

Homework Day 1 - FastQC

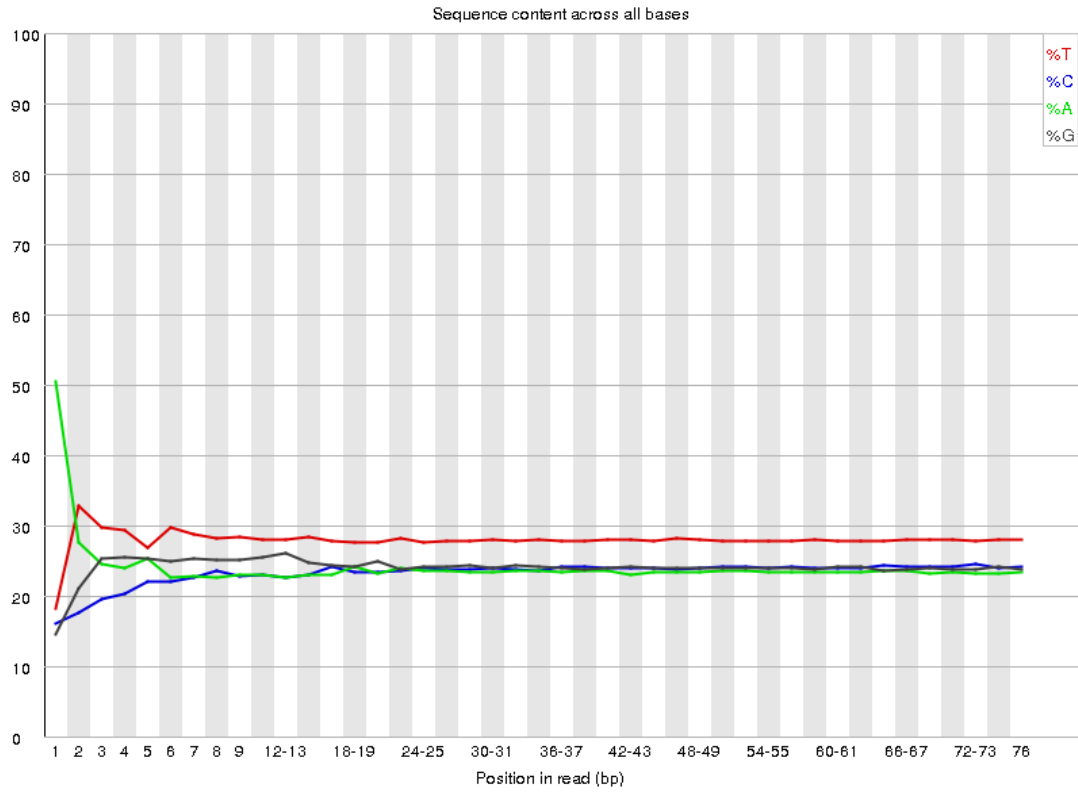
In class, we talked about how to read FastQC reports in the context of determining if there are overarching problems with a sequencing library.

Here, your job is to look at some FastQC reports to determine if a library looks good or whether it has problems (and what those problems might be). For each library, briefly answer the following questions:

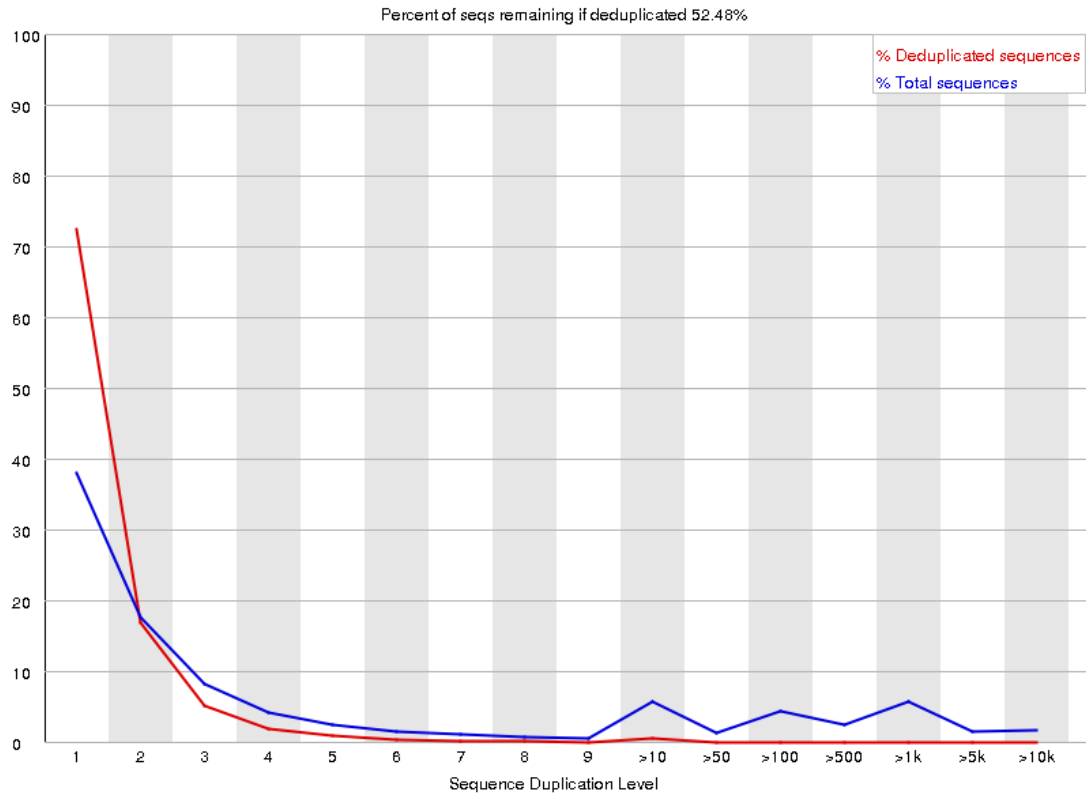
- 1) Does this library pass general QC?
- 2) If not:
 - 2a) What QC metric(s) show problems with the library?
 - 2b) What might be the biological or technological source of the problem(s)?

