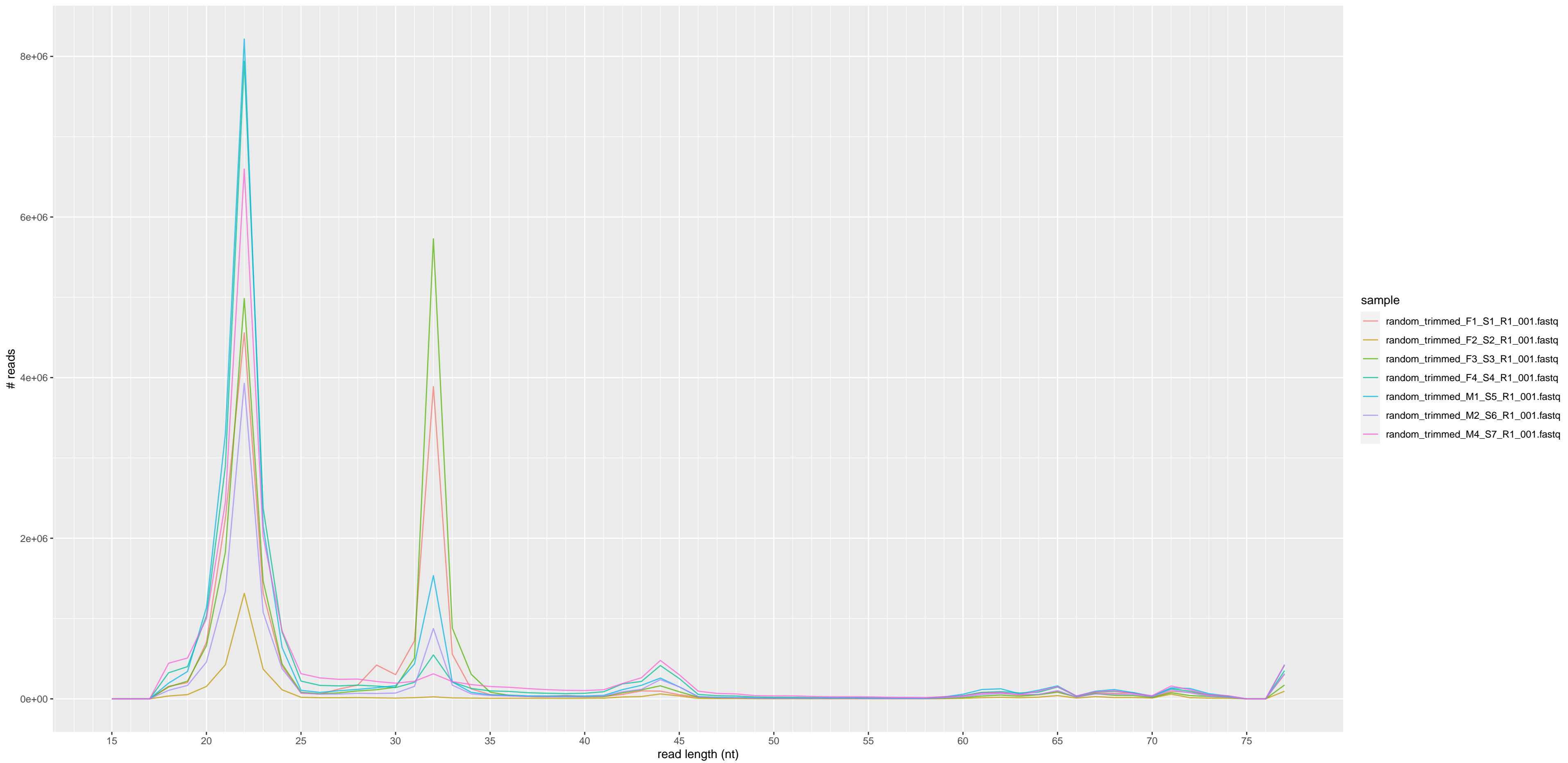
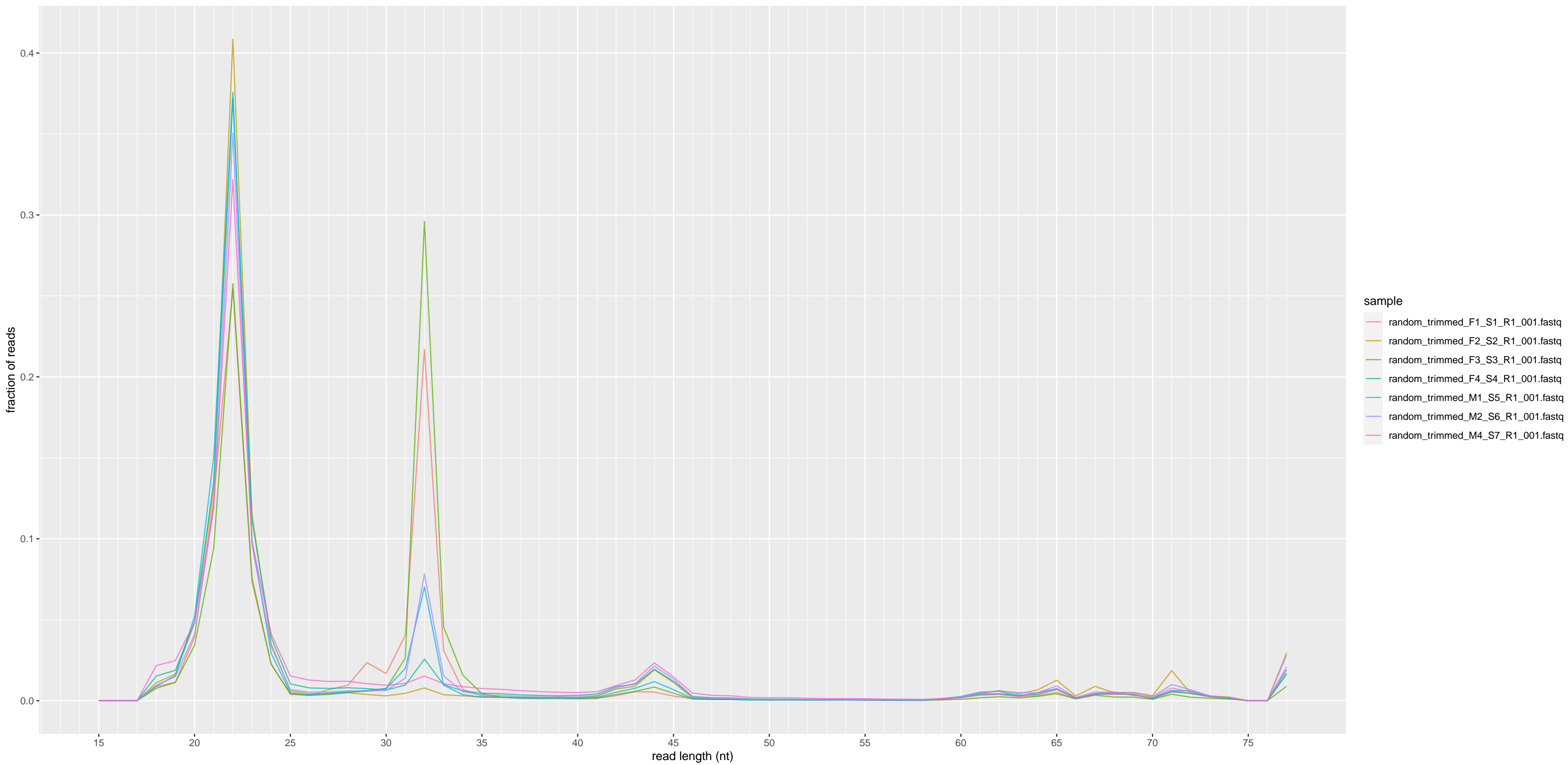


