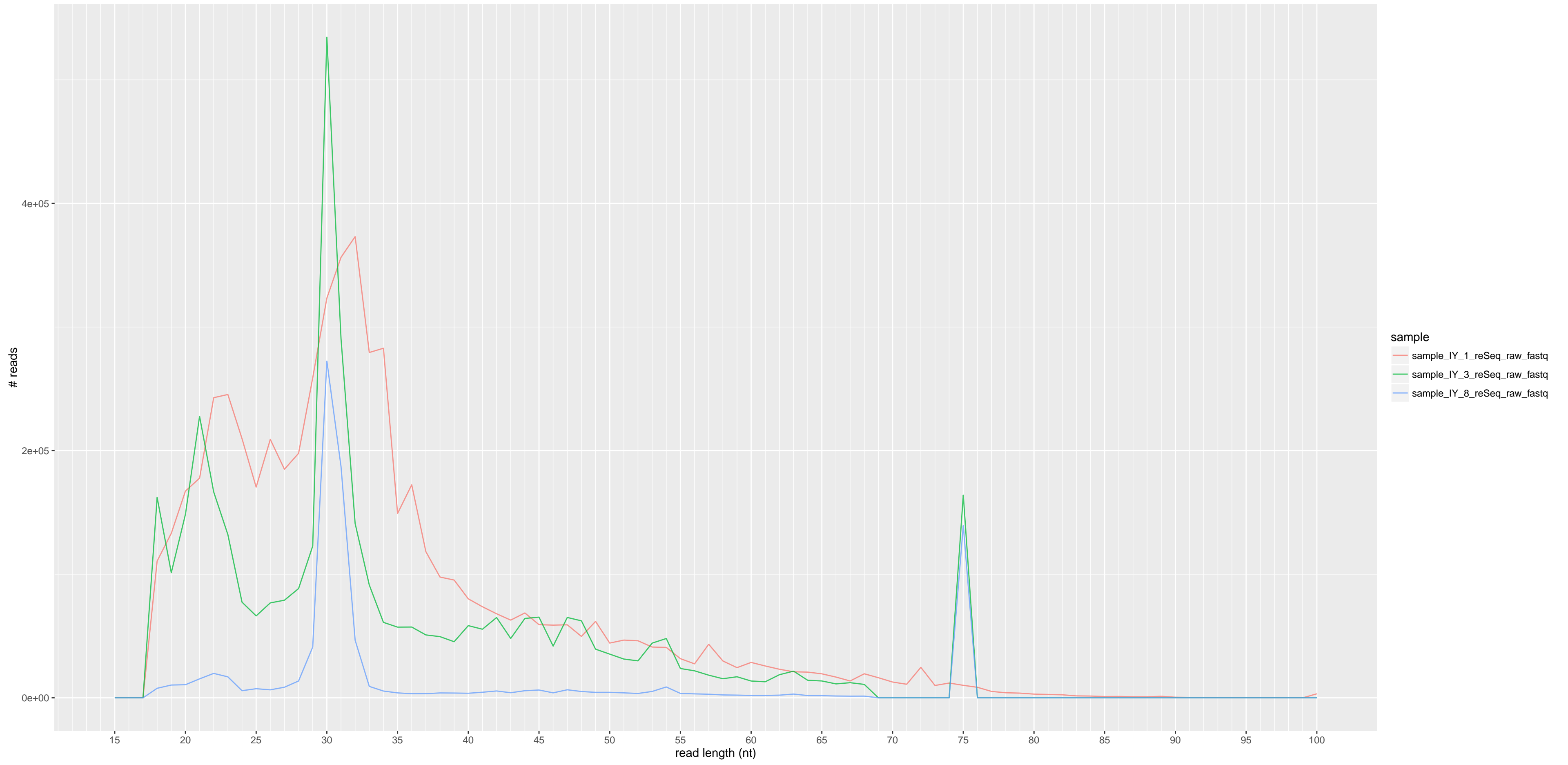
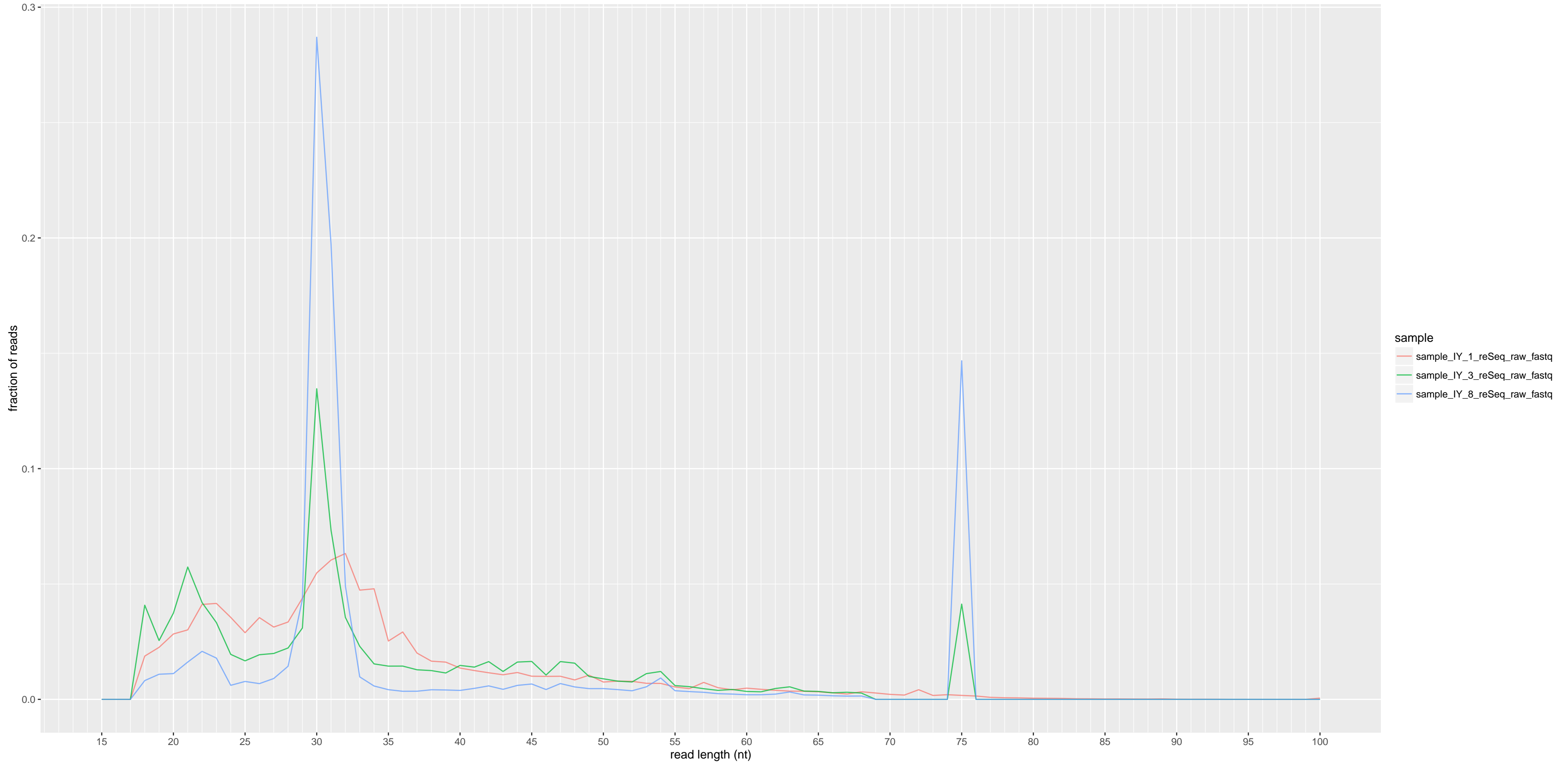


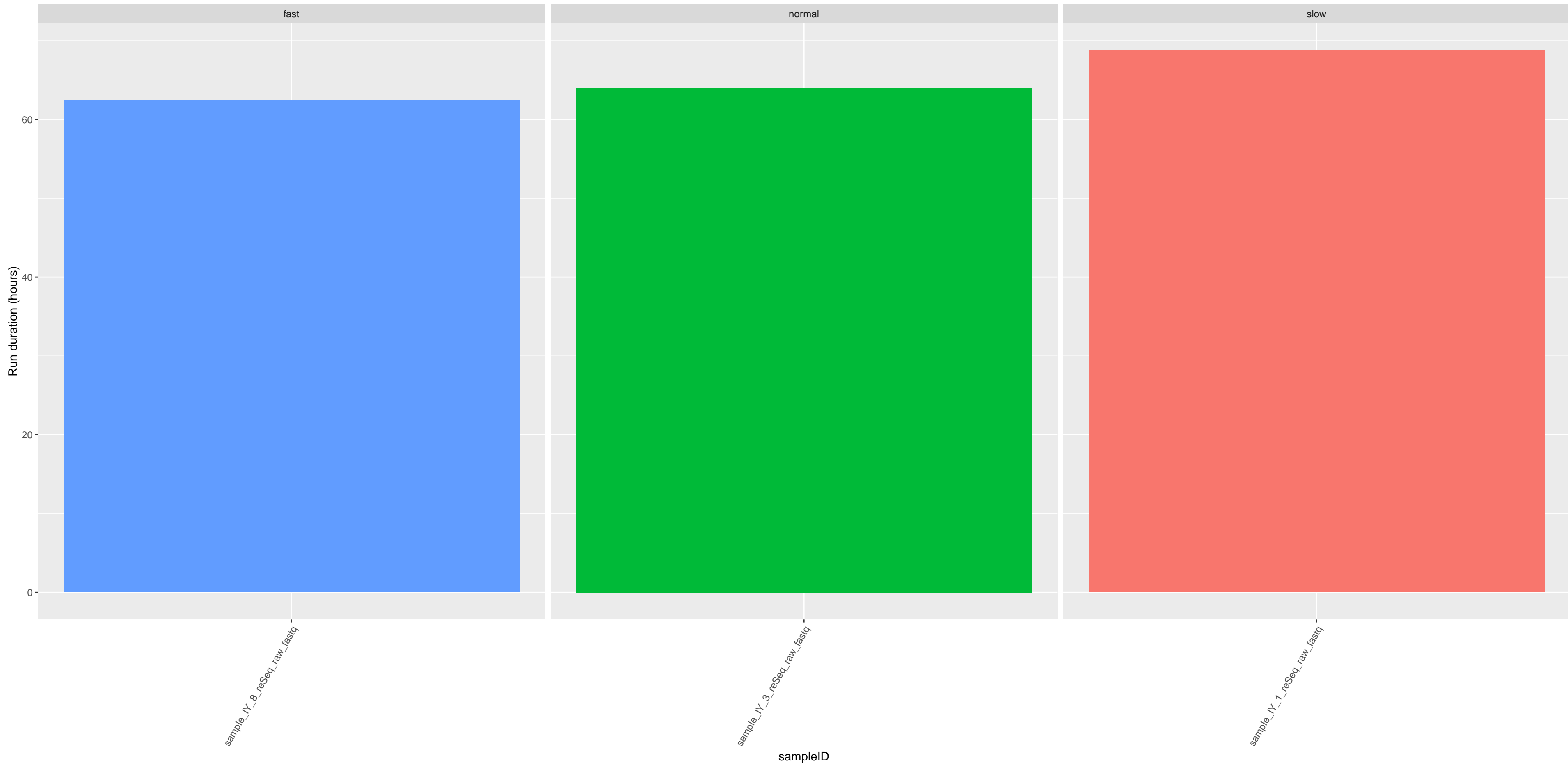
read-length distributions: raw read count



