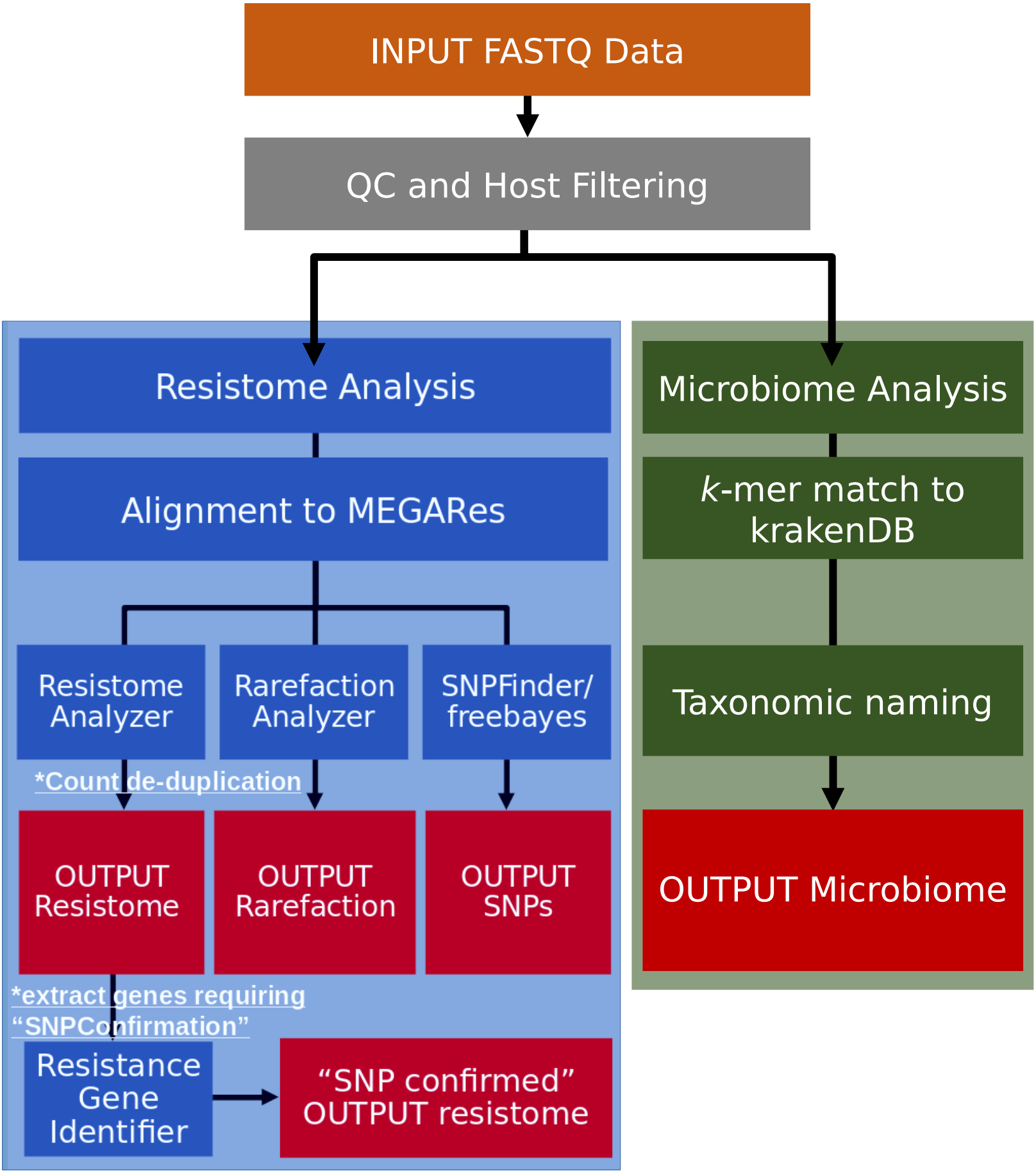
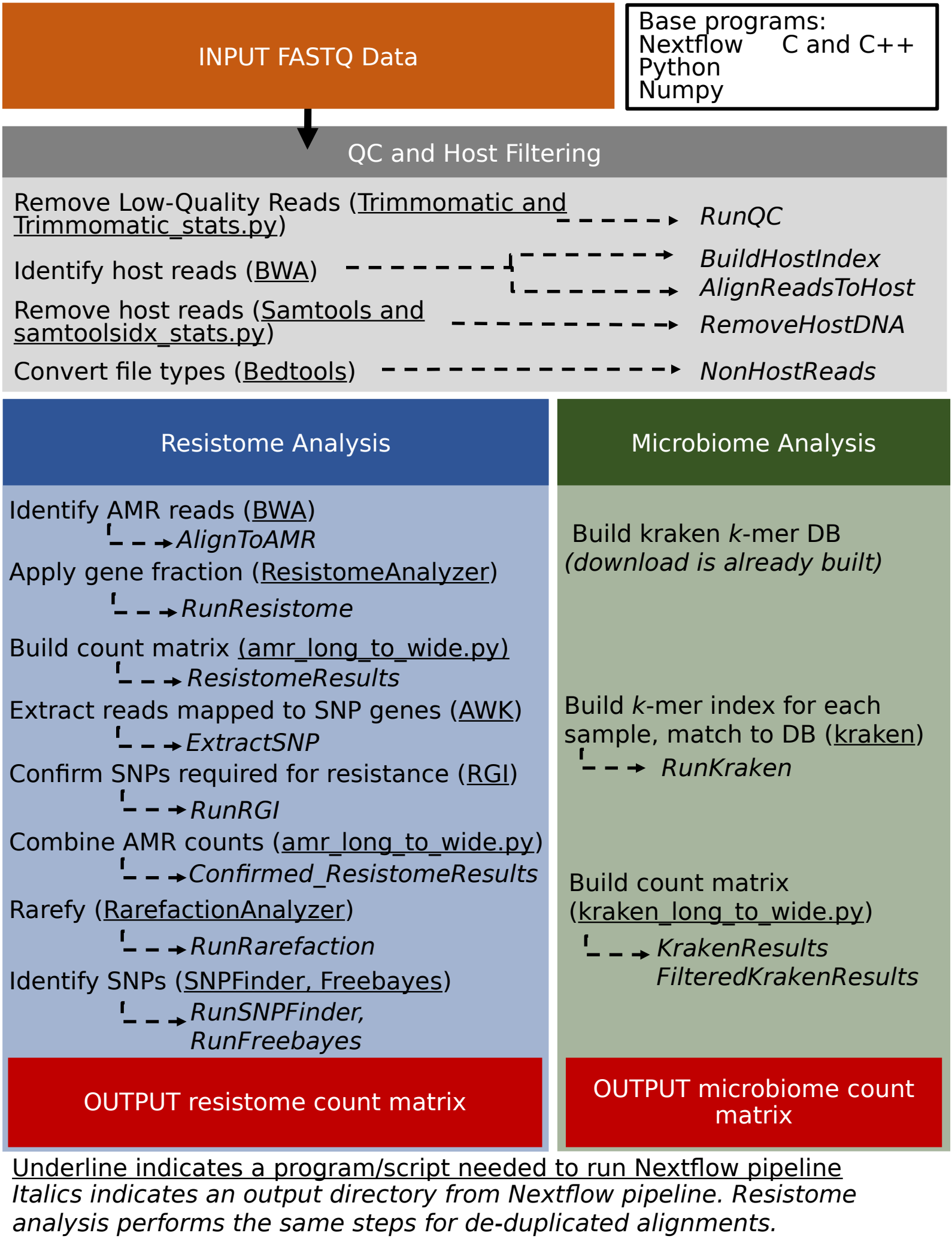

INPUT FASTQ Data
QC and Host Filtering
Resistome Analysis
Alignment to MEGARes
Resistome Analyzer
Rarefaction Analyzer
SNPFinder/ freebayes
*Count de-duplication
OUTPUT Resistome
OUTPUT Rarefaction
OUTPUT SNPs
*extract genes requiring "SNPConfirmation"
Resistance Gene Identifier
"SNP confirmed" OUTPUT resistome
Microbiome Analysis
k-mer match to krakenDB
Taxonomic naming
OUTPUT Microbiome



Underline indicates a program/script needed to run Nextflow pipeline

Italics indicates an output directory from Nextflow pipeline. Resistome analysis performs the same steps for de-duplicated alignments.