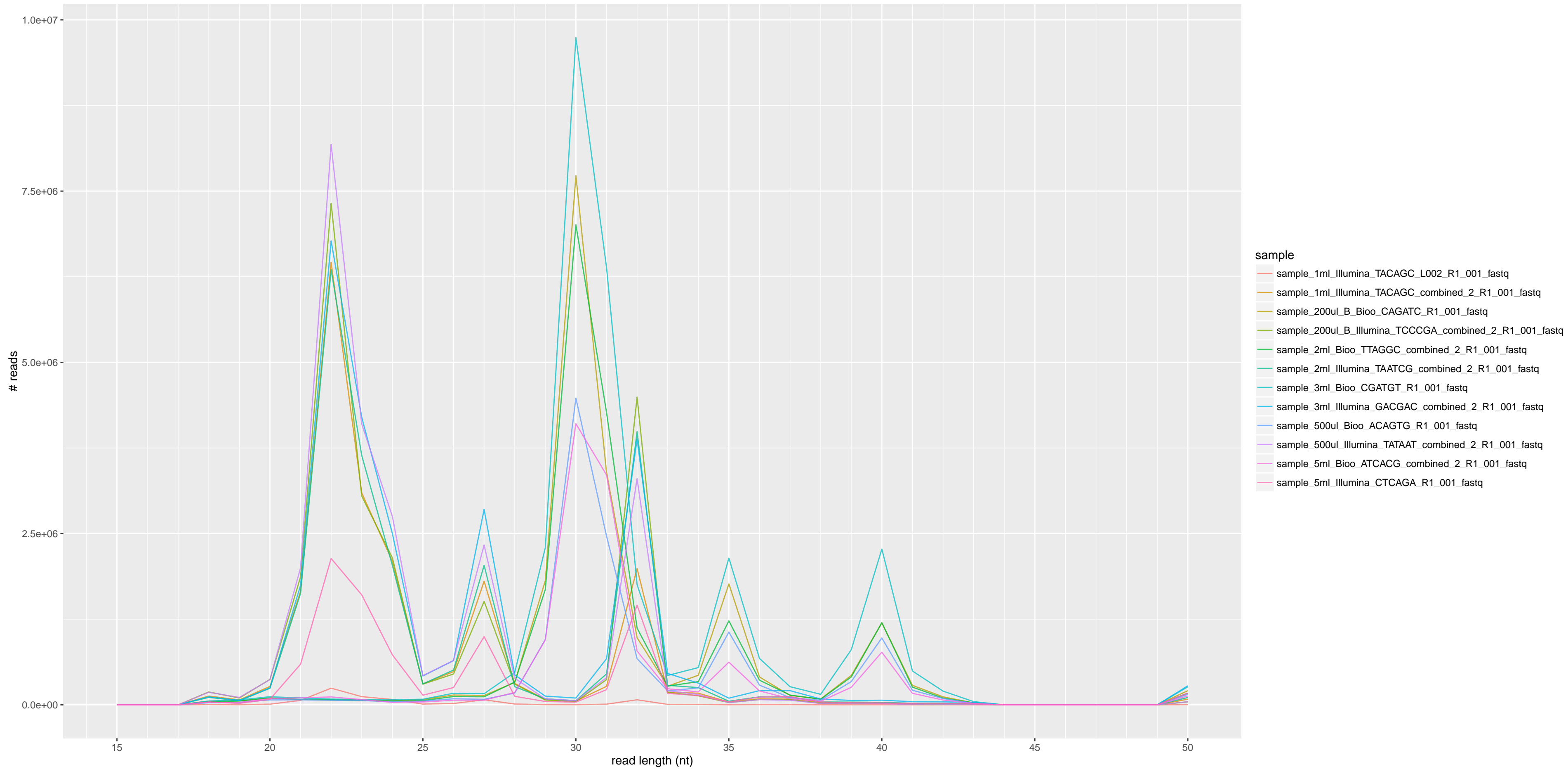
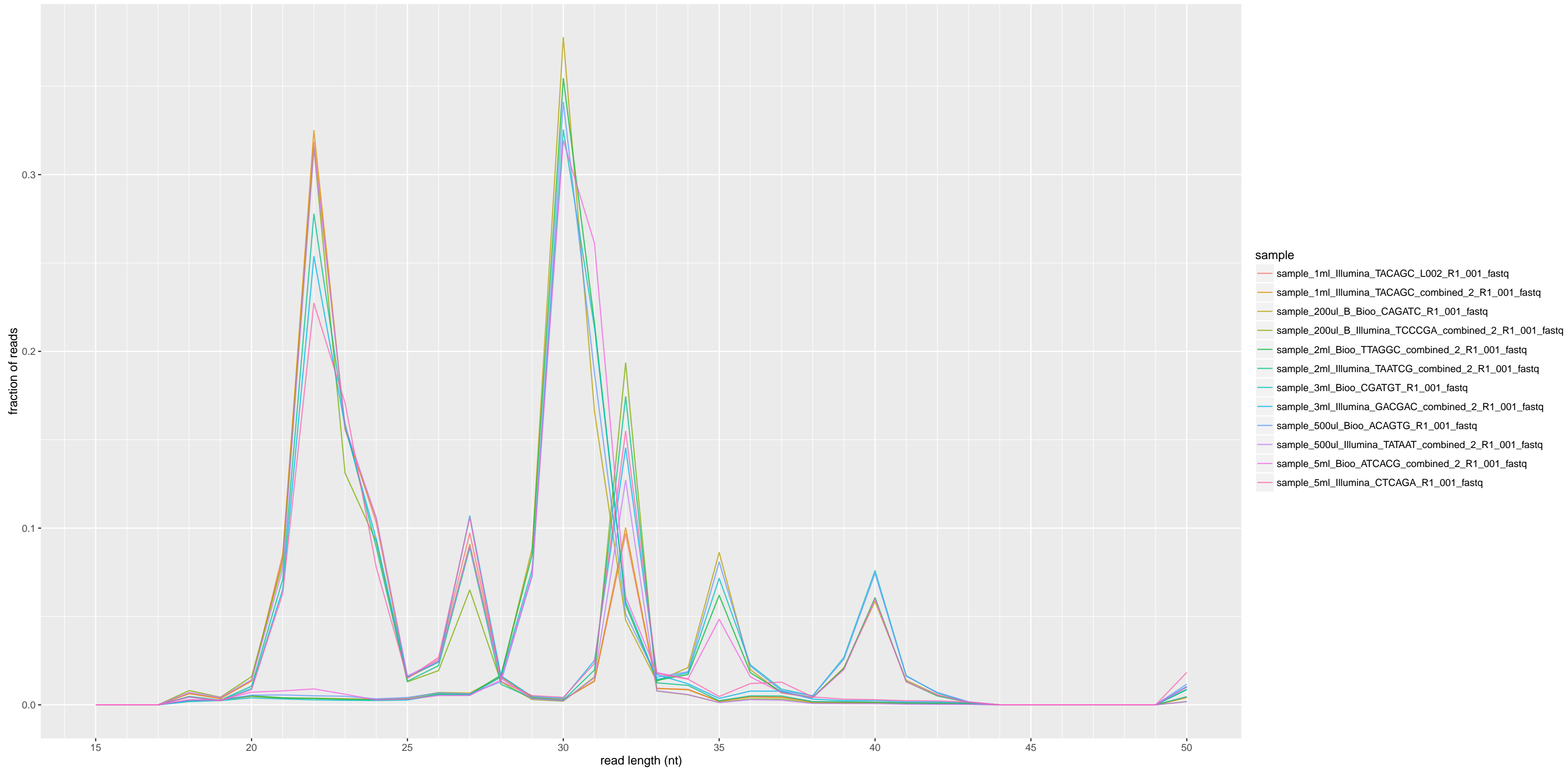


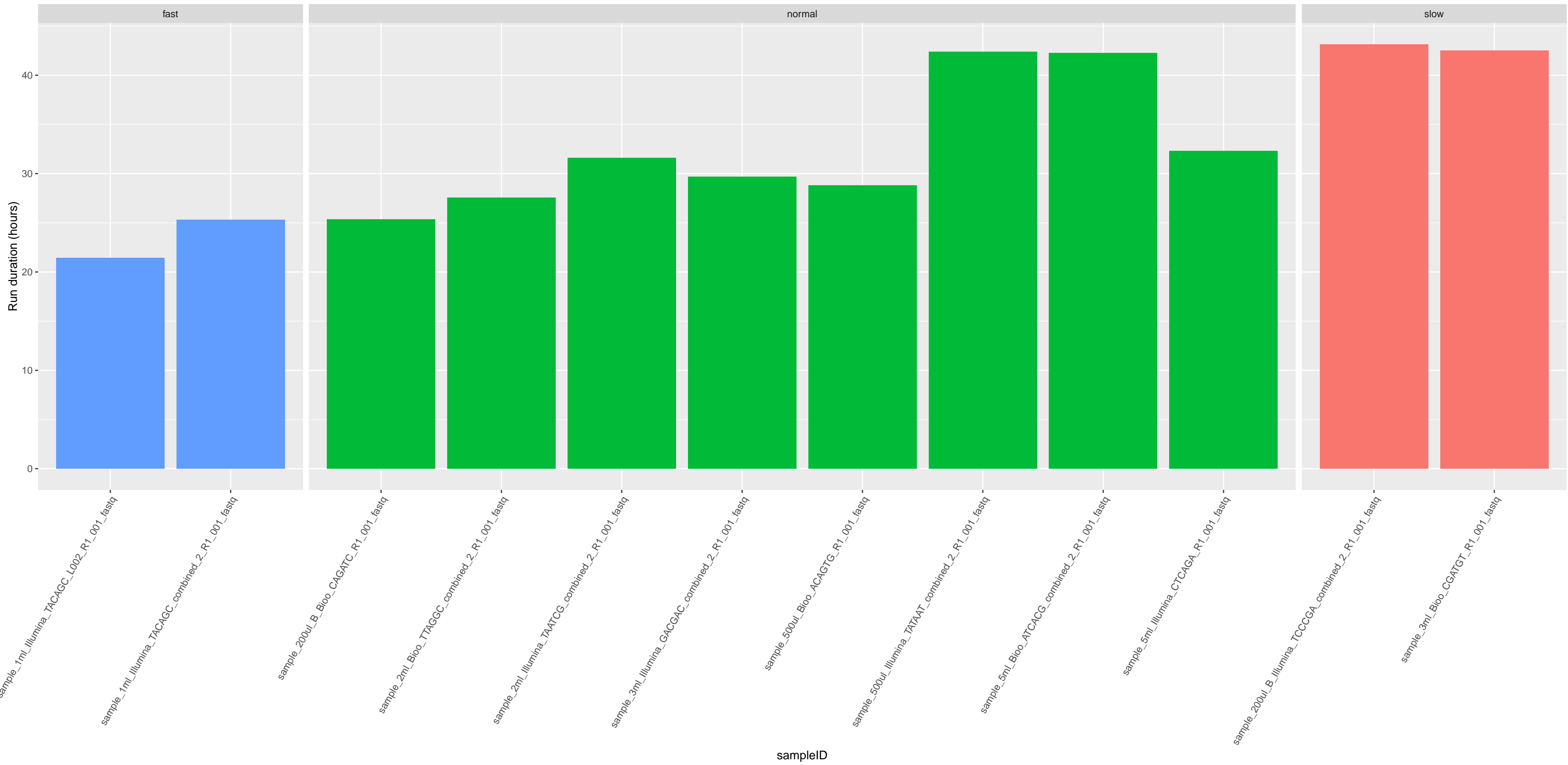
read-length distributions: raw read count



