Genotype distributions | n =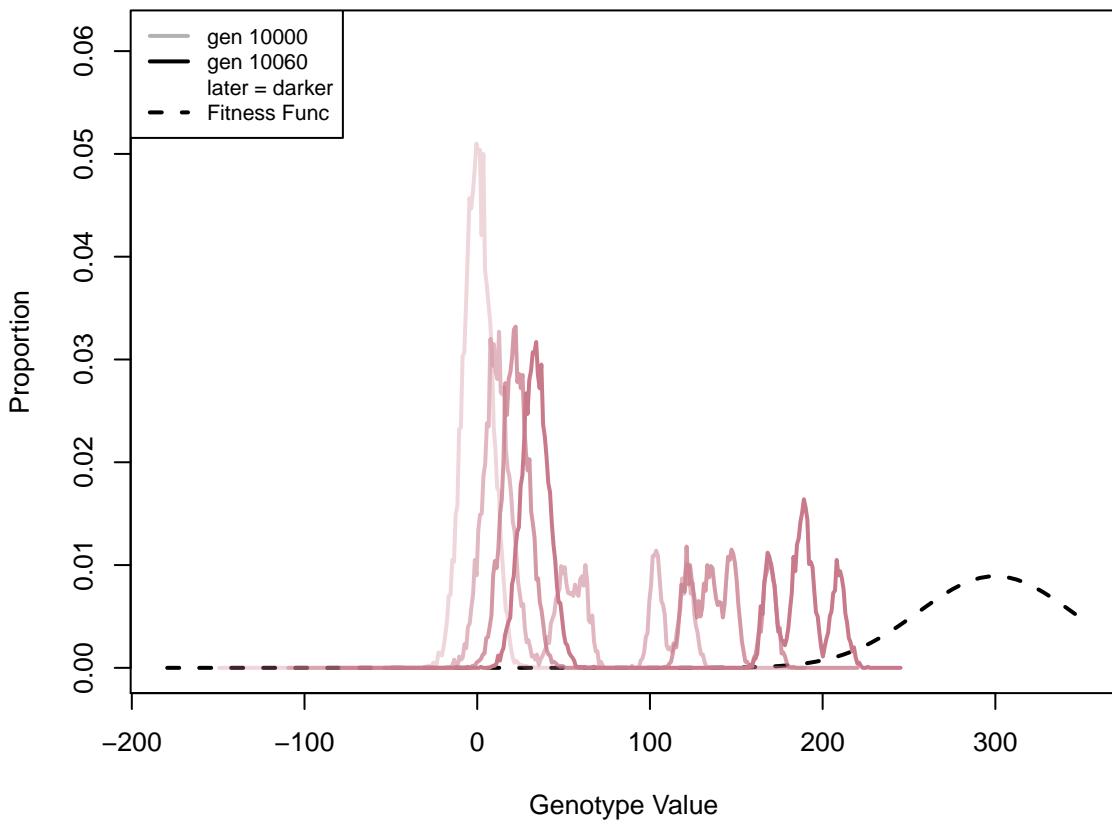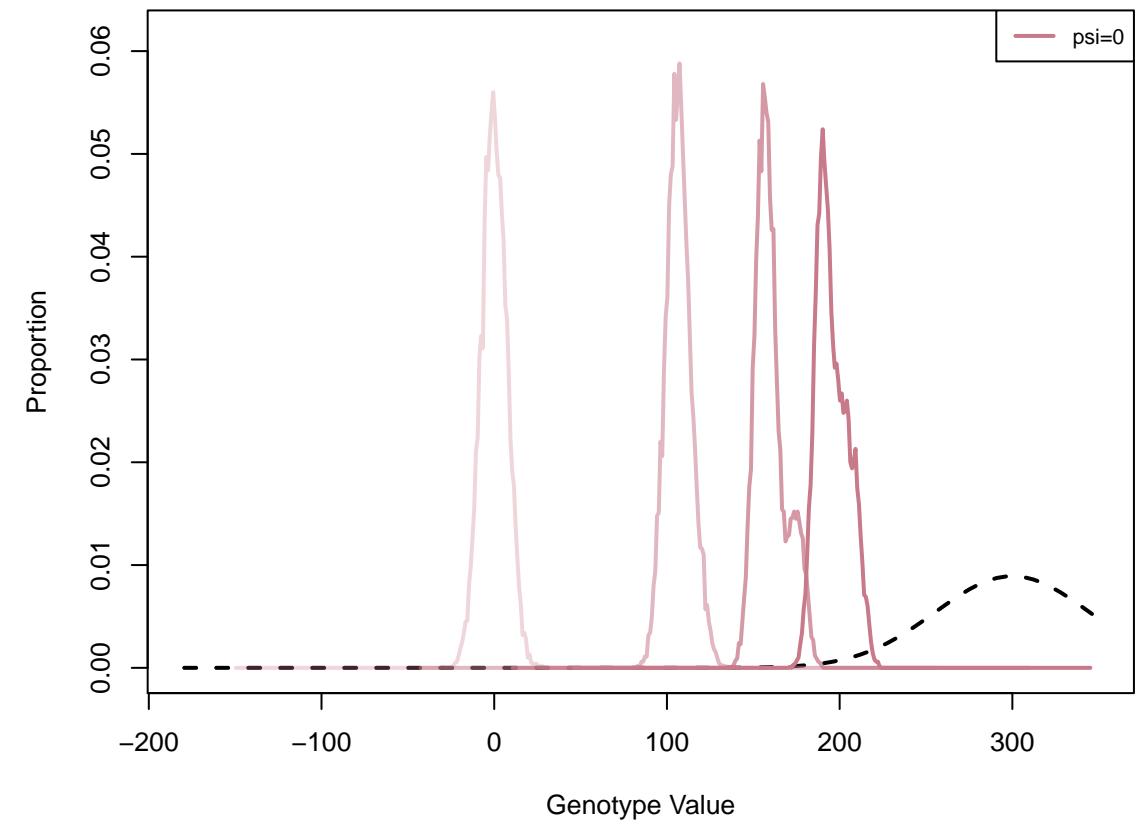 20 | shift_size = 300 by 20 | models: ave, ext, fit, inv