

Genome-wide scans for signatures of selection in Mangalarga Marchador horses using high-throughput SNP genotyping

Wellington B. Santos^{1*}, Gustavo P. Schettini¹, Amanda M. Maiorano¹; Fernando O. Bussiman², Júlio C. C. Balieiro², Guilherme C. Ferraz¹,
Guilherme L. Pereira³, Welder Angelo Baldassini³; Otávio R. M. Neto³, Henrique N. Oliveira¹ & Rogério A. Curi³

Supplementary material: Additional file 4

Analysis Summary

- **Batch Name:** DATA_MM_2019
- **Array Package Name:** Axiom_MNEc670.r3
- **Array Type Name:** Axiom_MNEc670
- **Array Display Name:** Axiom_MNEc670.r3
- **Workflow Type:** Best Practices Workflow
- **Date Created:** 7/14/2019 9:30:45 PM

Sample Summary

- Number of input samples: 192
- Samples passing DQC: 192 out of 192
- Samples passing DQC and QC CR: 192 out of 192
- Samples passing DQC, QC CR and Plate QC: 192 out of 192 (100%)
- Number of failing samples: 0
- Number of input samples without QC information: 0
- Number of Samples Genotyped: 192
- Average QC CR for the passing samples: 99.257
- Gender Calls Counts: female=130 male=62 unknown=0
- Inbred Penalty Applied: no

Plate QC Summary

Plate Barcode	Result	N° files in a batch	N° files failing dish QC	N° files failing QC Call rate	N° samples that passed	Percent of passing samples	Average call rate for passing samples	Filtered Call Rate
5505834338526080618058	PASSED	96	0	0	96	100	99.343	99.467
5505834338526080618064	PASSED	96	0	0	96	100	99.17	99.278

ProbeSet Metrics Summary

- Number of ProbeSets: 629474

ConversionType	Count	Percentage
PolyHighResolution	354473	56.313
NoMinorHom	128407	20.399
Other	66655	10.589
MonoHighResolution	62339	9.903
CallRateBelowThreshold	15948	2.534
OTV	1652	0.262

Marker Metrics Summary

- Number of Markers: 629474
- Number of BestandRecommended: 545219
- Percent BestandRecommended: 86.615

ConversionType	Count	Percentage
PolyHighResolution	354473	56.313
NoMinorHom	128407	20.399
Other	66655	10.589
MonoHighResolution	62339	9.903
CallRateBelowThreshold	15948	2.534
OTV	1652	0.262

Sample QC Thresholds

- DQC: ≥ 0.82
- QC call_rate: ≥ 97
- Percent of passing samples: ≥ 95
- Average call rate for passing samples: ≥ 98.5

SNP QC Thresholds

- species-type: Diploid
- cr-cutoff: ≥ 95
- fld-cutoff: ≥ 3.6
- het-so-cutoff: ≥ -0.1
- het-so-XChr-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
- hom-het: 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-2-XChr-cutoff: ≥ 0.05
- hom-ro-hap-2-MTChr-cutoff: ≥ 0.2
- aaf-XChr-cut: < 0.36
- fld-XChr-cut: ≥ 4
- homfld-XChr-cut: ≥ 6.5
- homfld-YChr-cut: ≥ 6.5
- min-YChr-samples-cut: ≥ 5
- sign-diff-hom-1-cutoff: ≥ 0.5
- sign-diff-hom-2-cutoff: ≥ 0.4
- min-mean-cp2-cutoff: ≥ 9
- max-mean-cp2-cutoff: ≤ 15
- priority-order: PolyHighResolution, NoMinorHom, OTV, MonoHighResolution, CallRateBelowThreshold
- recommended: PolyHighResolution, NoMinorHom, MonoHighResolution, Hemizygous
- y-restrict: ≤ 0.2

