Lohman et al. 2017 Frontiers in Immunology Supplementary Information

T obtain raw sequence data from UT Austin data archive, from the terminal:

wget http://web.corral.tacc.utexas.edu/Lohman_et_al_2017_FrontiersImmunology/Raw*

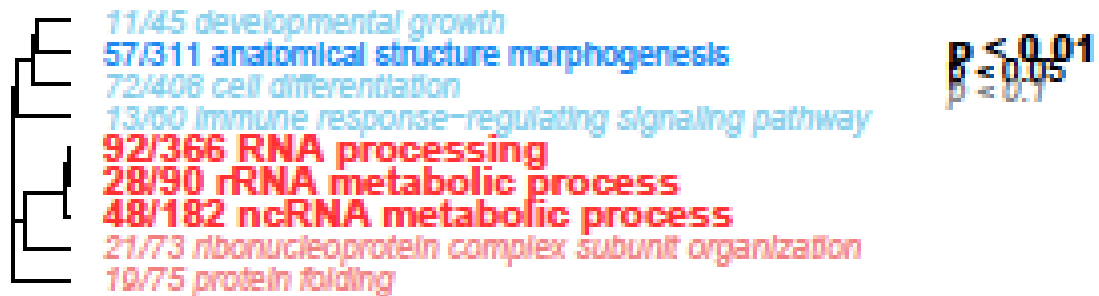To obtain code and data csv files from UT Austin data archive, from the terminal:

wget http://web.corral.tacc.utexas.edu/Lohman_et_al_2017_FrontiersImmunology/Code_Data*

**Supplementary Figure 1.** Population GO enrichment for Molecular Function (A) and Biological Processes (B).

A)

79/383 poly(A) RNA binding
3/7 RNA-dependent ATPase
7/31 ribonucleoprotein complex binding
6/33 ribonuclease
27/150 regulatory region nucleic acid binding
42/215 sequence–specific DNA binding
36/231 transcription factor, sequence–specific DNA binding
77/473 zinc ion binding
26/83 isomerase
5/17 snoRNA binding

$p < 0.01$
$p \leq 0.05$
$p \leq 0.1$

B)

11/45 developmental growth
57/311 anatomical structure morphogenesis
72/406 cell differentiation
13/60 immune response–regulating signaling pathway
92/366 RNA processing
28/90 rRNA metabolic process
48/182 ncRNA metabolic process
21/73 ribonucleoprotein complex subunit organization
19/75 protein folding

$p < 0.01$
$p \leq 0.05$
$p \leq 0.1$

Supplementary Figure 2. Gene-Trait correlations for a signed network with both Rob and Gos fish.
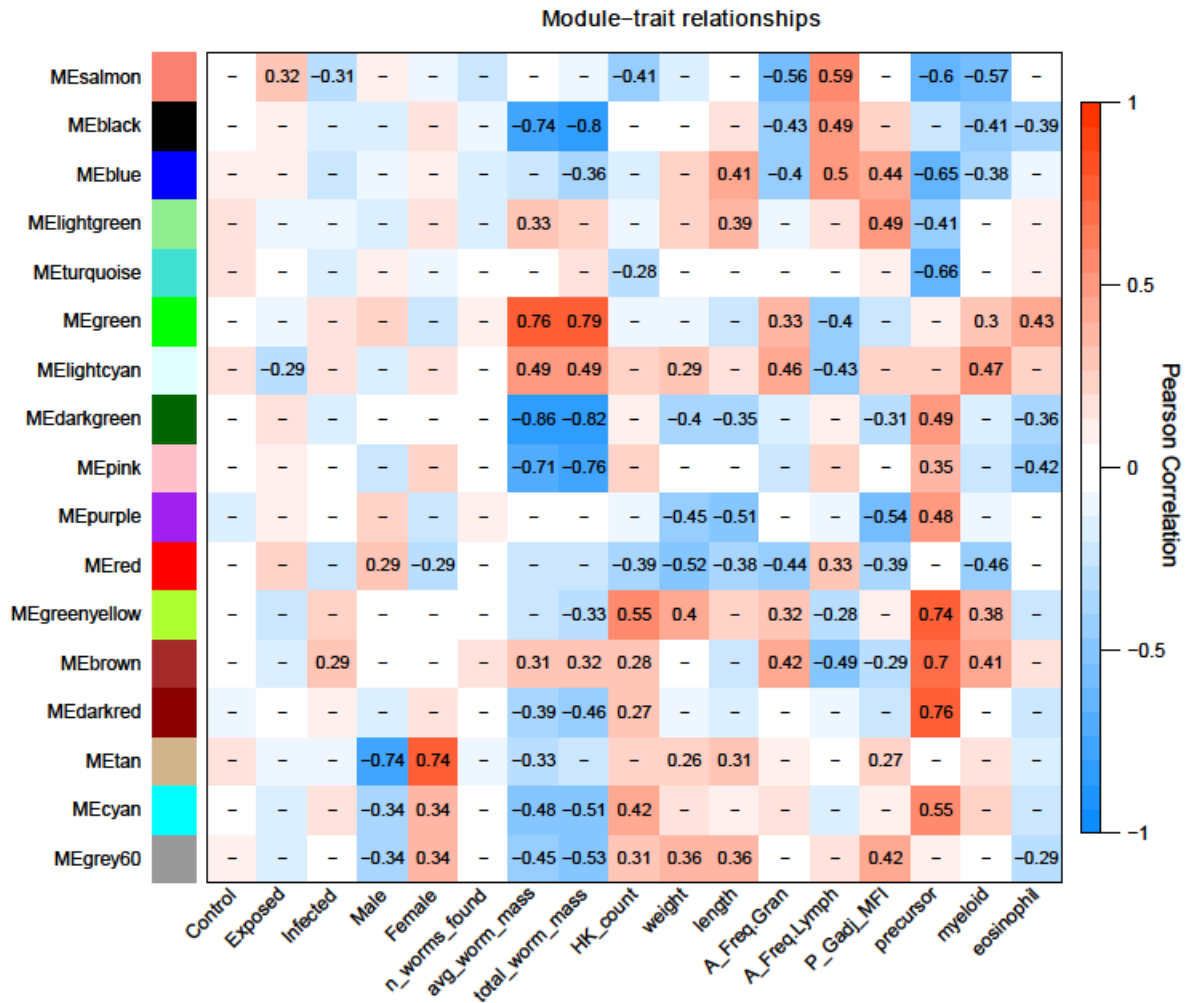

