Quality Control

样品信息

样品名	来源	样品类型	实验处理
CHo 1 replicate	Zeng lab	细胞	细胞的重复1
CHo 2 replicate	Zeng lab	细胞	细胞的重复2
Col-O(DMSO)	Xie Daoxin	拟南芥	野生型对照组
Col-O(SL)	Xie Daoxin	拟南芥	野生型处理组
d14(DMSO)	Xie Daoxin	拟南芥	突变体对照组
d14(SL)	Xie Daoxin	拟南芥	突变体处理组
FLY-WT	wangtao	果蝇的眼睛	果蝇野生型
FLY-B	wangtao	果蝇的眼睛	果蝇处理组

总结

- 细胞 CHO-1 去完接头后，RPF建库长度分布异常。
- 细胞 CHO-2 去完接头后，RPF建库长度分布异常。
- 植物 col-dmso 去完接头后，RPF建库长度分布正常，主峰为31nt。
- 植物 col-sl 去完接头后，RPF建库长度分布正常，主峰为31nt。
- 植物突变体 d14-dmso 去完接头后，RPF建库长度分布正常，主峰为31nt。
- 植物突变体 d14-sl 去完接头后，RPF建库长度分布正常，主峰为31nt。
- FLY-WT 去完接头后，RPF建库长度分布出现双峰，主峰为28nt。
- FLY-B 去完接头后，RPF建库长度分布出现双峰，主峰为28nt。

由于每个样品的建库的测序结果都很少（约0.1M），去除接头后只剩下几千个reads，没有进行后续的分析过程。

结果

- 在同一批次下，植物建库长度分布全部正常，而细胞 CHO 长度分布异常, 果蝇的眼睛的长度分布出现双峰。
- 植物的建库方法成熟，但是主峰为31nt,可能和RNase 酶的降解步骤相关，不知道是否需要将主峰优化到28nt。
- 细胞建库有问题，可能是样品的问题。
- 果蝇的眼睛建库出现双峰，可能是样品的问题。

建议

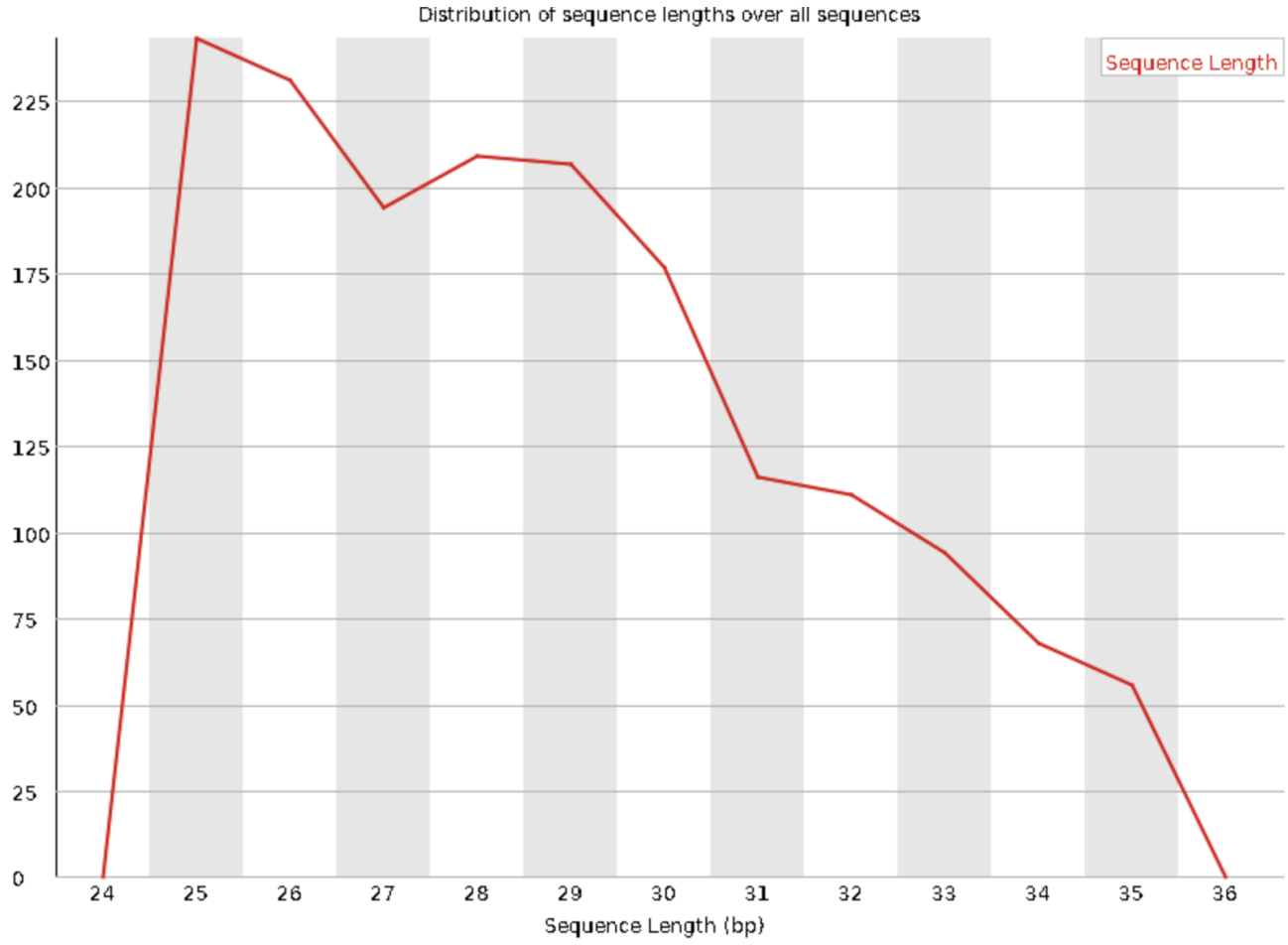
- 植物的建议大规模测序。
- 细胞建议重新提供样品建库。
- 果蝇的眼睛建议重新提供样品建库。

