

Splice region in PMCA1 gene (ID: ENSG00000070961)

Legend:

GGCGTGTGGGTGTGG - exon

TTTCCC - NFAT binding motif

GGAAA - NFAT binding motif

TATAAA - TATA box

alternative splicing region

R - altered nucleotides recognized during splicing

SEQUENCE BEFORE SPLICED EXON 39 bp

Intron 1 - 2

GAGGGGCCCCAGGTGAAGGGCGCCCGCACTTCTCCTGCGGCAATCATCGCTCTCCTGCCT
CCACACGTCGCGGCAGCGGCCCGGCCCGCGCCGAAACAGCAGCTGTGACTGACGGAGTC
ACCTCCCCGCGCGCCTGGCCACCCCTCCTCCCCCGCGCTCCCTCCTGCACCAACACGT
CATGGAAACACGGACGTCAGAGCCTCTCAGCCAATCGCAGGCTGCGGCAGGAGGGAAGGG
GCGCGCTGGAGGGGGCGGGGCGAGCGCAAGCCAAGGCGCTCAGGGGAAGGAAGAAAGGG
AGGGGCGTGCGGAGGCGCAAGTCCCCACCTCCGCCCTCACTCCGGCCACCC**TTTCCC**GA
CCGCGCGGCAAGTTCTAATCGCCAGGCGCGCTCGCCAGCCGAGGGCGCGCTCGCCGGG
TCCTCCCTTTAAACGCCCTCCCAGTGCCGCTCAGCTCCCAGTCCCGGTCCGAGCCGCGGT
TCCTCCGCGCGCGCGCGCAGTCCCGCCCCAGGCTCCCGCGGATCGCGTCACG
TGACCGCGCTCAGCCAAGGCGGCAGCGCGGCGGCGAGCTTCGGCGGCGGTGGCGGCT
GTGGCAGCGGGAGCAGCTGCGCCGCCAGCGTGGAGCGGGAGGCGTGTGGGTGTGGAGAAA
AGGGAGCGCCAGACC**CGA****ACGG**GTGAGCGTTCTCCTCCCCCTGCCTACCCGGCAATCTT
GCAGGCCACCCGGTGCAGACGGGGTCCCTGCCCGGAGCTGCGCGCAGCCCCCTCGTGCTC
GGCCGTCCGCTCTCCGGTGCCCGCGGGCCCCGCCCGAGTGGGGCGGGCTGCGGCGCTCA
CGGAGGTGGCTGCACCCCGCCCGCGGCTGCTGTTGCGGACGGCGGGGTGAGGCCGGCTGA
GCTGCCCGTGCCGAGCGAGCGCGGCGCGCCCTGTGTGCCGCTCTGCGGAGCCGAGGAGGC
GGGTCTTGCGGGGACGCGGGCGGCCACTCGGTGGCTGCCGGGCTCTGGGCGGGGACGGCC

Intron 5 - 6

CATTGTGTAACAACACTGTTATAGAAATGTGAACTACTTCTGCATAATTTAGCATGGCTGTA
TTCATTTCTTTT**GGAAA**GCTTTAATTCCCATTTTGTTCCT**R**CAG**ATAAGAAACAAGATGG**
AGCTATTGAGAATCGCAACAAAGGTAAATTTAGGAGGACAAAAGTACAGTGAGCTTGT
TCATTATATCCAAAATCTACTGTATACCATATTTATTCAAAGTAAGATACATGTGGCA
GGAAAATCAACAATATACGTTAGCTTGGGTAAACCTTTCTTCTTCCGGTGTCTTAGTC

SEQUENCE BEFORE SPLICED EXONS 154 bp

Intron 19 - 20

GACTTTTAACTGATTATGAAAGAATGTGTCTATATGCCCTAAGCTCCTTTTTTTCCTAGC
TCCCCCATCCCCACTTCATCTCAAAATGCTATTCTTGCCTATATGCTGTGTAAGAAAGTG
CCTTTTTCTTTTTATATGTTGATAGATGGAATGGTCCCTTTCTTCTTCTCTCTCTCT
TGCTGAGCAAGCTGTCACAATCTCTGATTCTTGCAG**ATGGATGTAGTGAATGCTTTCCA**
GAGTGGAAGTTCATT**CAGGGGGCTCTAAGGCGGCAACCCTCCATCGCCAGCCAGCATCA**
TGATGTAACAAATATTTCTACCCTACACATGTAGTGTTCCTCTTCTACTGCTTCTAC
TACTGTGGGGTGTGAGTGTGTGTTCCCTAAGTGCATGAAATTAACATTTCTACTTACAC
ACCTAACGTTTCTCATTTTCTCCTTAATGTTTGAATTCATTGTTTCAGGCTTTTTTCATAAA
GCTTCTTTTCGTAAAGTGGATTGAGACCTCAAAGTGTGTCGTTGTTGTTTATTTCTT