Gene−trait relationships
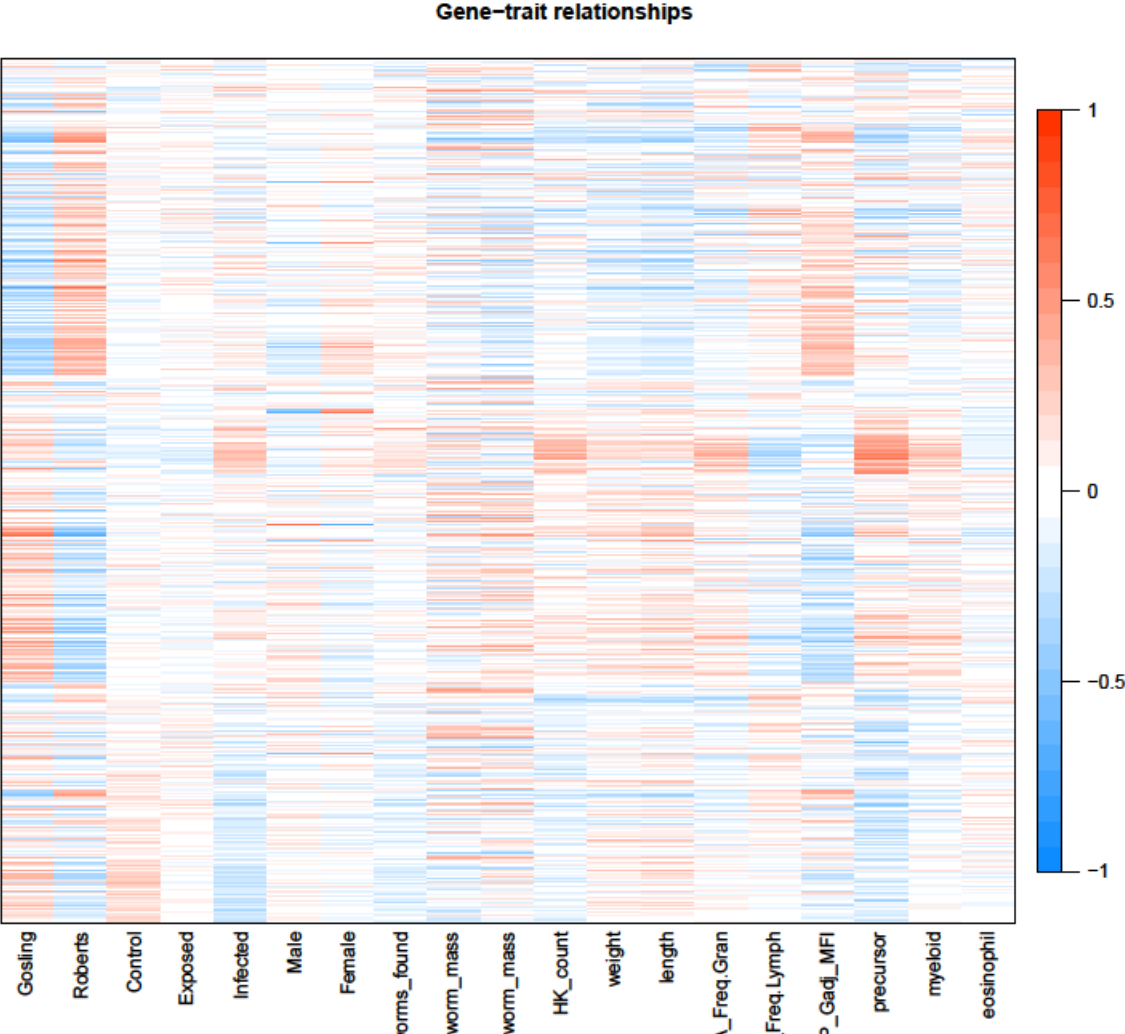
Supplementary Figure 3. Cluster dendrogram from a signed