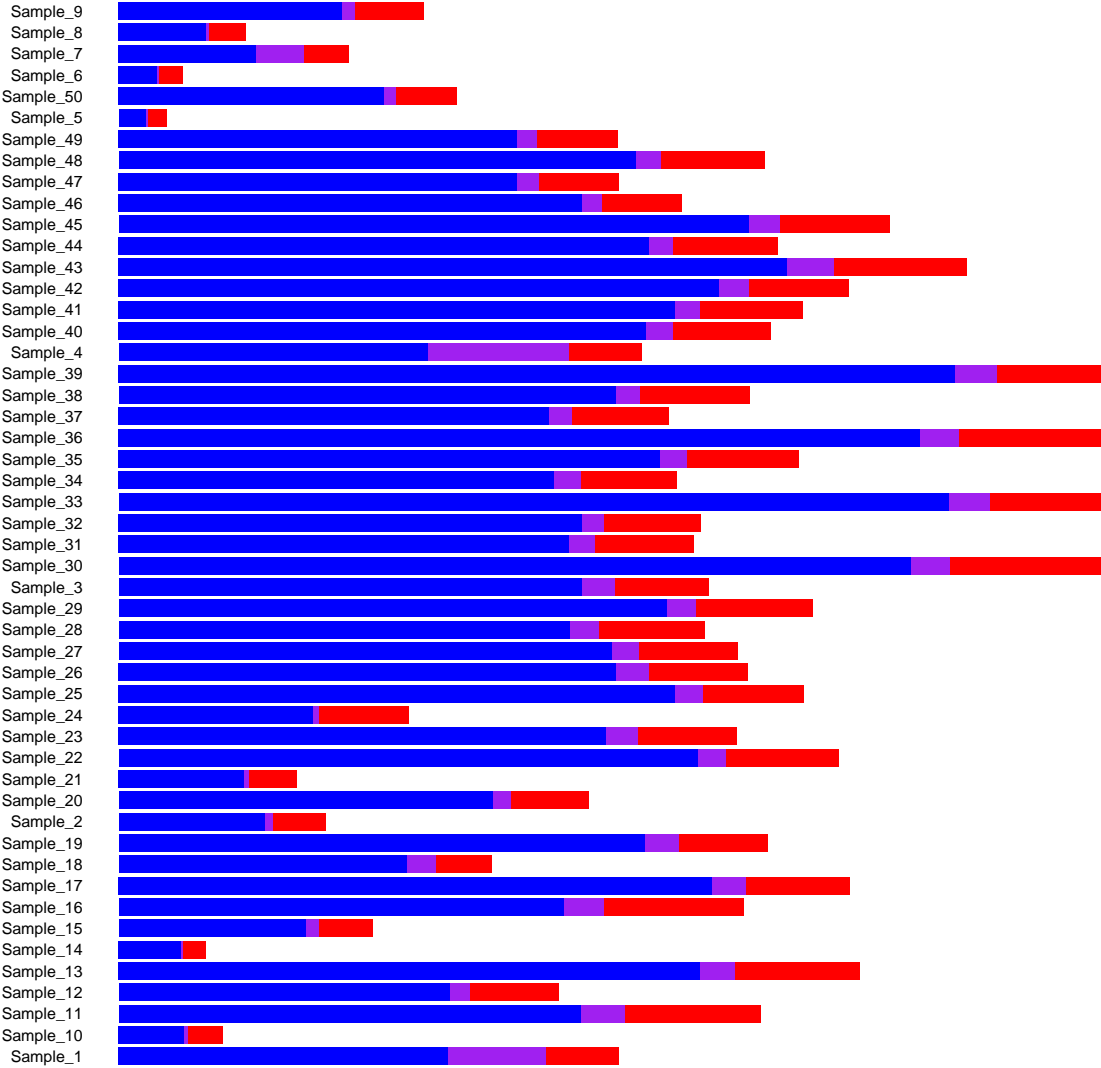


Sequencing Reads

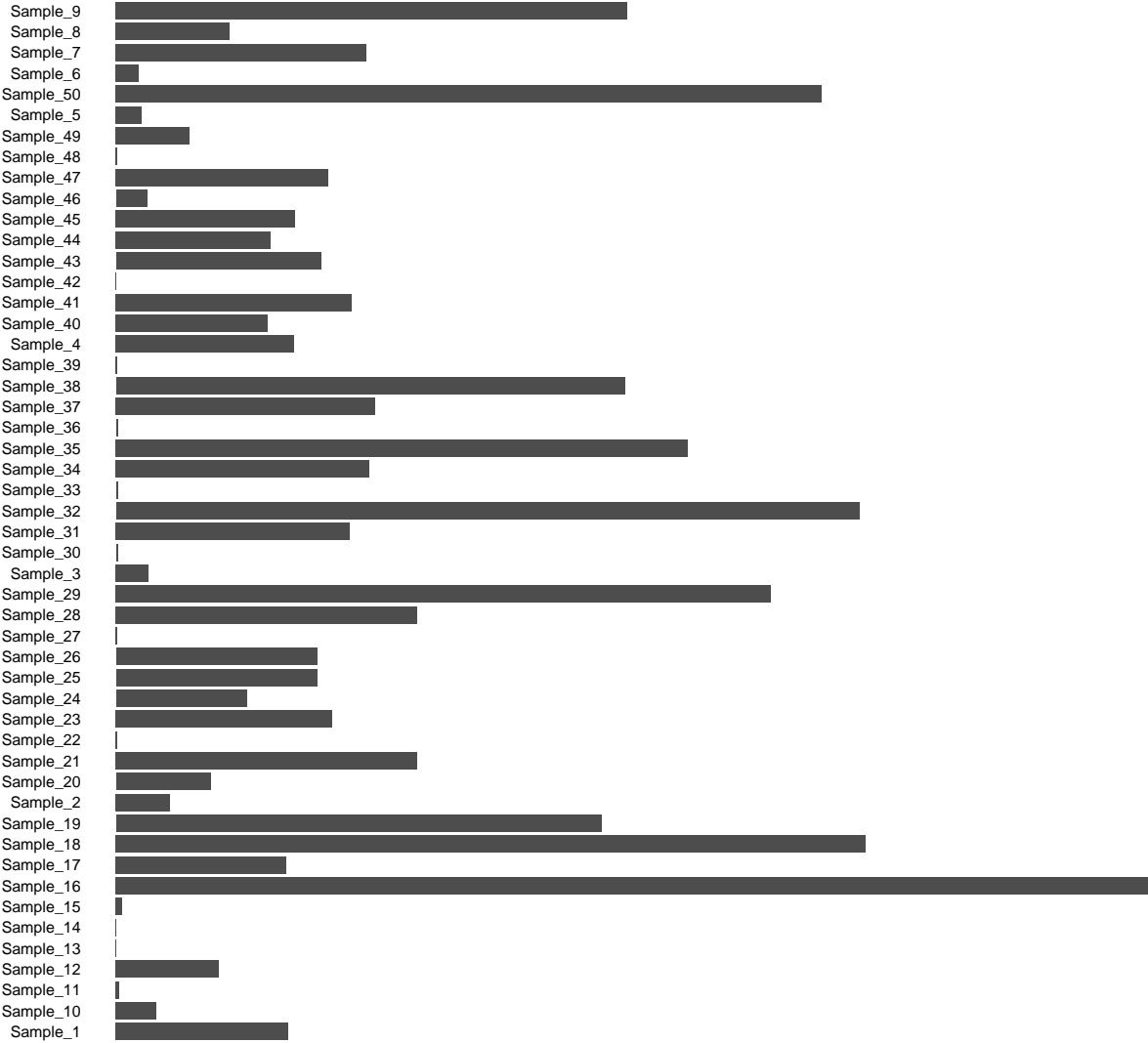
Unaligned Duplicated Unaligned



0 10 20 30 40 50

Number of reads (millions)

SamplePeaks\_MACS2



0 20000 40000 60000 80000

Number of peaks