Intron 20 - 21

GCTGAACTGGCCTAGTAACGTGCTGAAACTAACCAGACATATGGCTTAAATAGATGTGTC
AGACAAAGGAAGCATTAAACCTTAATCTTATGGAATGTTTTATTCAAGTGAAGTTAGGGAT
AAAGTAAATGATCGTATGTTTTTGTCTTCTCTTACTTCCAAGGAACCTGGAATTGGGAG
CCCAGAAACCTAGGTTTTAAGACTCTTTAGCACTAATTAGGAGTTCCTTAACAAGTCAGC
CACCCATCCTCTCTGTTGCTCAGTTTTATTATTTATGAAGTGGTTAGAAAAAAAAAATCT
CTAATATTGTTCAACAAATTCAGATA**GGAAA**AATCTTCTCAGAATTGAAGTTTTGCTAAG
AAGGGATTTAATCTTTCTTTGCCTGCCACCGGTGTATGTGTGTGATTGTGTGTGCACATA
TACTTGTGTCCTCACCTTTACACTCTGCCCTCTTAGAGCTTCACTAACTCTCAAATCT
CTAACTTAAGTTTACACTTTTCTTCTGAGCTCTAGATATTTTCCAAATTTAACATGTTTA
AAAAGTACATTTA**TTTCC**CCCCGATTCTTCACTGCTCACTTTTATACCGACTGATTACAA
AGAAAAACAGAT**GGAAA**ACACACACATACACAGAAAGCTTAACTGTTGTTCTATCTTCAG
TAGCAGCAGCACCAGCAACCTTATCAAATAAGCAACATCTTCAGGGTTGTCTTGAACAGT
TCTCATCACCCATCAAGTTTGCTGGCTGATCCTCTAATTTGTATTCTCCTCCGTGCCTAC
GGGCTGCTGATACCAACAAATTTTTTTTTTAGAAAGTTATCTTTTTTGCATTTTAAAGCTTTA
CAGTTTGTATTATTAGGACAGTCAGGATACTTGCTGAATGTTCACATG**TATAAAA**ATGTGAAT
TTTAAGACTTCAACAATAAAACACTGAATGAATTACTATAACGTTATATTTAGCAAACATT
GTTTACATTCCATATGTAGAACACTTTACATCTTAGTAAAGGGGAAGAGGAACAAGAGCA
ATAAAAGAAGTTGAAAAATATTTGCTGCTATTCATCAGTCAAATTAAGGAACTGAAGTAC
AAGCAATCAAATAGAATGGAAT**TATAAAA**AGATGGTAAAGCTGCAAGACATTAATAGAATA
GATGCTTGCTGCTCCAAGTGTGGATCATGGACCAGCAGCTTTAGCATCACCTTGGAGGTT
GTTAGAAATGCAGGACTTTAGGCCCTGCTGAATCAGAATCTGCATTTTAAACAAGATCCC
CAACTAATTTGTATGCACATTAAGTTCGAGAAGCCCTGGCCTCGATACTTGTGACCTAA
CATTGTTTTAAGTTTGTAGTGTGCTAACGAATTTAATCTCCCACAACAACCCCGTAAGGC
AAGTACCATTGCTATTTCCCATTTTATAGTTGAAGAAACCTGTTTGACCGAGGTTCTCTCA

PMCA1: 6 NFAT motifs

Splice region in PMCA2 gene (ID: ENSG00000157087)

Legend:

- GGCGTGTGGGTGTGG** - exon
- TTTCCC** - NFAT binding motif
- GGAAA** - NFAT binding motif
- TATAAA** - TATA box
- alternative splicing region
- R** - Altered nucleotides recognized during splicing

SEQUENCE BEFORE SPLICED EXONS: 33 bp, 60 bp, and 42 bp

Intron 1 - 2

GTCTCACTACCAGTCT
ATCAAGGTAACACTGAAATATCACCATTAATTCTTTTTCTCATAGAGAACTTTCTGCTAGCT
CTCTAAAGGAATGAAAATAACCTTGGGTAGGTAATGGGACAGGGAGAATCCTAAGTCATC
AGCCAAATTTATTATTCATTGACATCTCCATTCATCCATTTATTCACTCATCCTTTTTCTC
CATCTATTCATTTATCAGCCTCTCTAACTACCAATTCATCCACCAGTCCATCCATCCATC
CACCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCCCTTCTCTCTC
CATCTGTATCTCCATATATCCACTTTTCTTTCTAGCCATCCATTCATCCATCTATCCTTT
CACCAGGTTCCTCACTAAGCATCAATTCTGTGACTGGCTCTGTGGGGTAGAGATGAAAAGG
CTCACTCAGTTCAGCCCCTGCAGATCCCCCAGGACCCTGGCAGCAGCAGATCTATGAGC
CCACATTTTCCCCTGCTTGTGAGGATCACACCAAGAGAGACATTACATCCTGGCCTCAC
AAAGAAGAGATGGCAAAGTGGAAAAGGCCGGAGTCCCCAACCTGAGCCCTTTACCCTG
TCTCAGTCTTTTTATAACGAGGTGTGTGTGCTTGGGCAATGCCTCTCTCTTTCTGGGACTCA
GTGTACCCATCTCTGCTGTGGGGAGGTGGACTAGATGAGAGTTTCCCAAACTCCAGTTG
TTTTTTTCCCCTCCACACCTGGAGATCAGAACACCTGTACTAAAAAGTACTGAAAAT
CTTTATTCAAATGAGCTCACTTTTTTTTCAACCAAATAAATTTATTGAGTGAAGTGA
TATTGCTACCATAAATGGAAAATAAATGGTAACAGCTGTCATAAATAGAAAGTAAACAATT

