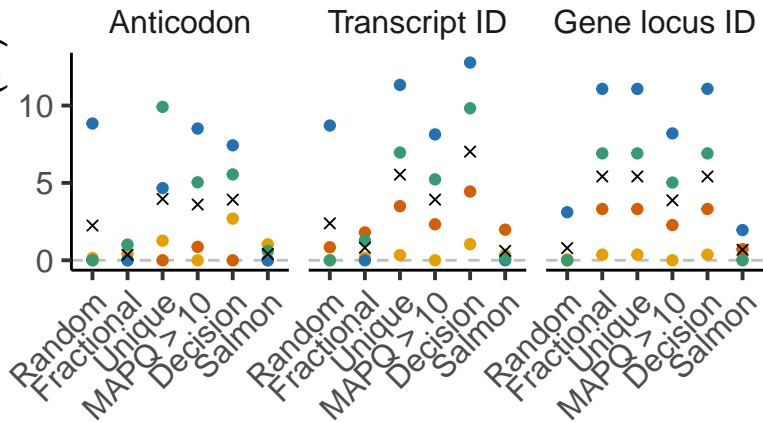


Variance explained  
by fold-change in  
simulation (%)



tRNA-Seq method

- QuantM-tRNA-seq
- mim-tRNAseq
- YAMAT-seq
- ALL-tRNAseq