SUPPLEMENTAL FILE 1

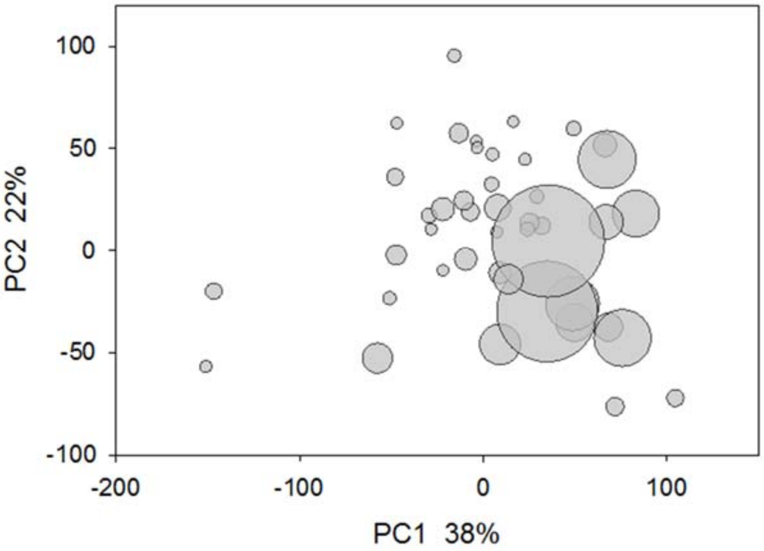

Fig. S1. Principal Coordinate Analysis based on KEGG level 2 functional categories. Datapoints located in close proximity have functionally similar metagenomes. The size of the circles is proportional to oocyst concentration. Metagenome gene abundance from experiment 2 was inferred from 16S sequence data using PICRUSt for 44 fecal samples analyzed by 16S amplicon sequencing and by flow cytometry.

Table S2 Metagenomic differences grouped by KEGG level 2 pathways between severely infected and mildly infected mice.

Group	**KEGG pathway**	**log(abundance)**	**LDA score**	**p**
Severely infected	Poorly Characterized	4.704	2.80	0.034
	Cellular Processes and Signaling	4.629	3.23	0.001
	Metabolism of Cofactors and Vitamins	4.592	2.96	0.041
	Cell Motility	4.540	3.59	0.001
	Genetic Information Processing	4.466	2.92	0.010
	Metabolism unclassified	4.439	2.71	0.002
	Folding Sorting and Degradation	4.341	2.67	0.023
	Signal Transduction	4.332	3.28	0.000
	Glycan Biosynthesis and Metabolism	4.306	2.86	0.002
	Infectious Diseases	3.656	2.61	0.001
	Circulatory System	0.665	2.11	0.008
	Cardiovascular Diseases	0.148	2.60	0.008
Mildly infected	Carbohydrate Metabolism	5.039	3.59	0.005
	Amino Acid Metabolism	4.939	2.89	0.016
	Replication and Repair	4.924	3.38	0.003
	Translation	4.722	3.27	0.002
	Nucleotide Metabolism	4.586	3.04	0.005
	Lipid Metabolism	4.484	2.91	0.002
	Xenobiotics Biodegrad. & Metabolism	4.336	3.05	0.003
	Metabolism of other Amino Acids	4.200	2.53	0.028
	Cell Growth and Death	3.685	2.38	0.001
	Signaling Molecules and Interaction	3.353	2.25	0.001