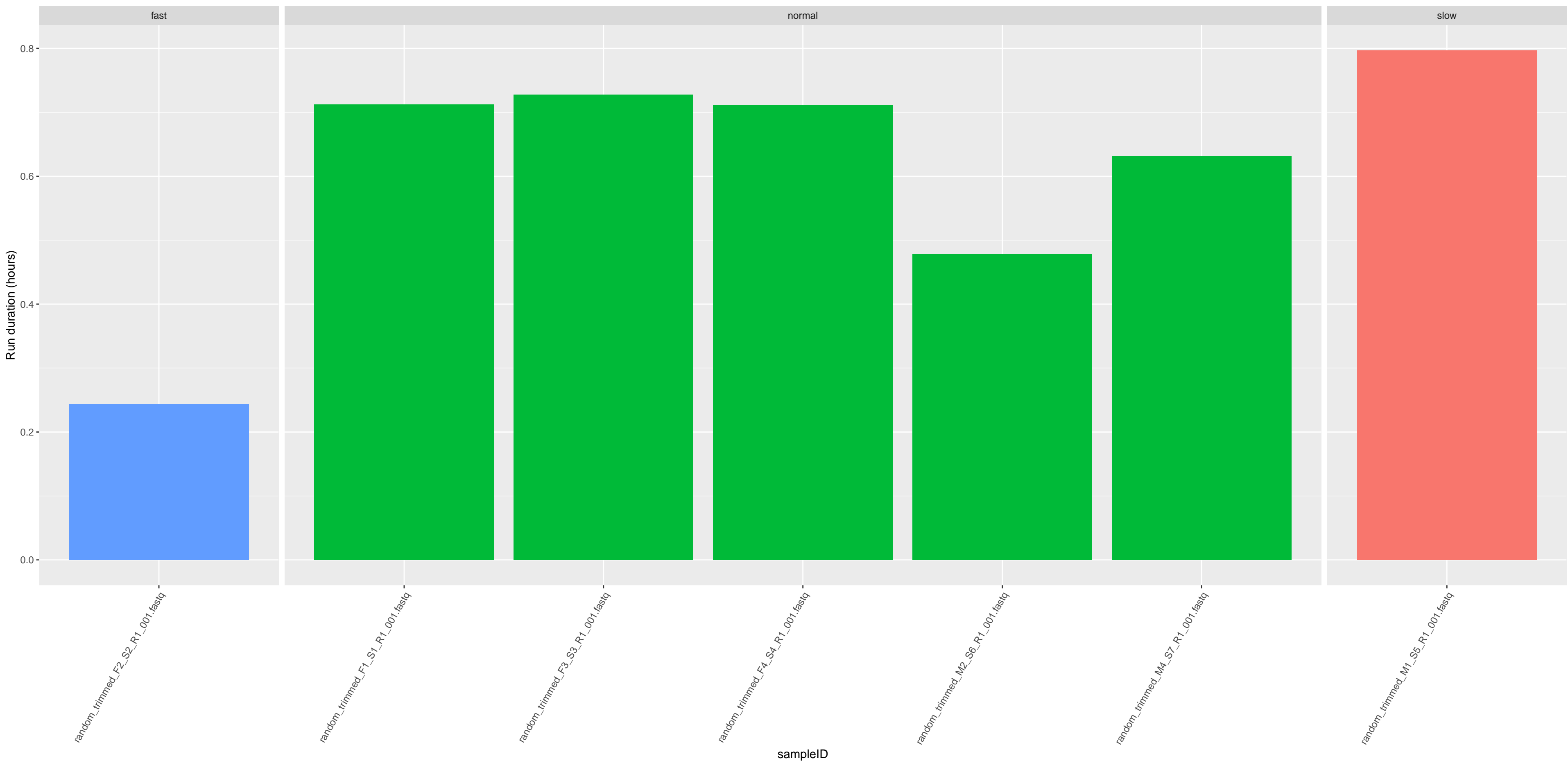
read-length distributions: raw read count



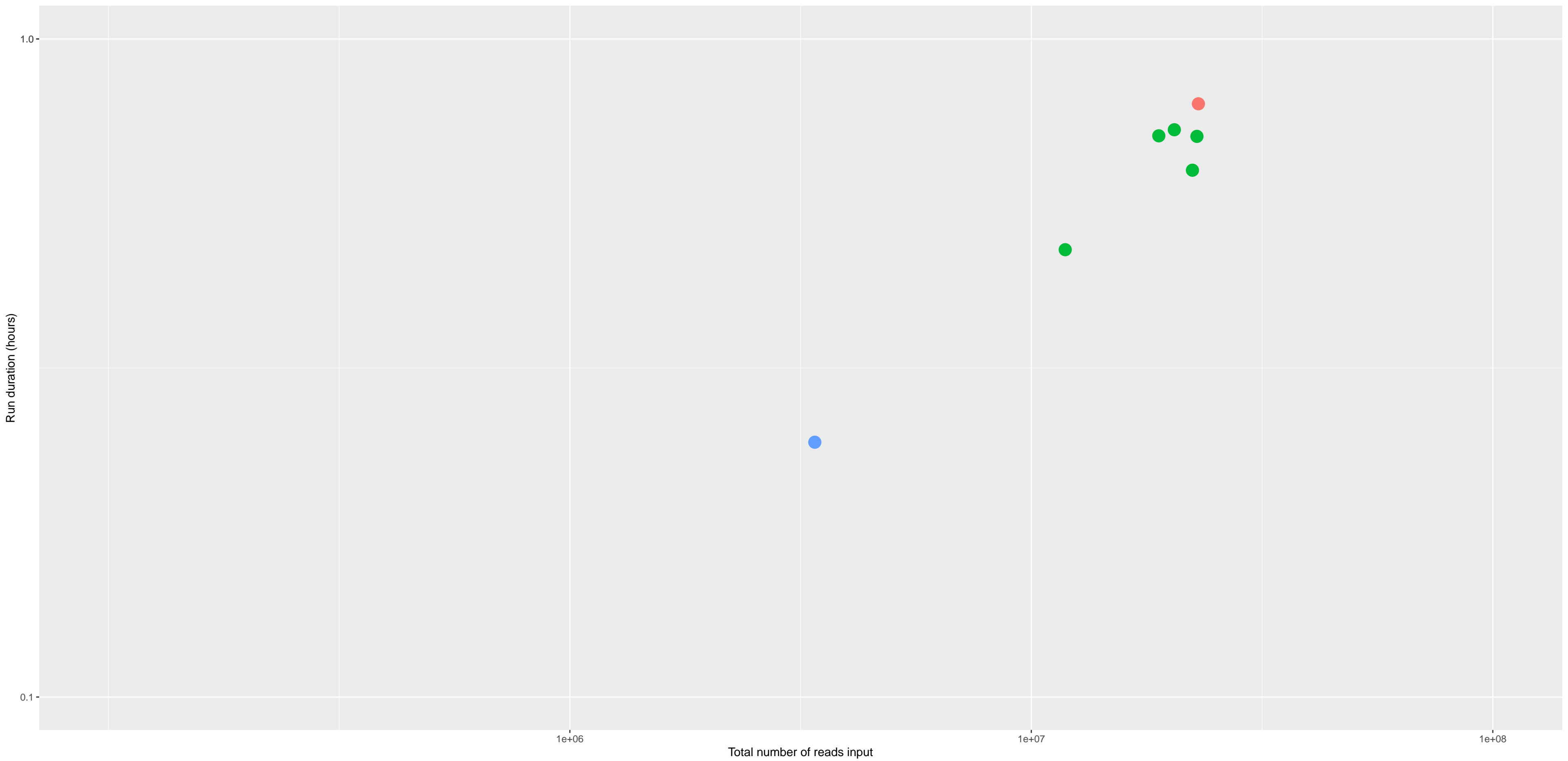
read-length distributions: normalised read fraction



