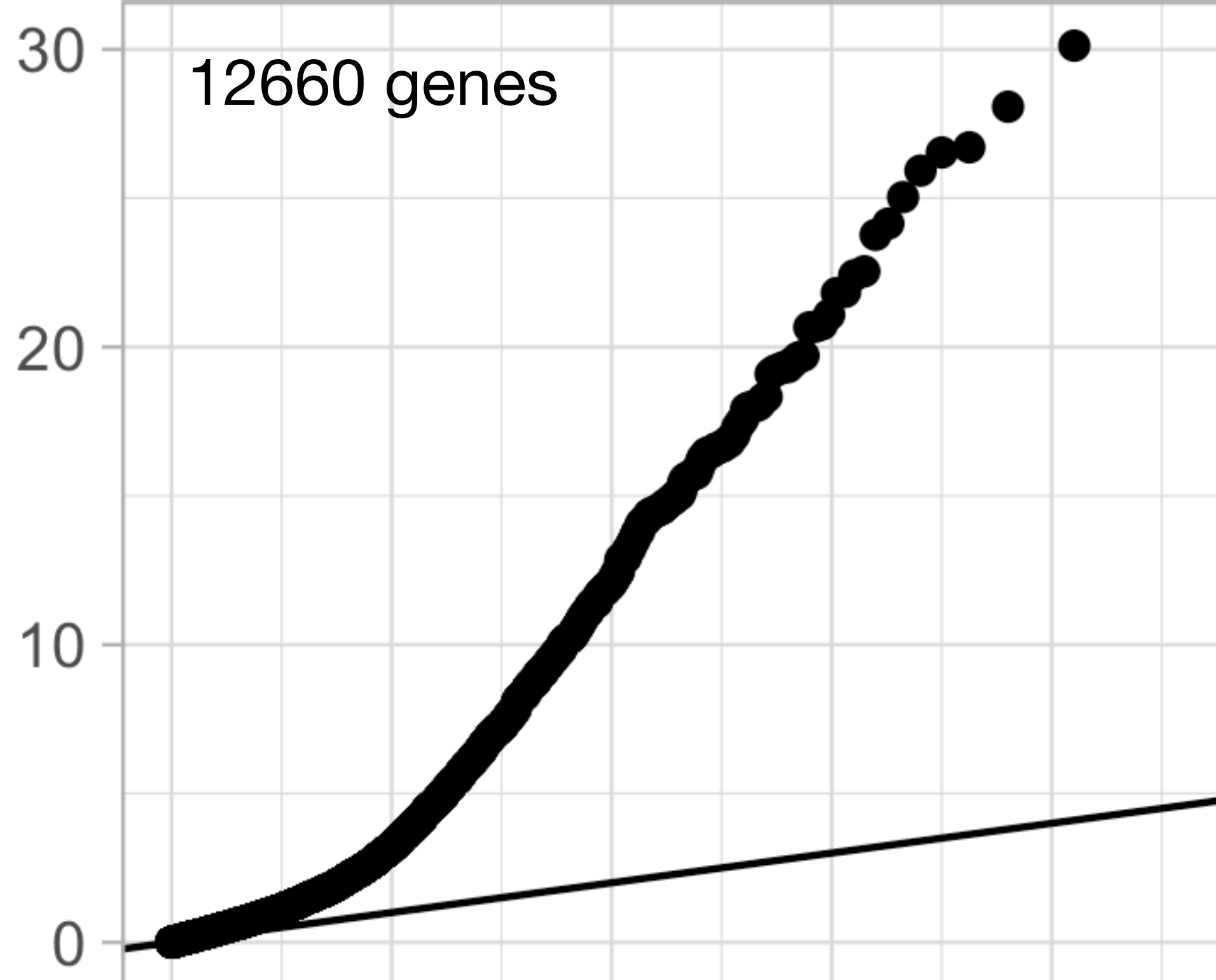


Log₁₀ permutation p-value (beta approximation)

