

Figure S1 - Patterns and levels of nucleotide variation in ANCs, comparison to alternatively defined fast evolving CNCs.

(A) The comparative DAF spectra for phase II HapMap SNPs in non-accelerated CNCs ($n = 48,811$), ANCs ($n = 682$), ANCs outside of SDs, CNVs, retroposed genes or pseudogenes ($n = 610$), in the two controls ($n = 28,408$ and $n = 28,722$) in the *power CNCs* ($n = 10,882$), in the HARs from Pollard et al. ($n = 84$), and in the accelerated CNSs of Prabhakar et al. ($n = 328$) in the 60 individuals of the Yoruban (YRI) population.

(B) The comparative distributions of F_{ST} values for all phase II HapMap SNPs in ANCs ($n = 688$), ANCs outside of SDs, CNVs, retroposed genes or pseudogenes ($n = 620$), *power CNCs* ($n = 11,267$), non-accelerated CNCs ($n = 52,210$), HARs ($n = 82$) and accelerated CNSs ($n = 340$).