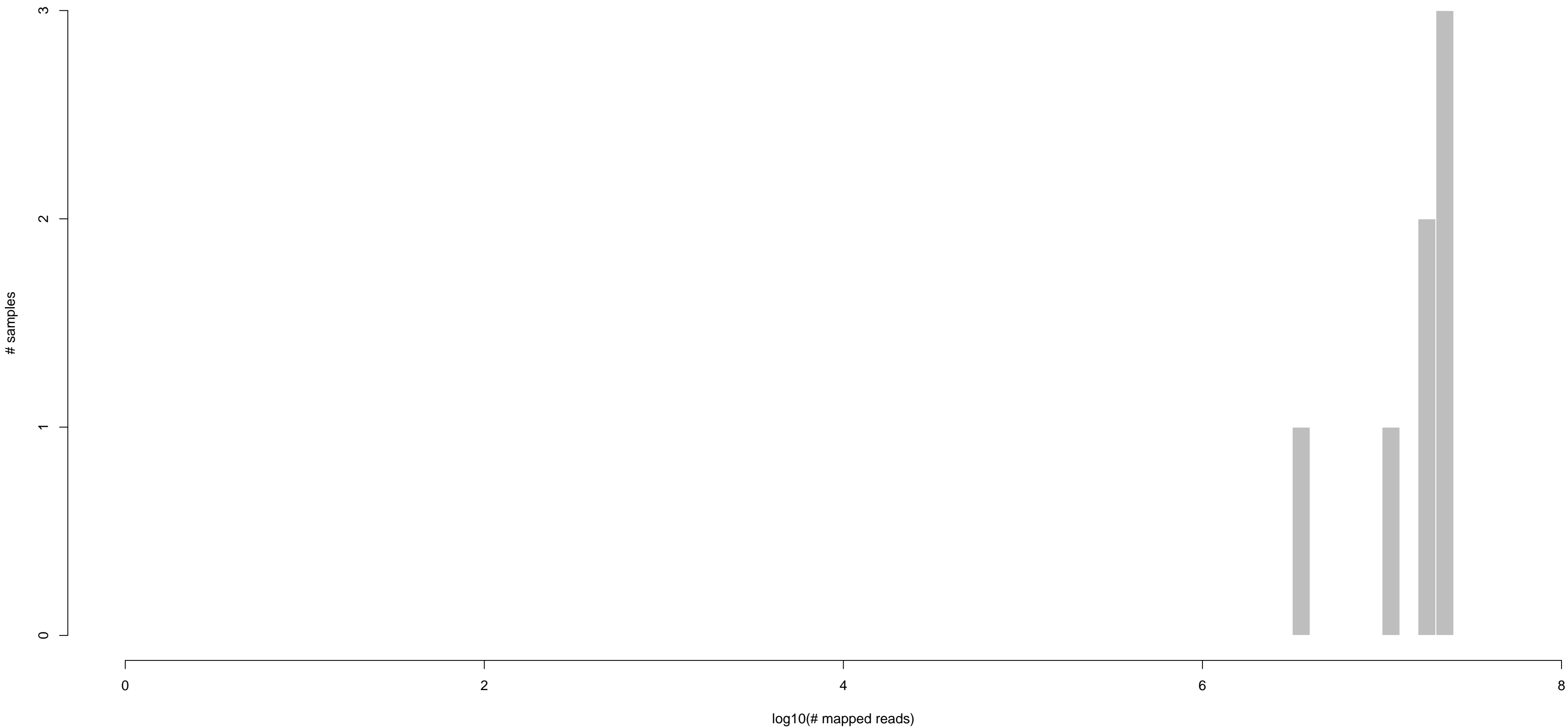
Duration of exceRpt run for each sample



Duration of exceRpt run per sequencing yield



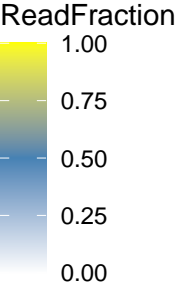
Library size (all mapped reads)



fraction aligned reads (normalised by # input reads)

Stage

input	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
successfully_clipped	98.3%	98.5%	95.3%	98.4%	98.2%	98.2%	96.9%
failed_quality_filter	3.3%	3.6%	3.5%	3.3%	3.5%	3.3%	3.4%
failed_homopolymer_filter	0.1%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%
calibrator	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
UniVec_contaminants	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
rRNA	6.1%	6.2%	28.4%	7.9%	13.1%	10.3%	17.3%
reads_used_for_alignment	88.8%	88.6%	63.3%	87.1%	81.5%	84.4%	76.1%
genome	87.5%	87.6%	62.1%	85.8%	80.2%	83.1%	74.7%
miRNA_sense	47.2%	44.6%	51.4%	65.6%	58.5%	68.4%	62.1%
miRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
miRNAprecursor_sense	0.1%	0.1%	0.1%	0.2%	0.2%	0.2%	0.2%
miRNAprecursor_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
tRNA_sense	31.0%	36.3%	1.2%	9.8%	9.6%	1.0%	3.2%
tRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRNA_sense	0.1%	0.1%	0.2%	0.2%	0.2%	0.2%	0.2%
piRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
gencode_sense	8.0%	5.6%	7.8%	8.9%	10.5%	11.8%	7.7%
gencode_antisense	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%
circularRNA_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
circularRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
not_mapped_to_genome_or_libs	1.3%	1.0%	1.2%	1.3%	1.3%	1.3%	1.4%



