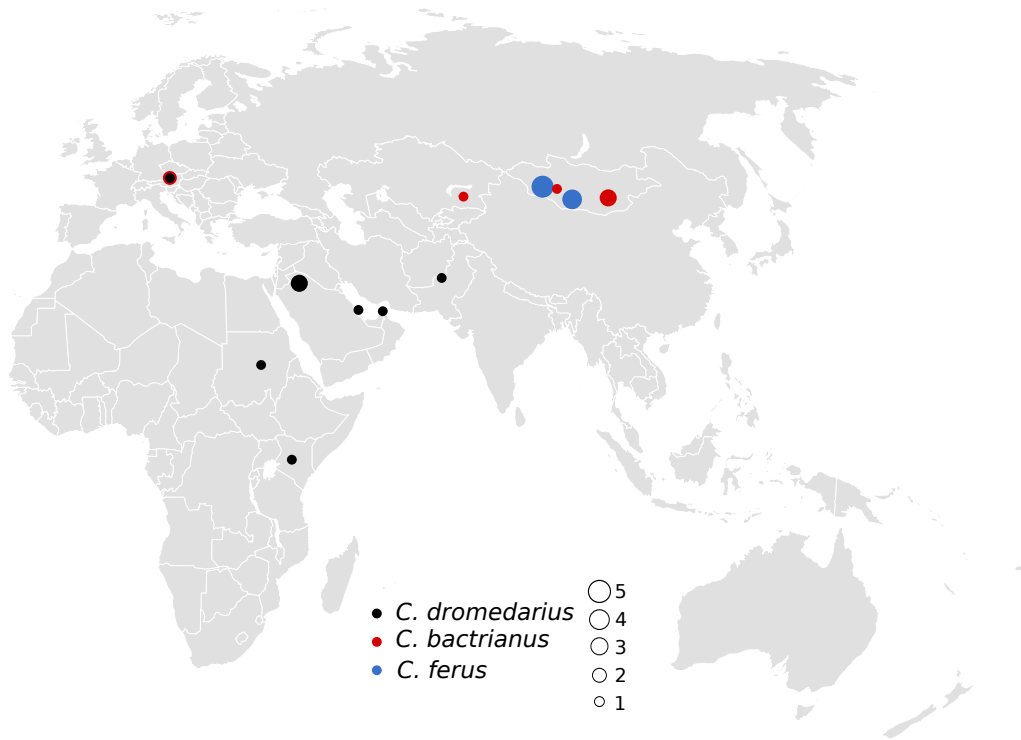
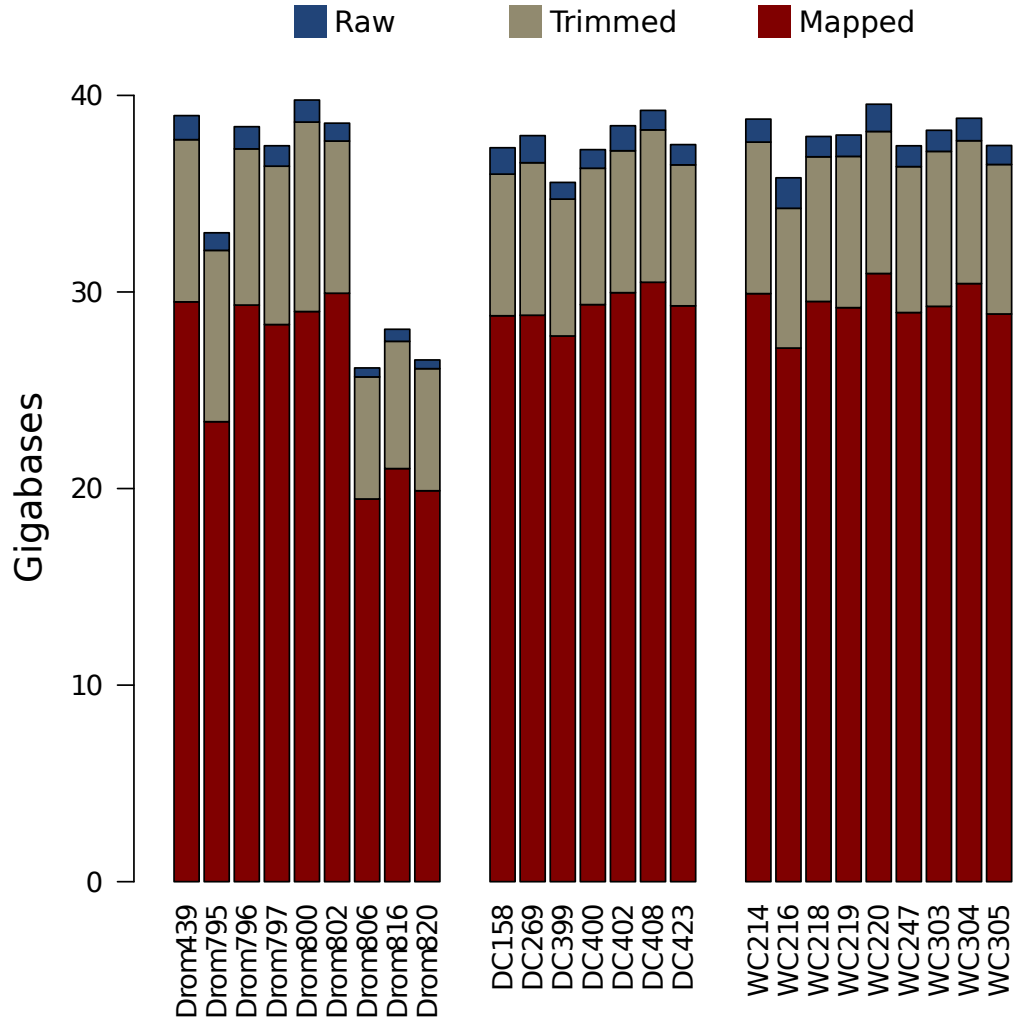


