1. (a) $\chi^2 = 20.5$ on 7 degress of freedom, so $P \approx 0.0046$. A permutation test with 1000 permutations gave $P \approx 0.003$, with estimated SE 0.002. Increasing the number of permutations to 10,000 gave $P \approx 0.002$ with SE 0.0004.

   (b) Alleles 1–8 gave $\chi^2 = 2.85$, 0.07, 0.44, 2.99, 5.26, 4.00, 1.04 and 6.38, respectively. The maximum was 6.38, with a nominal P-value of 0.012. Applying a Bonferroni correction, one obtains $8P \approx 0.092$ or $1 - (1 - P)^8 \approx 0.089$. A permutation test with 1000 permutations gave $P \approx 0.067$ (SE 0.008); 10,000 permutations gave $P \approx 0.065$ (SE 0.003).

   (c) We like permutation tests, and (a) and (b) may give quite different answers. Note, however, that this is just one data set (and I made it up)!

2. Let p denote the frequency of allele 1. Then you can calculate that $\Pr(\text{kid is } 11 | \text{mom is } 12) = p/2$, assuming Hardy-Weinberg and random mating. Similarly, one gets probability $1/2$ for the kid being 12 and $(1 - p)/2$ for the kid being 22, given the mother's genotype. If we tossed out the cases where the kid was 12, and inferred that the 1 was transmitted when the kid was 11 and the 2 was transmitted when the kid was 22, we'd find apparent evidence for LD whenever $p \neq 1/2$.

   [Check out the following: D Curtis and P Sham (1995) A note on the application of the transmission disequilibrium test when a parent is missing. Am J Hum Genet 56:811-812.]