Library 1

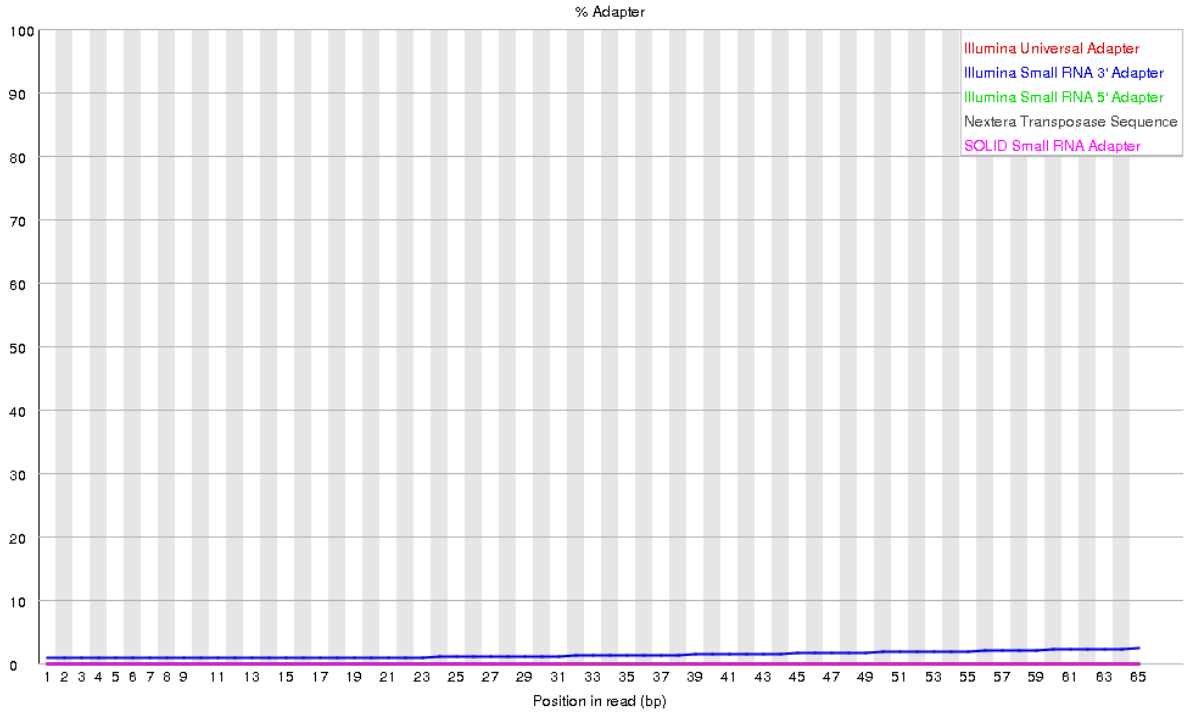
Per base sequence content



Sequence Duplication Levels

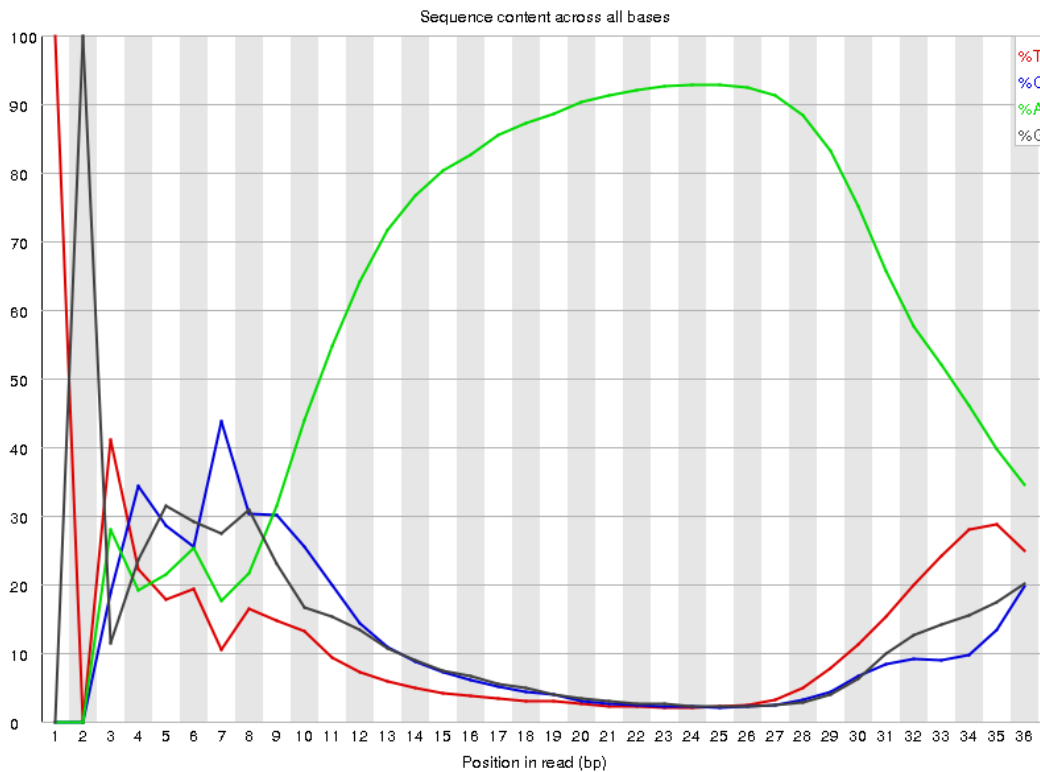


Adapter Content

