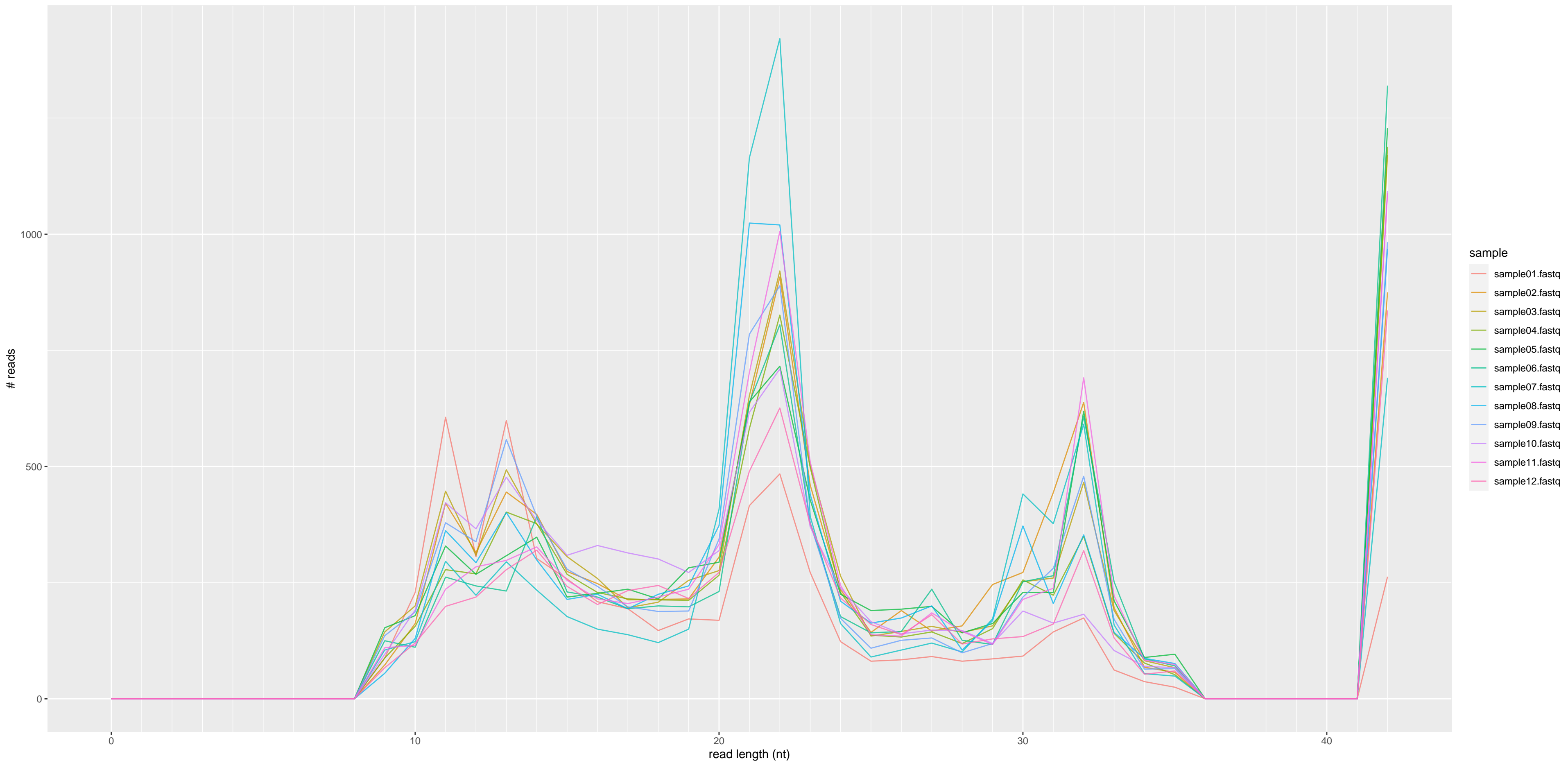
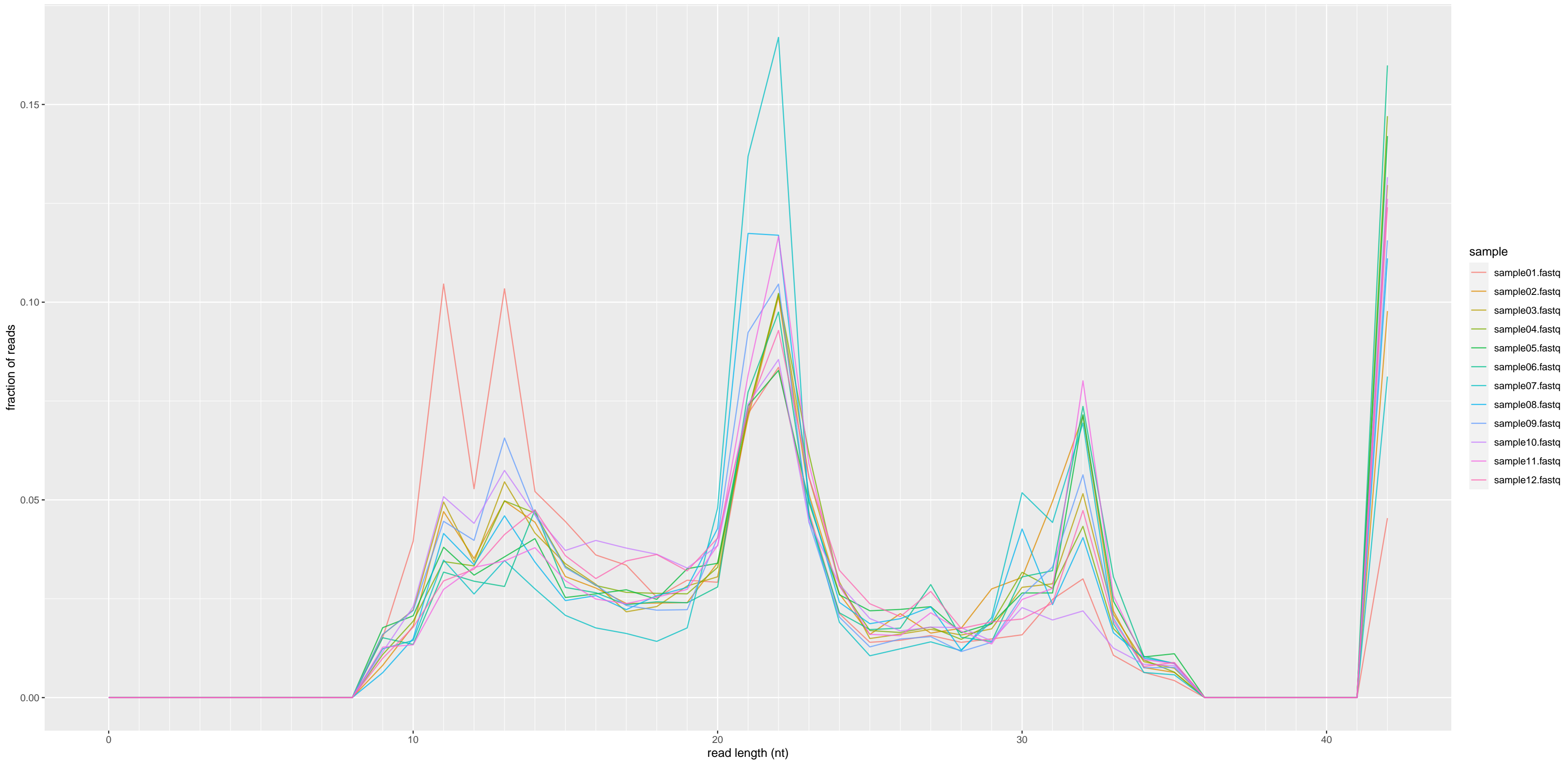
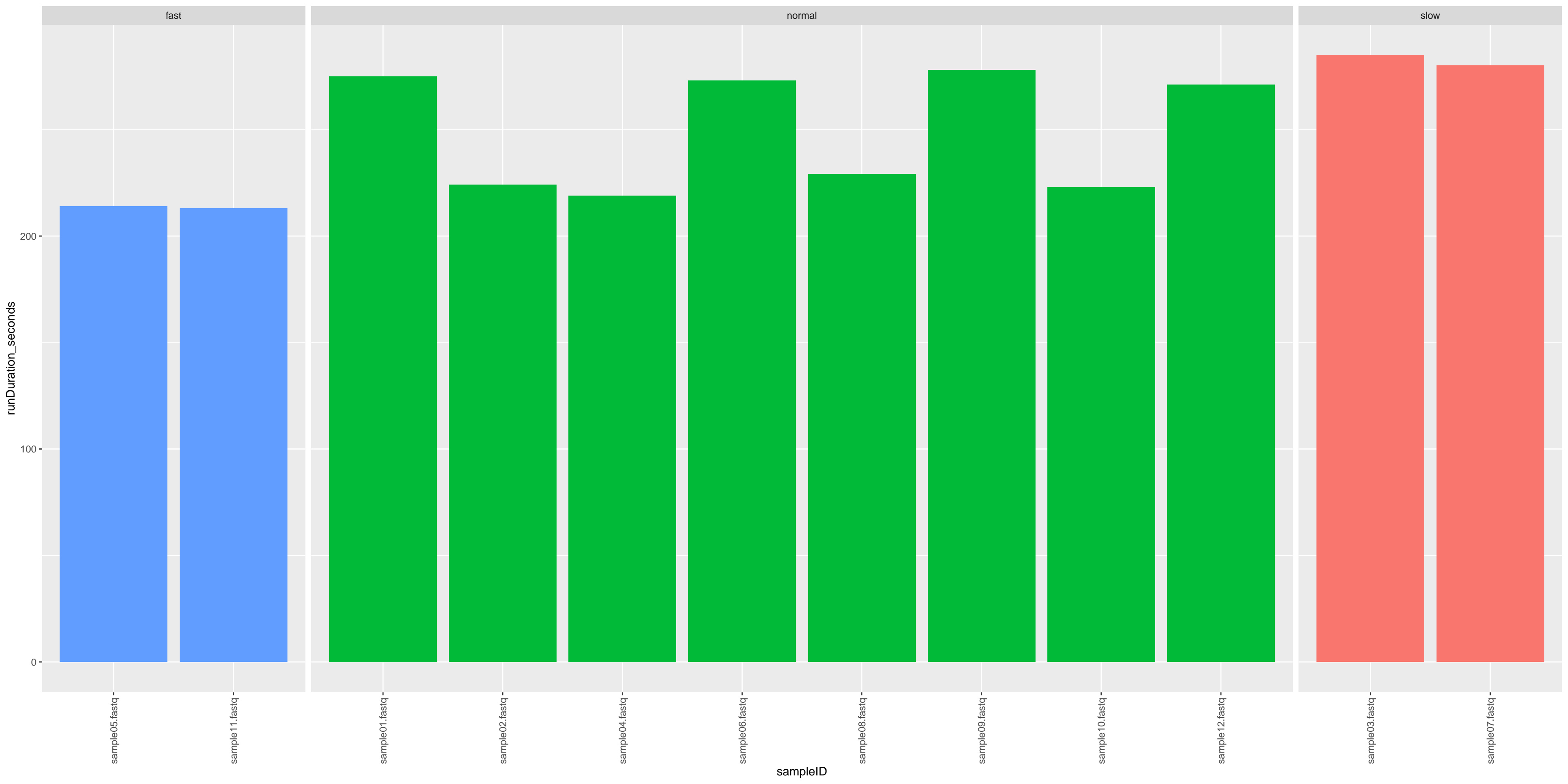


read-length distributions: raw read count



