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Cover In red, a region of looped chromatin is unraveled in order to reveal its intricate linkage disequilibrium (LD) structure (green and blue structures are duplicates). Haplotypes show sharp boundaries but remain connected through long tendrils of strong LD. The figure is generated with HapMap data (release #27, CEU) and taken from a section of the 17q24.3 locus containing prostate cancer risk variants rs8072254 and rs1859961. Bézier curves connecting single nucleotide polymorphisms (SNPs) encode r^2 values within the range of 0.5 to 1.0 in a color gradient between white and red. (Cover illustration by Richard Cowper-Sal·lari. [For details, see Zhang et al., pp. 1437–1446.])