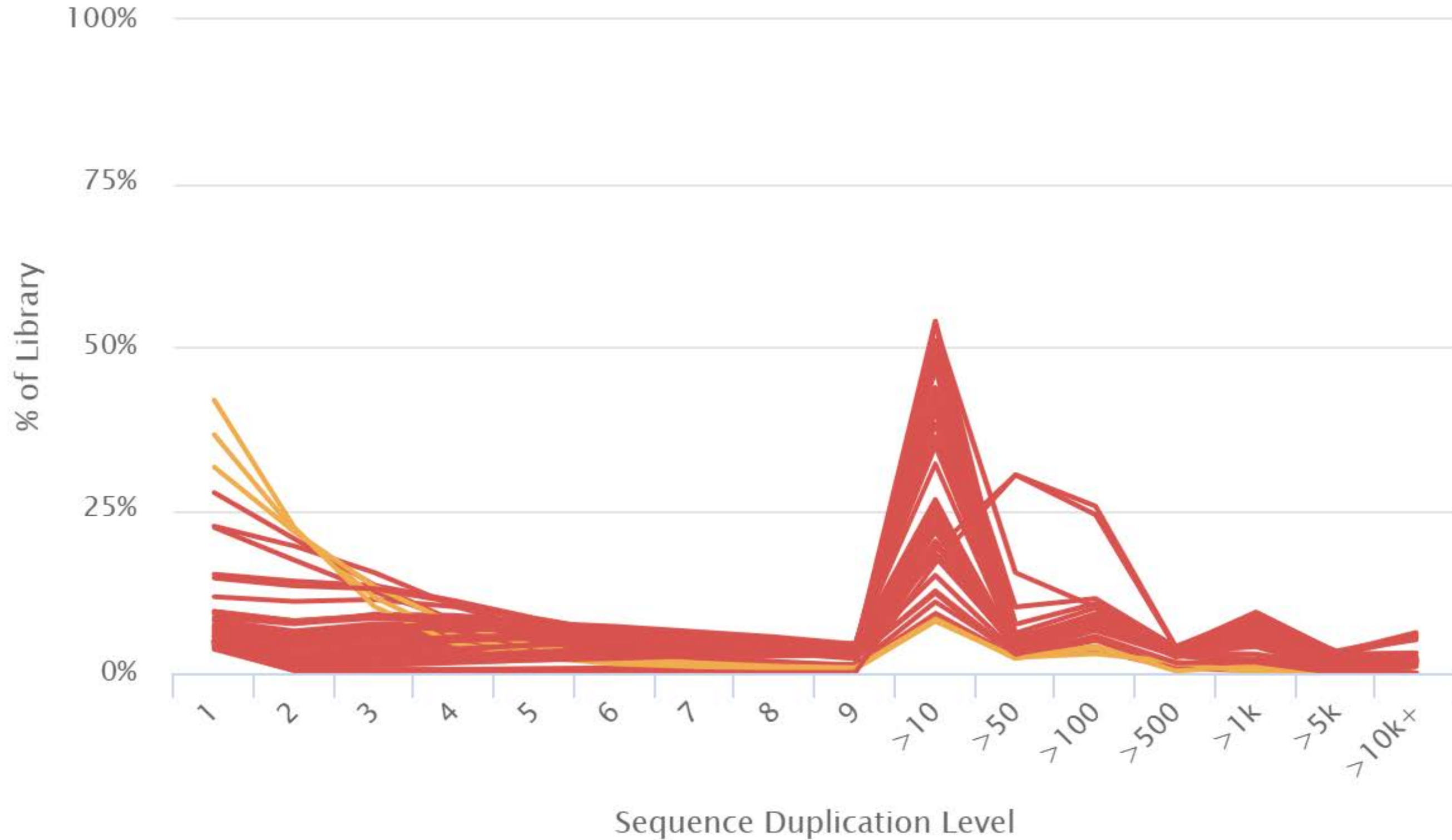
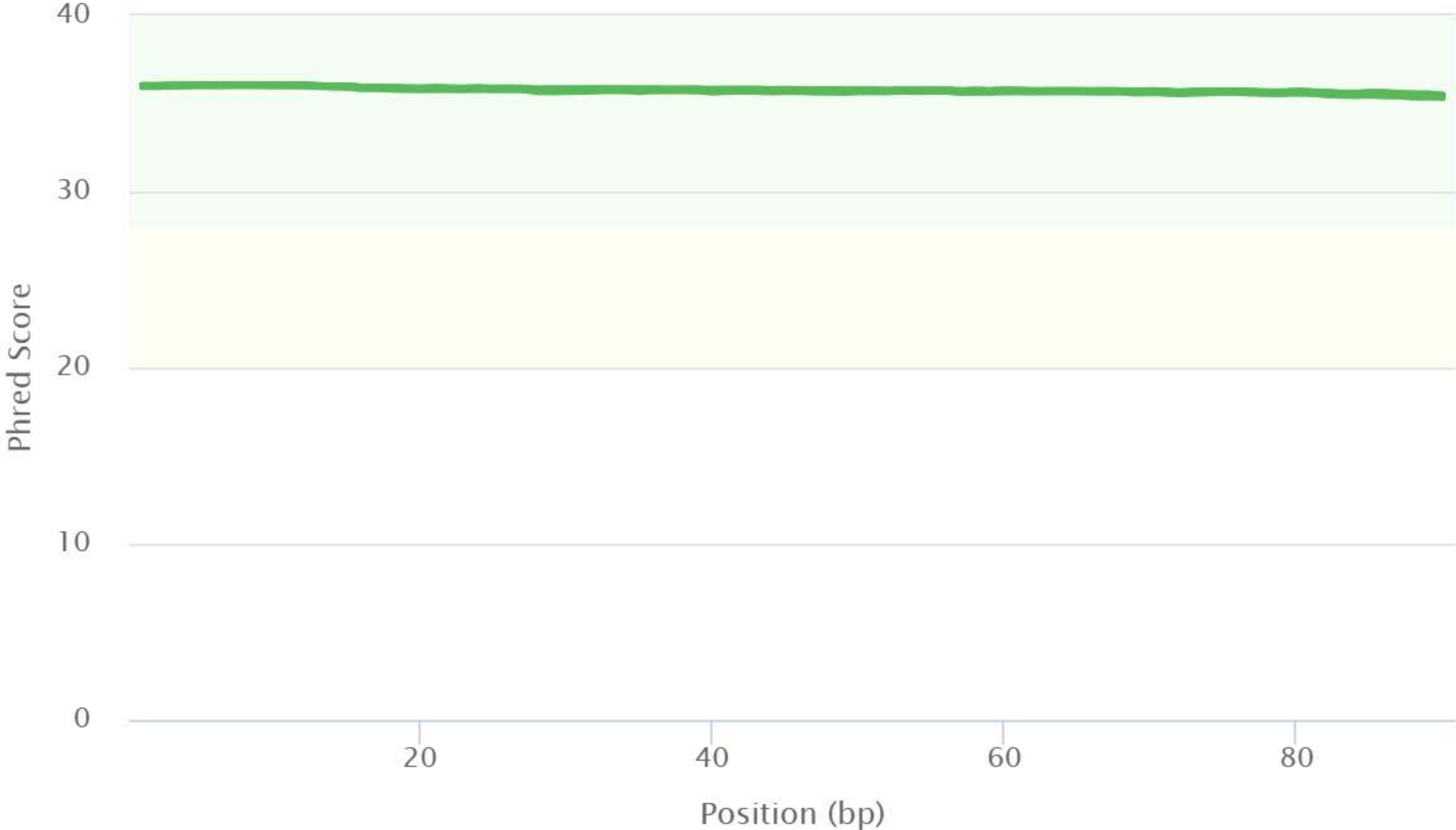


