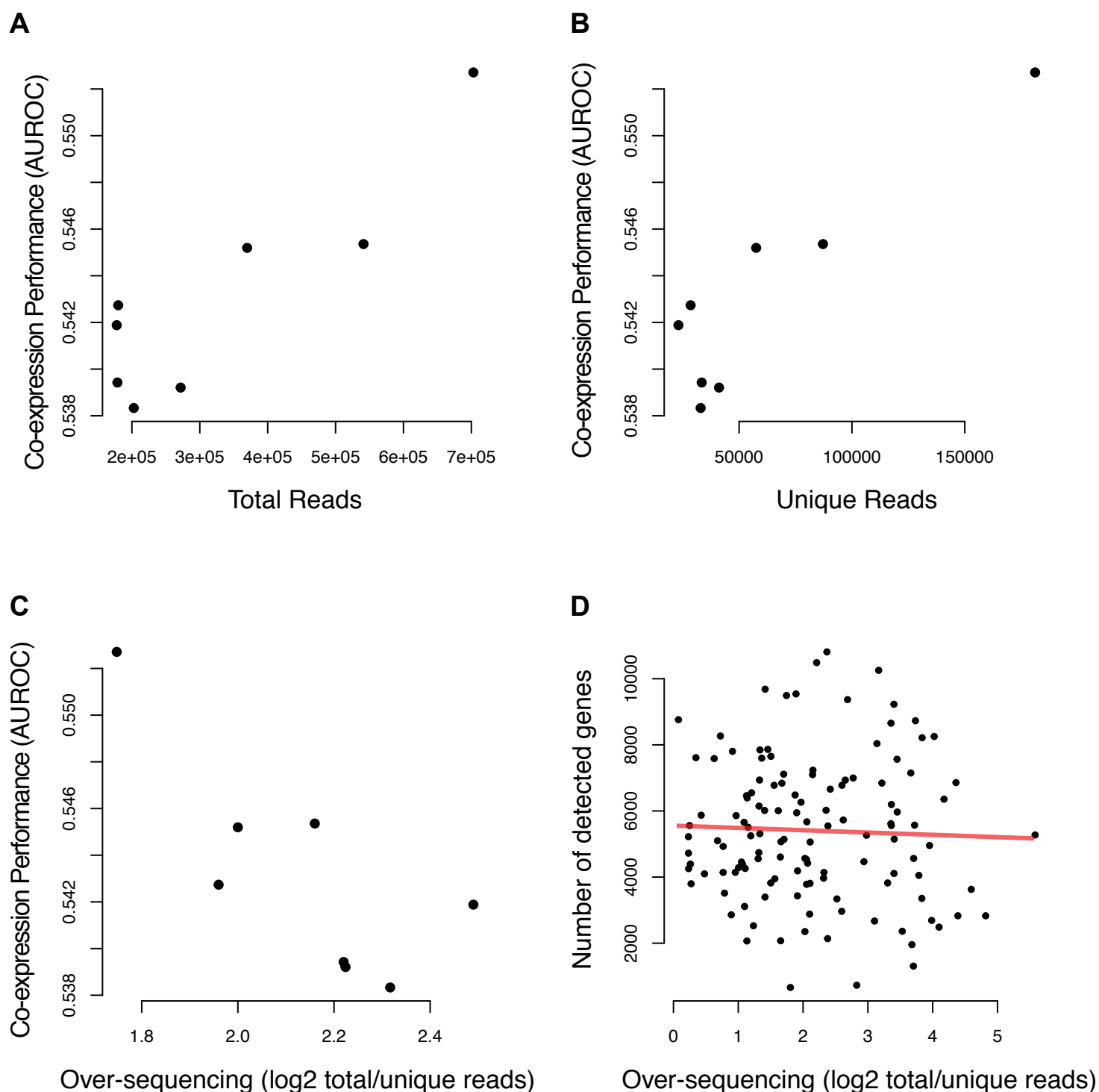


Additional file 6: Figure S3



Co-expression performance and sequencing depth.

A - Co-expression performance for GO slim is plotted against the average number of molecule counts for each batch, indicating a positive relationship ($r=0.62$). **B** - Co-expression performance for GO slim is plotted against the average unique molecule counts for each batch, indicating a positive relationship ($r=0.88$) and suggesting that the association between total reads and performance may be due to the number of detected genes. **C** - Co-expression performance for GO slim in each batch is plotted against over-sequencing level, indicating a negative relationship ($r=-0.76$). **D** - For each sample, the number of detected genes is plotted against over-sequencing level. No relationship is discernable when all samples are considered together ($r=-0.02$).