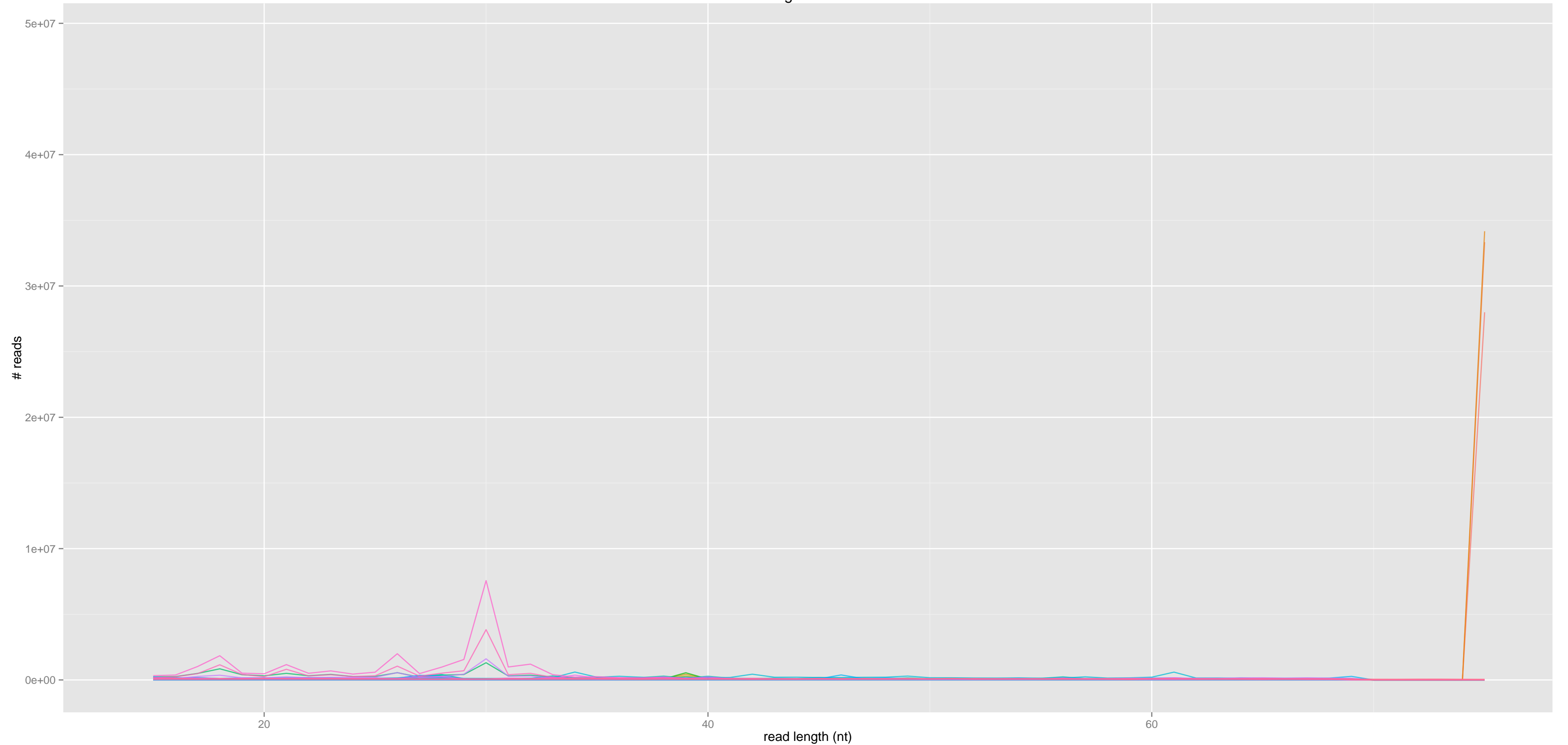
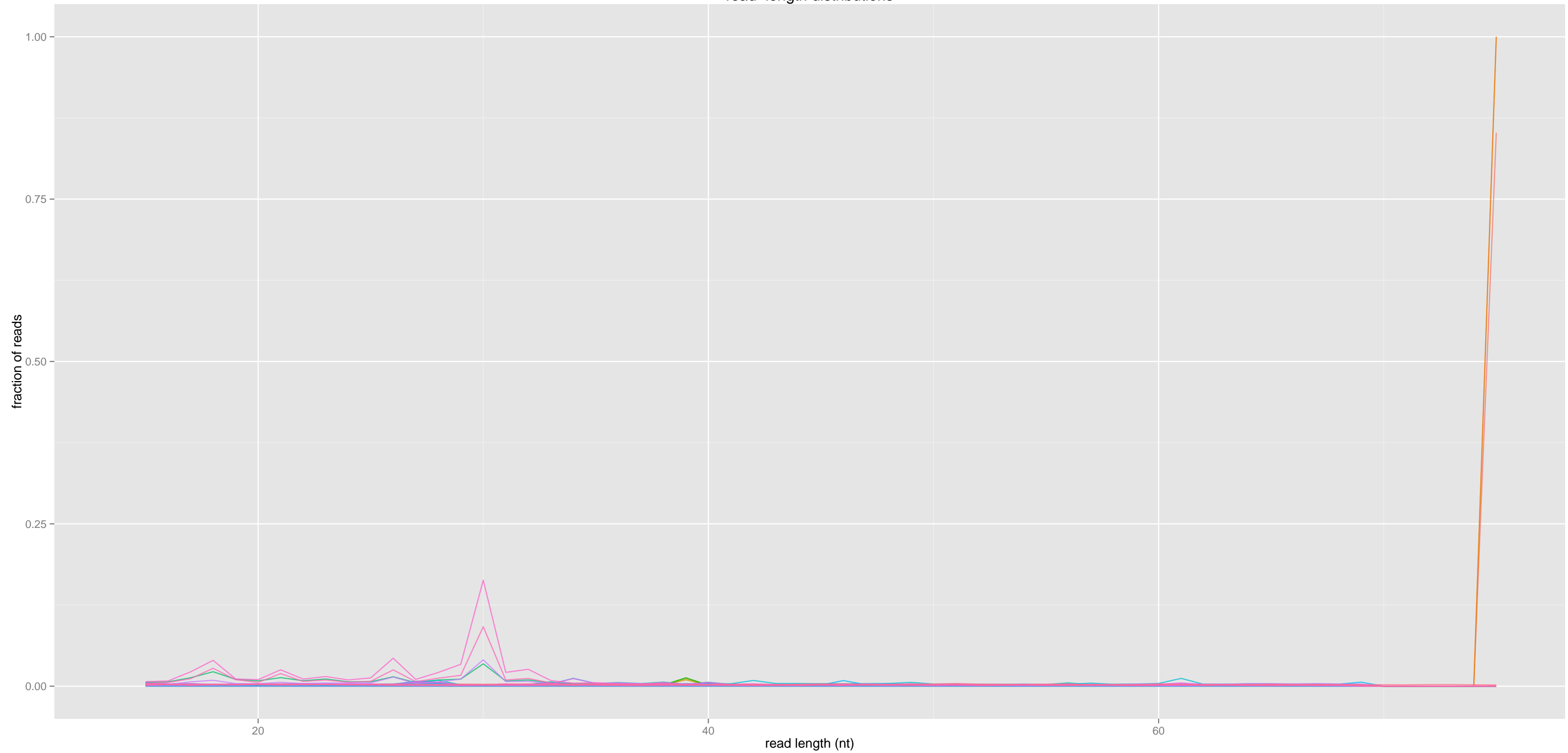
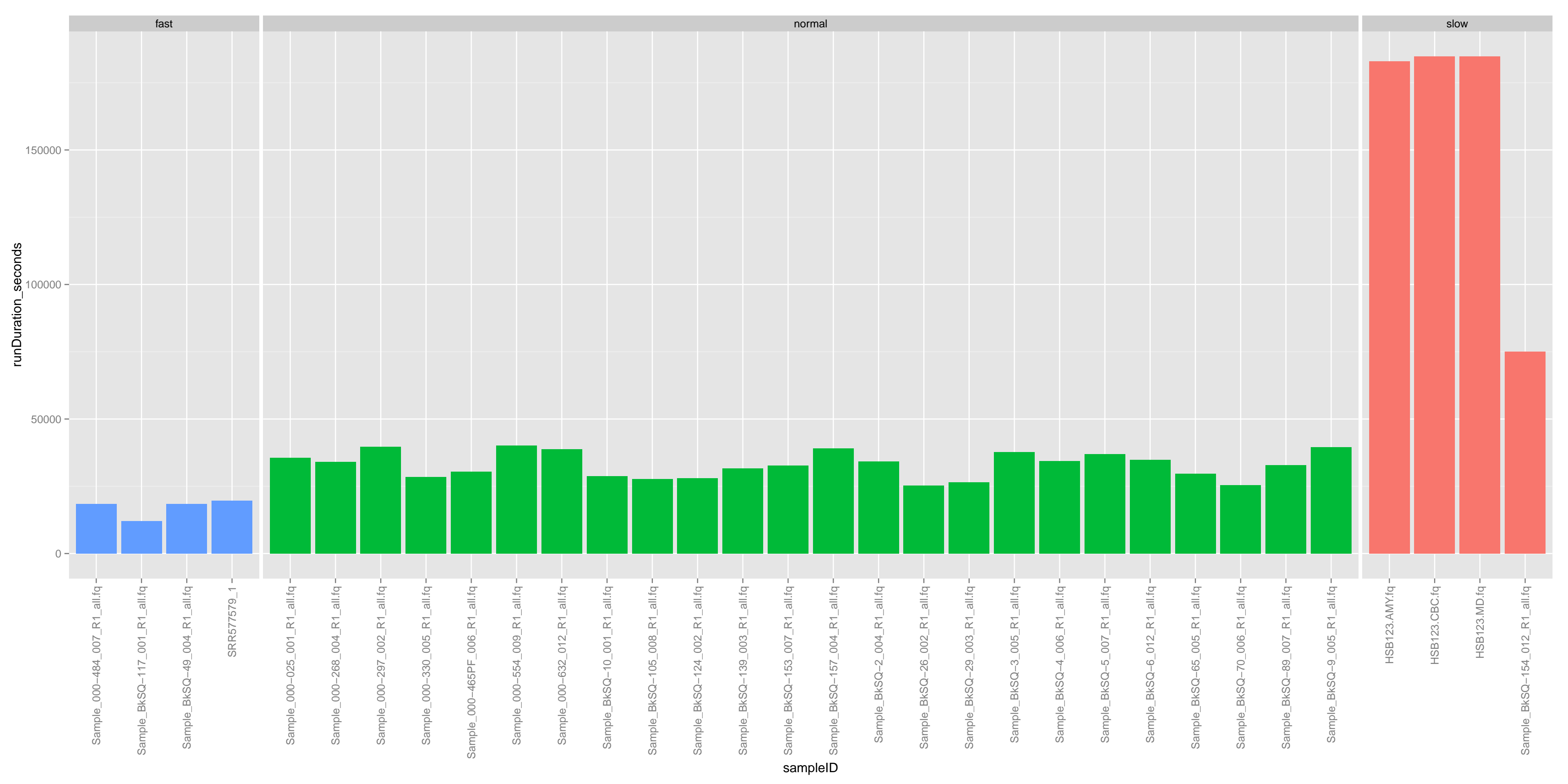


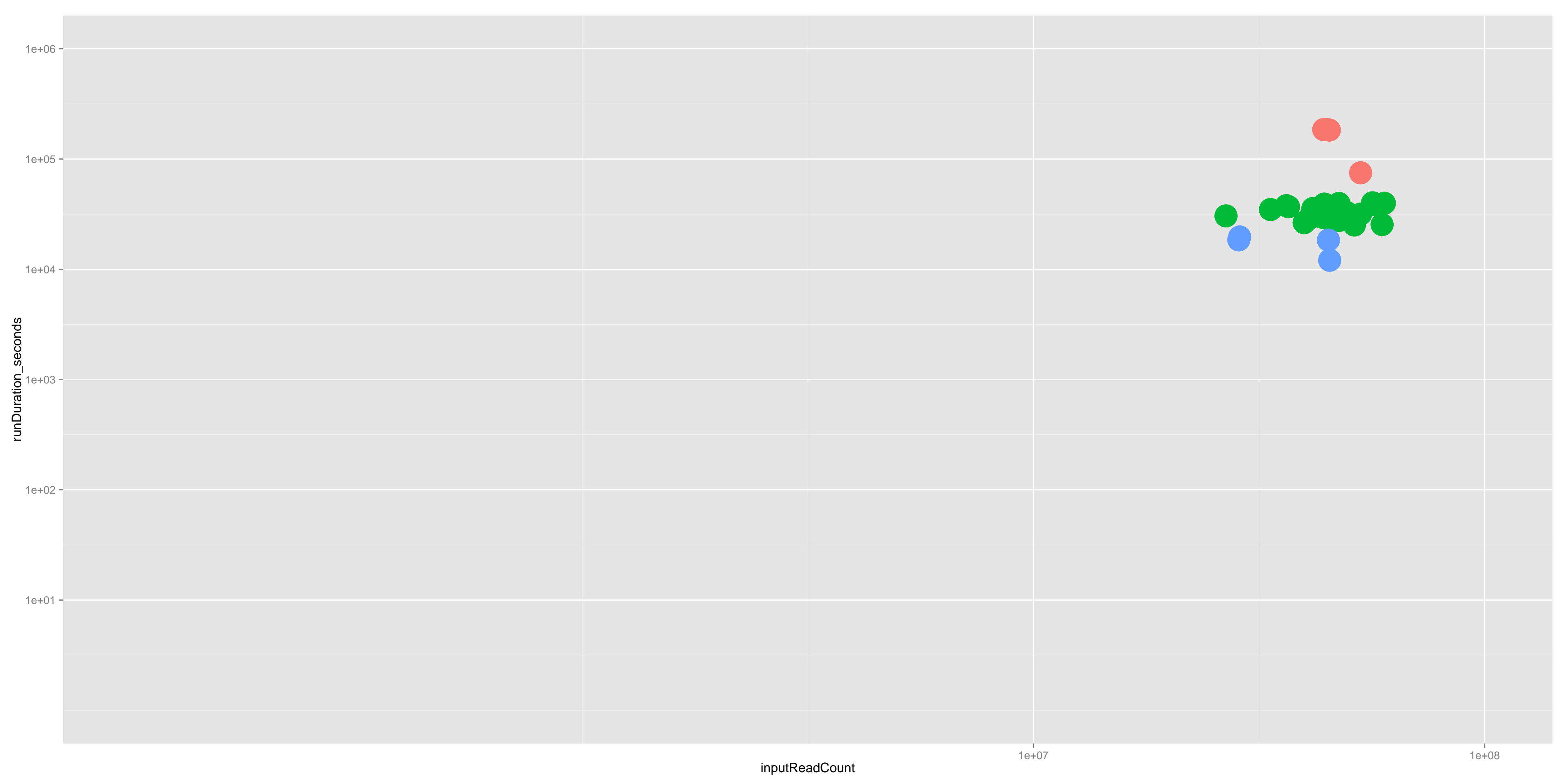
read-length distributions



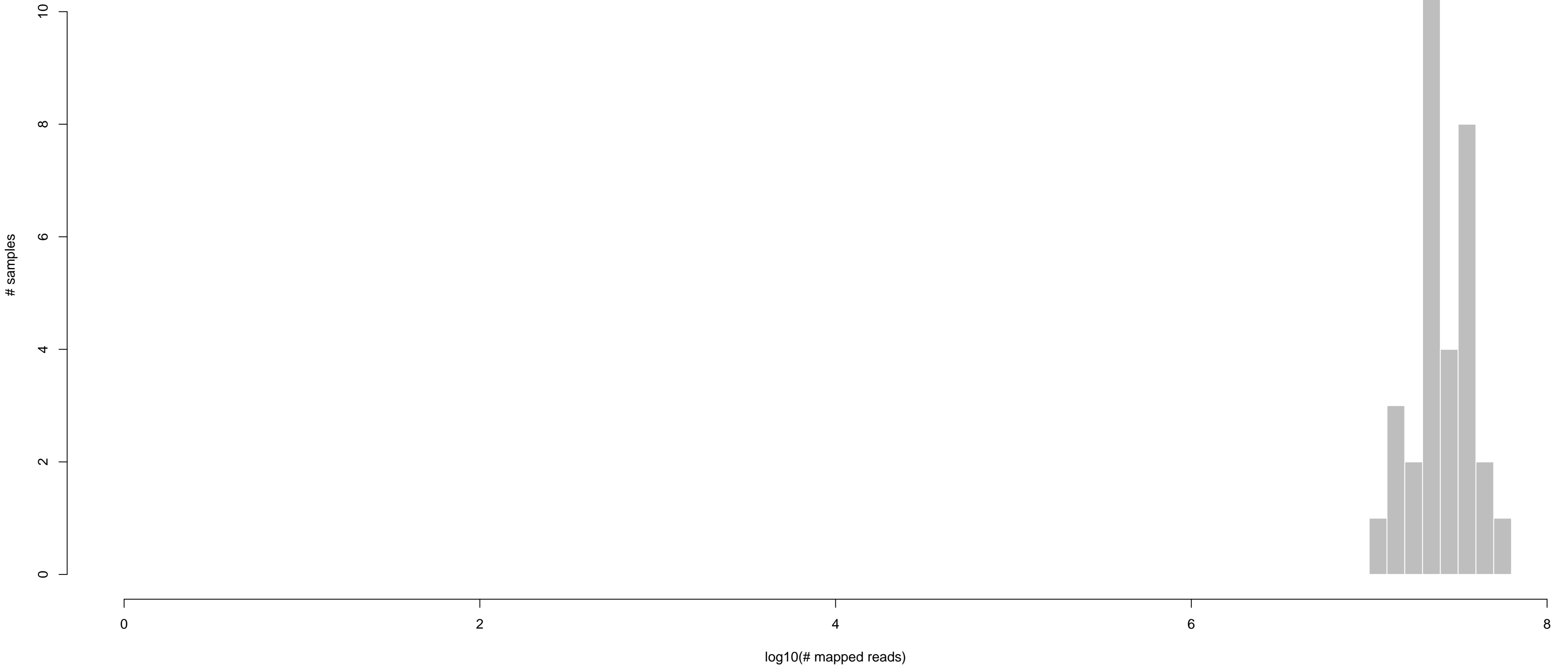
read-length distributions



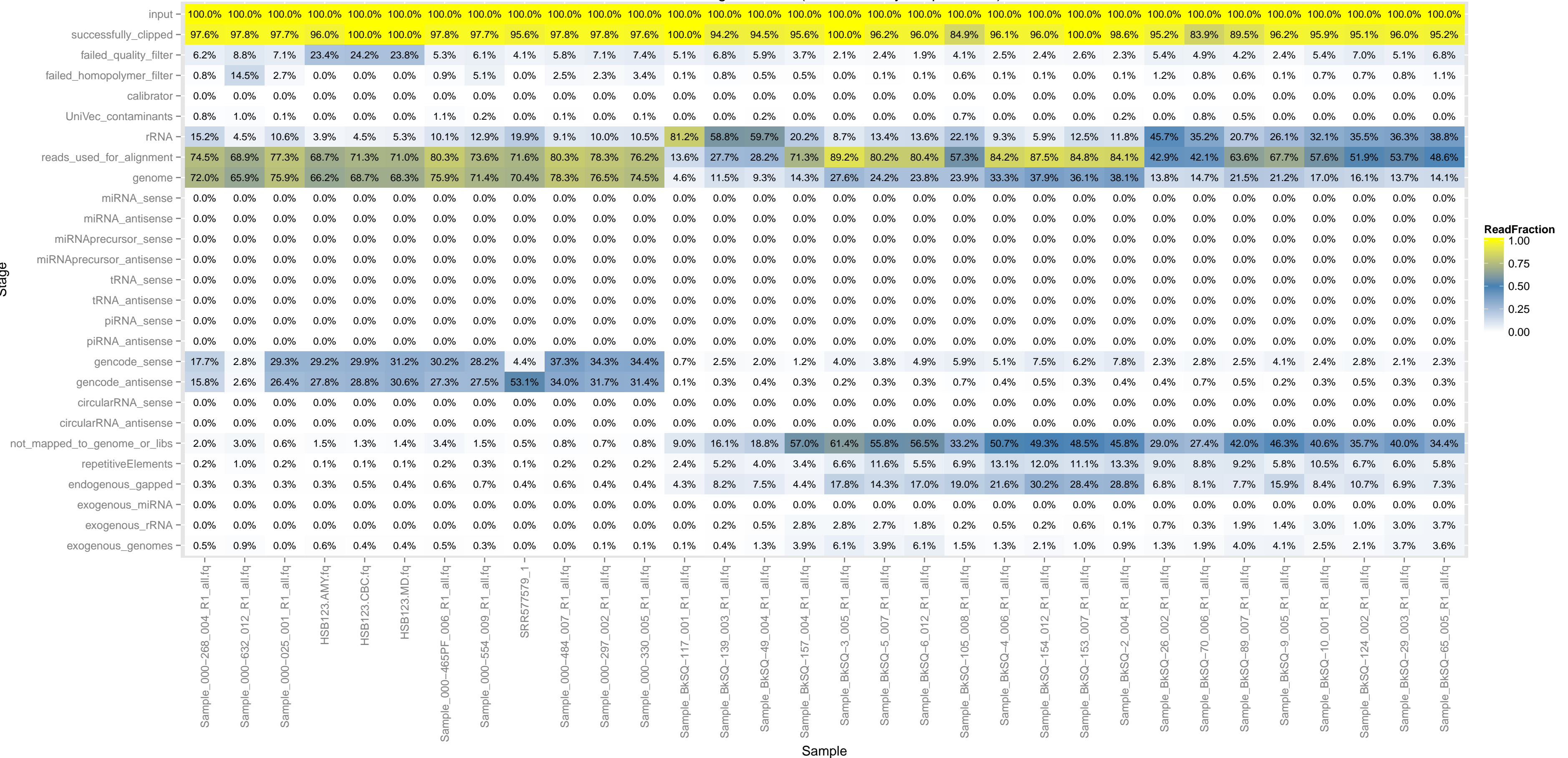




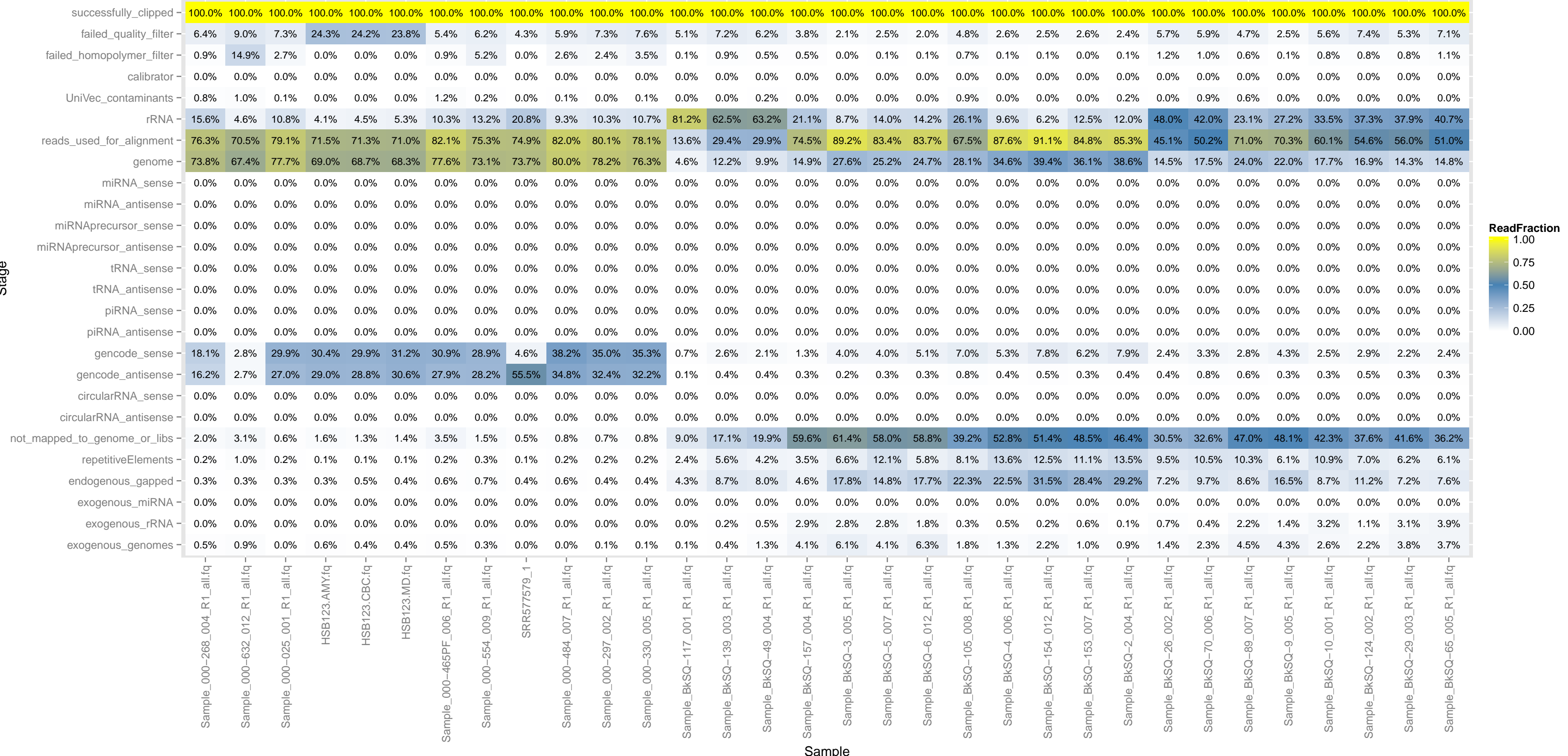
Library size (all mapped reads)



fraction aligned reads (normalised by # input reads)

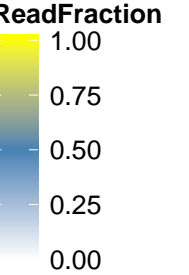


