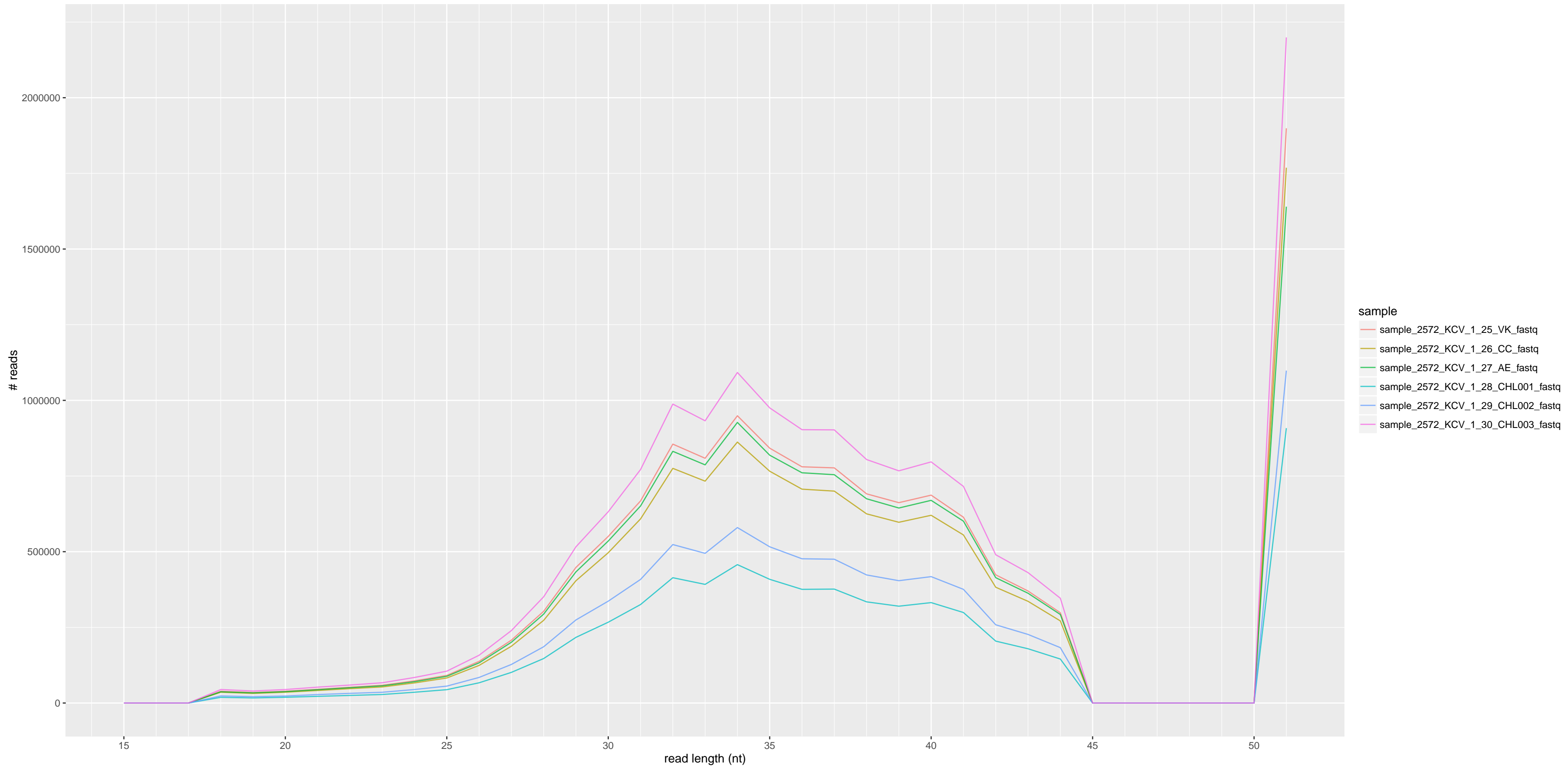
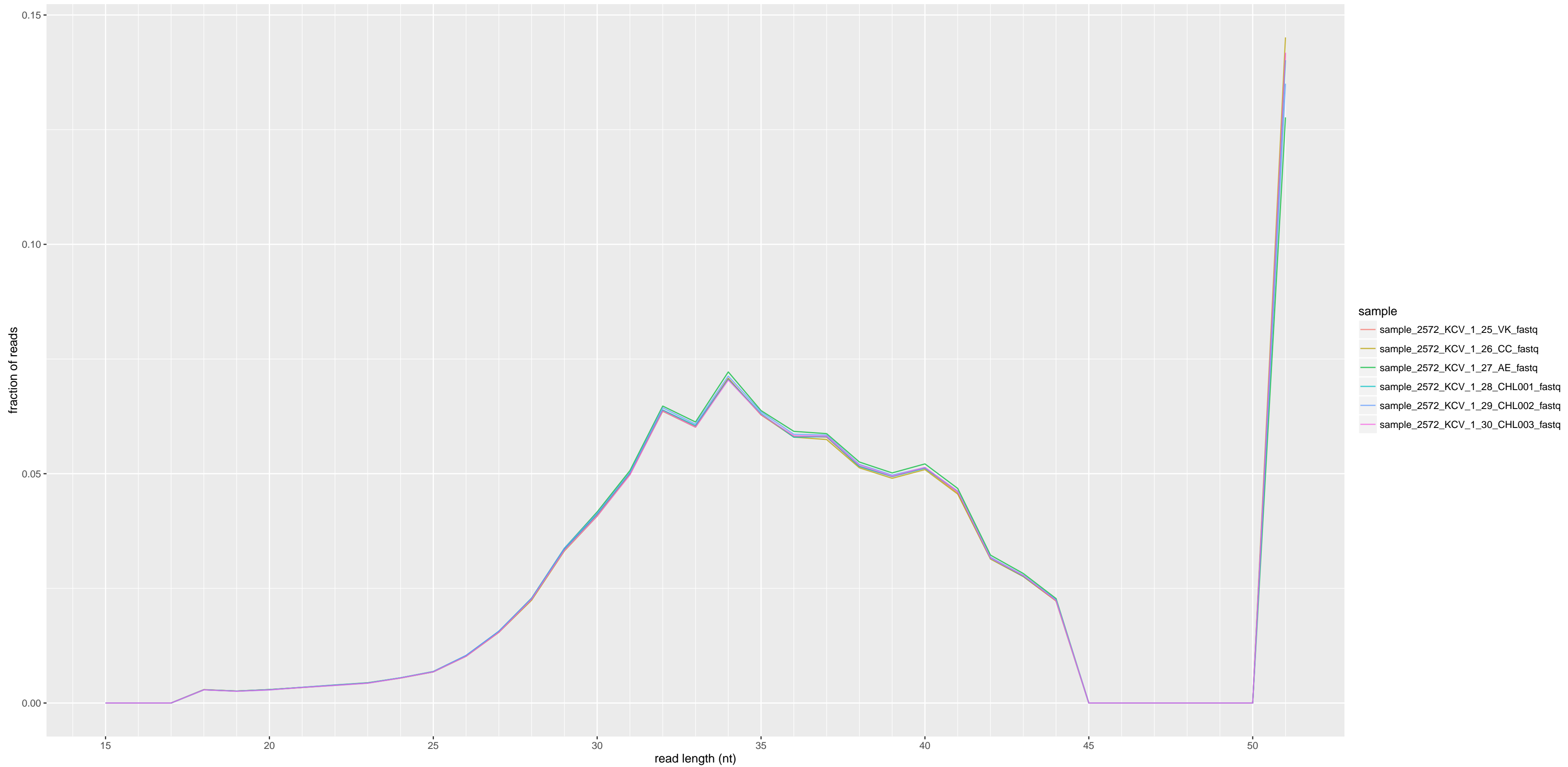


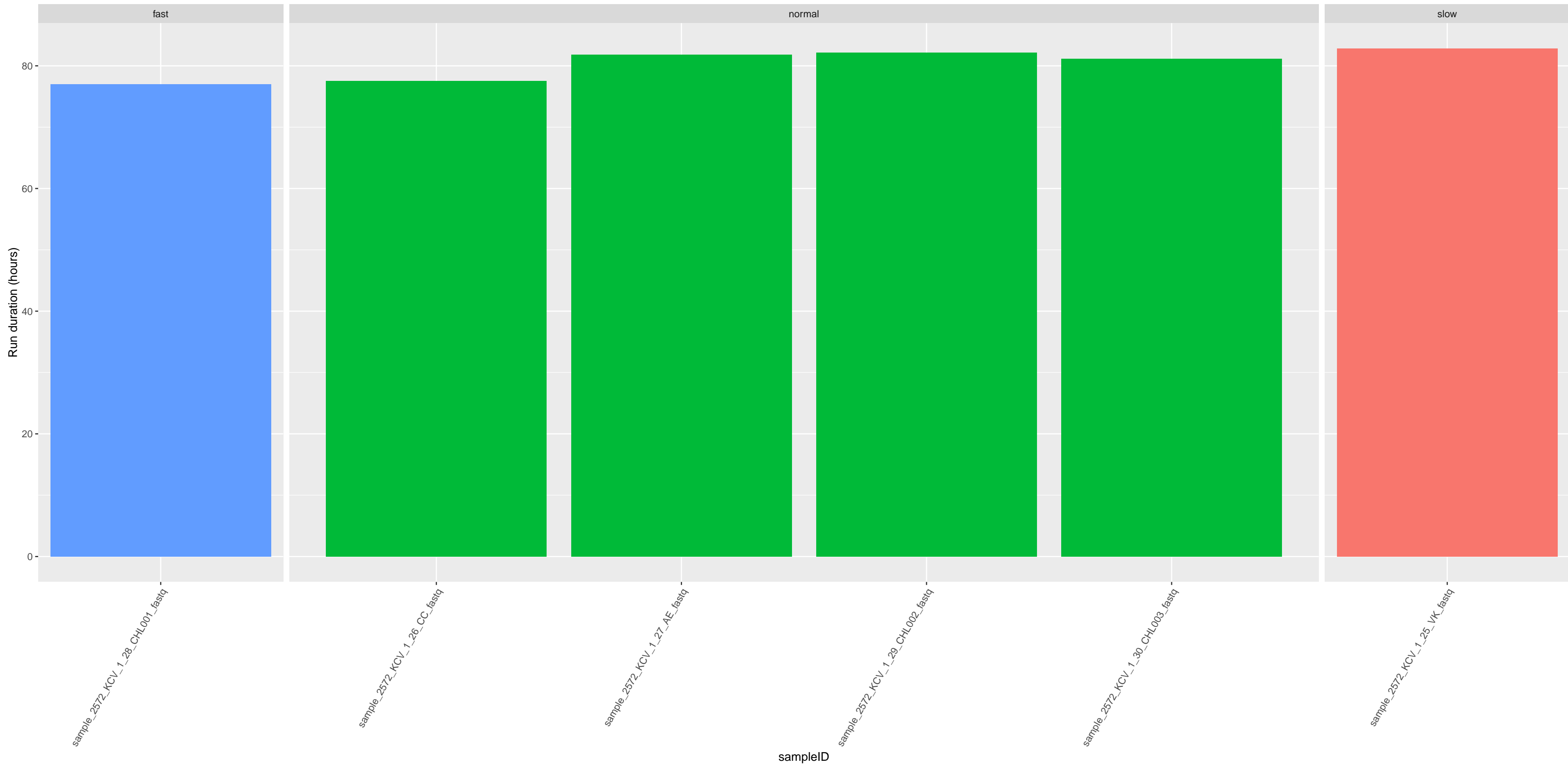
read-length distributions: raw read count



