FIGURE 26.5. Any short region of genome will share the same ancestral genealogy (bottom). Six sampled sequences are shown on the top. These carry any mutations that occurred on the lineages leading down to them (colored dots). Every mutation is assumed to occur at a unique place in the genome (i.e., the infinite-sites model). The sequences fall into two distinct haplotypes corresponding to the two main branches of the genealogy. The haplotype could be determined by scoring any one of the red or light blue mutations, which could therefore act as tagging single-nucleotide polymorphisms (tSNPs).