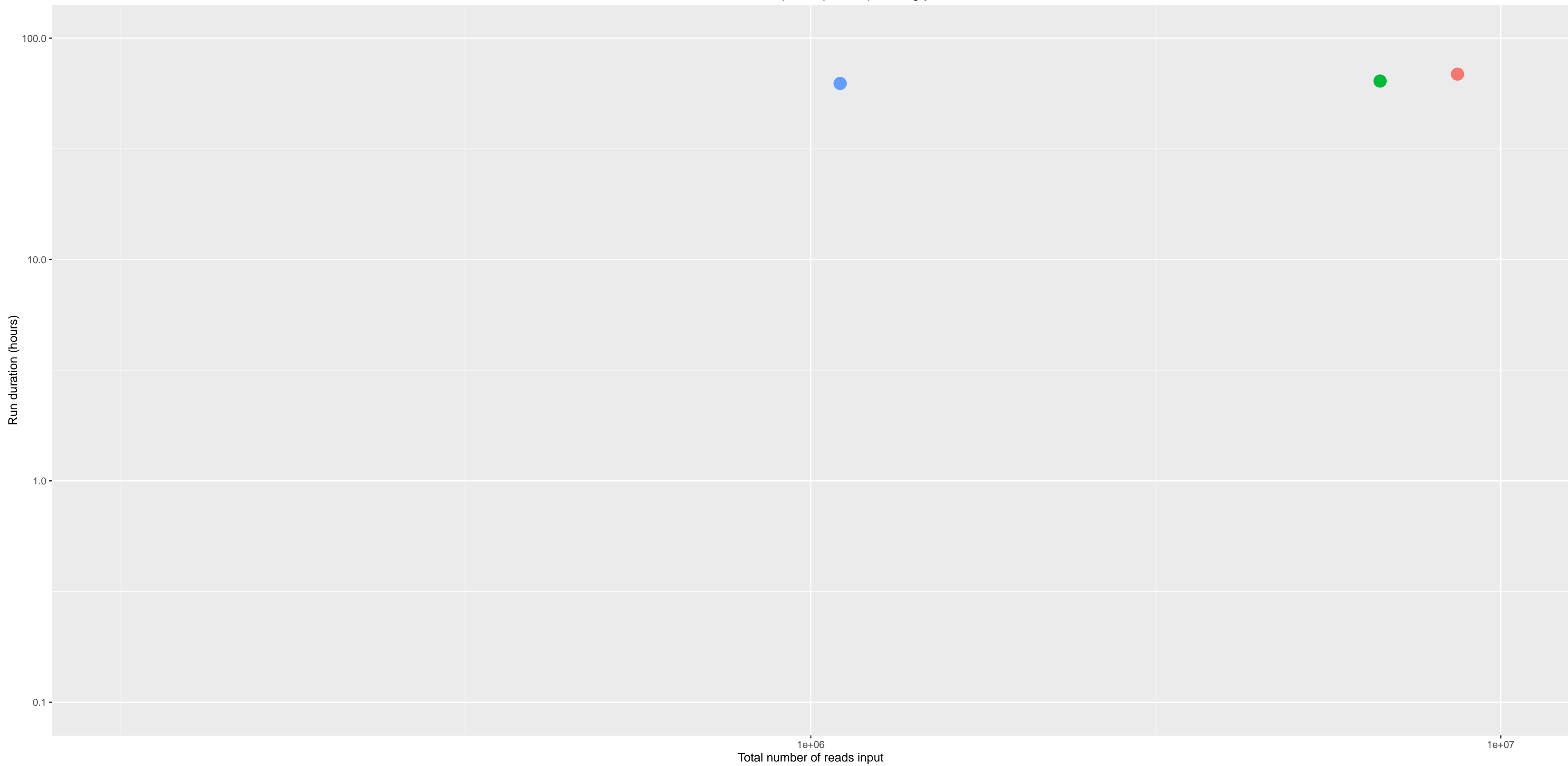
read-length distributions: normalised read fraction