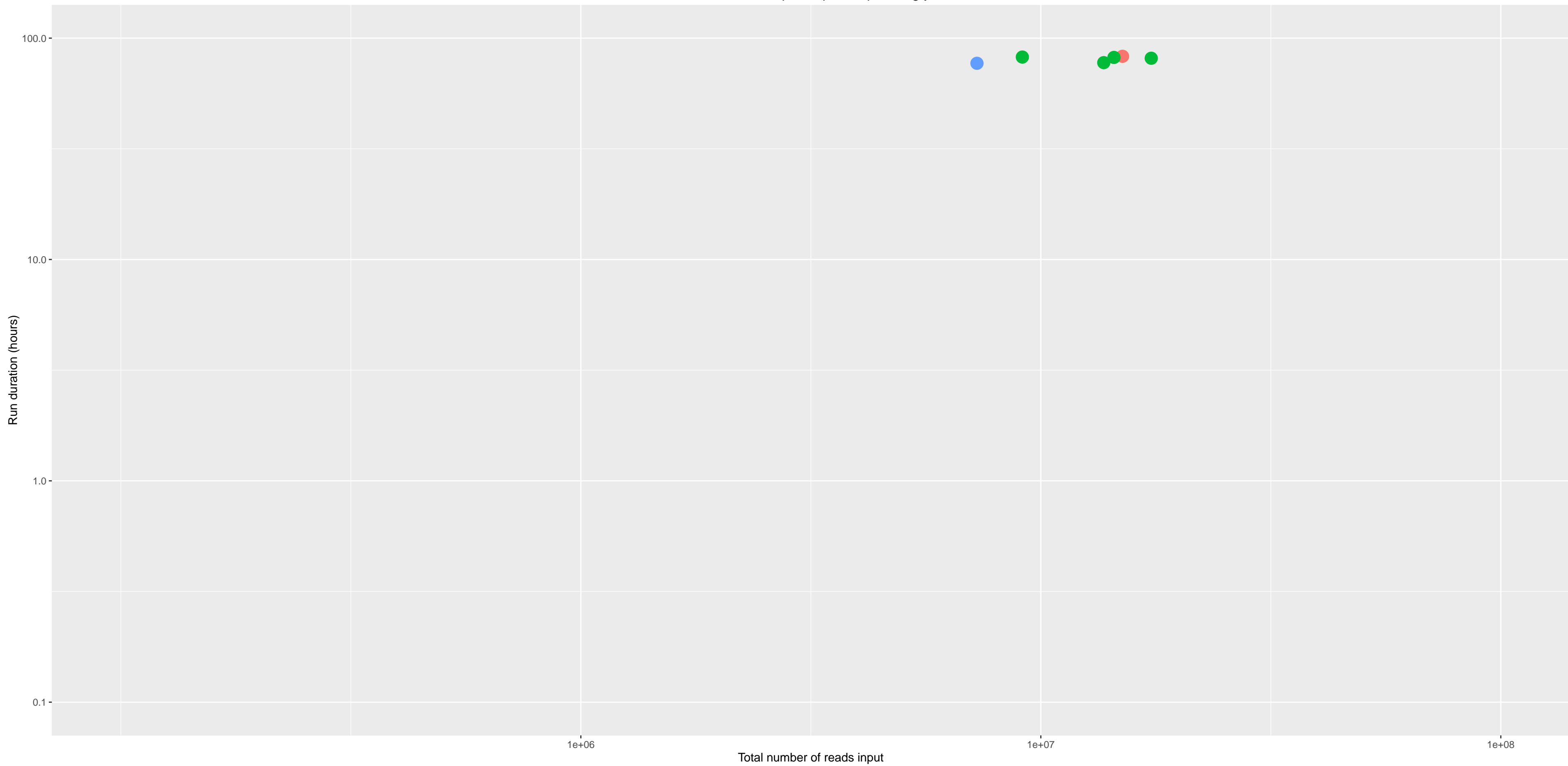
read-length distributions: normalised read fraction



