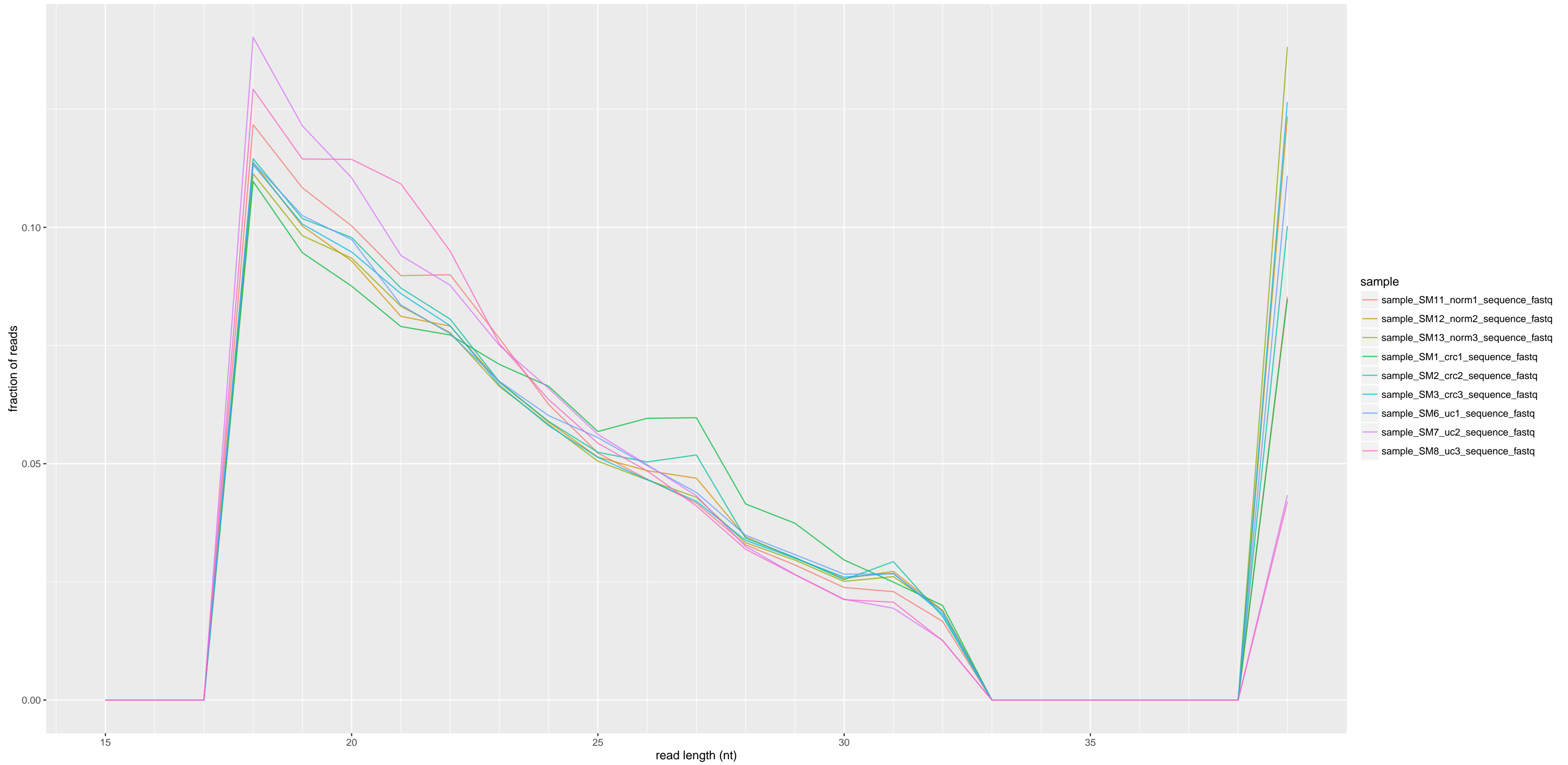
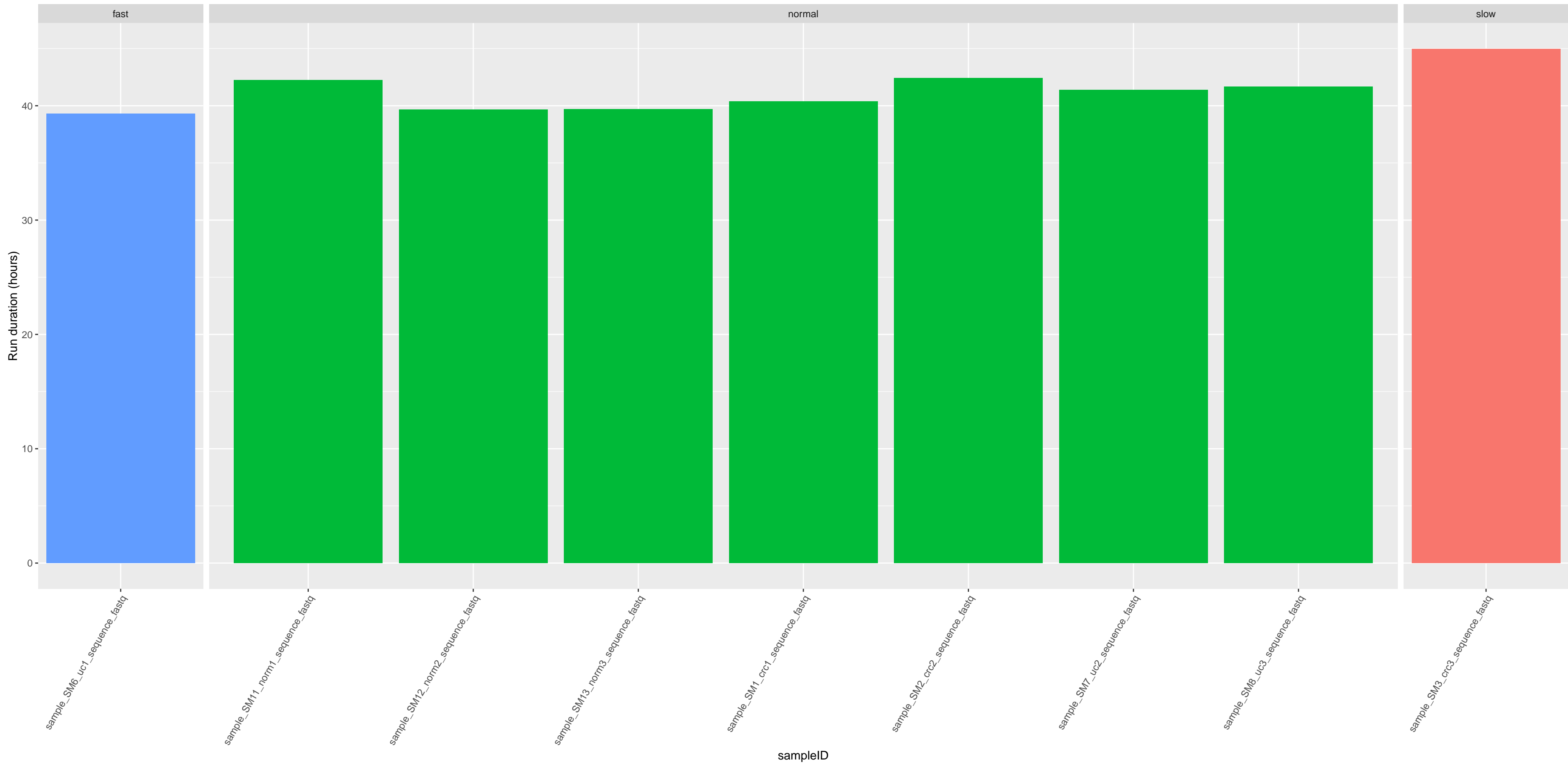


