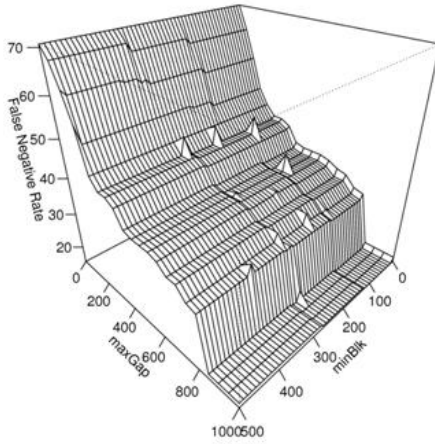


**Figure S1:** Box and whisker plots of the distribution of sequence similarity scores among genes within neighborhoods, stratified by the total neighborhood score computed from the Microarray Atlas data. Boxes show upper and lower quartiles and the dark line within the box is the median. The whiskers show the range of the data, while small circles denote outliers.

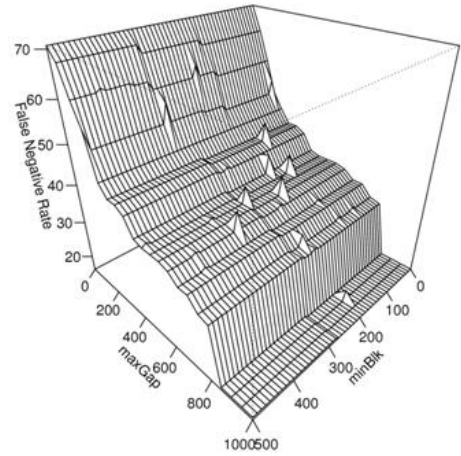
MOUSE  
Vs  
OPOSSUM

FN,  
Type II  
error

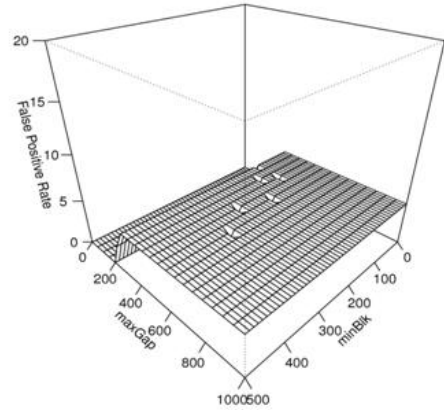
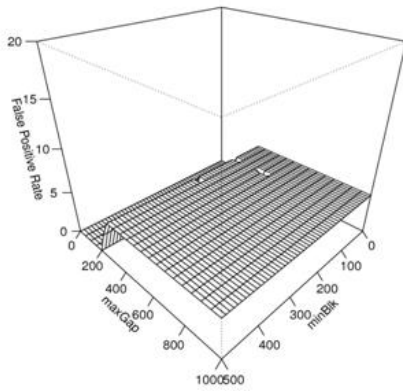
Minimum Number of Markers = 1