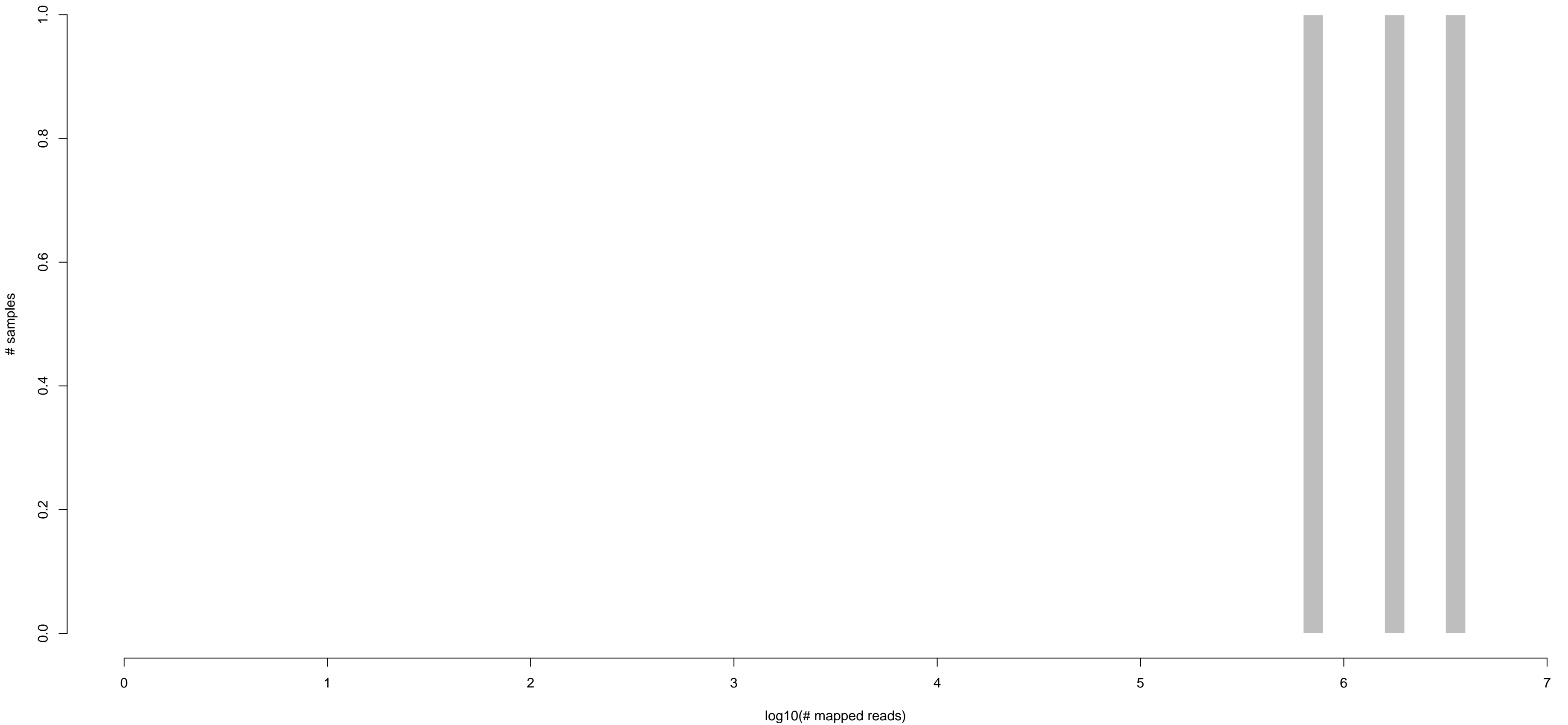
Duration of exceRpt run for each sample

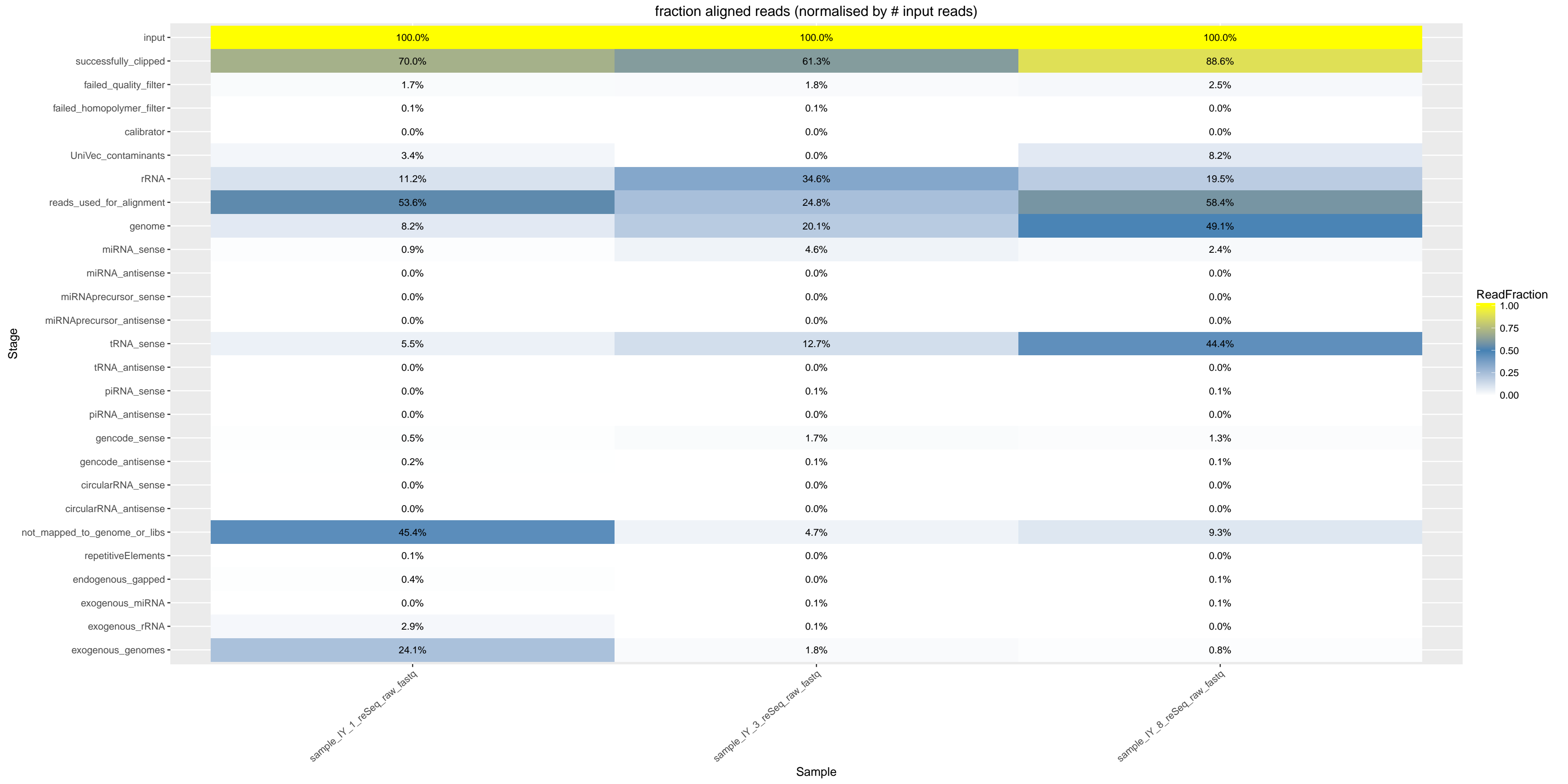


Duration of exceRpt run per sequencing yield

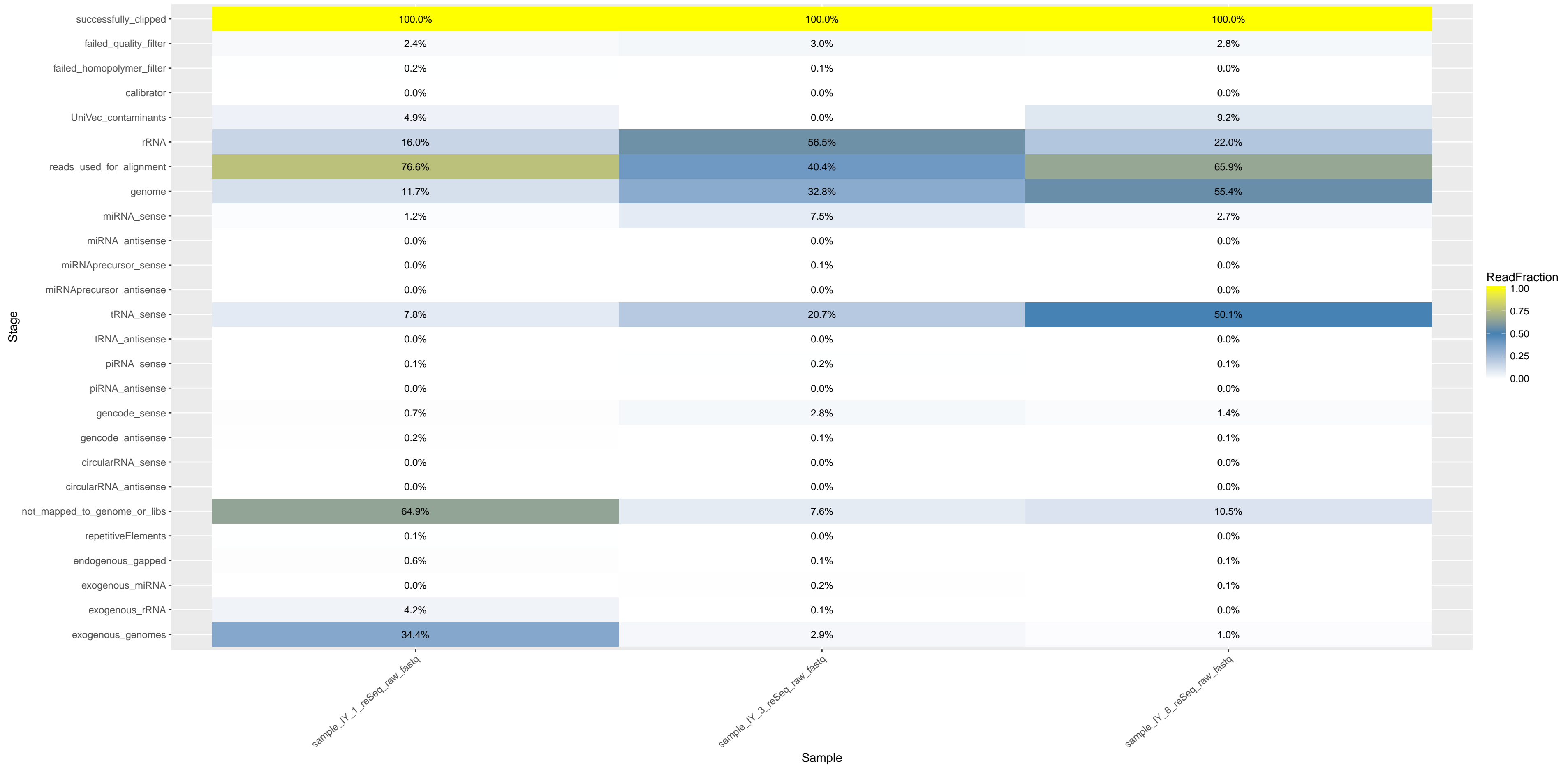