Supplement VIII

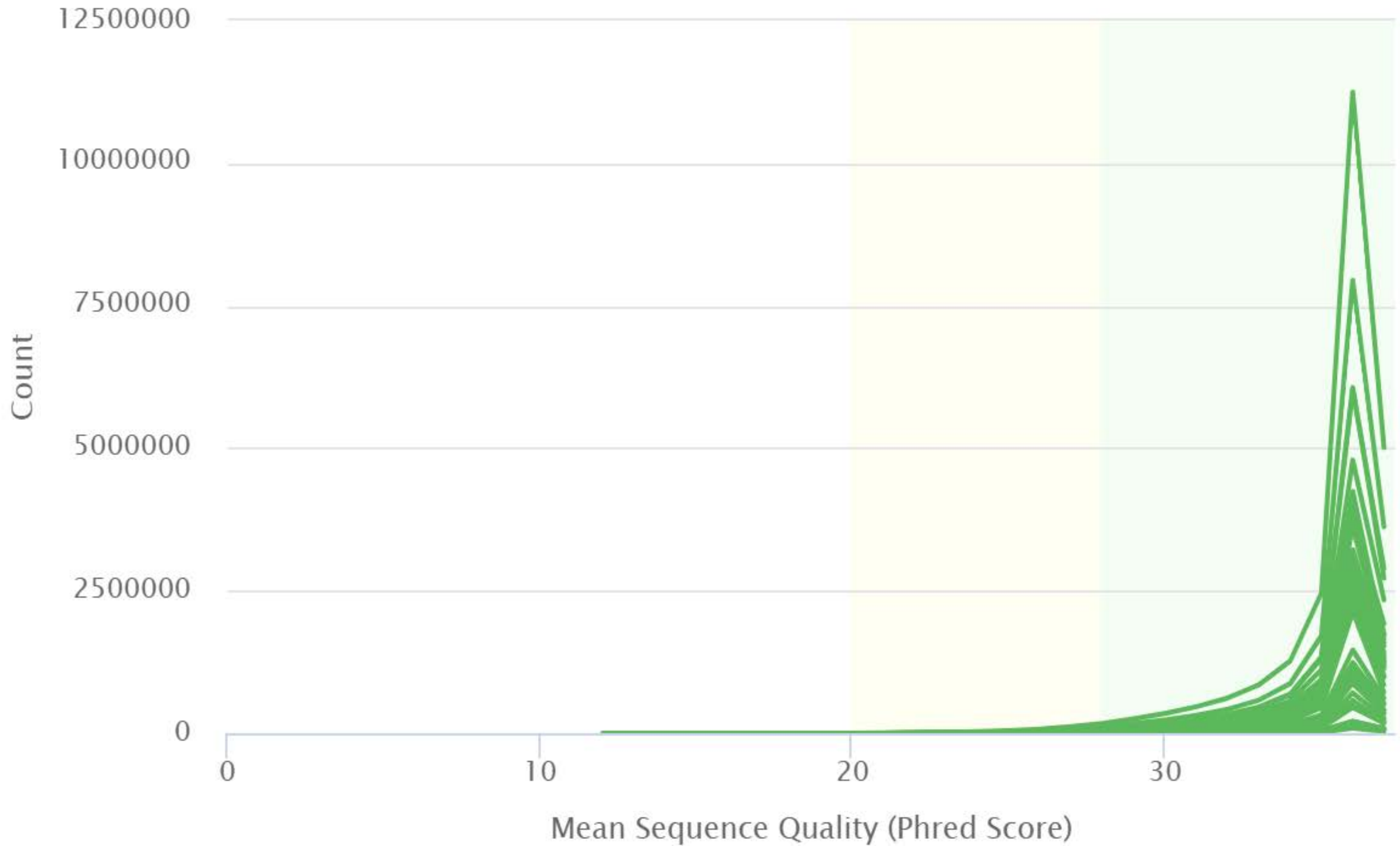
FastQC: Sequence Duplication Levels



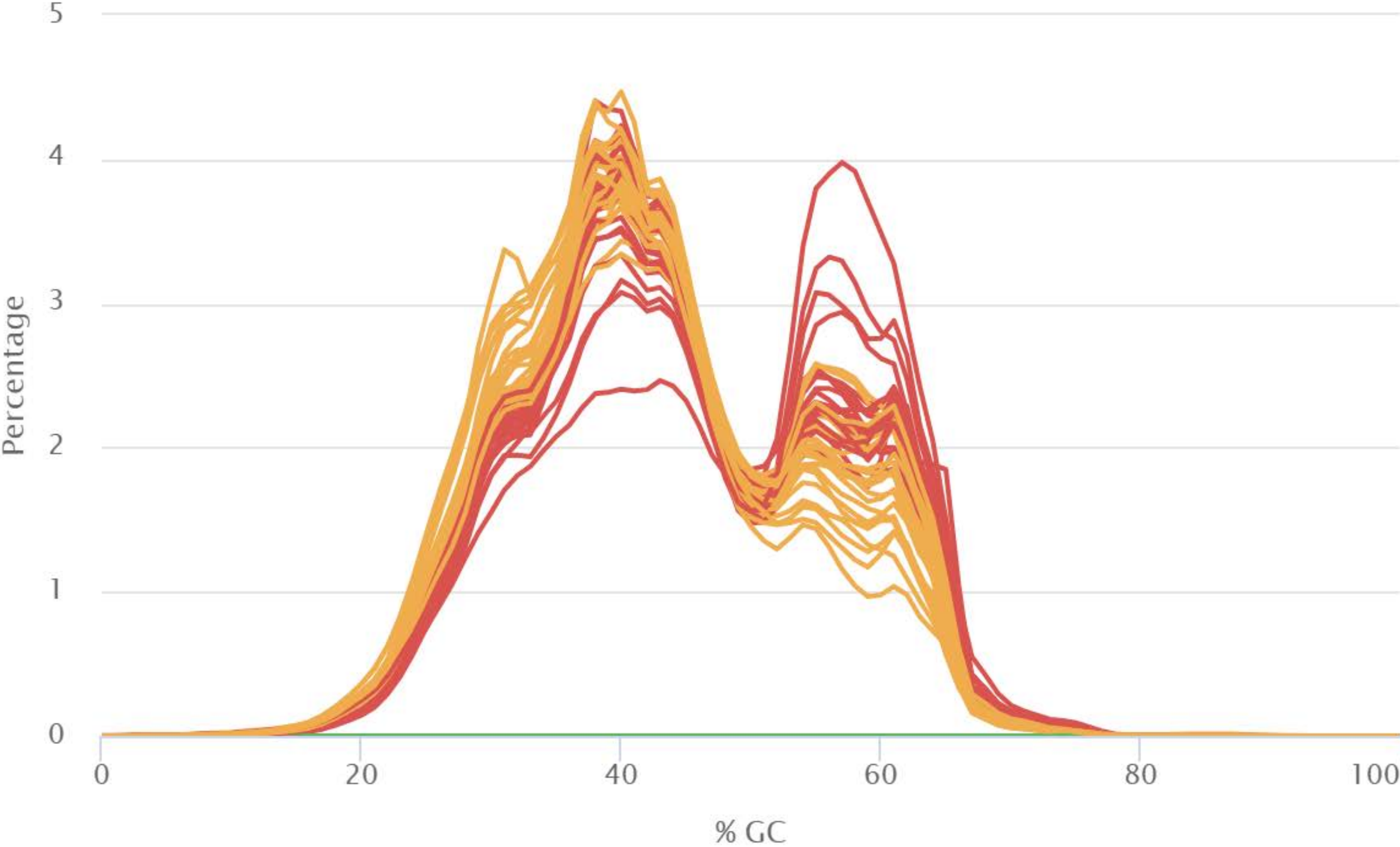
