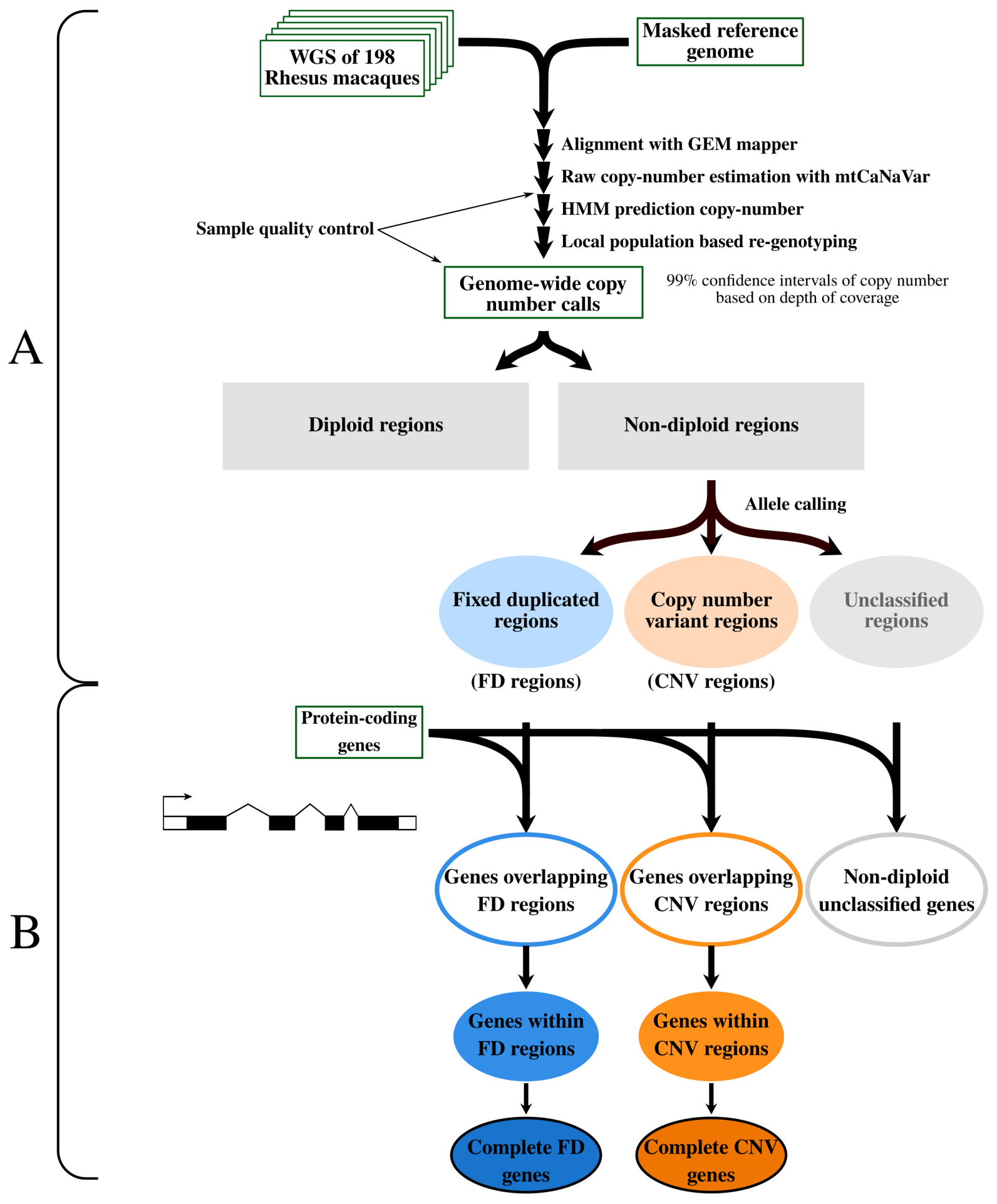
A
WGS of 198 Rhesus macaques
Masked reference genome
Alignment with GEM mapper
Raw copy-number estimation with mtCaNaVar
HMM prediction copy-number
Local population based re-genotyping
Sample quality control
Genome-wide copy number calls
99% confidence intervals of copy number based on depth of coverage
Diploid regions
Non-diploid regions
Allele calling
Fixed duplicated regions
Copy number variant regions
Unclassified regions
(FD regions)
(CNV regions)
B
Protein-coding genes
Genes overlapping FD regions
Genes overlapping CNV regions
Non-diploid unclassified genes
Genes within FD regions
Genes within CNV regions
Complete FD genes
Complete CNV genes