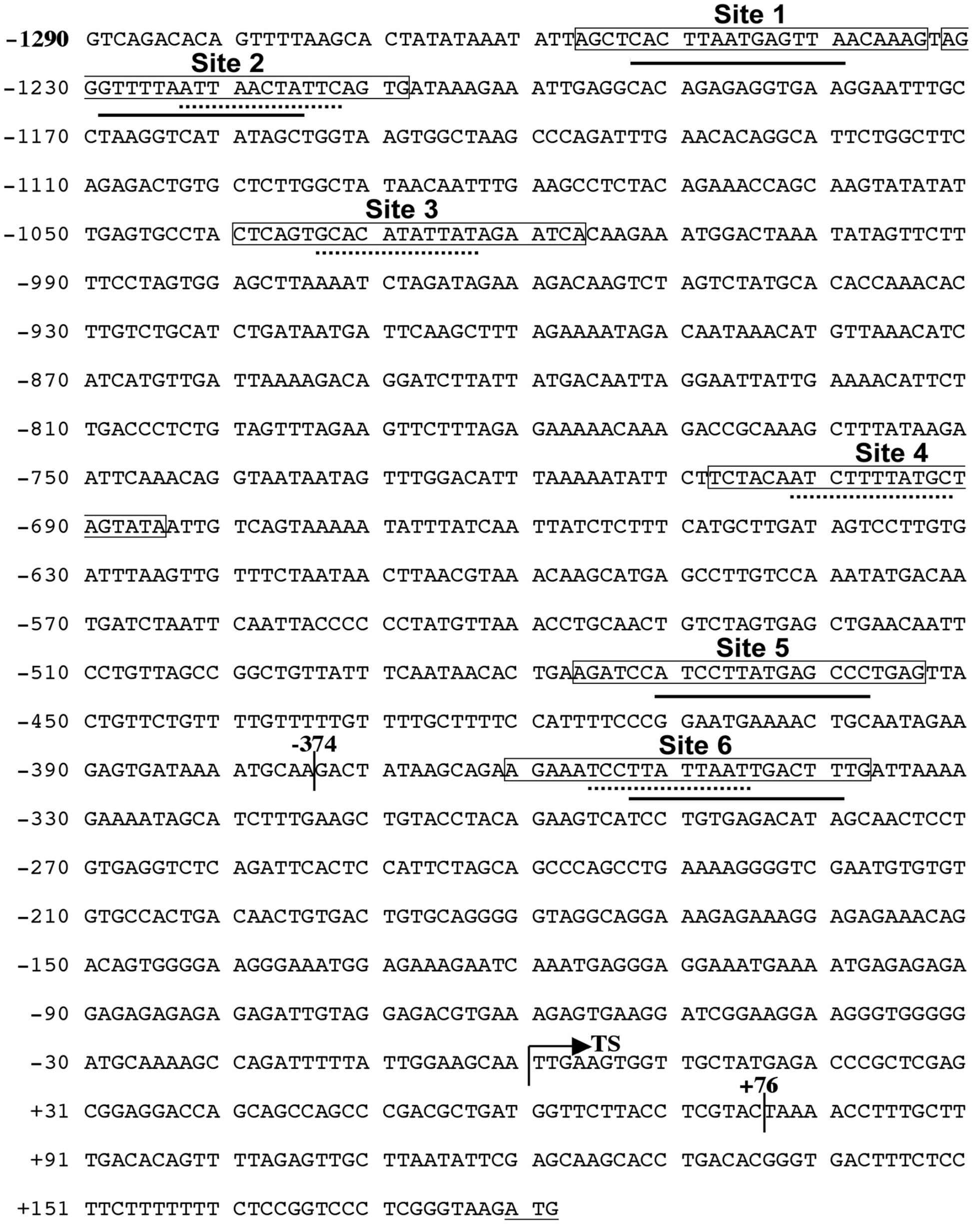
Supplemental Figure S2



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                                                              Site 1
-1290 GTCAGACACA GTTTTAAGCA CTATATAAAT ATTAGCTCAC TTAATGAGTT AACAAAGTAG
              Site 2
-1230 GGTTTTAATT AACTATTCAG TGATAAAGAA ATTGAGGCAC AGAGAGGTGA AGGAATTTGC