read-length distributions: raw read count

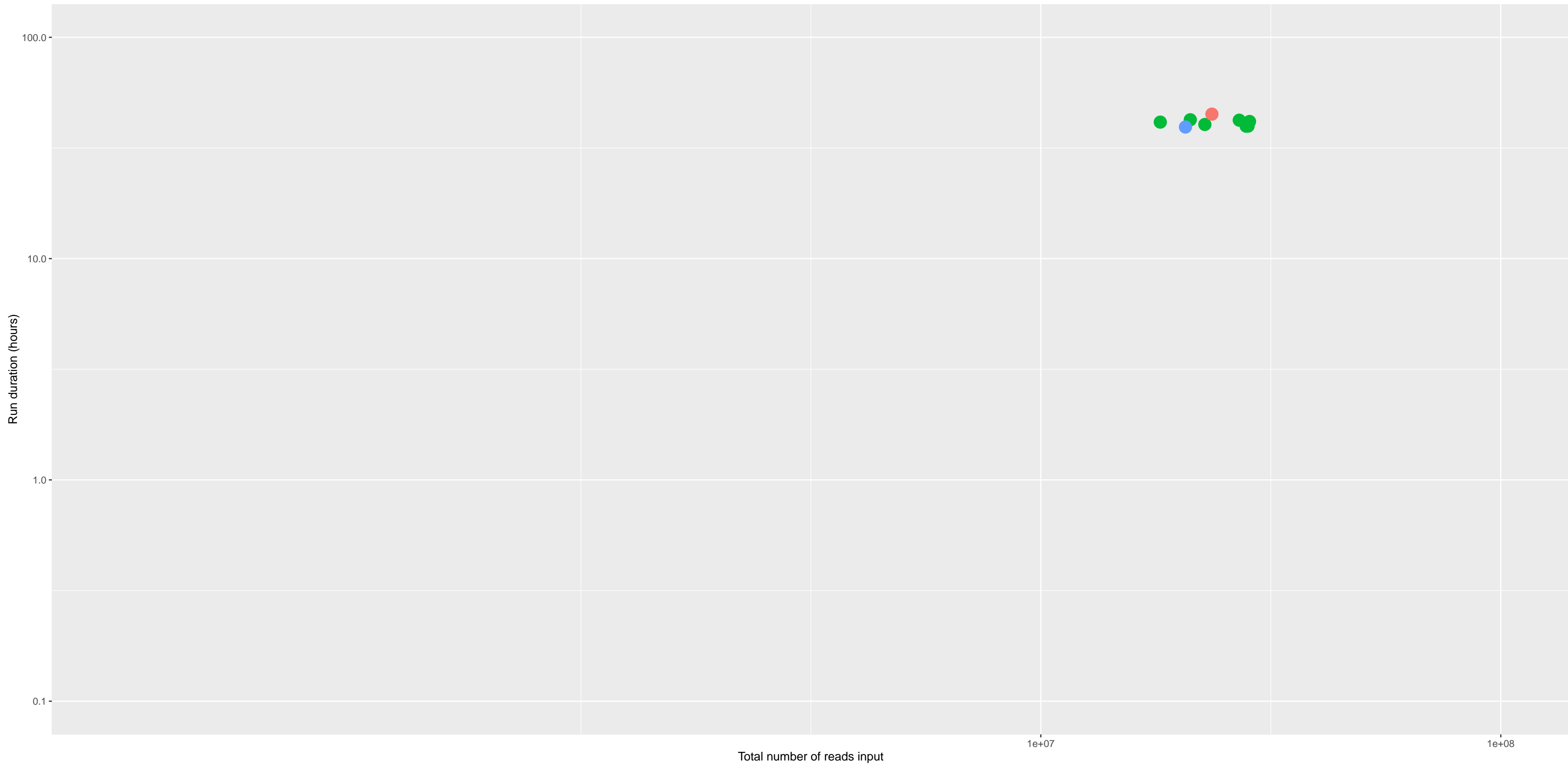
read-length distributions: normalised read fraction



