of lipogenic and immune function genes with depletion of SAMe.** Refers to **Figure 1**
3. **Table S3** (Microsoft Excel files), **Choline rescues gene expression after *sams-1(RNAi)*.** Refers to **Figure 3**
4. **Figure S1**. **Choline rescues upregulation of lipogenic or innate immune genes in *sams-1(lof)* animals on *E. coli*.** Refers to **Figure 3**.
5. **Table S4** (Microsoft Excel file). Reduced resistance to *Pseudomonas aeruginosa* in *sams-1(lof)* animals. Statistical data for survival assays. Refers to **Figure 4**.
6. **Figure S2. *sams-1(lof)* mutants fail to accumulate activating histone methylation marks on infection response genes when exposed to *Pseudomonas*.** Refers to **Figure 6**.
7. **Figure S3. *set-16/MLL* is important for expression of infection response genes upon *Pseudomonas* exposure.** Refers to **Figure 7.**

C. elegans	**Human**	**Description**	**Function**	**Class**
act-1	ACTB	Beta actin	Cytoskeleton	Control gene
ama-1	RBP1	RNA Polymerase 2, large subunit	Basal transcription	Control gene
arf-1.1	ARF1	ADP-ribosylation factor 1	GTPase	Intracellular transport
C17H12.6			CUB-like domain	Infection response
C32H11.1			CUB domain protein	Infection response
cyp-13A5	CYP3A5	Cytochrome P450 3A5	monooxygenases	Infection response
fat-7	SCD	Steroyl CoA desaturase	Produces oleic acid	Fatty acid biosynthesis
fbxa-74		F-box protein	Ubiquitin ligase	Infection response
ges-1	CES1	gut esterase	Intestine function	Intestinal control gene
gst-38	HPGDS	Hematopoietic prostaglandin D synthase	Glutathione-S transferase	Infection response
her-1		Male specific secreted protein	Secreted protein	Male specific control gene
hpo-6	MUC3A	Isoform 2 of Mucin-3A	Mucin	Infection response
irg-1				Infection response
irg-2			DUF1768 domain	Infection response
F49H6.13			Claudin-like	Infection response
F55G11.2			CUB domain protein	Infection response
mul-1			Mucin	Infection response
pcaf-1	PCAF	Histone acetyltransferase	Transcription	Control gene
pcyt-1	PCYT1	Choline-phosphate cytidylyltransferase	PC production	Phospholipid synthesis
pgp-5	ABCB5	ATP-binding cassette 5 isoform 1	Efflux pump	Infection response
pmk-1	MAPK14	Mitogen-activated protein kinase 14	p38 MAP kinase	Pathogenic stress response
pmt-1, pmt-1		phosphocholine methylatransferase	PC production	Phospholipid synthesis
rbp-2	RBP2	RNA Polymerase 2 subunit	Basal transcription	Control gene
sams-1	MAT1A/MAT2A	SAM synthase	SAM synthase	1-carbon cycle
sbp-1	SREBF1	Sterol Response Element binding protein-1	Transactivator	Fatty acid