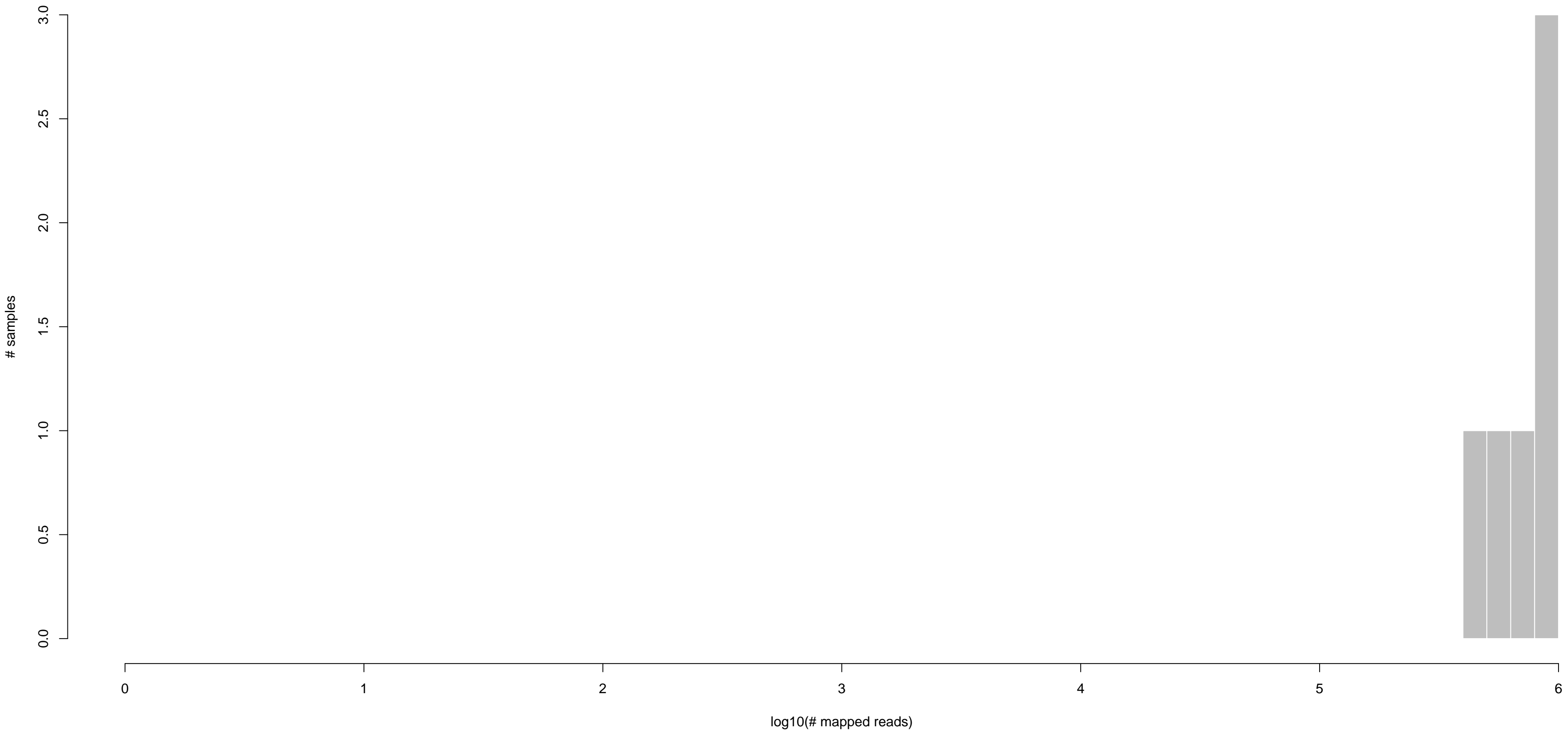
Duration of exceRpt run for each sample

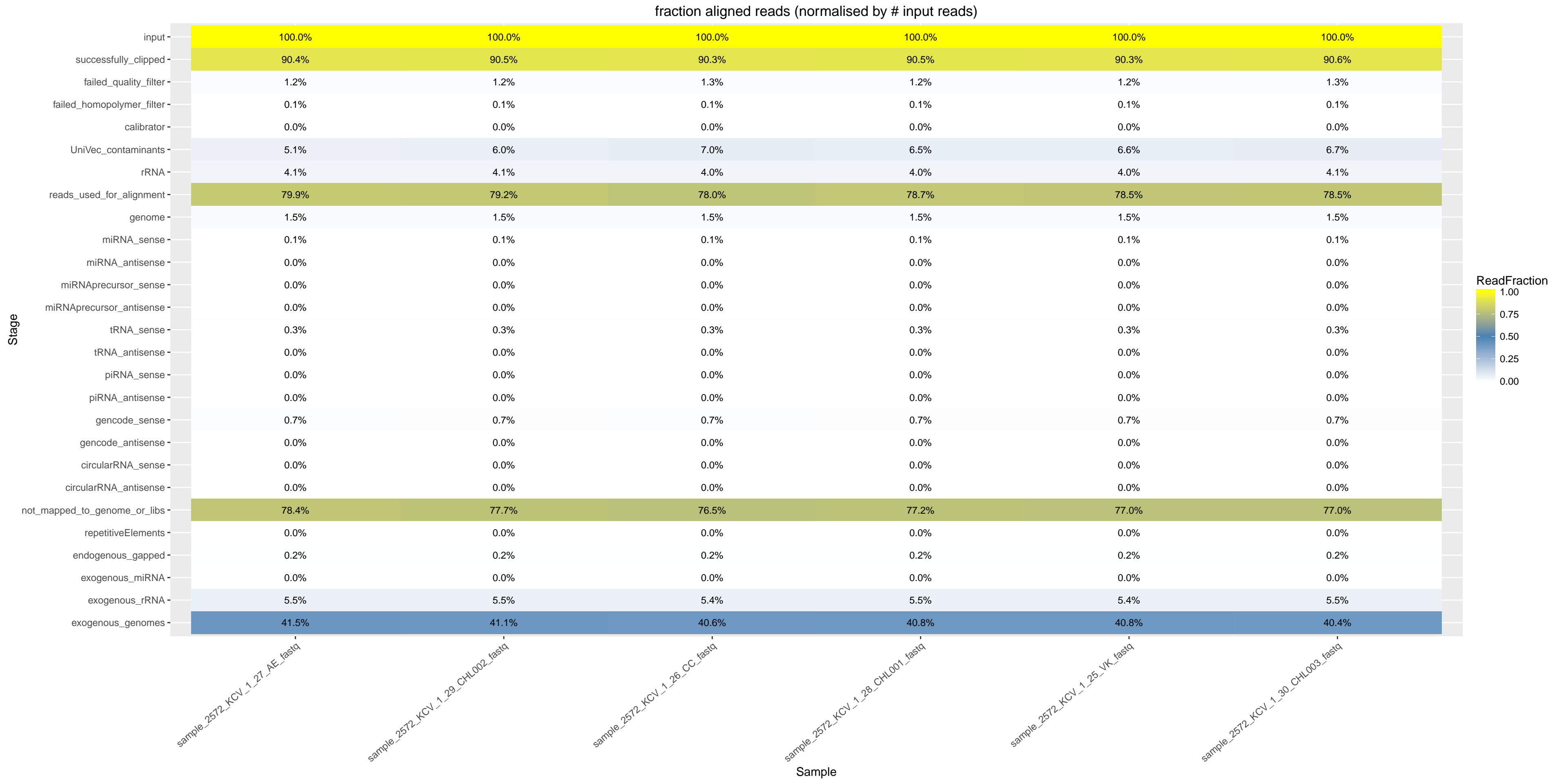


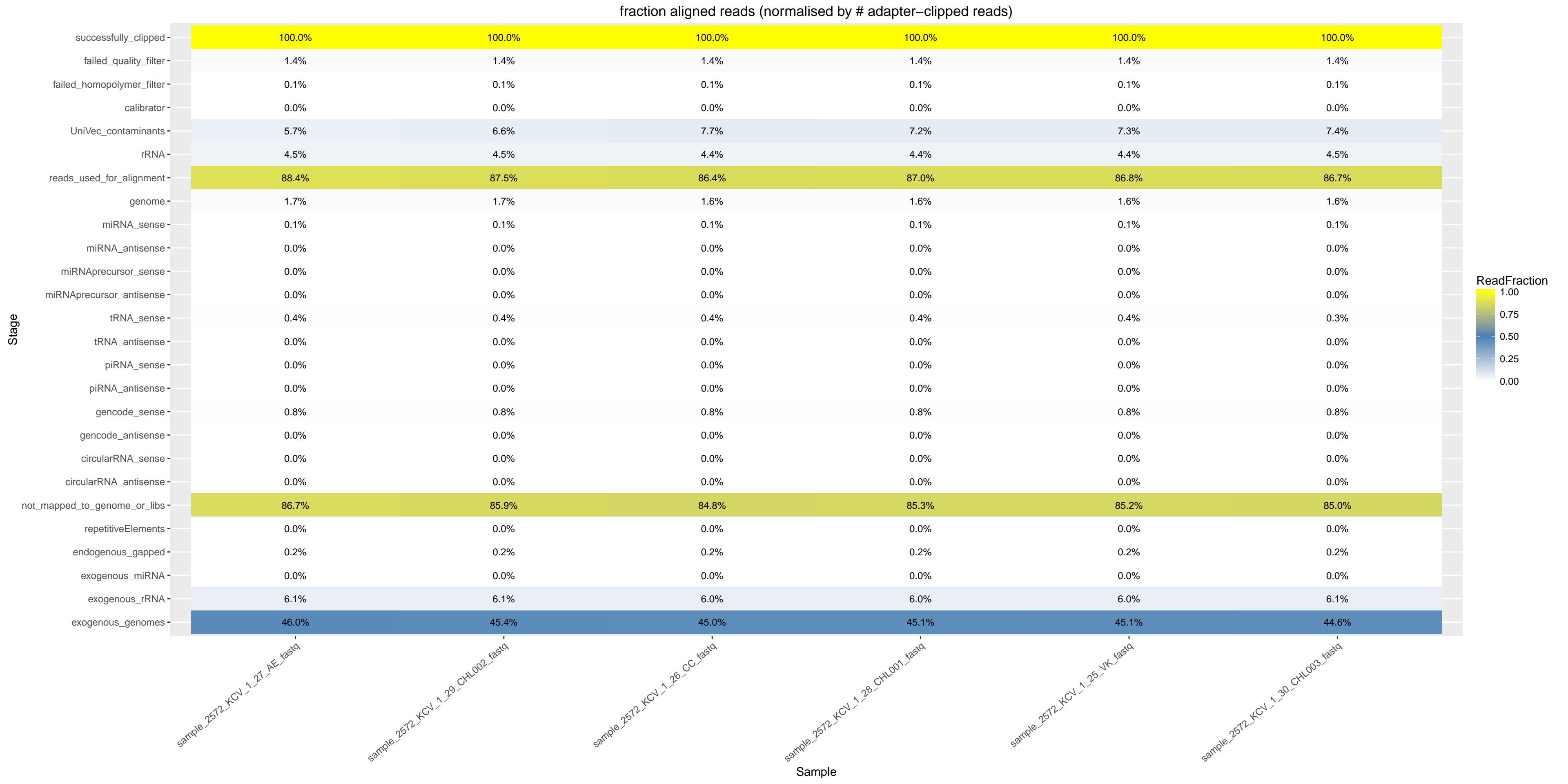
Duration of exceRpt run per sequencing yield

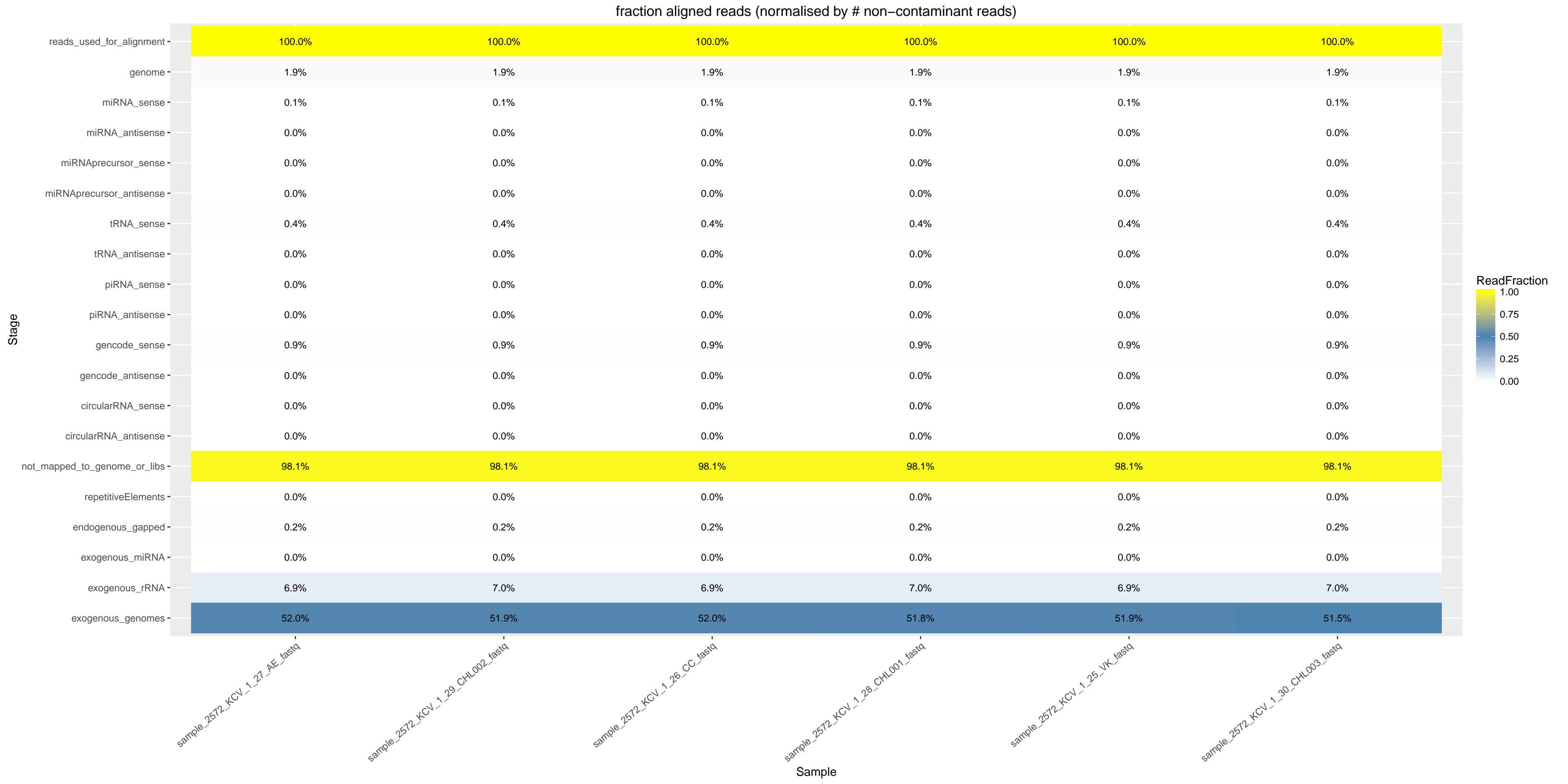


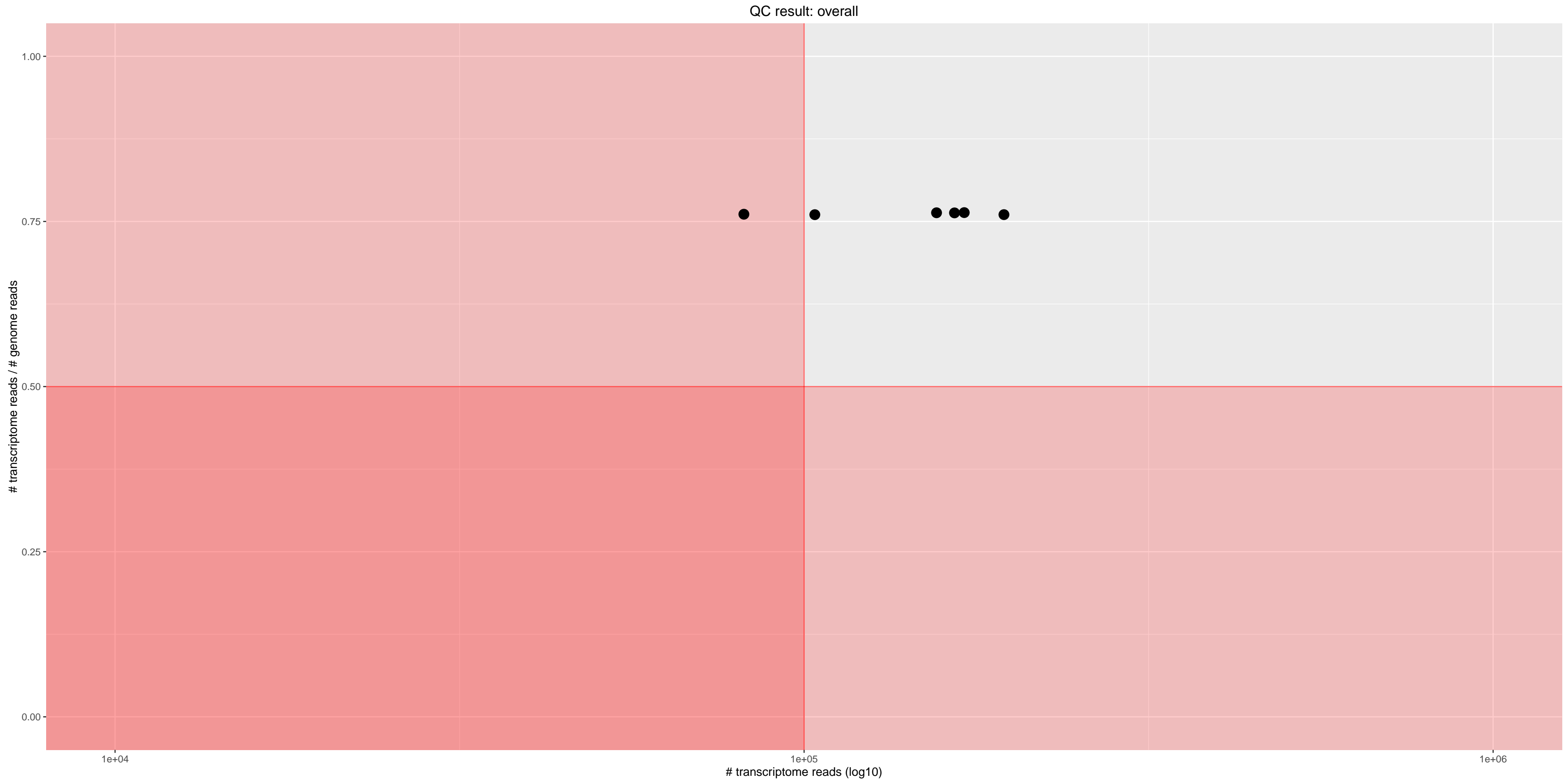
Library size (all mapped reads)



