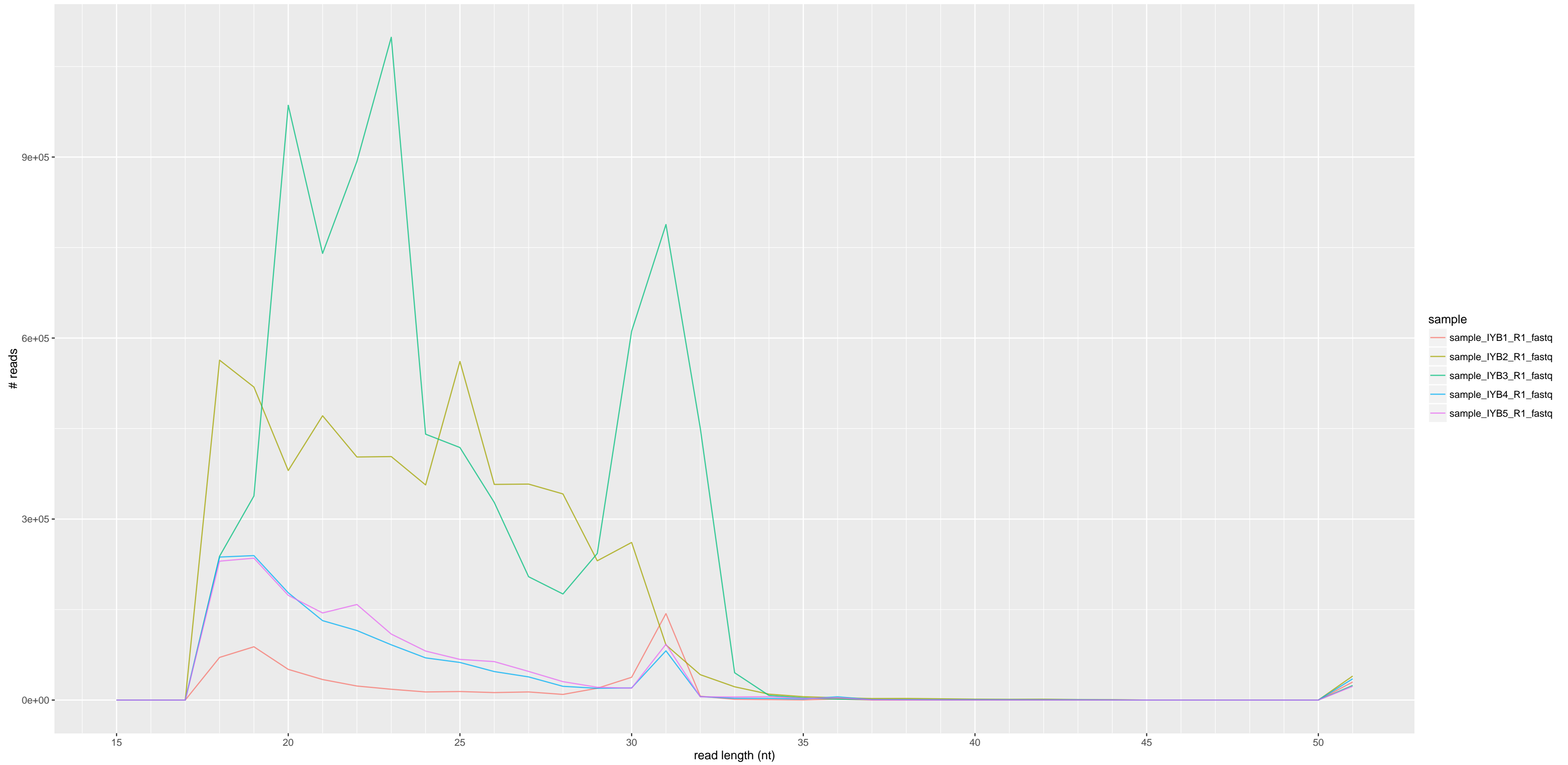
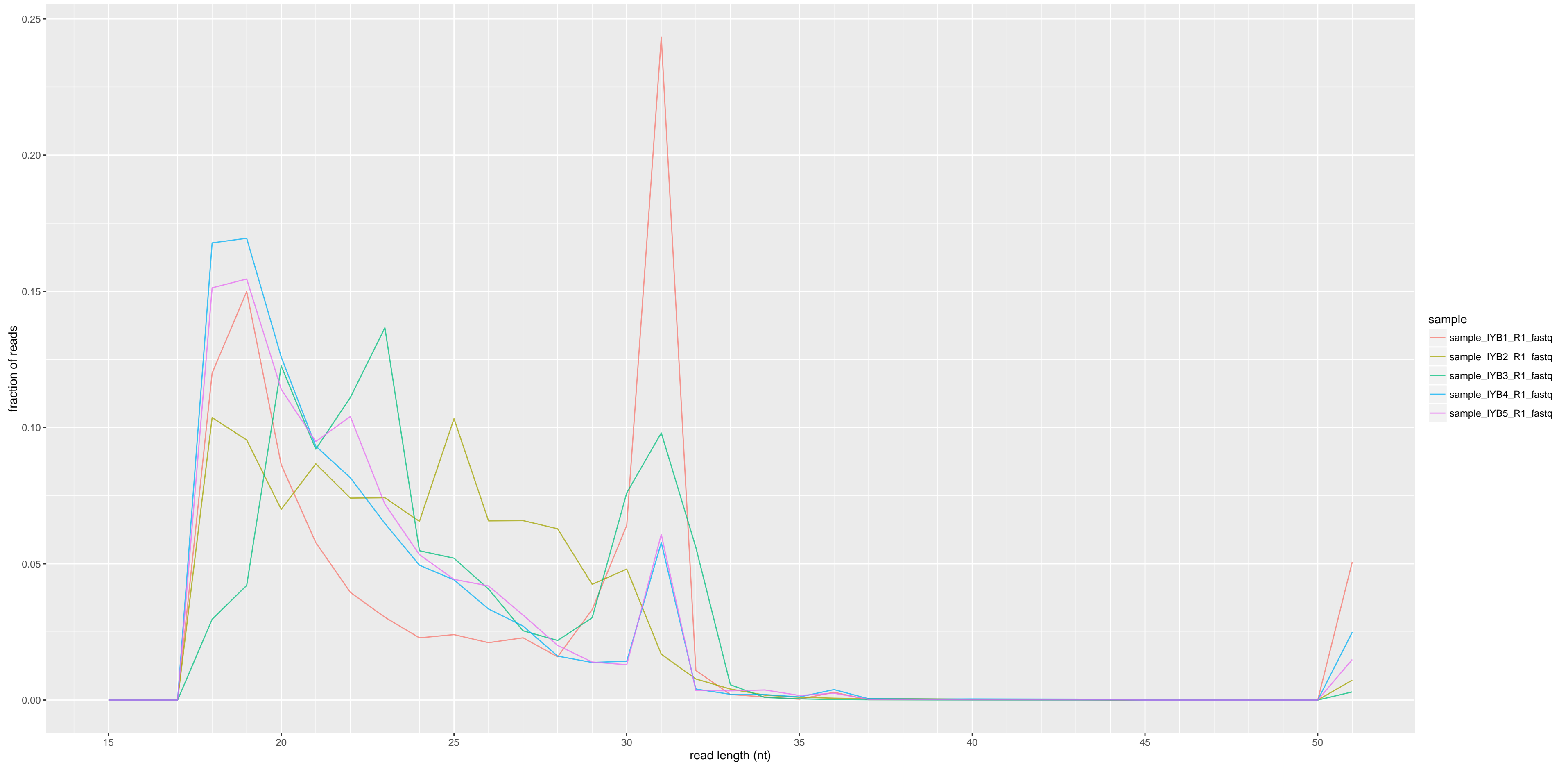


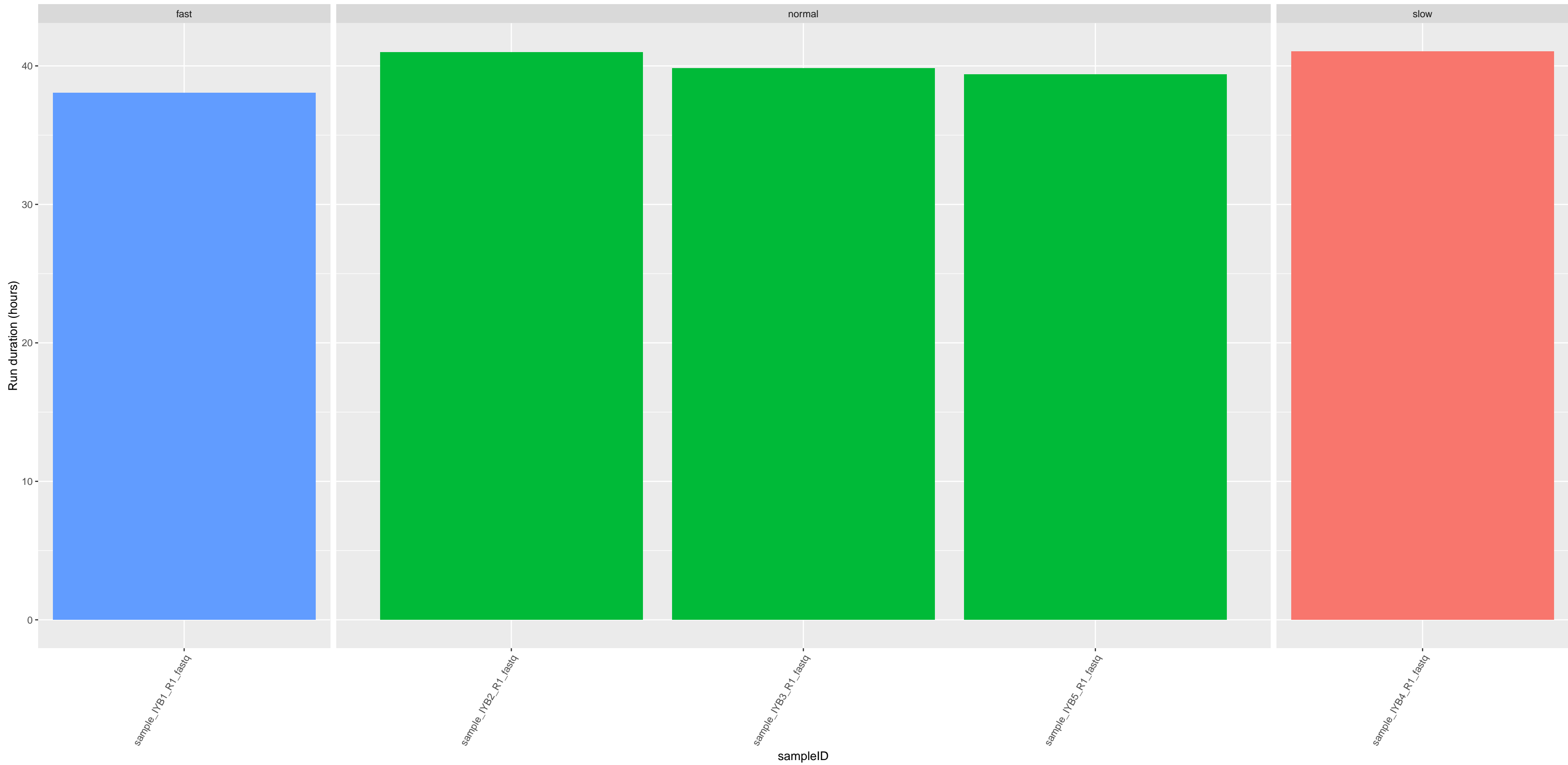
read-length distributions: raw read count



