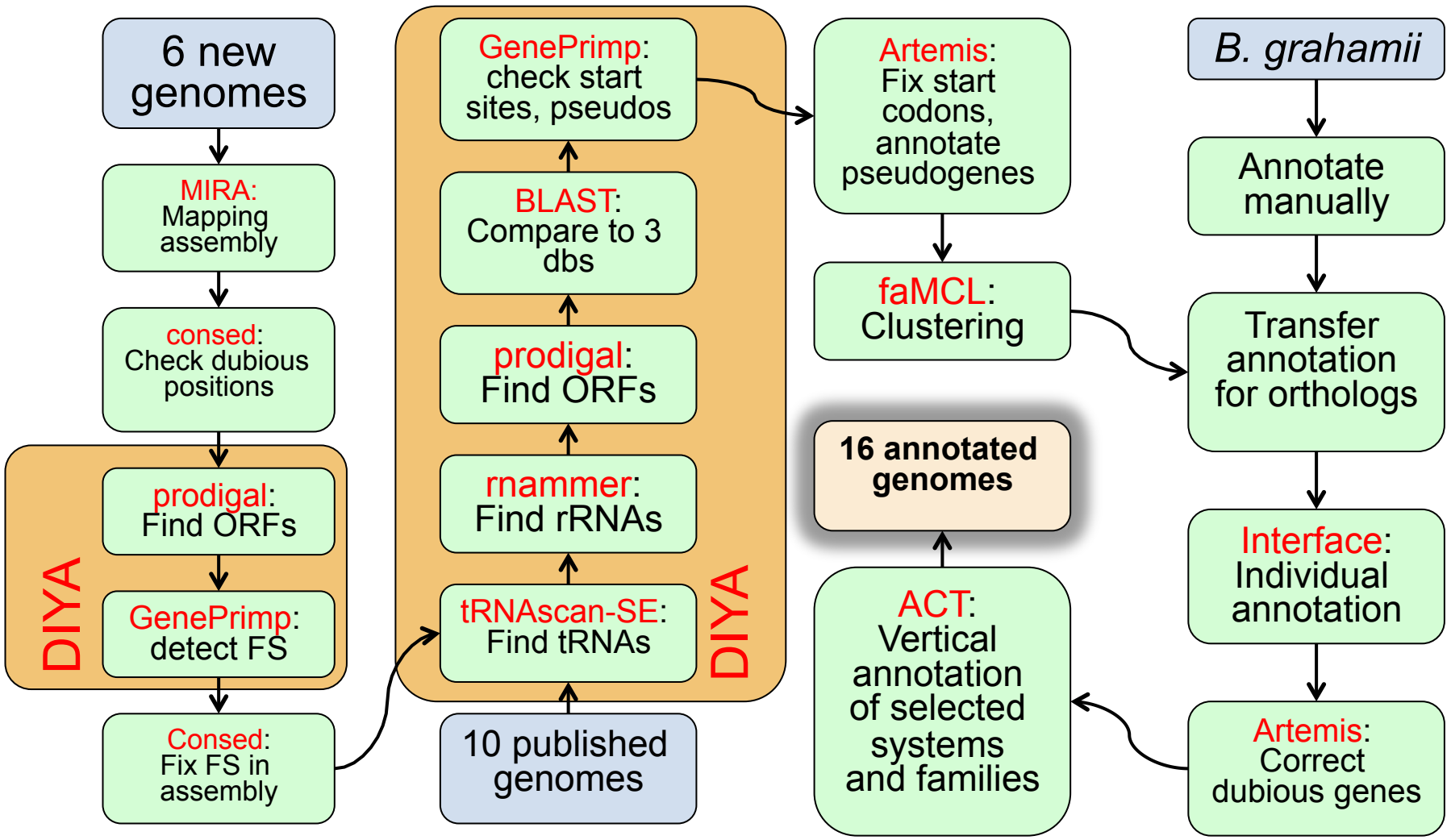
6 new genomes
MIRA: Mapping assembly
consed: Check dubious positions
DIYA
prodigal: Find ORFs
GenePrimp: detect FS
Consed: Fix FS in assembly
GenePrimp: check start sites, pseudos
BLAST: Compare to 3 dbs
prodigal: Find ORFs
rnammer: Find rRNAs
tRNAscan-SE: Find tRNAs
DIYA
10 published genomes
Artemis: Fix start codons, annotate pseudogenes
faMCL: Clustering
16 annotated genomes
ACT: Vertical annotation of selected systems and families
B. grahamii
Annotate manually
Transfer annotation for orthologs
Interface: Individual annotation
Artemis: Correct dubious genes