**Supplementary material**

**Figure S1 Cecal microbial profile across mouse samples.** Using 16S V4 rRNA gene sequence reads, a majority of cecum microbes belong to the Firmicutes phylum followed by Bacteroides. The other abundant phyla were Protobacteria (0.6%), Actinobacteria (0.6%).and Synergistetes (0.3%)

**Figure S2 eQTL map of cecum transcripts in CC mice.**

**Figure S3 Antibiotic Treatment.** Representative scatter-plot of *Odoribacter* vs sleep phenotype from Table 2. Cecums of control (left) and antibiotic treated (right) +/+ mice.

**Figure S4** **Sleep Phenotyping Summary** plot of sleep data from db/db antibiotic experiment.

**Table S1.** Founder strain intraclass correlations, sequences, and genus mapping based on Ribosomal Database Project for Operational Taxonomic Units found in at least 10% of CC mapping population.

**Table S2.** Heritability and eQTLs for cecal intestinal transcript abundance in CC founders and mapping population for probes with strain ICC >0.3.

**Table S3.** Raw sleep data for the 120 hours of sleep monitoring in the db and wt with and without antibiotic from the PiezoSleep system.

**Table S4.** Post-hoc comparison of mean sleep FFT peak amplitude in *db/db* and wild-type mice treated with broad spectrum antibiotic or vehicle control.

**Table S5**. Statistical analysis of plots in Figure S4.

**File S1-** Folder of the de-noised fasta sequences from the CC 454 pyro sequencing.

**File S2-** OTU Command line code