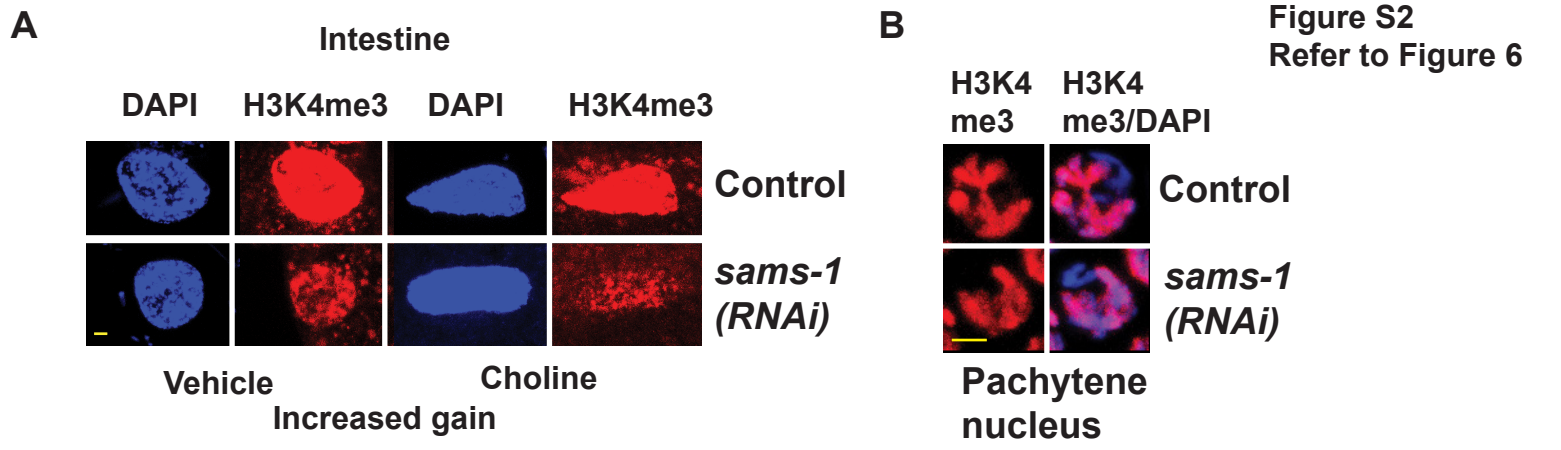
				biosynthesis
sod-3	SOD2	superoxide dismutase	oxidative stress	Oxidative Stress Response
T24C4.4			claudin-like	Infection response
taf-1	TAF1	TFIID component	Basal transcription	Control gene
tir-1	SARM1	Sterile alpha and TIR motif- protein	adaptor protein	Pathogenic stress response
ugt-16	UGT2B7	UDP-glucuronosyltransferase 2B7		Infection response
vhp-1	DUSP16	Dual Specificity Phosphatase	MAP Kinase Phosphatase	Stress response
vit-1		vitellogenin	Yolk transport	Lipid transport
vit-3		vitellogenin	Yolk transport	Lipid transport
Y41C4A.11	COPB2	subunit of the coatomer (COPI) complex	COP I transport	Intracellular transport
Y51B9A.8			CC domain, ShKT domain	Infection response
Y58A7A.5				Infection response

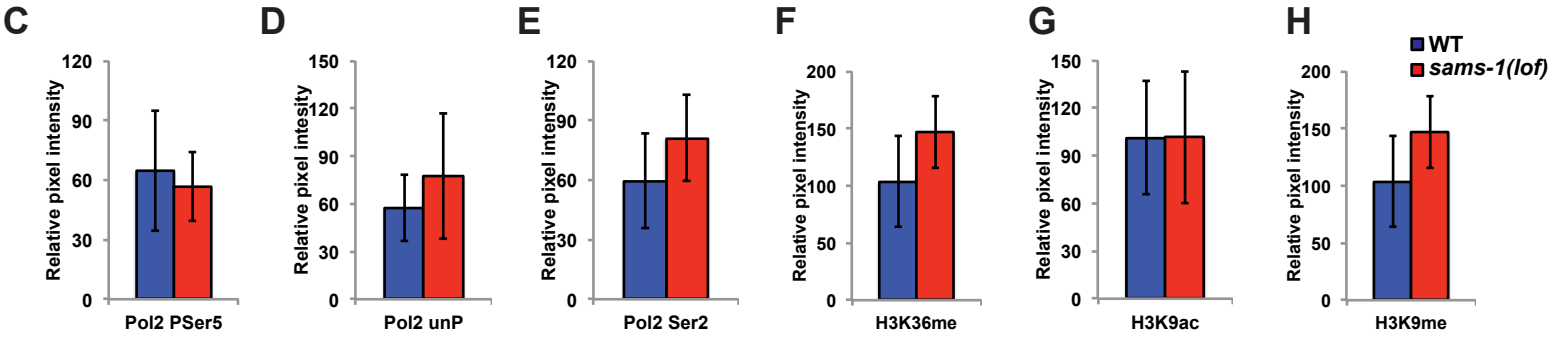
Genes mentioned, with human orthologs and functional classifications for use in our study.

