

Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch QC_150817KB: University of Hong Kong Lab Animal Unit-SPFBA

Percent Match of Allelic Profiles to Expected Profile for Strain

| Order-Set | Area | Colony | Ref Strain | N | Call Rate | % Match | # of Samples |
|---------------|---------|------------------|-----------------------|-----|-----------|---------|--------------|
| 2015049206-02 | Rm.207 | C57BL/6Nx CBA/Ca | B6CBACA: 0503 | 64 | 100.0% | 100.0% | 1 |
| 2015049206-03 | Rm.207 | 129x1/SvJ | 129X1SvJ: 0007 | 128 | 100.0% | 100.0% | 2 |
| 2015049206-04 | Rm.208 | FVB/N | FVB: 0110 | 128 | 100.0% | 100.0% | 2 |
| 2015049206-05 | Rm.208 | CBA/Ca | CBACa: 0041 | 192 | 100.0% | 100.0% | 3 |
| 2015049206-06 | Rm.209 | C57/BL/6N | B6: 0053 | 192 | 100.0% | 100.0% | 3 |
| 2015049206-07 | Rm.211 | BALB/cAnN-nu | BALBc: 0022 | 192 | 100.0% | 100.0% | 3 |
| 2015049206-08 | Rm.212 | C.B-17/lcr-scld | CB17: 0055 | 191 | 93.7% | 100.0% | 3 |
| 2015049206-09 | Rm.214 | BALB/c | BALBc: 0022 | 192 | 100.0% | 100.0% | 3 |
| 2015049206-10 | Rm.234B | SCID Beige | CB17: 0055 | 192 | 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 V V or F F at each SNP marker, whereas F1 hybrids may be heterozygous V F. 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: For all colonies, the Percent Match of the allelic profiles of the mice tested to their expected profiles were 100%, indicating that the test mice were authentic.

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
Order: 2015049206

Arrival: 2-Sep-2015
Approved: 22-Sep-2015

| Customer | | | | | | |
|----------|------|---------|---|----------|------|------------|
| Lab # | Code | Species | Strain/Line | Facility | Room | Colony |
| 3 | 311P | Mouse | F1 (C57BL/6N x CBA/Ca) | SPFBA | 207 | Issue |
| 4 | 316P | Mouse | 129X1/SvJ | SPFBA | 207 | Nucleus |
| 5 | 321P | Mouse | 129X1/SvJ | SPFBA | 207 | Issue |
| 6 | 326P | Mouse | FVB/N | SPFBA | 208 | Nucleus |
| 7 | 331P | Mouse | FVB/N | SPFBA | 208 | Issue |
| 8 | 336P | Mouse | CBA/Ca | SPFBA | 208 | Nucleus |
| 9 | 341P | Mouse | CBA/Ca | SPFBA | 208 | Production |
| 10 | 346P | Mouse | CBA/Ca | SPFBA | 208 | Issue |
| 11 | 351P | Mouse | C57BL/6N | SPFBA | 209 | Nucleus |
| 12 | 356P | Mouse | C57BL/6N | SPFBA | 209 | Production |
| 13 | 361P | Mouse | C57BL/6N | SPFBA | 209 | Issue |
| 14 | 366P | Mouse | BALB/cAnN-nu (Nude) | SPFBA | 211 | Nucleus |
| 15 | 371P | Mouse | BALB/cAnN-nu (Nude) | SPFBA | 211 | Production |
| 16 | 376P | Mouse | BALB/cAnN-nu (Nude) | SPFBA | 211 | Issue |
| 17 | 381P | Mouse | C.B-17/Icr-scld (SCID) | SPFBA | 212 | Nucleus |
| 18 | 386P | Mouse | C.B-17/Icr-scld (SCID) | SPFBA | 212 | Production |
| 19 | 391P | Mouse | C.B-17/Icr-scld (SCID) | SPFBA | 212 | Issue |
| 20 | 396P | Mouse | BALB/c | SPFBA | 214 | Nucleus |
| 21 | 401P | Mouse | BALB/c | SPFBA | 214 | Production |
| 22 | 406P | Mouse | BALB/c | SPFBA | 214 | Issue |
| 23 | 411P | Mouse | C.B-17/IcrHsd-Prkdc scld Lyst bg (SCID Beige) | SPFBA | 234B | Nucleus |
| 24 | 416P | Mouse | C.B-17/IcrHsd-Prkdc scld Lyst bg (SCID Beige) | SPFBA | 234B | Production |
| 25 | 421P | Mouse | C.B-17/IcrHsd-Prkdc scld Lyst bg (SCID Beige) | SPFBA | 234B | Issue |

