Viability Primary Screen IMPC_VIA_002

Purpose

To assess the postnatal viability, sub-viability, and lethality of mice of each zygosity and sex during cohort production.

Experimental Design

- Monitor genotypes of at least 28 live offspring from a specified breeding strategy (i.e. HetXHet). A single breeding strategy should be used per procedure so that totals of pups can be grouped together. If another breeding strategy is used for some litters, please submit a separate procedure, distinguished by sequence id.
- Record age of pups at genotype (P1-P28).
- (Optional) Record the age of the youngest and oldest female parents when cohort breeding starts.
- Record raw numbers of live pups of each sex/zygosity combination.
- Identify viability/subviability/lethality of zygosities/sexes by application of a percentage-based derivations.
- The viability calls are only made where the parental cross is Het x Het for autosomal genes and Het x Hemi for the X-linked genes. Hemizygous male viability is also calculated from WT x Hemi cross.
- If homozygous lethal: perform the embryonic lethal pipeline (if available).

Procedure

1. Determine gene category (see Notes below).
2. Select breeding strategy to generate phenotyping cohort for a colony.
3. Genotype all live pups and record numbers of each sex/zygosity for a minimum of 28 pups. If possible, record pups grouped by litter, along with the parental IDs and date of birth for each litter. Record all three parents for trio matings. Where litter data is not available, group these pups together as the “noLitter” group.
4. Submit numbers to seriesParameters. Include zeros for all categories where no pups were recorded, even if they were not expected. Do not submit values to the derived total or outcome parameters (see example submission file).
    a. Where litter data is available, submit each litter as a single increment of all “Number of…” parameters. Include parental IDs and dates of birth where possible. Use a unique identifier for each litter as the incrementValue. Trios matings are indicated by the presence of a second female parentID; otherwise, omit this ID.
    b. Where litter data is not available, submit pups grouped together as a single increment of all “Number of…” parameters, using incrementValue=”noLitter”. Omit the litter date of birth for this group. “unknown” can be submitted for parentalIDs for this group (or any litter where the parent cannot be identified).
5. Identify strains that produce no homozygous/hemizygous male or female pups.

   a. Homozygous animal viability call is calculated for both sexes of autosomal genes and females of X-linked genes.
   b. Heterozygous animal viability call is calculated for both sexes of autosomal genes.
   c. Hemizygous male viability call is calculated for males for X-linked genes based on the total number of pups.
   d. For sex specific homozygous viability calls, 28 pups of that particular sex are required.
6. Strains that produce <25% expected (#totalpups * 0.125 (3 for 28) (4 for 29-36) (5 for 37-52) homozygous pups will be considered SUBVIABLE (partial preweaning lethality [MP: 0011110]).

Notes

Anzygous is a term to describe the zygosity of a female animal for a gene on the Y-chromosome i.e. no copies of the gene expected. As with all sex/zygosity categories, please report zeros for all litters/colonies where no animals of this type were found, even if they were not expected from that breeding strategy.

Gene category should be available from production labs at each centre. It can be ascertained for most genes by searching NCBI gene. Any gene on a numbered chromosome is autosomal. Contact production labs or DCC data wranglers for assistance.

Parameters and Metadata

Gene category IMPC_VIA_034_001 | v1.0

procedureMetadata

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Description: Type of gene inheritance pattern

Options: Autosomal, X chromosome, Y chromosome, Pseudoautosomal,

---

Male parents genotype IMPC_VIA_035_001 | v1.0

procedureMetadata

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Description: Genotype of male parent(s)

Options: WT, Heterozygous, Homozygous, Hemizygous,

Female parents genotype IMPC_VIA_036_001 | v1.0

procedureMetadata

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Description: Genotype of female parent(s)

Options: WT, Heterozygous, Homozygous, Anzygous,

Litter male parent specimen id IMPC_VIA_037_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Description: ID of male parent of litter

Increments: Minimum 1

Litter female parent 1 specimen id IMPC_VIA_038_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Description: ID of female parent

Increments: Minimum 1

Litter female parent 2 specimen id IMPC_VIA_039_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Description: ID of optional second female parent for trio matings