Intron 2 - 3

AAGCTGACCTCACAGCTAAGCAGAGTGGGTGGTCGCCTTAGTGATGTGAGTCGAGGGGTG
CCAGGCAGCTCCCTCTGCTGCAAATCCCTCCCACTCACCAAACTGCTGCCGCCTGCAATT
CCACAATGAGCACTTTAGTCATCAAATCATAAAATGTCAGCTTGTAAATAGCCTTGGAAC
CTGTCTAGTTCAAATTTCCCAGCTCAGAGTGCTCTTGGAAAGATACCTGAACGGGCCCTTTA
TTTTTAGAGTGAATTAGTGGCAGAGCTGGAACCTCGAGTCTGACCCTGCACAGTGAAGGACG
CTAGAGGCATCTGCAGCTTCTTCAATGGGAAGGTGGGTTCTGAGTCACAAGATGGGCAGC
TCCCCAACAGAGGAAGGGTTCAGACATCAGGCATCCAAAGTAAATGACCAGTGTCCCTA
GTATTTATTTAGCCCTCACATCAAATGTCAACTTATAAAGAAAAGAGGCGACAATATTCC
GTTGAACGTTGCCTTCTCTTCAATCTAACTAATTCATCCCAAGTAGGATCCATTATCTG
ACTGTCTCATTATAGTCACACTGGAAAAGCACATCTTGTGTTGTTATAAATGACTTTTCAATT
TATTTCTCTTCTTTATTACAGTTGGGGCATCATATGCCTTTTTGAAATTATGTGTATTGG
TAGGTTATATGATGTGTGAATTTTCTTGGAAAGATAAAGAAAAAAAGTAAAAATGATGTTGG
ATCCAATGGGACCAAGAGCCACCAGCACAGTGGATAGAAACAAGGCCCTGTACTGAATC
CTGCCCTGCCTCCTAATTAGCTAGGACCTTGTCATATGAGCATGAACATCAGCTCTTACCC
CGGGTCTCTGAAGTCATTTATTGAACTTGGTTTCCCCTCACTAAGTGGGGTGAACAGTGG

Intron 3 - 4

CTACCGCGCACCAACTGAGCTGGGCAGTGGGATTTTACAGCAAATGAAAGCAGTCTAG
GGGACTAACGTGTCCAGGTTTGTCTGGGACATTCCTGATTTTAACTGAAAGTCCCAC
ATCCCAGGACACCCCTCAGTCCGAGGCAAACCAGGACAGTTGGTTCATCCTAACACAATCT

CTGCCCTCATGGATTTACAGTTTAGTGGAGGGACATAGACAATAAGTAAATATATAACAT

Intron 7 - 8

GACTGCAGAAGGCCAGTCTGCTACTCGGC **CCGCACTCTCTCCATTACACTACCCTGCCT**
CTTCTCCATGAGAGGCAGCGGGGTGTAGTGGATAGAGCACGGGTTCAAGTCCCGGCTCCA
CCACTCACAGCTGTGTGACCCTGGGCCATCACTCAAGCTCTCTGAGCCAGAAAGTGGTGG

Intron 8 - 9

AGAAACCTCCCTCCTGAGTCCCCTGGAGAATCAAGAGTTGCCCGGCTGGCAGGCCCCACA
GCTAAGGTGCGGCCAGGCCTGCTCCTGCTTCAGGGCCCTCCCCAACCCGTATCCCCACAC
AGAGGGATGCAGTCAGCACGGCCCGCCCTTCATCTGTGACATTAATGTCTGTGGCCTGTT
GCGTCTTCGTGATGACCGACCATGTGTTGTCTGTTCTCTGTTGTCTGTTAAAATTCTTTG
TCGTGTA **GTAAAATGCAGGATGGCAATGTGGACGCCAGCCAGAGCAAAG** GTAACC **M**TTT
TGTTTTAACC GGCGTTTGTGCTCCCTGAGGCCCTCCCCACCGGCTCTGACAGTCACACC
AGAGACAGAGACTGGCAAGGGCCAGAGGCAGACACATCCACTCCTACAGGTGTCTGACGA
CCTTGGGGGTGTAGCTGTGATTTGCATGGTGCCAGGCCAAATAAAGAGGTGTCCACCGGT
GAGGAGGGGGATACCCATGGGCCAGCATCTCCCTAGCCTTTGAACTCTGCGCCCCATTCA
GCTGAAGACTTTGAGATCCTTAGAGGTTGAGGGGTAGGGAGTTTGGCTCAGTCTCTGTCC
AAAAGGGTCACGGGCCCTCCAGTCCATCCTGCATGAAGAGGCCACGCCAACTGGGATAGT

