

Grapevine clonal genetic testing



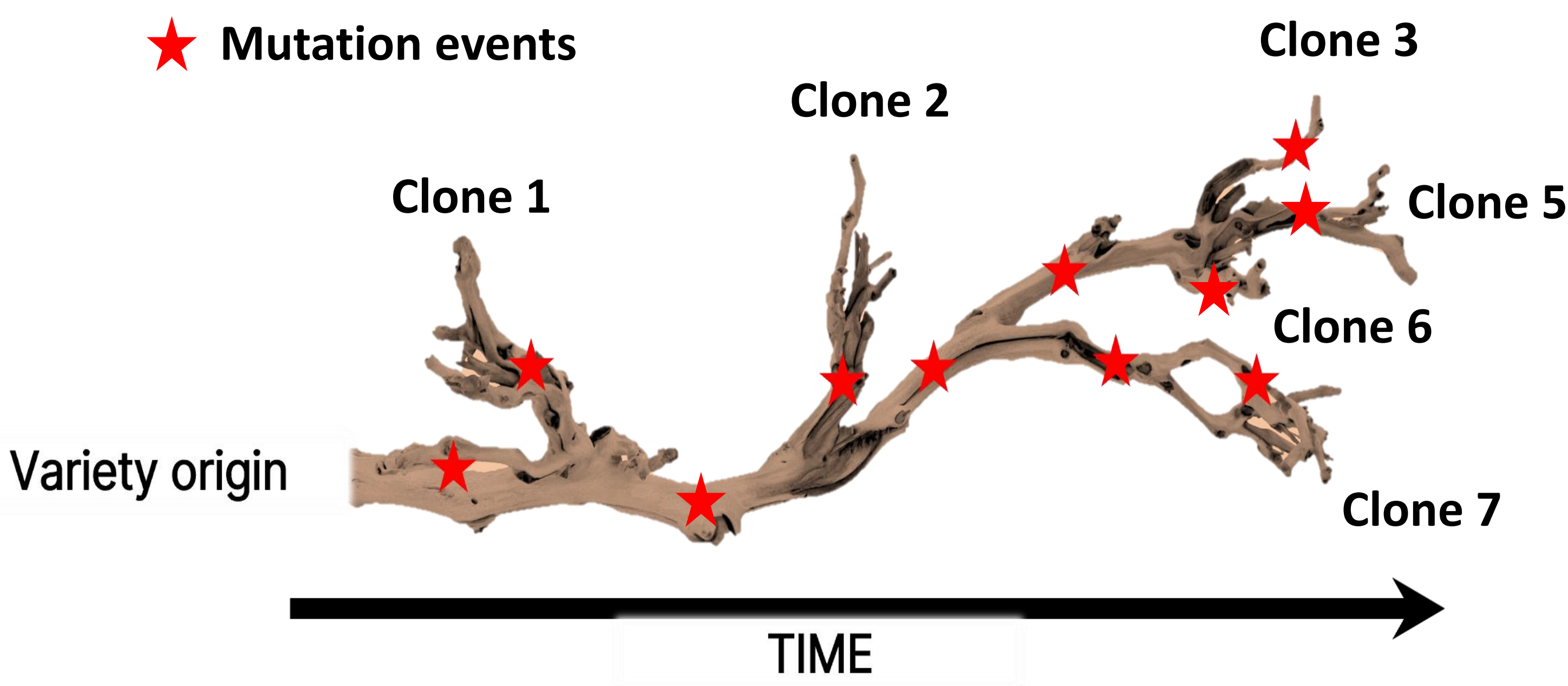
Chris Ward¹, Cristobal Onetto¹, Anthony Borneman¹

¹ The Australian Wine Research Institute, PO Box 46, Glenside (Adelaide) SA 5065, Australia