random\_trimmed\_F1\_S1\_R1\_001.fastq

random\_trimmed\_F3\_S3\_R1\_001.fastq

random\_trimmed\_M4\_S7\_R1\_001.fastq

random\_trimmed\_M1\_S5\_R1\_001.fastq

random\_trimmed\_M2\_S6\_R1\_001.fastq

random\_trimmed\_F2\_S2\_R1\_001.fastq

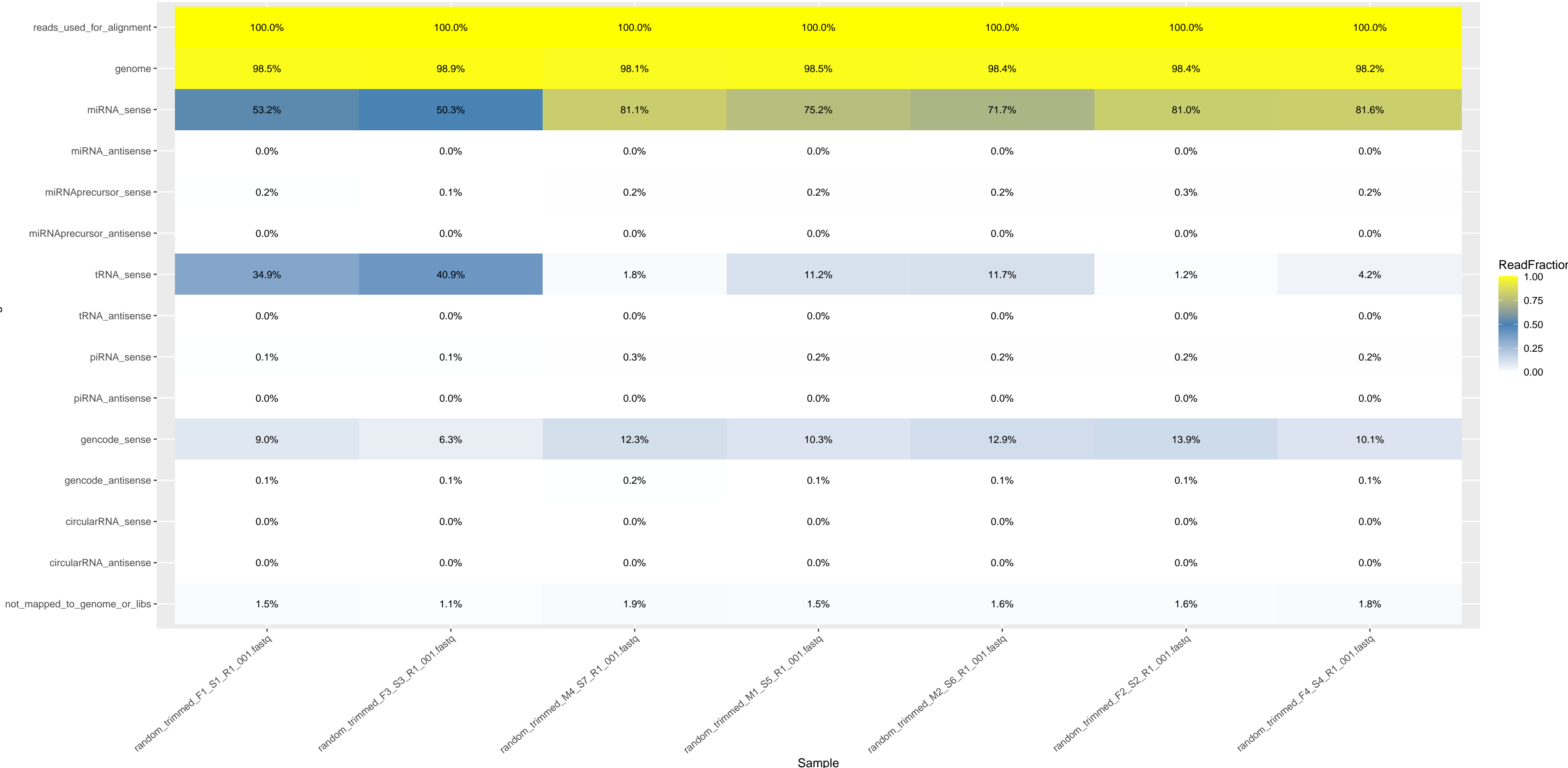
random\_trimmed\_F4\_S4\_R1\_001.fastq

Sample

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



fraction aligned reads (normalised by # non-contaminant reads)