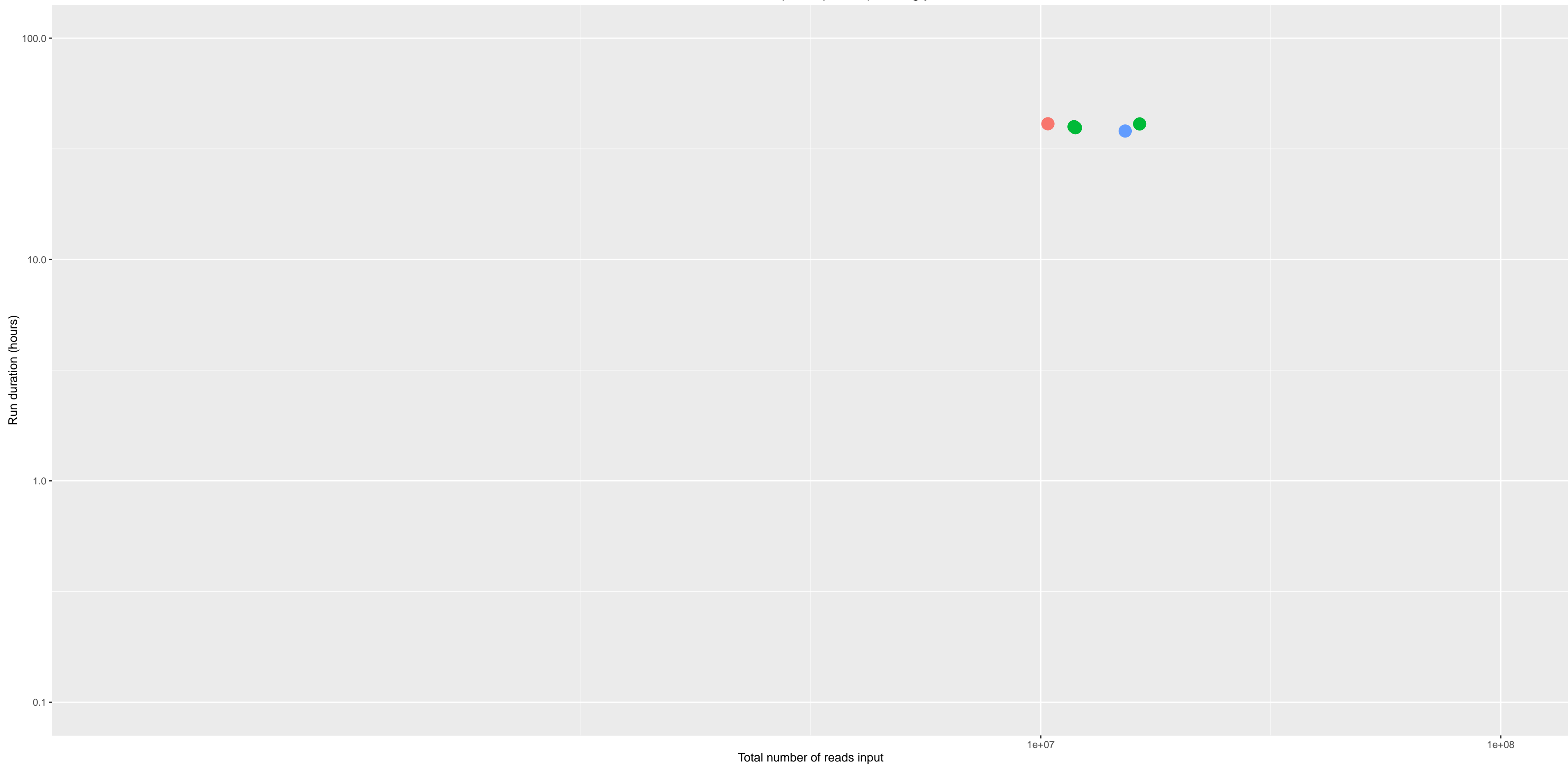
read-length distributions: normalised read fraction