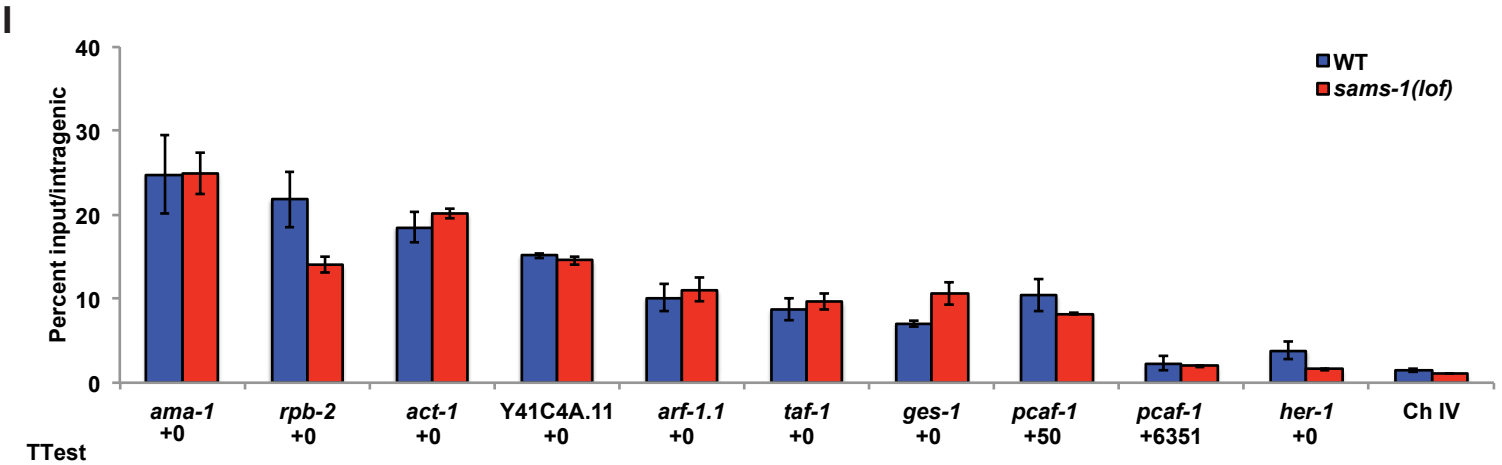
Ding, et al.
Figure S1
Refer to Figure 3



Ding, et al.
Figure S2
Refer to Figure 6

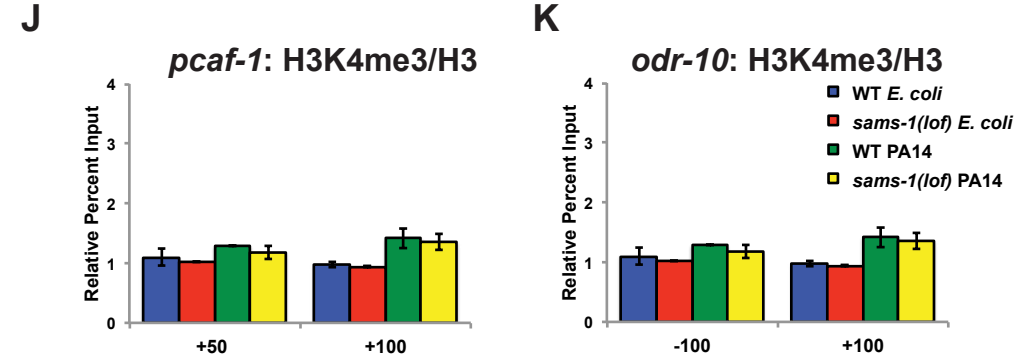






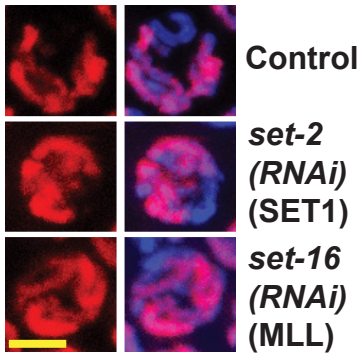
TTest to Ch IV

	ama-1 +0	rpb-2 +0	act-1 +0	Y41C4A.11 +0	arf-1.1 +0	taf-1 +0	ges-1 +0	pcaf-1 +50	pcaf-1 +6351	her-1 +0
WT	0.0019	0.0127	0.0056	0.0003	0.0176	0.0157	0.0026	0.0025	NS	NS
sams-1 (lof)	0.0053	0.0025	0.0004	0.0007	0.0094	0.0061	0.0100	0.0002	NS	NS