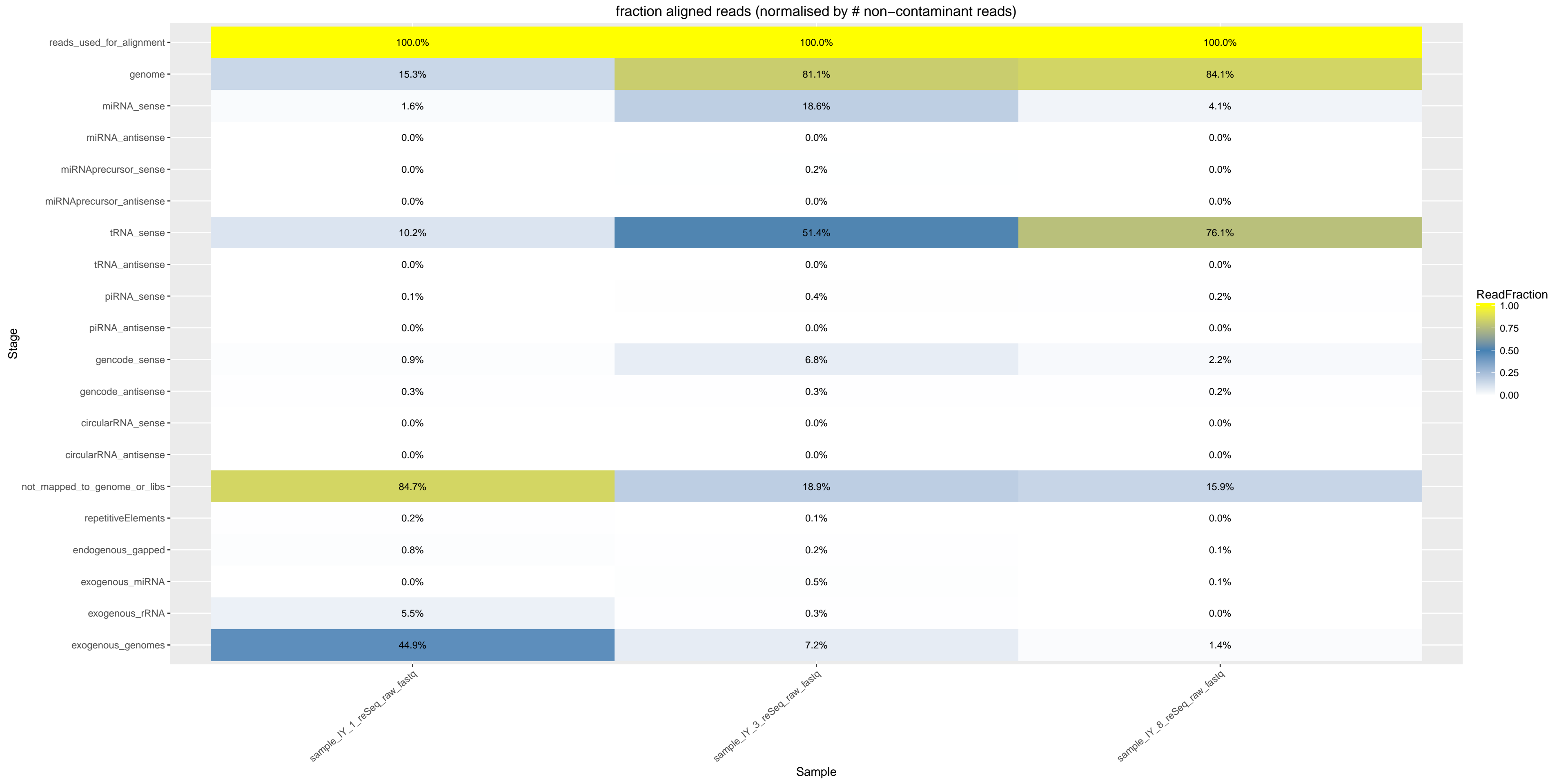
Library size (all mapped reads)



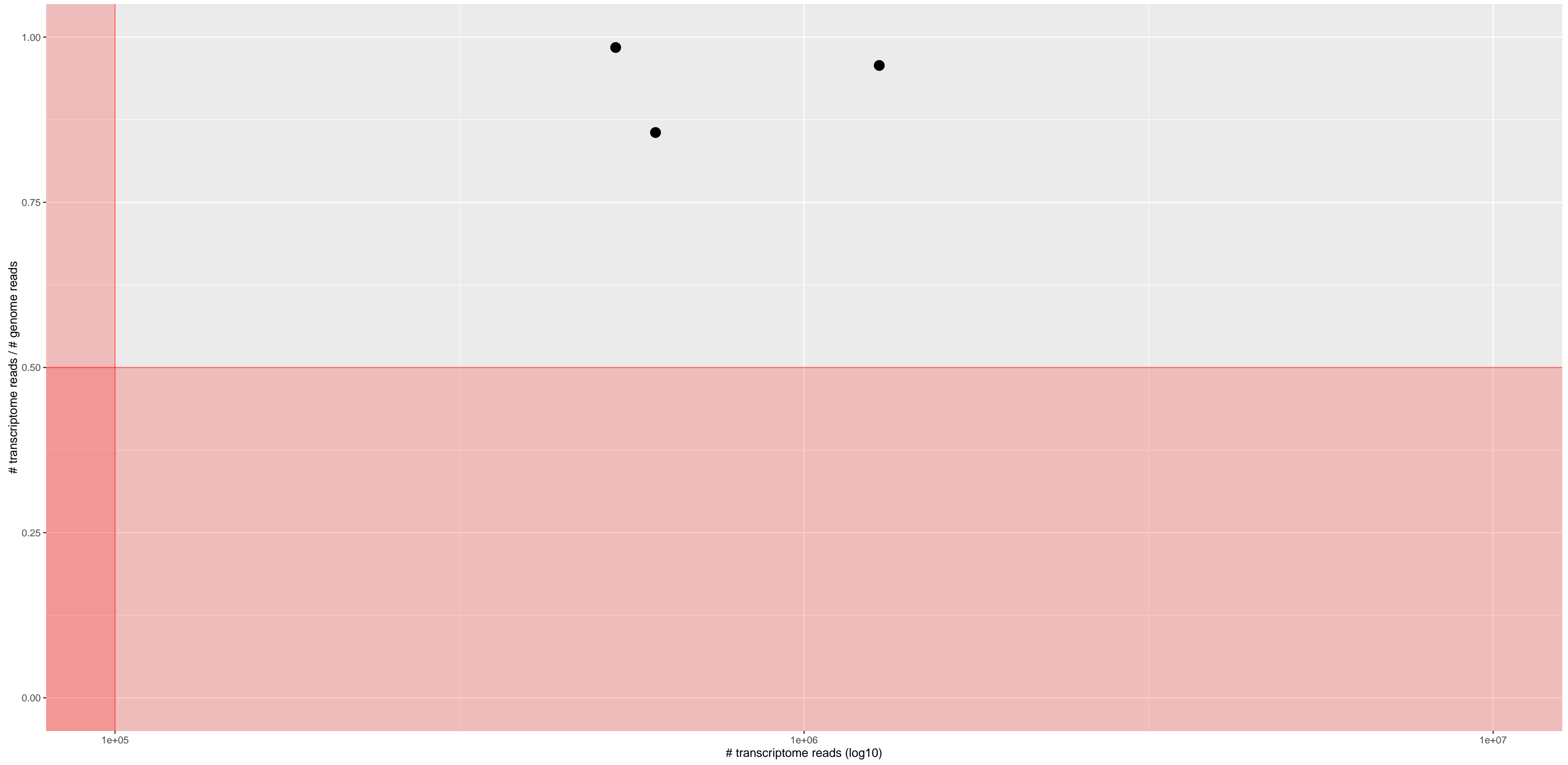


fraction aligned reads (normalised by # adapter-clipped reads)