network with both Rob and Gos fish. Colored bars below are groups of genes, or modules.
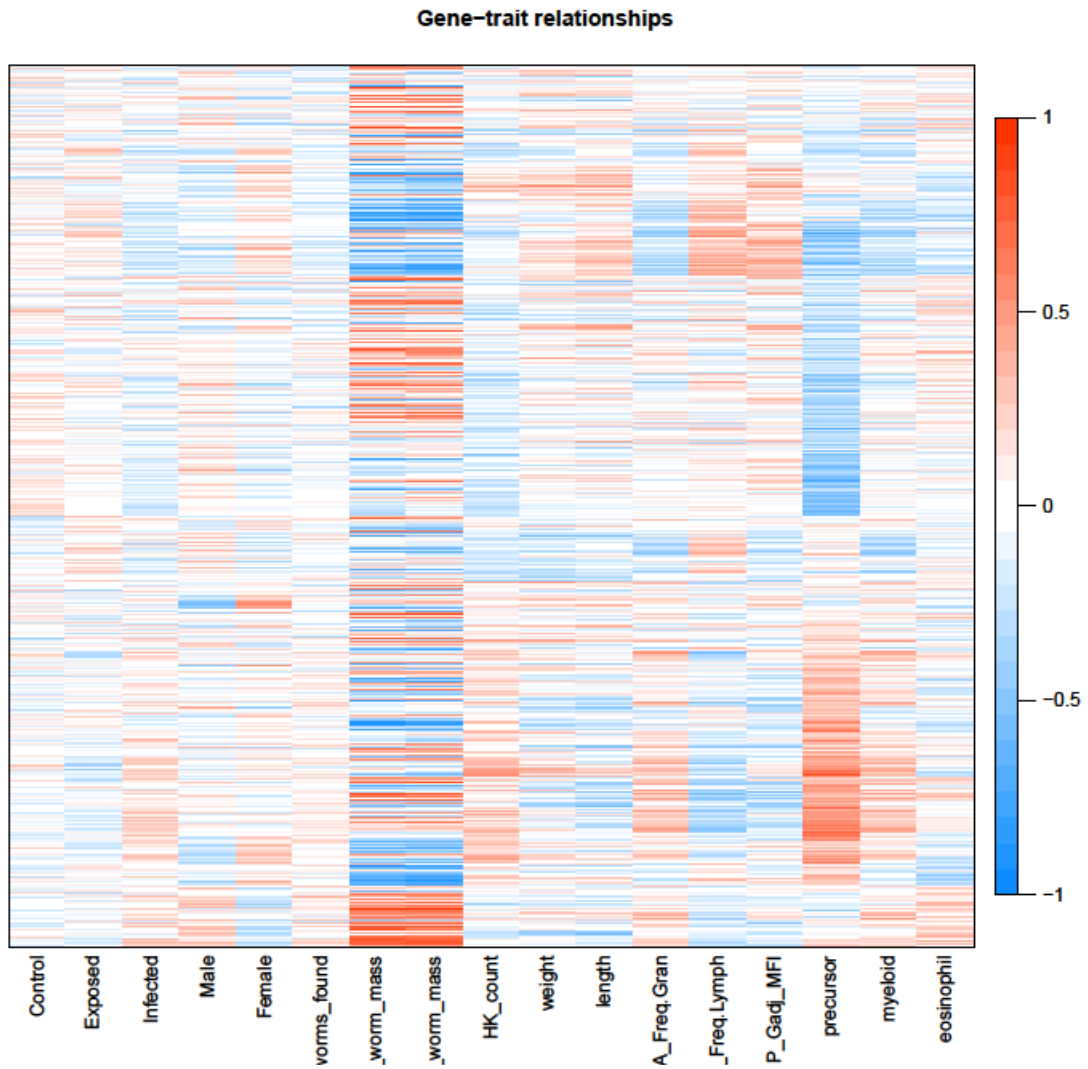