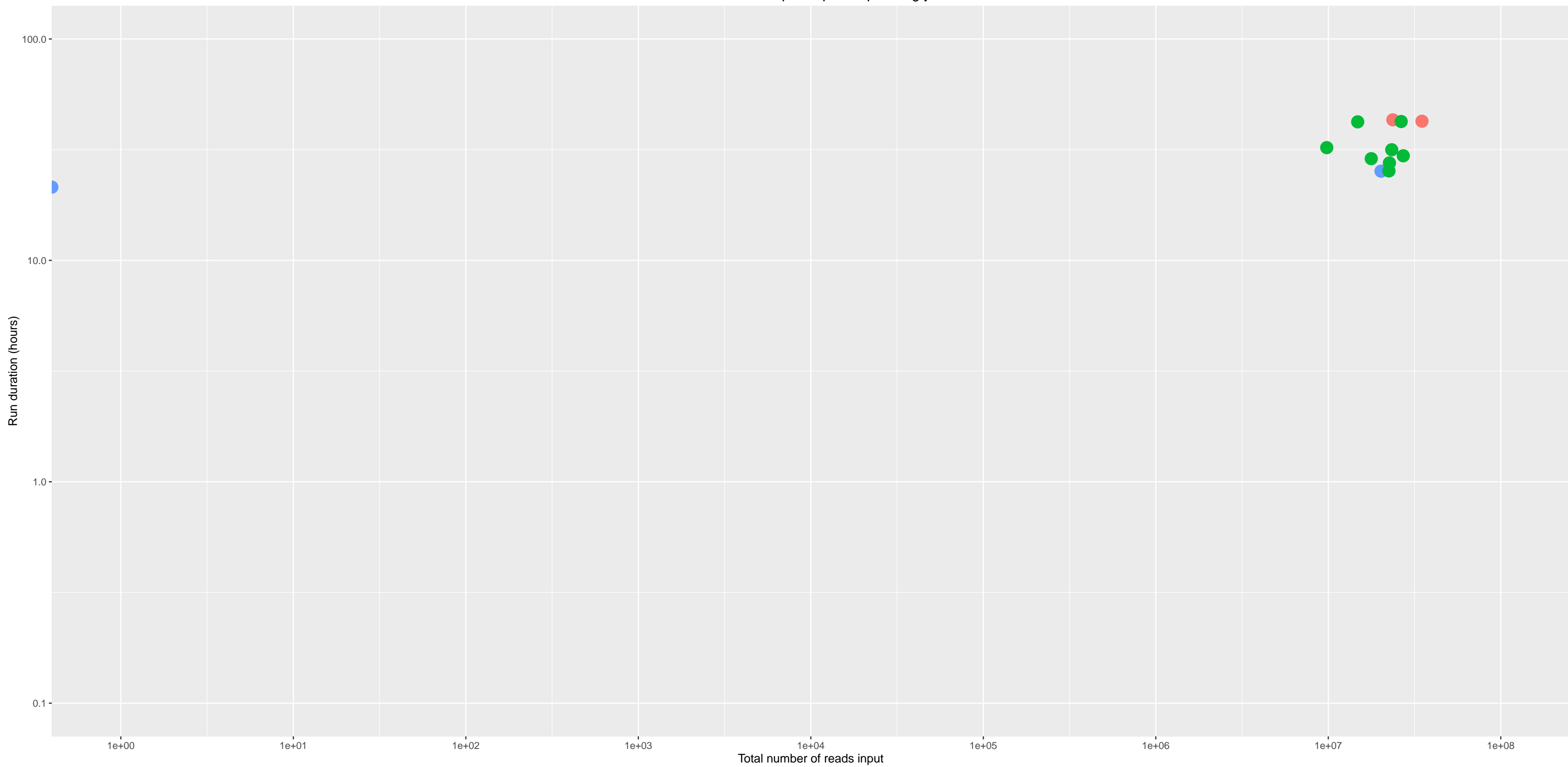
read-length distributions: normalised read fraction



