

A

>EGFPm_art3

ATGGTGAGCAAGGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTTCGAG
 CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGGCGAGGGC
 GATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC
 CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAG
 CCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA
 GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC
 GCGCCGAGGTGAAGTTCGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG
 GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
 ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGG
 TGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGGTAAACATCA
 TAACGAAGAAGGGTAGCATCATTAGAGCCAGAGCTCTGTCTCAGCTCCCTTCTTC
 CTTATCATCTTTTCAGCTGGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG
 GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAA
 AGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCC
 GGGATCACTCTCGGCATGGACGAGCTGTACAAGTAA

B

Acceptor (AG) sites. Threshold 0.000 (100%).
 1 P: 210 W: 4.10 Seq: tacggcggtgcAGtgcttcagcc
 2 P: 306 W: 0.23 Seq: atcttcttcaAGgacgacggca
3 P: 614 W: 11.43 Seq: atcatctttcAGctggccgacc
 4 P: 635 W: 0.10 Seq: cactaccagcAGaacacccccca
 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: ccgcgcgcgagGTgaagtccgag
 4 P: 361 W: 1.90 Seq: cgacaccctgGTgaaccgcatc
 5 P: 490 W: 6.94 Seq: cggcatcaagGTgaacttcaag
6 P: 535 W: 12.40 Seq: cagcgtgcagGTaaacatcata
 7 P: 557 W: 1.62 Seq: acgaagaaggGTtagcatcatta
 8 P: 797 W: 4.10 Seq: agctgtacaaGTaa-----

C

