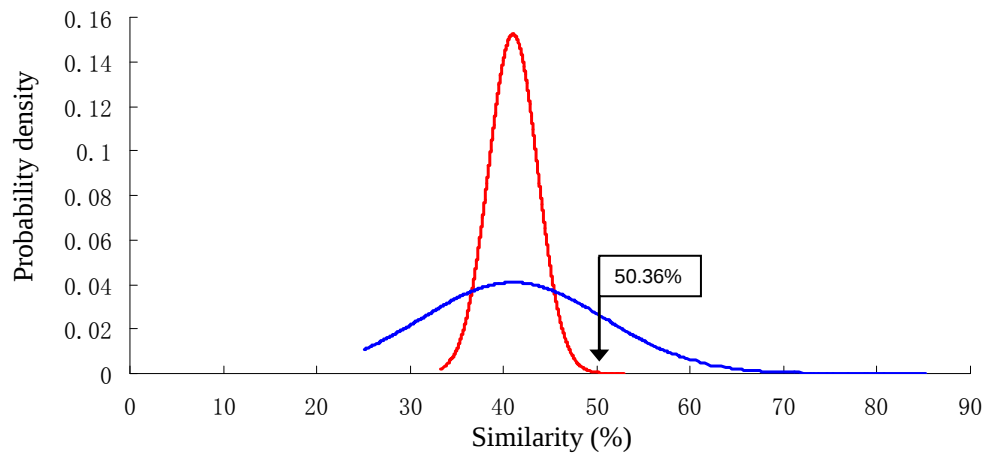




Additional file 7

Average similarity between detected HTGs and predicted donor sequences are significant larger. Red curve indicates the normal distribution (mean, 41.03%; s.d., 2.62%) of sequence similarity based on random sampling results. Blue curve indicates the normal distribute (mean, 41.02%; s.d., 9.76%) of sequence similarity between 1176 silkworm genes and their bacterial homologs. Arrow indicates the position of mean value (50.36%) of 14 types of HTGs.