

# Read lengths – for each sample in dataset

run\_name = bioprj\_PRJNA473221\_Bombus-bifarius

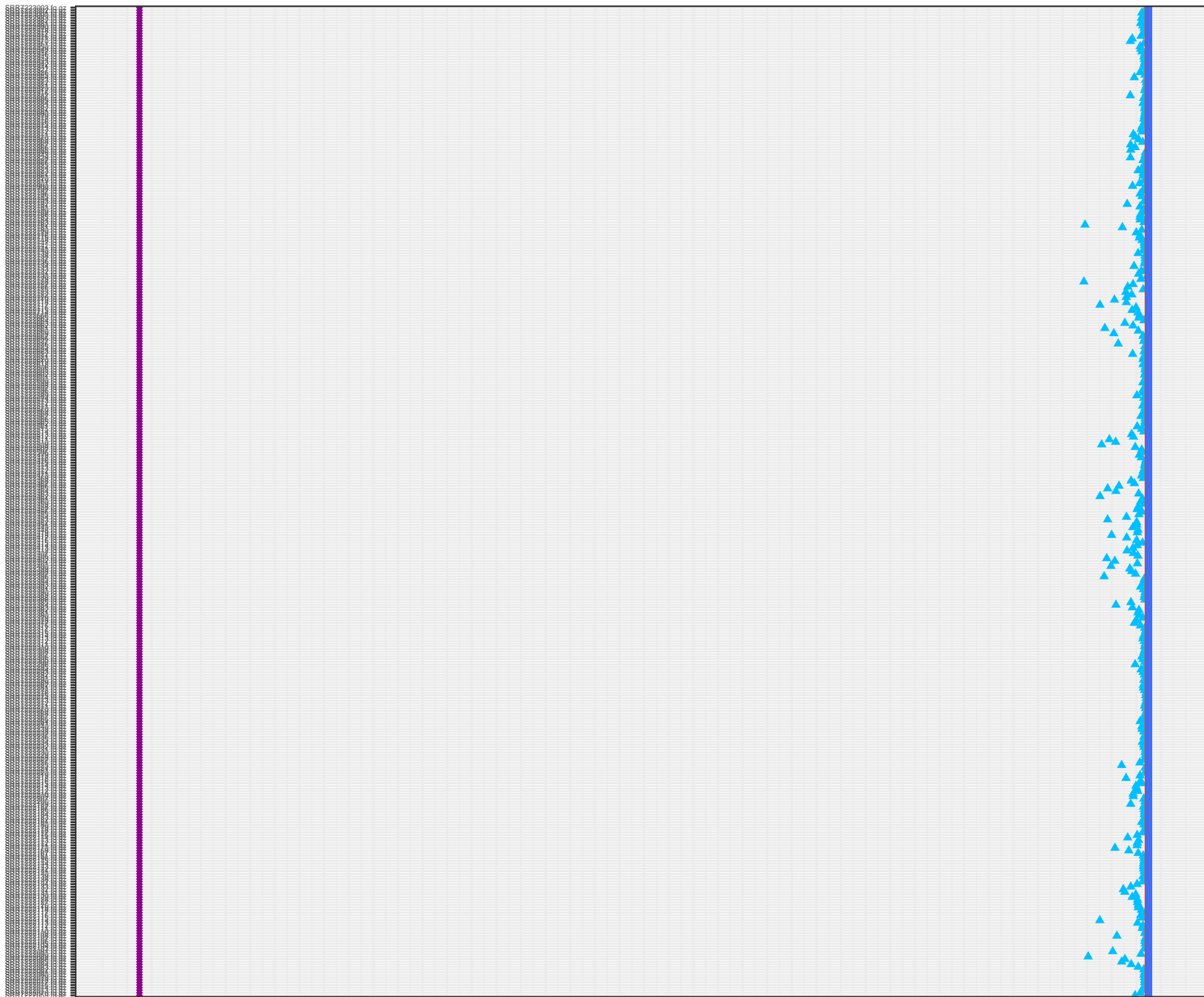
sample\_name

2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86

read lengths

type

- max\_length
- mean\_length
- median\_length
- min\_length



# Read length histogram – for each sample in dataset

run\_name = bioprj\_PRJNA473221\_Bombus-bifarius