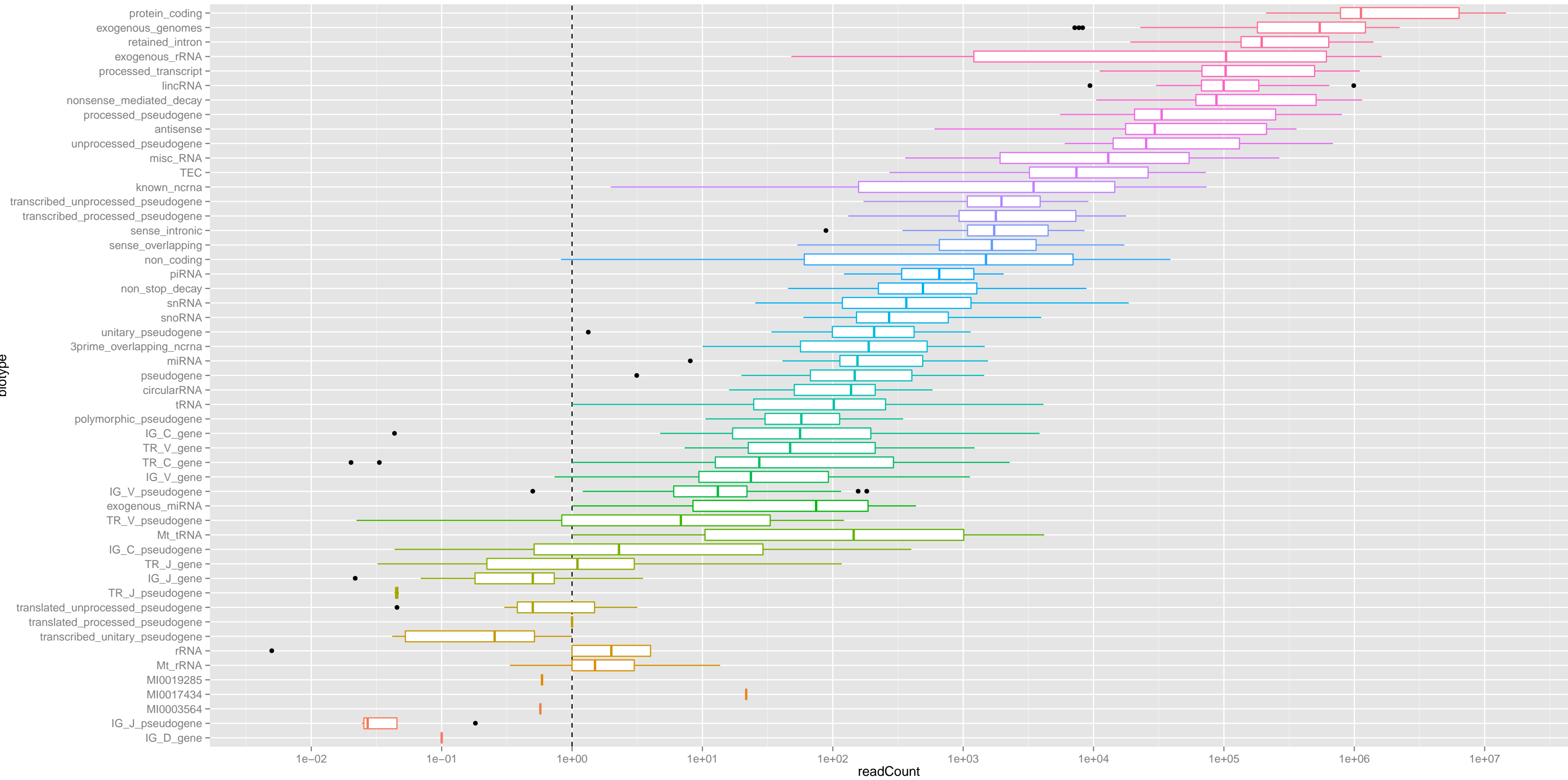
fraction aligned reads (normalised by # adapter-clipped reads)



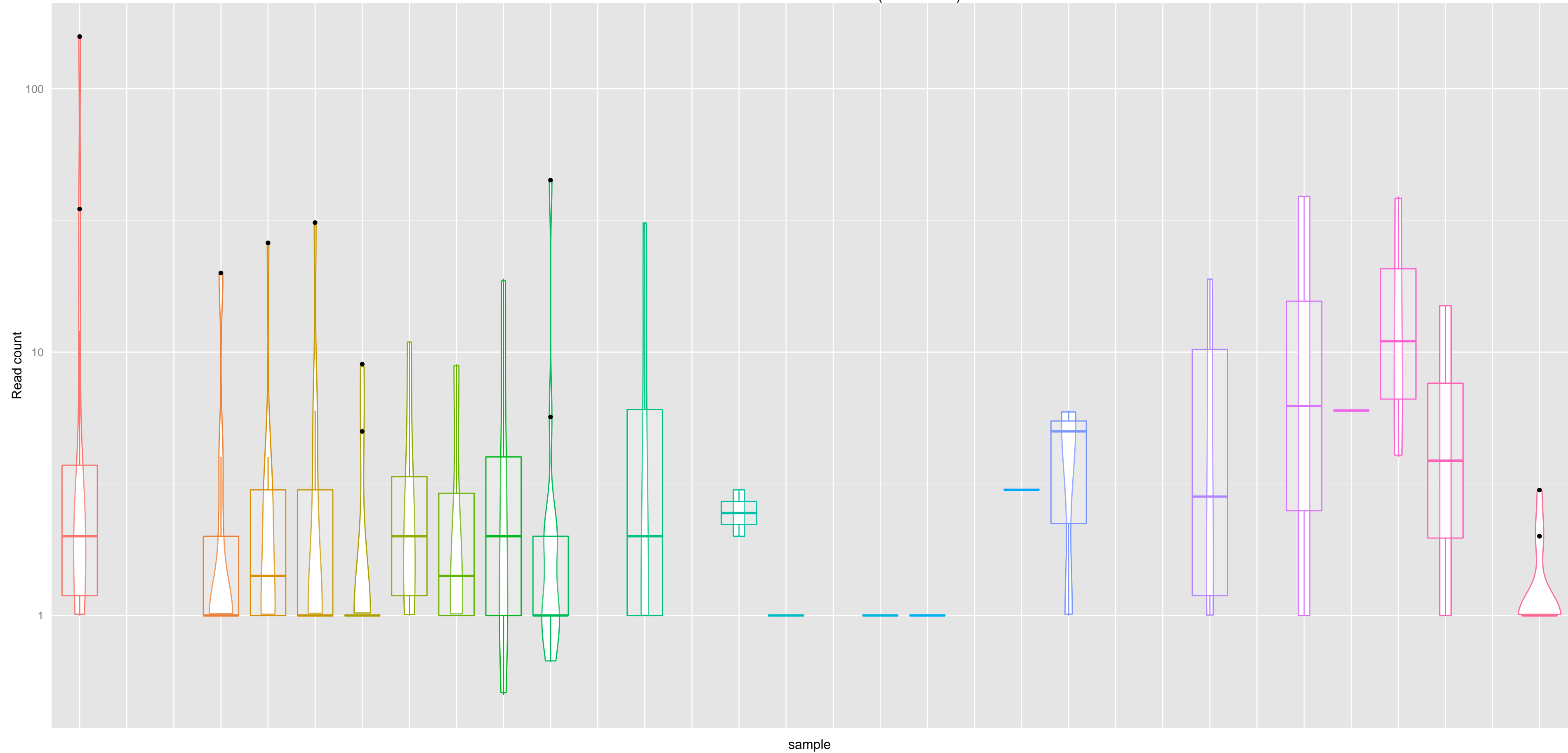
fraction aligned reads (normalised by # non-contaminant reads)

Stage	Sample_000-268_004_R1_all.fq	Sample_000-632_012_R1_all.fq	Sample_000-025_001_R1_all.fq	HSB123.AMY.fq	HSB123.CBC.fq	HSB123.MD.fq	Sample_000-465PF_006_R1_all.fq	Sample_000-554_009_R1_all.fq	SRR577579_1	Sample_000-484_007_R1_all.fq	Sample_000-297_002_R1_all.fq	Sample_000-330_005_R1_all.fq	