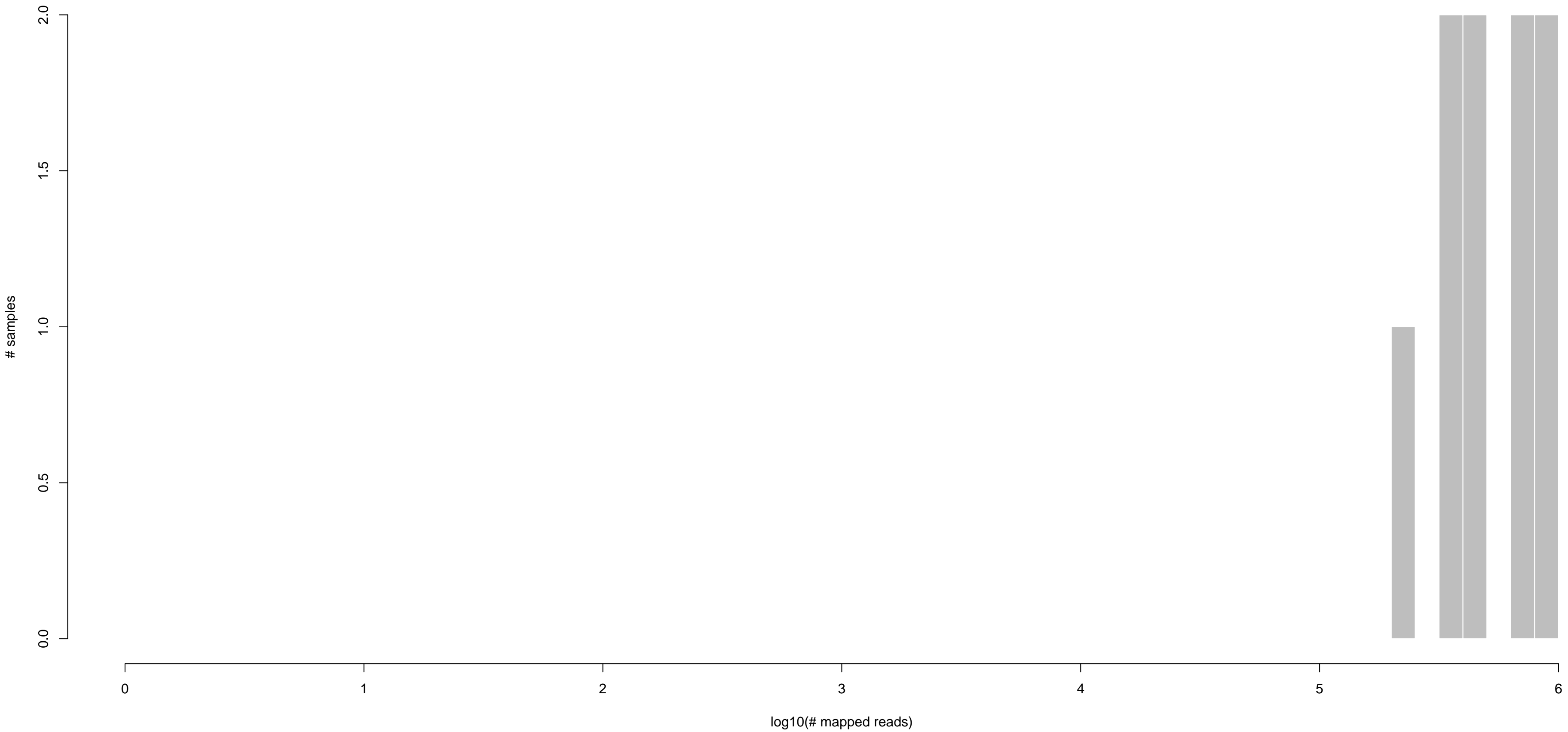
Duration of exceRpt run for each sample

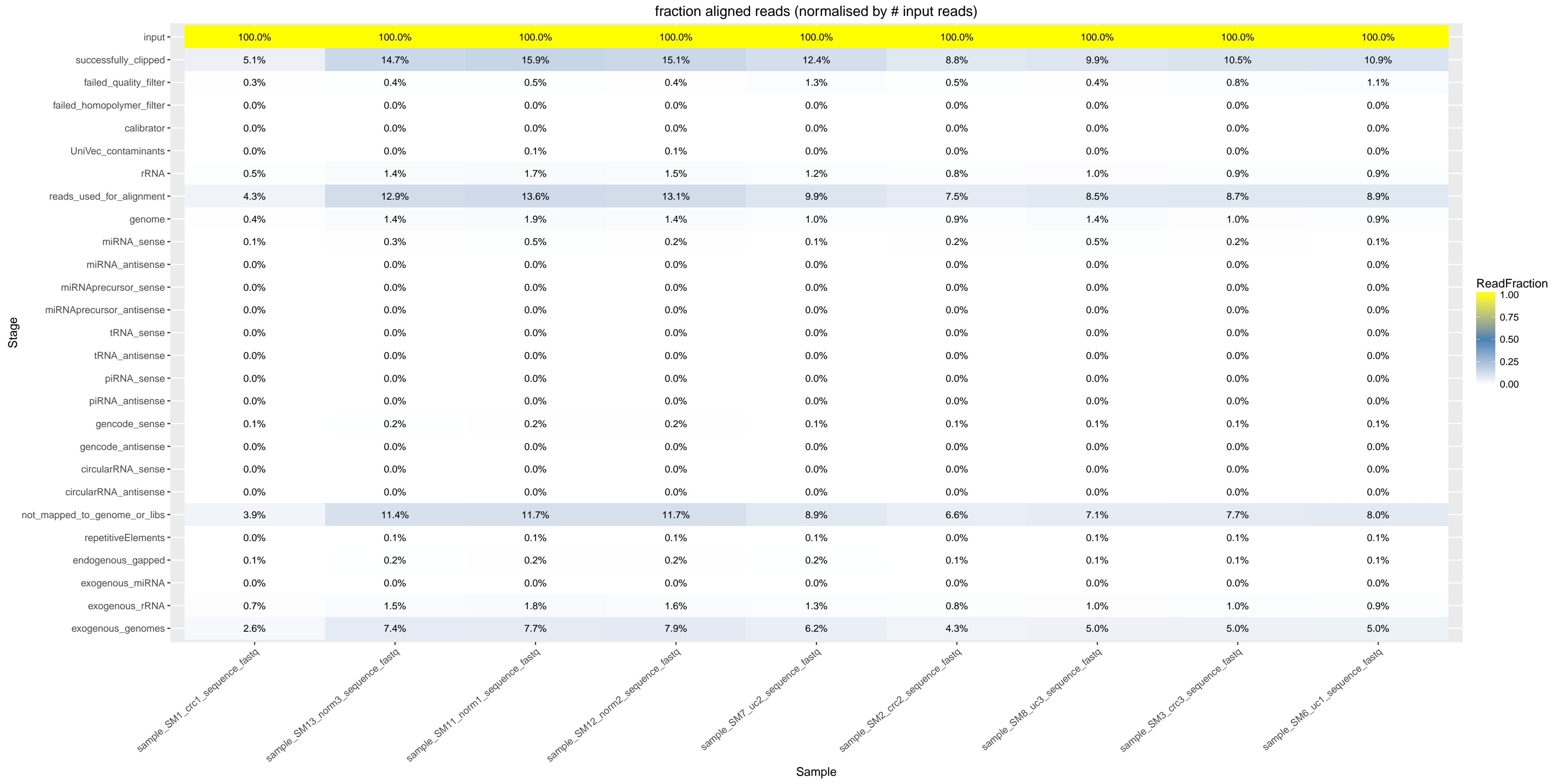


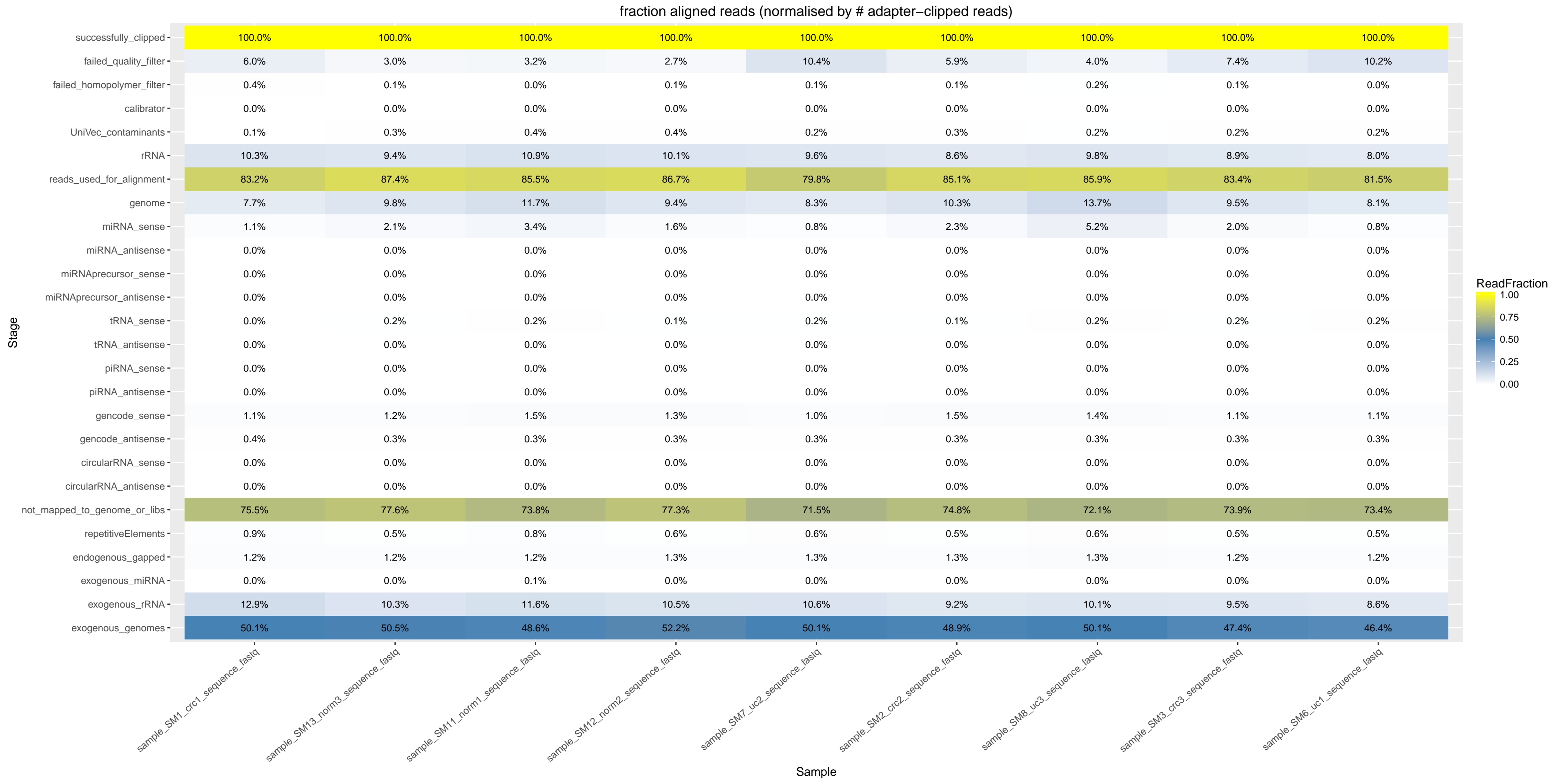
Duration of exceRpt run per sequencing yield



Library size (all mapped reads)



