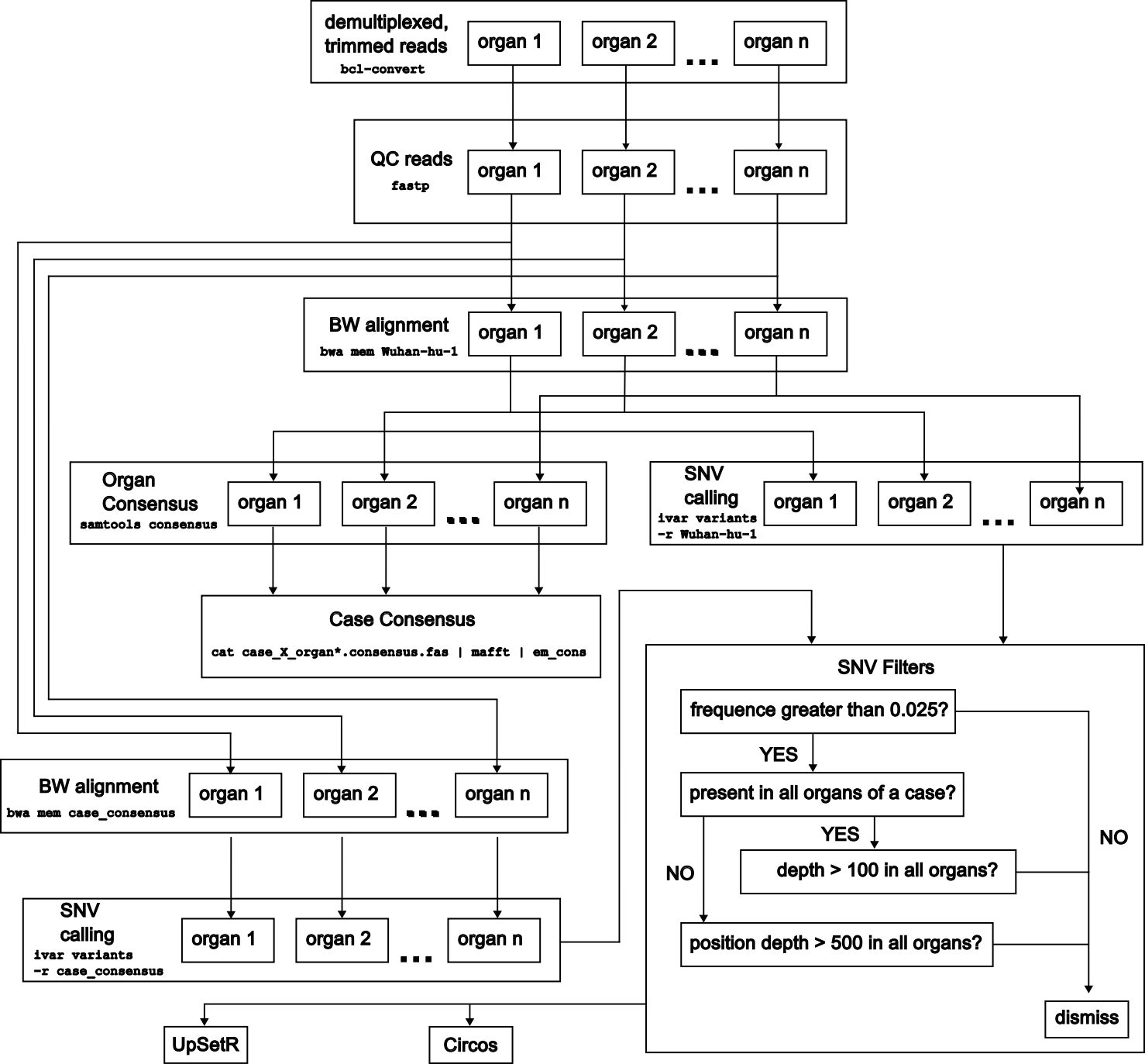
demultiplexed, trimmed reads
bcl-convert
organ 1
organ 2
organ n
QC reads
fastp
BW alignment
bwa mem Wuhan-hu-1
Organ Consensus
samtools consensus
SNV calling
ivar variants -r Wuhan-hu-1
Case Consensus
cat case_X_organ*.consensus.fas | mafft | em_cons
SNV Filters
frequence greater than 0.025?
YES
NO
present in all organs of a case?
YES
NO
depth > 100 in all organs?
position depth > 500 in all organs?
dismiss
BW alignment
bwa mem case_consensus
SNV calling
ivar variants -r case_consensus
UpSetR
Circos