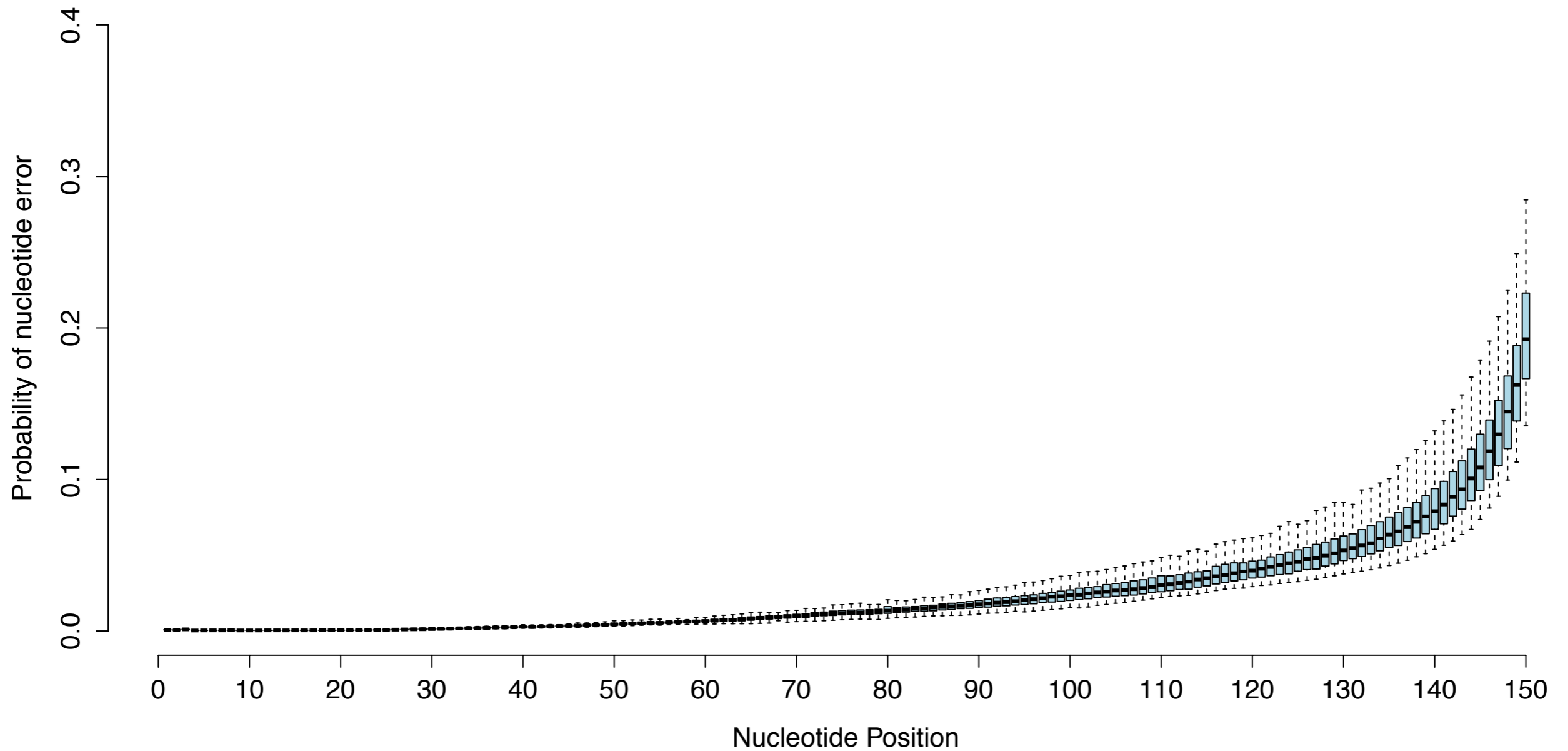
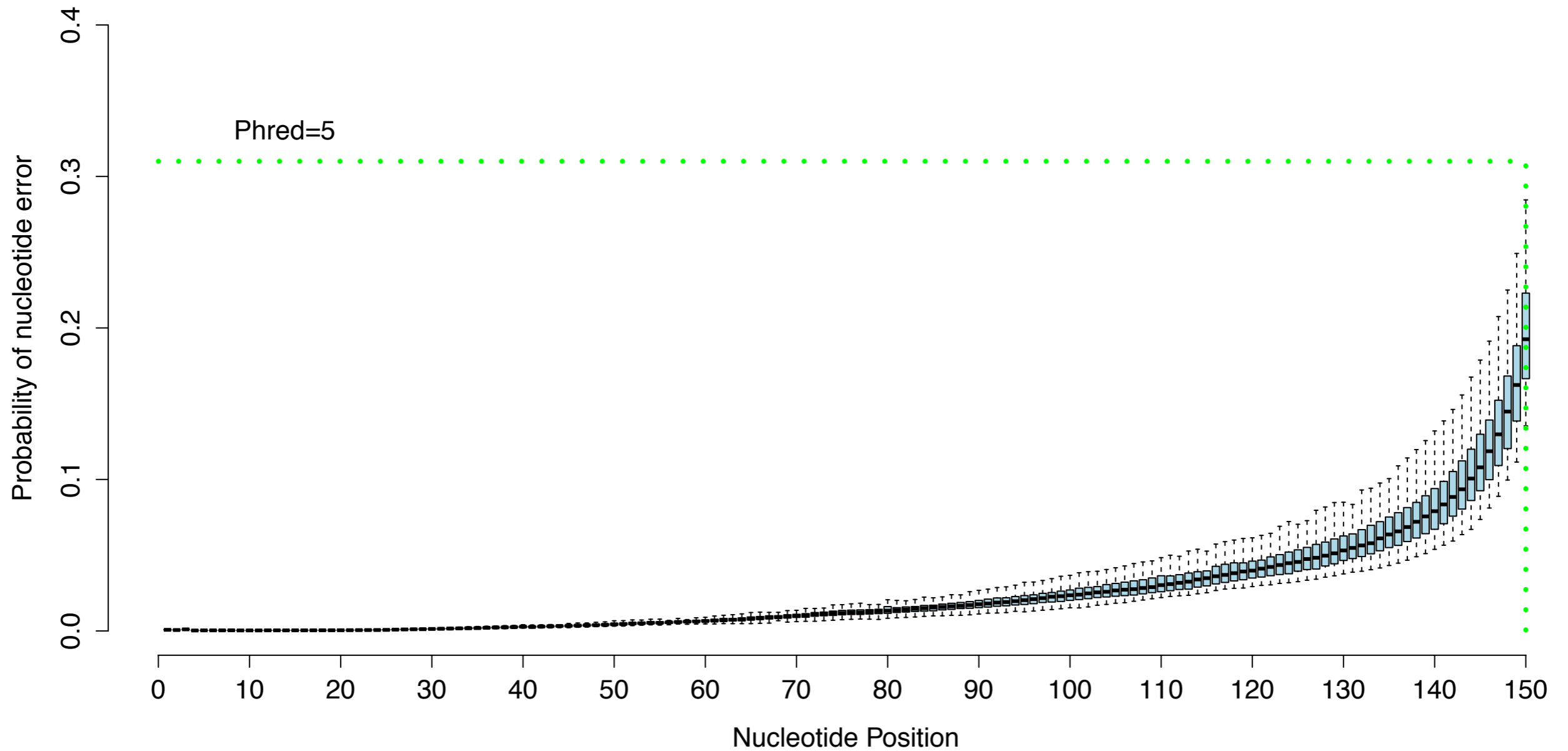


Quality trimming of NGS data

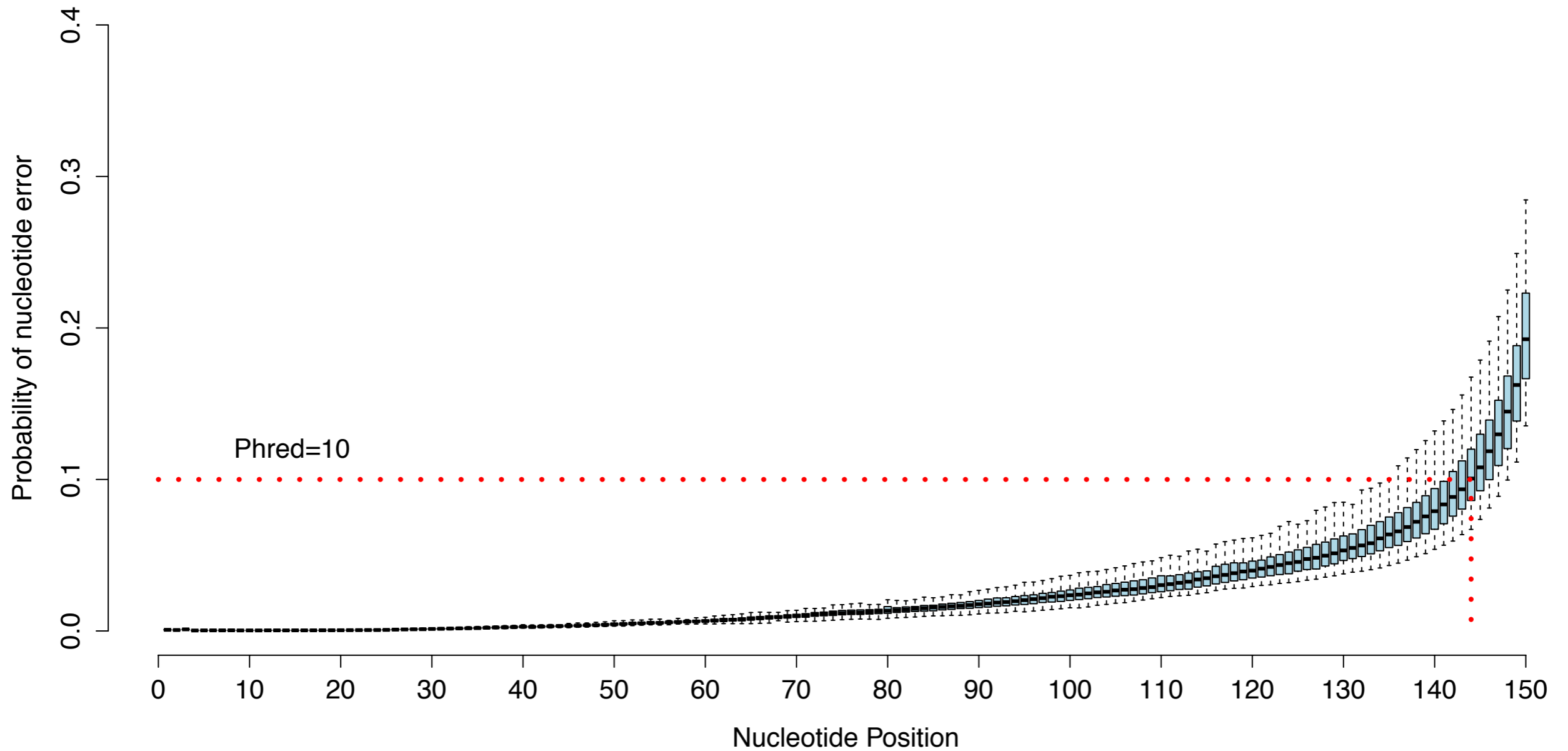
