# Supplementary File 1.

Supplementary File 1a. Genotypes of offspring from *Naa10+/-* female mice crossed to the *Naa10+/Y* male mice.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype****(Expected Mendelian %)** | **Naa10+/Y or Naa10+/+ (50%)** | **Naa10+/- (25%)** | **Naa10-/Y (25%)** |
| **E10.5 (n=134)** | **62 (46.3%)** | **39 (29.1%)** | **33 (24.6%)** |
| **E13.5 (n=98)** | **53 (54.1%)** | **22 (22.4%)** | **23 (23.4%)** |
| **E18.5 (n=170)** | **82 (48.2%)** | **49 (28.8%)** | **39 (23.0%)** |
| **Adults (n=733)** | **438 (59.8%)** | **207 (28.2%)** | **88 (12.0%)** |

Expected and observed Mendelian ratio of genotypes in offspring at E10.5, E13.5, E18.5 and adults from crosses of *Naa10+/-* female and *Naa10+/Y* male mice. The percentage of adult *Naa10-/Y*mice significantly decreases.

Supplementary File b. Genotypes of offspring from *Naa10+/tm1a* female mice crossed to the *Naa10+/Y* male mice.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype****(Expected Mendelian %)** | **Naa10+/Y or****Naa10+/+ (50%)** | **Naa10+/tm1a (25%)** | **Naa10tm1a/Y (25%)** |
| **E10.5 (n=109)** | **55 (50.46%)** | **26 (23.85%)** | **28 (25.69%)** |
| **E12.5 (n=45)** | **20 (44.4%)** | **12 (26.7%)** | **13 (28.9%)** |
| **E18.5 (n=53)** | **27 (51.0%)** | **13 (24.5%)** | **13 (24.5%)** |
| **Adults (n=260)** | **152 (58.5%)** | **85 (32.7%)** | **23 (08.8%)** |

Expected and observed Mendelian ratio of genotypes in offspring at E10.5, E13.5, E18.5 and adults from crosses of *Naa10+/tm1a* female and *Naa10+/Y* male mice. The percentage of adults *Naa10tm1a/Y* mice significantly decreases.

Supplementary File c. Cervical fusion skeletal analyses in *Naa10* KO mice.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **genotype** | **sample size** | **one or more****fusion events** | **two or more****fusion events** | **consecutive****fusion events** | **C1+2 fusion** | **C2+3 fusion** | **C3+4 fusion** | **C4+5 fusion** | **C5+6 fusion** | **C6+7 fusion** | **C7+ T1 fusion** | **T1+2 fusion** |
| ***Naa10+/Y*** | **19** | **2/17 (12%)** | **1/17 (6%)** | **0/17****(0%)** | **2/17 (12%)** | **0/18 (0%)** | **0/18 (0%)** | **0/19 (0%)** | **0/19 (0%)** | **0/19 (0%)** | **1/19 (5%)** | **0/19 (0%)** |
| ***Naa10+/+*** | **4** | **1/4 (25%)** | **0/4****(0%)** | **0/4****(0%)** | **1/4 (25%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** |
| ***Naa10+/-*** | **4** | **1/4 (25%)** | **0/4****(0%)** | **0/4****(0%)** | **1/4 (25%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** | **0/4****(0%)** |
| ***Naa10-/Y*** | **9** | **9/10 (90%)** | **3/9 (33%)** | **1/9****(11%)** | **7/10 (70%)** | **2/9 (22%)** | **2/9 (22%)** | **1/9 (11%)** | **0/9****(0%)** | **0/9****(0%)** | **1/9 (11%)** | **0/9****(0%)** |
| ***Naa10-/-*** | **1** | **1/1 (100%)** | **1/1 (100%)** | **1/1****(100%)** | **1/1 (100%)** | **1/1 (100%)** | **0/1****(0%)** | **0/1****(0%)** | **0/1****(0%)** | **0/1****(0%)** | **0/1****(0%)** | **0/1****(0%)** |

Supplementary File d. Matings and litter size analyses.