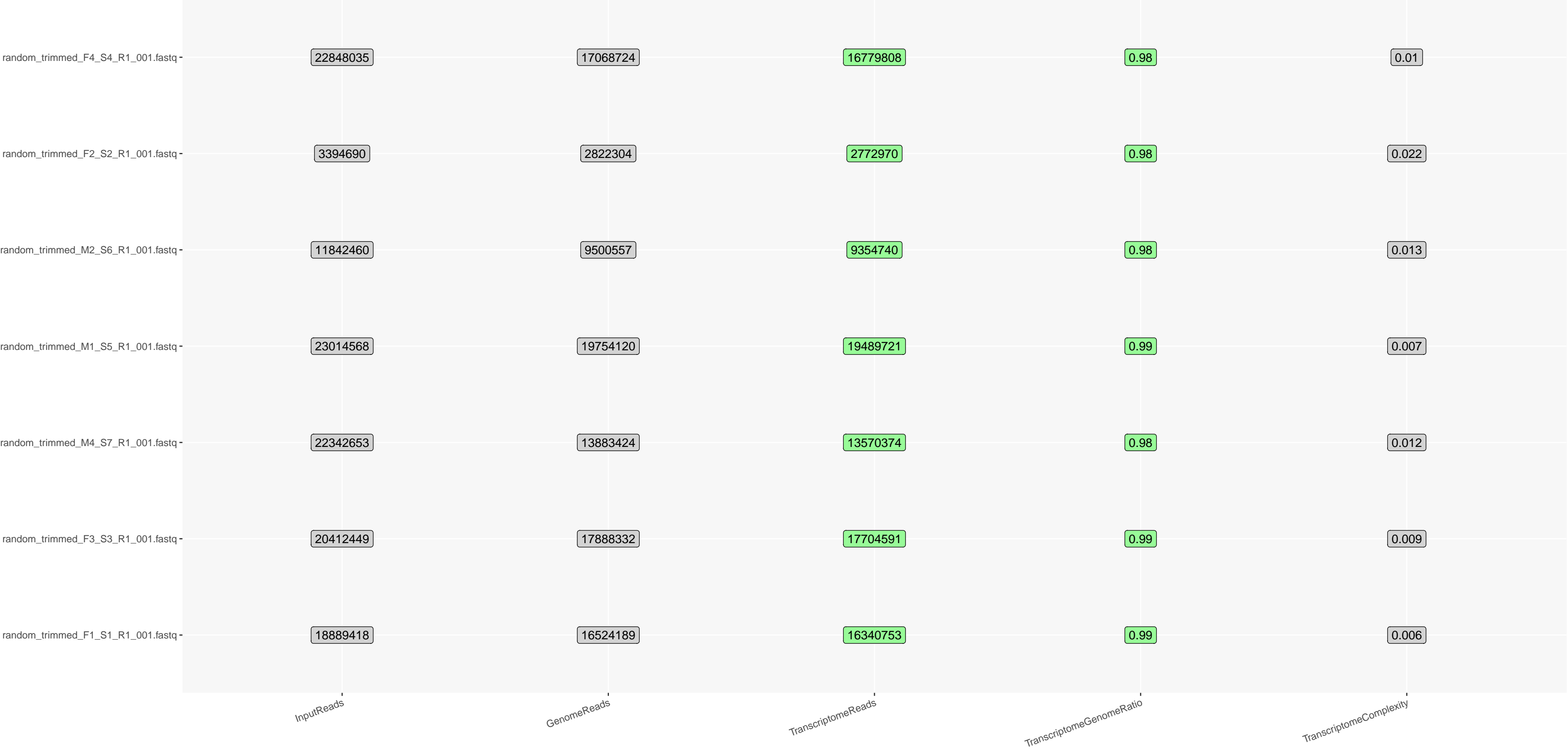




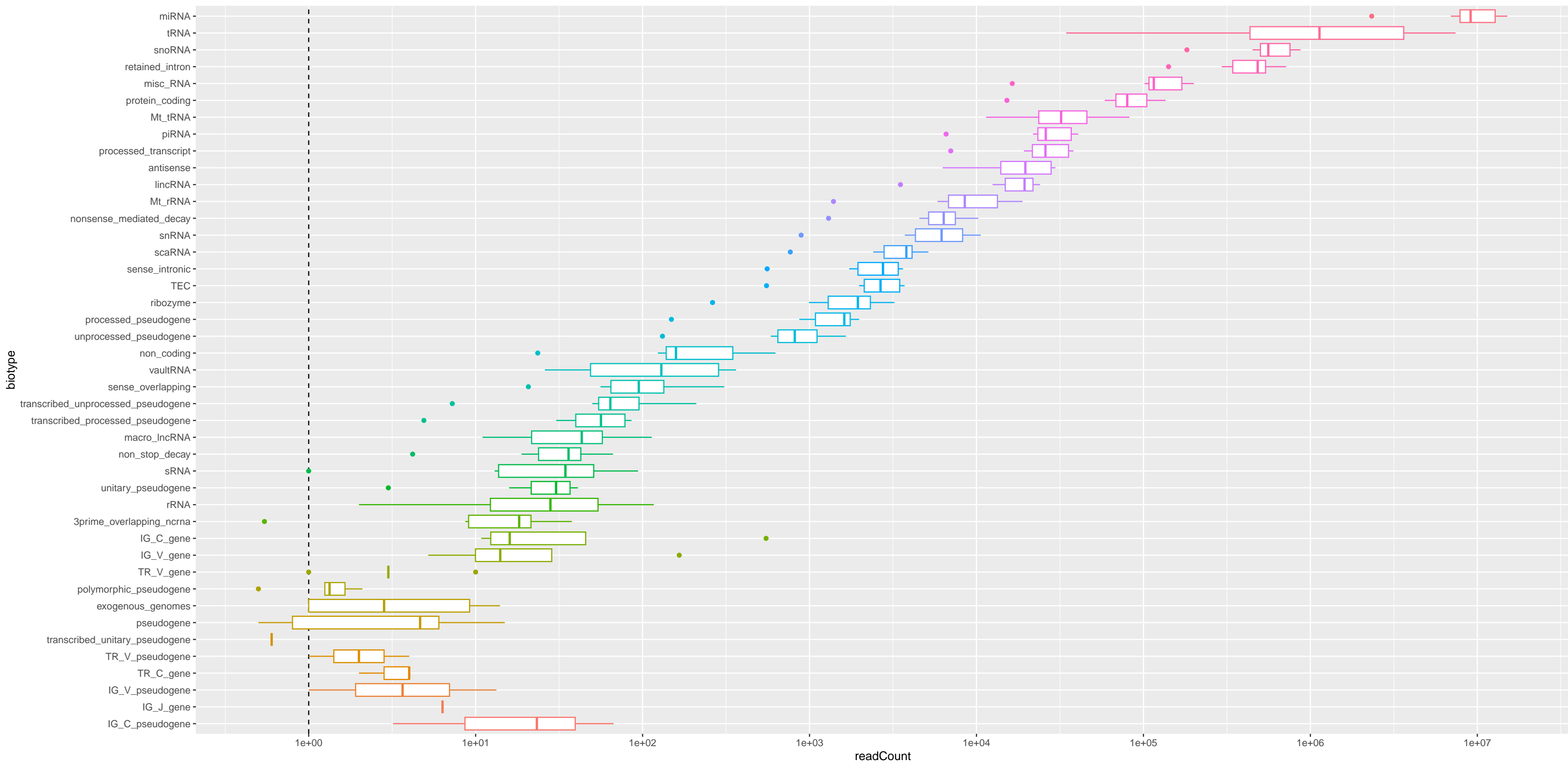
QC result: overall



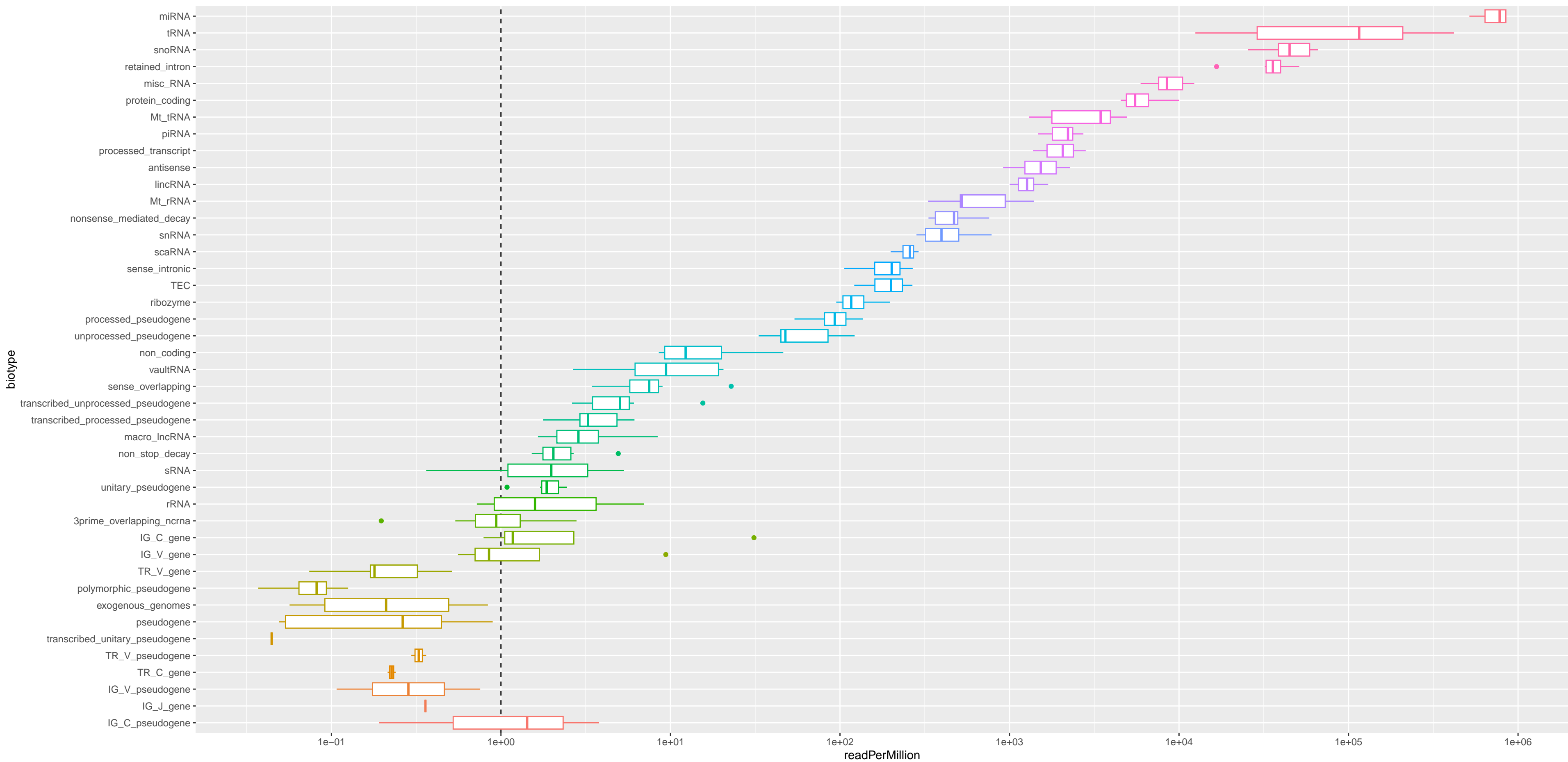
QC result: per-sample results



Biotypes: distributions, raw read-counts