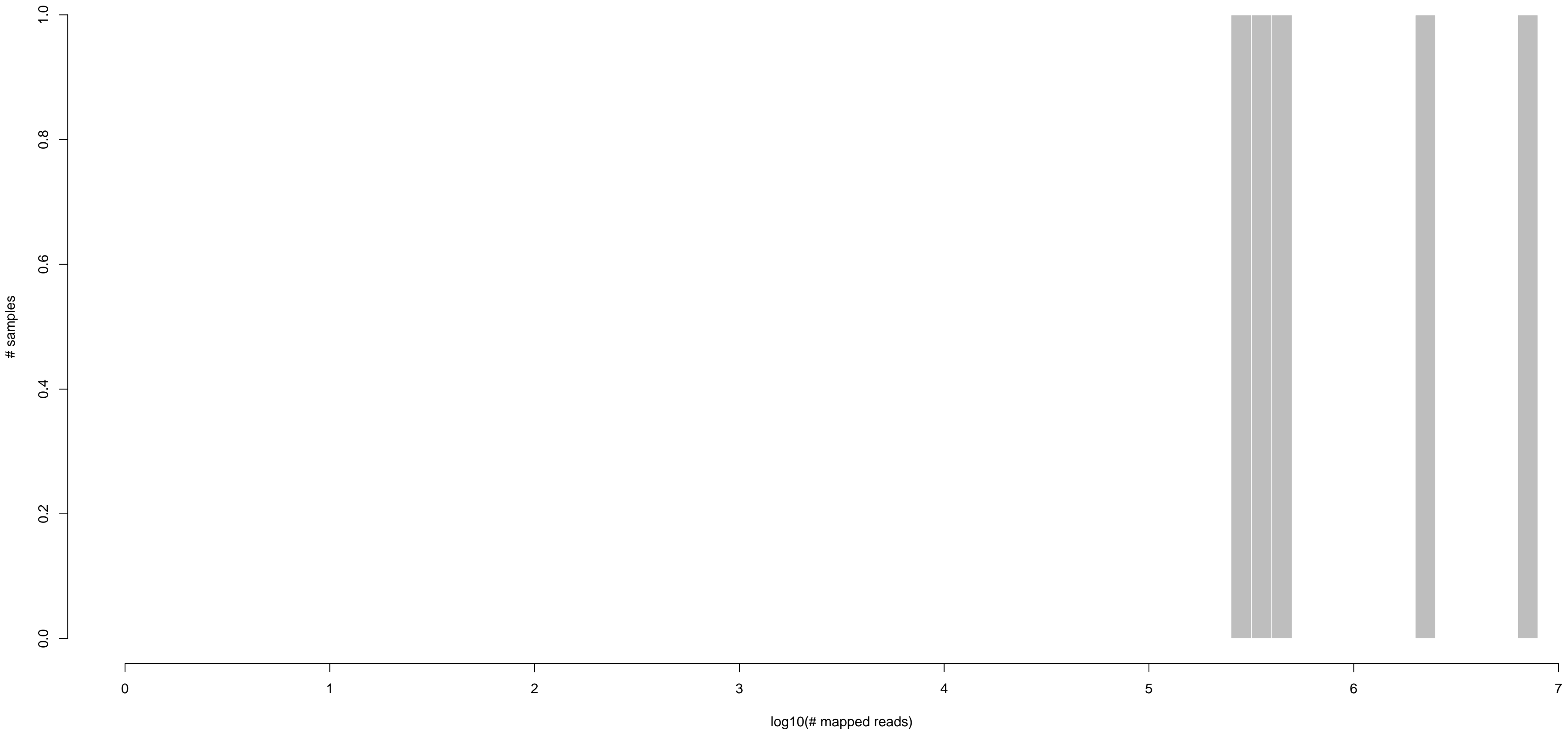
Duration of exceRpt run for each sample

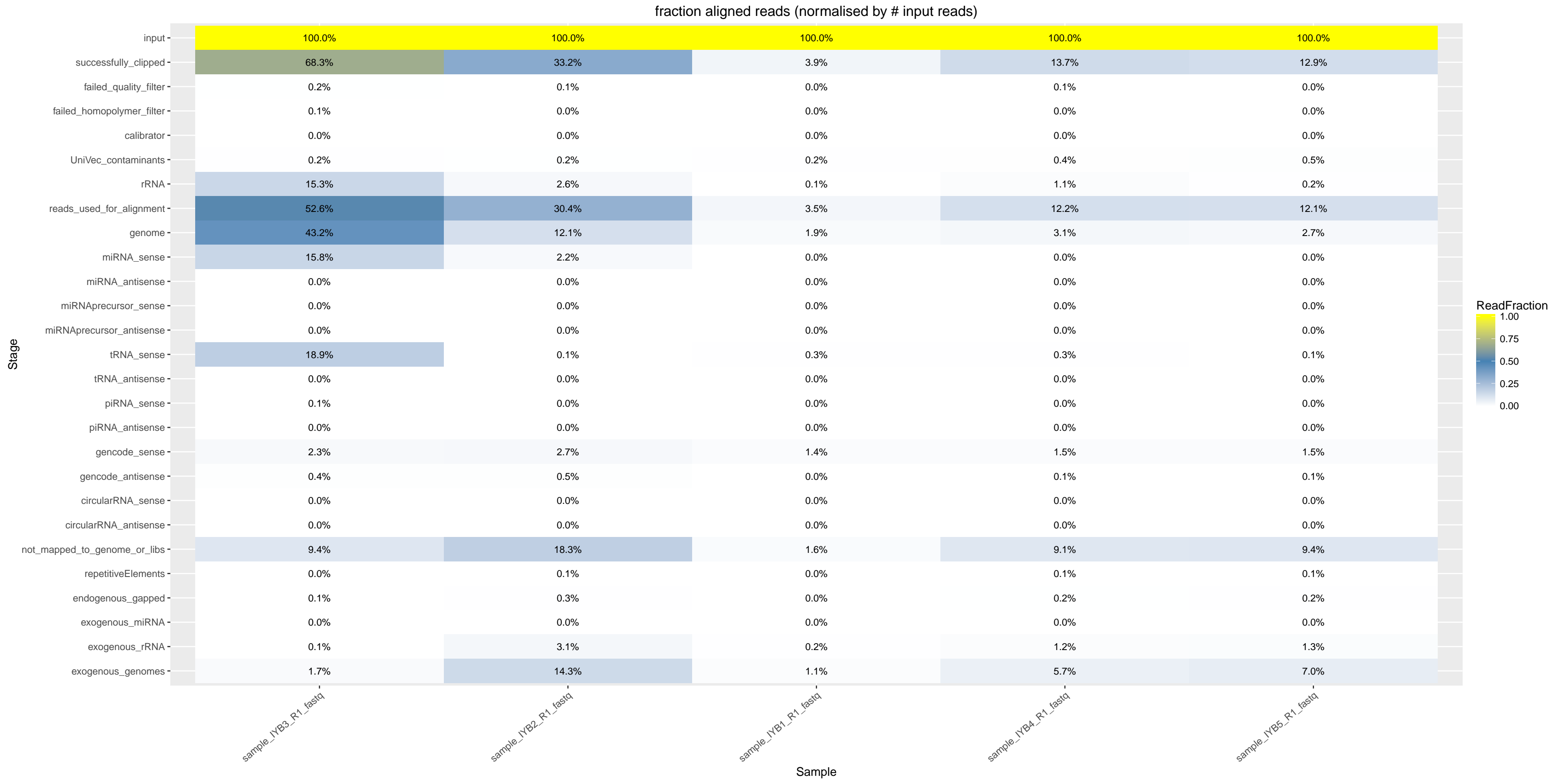


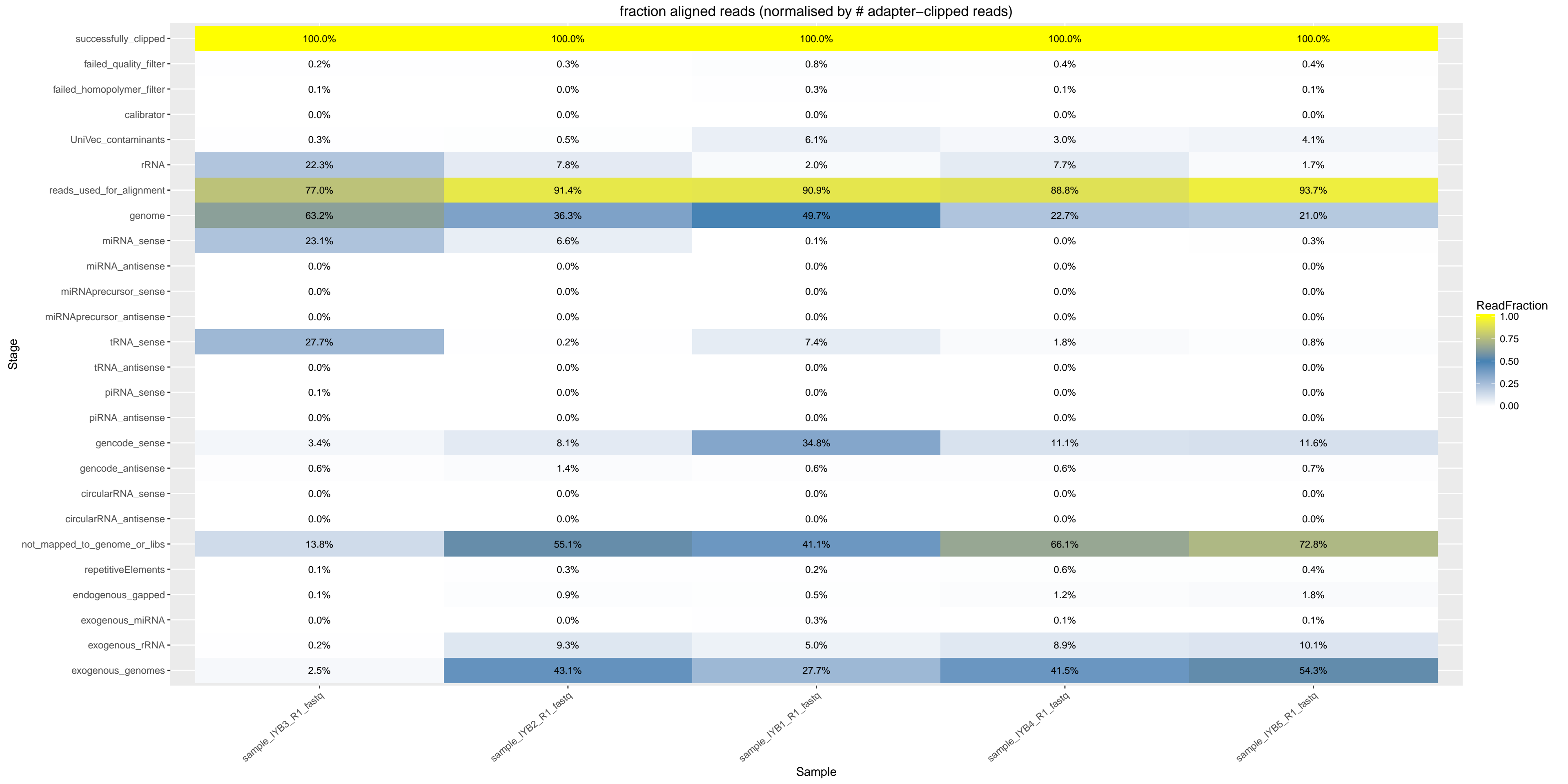
Duration of exceRpt run per sequencing yield

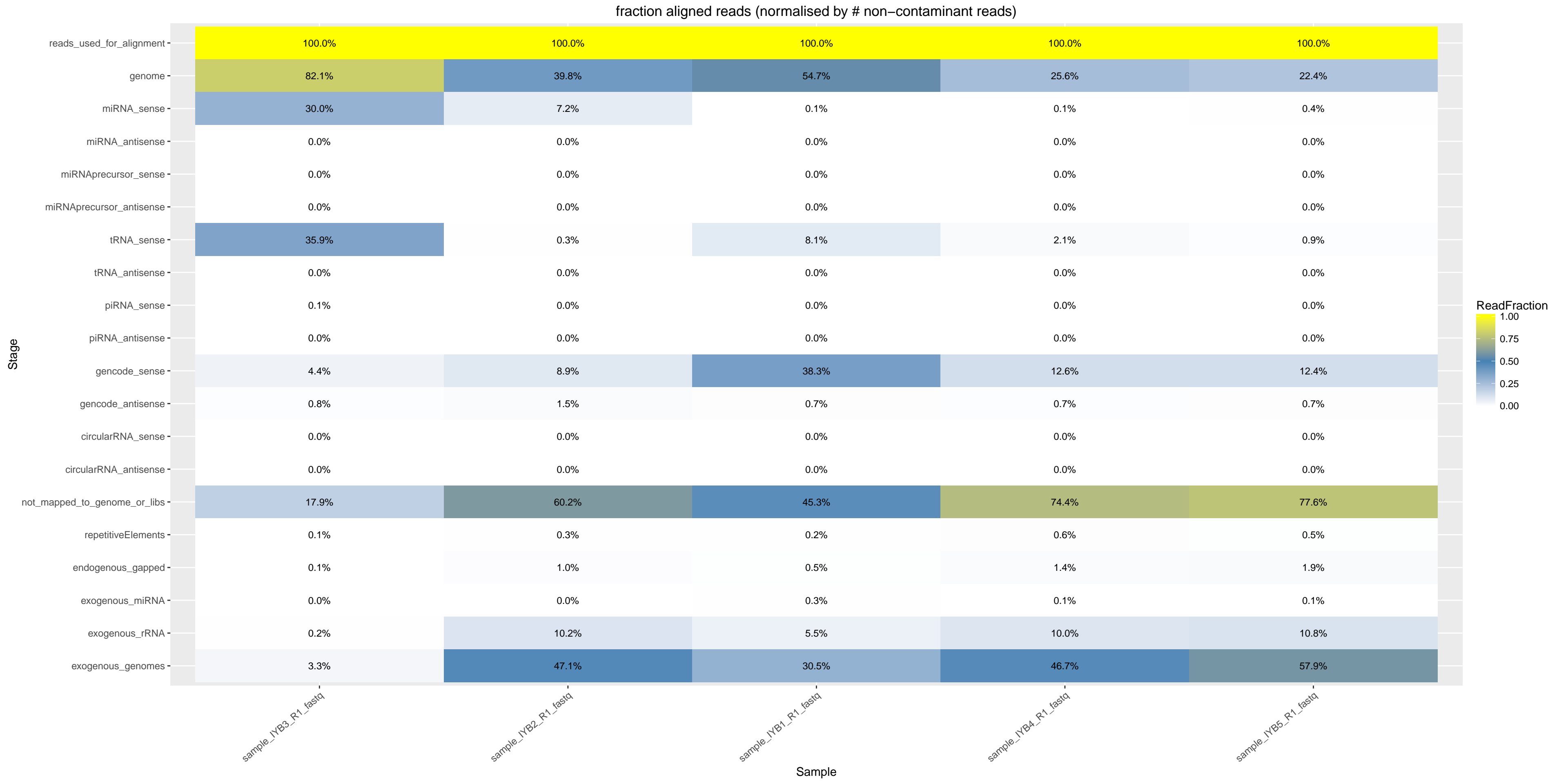


Library size (all mapped reads)