FastQC: Mean Quality Scores



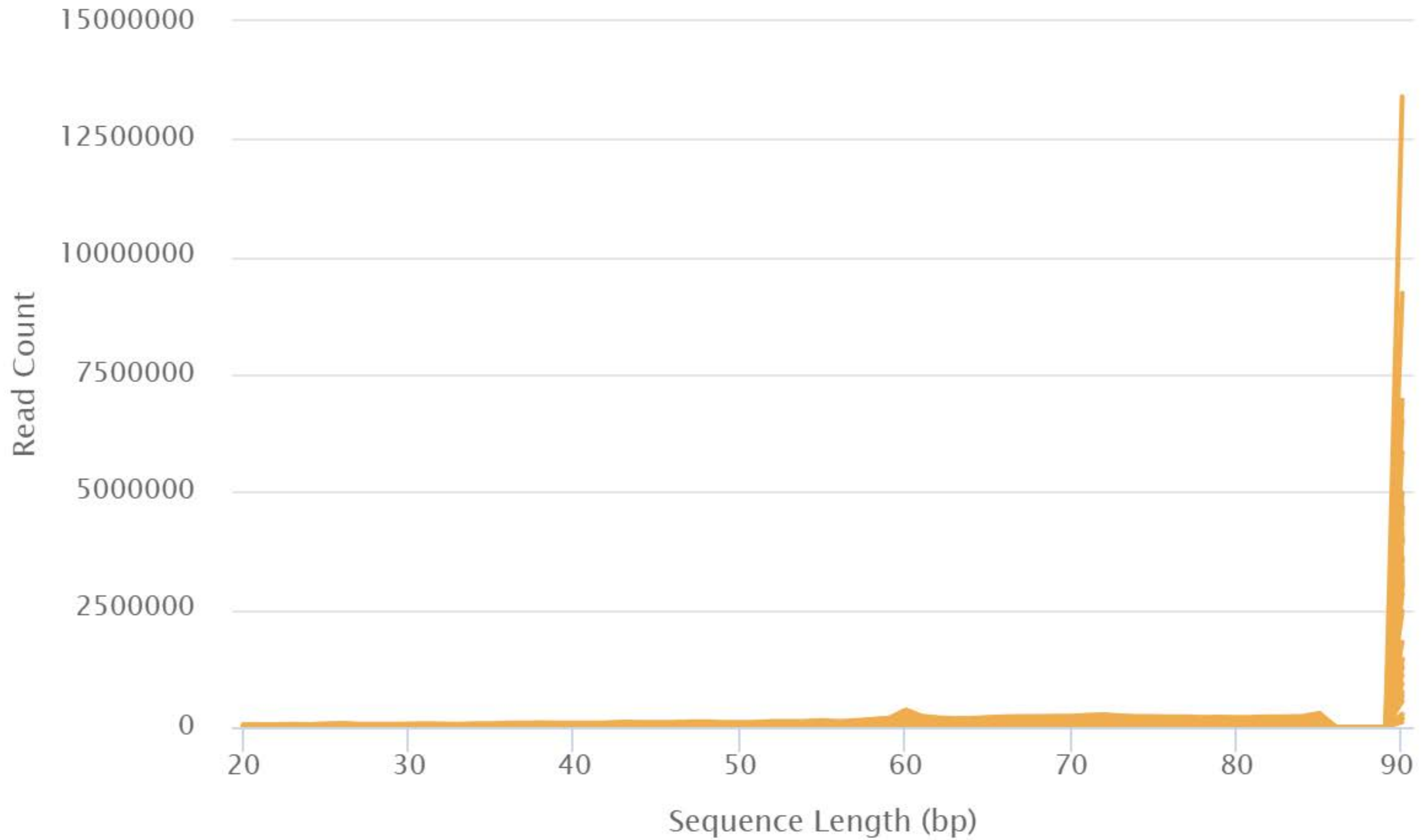
FastQC: Per Sequence Quality Scores