Introns and exons 7, 8, 9

ACCTGCACTCCTGTGAGATGGAGATGTCAGAAAAATAGCCTCATGTAGAAGGAAGATGGG
GAATGTGGAAGGGATGTGGCAGAGGAAGCCTGGGGGAGCAGTCCAGCATCTCAGGCCACC
ATGAGCAGCATGGCCTCAGCTGGGCCCCCTCTGCCCTCCCATCCCATCACCTCCACTAGG
AACATTGCTTAGAGCCCGCCACATGTCCCCATTTAGGATGACCCTAGGTGTATGGCCAT
GTGTGTATGCACATGTGTGTTTGTGTGTGTGCGCGTGCGCATGGGCAGATGAGGCTGTGT
GCTTCTCCTTCATTAACATGTCTCAAAAATCATCACA **Y**AG **GTGTGAAGAAGGGGGATGGC**
CTTCAGCTACCAGGTACAGTAAGACACCCTCAGGGTAGATGGGCTTTTAGAAATAGCAGC
AGGCTTTGGTCATTGGGCCCTGCCCCCTAGACCACCAGCACACAGCTGGAGGAGGCCACAT
GCCTGTGGGTGGCTCCACCCCCAGACCCTCCTTTGTGCCCTCCTGTGATGCCAGCCCTG
TGGGACAAGCCAACACCCCACTCCACCCTCTTGCCCTTACAGTGCCTCACCCCTACCAGCC
AATGCCAAGTGGTACCACCCCATCTCTACACCACCCTTAGCCCTGCGTACCAGCATGCA
AAGCTTGCTCACCATCATAGGACCCTCCCCTCAGGCCCTGCTCTCCCCACCAGCACCCCT
GGGAGCCCATGCCCTCACGCAACAGTGTGCTTCACCCAGTGGGGCCTCTTCTGCCCAT
AGAACACTATTCCCTACCCACAAGAAAGAGCAAAAGGTGTGAATTTAGCCATCTCATATC
ACTTTTAATTTCTAAATTAAGAAAAATTCAGTAGTGCT **TTTTCC**ATCCCATATACAAAAT
GCAACATGCTTGATGTCACCTTTTAAATTTGGGGGGCATCTCACATGGGAGTTCCCAAAG
CAGTCTCTGGAATGCCAGTTAAGGAAGGAGGCAATGGCCTGAATCAAGGGCATGAATCCA
GTTAAGTCAAAGTCATCACCATTAGCAAATGTTCTTCCAGAACACCCTGATGCACAGAGA
TGGTGGTCATGGAGAATACTCATTCTGAGTGGTCCGTGCCACGCTGCACTGCCTAGTGA
ATATTTTTTCCACTCCTGGCCCCAATGGGCAGCCAGATCTCCTCATTTTATGGAGCCCTC
TCTTCCAGGGGACTCTCTTGACTGGTTGGACCAGCAGGGTCCAGACCTCAGCACAGACCA
GCACCATCCCAGCTAACCACCCTGGTCATCCACCATGCTTTATTTGAAAGACCCTCCATG
TCTGAGTTTCTCCCCTCAACCTCTGCGGCATCTCTATGGAACATTTACACCCCAACCCCAA
ATTTGAGTTTCTTGGTTTCCAAAGGATAATTTTTTTTTTTAAGAATAGAGTCATGTTATC
TCCCACAAGTTGGTTCATGTCTTTGTGCTTGTGCTTTTCTCCATTGTGACACTGCATT
TTCCATCCCTCCACCC **YSS**TG **Y**AG **CAGCAGACGGTGCGGCAGCTTCAAATGCTGCAGAT**
AGTGCGAATGCCAGCCTAGTCAATGR **T**ATGTCTCCACGGCGAGCTCCTGGTCATGGTTG
GATGGGCGTCTCTCACCCCAACCTTTGGGCTTTCTTTCTTCTGTTCTGGACTGCAC
AGATCTCGGATGTGCATGGGCCGCTGGGACAGTCACCTTCTCACATGGGGCAGGCGCTTA

