

General Statistics

18 samples

Custom content: DupRadar
dupInt



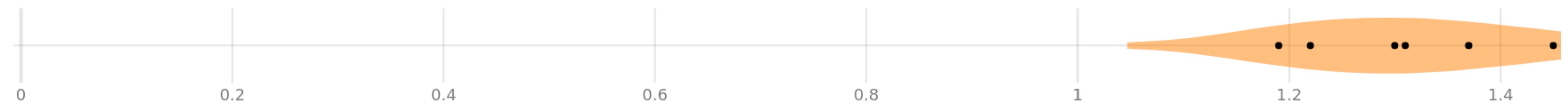
Custom content: Biotype Counts
% rRNA



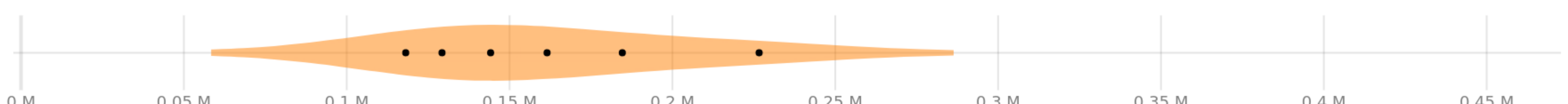
Picard: Mark Duplicates
Duplication



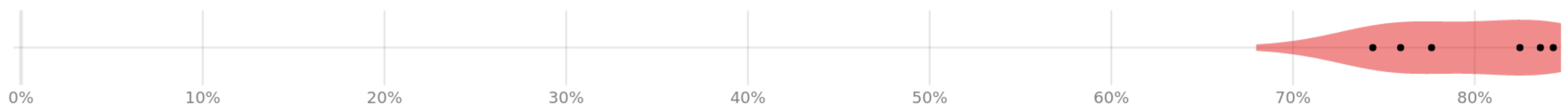
QualiMap: RNASeq
5'-3' bias



QualiMap: RNASeq
M Aligned



RSeQC: Bam Stat
Proper Pairs



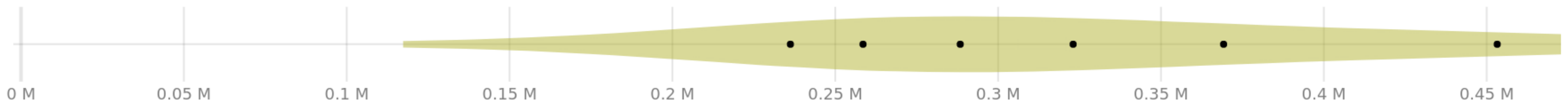
Samtools: stats
Error rate



Samtools: stats
Non-primary



Samtools: stats
Reads mapped



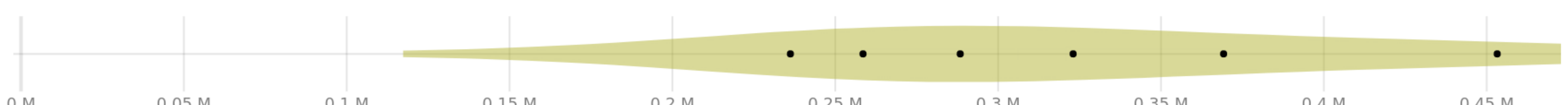
Samtools: stats
% Mapped



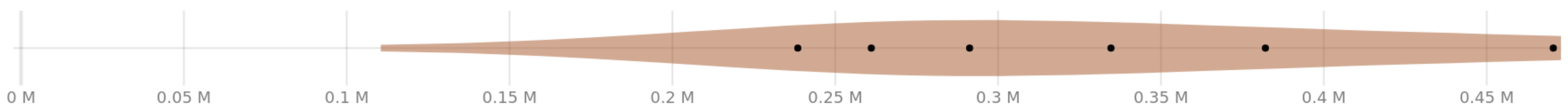
Samtools: stats
% Proper pairs



Samtools: stats
Total seqs



Samtools: flagstat
Reads mapped



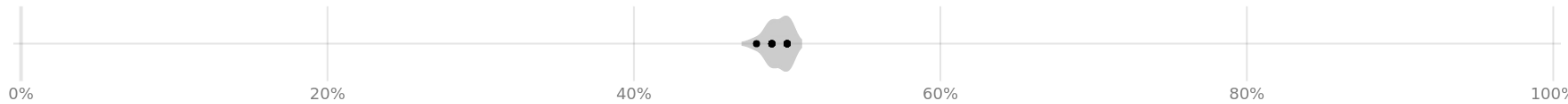
STAR
Aligned



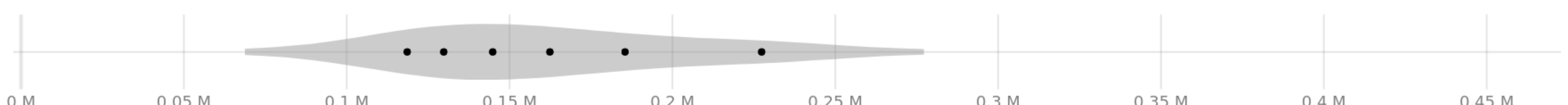
STAR
Uniq aligned



FastQC (raw)
% GC



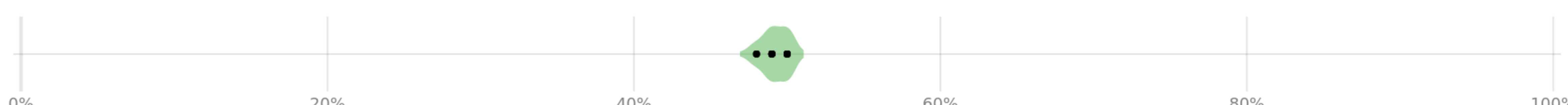
FastQC (raw)
M Seqs



Cutadapt
% BP Trimmed



FastQC (trimmed)
% GC



FastQC (trimmed)
M Seqs