Sample_BkSQ-117_001_R1_all.fq	Sample_BkSQ-139_003_R1_all.fq	Sample_BkSQ-49_004_R1_all.fq	Sample_BkSQ-157_004_R1_all.fq	Sample_BkSQ-3_005_R1_all.fq	Sample_BkSQ-5_007_R1_all.fq	Sample_BkSQ-6_012_R1_all.fq	Sample_BkSQ-105_008_R1_all.fq	Sample_BkSQ-4_006_R1_all.fq	Sample_BkSQ-154_012_R1_all.fq	Sample_BkSQ-153_007_R1_all.fq	Sample_BkSQ-2_004_R1_all.fq	Sample_BkSQ-26_002_R1_all.fq	Sample_BkSQ-70_006_R1_all.fq	Sample_BkSQ-89_007_R1_all.fq	Sample_BkSQ-9_005_R1_all.fq	Sample_BkSQ-10_001_R1_all.fq	Sample_BkSQ-124_002_R1_all.fq	Sample_BkSQ-29_003_R1_all.fq	Sample_BkSQ-65_005_R1_all.fq		
reads_used_for_alignment	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	
genome	96.7%	95.6%	98.2%	96.4%	96.4%	96.3%	94.5%	97.1%	98.4%	97.6%	97.7%	97.7%	33.7%	41.6%	33.1%	20.0%	31.0%	30.2%	29.5%	41.7%	39.5%	43.3%	42.5%	45.3%	32.2%	34.8%	33.7%	31.3%	29.5%	30.9%	25.5%	29.0%		
miRNA_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
miRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