- Universal practice



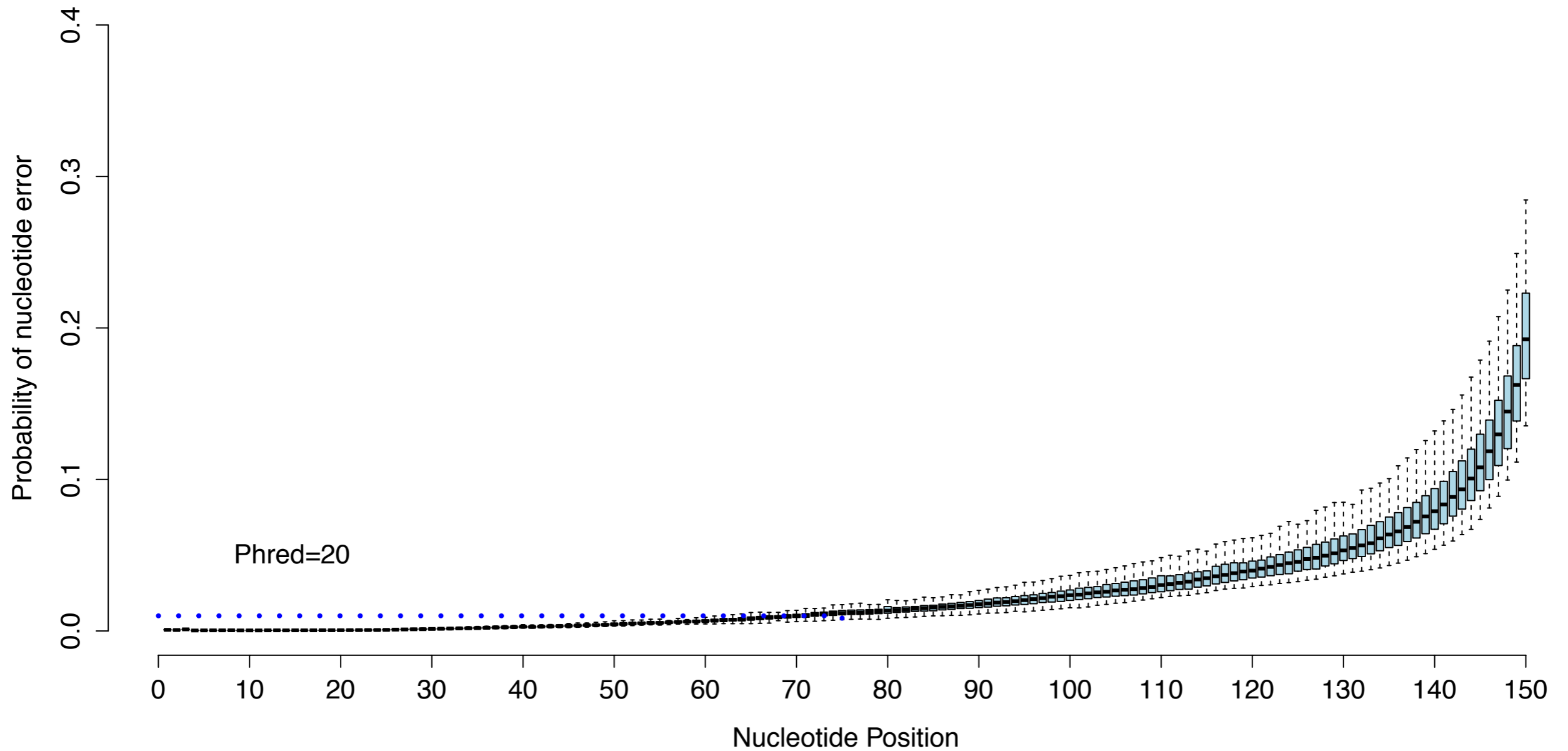
Quality trimming of NGS data