|  |  |
| --- | --- |
| ***Naa10* KO matings, all WT/WT for Naa12, all >99.6% C57BL/6J** | **Naa10 x Naa12 matings,****mixed genetic background** |
| **Genotypes of breeders (♀ x ♂)** | ***Naa10+/+* x*****Naa10+/Y*** | ***Naa10+/+* x*****Naa10-/Y*** | ***Naa10+/-* x *Naa10+/Y*** | ***Naa10+/-* x*****Naa10-/Y*** | ***Naa10-/-* x*****Naa10-/Y*** | ***Naa10-/-* x *Naa10+/Y*** | **Naa10+/- Naa12+/+****x****Naa10+/Y Naa12+/-** | **Naa10+/- Naa12+/+****x****Naa10+/Y Naa12-/-** |
| **#pups** | **255** | **18** | **330** | **59** | **59** | **127** | **214** | **252** |
| **#litters** | **39** | **2** | **66** | **13** | **11** | **31** | **43** | **64** |
| **#pups/****#litters, or litter size** | **6.5** | **9.0** | **5.0** | **4.5** | **5.4** | **4.1** | **5.0** | **3.9** |
| **SD of litter size** | **3.2** | **0.0** | **2.2** | **2.5** | **2.5** | **2.1** | **2.1** | **2.0** |
| **% Died in 1st three days of life** | **5.1%** | **5.6%** | **15.8%** | **13.6%** | **42.4%** | **36.0%** | **16.8%** | **36%** |
| **% of total that died by****weaning ~4 weeks** | **5.9%** | **11.1%** | **23.0%** | **32.2%** | **59.3%** | **44.0%** | **20.0%** | **42%** |
| **Avg Length of Mating till 1st****Litter:** | **29** | **22** | **34** | **25** | **35** | **28** | **26** | **34** |
| **Total number of unique****mating males:** | **7** | **1** | **12** | **5** | **6** | **7** | **13** | **16** |
| **Total number of mating pairs****set up:** | **8** | **1** | **>16** | **14** | **10** | **11** | **22** | **17** |
| **Total number of mating pairs with progeny** | **7** | **1** | **N/A** | **7** | **4** | **11** | **21** | **15** |
| **% females who became pregnant and gave birth at****least once:** | **87.5%** | **100.0%** | **N/A** | **50.0%** | **40.0%** | **100.0%** | **95.5%** | **88.2%** |

Supplementary File e. Genotypes of offspring from *Naa12+/-* female mice crossed to the *Naa12+/-* male mice.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype****(Expected Mendelian %)** | **Naa12+/+****(25%)** | **Naa12+/-****(50%)** | **Naa12-/-****(25%)** |
| **Adults (n=117)** | 26 (22%) | 62 (53%) | 29 (25%) |

Expected and observed Mendelian ratio of genotypes in offspring from crosses.

Supplementary File f. Genotypes of offspring from *Naa10+/-* *Naa12+/+* female mice crossed to the *Naa10+/y Naa12+/-* male mice.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Genotype****(Expected Mendelian %)** | ***Naa10(+/y)* *Naa12(+/-)* males****(12.5%)** | ***Naa10(-/y)*** ***Naa12(+/-)* males****(12.5%)** | ***Naa10(+/y)* *Naa12(+/+)* males****(12.5%)** | ***Naa10(-/y) Naa12(+/+)* males****(12.5%)** |
| **Newborn pups (n=214)** | 27 (12.6%) | 0 (0%) | 33 (15.4%) | 21 (9.8%) |
| **Genotype****(Expected Mendelian %)** | ***Naa10(+/-)* *Naa12(+/+)* females****(12.5%)** | ***Naa10(+/+)*** ***Naa12(+/+)* females****(12.5%)** | ***Naa10(+/-)******Naa12(+/-)* females****(12.5%)** | ***Naa10(+/+)* *Naa12(+/-)* females****(12.5%)** |
|  | 31 (14.5%) | 33 (15.4%) | 9 (4.2%) | 41 (19.2%) |
| **Early neonatal death, unable to genotype = 19 (8.9%)** |

Expected and observed Mendelian ratio of genotypes in offspring from crosses.

Supplementary File g. Genotypes of offspring from *Naa10+/-* *Naa12+/+* female mice crossed to the *Naa10+/y Naa12-/-* male mice.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Genotype****(Expected Mendelian %)** | **NAA10+/Y NAA12+/-****male (25%)** | **NAA10-/Y NAA12+/-****male (25%)** | **NAA10+/+ NAA12+/-****female (25%)** | **NAA10+/- NAA12+/-female (25%)** |
| **Newborn pups (n=252\*)** | 78 (31%) | 0 (0%) | 83 (33%) | 36 (14%) |
| **\*Early neonatal death, unable to genotype = 55 (22%)** |

Expected and observed Mendelian ratio of genotypes in offspring from crosses.