CHO-1-R_FKDL202558030-1a-29

=== Summary ===

Name	Percentage
Total reads processed:	143,342
Reads with adapters:	43,952 (30.7%)
Reads that were too short:	39,459 (27.5%)
Reads that were too long:	102,177 (71.3%)
Reads written (passing filters):	1,706 (1.2%)

Read length distribution



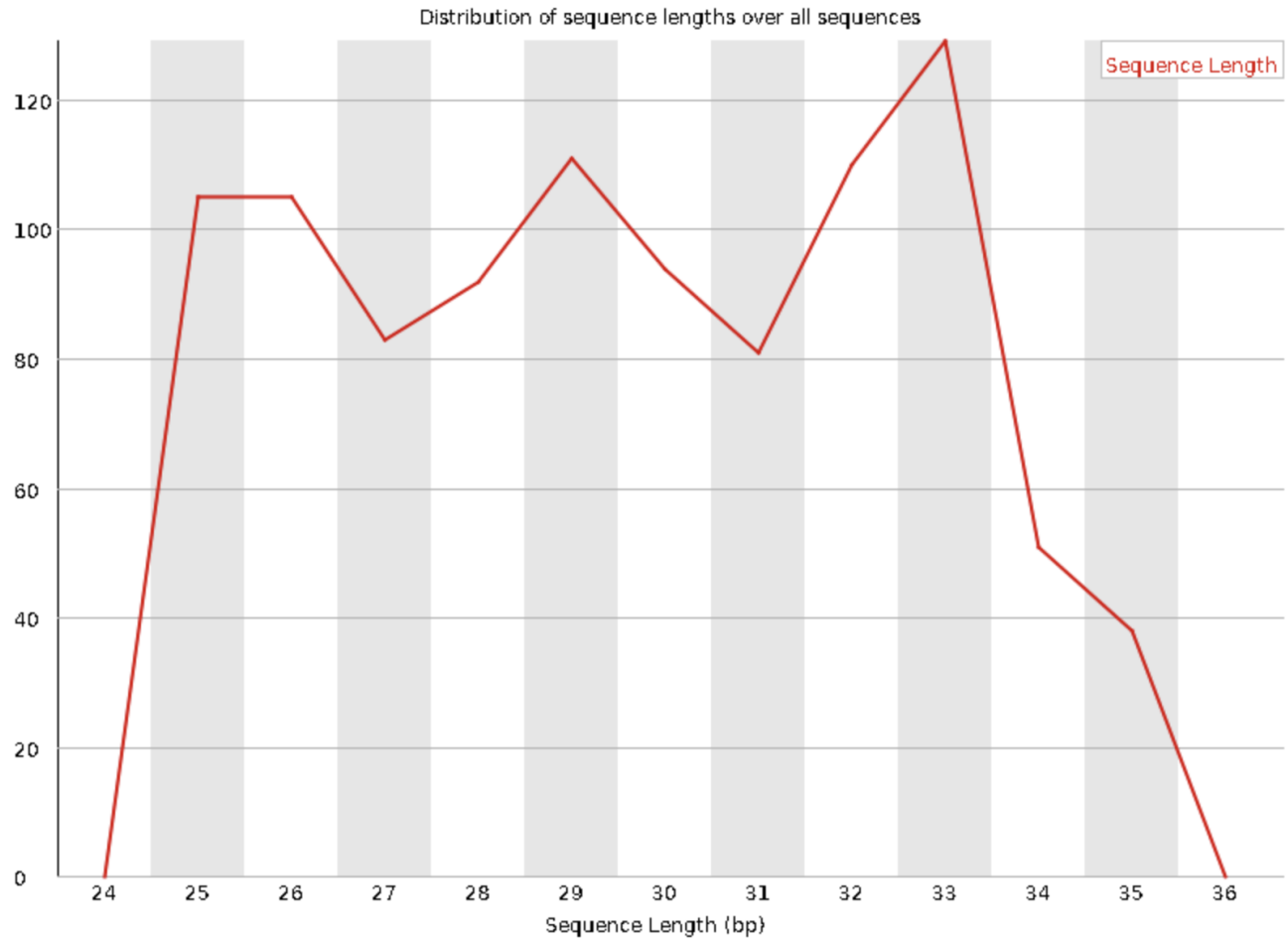
CHO-2-R_FKDL202558030-1a-30

=== Summary ===

Name	Percentage
Total reads processed:	136,314
Reads with adapters:	102,996 (75.6%)

Name	Percentage
Reads that were too short:	100,967 (74.1%)
Reads that were too long:	34,348 (25.2%)
Reads written (passing filters):	999 (0.7%)