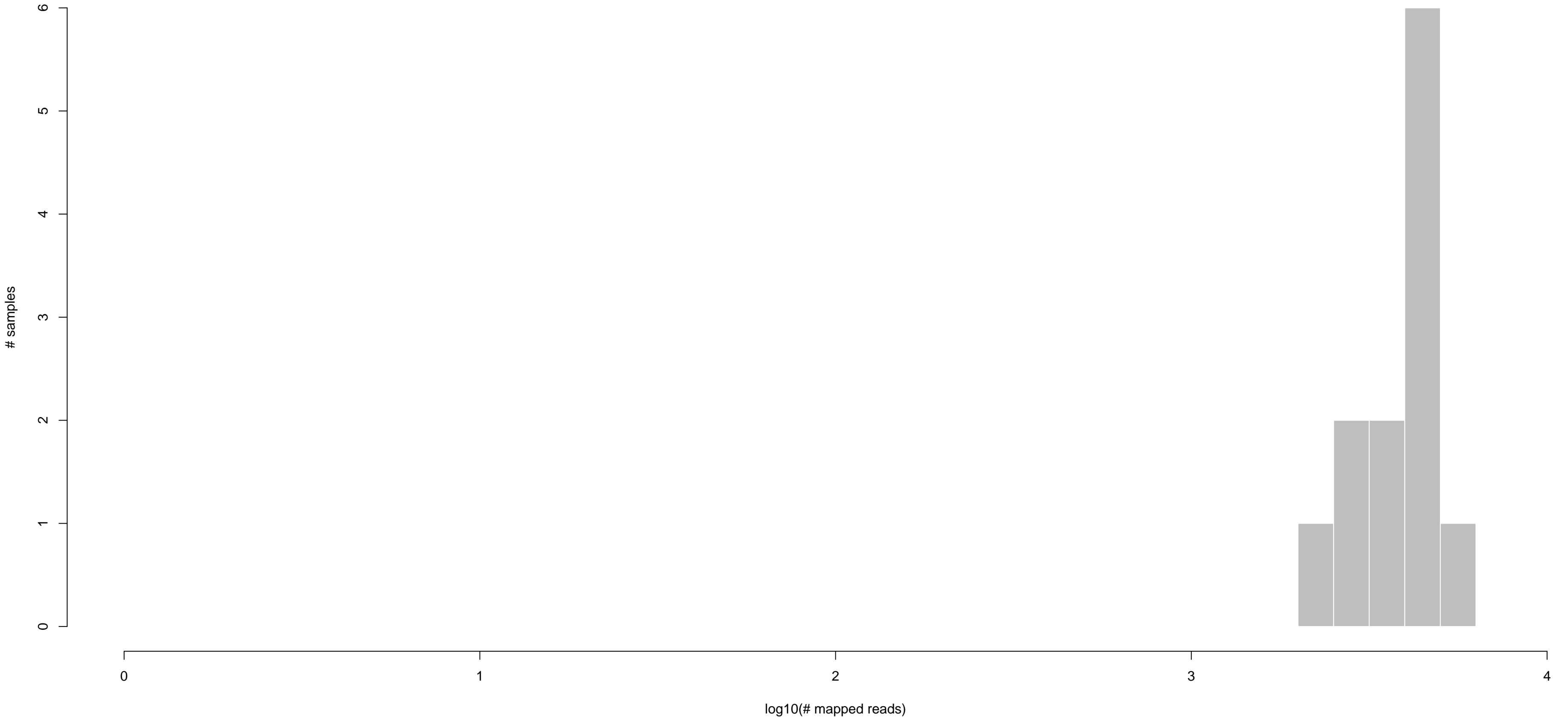
read-length distributions: normalised read fraction



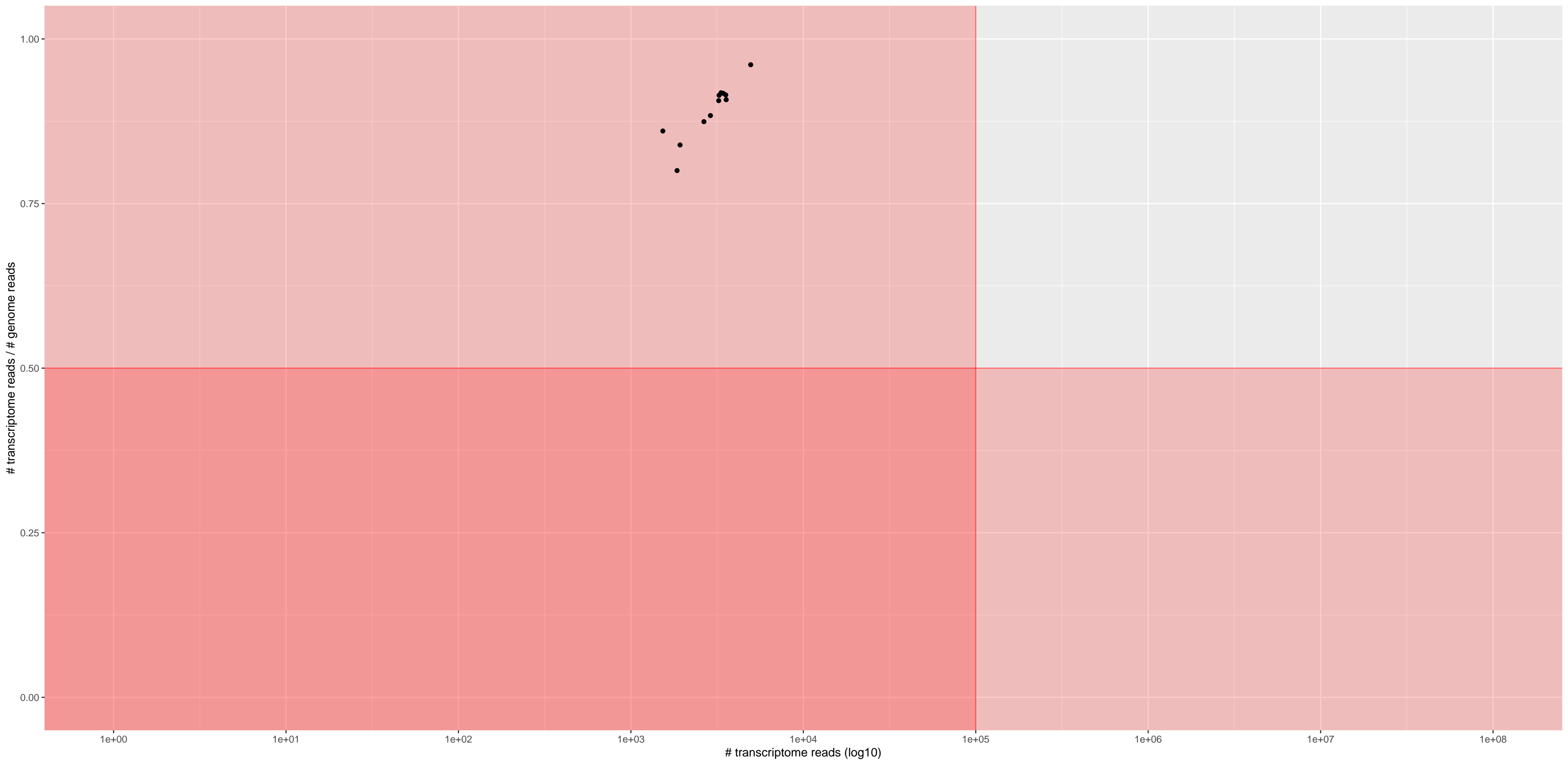




Library size (all mapped reads)

