Charles River Genetic Testing Services, Wilmington

Agena-MUS032-210827: U Hong Kong Ctr for Comparative Med Research Order 2021011054: NULL-B6 vs B6 Ref

Call Rate and Percent Match to Reference Allelic Profile

Colony Strain	Reference Strain	Sample #	Sex	DOB	Breed Colony		# of 32 Called	Percent Called	Percent Match
B6	**B6**	005-21P		0	0		32	100.0%	100.0%
		006-26P		0	0		32	100.0%	100.0%
		007-31P		0	0		32	100.0%	100.0%
Average:							**96**	**100.0%**	**100.0%**

RESULTS SUMMARY:
Passing Sample Results: % Match averages > 98% for inbreds and >95% for F1 hybrids samples provided call rate exceeds 60%.

To discuss results, please contact Bill Shek, DVM, PhD (O: 781-222-6442; email: william.shek@crl.com)

GENERAL INFORMATION: Mouse sample genotypes at 32 single-nucleotide-polymorphism (SNP) loci (on autosomes 1 through 19 and the X chromosome) were determined by the Agena iPLEX PCR MassARRAY assay. The genetic profile of each sample was analyzed to determine the call rate (i.e., the percentage of SNP loci to which genotypes were assigned) and percen t match (or conformity) to its strain reference profile.

Charles River Genetic Testing Services, Wilmington

Agena-MUS032-210827: U Hong Kong Ctr for Comparative Med Research Order 2021011054: NULL-BALB/C vs BALBc Ref

Call Rate and Percent Match to Reference Allelic Profile

Colony Strain	Reference Strain	Sample #	Sex	DOB	Breed Colony		# of 32 Called	Percent Called	Percent Match
BALB/C	**BALBc**	008-36P			0	0	32	100.0%	100.0%
		009-41P			0	0	32	100.0%	100.0%
		010-46P			0	0	32	100.0%	100.0%
		011-51P			0	0	32	100.0%	100.0%
		012-56P			0	0	32	100.0%	100.0%
		013-61P			0	0	32	100.0%	100.0%
		014-66P			0	0	32	100.0%	100.0%
		018-86P			0	0	32	100.0%	100.0%
		019-91P			0	0	32	100.0%	100.0%
		020-96P			0	0	32	100.0%	100.0%
		021-101P			0	0	32	100.0%	100.0%
Average:							**352**	**100.0%**	**100.0%**

RESULTS SUMMARY:
Passing Sample Results: % Match averages > 98% for inbreds and >95% for F1 hybrids samples provided call rate exceeds 60%.

To discuss results, please contact Bill Shek, DVM, PhD (O: 781-222-6442; email: william.shek@crl.com)

GENERAL INFORMATION: Mouse sample genotypes at 32 single-nucleotide-polymorphism (SNP) loci (on autosomes 1 through 19 and the X chromosome) were determined by the Agena iPLEX PCR MassARRAY assay. The genetic profile of each sample was analyzed to determine the call rate (i.e., the percentage of SNP loci to which genotypes were assigned) and percen t match (or conformity) to its strain reference profile.

Charles River Genetic Testing Services, Wilmington

Agena-MUS032-210827: U Hong Kong Ctr for Comparative Med Research Order 2021011054: NULL-CB17 vs CB17 Ref

Call Rate and Percent Match to Reference Allelic Profile

Colony Strain	Reference Strain	Sample #	Sex	DOB	Breed Colony		# of 32 Called	Percent Called	Percent Match
CB17	**CB17**	015-71P		0	0		32	100.0%	96.9%
		016-76P		0	0		32	100.0%	100.0%
		017-81P		0	0		32	100.0%	100.0%
Average:							**96**	**100.0%**	**99.0%**

RESULTS SUMMARY:
Passing Sample Results: % Match averages > 98% for inbreds and >95% for F1 hybrids samples provided call rate exceeds 60%.

To discuss results, please contact Bill Shek, DVM, PhD (O: 781-222-6442; email: william.shek@crl.com)

GENERAL INFORMATION: Mouse sample genotypes at 32 single-nucleotide-polymorphism (SNP) loci (on autosomes 1 through 19 and the X chromosome) were determined by the Agena iPLEX PCR MassARRAY assay. The genetic profile of each sample was analyzed to determine the call rate (i.e., the percentage of SNP loci to which genotypes were assigned) and percen t match (or conformity) to its strain reference profile.