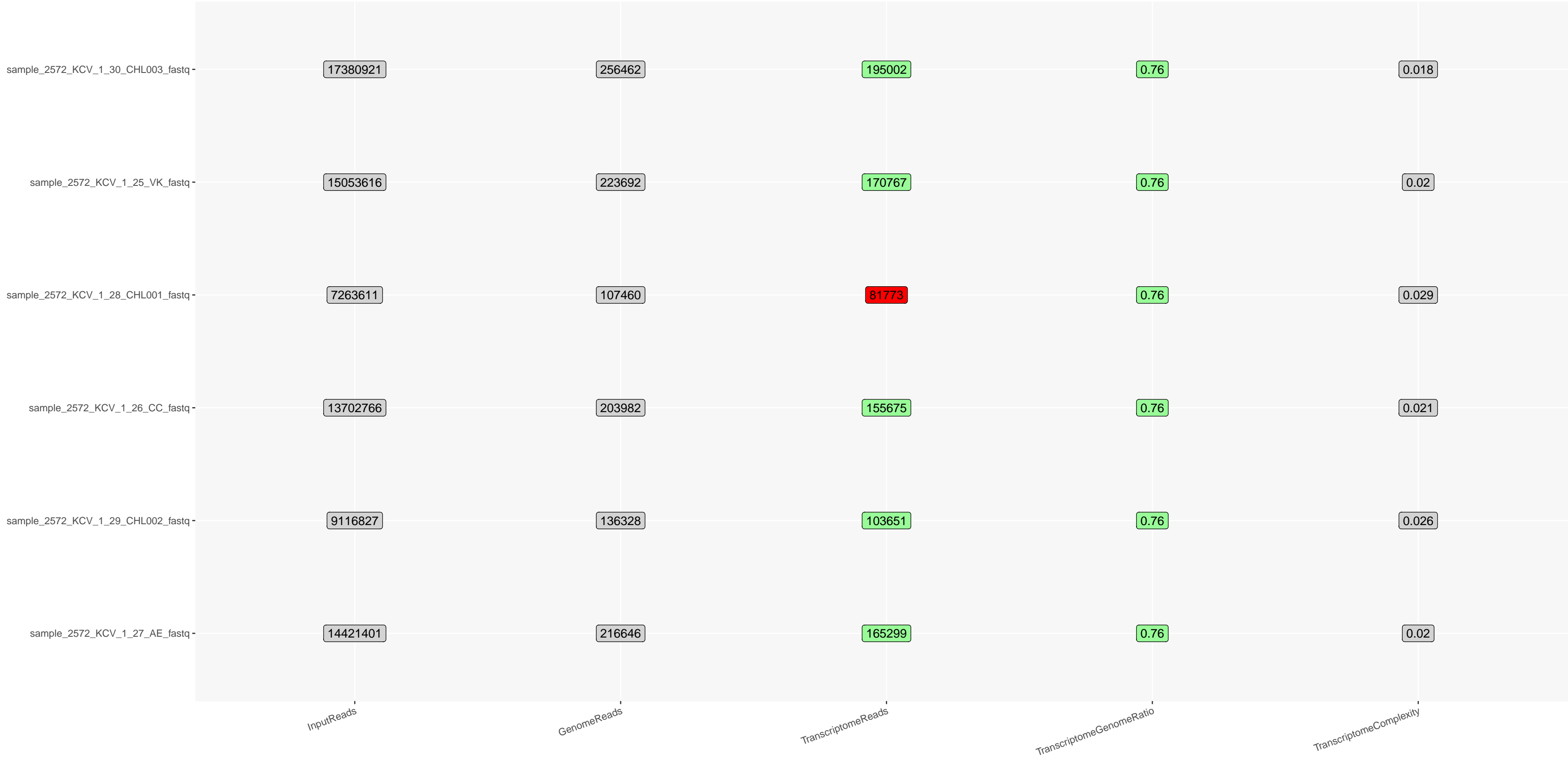




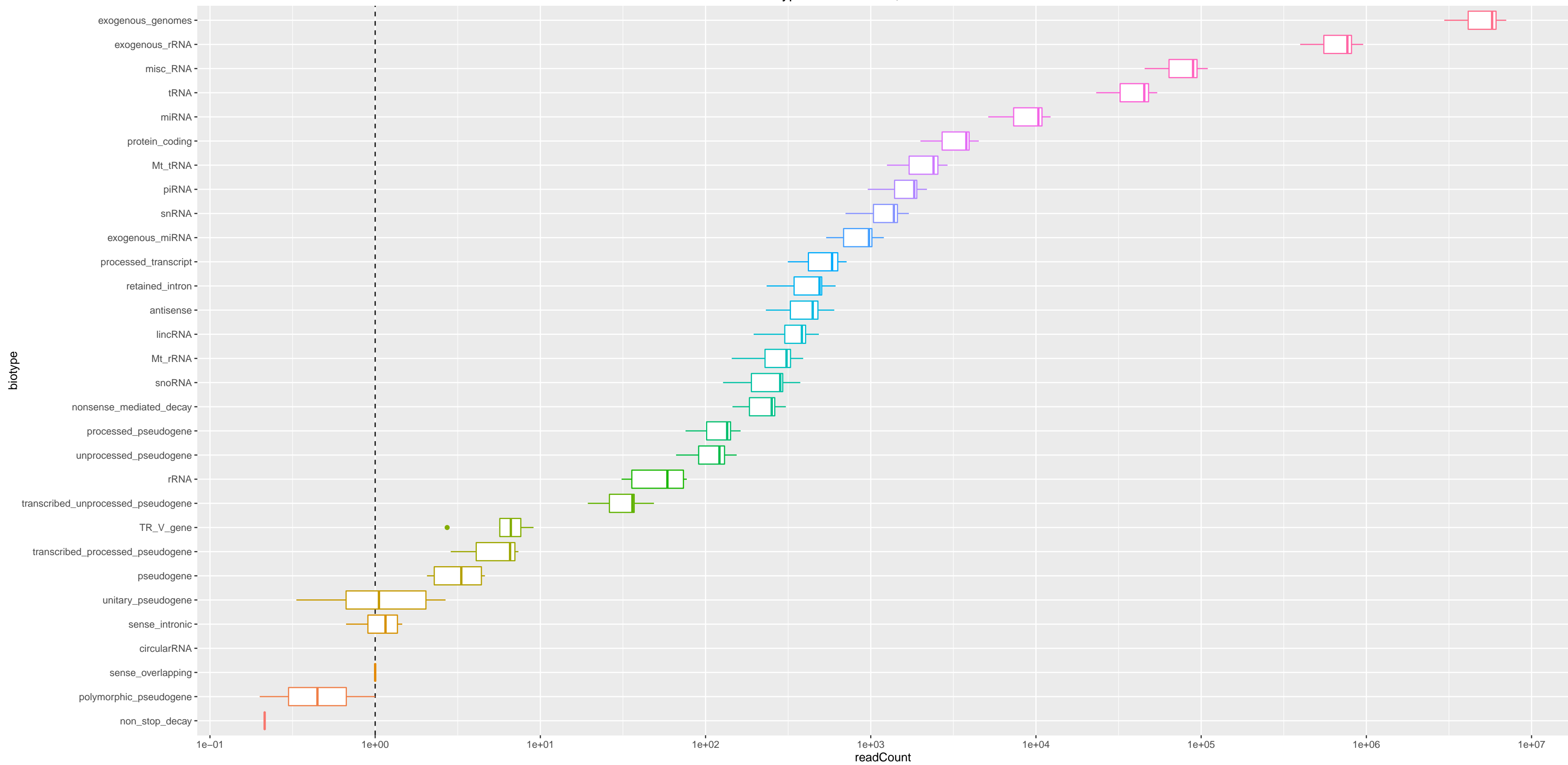




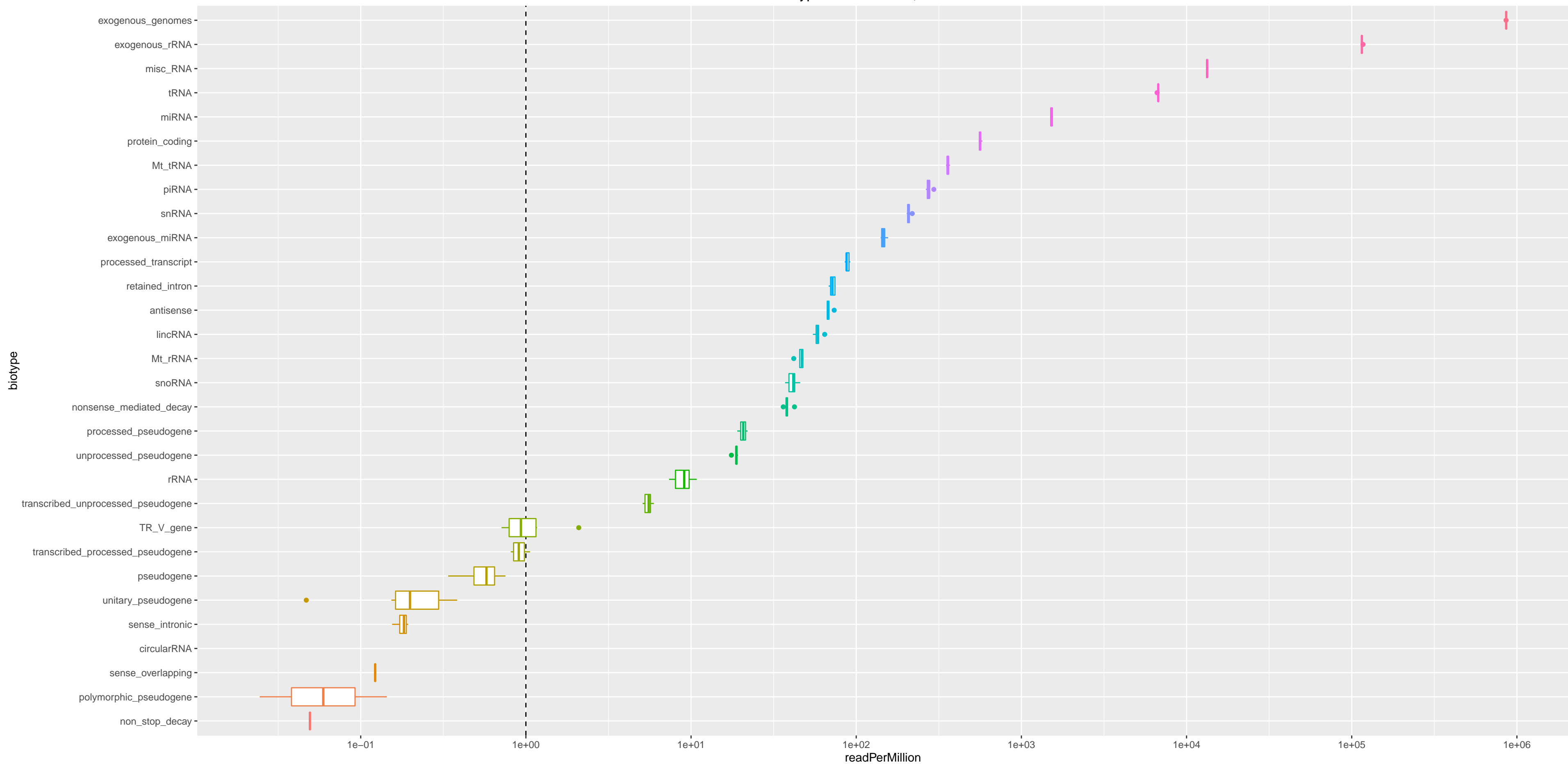
QC result: per-sample results



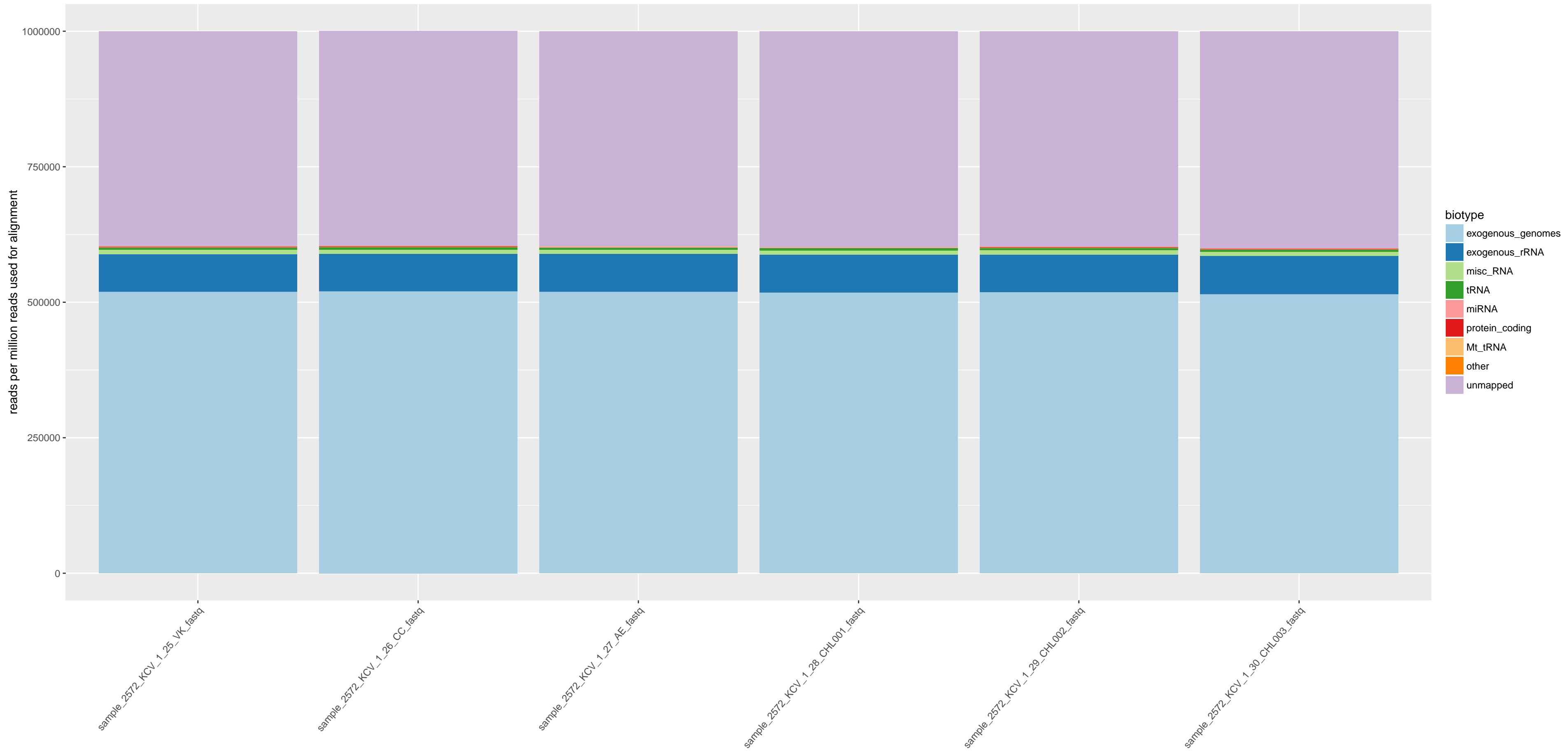
Biotypes: distributions, raw read-counts



