

Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch QC_160826KB: University of Hong Kong Lab Animal Unit-SPFBA Order 2016052026

Percent Match of Allelic Profiles to Expected Profile for Strain

Order-Set	Area	Colony Strain	Ref Strain	N	Call Rate	% Match	# of
2016051945-01	Rm. 207	F1 (C57BL/6N x CBA/Ca)	B6CBACA: 0503	64	100.0%	96.9%	1
2016051945-02	Rm. 208	C57BL/6J	B6: 0053	192	99.5%	100.0%	3
2016051945-03	Rm. 208	FVB/N	FVB: 0110	128	100.0%	100.0%	2
2016051945-04	Rm. 208	CBA/Ca	CBACa: 0041	128	100.0%	100.0%	2
2016051945-05	Rm. 209	C57BL/6N	B6: 0053	192	100.0%	100.0%	3
2016051945-06	Rm. 212	BALB/cAnN-nu (Nude)	BALBc: 0022	192	100.0%	100.0%	3
2016051945-07	Rm. 211	C.B-17/Icr-scid (SCID)	CB17: 0055	192	100.0%	100.0%	3
2016051945-08	Rm. 214	BALB/c	BALBc: 0022	191	100.0%	100.0%	3
2016051945-09	Rm. 234B	C.B-17/IcrHsd-Prkdc<scid>Lyst<bg> (SCID Beige)	CB17: 0055	191	100.0%	100.0%	3

GENERAL INFORMATION: A 32 single nucleotide polymorphism (SNP) panel was employed to generate allelic profiles of the test mice for comparison to the reference strain profiles. Each SNP has 2 alleles, i.e., is dimorphic. One allele is identified with a complementary oligonucleotide (TaqMan) probe labeled with the fluorescent dye FAM. The probe complementary to the other allele is labeled with the fluorescent dye VIC. Therefore, genotypes are reported as F F or V V for homozygotes and V F for heterozygotes. Inbred strains are expected to be homozygous VV or FF at each SNP marker, whereas F1 hybrids may be heterozygous VF. Deviation from the reference profile is indicative of subline divergence due to genetic contamination

The *Percent Match* of an animal with the reference strain is determined by comparing the genotype at each marker. A heterozygous V F genotype = 0.5 (i.e., a half match); a homozygous genotype (i.e., V V or FF) = 1 if it matches that of the reference strain or 0 if it doesn't. NC (for No Call) is shown if the marker could not be classified (e.g., if it wasn't amplified). NC results are not compared to the reference. An NC result occurs when the sample is not adequately amplified or shows a fluorescence pattern not assignable by the analysis software or the analyst to one of the three genotypes. The *Call Rate* in the above table is the percentage of assays in which a sample was assigned a genotype. Repeat testing, preferably of a new tissue specimen, is recommended when the call rate falls below 90%.

RESULT COMMENTS: The Percent Match of the sample allelic profiles to their expected profiles were 100% for the inbred mouse samples in sets 2 to 9 and 96.9% for the F1 (C57BL/6N x CBA/Ca) sample in set 1. The latter 3.1% difference from the reference profile is expected for a male, which is hemizygous at the X-linked SNP loci 31 and 32. In summary, all mice tested as authentic members of their respective strains.