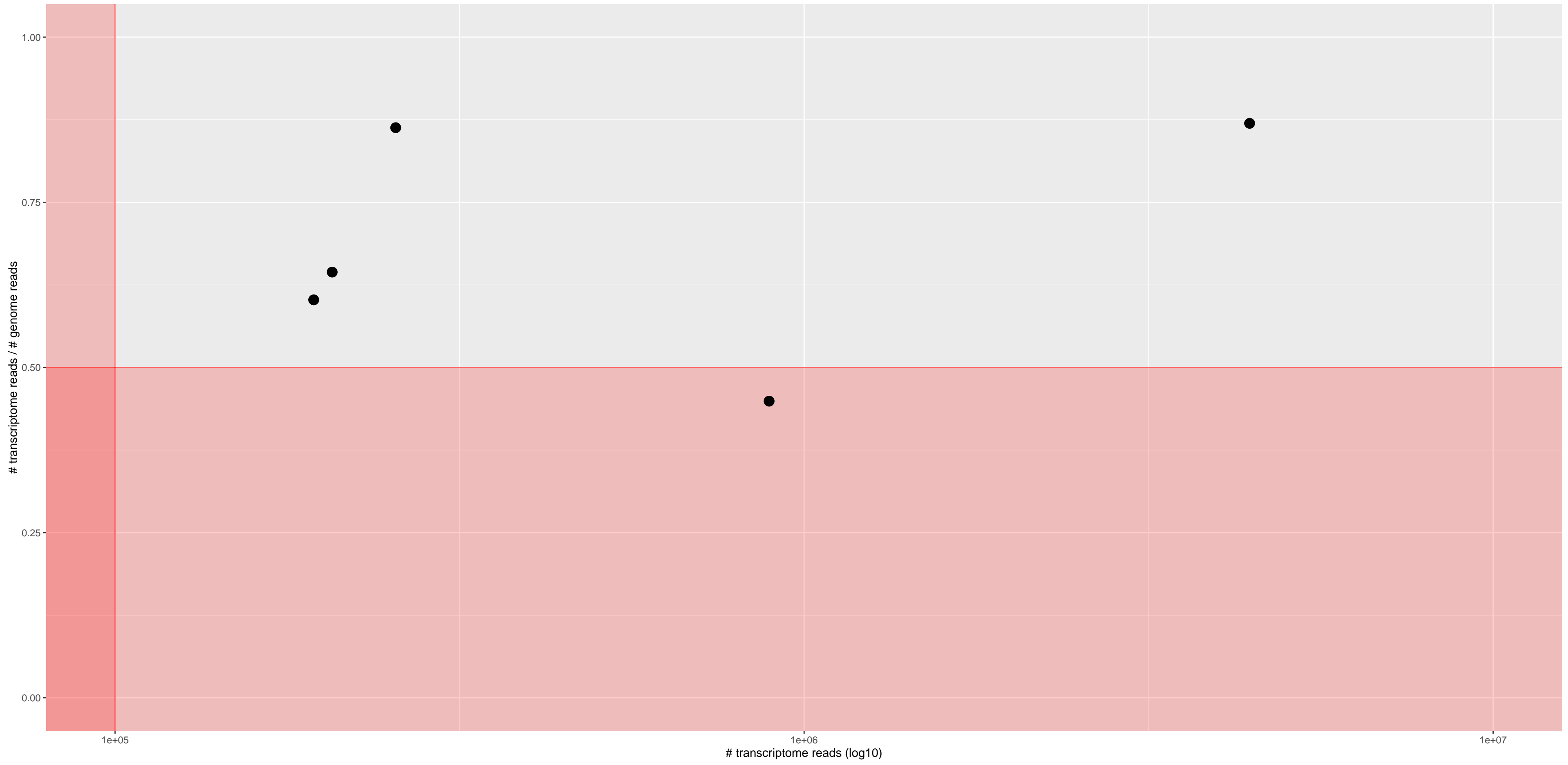




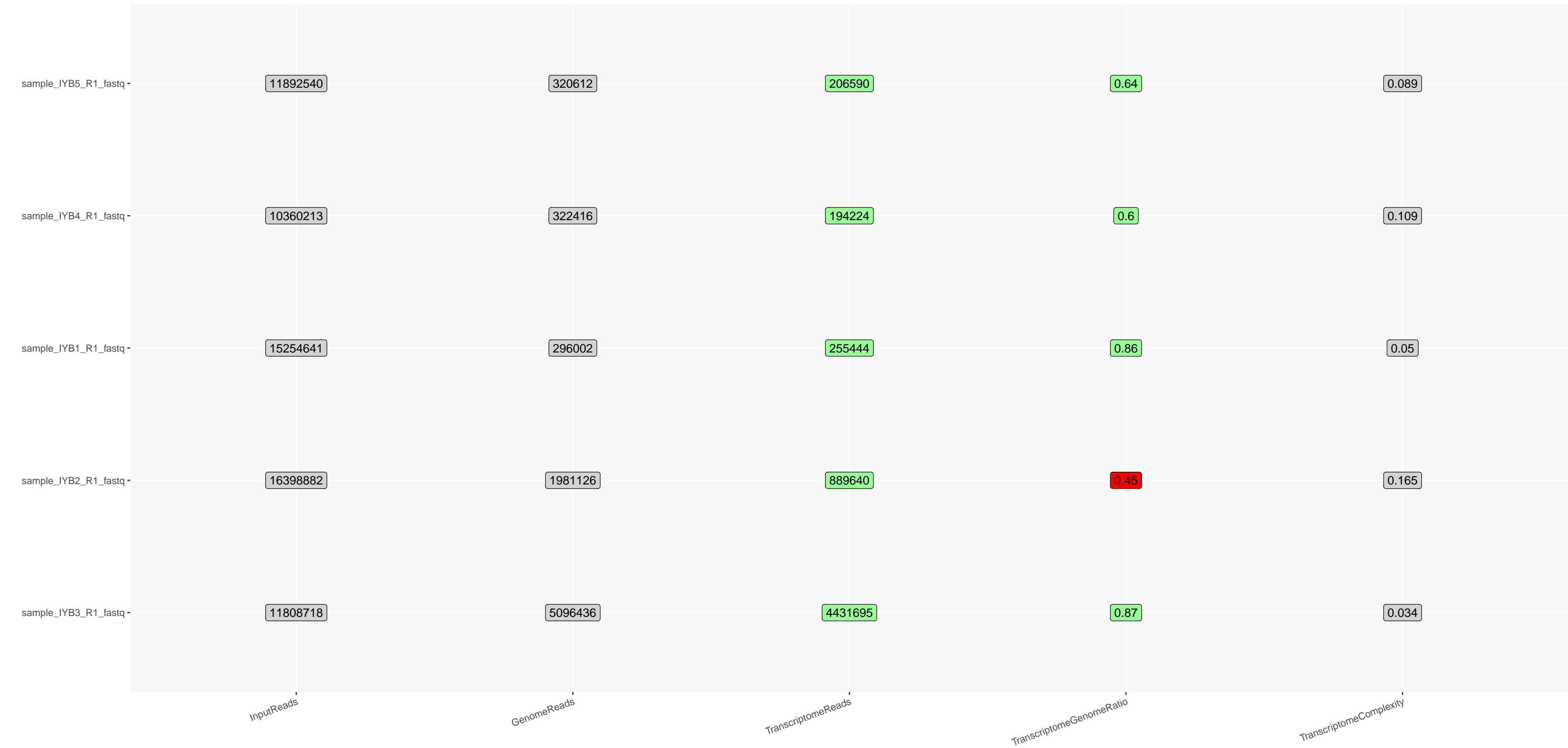




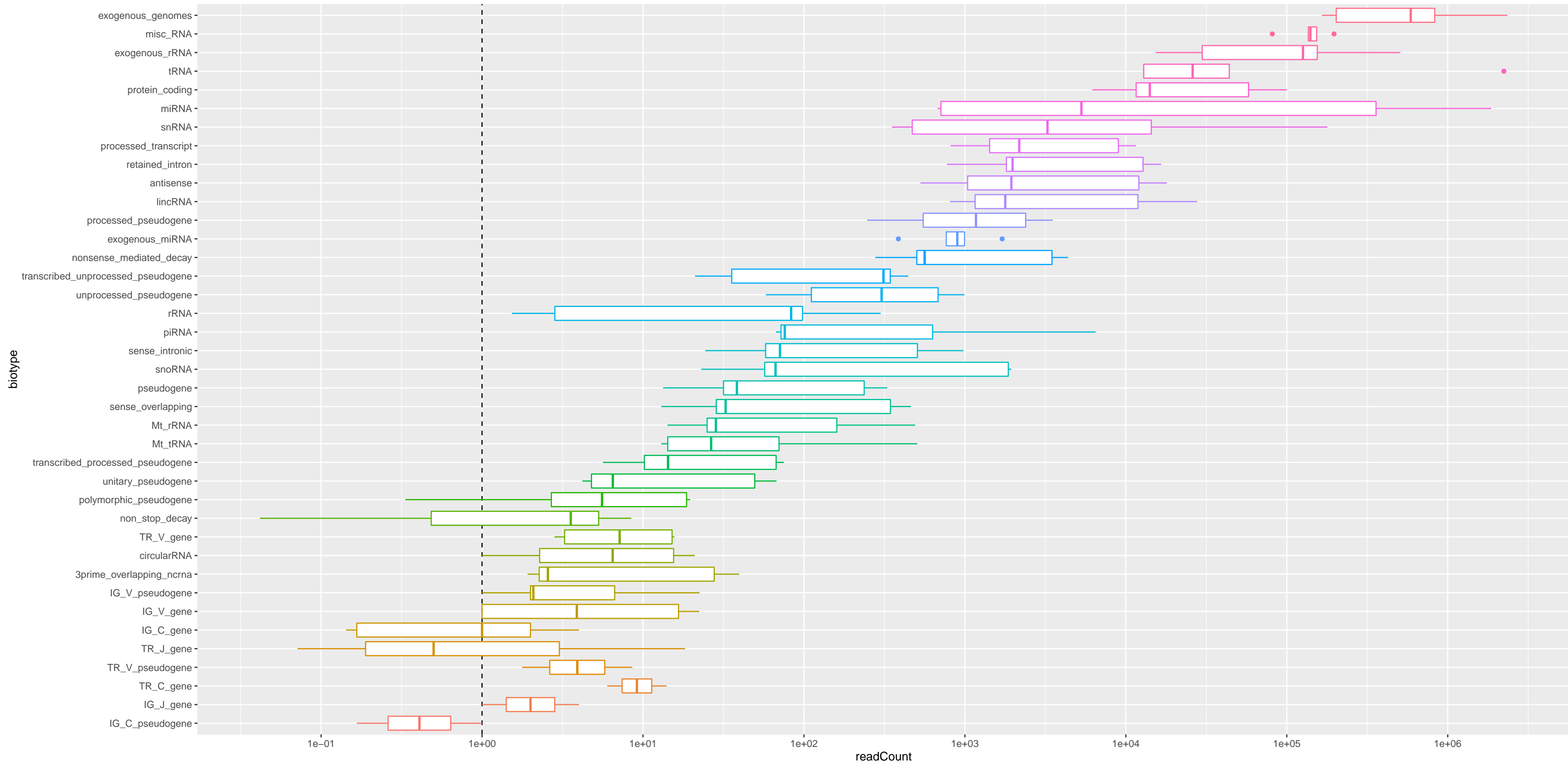
QC result: overall



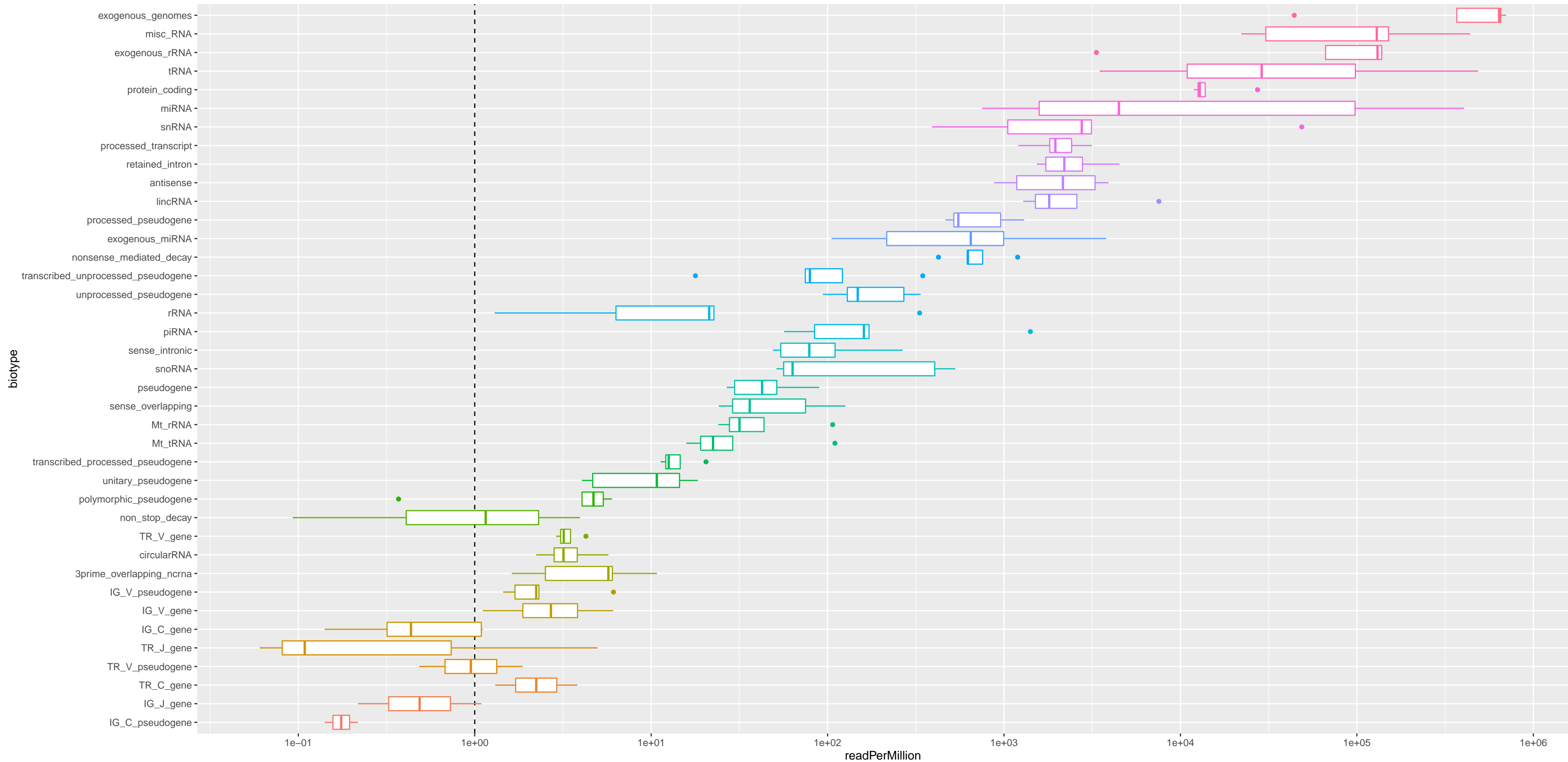
QC result: per-sample results



Biotypes: distributions, raw read-counts

