**Alignment of *UKAR cDNA*,genomic sequence and sequence over the small deletion (#8)**

RE13419 25 TCAACTGGTATTCGGTTATCCGTGTTAAACAAATATCTAAATTTTATATATTGTATATTA 84

CG11155 gene 27 TCAACTGGTATTCGGTTATCCGTGTTAAACAAATATCTAAATTTTATATATTGTATATTA 86

8-UKAR-seq 291 181 TCAACTGGTATTCGGTTATCCGTGTTAAACAAATATCTAAATTTTATATATTGTATATTA 240

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RE13419 85 TATAAATAAATTATAACTAAGTGTTTCGGAATGTAATTAAGCAGCATTATCCACATAAAA 144

CG11155 gene 87 TATAAATAAATTATAACTAAGTGTTTCGGAATGTAATTAAGCAGCATTATCCACATAAAA 146

8-UKAR-seq 291 241 TATAAATAAATTATAACTAAGTGTTTCGGAATGTAATTAAGCAGCATTATCCACATAAAA 300

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RE13419 145 TAATGGTA---------------------------------------------------- 152

CG11155 gene 147 TAATGGTAAAAAAAGCCATCAGTACCTTTACTAAAATAATATACGTATATATGCTCTTTA 206

8-UKAR-seq 291 301 TAATGGTAAAAAAAGCCATCAGTACCTTTACTAAAATAATATACGTATACATGCTCTTTA 360

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RE13419 153 ----CGAAAAAAACGAGAAATCGTAATAAAGGAAAATATTCAAGGACGAAGTTACCTTAA 208

CG11155 gene 207 GGTACGAAAAAAACGAGAAATCGTAATAAAGGAAAATATTCAAGGACGAAGTTACCTTAA 266

8-UKAR-seq 291 361 GGTACGAAAAAAACGAGAAATCGTAATAAAGGAAAATATTCAAGGACGAAGTTACCTTAA 420

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RE13419 209 AAAAATATGTTGTTCGTATATAATACTGTCCATCCTCGTAATTTCTAATGCCTTGCCCCC 268

CG11155 gene 267 AAAAATATGTTGTTCGTATATAATACTGTCCATCCTCGTAATTTCTAATGCCTTGCCCCC 326

8-UKAR-seq 291 421 AAAAATATGTTGTTCGTATATAATACTGTCCATCCTCGTAATTTCTAATGCCTTGCCCCC 480

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RE13419 269 AGTAATACGAGTAGGT-------------------------------------------- 284

CG11155 gene 327 AGTAATACGAGTAGGTAAGTTTAATGTGAAGTTTATTTGTTTTGACAATTTATGCTCTTG 386

8-UKAR-seq 291 481 AGTAATACGAGTAGGTAAGTTTAATGTGAAGTTTATTTGTTTTGACAATTTATGCTCTTG 540

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RE13419 285 ----------------GCCATATTTACGGAAGATGAACGCGAAAGCAGTATTGAATCTGC 328

CG11155 gene 387 ATGTATTACCCCAGGTGCCATATTTACGGAAGATGAACGCGAAAGCAGTATTGAATCTGC 446

8-UKAR-seq 291 541 ATGTATTACCCCA---GCCATATTTACGGAAGATGAACGCGAAAGCAGTATTGAATCTGC 597

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RE13419 329 ATTTAAATACGCAATATACCGTATAAATAAGGAAAAGACTCTTCTTCCCAATACACAATT 388

CG11155 gene 447 ATTTAAATACGCAATATACCGTATAAATAAGGAAAAGACTCTTCTTCCCAATACACAATT 506

8-UKAR-seq 291 598 ATTTAAATACGCAATATACCGTATAAATAAGGAAAAGACTCTTCTTCCCAATACACAATT 657

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Del#8 has a very good splice donor but no splice acceptor.

Theoretically, there should be a big chunk missing (magenta) until the next decent splice acceptor. In this case, there will be frame shift and early STOP- therefore, a genetic null.

Or this intron should no longer be spliced, which again will induce frame shift and early STOP/ also genetic null.