Charles River Genetic Testing Services, Wilmington

Agena-MUS032-210827: U Hong Kong Ctr for Comparative Med Research Order 2021011054: NULL-NODSCID vs NODSCID Ref

Call Rate and Percent Match to Reference Allelic Profile

Colony Strain	Reference Strain	Sample #	Sex	DOB	Breed Colony		# of 32 Called	Percent Called	Percent Match
NODSCID	**NODSCID**	001-1P		0	0		32	100.0%	100.0%
		002-6P		0	0		32	100.0%	100.0%
		003-11P		0	0		32	100.0%	100.0%
		004-16P		0	0		32	100.0%	100.0%
Average:							**128**	**100.0%**	**100.0%**

RESULTS SUMMARY:
Passing Sample Results: % Match averages > 98% for inbreds and >95% for F1 hybrids samples provided call rate exceeds 60%.

To discuss results, please contact Bill Shek, DVM, PhD (O: 781-222-6442; email: william.shek@crl.com)

GENERAL INFORMATION: Mouse sample genotypes at 32 single-nucleotide-polymorphism (SNP) loci (on autosomes 1 through 19 and the X chromosome) were determined by the Agena iPLEX PCR MassARRAY assay. The genetic profile of each sample was analyzed to determine the call rate (i.e., the percentage of SNP loci to which genotypes were assigned) and percen t match (or conformity) to its strain reference profile.

PDF Title: U Hong Kong Ctr for Comparative Med Research Order 2021011054: NULL-Not specified vs CB17 Ref

Agena-MUS032-210831: U Hong Kong Ctr for Comparative Med Research Order 2021011054: NULL-Not specified vs CB17 Ref

Call Rate and Percent Match to Reference Allelic Profile

Order-Set-Colony	2021011054-01-0048347
CRL SNP #	(Multiple Items)
Quality-Warning	(Multiple Items)
Exclude Sample	(All)
Exclude SNP	(All)

						Values		
Colony Strain	Reference Strain	Sample #	Sex	DOB	Breed Colony	# of 32 Called	Percent Called	Percent Match
Not specified	**CB17**	015-71P		0	6J	32	100.0%	96.9%
Average:						**32**	**100.0%**	**96.9%**

Print End

GENERAL INFORMATION: Mouse sample genotypes at 32 single-nucleotide-polymorphism (SNP) loci (on autosomes 1 through 19 and the X chromosome) were determined by the Agena iPLEX PCR MassARRAY assay. The genetic profile of each sample was analyzed to determine the call rate (i.e., the percentage of SNP loci to which genotypes were assigned) and percent match (or conformity) to its strain reference profile.

RESULTS SUMMARY:
Passing Sample Results: % Match averages > 98% for inbreds and >95% for F1 hybrids samples provided call rate exceeds 60%.

To discuss results, please contact Bill Shek, DVM, PhD (O: 781-222-6442; email: william.shek@crl.com)

PDF Title: U Hong Kong Ctr for Comparative Med Research Order 2021013166: NULL-Not specified vs CB17 Ref

Agena-MUS032-211006: U Hong Kong Ctr for Comparative Med Research Order 2021013166: NULL-Not specified vs CB17 Ref

Call Rate and Percent Match to Reference Allelic Profile

Order-Set-Colony	2021013166-01-0048347
CRL SNP #	(Multiple Items)
Quality-Wa	(Multiple Items)
Exclude San	(All)
Exclude SN	(All)

Colony Strain	Reference Strain	Sample #	Sex	DOB	Breed Colony	Values # of 32 Called	Percent Called	Percent Match
Not speci	**CB17**	001-A1 71		0	Nucleus	32	100.0%	100.0%
		002-B1 72		0	Nucleus	32	100.0%	100.0%
		003-C1 73		0	Nucleus	32	100.0%	100.0%
		004-D1 74		0	Nucleus	32	100.0%	100.0%
		005-E1 75		0	Nucleus	32	100.0%	100.0%
Average:						**160**	**100.0%**	**100.0%**

GENERAL INFORMATION: Mouse sample genotypes at 32 single-nucleotide-polymorphism (SNP) loci (on autosomes 1 through 19 and the X chromosome) were determined by the Agena iPLEX PCR MassARRAY assay. The genetic profile of each sample was analyzed to determine the call rate (i.e., the percentage of SNP loci to which genotypes were assigned) and percent match (or conformity) to its strain reference profile.

RESULTS SUMMARY:
Passing Sample Results: % Match averages > 98% for inbreds and >95% for F1 hybrids samples provided call rate exceeds 60%.

To discuss results, please contact Bill Shek, DVM, PhD (O: 781-222-6442; email: william.shek@crl.com)