Corresponding author’s email: chris.ward@awri.com.au

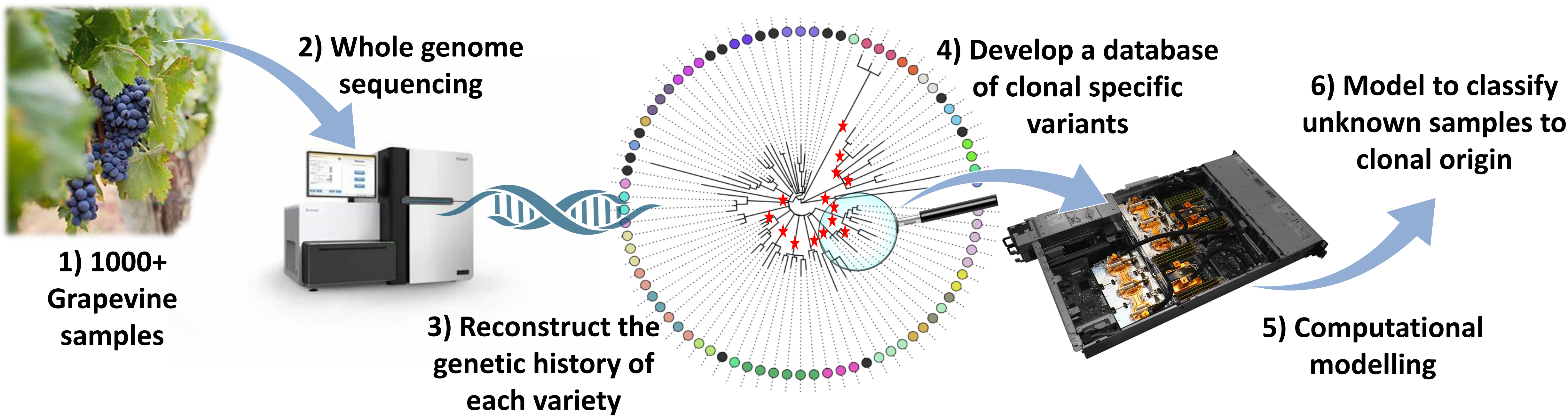
Background

- Grapevines are propagated clonally without sexual reproduction.
- Mutations occur within somatic (non-sexual) tissues and accumulate as the plant grows.
- When a sport is selected for propagation, the mutations that have accumulated are transferred to the next ‘generation’ giving rise to genetically distinct clones.
- Clones can have important, but subtle differences in traits (e.g. drought tolerance, aroma, bunch architecture) leading to growers favouring a subset of clones.
- As the desired traits often require substantial time to develop, nurseries and growers need to trace supply records to the point of origin to confidently determine if the material they are purchasing or selling is 100% the desired clone.
- These records are not always available or reliable, particularly for older accessions.

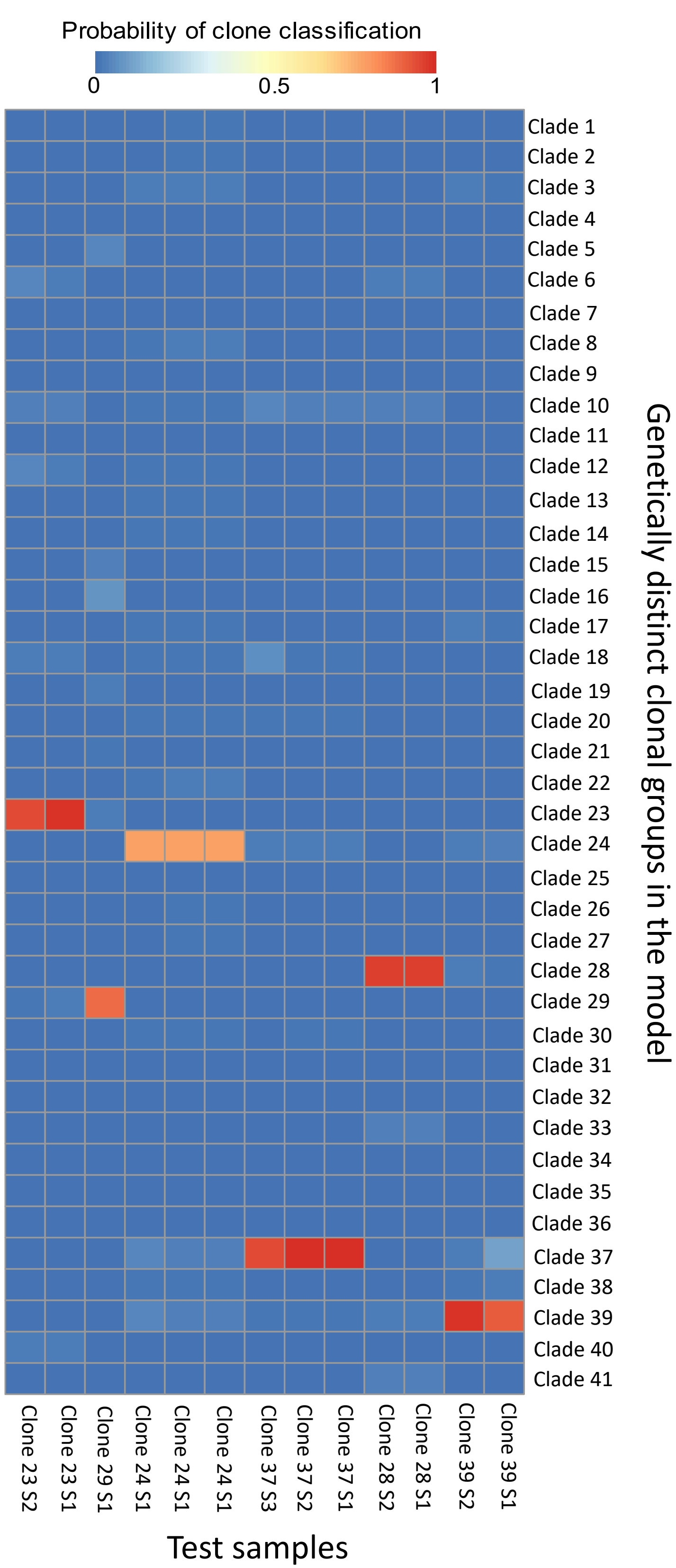


Methodology

Aim: To quantify the total genetic variation within seventeen grapevine varieties and develop a rapid methodology to determine clonal identity of unknown samples



Results



Classification of Pinot grapevines (left)

- The genetic variation between Pinot grapevines was used to build a computational model.
 - 189 Pinot vines from 41 genetically distinct clones.
 - 4961 genetic variants separate clones used to train the model.
 - Pinot grapevines with known clone origin, were then classified based on their patterns of variation present within the model.
 - Returns a classification probability against each clonal group for each sample.
- This revealed:
- 100% correctly classified ‘test’ samples to their clone of origin.
 - The model is highly discriminatory with no false positive classifications within the data tested.

Classification of Chardonnay grapevine genome sequence data sourced from NCBI (right)

- The total genetic variation (3037 variants) between Chardonnay clones was used to build a computational model.
 - 97 Chardonnay grapevines from 21 genetically distinct clones.
- Whole genome sequence data (n = 7) was then sourced from a public repository (NCBI) and tested against the model.
- 5/7 accessions from outside of Australia were classified to a putative clonal origin, the remaining accessions are clones not found in Australia.
- Robust classification (although at lower probability) was possible even with samples with very low (~10x) sequencing coverage.