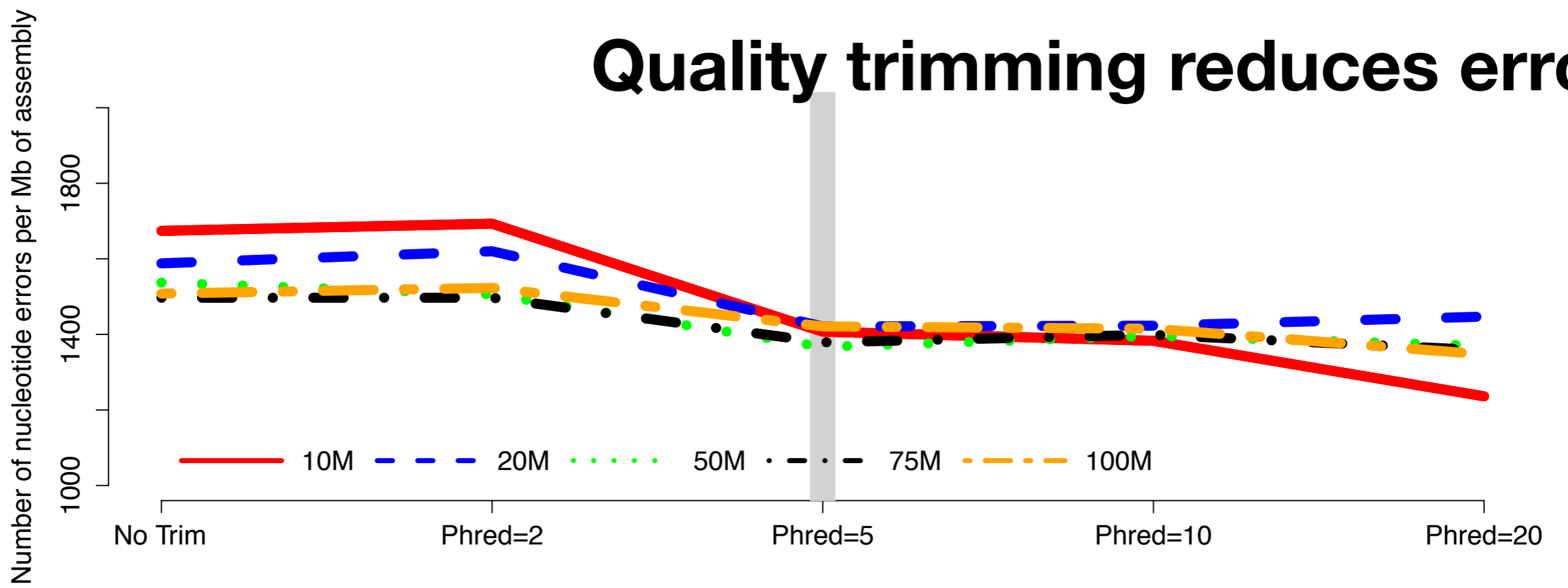
Quality trimming of NGS data



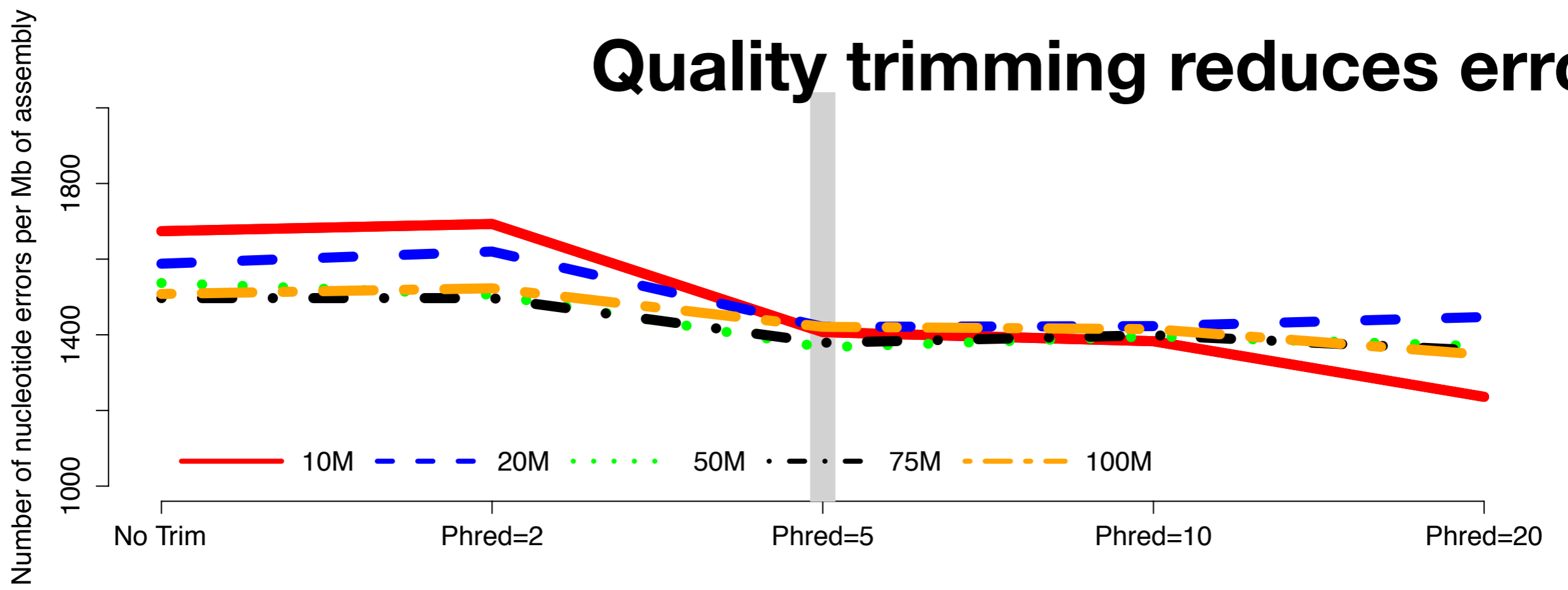
Quality trimming of NGS data