Read length distribution

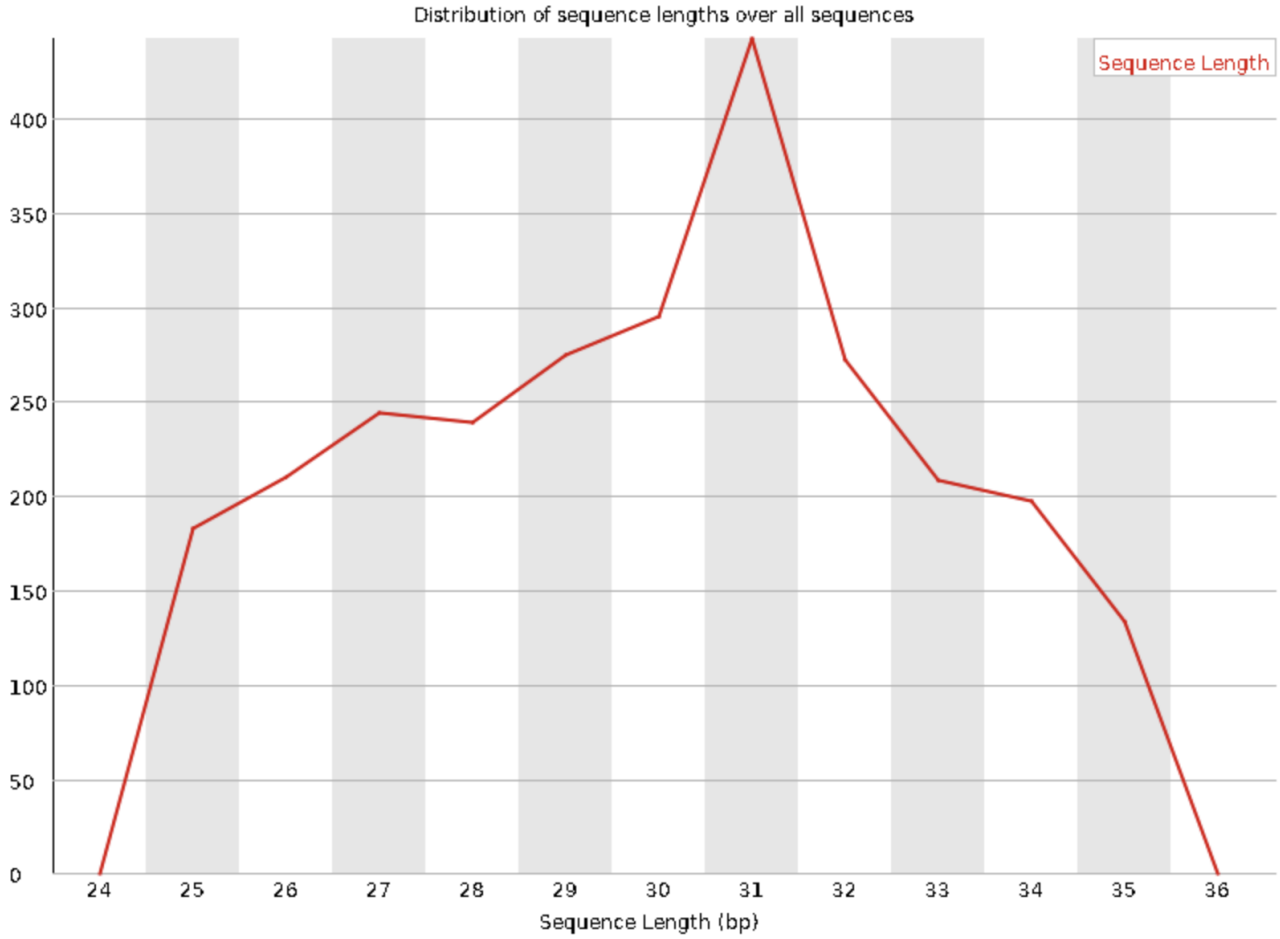


COL-O-DMSO-R_FKDL202558030-1a-33

=== Summary ===

Name	Percentage
Total reads processed:	278,740
Reads with adapters:	242,586 (87.0%)
Reads that were too short:	238,741 (85.7%)
Reads that were too long:	37,298 (13.4%)
Reads written (passing filters):	2,701 (1.0%)

