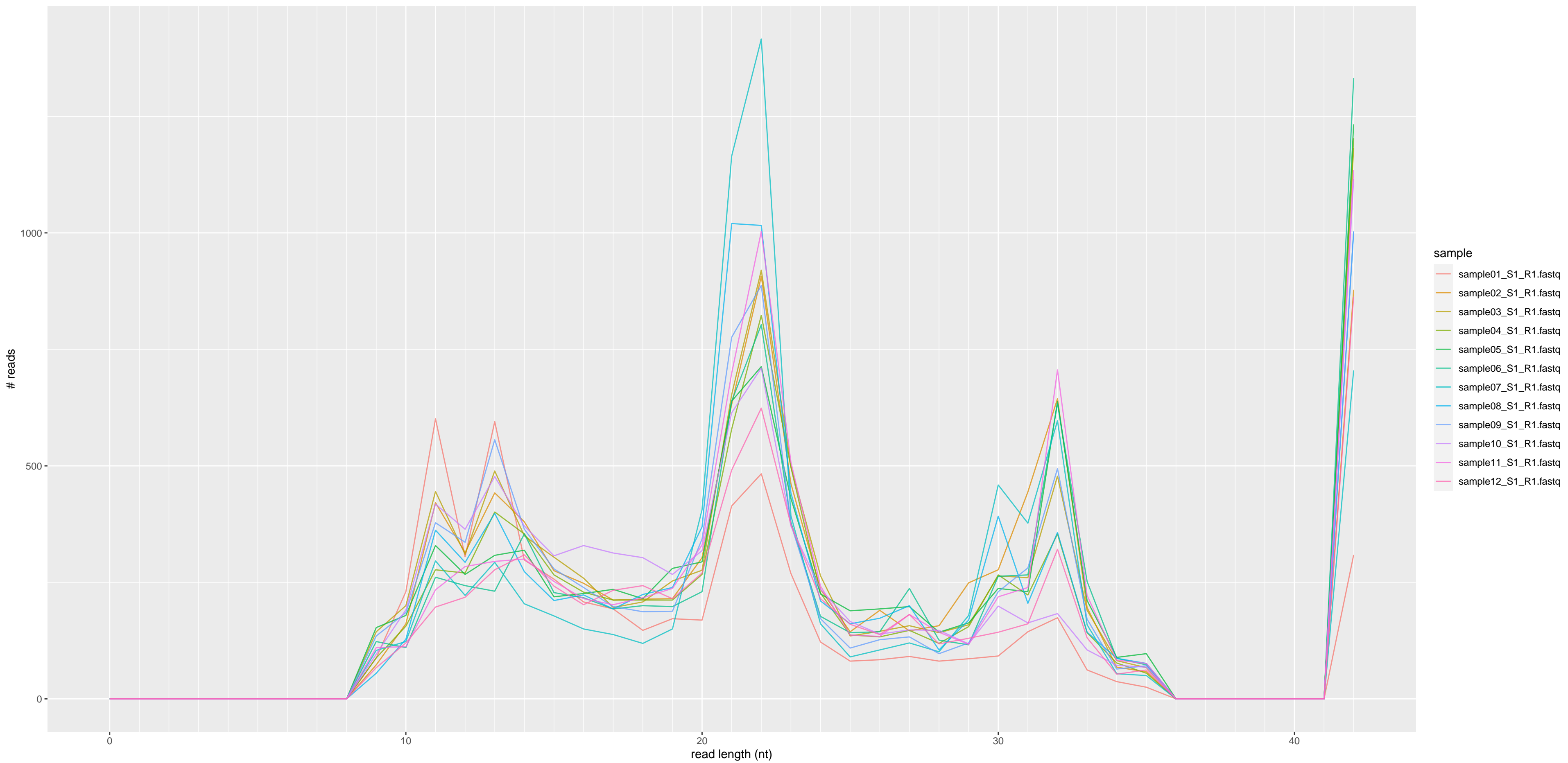
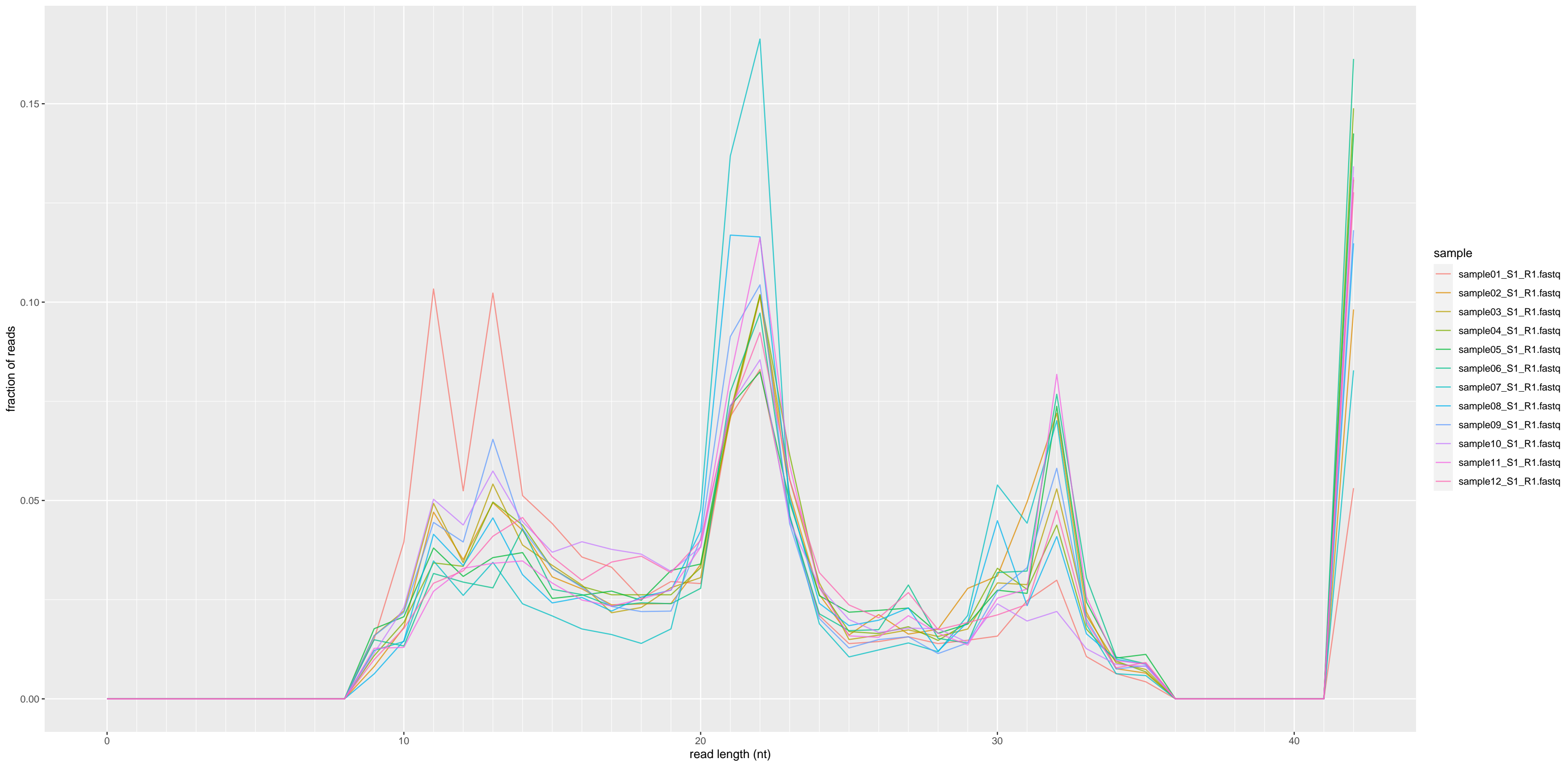
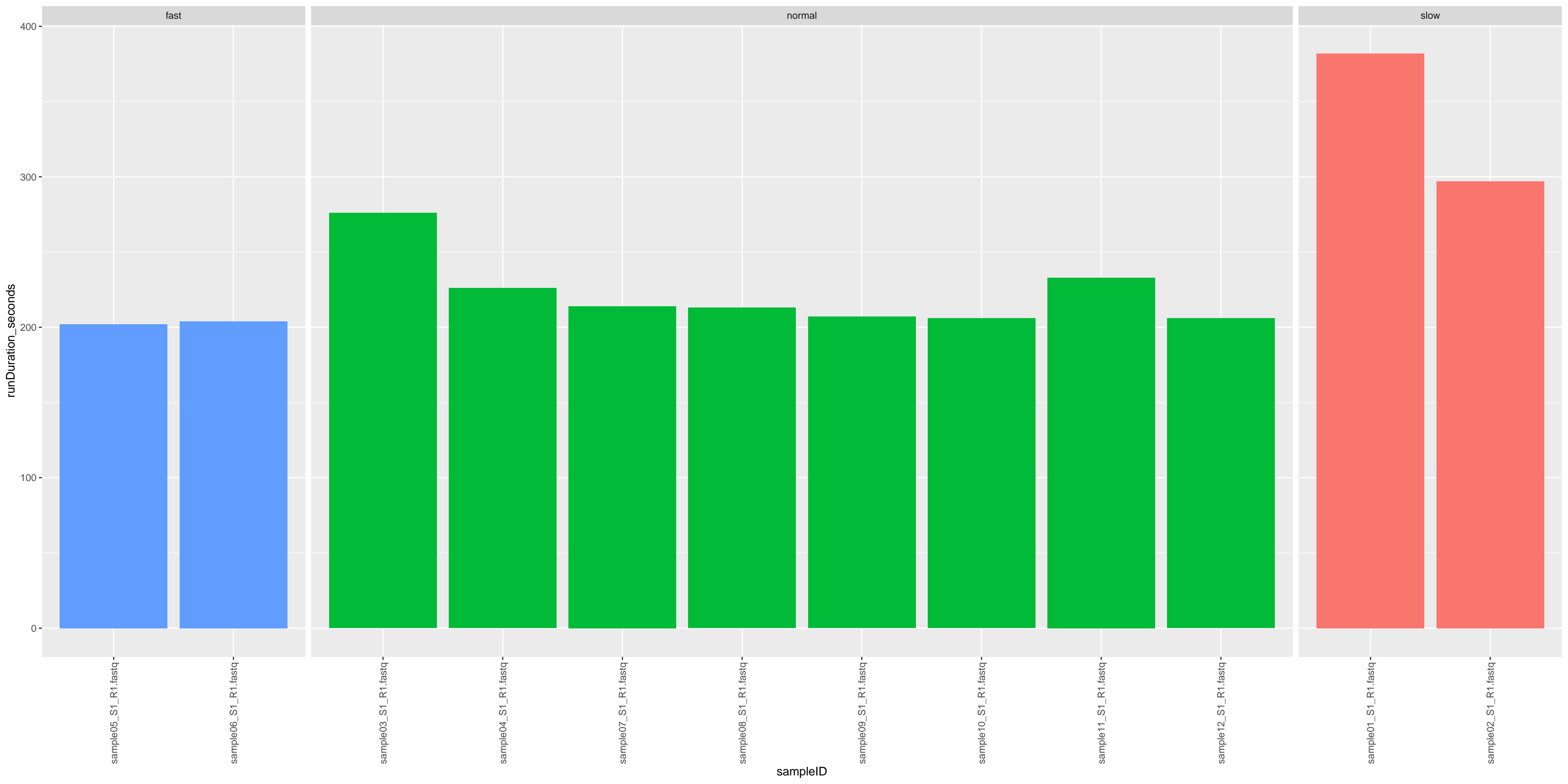