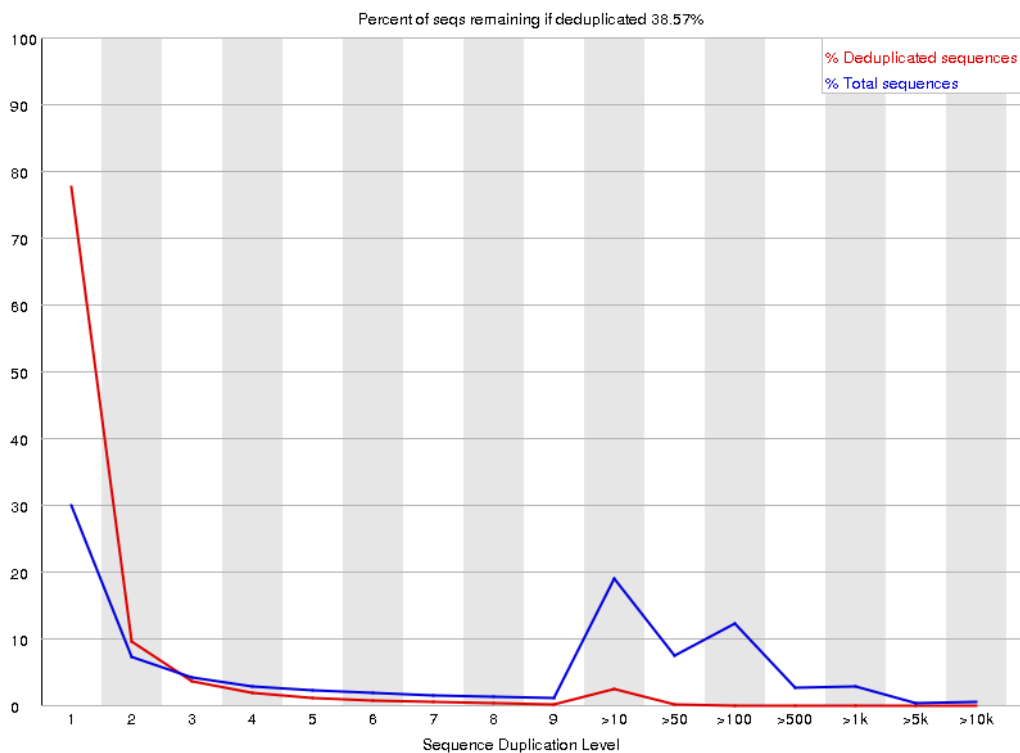


Library 2

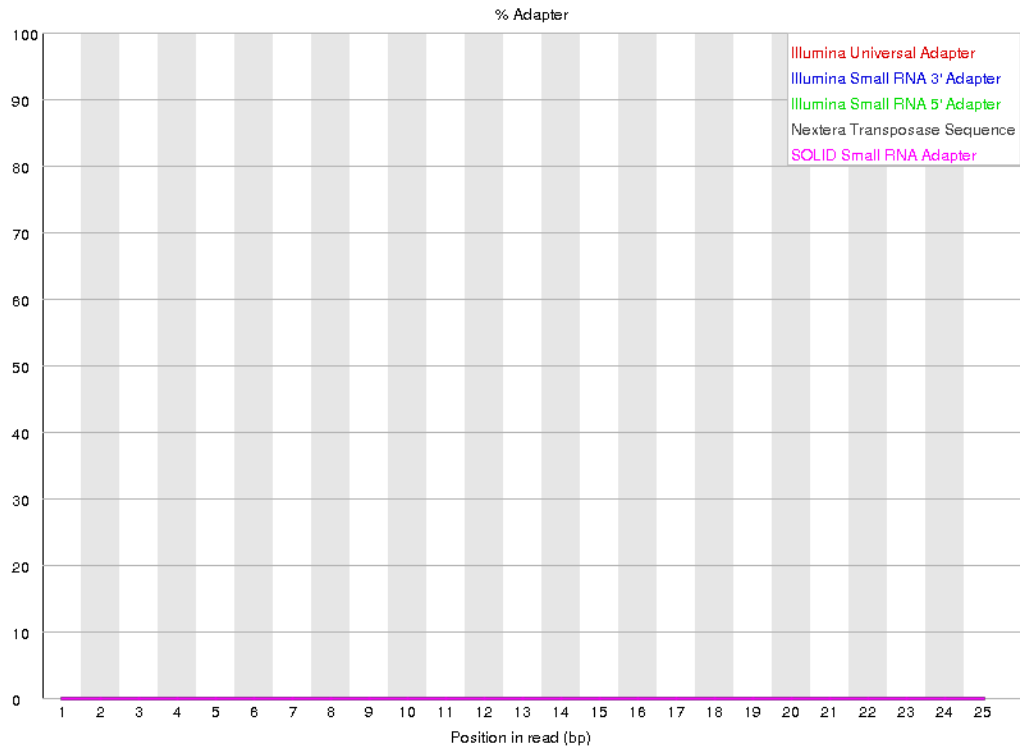
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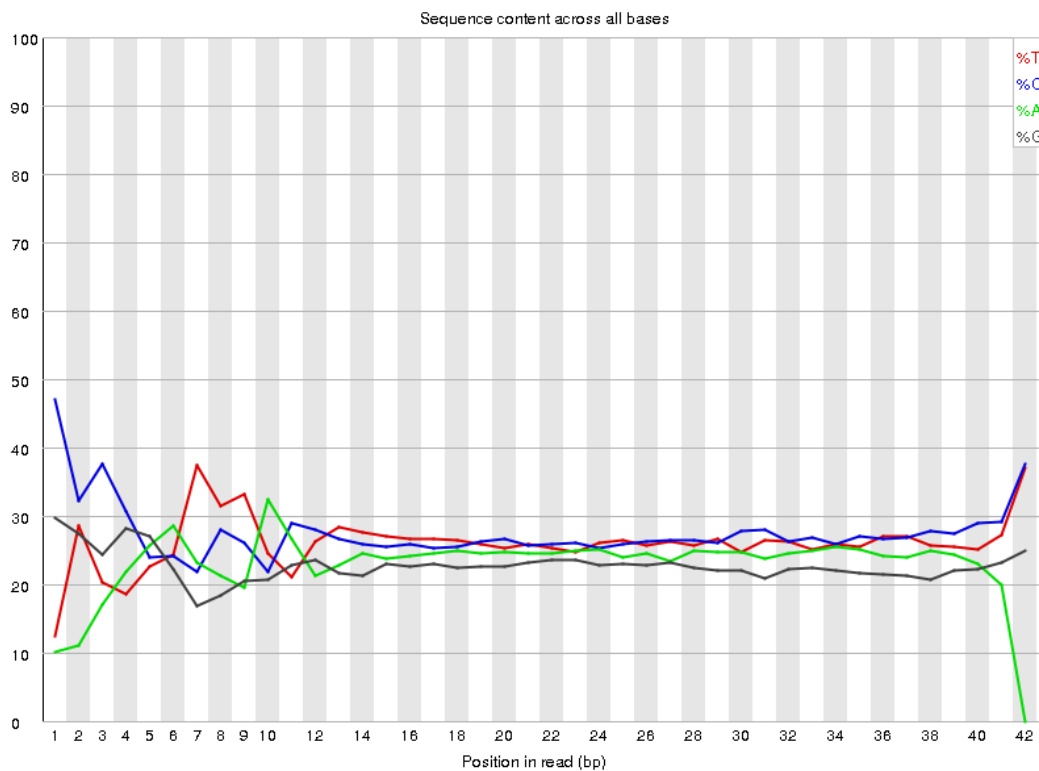