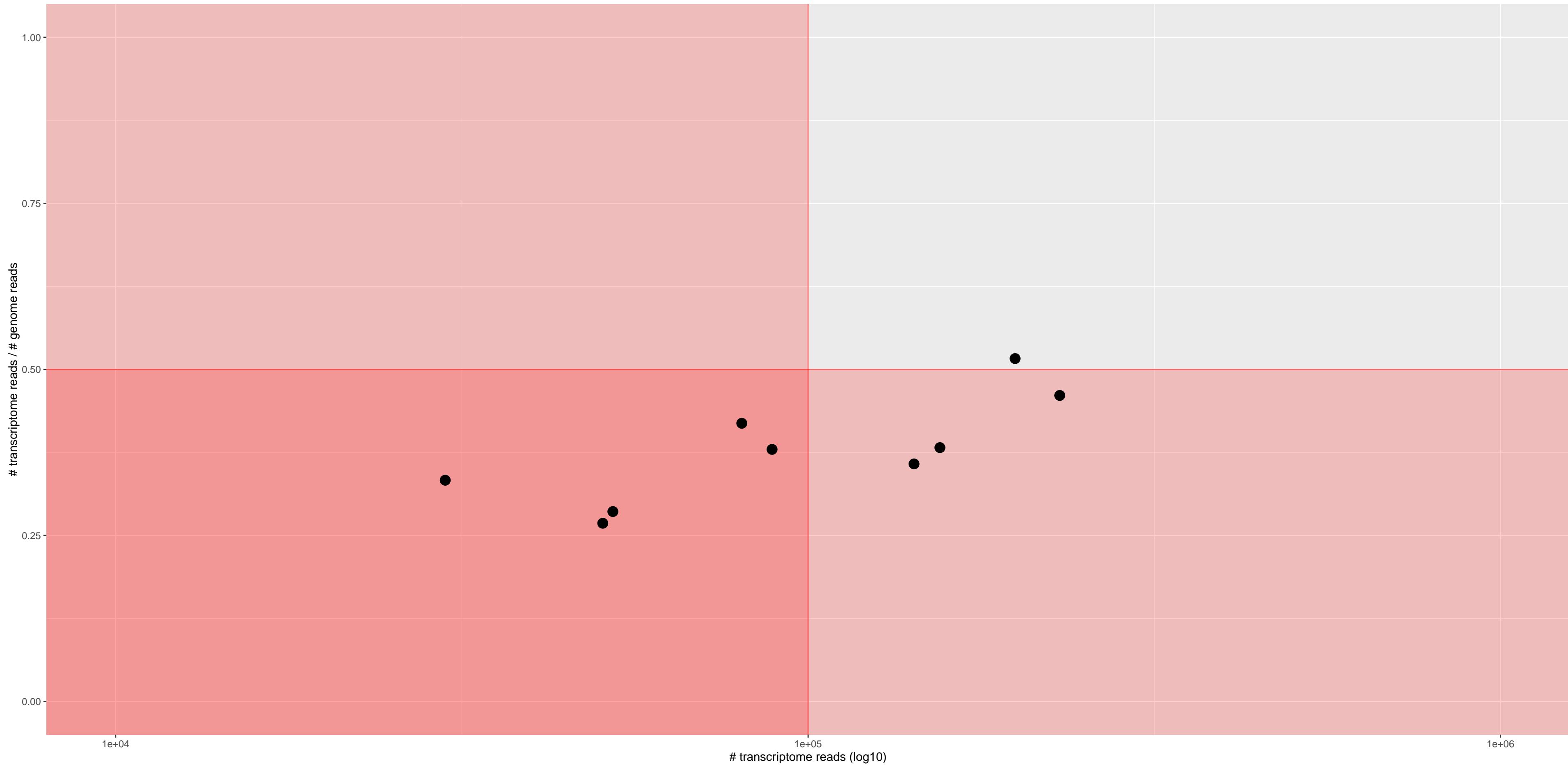




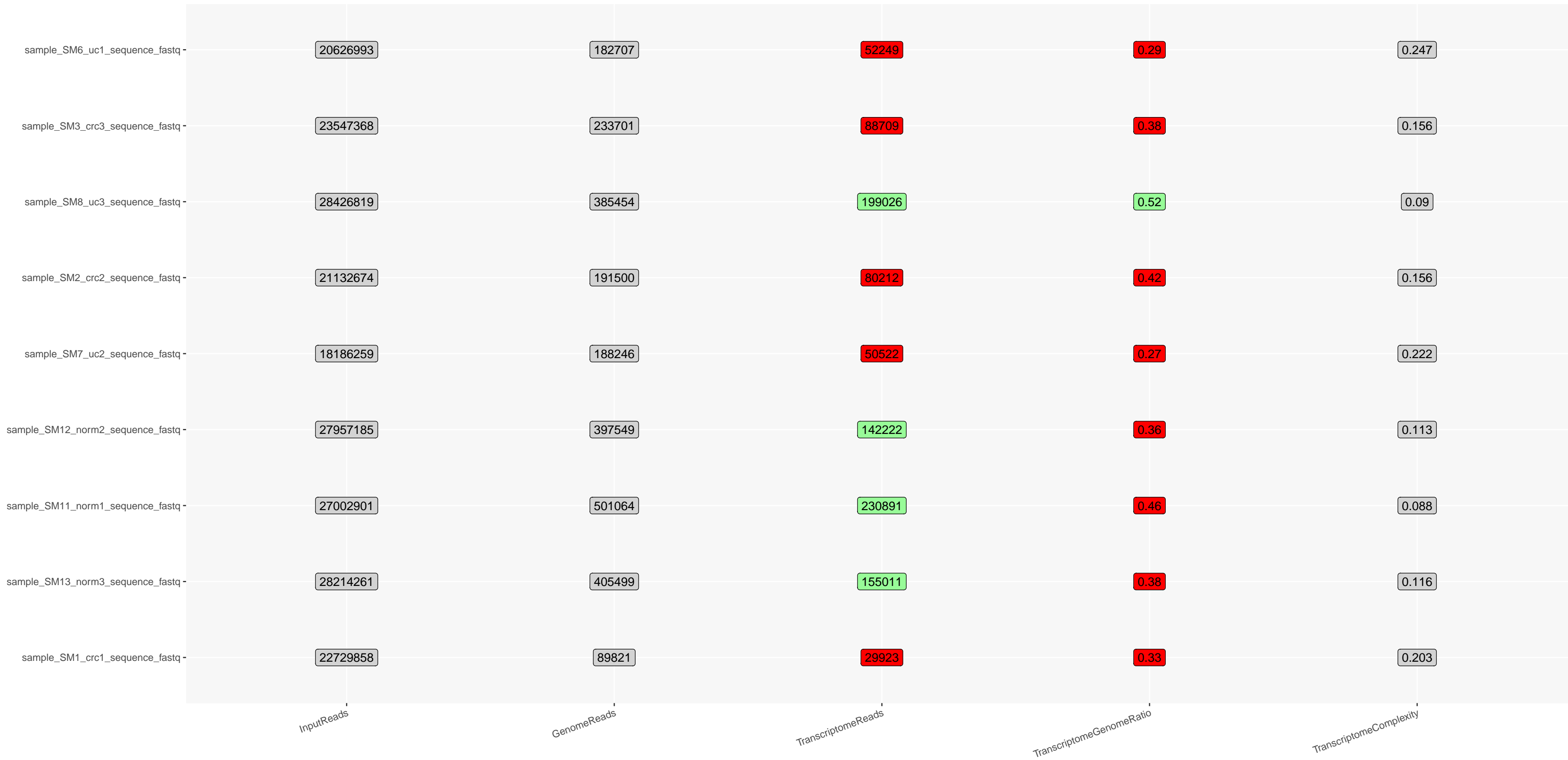




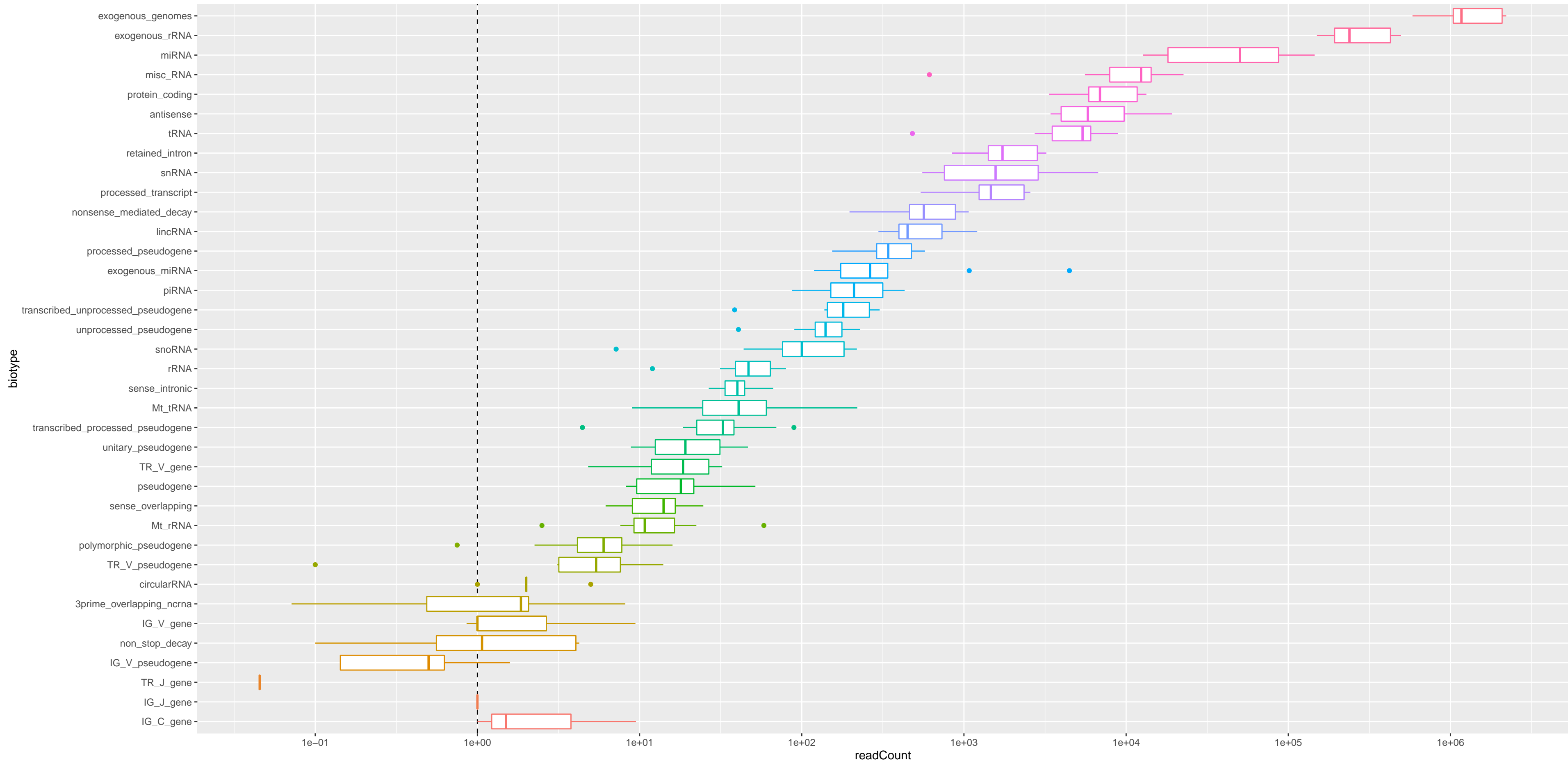
QC result: overall



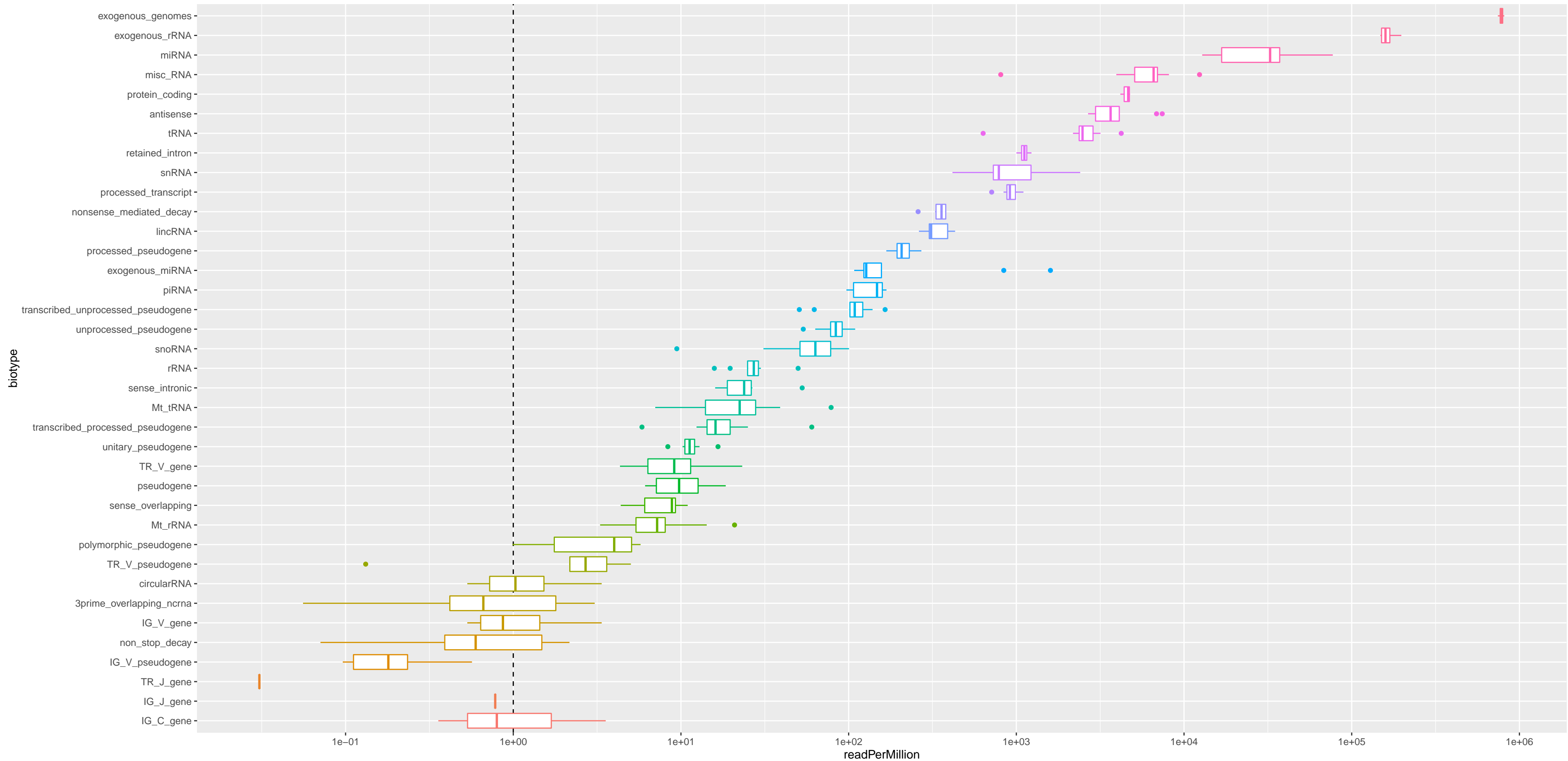
QC result: per-sample results