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TCTGGGTCCCCAGCAAAGGCTCTAGTCCTCGACTCTAAAATTTCTCGAGGCAAGGGGAC
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GTTCTGTCTTTCGGATGTGGACTGGTGTTCCTTGTCTGTTGCCTGTGCTGGAGCGTTTGTG
CTGGGTACAGGGGTGGAGGGTGGGGGAGAGGGGCTGGCACTGTGTACTGGTGTCTGCAT
CTTAATCTCCTTACACGCAAGCAAGAAGGAGTTCATTCACTTGCCCCCAAAGCCTTTAG
AAGATTTTCGGATTTCTATCCCCCTTCTGGCTTCAGAGCAACAGACAAGGCTTTTGTACT
CAGATACCACCCCTATCCCCAAATAAAGTGACATAATAGTCCCCCAGGCTACTCCTGAAC
TGTTGAGAGCCATTAGGGCTCCATCATGAAAACATTGCCCCAGAGGAGCTGAGGGCAGGG
GAAAATCTTTTTCCACCGTCTCTGCATAACCAGGCACTGGGCTGTGGGTTTCTCATCCAT
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CTCCCATCCCCTGCCCTAGACCTCTCCCCAAGCCACCTGCATTCAAAGTGCCCAAAGATG
GAAGCACCTAGTAGGTGTCGGGGCTGAGTAAGGCACTTCTGCGAGCAGTGCCTTGCCAAG
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GGAGTGGGAGGTGTCATGCCTCAGGGAGGGGTGGCTGAGGGTGACAAGGAGAACCCATGT
GGGCAAACCCATGGCTGAGAGAGAAGGAACCTAGAGGGGGCACCCACTTCACCCCGGCAG
TGAGCCTGCTGAGCTTTGTGAACATAACAGACCCCATCCAGGCTGGCCAGTCTCAGAAAA
AGGGCAGCTTTACTTCCAGACTGCAGCAGAAAACCCCAAATATCCCAAGAGAACTGTAG
GAAACGTTCAATTTCTTGACCACCTACTGTATAACCAGGCACTGCTGAAAGCATTTTCATATT
CACCATCTCATTTAATCCTCATGACACCCCATGATACAGGTTTTTATTGTCCCCACTTTA
AAGATGAGGAGACTGAGGCTCAAGGAGACCAAGACACTAGCCTAAGGTCACAGAGCTAGA
AAGTAGCAGAGCTGGGATTTGAACCCAGAACCAGACCTGGCTGGCTCTAAAGTGTGTGC
TTCTCCTCCTGATCCAGGATTTCCAGTGGAGTGTGTCTTGTAAAGTTTCACAAGGATGTT
AAGAGGGCTTTACCCCAAGAAAAGGATTTCTGTGGTCAAAGATGTTTGAGAACCCTGGAT
TGAATTGATCTCTTCTGGTTACAGAAATTAGTCCTGGTTACAGGACTGCTCAGAGCCTTG
AATATGCTGGTGTGTAGCGGAGAGTTACAGAGTCACATAGAGTTTCCTAGGCTGATTTGA
CTGCAAGACCTTTCTGGCTGAATCCTGTGGAATTGGTCTGCCCCATAATATACTCTGGG
AAATAATGCTCTAAGCCATTGCTATTTCAAATGTGATCACAGGACCCAAAGCCTGCACAT
CACCTGGGAGCTCCTTAGAAATGCAGAATCTCAGTTTTTTTATTTTATTATTATACTT
TAAGTTTTAGGGTGCACACGTACCCTAAAACCTTAAAGTATAATAATAATAAAAATAAAAAT
TAAAATTAAAAAATTAAAAAAAAGAAATGCAGAATCTCAGACCCCAACCCAGACCAACT
GAAGGAGAATCTGCATTTTAAACAGGCTTTCCAGACTCCAGGTGAGAGCACATTACAGGTG
GAGAGGCACAAGGTGGAACCTTGCCGATTGAGAGAGAATTAAGTGTCTTTCCCTCCTT
CCTCTGAGCCAGATCACAATGACTTGGATATGGAAAATAAATAAATAAATAAATAAATAA
CCCTTTGACCCTGCTCCCCAAGCCCCCAACTGAAAAATGGGTGTGGTCCATTCATCTTG
GAAGCATTATGATTGCCATTATTATTTAGTTATTTTTCTTTTACATTACTAGTGTGTAC
TATGTAATACATGACCTGTAATCATGGTTATAATCACAGTTAATTATAACATCATGAGGCC
GGCGCAATGACTCATGCCTGAAATCCCAGCACTTTGGGAGGCCAAGGCAGGTGGATTGC
TTGAGGTCAGGAGTTGGAGACCAGCCTGGGCAACATGGTGAAACTCTGTCTCTACTAAA
ATACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
TAGGAGGATGAGGCAGGAGAATTGCTTGAACCCAGGAAGTGGAGGTGCACTGAGCTGAG
ATCATGCCACTGCACTCCAGCCTAGGAGACAGAGTGAGACTCTGTCTCAAAAAAGAAAA
AAAAATTATACATCATGGGCTGGGTACAGTGCTTCATGCCTATAATCCCAACACTTTGGG
AGGCCGAAGCAGGAGAATCACTTGAAGTCAAGAGTTTGAAGTGGAGGTTGCACTGAGCTGAG
GAGACCACATCTCTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ACATCTATATTCCCAGCAACTCAGGAAGCTGAAGTAGGAGGATTGCTTGAAGCCAGGAGT
TCAACGTTGCAGTGAACCAAGATCACGCCACTGCACTCCAGCCTGGGCAACAATAAATAA