Cluster Dendrogram
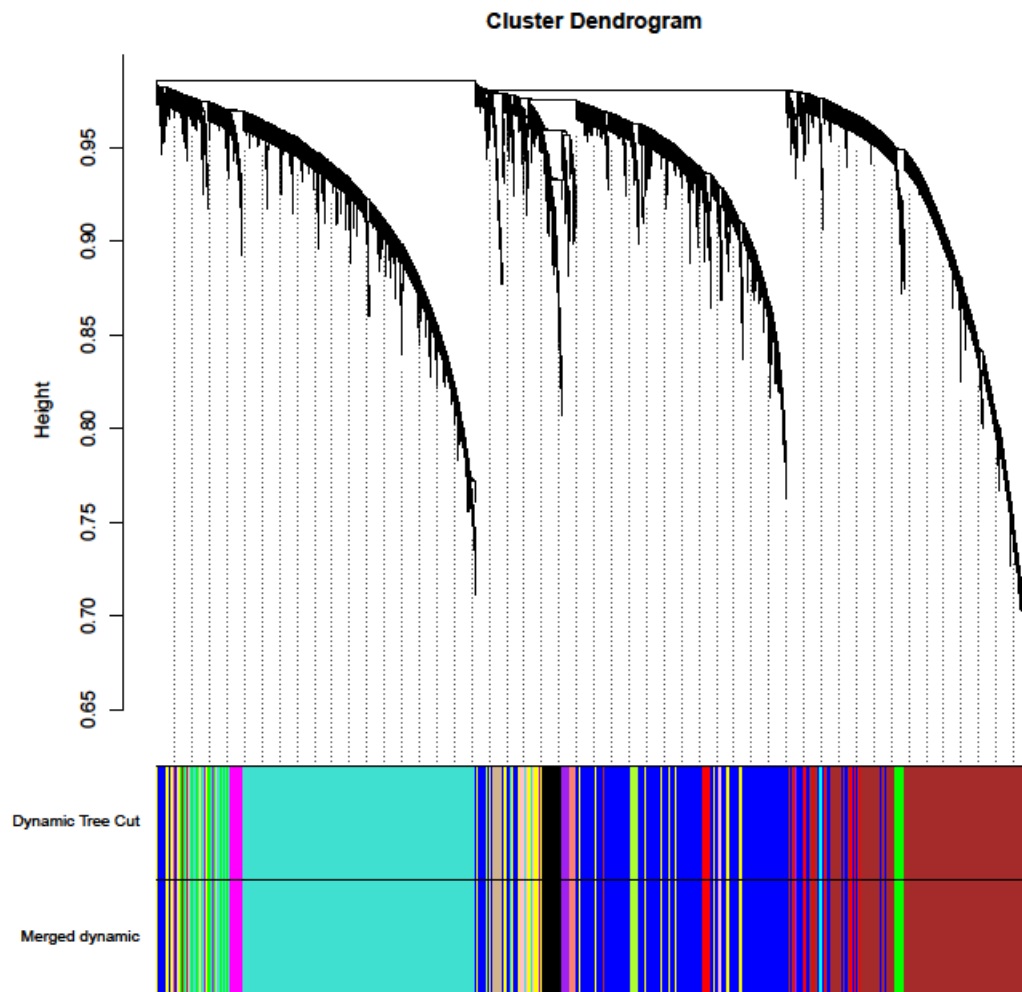
Supplementary Figure 4. Comparison of module membership between signed networks built from Rob only and Gos only fish (see below for additional details on population specific networks). Cell intensity indicates the percent similarity between any two