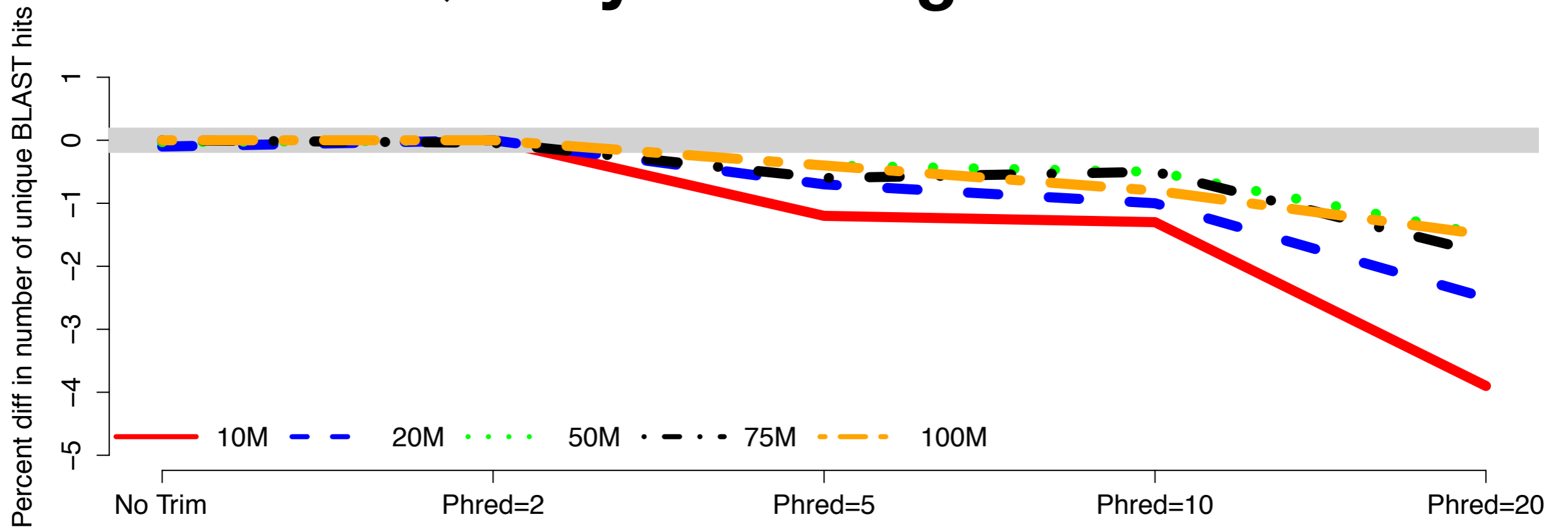
Quality trimming reduces error



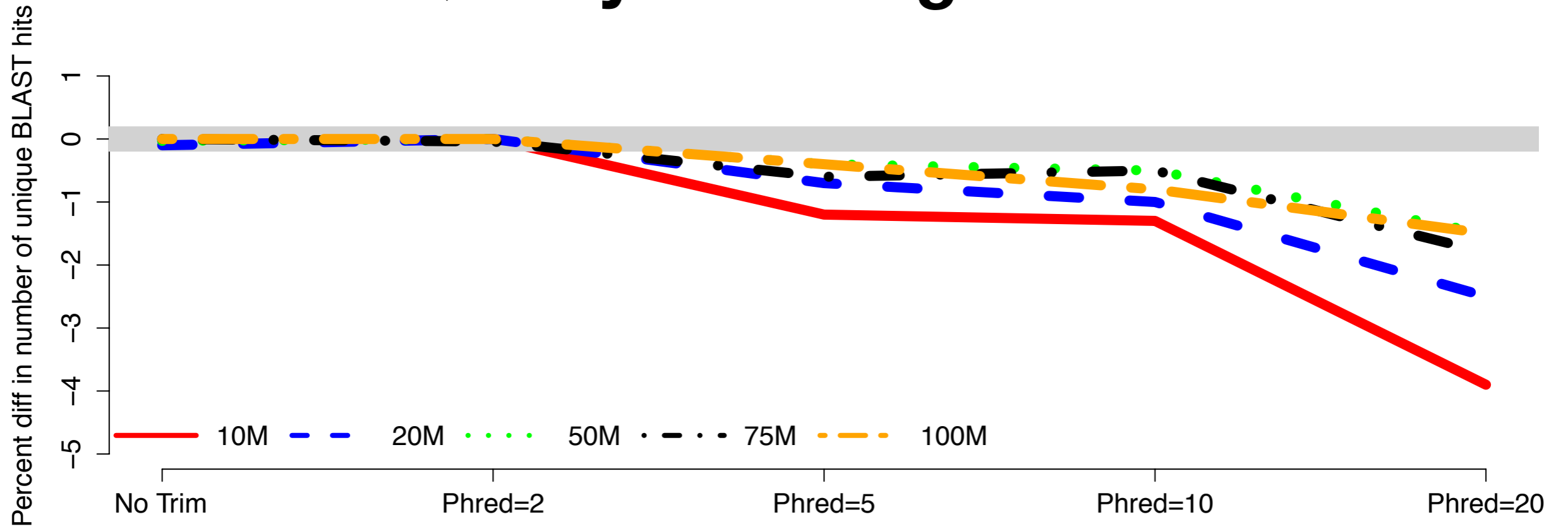
Quality trimming reduces error