AACACATTACTACTAACTCCCAACGTTTACACAGTGATTTTCCAGTGCCTTTCATAAACA
TCACCTTAGTTGATATCCATTTACAGAGGAGAAAATGGAGGCACAGGGAAGAGAAGTGG
TATTTCCCAAGTCTCCCAGGTAGTGGTCTCTCTCCCAGAGCTTGTGTATCAGGTCAGCT
TACCAGGAATCCTCCCAATCCATGCACTTACACCCATGCCCTTGTGTATGCACAGAGAG
AATAGACCCATTT**GGAAA**AGGTGCATCTGACTCCAGATACAGAGAAGGGCCTCTGAGACC
CCACCTGAGGGCTCAGTCTTGGACCCCATTCCTAGCTCTCCTGAAATACAGCCCATCTCC
AGATCCCACATGGGGCCAAAGCTGGCTGTTCCACCATAGTTTCAGGGCCAGGCGAGCACCA
GTTTGGCCAGGAGAGCCCCAAATAAGTCCCTCGCTTCTGAGAAACCAGGCCATCTGTGCC
TCAGCACTCCCAGAACATCCTTCCCTTCCCTCCAGCATATGCATTGGTGATTATTTTTCTG
ATCACGTGTTCACTCT**GGAAA**TAAAAGAGGAAAGTGCTAGCTGGGCTTAATGAGTGCACA
CACCGGCTATTGCATCTGATAAATATGCAATGCAAATAAAGGCCCTTTGAGCCTTCTAAA
ACCAACTATTGAAGTGGAGTCCCCTGGTGCCCCTGAGCCCAGTCAGTAAAATTATTTTAG
AAAATAAAAATAATTGTTGTTATTCATTCCTGCTTACTCTAAAAGCTTTTTTCTCTTGT
GTTTTTTAATCCAGTAGAAAGAATTTTACAGTAGAGACACAGGGGGTCTTTCACCTTAAA
GCCCAGGATGGGCAACTGATCCTTTGCCATGGGAGGCCATGGGGACAGCTCTGCACTTAC
CCTTGAACAGACAGTGTGGGCGAGGTTCCGGGAAGCCACTTCTCCCCTCTGAGTCACCC
AGAAAGTGGGCACAGTGACAGTGATGAACTAATCCTGCAGCCATGGGGCTATTCCGAGGA
TGCTCCTAAATTCAGGCTGCCTCTGAACTTCCCTTGGCCTCAGTTTCCCCTCTATAAAA
TGAGAGTGATGAAAATCCCTCCTGCCCCACCTTGCAGGGATACTGGGAAGACTGACAAGA
GATGACACTTGCAAAGCCCTTTGAAACTGCAAAGGCTGAACCGTGCAAGTGATTATGA
TGAAGGTAAGTGGGACACTCTGGGAGGTGAATGTCTCATCCTGTTTTATGAAAGTGGAA
CTTGATGAGATTGGGAGATAGAAAGCCAGCAGCTAGTTGGTGGTGAAATGAAGACTTCAG
GAACCCTGTGCGCAGCAGTGCCACCTCAACTTCCCTCCCCTGGGCTCAGAGGGGGCTGAGGG
GTGTCCATGGTCTCCCTGACGGCAGCTTCTGGAGAAGCAATGGCAGGACGGAAGTAGGCA
CGCACTTTGGGGCCAGCTCTCCATTTACCCATTGAGACCCAAGCAGCTCATCTCCCTCTC
TGAGCCTCAGTTTCTCATCCATAAATGGGTATAATACAAGCACACCCTTCATAGGTGAGG
CTGTGGCGAGGATTAGATGGAATCTCAGAGCTTATGTGTGTGCCCAGCACATGGTGGTGG
ACTGTCCCTGGAATGTGAGCTGTGAGAATCACCATTCAGCCATCATCCAAGGGTGGCCAA
CCTTCTCAGACCCCTCCCAAGGGGGCGAGGCCGTGTTGGCAGAGCAGGCAGAGCTCTGGGT
GAGCGTGCAGGCCCAGTAGATGGGAGGGTGTGCTGGCGAAGGCAGGTGTGCTAGGCAAGAGA
CAGAGGCCTCCATTGCCACATTCACACCCAGCCACAAGCTCCTGGCCAAGGCTGGAG
TGGGGGCCTCCCAGGCAGCTCTGATGAGTCCGGTGGGGGGCAGCCAGATGCAGCACCAGGC
CCTGGTATGGAAGGGGATGCCACGGACACTACTTAGCCTGCTGCTGTAGCCTGAGCCAT
ACCCCTACCAAGGGGTCAGCACCCCCATTGGGGACCAGAGCACTTCATCAAGAACCCGGC
CACACTTGAGGTCCCTCGTATAACCACCATGGGGACCCCTGATCACTCTTTGTTCTGGTCA
CTCTCAGGGGCATTGGGCAAGGGGTATCCTTGGGTGGCTTACACTCTTCAGAGTGTGA
AGGAGAAAAGATCATCCCTCTTGAAGGCCAAAATAAGGAACACATTGACCTCAGTGCCTT
GTCCAAACTCCTCTCCATTCTAGAAACACTCTCTCCTCTCTCTCTGTCTCTCTTTCTCTC
TCTCTCCCCTCTCCCCTCTCTCTACTGCATGTTTTCTTTTGTG**GGAAA**ATGAAAAGGAC
GTAAGTGAACAAGCTTCCCTTTGCCTTCTCTCAACCAGAAAACACCAAATCGGTCACAA
AAAGCTTGGTGTGGGGGCCTGAGTGTCTCTGCTGCCTCCTCCAGCAGACTCTAATCCC
CTGCACCCTCTGATACTTCCCTTTGATCTGTAACACGCTCAAGGCCAAAAGTATTCCAGC
AGAAACCTCCCTCCTGAGTCCCCTGGAGAATCAAGAGTTGCCCGGCTGGCAGGCCCCACA
GCTAAGGTGCGGCCAGGCCTGCTCCTGCTTCAGGGCCCTCCCCAACCCGTATCCCCACAC
AGAGGGATGCAGTCAGCACGGCCCCGCCCTTCATCTGTGACATTAATGTCTGTGGCCTGTT
GCGTCTTCGTGATGACCGACCATGTGTTGTCTGTTCTCTGTTGTCTGTTAAAATTCTTTG
TCGTGTA**RGTAAAATGCAGGATGGCAATGTGGACGCCAGCCAGAGCAAAG**GTAACC**M**TTT
TGTTTTAACC GGCGTTTGTGCTCCCTGAGGCCCTCCCCACCGGCTCTGACAGTCACACC
AGAGACAGAGACTGGCAAGGGCCAGAGGCAGACACATCCACTCCTACAGGTGTCTGACGA
CCTTGGGGGTGTAGCTGTGATTGTCATGGTGCCAGGCCAAAATAAAGAGGTGTCCACCGGT
GAGGAGGGGGATACCCATGGGCCAGCATCTCCCTAGCCTTTGAACTCTGCGCCCCATTCA

