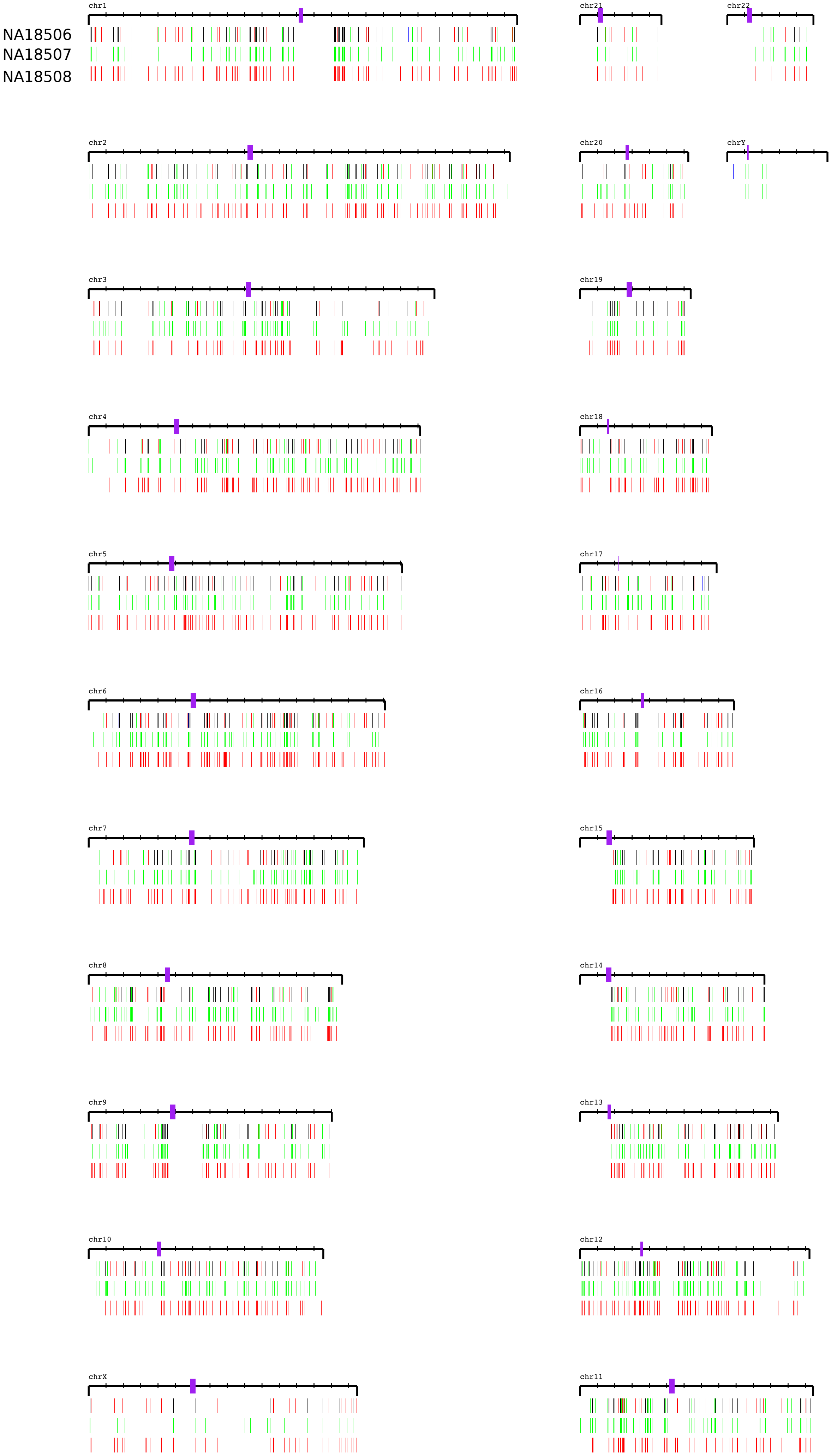
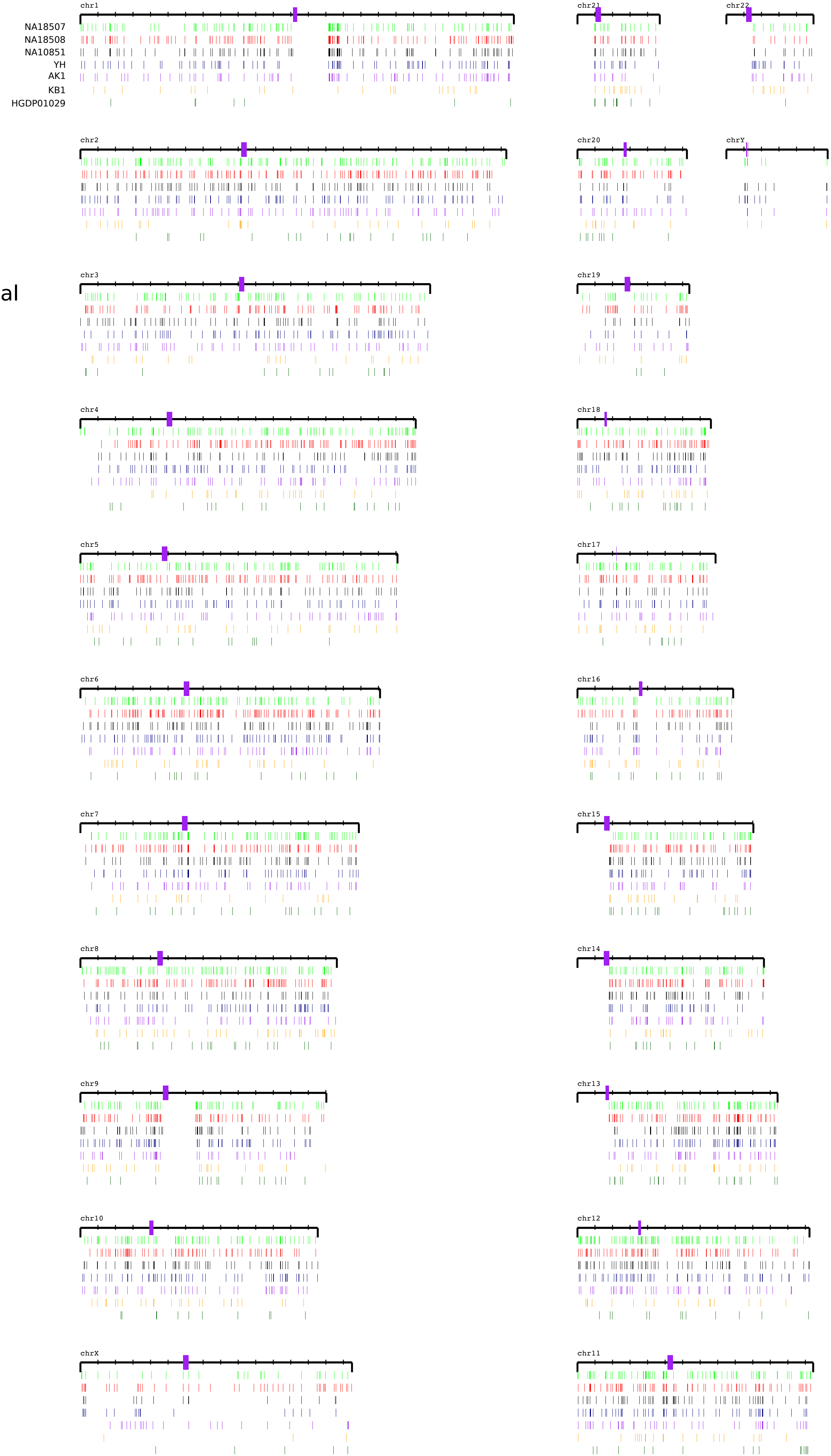
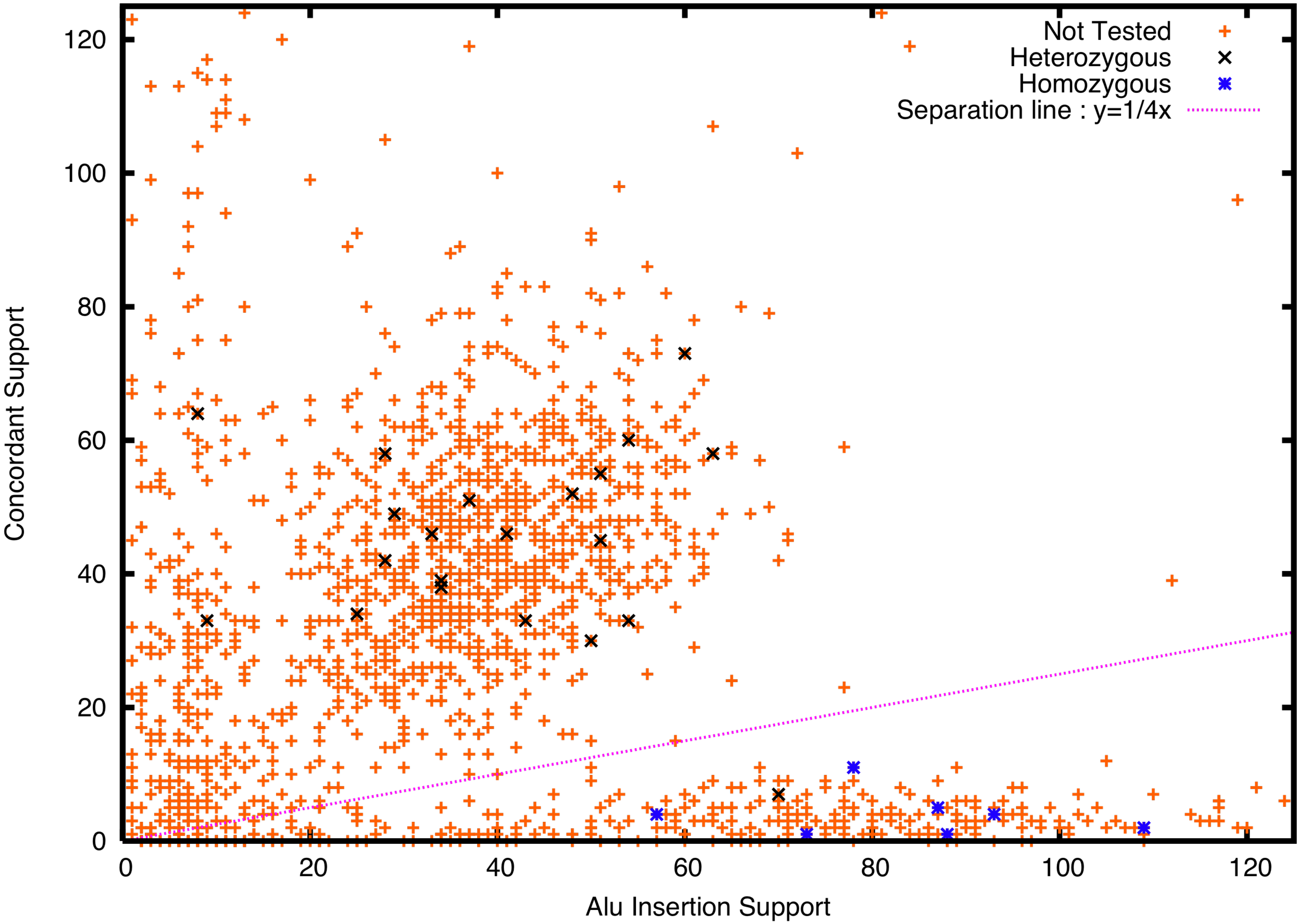
Supplemental Fig. S1



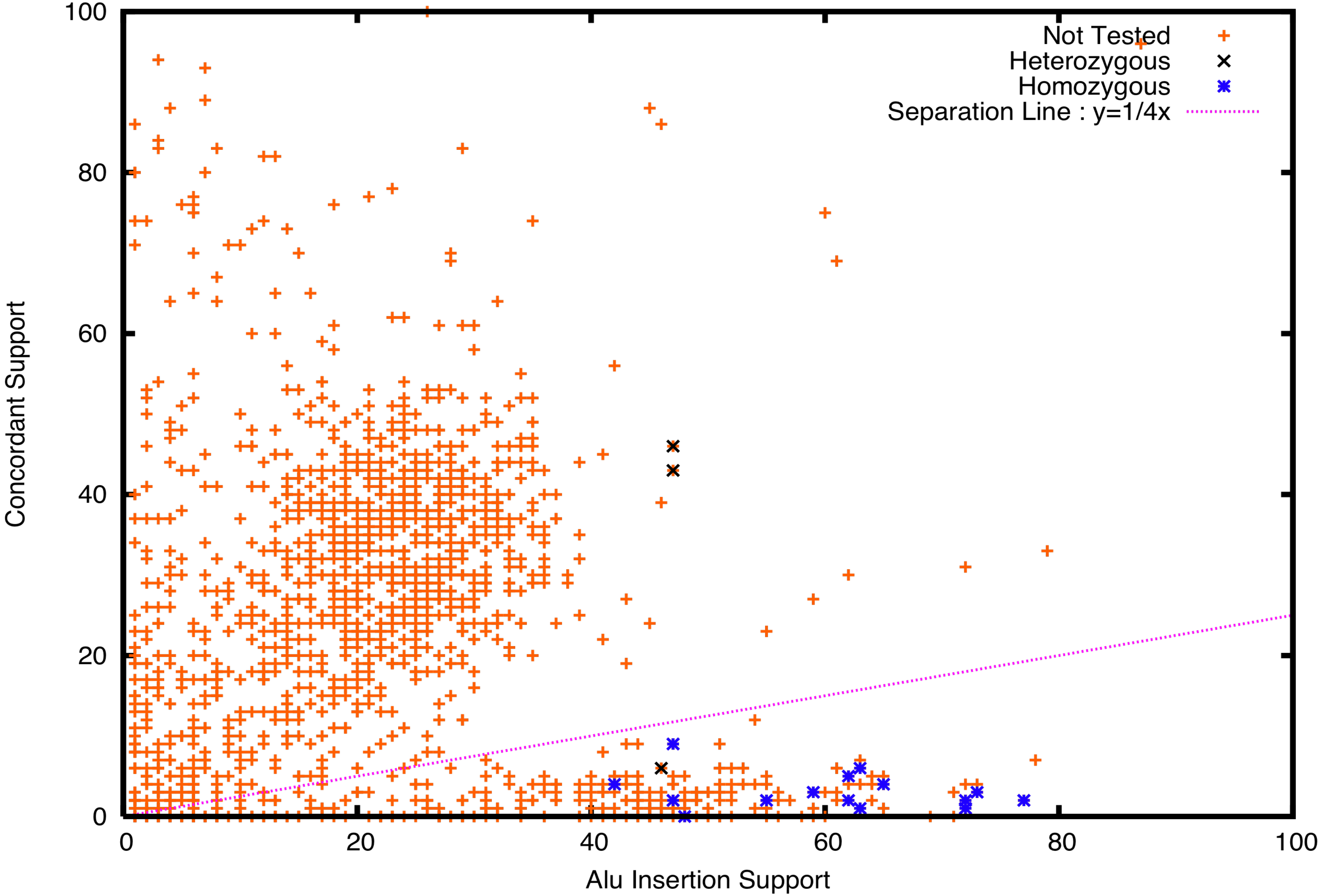
Supplemental
Fig. S2



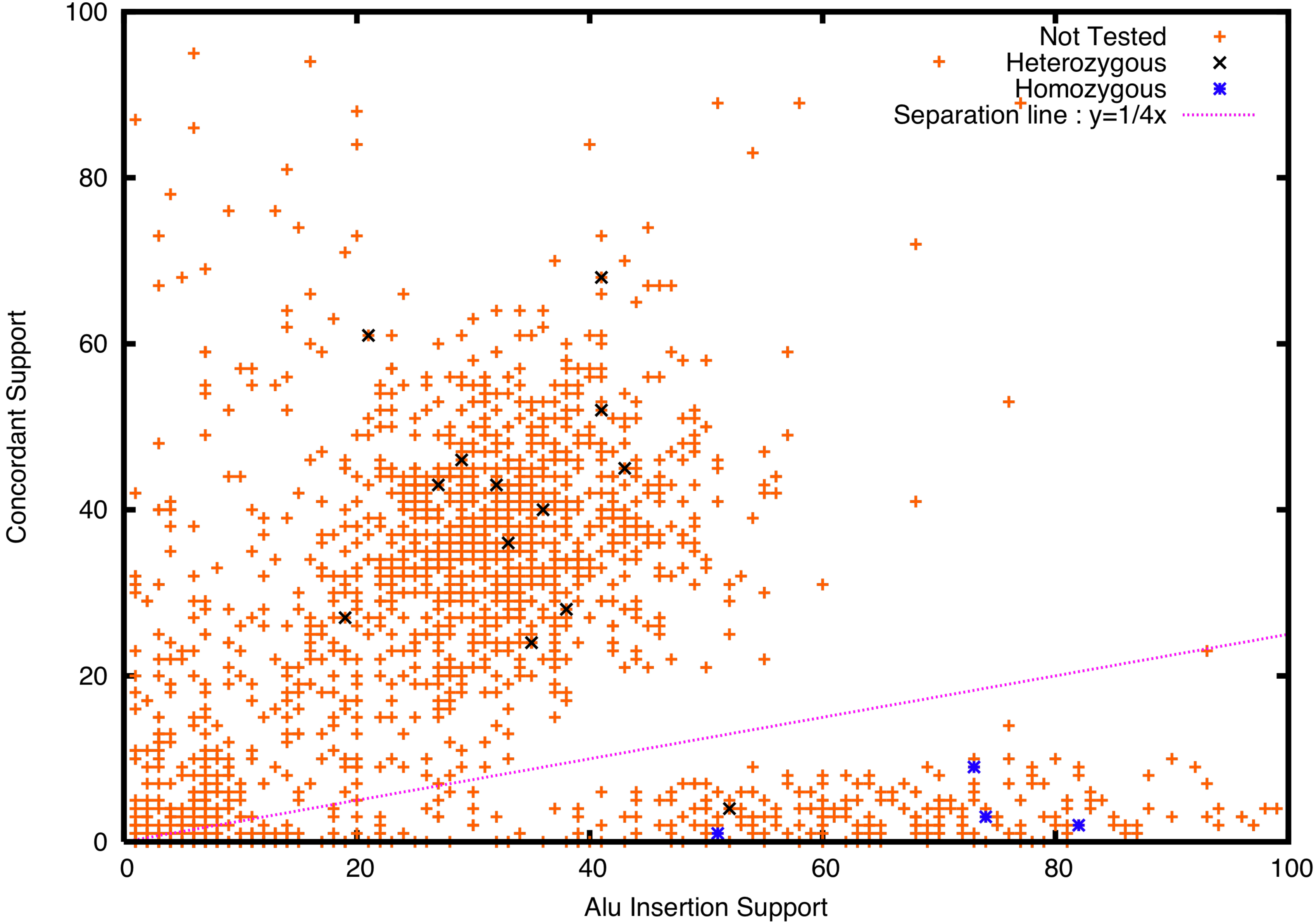
