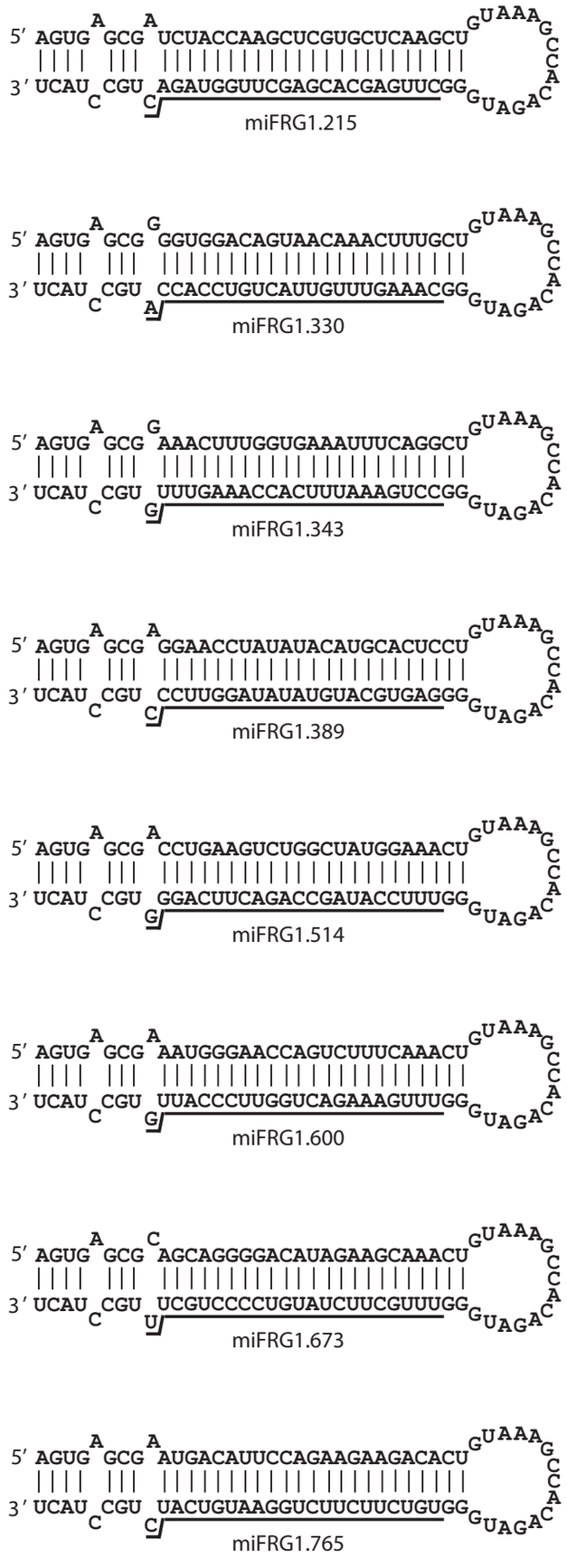
a



b

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        90        100        110        120        130        140        150        160
GGAGTGTTTA TTTCGCGTCC GCTTCTGTTT CTCCGCGCCC CTGTGCTGCC CCGACTCACA TACTCGTCCA GAACCGGCCT
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       170        180        190        200        210        220        230        240
CAGCCTCTCC GCGCAGAAGT TTCCCGGAGC CATGGCCGAG TACTCCTACG TGAAGTCTAC CAAGCTCGTG CTCAAGGGAA
GTCGGAGAGG CGCGTCTTCA AAGGGCCTCG GTACCGGCTC ATGAGGATGC ACTTCAGATG GTTCGAGCAC GAGTTCCCTT
                                  M  A  E   Y  S  Y   V  K  S  T   K  L  V   L  K  G

       250        260        270        280        290        300        310        320
CCAAGACGAA GAGTAAGAAG AAAAAGAGCA AAGATAAGAA AAGAAAAAGA GAAGAAGATG AAGAAACCCA GCTTGATATT
GGTTCTGCTT CTCATTCTTC TTTTTCTCGT TTCTATTCTT TTCTTTTTCT CTTCTTCTAC TTCTTTGGGT CGAACTATAA
T  K  T  K   S  K  K   K  K  S   K  D  K  K   R  K  R   E  E  D   E  E  T  Q   L  D  I

       330        340        350        360        370        380        390        400
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CAACCTTAGA CCACCTGTCA TTGTTTGAAA CCACTTTAAA GTCCTTGGTA TCGGTAACTT TACCTATTCC CTTGGATATA
 V  G  I   W  W  T  V   T  N  F   G  E  I   S  G  T  I   A  I  E   M  D  K   G  T  Y  I