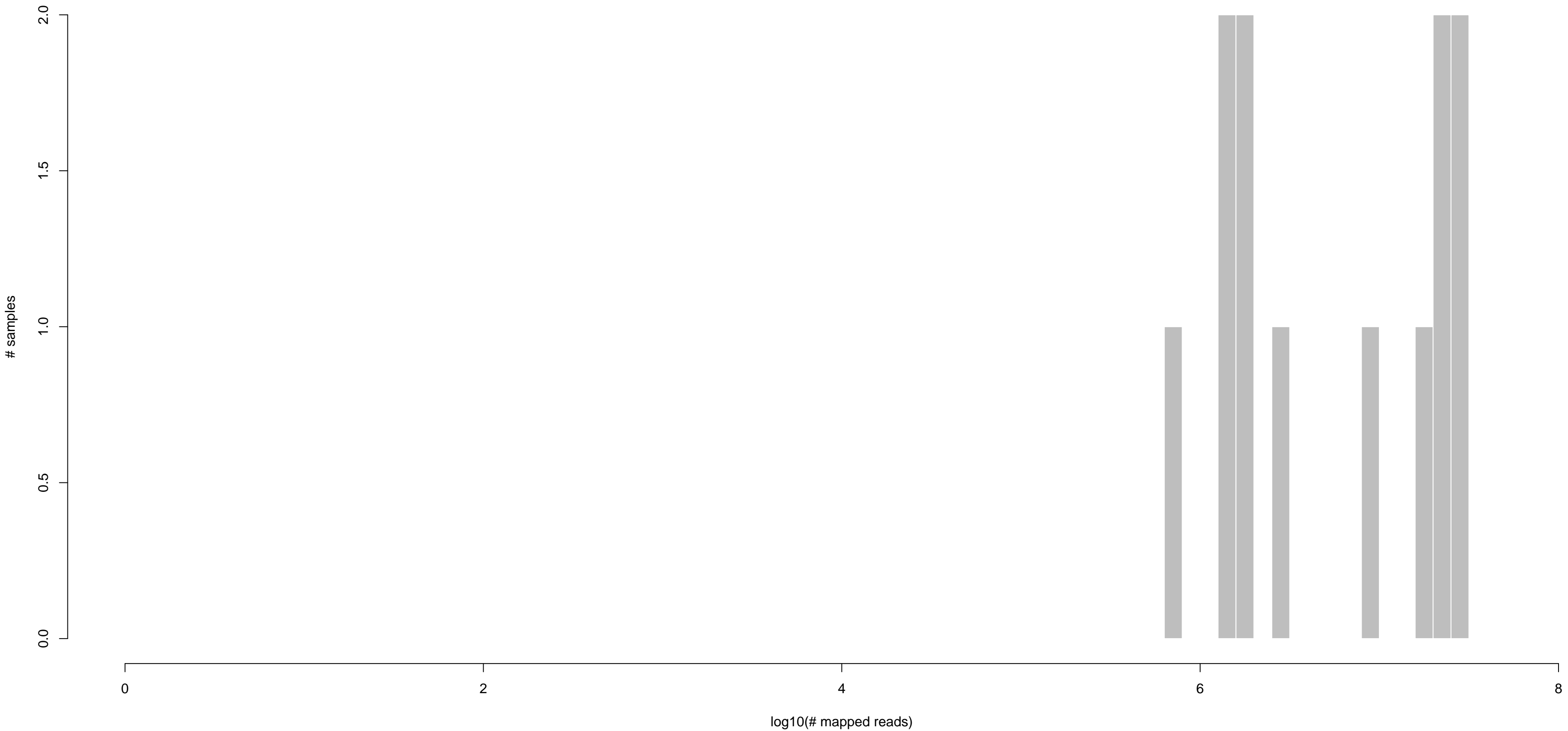
Duration of exceRpt run for each sample

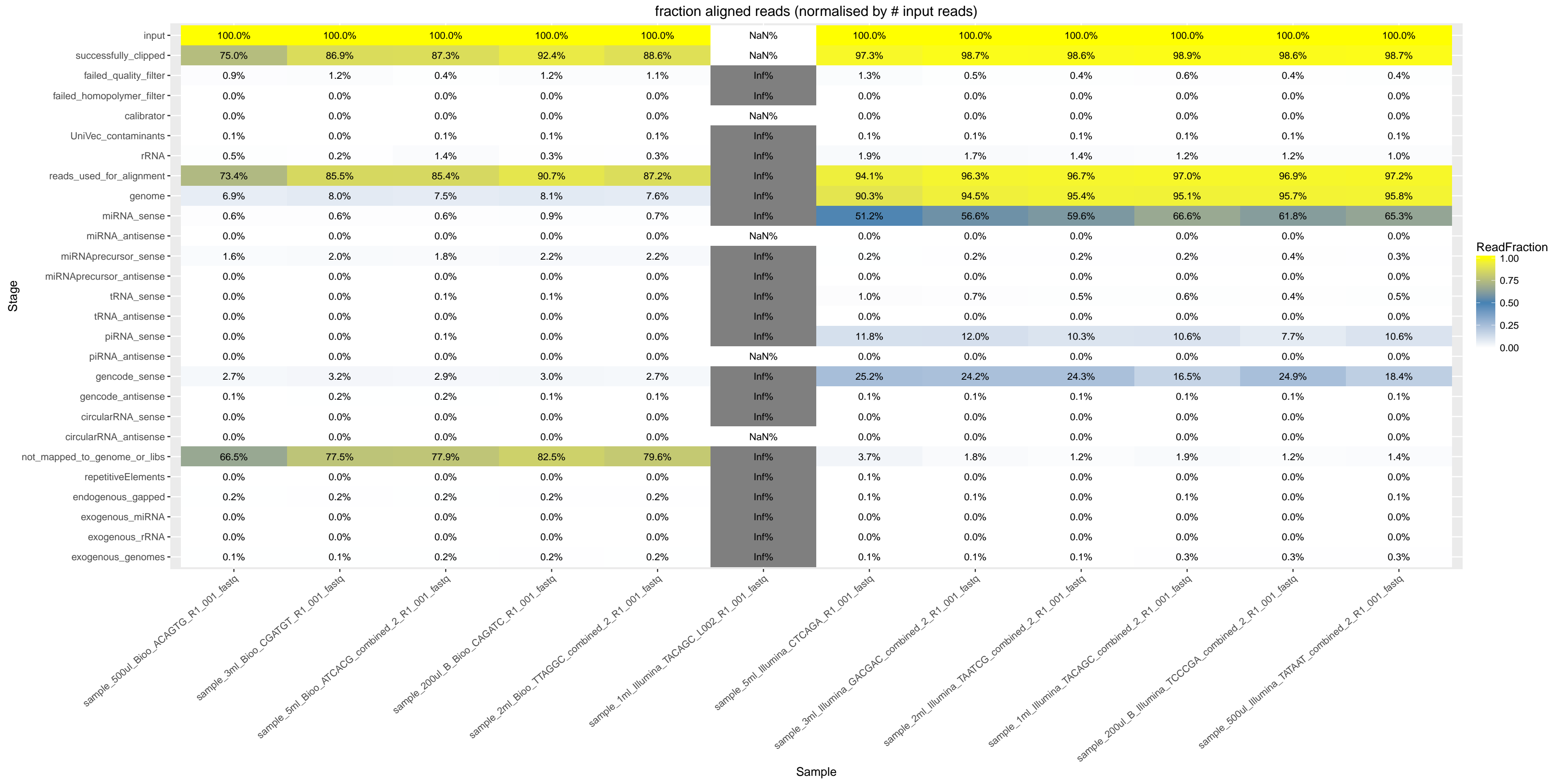


Duration of exceRpt run per sequencing yield

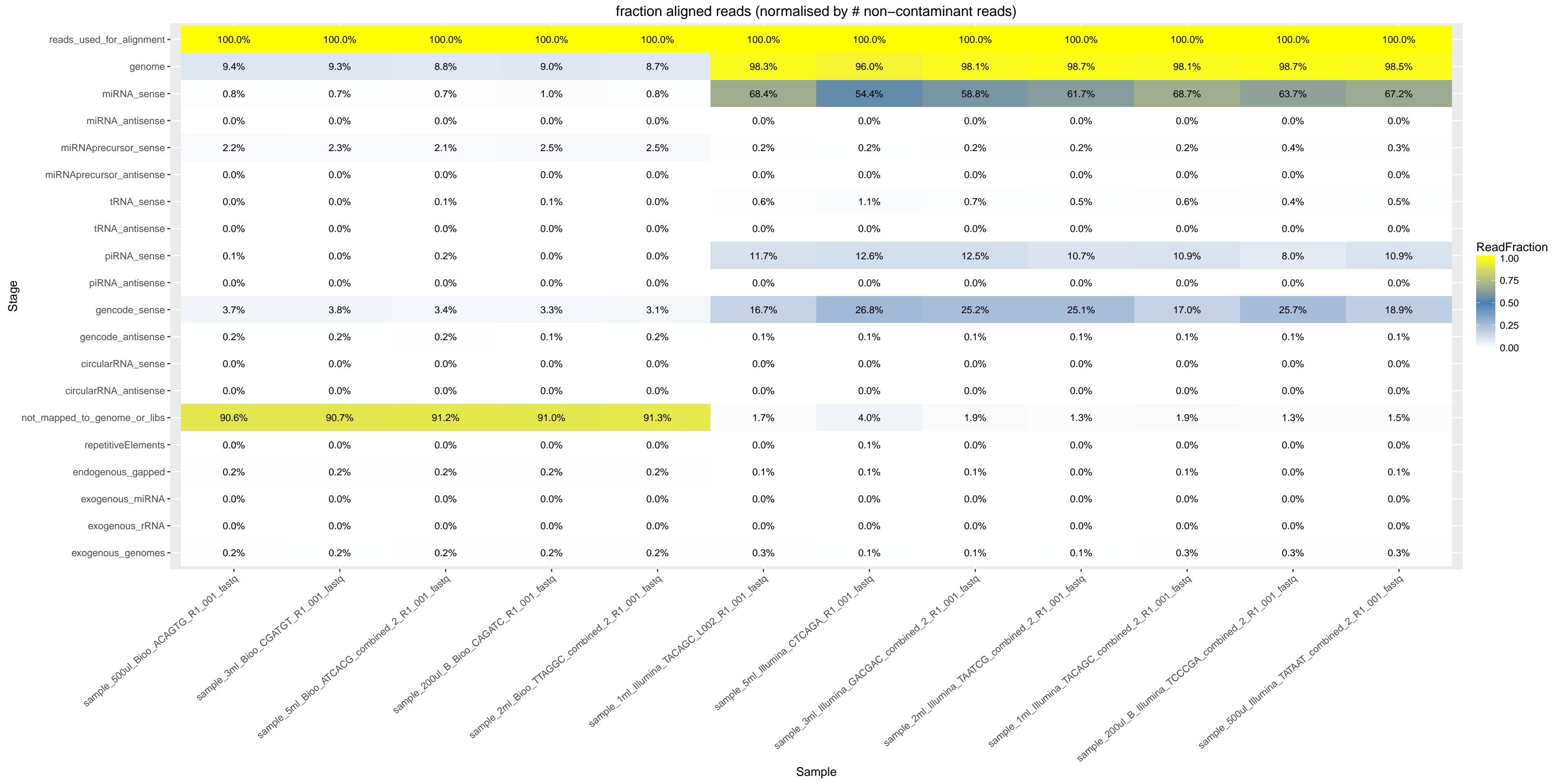


Library size (all mapped reads)