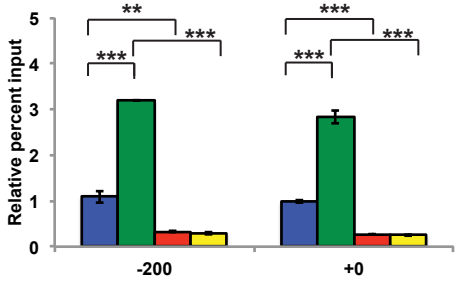
Ding, et al.
Figure S3
Refer to Figure 7

A



Pachytene nucleus

B



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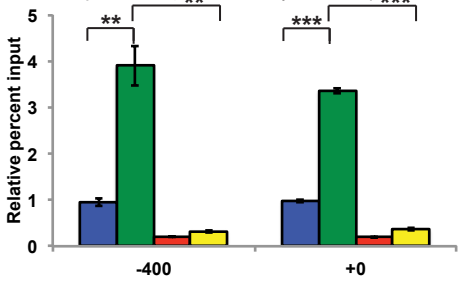

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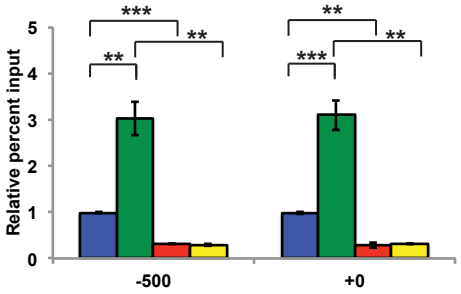

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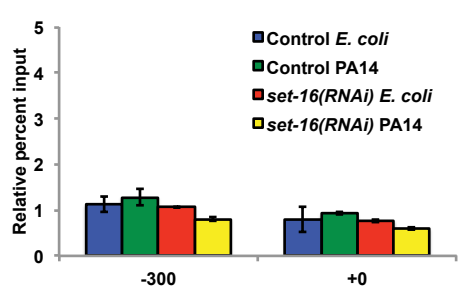

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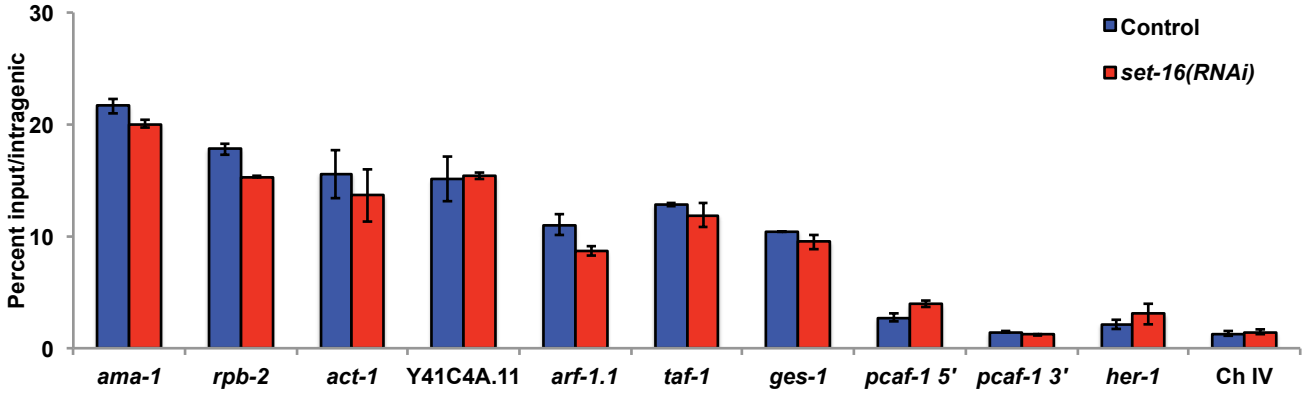

TTest RNAi to Ch IV	ama-1 +0	rpb-2 +0	act-1 +0	Y41C4A.11 +0	arf-1.1 +0	taf-1 +0	ges-1 +0	pcaf-1 5' +50	pcaf-1 3' +6351	her-1 +0
Control	0.0006	0.0006	0.0116	0.0101	0.0047	0.0003	0.0004	0.0488	NS	NS
set-16	0.0002	0.0002	0.0180	0.0003	0.0021	0.0057	0.0036	0.0110	NS	NS

