



Figure S39: The effect of migration on distributions of F_{ST} and their random overlap. Data are plotted for F_{ST} calculated over the 20 iterations of 100 genomic windows under neutrality. Shown are the overlap between two treatments with (A) and without (B) migration. In each figure, 95% quantiles are plotted for each distribution as dashed lines. Distributions for x and y data are plotted in axis margins.