-1170 CTAAGGTCAT ATAGCTGGTA AGTGGCTAAG CCCAGATTTG AACACAGGCA TTCTGGCTTC

-1110 AGAGACTGTG CTCTTGGCTA TAACAATTTG AAGCCTCTAC AGAAACCAGC AAGTATATAT
                            Site 3
-1050 TGAGTGCCTA CTCAGTGCAC ATATTATAGA ATCACAAGAA ATGGACTAAA TATAGTTCTT

 -990 TTCCTAGTGG AGCTTAAAAT CTAGATAGAA AGACAAGTCT AGTCTATGCA CACCAAACAC

 -930 TTGTCTGCAT CTGATAATGA TTCAAGCTTT AGAAAATAGA CAATAAACAT GTTAAACATC

 -870 ATCATGTTGA TTAAAAGACA GGATCTTATT ATGACAATTA GGAATTATTG AAAACATTCT

 -810 TGACCCTCTG TAGTTTAGAA GTTCTTTAGA GAAAAACAAA GACCGCAAAG CTTTATAAGA
                                                                 Site 4
 -750 ATTCAAACAG GTAATAATAG TTTGGACATT TAAAAATATT CTTCTACAAT CTTTTATGCT

 -690 AGTATAATTG TCAGTAAAAA TATTTATCAA TTATCTCTTT CATGCTTGAT AGTCCTTGTG

 -630 ATTTAAGTTG TTTCTAATAA CTTAACGTAA ACAAGCATGA GCCTTGTCCA AATATGACAA

 -570 TGATCTAATT CAATTACCCC CCTATGTTAA ACCTGCAACT GTCTAGTGAG CTGAACAATT
                                                     Site 5
 -510 CCTGTTAGCC GGCTGTTATT TCAATAACAC TGAAGATCCA TCCTTATGAG CCCTGAGTTA

 -450 CTGTTCTGTT TTGTTTTTGT TTTGCTTTTC CATTTTCCCG GAATGAAAAC TGCAATAGAA
                  -374                             Site 6
 -390 GAGTGATAAA ATGCAAGACT ATAAGCAGAA GAAATCCTTA TTAATTGACT TTGATTAAAA

 -330 GAAAATAGCA TCTTTGAAGC TGTACCTACA GAAGTCATCC TGTGAGACAT AGCAACTCCT

 -270 GTGAGGTCTC AGATTCACTC CATTCTAGCA GCCCAGCCTG AAAAGGGGTC GAATGTGTGT

 -210 GTGCCACTGA CAACTGTGAC TGTGCAGGGG GTAGGCAGGA AAGAGAAAGG AGAGAAACAG

 -150 ACAGTGGGGA AGGGAAATGG AGAAAGAATC AAATGAGGGA GGAAATGAAA ATGAGAGAGA

  -90 GAGAGAGAGA GAGATTGTAG GAGACGTGAA AGAGTGAAGG ATCGGAAGGA AGGGTGGGGG
                                        TS
  -30 ATGCAAAAGC CAGATTTTTA TTGGAAGCAA TTGAAGTGGT TGCTATGAGA CCCGCTCGAG
                                                   +76
  +31 CGGAGGACCA GCAGCCAGCC CGACGCTGAT GGTTCTTACC TCGTACTAAA ACCTTTGCTT

  +91 TGACACAGTT TTAGAGTTGC TTAATATTCG AGCAAGCACC TGACACGGGT GACTTTCTCC

 +151 TTCTTTTTTT CTCCGGTCCC TCGGGTAAGA TG
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Figure S2. Bioinformatic prediction of POU4 protein binding sites in the *RIT2* promoter. Nucleotide sequence of the *RIT2* 5'-upstream region from –1290 to +76 bp was scanned for the presence of potential binding sites for POU4 transcription factors using Patser [http://rsat.ulb.ac.be/rsat] with position-specific scoring matrices for POU4F1/F2 (Matrix 1) and POU4F2 (Matrix 2). The transcription start site (TS, numbered +1) is indicated by an angled arrow, and the numbers on the left are the nucleotide positions relative to it. The positions of –374 and +76 bp are indicated by vertical lines. The initiation ATG is underlined. Core binding sequences predicted by Matrix 1 and Matrix 2 with scores higher than 3.0 are marked by dotted and solid underlines, respectively (see also Fig. 4). Note that Sites 2 and 6 are predicted with both matrices. The positions and sequences of oligonucleotides containing the predicted sites (Sites 1-6) in the middle that were used for EMSA as probes (Probes 1-6) or competitors are boxed.