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

Charles River Genetic Testing Services, Wilmington

Order Sample Detail

Customer: University of Hong Kong Lab Animal Unit

Facility: SPFBA

LTM Order: 2016051945

Received: 17-Aug-2016

Tested: 26-Aug-2016

Sample #-			
Code	Room	Strain-Line	Breed Colony
001-11P	Rm. 207	F1 (C57BL/6N x CBA/Ca)	Issue
002-16P	Rm. 208	C57BL/6J	Nucleus
003-21P	Rm. 208	C57BL/6J	Production
004-26P	Rm. 208	C57BL/6J	Issue
005-31P	Rm. 208	FVB/N	Nucleus
006-36P	Rm. 208	FVB/N	Issue
007-41P	Rm. 208	CBA/Ca	Nucleus
008-46P	Rm. 208	CBA/Ca	Issue
009-51P	Rm. 209	C57BL/6N	Nucleus
010-56P	Rm. 209	C57BL/6N	Production
011-61P	Rm. 209	C57BL/6N	Issue
012-66P	Rm. 212	BALB/cAnN-nu (Nude)	Nucleus
013-71P	Rm. 212	BALB/cAnN-nu (Nude)	Production
014-76P	Rm. 212	BALB/cAnN-nu (Nude)	Issue
015-81P	Rm. 211	C.B-17/Icr-scid (SCID)	Nucleus
016-86P	Rm. 211	C.B-17/Icr-scid (SCID)	Production
017-91P	Rm. 211	C.B-17/Icr-scid (SCID)	Issue
018-96P	Rm. 214	BALB/c	Nucleus
019-101P	Rm. 214	BALB/c	Production
020-106P	Rm. 214	BALB/c	Issue
021-111P	Rm. 234B	C.B-17/IcrHsd-Prkdc<scid>Lyst<bg> (SCID Beige)	Nucleus
022-116P	Rm. 234B	C.B-17/IcrHsd-Prkdc<scid>Lyst<bg> (SCID Beige)	Production
023-121P	Rm. 234B	C.B-17/IcrHsd-Prkdc<scid>Lyst<bg> (SCID Beige)	Issue

Charles River Genetic Testing Services, Wilmington

Rat 32-SNP Panel Batch QC_160826KB: University of Hong Kong Lab Animal Unit-SPFBA

Percent Match of Allelic Profiles to Expected Profile for Strain

Order-Set	Area	Colony Strain	Ref Strain	N	Call Rate	% Match
2016052069-01	Rm. 213	LEW (Lewis)	LEW: 0011	64	100.0%	100.0%
				64	100.0%	100.0%
2016052069-02	Rm. 213	DA (Dark Agouti)	DA-HK: 0045	64	96.9%	100.0%
				64	96.9%	100.0%

GENERAL INFORMATION: A 32 single nucleotide polymorphism (SNP) panel was employed to generate allelic profiles of the test mice for comparison to the reference strain profiles. Each SNP has 2 alleles, i.e., is dimorphic. One allele is identified with a complementary oligonucleotide (TaqMan) probe labeled with the fluorescent dye FAM. The probe complementary to the other allele is labeled with the fluorescent dye VIC. Therefore, genotypes are reported as F F or V V for homozygotes and V F for heterozygotes. Inbred strains are expected to be homozygous VV or FF at each SNP marker, whereas F1 hybrids may be heterozygous VF. Deviation from the reference profile is indicative of subline divergence due to genetic contamination

The *Percent Match* of an animal with the reference strain is determined by comparing the genotype at each marker. A heterozygous V F genotype = 0.5 (i.e., a half match); a homozygous genotype (i.e., V V or FF) = 1 if it matches that of the reference strain or 0 if it doesn't. NC (for No Call) is shown if the marker could not be classified (e.g., if it wasn't amplified). NC results are not compared to the reference. An NC result occurs when the sample is not adequately amplified or shows a fluorescence pattern not assignable by the analysis software or the analyst to one of the three genotypes. The *Call Rate* in the above table is the percentage of assays in which a sample was assigned a genotype. Repeat testing, preferably of a new tissue specimen, is recommended when the call rate falls below 90%.

RESULTS SUMMARY: The Percent Match of the inbred rat allelic profiles to their respective strain reference profiles were 100%, indicating that the rats were purebred.

Note that the reference allelic profile for the DA, designated DA-HK for Hong Kong, is based on prior testing of the University of Hong Kong colony. This profile differs from the standard Charles River DA profile at a single SNP locus (i.e., locus 3 on chromosome 2).

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

**Rat 32-SNP Panel Batch QC_160826KB: University of Hong Kong Lab Animal Unit-
SPFBA Room 213**

Allelic Profiles (Red = Mismatch)