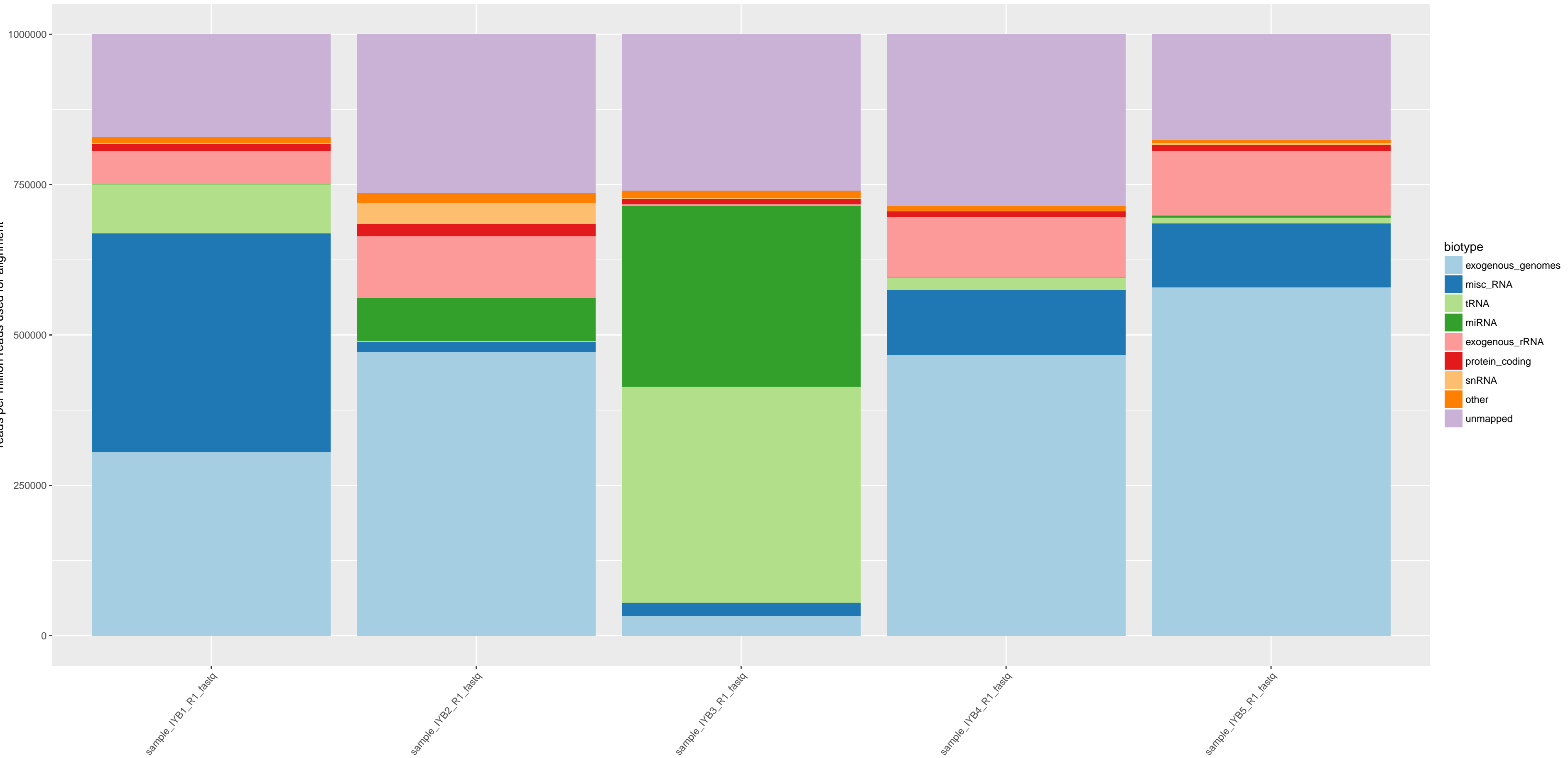


Biotypes: distributions, normalised

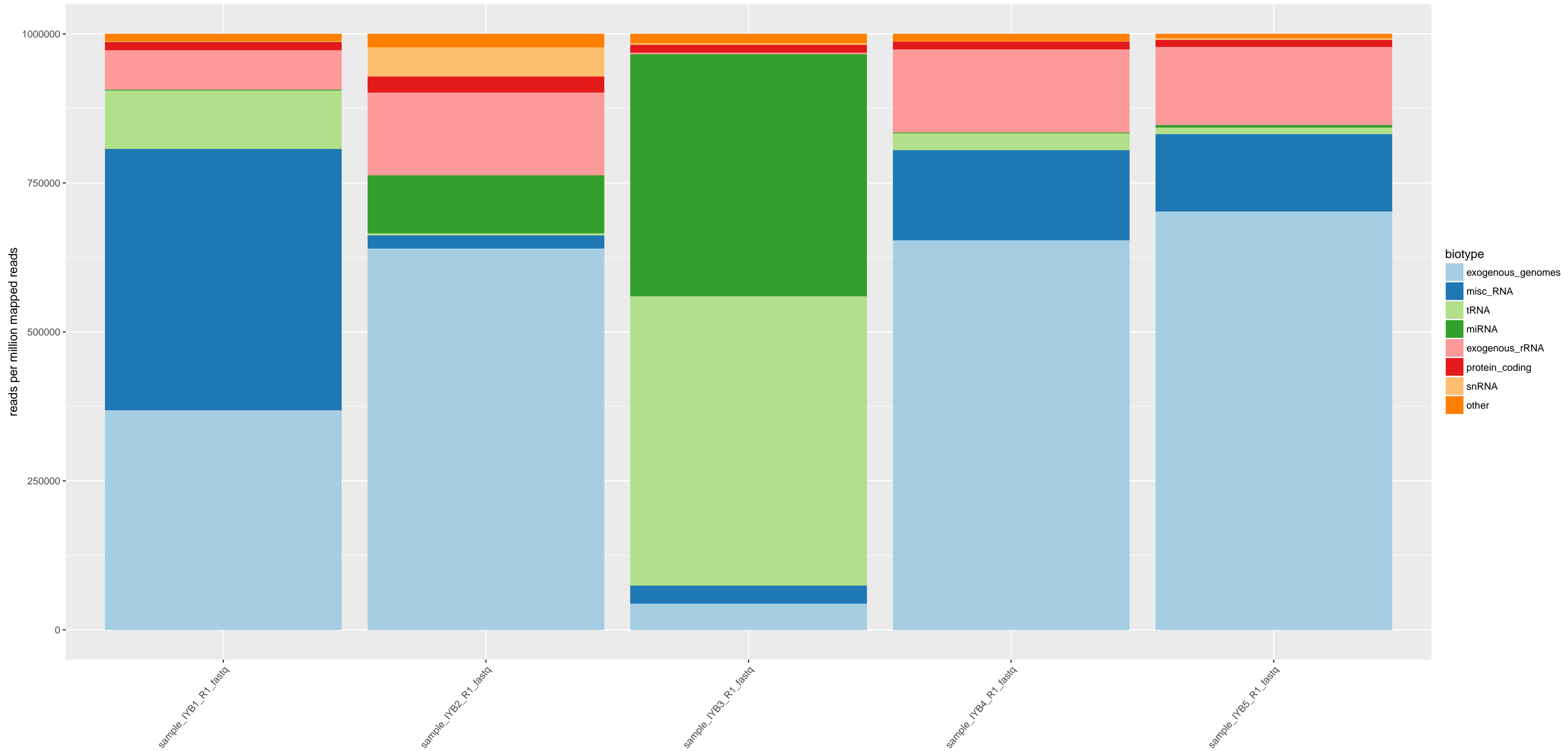


Biotypes: per-sample, normalised

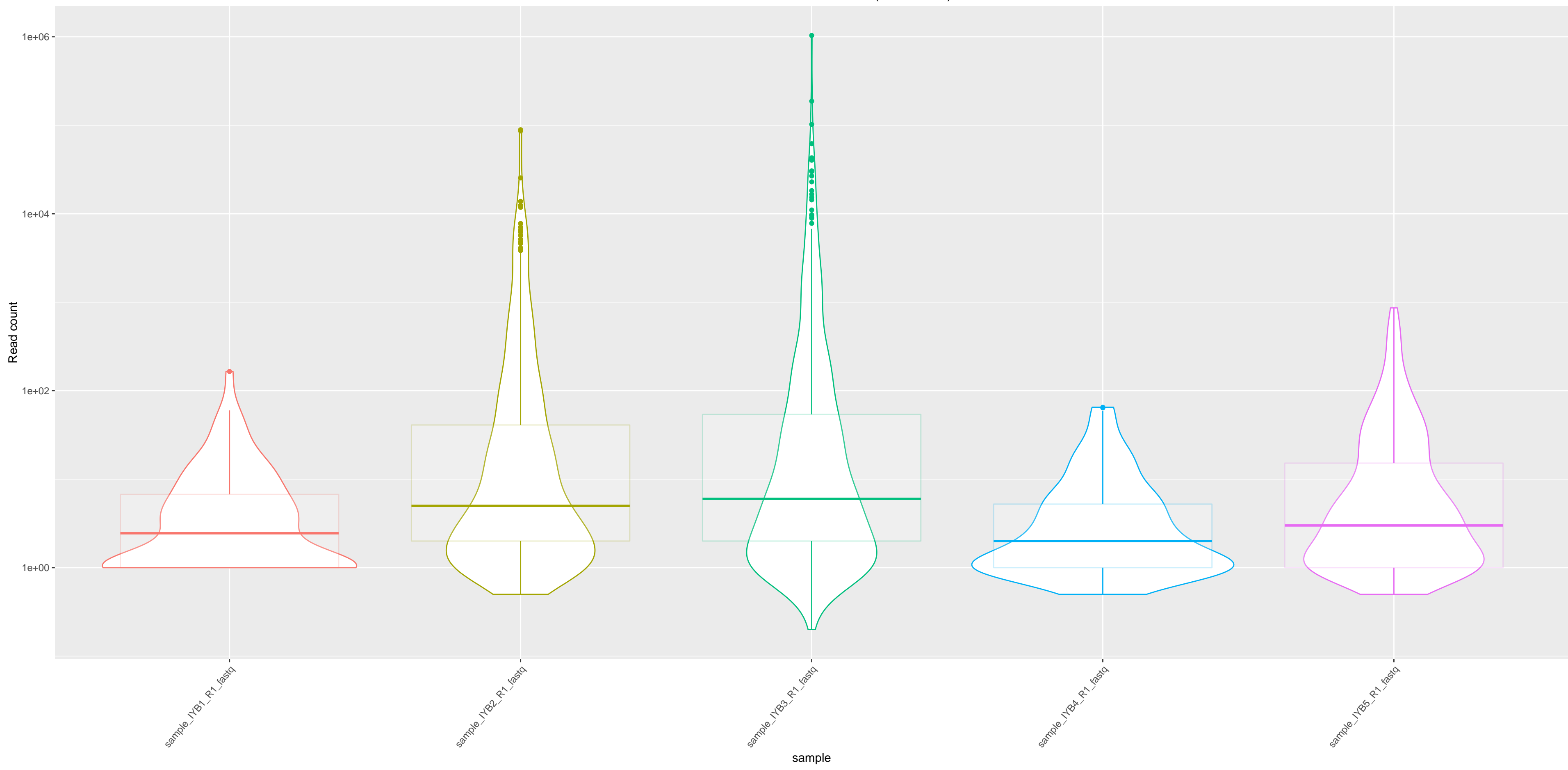
reads per million reads used for alignment