Read length distribution

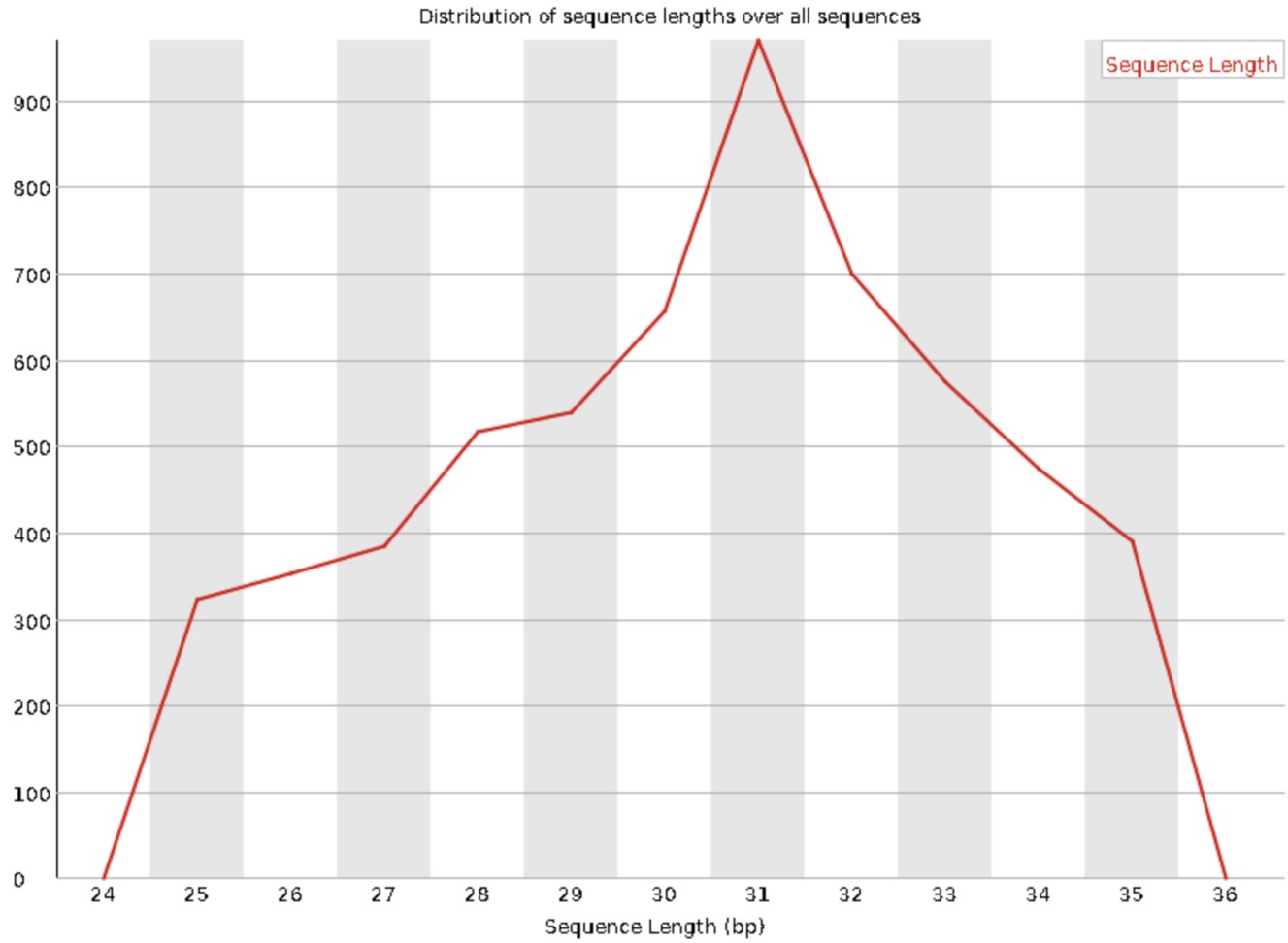


COL-O-SL-R_FKDL202558030-1a-34

=== Summary ===

Name	Percentage
Total reads processed:	238,150
Reads with adapters:	162,247 (68.1%)
Reads that were too short:	153,838 (64.6%)
Reads that were too long:	78,431 (32.9%)
Reads written (passing filters):	5,881 (2.5%)