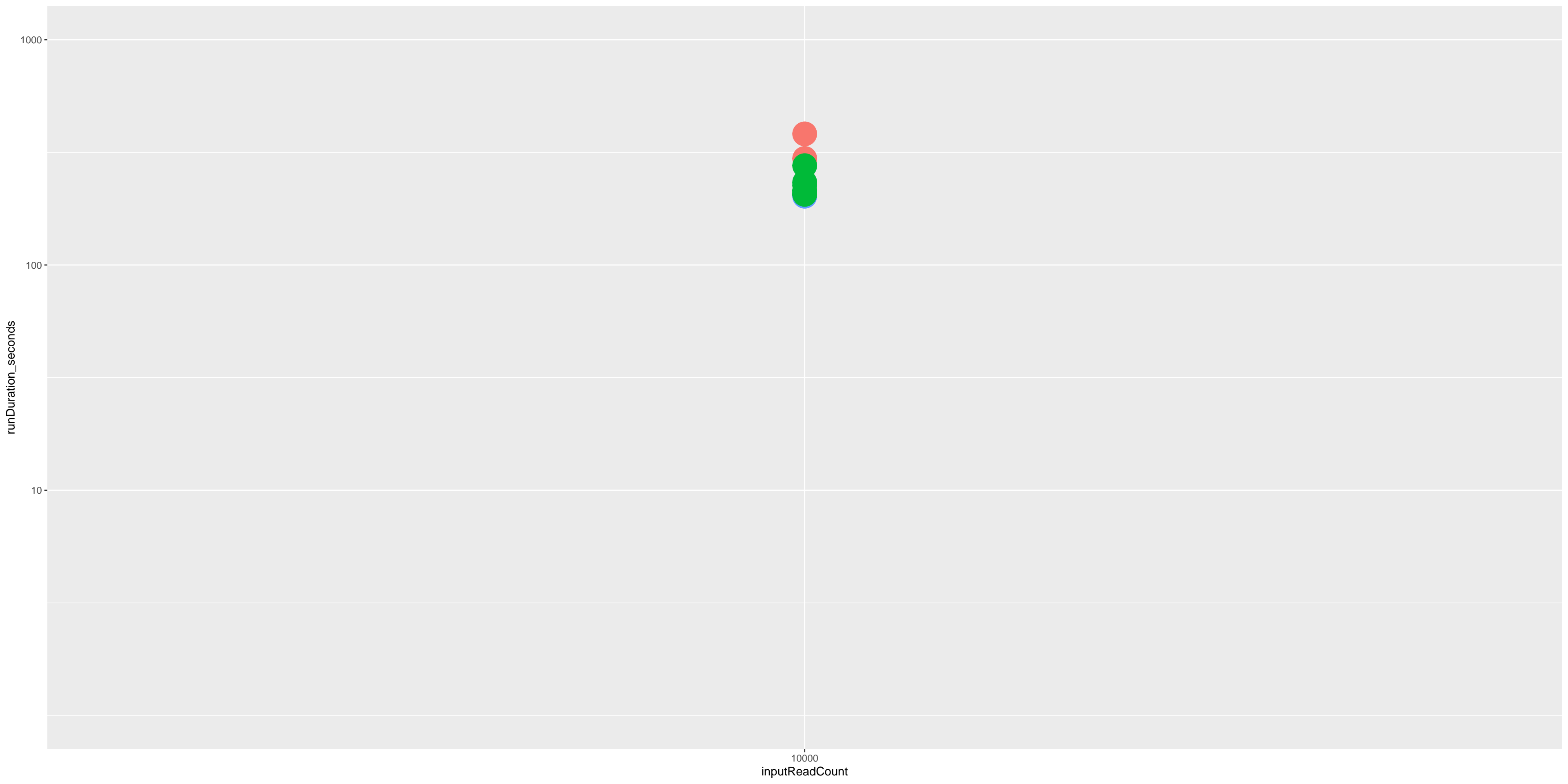
read-length distributions: raw read count