Rat 32-SNP Panel Batch QC_150918KB: University of Hong Kong Lab Animal Unit-SPFBA
Percent Match of Allelic Profiles to Expected Profile for Strain

Facility University of Hong Kong Lab Animal Unit-SPFBA
Call Max (Multiple Items)

| Order-Set | Room | Colony | Reference Strain Code | Sample ID- | Values | | |
|---------------|---------|------------------|-----------------------|------------|--------|-----------|---------|
| | | | | | N | Call Rate | % Match |
| 2015049207-01 | Rm. 213 | LEW (Lewis) | LEW: 0011 | 001-426P | 64 | 98.4% | 100.0% |
| | | | | 002-431P | 64 | 96.9% | 100.0% |
| 2015049207-02 | Rm. 213 | DA (Dark Agouti) | DA: 0036 | 003-436P | 64 | 96.9% | 96.7% |
| | | | | 004-441P | 64 | 96.9% | 96.7% |

GENERAL INFORMATION: A 32 single nucleotide polymorphism (SNP) panel was employed to generate allelic profiles of the test rats 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 COMMENTS: The Percent Match of the allelic profiles of rats 001-426P and 002-431P to the LEW reference profile were both 100%, indicating that these rats were authentic. The DA rats 003-436P and 004-441P had identical allelic profiles consisting of 17 FF, 14 VV, and 0 VF genotypes and 1 no-call (NC) at SNP 31; the common allelic profile of rats 003-436P and 004-441P showed a 96.7% match with our DA reference profile, with a single mismatch at SNP marker 3.

To discuss results, please contact Bill Shek, DVM, PhD (Office: +1-781-222-6442; email: william.shek@crl.com)

Rat 32-SNP Panel Batch QC_150918KB: University of Hong Kong Lab Animal Unit-SPFBA

Allelic Profiles (**Red = Mismatch**)

| SNP # | Chr # | LEW: 0011 | DA: 0036 | SNP # | LEW (Lewis) | | DA (Dark Agouti) | |
|-------|--------|-----------|----------|-------|-------------|----------|------------------|-----------|
| | | | | | 001-426P | 002-431P | 003-436P | 004-441P |
| 1 | Chr-01 | FF | FF | 1 | FF | FF | FF | FF |
| 2 | Chr-01 | VV | FF | 2 | VV | VV | FF | FF |
| 3 | Chr-02 | VV | VV | 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 | NC | 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
Order: 2015049207

Arrival: 2-Sep-2015
Approved: 22-Sep-2015

| Lab # | Customer Code | Species | Strain/Line | Facility | Room | Colony |
|--------------|----------------------|----------------|---------------------------|-----------------|-------------|---------------|
| 26 | 426P | Rat | LEW (<i>Lewis</i>) | SPFBA | 213 | Nucleus |
| 27 | 431P | Rat | LEW (<i>Lewis</i>) | SPFBA | 213 | Nucleus |
| 28 | 436P | Rat | DA (<i>Dark Agouti</i>) | SPFBA | 213 | Nucleus |
| 29 | 441P | Rat | DA (<i>Dark Agouti</i>) | SPFBA | 213 | Nucleus |

Charles River Genetic Testing Services, Wilmington

Mouse 32-SNP Panel Batch QC_150817KB: University of Hong Kong Lab Animal Unit-MDA-LAU

Percent Match of Allelic Profiles to Expected Profile for Strain

| Order-Set | Area | Colony | Ref Strain | N | Call Rate | % Match | # of Samples |
|---------------|--------|----------|---------------|-----|-----------|---------|--------------|
| 2015049206-01 | Rm.118 | 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 V V or F F at each SNP marker, whereas F1 hybrids may be heterozygous V F. 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 allelic profiles of the NOD SCID mice tested to the expected profile were 100%, indicating that the mice were authentic.

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
Order: 2015049206

Arrival: 2-Sep-2015
Approved: 22-Sep-2015

| Customer | | | | | | |
|-----------------|-------------|----------------|----------------------------------|-----------------|-------------|---------------|
| Lab # | Code | Species | Strain/Line | Facility | Room | Colony |
| 1 | 301P | Mouse | NOD.CB17-Prkdc scid/J (NOD SCID) | MDA-LAU | 118 | Nucleus |
| 2 | 306P | Mouse | NOD.CB17-Prkdc scid/J (NOD SCID) | MDA-LAU | 118 | Issue |