

Analysis Summary

- **Batch Name:** autogenous\_np\_oct27\_2023
- **Array Package Name:** Axiom\_Aealbo.r1
- **Array Display Name:** Axiom\_Aealbo.r1
- **Workflow Type:** Best Practices Workflow
- **Date Created:** 10/27/2023 2:06:31 PM

Sample Summary

- Number of input samples: 61
- Samples passing DQC: 61 out of 61
- Samples passing DQC and QC CR: 61 out of 61
- Samples passing DQC, QC CR and Plate QC: 61 out of 61 (100%)
- Number of failing samples: 0
- Number of Samples Genotyped: 61
- Average QC CR for the passing samples: 99.468
- Inbred Penalty Applied: no
- Prior Model File: Axiom\_Aealbo.r1.20231027.autogenous.models
- SNP List File: none

Plate QC Summary

Plate Barcode	Result	Number of files in a batch	Number of files failing dish QC	Number of files failing QC Call rate	Number of samples that passed	Percent of passing samples	Average call rate for passing samples	Filtered Call Rate
5513584436722042923432	PASSED	51	0	0	51	100	99.484	97.246
5513584436722042923435	PASSED	10	0	0	10	100	99.386	96.268

ProbeSet Metrics Summary

- Number of ProbeSets: 175396

ConversionType	Count	Percentage
PolyHighResolution	97883	55.807
Other	26710	15.228
NoMinorHom	20678	11.789
OTV	16700	9.521
MonoHighResolution	12487	7.119
CallRateBelowThreshold	938	0.535

Marker Metrics Summary

- Number of Markers: 175396
- Number of BestandRecommended: 131048
- Percent BestandRecommended: 74.716

ConversionType	Count	Percentage
PolyHighResolution	97883	55.807
Other	26710	15.228
NoMinorHom	20678	11.789
OTV	16700	9.521
MonoHighResolution	12487	7.119
CallRateBelowThreshold	938	0.535

**Sample QC Thresholds**

- DQC:  $\geq 0.82$
- QC call\_rate:  $\geq 90$
- Average call rate for passing samples:  $\geq 90$
- Percent of passing samples:  $\geq 90$

**SNP QC Thresholds**

- species-type: Diploid
- cr-cutoff:  $\geq 90$
- fld-cutoff:  $\geq 3.6$
- het-so-cutoff:  $\geq -0.1$
- het-so-XChr-cutoff:  $\geq -0.1$
- het-so-ZChr-cutoff:  $\geq -0.1$
- het-so-otv-cutoff:  $\geq -0.3$
- hom-ro-1-cutoff:  $\geq 0.6$
- hom-ro-2-cutoff:  $\geq 0.3$
- hom-ro-3-cutoff:  $\geq -0.9$
- hom-ro: true
- num-minor-allele-cutoff:  $\geq 2$
- hom-ro-hap-1-XChr-cutoff:  $\geq 0.1$
- hom-ro-hap-1-MTChr-cutoff:  $\geq 0.4$
- hom-ro-hap-1-ZChr-cutoff:  $\geq 0.1$
- hom-ro-hap-2-XChr-cutoff:  $\geq 0.05$
- hom-ro-hap-2-MTChr-cutoff:  $\geq 0.2$
- hom-ro-hap-2-ZChr-cutoff:  $\geq 0.05$
- aaf-XChr-cut:  $< 0.36$
- aaf-ZChr-cut:  $< 0.36$
- fld-XChr-cut:  $\geq 4$
- fld-ZChr-cut:  $\geq 4$
- homfld-XChr-cut:  $\geq 6.5$
- homfld-ZChr-cut:  $\geq 6.5$
- homfld-YChr-cut:  $\geq 6.5$
- homfld-WChr-cut:  $\geq 6.5$
- min-YChr-samples-cut:  $\geq 5$
- min-WChr-samples-cut:  $\geq 5$
- priority-order: PolyHighResolution, NoMinorHom, MonoHighResolution, OTV, UnexpectedGenotypeFreq, CallRateBelowThreshold, Other, OtherMA
- recommended: PolyHighResolution, NoMinorHom, MonoHighResolution, Hemizygous
- y-restrict:  $\leq 0.2$

- min-genotype-freq-samples:  $\geq 20$
- genotype-p-value-cutoff:  $\geq 1E-06$

### **Multi-Allelic SNP QC Thresholds**

- HomMMA-cutoff:  $> 10$
- FLD-MA-cutoff:  $> 5.2$
- FLD-MA-2-cutoff:  $> 5.2$
- Min-FLD-MA-cutoff:  $> 0$
- Min-FLD-MA-2-cutoff:  $> 0$
- HetSO-MA-2-cutoff:  $> -0.1$
- HomRO-MA-cutoff:  $> 0.5$
- HomRO-MA-2-cutoff:  $> 0.5$
- HomRO-MA-1-cutoff:  $> 1$
- priority-order-MA: PolyHighResolution, NoMinorHom, MonoHighResolution, Hemizygous, UnexpectedGenotypeFreq, CallRateBelowThreshold, Other, OtherMA
- Best-CR-MA-cutoff:  $> 90$