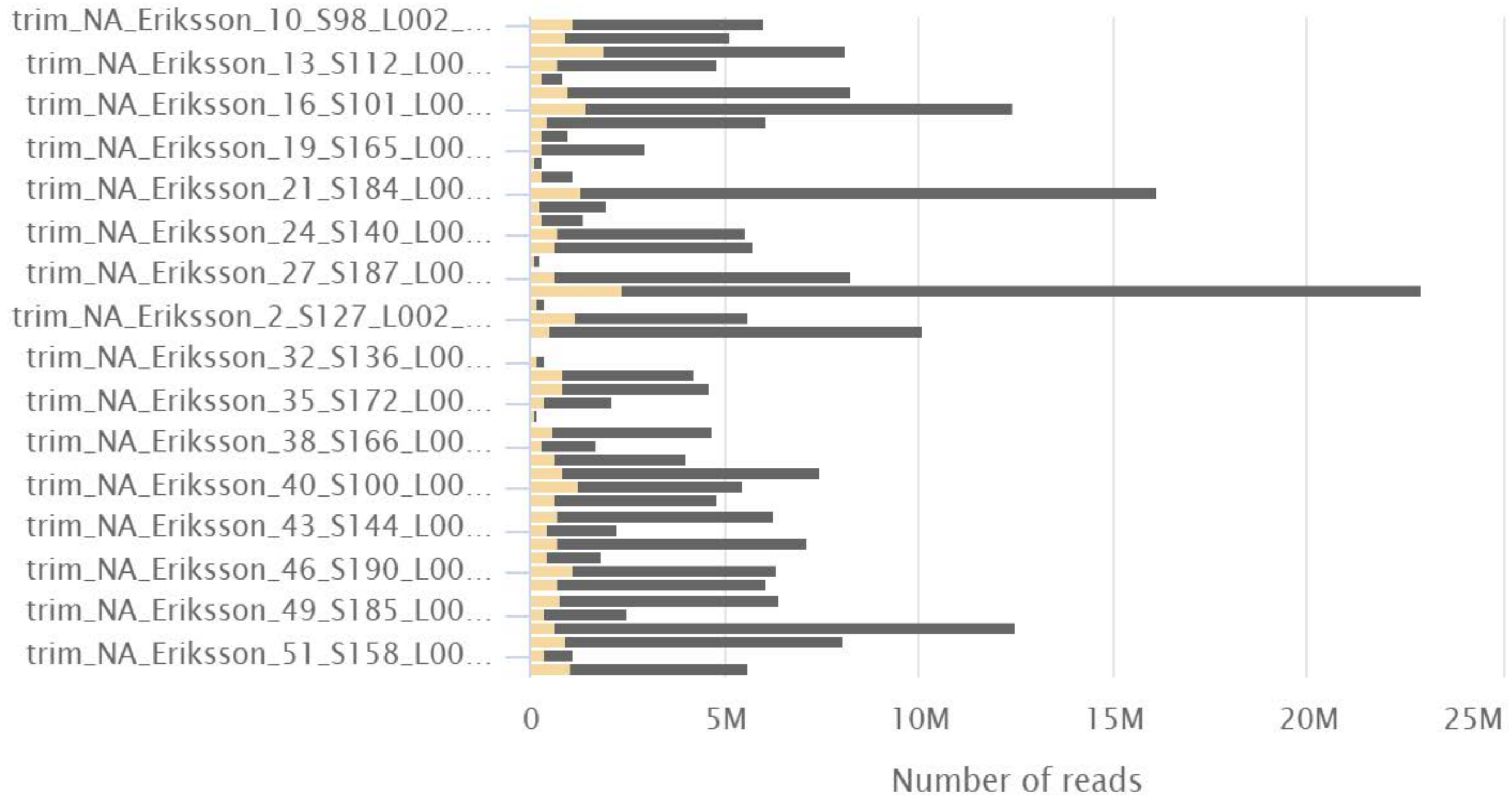
FastQC: Per Sequence GC Content



FastQC: Sequence Length Distribution

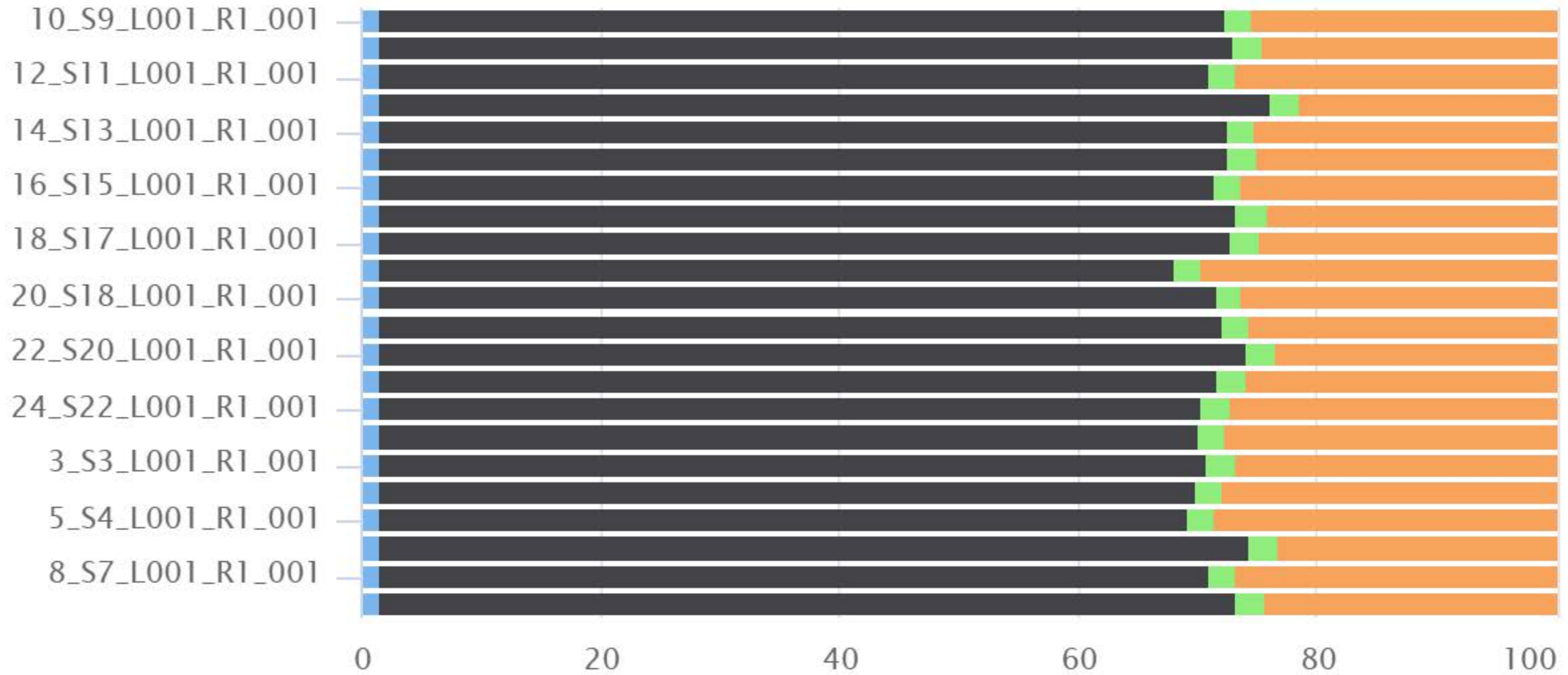


