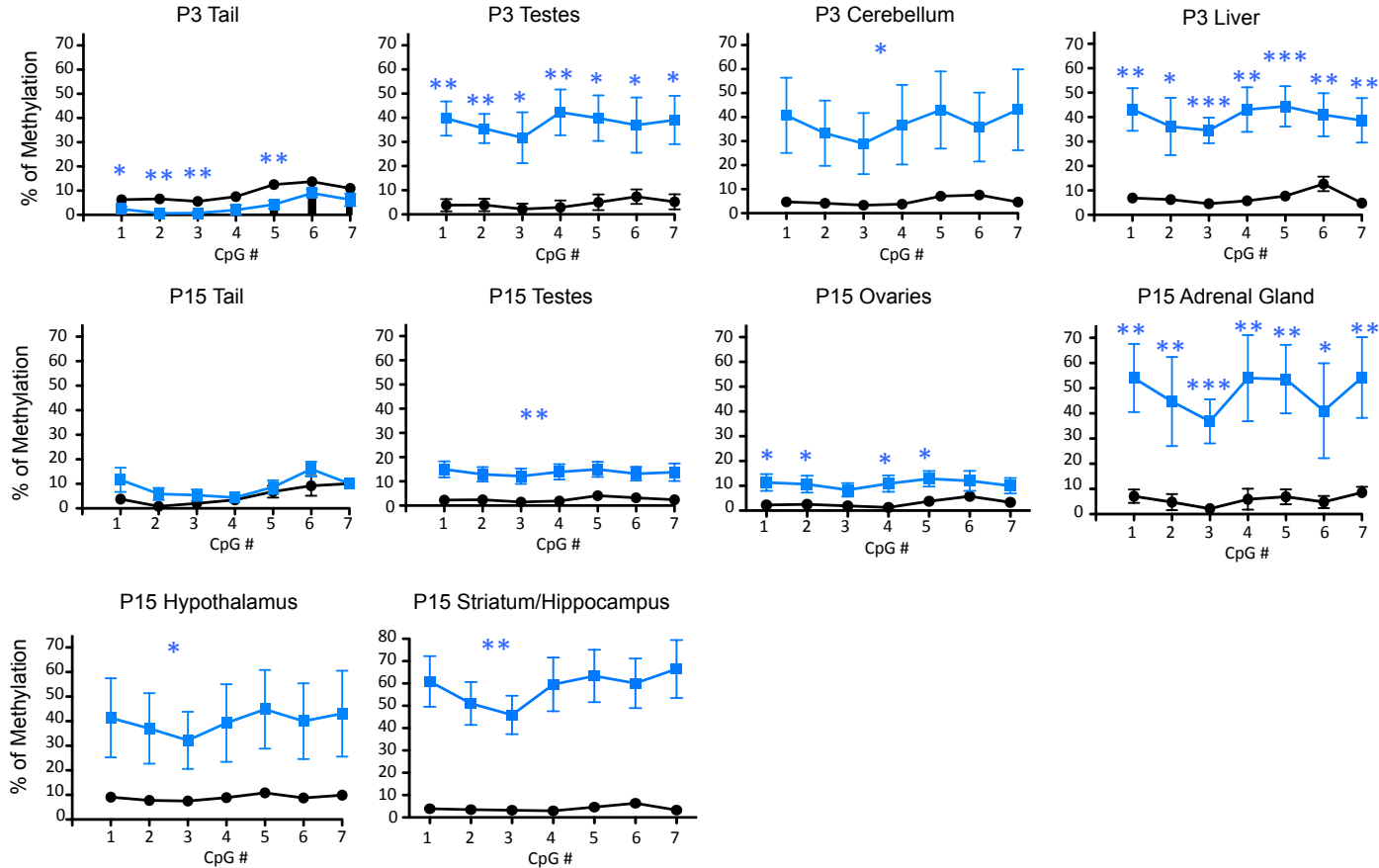


CpG Residues Analyzed in *Meg3* Promoter Region

TACTAGCCGTTTCCTGACGCAGCTACTTTAACAGCGGAAAGAGAGGGCGTCAAAGGCAAATCTAGCCGGAGACCCCCAGATCACAGAGAAGGCTGCGGAACCGGGGGGCA

● *Dio3* +/+ (F0 *Dio3* +/+) ■ *Dio3* +/+ (F0 Paternal grandfather *Dio3* -/-)