Biotypes: distributions, raw read-counts



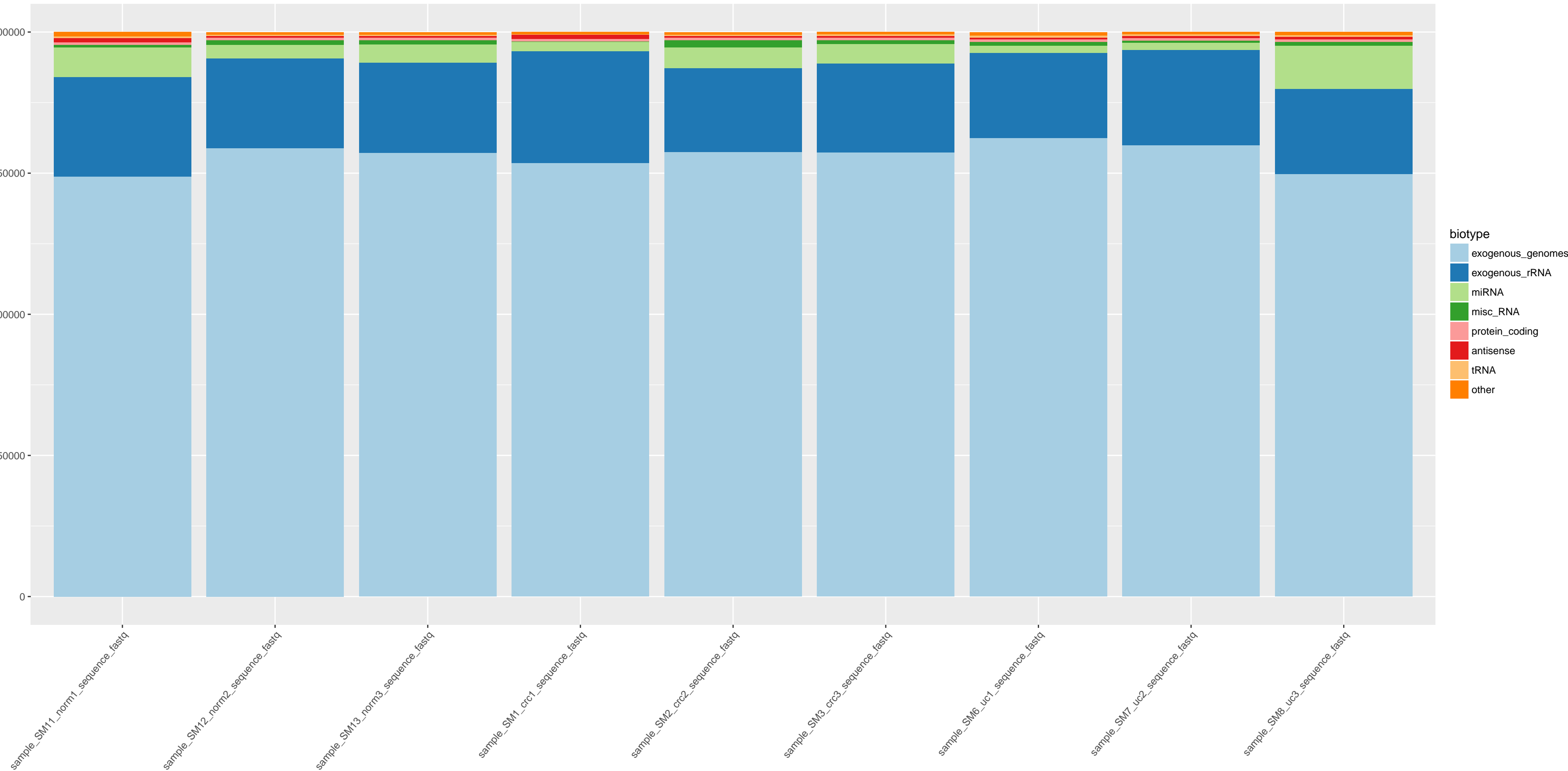
Biotypes: distributions, normalised



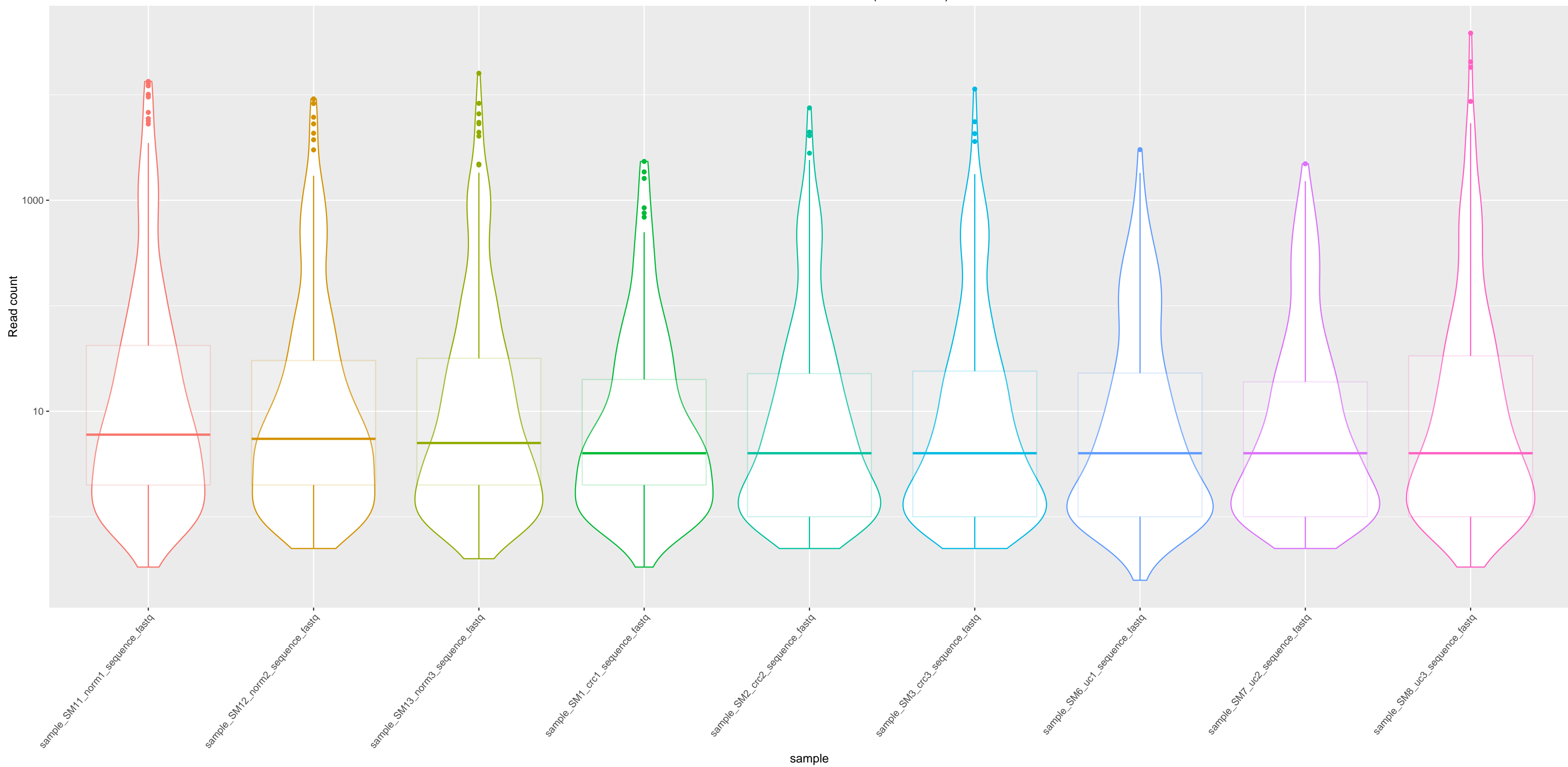


Biotypes: per-sample, normalised

