

## Charles River Genetic Testing Services, Wilmington

**Mouse 32-SNP Panel Batch QC\_171221BS: University of Hong Kong, Lab Animal Unit - LTM Order 2017009560**

### *Percent Match of Allelic Profiles to Expected Profile for Strain*

Order-Set	Facility-Room	Colony Strain	Ref Strain	N	Call Rate	% Match	# of Samples
2017009560-01	MDA-LAU 118	NOD.CB17-Prkdscid/J (NOD SCID)	<b>NODSCID: 0142</b>	128	91.4%	<b>100.0%</b>	2
2017009560-02	SPFBA 207	C57BL/6N x CBA/Ca F1	<b>B6CBACA: 0503</b>	64	100.0%	<b>100.0%</b>	1
2017009560-03	SPFBA 208	C57BL/6J	<b>B6: 0053</b>	192	100.0%	<b>100.0%</b>	3
2017009560-04	SPFBA 208	FVB/N	<b>FVB: 0110</b>	127	100.0%	<b>100.0%</b>	2
2017009560-05	SPFBA 208	CBA/Ca	<b>CBACa: 0041</b>	128	100.0%	<b>100.0%</b>	2
2017009560-06	SPFBA 209	C57BL/6N	<b>B6: 0053</b>	192	99.0%	<b>100.0%</b>	3
2017009560-07	SPFBA 210	BALB/cAnN-nu (Nude)	<b>BALBc: 0022</b>	128	97.7%	<b>100.0%</b>	2
2017009560-08	SPFBA 212	BALB/cAnN-nu (Nude)	<b>BALBc: 0022</b>	128	100.0%	<b>100.0%</b>	2
2017009560-09	SPFBA 211	CB17/Icr-scid (SCID)	<b>CB17: 0055</b>	192	100.0%	<b>100.0%</b>	3
2017009560-10	SPFBA 214	BALB/c01aHsd	<b>BALBc: 0022</b>	192	100.0%	<b>100.0%</b>	3
2017009560-11	SPFBA 234B	CB17/IcrHsd-PrkdscidLystbg (SCID Beige)	<b>CB17: 0055</b>	192	100.0%	<b>100.0%</b>	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 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%.

**RESULT SUMMARY:** The Percent Match of the sample allelic profiles to their respective strain reference profiles were 100%, indicating that the mice tested were purebred.

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# Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch QC\_171221BS: University of Hong Kong, Lab Animal  
Unit - LTM Order 2017009560

## Order Sample Detail

Date Samples Received: 13-Dec-2017

Date Samples Tested: 21-Dec-2017

Sample #-Code	Room	Strain-Line	Breed Colony
001-301P	MDA-LAU 118	NOD.CB17-Prkdescid/J (NOD SCID)	Nucleus
002-306P	MDA-LAU 118	NOD.CB17-Prkdescid/J (NOD SCID)	Issue
003-311P	SPFBA 207	C57BL/6N x CBA/Ca F1	Issue
004-316P	SPFBA 208	C57BL/6J	Nucleus
005-321P	SPFBA 208	C57BL/6J	Production
006-326P	SPFBA 208	C57BL/6J	Issue
007-331P	SPFBA 208	FVB/N	Nucleus
008-336P	SPFBA 208	FVB/N	Issue
009-341P	SPFBA 208	CBA/Ca	Nucleus
010-346P	SPFBA 208	CBA/Ca	Issue
011-351P	SPFBA 209	C57BL/6N	Nucleus
012-356P	SPFBA 209	C57BL/6N	Production
013-361P	SPFBA 209	C57BL/6N	Issue
014-366P	SPFBA 210	BALB/cAnN-nu (Nude)	TL*
015-371P	SPFBA 212	BALB/cAnN-nu (Nude)	Nucleus
016-376P	SPFBA 212	BALB/cAnN-nu (Nude)	Production
017-381P	SPFBA 210	BALB/cAnN-nu (Nude)	Issue
018-386P	SPFBA 211	CB17/Icr-scid (SCID)	Nucleus
019-391P	SPFBA 211	CB17/Icr-scid (SCID)	Production
020-396P	SPFBA 211	CB17/Icr-scid (SCID)	Issue
021-401P	SPFBA 214	BALB/c01aHsd	Nucleus
022-406P	SPFBA 214	BALB/c01aHsd	Production
023-411P	SPFBA 214	BALB/c01aHsd	Issue
024-416P	SPFBA 234B	CB17/IcrHsd-PrkdescidLystbg (SCID Beige Nucleus	
025-421P	SPFBA 234B	CB17/IcrHsd-PrkdescidLystbg (SCID Beige Production	
026-426P	SPFBA 234B	CB17/IcrHsd-PrkdescidLystbg (SCID Beige Issue	

\* Traffic Light Animals

## Charles River Genetic Testing Services, Wilmington

Rat 32-SNP Panel Batch QC\_171219BS: University of Hong Kong, Lab Animal Unit - LTM Order 2017009845

### *Percent Match of Allelic Profiles to Expected Profile for Strain*

Order-Set	Area	Colony Strain	Ref Strain	Sample	Breed Colony	Values		
						N	Call Rate	% Match
2017009845-01	SPFBA	LEW (Lewis)	LEW: 0011	001-431P	N	64	100.0%	100.0%
				002-436P	I	64	100.0%	100.0%
2017009845-02	SPFBA	DA (Dark Agouti)	DA-HK: 0045	003-441P	N	64	96.9%	100.0%
				004-446P	I	64	93.8%	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.

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**Rat 32-SNP Panel Batch QC\_171219BS: University of Hong Kong, Lab  
Animal Unit - LTM Order 2017009845**

**Allelic Profiles (Red = Mismatch)**

SNP #	Chr #	LEW: 0011	DA-HK: 0045	SNP #	LEW (Lewis)		DA (Dark Agouti)	
					002-436P	001-431P	003-441P	004-446P
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	NC
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

**Rat 32-SNP Panel Batch QC\_171219BS: University of Hong Kong, Lab  
Animal Unit - LTM Order 2017009845**

## *Order Sample Detail*

**Date Samples Received: 13-Dec-2017**

**Date Samples Tested: 19-Dec-2017**

<b>Sample #-Code</b>	<b>Room</b>	<b>Strain-Line</b>	<b>Breed Colony</b>
<b>001-431P</b>	<b>SPFBA 213</b>	LEW (Lewis)	Nucleus
<b>002-436P</b>	<b>SPFBA 213</b>	LEW (Lewis)	Issue
<b>003-441P</b>	<b>SPFBA 213</b>	DA (Dark Agouti)	Nucleus
<b>004-446P</b>	<b>SPFBA 213</b>	DA (Dark Agouti)	Issue