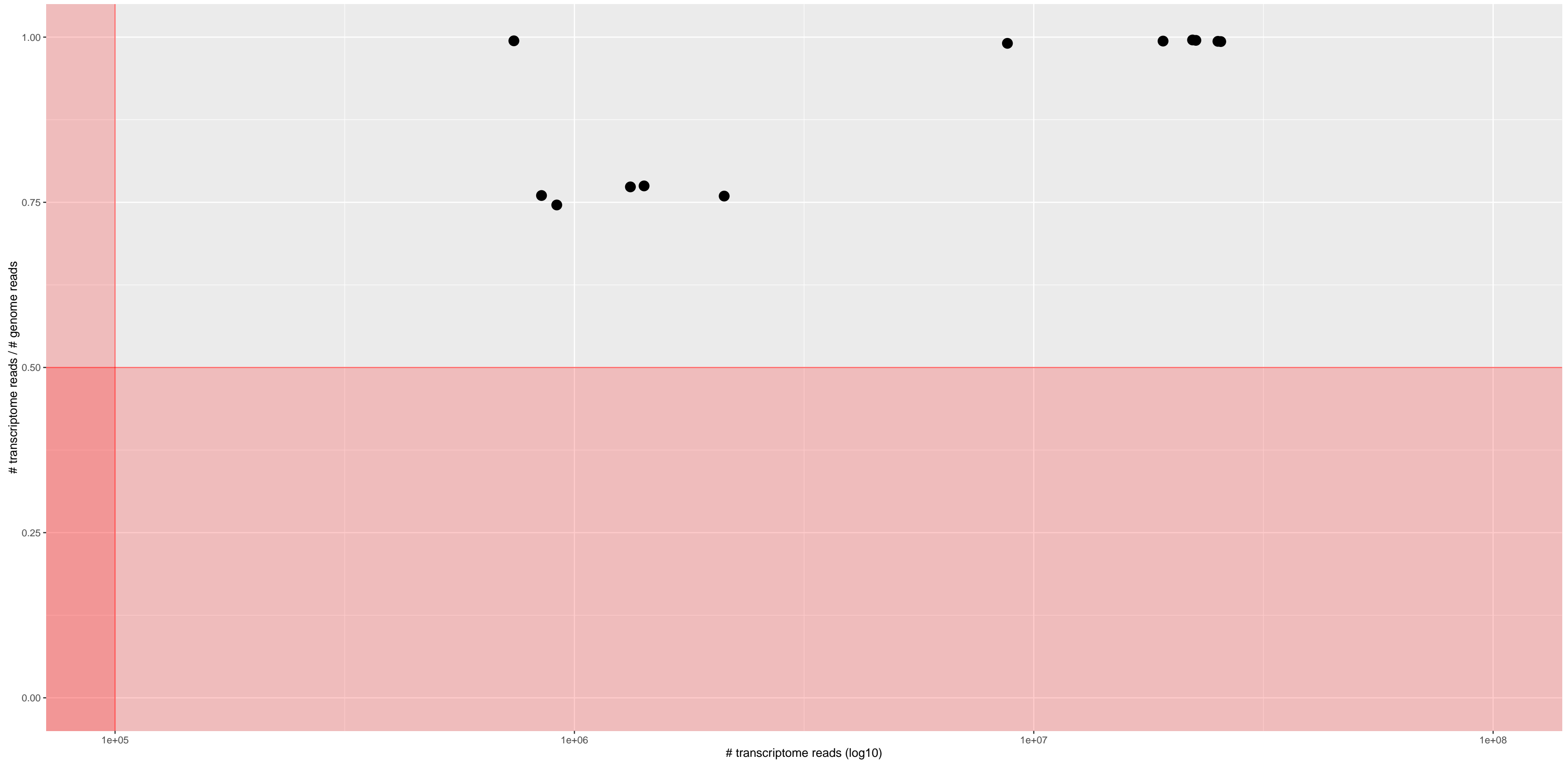








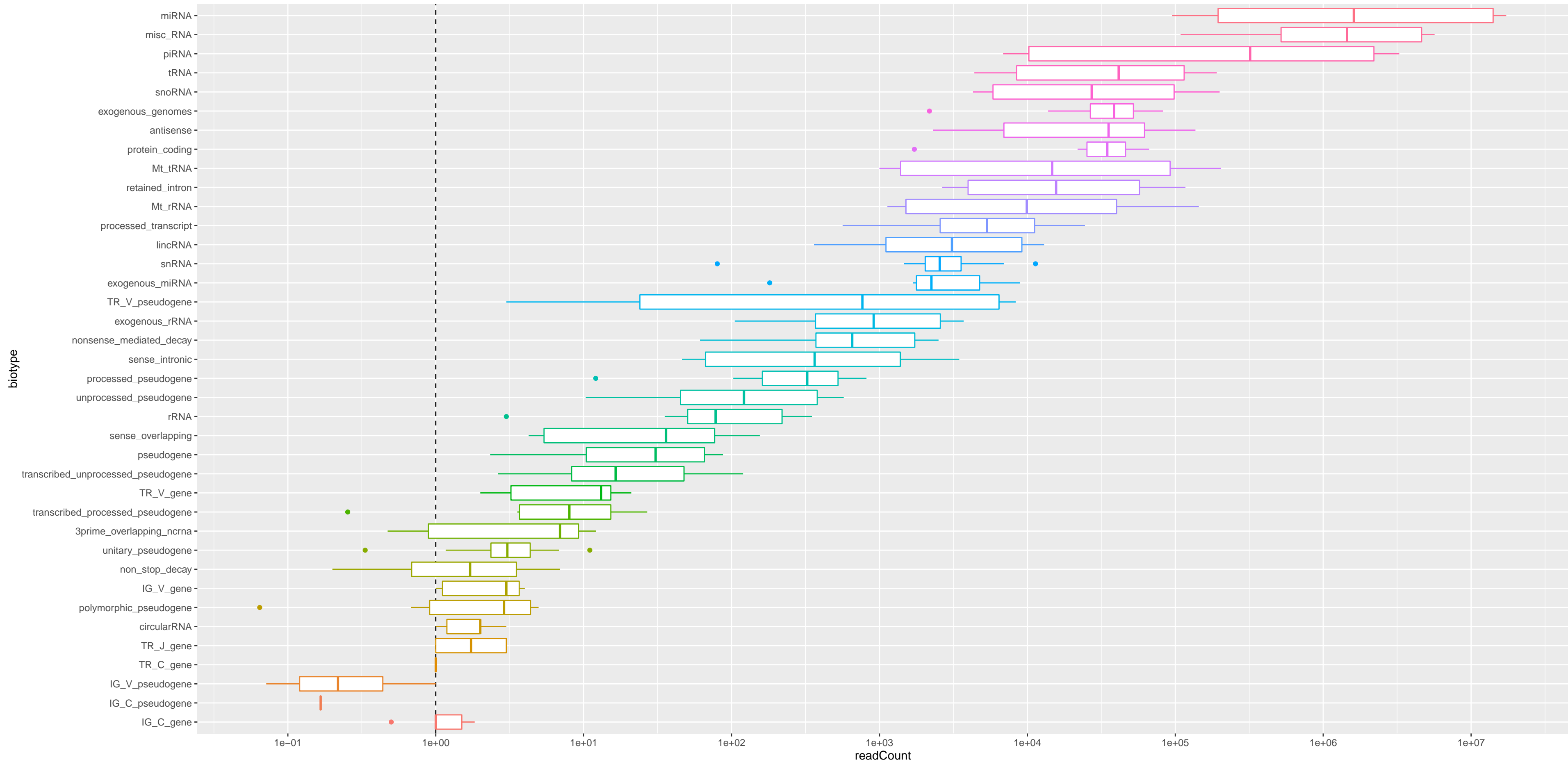
QC result: overall



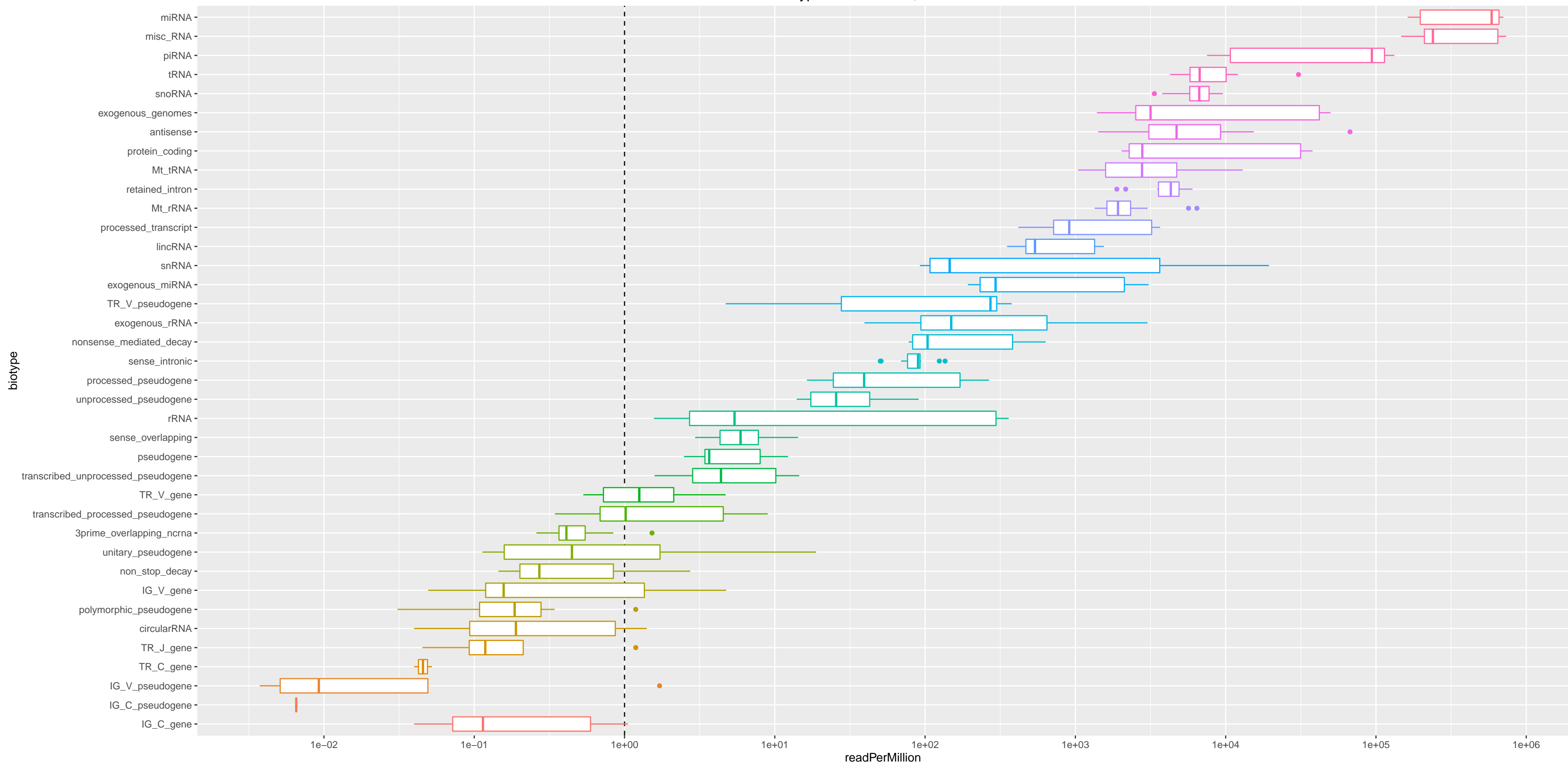
QC result: per-sample results

sample_500ul_Illumina_TATAAT_combined_2_R1_001_fastq	26453715	25329803	25169378	0.99	0.005
sample_200ul_B_Illumina_TCCCGA_combined_2_R1_001_fastq	23670707	22645125	22535422	1	0.005
sample_1ml_Illumina_TACAGC_combined_2_R1_001_fastq	20215352	19233229	19118879	0.99	0.007
sample_2ml_Illumina_TAATCG_combined_2_R1_001_fastq	23321450	22258376	22163485	1	0.006
sample_3ml_Illumina_GACGAC_combined_2_R1_001_fastq	27204745	25700929	25529014	0.99	0.007
sample_5ml_Illumina CTCAGA_R1_001_fastq	9795441	8845828	8762956	0.99	0.013
sample_1ml_Illumina_TACAGC_L002_R1_001_fastq	12061	742376	738259	0.99	0.023
sample_2ml_Bioo_TTAGGC_combined_2_R1_001_fastq	22607435	1711974	1323994	0.77	0.184
sample_200ul_B_Bioo_CAGATC_R1_001_fastq	22463898	1829852	1417869	0.77	0.105
sample_5ml_Bioo_ATCACG_combined_2_R1_001_fastq	14802519	1115150	847868	0.76	0.106
sample_3ml_Bioo_CGATGT_R1_001_fastq	34924879	2789562	2118550	0.76	0.142
sample_500ul_Bioo_ACAGTG_R1_001_fastq	17741337	1226940	915301	0.75	0.131

