

## Prmt2 (MARU; EPD0197\_1\_C09)

Allele: *Prmt2*<sup>tm1a(EUCOMM)Wtsi</sup>

### Genotyping Information

#### Genotyping by short range PCR (srPCR)

These mice may be genotyped through a combination of separate PCR reactions that detect *LacZ*, the gene-specific wild type allele, and a mutant allele-specific short range PCR. Interpretation of the consolidated results produces the genotype of the mice.

For example: *LacZ* positive, mutant positive, wild type positive = heterozygous.

#### ➤ PCRs primer pairs and expected size bands

| PCR type      | Forward primer | Reverse primer | Expected size band (bp) |
|---------------|----------------|----------------|-------------------------|
| Mutant PCR    | Prmt2_40870_F  | CAS_R1_Term x  | 274                     |
| Wild type PCR | Prmt2_40870_F  | Prmt2_R3       | 357                     |
| LacZ PCR      | LacZ_2_small_F | LacZ_2_small_R | 108                     |

#### ➤ Primer sequences

| Primer name    | Primer sequence (5' > 3') |
|----------------|---------------------------|
| CAS_R1_Term    | TCGTGGTATCGTTATGCGCC      |
| Prmt2_40870_F  | GATCGTCCAGTTCCTACGGG      |
| Prmt2_R3       | GGTCCCTTAGAAGCACAGGT      |
| LacZ_2_small_F | ATCACGACGCGCTGTATC        |
| LacZ_2_small_R | ACATCGGGCAAATAATATCG      |

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➤ **Reaction**

| Reagent                           | μl          |
|-----------------------------------|-------------|
| DNA (~50-100 ng)                  | 1.0         |
| 10x Buffer                        | 2.0         |
| MgCl <sub>2</sub> (50 mM)         | 0.6         |
| PtTaq (Platinum Taq (Invitrogen)) | 0.2         |
| dNTPs (100 mM)                    | 0.2         |
| Primer 1 (10 μM)                  | 0.4         |
| Primer 2 (10 μM)                  | 0.4         |
| H <sub>2</sub> O                  | <u>15.2</u> |
| <b>Total</b>                      | <b>20.0</b> |

➤ **Cycling conditions**

**Wild type and mutant PCRs**

| Cycle | Temp                  | Time    |
|-------|-----------------------|---------|
| 1     | 94 °C                 | 5 min   |
| 2     | 94 °C                 | 30 sec  |
| 3     | 58 °C                 | 30 sec  |
| 4     | 72 °C                 | 45 sec  |
| 5     | Go to '2' + 34 cycles |         |
| 6     | 72 °C                 | 5 min   |
| 7     | 12 °C                 | forever |

**LacZ PCR**

| Cycle | Temp                  | Time    |
|-------|-----------------------|---------|
| 1     | 94 °C                 | 5 min   |
| 2     | 94 °C                 | 30 sec  |
| 3     | 60 °C                 | 30 sec  |
| 4     | 72 °C                 | 30 sec  |
| 5     | Go to '2' + 34 cycles |         |
| 6     | 72 °C                 | 5 min   |
| 7     | 12 °C                 | forever |

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## Genotyping by loss of WT allele qPCR Assay (gene-specific assay)

The wild type loss of allele (WTLoA) qPCR assay uses a hydrolysis probe assay (for example Applied Biosystems TaqMan® technology) to determine the copy number of the wild type allele in a sample. Homozygotes will show no amplification, heterozygotes one copy and wild type mice will show two copies when compared to a wild type control.

The number of copies of the Prmt2 allele can be detected using a FAM-labelled custom qPCR TaqMan® assay. These are multiplexed with a VIC® labelled endogenous control assay (for example TaqMan® Copy Number Reference Assay, Mouse, Tfrc; Applied Biosystems part #4458366). Reference DNA controls of known genotypes should also be included to facilitate correct analysis.

| Forward Primer Name | Forward Primer Seq.      |
|---------------------|--------------------------|
| PRMT2_WT_F          | GCTCATCAATAGTCTCCAGTAGGT |

| Reverse Primer Name | Reverse Primer Seq.     |
|---------------------|-------------------------|
| PRMT2_WT_R          | TGCTTCTAAGGGACCCACAGTTA |

| Reporter 1 Name | Reporter 1 Sequence | Reporter 1 Dye |
|-----------------|---------------------|----------------|
| PRMT2_WT_M      | CCTCTGGTCAAGCGCA    | FAM            |

### ➤ Reaction setup

Reactions are performed in a 10µl volume using an Applied Biosystems 7900HT Fast Real-Time PCR System with DNA prepared using the Sample-to-SNP™ kit (Applied Biosystems) from mouse ear biopsies. GTXpress™ buffer is also used (Applied Biosystems)

|                     | Volume µl |
|---------------------|-----------|
| 2x GTXpress™ buffer | 5         |
| Prmt2_WT 20x assay  | 0.5       |
| ddH2O               | 3         |
| Tfrc 20x assay      | 0.5       |
| DNA                 | 1         |

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➤ **qPCR Cycling conditions**

| Cycle |                       |       |
|-------|-----------------------|-------|
| 1     | 95°C                  | 20sec |
| 2     | 95°C                  | 10sec |
| 3     | 60°C                  | 30sec |
| 4     | Go to '2' + 34 cycles |       |

Results can be analysed using CopyCaller™ software (Applied Biosystems) or RQ Manager (Applied Biosystems). Both packages use the comparative Ct (ddCt) method to perform the analysis.

Other instrument systems will have their own analysis software – please see the manufacturer's guidelines for information about your system.

**Genotyping by Neomycin copy number qPCR Assay (universal assay)**

The *neo* count qPCR assay uses a hydrolysis probe assay (eg Applied Biosystems TaqMan technology) to determine the copy number of the *neo* cassette in a sample. Homozygotes will possess two copies of *neo*, heterozygotes one copy and wild type mice will show no amplification.

Please note that this assay is not gene-specific – other information should be used in conjunction with the *neo* count (for example the mutant-specific srPCR) when assigning the genotype.

| Forward Primer Name | Forward Primer Seq. |
|---------------------|---------------------|
| NeoF                | GGTGGAGAGGCTATTCGGC |

| Reverse Primer Name | Reverse Primer Seq. |
|---------------------|---------------------|
| NeoR                | GAACACGGCGGCATCAG   |

| Reporter 1 Name | Reporter 1 Sequence     | Reporter 1 Dye |
|-----------------|-------------------------|----------------|
| NeoM1           | TGGGCACAACAGACAATCGGCTG | FAM            |

Reaction setup and amplification conditions are the same as those used for the LoA qPCR assay, with the *neo* taking the place of the Prmt2 probe and primers.

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