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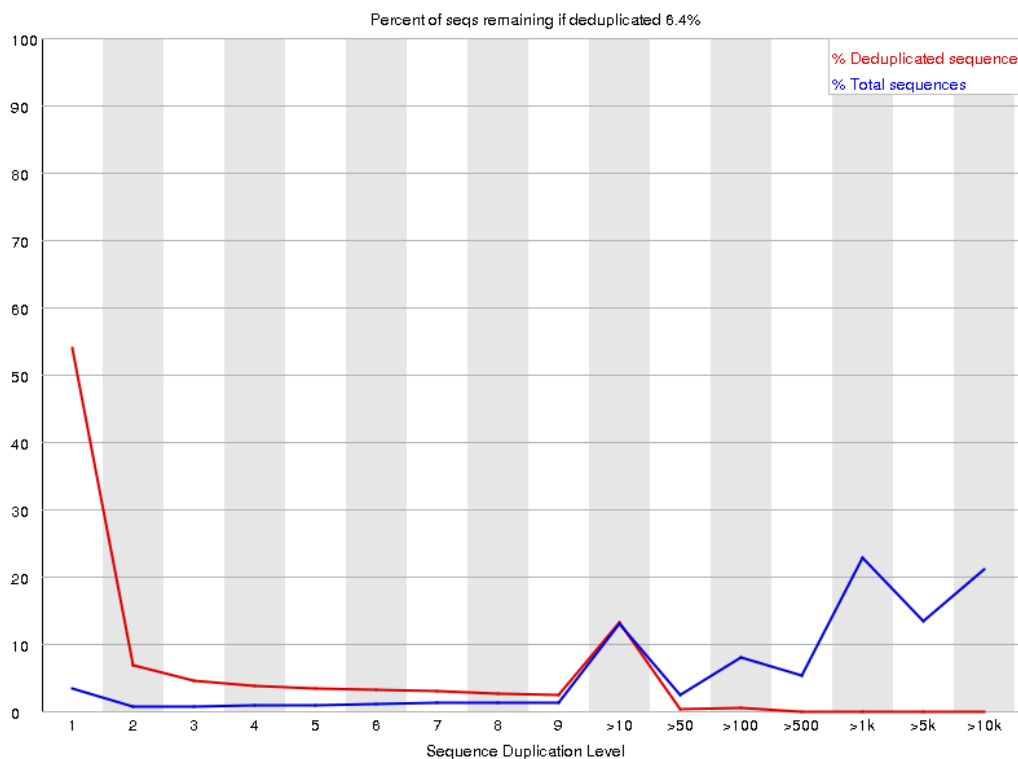