pairs of modules as determined by the fraction of genes shared by both modules.
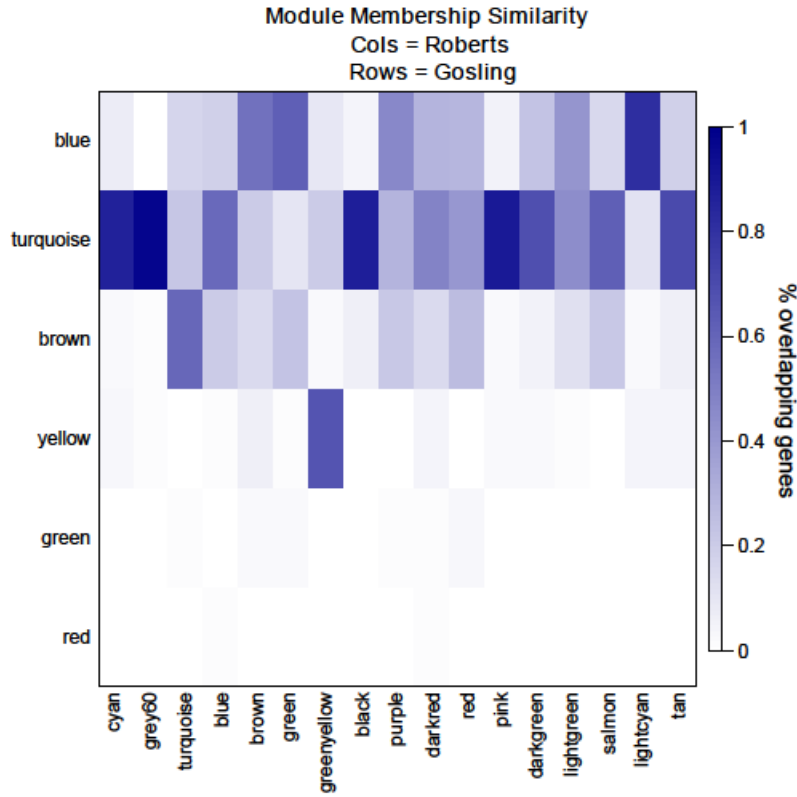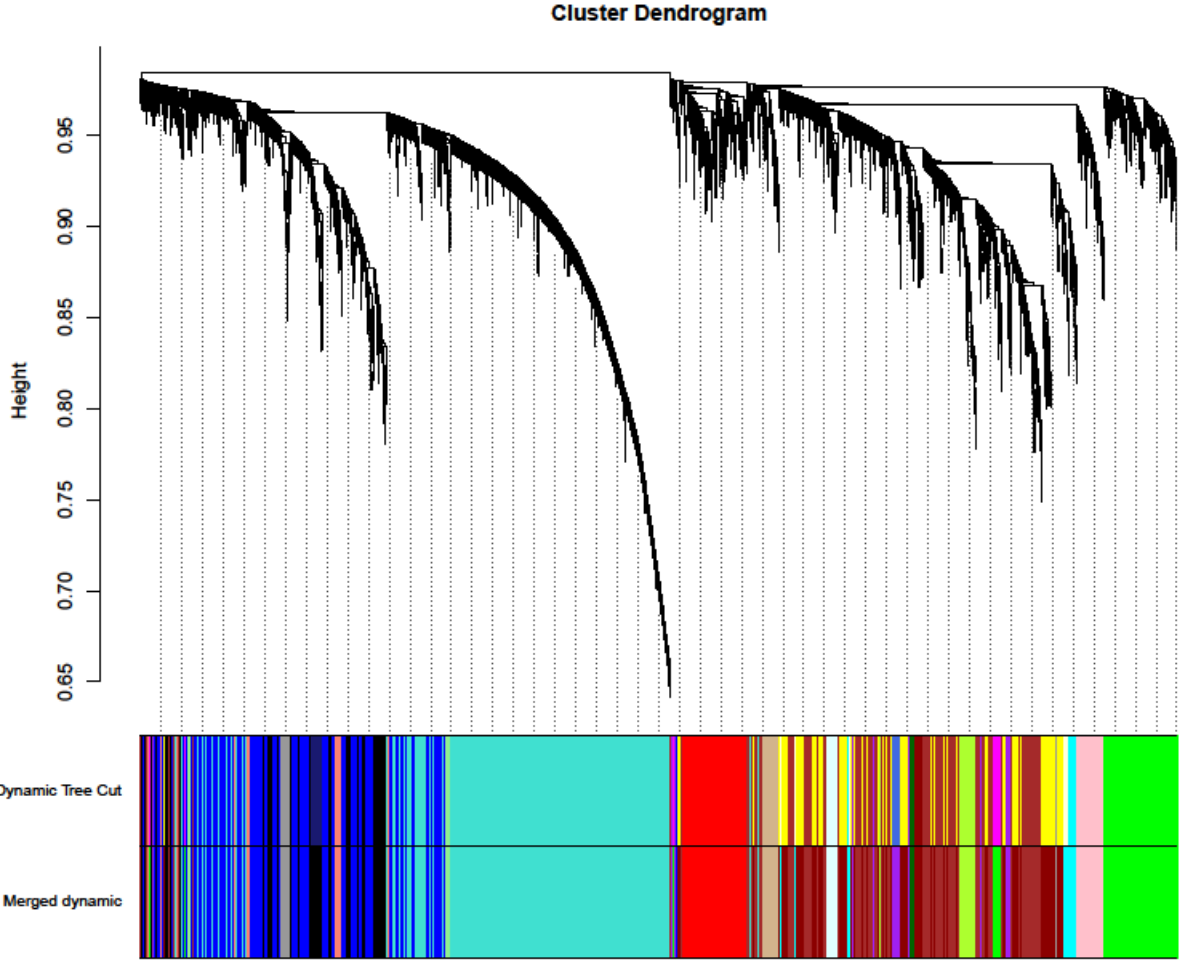
Supplementary Figure 5. Module-trait correlations based on a signed network of only Rob fish. Correlations with p-values greater than 0.1 are omitted.