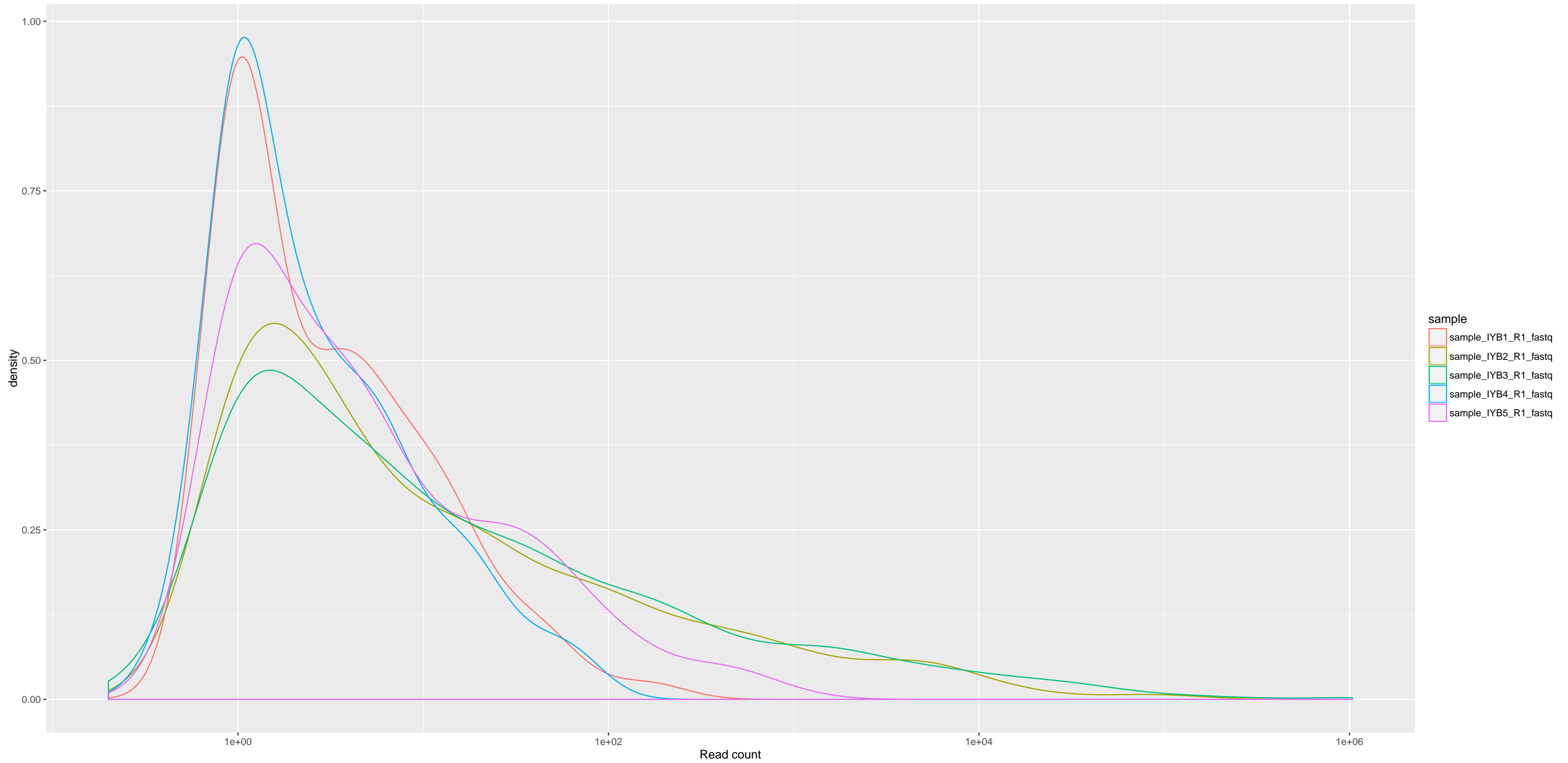
Biotypes: per-sample, normalised



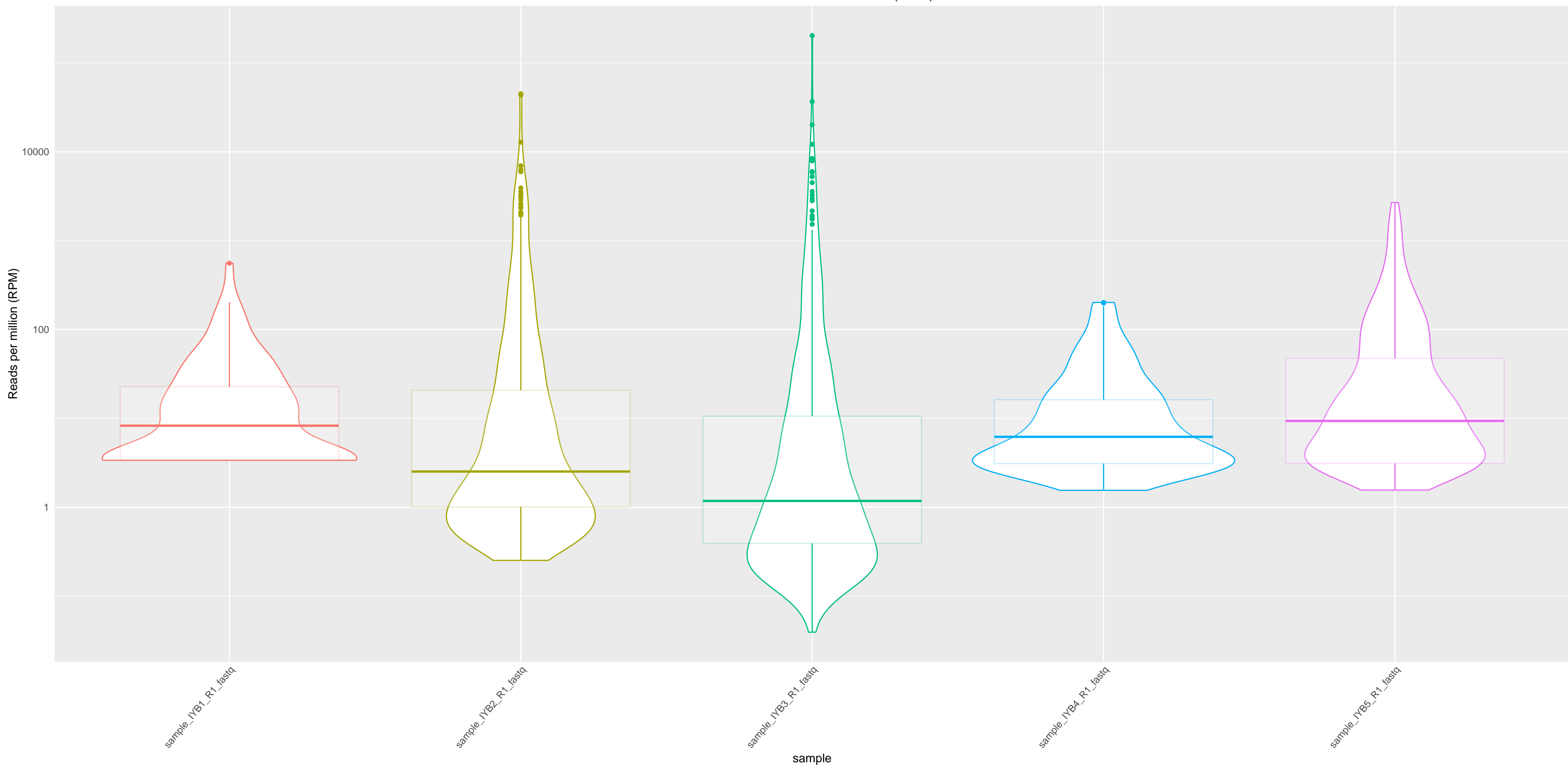
miRNA abundance distributions (raw counts)



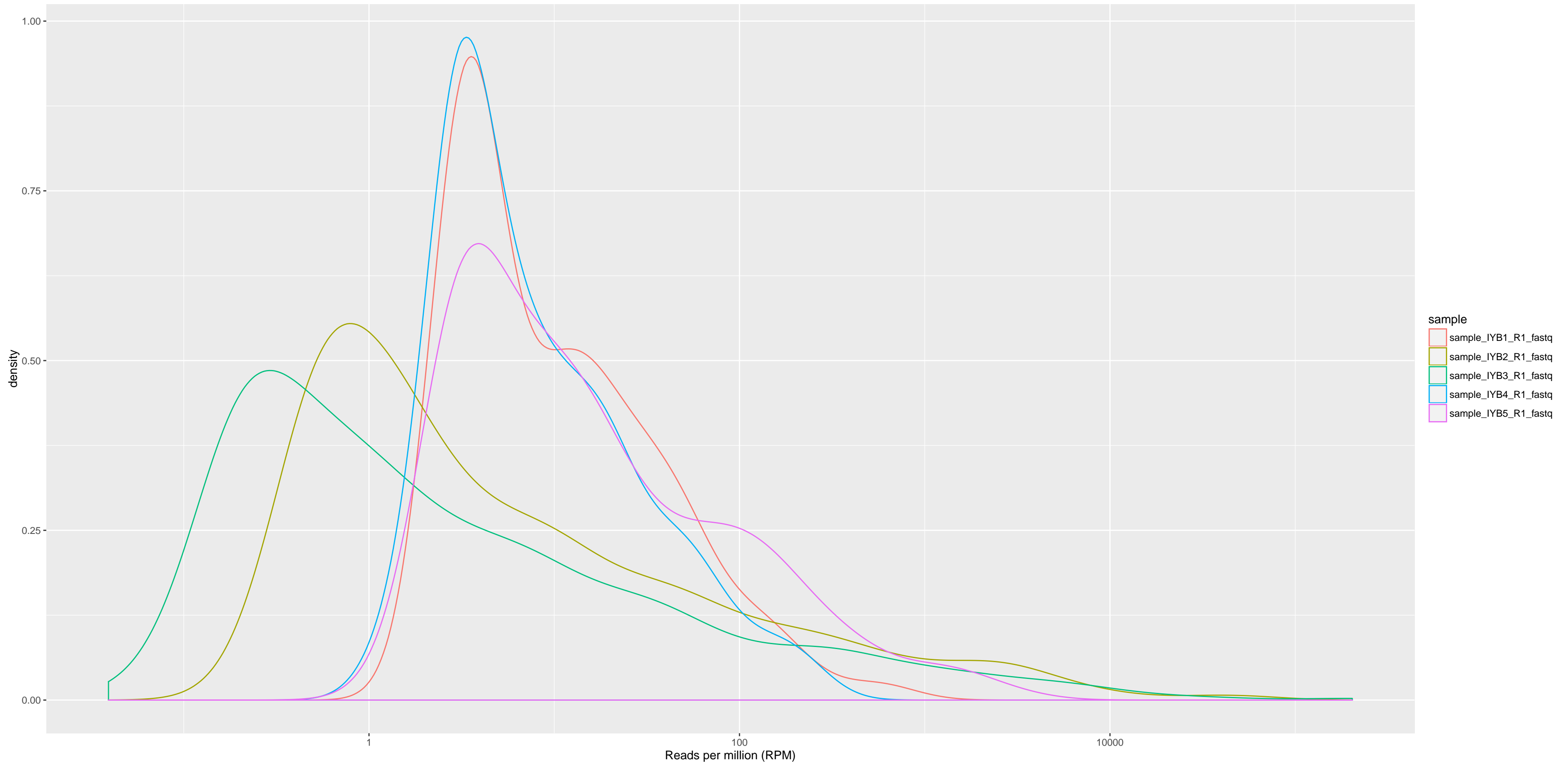
miRNA abundance distributions (raw counts)



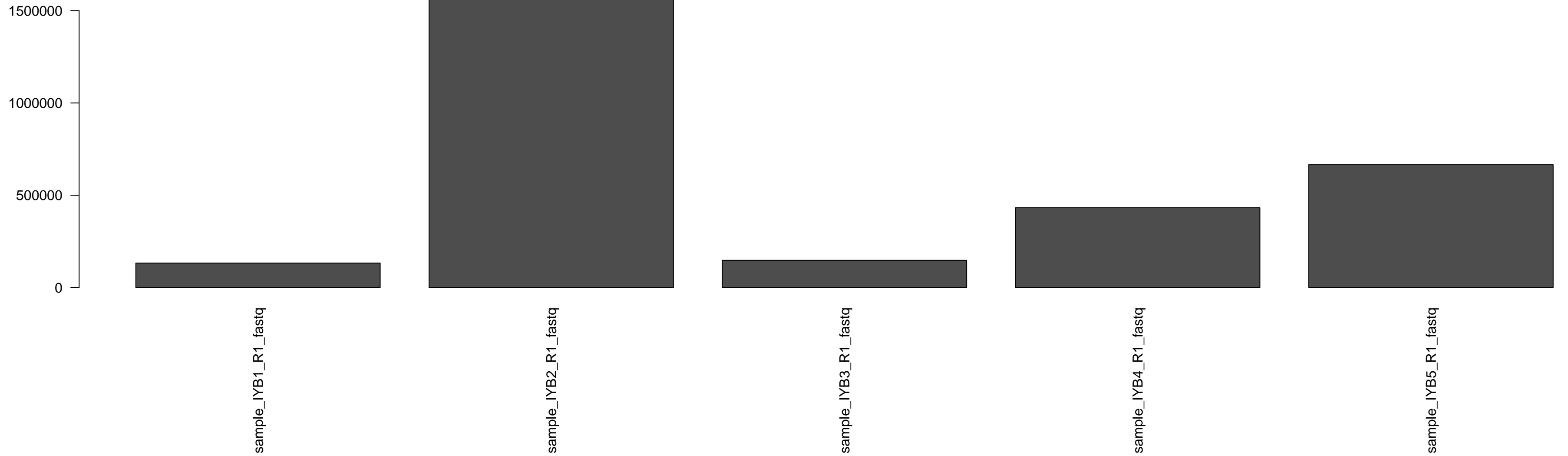
miRNA abundance distributions (RPM)

