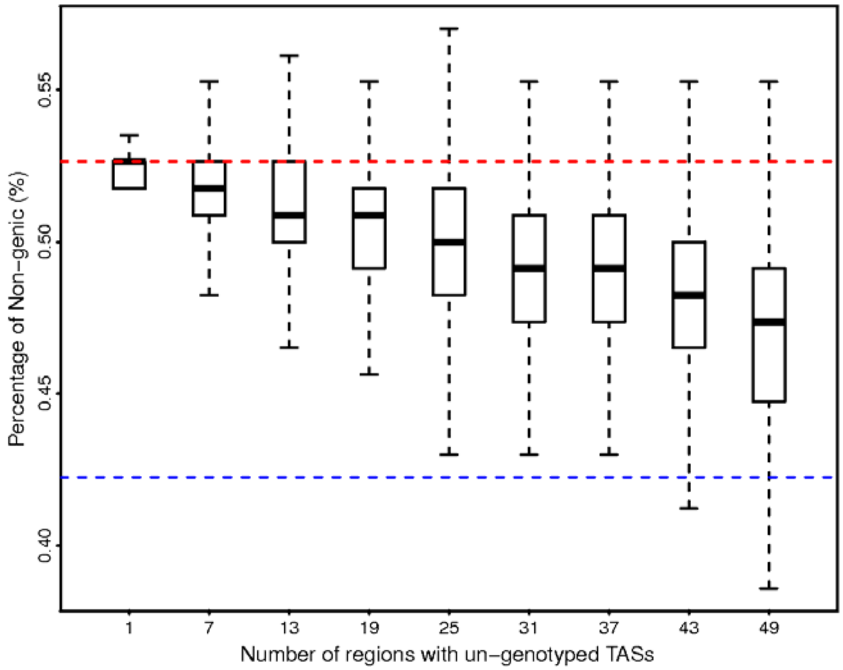
Supplementary Figure 5. The consistency of the genic and non-genic TAS distributions supported by simulations. In each simulation, a set of discovered TASs were randomly dropped out of the merged SNP data and the next highly associated SNPs within each target region were tabulated as the TASs. Even with missing over one-third of the TASs, the estimates of the percentage of non-genic TASs are still consistent with the findings from the whole dataset (red line). 1000 simulations were conducted for each case. Percentage of the non-genic SNP in the whole dataset is shown with the blue line



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