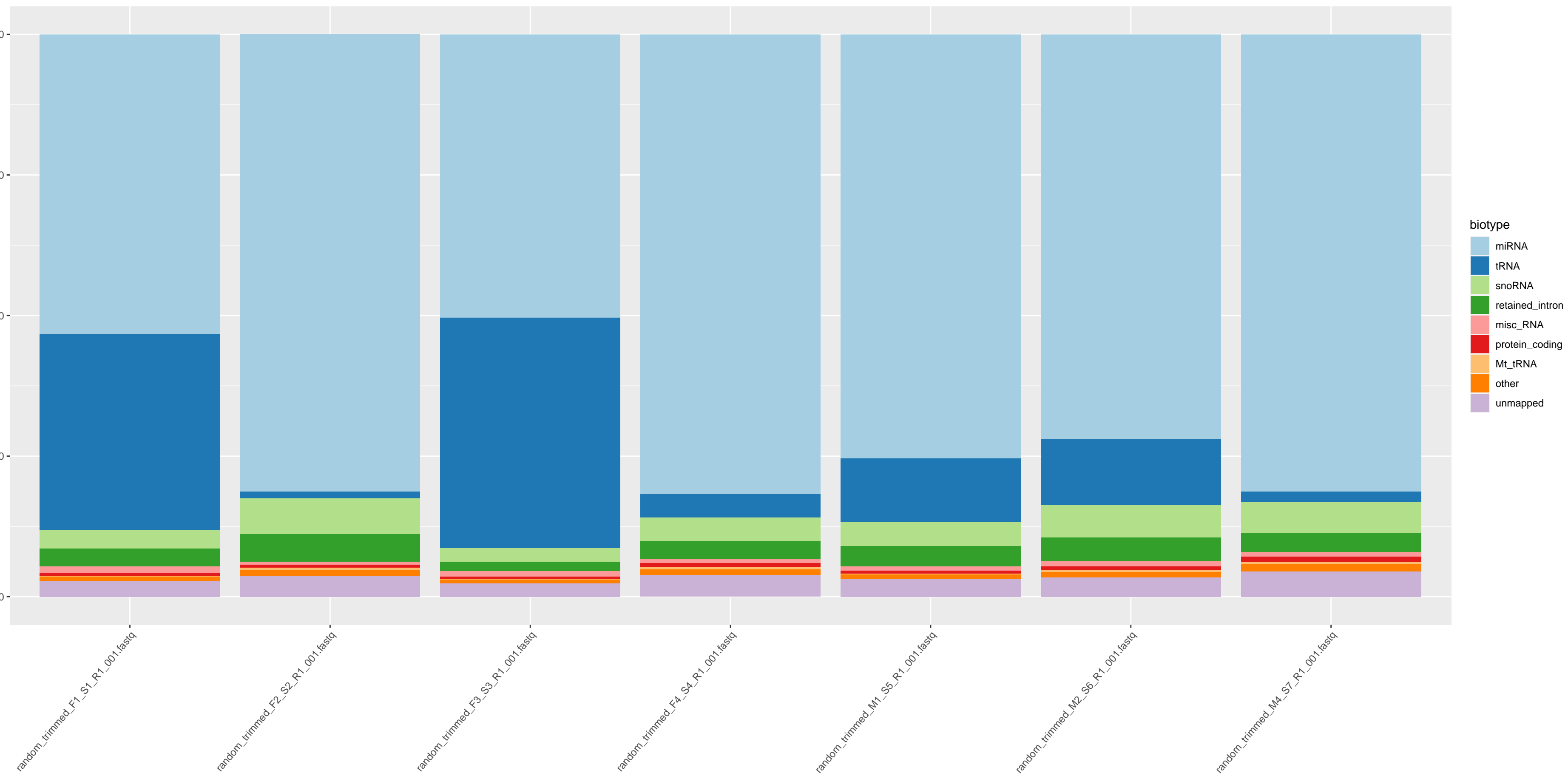


Biotypes: distributions, normalised



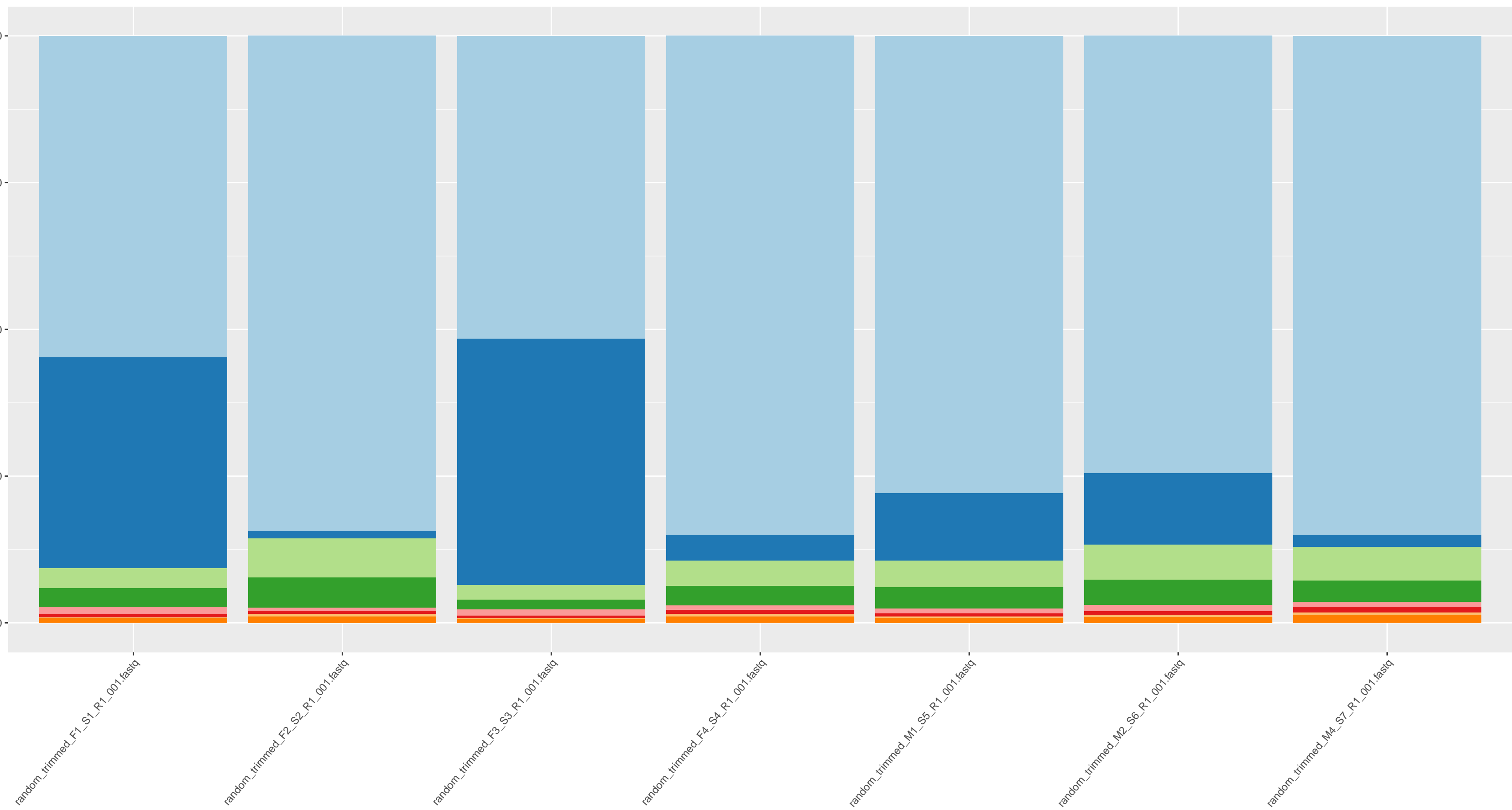
Biotypes: per-sample, normalised

reads per million reads used for alignment



Biotypes: per-sample, normalised