GCTGAAGACTTTGAGATCCTTAGAGGTTGAGGGGTAGGGAGTTTGGCTCAGTCTCTGTCC
AAAAGGGTCACGGGCCCTCCAGTCCATCCTGCATGAAGAGGCCACGCCAACTGGGATAGT
GACTTGGCTCCCATGGCTGCCCTCTTTTACGTTCTAAGCCTCCTTTTTTGTCCCTCCTGT
CGAGTGGCTACTTAATATCCACACAACAGGTCCCAAGGACCAGCTGGGTAGAGCCCAAGCC

SEQUENCE BEFORE SPLICED EXONS: 172 bp, 55 bp

Intron 22 - 23

TCAAAAAAAAAAAAAAAAAAAAAAAAAAAGACATTGTCAAAGACTGGGCTGAGGAACAGGTGA
GGTGGGTGAAGGAGTAGATTGATCACATGCCTGGGTGAGCGGGTAGGAGGAGGGAGGTAG
AGGAGCGGGTGTGAGGGAGAGAAGGCCACTGGGAAGGACAGCCCCACCGTCCTGACAGAC
AGGGTCCCTTGCAG**GTCATCGCCACCATCCCGACCAGCAGACTCAAGTTCCTCAAGGAGG
CAGGCAGGCTCACACAGAAGGAGGAGATCCCGGAGGAGGAGCTCAACGAGGACGTGGAGG
AGATCGACCACGCGGAGCGGGAGCTGCGGCGGGGCCAGATCCTGTGGTTCCGAGGCCTGA
ATCGGATCCAGACACAG**GTAYAGGAGGCTCTTGGGGGCTGGGCCAGGCCTGGCCGGGGC
GGGCCAGGGGATGGAGGTGAGTGTGCTTGTGCTGCCCCCAGGGCCAGCTCTGGTGCTG
AGGGAGGGTGGCTACAGAGGGGTCCCGGCCAGCTCTCACCAGCCACTTGCACACCCACTC
CTGTGGCTGCTAAGGAACAGCACGGCCTCCTCAGAGAGGTCCCATTGTGCCCTCTCAGGG
CAGCACGGGGAAGTGGTAGGGGTCACACCCACCATGGTCTCCAGGGGGA**TTTCC**TGAGA
TGTCCACAGTCAAGGCACCAGATGTGGCAGAGCCAGGATGCAAGTTGGGTCTTTCTGCCT
CCAAGTCCAGTGCTC**TTTCC**ACTAGCCTTGAAGACTCAATGACCAGCCTCCTCCCATTCT