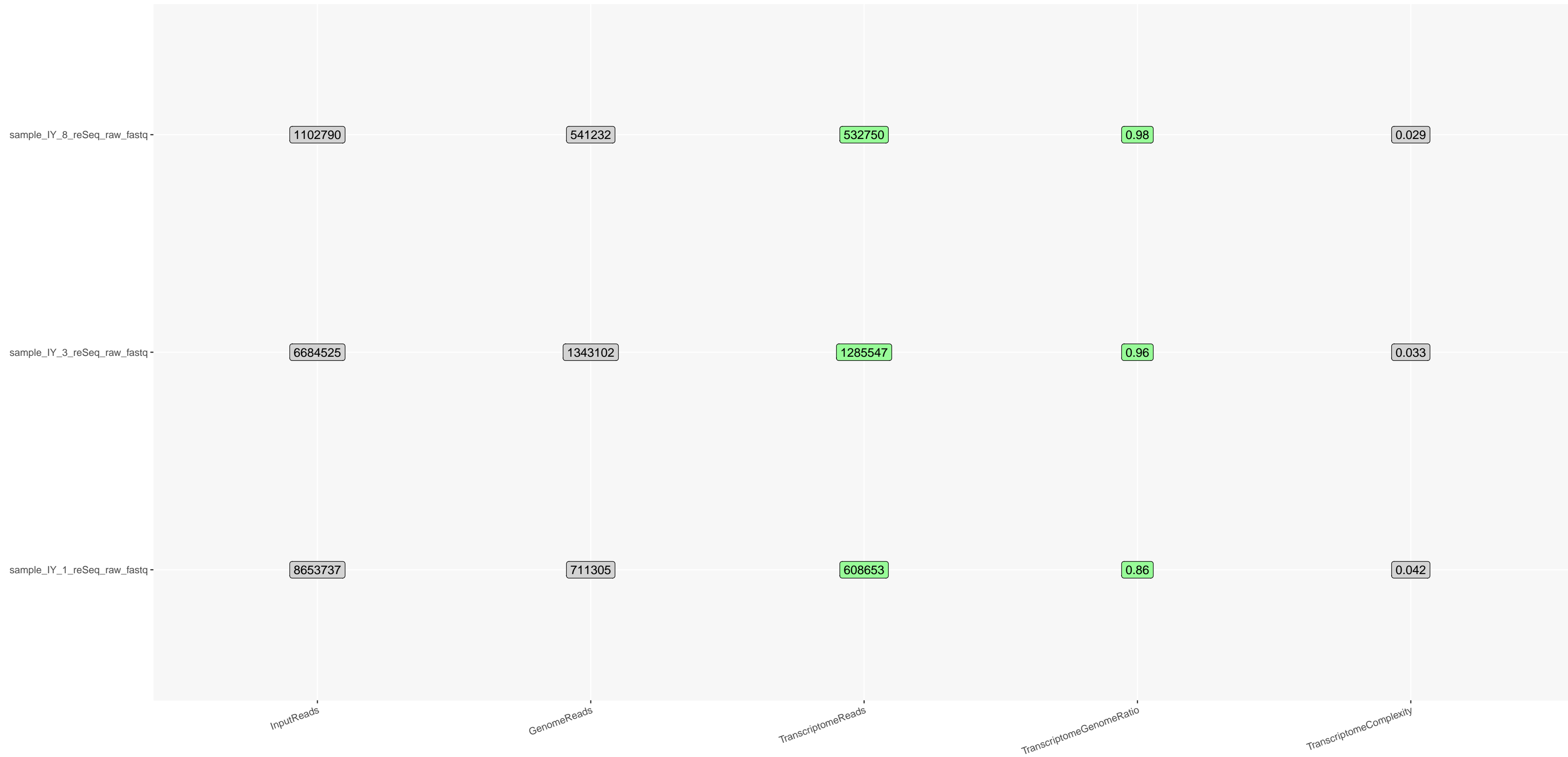




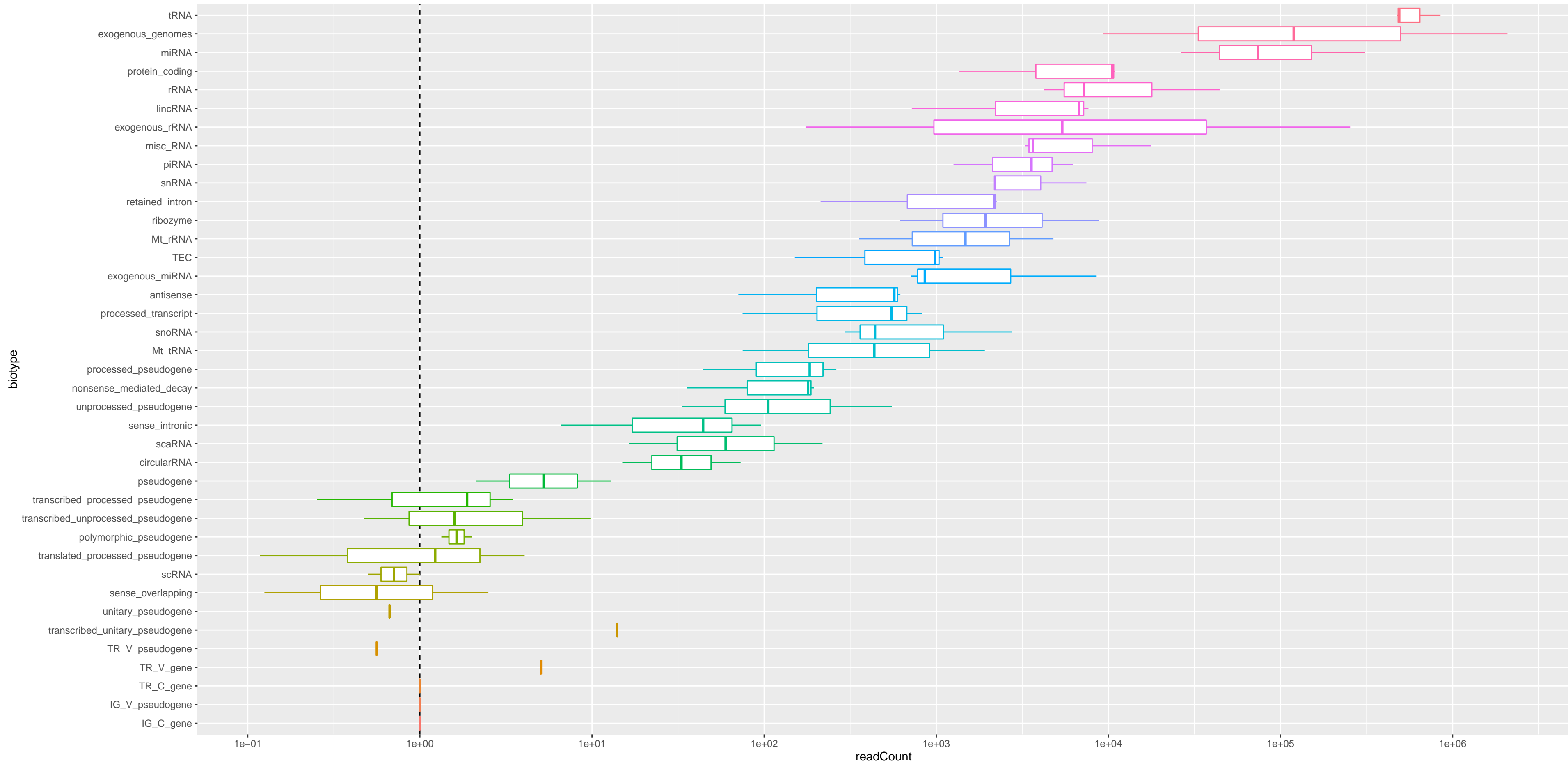
QC result: overall



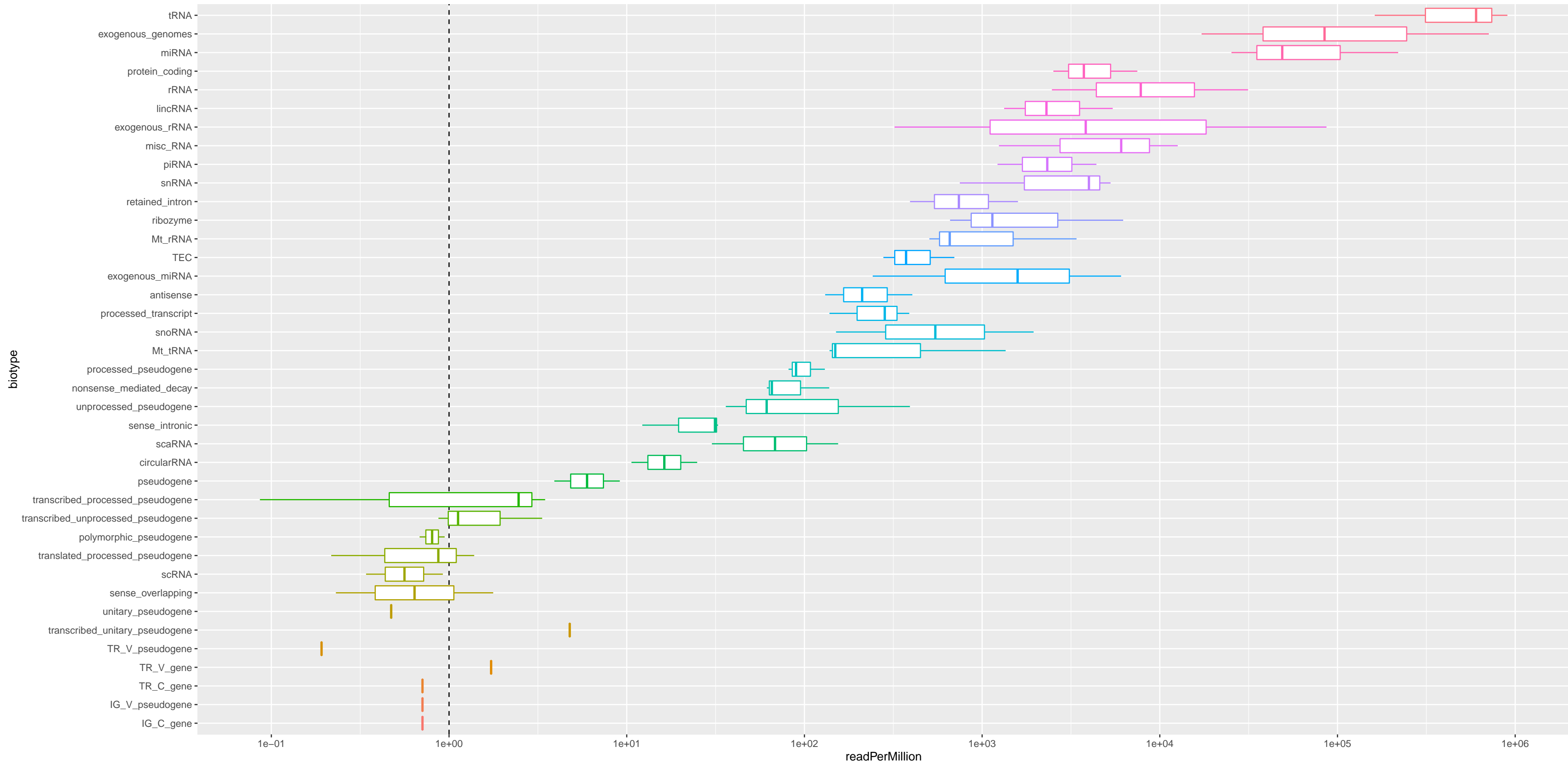
QC result: per-sample results



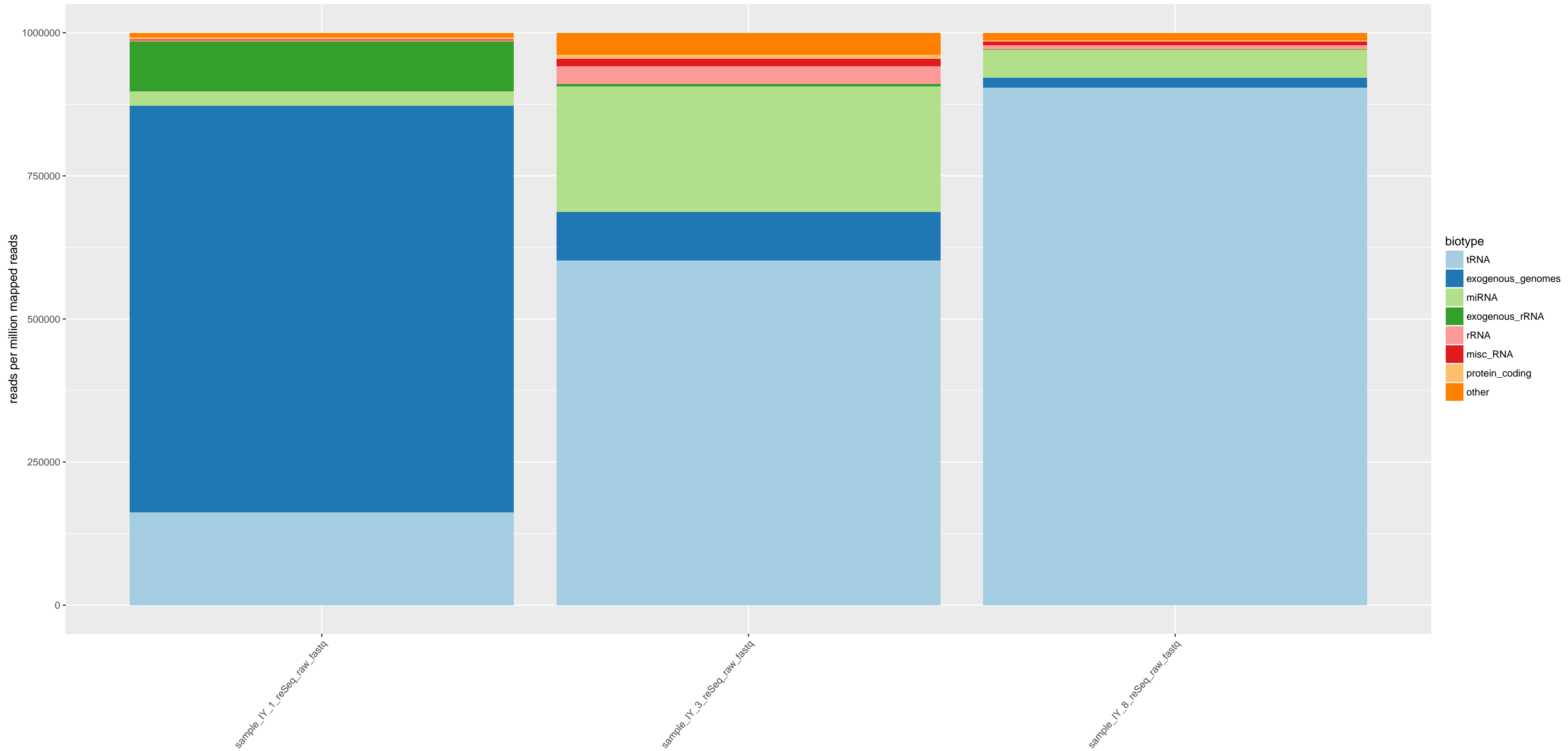
Biotypes: distributions, raw read-counts