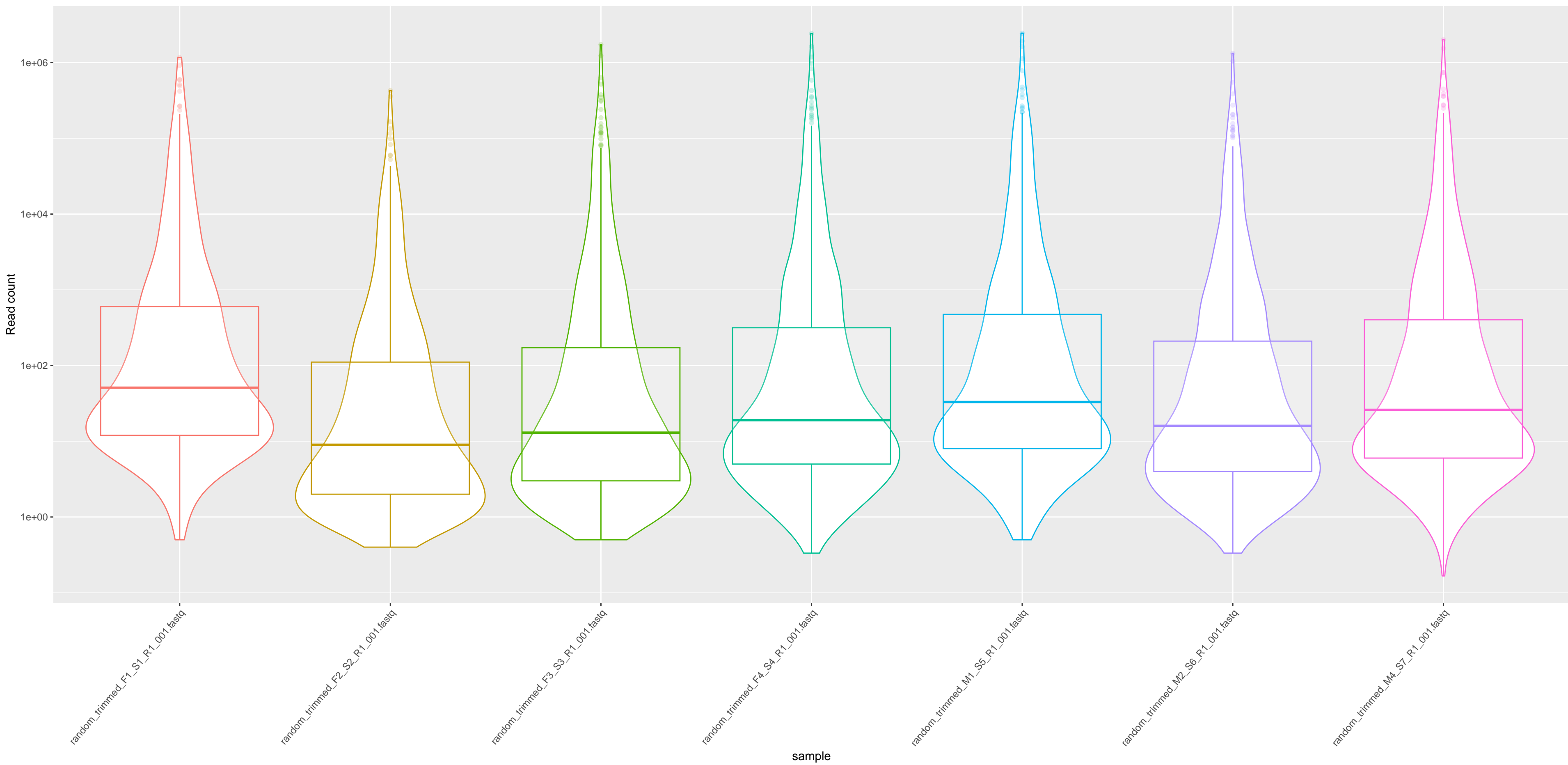
reads per million mapped reads



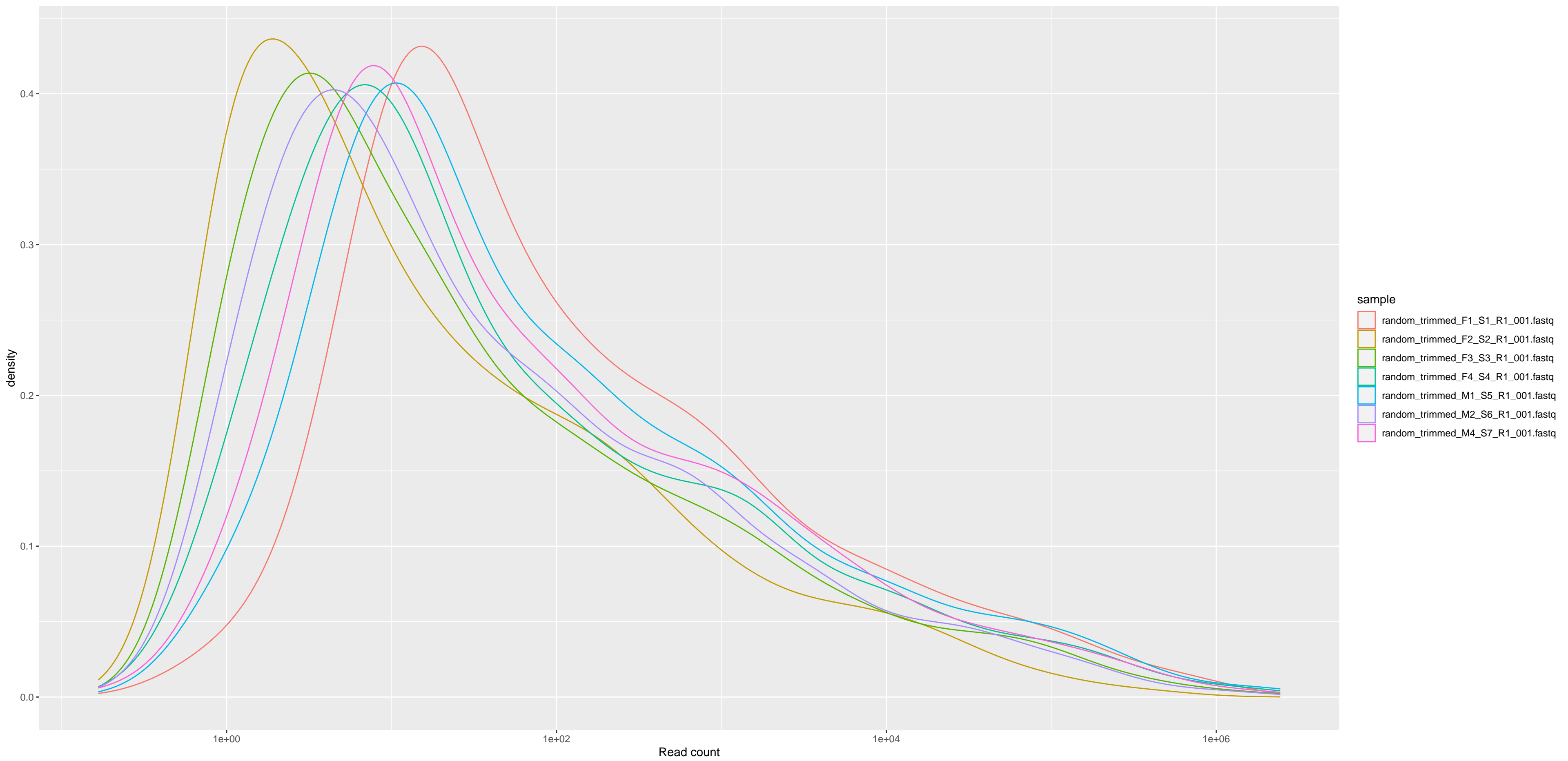
biotype

- miRNA
- tRNA
- snoRNA
- retained\_intron
- misc\_RNA
- protein\_coding
- Mt\_tRNA