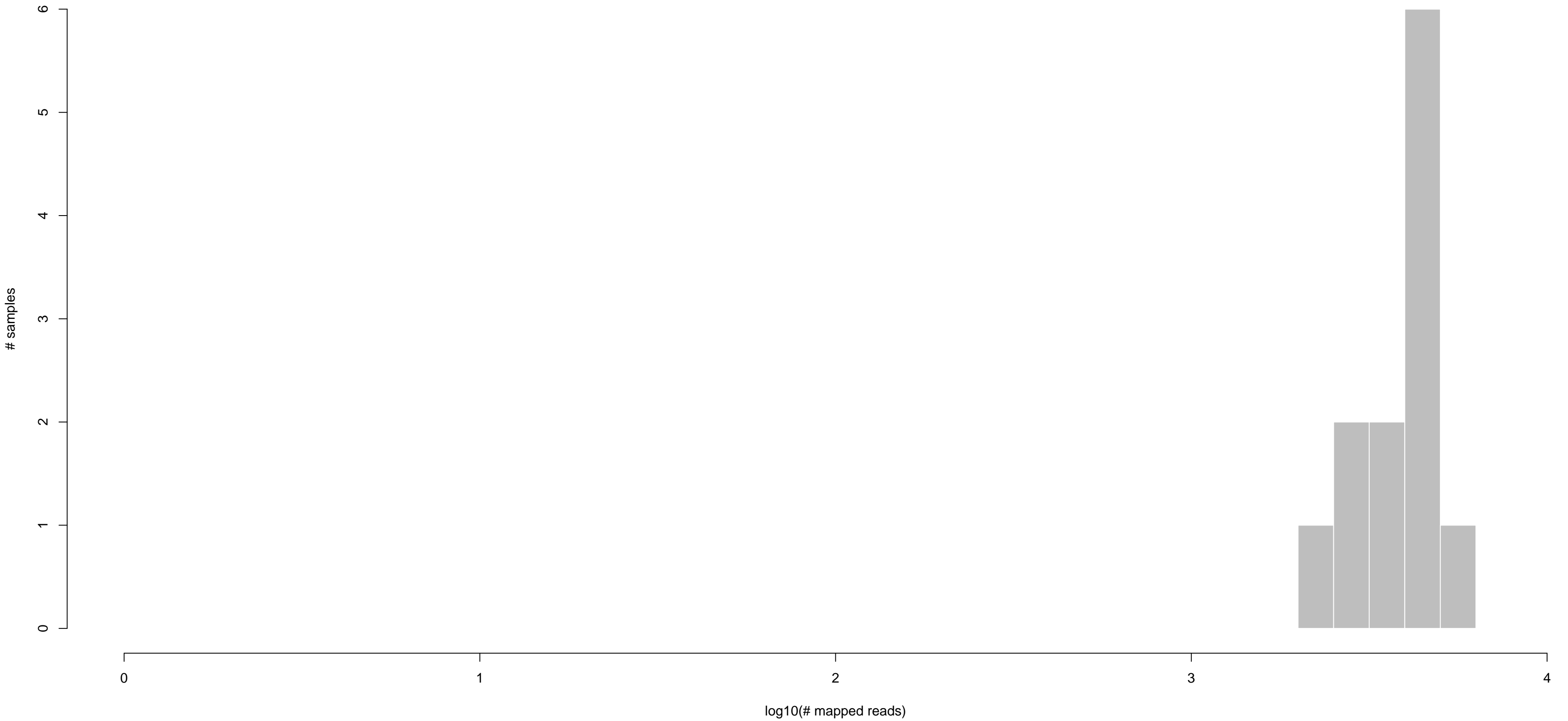
read-length distributions: normalised read fraction



