

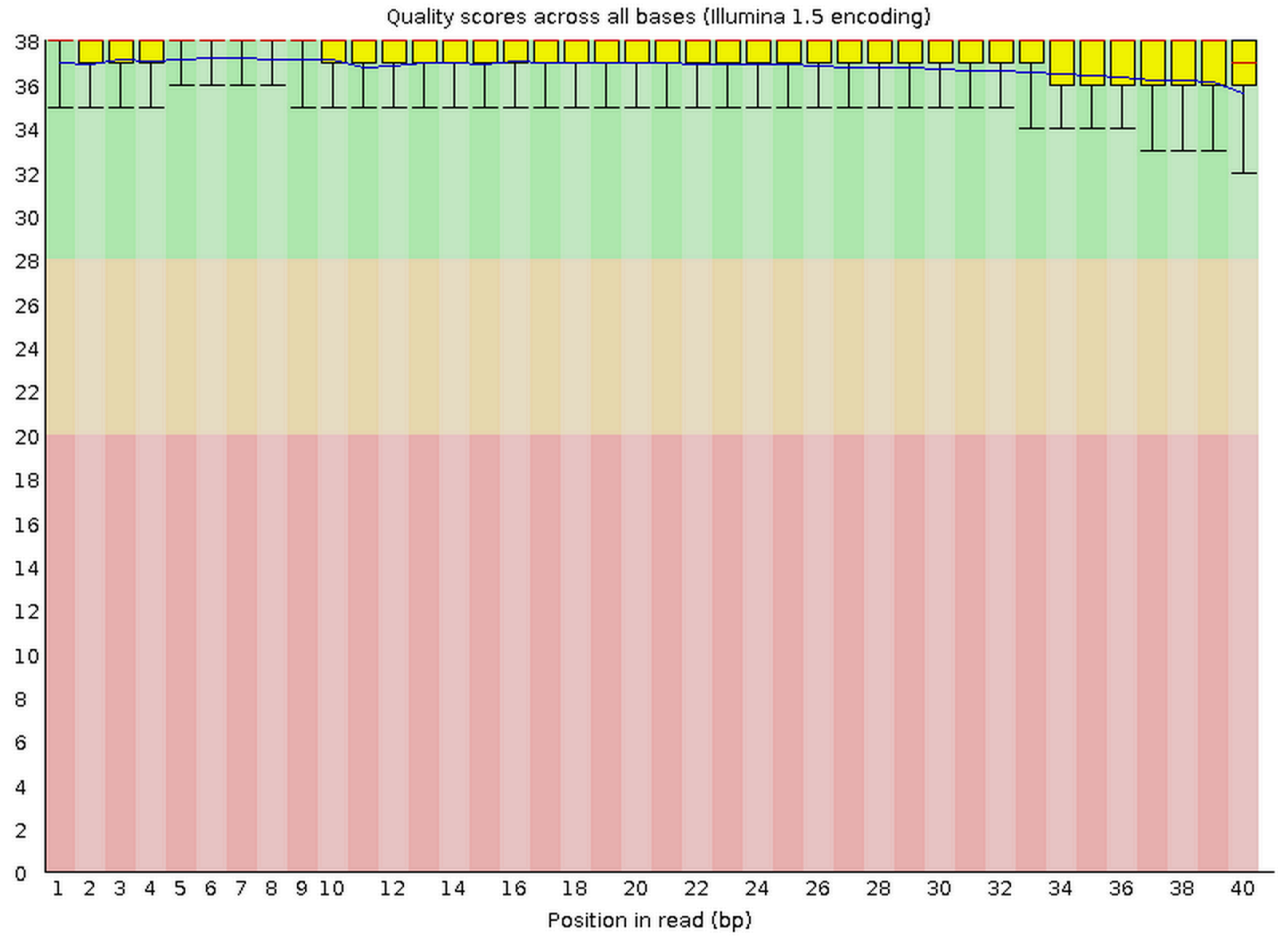
# FastQC Report

Wed 25 Mar 2015  
good\_sequence\_short.txt

## Summary

- ✔ [Basic Statistics](#)
- ✔ [Per base sequence quality](#)
- ✔ [Per tile sequence quality](#)
- ✔ [Per sequence quality scores](#)
- ! [Per base sequence content](#)
- ✔ [Per sequence GC content](#)
- ✔ [Per base N content](#)
- ✔ [Sequence Length Distribution](#)
- ✔ [Sequence Duplication Levels](#)
- ✔ [Overrepresented sequences](#)
- ✔ [Adapter Content](#)
- ! [Kmer Content](#)

