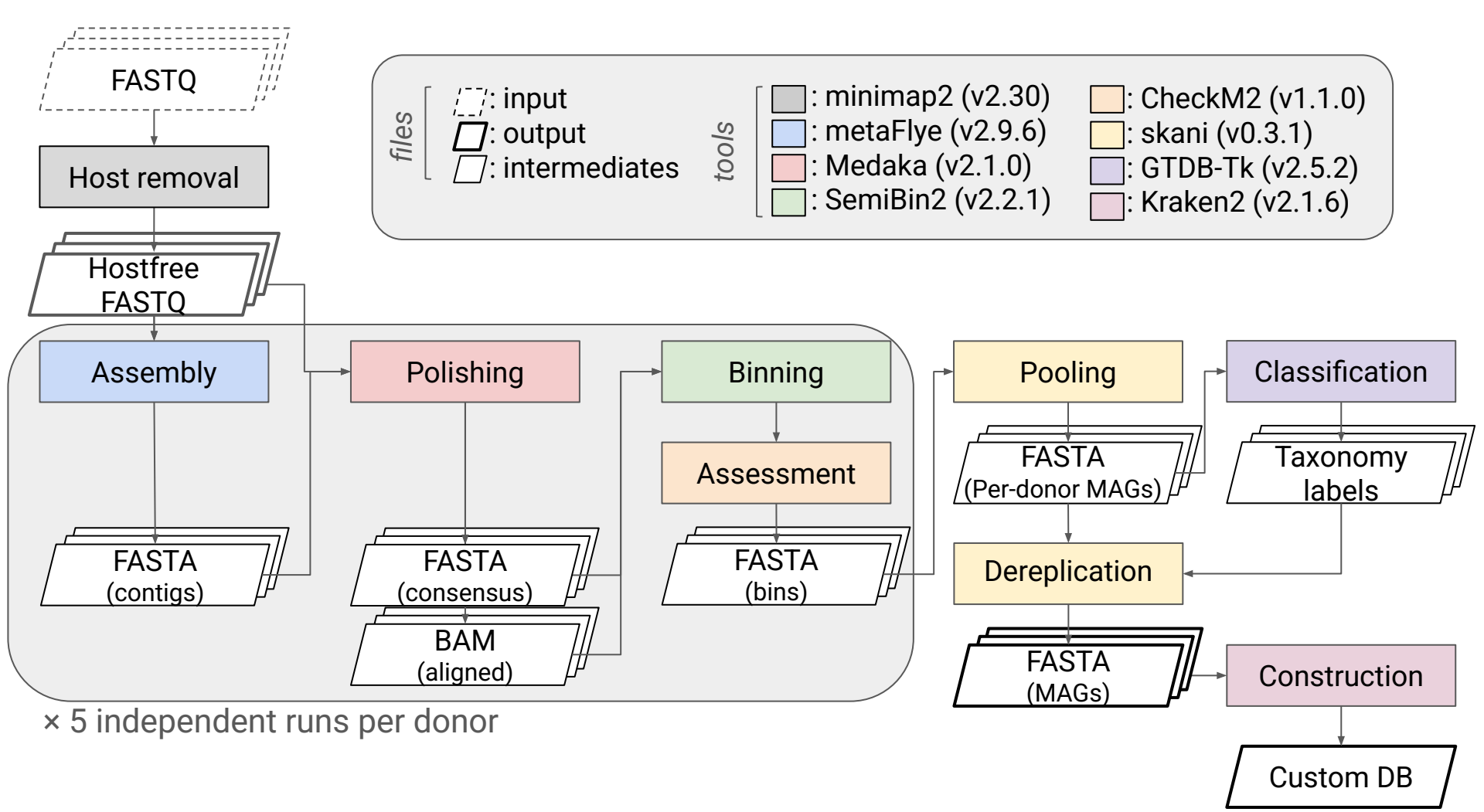

FASTQ
Host removal
Hostfree FASTQ
Assembly
Polishing
Binning
Assessment
FASTA (contigs)
FASTA (consensus)
BAM (aligned)
FASTA (bins)
× 5 independent runs per donor
files
: input
: output
: intermediates
tools
: minimap2 (v2.30)
: metaFlye (v2.9.6)
: Medaka (v2.1.0)
: SemiBin2 (v2.2.1)
: CheckM2 (v1.1.0)
: skani (v0.3.1)
: GTDB-Tk (v2.5.2)
: Kraken2 (v2.1.6)
Pooling
Classification
FASTA (Per-donor MAGs)
Taxonomy labels
Dereplication
FASTA (MAGs)
Construction
Custom DB