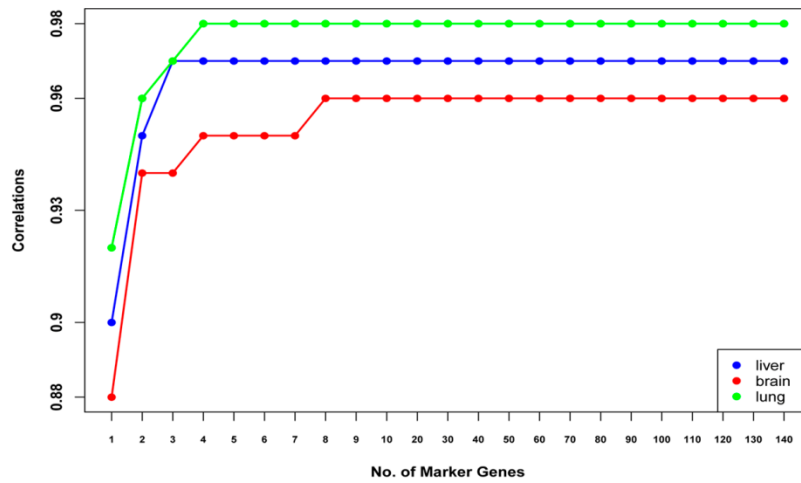
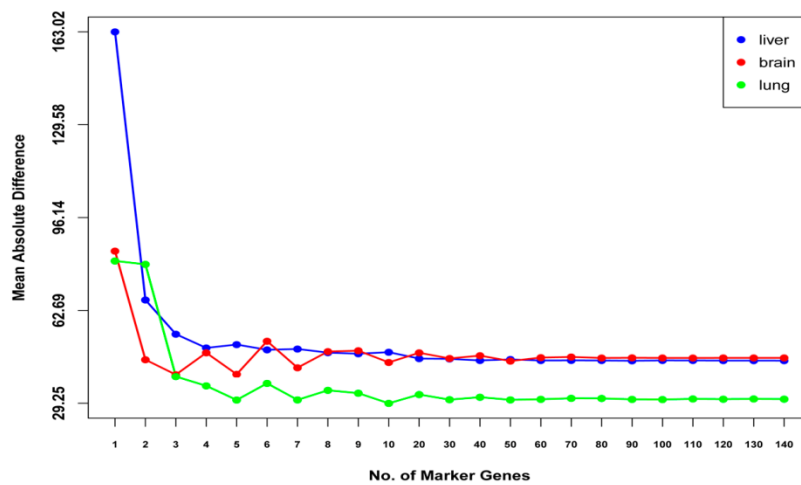


(A)



(B)



Marker genes were randomly selected from the TIGER list at different sizes, for 100 times on each size. In each repetition, the estimated weight matrix using the sampled marker genes was then used to estimate the cell-type specific signals. Correlation and mean absolute difference (MAD) between the original and estimated signals were measured. (A) shows the average correlation and (B) shows the average MAD from the 100 iterations using different number of marker genes.