Biotypes: distributions, normalised



Biotypes: per-sample, normalised



Biotypes: per-sample, normalised

reads per million mapped reads

sample_2572_KCV_1_25_VK_fastq

sample_2572_KCV_1_26_CC_fastq

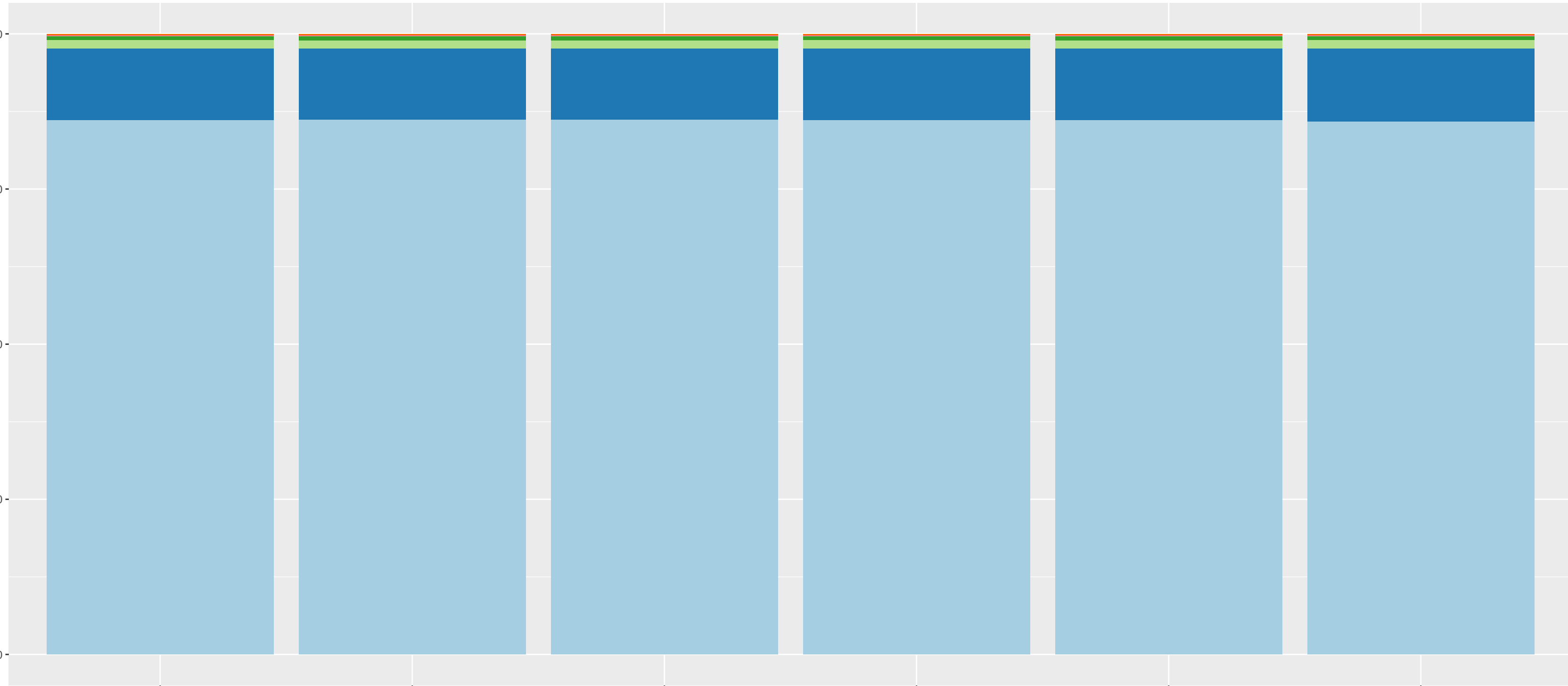
sample_2572_KCV_1_27_AE_fastq

sample_2572_KCV_1_28_CHL001_fastq

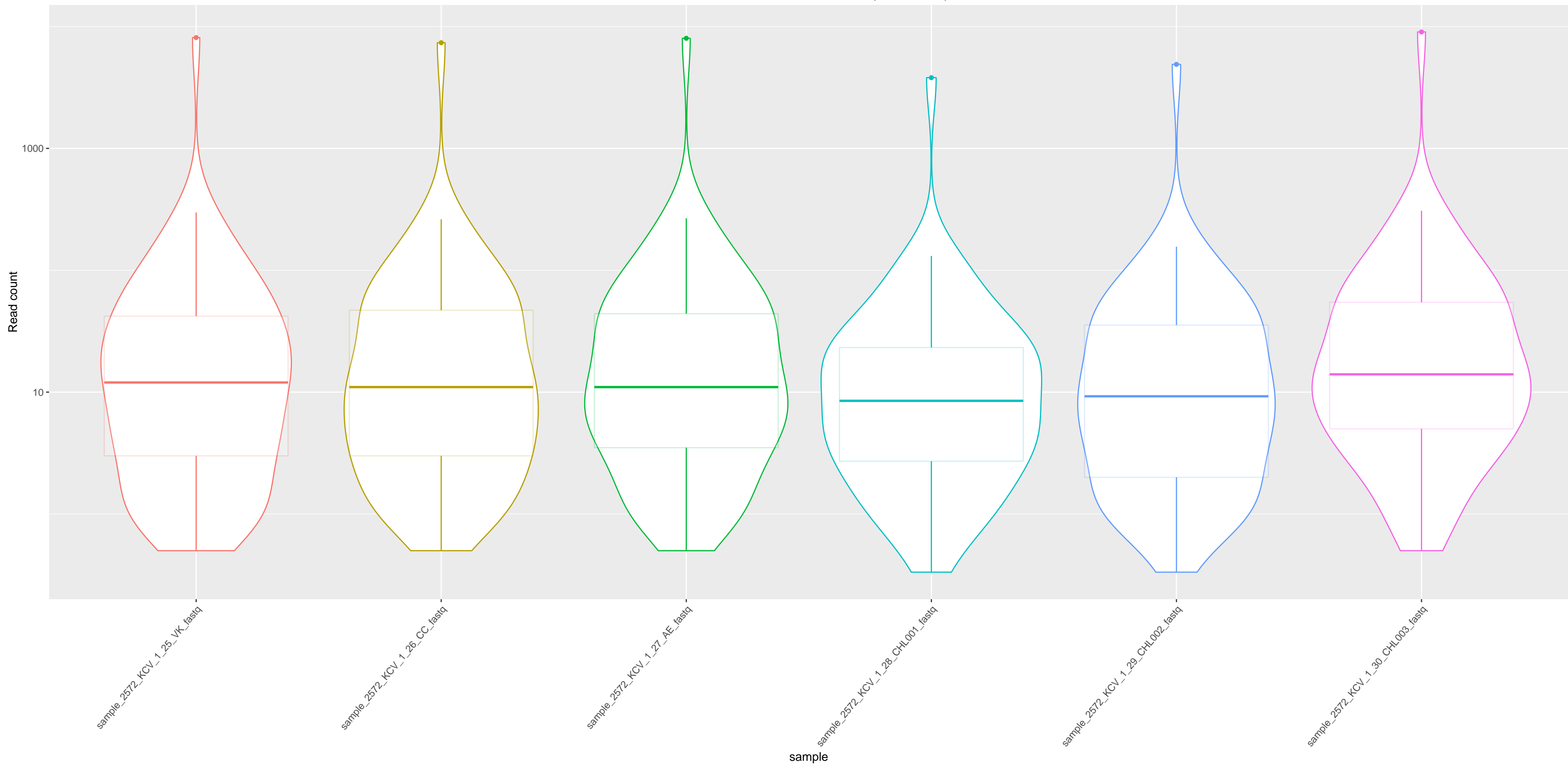
sample_2572_KCV_1_29_CHL002_fastq

sample_2572_KCV_1_30_CHL003_fastq