Increments: Minimum 1

Litter date of birth IMPC_VIA_040_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Description: Date of birth of litter

Increments: Minimum 1

Number of WT males IMPC_VIA_041_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of wild-type males in litter, or total wild-type males if litter data is not available

Increments: Minimum 1

Number of WT females IMPC_VIA_042_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of wild-type females in litter, or total wild-type females if litter data is not available

Increments: Minimum 1

Number of heterozygous males IMPC_VIA_043_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of heterozygous males in litter, or total heterozygous males if litter data is not available

Increments: Minimum 1

Number of heterozygous females IMPC_VIA_044_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of heterozygous females in litter, or total heterozygous females if litter data is not available

Increments: Minimum 1

Number of homozygous males IMPC_VIA_045_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of homozygous males in litter, or total homozygous males if litter data is not available

Increments: Minimum 1

Number of homozygous females IMPC_VIA_046_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of homozygous females in litter, or total homozygousfe males if litter data is not available

Increments: Minimum 1

Number of hemizygous males IMPC_VIA_047_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of hemizygous males in litter, or total hemizygous males if litter data is not available

Increments: Minimum 1

Number of anzygous females IMPC_VIA_048_001 | v1.0

seriesParameter

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: count

Description:
Number of anzygous (i.e. no copies of gene as it is Y-chromosome) females in litter, or total anzygous females if litter data is not available

Increments: Minimum 1

Total WT males IMPC_VIA_049_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total wild-type males

Derivation: sumOfIncrements('IMPC_VIA_041_001', 1)

Total WT females IMPC_VIA_050_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total wild-type females

Derivation: sumOfIncrements('IMPC_VIA_042_001', 1)

Total heterozygous males IMPC_VIA_051_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total heterozygous males

Derivation: sumOfIncrements('IMPC_VIA_043_001', 1)

Total heterozygous females IMPC_VIA_052_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total heterozygous females

Derivation: sumOfIncrements('IMPC_VIA_044_001', 1)

Total homozygous males IMPC_VIA_053_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total homozygous males

Derivation: sumOfIncrements('IMPC_VIA_045_001', 1)

Total homozygous females IMPC_VIA_054_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total homozygous males

Derivation: sumOfIncrements('IMPC_VIA_046_001', 1)

Total of hemizygous males IMPC_VIA_055_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total hemizygous males

Derivation: sumOfIncrements('IMPC_VIA_047_001', 1)

Total anzygous females IMPC_VIA_056_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total anzygous (i.e. no copies of gene as it is Y-chromosome) females

Derivation: sumOfIncrements('IMPC_VIA_048_001', 1)

Total pups IMPC_VIA_057_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total pups

Derivation:
sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1))

Total WTs IMPC_VIA_058_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total wild-type pups

Derivation:
sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1))

Total heterozygotes IMPC_VIA_059_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total heterozygous pups

Derivation:
sum(sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1))

Total homozygotes IMPC_VIA_060_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total homozygous pups

Derivation:
sum(sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1))

Total males IMPC_VIA_061_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total male pups

Derivation:
sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1))

Total females IMPC_VIA_062_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: count

Description: Total female pups

Derivation:
sum(sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1))

Female age earliest start IMPC_VIA_026_001 | v1.1

procedureMetadata

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: Weeks

Female age oldest end IMPC_VIA_027_001 | v1.1

procedureMetadata

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Unit Measured: Weeks

Age of pups at genotype IMPC_VIA_030_001 | v1.1

procedureMetadata

Req. Analysis: false **Req. Upload:** true **Is Annotated:** false

Unit Measured: Weeks

Homozygous males viability IMPC_VIA_063_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** true

Description: Outcome of viability assessment for homozygous males

Derivation:
ifElse(sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1)) >= 28, ifElse(strEquals('IMPC_VIA_035_001' , 'Heterozygous')=='true' && strEquals('IMPC_VIA_036_001' , 'Heterozygous')=='true' , ifElse(sumOfIncrements('IMPC_VIA_045_001', 1) == 0, 'Homozygous - Lethal', ifElse(mul(div(sumOfIncrements('IMPC_VIA_045_001', 1), sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1))), 100) > 12.5, 'Homozygous - Viable', 'Homozygous - Subviable')), 'Cannot be calculated'), 'Insufficient numbers to make a call')