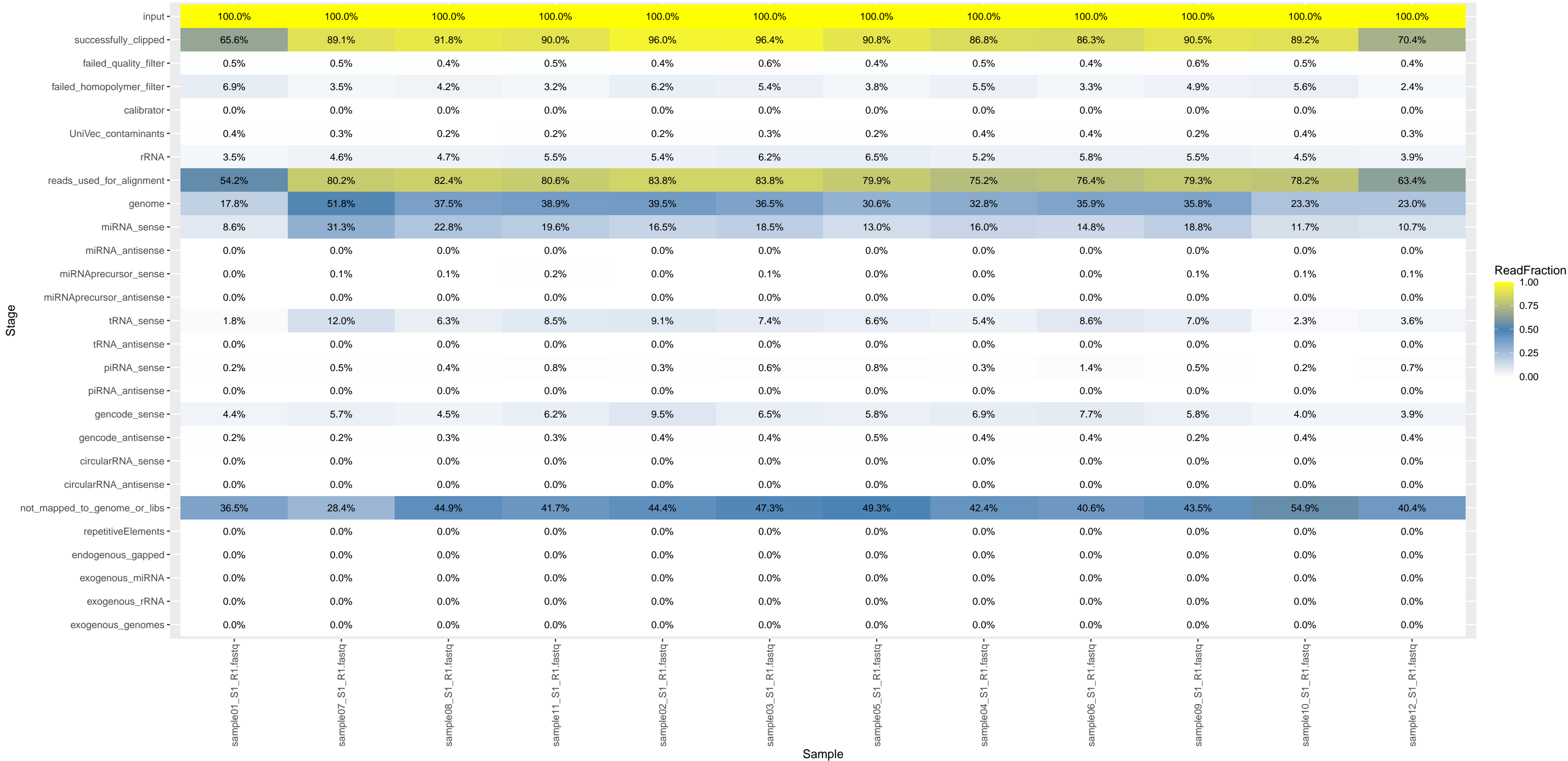


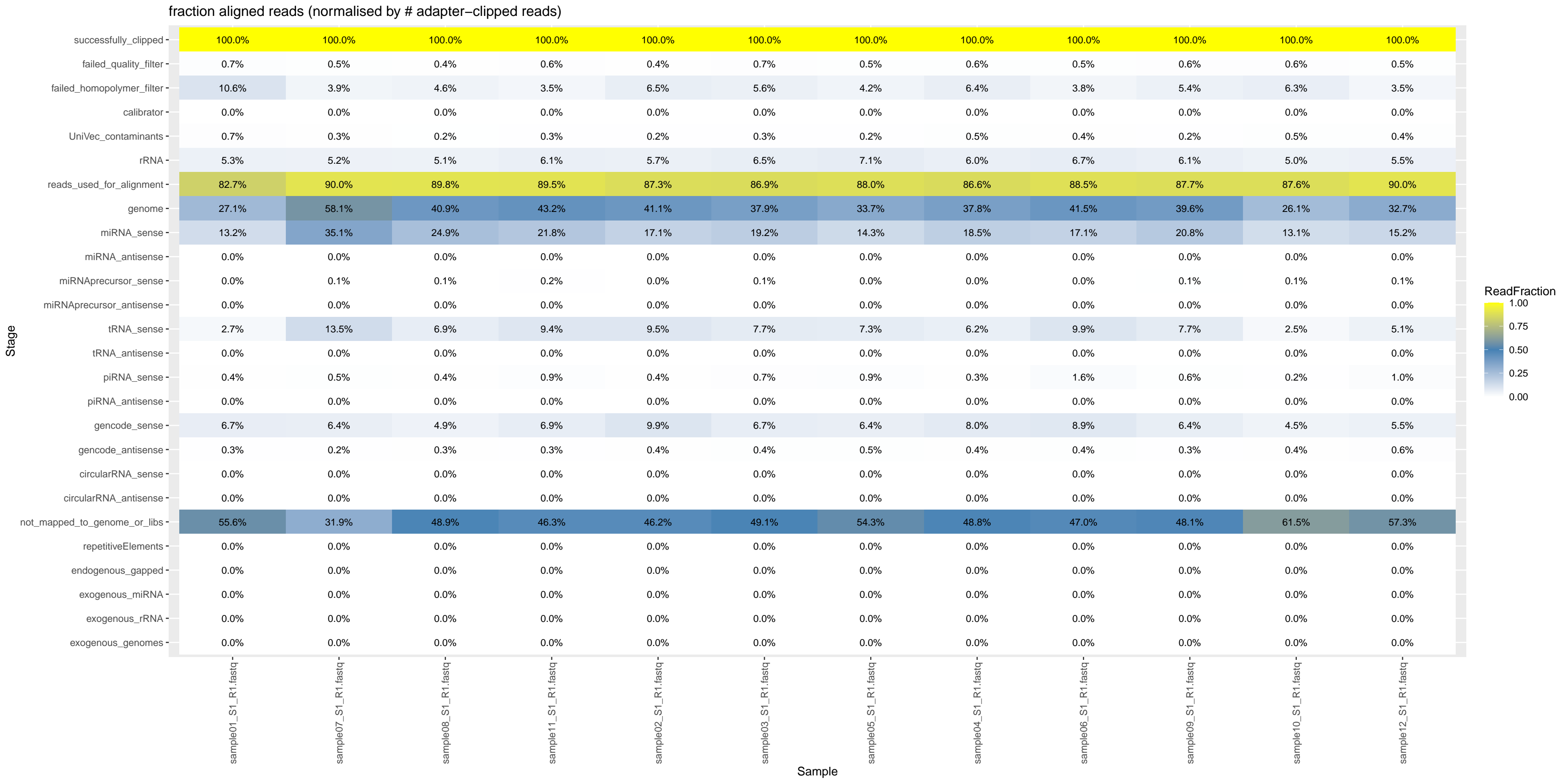


Library size (all mapped reads)

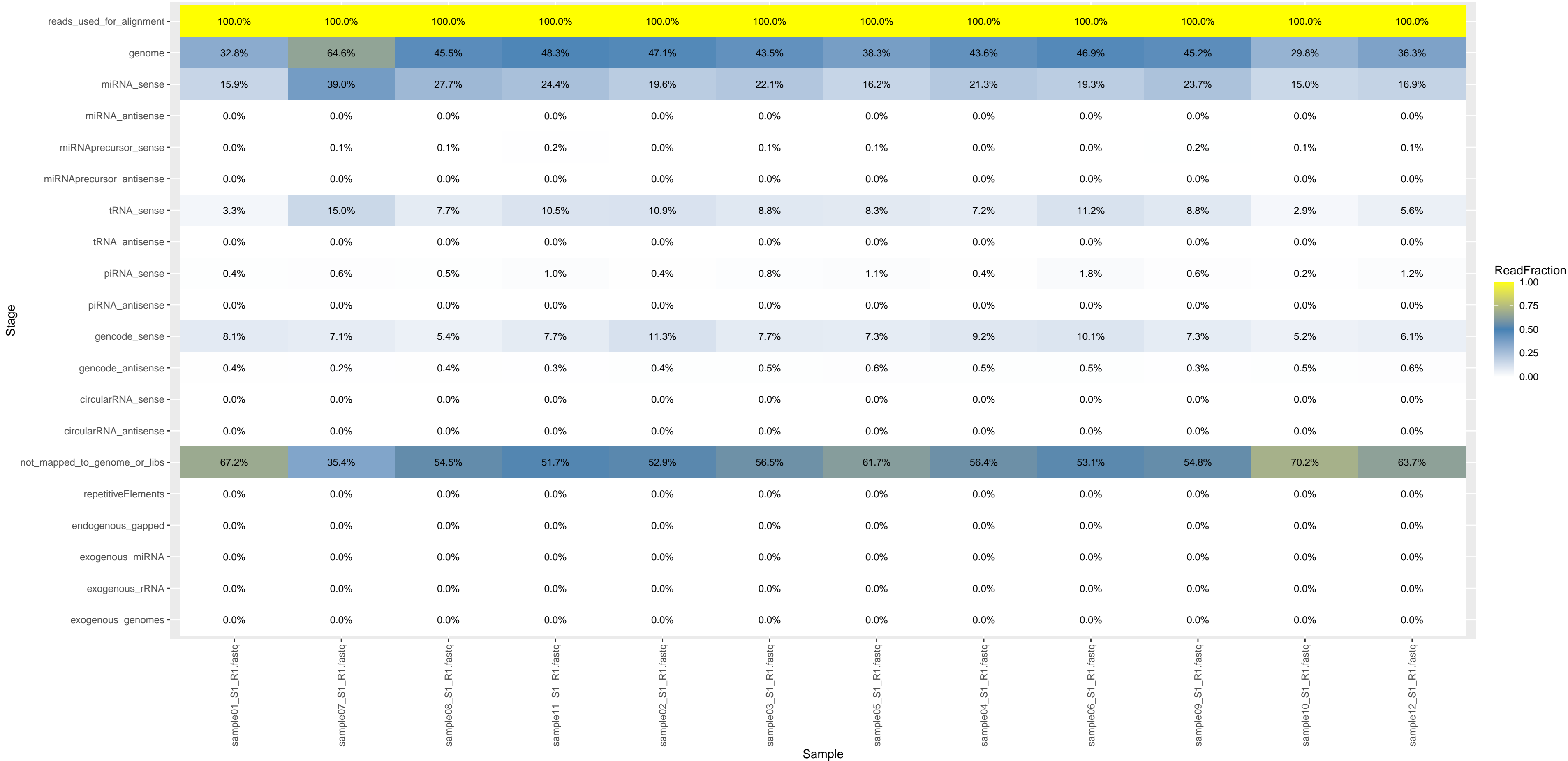


fraction aligned reads (normalised by # input reads)

