

## ***Egr1* (genomic region of exon 2)**

2691 GCTGCGTGGG TGGCTGGAGG GGGTGGGGGG GAGGGTTTGT TTTGATGAGC  
CGACGCACCC ACCGACCTCC CCCACCCCCC CTCCCAAACA AAACACTCG

2741 GGGGTTGCCC CCTCCCCCGC GCGCGCGGTG TCGCGCGCCT TGTTCGAGA  
CCCCAACGGG GGAGGGGGCG CGCGCGCCAC AGCGCGCGGA ACAAACGTCT

2791 TTGTTCCCA AGGCAGGGCT GAAATCTGTG ACCAGGGATG TCCCGCCGCC  
ACAAGGGGT TCCGTCCCGA CTTTAGACAC TGGTCCCTAC AGGGCGGC**GG**

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2841 CAGGGTCGGG GCGCGCATT AGCTGTAGCC ACTAGGGTGC TGGCGGGATT  
**GTCCCAGCCC CCGCGCGTAA T**CGACATCGG TGATCCCACG ACCGCCCTAA

2891 CCCTCGCCCG CGCAGCCTCG CTGCGGAGCG CTCTCGGAGC TGCAGTAGAG  
GGGAGCGGGC GCGTCGGAGC GACGCCTCGC GAGAGCCTCG ACGT CATCTC

2941 GGGGATTCT CTGTTTTCGT CAGCTGTTGA AATGGGCTCT GCCACTGGAG  
CCCCCTAAGA GACAAACGCA GTCGACAACT TTACCCGAGA CGGTGACCTC

2991 CAGGTCCAGG AACATTGCAA TCTGCTGCTA TCAATTATTA ACCACATCGG  
GTCCAGGTCC TTGTAACGTT AGACGACGAT AGTTAATAAT TGGTGTAGCC

3041 GAGTCAGTGG TAGCCGGGCG ACCTCTTGCC AGGCCGCTTC GGGTCTCATC  
CTCAGTCACC ATCGGCCCGC TGGAGAACGG TCCGGCGAAG CCCAGAGTAG

3091 GTCCAGTGAT TCCTCTCCAG TAACCAGGCC TCTCTGTTCC CTTTCCT GCC  
CAGGTCAC TA AGGAGAGGTC ATGGTCCGG AGAGACAAGG GAAAGGACGG

Exon 2

3141 AG**AGTCC**TTT TCTGACATCG CTCTGAATAA TGAGAAGGCG ATGGTGGAGA  
TC**TCAGG**AAA AGACTGTAGC GAGACTTATT ACTCTTCCGC TA CCACC TCT