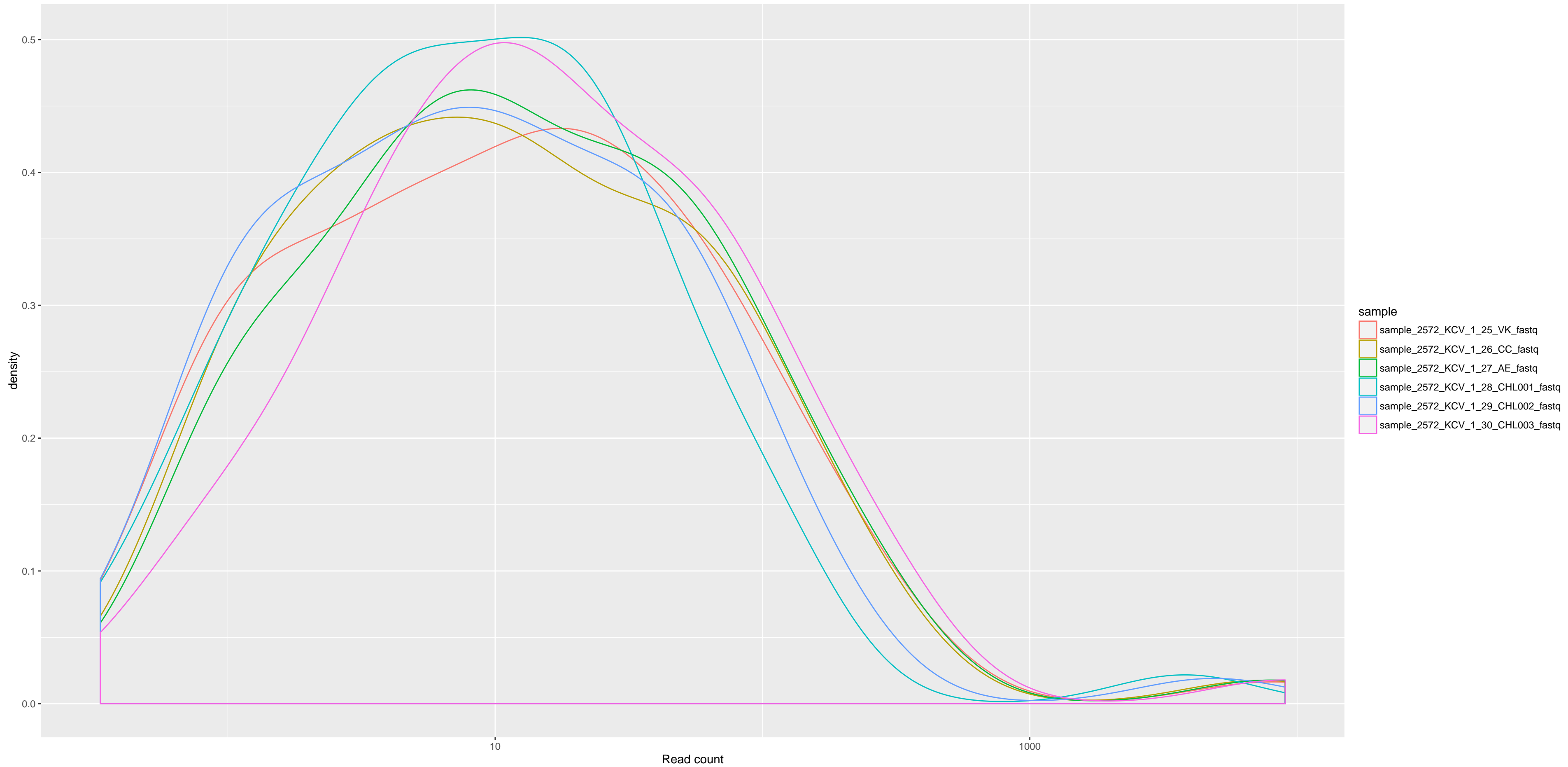
- biotype
- exogenous_genomes
 - exogenous_rRNA
 - misc_RNA
 - tRNA
 - miRNA
 - protein_coding
 - Mt_tRNA
 - other



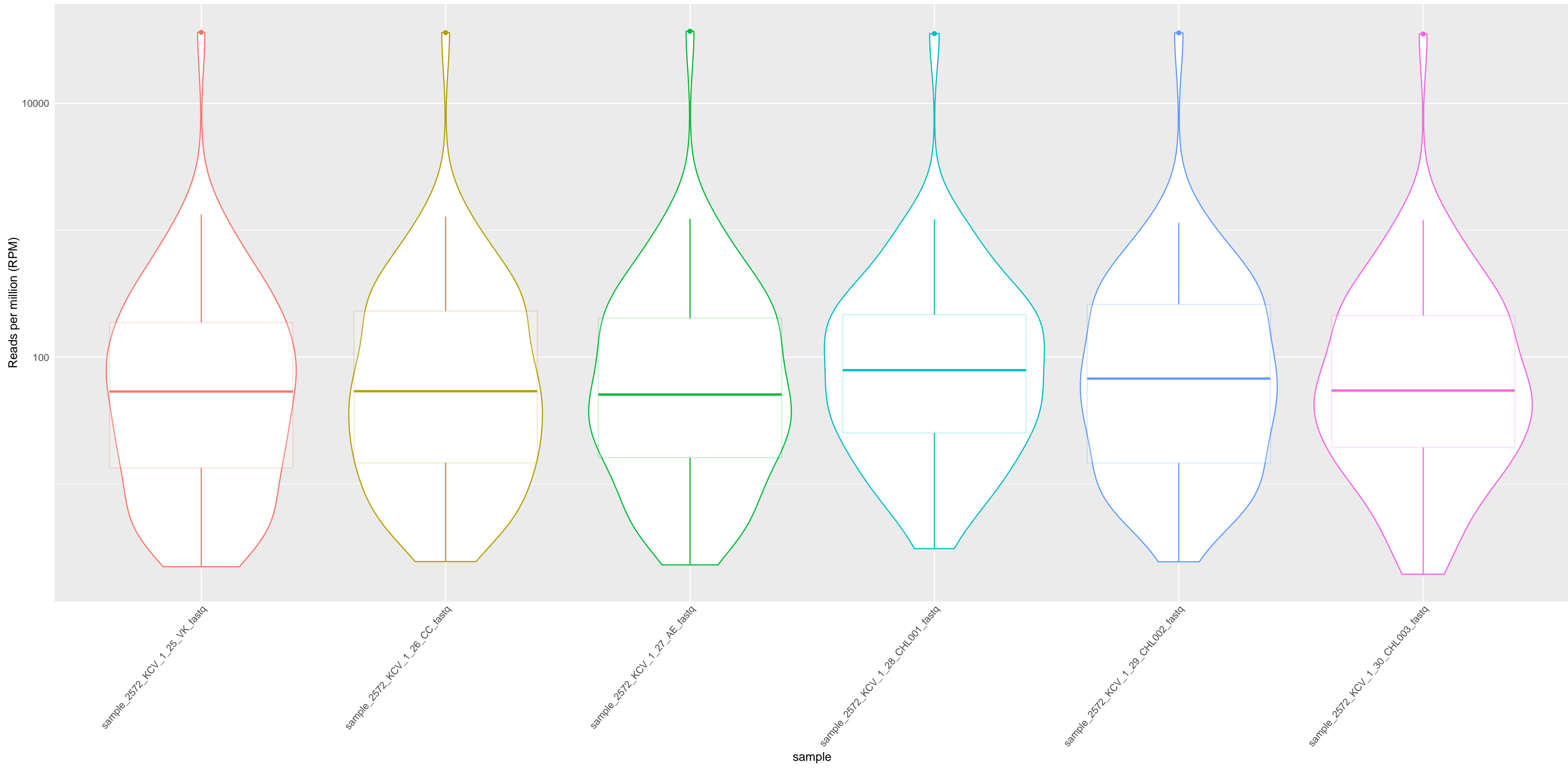
miRNA abundance distributions (raw counts)



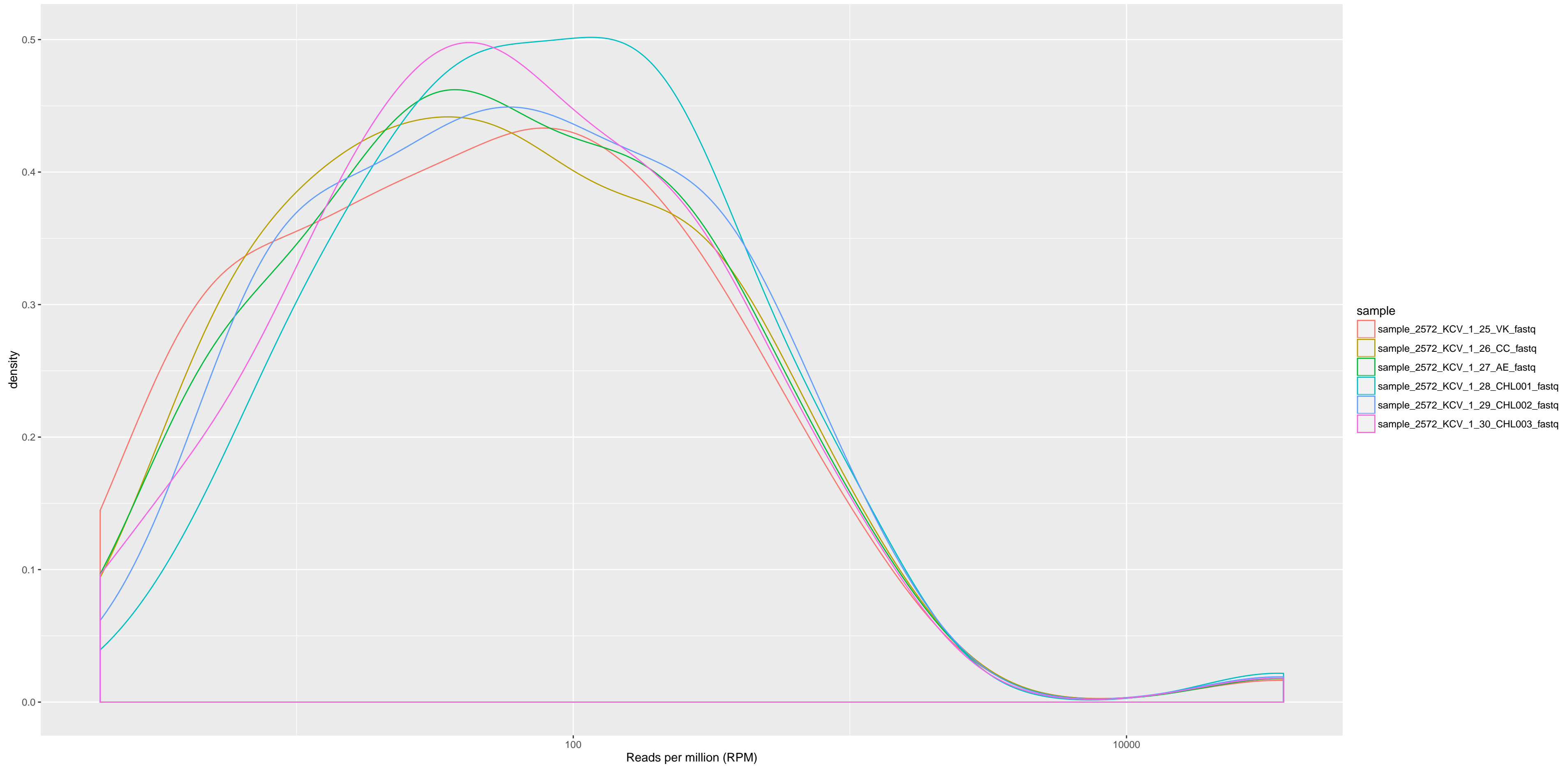
miRNA abundance distributions (raw counts)



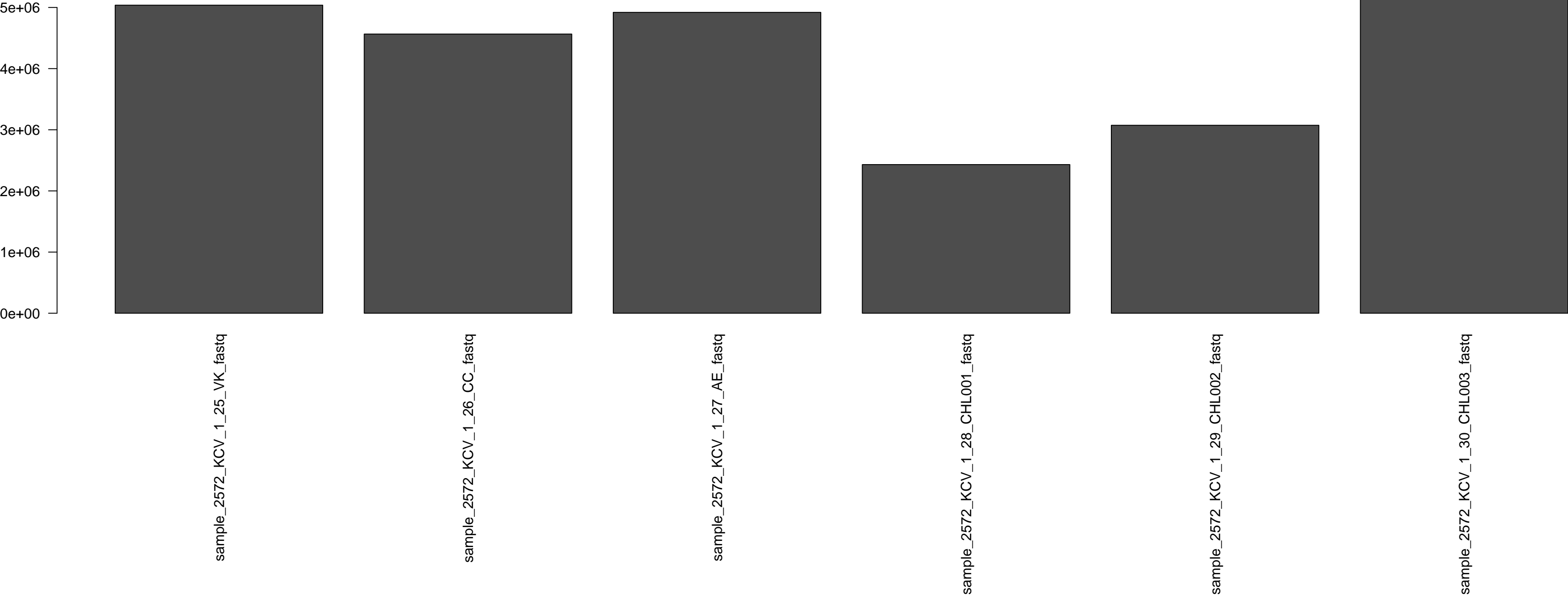
miRNA abundance distributions (RPM)