Read length distribution

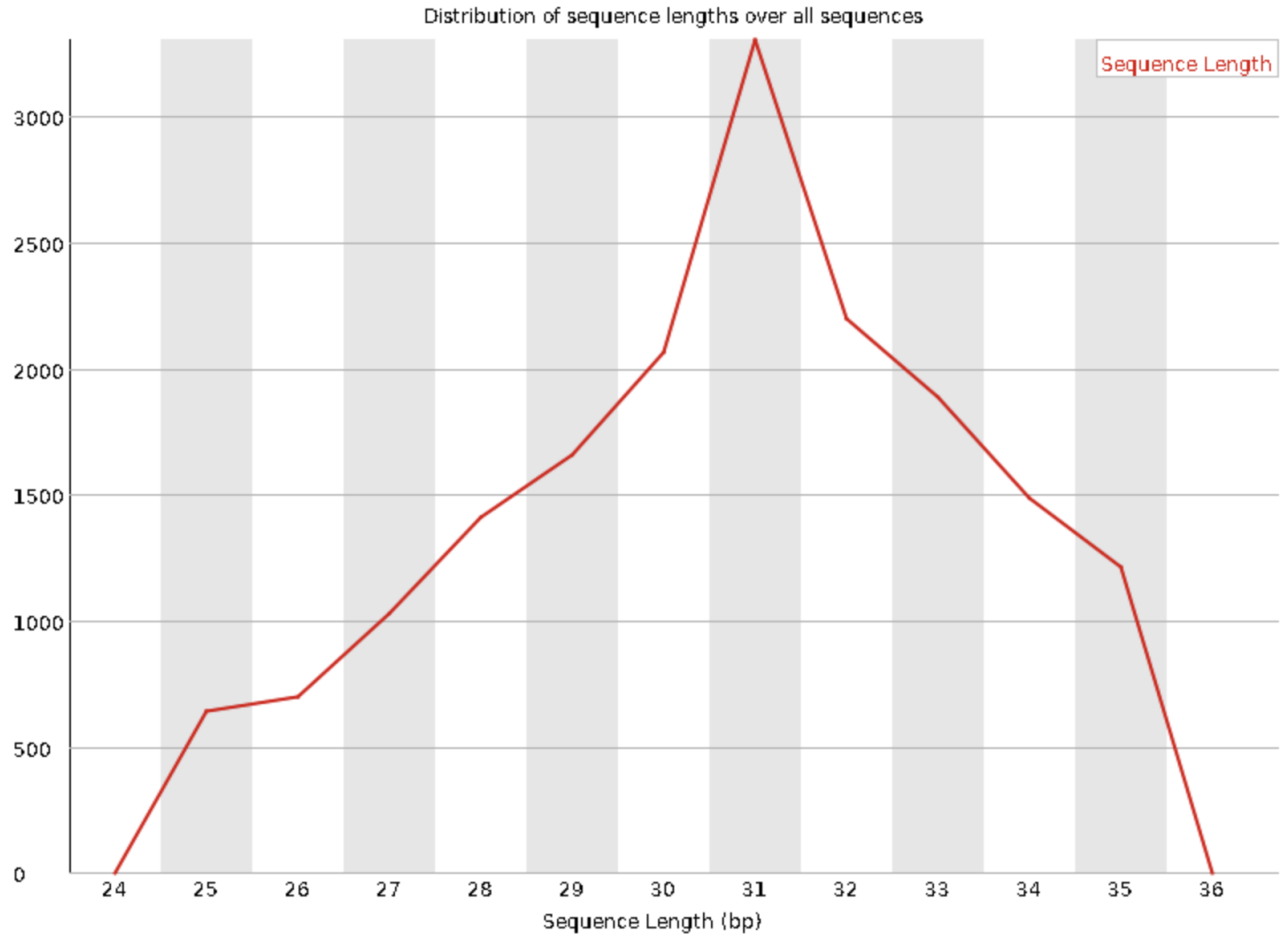


D14-DMSO-R_FKDL202558030-1a-35

=== Summary ===

Name	Percentage
Total reads processed:	337,480
Reads with adapters:	220,978 (65.5%)
Reads that were too short:	198,600 (58.8%)
Reads that were too long:	121,251 (35.9%)
Reads written (passing filters):	17,629 (5.2%)

