

# 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 zygositys/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 parentallIDs 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,

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## 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,

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## 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

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## 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

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## **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

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**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

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**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

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## 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

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## 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

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**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

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**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

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**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)

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**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)

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## 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)

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## 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)

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## 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)

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## 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)

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## 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)

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## 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)

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## 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))

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## 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))

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## 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))

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## 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))

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## 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))

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## 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))

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## Female age earliest start IMPC\_VIA\_026\_001 | v1.1

procedureMetadata

Req. Analysis: false

Req. Upload: false

Is Annotated: false

Unit Measured: Weeks

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## Female age oldest end IMPC\_VIA\_027\_001 | v1.1

procedureMetadata

Req. Analysis: false

Req. Upload: false

Is Annotated: false

Unit Measured: Weeks

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## Age of pups at genotype IMPC\_VIA\_030\_001 | v1.1

procedureMetadata

Req. Analysis: false

Req. Upload: true

Is Annotated: false

Unit Measured: Weeks

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## Homozygous males viability IMPC\_VIA\_063\_001 | v1.0

simpleParameter

Req. Analysis: false

Req. Upload: false

Is Annotated: false

**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')
```

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## Homozygous females viability IMPC\_VIA\_064\_001 | v1.0

simpleParameter

**Req. Analysis:** false

**Req. Upload:** false

**Is Annotated:** false

**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')
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## Hemizygous males viability IMPC\_VIA\_065\_001 | v1.0

simpleParameter

Req. Analysis: false

Req. Upload: false

Is Annotated: false

**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')
```

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## Heterozygous animals viability IMPC\_VIA\_066\_001 | v1.0

simpleParameter

Req. Analysis: false

Req. Upload: false

Is Annotated: false

**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')
```

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## Homozygous animals viability IMPC\_VIA\_067\_001 | v1.0

simpleParameter

Req. Analysis: false

Req. Upload: false

Is Annotated: false

**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')
```

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## 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

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