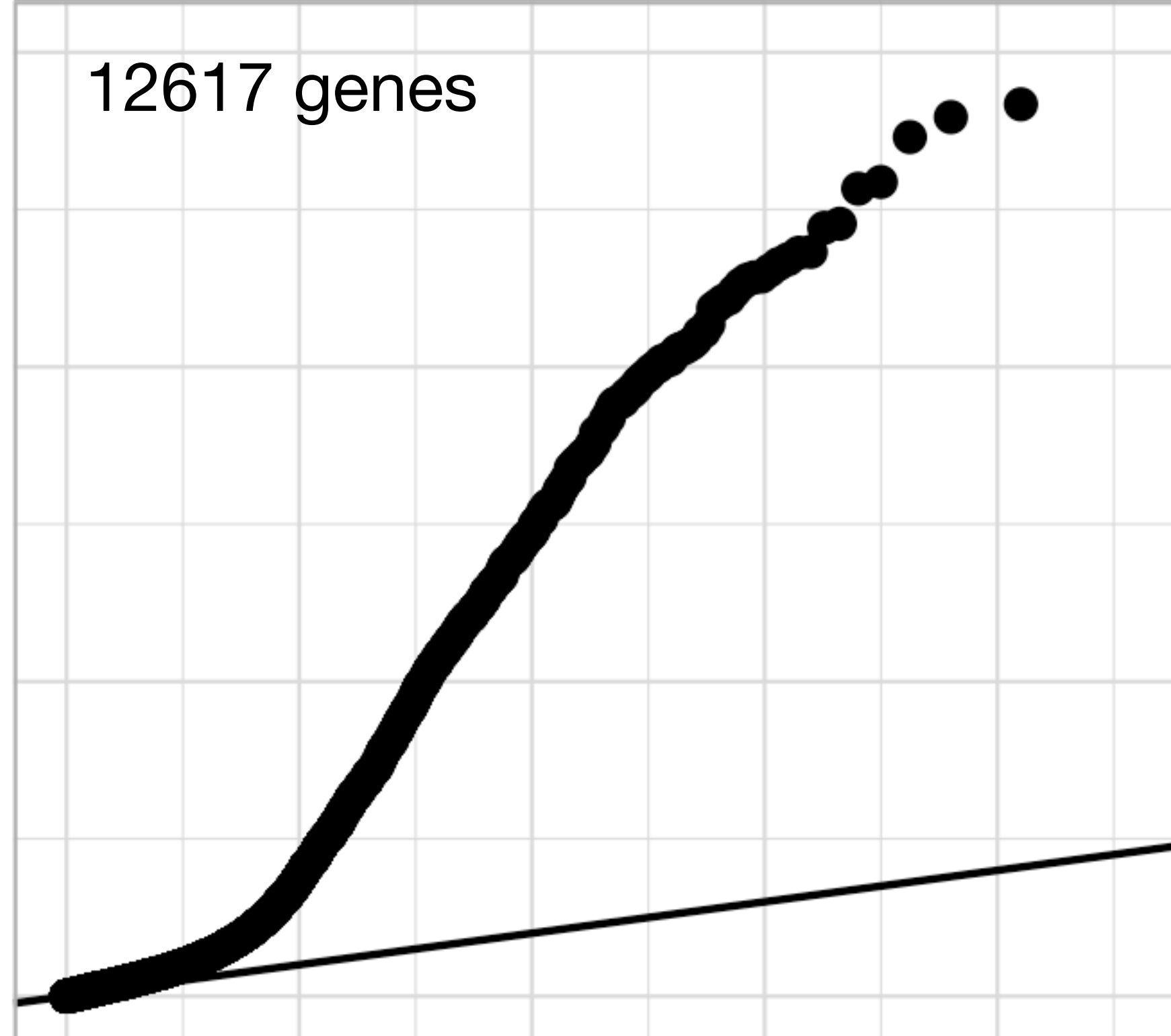
read count

12660 genes



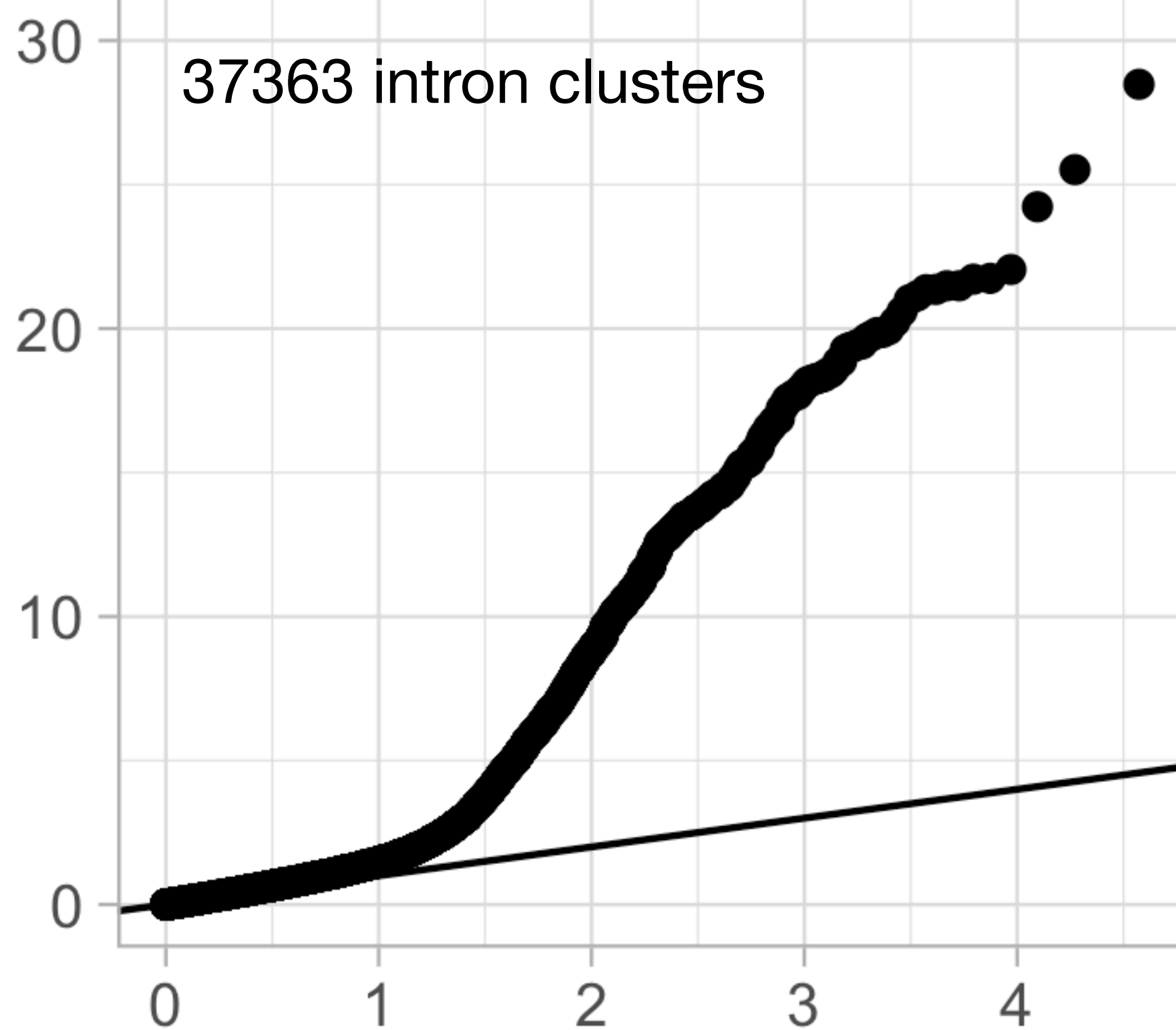
