



Figure 2: Posterior membership probability plots from Admixture based on the 41,268 SNPs and considering two to four genetic clusters (K). Each individual ($n = 231$) is represented by a single vertical line colored proportionally to its posterior membership probability to one of the eight genetic clusters considered for this analysis. Samples are wrapped by sampling sites. After $K = 4$, only one sampling site is being differentiated from the others when increasing the K value. The 3 genetic gaps detected in the study are identified.