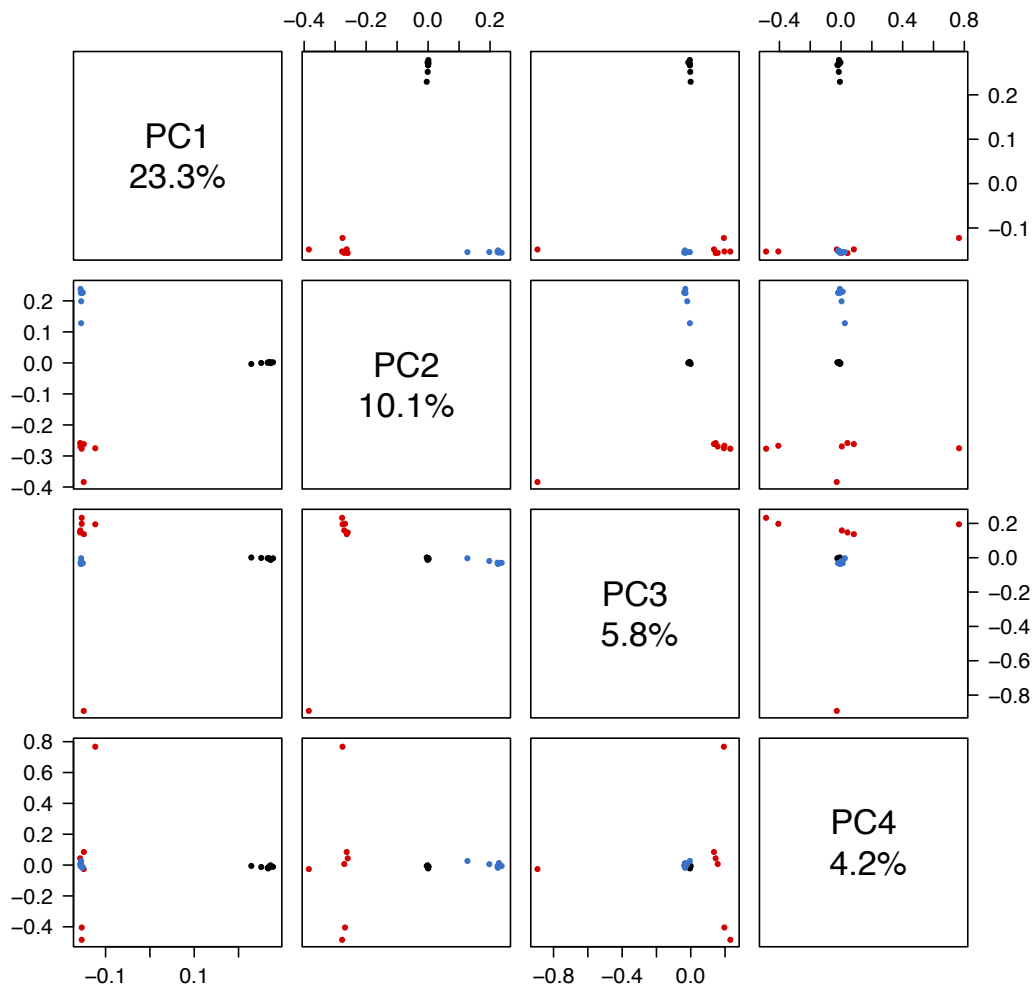
## Supplementary Figures



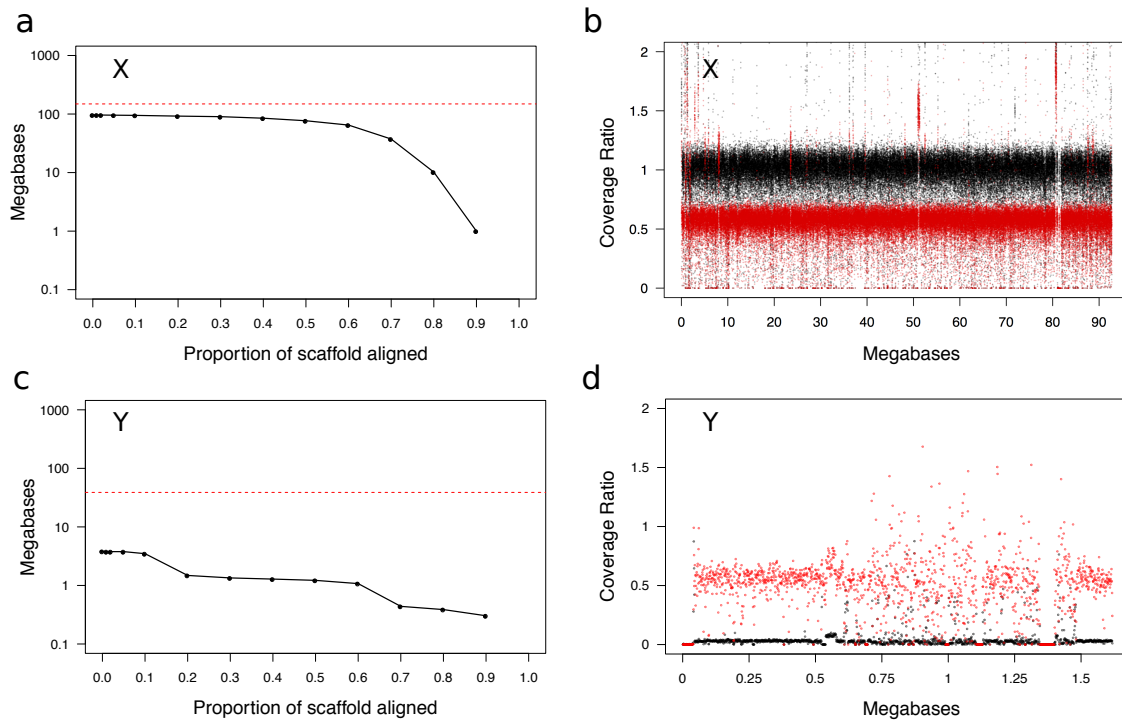
**Supplementary Figure 1. Map illustrating the samples used in this study for genome sequencing.** The size of each circle is proportional to the sample size for that location. Colors correspond to the three Old World camel species.



**Supplementary Figure 2. The number of raw, trimmed, and mapped bases for each individual.** See Supplementary Table 1 for the list of sequenced camels.



**Supplementary Figure 3. Principal components analysis of genetic variation in Old World camels.** The first four principal components (PC) are shown as pairwise plots, with the diagonal stating the variation explained by the PC. Dromedaries (*Camelus dromedarius*) are shown as black, domestic Bactrian camels (*Camelus bactrianus*) as red, and wild camels (*Camelus ferus*) as blue circles.



**Supplementary Figure 4. Identification of X and Y putative scaffolds.** (a,b) Total number of megabases contained in scaffolds that aligned to the cow (*Bos taurus*) reference X (a) and Y (b) chromosome sequences. (c,d) The ratio of sequencing coverage in putative X (c) and Y (d) scaffolds relative to the genome-wide background in female (black) and male (red) individuals. Notice male coverage is  $\sim 0.5$  the genome-wide background for the putative X scaffolds, and approximately 0 and 0.5 the genome-wide background for the putative Y scaffolds in females and males, respectively.