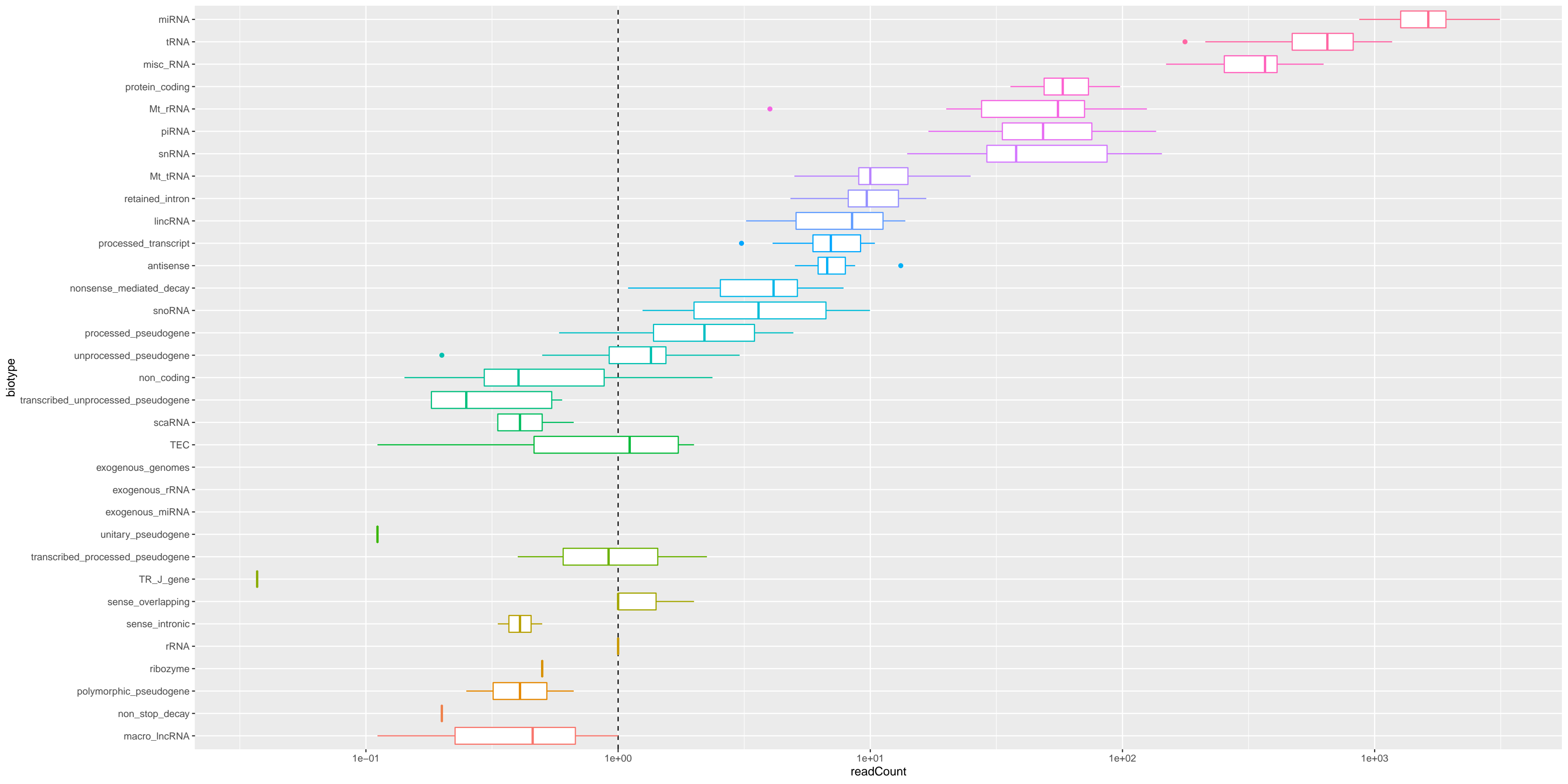


QC result: overall

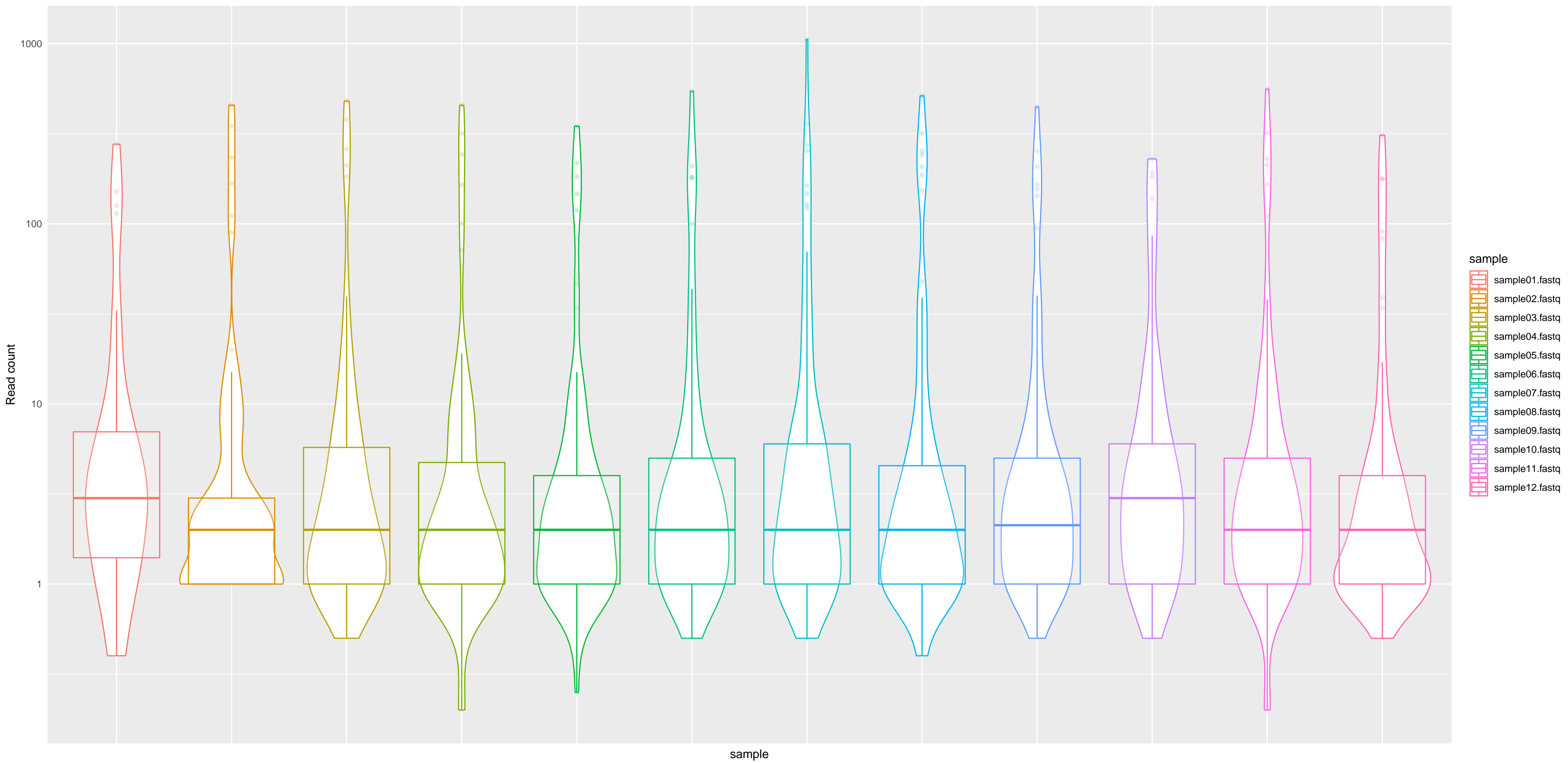


QC result: per-sample results