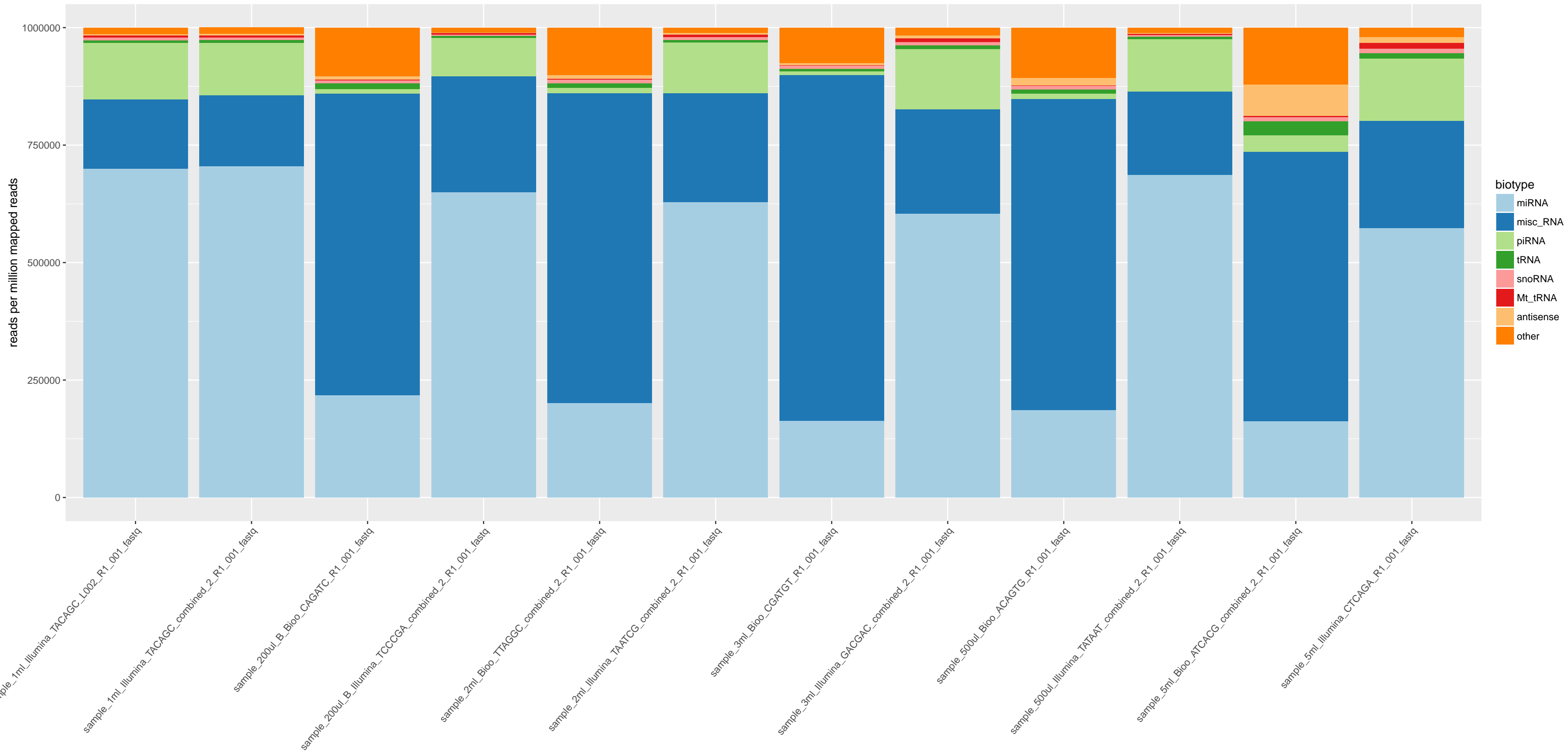
Biotypes: distributions, raw read-counts



