RSEM vs. STAR (estimating gene expression)
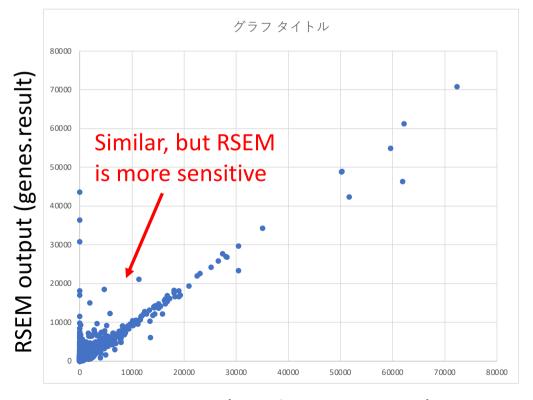
2022.06.10
KIM JS

- There are two ways of estimate the gene_count from mRNA-seq
  (1) native STAR "GeneCounts" (2) STAR "TranscriptomeSAM" -> RSEM

- The later doubles analyzing time, so which one is better?

(Barley mRNA-seq)

Similar, but RSEM is more sensitive