FastQC: Sequence Counts



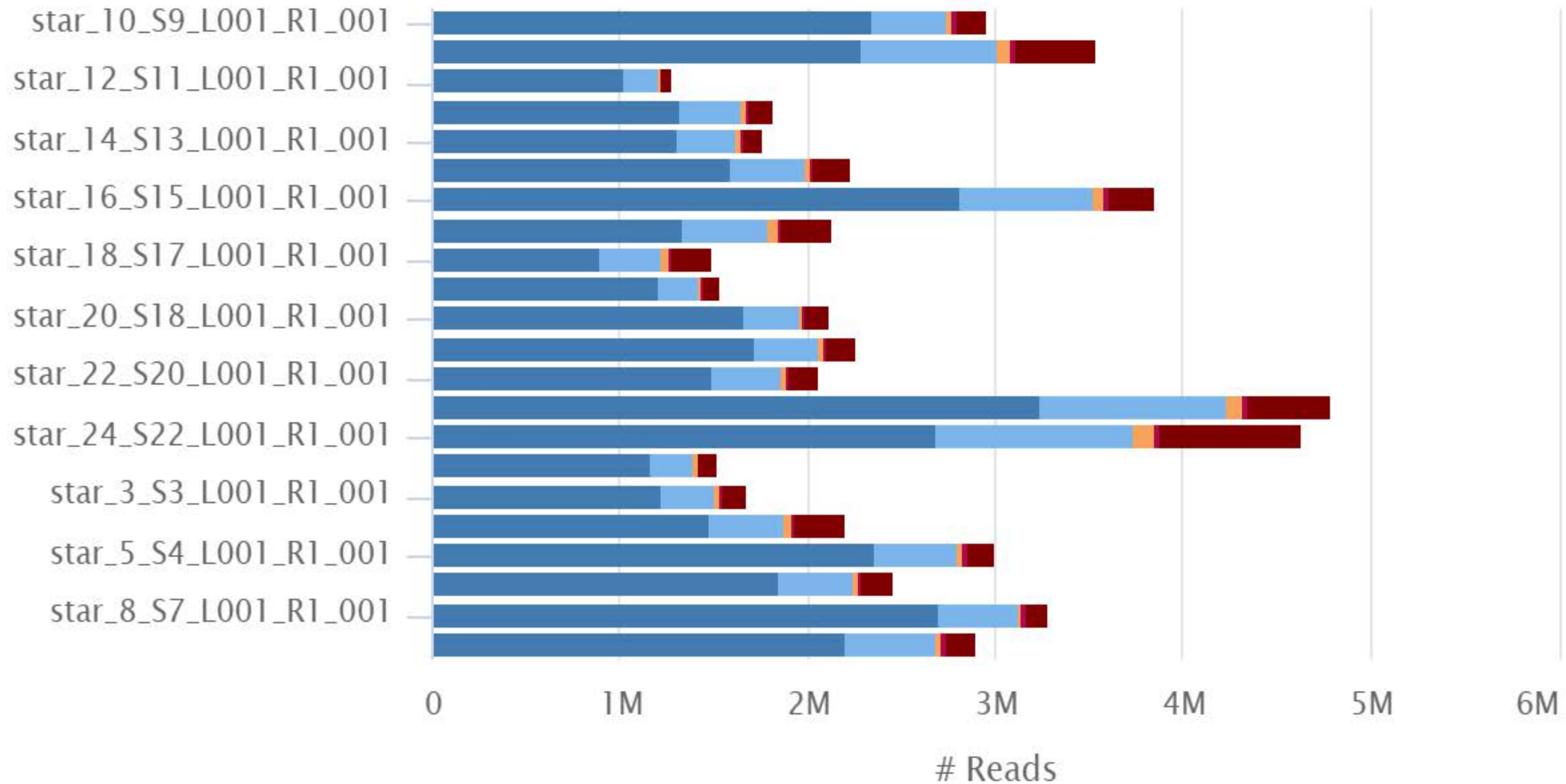
● Unique Reads ● Duplicate Reads

QoRTs: Strand Test