Library 3

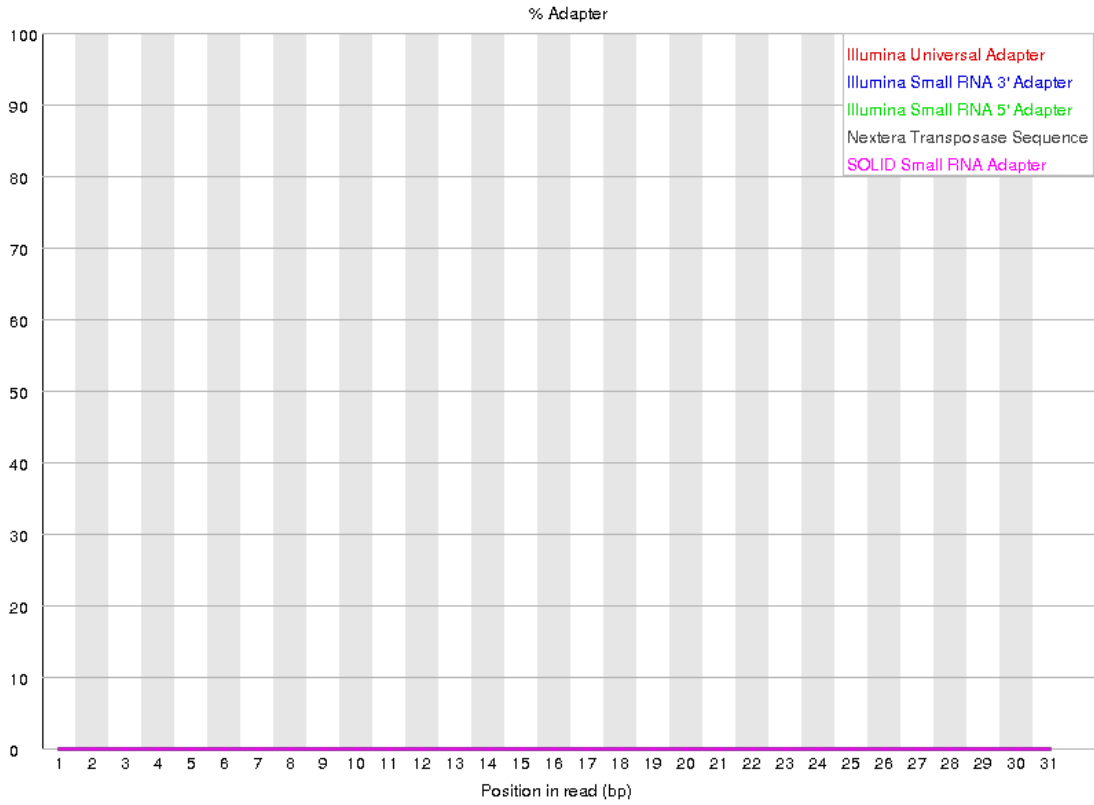
Per base sequence content



Sequence Duplication Levels