3191 CGAGTTATCC CAGCCAAACG ACTCGGTTGC CTCCATCAC CTATACTGGC  
GCTCAATAGG GTCGGTTTGC TGAGCCAACG GAGGGTAGTG GATATGACCG

3241 CGCTTCTCCC TGGAGCCCGC ACCCAACAGT GGCAACACTT TGTGGCCTGA  
GCGAAGAGGG ACCTCGGGCG TGGGTTGTCA CCGTTGTGAA ACACCGGACT

3291 ACCCC TTTTC AGCCTAGTCA GTGGCCTCGT GAGCATGACC AATCCTCCGA  
TGGGGAAAAG TCGGATCAGT CACCGGAGCA CTCGTAC TGG TTAGGAGGCT

3341 CCTCTTCATC CTCGGCGCCT TCTCCAGCTG CTTTCATCGTC TTCCTCTGCC  
GGAGAAGTAG GAGCCGCGGA AGAGGTCGAC GAAGTAGCAG AAGGAGACGG

3391 TCCAGAGCC CGCCCCTGAG CTGTGCCGTG CCGTCCAACG ACAGCAGTCC  
AGGGTCTCGG GCGGGGACTC GACACGGCAC GGCAGGTTGC TGTCGTCAGG

## **SUPPORT INFORMATION FIGURE S1**

3441 CATCTACTCG GCTGCGCCCA CCTTTCCTAC TCCCAACACT GACATTTTTC  
 GTAGATGAGC CGACGCGGGT GGAAAGGATG AGGGTTGTGA CTGTAAAAAG

3491 CTGAGCCCCA AAGCCAGGCC TTTCTT GGCT CGGCAGGCAC AGCCTTGCAG  
 G ACTCGGGGT TTCGGTCCGG AAAGGACCGA GCCGTCCGTG TCGGAACGTC

3541 TACCCGCCTC CTGCCTACCC TGCCACCAA GGTGGTTTCC AGGTTCCCAT  
 ATGGGCGGAG GACGGATGGG ACGGTGGTTT CCACCAAAGG TCCAAGGGTA

3591 GATCCCTGAC TATCTGTTTC CACAACAACA GGGAGACCTG AGCCTGGGCA  
 CTAGGGACTG ATAGACAAAG GTGTTGTTGT CCCTC TGGAC TCGGACCCGT

3641 CCCCAGACCA GAAGCCCTTC CAGGGTCTGG AGAACCGTAC CCAGCAGCCT  
 GGGGTCTGGT CTTCCGGGAAG GTCCCAGACC TCTTGGCATG GGTCGTCGGA

3691 TCGCTCACTC CACTATCCAC TATTAAGCC TTCGCCACTC AGTCGGGCTC  
 AGCGAGTGAG GTGATAGGTG ATAATTTCCG AAGCGGTGAG TCAGCCCGAG

3741 CCAGGACTTA AAGGCTCTTA ATACCACCTA CCAATCCCAG CTCATCAAAC  
 GTCCCTGAAT TTCCGAGAAT TATGGTGGAT GGTTAGGGTC GAGTAGTTTG

3791 CCAGCCGCAT GCGCAAGTAC CCCAACCGGC CCAGCAAGAC ACCCCCCAT  
 GGTCGGCGTA CGCGTTCATG GGGTTGCCG GGTCGTTCTG TGGGGGGTA

3841 GAACGCCCAT ATGCTTGCCC TGTCGAGTCC TCGGATCGCC GCTTTTCTCG  
 CTTGCGGGTA TACGAACGGG ACAGCTCAGG ACGCTAGCGG CGAAAAGAGC

3891 CTCGGATGAG CTTACCCGCC ATATCCGCAT CCACACAGGC CAGAAGCCCT  
 GAGCCTACTC GAATGGGCGG TATAGGCGTA GGTGTGTCCG GTCTTCGGGA

3951 TCCAGTGTCG AATCTGCATG CGTAACTTCA GTCGTAGTGA CCACCTT ACC  
 AGGTCACAGC TTAGACGTAC GCATTGAAGT CAGCATCACT GGTGGAATGG

3991 ACCCACATCC GCACCCACAC AGGCGAGAAG CTTTTGCCT GTGACATTTG  
 TGGGTGTAGG CGTGGGTGTG TCCGCTCTTC GAAAACGGA CACTGTAAAC

4041 TGGGAGGAAG TTTGCCAGGA GTGATGAACG CAAGAGGCAT ACCAAAATCC  
 ACCCTCCTTC AAACGGTCCT CACTACTTGC GTTC TCCGTA TGGTTTTAGG

4091 ATTTAAGACA GAAGGACAAG AAAGCAGACA AAAGTGTGGT GGCCTCCCCG  
 TAAATTCTGT CTTCTGTTC TTT CGTCTGT TTTCA CACCA CCGGAGGGGG

4141 GCTGCCTCTT CACTCTCTTC TTACCCATCC CCAGTGGCTA CCTCCTACCC  
 CGACGGAGAA GTGAGAGAAG AATGGGTAGG GGTCACCGAT GGAGGATGGG

4191 ATCCCCTGCC ACCACCTCAT TCCCATCCCC TGTGCCCACT TCCTACTCCT  
 TAGGGGACGG TGGTGGAGTA AGGGTAGGGG ACACGGGTGA AGGATGAGGA

## SUPPORT INFORMATION FIGURE S1

4241 CTCCTGGCTC CTCCACCTAC CCATCTCCTG CGCACAGTGG CTT CCCGTCCG  
