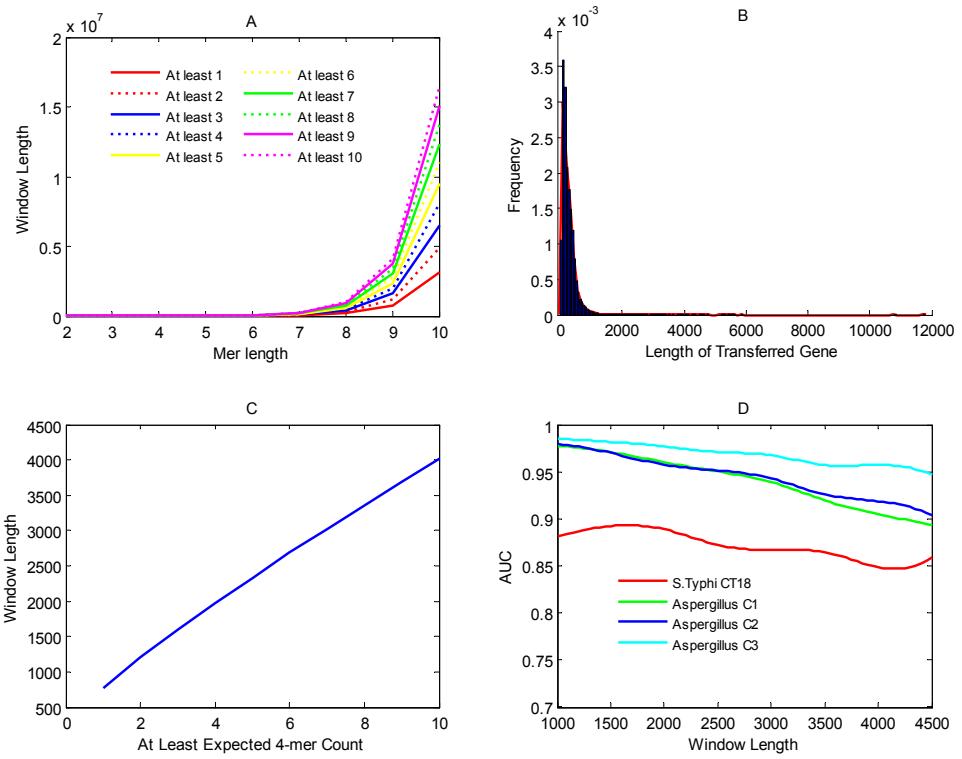


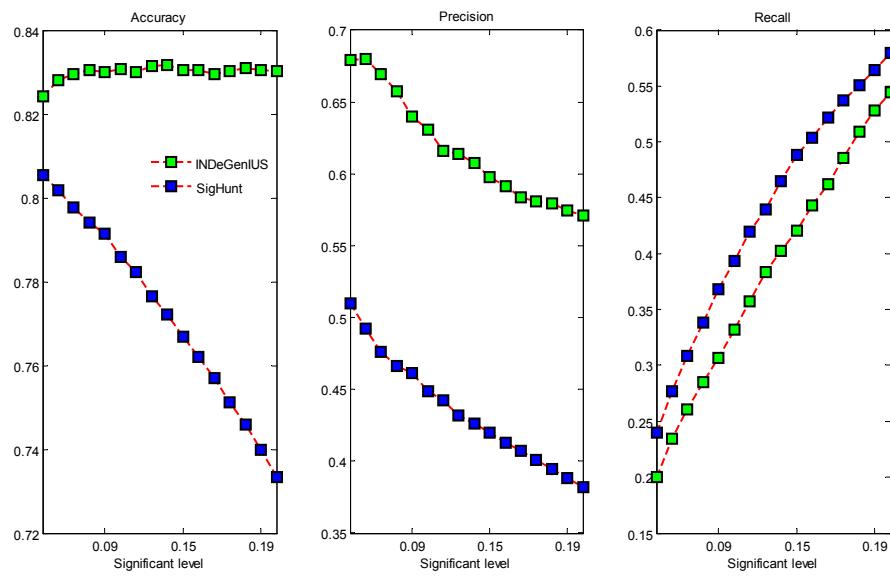
List of Figures

Supp Fig. 1. Relationships between the window size and mer size as well as their expected counts. A) Window sizes for the mers with lengths from 2 to 10, and their expect counts are at least from 1 to 10; B) Length distribution of 118131 horizontally transferred genes with lengths from 15 bp to 11792 bp downloaded from Horizontal Gene Transfer Database; C) Window size for the 4-mer with the expected counts from 1 to 10; D) AUC scores for three chromosomes of *Aspergillus fumigatus* and *S. enterica* serovar CT18 genome, in which genome sequence is scored using the IST-LFS without iteration, and the non-overlapping window sizes are from 1 kb to 4.5 kb.

Supp Fig. 2. Precision, recall and overall accuracy of SigHunt and INDeGenIUS, in which 0.05-0.2 significance levels are used as cut-off values to evaluate their performances. All evaluation indexes are calculated at the nucleotide level.



Supp Fig. 1. Relationships between the window size and mer size as well as their expected counts. A) Window sizes for the mers with lengths from 2 to 10, and their expect counts are at least from 1 to 10; B) Length distribution of 118131 horizontally transferred genes with lengths from 15 bp to 11792 bp downloaded from Horizontal Gene Transfer Database; C) Window size for the 4-mer with the expected counts from 1 to 10; D) AUC scores for three chromosomes of *Aspergillus fumigatus* and *S. enterica* serovar CT18 genome, in which genome sequence is scored using the IST-LFS without iteration, and the non-overlapping window sizes are from 1 kb to 4.5 kb.



Supp Fig. 2. Precision, recall and overall accuracy of SigHunt and INDeGenIUS, in which 0.05-0.2 significance levels are used as cut-off values to evaluate their performances. All evaluation indexes are calculated at the nucleotide level.