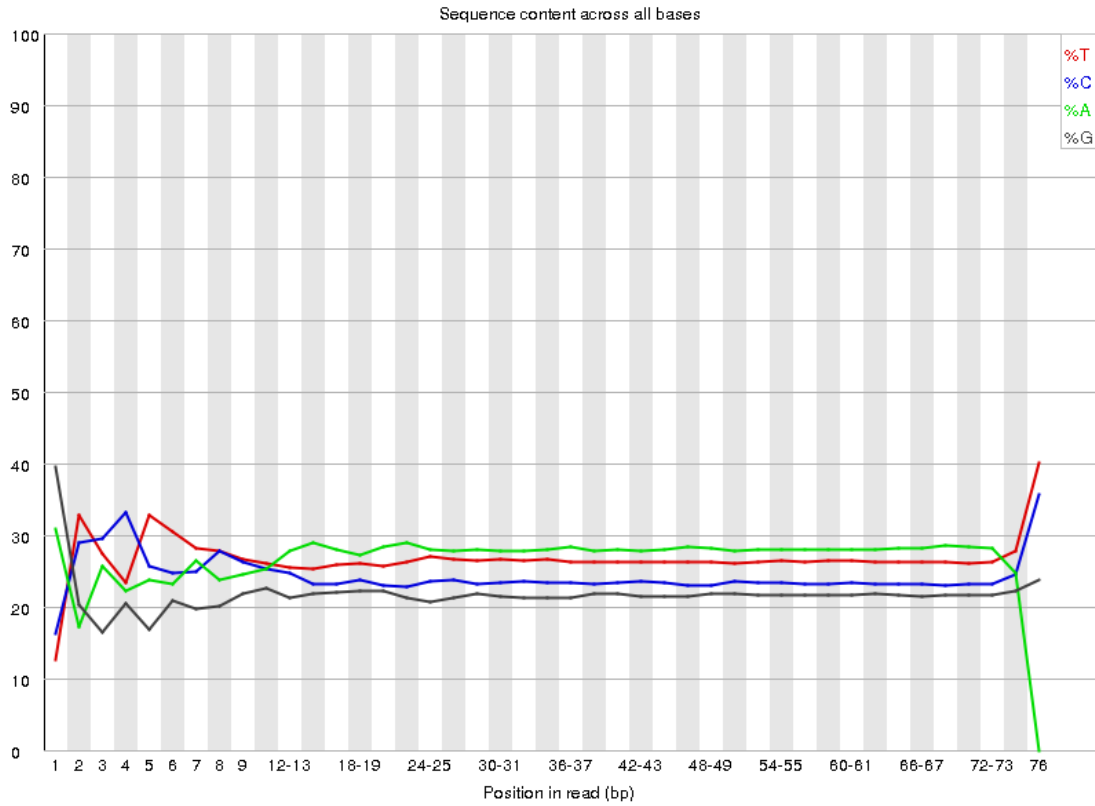


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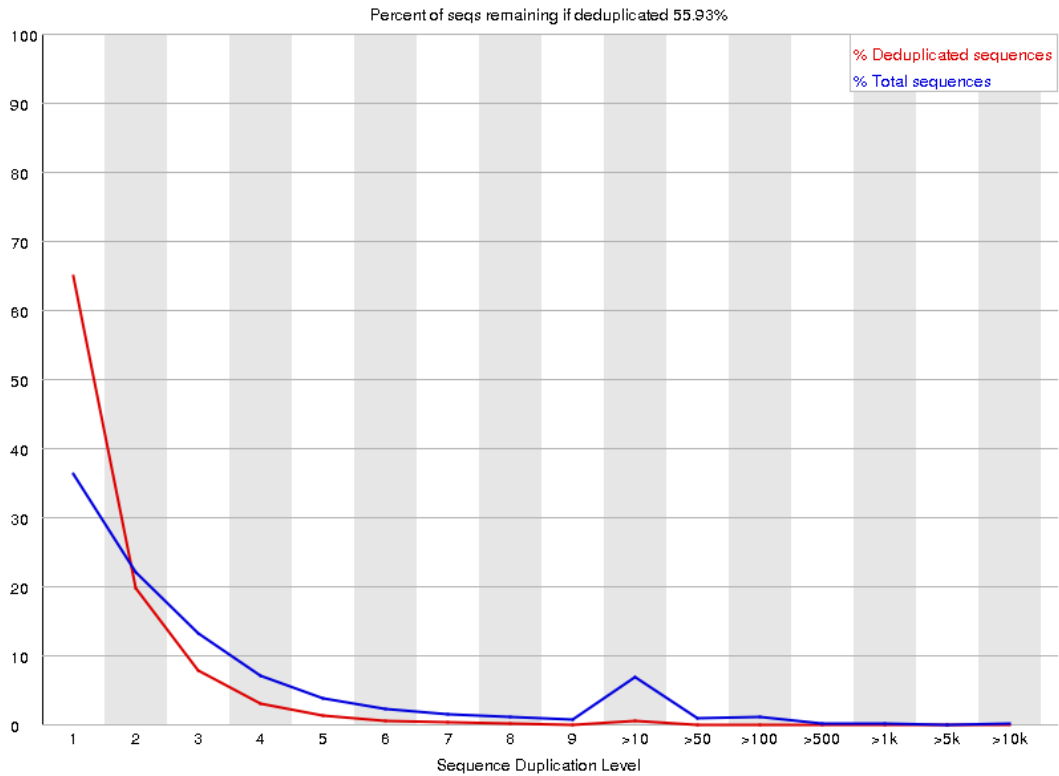


