

Supplementary Fig. 1. Design of TALENs used in this study. The target sequences of left and right TALENs are underlined. Red letters indicate start codon.

A

Left *bL* TALEN

5' - TTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCA - 3'

3' - AAAAACGAGTGGGTCTTTGCGACCACTTTCATTTTTCTACGACTTCTAGT - 5'

Right *bL* TALEN

B

Left *Clec4b1* TALEN

5' - TGCACATAGACCTCAATA**ATG**GTTTCAGGAAAGACAGCTACAAGGTA - 3'

3' - ACGTGTATCTGGAGTTATTACCAAGTCCTTTCTGTTCGATGTTCCAT - 5'

Right *Clec4b1* TALEN

Supplementary Fig. 2 Sequencing analysis of PCR products from founders injected with *bL* TALENs. Founder numbers shown on the left side are identical to Supplementary Table 2. The original *bL* sequence is shown at the top (bL) with the TALEN target sequences (underlined). Deletions are indicated by dashes, and insertions or substitutions are enclosed in a black box. Founders MU2, IUF6, IUF9 and IFF4 had two types of mutations.

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bL      CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU1     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----TAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU2-1  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----AAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU2-2  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAA-----AGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU3     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----ATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU4     CCT-----GAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU6     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGC-----GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU7     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGC-----GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MU8     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGG-----ACTCTCAACAGCG
MU9     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----AAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF2     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAA-----AAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF6     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----AAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF8     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----AAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF9     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAG-----TTTTTGTCTCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF12    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG--TGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF16    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGGT--AAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
MF17    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCT-----ACATCGAACTGGATCTCAACAGCG
MF18    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF2    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCT---AAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF3    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGG--AAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF4    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGGTTGAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGC
IUF6-1  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCT-----GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF6-2  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCT-----AGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF8     CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----AAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF9-1  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG---AAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF9-2  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGGTAAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGC
IUF11   CC-----TGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF16   CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTG-----TAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF19   CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACG-----TTTGTCTGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IUF20   CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACG-----TAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IFF4-1  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGCTGG--AAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IFF4-2  CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACG-----TAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
IFF6    CCTTTTTTGCGGCATTTGCGCTTCCCTGTTTTTGTCTACCCAGAAACGTTTTTCATGACATTAACTATAAAAATAGGCGTATCACGAGGCCCTTTTCAGATCAGTTGGGTGCACGAGTGGGTT

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Supplementary Fig. 3 Sequencing analysis of PCR products from founders injected with *Clec4b1* TALENs which unfrozen mature oocytes (A), unfrozen immature oocytes (B), frozen mature oocytes (C), and frozen immature oocytes (D) were used. Founder numbers shown on the left side are identical to Supplementary Table 4. The original *Clec4b1* sequence is shown at the top (WT) with the TALEN target sequences (underlined). Start codon is enclosed in a red box. Deletions are indicated by dashes and insertions or substitutions are enclosed in a black box.