GAGGACCGAG GAGGTGGATG GGTAGAGGAC GCGTGTACC GAAGGGCAGC

4291 CCGTCAGTGG CCACCA CTT TGCCTCCGTT CCACCTGCTT TCCCCACCCA  
GGCAGTCACC GGTGGTGGAA ACGGAGGCAA GGTGGACGAA AGGGGTGGGT

4341 GGTCAGCAGC TTCCCGTCTG CGGGCGTCAG CAGCTCCTTC AGCACCTCAA  
CCAGTCGTCC AAGGGCAGAC GCCCGCAGTC GTCGAGGAAG TCGTGGAGTT

4391 CTGGT CTTTC AGACATGACA GCGACCTTTT CTCCAGGAC AATTGAAATT  
GACCAGAAAG TCTGTACTGT CGCTGGAAAA GAGGGTCCTG TTAACCTTAA

4441 TGCTAAAGGG AATAAAAGAA AGCAAAGGGA GAGGCAGGAA AGACATAAAA  
ACGATTTCCC TTATTTT C TT TCGTTTCCCT CTCCGTCCTT TCTGTA TTTT

4491 GCACAGGAGG GAAGAGATGG CCGCAAGAGG GGCCACCTCT TAGGTCAGAT  
CGTGTCTCC CTC TCTACC GGC GTTCTCC CCGGTGGAGA ATCCAGTCTA

4541 GGAAGATCTC AGAGCCAAGT CTTTCTACTC ACGAGTAGAA GGACCGTTGG  
CCTTCTAGAG TCTC GGTTCA GGAAGATGAG TGCTCATCTT CCT GGCAACC

4591 CCAACAGCCC TTTCACTTAC CATCCCTGCC TCCCCGTCC TGTT CCCTTT  
GTTTGTCCGGG AAAGTGAATG GTAGGGACGG AGGGGGCAGG ACAAGGGAAA

4641 GACTTCAGCT GCCTGAAACA GCCATGTCCA AGTTCTTAC CTCTATCCAA  
CTGAAGTCGA CGGACTTTGT CCGTACAGGT TCAAGAAGTG GAGATAGGTT

4691 AGGACTTGAT TTGCATGGTA TTGGATAAAT CATTTCAGTA TCCTCT CCAT  
TCCTGAACTA AACGTACCAT AACCTATTTA GTAAAGTCAT AGGAGAGGTA

4741 CACATGCCTG GCC TTGCTC CTTTACGCG TAGACCATCA AGTTGGCATA  
GTGTACGGAC CGGGAACGAG GGAAGTCGCG ATCTGGTAGT TCAACCGTAT

4791 AAGAAAAAAA AATGGGTTTG GGCCCTCAGA ACCCTGCCCT GCATCTTTGT  
TTCTTTTTTT T TACCCAAAC CCGGGAGTCT TGGGACGGGA CGTAGAAACA

4841 ACAGCATCTG TGCCATGGAT TTTGTTTTCC TTGGGGTATT CTTGATGTGA  
TGTCGTAGAC ACGGTACCTA AAACAAAAGG AACCCATAA GAACTACACT

4891 AGATAATTTG CATACTCTAT TGTATTATTT GGAGTTAAAT CCTCACTTTG  
TCTATTAAC GTATGAGATA ACAT AATAAA CCTCAATTTA GGAGTGAAC

4941 GGGGAGGGGG GAGCAAAGC CAAGCAAACC AATGATGATC CTCTATTTTGT  
CCCC TCCCC C CTCGTTTCG GTTCGTTTGG TTACTIONTAG GAGATAAAACA

4991 GATGACTCTG CTGTGACATT AGGTTTGAAG CATTTTTTTT TTCAAGCAGC  
CTACTGAGAC GACTGTAA TCCAACTTC GTAAAAAAA AAGTTCGTCC

## SUPPORT INFORMATION FIGURE S1

5041 AGTCCTAGGT ATTA ACTGGA GCATGTGTCA GAGTGTGTT CCGTTAATTT  
 TCAGGATCCA TAATTGACCT CGTACACAGT CTCACAACAA GGCAATTA AA

5091 TGTA AACT GCTCGACTGT AACTCTCACA TGTGACAAAG TATGGTTTGT  
 ACATTTATGA CGAGCTGACA TTG AGAGTGT ACACTGTTTC ATACCAAACA

5141 TTGGTTGGGT TTTGTTTTTG AGAATTTTTT TGCCCGTCCC TTTGGTTTCA  
 AACCAA CCA AACAAAAAC TCTTAAAAAAA CGGGCAGGG AAACCAAAGT

5191 AAAGTTTCAC GTCTTGGTGC CTTTTGTGTG ACACGCCTTG CCGATGGCTT  
 TTTCAAAGTG CAGAACCACG GAAAACACAC TGTGCGGAAC GGCTACCGAA

5241 GACATGCGCA GATGTGAGGG ACACGCTCAC CTTAGCCTTA AGGGGGTAGG  
 CTGTACGCGT CTACACTCCC TGTGCGAGTG GAATCGGAAT TCCCC ATCC

5291 AGTGATGTTT TGGGGGAGGC TTTGAGAGCA AAAACGAGGA AGAGGGGCTGA  
 TCACTACAAA ACCCCC TCCG AA ACTCTCGT T TTTGC TCCT TCTC CCGACT