## ✔ Per base sequence quality

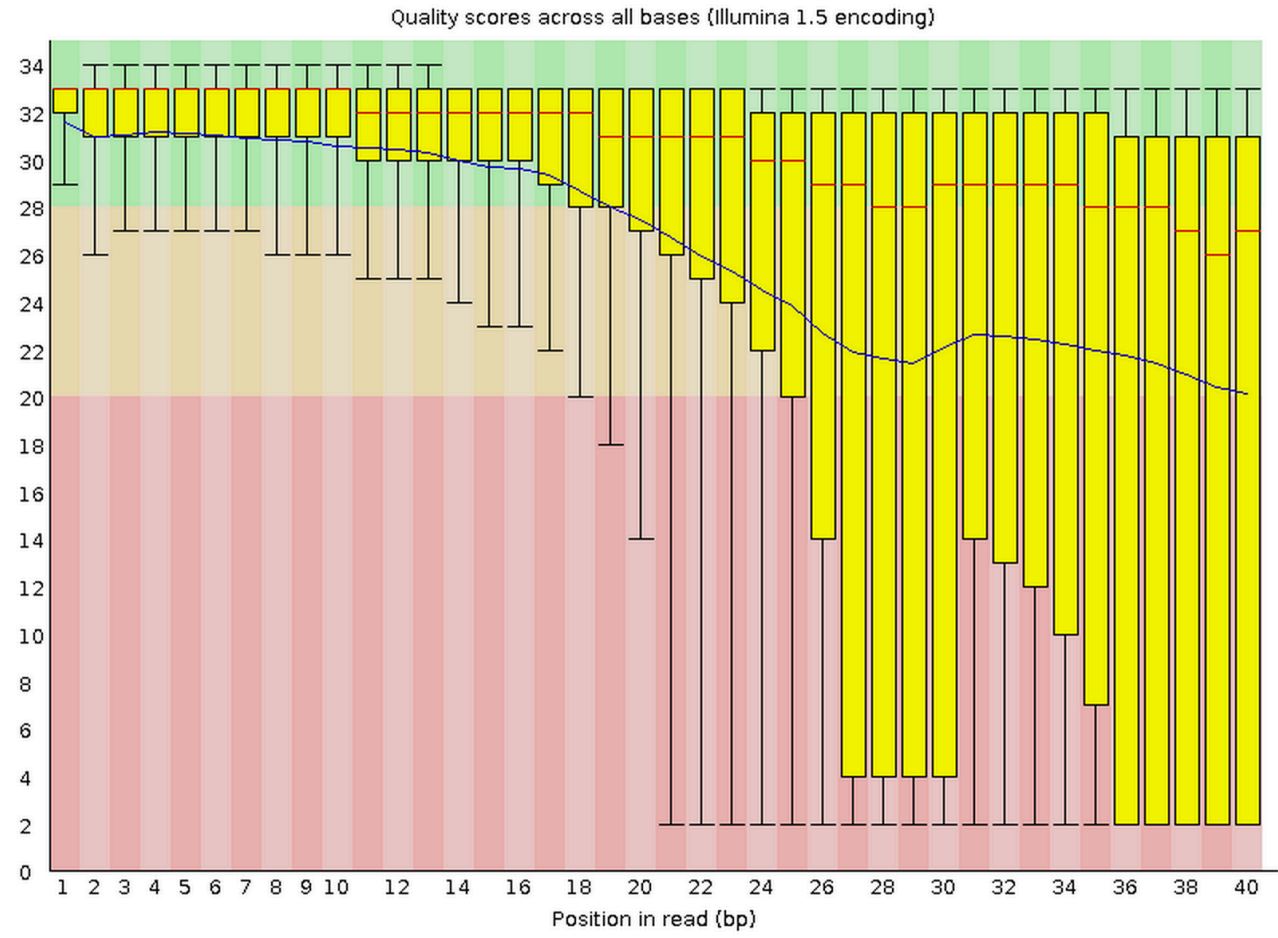


# FastQC Report

## Summary

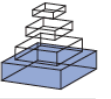
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## ✘ Per base sequence quality



# What to do?

- Trim the reads?
- Start over – try sequencing it again?