full-length txs

12617 genes



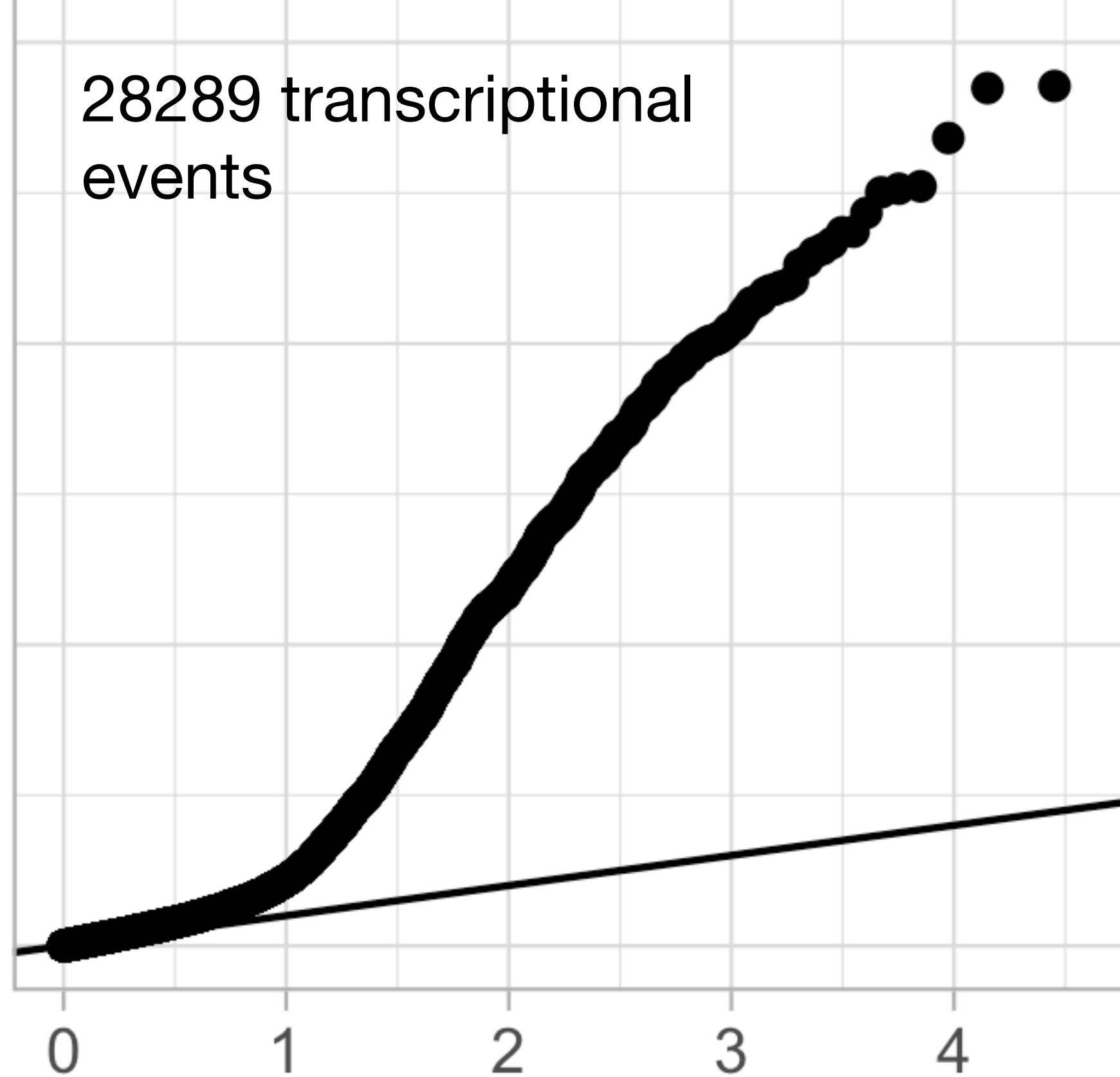
Leafcutter

37363 intron clusters



txrevise

28289 transcriptional
events



Log₁₀ expected p-value