

## Supplementary Figure 2. Separation of Continental Populations Using Genotyping SNPs.

We created a neighbor-joining tree for 66 samples for which we have at least 137 successfully genotyped SNPs, to examine genetic relatedness among parasite lines (Supplementary Methods). Even with this limited data, we found good support for Asian and American clades that were distinct from African parasites. The results show substantial population differentiation between continental groups [Asian vs. African  $F_{ST} = 0.23$  ( $p = 0.35$ ); Asian vs. American  $F_{ST} = 0.28$  ( $p = 0.20$ ); African vs. American  $F_{ST} = 0.12$  ( $p = 0.41$ )], although these  $F_{ST}$  values are not significant with our limited data<sup>1</sup>. These results are consistent with previous observations<sup>2,3</sup> that population-specific variation exists, which seems likely to have biological significance. With more data we hope to further distinguish within and between continental differences. Details on the SNPs used in this analysis are available at <http://www.broad.mit.edu/mpg/pubs/>

1. Lewontin, R.C. & Krakauer, J. Distribution of gene frequency as a test of the theory of the selective neutrality of polymorphisms. *Genetics* 74, 175-95 (1973).
2. Wootton, J.C. et al. Genetic diversity and chloroquine selective sweeps in *Plasmodium falciparum*. *Nature* 418, 320-3 (2002).
3. Mu, J. et al. Recombination hotspots and population structure in *Plasmodium falciparum*. *PLoS Biol* 3, e335 (2005).