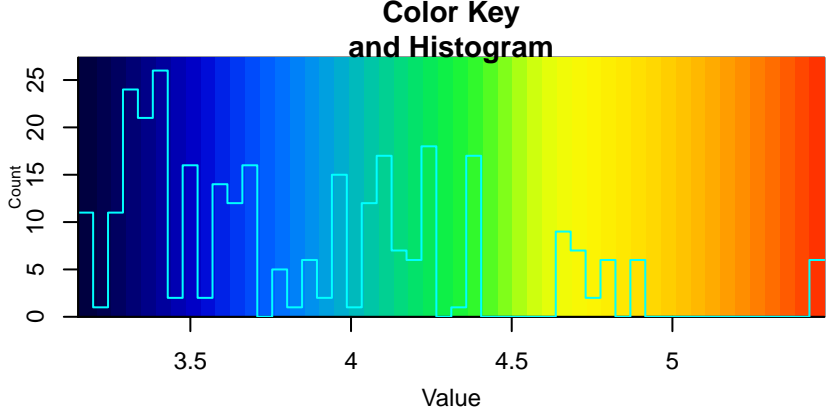


miRNA abundance distributions (RPM)

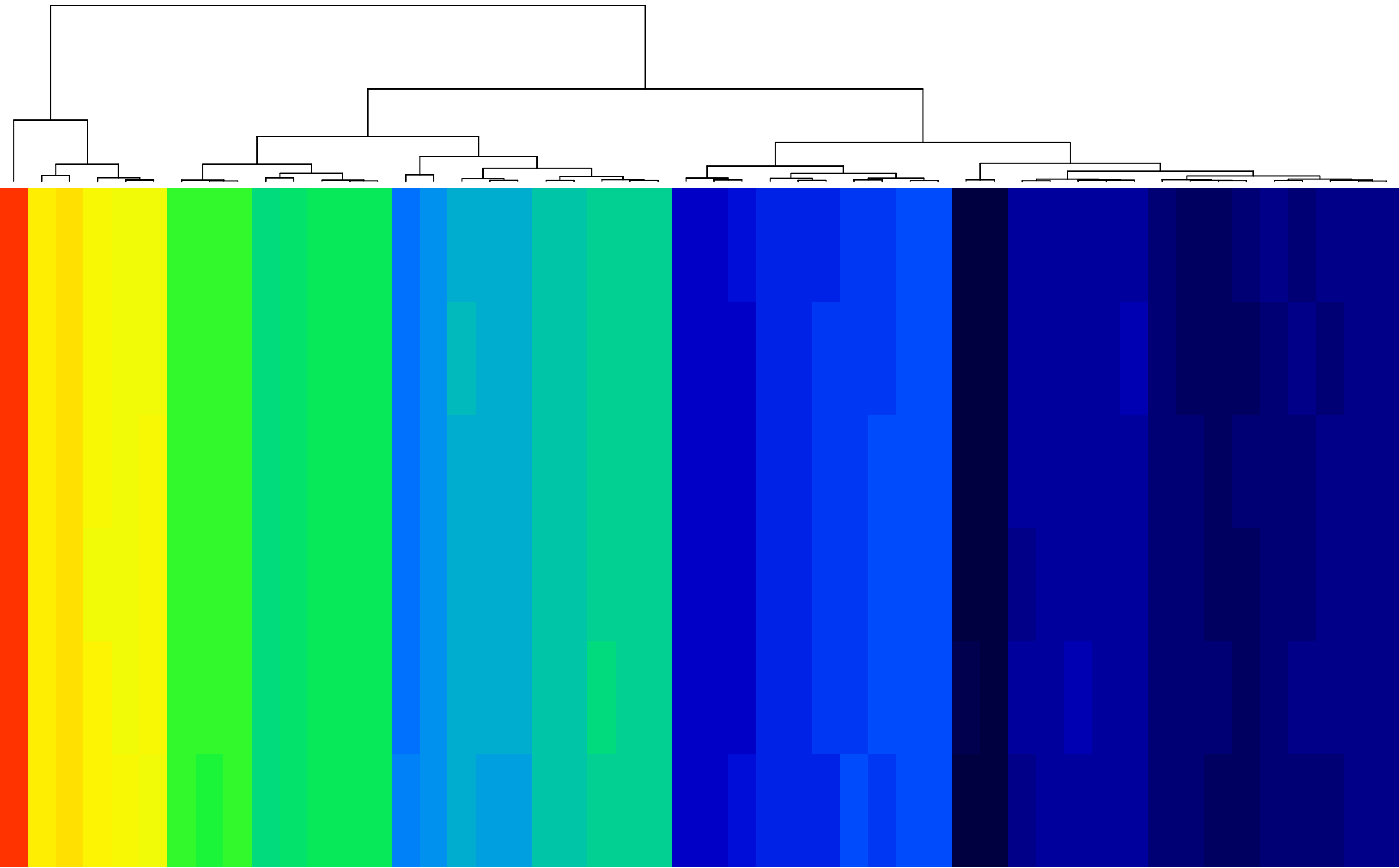
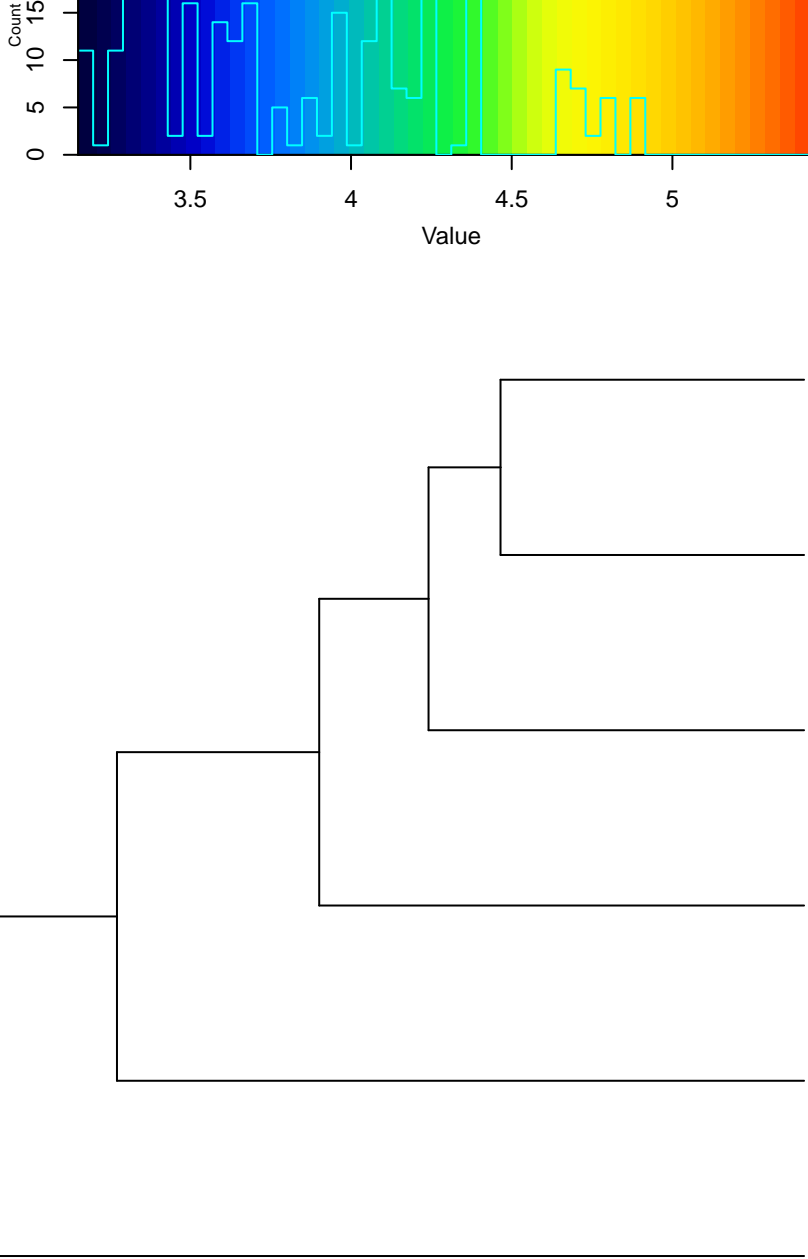


