



2022015873

Notes: Lab. No. 1P, 6P, Location: Minimal Disease Experimental Holding Area – (MDA) Resubmission of Order #2022011008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (13-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|------------------------------|--------------|------------|-----|--------------|------------|------------------|-----------------------|
| 13 A3, 13 B2, 13 C3 | Male | | | | | 1P, Rm.G10 (NSG) | pass |
| 13 A2-4, 13 B1-2, 13 C2-2 | Male, Female | | | | | 6P, Rm.G10 (NSG) | pass |

Remarks

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. A "Pass" results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively.

Referenced to strain NODSCID. 11Jan2023 RM.



2022015874

Notes: Lab. No. 11P, 16P, Location: Minimal Disease Experimental Holding Area – (MDA) Resubmission of Order #202211008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (13-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|---------------------------------------------------------|--------------|------------|-----|--------------|------------|------------------------|-----------------------|
| 11 A1, 11 B3, 11 C3, 11 D1, 11 E3 | Male, Female | | | | | 11P, Rm.G10 (NOD SCID) | pass |
| 11 A3-4, 11 B4-1, 11 C2-5, 11 D3-5, 11 E2-5 | Male, Female | | | | | 16P, Rm.G10 (NOD SCID) | pass |

Remarks 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. A “Pass” results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively.

Referenced to strain NODSCID. 11Jan2023 RM.



2022015875

Notes: Lab. No. 21P, 26P, Location: Specific Pathogen Free Breeding Area– (SPFBA)Resubmission of Order #202211008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (29-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|---------------------------------------------------------------------------------------|--------|------------|-----|--------------|------------|----------------------|-----------------------|
| Code: 66A3, Code: 66B4, Code: 66C1, Code: 66D2, Code: 66E2 | Male | | | | | 21P, Rm.207 (CBA/Ca) | pass |
| P. Code: 66A3, P. Code: 66B4, P. Code: 66C1, P. Code: 66D2, P. Code: 66E2 | Female | | | | | 26P, Rm.207 (CBA/Ca) | pass |

Remarks 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. A “Pass” results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively

Referenced to strain CBACa. 26Jan2023 RM.



2022015876

Notes: Lab. No. 31P, 36P, 41P, Location: Specific Pathogen Free Breeding Area– (SPFBA) Resubmission of Order #202211008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (29-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|--------------------------------------------------------------------------------------------------|--------------|------------|-----|--------------|------------|------------------------|-----------------------|
| Code: 17A5, Code: 17B2, Code: 17C3, Code: 17D4, Code: 17E1 | Male | | | | | 31P, Rm.208 (C57BL/6J) | pass |
| Code: TL17A3, Code: TL17B5, Code: TL16C8R, Code: TL16D1, Code: TL16E8 | Male, Female | | | | | 36P, Rm.208 (C57BL/6J) | pass |
| P. Code: TL17A3, P. Code: TL17B5, P. Code: TL16C8R, P. Code: TL16D1, P. Code: TL16E8 | Female | | | | | 41P, Rm.208 (C57BL/6J) | pass |

Remarks

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. A “Pass” results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively.

Referenced to strain B6. 26Jan2023 RM.



2022015877

Notes: Lab. No. 46P, 51P, 56P, Location: Specific Pathogen Free Breeding Area– (SPFBA)Resubmission of Order #2022011008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (29-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|--------------------------------------------------------------------------------------|--------------|------------|-----|--------------|------------|--------------------|-----------------------|
| Code: 49A5, Code: 49B3, Code: 49C5, Code: 49D3, Code: 49E4 | Male, Female | | | | | 46P, Rm.211 (SCID) | pass |
| Code: TL37A3, Code: TL37B10, Code: TL37C7, Code: TL37D8, Code: TL37E9 | Male, Female | | | | | 51P, Rm.211 (SCID) | pass |
| P. Code: TL37A3, P. Code: TL37B10, P. Code: TL37C7, P. Code: TL37D8, P. Code: TL37E9 | Female | | | | | 56P, Rm.211 (SCID) | pass |

Remarks 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. A “Pass” results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively.

Referenced to strain CB17. 26Jan2023 RM.



2022015878

Notes: Lab. No. 61P, 66P, Location: Specific Pathogen Free Breeding Area– (SPFBA)Resubmission of Order #2022011008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (29-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|-----------------------------------------------------------------------------------|--------|------------|-----|--------------|------------|------------------------|-----------------------|
| Code: 1N6, Code: 1N9, Code: 1N4, Code: 1N2, Code: 1N1 | Male | | | | | 61P, Rm.204 (IVC SCID) | pass |
| P. Code: 1N6, P. Code: 1N9, P. Code: 1N4 , P. Code: 1N2, P. Code: 1N1 | Female | | | | | 66P, Rm.204 (IVC SCID) | pass |

Remarks 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. A “Pass” results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively.

Referenced to strain CB17. 26Jan2023 RM.



2022015879

Notes: Lab. No. 76P, 81P, 86P, 91P, Location: Specific Pathogen Free Breeding Area– (SPFBA)Resubmission of Order #2022011008

Samples Arrived: 20-Dec-2022

Service: GM

Approved By: Crispo, Nancy (29-Jan-2023) Nancy.Crispo@crl.com

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| Parental ID | Sex | Generation | DOB | Breed Scheme | Coat Color | Sample | Mouse 32-SNP QC Panel |
|-------------------------------------------------------------------------------------|--------|------------|-----|--------------|------------|------------------------|-----------------------|
| Code: 1N12, Code: 1N23, Code: 1N13, Code: 1N42, Code: 1N39 | Male | | | | | 76P, Rm.204 (IVC Nude) | pass |
| Code: TL1F1, Code: TL1F4, Code: TL1F5, Code: TL1F6, Code: TL1F7 | Male | | | | | 81P, Rm.204 (IVC Nude) | pass |
| Code: SH5, Code: S16, Code: SJ5, Code: SK4, Code: SL10 | Male | | | | | 86P, Rm.204 (IVC Nude) | pass |
| P. Code: SH5a, P. Code: S16b, P. Code: SJ5a, P. Code: SK4a, Code: SL10a | Female | | | | | 91P, Rm.204 (IVC Nude) | pass |

Remarks

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. A “Pass” results indicates that the sample tested purebred based on the call rate and percent match levels exceeding 60% and 98.0%, respectively.

Referenced to strain BALB/c. 11Jan2023 RM.