A

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WT      GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGGTTTCAGGAAAGACAGCTACAAGGTAGGGTGA
MUM1-1  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA
MUM1-2  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAG-----ACAGCTACAAGGTAGGGTGA
MUM2    GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG-----GACAGCTACAAGGTAGGGTGA
MUM3-1  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG-----AAAGACAGCTACAAGGTAGGGTGA
MUM3-2  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAAT-----AAGACAGCTACAAGGTAGGGTGA
MUM4-1  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCA-----GGAAAGACAGCTACAAGGTAGGGTGA
MUM4-2  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATA-----AAGACAGCTACAAGGTAGGGTGA
MUM5    GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----GACAGCTACAAGGTAGGGTGA
MUM6    GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG-----AAAGACAGCTACAAGGTAGGGTGA
MUM7    GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA
MUM9    GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGAC-----AGCTACAAGGTAGGGTGA
MUM10   GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---CAGGAAAGACAGCTACAAGGTAGGGTGA
MUM11-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT----AGGAAAGACAGCTACAAGGTAGGGTGA
MUM11-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----GGAAAGACAGCTACAAGGTAGGGTGA
MUM12-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---TCAGGAAAGACAGCTACAAGGTAGGGTGA
MUM12-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG---AAAGACAGCTACAAGGTAGGGTGA
MUM13-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG---AGGAAAGACAGCTACAAGGTAGGGTGA
MUM13-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA
MUM13-3 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---CAGGAAAGACAGCTACAAGGTAGGGTGG
MUM14-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT--TTGAGGAAAGACAGCTACAAGGTAGGGTGA
MUM14-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCT-----AGGAAAGACAGCTACAAGGTAGGGTGA
MUM15   GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGAC-----AGCTACAAGGTAGGGTGA
MUM16-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---TCAGGAAAGACAGCTACAAGGTAGGGTGA
MUM16-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT-----AGACAGCTACAAGGTAGGGTGA
MUM16-3 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCT-----AGGAAAGACAGCTACAAGGTAGGGTGA
MUM17-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA
MUM17-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGAC-----AGCTACAAGGTAGGGTGA
MUM18-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT---TTGAGGAAAGACAGCTACAAGGTAGGGTGA
MUM18-2 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG-----AAAGACAGCTACAAGGTAGGGTGA
MUM19-1 GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATA-----GGAAAGACAGCTACAAGGTAGGGTGA
MUM19-2 GACTG-----TAGCTGCTACAAGGTAGGGTGA
MUM20  GACTGAGTTCTGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG-----AAGACAGCTACAAGGTAGGGTGA
  
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C

WT TACAAGAAACCATTGACCTGCACATAGACCTCAATAATGGTTCAGGAAAGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM1 TACAAGAAACCATTGACCTGCACATAG-----GAAAGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM2-1 TACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG-----AAAGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM2-2 TACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM2-3 TACAAGAAACCATTGACCTGCACAT-----AGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM2-4 TACAAGAAACCATTGACCTGCACATAGAC-----AGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM3 TACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG-----AAAGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM4-1 TACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM4-2 TACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AATAAAATAAATAAAATAAATGAGGTCCTT

MFM5 TACAAGAAACCATTGACCTGCACA-----AAGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

MFM6 TACAAGAAACCATTGACCTGCACATAGACCTCAATAATGG---AGGAAAGACAGCTACAAGGTAGGGTGAGCATTCTGTCTTAGTCCATAGGACACGGTTGGAGTGAGTGATGCAATGAGGAGGTCCCTT

D

WT TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATGGTTCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---CAGGAAAGACAGCTACAAGGTAGGGTGA

MFI2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAG-----GTACAAGGTAGGGTGA

MFI3-1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG--TCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI3-2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAAT-----TATTGAAAGACAGCTACAAGGTAGGGTGA

MFI3-3 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATATAT-----TTGAAAGACAGCTACAAGGTAGGGTGA

MFI4 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA

MFI5-1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAAT-----TCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI5-2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAA-----TCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI5-3 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAAT-----CAGGAAAGACAGCTACAAGGTAGGGTGA

MFI6 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----GGAAAGACAGCTACAAGGTAGGGTGA

MFI7 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA

MFI8 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----AGACAGCTACAAGGTAGGGTGA

MFI9-1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---TCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI9-2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT-----AGGAAAGACAGCTACAAGGTAGGGTGA

MFI10-1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT---TCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI10-2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT---CAGGAAAGACAGCTACAAGGTAGGGTGA

MFI10-3 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATA-----TTAGACAGCTACAAGGTAGGGTGA

MFI10-4 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAAT-----AAGGTAGGGTGA

MFI10-5 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGAC-----AGCTACAAGGTAGGGTGA

MFI11-1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCA-----GGAAAGACAGCTACAAGGTAGGGTGA

MFI11-2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA-----ACAGCTACAAGGTAGGGTGA

MFI12-1 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAATG---AGGAAAGACAGCTACAAGGTAGGGTGA

MFI12-2 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCAATAA---TCAGGAAAGACAGCTACAAGGTAGGGTGA

MFI12-3 TGGCCTGTTTGAAGAAGCAAGTCCCTGAGTCATATCTTCAAGAGTCAGATACAAGAAACCATTGACCTGCACATAGACCTCA-----GGAAAGACAGCTACAAGGTAGGGTGA