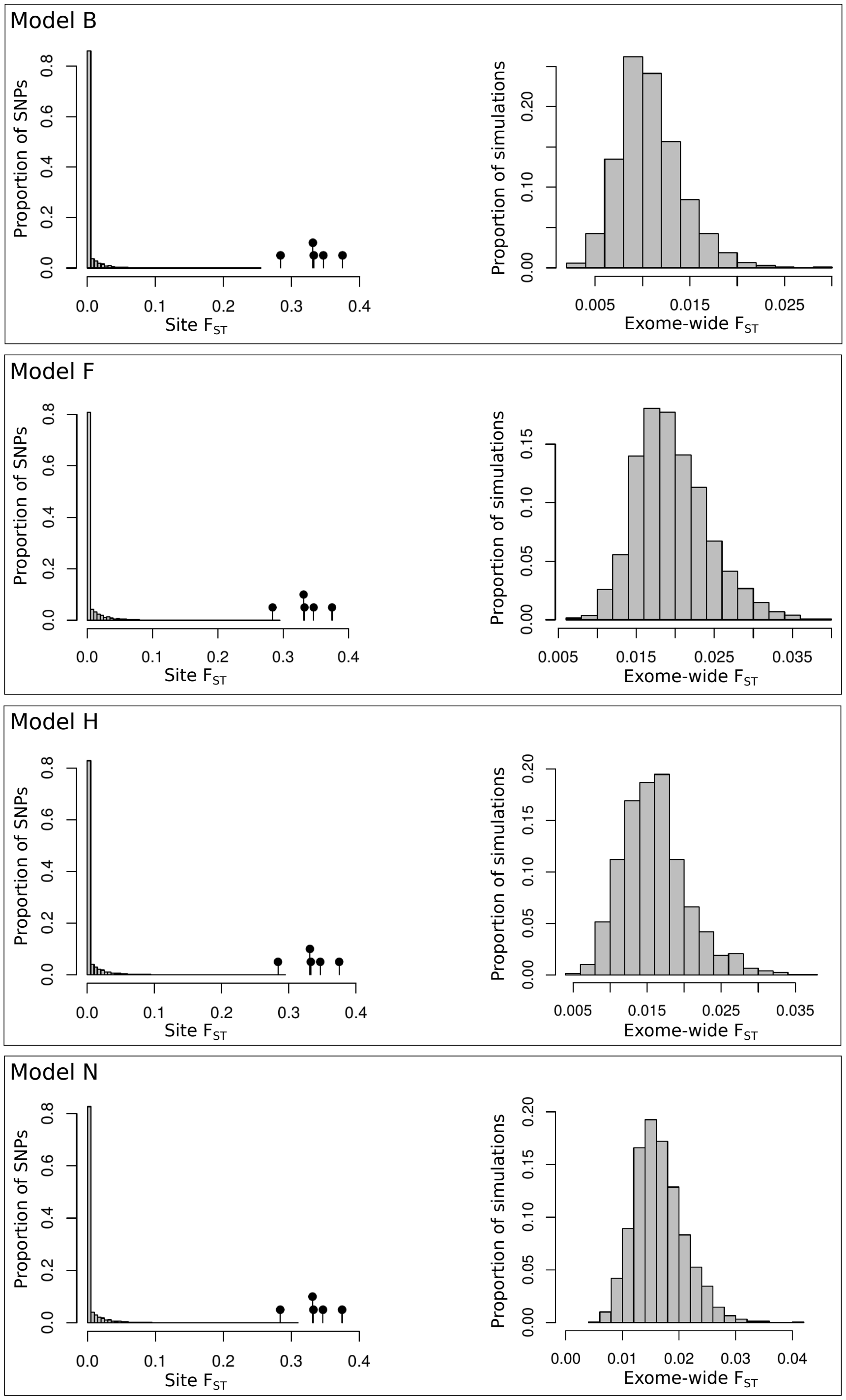

S9 Fig. Expected F_{ST} distribution for YNP *T. alpinus* under histories inferred with ABC. The expected distribution of neutral F_{ST} per site and exome-wide under the best fitting demographic histories for YNP *T. alpinus* inferred with ABC. Each F_{ST} distribution was generated from 1,500 simulations under the maximum likelihood histories for the best fitting demographic models for YNP *T. alpinus*, B, F, H, and N. The positions of the five observed F_{ST} outlier SNPs (see Fig 4) are plotted onto the expected per site F_{ST} distributions.