Library 4

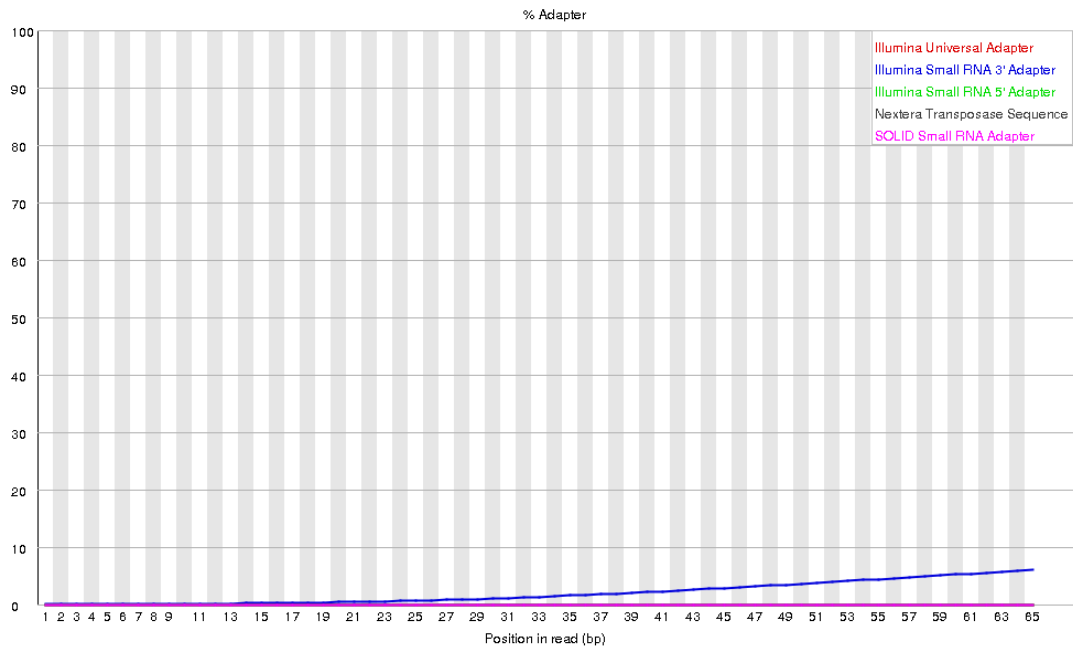
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Sequence Duplication Levels