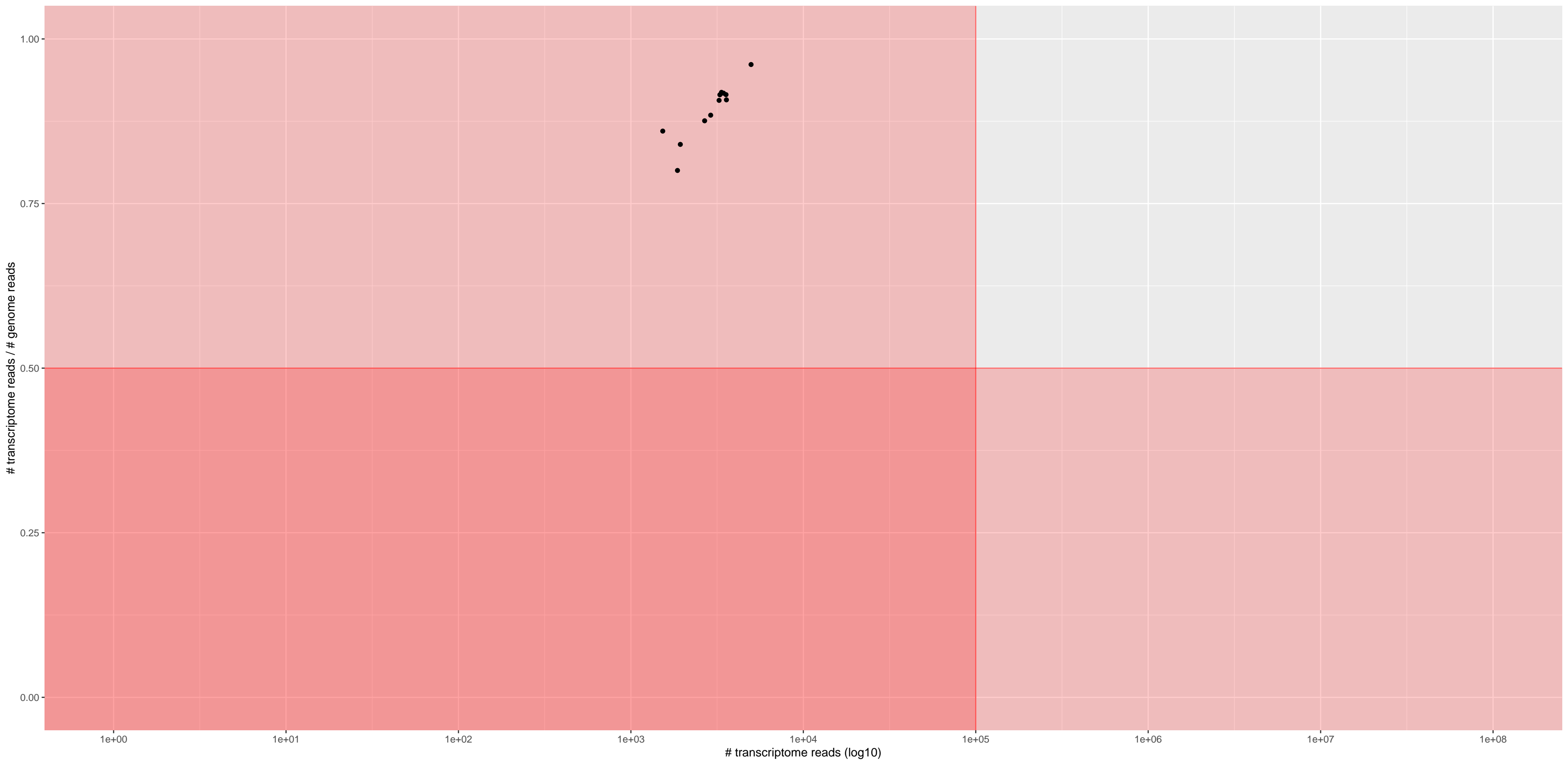




fraction aligned reads (normalised by # non-contaminant reads)