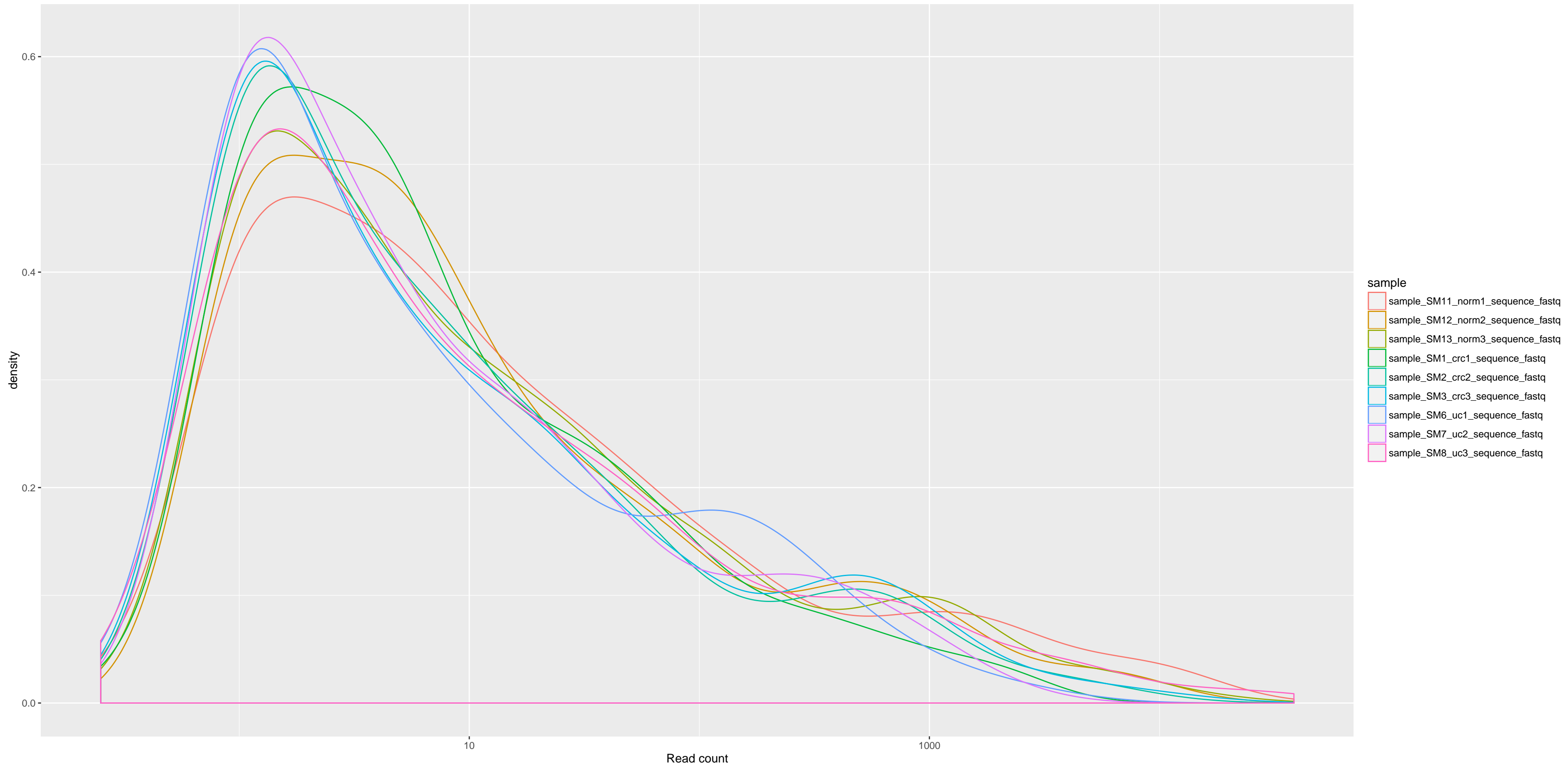
reads per million mapped reads



miRNA abundance distributions (raw counts)

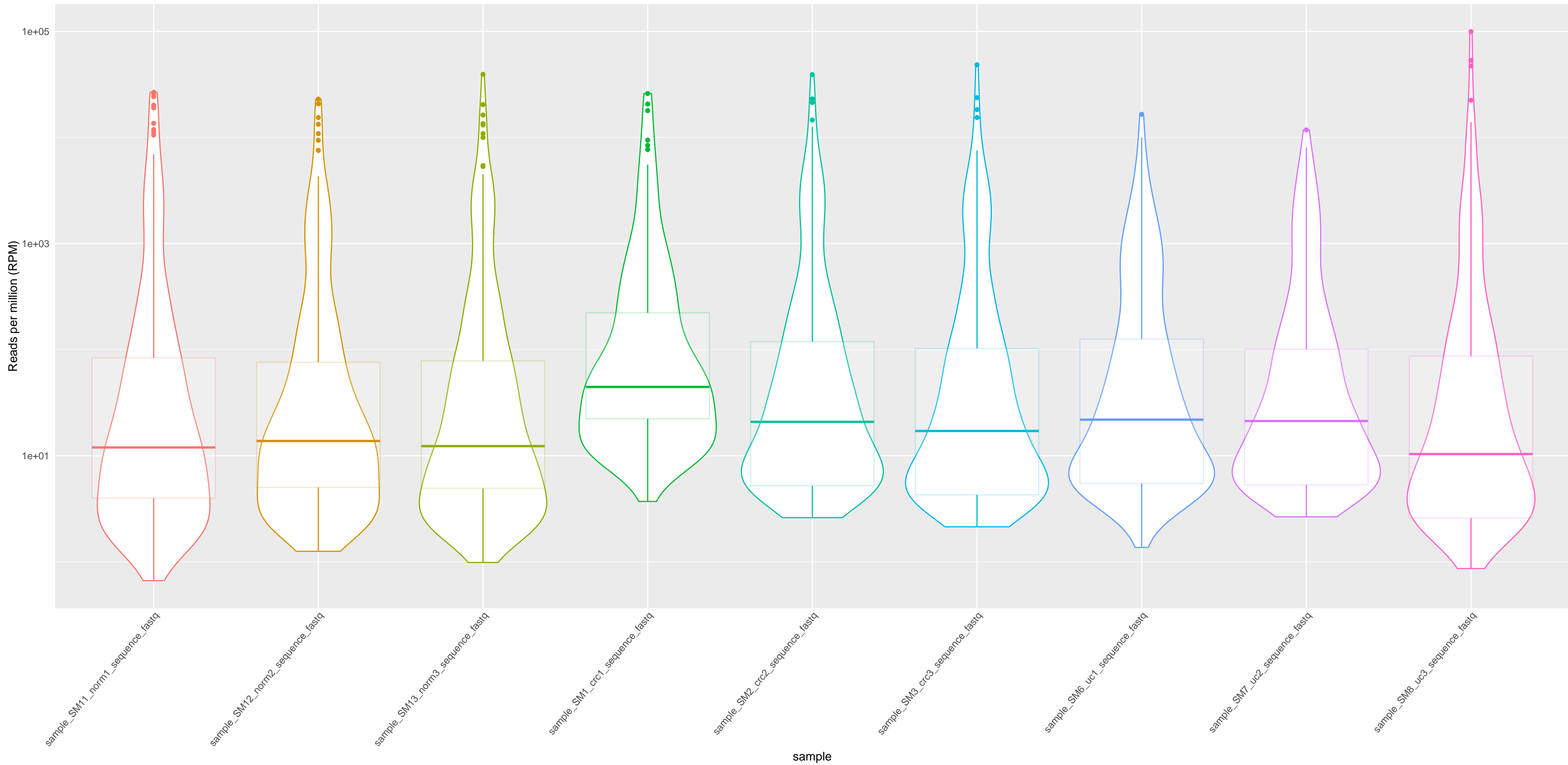


miRNA abundance distributions (raw counts)