Supplementary File h. Mendelian and Observed Offspring Distributions from Naa10(+/Y); Naa12(+/-) Male and Naa10(+/-); Naa12(+/-) Female Breeding

|  |  |  |
| --- | --- | --- |
|  | **Mendelian Genotype Distribution (%)** | **Observed Number (% Genotyped)** |
| **#\*** | **Offspring Genotypes** | **F** | **M** | **Total** | **E10.5** | **E18.5** | **Postnatal** |
| 1 | Naa10 (+/+), Naa12 (+/+) | 6.25 |  | 6.25 |  2 (6.9) |  5 (15.2) |  16 (10.2) |
| 2 | Naa10 (+/+), Naa12 (+/-) | 12.50 |  | 12.50 |  4 (13.8) |  7 (21.2) |  28 (17.8) |
| 3 | Naa10 (+/+), Naa12 (-/-) | 6.25 |  | 6.25 |  3 (10.3) |  1 (3.0) |  16 (10.2) |
| 4 | Naa10 (+/-), Naa12 (+/+) | 6.25 |  | 6.25 |  3 (10.3) |  1 (3.0) |  14 (8.9) |
| 5 | Naa10 (+/-), Naa12 (+/-) | 12.50 |  | 12.50 |  6 (20.7) |  5 (15.2) |  5 (3.2) |
| 6 | Naa10 (+/-), Naa12 (-/-) | 6.25 |  | 6.25 |  2 (6.9) |  0 (0.0) |  0 (0.0) |
| 7 | Naa10 (+/Y), Naa12 (+/+) |  | 6.25 | 6.25 |  1 (3.4) |  4 (12.1) |  17 (10.8) |
| 8 | Naa10 (+/Y), Naa12 (+/-) |  | 12.50 | 12.50 |  1 (3.4) |  5 (15.2) |  31 (19.7) |
| 9 | Naa10 (+/Y), Naa12 (-/-) |  | 6.25 | 6.25 |  3 (10.3) |  3 (9.1) |  17 (10.8) |
| 10 | Naa10 (-/Y), Naa12 (+/+) |  | 6.25 | 6.25 |  0 (0.0) |  1 (3.0) |  17 (8.3) |
| 11 | Naa10 (-/Y), Naa12 (+/-) |  | 12.50 | 12.50 |  4 (13.8) |  1 (3.0) |  0 (0.0) |
| 12 | Naa10 (-/Y), Naa12 (-/-) |  | 6.25 | 6.25 |  0 (0.0) |  0 (0.0) |  0 (0.0) |
|  | **TOTAL (% Genotyped)** | **50.0** | **50.0** | **100.0** |  **29 (99.8)** |  **33 (100.0)** |  **157 (99.9)** |
|  | **Not Genotyped (% Total)** |  |  |  |  **3 (9.4)** |  **23 (41.1)** |  **0 (0.0)** |
|  | **TOTAL**  | **50.0** | **50.0** | **100.0** |  **32** |  **56** |  **157**  |

F = Female; M = Male
\*Genotypes in subsequent tables are numbered according to this table, which includes all possible genotypes from all crosses considered.

Supplementary File i. Mendelian and Observed Offspring Distributions from Naa10(+/Y); Naa12(-/-) Male and Naa10(+/-); Naa12(+/-) Female Breeding

|  |  |  |
| --- | --- | --- |
|  | **Mendelian Genotype Distribution (%)** | **Observed Number (% Genotyped)** |
| **#\*** | **Offspring Genotypes** | **F** | **M** | **Total** | **E8.5** | **E10.5** | **E12.5** | **E18.5** | **Postnatal** |
| 2 | Naa10 (+/+), Naa12 (+/-) | 12.5 |  | 12.5 |  4 (19.0) |  3 (10.7) |  4 (16.0) |  2 (18.2) |  45 (25.1) |
| 3 | Naa10 (+/+), Naa12 (-/-) | 12.5 |  | 12.5 |  6 (28.6) |  8 (28.6) |  1 (4.0) |  2 (18.2) |  35 (19.6) |
| 5 | Naa10 (+/-), Naa12 (+/-) | 12.5 |  | 12.5 |  2 (9.5) |  8 (28.6) |  7 (28.0) |  3 (27.3) |  12 (6.7) |
| 6 | Naa10 (+/-), Naa12 (-/-) | 12.5 |  | 12.5 |  1 (4.8) |  1 (3.6) |  0 (0.0) |  0 (0.0) |  0 (0.0) |
| 8 | Naa10 (+/Y), Naa12 (+/-) |  | 12.5 | 12.5 |  1 (4.8) |  3 (10.7) |  7 (28.0) |  0 (0.0) |  40 (22.3) |
| 9 | Naa10 (+/Y), Naa12 (-/-) |  | 12.5 | 12.5 |  7 (33.3) |  4 (14.3) |  6 (24.0) |  4 (36.4) |  47 (26.3) |
| 11 | Naa10 (-/Y), Naa12 (+/-) |  | 12.5 | 12.5 |  0 (0.0) |  1 (3.6) |  0 (0.0) |  0 (0.0) |  0 (0.0) |
| 12 | Naa10 (-/Y), Naa12 (-/-) |  | 12.5 | 12.5 |  0 (0.0) |  0 (0.0) |  0 (0.0) |  0 (0.0) |  0 (0.0) |
| **TOTAL (% Genotyped)** | **50.0** | **50.0** | **100.0** |  **21 (100.0)** |  **28 (100.1)** |  **25 (100.0)** |  **11 (100.1)** |  **179 (100.0)** |
| **Not Genotyped (% Total)** |  |  |  |  **4 (16.0)** |  **12 (30.0)** |  **19 (43.2)** |  **7 (38.9)** |  **2 (1.1)** |
| **TOTAL**  | **50.0** | **50.0** | **100.0** |  **25** |  **40** |  **44** |  **18** |  **181**  |

