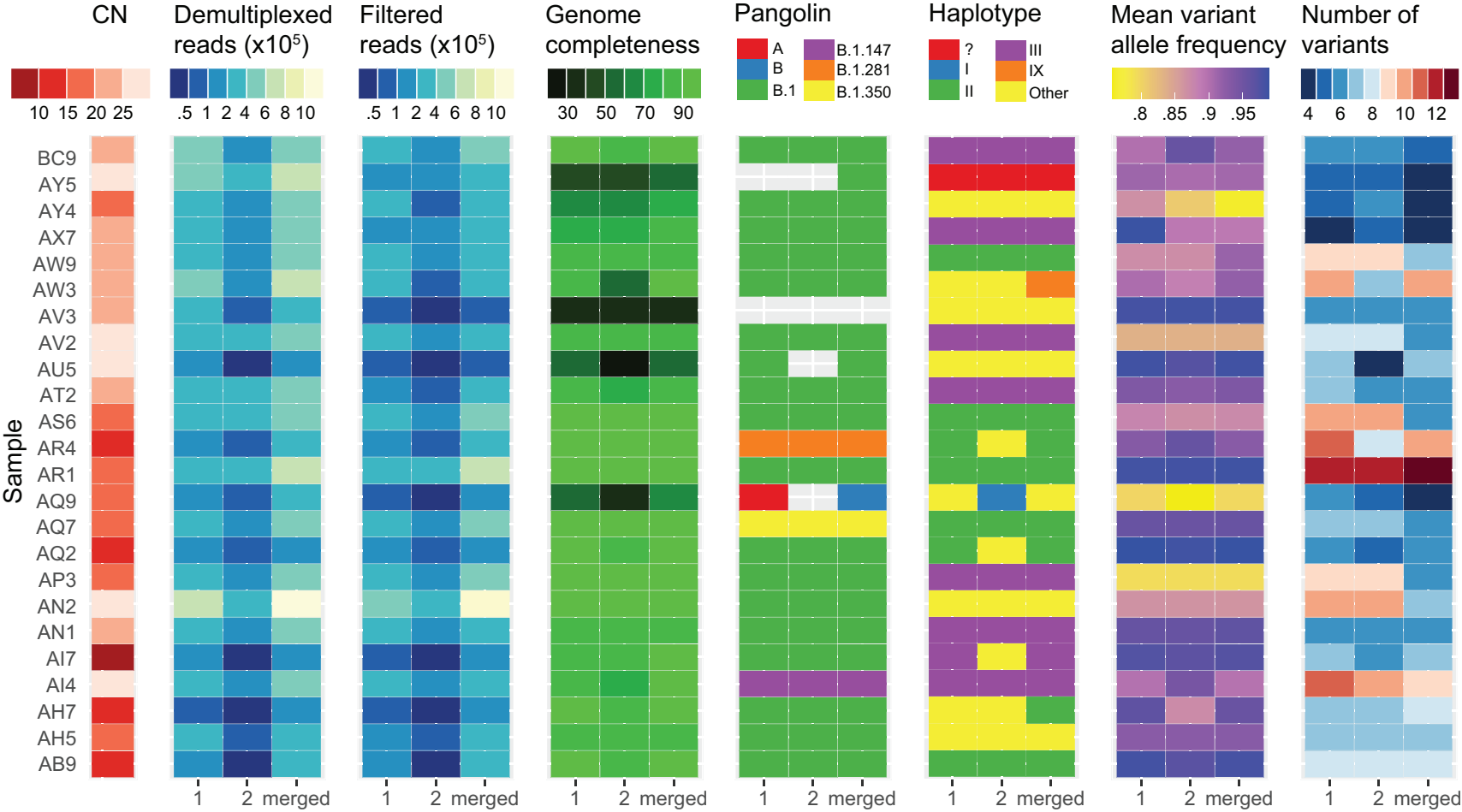
CN
10 15 20 25
Demultiplexed reads (x10^5)
.5 1 2 4 6 8 10
Filtered reads (x10^5)
.5 1 2 4 6 8 10
Genome completeness
30 50 70 90
Pangolin
A
B
B.1
B.1.147
B.1.281
B.1.350
Haplotype
?
I
II
III
IX
Other
Mean variant allele frequency
.8 .85 .9 .95
Number of variants
4 6 8 10 12
Sample
BC9
AY5
AY4
AX7
AW9
AW3
AV3
AV2
AU5
AT2
AS6
AR4
AR1
AQ9
AQ7
AQ2
AP3
AN2
AN1
AI7
AI4
AH7
AH5
AB9
1 2 merged