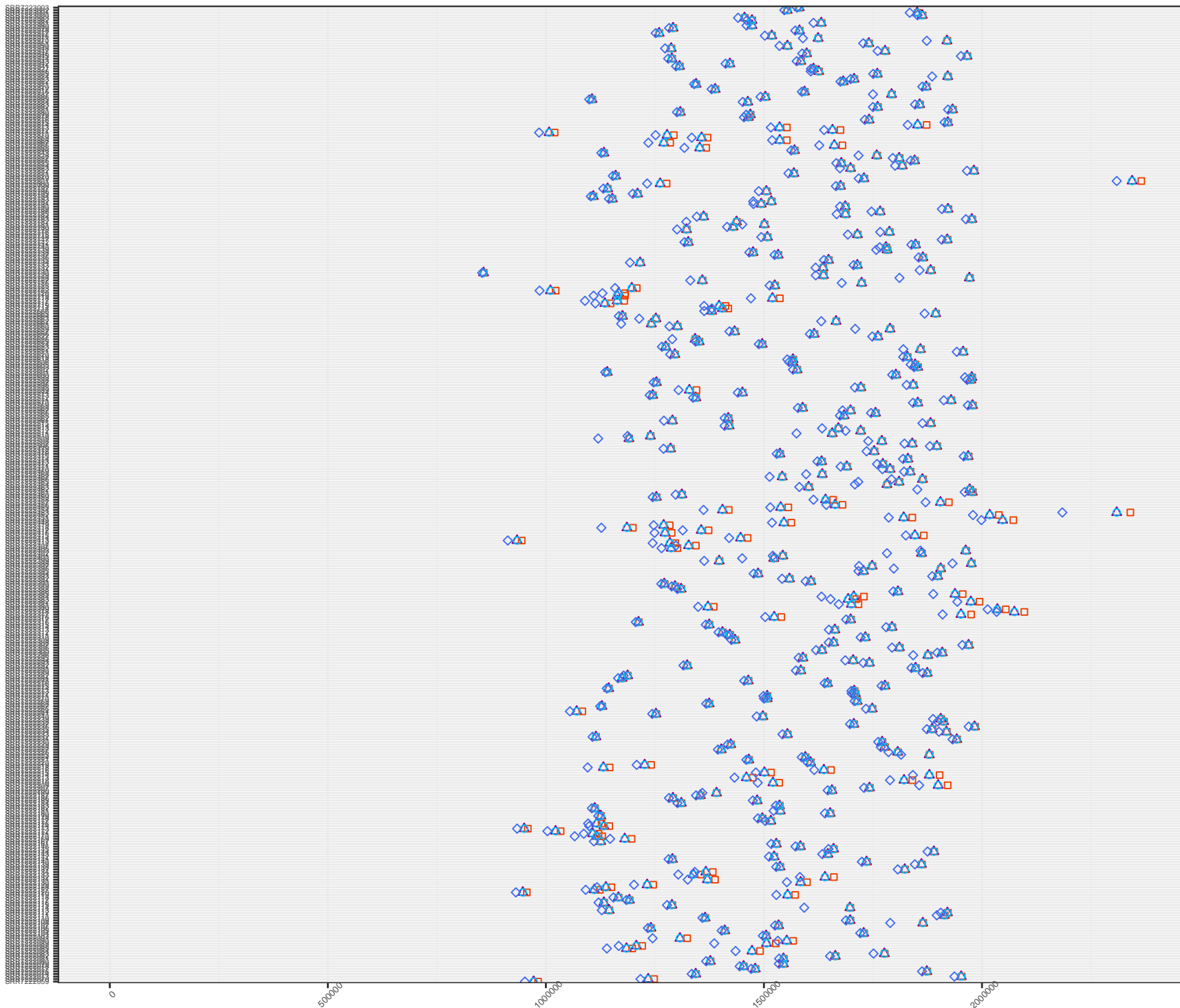


Read counts from NCBI download thru final cleaning – for each sample in dataset

run_name = bioprj_PRJNA473221_Bombus-bifarius

sample_name



