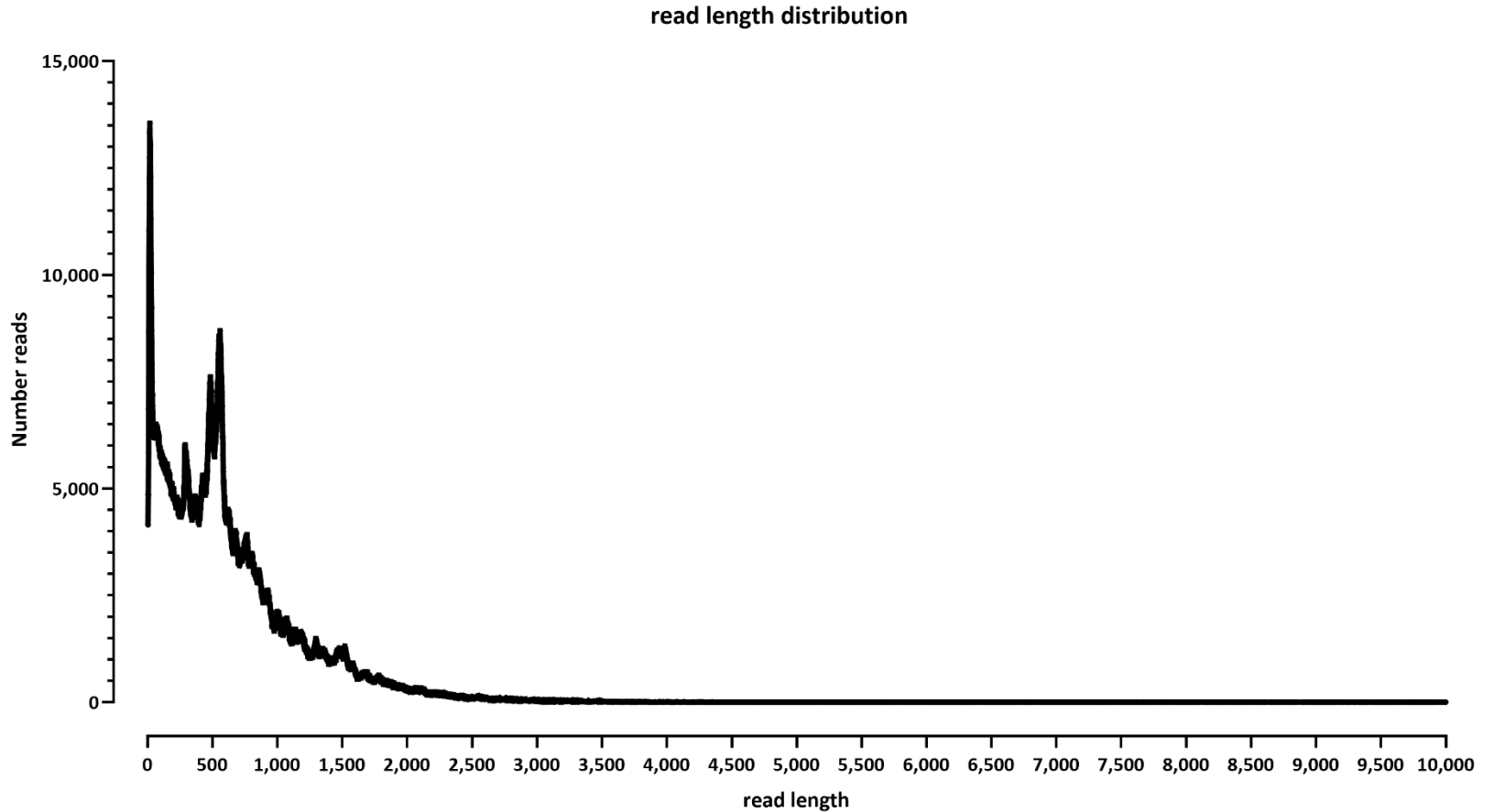


# READ LENGTH DISTRIBUTION

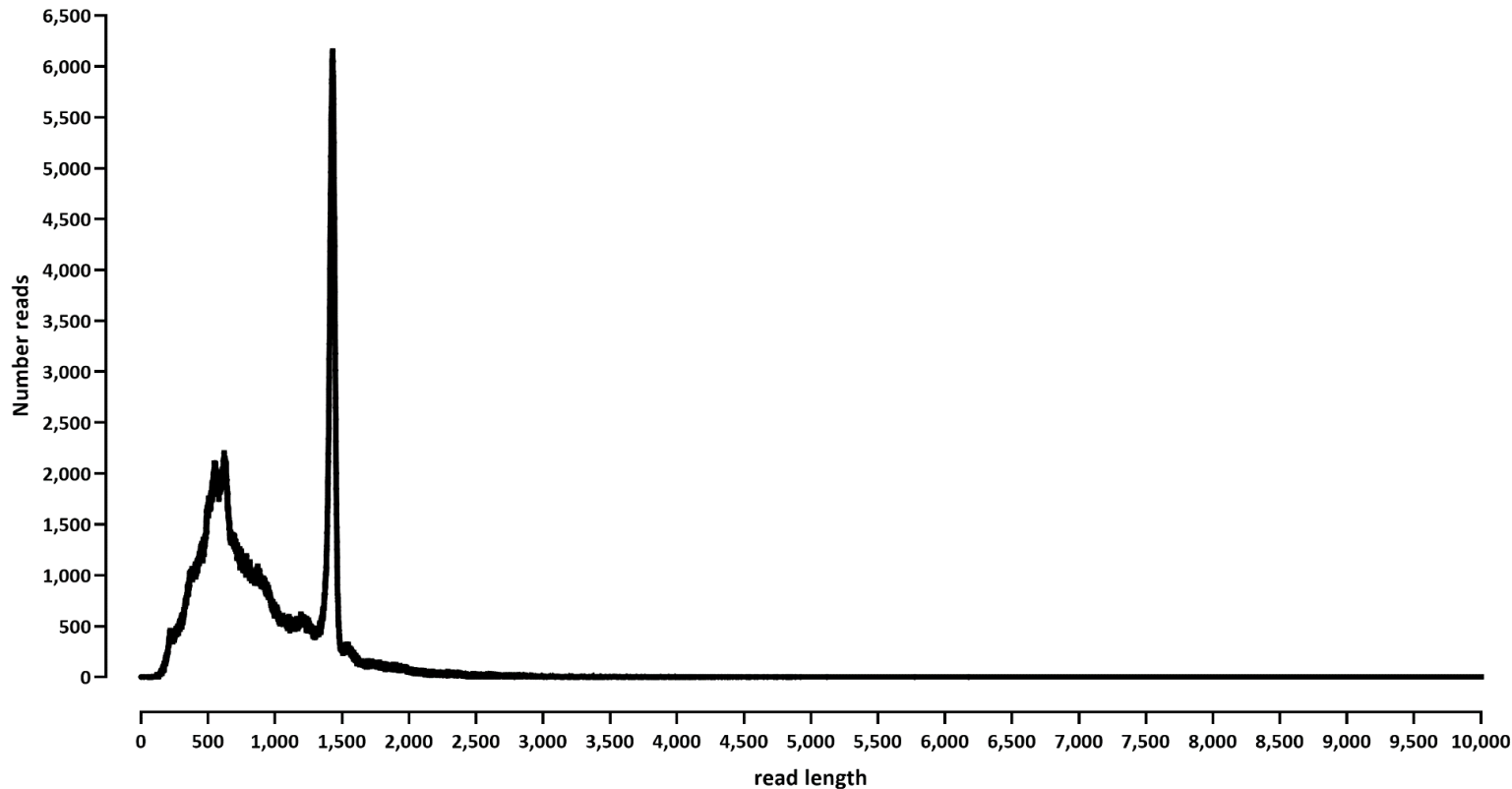


1

Note: this has way too many very short reads for my taste

# LAST TIME FOR COMPARISON

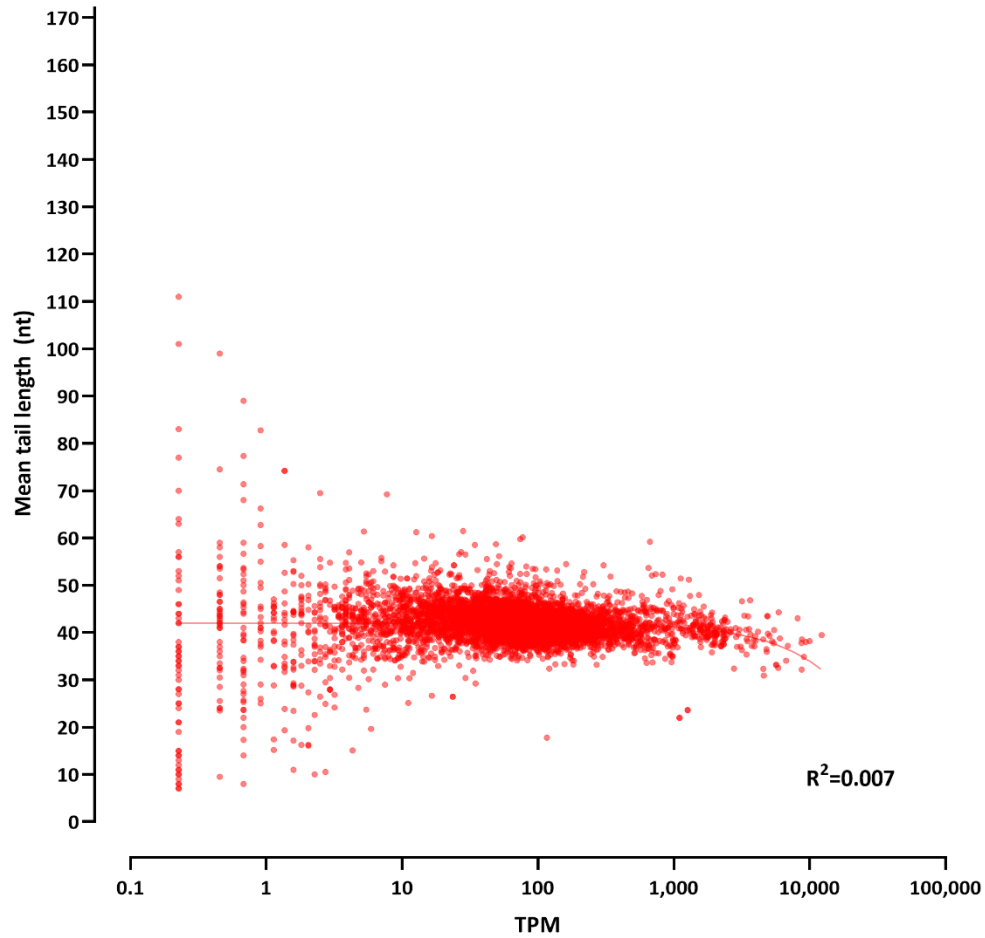
read length distribution



## **NEW PIPELINE:**

- dorado for rebasecalling and poly-A tail length estimation
- Minimap2 alignment against the transcriptome
- Post-processing by me to get TPMs and mean poly-A tail lengths

250221\_exp240718\_MS798\_S2



250221\_exp240718\_MS798\_S2 reads >= 100bp