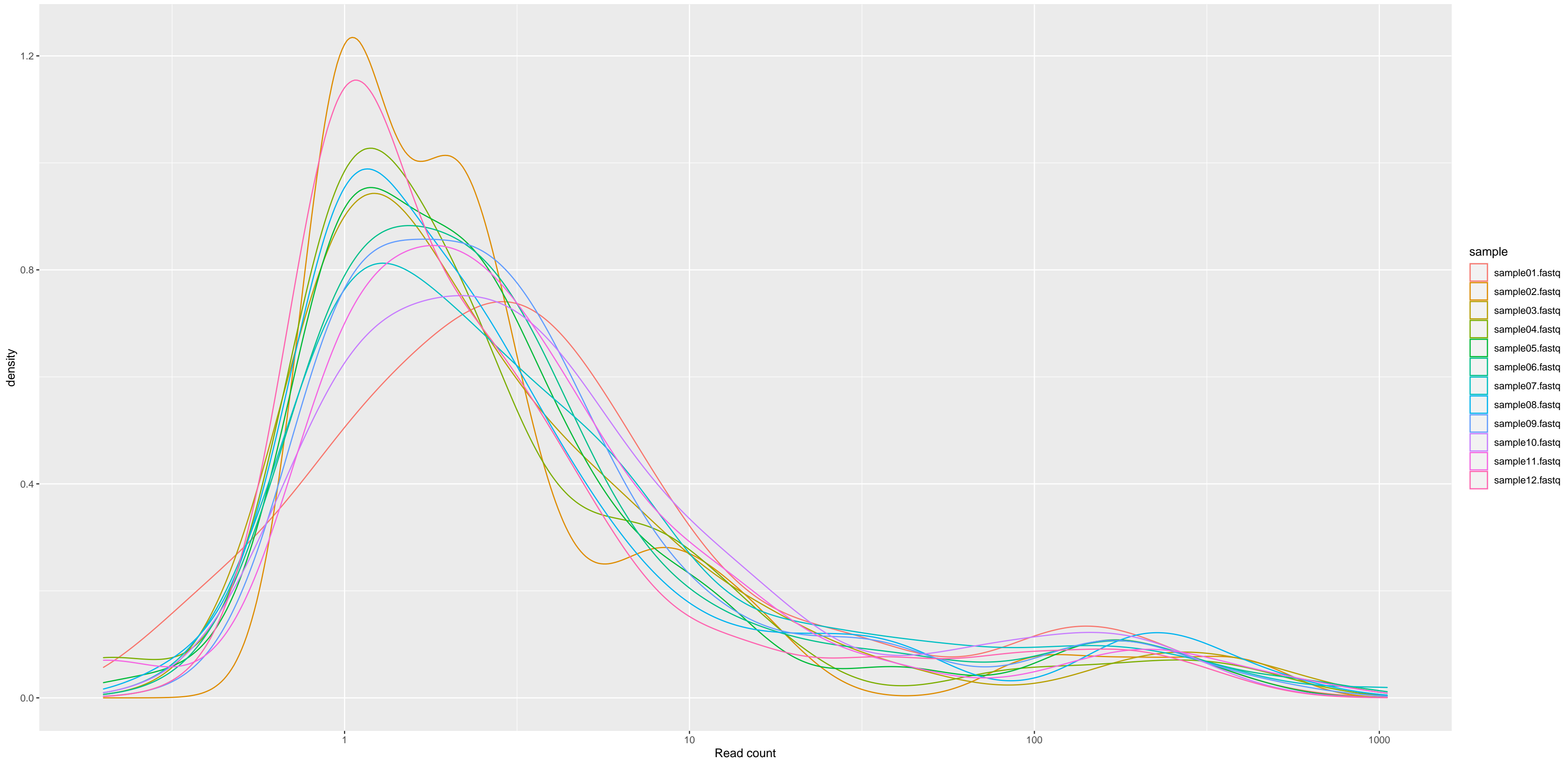
Sample	InputReads	GenomeReads	TranscriptomeReads	TranscriptomeGenomeRatio	TranscriptomeComplexity
sample12.fastq	10000	2298	1928	0.84	0.228