F = Female; M = Male
\*Genotypes in this table are numbered according to **Supplement File 1h**, which includes all possible genotypes from all crosses considered.

Supplementary File j. Mendelian and Observed Postnatal Offspring Distributions from Naa10(+/Y); Naa12(+/-) Male and Naa10(+/-); Naa12(+/+) Female Breeding

|  |  |  |
| --- | --- | --- |
|  | **Mendelian Genotype Distribution (%)** | **Observed Number (% Genotyped)** |
| **#\*** | **Offspring Genotypes** | **F** | **M** | **Total** | **Postnatal** |
| 1 | Naa10 (+/+), Naa12 (+/+) | 12.5 |  | 12.5 |  33 (16.9) |
| 2 | Naa10 (+/+), Naa12 (+/-) | 12.5 |  | 12.5 |  41 (21.0) |
| 4 | Naa10 (+/-), Naa12 (+/+) | 12.5 |  | 12.5 |  31 (15.9) |
| 5 | Naa10 (+/-), Naa12 (+/-) | 12.5 |  | 12.5 |  9 (4.6) |
| 7 | Naa10 (+/Y), Naa12 (+/+) |  | 12.5 | 12.5 |  33 (16.9) |
| 8 | Naa10 (+/Y), Naa12 (+/-) |  | 12.5 | 12.5 |  27 (13.8) |
| 10 | Naa10 (-/Y), Naa12 (+/+) |  | 12.5 | 12.5 |  21 (10.8) |
| 11 | Naa10 (-/Y), Naa12 (+/-) |  | 12.5 | 12.5 |  0 (0.0) |
| **Total (% Genotyped)** |  |  |  |  **195 (99.9)** |
| **Not Genotyped (% Total)** |  |  |  |  **19 (8.9)** |
| **TOTAL** | **50.0** | **50.0** | **100.0** |  **214** |

F = Female; M = Male
\*Genotypes in this table are numbered according to **Supplement File 1h**, which includes all possible genotypes from all crosses considered.

Supplementary File k. Mendelian and Observed Postnatal Offspring Distributions from Naa10(+/Y); Naa12(-/-) Male and Naa10(+/-); Naa12(+/+) Female Breeding

|  |  |  |
| --- | --- | --- |
|  | **Mendelian Genotype Distribution (%)** | **Observed Number (% Genotyped)** |
| **#\*** | **Offspring Genotypes** | **F** | **M** | **Total** | **Postnatal** |
| 2 | Naa10 (+/+), Naa12 (+/-) | 25.0 |  | 25.0 |  83 (42.1) |
| 5 | Naa10 (+/-), Naa12 (+/-) | 25.0 |  | 25.0 |  36 (18.3) |
| 8 | Naa10 (+/Y), Naa12 (+/-) |  | 25.0 | 25.0 |  78 (39.6) |
| 11 | Naa10 (-/Y), Naa12 (+/-) |  | 25.0 | 25.0 |  0 (0.0) |
| **Total (% Genotyped)** |  |  |  |  **197 (100.0)** |
| **Not Genotyped (% Total)** |  |  |  |  **55 (21.8)** |
| **TOTAL** | **50.0** | **50.0** | **100.0** |  **252** |

F = Female; M = Male
\*Genotypes in this table are numbered according to **Supplement File 1h**, which includes all possible genotypes from all crosses considered.