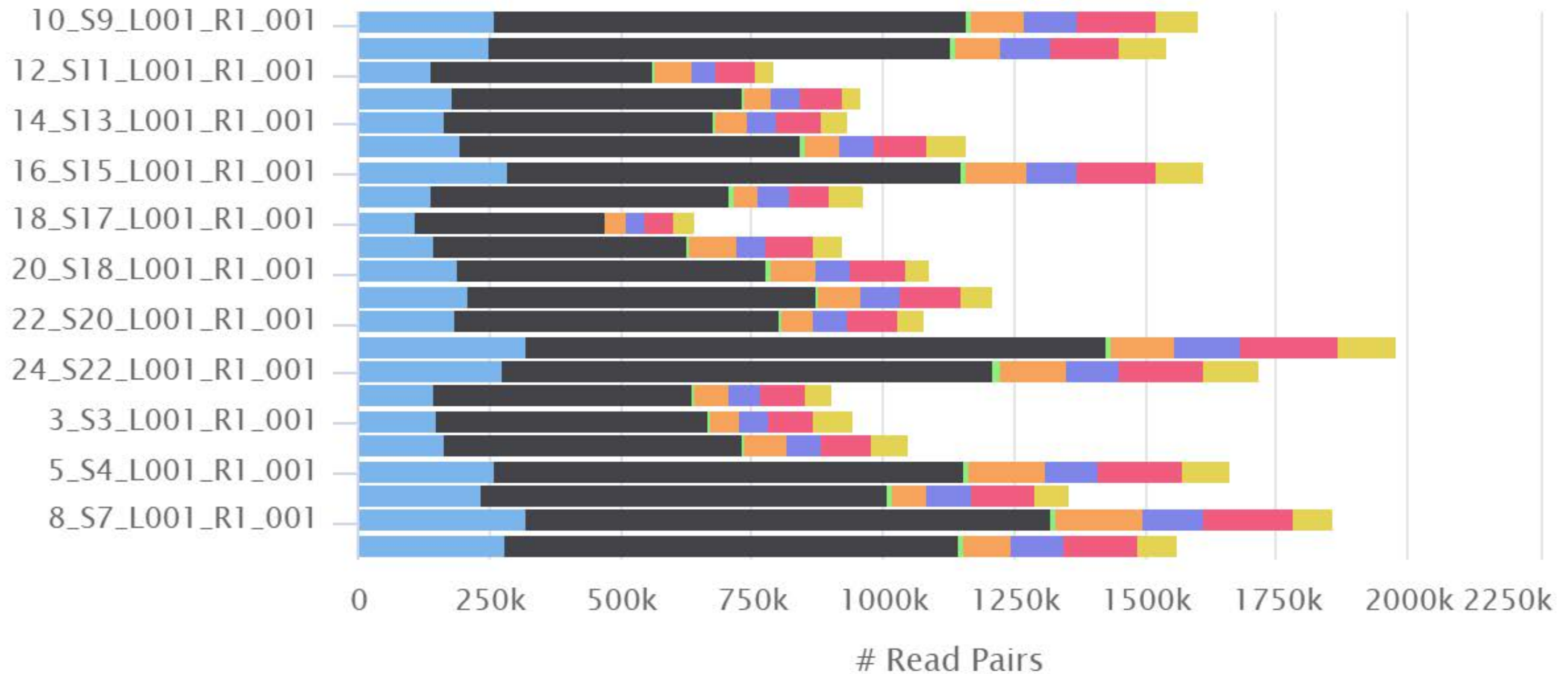
- Fr First Strand
- Fr Second Strand
- Ambig: Genes Found On Both Strands
- Ambig: No Genes