miRNAprecursor_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
miRNAprecursor_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
tRNA_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
tRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRNA_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
gencode_sense	23.7%	4.0%	37.8%	42.5%	42.0%	44.0%	37.6%	38.4%	6.1%	46.5%	43.7%	45.2%	5.0%	9.0%	6.9%	1.7%	4.5%	4.7%	6.1%	10.3%	6.0%	8.6%	7.3%	9.2%	5.3%	6.7%	3.9%	6.1%	4.1%	5.3%	3.9%	4.7%		
gencode_antisense	21.2%	3.8%	34.1%	40.5%	40.4%	43.1%	33.9%	37.4%	74.1%	42.4%	40.4%	41.2%	0.4%	1.2%	1.2%	0.4%	0.2%	0.4%	0.4%	1.2%	0.4%	0.6%	0.4%	0.5%	0.9%	1.7%	0.8%	0.4%	0.5%	0.9%	0.5%	0.6%		
circularRNA_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
not_mapped_to_genome_or_libs	2.7%	4.4%	0.8%	2.2%	1.8%	1.9%	4.3%	2.0%	0.7%	1.0%	0.9%	1.1%	66.2%	58.1%	66.7%	80.0%	68.9%	69.6%	70.2%	58.0%	60.3%	56.4%	57.2%	54.4%	67.6%	65.0%	66.1%	68.4%	70.4%	68.9%	74.3%	70.9%		