Supplementary File l. Mendelian and Observed Age-Specific Offspring Distributions from Four Crosses

|  |  |
| --- | --- |
|  | **Observed Number at Age (% Genotyped)** |
| **#\*** | **Offspring Genotypes** | **E8.5** | **E10.5** | **E12.5** | **E18.5** | **Postnatal** |
| 1 | Naa10 (+/+), Naa12 (+/+) |  |  2 (3.5) |  |  5 (11.4) |  16 (4.8) |
| 2 | Naa10 (+/+), Naa12 (+/-) |  4 (19.0) |  7 (12.3) |  4 (16.0) |  9 (20.5) |  73 (21.7) |
| 3 | Naa10 (+/+), Naa12 (-/-) |  6 (28.6) |  11 (19.3) |  1 (4.0) |  3 (6.8) |  51 (15.2) |
| 4 | Naa10 (+/-), Naa12 (+/+) |  |  3 (5.3) |  |  1 (2.3) |  14 (4.2) |
| 5 | Naa10 (+/-), Naa12 (+/-) |  2 (9.5) |  14 (24.6) |  7 (28.0) |  8 (18.2) |  17 (5.1) |
| 6 | Naa10 (+/-), Naa12 (-/-) |  1 (4.8) |  3 (5.3) |  0 (0.0) |  0 (0.0) |  0 (0.0) |
| 7 | Naa10 (+/Y), Naa12 (+/+) |  |  1 (1.8) |  |  4 (9.1) |  17 (5.1) |
| 8 | Naa10 (+/Y), Naa12 (+/-) |  1 (4.8) |  4 (7.0) |  7 (28.0) |  5 (11.4) |  71 (21.1) |
| 9 | Naa10 (+/Y), Naa12 (-/-) |  7 (33.3) |  7 (12.3) |  6 (24.0) |  7 (15.9) |  64 (19.0) |
| 10 | Naa10 (-/Y), Naa12 (+/+) |  |  0 (0.0) |  |  1 (2.3) |  13 (3.9) |
| 11 | Naa10 (-/Y), Naa12 (+/-) |  0 (0.0) |  5 (8.8) |  0 (0.0) |  1 (2.3) |  0 (0.0) |
| 12 | Naa10 (-/Y), Naa12 (-/-) |  0 (0.0) |  0 (0.0) |  0 (0.0) |  0 (0.0) |  0 (0.0) |
| **TOTAL (% Genotyped)** |  **21 (100.0)** |  **57 (100.2)** |  **25 (100.0)** |  **44 (100.2)** |  **336 (100.0)** |

F = Female; M = Male
\*Genotypes in this table are numbered according to **Supplement File 1h**, which includes all possible genotypes from all crosses considered.

Supplementary File m. Mendelian and Observed Cumulative Offspring Distributions from All Four Crosses

|  |  |
| --- | --- |
|  | **Cumulative Observed Number (% Genotyped)** |
| **#\*** | **Offspring Genotypes** | **E8.5** | **E10.5** | **E12.5** | **E18.5** | **Postnatal** |
| 1 | Naa10 (+/+), Naa12 (+/+) |  |  2 (2.6) |  2 (1.9) |  7 (4.8) |  23 (4.8) |
| 2 | Naa10 (+/+), Naa12 (+/-) |  4 (19.0) |  11 (14.1) |  15 (14.6) |  24 (16.3) |  97 (20.1) |
| 3 | Naa10 (+/+), Naa12 (-/-) |  6 (28.6) |  17 (21.8) |  18 (17.5) |  21 (14.3) |  72 (14.9) |
| 4 | Naa10 (+/-), Naa12 (+/+) |  |  3 (3.8) |  3 (2.9) |  4 (2.7) |  18 (3.7) |
| 5 | Naa10 (+/-), Naa12 (+/-) |  2 (9.5) |  16 (20.5) |  23 (22.3) |  31 (21.1) |  48 (9.9) |
| 6 | Naa10 (+/-), Naa12 (-/-) |  1 (4.8) |  4 (5.1) |  4 (3.9) |  4 (2.7) |  4 (0.8) |
| 7 | Naa10 (+/Y), Naa12 (+/+) |  |  1 (1.3) |  1 (1.0) |  5 (3.4) |  22 (4.6) |
| 8 | Naa10 (+/Y), Naa12 (+/-) |  1 (4.8) |  5 (6.4) |  12 (11.7) |  17 (11.6) |  88 (18.2) |
| 9 | Naa10 (+/Y), Naa12 (-/-) |  7 (33.3) |  14 (17.9) |  20 (19.4) |  21 (18.4) |  91 (18.8) |
| 10 | Naa10 (-/Y), Naa12 (+/+) |  |  0 (0.0) |  0 (0.0) |  1 (0.7) |  14 (2.9) |
| 11 | Naa10 (-/Y), Naa12 (+/-) |  0 (0.0) |  5 (6.4) |  5 (4.9) |  6 (4.1) |  6 (1.2) |
| 12 | Naa10 (-/Y), Naa12 (-/-) |  0 (0.0) |  0 (0.0) |  0 (0.0) |  0 (0.0) |  0 (0.0) |
| **TOTAL (% Genotyped)** |  **21 (100.0)** |  **78 (99.9)** |  **103 (100.0)** |  **147 (100.2)** |  **483 (99.9)** |