5341 GCTGAGCTTT CGGTCTCCAG AATGTAAGAA GAAAAAATTT AAACAAAAT  
 CGACTCGAAA GCCAGAGGTC TTACATT CTT CTTTTT AAA TTT GTTTT A

5391 CTGAACTCTC AAAAGTCTAT TTTTCT AAAC TGAAAATGTA AATTTATACA  
 GACT TGAGAG TTT TCAGATA AAAAGATTTG ACTTTTA CAT TAAATATGT

5441 TCTATTCAGG AGTTGGAGTG TTGTGTTAC CTA CTGAGTA GGCTGCAGTT  
 AGATAAGTCC TCAA CCTCAC AACACC AATG GATGACTCAT CCGACGTCAA

5491 TTTGTATGTT ATGAACATGA AGTTCATTAT TTT GTGGTTT TATTTT ACTT  
 AAACATACAA TACTTGTACT TCAAGTAATA AAACACCAA ATAAAATGAA

5541 TGTA CTGTG TTTGCTTAAA CAAAGTAACCT GTTTGGCTTA TAAACACAT  
 ACATGAACAC AAACGAATTT GTTTC ATTGGA CAAACCGAAT ATTTGTGTA

5591 TGAATGCGCT CTATTGCCCA TGGGATATGT GGTGTGTATC CTTCAGAAAA  
 ACTT ACGCGA GATAACGGGT ACCCT ATACA CCACACATAG GAAGTCTTTT

5641 ATTA AAAGGA AAAATAAAGA AA CTGTAGCC TGTTGTTTCT CCTGGGCTTG  
 TAATTTTCC T TTTTATT C T TTGACATCGG ACAACAAAGA GGACCCGAAC

5691 GGGTAGGGCT GCGGAGTACC CGTTCCTGCC TAAAGGGGG TCAAGGTGTT  
 CCCAT CCCGA CGCCTCATGG GCAAGGACGG ATTTT CCCCC AGTTCCACAA

5741 TTTCAGCCTG AGTCCTTACC CATGTGTGGT GGTTCTGGGA ACTGACCATG  
 AAAGTCGGAC TCAGGAATGG GTACACACCA CCAAGACCCT TGA CTGGTAC

5791 CACGTGTTAA ACAGACCTGG GCCAGTGTTT GTTCTGCTTC GGGCTGGTCA  
 GTGCACAATT TGTCTGGACC CGGTCACAAA CAAGACGAAG CCCGACCAGT

## SUPPORT INFORMATION FIGURE S1

5841 ACTATAGCTT TGTGTTGATG AATTGGAGCC AGAGGCCACG TGGCCAGAGG  
TGATATCGAA ACACAACACTAC TTAAC CTCGG TCT CCGGTGC ACCGGTCTC C

5891 TGGTGGCCAA TCCAATCCCT TAT CTCTA CC CAATATTCGA GAAATCTGCT  
ACCACCGGTT AGGTTAGGGA ATAGAGATGG GTTATAAGCT CTTT AGACGA

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5941 CCAGGCCAGA TGTGCTCATA GGAGATAAGA GGTAGACAAC ACAGGCTTTA  
CGTCCGGTCT ACACGAGTAT CC TCTATTCT CCATCTGT TG TGTCCGAAAT

5991 GGAAACAGTT ACAAGGCTAA GGGTGACTCA ACTTCTCCCT CCTT GCATGT  
CCTTT GTCAA TGTTCCG ATT CCCACTGAGT TGAAGAGGGA GGAACGTACA

6041 CCCCAGCAAC TTAAAAACAA GGGCTAGTTG TCCAGCCAAG AATCCAGGAA  
GGGGTCGTTG AATTT TTGTT CC CGATCAAC AGGTCGGTTC TTAGGTCCT T

6091 GCAGAGCTCA TCCCTTTGCC AGTTGGAATG GCCATTCTTG GCAGCTTCCT  
CGTCTCG AGT AGGGAAACGG TCAACCTTA C CGGTAAGAAC CGTCGAAGGA

6141 GGGA  
CCCT

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