repetitiveElements	0.3%	1.4%	0.3%	0.1%	0.1%	0.1%	0.3%	0.4%	0.1%	0.2%	0.2%	0.3%	17.8%	18.9%	14.0%	4.8%	7.4%	14.5%	6.9%	12.0%	15.5%	13.7%	13.0%	15.8%	21.1%	20.9%	14.5%	8.6%	18.2%	12.9%	11.1%	12.0%		
endogenous_gapped	0.4%	0.5%	0.4%	0.5%	0.7%	0.6%	0.7%	0.9%	0.5%	0.7%	0.5%	0.5%	31.9%	29.6%	26.6%	6.2%	20.0%	17.8%	21.1%	33.1%	25.7%	34.5%	33.5%	34.2%	15.9%	19.3%	12.2%	23.5%	14.5%	20.6%	12.8%	15.0%		
exogenous_miRNA	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenous_rRNA	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.6%	1.8%	4.0%	3.1%	3.3%	2.2%	0.4%	0.6%	0.2%	0.7%	0.1%	1.6%	0.8%	3.0%	2.1%	5.3%	2.0%	5.5%	7.6%		
exogenous_genomes	0.7%	1.3%	0.0%	0.9%	0.6%	0.6%	0.7%	0.4%	0.0%	0.0%	0.1%	0.1%	0.4%	1.4%	4.5%	5.4%	6.9%	4.9%	7.6%	2.6%	1.5%	2.5%	1.2%	1.1%	3.1%	4.6%	6.3%	6.1%	4.3%	4.1%	6.9%	7.3%		

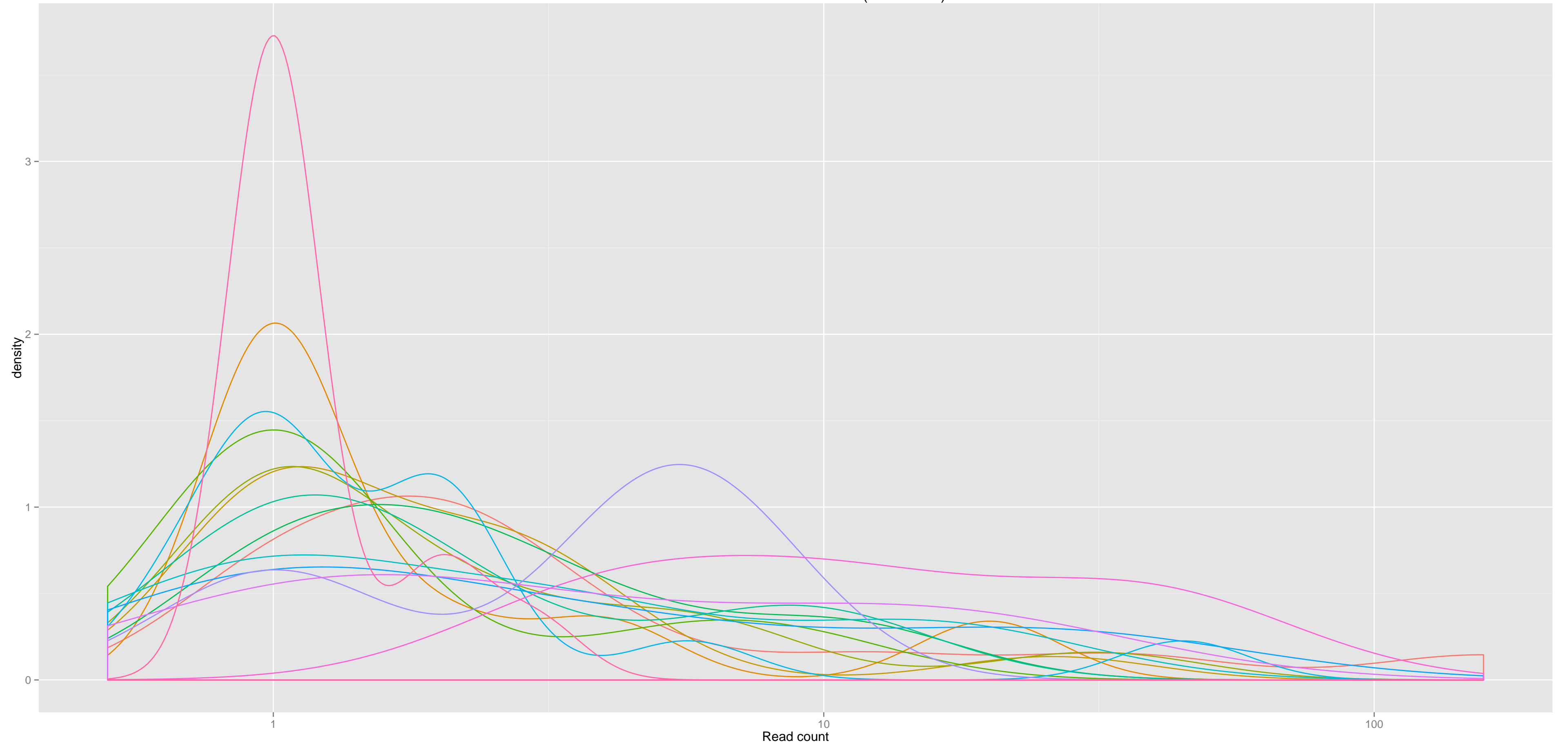




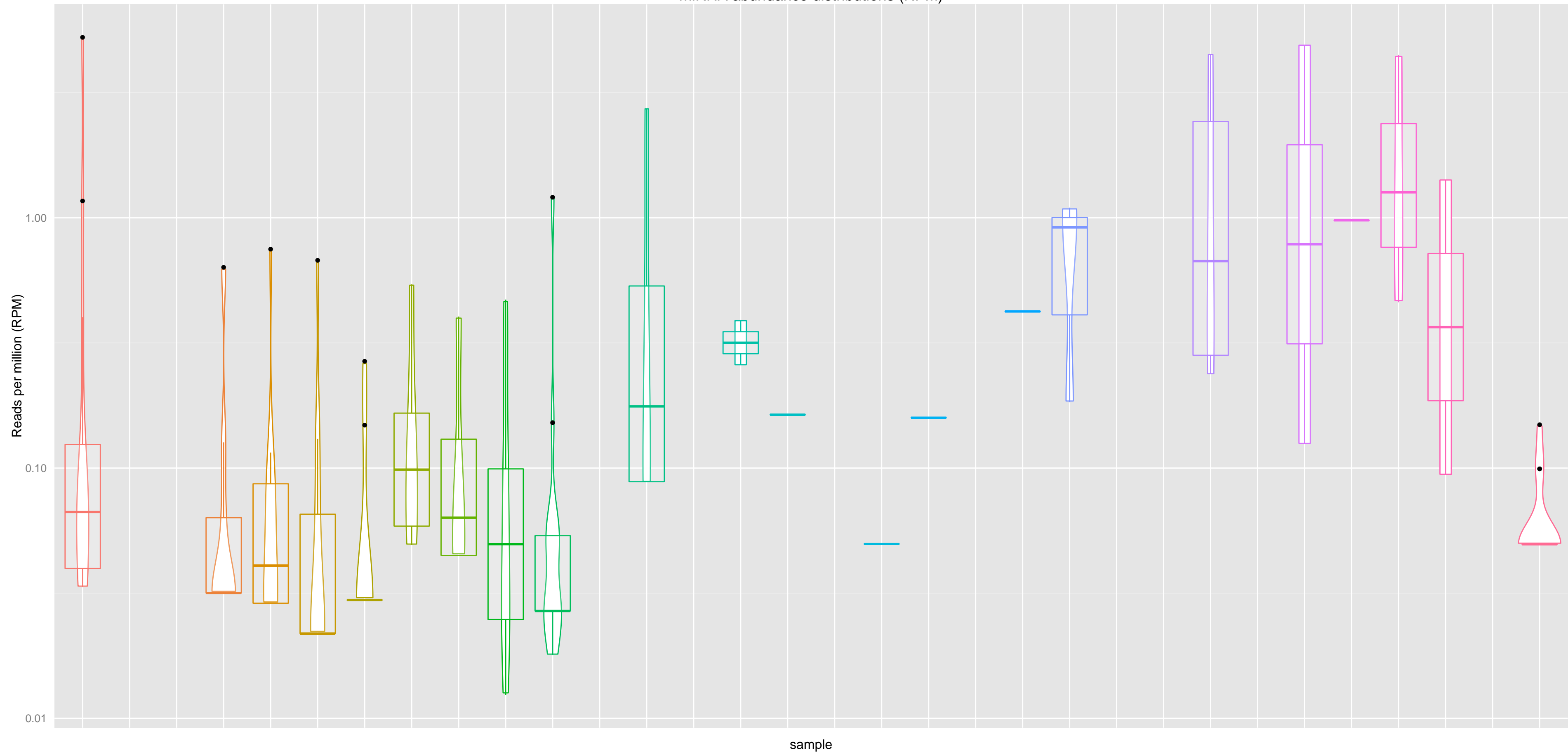
miRNA abundance distributions (raw counts)



miRNA abundance distributions (raw counts)



miRNA abundance distributions (RPM)



miRNA abundance distributions (RPM)