STAR: Alignment Scores



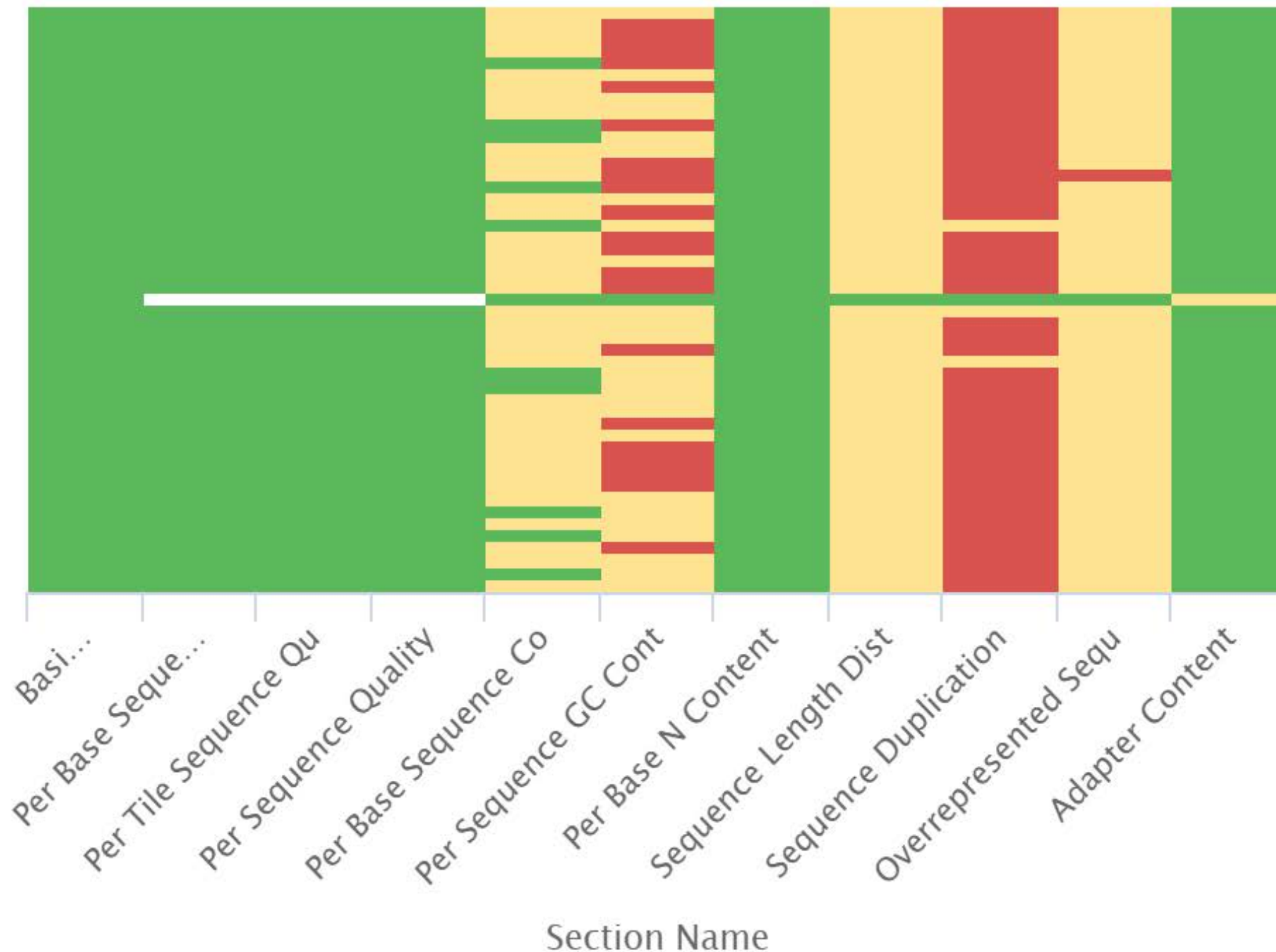
- Uniquely mapped
- Mapped to multiple loci
- Mapped to too many loci
- Unmapped: too short
- Unmapped: other

QoRTs: Alignment Locations



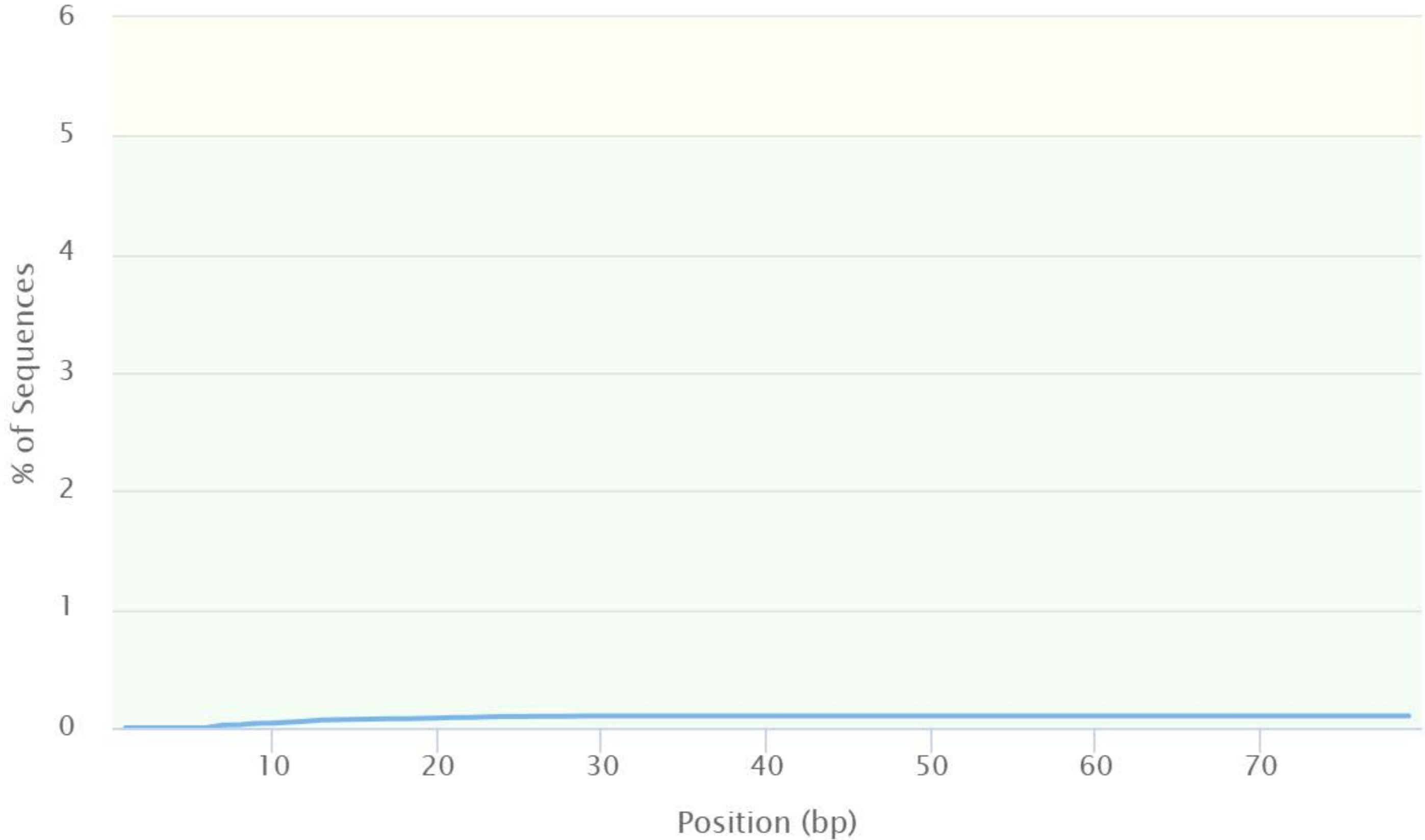
- Unique Gene: CDS
 ● Unique Gene: UTR
● Ambig Gene
● No Gene: Intron
- No Gene: One Kb From Gene
 ● No Gene: Ten Kb From Gene
- No Gene: Middle Of Nowhere

