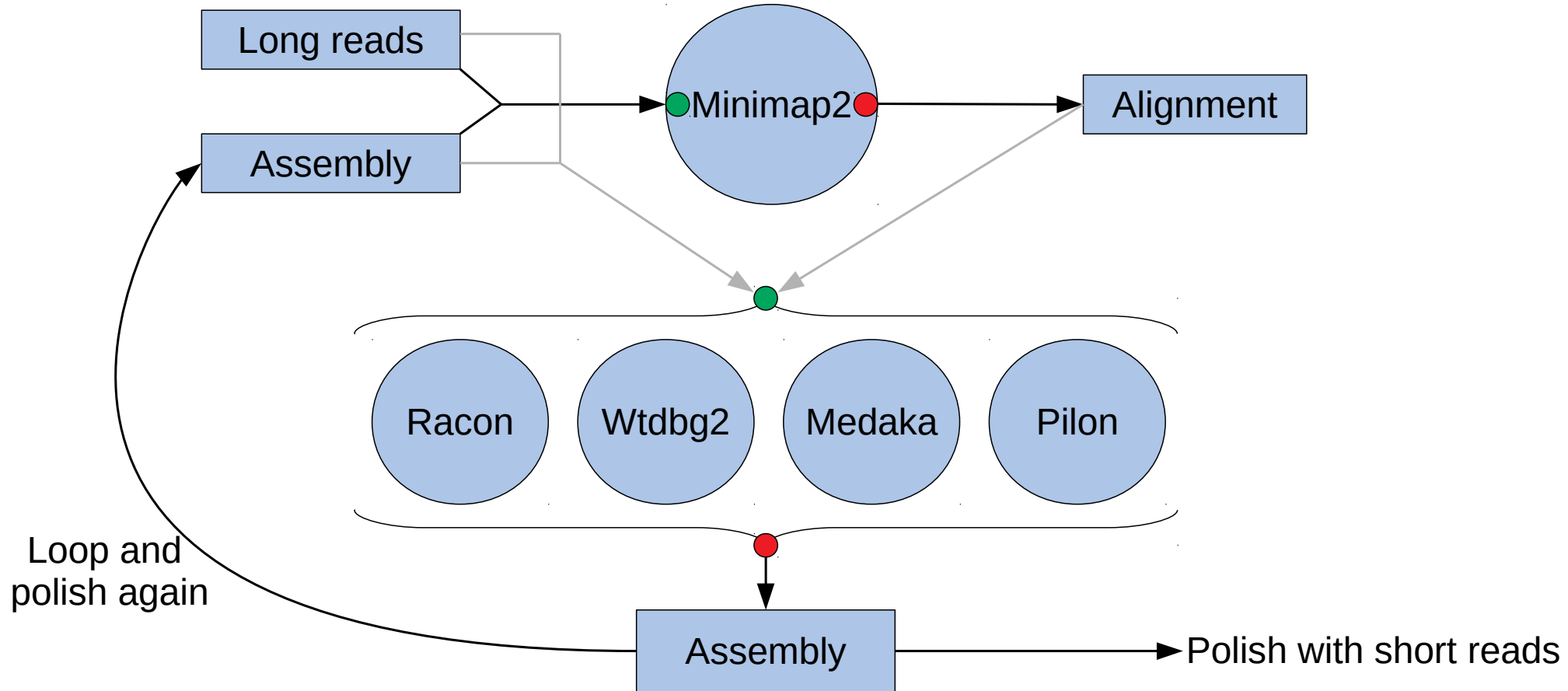


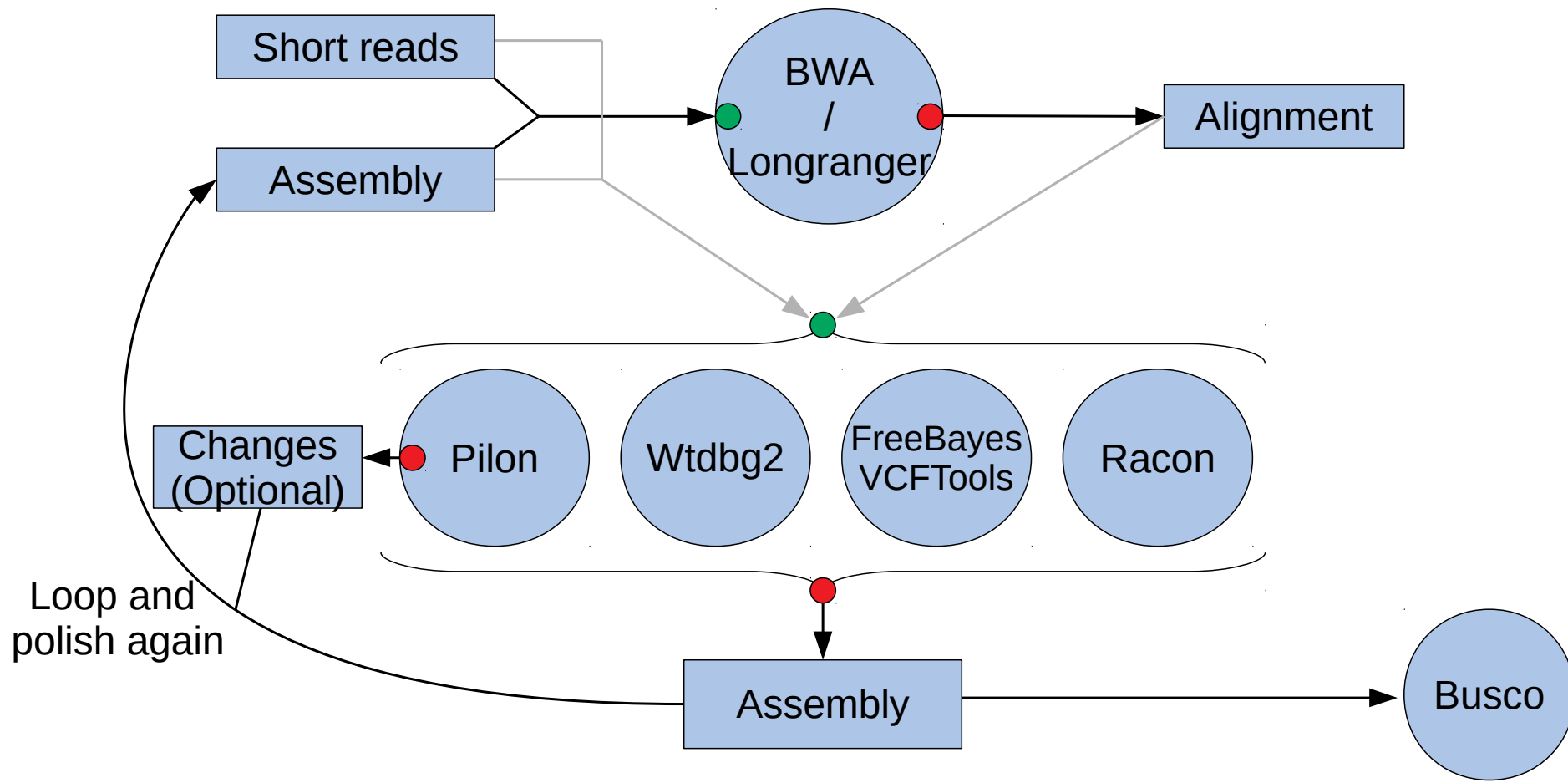
# Genome polishing Pipeline

**nextflow**

# Long reads polishing



# Short reads polishing



# Use of the pipeline

Nextflow run main.nf

**--longReads**

Path to long reads fasta or fastq .gz file

or/and

**--shortReads**

Path to short reads fasta or fastq .gz file

**--assembly**

Fasta file of genome assembly to polish

(Optional)

**--LRPolish**

Polisher to use for long reads: wtdbg2, racon, pilon, medaka (default : **racon**)

**--LRNum**

Number of long reads polishing (default: **2**)

**--SRPolish**

Polisher to use for short reads: pilon, racon, freebayes or wtdbg2 (default : **pilon**)

**--SRNum**

Number of short reads polishing (default: **2**)

**--NoChanges**

Short reads polishing with pilon until no more changes (default : **false**)

**--chunk**

Size for pilon parallelization (default : **10000000**)