Total # reads mapped to NCBI taxonomy



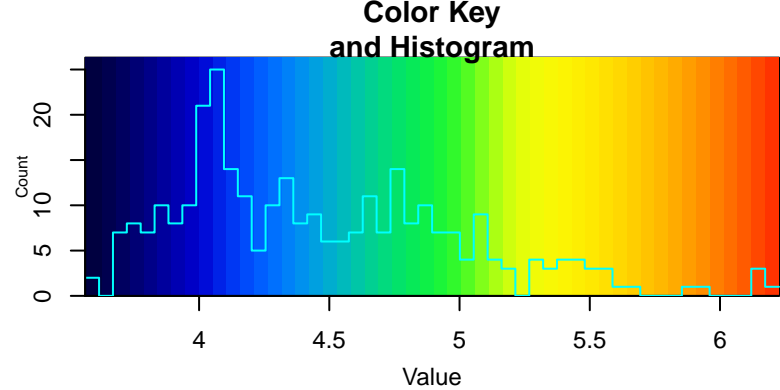


top taxa nodes: specific normalised read count

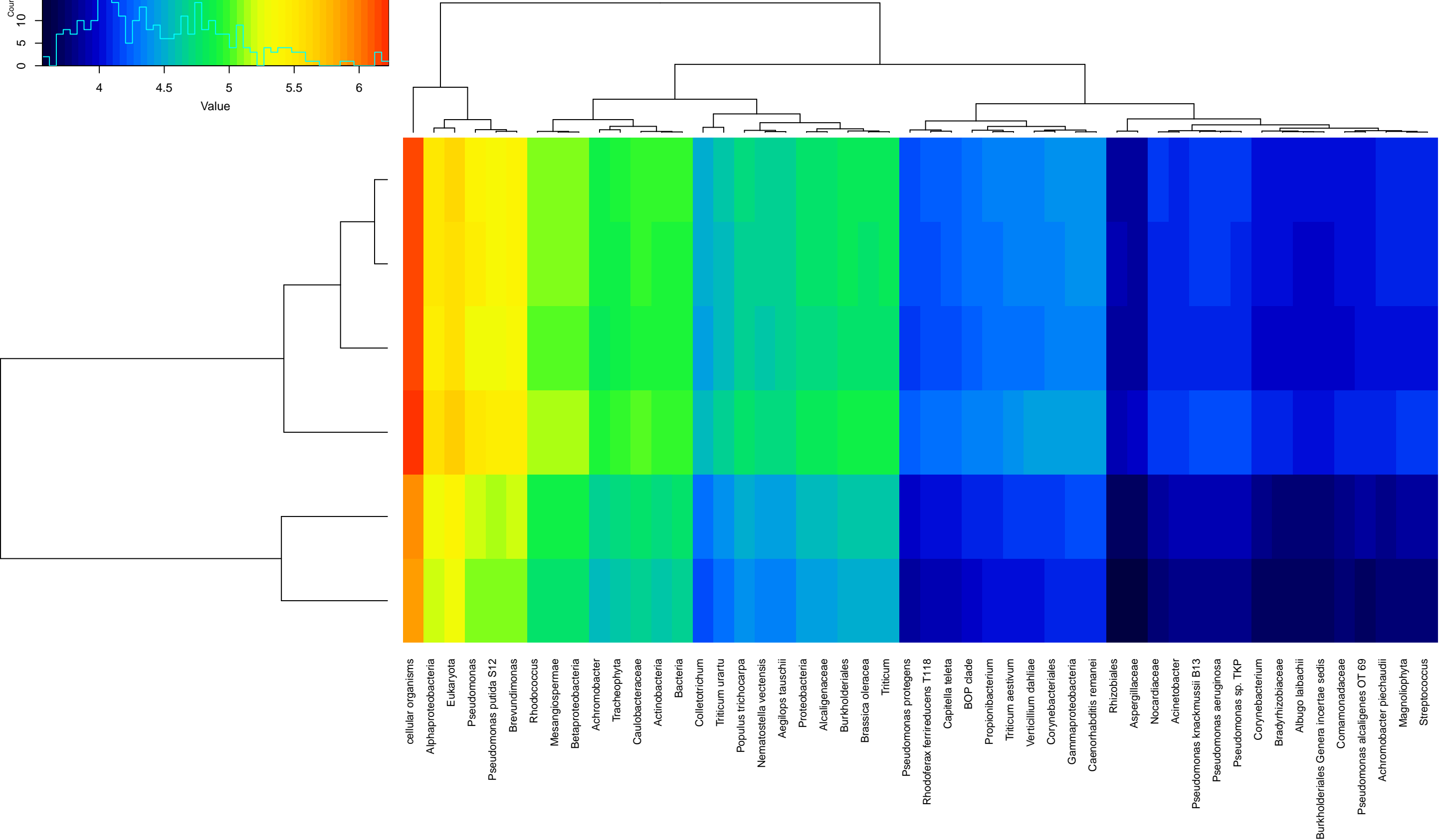


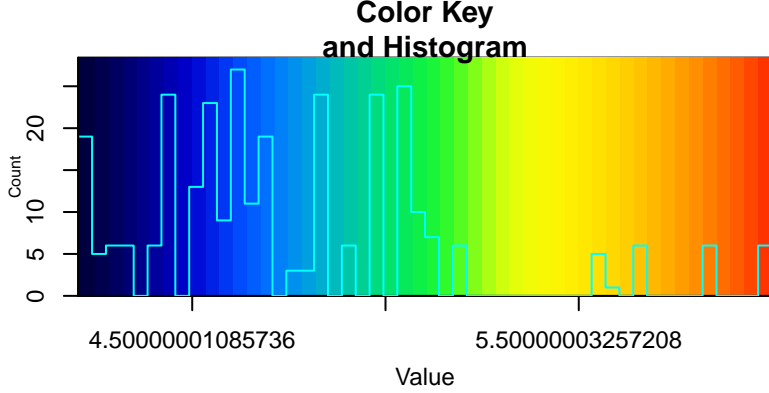
- cellular organisms
- Alphaproteobacteria
- Eukaryota
- Pseudomonas
- Pseudomonas putida S12
- Brevundimonas
- Rhodococcus
- Mesangiopermae
- Betaproteobacteria
- Achromobacter
- Tracheophyta
- Caulobacteraceae
- Actinobacteria
- Bacteria
- Colletotrichum
- Triticum urartu
- Populus trichocarpa
- Nematostella vectensis
- Aegilops tauschii
- Proteobacteria
- Alcaligenaceae
- Burkholderiales
- Brassica oleracea
- Triticum
- Pseudomonas protegens
- Rhodofarax ferrieducens T118
- Capitella teleta
- BOP clade
- Propionibacterium
- Triticum aestivum
- Verticillium dahliae
- Corynebacteriales
- Gammaproteobacteria
- Caenorhabditis remanei
- Rhizobiales
- Aspergillaceae
- Nocardia
- Acinetobacter
- Pseudomonas knackmussii B13
- Pseudomonas aeruginosa
- Pseudomonas sp. TKP
- Corynebacterium
- Bradyrhizobiaceae
- Albugo laibachii
- Burkholderiales Genera incertae sedis
- Comamonadaceae
- Pseudomonas alcaligenes OT 69
- Achromobacter piechaudii
- Magnoliophyta
- Streptococcus

- sample_2572_KCV_1_28_CHL001_fastq
- sample_2572_KCV_1_29_CHL002_fastq
- sample_2572_KCV_1_25_VK_fastq
- sample_2572_KCV_1_26_CC_fastq
- sample_2572_KCV_1_27_AE_fastq
- sample_2572_KCV_1_30_CHL003_fastq

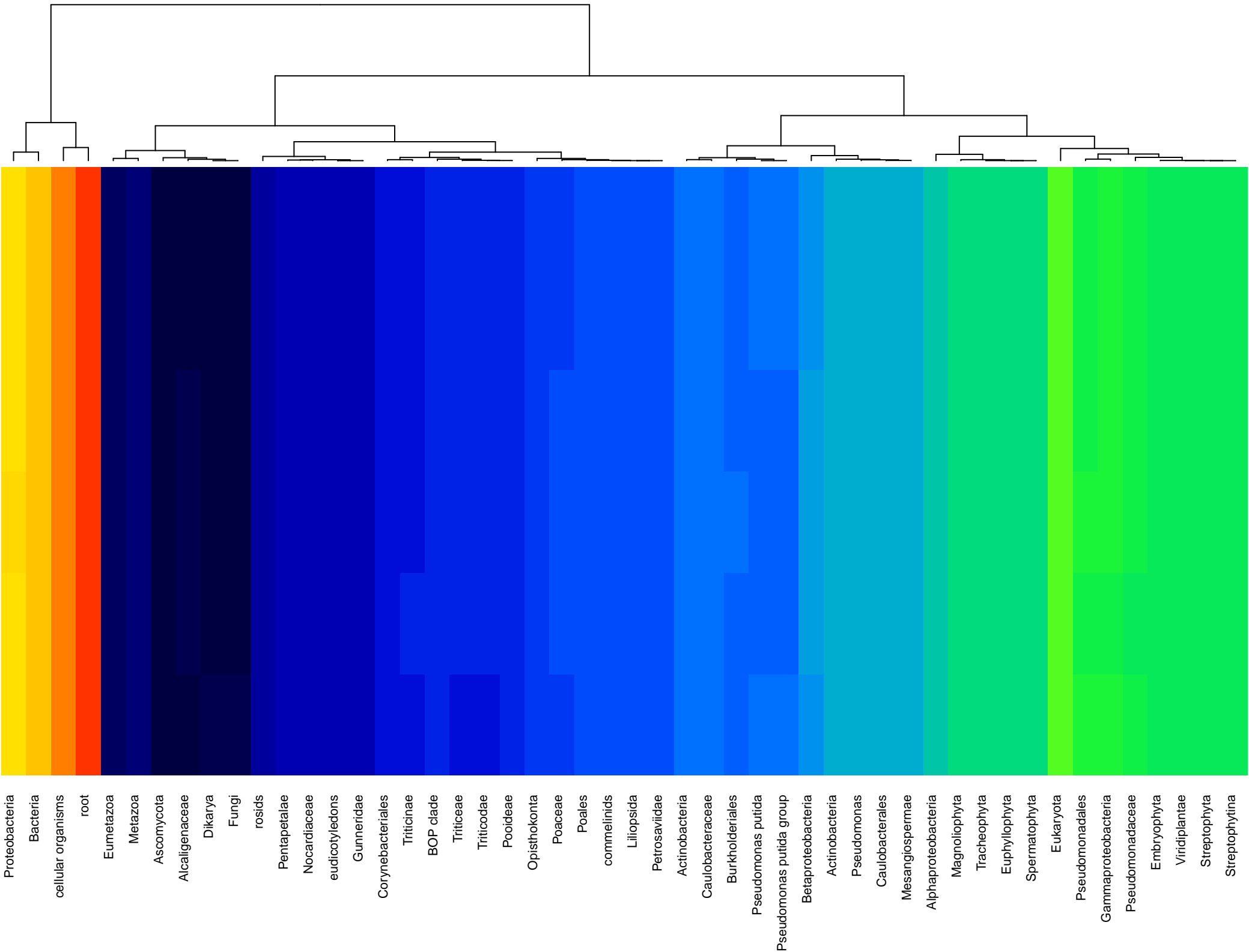
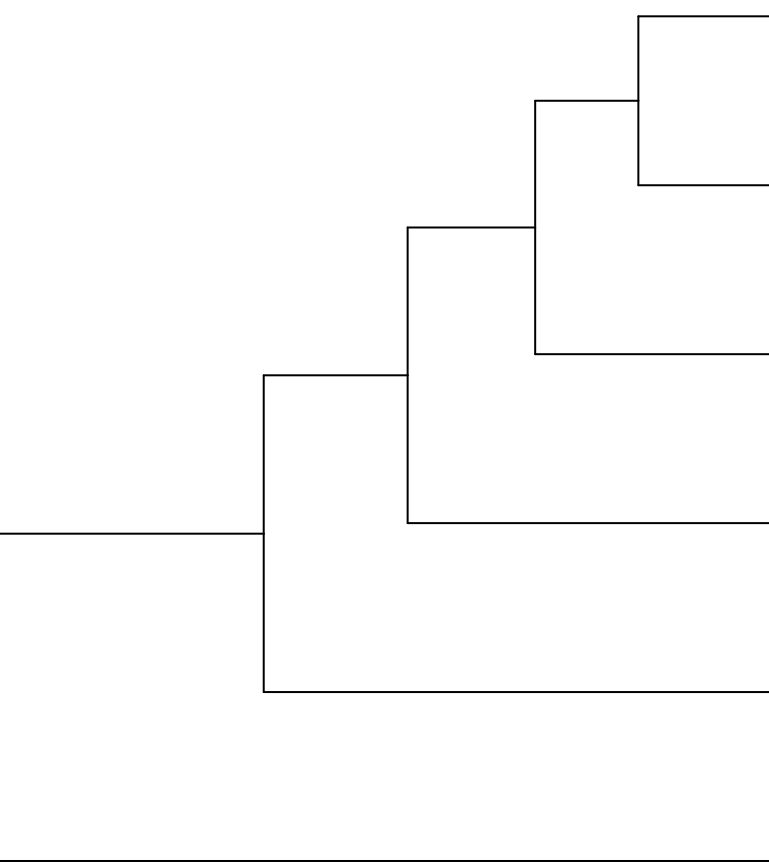


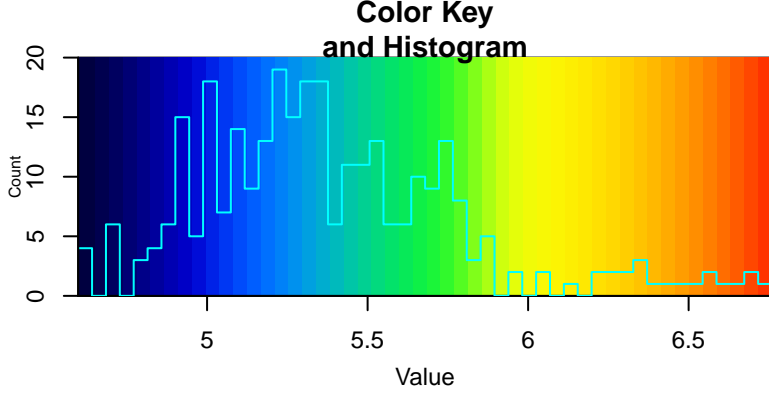
top taxa nodes: specific absolute read count





top taxa nodes: cumulative normalised read count





top taxa nodes: cumulative absolute read count