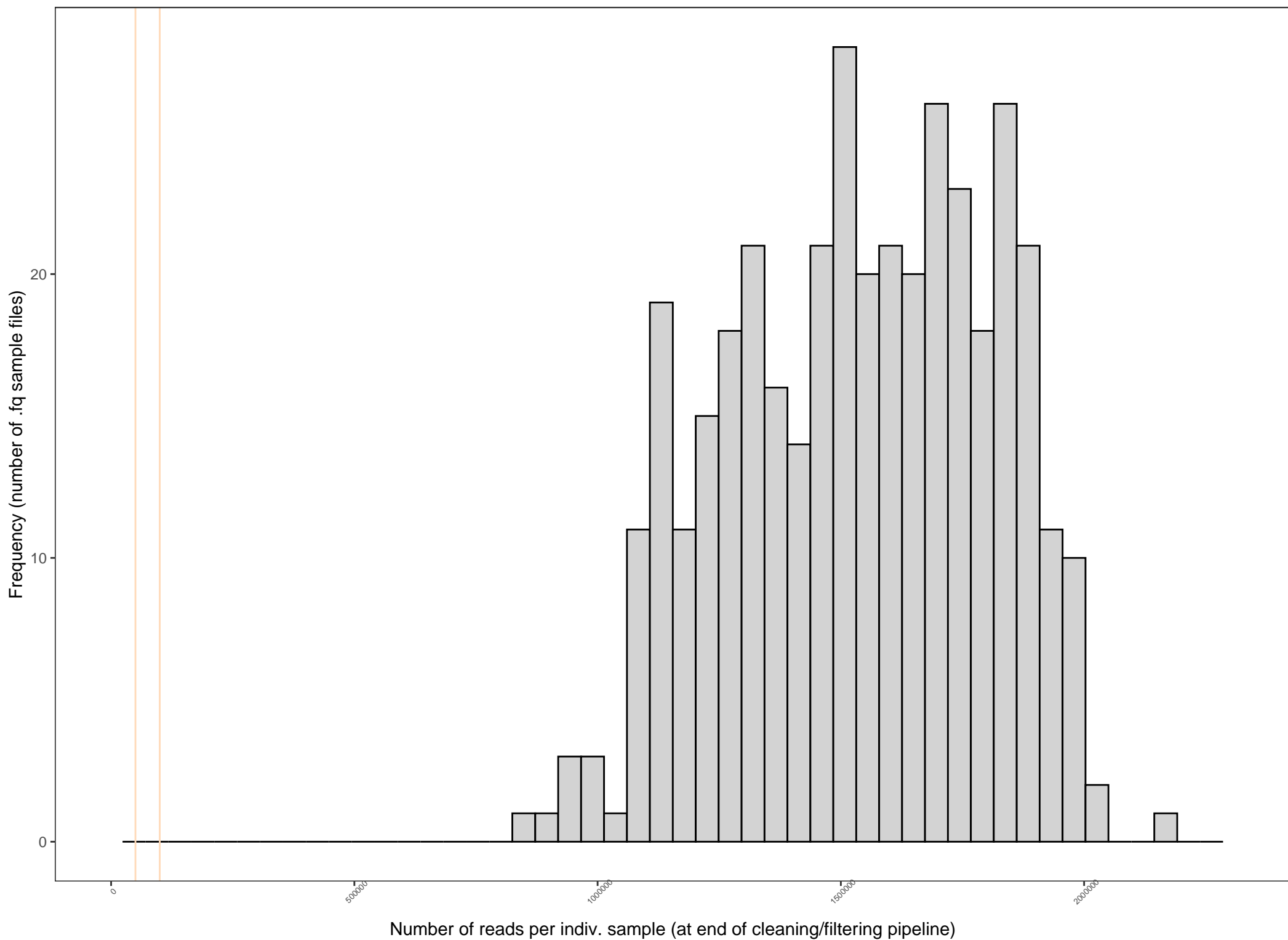
stage

- reads_downloaded
- reads_postlowqual
- reads_postadapter
- reads_posttrim

Number of reads per indiv. sample

