

Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch 181009SK: University of Hong Kong, Lab Animal Unit - LTM Order 2018008335

Percent Match of Allelic Profiles to Expected Profile for Strain

Order-Set	Facility-Room	Colony Strain	Ref Strain	N	Call Rate	% Match	# of Samples
2018008335-01	MDA-LAU 118	NOD.CB17-PrkdcScid (NOD-SCID)	NODSCID: 0142	124	94.4%	100.0%	2
2018008335-02	SPFBA 205	CAnN.Cg-Foxan1nu/Crl	BALBc: 0022	183	99.5%	100.0%	3
2018008335-03	SPFBA 207	F1 (C57BL/6N x CBA/Ca)	B6CBACA: 0503	63	100.0%	100.0%	1
2018008335-04	SPFBA 208	C57BL/6J	B6: 0053	190	99.5%	100.0%	3
2018008335-05	SPFBA 208	CBA/Ca	CBACa: 0041	122	100.0%	100.0%	2
2018008335-06	SPFBA 209	C57BL/6N	B6: 0053	186	100.0%	100.0%	3
2018008335-07	SPFBA 210	BALB/cAnN-nu (Nude)	BALBc: 0022	122	100.0%	100.0%	2
2018008335-08	SPFBA 212	BALB/cAnN-nu (Nude)	BALBc: 0022	122	100.0%	100.0%	2
2018008335-09	SPFBA 211	C.B-17/Icr-scid (SCID)	CB17: 0055	183	100.0%	100.0%	3
2018008335-10	SPFBA 214	BALB/C	BALBc: 0022	187	100.0%	100.0%	3
2018008335-11	SPFBA 234B	C.B-17/Icr-scid-bg (SCID Beige)	CB17: 0055	186	99.5%	100.0%	3
2018008335-12	SPFBA 208	FVB/N	FVB: 0110	126	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 profile. 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 FF or VV for homozygotes and VF 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 VF genotype = 0.5 (i.e., a half match); a homozygous genotype (i.e., VV 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 sample allelic profiles to their respective strain reference profiles were 100%, indicating that the mice tested were purebred.

W. Shek, DVM, PhD, 05-Nov-2018; william.shek@crl.com, +1 (781) 222-6442

Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch 181009SK: University of Hong Kong, Lab Animal Unit
- LTM Order 2018008335

Order Sample Detail

Date Samples Received: 30-Aug-2018

Date Samples Tested: 9-Oct-2018

Sample #-Code	Room	Strain-Line	Breed Colony
001-1P	MDA-LAU 118	NOD.CB17-PrkdcScid (NOD-SCID)	Nucleus
002-6P	MDA-LAU 118	NOD.CB17-PrkdcScid (NOD-SCID)	Issue
003-16P	SPFBA 205	CAnN.Cg-Foxan1nu/Crl	Nucleus
004-21P	SPFBA 205	CAnN.Cg-Foxan1nu/Crl	Production
005-26P	SPFBA 205	CAnN.Cg-Foxan1nu/Crl	Issue
006-31P	SPFBA 207	F1 (C57BL/6N x CBA/Ca	Issue
007-36P	SPFBA 208	C57BL/6J	Nucleus
008-41P	SPFBA 208	C57BL/6J	Production
009-46P	SPFBA 208	C57BL/6J	Issue
010-51P	SPFBA 208	CBA/Ca	Nucleus
011-56P	SPFBA 208	CBA/Ca	Issue
012-61P	SPFBA 209	C57BL/6N	Nucleus
013-66P	SPFBA 209	C57BL/6N	Production
014-71P	SPFBA 209	C57BL/6N	Issue
015-76P	SPFBA 210	BALB/cAnN-nu (Nude)	Traffic Light
016-81P	SPFBA 210	BALB/cAnN-nu (Nude)	Issue
017-86P	SPFBA 212	BALB/cAnN-nu (Nude)	Nucleus
018-91P	SPFBA 212	BALB/cAnN-nu (Nude)	Production
019-96P	SPFBA 211	C.B-17/Icr-scid (SCID)	Nucleus
020-101P	SPFBA 211	C.B-17/Icr-scid (SCID)	Production
021-106P	SPFBA 211	C.B-17/Icr-scid (SCID)	Issue
022-111P	SPFBA 214	BALB/C	Nucleus
023-116P	SPFBA 214	BALB/C	Production
024-121P	SPFBA 214	BALB/C	Issue
025-126P	SPFBA 234B	C.B-17/Icr-scid-bg (SCID Beige)	Nucleus
026-131P	SPFBA 234B	C.B-17/Icr-scid-bg (SCID Beige)	Production
027-136P	SPFBA 234B	C.B-17/Icr-scid-bg (SCID Beige)	Issue
028-161P	SPFBA 208	FVB/N	Nucleus
029-166P	SPFBA 208	FVB/N	Issue

Charles River Genetic Testing Services, Wilmington

Rat 32-SNP Panel Batch 180831NGC: University of Hong Kong, Lab Animal Unit - LTM Order 2018008423

Percent Match of Allelic Profiles to Expected Profile for Strain

Order-Set	Area	Colony Strain	Ref Strain	Sample	Values		
					N	Call Rate	% Match
2018008423-01	SPFBA 213	LEW (Lewis)	LEW: 0011	001-141P	64	100.0%	100.0%
				002-146P	64	100.0%	100.0%
2018008423-02	SPFBA 213	DA (Dark Agouti)	DA-HK: 0045	003-151P	64	100.0%	100.0%
				004-156P	64	100.0%	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 80%.

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

W. Shek, DVM, PhD, 05-Nov-2018; william.shek@crl.com, +1 (781) 222-6442

**Rat 32-SNP Panel Batch 180831NGC: University of Hong Kong, Lab Animal Unit -
LTM Order 2018008423**

No Order Match

Allelic Profiles (with mismatches highlighted in red)

SNP #	Chr #	LEW (Lewis)			DA (Dark Agouti)			
		LEW: 0011	DA-HK: 0045	SNP #	001-141P	002-146P	003-151P	004-156P
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	VV	VV
32	Chr-0X	FF	VV	32	FF	FF	VV	VV

Charles River Genetic Testing Services, Wilmington

**Rat 32-SNP Panel Batch 180831NGC: University of Hong Kong,
Lab Animal Unit - LTM Order 2018008423**

Order Sample Detail

Date Samples Received: 30-Aug-2018

Date Samples Tested: 31-Aug-2018

Sample #-Code	Room	Strain-Line	Breed Colony
001-141P	SPFBA 213	LEW (Lewis)	Nucleus
002-146P	SPFBA 213	LEW (Lewis)	Issue
003-151P	SPFBA 213	DA (Dark Agouti)	Nucleus
004-156P	SPFBA 213	DA (Dark Agouti)	Issue