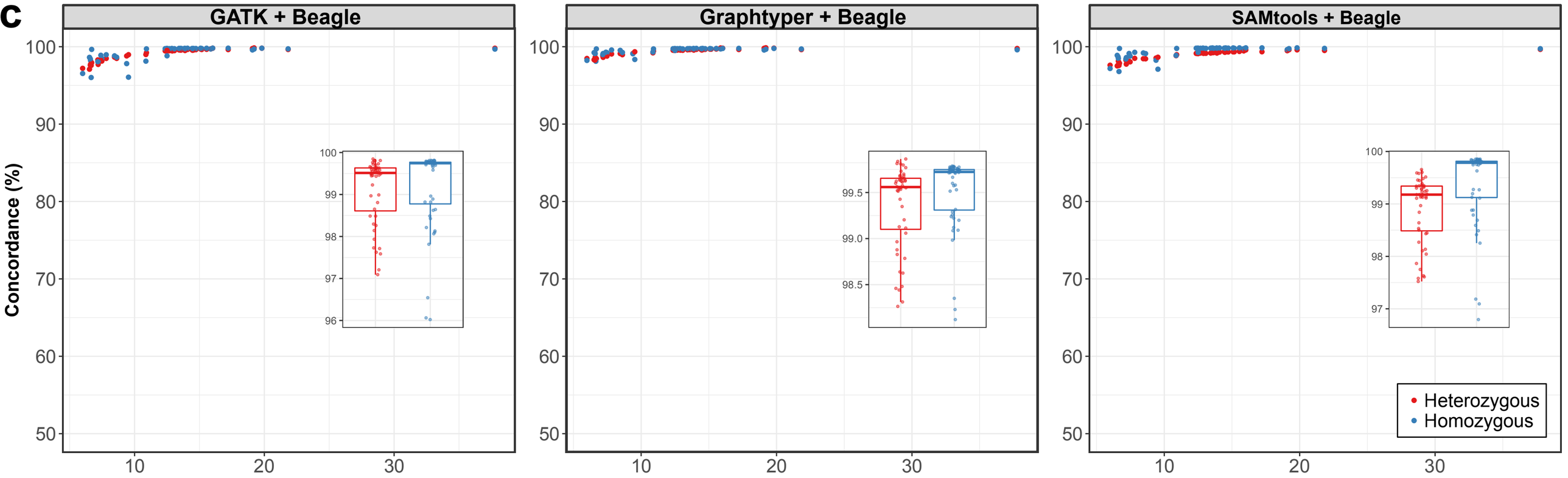
c
GATK + Beagle
Graphtyper + Beagle
SAMtools + Beagle
Concordance (%)
100
90
80
70
60
50
10
20
30
Heterozygous
Homozygous