# On the optimal trimming of high-throughput mRNA sequence data

**Matthew D. MacManes**<sup>1,2\*</sup>

<sup>1</sup> Department of Molecular, Cellular and Biomedical Sciences, University of New Hampshire, Durham, NH, USA

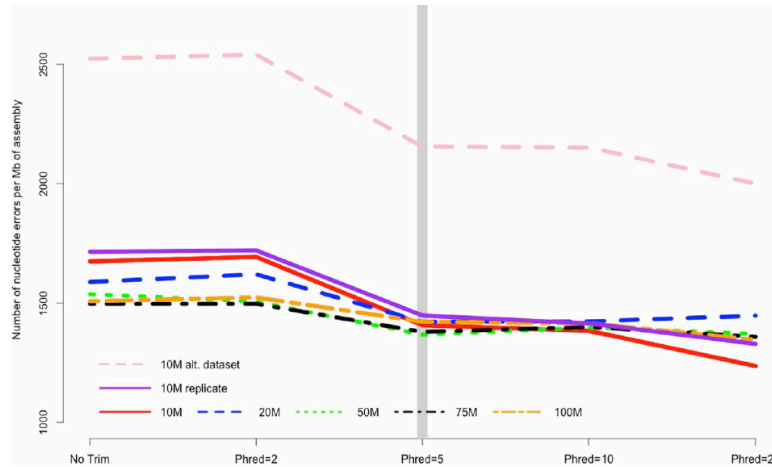
<sup>2</sup> Hubbard Center for Genome Studies, Durham, NH, USA

“... researchers interested in assembling transcriptomes de novo should elect for a much gentler quality trimming, or no trimming at all.”

“... trimming at PHRED=2 or PHRED=5 optimizes assembly quality.”

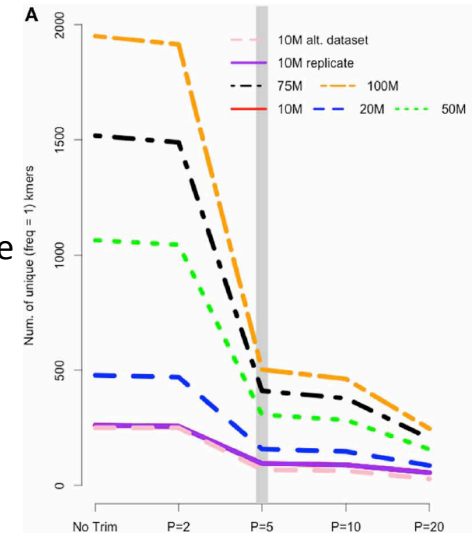
# Aggressive Trimming may be harmful, whereas light trimming could be beneficial