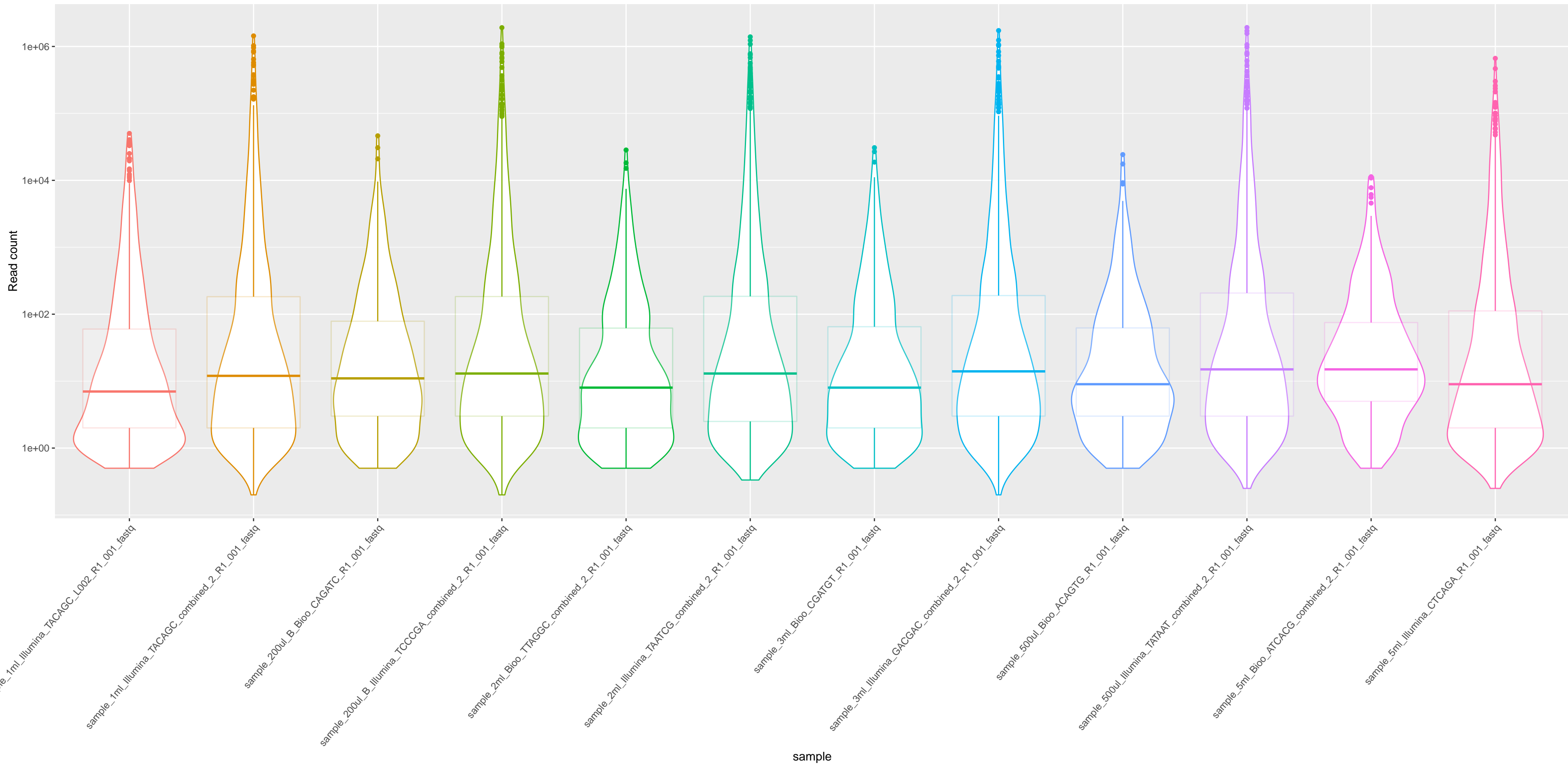
Biotypes: distributions, normalised



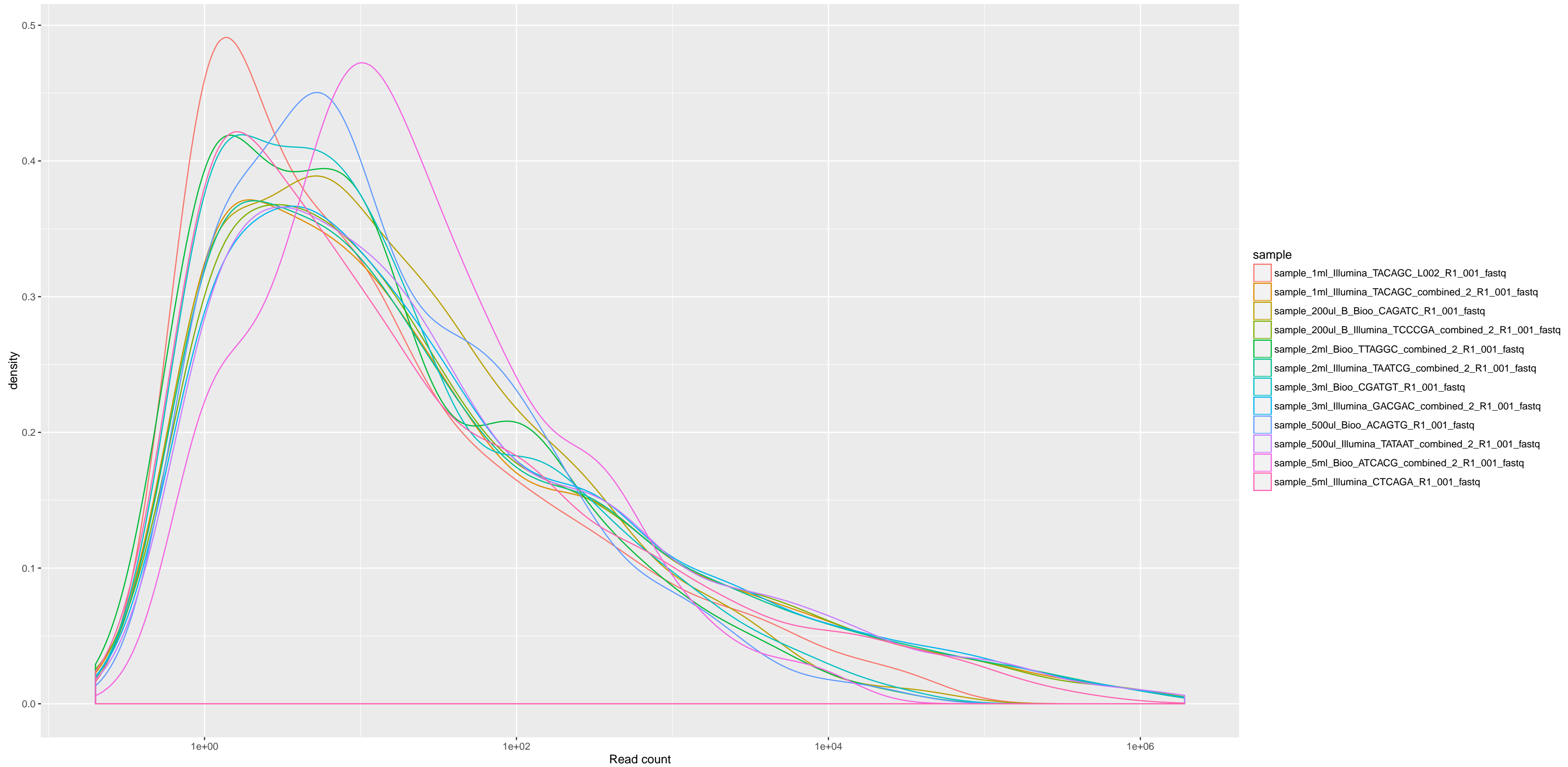
Biotypes: per-sample, normalised



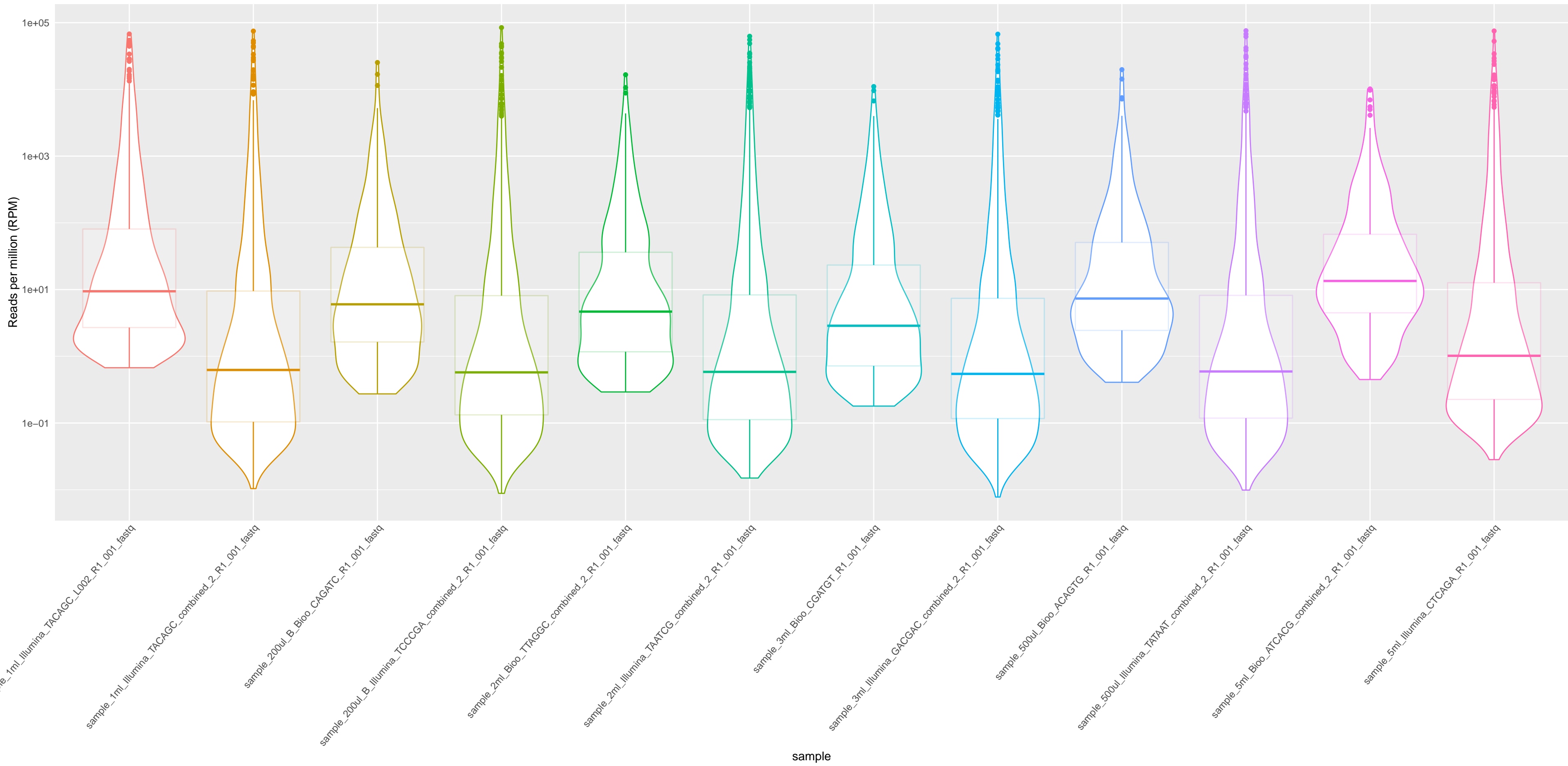
miRNA abundance distributions (raw counts)



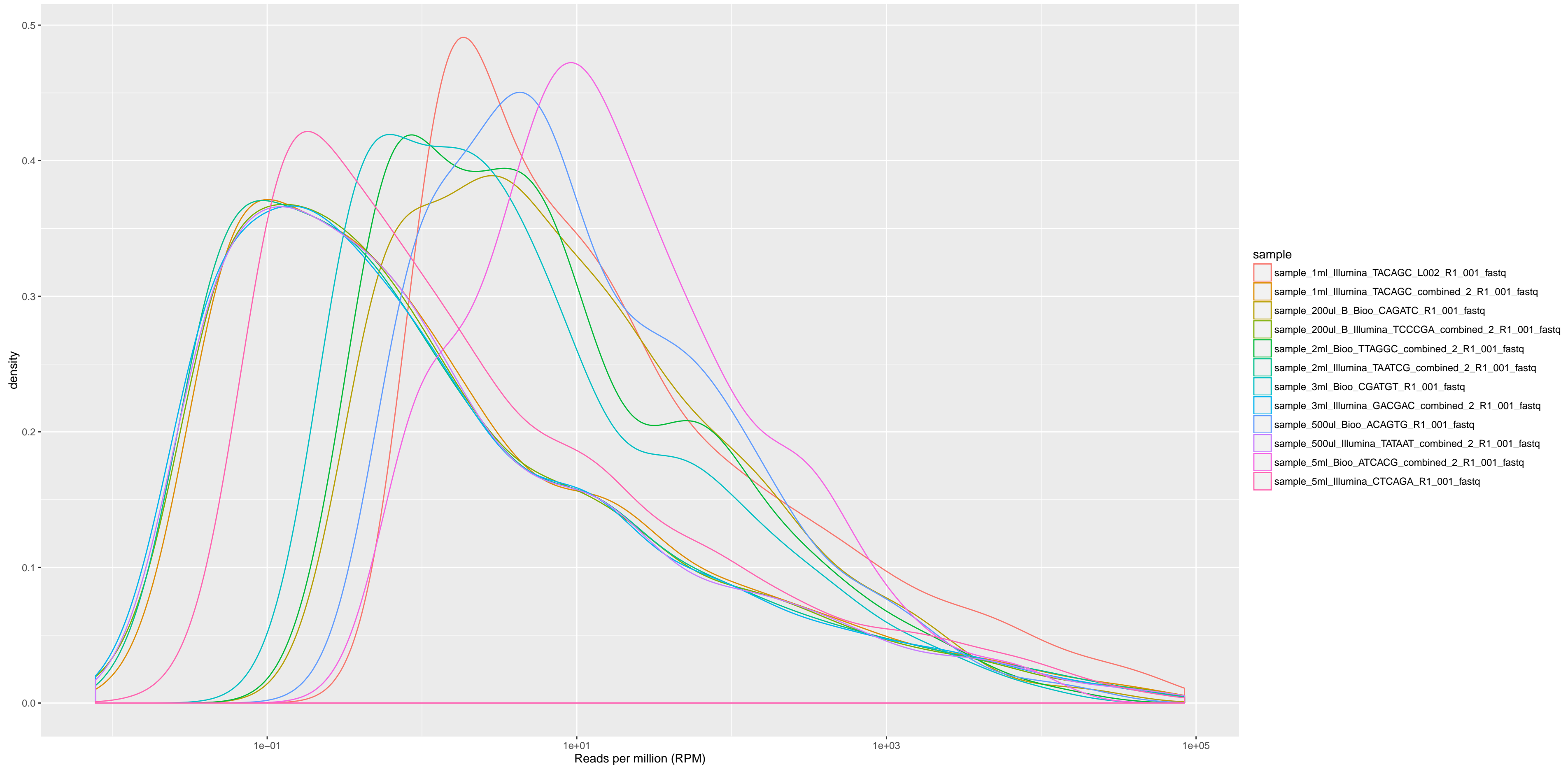
miRNA abundance distributions (raw counts)



