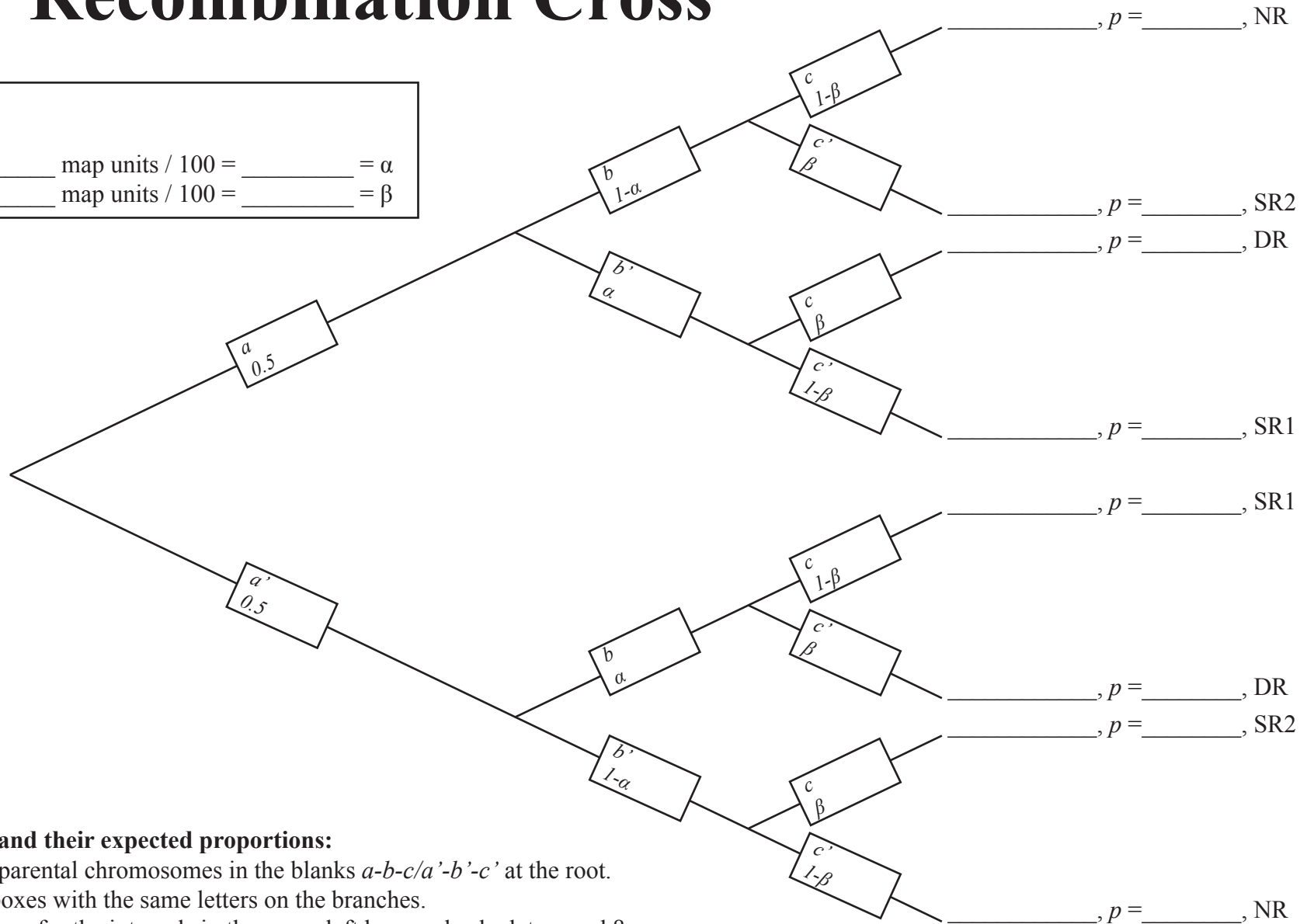
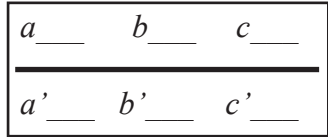


# 3-Marker Recombination Cross

## Known Map Distances:

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

Interval 2 (b \_\_\_ to c \_\_\_): \_\_\_\_\_ map units / 100 = \_\_\_\_\_ =  $\beta$



## To determine gamete classes and their expected proportions:

- 1) Write the alleles on the two parental chromosomes in the blanks  $a-b-c/a'-b'-c'$  at the root.
- 2) Copy those alleles into the boxes with the same letters on the branches.
- 3) Write the known map distances for the intervals in the upper left box, and calculate  $\alpha$  and  $\beta$ .
- 4) Write the values of  $\alpha$ ,  $(1-\alpha)$ ,  $\beta$ , and  $(1-\beta)$  in the boxes 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 is a recombination event. Classes are labeled NR (non-recombinant) SR (single-recombinant, interval 1 or 2) or DR (double-recombinant).
- 8) If doing a  $\chi^2$  test, multiply each  $p$  by the total number of progeny observed to get expected values.