## Fewer errors in the assembly



# Nucleotide errors / Mb

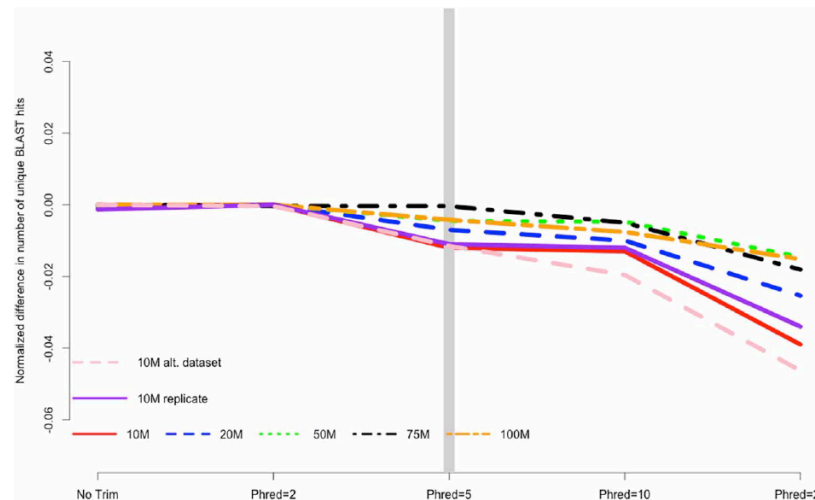
## Fewer unique kmers



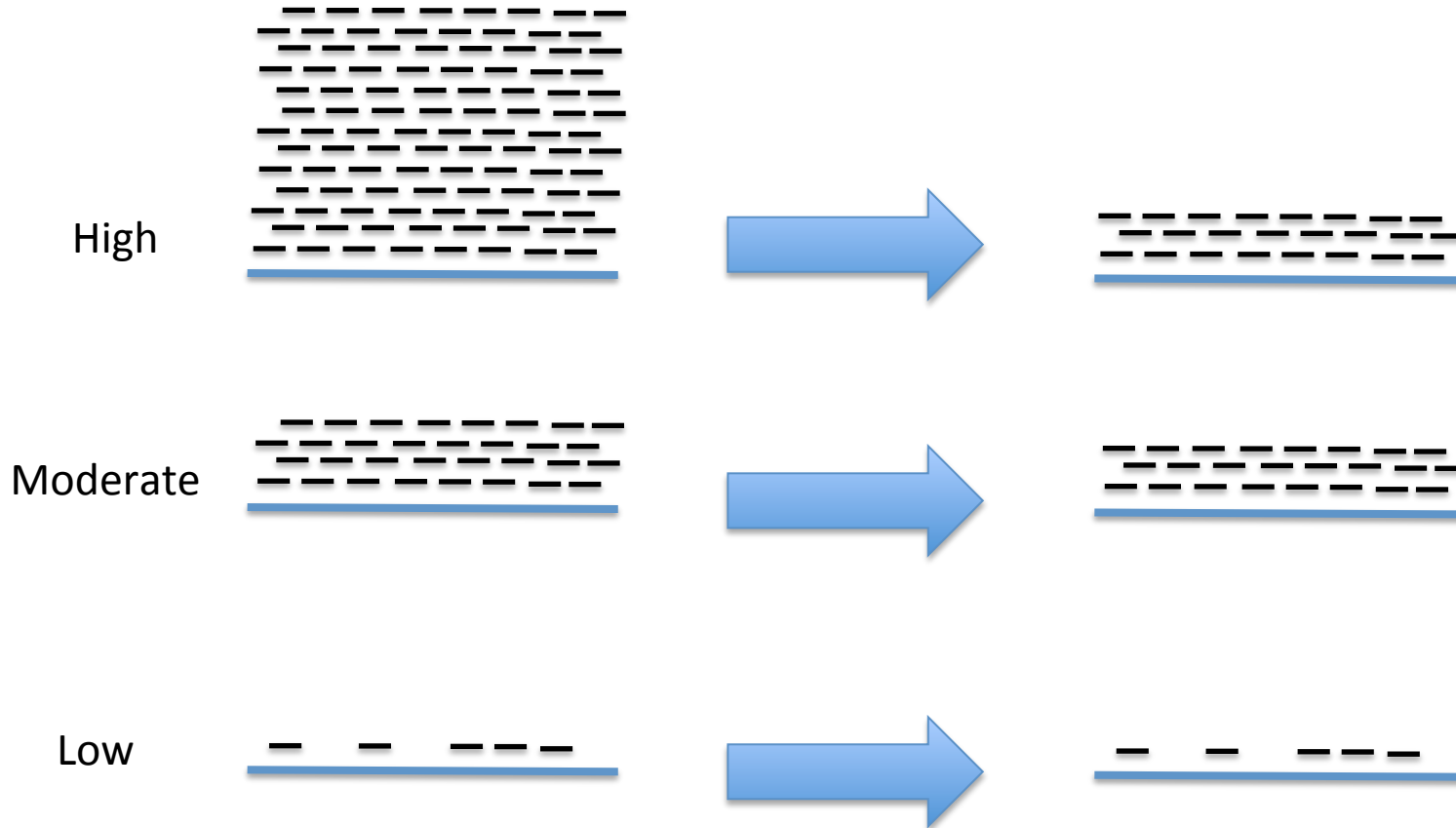
# unique kmers

Light trimming doesn't reduce number of blast matches w/ higher sequencing depths.