SNP #	Chr #			LEW (Lewis)		DA (Dark Agouti)		
		LEW: 0011	DA-HK: 0045	SNP #	002-131P	001-126P	004-141P	003-136P
1	Chr-01	FF	FF	1	FF	FF	FF	FF
2	Chr-01	VV	FF	2	VV	VV	FF	FF
3	Chr-02	VV	FF	3	VV	VV	FF	FF
4	Chr-02	FF	FF	4	FF	FF	FF	FF
5	Chr-03	VV	VV	5	VV	VV	VV	VV
6	Chr-03	FF	VV	6	FF	FF	VV	VV
7	Chr-04	VV	VV	7	VV	VV	VV	VV
8	Chr-04	FF	FF	8	FF	FF	FF	FF
9	Chr-05	VV	VV	9	VV	VV	VV	VV
10	Chr-05	FF	FF	10	FF	FF	FF	FF
11	Chr-06	VV	VV	11	VV	VV	VV	VV
12	Chr-06	VV	VV	12	VV	VV	VV	VV
13	Chr-07	FF	FF	13	FF	FF	FF	FF
14	Chr-07	FF	FF	14	FF	FF	FF	FF
15	Chr-08	VV	VV	15	VV	VV	VV	VV
16	Chr-08	VV	VV	16	VV	VV	VV	VV
17	Chr-09	FF	VV	17	FF	FF	VV	VV
18	Chr-09	FF	FF	18	FF	FF	FF	FF
19	Chr-10	VV	FF	19	VV	VV	FF	FF
20	Chr-10	VV	VV	20	VV	VV	VV	VV
21	Chr-11	VV	FF	21	VV	VV	FF	FF
22	Chr-11	FF	FF	22	FF	FF	FF	FF
23	Chr-12	VV	VV	23	VV	VV	VV	VV
24	Chr-13	VV	VV	24	VV	VV	VV	VV
25	Chr-14	FF	FF	25	FF	FF	FF	FF
26	Chr-15	VV	VV	26	VV	VV	VV	VV
27	Chr-16	FF	FF	27	FF	FF	FF	FF
28	Chr-17	FF	FF	28	FF	FF	FF	FF
29	Chr-18	FF	FF	29	FF	FF	FF	FF
30	Chr-19	VV	FF	30	VV	VV	FF	FF
31	Chr-20	VV	VV	31	VV	VV	NC	NC
32	Chr-0X	FF	VV	32	FF	FF	VV	VV

Charles River Genetic Testing Services, Wilmington

Order Sample Detail

Customer: University of Hong Kong Lab Animal Unit
Facility: SPFBA
LTM Order: 2016052069
Received: 17-Aug-2016
Tested: 26-Aug-2016

Sample #-			
Code	Room	Strain-Line	Breed Colony
001-126P	Rm. 213	LEW (Lewis)	Nucleus
002-131P	Rm. 213	LEW (Lewis)	Issue
003-136P	Rm. 213	DA (Dark Agouti)	Nucleus
004-141P	Rm. 213	DA (Dark Agouti)	Issue

Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch QC_160826KB: University of Hong Kong Lab Animal Unit-MDA-LAU Order 2016052026

Percent Match of Allelic Profiles to Expected Profile for Strain

Order-Set	Area	Colony Strain	Ref Strain	N	Call Rate	% Match	# of
2016052026-01	Rm. 118	NOD.CB17-Prkdc<scid>/J (NOD/SCID)	NODSCID: 0142	128	100.0%	100.0%	2

GENERAL INFORMATION: A 32 single nucleotide polymorphism (SNP) panel was employed to generate allelic profiles of the test mice for comparison to the reference strain profiles. Each SNP has 2 alleles, i.e., is dimorphic. One allele is identified with a complementary oligonucleotide (TaqMan) probe labeled with the fluorescent dye FAM. The probe complementary to the other allele is labeled with the fluorescent dye VIC. Therefore, genotypes are reported as F F or V V for homozygotes and V F for heterozygotes. Inbred strains are expected to be homozygous VV or FF at each SNP marker, whereas F1 hybrids may be heterozygous VF. Deviation from the reference profile is indicative of subline divergence due to genetic contamination

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RESULT COMMENTS: The Percent Match of the 2 NOD/SCID sample allelic profiles to the reference profile were 100% , thus indicating that mice tested were authentic (i.e., not genetically contaminated).

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

Charles River Genetic Testing Services, Wilmington

Order Sample Detail

Customer: University of Hong Kong Lab Animal Unit
Facility: MDA-LAU
LTM Order: 2016052026
Received: 17-Aug-2016
Tested: 26-Aug-1916

Sample #-Code	Room	Strain-Line	Breed Colony
001-1P	Rm. 118	NOD.CB17-Prkdc<scid>/J (NOD/SCID)	Nucleus
002-6P	Rm. 118	NOD.CB17-Prkdc<scid>/J (NOD/SCID)	Issue