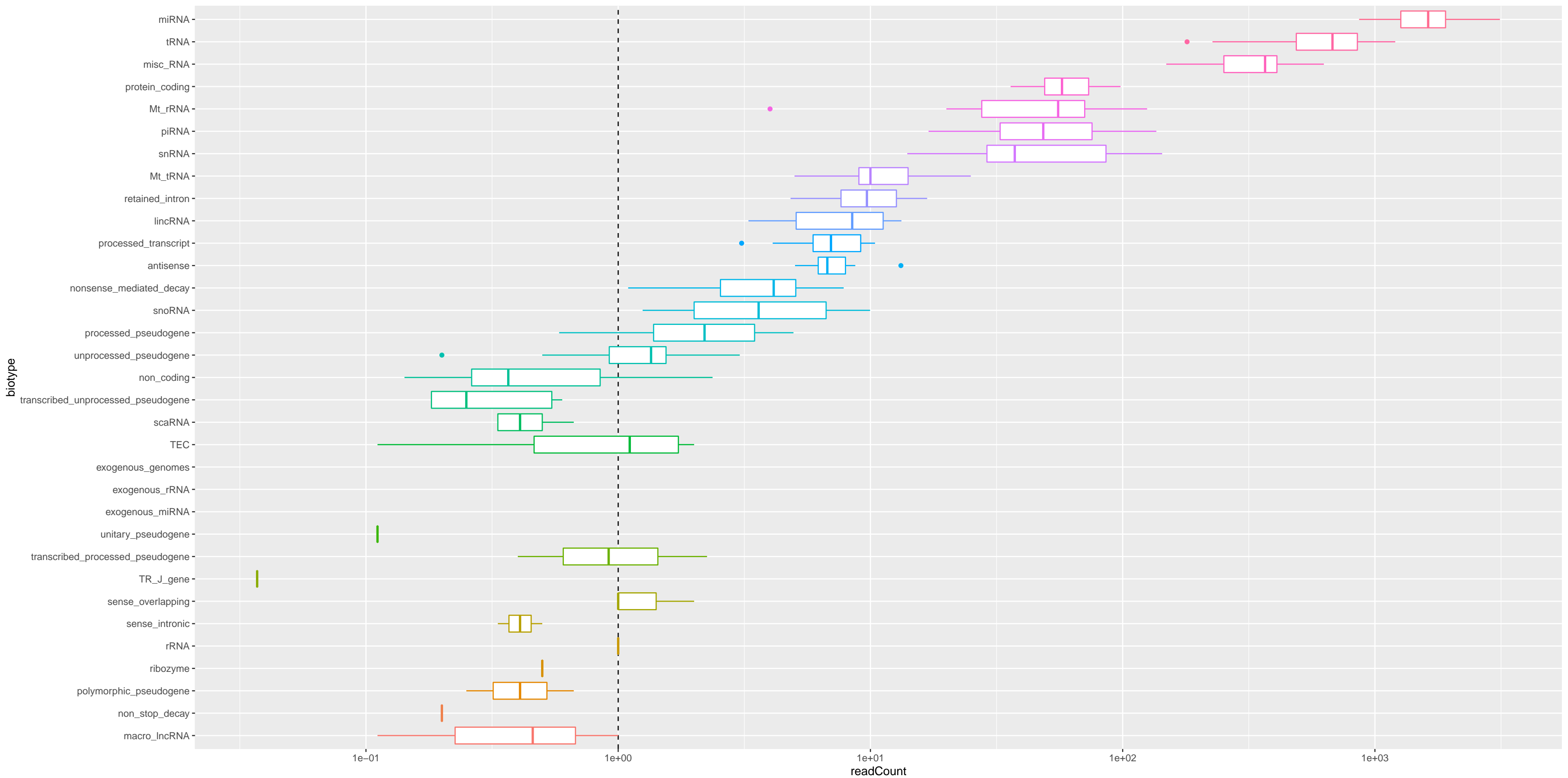


QC result: overall

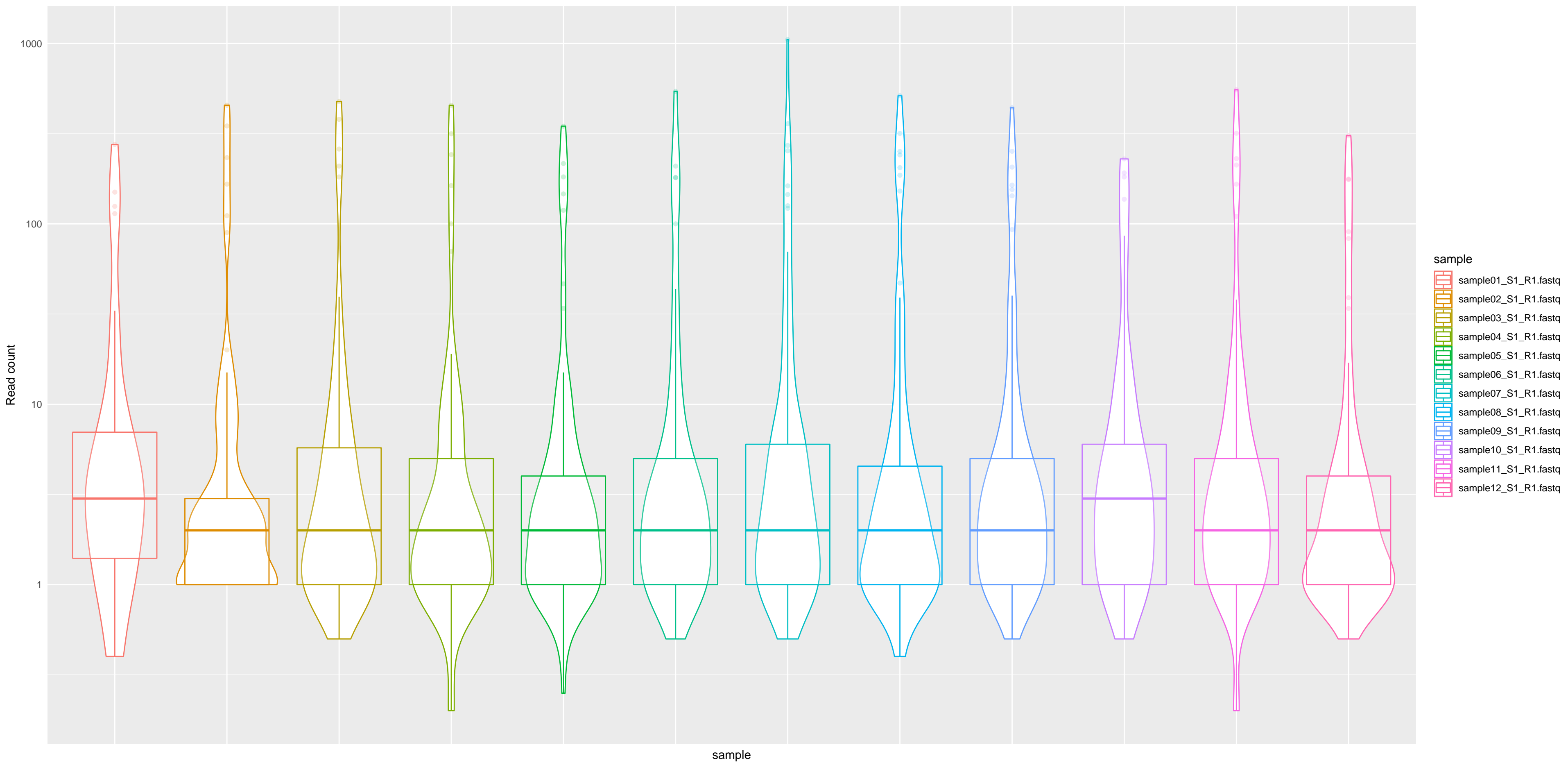


QC result: per-sample results

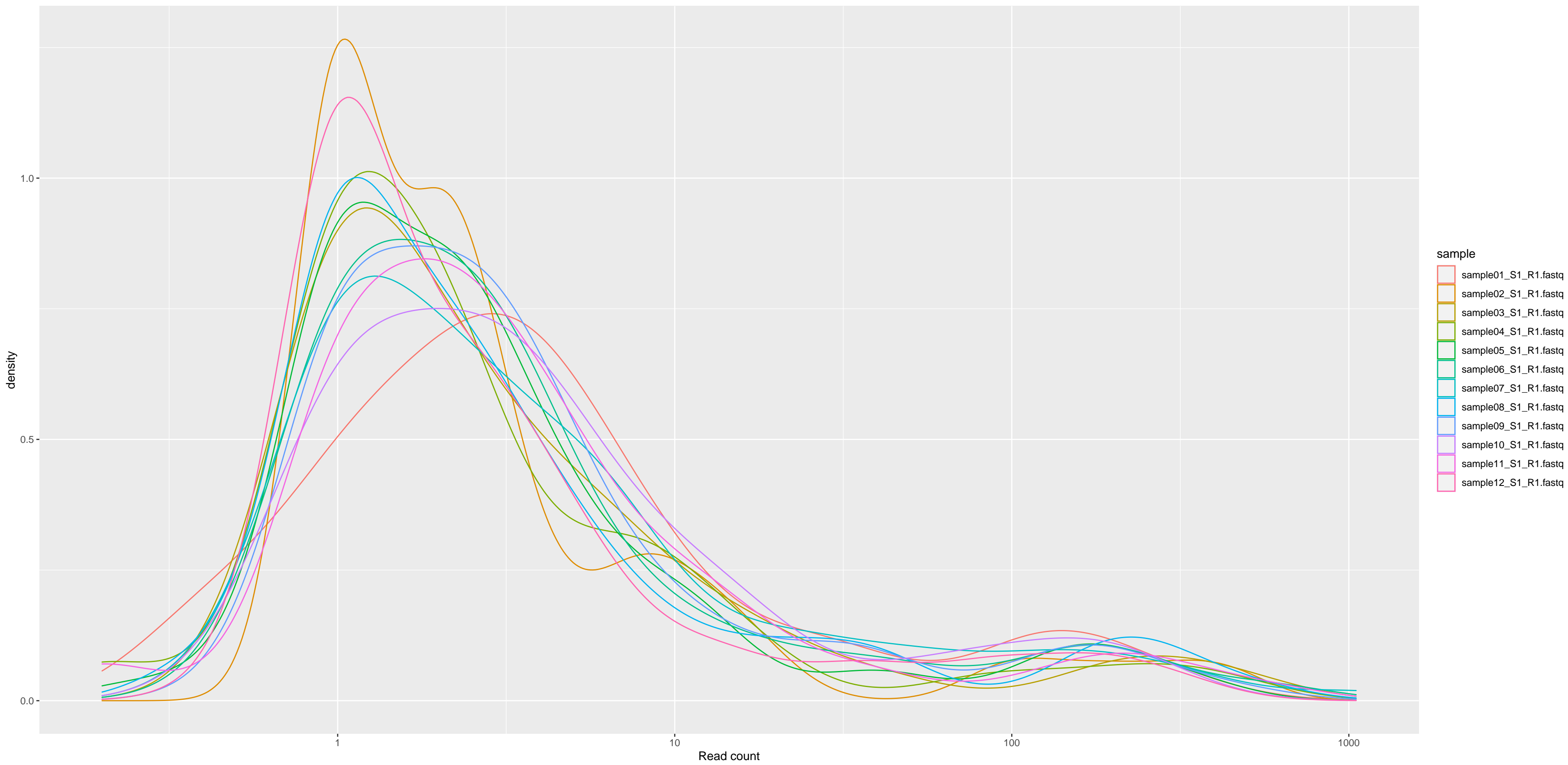
sample12_S1_R1.fastq -	10000	2304	1935	0.84	0.226
sample10_S1_R1.fastq -	10000	2328	1863	0.8	0.221
sample09_S1_R1.fastq -	10000	3581	3247	0.91	0.215
sample06_S1_R1.fastq -	10000	3586	3282	0.92	0.178
sample04_S1_R1.fastq -	10000	3282	2902	0.88	0.222
sample05_S1_R1.fastq -	10000	3057	2677	0.88	0.205
sample03_S1_R1.fastq -	10000	3649	3353	0.92	0.211
sample02_S1_R1.fastq -	10000	3946	3581	0.91	0.195
sample11_S1_R1.fastq -	10000	3890	3561	0.92	0.168
sample08_S1_R1.fastq -	10000	3753	3444	0.92	0.175
sample07_S1_R1.fastq -	10000	5177	4976	0.96	0.156
sample01_S1_R1.fastq -	10000	1779	1530	0.86	0.2
	InputReads -	GenomeReads -	TranscriptomeReads -	TranscriptomeGenomeRatio -	TranscriptomeComplexity -



