Supplementary Figure 3: Plot of the predictions of the threshold (A) and HMM (B) methods as the threshold is varied from the lowest to highest threshold value in the aCGH experiment with *Dda*3937 against a *Pba*1043 gDNA reference, taking log-transformed hybridisation ratios. Both methods predict a mixture of CDS with and without orthologues at the lowest threshold value. As the threshold increases from a minimum to a maximum, the proportion of CDS predicted to have no orthologue increases to 100% for the threshold method. At large threshold values, the HMM uniformly predicts the dominant state of the training data, which in this case is that all *Pba*1043 CDS have an orthologue in *Dda*3937.