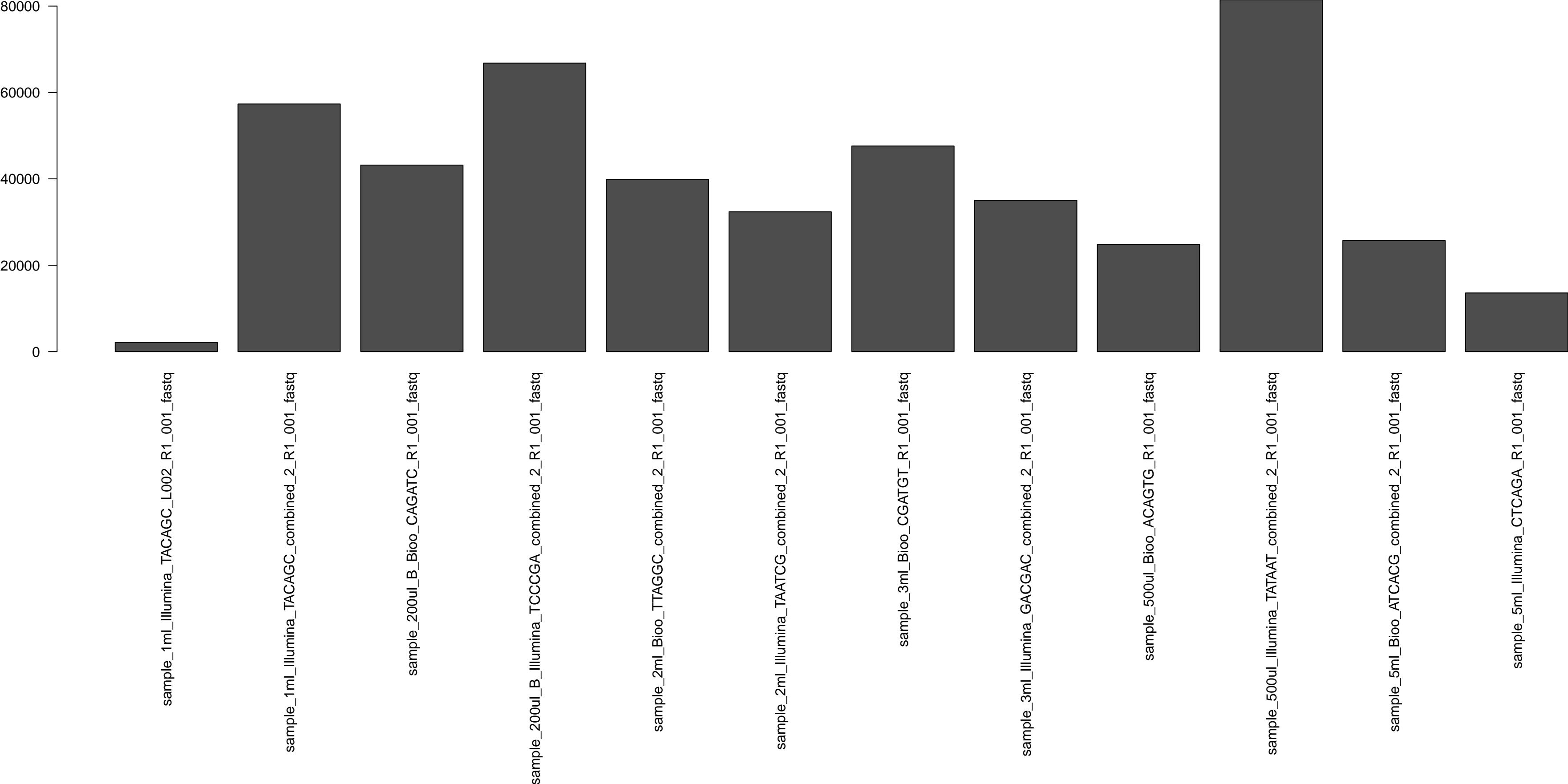
miRNA abundance distributions (RPM)

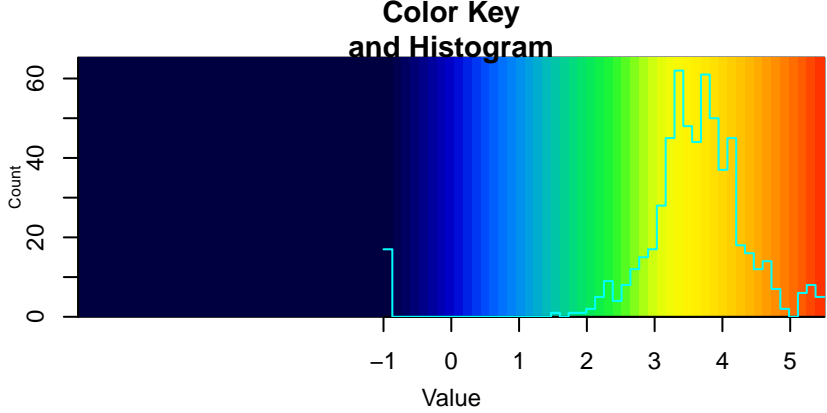


miRNA abundance distributions (RPM)