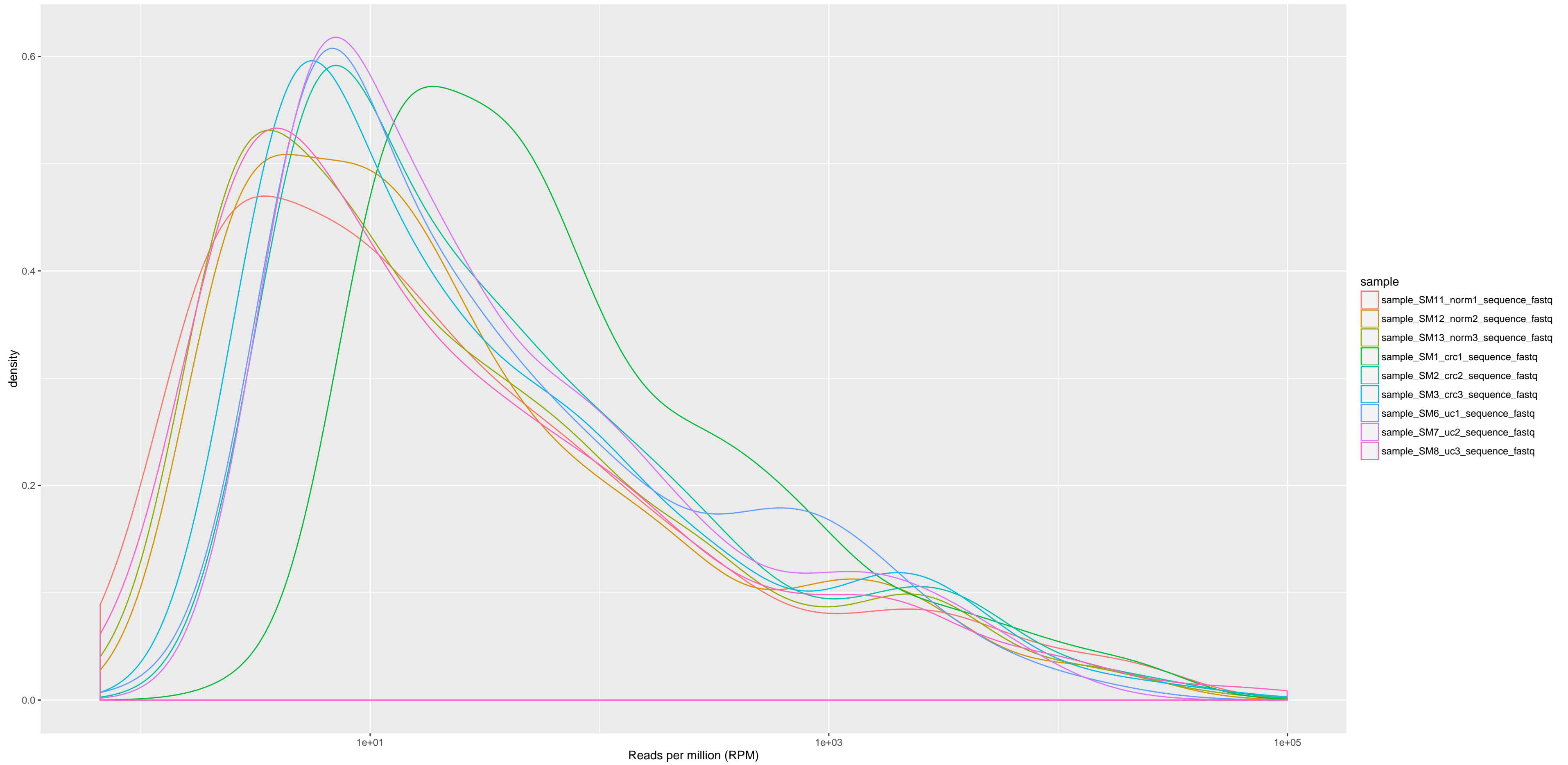




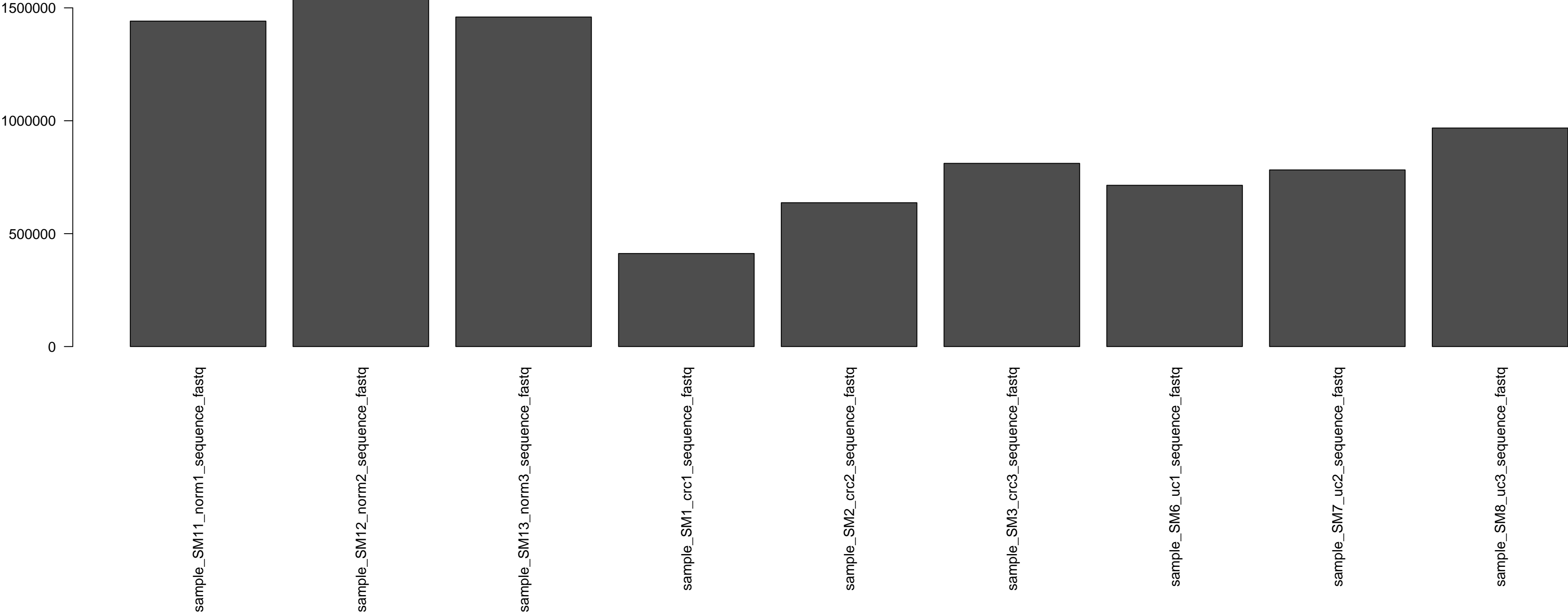
miRNA abundance distributions (RPM)

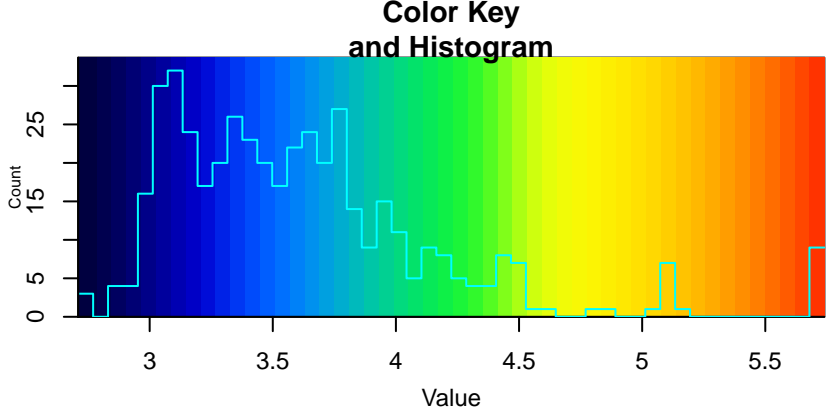


miRNA abundance distributions (RPM)