Read length distribution

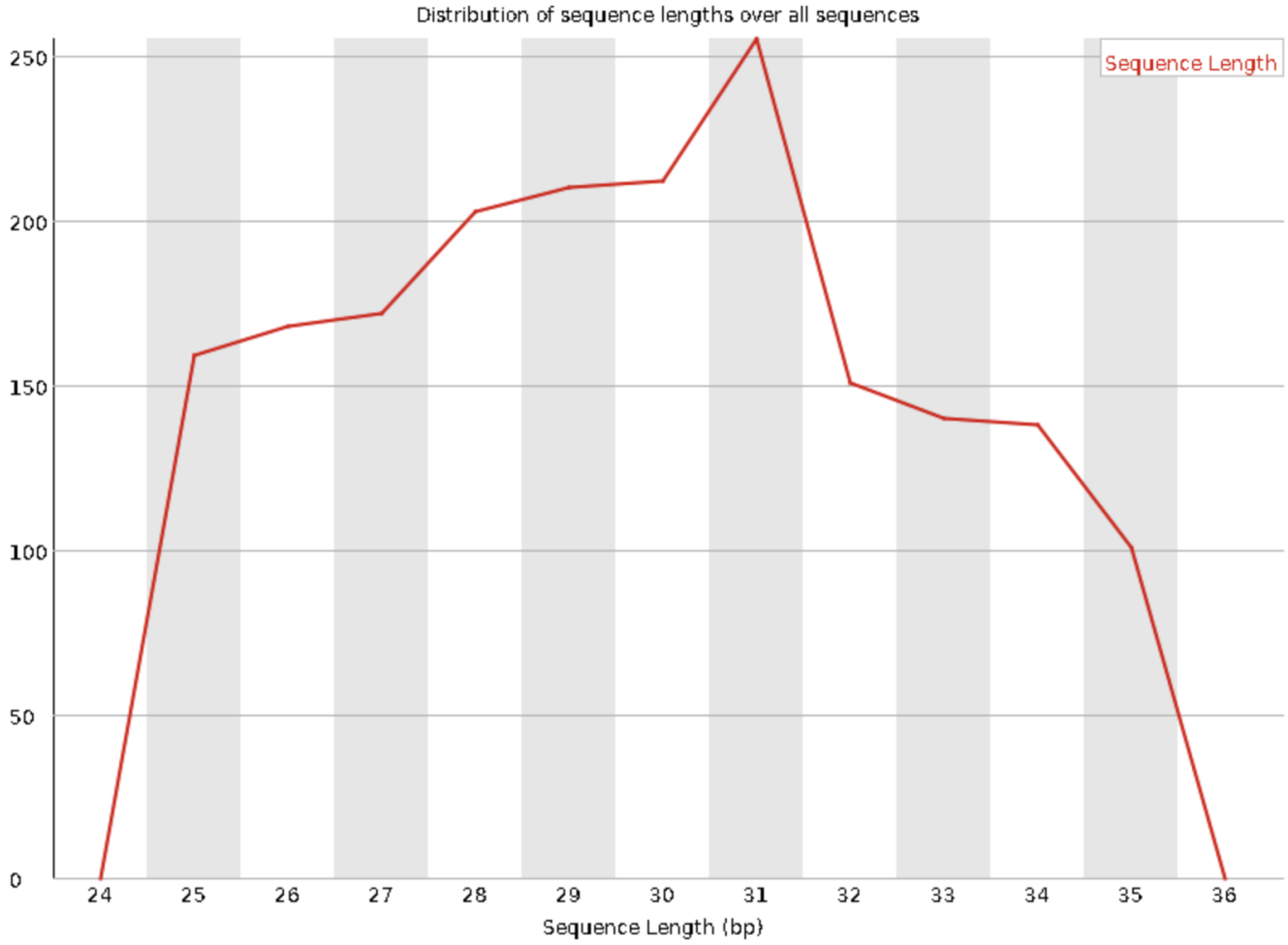


D14-SL-R_FKDL202558030-1a-36

=== Summary ===

Name	Percentage
Total reads processed:	91,677
Reads with adapters:	28,611 (31.2%)
Reads that were too short:	24,861 (27.1%)
Reads that were too long:	64,907 (70.8%)
Reads written (passing filters):	1,909 (2.1%)

