

Applied Biosystems™ Axiom™ Genotyping Services Summary Report

Project Name PRO100881 BFW881 SAX
Customer Dr. Heino Konrad (Austrian Research Centre for Forests, Vienna, Austria)
Array Name Axiom™ 4TREE
Analyst Jonah Ho

Sample QC Summary & Genotyping Metrics

For this analysis, het-so-cutoff was set to -0.3, supplemental SNP filtering was performed, and OTV caller was used.

Overall Project	
Total number of samples	1,152
Passed samples	1,107
Failed samples	45
% Passed samples	96.09%
% Samples meeting concentration spec. passed	97.18%
Average Cluster Call Rate	99.53%
Sample Reproducibility	99.95%

SNP QC Summary

For this cluster, the PolyHighResolution, NoMinorHom, MonoHighResolution categories are considered recommended for downstream analysis.

	# of markers	% of markers
PolyHighResolution	10,499	78.31
NoMinorHom	669	4.99
MonoHighResolution	414	3.09
CallRateBelowThreshold	312	2.33
OffTargetVariant	103	0.77
Other	531	3.96
AAvarianceX	149	1.11
AAvarianceY	120	0.90
ABvarianceX	186	1.39
ABvarianceY	115	0.86
BBvarianceX	174	1.30
BBvarianceY	135	1.01
Total	13,407	100.00
Total recommended	11,582	86.39

Sample Tracking

Replicate analysis was done by comparing calls over a subset of markers from the PolyHighRes category. 1 set(s) of known replicates were confirmed. The details are available in the Axiom Analysis Suite files in the cluster data folder.

Deliverables

A complete list of deliverables is provided in the Axiom_ReadMe.pdf file, under the "Reference" folder. Full list of samples, QC metrics and analysis settings can be accessed in Axiom Analysis Suite files by loading the cluster data folder in Axiom Analysis Suite Software (More information on the software can be found on the [Thermo Fisher website](#)).