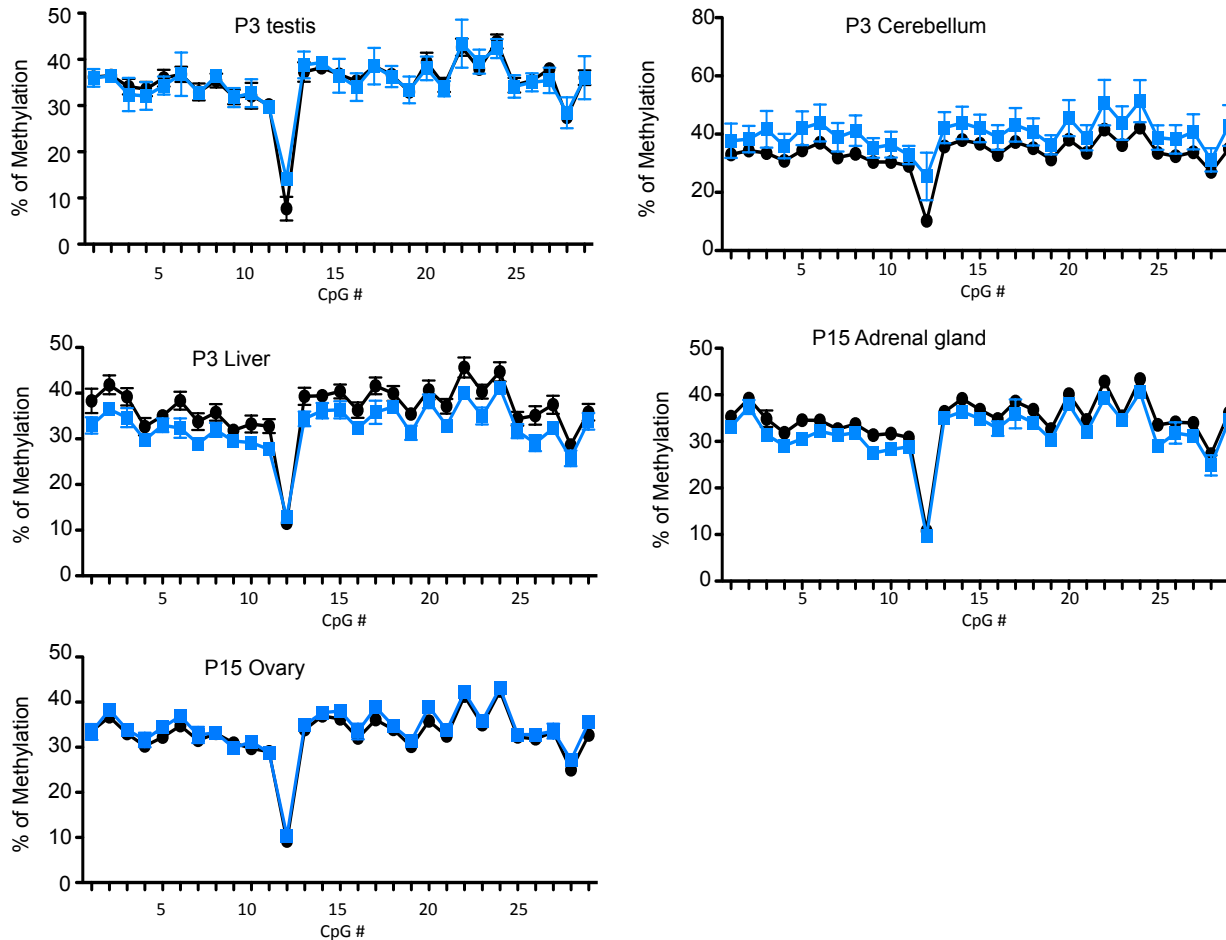


Supplemental Figure 1. Methylation status of individual CpG residues of *Meg3* promoter region. DNA methylation in seven CpG residues of the *Meg3* gene (sequence indicated) in P3 and P15 tissues of wild type control and wild-type PGF mice. Data represent the mean \pm SEM of three to five biological samples from at least three different litters. ***, ** and * indicate $P < 0.001$, $P < 0.01$ and $P < 0.05$, respectively, for individual CpG residues, or for all CpG residues analyzed, as determined by the Student's t-test.

