

A

>EGFPm_art1

ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAG
 CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC
 GATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC
 CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGACGTGCTTCAG
 CCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA
 GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC
 GcGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG
 GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
 ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGG
 TGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGAGGTGGGTAATA
 AAGGAGATGACAGGTAGCATCATTAGAGCCAGAGCTCTGTCTCAGCTCCTCTTAT
 CTCTTTTATTACCCAGCTGGCCGACCACTACCAGCAGAACACCCCCATCGGCGAC
 GGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCA
 AAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCG
 CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAA

B

Acceptor (AG) sites. Threshold 0.000 (100%).
 1 P: 210 W: 4.10 Seq: tacggcgtgcAGtgcttcagcc
 2 P: 306 W: 0.23 Seq: atcttcttcaAGgacgacggca
3 P: 615 W: 10.47 Seq: tttattacccAGctggccgacc
 Donor (GT) sites. Threshold 0.079 (100%).
 1 P: 4 W: 10.02 Seq: -----atgGTgagcaagggc
 2 P: 67 W: 3.30 Seq: ggacggcgacGTaaacggccac
 3 P: 337 W: 5.96 Seq: ccgcgccgagGTgaagtccgag
 4 P: 361 W: 1.90 Seq: cgacaccctgGTgaaccgcatc
 5 P: 490 W: 6.94 Seq: cggcatcaagGTgaacttcaag
6 P: 535 W: 11.28 Seq: cagcgtgcagGTgggtaataaa
 7 P: 539 W: 1.34 Seq: gtgcaggtggGTaataaaggag
 8 P: 558 W: 8.20 Seq: gagatgacagGTagcatcatta
 9 P: 798 W: 4.10 Seq: agctgtacaaGTaa-----

C

