Supplementary Figure 5: Plot of the Pba1043 CDS with (copper) and without (black) a predicted orthologue in A) Pba1039 and B) Pcc193. The indicated analytical methods are HMM and HMM(lacto): hidden Markov models as described in the manuscript, trained on the Pba1043:Dda3937 and L. lactis comparisons, respectively; GACK_100, GACK_50, GACK_0: GACK with the EPP parameter set to 100%, 50% and 0%, respectively; MPP(BPP), MPP(EPP), MPP(MJ); MPP's BPP, EPP and MJ gene entry vector results, respectively. A consensus of Pba1043 CDS predicted to have no orthologue in each comparator organism is also indicated. All methods agree on the approximate location and size of the major genomic islands, but differ in the number and size of smaller islands. In particular, GACK appears to overpredict the number of Pba1043 CDS with no orthologue in Pcc193. For the Pba1043:Pba1039 comparison, the HMM derived from the Lactococcus comparison data appears to unite some neighbouring islands that are predicted by the HMM derived from the Pba1043:Dda3937 comparison; otherwise, their predictions are very similar.