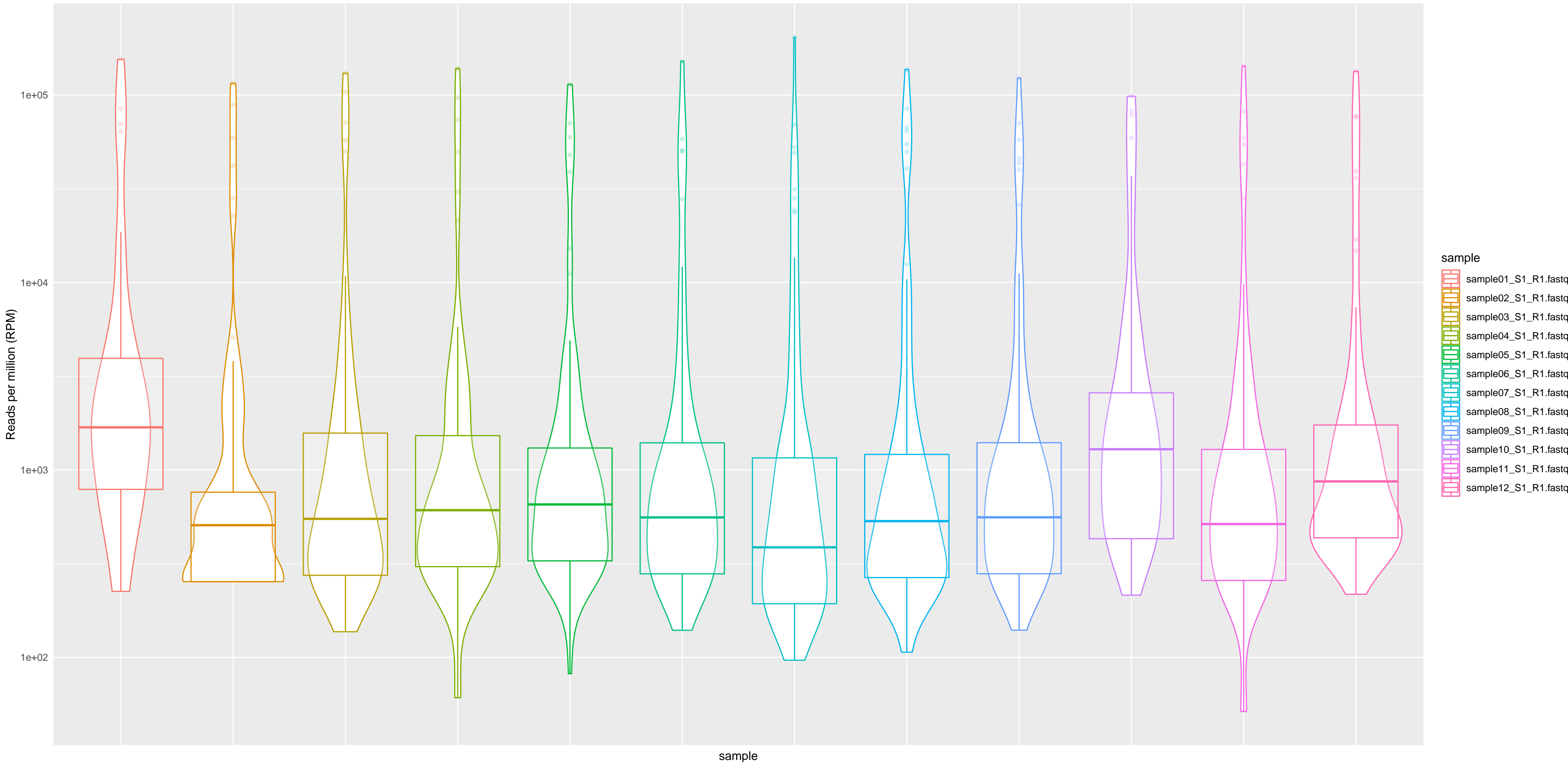
miRNA abundance distributions (raw counts)



miRNA abundance distributions (raw counts)



miRNA abundance distributions (RPM)



miRNA abundance distributions (RPM)

