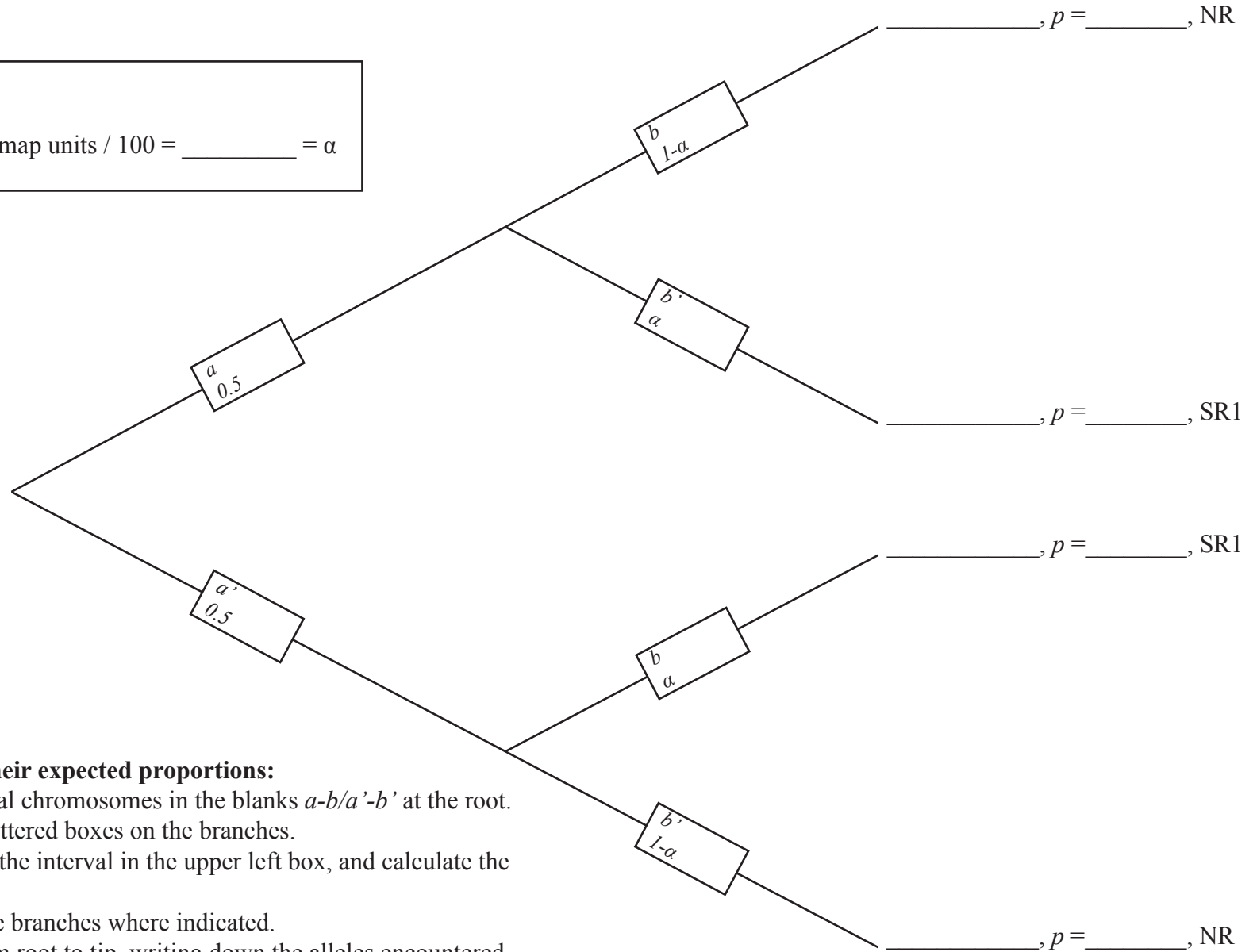


# 2-Marker Recombination Cross

**Known Map Distance:**

Interval 1 (a \_\_\_ to b \_\_\_): \_\_\_\_\_ map units / 100 = \_\_\_\_\_ =  $\alpha$

$\frac{a \quad b}{a' \quad b'}$



**To determine gamete classes and their expected proportions:**

- 1) Write the alleles on the two parental chromosomes in the blanks  $a-b/a'-b'$  at the root.
- 2) Copy those alleles into the same lettered boxes on the branches.
- 3) Write the known map distance for the interval in the upper left box, and calculate the map proportion  $\alpha$ .
- 4) Write the value of  $\alpha$  or  $(1-\alpha)$  on the branches where indicated.
- 5) For each tip on the right, trace from root to tip, writing down the alleles encountered along the way. This gives the genotype of that gamete class.
- 6) For each tip on the right, trace from root to tip, multiplying all numbers along the way. This gives the expected proportion  $p$  for that gamete class.
- 7) Each change of direction from root to tip is a recombination event. The gamete classes are labeled NR (non-recombinant) or SR (single-recombinant).
- 8) If doing a  $\chi^2$  test, multiply each  $p$  by the total number of progeny observed to get the expected numbers of progeny for each gamete class.