**--lineage**

Lineage dataset used for BUSCO

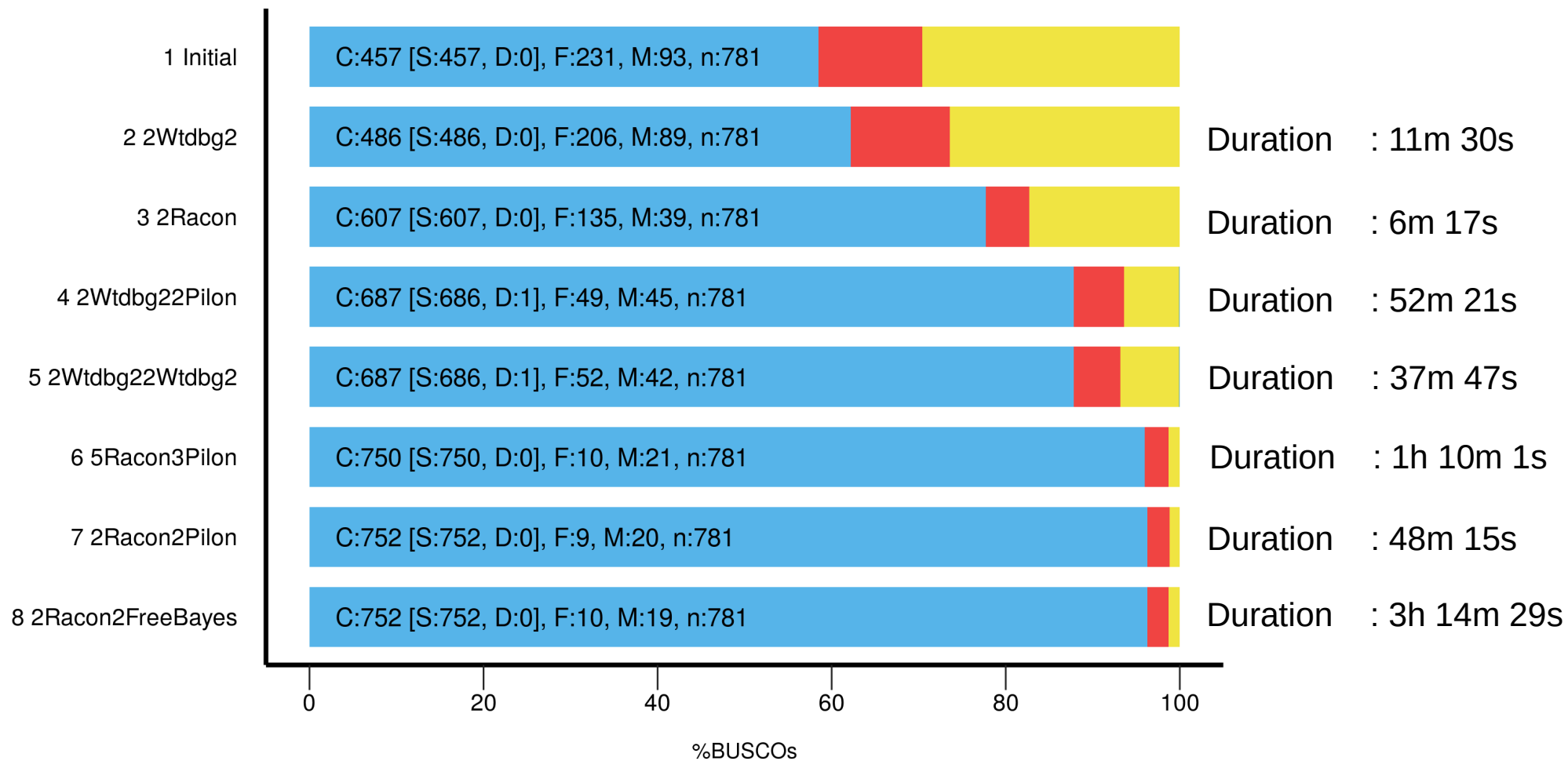
**--species**

Reference species for BUSCO (default: **generic**)

**--outdir**

The output directory where the results will be saved (default: **./results/**)

# BUSCO Polishing pipeline E.coli Results





Duration : 3h 14m 29s

CPU hours : 24.0

Duration : 48m 15s

CPU hours : 5.7

Duration : 52m 21s

CPU hours : 6.5

Duration : 37m 47s

CPU hours : 4.1

Duration : 1h 10m 1s

CPU hours : 8.6

BUSCO Polishing pipeline E.coli Results