F = Female; M = Male
\*Genotypes in this table are numbered according to **Supplement File 1h**, which includes all possible genotypes from all crosses considered.

Supplementary File n. Mice analyzed by weighing, according to genotype.

|  |
| --- |
| **Females** |
|  | **Naa12 status** |
| **WT/WT** | **WT/KO** | **KO/KO** | **Total** |
| **Naa10 status** | **Pure C57BL/6J background****Naa10 mice** | **WT/WT** | **67** | **N/A** | **N/A** | **67** |
| **WT/KO** | **125** | **N/A** | **N/A** | **125** |
| **KO/KO** | **15** | **N/A** | **N/A** | **15** |
| **Subtotal** | **207** | **N/A** | **N/A** | **207** |
| **mixed genetic background Naa10 and Naa12 mice** | **WT/WT** | **32** | **82** | **10** | **124** |
| **WT/KO** | **35** | **23** | **0** | **58** |
| **KO/KO** | **0** | **0** | **0** | **0** |
| **Subtotal** | **67** | **105** | **10** | **182** |
| **Total** | **274** | **105** | **10** | **389** |

|  |
| --- |
| **Males** |
|  | **Naa12 status** |
| **WT/WT** | **WT/KO** | **KO/KO** | **Total** |
| **Naa10 status** | **Pure C57BL/6J background****Naa10 mice** | **WT** | **97** | **N/A** | **N/A** | **97** |
| **KO** | **70** | **N/A** | **N/A** | **70** |
| **Subtotal** | **167** | **N/A** | **N/A** | **167** |
| **mixed genetic background Naa10 and Naa12 mice** | **WT** | **44** | **63** | **11** | **118** |
| **KO** | **14** | **0** | **0** | **14** |
| **Subtotal** | **58** | **63** | **11** | **132** |
| **Total** | **225** | **63** | **11** | **299** |

Supplementary File o. Effects of *Naa10* KO on growth rate of *Naa10* mice on pure genetic background.

|  |  |
| --- | --- |
|  | **C57BL/6J inbred females (N = 207)** |
| **Effect of age and age2** | **Effect of Naa10 KO** | **Effect of age and Naa10 KO** | **Effect of age,** **Naa10 KO,****and interaction** |
| **Coeff.** | **SE** | **z** | **p > |z|** | **Coeff.** | **SE** | **z** | **p > |z|** | **Coeff.** | **SE** | **z** | **p > |z|** | **Coeff.** | **SE** | **z** | **p > |z|** |
| **Age in days** | **0.349** | **0.006** | **59.49** | **< 0.001** |  |  |  |  | **0.349** | **0.006** | **59.38** | **< 0.001** | **0.344** | **0.010** | **34.59** | **< 0.001** |
| **Age2** | **- 0.001** | **0.00003** | **- 40.59** | **< 0.001** |  |  |  |  | **- 0.001** | **0.00003** | **- 40.56** | **< 0.001** | **- 0.001** | **0.00005** | **- 24.53** | **< 0.001** |
| **Naa10 KO** |  |  |  |  | **- 2.92** | **0.847** | **- 3.45** | **0.001** | **- 0.252** | **0.248** | **- 1.01** | **ns** | **- 0.219** | **0.451** | **- 0.49** | **ns** |
| **Age x KO** |  |  |  |  |  |  |  |  |  |  |  |  | **0.009** | **0.012** | **0.75** | **ns** |
| **Age2 x KO** |  |  |  |  |  |  |  |  |  |  |  |  | **-0.00009** | **0.00007** | **-1.27** | **ns** |
| **(constant)** | **2.518** | **0.204** | **12.35** | **< 0.001** | **17.23** | **0.690** | **24.96** | **< 0.001** | **2.697** | **0.272** | **9.93** | **< 0.001** | **2.633** | **0.382** | **6.90** | **< 0.001** |
| **Wald *X*2 a** | **6547.29, p < 0.0001** | **11.93, p = 0.0006** | **6552.24, p < .0001** | **6611.63, p < 0.0001** |

