

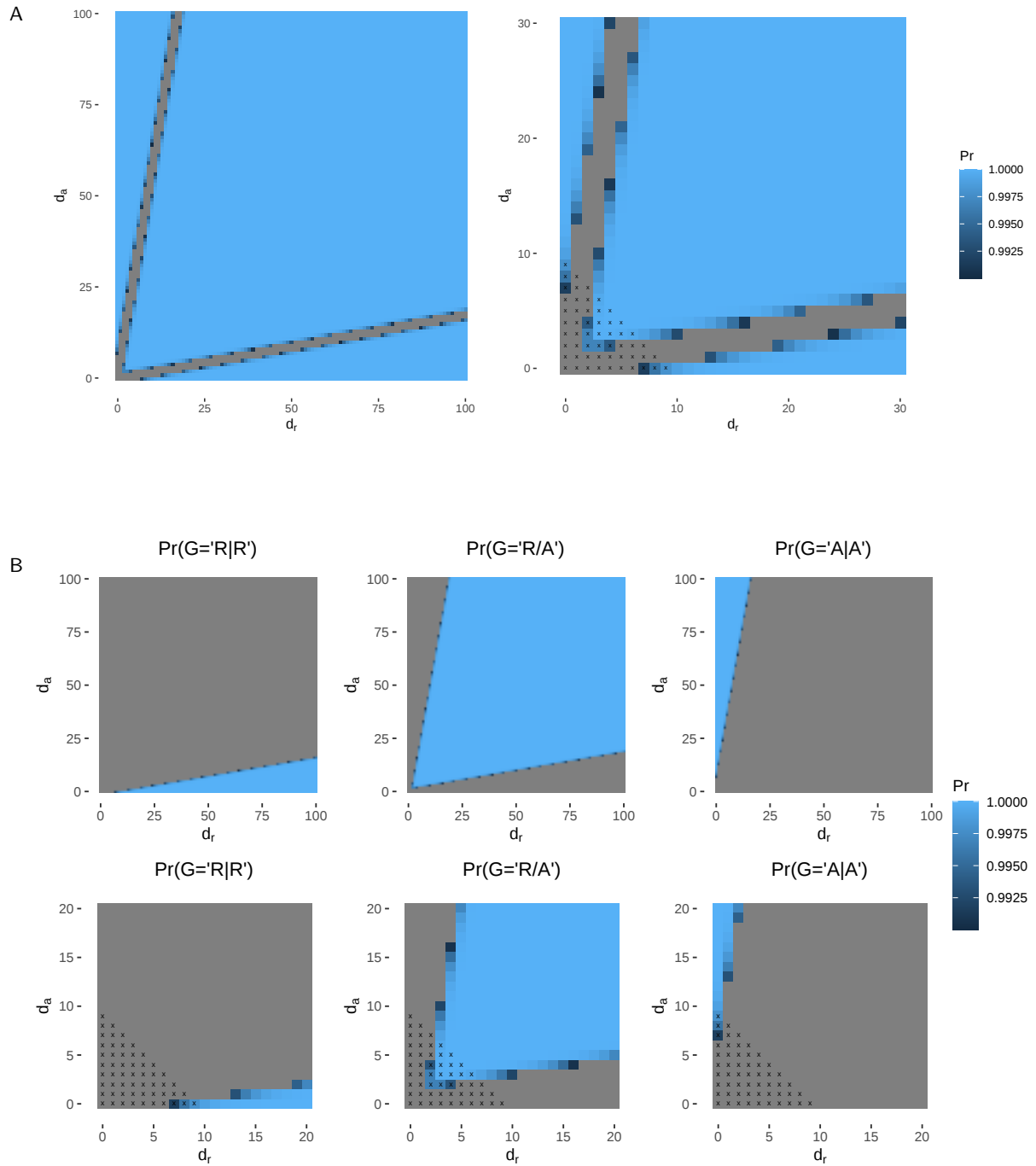


Fig S5. Power of TSM genotyping function. **(A)** The TSM genotype is inferred from mapping coverage of the alternative alleles using a strategy similar to base calling. The heatmaps show the posterior probability of the best genotype for different combinations of REF (d_r) and ALT (d_a) mapping depths; the combinations indicated with gray have posterior probability < 0.99 and are considered unknown. The plot on the right shows the values for low depths: the values indicated with crosses are rejected because of low total coverage (< 10). **(B)** The heatmaps show the posterior probability of the three different genotypes.