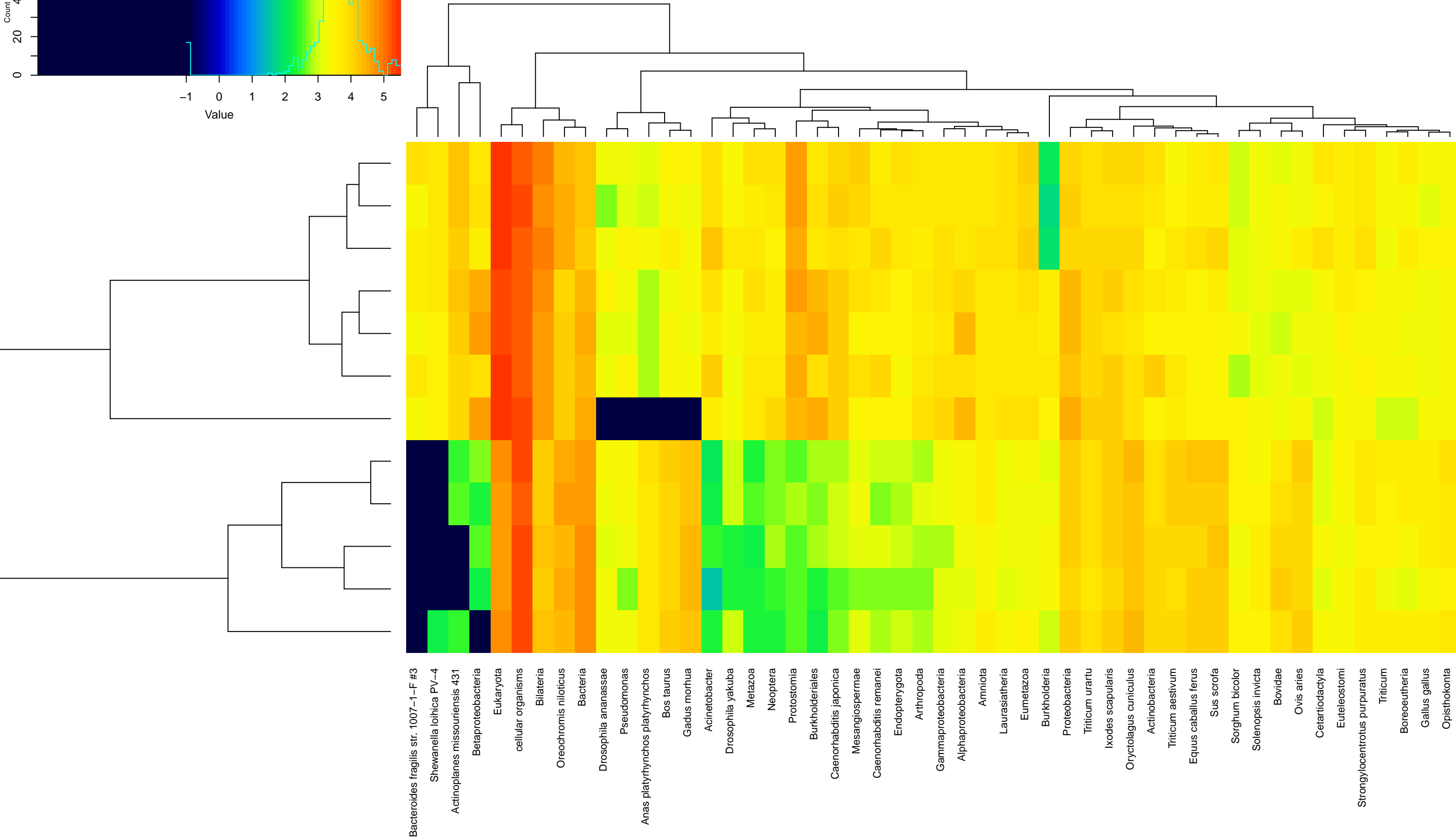


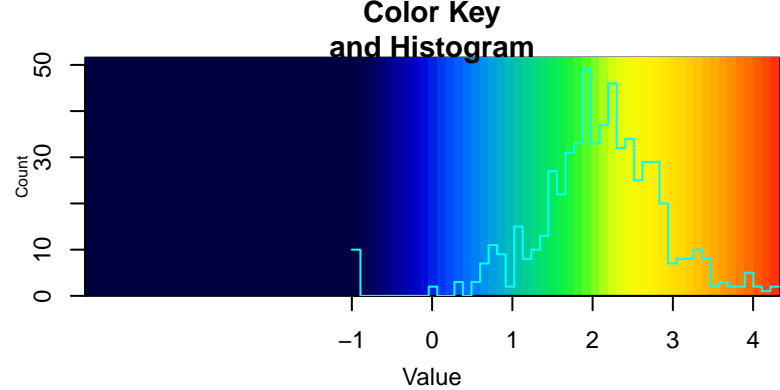
Total # reads mapped to NCBI taxonomy



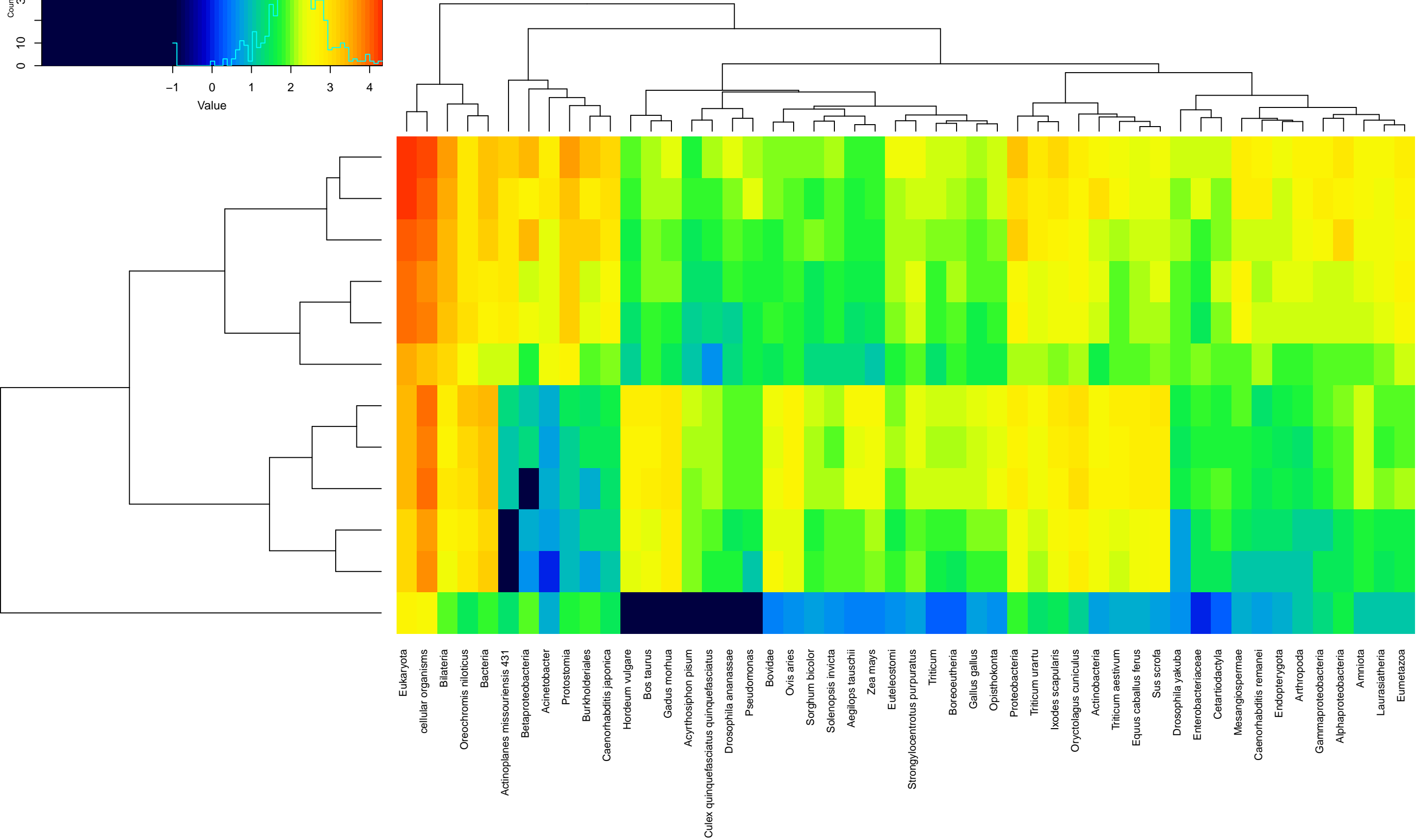


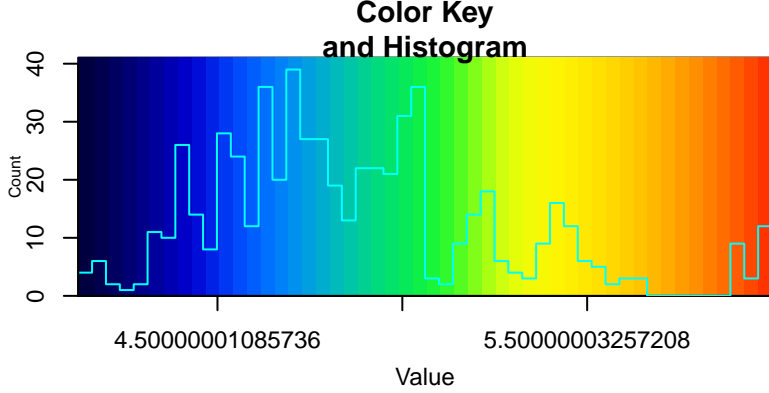
top taxa nodes: specific normalised read count



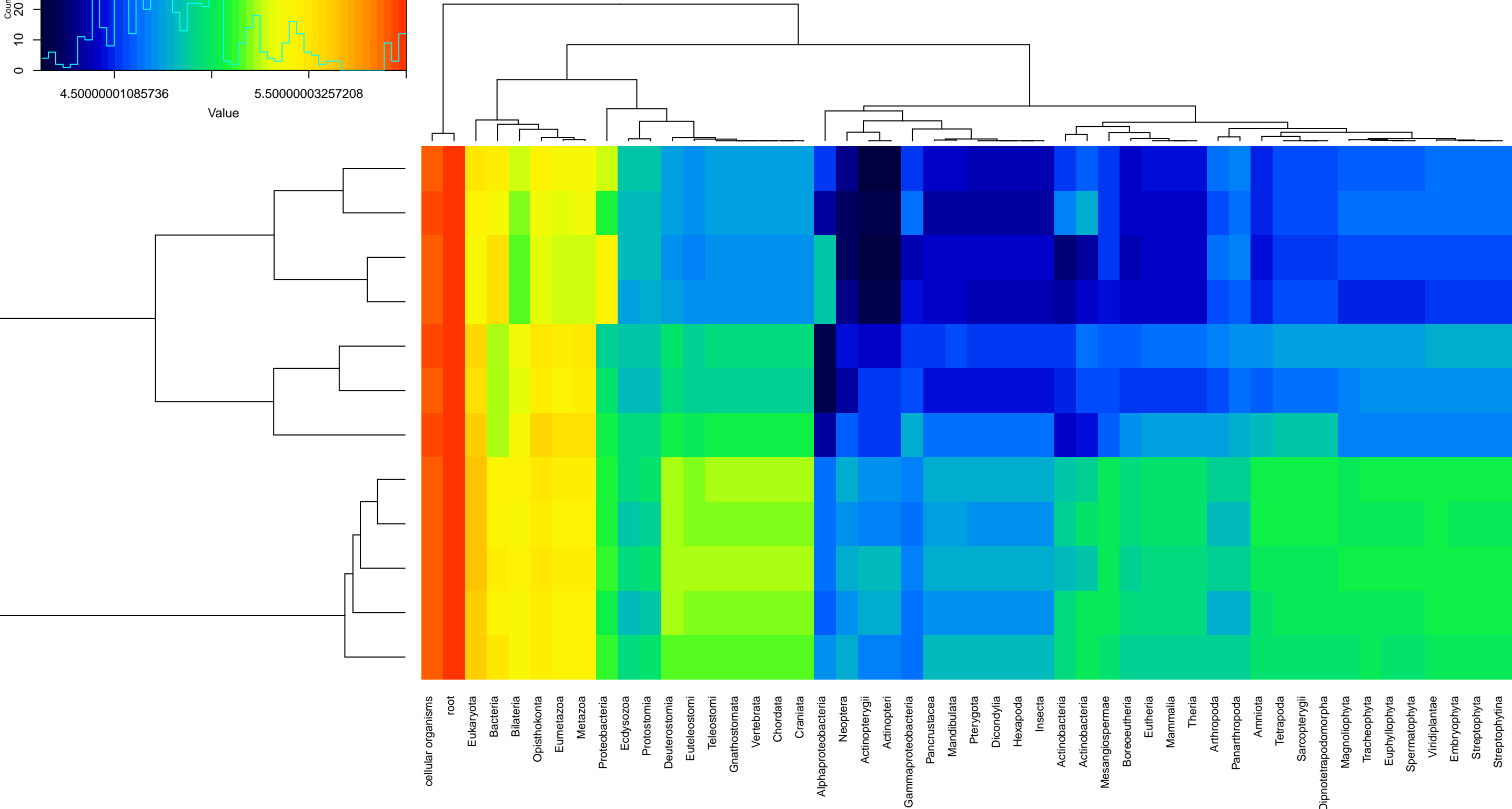


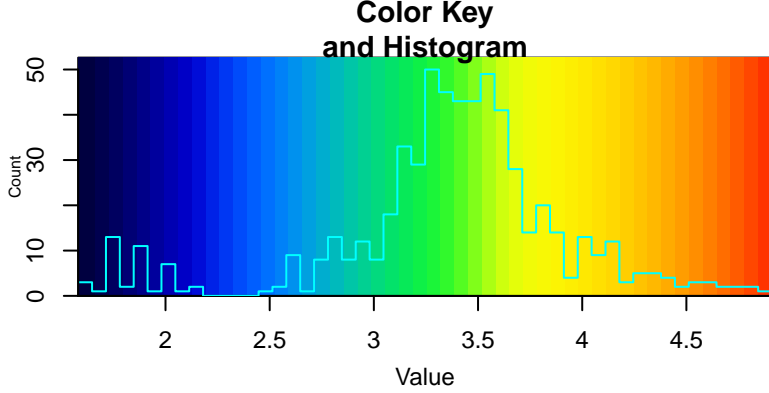
top taxa nodes: specific absolute read count





top taxa nodes: cumulative normalised read count





top taxa nodes: cumulative absolute read count