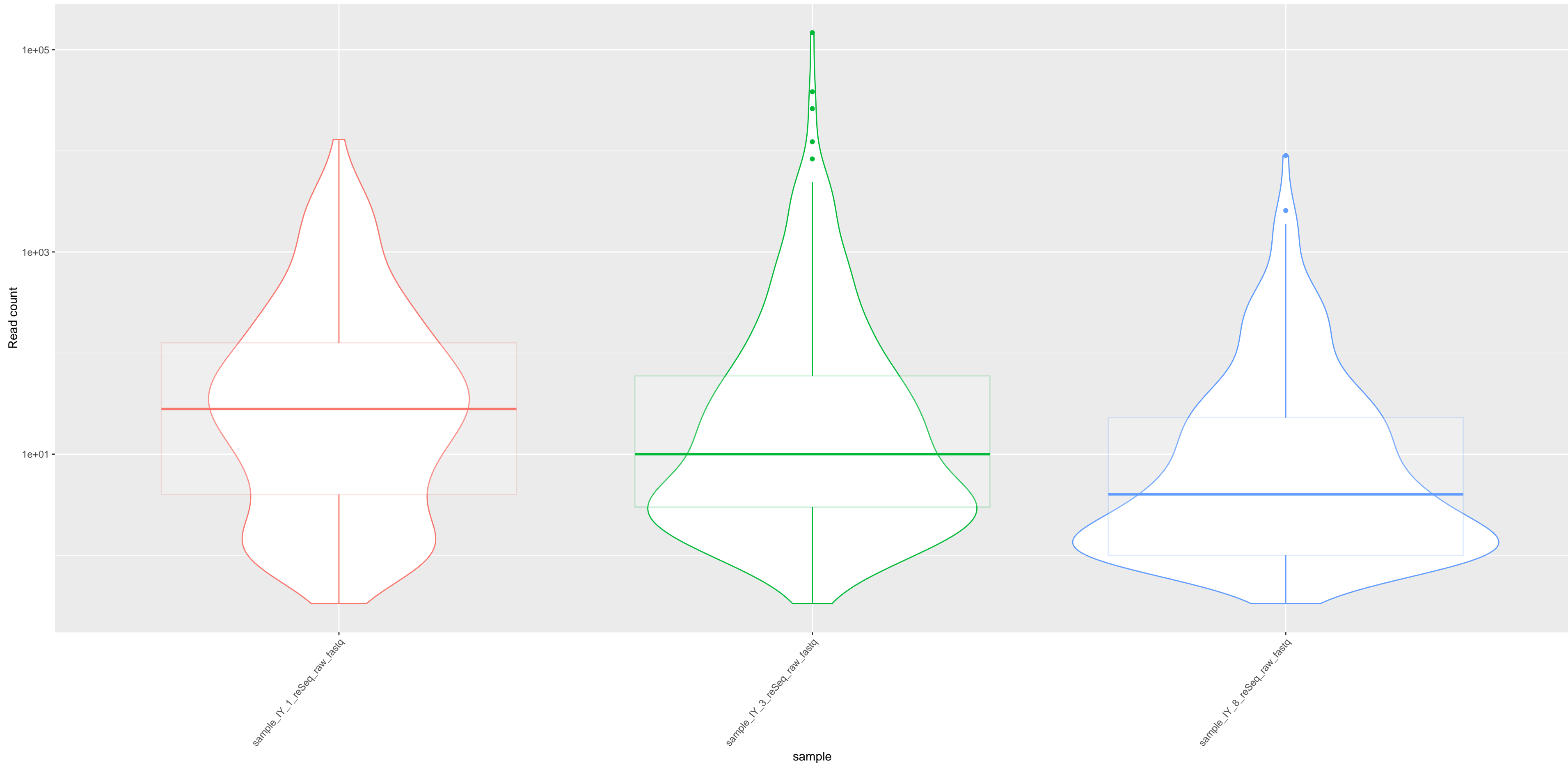
Biotypes: distributions, normalised



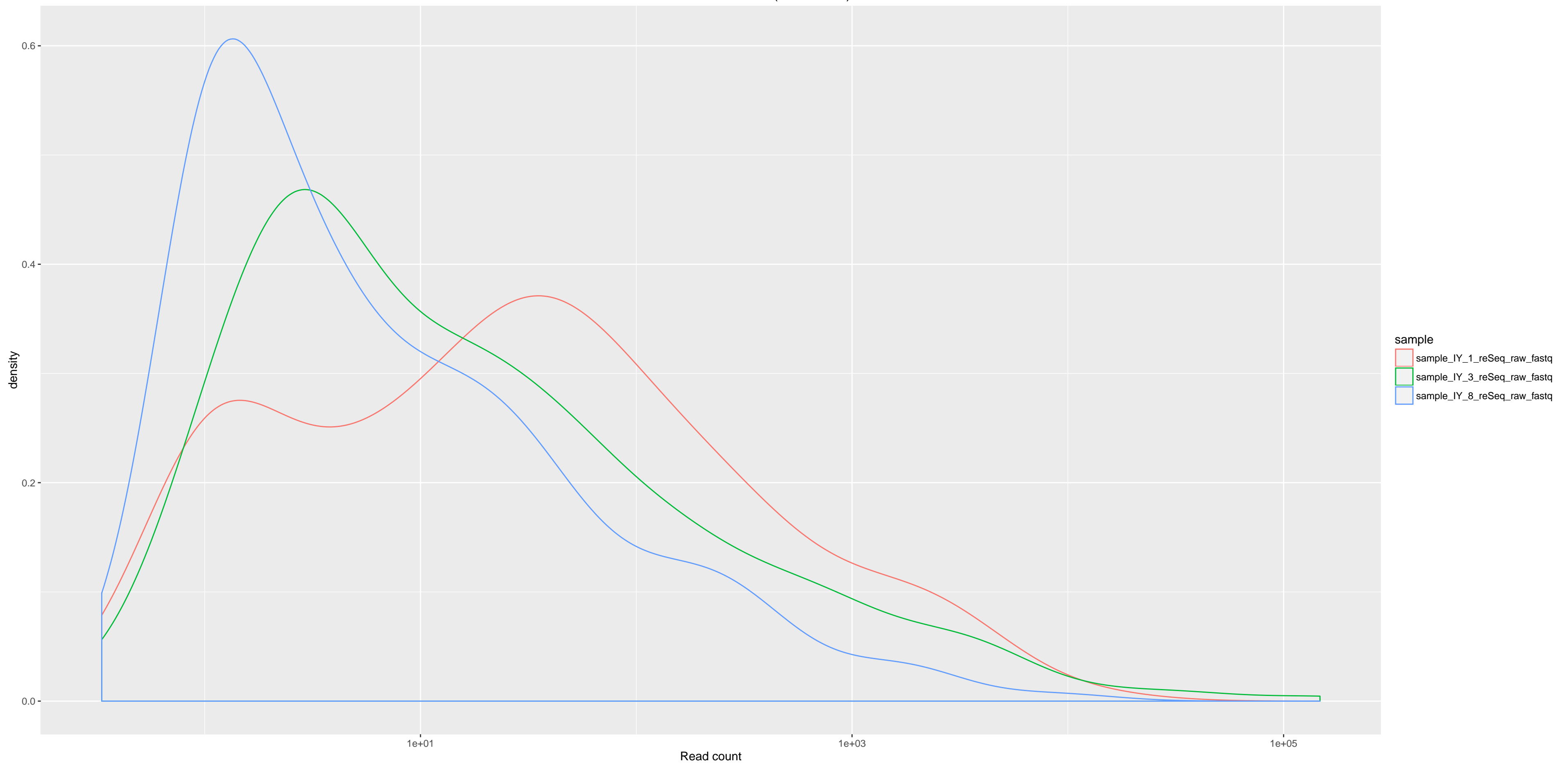
Biotypes: per-sample, normalised



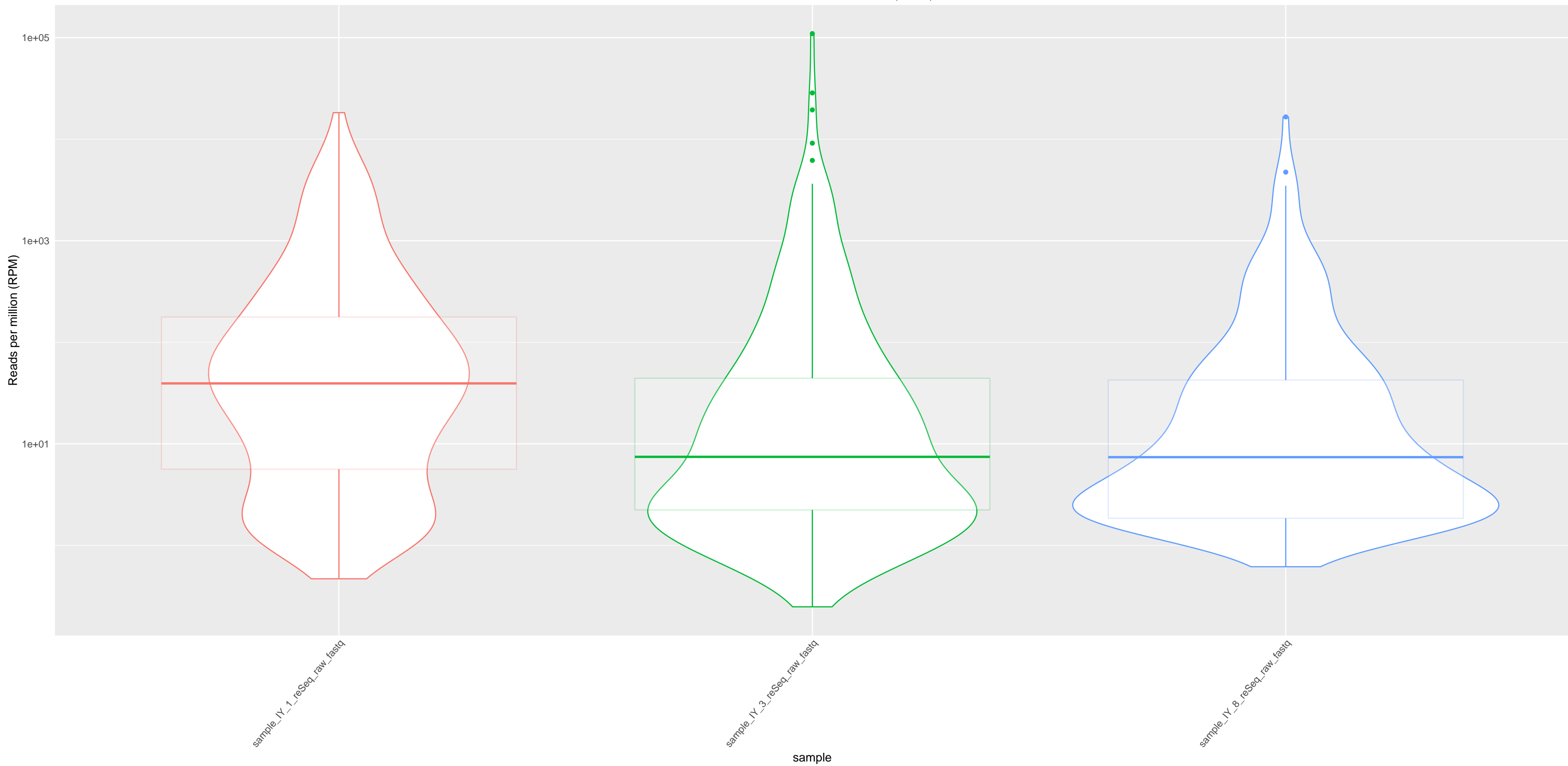
miRNA abundance distributions (raw counts)



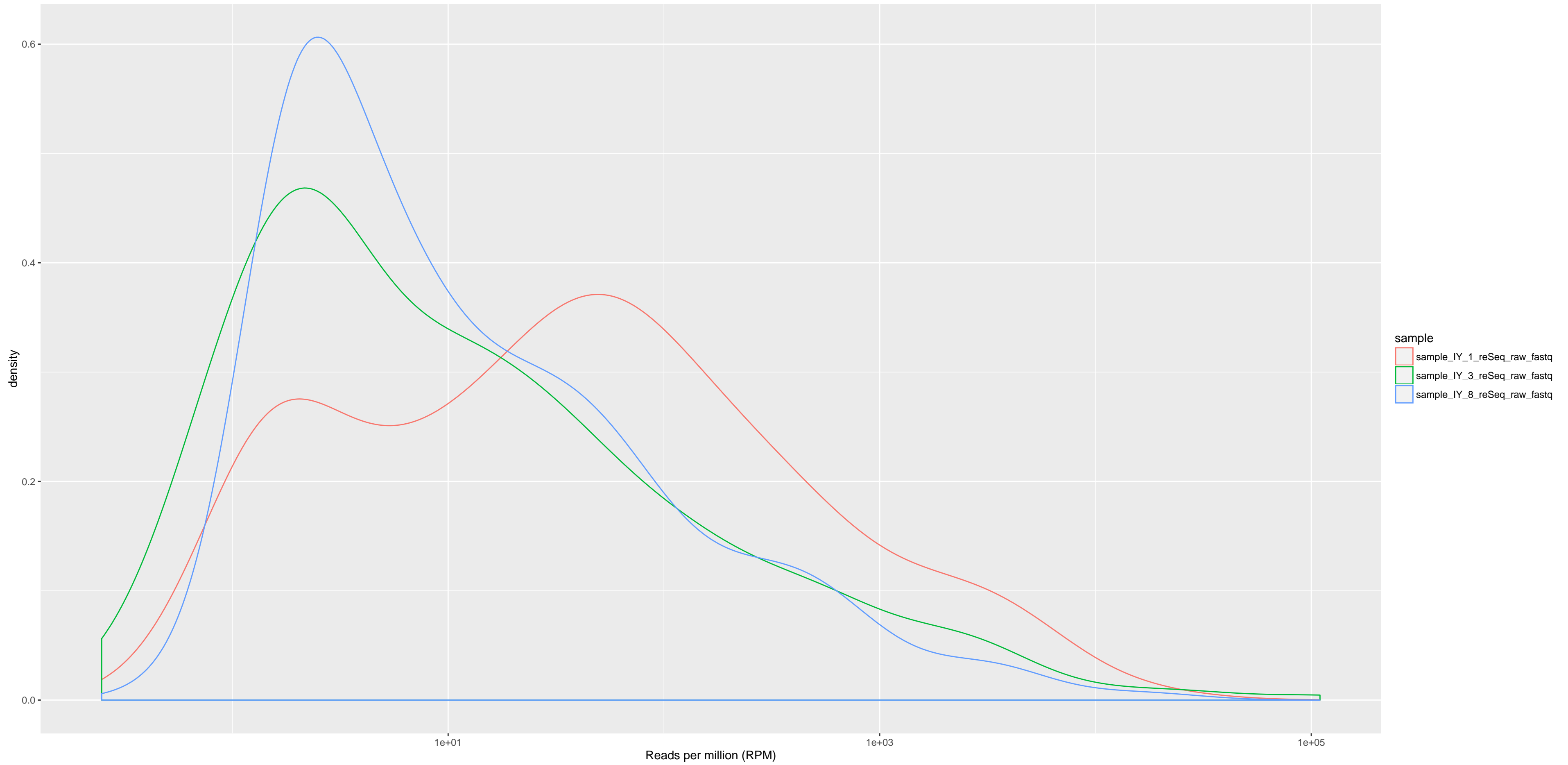
miRNA abundance distributions (raw counts)



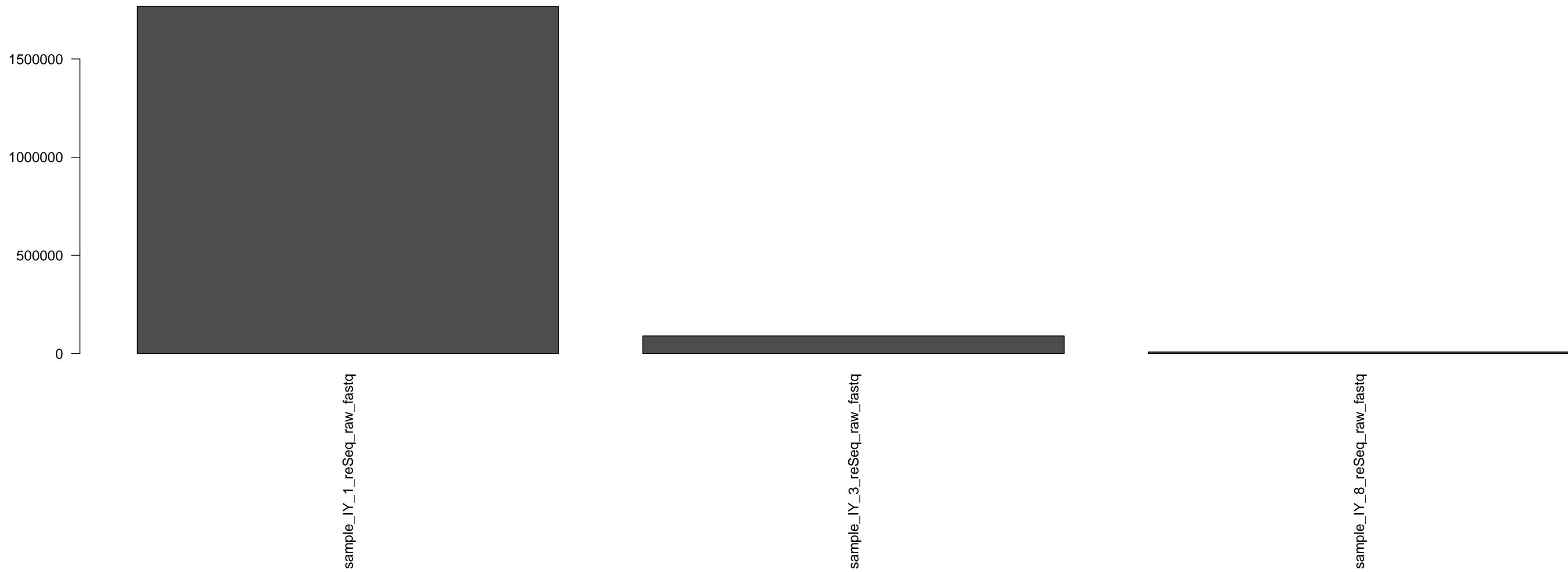
miRNA abundance distributions (RPM)

