STRUCTURE all data.txt
This is the input file for the program STRUCTURE
The first row contains the marker names
Each individual is represented by two rows; if the individual is homozygous at a marker then the two rows will be identical, if the individual is heterozygous at a marker then the two rows will differ for that marker, if the individual is haploid (male) then the second row of data for that individual will consist of missing data at each marker
1 represents A
2 represents T
3 represents C
4 represents G
-9 represents missing data (due to an individual being haploid, or due to no genotype recorded for that individual at that marker)
The first column contains the individual identifier
The second column is the 'population flag' (POPFLAG) that indicates to structure which samples should be used for the burnin phase; 1 for reference population, 0 for test population
Column 3 indicates which population the sample came from, Column 4 indicates where the sample was collect from, Column 5 represents the extraction ID of the sample, Column 6 represents the collection from which samples were taken and Column 7 indicates whether the samples was a worker (diploid) or drone (haploid)
To repeat our analysis: Select new project. Number of individuals is 829. Number of loci is 95. Missing data value is -9. In Step 3 of 4 select "row of marker names". In step 4 of 4 select "Individual ID for each individual", "Use pop info" and "Other extra columns". There are 5 extra columns.
Create a new parameter set by selecting "Parameter Set". Under "Run Length" make "Length of Burnin Period" 50,000 and "Number of MCMC Reps after Burnin" to 100,000. Under "Ancestry Model" select "Use Admixture Model". Under "Allele Frequency Model" select "Allele Frequencies Independent". Under "Advanced" select "Update allele frequencies using only individuals with POPFLAG=1 data, leave "Compute probability of the data (for estimating K)" selected.

genepop.txt
This is the input file for GENEPOP
11 represents A
22 represents T
33 represents C
44 represents G
00 represents missing data (due to an individual being haploid, or due to no genotype recorded for that individual at that marker)
Abbreviations: Brazil Africanized (BRAZILAF), USA Africanized (USAAF), Canadian Commercial (Canada), Capensis (Capensis), Capensis Clone (Clone), Australian Commercial (Commercial), Australian Feral (Feral), Scutellata-Capensis Hybrid (Hybrid), Eastern Europe (EasternE), Western Europe (WesternE), USA Varroa Resistant (Resistant), Africa (Scutellata), USA Commercial (USAEuro)

phylip.txt
This is the input file for PHYLIP
The table gives the mean pairwise F_{ST} among the 3 reference populations (African, Eastern Europe and Western Europe) and the 10 test populations calculated in Genepop
The first row indicates the number of populations
Abbreviations: Brazil Africanized (Br), USA Africanized (UA), Canadian Commercial (Ca), Capensis (Cap), Capensis Clone (Clo), Australian Commercial (AuC), Australian Feral (AuF), Scutellata-Capensis hybrid (H), Eastern Europe (C), Western Europe (M), Varroa Resistant (VR), Africa (A), USA Commercial (US)
Open Neighbor in Phylip.
Enter file name (phylip.txt)
Select UPGMA tree (N), Lower-triangular data matrix (L), Randomize input order of species (J), choose a random seed (odd number).
An outfile will be produced (tree.txt)

tree.txt
This is a tree file for use in Phylip (TreeDraw). Simply open the file in the program.
Abbreviations: Brazil Africanized (Br), USA Africanized (UA), Canadian Commercial (Ca), Capensis (Clo), Australian Commercial (AuC), Australian Feral (AuF), Scutellata-Capensis hybrid (H), Eastern Europe (C), Western Europe (M), Varroa Resistant (VR), African (A), USA Commercial (US)