Homozygous females viability IMPC_VIA_064_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** true

Description: Outcome of viability assessment for homozygous females

Derivation:
ifElse(sum(sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1)) >= 28, ifElse((strEquals('IMPC_VIA_035_001' , 'Heterozygous')=='true' || strEquals('IMPC_VIA_035_001','Hemizygous')=='true') && strEquals('IMPC_VIA_036_001' , 'Heterozygous')=='true', ifElse(sumOfIncrements('IMPC_VIA_046_001', 1) == 0, 'Homozygous - Lethal', ifElse(mul(div(sumOfIncrements('IMPC_VIA_046_001', 1), sum(sumOfIncrements('IMPC_VIA_042_001', 1),   sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1))), 100) > 12.5, 'Homozygous - Viable', 'Homozygous - Subviable')), 'Cannot be calculated'), 'Insufficient numbers to make a call')

Hemizygous males viability IMPC_VIA_065_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** true

Description: Outcome of viability assessment for hemizygous males

Derivation:
ifElse(sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1)) >= 28, ifElse((strEquals('IMPC_VIA_035_001','Hemizygous')=='true' || strEquals('IMPC_VIA_035_001','WT')=='true') && strEquals('IMPC_VIA_036_001' , 'Heterozygous')=='true', ifElse(sumOfIncrements('IMPC_VIA_047_001', 1) == 0, 'Hemizygous - Lethal', ifElse(mul(div(sumOfIncrements('IMPC_VIA_047_001', 1), sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1))), 100) > 12.5, 'Hemizygous - Viable', 'Hemizygous - Subviable')), 'Cannot be calculated'), 'Insufficient numbers to make a call')

Heterozygous animals viability IMPC_VIA_066_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** true

Description: Outcome of viability assessment for heterozygous animals

Derivation:
ifElse(sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1)) >= 28, ifElse(strEquals('IMPC_VIA_035_001' , 'Heterozygous')=='true' && strEquals('IMPC_VIA_036_001' , 'Heterozygous') =='true' , ifElse(sum(sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1)) == 0, 'Heterozygous - Lethal', ifElse(mul(div(sum(sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1)), sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1))), 100) > 25, 'Heterozygous - Viable', 'Heterozygous - Subviable')), 'Cannot be calculated'), 'Insufficient numbers to make a call')

Homozygous animals viability IMPC_VIA_067_001 | v1.0

simpleParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** true

Description: Outcome of viability assessment for homozygous animals

Derivation:
ifElse(sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1)) >= 28, ifElse((strEquals('IMPC_VIA_035_001' , 'Heterozygous')=='true' || strEquals('IMPC_VIA_035_001','Hemizygous')=='true') && strEquals('IMPC_VIA_036_001' , 'Heterozygous')=='true' , ifElse(sum(sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1)) == 0, 'Homozygous - Lethal', ifElse(mul(div(sum(sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1)), sum(sumOfIncrements('IMPC_VIA_041_001', 1), sumOfIncrements('IMPC_VIA_042_001', 1), sumOfIncrements('IMPC_VIA_043_001', 1), sumOfIncrements('IMPC_VIA_044_001', 1), sumOfIncrements('IMPC_VIA_045_001', 1), sumOfIncrements('IMPC_VIA_046_001', 1), sumOfIncrements('IMPC_VIA_047_001', 1), sumOfIncrements('IMPC_VIA_048_001', 1))), 100) > 12.5, 'Homozygous - Viable', 'Homozygous - Subviable')), 'Cannot be calculated'), 'Insufficient numbers to make a call')

Embryo Vignette IMPC_VIA_068_001 | v1.0

mediaParameter

Req. Analysis: false **Req. Upload:** false **Is Annotated:** false

Description: Poster style vignette to highlight the embryo development for a line

---