Module−trait relationships

Module	Control	Exposed	Infected	Male	Female	n_worms_found	avg_worm_mass	total_worm_mass	HK_count	weight	length	A_Freq_Gran	A_Freq_Lymph	P_Gadj_MFI	precursor	myeloid	eosinophil
MEsalmon	−	0.32	−0.31	−	−	−	−	−	−0.41	−	−	−0.56	0.59	−	−0.6	−0.57	−
MEblack	−	−	−	−	−	−	−0.74	−0.8	−	−	−	−0.43	0.49	−	−	−0.41	−0.39
MEblue	−	−	−	−	−	−	−	−0.36	−	−	0.41	−0.4	0.5	0.44	−0.65	−0.38	−
MElightgreen	−	−	−	−	−	−	0.33	−	−	−	0.39	−	−	0.49	−0.41	−	−
MEturquoise	−	−	−	−	−	−	−	−	−0.28	−	−	−	−	−	−0.66	−	−
MEgreen	−	−	−	−	−	−	0.76	0.79	−	−	−	0.33	−0.4	−	−	0.3	0.43
MElightcyan	−	−0.29	−	−	−	−	0.49	0.49	−	0.29	−	0.46	−0.43	−	−	0.47	−
MEdarkgreen	−	−	−	−	−	−	−0.86	−0.82	−	−0.4	−0.35	−	−	−0.31	0.49	−	−0.36
MEpink	−	−	−	−	−	−	−0.71	−0.76	−	−	−	−	−	−	0.35	−	−0.42
MEpurple	−	−	−	−	−	−	−	−	−	−0.45	−0.51	−	−	−0.54	0.48	−	−
MEred	−	−	−	0.29	−0.29	−	−	−	−0.39	−0.52	−0.38	−0.44	0.33	−0.39	−	−0.46	−
MEgreenyellow	−	−	−	−	−	−	−	−0.33	0.55	0.4	−	0.32	−0.28	−	0.74	0.38	−
MEbrown	−	−	0.29	−	−	−	0.31	0.32	0.28	−	−	0.42	−0.49	−0.29	0.7	0.41	−
MEdarkred	−	−	−	−	−	−	−0.39	−0.46	0.27	−	−	−	−	−	0.76	−	−
MEtan	−	−	−	−0.74	0.74	−	−0.33	−	−	0.26	0.31	−	−	0.27	−	−	−
MEcyan	−	−	−	−0.34	0.34	−	−0.48	−0.51	0.42	−	−	−	−	−	0.55	−	−
MEgrey60	−	−	−	−0.34	0.34	−	−0.45	−0.53	0.31	0.36	0.36	−	−	0.42	−	−	−0.29

Pearson Correlation

Supplementary Figure 6. Gene-trait correlations based on a signed network of only Rob fish. Each row is 1 gene.

Gene−trait relationships

Supplementary Figure 7. Cluster dendrogram for signed network with Rob only fish. Colored bars below are groups of genes, or modules.