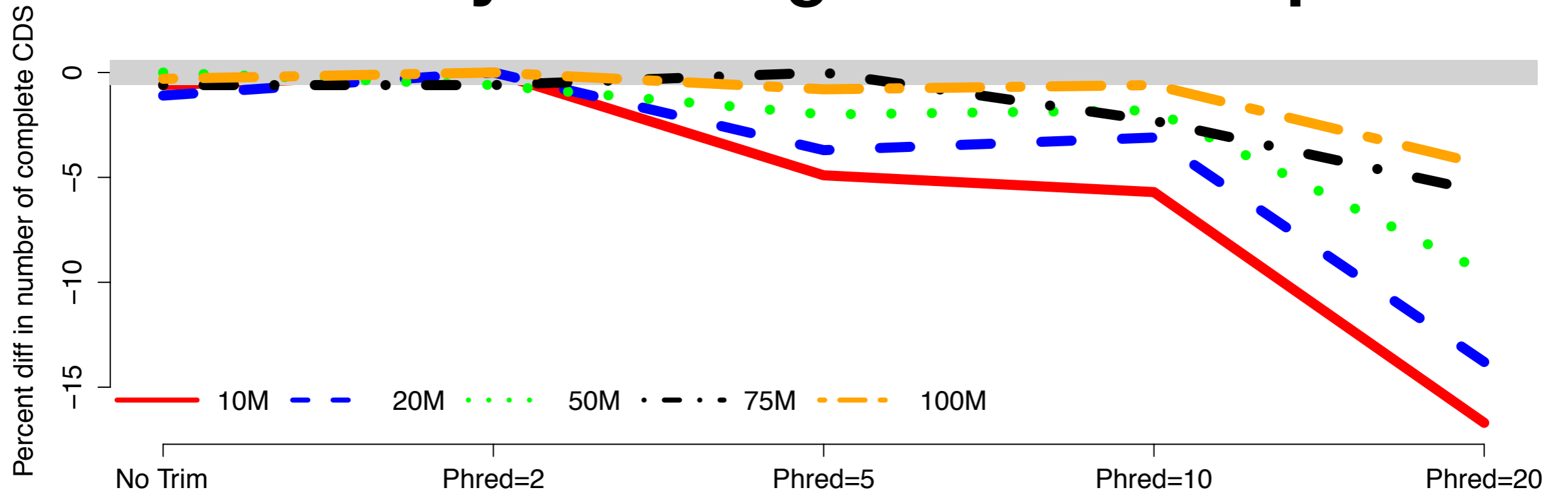
Quality trimming reduces BLAST hits



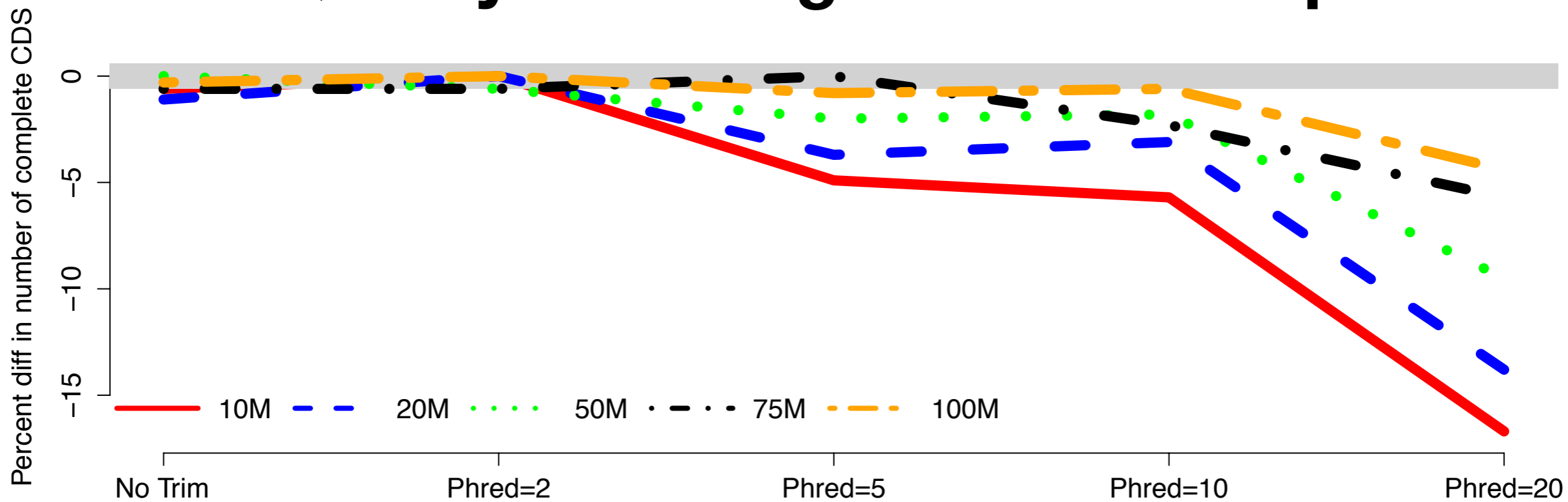
Quality trimming reduces BLAST hits



Quality trimming reduces complete CDS



Quality trimming reduces complete CDS



Summary

- Trimming does reduce assembly error, but at the cost of content & contiguity.
- **Proposed guidelines.**
 1. To max transcriptome assembly content & contiguity \Rightarrow Trim at 0 or 2
 2. If concerned about error \Rightarrow Trim at Phred=5
 3. Usually probably never trim at Phred ≥ 10