Additional File 1 : Sequence alignment for R_1 (SR) and R_2 (SRQ). The primers used for the PCR amplification are indicated (light gray), as well as the restriction sites for the *BfaI* and *AluI* enzymes (darker gray, the triangles indicate where restriction cuts). Mutations between the two sequences are bolded.

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         1                                                  50
R1-SR    GCGCGAGCAT ATCCATAGCA CTACGACCCG GCGGCGTGGC CTGACCCGGA
R2-SRQ   GCGCGAGCAT ATCCATAGCA CTACGACCCG GCGGCGTGGC CTAACCCGGA
         Primer Intron2dir1
         51                                                100
R1-SR    GGGAGTCCAG CTCCGGTGAG TTCTGGGAGG GG........ GCCATTT.CC
R2-SRQ   GGGAGTCCAG CTCCGGTGAG TTCTAGGAGG GGCTTTTGGG GTCATTTGCC
                                 BfaI
         101                                               150
R1-SR    CTTTGCTAAC TAATTTACTC CAATTTTCGT AGATGCCACC GACTCGGACC
R2-SRQ   CTTTGCTAAC TAATTCACTC CAATTTTCGT AGATGCCACC GACTCGGACC

         151                                               200
R1-SR    CACTGGTAAT AACGACGGAC AAGGGCAAAA TCCGTGGAAC GACACTGGAA
R2-SRQ   CACTGGTCAT AACGACGGAC AAAGGCAAAA TCCGTGGAAC GACACTGGAA

         201                                               250
R1-SR    GCGCCAAGTG GAAAGAAGGT GGACGCATGG ATGGGCATTC CGTACGCGCA
R2-SRQ   GCGCCTAGCG GAAAGAAGGT GGACGCATGG ATGGGCATTC CGTACGCGCA
              BfaI
         251                                               300
R1-SR    GCCCCCGCTG GGTCCGCTCC GGTTTCGACA TCCGCGACCC GCCGAAAGAT
R2-SRQ   GCCTCCGCTG GGTCCGCTCC GGTTTCGACA TCCGCGACCC GCCGAAAGAT

         301                                               350
R1-SR    GGACCGGTGT GCTGAACGCG ACCAAACCAC CCAACTCCTG CGTCCAGATC
R2-SRQ   GGACCGGTGT GCTGAACGCG ACCAAACCGC CCAACTCCTG CGTCCAGATC

         351                                               400
R1-SR    GTGGACACCG TGTTCGGTGA CTTCCCGGGG GCCACCATGT GGAACCCGAA
R2-SRQ   GTGGACACCG TGTTCGGTGA CTTCCCGGGG GCCACCATGT GGAACCCGAA

         401                                               450
R1-SR    CACACCCCTC TCGGAGGACT GTCTGTACAT CAACGTGGTC GTGCCAAGGC
R2-SRQ   CACACCGCTC TCGGAGGACT GTCTGTACAT CAACGTGGTC GTGCCACGGC

         451                                               500
R1-SR    CGAGGCCCAA GAATGCCGCT GTCATGCTGT GGATCTTTGG GGGTAGCTTC
R2-SRQ   CCAGGCCCAA GAATGCCGCC GTCATGCTGT GGATCTTCGG GGGTAGCTTC
                                                      AluI
         501                                               550
R1-SR    TACTCCGGGA CTGCCACGTT GGACGTGTAC GATCATCGGA CGCTGGCCTC
R2-SRQ   TACTCCGGGA CTGCCACGCT GGACGTGTAC GACCACCGGA CGCTGGCCTC

         551                                           597
R1-SR    GGAGGAGAAC GTGATCGTGG TTTCGCTGCA GTACCGTGTC GCAAGTC
R2-SRQ   GGAGGAGAAC GTGATCGTAG TTTCGCTGCA GTACCGTGTC GCAAGTC
                                          Primer CpEx3rev
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