Supplemental Fig. S3A



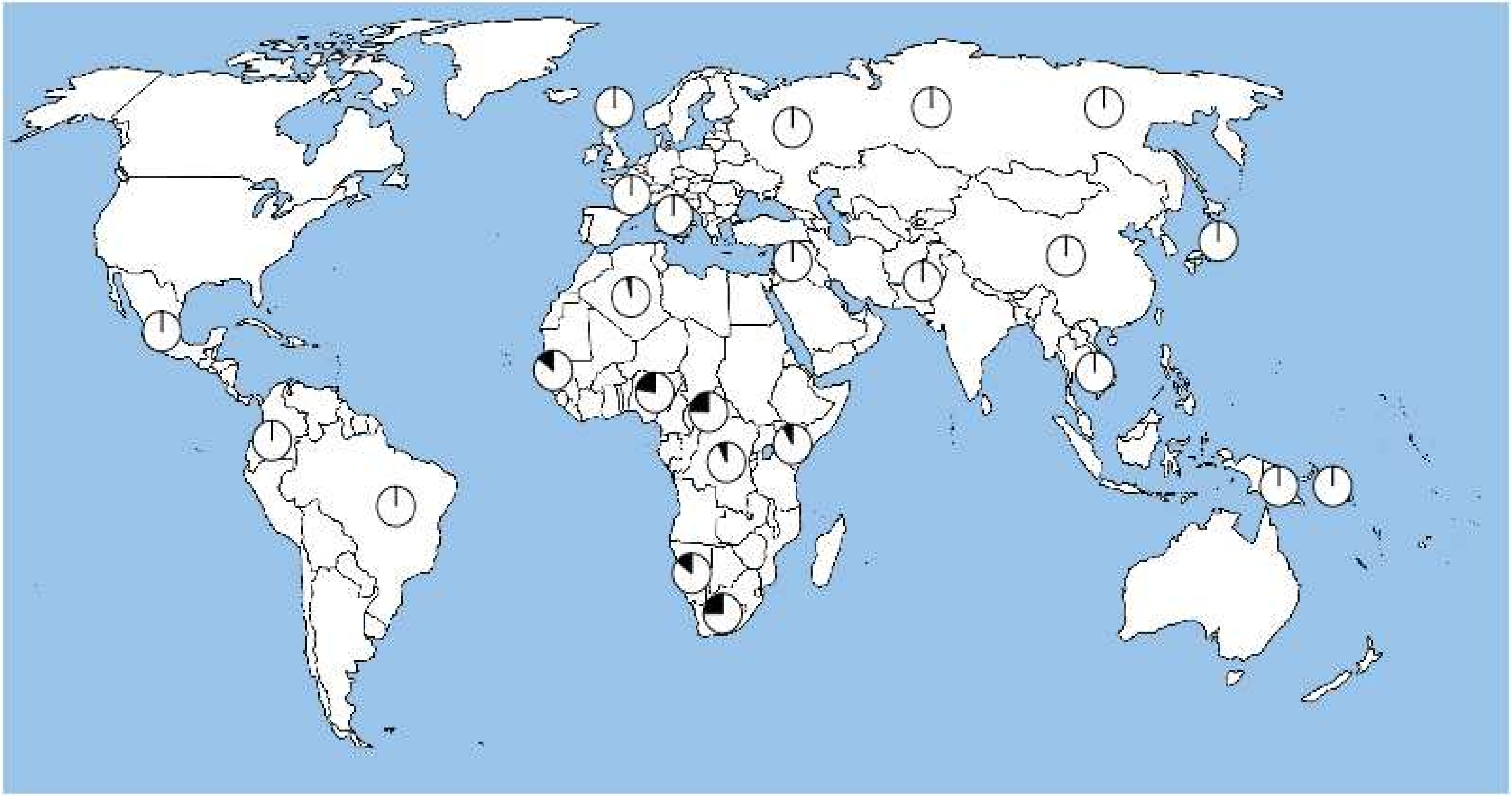
Supplemental Fig. S3B



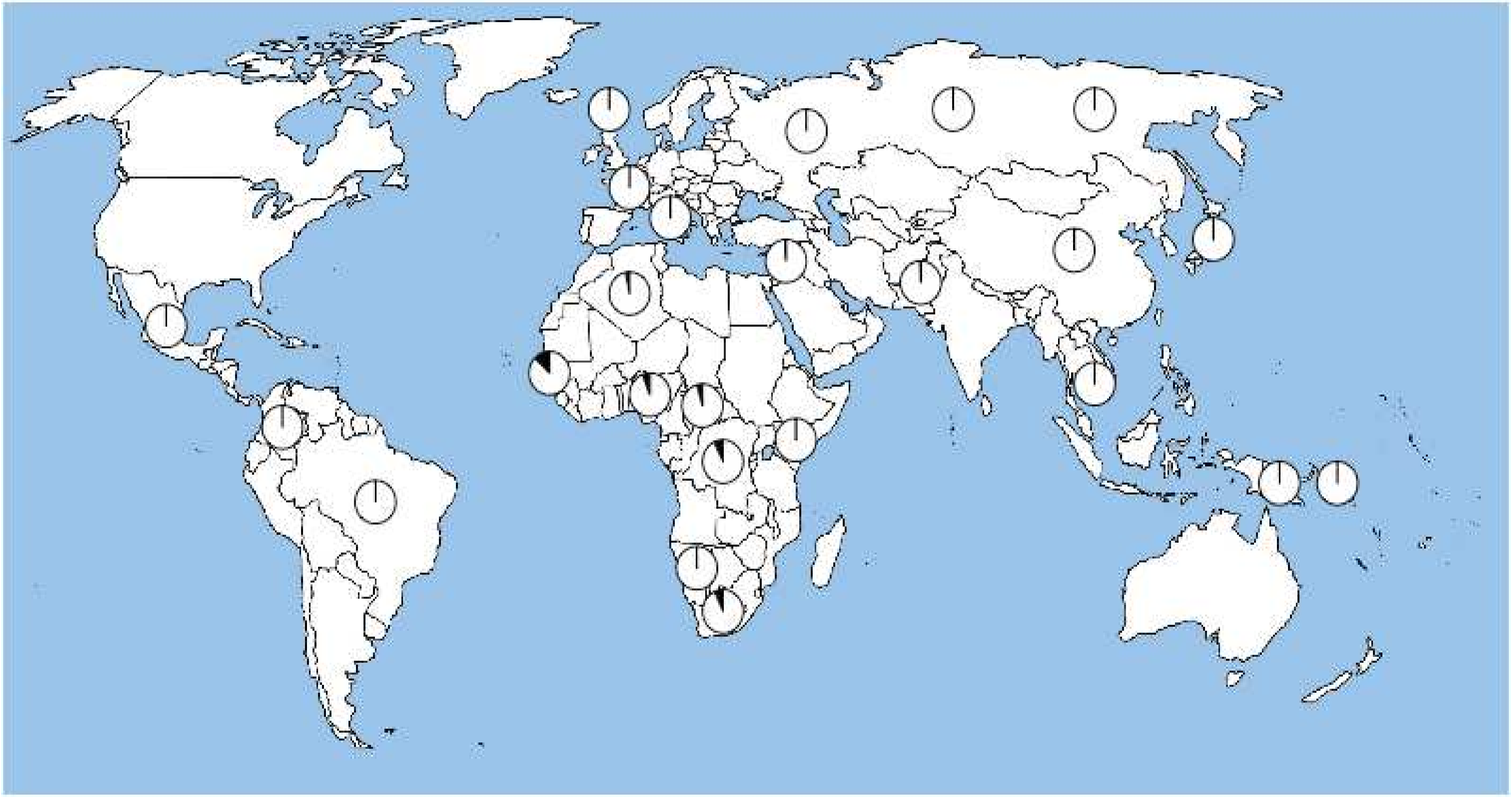
Supplemental Fig. S3C



Supplemental Fig. S4A



Supplemental Fig. S4B



Supplemental Fig. S1. The *Alu* insertion map in the YRI trio genomes. The *Alu* insertion loci are shown for the YRI trio in the order of NA18506, NA18507 and NA18508.

Supplemental Fig. S2. The *Alu* insertion map in seven human genomes. The *Alu* insertion map of all the samples we studied in the order of NA18507, NA18508, NA10851, YH, AK1, KB1 and HGDP01029.

Supplemental Fig. S3. Genotyping insertions in the genomes of YRI trio. The classifier compares the number of reads consistent with the reference genome (concordant) when compared to the number of reads supporting an *Alu* insertion polymorphism. Experimentally confirmed heterozygous insertions (black dots) are compared to homozygous insertions (blue dots) with classifier ($y = 1/4x$). We correctly genotyped 27/28 loci for each *(A)* NA18506 *(B)* NA18507 and *(C)* NA18508 as homozygous and heterozygous.

Supplemental Fig. S4. Global genome-wide distribution of *Alu*18507_11 and *Alu*18508_6 polymorphisms. Allele frequency as determined by PCR of 1,054 samples from 52 HGDP populations. Insertion polymorphism frequency (black portion of the pie chart) for *A) Alu*18507_11 and *B) Alu*18508_6 is depicted.