

P002 The first genome-wide linkage disequilibrium map
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We used a subset of the phase 1 HapMap data, consisting of parental genotypes for approximately 750,000 SNPs from 60 CEPH (CEU), 60 Yoruban (YRI), 45 Chinese (CHB) and 44 Japanese (JPT) individuals, to create the first genome wide LDU maps which cover 99.7% (2,934 Mb) of the euchromatin. Comparison between these LDU maps and the linkage map shows that recombination accounts for 99% of the LDU variance in chromosome arms and 98% in their deciles. Furthermore, the close correspondence between several sites of meiotic recombination determined by sperm typing and specific LDU steps demonstrate their ability to identify novel hotspots and enhance the resolution of linkage maps. Since coalescent methods such as LDhat provide similar information, we use regression and variance to determine whether recombination rates from LDhat or LDU are closest to the linkage map. Rates of recombination from LDU maps share a closer correspondence with the linkage map across the entire genome and on sixteen of the twenty three chromosomes. These genome wide LDU maps are available from our LD database (http://cedar.genetics.soton.ac.uk/public_html/) as integrated maps that can be viewed as tables or graphs to determine the pattern of LD in any genomic region.