Cluster Dendrogram

Supplementary Figure 8. Module-trait correlations based on a signed network of only Gos fish. Correlations with p-values greater than 0.1 are omitted.
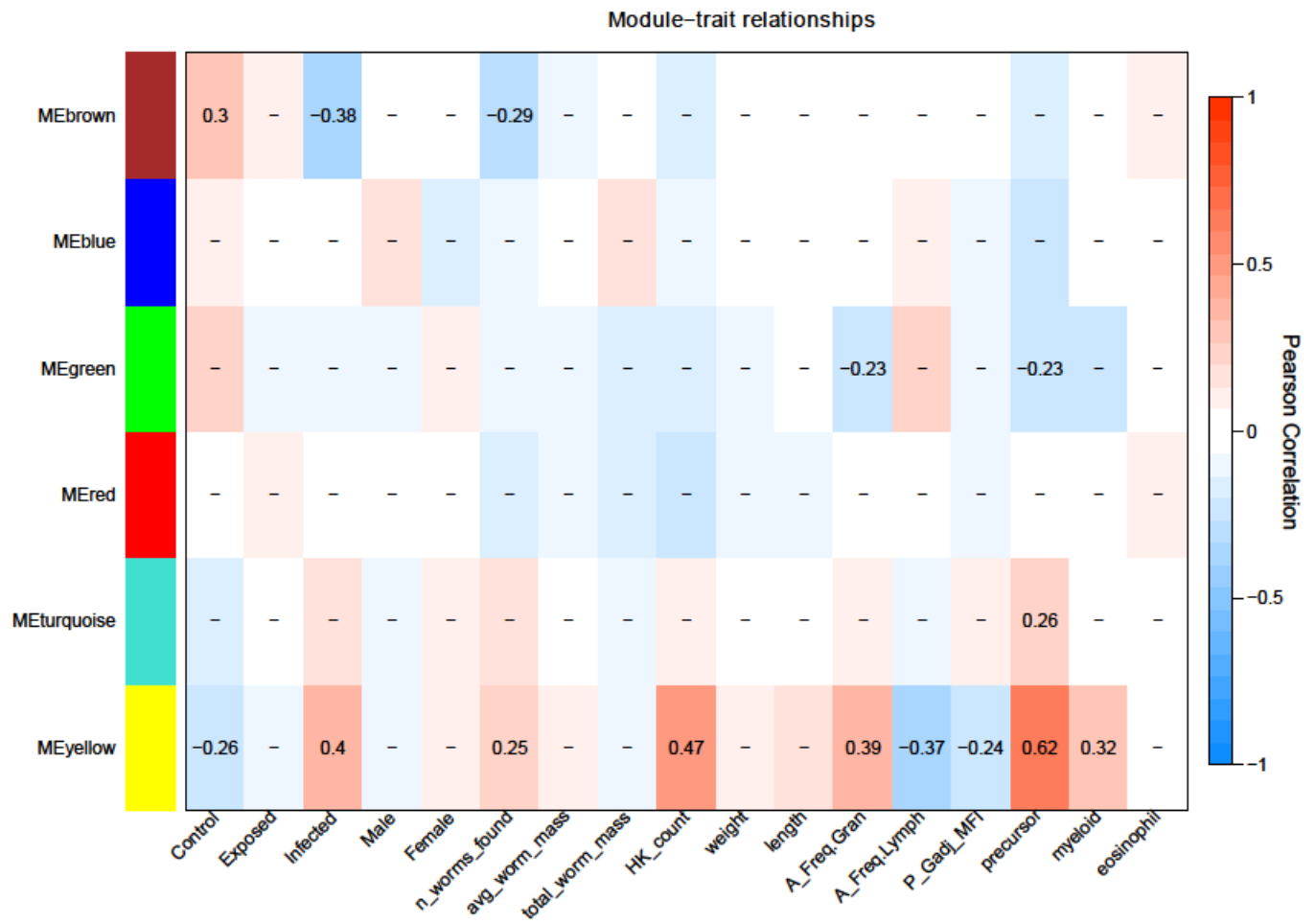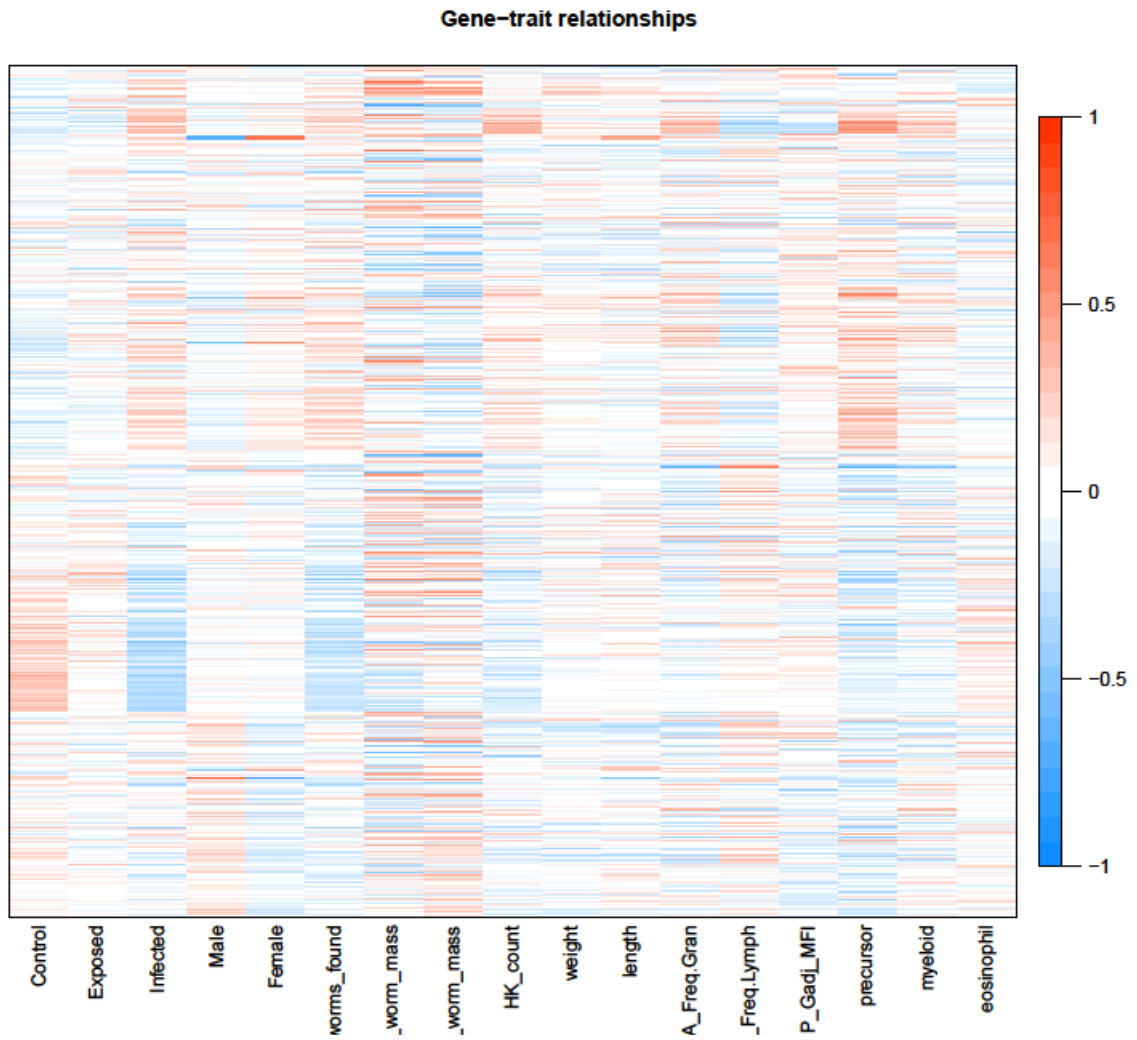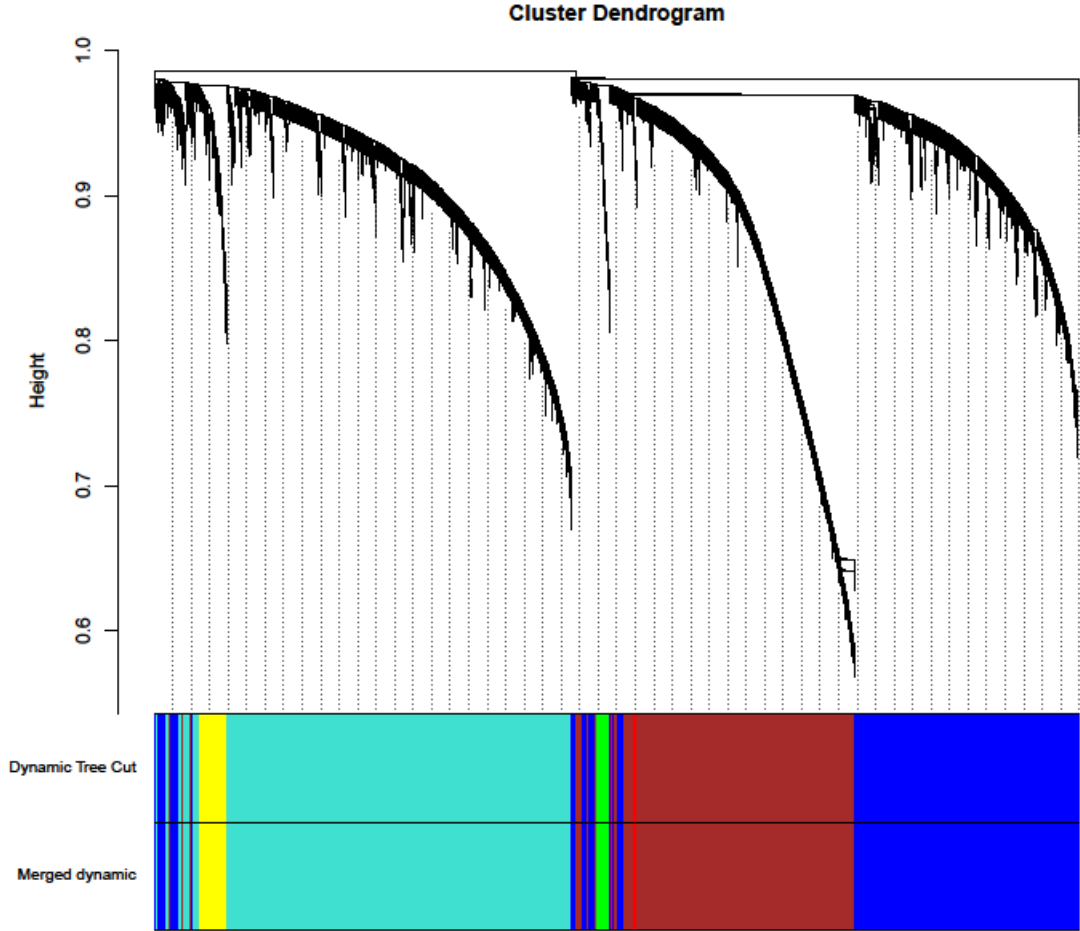
Supplementary Figure 9. Gene-trait correlations based on a signed network of only Gos fish. Each row is 1 gene.

Gene−trait relationships

Supplementary Figure 10. Cluster dendrogram for signed network with Gos only fish. Colored bars below are groups of genes, or modules.

Cluster Dendrogram

Supplementary Table 1. Family and infection status sample sizes, post outlier removal, for TagSeq libraries. RRXX are Rob families and GGXX are Gos families. The infected fish for GG49 was removed as part of outlier analysis.

Family	Control	Exposed	Infected
GG12	2	2	3
GG13	2	2	1
GG15	1	2	1
GG16	1	1	4
GG17	1	2	2
GG22	2	2	1
GG32	2	2	1
GG42	2	2	1
GG47	2	2	2
GG49	2	2	0
GG8	2	2	1
RR10	2	2	1
RR12	2	2	1
RR13	2	2	1
RR15	2	2	1
RR18	2	2	1
RR30	2	2	1
RR44	2	2	2
RR52	2	2	1