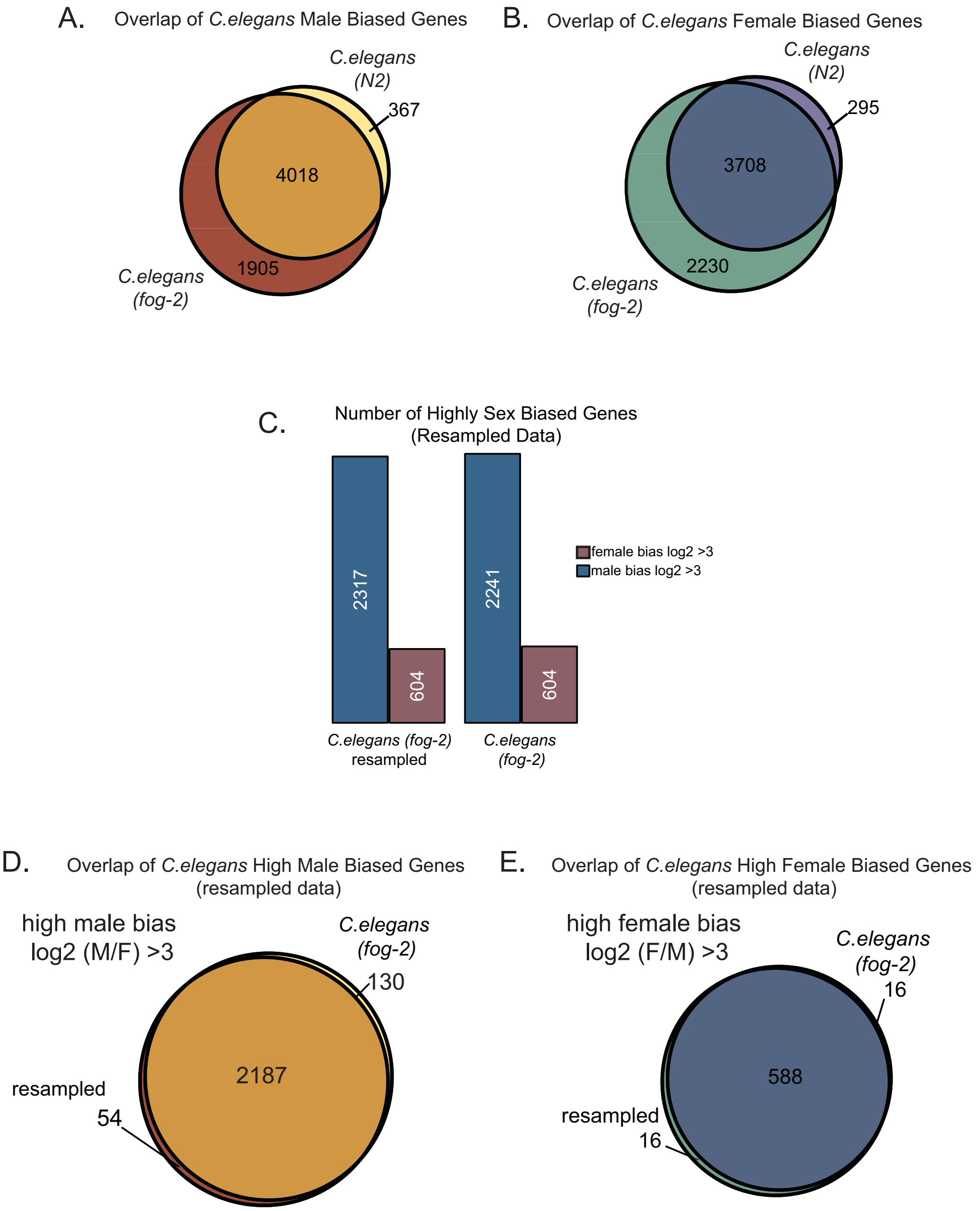

Figure S3 **A)** Sets of male and female-biased genes were determined individually using *C. elegans* (*N2)* (male-hermaphrodite) and (*fog-2)* (male-female) data. Sex-biased genes (including sex-specific genes) are those called differentially expressed by DESeq (q value < 0.05) and with FPKM > 1 in at least one sex. Overlap of male-biased genes is plotted. **B)** Same as in **A** but overlap of female-biased genes is plotted. **C)** *C. elegans (fog-2)* mapped reads were resampled to match the number of mapped reads in *P. pacificus*. Using the resampled data, we identified genes with sex-biased expression. Plot indicates the number of genes with high male and high female-bias (log2 sex expression ratio > 3) for the resampled data (left) and for the original *C. elegans (fog-2)* data. **D)** Overlap of high male-biased genes in the original and the resampled *C. elegans (fog-2)* data. **E)** Same as in **D** but for high female-biased genes**.**