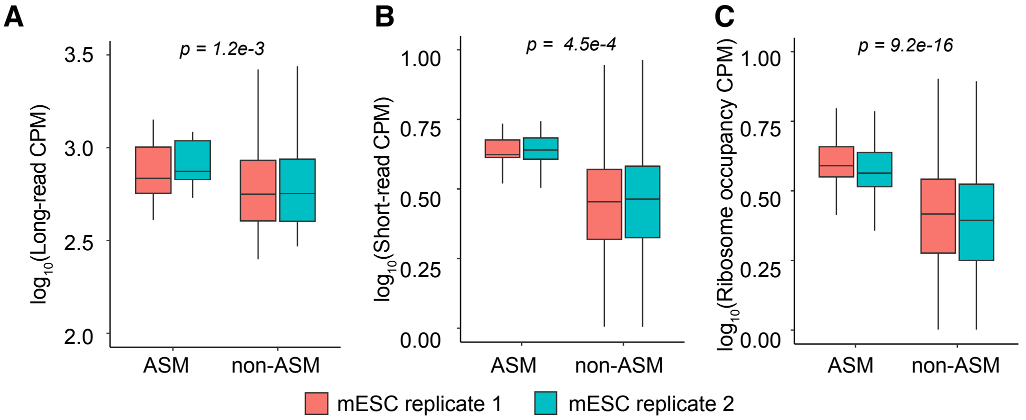

Supplemental Figure. 4 | Detection of ASM is biased towards more highly expressed genes

Comparison of RNA expression and ribosome occupancy of transcripts harboring sites with ASM or without ASM. RNA expression and ribosome occupancy were calculated using counts per million reads (CPM) from long-read sequencing (A), short-read sequencing (B), and ribosome profiling data (C). The boxplot compared RNA expression level and ribosome occupancies of the transcripts which contain ASM or not. P-values were obtained using a two-sided Wilcoxon Rank-Sum Test.