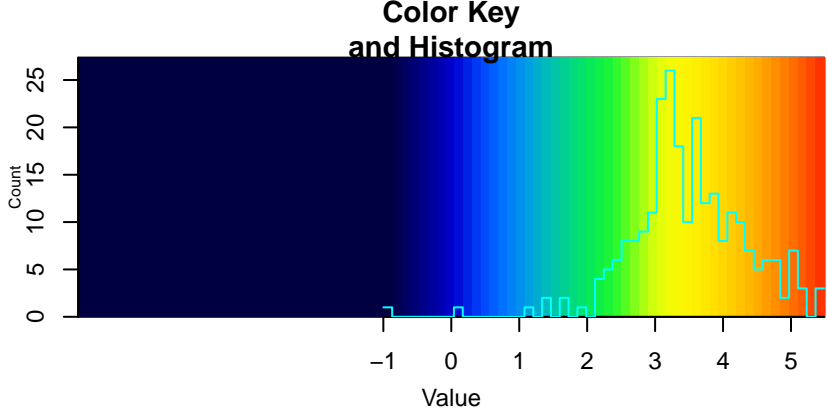


miRNA abundance distributions (RPM)

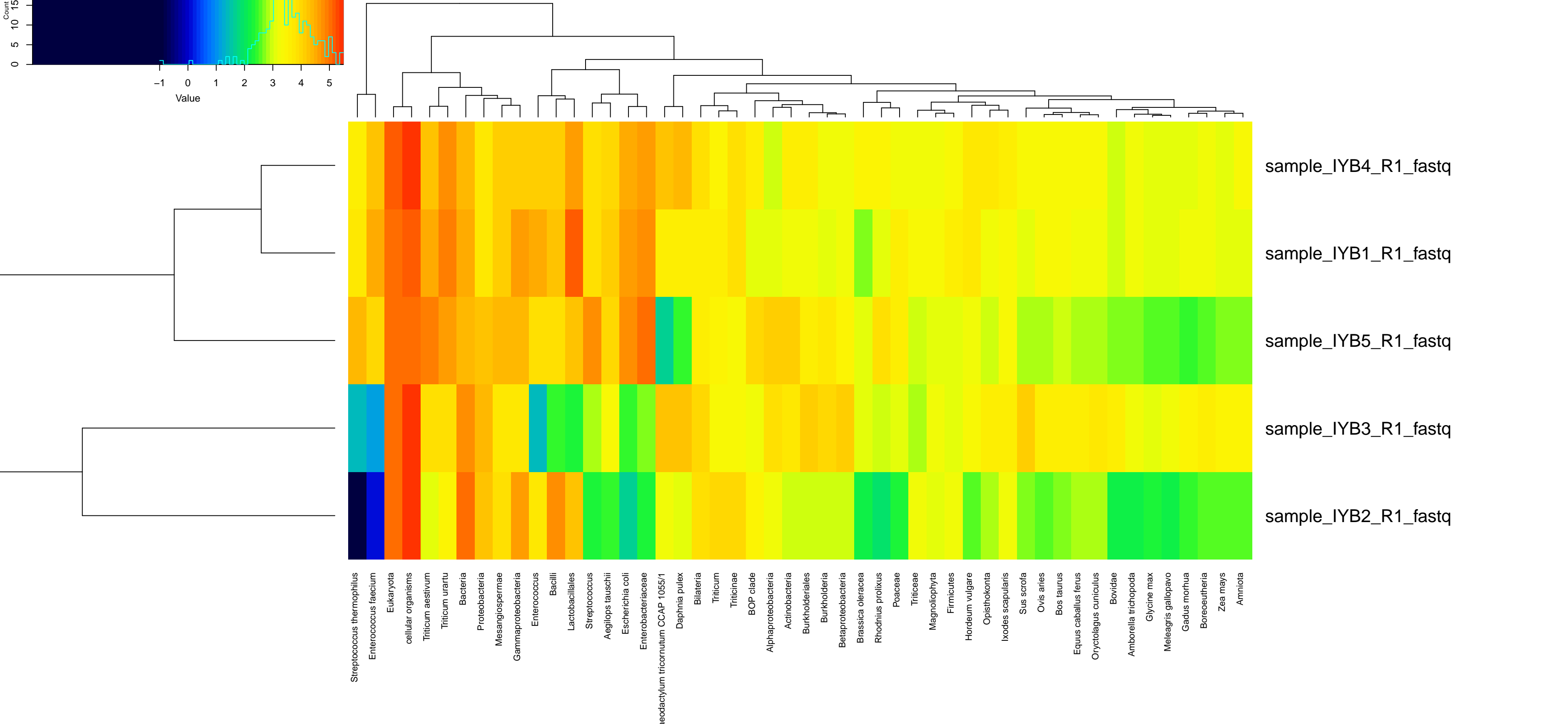


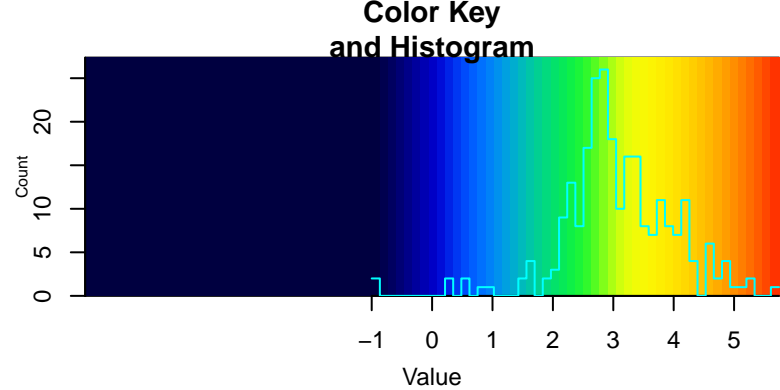
Total # reads mapped to NCBI taxonomy



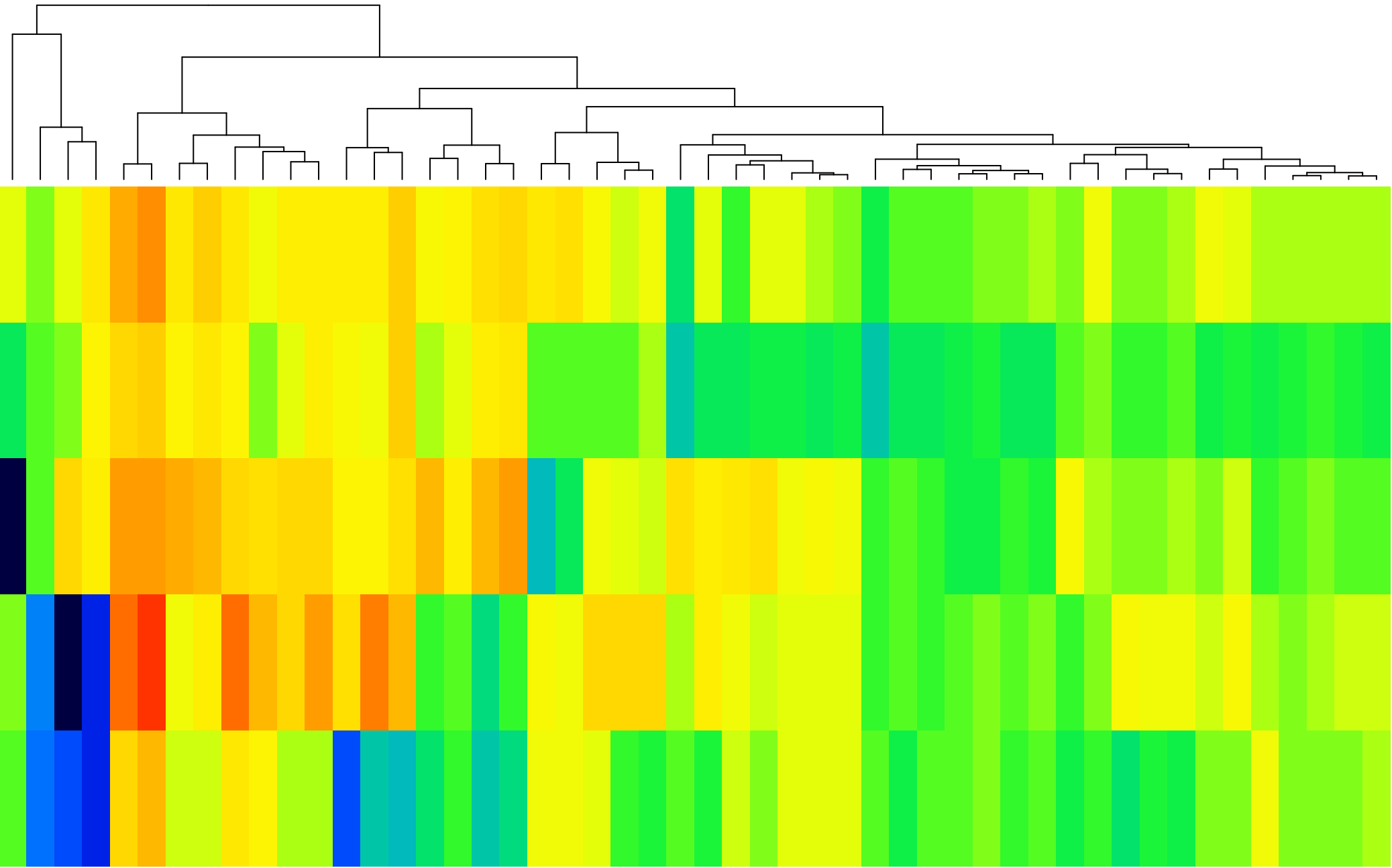
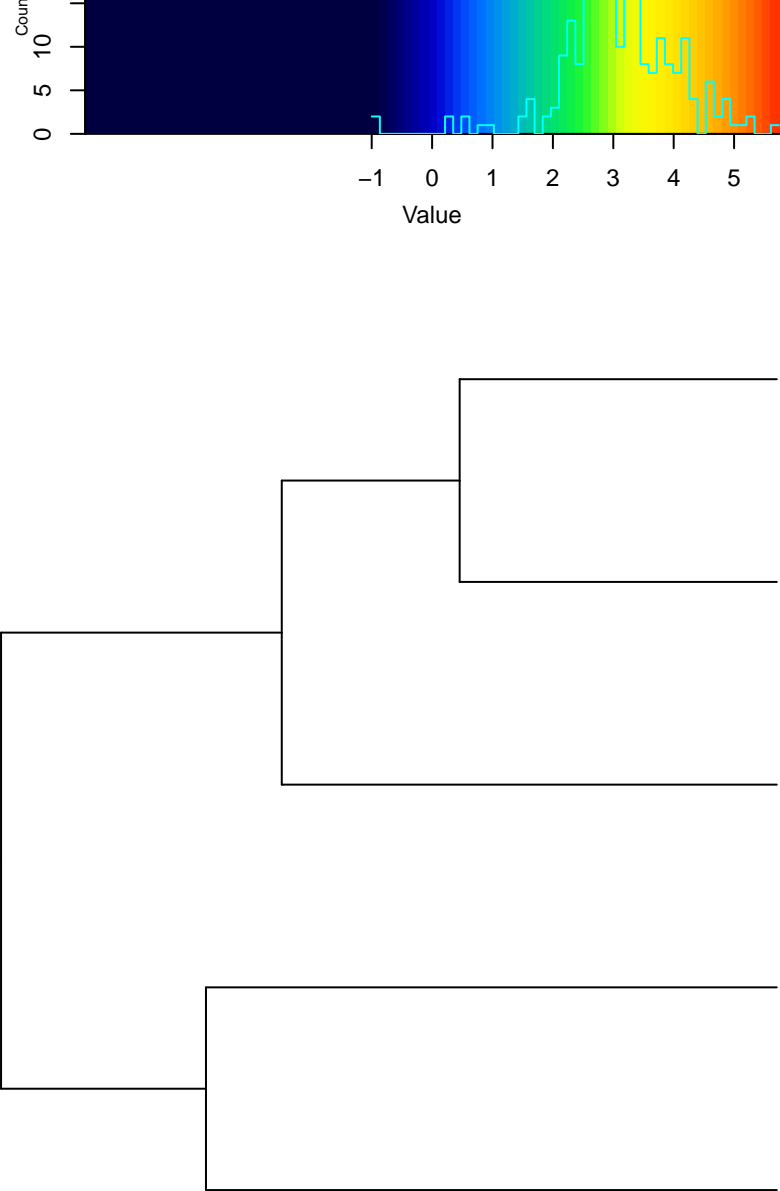


