

A

>EGFPm_art4

ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGGCCATCCTGGTTCGAG
 CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC
 GATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC
 CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAG
 CCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA
 GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC
 GcGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG
 GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
 ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGG
 TGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGGTAAACATCA
 TAGCGAGGTAGGGTAGCATCATTAGAGCCAGAGCTCTGTCTCAGCTCCCTACTTC
 CTTATTATGTTTCAGCTGGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG
 GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAA
 AGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCC
 GGGATCACTCTCGGCATGGACGAGCTGTACAAGTAA

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: 614 W: 10.43 Seq: attatgtttcAGctggccgacc
 Donor (GT) sites. Threshold 0.079 (100%).
 1 P: 4 W: 10.02 Seq: -----atgGTgagcaagggc
 2 P: 67 W: 3.30 Seq: ggacggcgcacGTaaacggccac
 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: 552 W: 9.60 Seq: tcatagcgcagGTagggtagcat
 8 P: 557 W: 1.62 Seq: gcgaggtaggGTagcatcatta
 9 P: 797 W: 4.10 Seq: agctgtacaaGTaa-----

C

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 Output of sir_great (6)
 mink_art4.7

