Quake 2013

454 → 200bp COR3 → 1-3 Errors
Illumina → 200bp COR3 → 0.25 Errors

100,000 B cells → 10 IGH transcripts
→ 1,000,000 IGH transcripts
→ 454 → ~ < 100,000 Reads ⇒ Every Read from unique IGH transcript

→ Illumina → > 5,000,000 Reads

1,000,000 original IGH Transcripts
+ 1,000,000 Reads that look original Transcripts with Mutation
RT Error, 10^-5
Sequencing, 10^-3 \text{ Impared} \xrightarrow{+} 10^-3
PCR, 10^-6

Sample Prep
4 \times 4 = 41 \text{ Billion}

\text{Geneic Reference}