|  |  |
| --- | --- |
|  | **C57BL/6J inbred males (N = 167)** |
| **Effect of age and age2** | **Effect of Naa10 KO** | **Effect of age and Naa10 KO** | **Effect of age,** **Naa10 KO,****and interaction** |
| **Coeff.** | **SE** | **z** | **p > |z|** | **Coeff.** | **SE** | **z** | **p > |z|** | **Coeff.** | **SE** | **z** | **p > |z|** | **Coeff.** | **SE** | **z** | **p > |z|** |
| **Age in days** | **0.454** | **0.008** | **60.16** | **< 0.001** |  |  |  |  | **0.454** | **0.007** | **62.20** | **< 0.001** | **0.467** | **0.009** | **51.68** | **< 0.001** |
| **Age2** | **- 0.002** | **0.00005** | **- 39.76** | **< 0.001** |  |  |  |  | **-0.002** | **0.00004** | **- 41.16** | **< 0.001** | **- 0.002** | **0.00005** | **- 34.53** | **< 0.001** |
| **Naa10 KO** |  |  |  |  | **- 4.721** | **1.040** | **- 4.54** | **< 0.001** | **-2.578** | **0.304** | **- 8.47** | **< 0.001** | **- 1.351** | **0.504** | **- 2.68** | **0.007** |
| **Age x KO** |  |  |  |  |  |  |  |  |  |  |  |  | **- 0.035** | **0.015** | **- 2.32** | **0.020** |
| **Age2 x KO** |  |  |  |  |  |  |  |  |  |  |  |  | **0.0001** | **0.00009** | **1.46** | **ns** |
| **(constant)** | **1.303** | **0.271** | **4.81** | **< 0.001** | **19.56** | **0.668** | **29.28** | **< 0.001** | **2.430** | **0.283** | **8.58** | **< 0.001** | **1.931** | **0.321** | **6.01** | **< 0.001** |
| **Wald *X*2 a** | **7220.56, p < 0.0001** | **20.60, p < 0.0001** | **8007.09, p < 0.0001** | **8185.75, p < 0.0001** |

a The Wald *X*2 is a measure of the overall goodness of fit of the complete model.

Supplementary File p. Effects of *Naa10* and *Naa12* Kos on growth rate on mixed genetic background

|  |  |
| --- | --- |
|  | **females (N = 182): effects of age and knockouts on weight** |
| **Effect of age and age2** | **Effects of age****and Naa10 KO** | **Effects of age****and Naa12 KO** | **Effects of age,****Naa10 & Naa12 Kos** | **Effects: age,****Naa10, Naa12, both Kos** |
|  | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** |
| **Age** | **.** | **0.011** | **43.10** | **< 0.001** | **0.489** | **0.011** | **45.02** | **< 0.001** | **0.489** | **0.011** | **43.25** | **< 0.001** | **0.491** | **0.011** | **46.16** | **< 0.001** | **0.492** | **0.011** | **46.49** | **< 0.001** |
| **Age2** | **-0.003** | **0.0001** | **-24.47** | **< 0.001** | **-0.003** | **0.0001** | **-25.58** | **< 0.001** | **-0.003** | **0.0001** | **-24.55** | **< 0.001** | **-0.003** | **0.0001** | **-26.21** | **< 0.001** | **-0.003** | **0.0001** | **-26.45** | **< 0.001** |
| **Naa10** |  |  |  |  | **-1.117** | **0.254** | **-4.40** | **< 0.001** |  |  |  |  | **-1.424** | **0.267** | **-5.33** | **< 0.001** | **-0.368** | **0.335** | **-1.10** | **ns** |
| **Naa12-****Het** |  |  |  |  |  |  |  |  | **-0.377** | **0.247** | **-1.53** | **ns** | **-0.789** | **0.255** | **-3.09** | **0.002** | **0.039** | **0.287** | **0.14** | **ns** |
| **Naa12-****Ho** |  |  |  |  |  |  |  |  | **-0.659** | **0.625** | **-1.05** | **ns** | **-1.376** | **0.621** | **-2.21** | **0.027** |  |  |  |  |
| **Naa10-Naa12-****Het** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | **-2.143** | **0.510** | **-4.20** | **< 0.001** |
| **(constant)** | **0.616** | **0.264** | **2.33** | **0.020** | **0.966** | **0.267** | **3.61** | **< 0.001** | **0.825** | **0.291** | **2.83** | **0.005** | **1.508** | **0.307** | **4.91** | **< 0.001** | **0.879** | **0.307** | **2.86** | **0.004** |
| **Wald *X*2 a** | **4692.14, p < 0.0001** | **5116.03, p < 0.0001** | **4752.14, p < 0.0001** | **5396.11, p < 0.0001** | **5461.46, p < 0.0001** |

