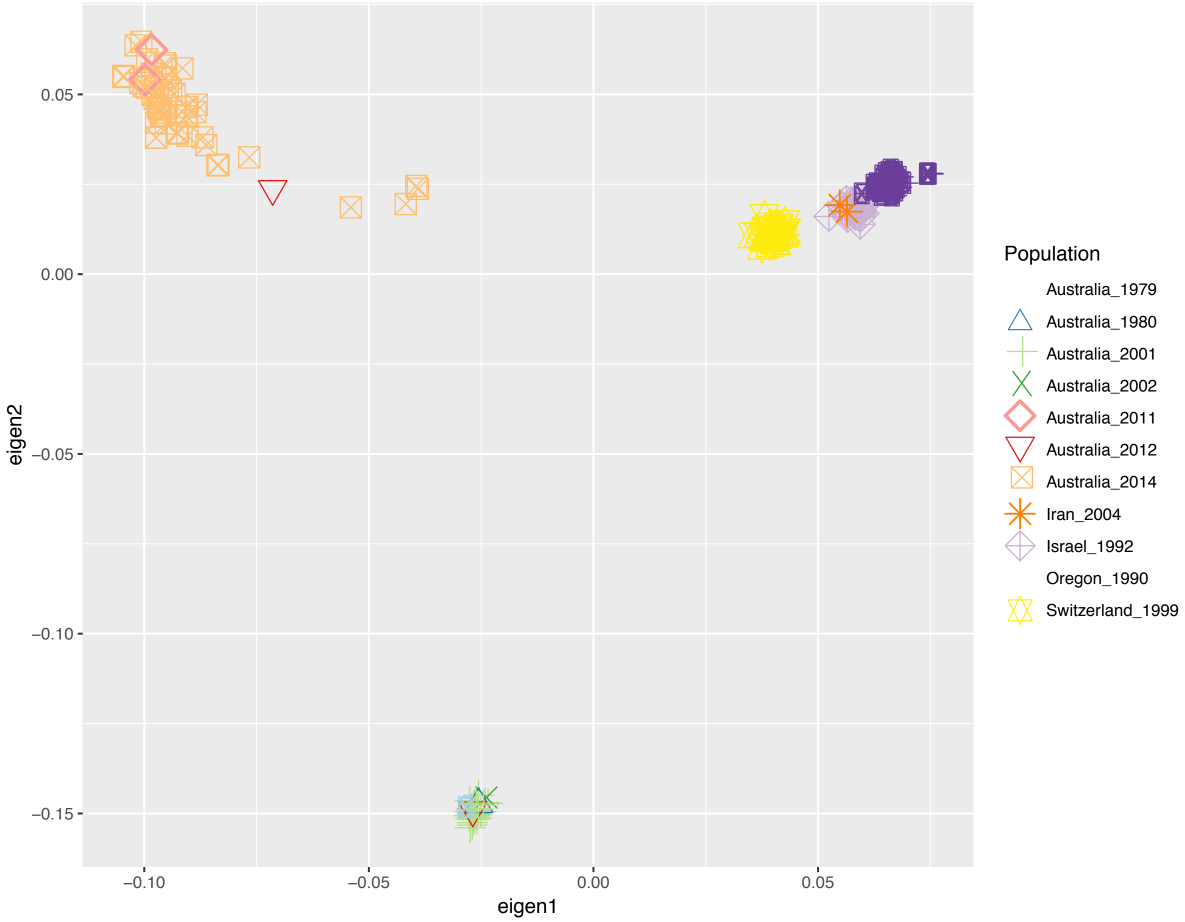
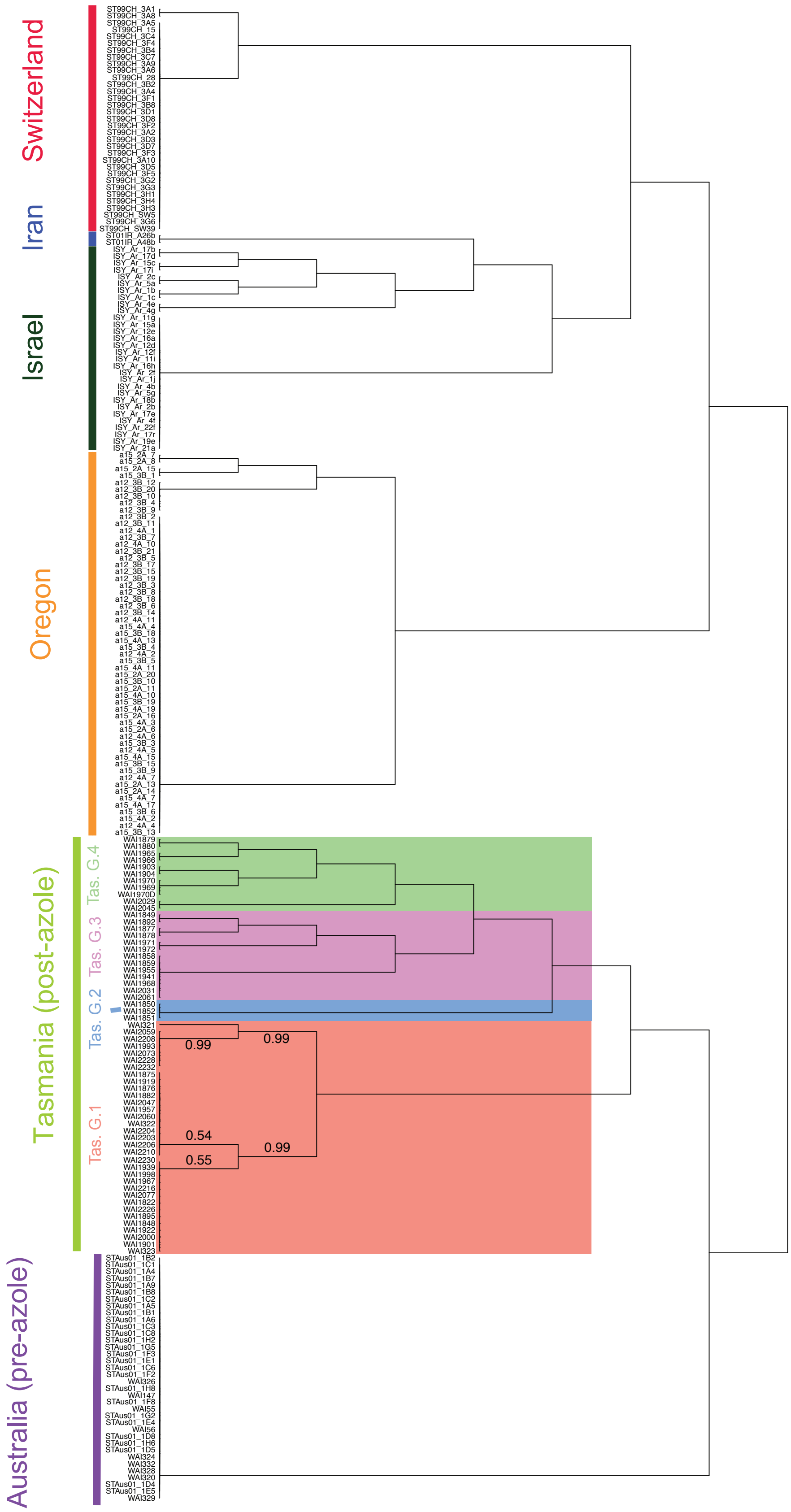
Supplemental Figure 1- Principal components analysis of genome wide SNP markers for 5 populations. Population of origin is shown in the legend to the right of the figure. The Australian samples from 1979, 1980 and 2002 group together at the bottom of the plot with the larger population sampled in Australia in 2001.



Supplementary Figure 2A: Population dendrogram shown at the top of Figure 1. Included here to show the isolates in the order they occur in Figure 1 and Supplemental Figure 2B. Isolate names are visible when zooming in on PDF document. For ease of viewing the major clusters are colored according to population of origin. Posterior support values are only drawn on branches where they were less than 1. The sub-groups found within the Tasmanian population are also colored (G1-G4).



Supplementary Figure 2B: The pairwise co-incidence matrix as estimated by fineStructure. The color represents the posterior coincidence probability and the black dots indicate the maximum *a posteriori* probability state for each pair-wise comparison between isolates. This heatmap shows good convergence for the FineStructure run (most posterior coincidence values close to 1).