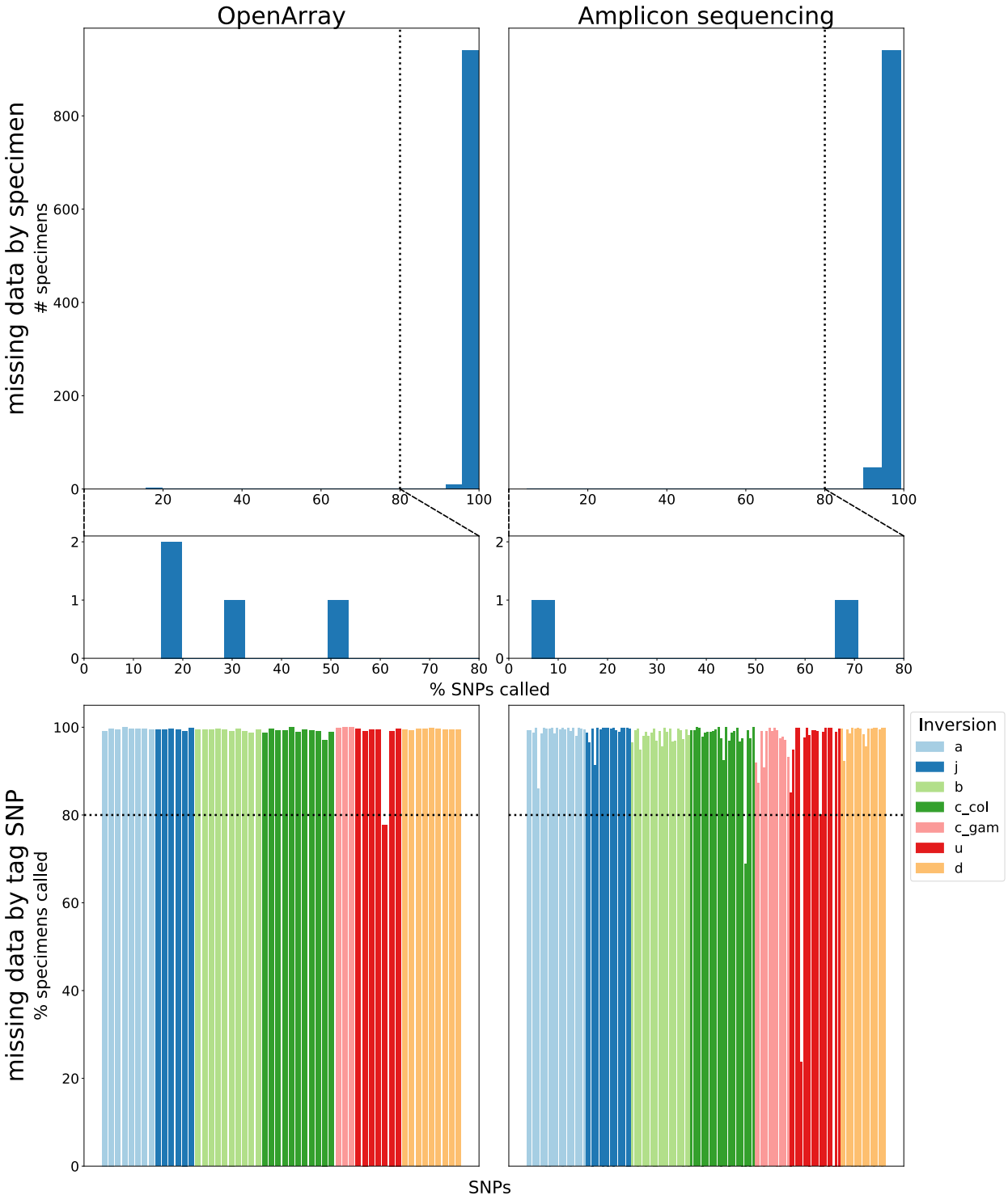
OpenArray
Amplicon sequencing
missing data by specimen
specimens
% SNPs called
missing data by tag SNP
% specimens called
SNPs
Inversion
a
j
b
c_col
c_gam
u
d

Figure S1. Tag SNP and specimen call rates for OpenArray and amplicon sequencing (GT-seq) approaches. Top panels show histograms of the percentage of all tag SNPs that could be called for each specimen used for OpenArray or GT-seq. The dotted line indicates the 80% threshold below which specimens were removed from further analysis. The portion of the plot showing specimens with call rates below 80% is enlarged to show detail. Bottom panels show the percentage of specimens that could be called for each individual tag SNP used for OpenArray or GT-seq, grouped and colored by inversion. The dotted line indicates the 80% threshold below which tag SNPs were removed from further analysis.

Table S1. OpenArray tag SNPs. Details of the final 53 tag SNPs used for OpenArray, including positions, assay names, reference and alternate alleles, sequences of forward and reverse primers, and sequences of probes for both alleles. (Table S1 is included separately as Table_S1.csv.)

Table S2. GT-seq tag SNPs. Details of the final 131 tag SNPs used for GT-seq, including positions, reference and alternate alleles, and the sequences of forward and reverse primers. (Table S2 is included separately as Table_S2.csv.)

Table S3. Cytogenetic and molecular karyotypes. Specimen IDs, villages of origin, species, and cytogenetic ("_cyto"), GT-seq ("_amp"), and OpenArray ("_oa") inversion genotypes for the 957 specimens used for either OpenArray or GT-seq analysis. Please note that while inversion genotypes are included for all inversions for all specimens, some groups of tag SNPs are not applicable to all specimens (see text for further details). (Table S3 is included separately as Table_S3.csv.)