Supplementary Figure S9. Number of “contaminated” genome scaffolds that contain regions with hits to bacterial or viral genomes, shown at different threshold of percentage sequence cover in the scaffolds for (A) *S. goreau* and (B) *S. kawagutii*. The implicated gene models in the corresponding scaffolds in *S. goreau* and *S. kawagutii* are shown in (C) and (D) respectively.