Supplemental Figure Legends

Figure S1. Choline rescues upregulation of lipogenic or innate immune genes in *sams-1(lof)* animals on *E. coli*. (A) Indirect ELISA assay (Artus Biosystems) showing SAM levels normalized to protein concentration in control or *sams-1(RNAi)* animals. qRT-PCR showing expression of genes involved in lipogenesis, or an unrelated, highly expressed gene (**B**) or innate immune genes (**C**) compared between control and choline treated (CH) groups in wild type and *sams-1(lof)* mutants. **D.** GC/MS assays comparing major lipid classes in control and *sams-1(RNAi)* with choline treated samples. PE: phosphatidylethanolamine; PS: phosphatidylserine, PI; phosphatidylinostitol; CL: cardiolipin; TG: triglyceride. RT-PCR comparing choline rescue of *sams-1(RNAi)* with *pcyt-1(RNAi)* for a lipogenic gene (**E**), a highly expressed gene (**F**) or immune function genes (**H-J**). Legend refers to **E-I**. Error bars show standard deviation. Results from Student's T test shown by * <0.05, ** <0.01, *** <0.005.

Figure S2. *sams-1(lof)* mutants fail to accumulate activating histone methylation marks on infection response genes when exposed to *Pseudomonas*. H3K4me3 is diminished in nuclei of intestinal cells (**A**) after *sams-1(RNAi)* and also in choline treated *sams-1(RNAi).* Yellow bar shows 2 microns. Image is identical to **Figure 6A** with levels increased to visualize staining in *sams-1(RNAi)* nuclei. **B.** Immunoflourescence showing H3K4me3 staining is specific to the transcriptionally active autosomes in pachytene nuclei of *sams-1(RNAi)* germlines. Quantitation of immuoflourescence showing an average of pixel intensity over area for 8-12 nuclei per sample for Pol II PSer5 (**C**), Pol II unP (**D**), Pol II Pser2 (**E**), H3K36 (**F**), H3K9ac (**G**) or H3K9me3 (**H**). **I.** Control chromatin immunoprecipitation comparing enrichment of H3K4me3 in control or *sams-1(lof)* animals grown on *E. coli* at the

promoter regions of genes expressed in the intestine and other tissues (*ama-1, rpb-2, act-1, Y41C4A.11, arf-1.1, taf-1 or pcaf-1*), an intestinal specific gene (*ges-1*) or a gene that is not expressed in hermaphrodites (*her-1*). Values are relative to an intragenic sequence on chromosome IV. Chromatin immunoprecipitation comparing levels of H3K4me3 around the start site of control genes grown on *E. coli* (OP50) or *Pseudomonas* (PA14) in wild-type (WT) or *sams-1(lof)* mutants for *pcaf-1* (**K**) and *odr-10* (**J**). Input levels are normalized to the WT *E. coli* value on the upstream primer pair. Data from **Figure 6 E-J, Figure S2 C, J-K** are from the same representative chromatin immunoprecipation, separate qPCRs for *pcaf-1* were used in **Figure S2C** and **S2J** to allow comparison to relative gene sets. Error bars show standard deviation. Results from Student's T test shown by * <0.05, ** <0.01, *** <0.005.

Figure S3: *set-16/MLL* is important for expression of infection response genes upon *Pseudomonas* exposure. A. Immunoflourescence showing H3K4me3 staining is specific to the transcriptionally active autosomes in pachytene nuclei after RNAi of *set-2* or *set-16* from hatching to young adulthood. **B**. Control chromatin immunoprecipitation comparing enrichment of H3K4me3 in control or *set-16* animals grown on *E. coli* at the promoter regions of genes expressed in the intestine and other tissues (*ama-1, rpb-2, act-1, Y41C4A.11, arf-1.1, taf-1 or pcaf-1*), an intestinal specific gene (*ges-1*) or a gene that is not expressed in hermaphrodites (*her-1*). Values are relative to an intragenic sequence on Chromosome IV. Representative chromatin immunoprecipitations comparing induction of infection response genes (**C-E**) and a control gene (**F**) in response to PA14 after control or *set-16 RNAi.* Error bars show standard deviation. Results from Student's T test shown by * <0.05, ** <0.01, *** <0.005.

Supplemental Experimental Procedure

SAM measurements: 1 gram of young adult *C. elegans* were frozen liquid nitrogen, then ground to a fine powder in a -80 degree mortar. After solubilization in 2 milliliters of phospho-buffered saline, extracts were sheared in a Dounce homogenizer with pestle B before sonication for 2-5 20 second bursts. Lysates were cleared, then 30 microliters was used a SAM measurement ELISA kit (Artus Bioscience).