FastQC: Status Checks

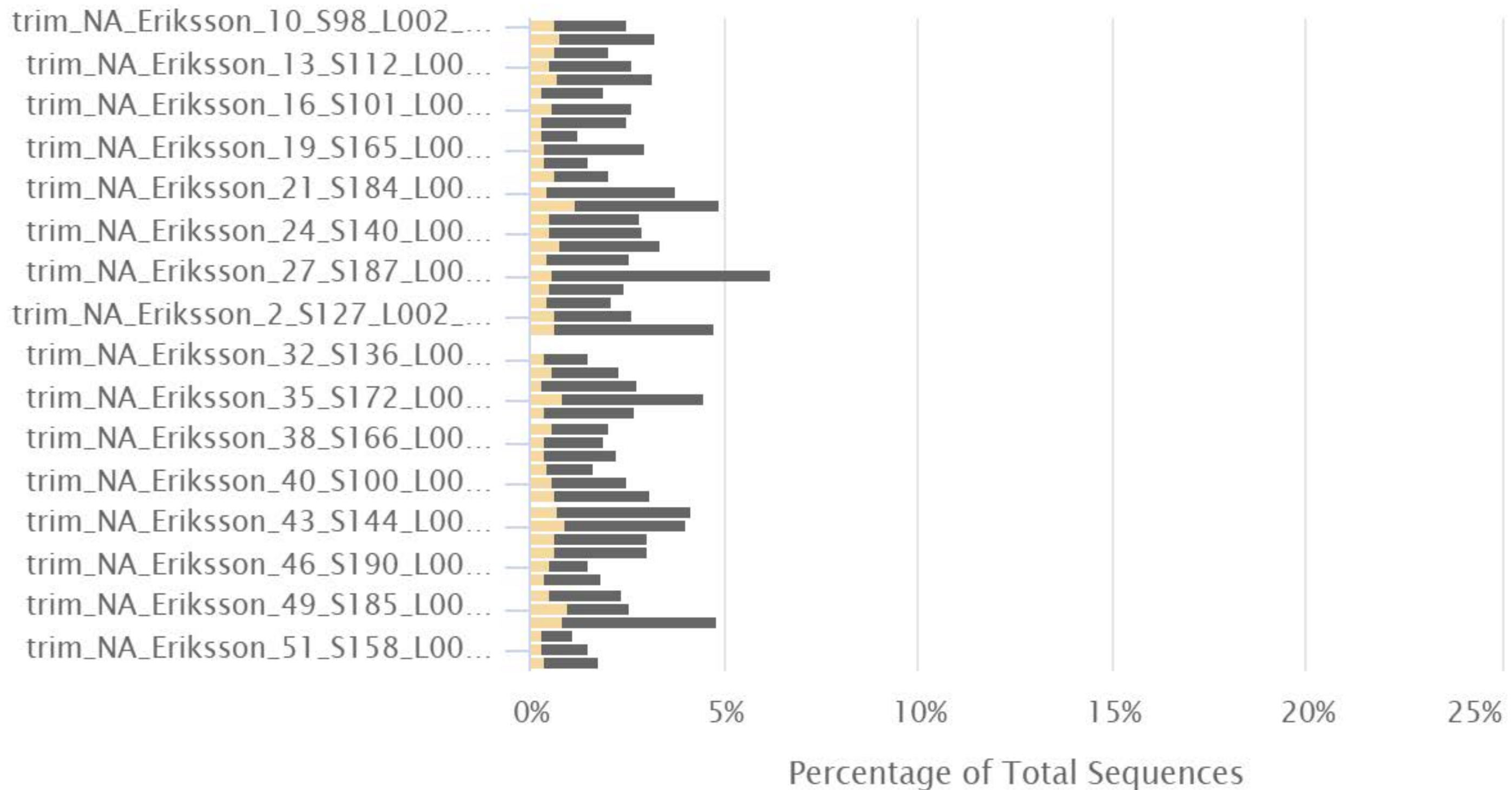


trim_NA_Eriksson_10_
 trim_NA_Eriksson_14_
 trim_NA_Eriksson_18_
 trim_NA_Eriksson_21_
 trim_NA_Eriksson_25_
 trim_NA_Eriksson_29_
 trim_NA_Eriksson_32_
 trim_NA_Eriksson_36_
 trim_NA_Eriksson_3_S
 trim_NA_Eriksson_43_
 trim_NA_Eriksson_47_
 trim_NA_Eriksson_50_

FastQC: Adapter Content



FastQC: Overrepresented sequences



● Top over-represented sequence

● Sum of remaining over-represented sequences

FastQC: Per Base N Content

