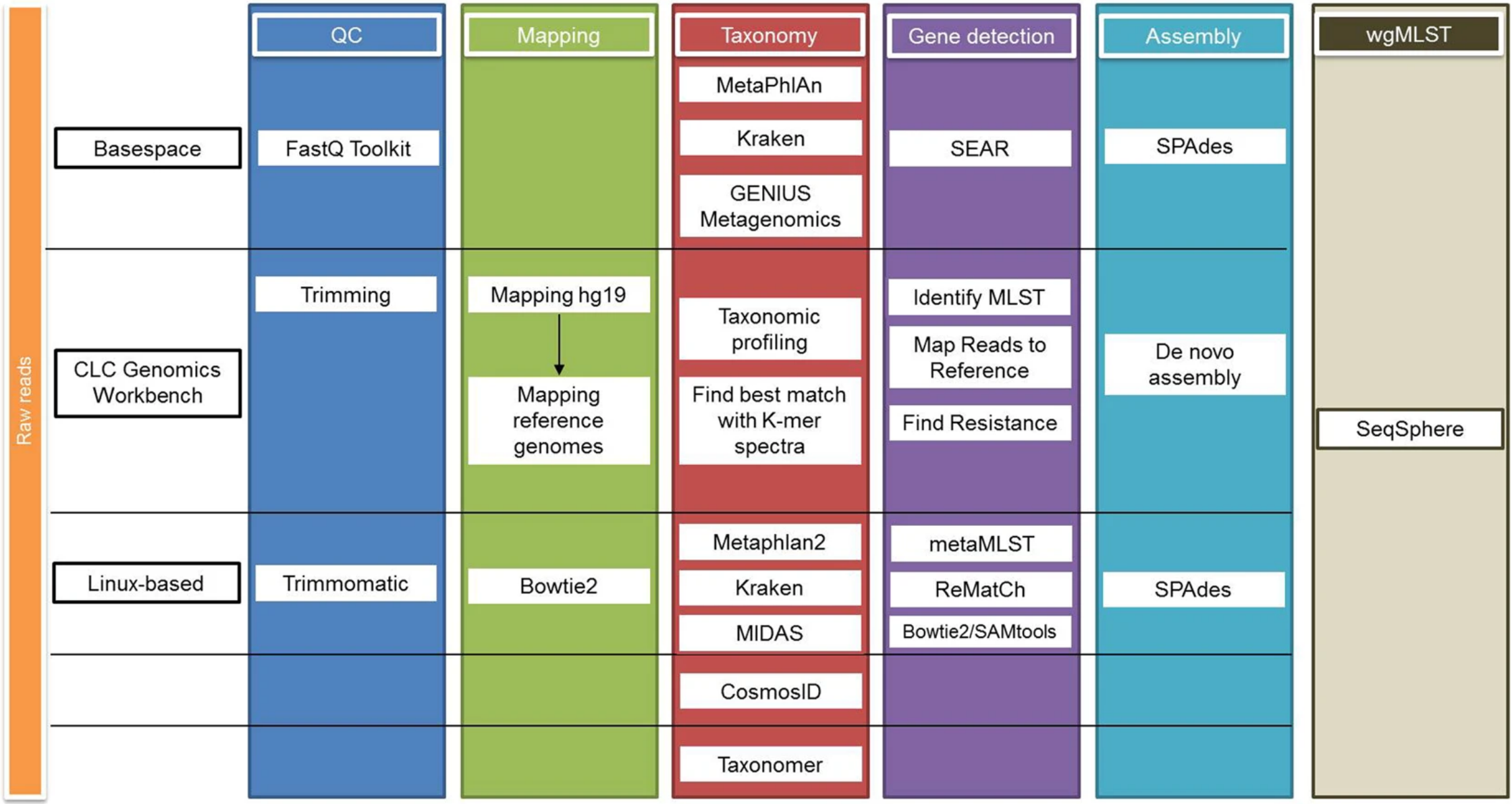
Raw reads
QC
Mapping
Taxonomy
Gene detection
Assembly
wgMLST
Basespace
FastQ Toolkit
MetaPhlAn
Kraken
GENIUS Metagenomics
SEAR
SPAdes
CLC Genomics Workbench
Trimming
Mapping hg19
Mapping reference genomes
Taxonomic profiling
Find best match with K-mer spectra
Identify MLST
Map Reads to Reference
Find Resistance
De novo assembly
SeqSphere
Linux-based
Trimmomatic
Bowtie2
Metaphlan2
Kraken
MIDAS
metaMLST
ReMatCh
Bowtie2/SAMtools
SPAdes
CosmosID
Taxonomer