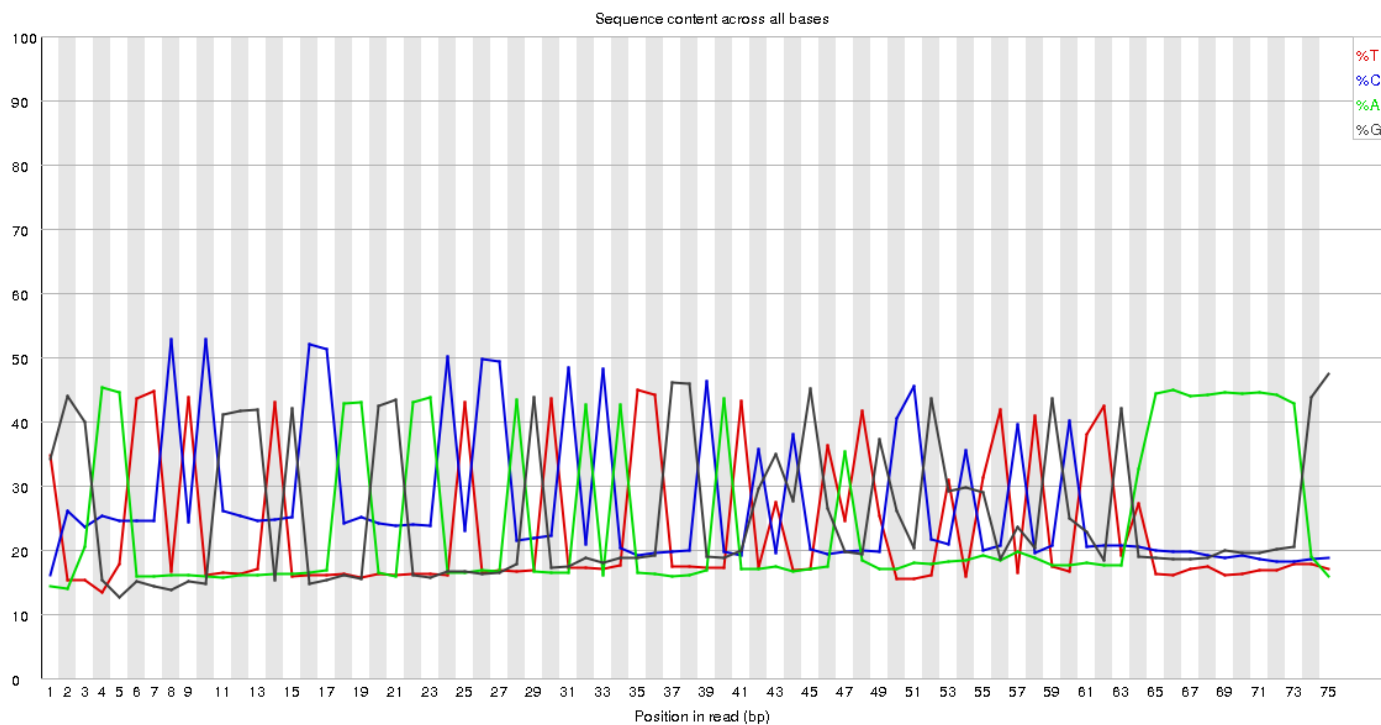


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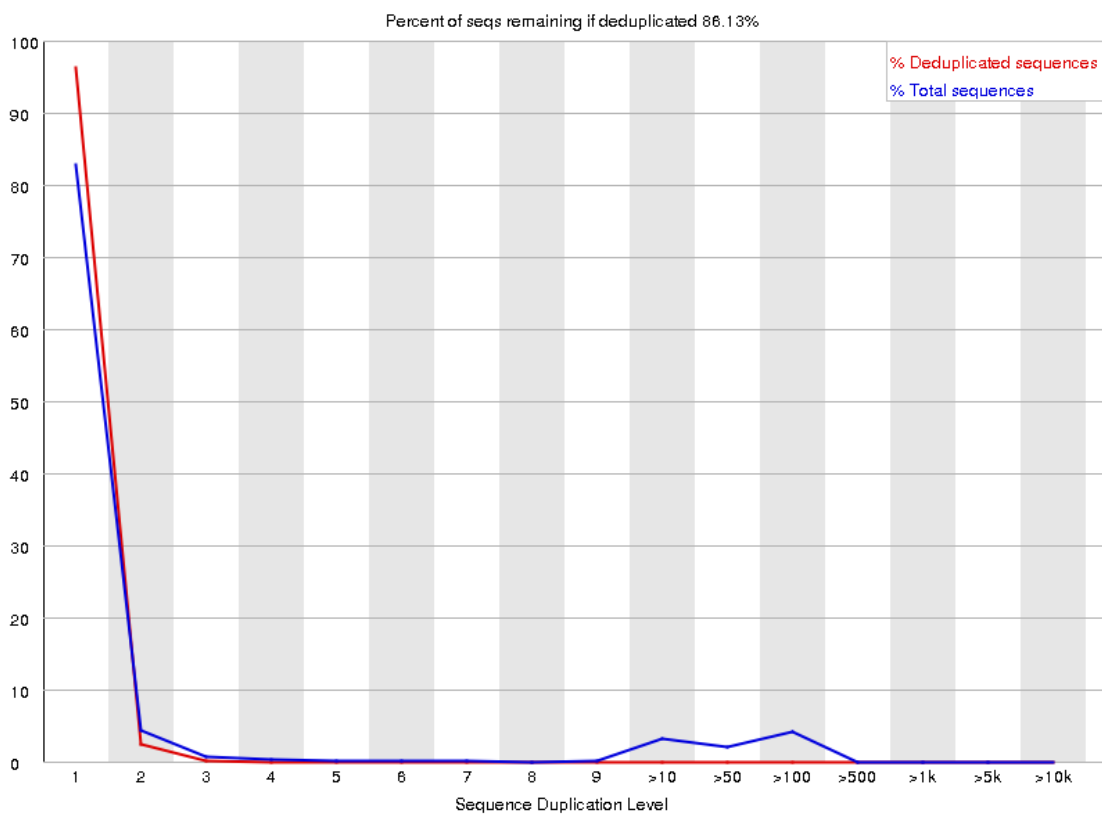


Library 5

Per base sequence content



Sequence Duplication Levels



Adapter Content

