PYY 3’-UTR variant C+1134A: Sequence alignments.

a. Mammalian inter-species sequence conservation (by Clustal-W alignment).

```
H.sapiens WT    GC-------GGCCCTCCGCCCGCGTCTCGGTGCCCCCGCCCCCTGGGCTGGAGGGCTGTGTGTGGT
H.sapiens var   GC-------GGCCCTCCGCCCGCGTCTCGGTGCCCCAGCCCCCTGGGCTGGAGGGCTGTGTGTGGT
M.mulatta       GC-------GGCCCTCCGCCCGCATCTCGGTGCCCCCGCCCCCTGGGCTGGAGGGCTGTGTGTGGT
P.troglodytes   GC-------GGCCCTCCGCCCGCGTCTCGGTGCCCCCGCCCCCTGGGCTGGAGGGCTGTGTGTGGT
P.pygmaeus      GC-------GGCCCTCCGCCCGCGTCTCGGTGCCCCCGCCCCCTGGGCTGGAGGGCTGTGTGTGGT
C.familiaris    GG-GGATGGGGTCTTCATTCCACTTCTCCGTGTCCCCAGCCCCTGGGCTGGCGGGCTGTGTGTGGT
F.catus         GCTGGATGGGGTCTTCATCCCATTTCTCCGTGCCCCCGGCCCCTGGGCTGGAGGGCTGTGTGTGGT
R.norvegicus    AC----------------TTC--------GTGTCTCAGACACCCAGGCTGGAGGGCTGTGTGTGTT
M.musculus      AC----------------TTCATATCTCGGTGTCTCGGACACCCAGACTGGAGGGCTGTGTGTGTT
Conserved                           *          *** * * * **  * **** ************ *
                                                    ↑
                                                 C+1134A
```

b. Occurrence within a microRNA recognition motif: hsa-miR663.

C1134 (wild-type) allele
Match: 14.2/22

```
hsa-miR663: CGCCAGGGCGCCGCGGGGCGGA
               |||:||  || |||||||
     C1134: CGCGTCTCGGTGC-CCCCGCCC
```

1134A (variant) allele
Match: 13.2/22

```
hsa-miR663: CGCCAGGGCGCCGCGGGGCGGA
               |||:||  || ||| |||
     1134A: CGCGTCTCGGTGC-CCCAGCCC
```

Online Supplemental Figure 4. ***PYY*** **3’-UTR variant C+1134A: Sequence alignments**.