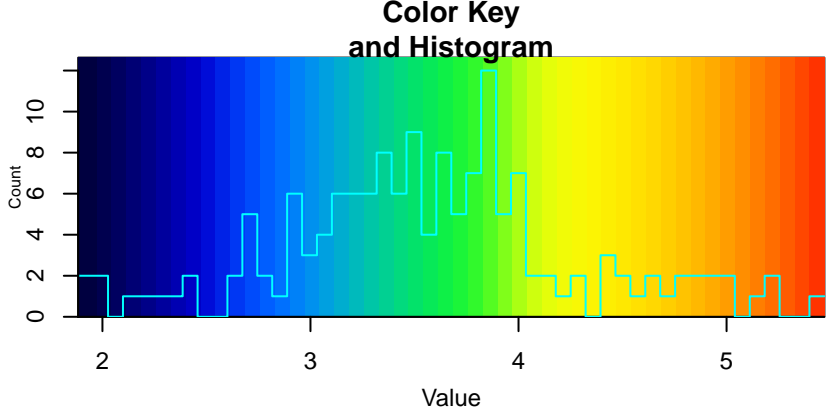


miRNA abundance distributions (RPM)

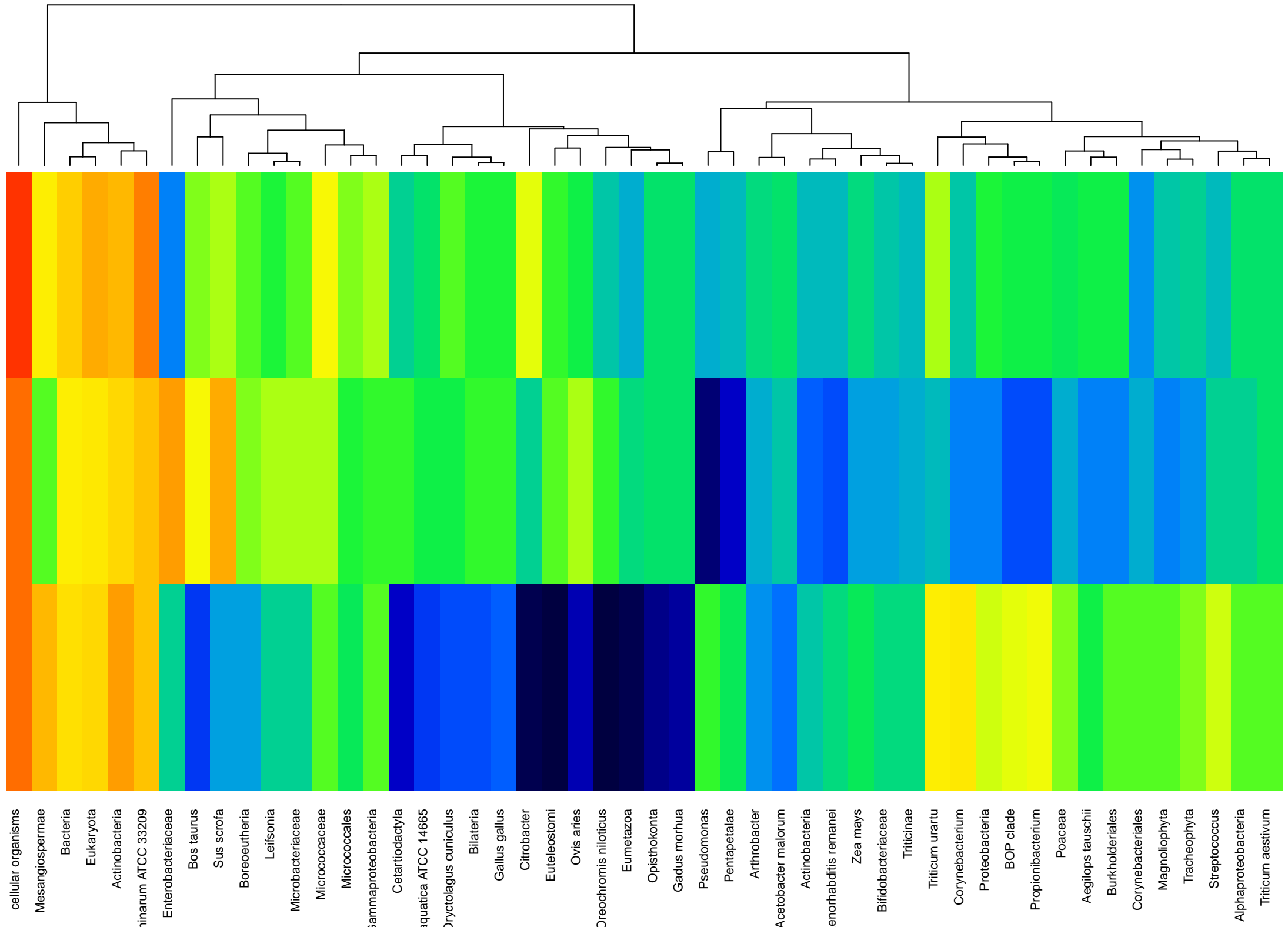
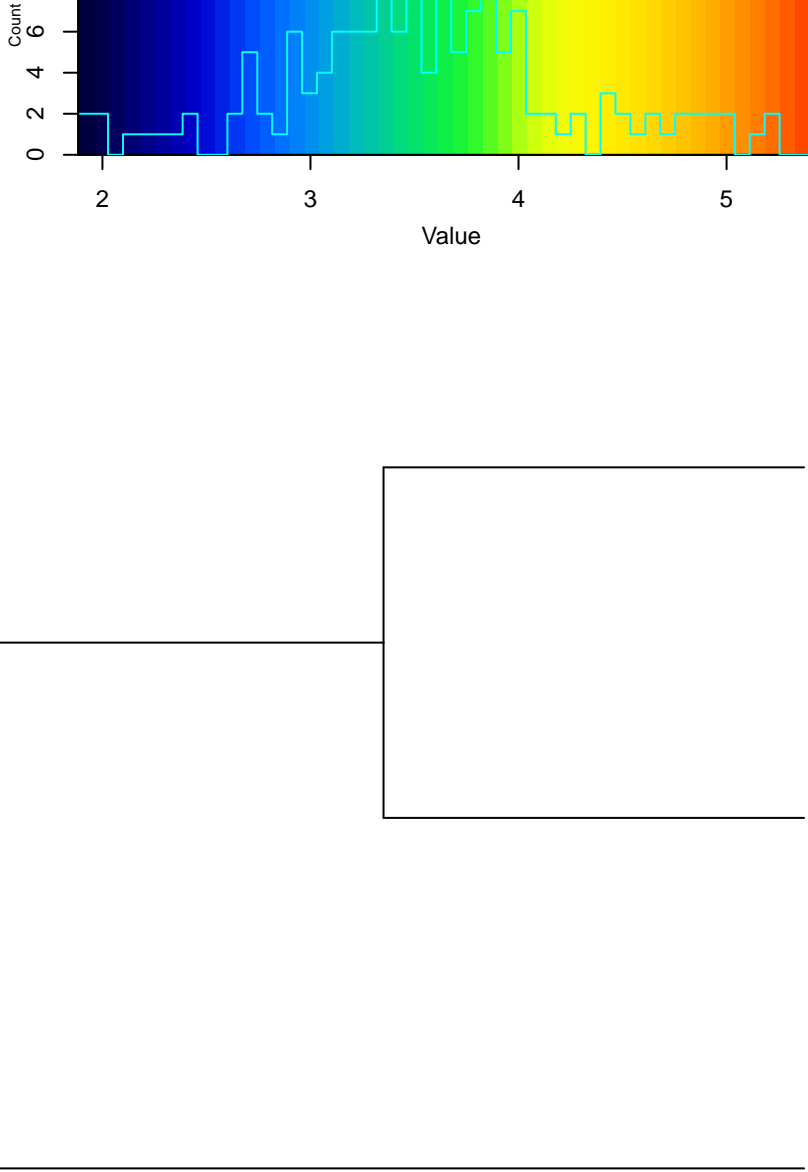


