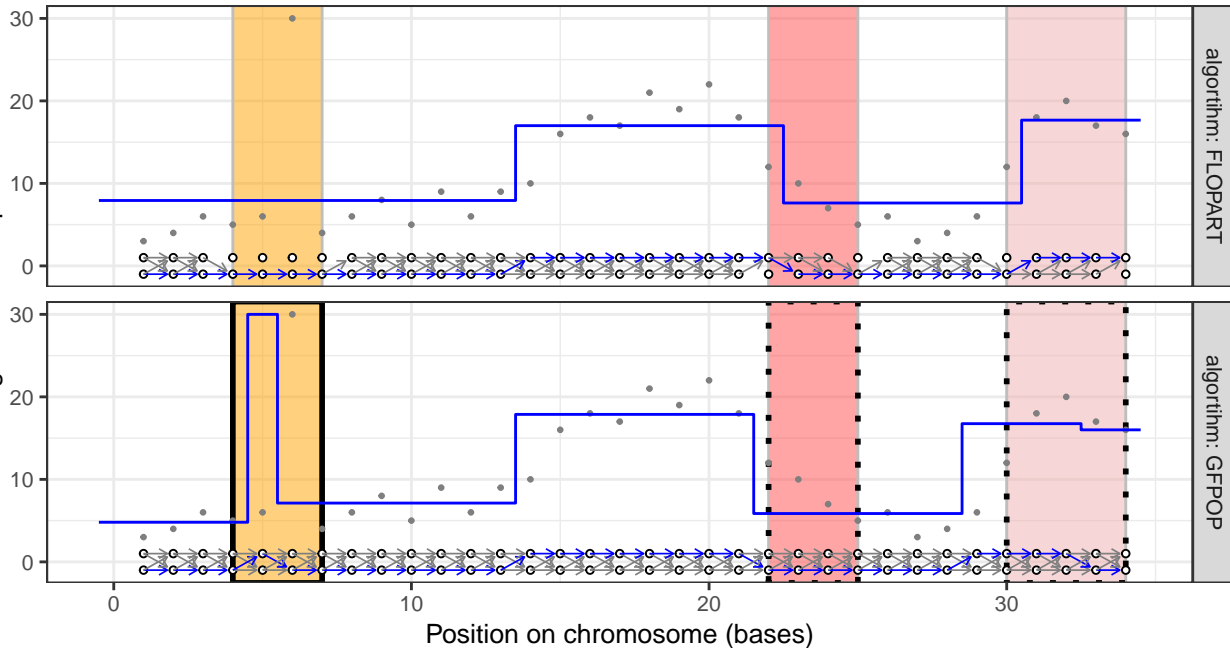


Count of aligned DNA sequence reads



error type

- correct
- false negative
- false positive

annotation

- noPeaks
- peakStart
- peakEnd

path

- Optimal
- Possible