Read length distribution

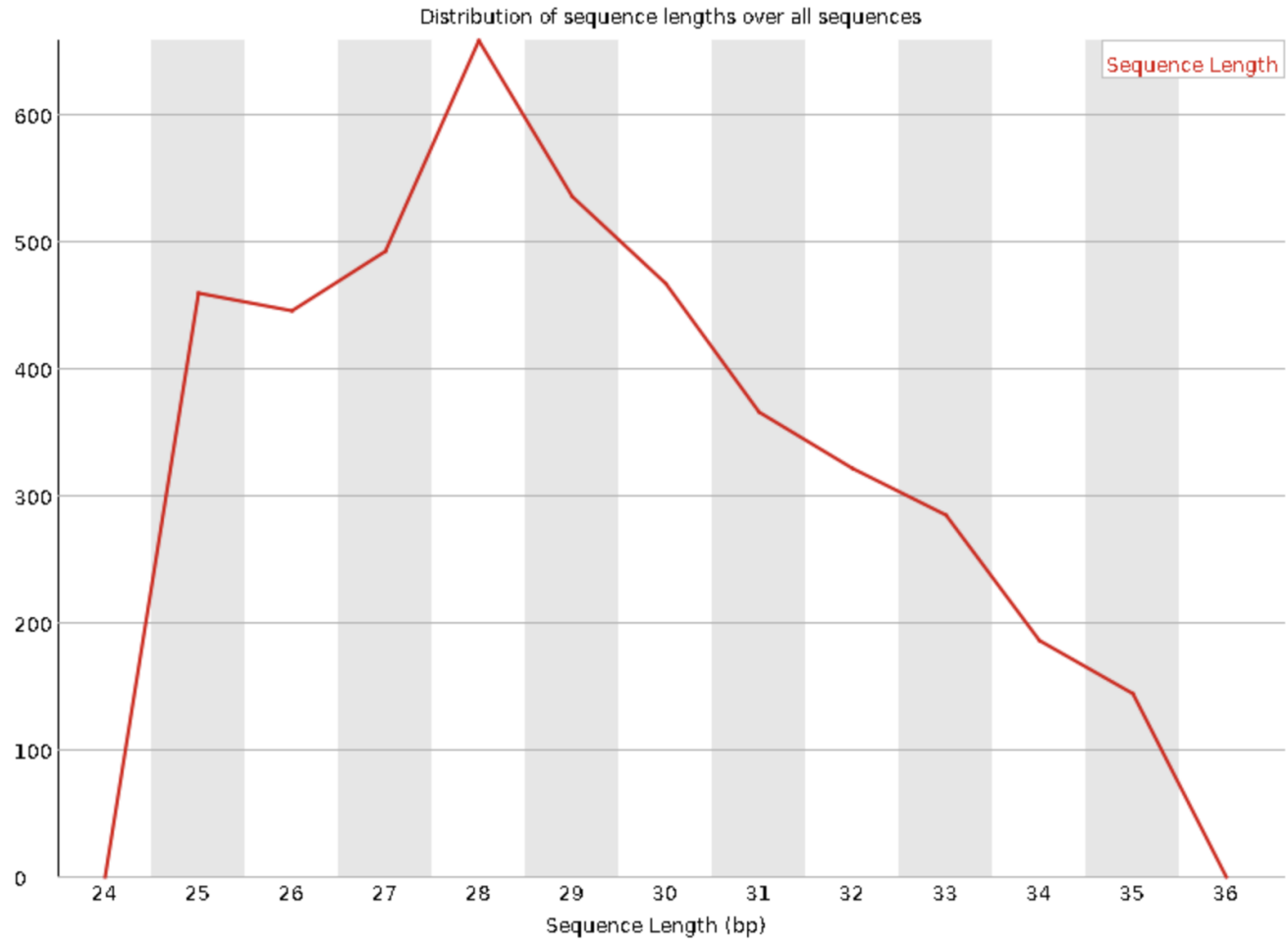


FLY-WT-R_FKDL202558030-1a-32

=== Summary ===

Name	Percentage
Total reads processed:	468,578
Reads with adapters:	370,766 (79.1%)
Reads that were too short:	363,265 (77.5%)
Reads that were too long:	100,948 (21.5%)
Reads written (passing filters):	4,365 (0.9%)

