FIGURE 13.12. Unique mutations in a nonrecombining DNA sequence can be used to reconstruct their genealogy. This example shows four sequences (nos. 2–5) sampled from a population, together with a more distantly related sequence (1) termed an outgroup. Each unique mutation defines a group of related sequences, or clade; for example, sequences 3, 4, and 5 all share an A→T substitution (green), which shows that they form a single clade, and sequences 4 and 5 share a G→C substitution (dark blue), which shows that they also form a clade. In this example, enough mutations have occurred that the genealogy can be reconstructed unambiguously. Mutations that occurred between the outgroup and sequences 2–5 are represented by brown dots. However, these are of no use in reconstructing the genealogy that relates 2–5. Only variable positions in the sequence are shown: in the full sequence, the great majority of sites would not vary. See Chapter 27 (online) for a full discussion.