- other

miRNA abundance distributions (raw counts)

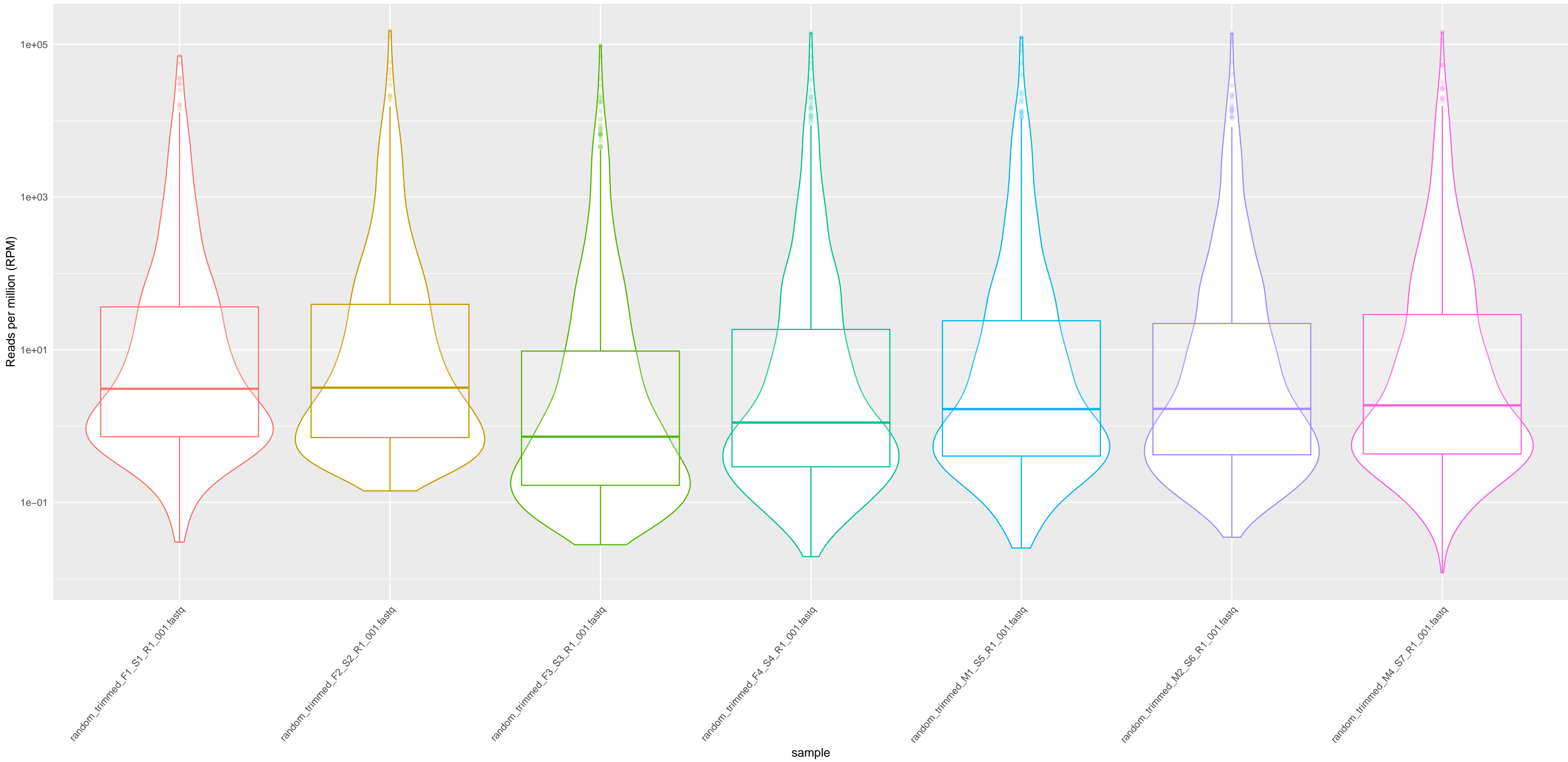


miRNA abundance distributions (raw counts)





miRNA abundance distributions (RPM)



miRNA abundance distributions (RPM)