|  |  |
| --- | --- |
|  | **females (N = 182): effects of age and knockouts on growth rate** |
| **Effects of age, Naa10 KO, interaction with age** | **Effects of age, Naa12 KO, interaction with age** | **Effects of age, both Kos & interaction with age** | **Effects: age, Kos & interaction with ea. Other** |
|  | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** | **Coeff** | **SE** | **z** | **p > |z|** |
| **Age** | **0.508** | **0.013** | **39.24** | **< 0.001** | **0.491** | **0.015** | **32.64** | **< 0.001** | **0.523** | **0.018** | **29.09** | **< 0.001** | **0.496** | **0.011** | **46.35** | **< 0.001** |
| **Age2** | **-0.003** | **0.0001** | **-22.76** | **< 0.001** | **-0.003** | **0.0002** | **-17.97** | **< 0.001** | **-0.003** | **0.0002** | **-16.71** | **< 0.001** | **-0.003** | **0.0001** | **-26.24** | **< 0.001** |
| **Naa10** | **0.109** | **0.547** | **0.20** | **ns** |  |  |  |  | **0.030** | **0.582** | **0.05** | **ns** | **-0.364** | **0.336** | **-1.08** | **ns** |
| **Agex Naa10** | **-0.059** | **0.023** | **-2.51** | **0.012** |  |  |  |  | **-0.068** | **0.025** | **-2.76** | **0.006** |  |  |  |  |
| **Age2 x Naa10** | **0.0006** | **0.0002** | **2.25** | **0.024** |  |  |  |  | **0.0006** | **0.0003** | **2.46** | **0.014** |  |  |  |  |
| **Naa12-Het** |  |  |  |  | **-0.175** | **0.547** | **-0.32** | **ns** | **-0.099** | **0.557** | **-0.18** | **ns** | **0.036** | **0.288** | **0.13** | **ns** |
| **Agex Naa12-Het** |  |  |  |  | **-0.005** | **0.023** | **-0.23** | **ns** | **-0.029** | **0.023** | **-1.23** | **ns** |  |  |  |  |
| **Age2 x Naa12-****Het** |  |  |  |  | **0.000004** | **0.0002** | **0.02** | **ns** | **0.0002** | **0.0002** | **0.97** | **ns** |  |  |  |  |
| **Naa12-Ho** |  |  |  |  | **-0.882** | **1.584** | **-0.56** | **ns** | **-0.916** | **1.551** | **-0.59** | **ns** |  |  |  |  |
| **Agex Naa12-Ho** |  |  |  |  | **0.003** | **0.073** | **0.04** | **ns** | **-0.029** | **0.071** | **-0.41** | **ns** |  |  |  |  |
| **Age2 x Naa12-Ho** |  |  |  |  | **0.00003** | **0.0007** | **0.04** | **ns** | **0.0003** | **0.001** | **0.47** | **ns** |  |  |  |  |
| **Naa10-Naa12-Het** |  |  |  |  |  |  |  |  |  |  |  |  | **0.784** | **1.303** | **0.60** | **ns** |
| **Agex** **Naa10-Naa12-Het** |  |  |  |  |  |  |  |  |  |  |  |  | **-0.113** | **0.052** | **-2.15** | **0.031** |
| **Age2 x** **Naa10-Naa12-Het** |  |  |  |  |  |  |  |  |  |  |  |  | **0.0009** | **0.0005** | **1.73** | **ns** |
| **(constant)** | **0.588** | **0.305** | **1.93** | **ns** | **0.756** | **0.348** | **2.17** | **0.030** | **0.790** | **0.426** | **1.85** | **ns** | **0.774** | **0.309** | **2.50** | **0.012** |
| **Wald *X*2 a** | 5224.04, p < 0.0001 | 4758.89, p < 0.0001 | 5526.71, p < 0.0001 | 5586.86, p < 0.0001 |

Het : heterozygous
Ho : homozygous
a The Wald *X*2 is a measure of the overall goodness of fit of the complete model.