

Analysis Summary

- **Batch Name:** manuscript_august10_2023
- **Array Package Name:** Axiom_Aealbo.r1
- **Array Display Name:** Axiom_Aealbo.r1
- **Workflow Type:** Best Practices Workflow
- **Date Created:** 8/10/2023 10:52:37 AM

Sample Summary

- Number of input samples: 266
- Samples passing DQC: 245 out of 266
- Samples passing DQC and QC CR: 243 out of 266
- Samples passing DQC, QC CR and Plate QC: 243 out of 266 (91.353%)
- Number of failing samples: 23
- Number of Samples Genotyped: 243
- Average QC CR for the passing samples: 98.744
- Inbred Penalty Applied: no
- Prior Model File: Axiom_Aealbo.r1.20230809_manuscript.models.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
5513584436722042923427	PASSED	45	7	1	37	82.222	98.926	96.325
5513584452328010824440	PASSED	53	8	0	45	84.906	98.877	96.93
5513584452328010824441	PASSED	24	0	0	24	100	99.127	96.844
5513584452328010824444	PASSED	31	0	0	31	100	98.969	96.861
5513584452328010824445	PASSED	32	1	1	30	93.75	97.929	95.551
5513584452328010824447	PASSED	32	5	0	27	84.375	98.749	96.734
5513584452328010824448	PASSED	37	0	0	37	100	98.639	96.521
5513584478174020425867	PASSED	12	0	0	12	100	98.69	96.083

ProbeSet Metrics Summary

- Number of ProbeSets: 175396

ConversionType	Count	Percentage
PolyHighResolution	105117	59.931
Other	35588	20.29
OTV	23600	13.455
NoMinorHom	7590	4.327
MonoHighResolution	2639	1.505
CallRateBelowThreshold	862	0.491

Marker Metrics Summary

- Number of Markers: 175396
- Number of BestandRecommended: 115346
- Percent BestandRecommended: 65.763

ConversionType	Count	Percentage
PolyHighResolution	105117	59.931
Other	35588	20.29
OTV	23600	13.455
NoMinorHom	7590	4.327
MonoHighResolution	2639	1.505
CallRateBelowThreshold	862	0.491

Sample QC Thresholds

- DQC: ≥ 0.82
- QC call_rate: ≥ 90
- Average call rate for passing samples: ≥ 90
- Percent of passing samples: ≥ 90

SNP QC Thresholds

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

- min-genotype-freq-samples: ≥ 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