CpG Residues Analyzed in the IG-DMR

AATGCTGCCGTTCCGCTATGAACTACCGCTACCGGTTTCATAGTGGACAGTCAGTGC CGCAGATCGCTATGGACTGGTGCCAAGGTTCCGCCATGGACTAGT
 GC CGCGGACCTCCGTTGAACTAGCGAGGAGGTTCCGCGTGTACTAATGCCGCTT CGCGTACCGCTGTGTA CGCGTGCCCGGAACCGCGTGGAAATTGT
 GCCCGCGTTCCCGTGGAGTAGCGCTGCAGCCGCT

● *Dio3* +/+ (F0 *Dio3* +/+) ■ *Dio3* +/+ (F0 Paternal grandfather *Dio3* -/-)

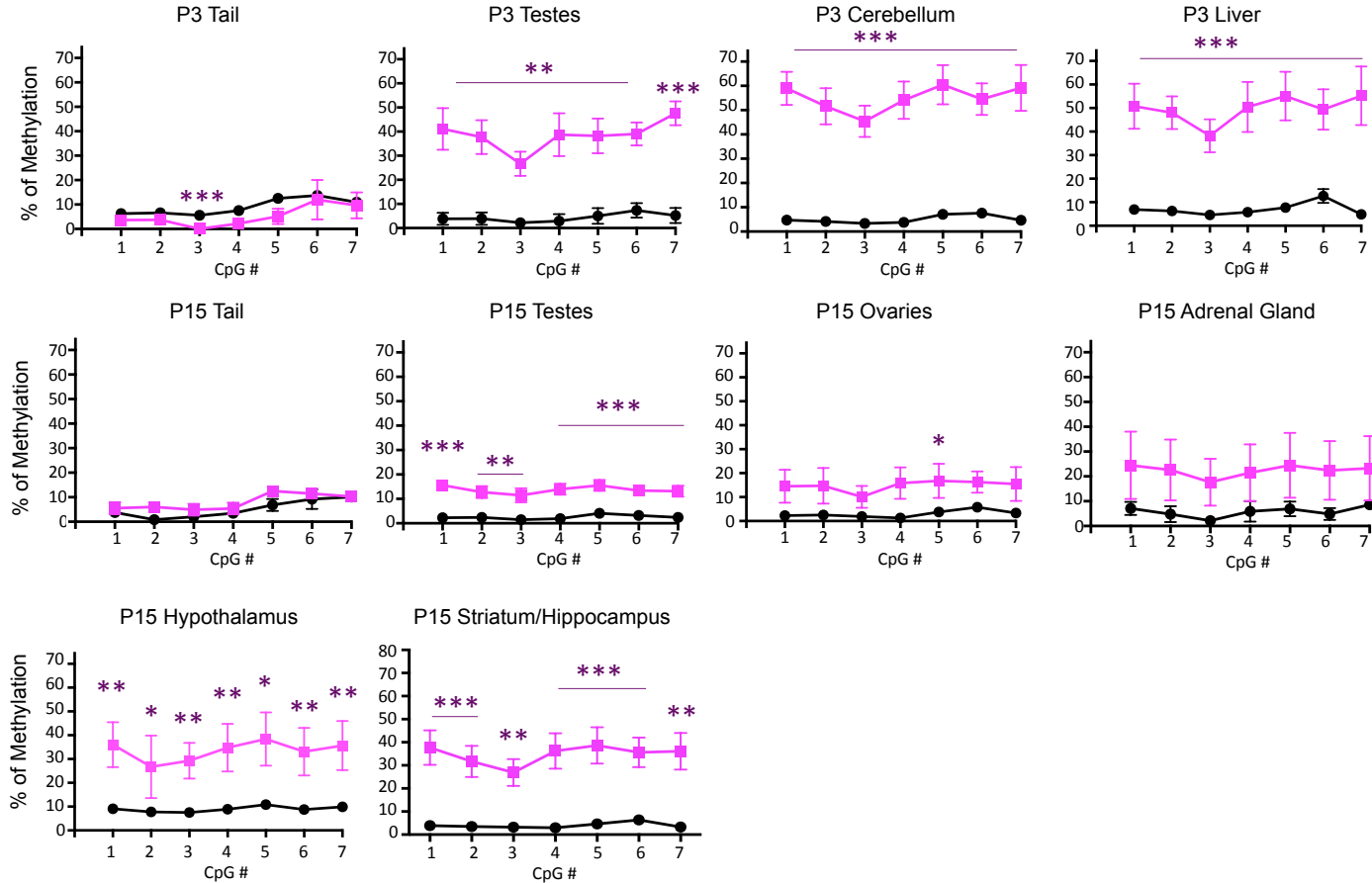


Supplemental Figure 2. Methylation status of individual CpG residues of the intergenic differentially methylated region (IG-DMR). DNA methylation in 29 CpG residues of the IG-DMR gene (sequence indicated) in P3 and P15 tissues of wild type control and wild-type PGF mice. Data represent the mean \pm SEM of three to five biological samples from at least three different litters. We observed no statistically significant difference for any CpG residue in any given tissue, as determined by the Student's t-test.

