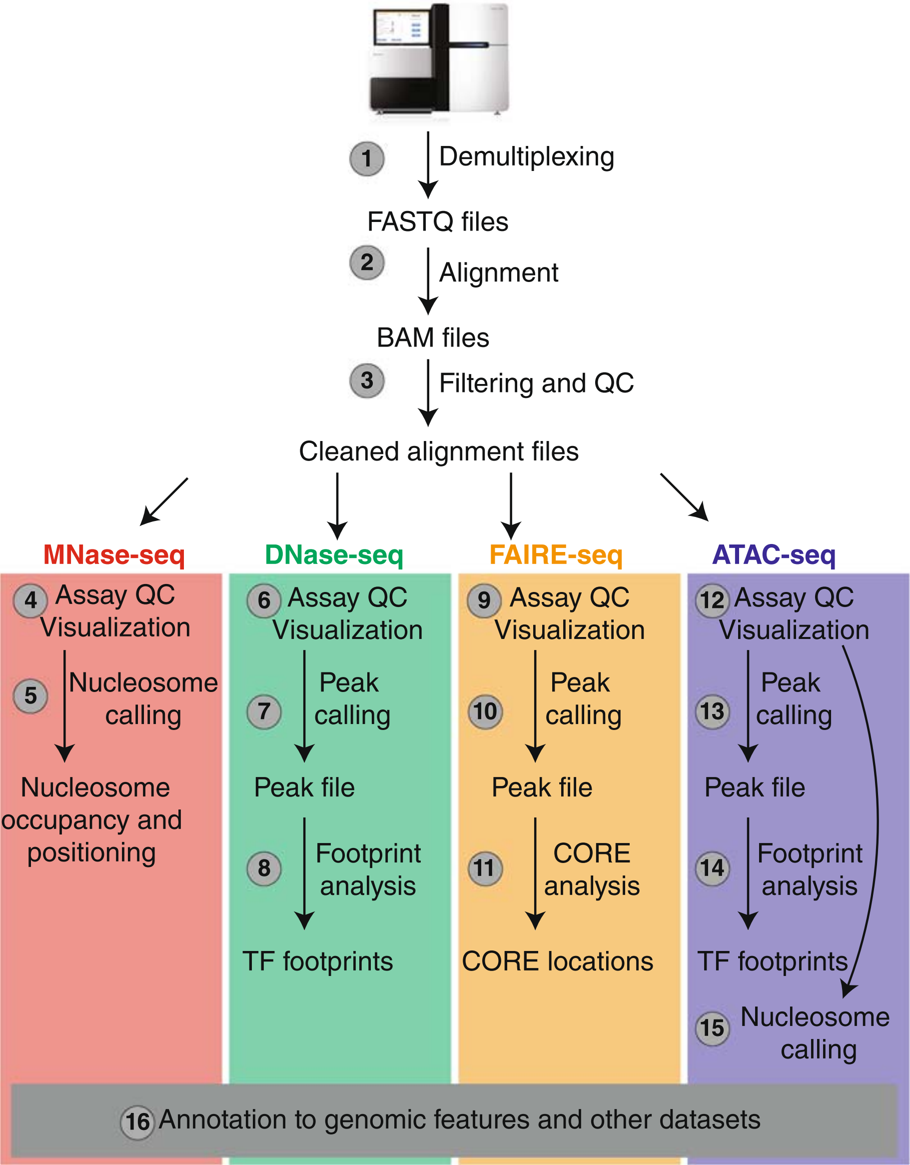
1
Demultiplexing
FASTQ files
2
Alignment
BAM files
3
Filtering and QC
Cleaned alignment files
MNase-seq
DNase-seq
FAIRE-seq
ATAC-seq
4
Assay QC
Visualization
5
Nucleosome calling
Nucleosome occupancy and positioning
6
Assay QC
Visualization
7
Peak calling
Peak file
8
Footprint analysis
TF footprints
9
Assay QC
Visualization
10
Peak calling
Peak file
11
CORE analysis
CORE locations
12
Assay QC
Visualization
13
Peak calling
Peak file
14
Footprint analysis
TF footprints
15
Nucleosome calling
16
Annotation to genomic features and other datasets