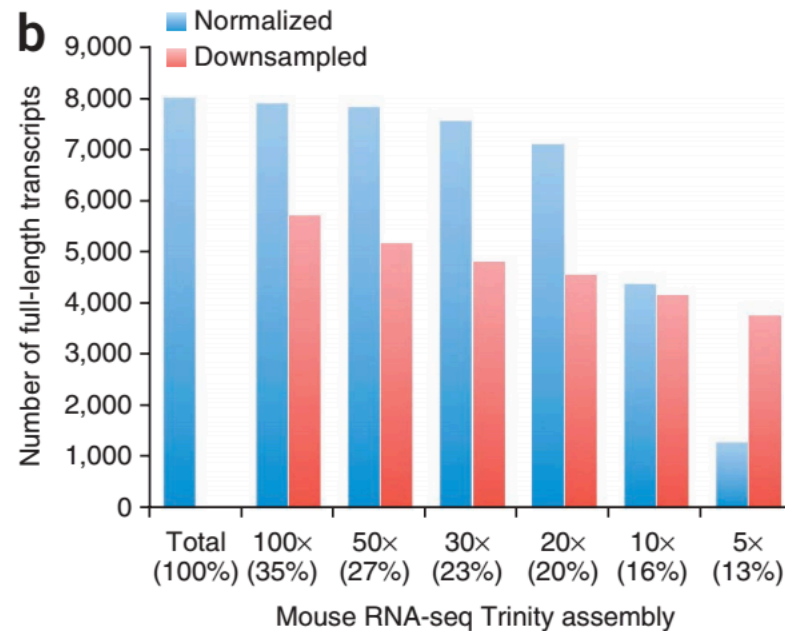
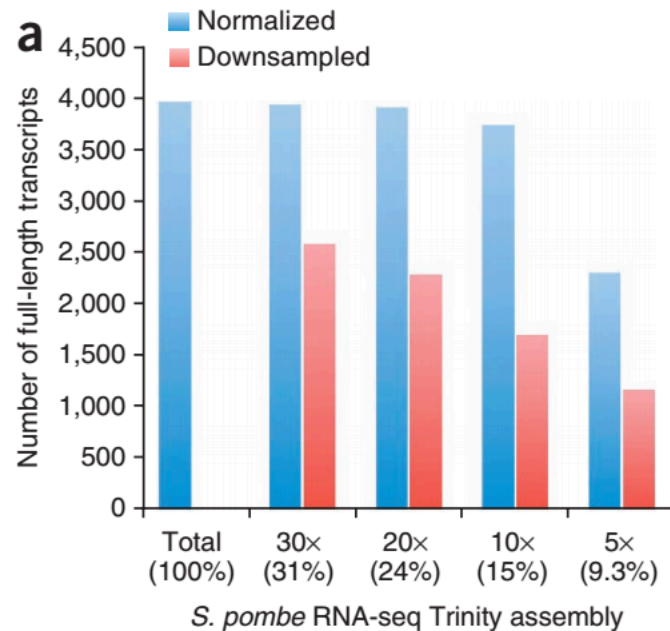
Normalized # of blast matches



# *In silico* normalization of reads



# Impact of Normalization on *De novo* Full-length Transcript Reconstruction



Largely retain full-length reconstruction, but use less RAM and assemble much faster.

# Quality Trimming and Normalization via Trinity

- Quality Trimming using Trimmomatic:
  - Trinity --trimmomatic
- Normalization of reads:
  - Trinity --normalize\_reads *(now on by default!)*
- You can do both in a single Trinity assembly run:
  - Trinity --trimmomatic --normalize\_reads



# Fastqc, trimming, and normalization practical