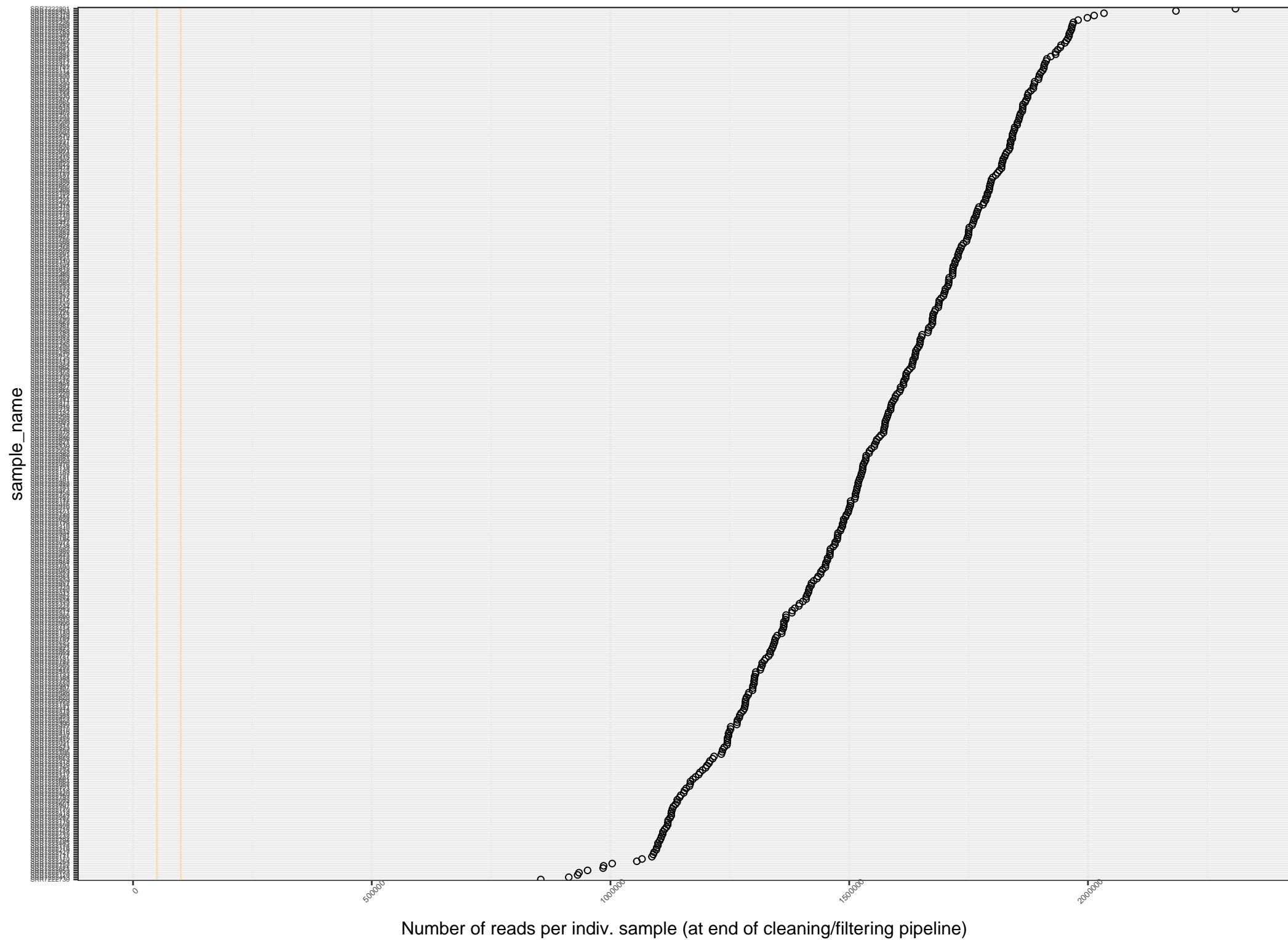
Histogram of pre-assembly read counts

run_name = bioprj_PRJNA473221_Bombus-bifarius



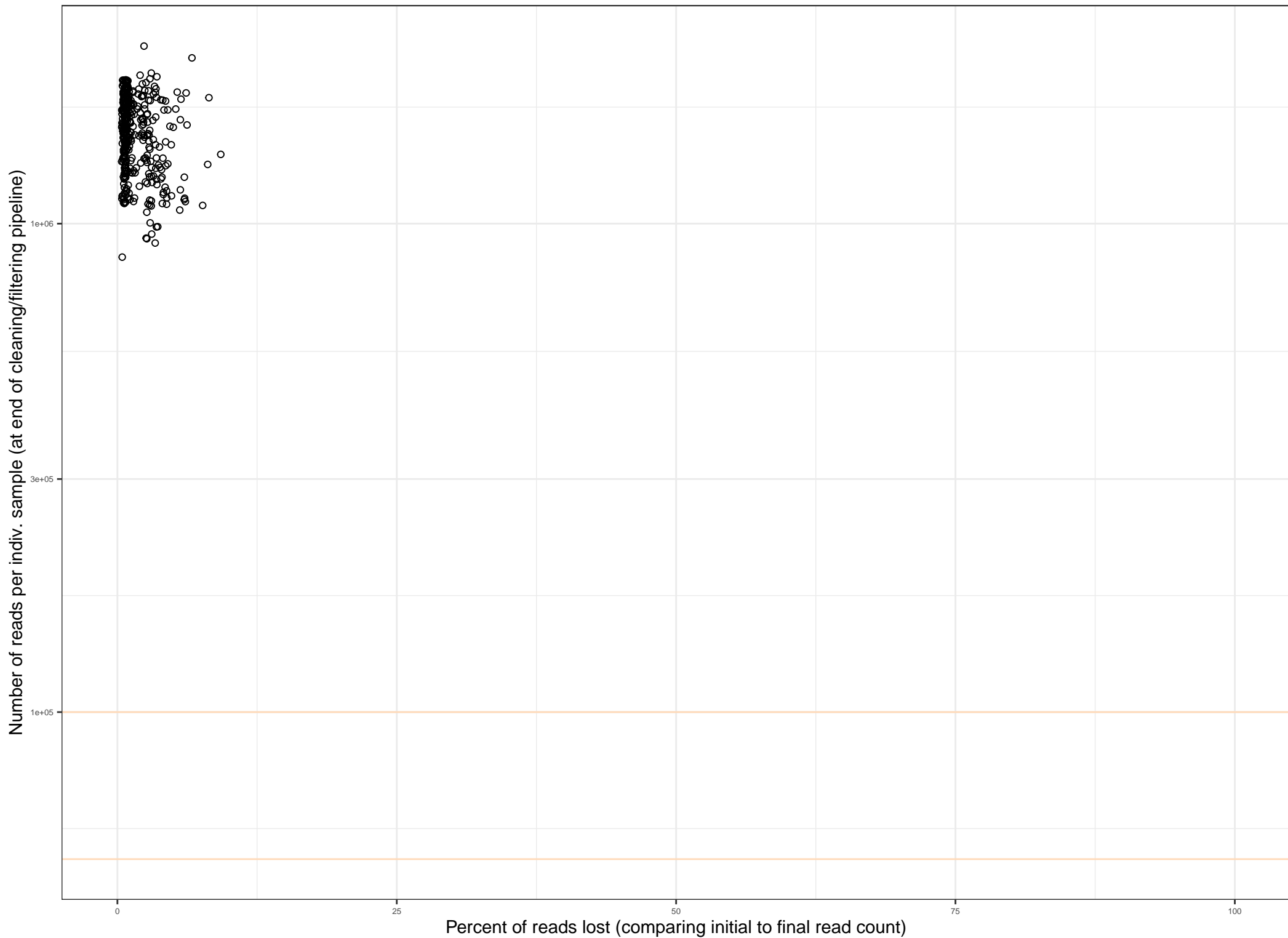
Dot plot of pre-assembly read counts

```
run_name = bioprj_PRJNA473221_Bombus-bifarius
```



Read Loss

run_name = bioprj_PRJNA473221_Bombus-bifarius



```
run_name = bioprj_PRJNA473221_Bombus-bifarius
```