top taxa nodes: specific normalised read count





top taxa nodes: specific absolute read count



Bacillariophyta
Lactobacillus delbrueckii
Streptococcus thermophilus
Enterococcus faecium
Eukaryota
cellular organisms
Triticum aestivum
Triticum urartu
Bacteria
Proteobacteria
Mesangiospermae
Gammaproteobacteria
Enterococcus
Bacilli
Lactobacillales
Streptococcus
Aegilops tauschii
Escherichia coli
Enterobacteriaceae
Phaeodactylum tricornutum CCAP 1055/1
Daphnia pulex
Bilateria
Triticum
Triticinae
Rhizobiales
BOP clade
Alphaproteobacteria
Actinobacteria
Burkholderiales
Burkholderia
Betaproteobacteria
Burkholderiaceae
Aedes aegypti aegypti
Bovidae
Gadus morhua
Boreoeutheria
Zea mays
Amniota
Poaceae
Hordeum vulgare
Triticeae
Magnoliophyta
Firmicutes
Opisthokonta
Ixodes scapularis
Sus scrofa
Ovis aries
Bos taurus
Equus caballus ferus
Oryctolagus cuniculus

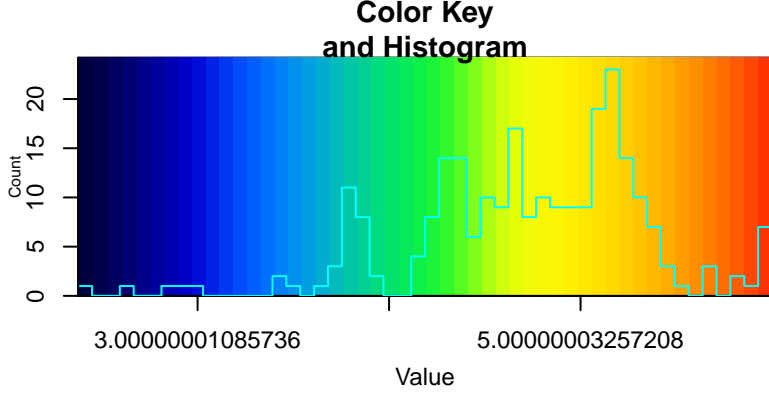
sample_IYB4_R1_fastq

sample_IYB1_R1_fastq

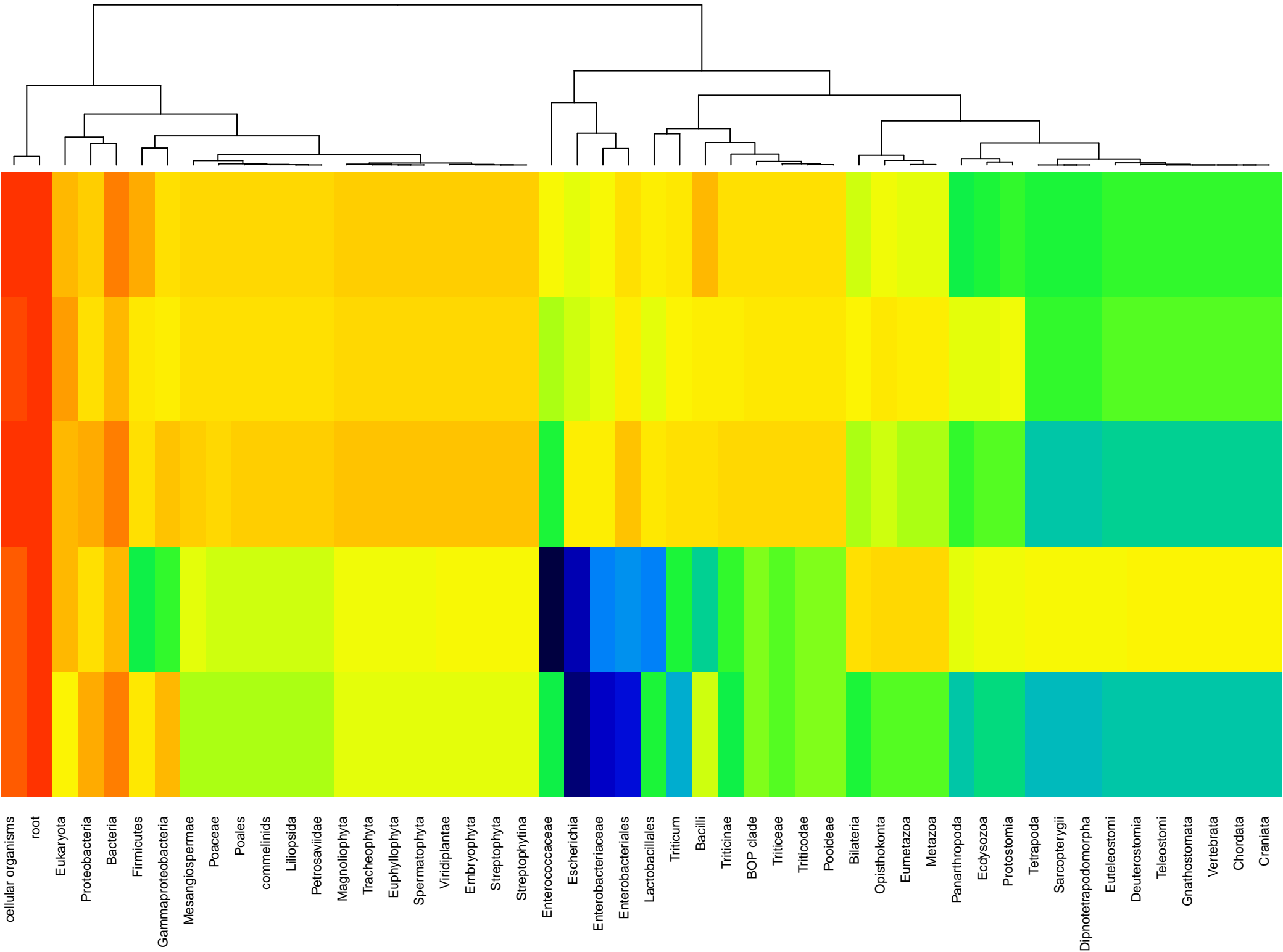
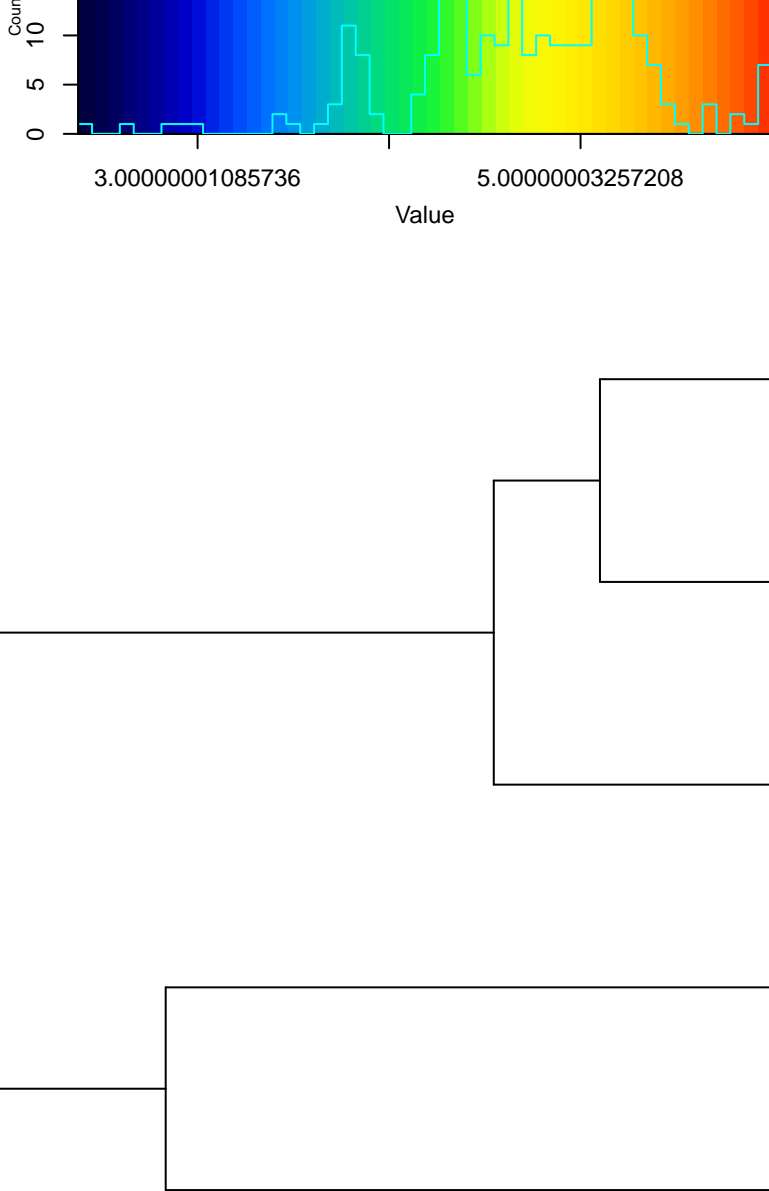
sample_IYB5_R1_fastq

sample_IYB2_R1_fastq

sample_IYB3_R1_fastq



top taxa nodes: cumulative normalised read count



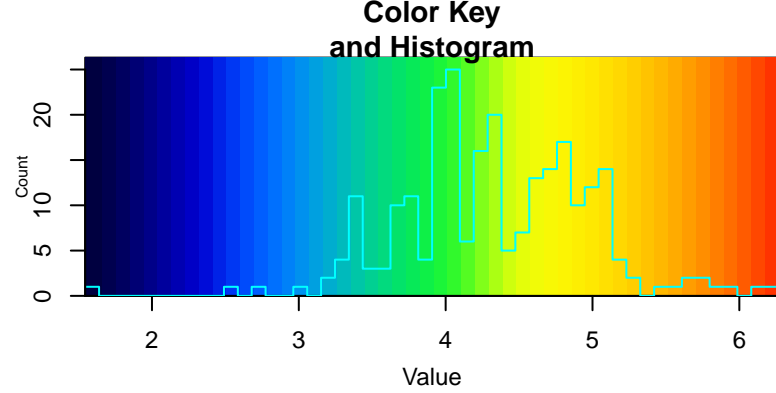
sample_IYB1_R1_fastq

sample_IYB4_R1_fastq

sample_IYB5_R1_fastq

sample_IYB3_R1_fastq

sample_IYB2_R1_fastq



top taxa nodes: cumulative absolute read count