CpG Residues Analyzed in *Meg3* Promoter Region

TACTAGCCCGTTTCCTGACCGCAGCTACTTTAACAGCGGAAAGAGAGGGCGTCAAAGGCCAAATCTAGCCCGGAGACCCCCAGATCACAGAGAAGGCTGCGGAACCGGGGGGCA

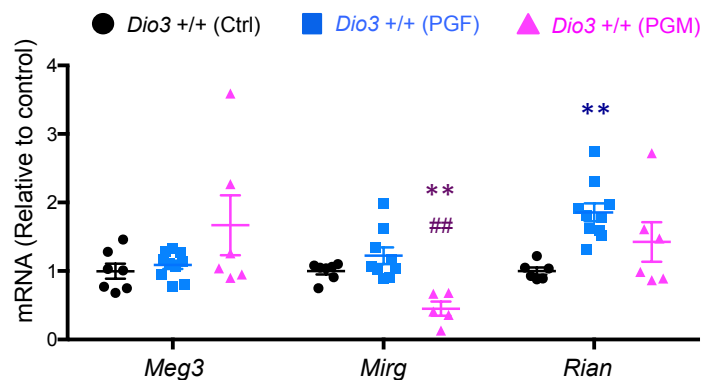
● *Dio3* +/+ (F0 *Dio3* +/+) ■ *Dio3* +/+ (F0 Paternal grandmother *Dio3* -/)



Supplemental Figure 3. Methylation status of individual CpG residues of *Meg3* promoter region. DNA methylation in seven CpG residues of the *Meg3* gene (sequence indicated) in P3 and P15 tissues of wild type control and wild-type PGM mice. Data represent the mean \pm SEM of three to five biological samples from at least three different litters. ***, ** and * indicate $P < 0.001$, $P < 0.01$ and $P < 0.05$, respectively, for individual CpG residues or for all CpG residues analyzed, as determined by the Student's t-test.