       410        420        430        440        450        460        470        480
ACATGCACTC GACAATGGTC TTTTTACCCT GGGAGCTCCA CACAAAGAAG TTGATGAGGG CCCTAGTCCT CCAGAGCAGT
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  H  A  L   D  N  G   L  F  T  L   G  A  P   H  K  E   V  D  E  G   P  S  P   P  E  Q

       490        500        510        520        530        540        550        560
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F  T  A  V   K  L  S   D  S  R   I  A  L  K   S  G  Y   G  K  Y   L  G  I  N   S  D  G

       570        580        590        600        610        620        630        640
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GAACAACAAC CCGCAAGTCT ACGTTAACCT GGTTCTCTTG TTACCCTTGG TCAGAAAGTT TTACCCTTTT ACCGAAACAA
 L  V  V   G  R  S  D   A  I  G   P  R  E   Q  W  E  P   V  F  Q   N  G  K   M  A  L  L

       650        660        670        680        690        700        710        720
GGCCTCAAAT AGCTGCTTTA TTAGATGCAA TGAAGCAGGG GACATAGAAG CAAAAAGTAA AACAGCAGGA GAAGAAGAAA
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  A  S  N   S  C  F   I  R  C  N   E  A  G   D  I  E   A  K  S  K   T  A  G   E  E  E

       730        740        750        760        770        780        790        800
TGATCAAGAT TAGATCCTGT GCTGAAAGAG AAACCAAGAA AAAAGATGAC ATTCCAGAAG AAGACAAAGG AAATGTAAAA
ACTAGTTCTA ATCTAGGACA CGACTTTCTC TTTGGTTCTT TTTTCTACTG TAAGGTCTTC TTCTGTTTCC TTTACATTTT
M  I  K  I   R  S  C   A  E  R   E  T  K  K   K  D  D   I  P  E   E  D  K  G   N  V  K

       810        820        830        840        850        860        870        880
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GTTACACTTT AGTTAATACA TTTCTTTAAA GTCTCGAAGG TTCTGGTGTT TGAATTTTAT TCATTTCTTC TGTCATTTTA
 Q  C  E   I  N  Y  V   K  K  F   Q  S  F   Q  D  H  K   L  K  I   S  K  E   D  S  K  I

       890        900        910        920        930        940        950        960
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AGAATTTTTC CGAGCCTTTC TACCTAAAAA CGTACTCTGC GAAGACCTGT CCTCTCGGTT TAACTTTCGG CTGTCTATGA
  L  K  K   A  R  K   D  G  F  L   H  E  T   L  L  D   R  R  A  K   L  K  A   D  R  Y

       970        980        990       1000       1010       1020       1030       1040
GCAAGTGACT GGGATTTTTG TTTCTGCCTT ATCTTTCTGT GTTTTTTTCT GAATAAAATA TTCAGAGGAA ATGCTTTTACAG
CGTTCACTGA CCCTAAAAAC AAAGACGGAA TAGAAAGACA CAAAAAAAGA CTTATTTTAT AAGTCTCCTT TACGAAAATGTC
C  K  *
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c

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Human FRG1
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miFRG1.948

Mouse FRG1
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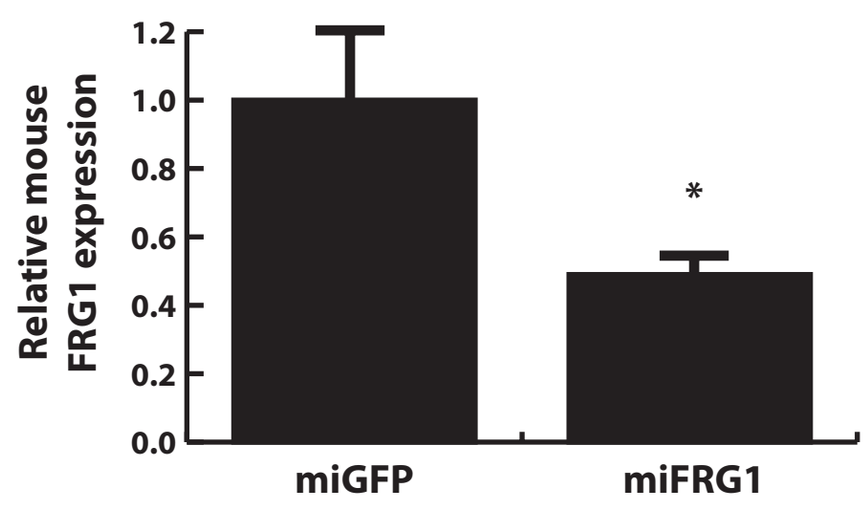
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