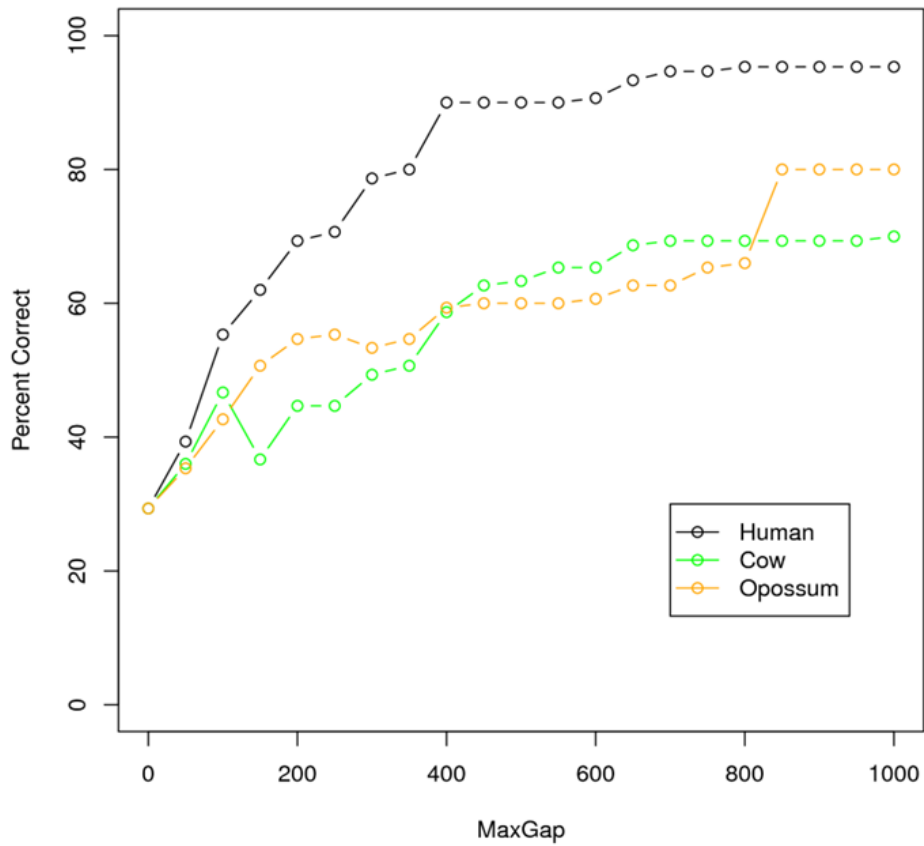
Minimum Number of Markers = 2



FP,  
Type I  
error



**Figure S2.** Effects of syntenic block parameter settings on error rates of gene neighborhood synteny detection between the Mouse and Opossum genomes



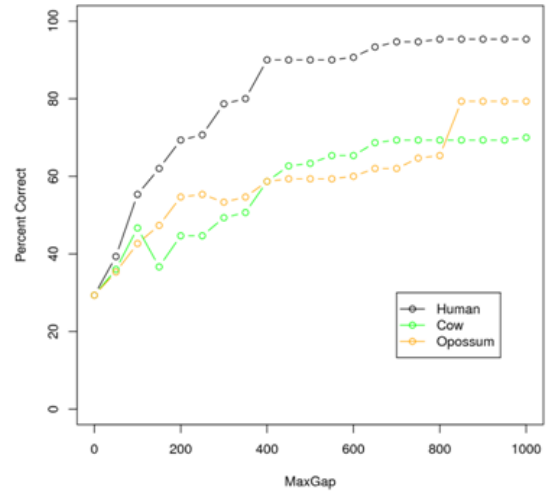
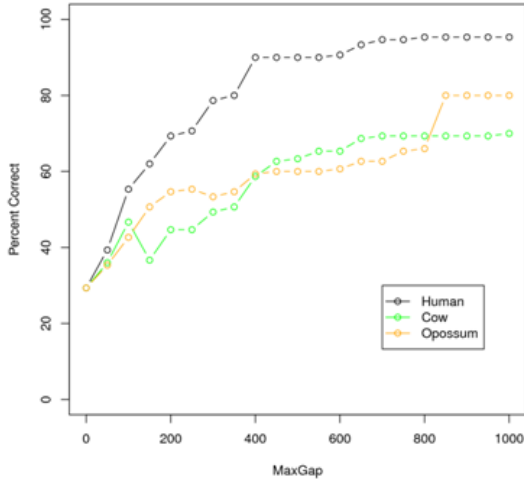
**Figure S3.** Effect of MaxGap parameter (in kb) on accuracy of gene neighborhood synteny

Total  
Percent  
Correct

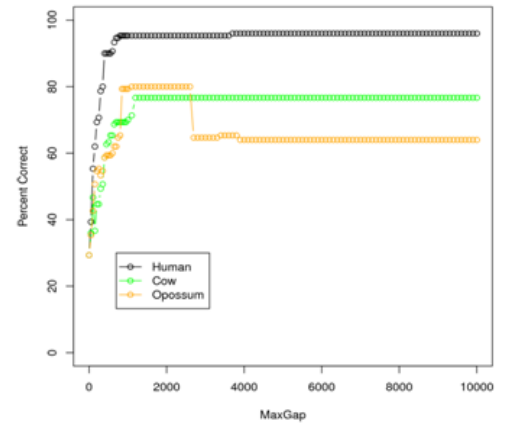
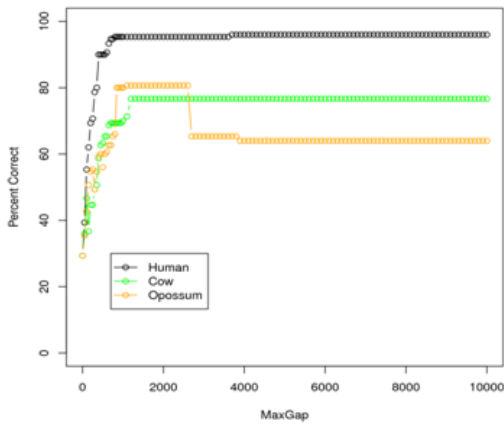
Minimum Number of Markers = 1

Minimum Number of Markers = 2

MaxGap  
Up to  
1 MB



> 1MB  
MaxGap



**Figure S4.** Effect of MaxGap parameter settings (in kb) on accuracy of gene neighborhood synteny