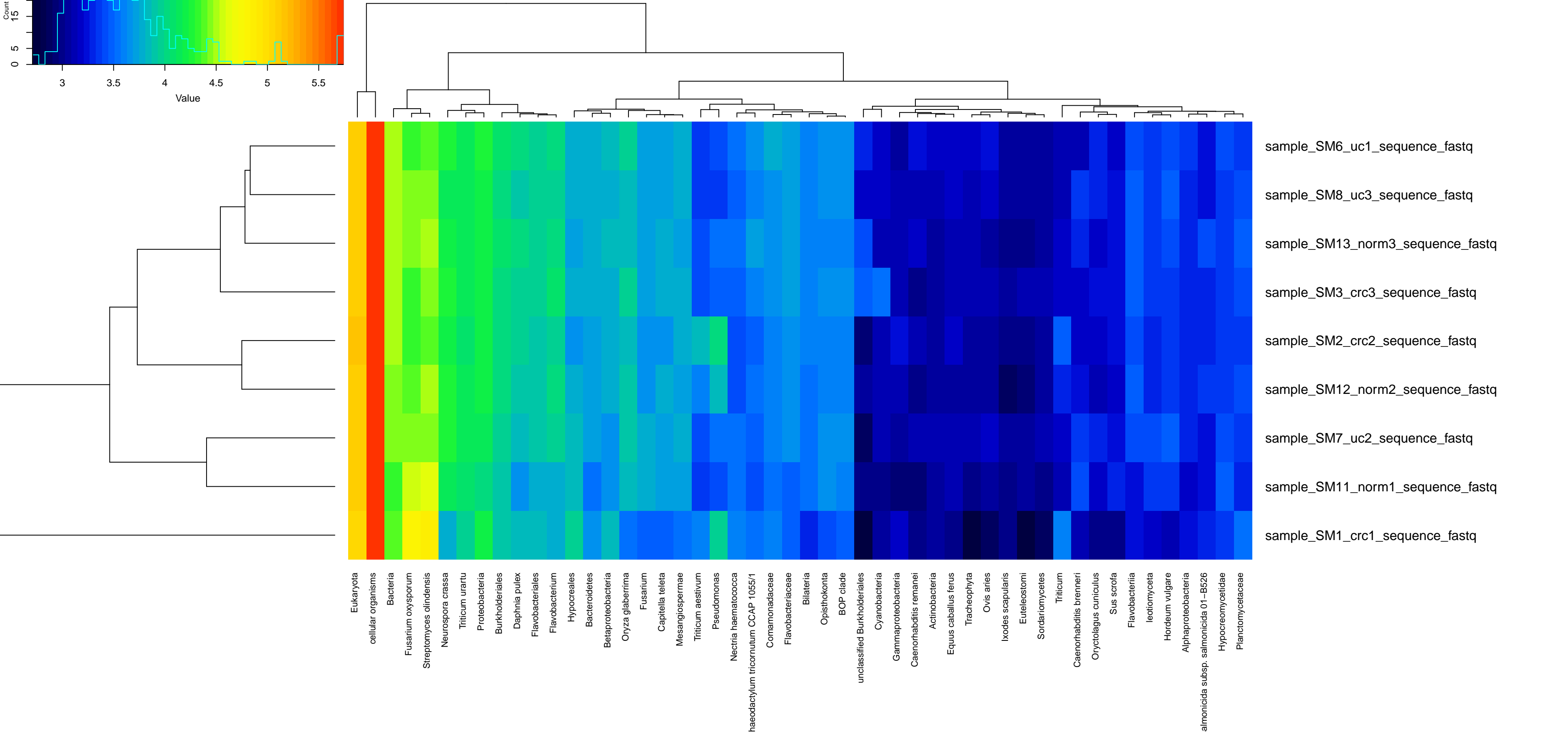


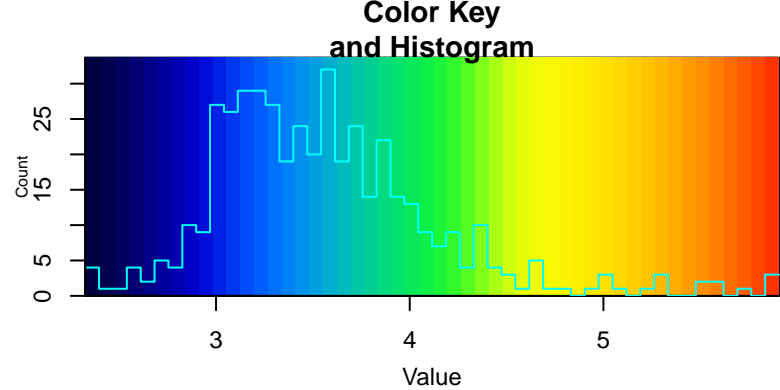
Total # reads mapped to NCBI taxonomy



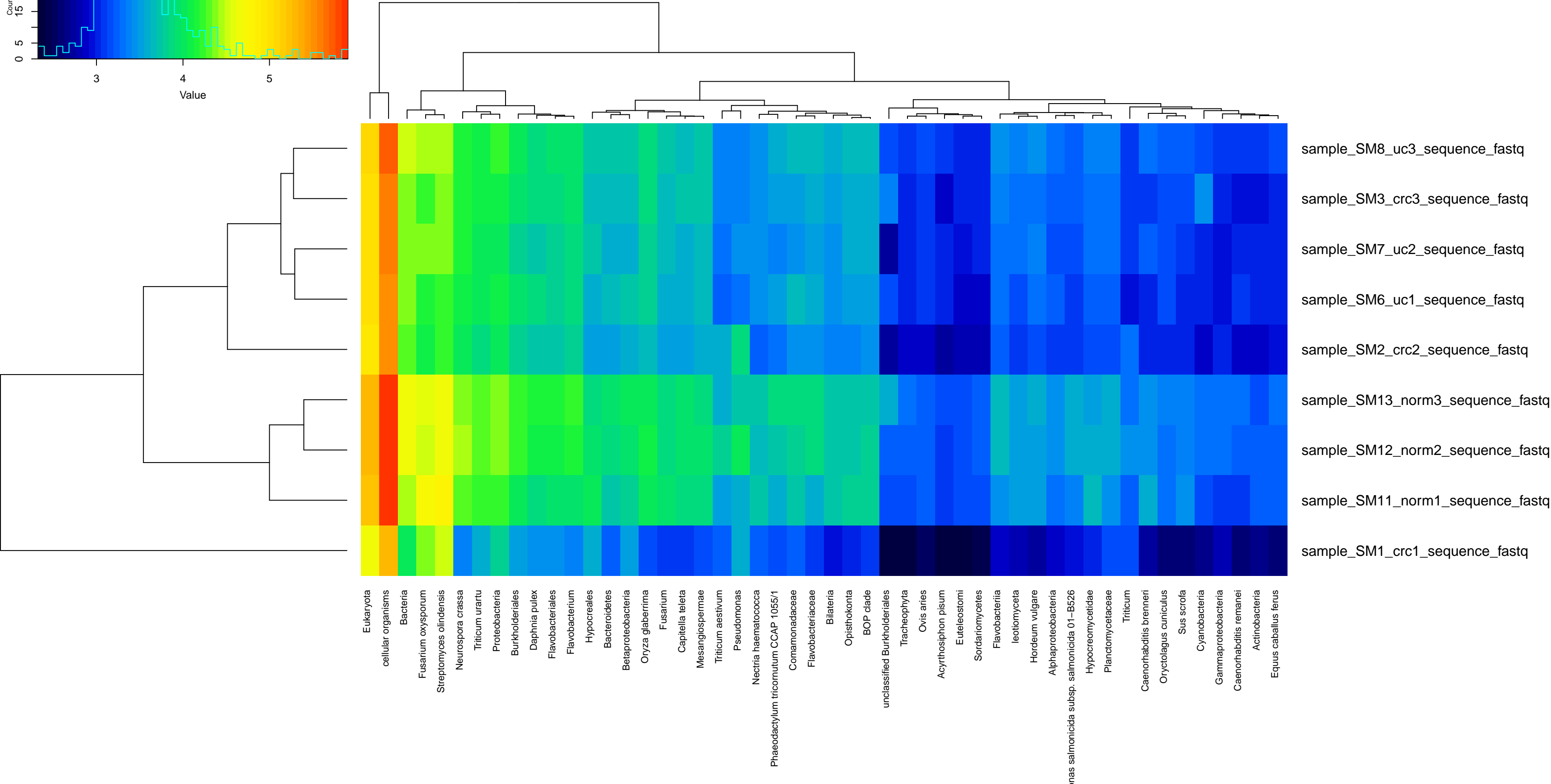


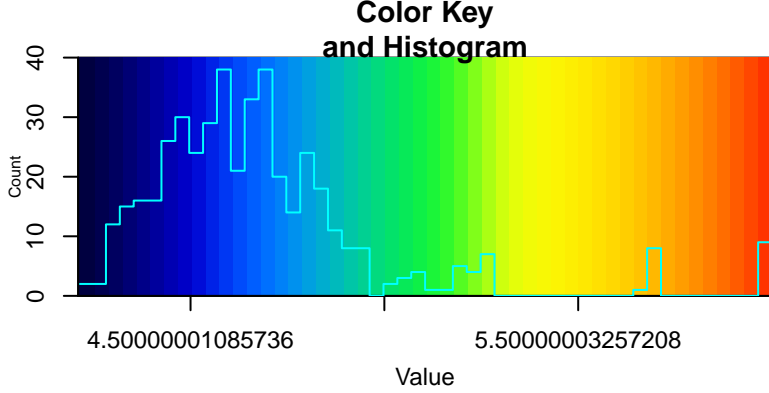
top taxa nodes: specific normalised read count



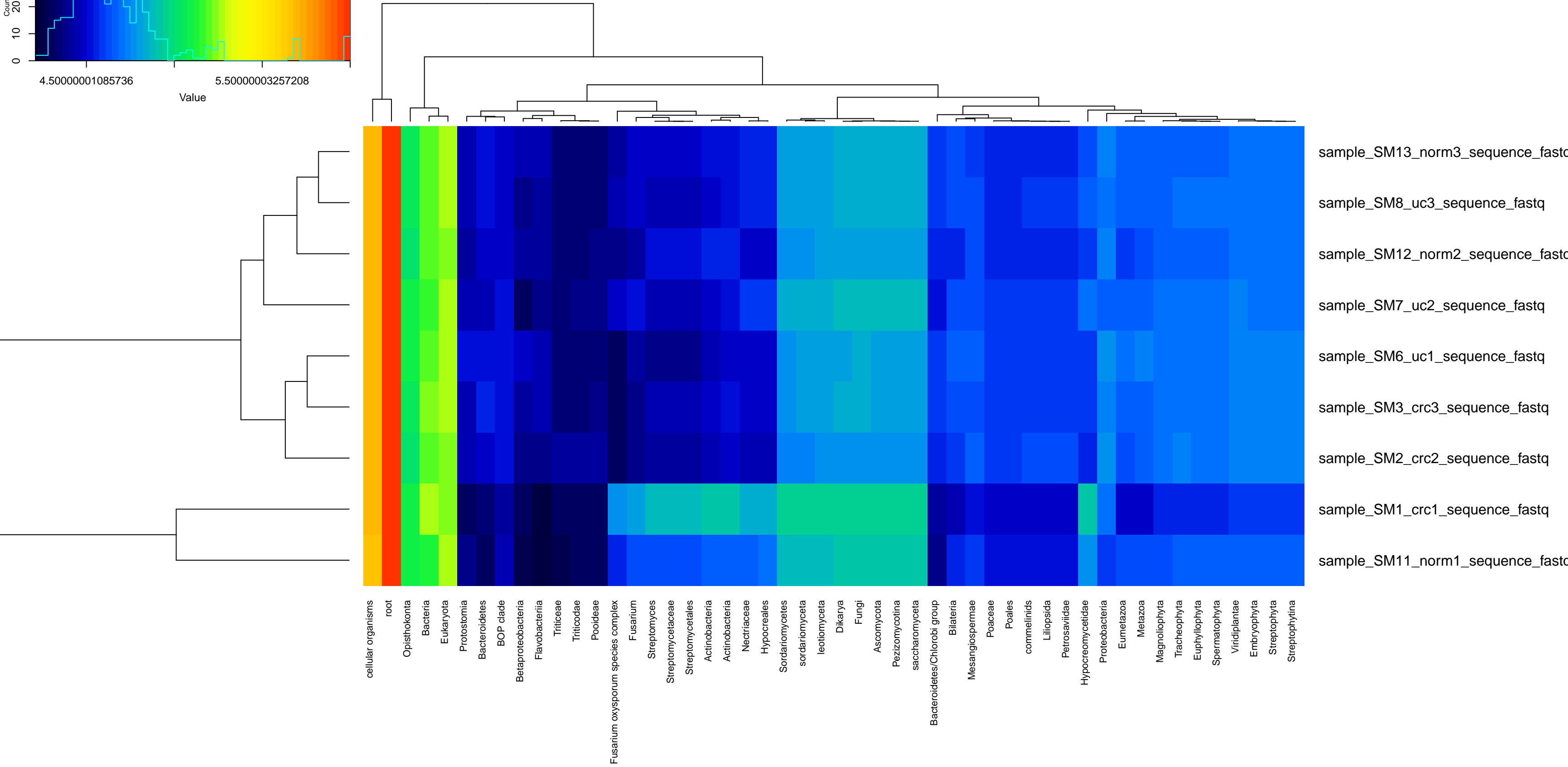


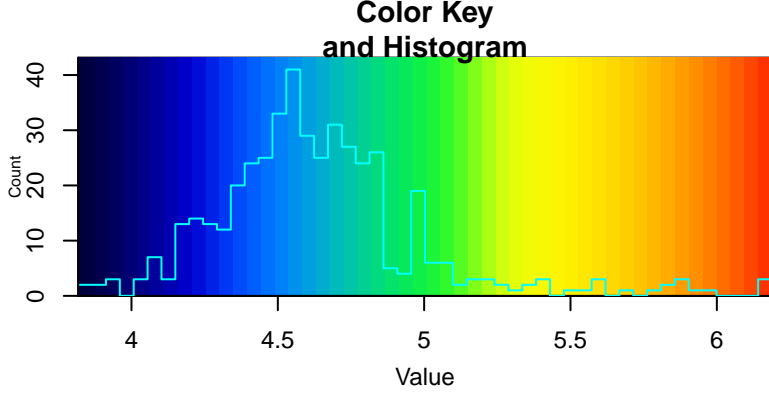
top taxa nodes: specific absolute read count





top taxa nodes: cumulative normalised read count





top taxa nodes: cumulative absolute read count