Read length distribution

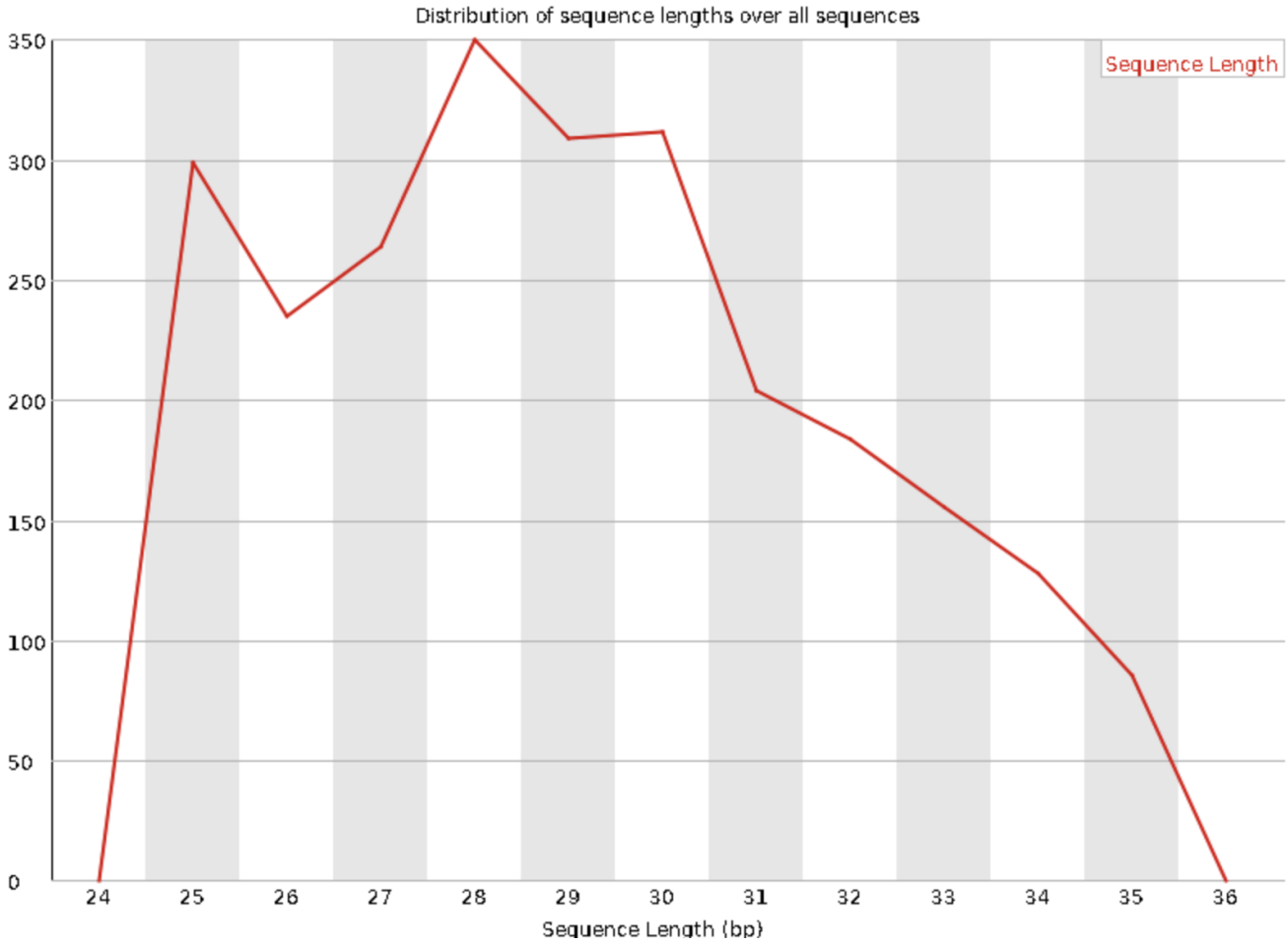


FLY-B-R_FKDL202558030-1a-31

=== Summary ===

Name	Percentage
Total reads processed:	291,994
Reads with adapters:	220,983 (75.7%)
Reads that were too short:	216,291 (74.1%)
Reads that were too long:	73,176 (25.1%)
Reads written (passing filters):	2,527 (0.9%)

Read length distribution


Distribution of sequence lengths over all sequences
Sequence Length
350
300
250
200
150
100
50
0
24
25
26
27
28
29
30
31
32
33
34
35
36
Sequence Length (bp)