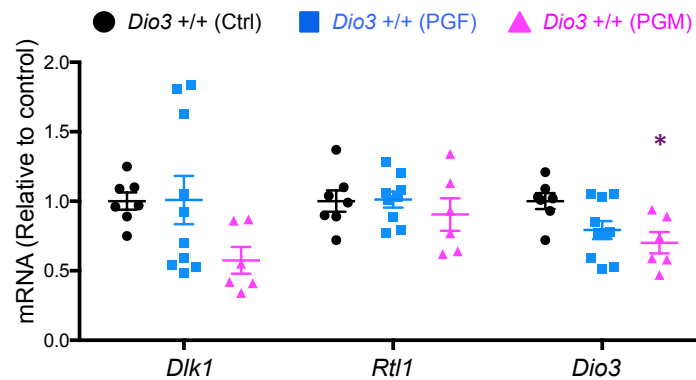
A

P15 testis expression of maternally expressed genes



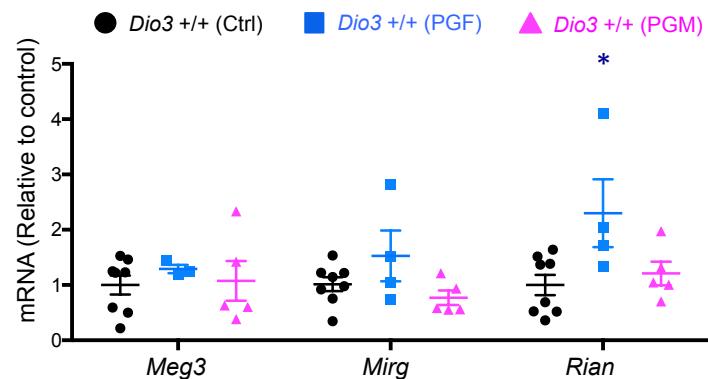
B

P15 testis expression of paternally expressed genes



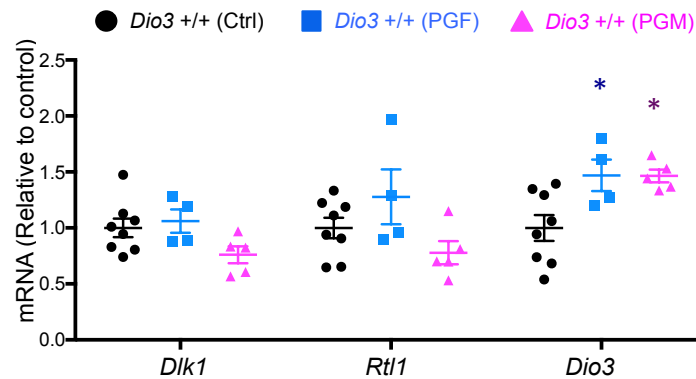
C

P15 Adrenal gland expression of maternally expressed genes



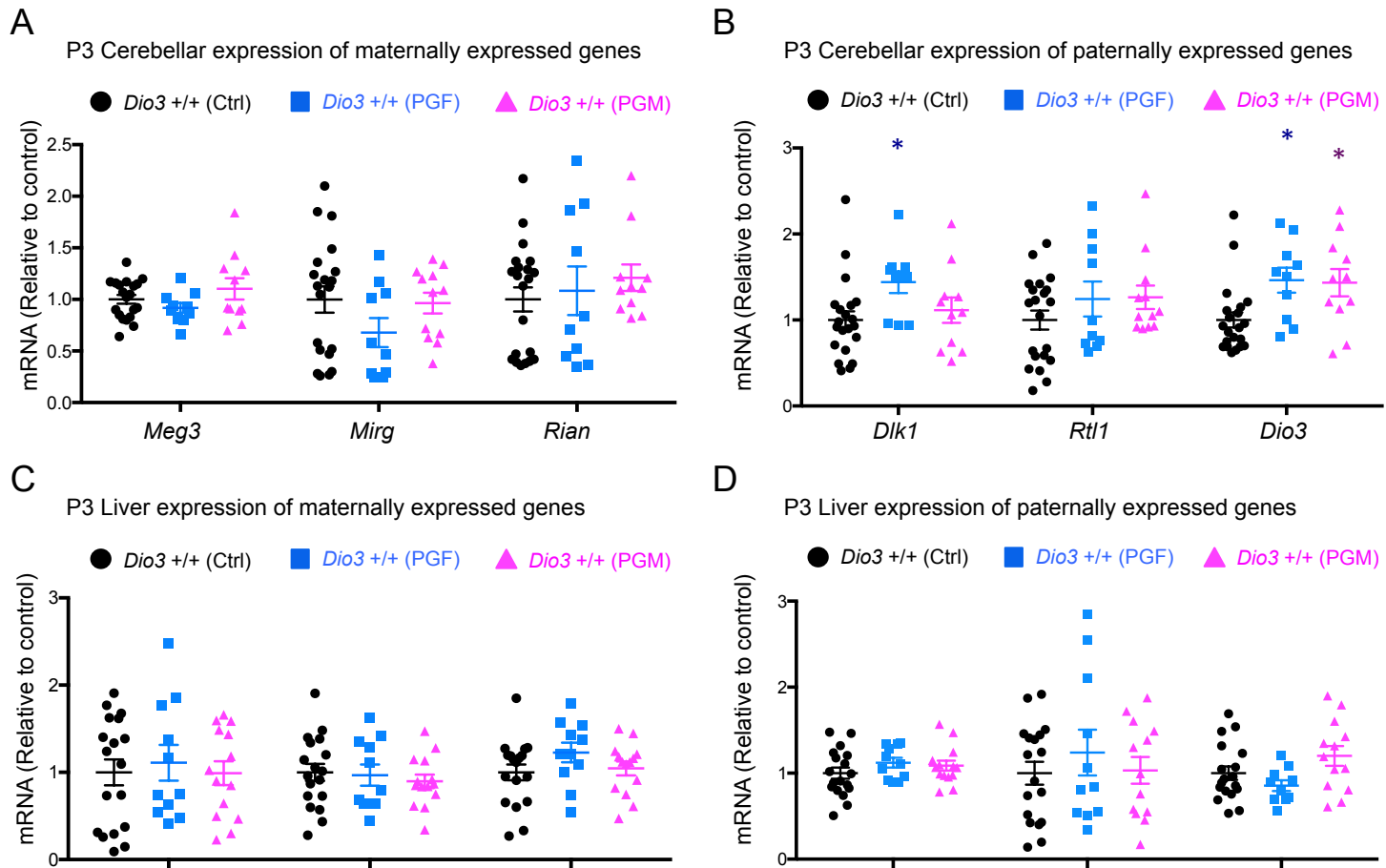
D

P15 Adrenal gland expression of paternally expressed genes



Supplemental Figure 4. Expression of *Dlk1-Dio3* domain genes in PGF and PGM tissues.

(A) Expression of maternally expressed genes in the P15 testis. (B) Expression of paternally expressed genes in the P15 testis. (C) Expression of maternally expressed genes in the P15 adrenal gland. (D) Expression of paternally expressed genes in the P15 adrenal gland. Data represent the mean \pm SEM of 6-10 individual animals (A and B), or of 4-8 pools of two mice each (C and D). Samples represent at least three different litters. ** and * indicate $P < 0.01$ and $P < 0.05$, respectively, when compared to controls; and ## indicate $P < 0.01$ when compared to PGF, as determined by one-way ANOVA and Tukey's *post hoc* test.



Supplemental Figure 5. Expression of *Dlk1-Dio3* domain genes in PGF and PGM tissues.