sample10.fastq	10000	2316	1853	0.8	0.221
sample09.fastq	10000	3564	3230	0.91	0.216
sample06.fastq	10000	3552	3248	0.91	0.181
sample04.fastq	10000	3273	2892	0.88	0.224
sample05.fastq	10000	3032	2651	0.87	0.207
sample03.fastq	10000	3630	3333	0.92	0.212
sample02.fastq	10000	3933	3570	0.91	0.195
sample11.fastq	10000	3880	3550	0.91	0.17
sample08.fastq	10000	3741	3432	0.92	0.177
sample07.fastq	10000	5155	4953	0.96	0.157
sample01.fastq	10000	1781	1532	0.86	0.2



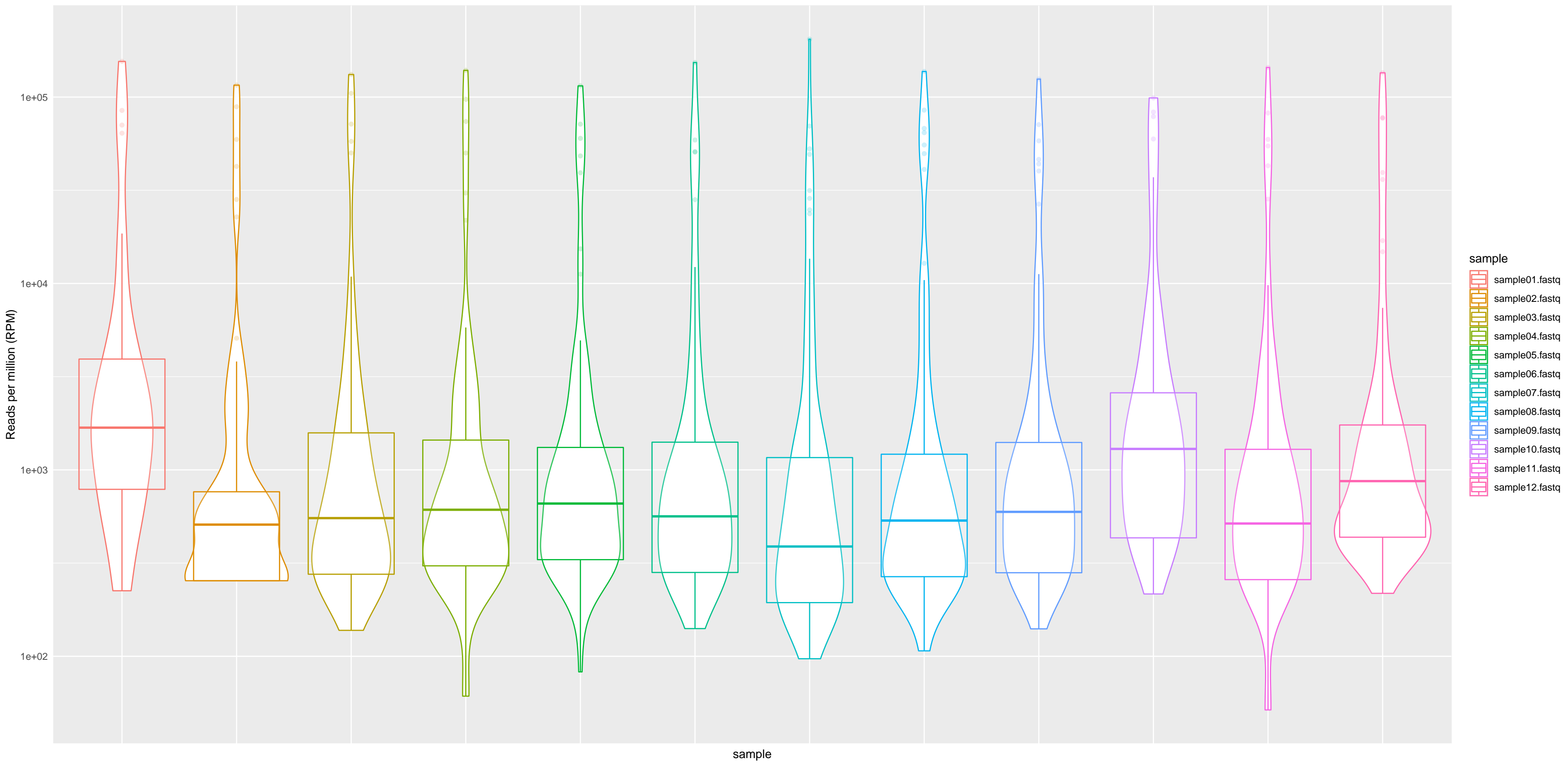
miRNA abundance distributions (raw counts)



miRNA abundance distributions (raw counts)



miRNA abundance distributions (RPM)



miRNA abundance distributions (RPM)