Total # reads mapped to NCBI taxonomy





top taxa nodes: specific normalised read count

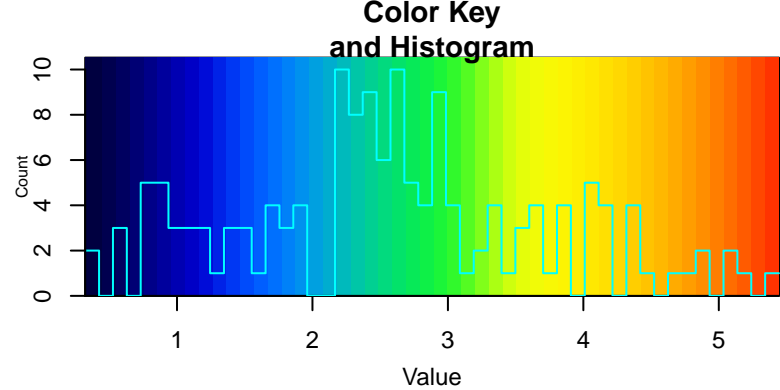


sample_IY_3_reSeq_raw_fa

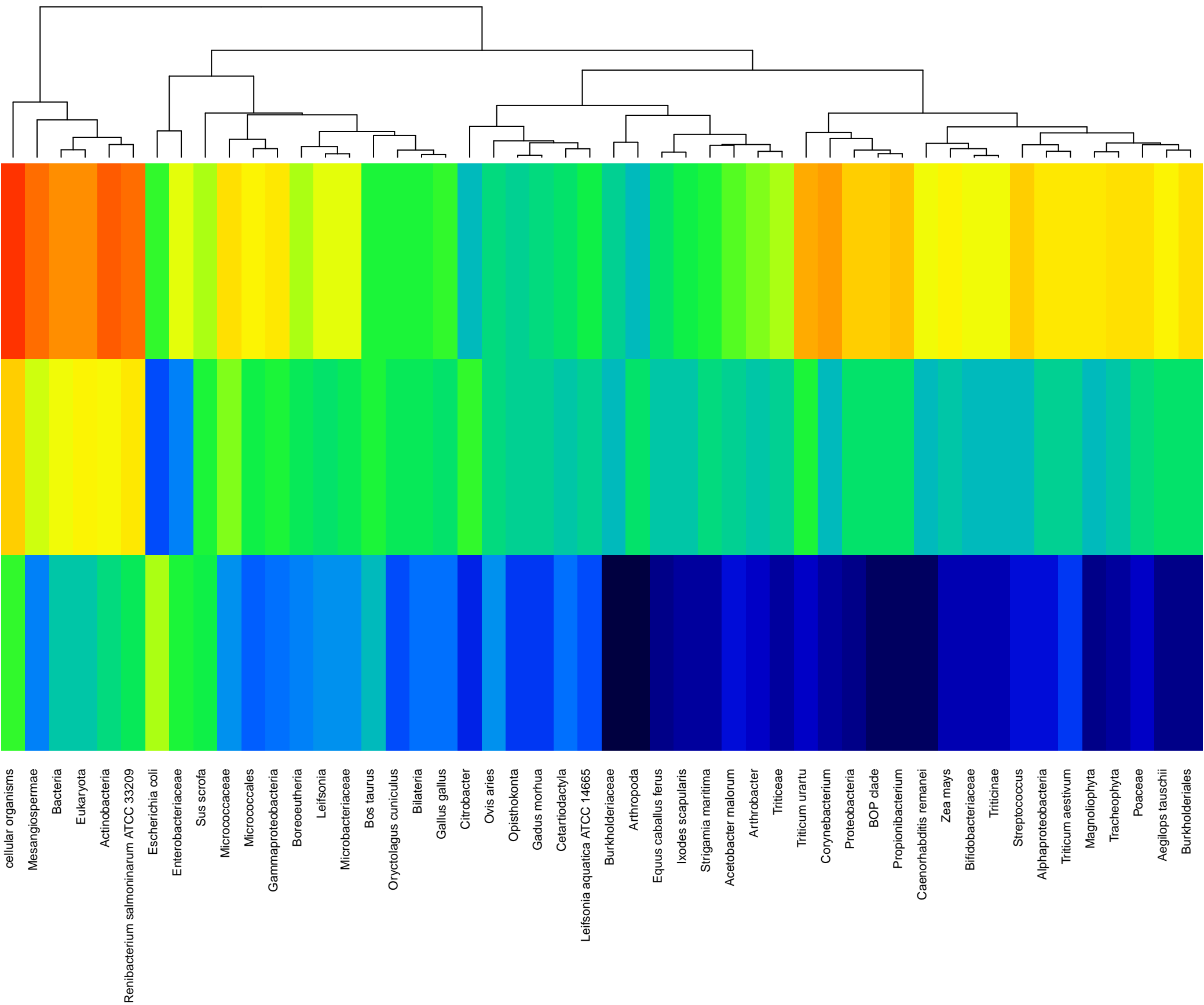
sample_IY_8_reSeq_raw_fa

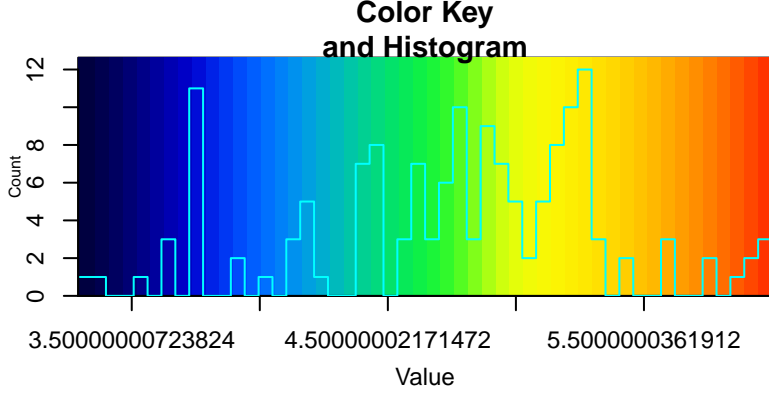
sample_IY_1_reSeq_raw_fa

- cellular organisms
- Mesangiopermae
- Bacteria
- Eukaryota
- Actinobacteria
- Actinobacterium ATCC 33209
- Enterobacteriaceae
- Bos taurus
- Sus scrofa
- Boreoeutheria
- Leifsonia
- Microbacteriaceae
- Micrococcales
- Microproteobacteria
- Cetartiodactyla
- Leifsonia aquatica ATCC 14665
- Oryctolagus cuniculus
- Bilateria
- Gallus gallus
- Citrobacter
- Euteleostomi
- Ovis aries
- Oreochromis niloticus
- Eumetazoa
- Opisthokonta
- Gadus morhua
- Pseudomonas
- Pentapetalae
- Arthrobacter
- Acetobacter malorum
- Actinobacteria
- Caenorhabditis remanei
- Zea mays
- Blifidobacteriaceae
- Triticinae
- Triticum urartu
- Corynebacterium
- Proteobacteria
- BOP clade
- Propionibacterium
- Poaceae
- Aegilops tauschii
- Burkholderiales
- Corynebacteriales
- Magnoliophyta
- Tracheophyta
- Streptococcus
- Alphaproteobacteria
- Triticum aestivum

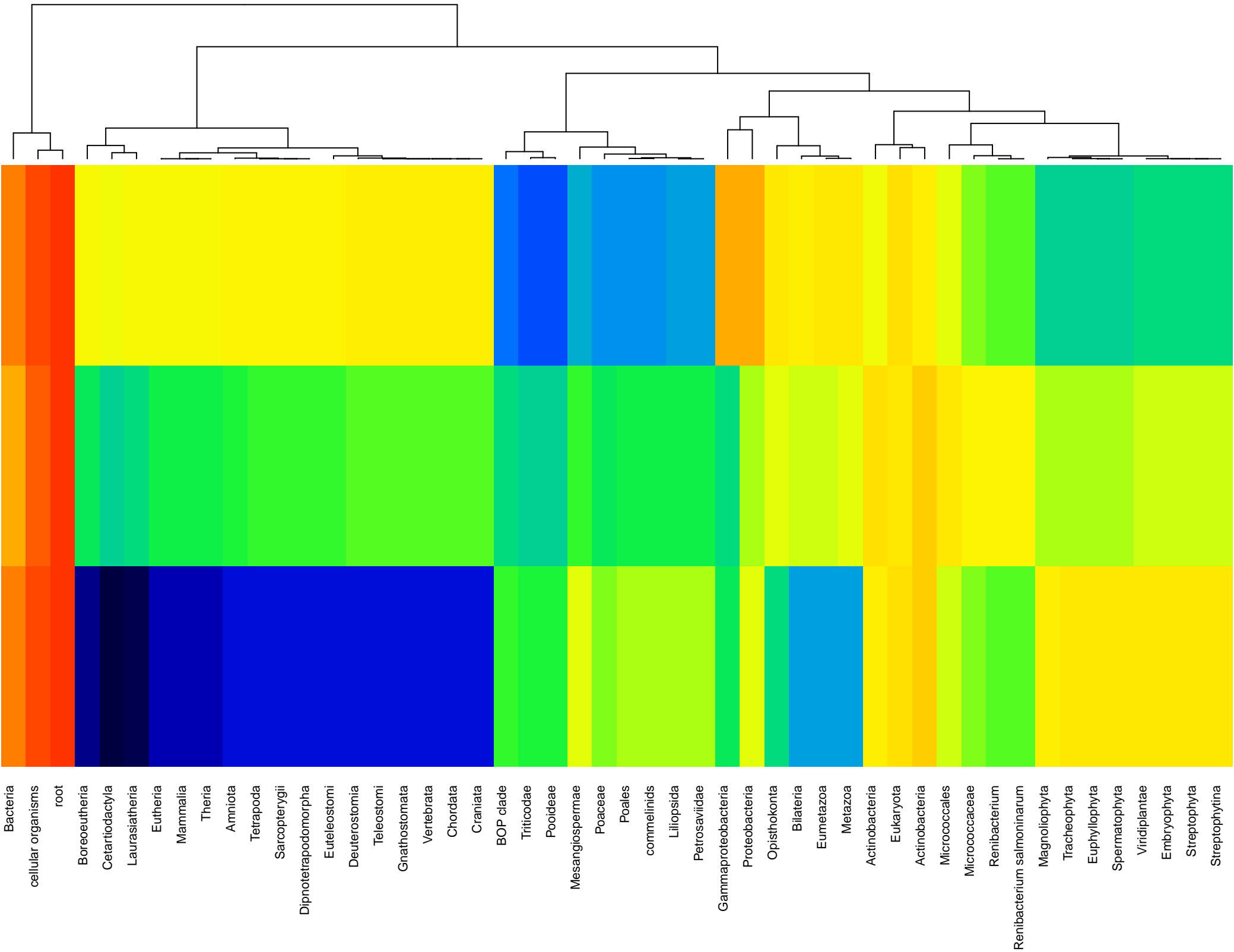
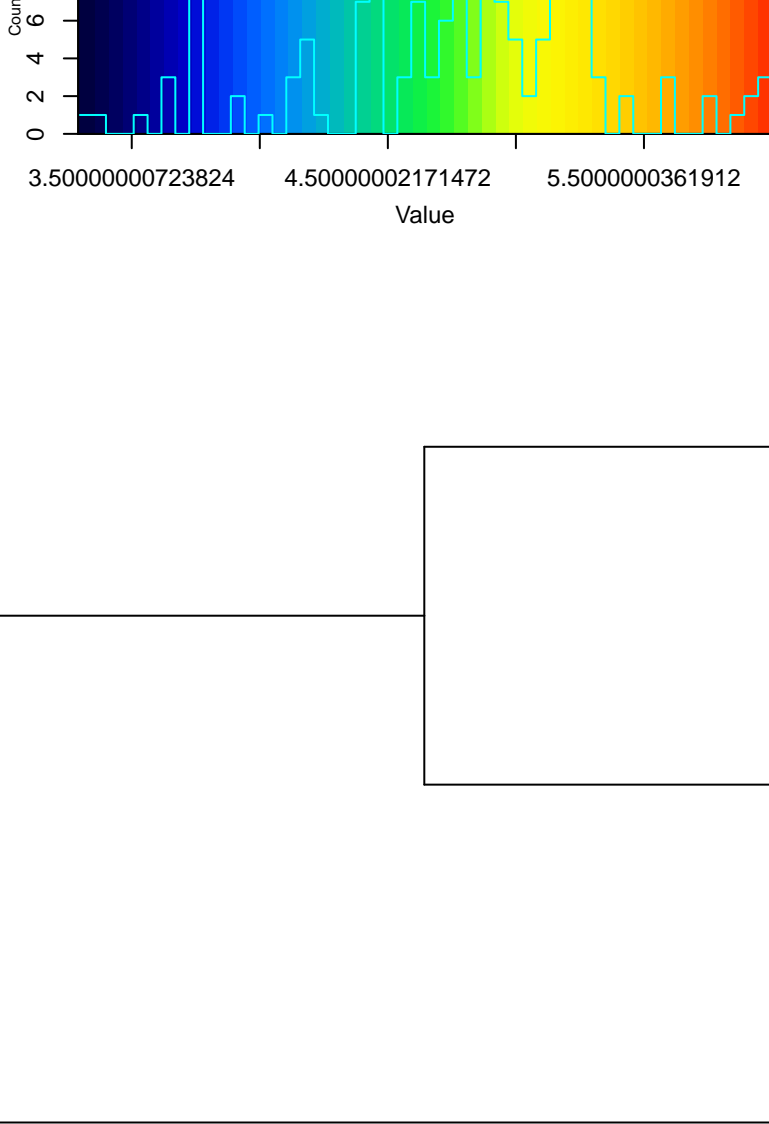


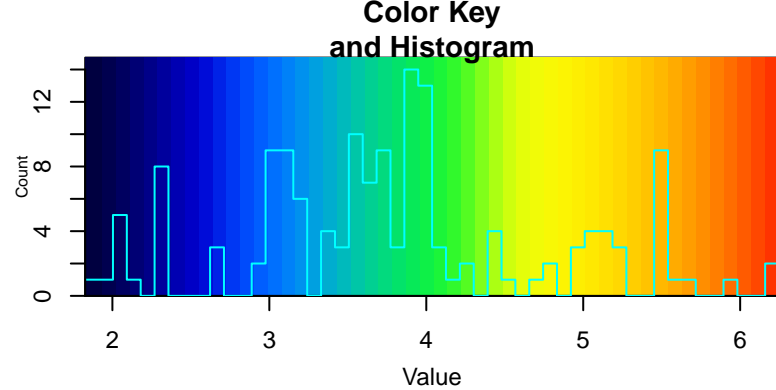
top taxa nodes: specific absolute read count





top taxa nodes: cumulative normalised read count





top taxa nodes: cumulative absolute read count