(A) Expression of maternally expressed genes in the P3 cerebellum. (B) Expression of paternally expressed genes in the P3 cerebellum. (C) Expression of maternally expressed genes in the P3 liver. (D) Expression of paternally expressed genes in the P3 liver. Data represent the mean \pm SEM of 11-18 individual animals representing at least three different litters. *, indicates $P < 0.05$, when compared to control group, as determined by one-way ANOVA and Tukey's *post hoc* test.

Supplemental Table 1. Sequences of primers used in qPCR for gene expression analyses.

Primer name	Primer Sequence (5' to 3')
<i>Begain-F</i>	GCTCTCCTACACCACGCATAA
<i>Begain-R</i>	CCGTCACCTTGTCTAGCTCCT
<i>Dio1-F</i>	GGCAGAGACTGGAAGACAGG
<i>Dio1-R</i>	ATCTGTGGCGTGAGCTTCTT
<i>Dio3-F</i>	TGAGCACAGCCACAGAACTC
<i>Dio3-R</i>	AAAGCTGTCAGTTCGAGCCA
<i>Dio3os-F</i>	CCGAAGTGGAGCCACCTTC
<i>Dio3os-R</i>	TTGAGGCCTTGACTTTACGC
<i>Dlk1-F</i>	GCTGGGACGGGAAATTCTG
<i>Dlk1-R</i>	CCTGGCCCTCATCATCCAC
<i>Gapdh-F</i>	AGGAGCGAGACCCCACTAAC
<i>Gapdh-R</i>	CGGAGATGATGACCCTTTTG
<i>Hr-F</i>	AGCACTGTGTGGCA GTGTT
<i>Hr-R</i>	AACCCTGCATCCAAGTAGCA
<i>Meg3-F</i>	GGACACACGGACACAGACA
<i>Meg3-R</i>	TGTCCCACAGGAAATGTGCAA
<i>Mirg-F</i>	CCACCATCATCAGAGAGCTTC
<i>Mirg-R</i>	GATGTAGCCTCTGGAGTCCTT
<i>Rian-F</i>	CTAAGTCACCATGGAGAACCAG
<i>Rian-R</i>	CAGATTTTCAGGGTGGCAGTAAG
<i>Rtl1/Rtl1as-F</i>	GAGAGTGGACCCCTACCACA
<i>Rtl1/Rtl1as-R</i>	GGCAAACCTCTCATCCATGT