PMCA2: 16 NFAT motifs

Splice region in PMCA3 gene (ID: ENSG00000067842)

Legend:

GGCGTGTGGGTGTGG - exon

TTTCCC - NFAT binding motif

GGGAAA - NFAT binding motif

TATAAA - TATA box

alternative splicing region

R - Altered nucleotides recognized during splicing

SEQUENCE BEFORE SPLICED EXON 42 bp

Intron 2 - 3

AAGGCTCCTGTCTAGAGGGAGAGCCAGGCGCTGGCCAGACGGCCCCAGAGGGCTGCTGCC
ACCCAGGAGCAGTCAGTCAGGGCCACATAGGAGGCCTGGGACACACAAGGCCGACCCGT
CCCATCCATCCTCCCTTCTGTGCTTCCGGGGCACCATGCAG**GCCTGGCGGACAACACC**
AATGACCTGGAGAAGCGCAGGCAGATCTACGGGCAGAACTTCATCCCCCAAAGCAACCC
AAGACCTTCTGCAGCTGGTGTGGGAGGCCCTGCAGGACGTGACCCTCATCATCCTGGAG
GTGGCTGCCATCGTCTCTCTGGGCTCTCGTTCTATGCGCCGCCAGGAGAGAGTGAA
GGTAA**RS**CCCGGGGGCCTGGGCTGGAAGGAGGAAGAGGAATGGGGCTTGAGATGAGGGAC
GGTCACAGGATGGTGATGTCTCCTCCACTGCT**TTCCC**TTCTGTCTCTCC**R**CACAG**CCTGTGG**
GAATGTGTCGGGAGGCGCAGAAGATGAGGGCGAGGCCGAAGCTGGCTGGATCGAGGGGGC
TGCCATCCTGCTGTCCGTCTGTGTGGTGTGGTGCACGGCCTTCAATGACTGGAGCAA
GGAGAAGCAGTTCCGAGGCCTGCAGAGCCGAATTGAGCAGGAGCAGAAGTTCACGGTCAT
CCGGAACGGGCAGCTCCTCCAGGTCCCCGTGGCTGCGCTGGTGGTGGGGGACATTGCCCA
GGTCAAGTAYGGTGAGTGCCCTGGTCTTACCCACCCTGTCAAGGAAGCTCGGCTCCTGC
TTCTGGGGAGGGTGAGCCAGAGGAGACCCCCAGCACAGGTTCTCCCCGGTGGCCTGCGTG
TCGTACCTGCCTTAGGAGGCGGGAGGTGGCGGGGGTGGGGGAGGTGGGGGAACACGGGG

Intron 3 - 4

CAGGGCAGAGTGGTTTCAGACACAGCAGGCCCCCGAAGAATCAACTGTCCCCACAGCCTC
CACGGCGGGCT**TTTCCC**CCCTACAAAGGATGCAAATGTCCTCG**TTCCC**CAGAAGGAGGAGG
GCTCCTGAGTCC**TTTCCC**AGGCGGCCATGGCACCTGACGGGACCTCCCCTGGGGCAGC
CGGGAGGAGGCGGTGGGGAGAAAGGCCTCTGC**TTCCC**GGTGCT**Y**TAG**GCGACCTGCTGCC**
AGCCGACGGCGTGCTCATCCAGGCCAATGACCTCAAGATCGACGAGAGCTCCCTGACGGG
CGAGTCTGACCACGTGCGCAAGTCAGCTGACAAAGATCCCATGCTGCTCTCAGGTGAGGG
CCACCCTCCGGGCCAGCCTGGCACCAAGGGGCGTCAGCAGCCGTGTGGCCAGCATCCTG
TCCAGGCTGCCTGCTGGGCTCAGCCTCCACCTCCACCAGGGCCTTCCAGCATAACCTTCA
GGTTGGGAATCTGAAGACTCCGCCCGTCTTGAGGCCTGATGGTGGCAGCTCCAGCCACAG

Intron 6 - 7

GTGCTGGGAGGTGGTGACGGGGTGAGCCTGGAGAGGACGGGGCATGAAGAAGGCCACCAG
CAATCAGGCCCTCCTCCCCACCCCTCTGCCACGCGGGCCCCAGGCTGGTGTCTCAAG
CCTTCGTGTCTGTCATCCCTCTTCCATTGTAG**GCAAGCAGCAGGATGGGGCCATGGAGAG**
TAGCCAGACCAAAGGTAACG**R**GCGCCGCTGCTTGGGCACAACAAGCTTGAGCCCTGGGG
GTGGGGCTGGTGGAGGGCACAGTGTGGGGGAGGTTACCTGCCTCGGTGG**CAGGAGCAA**
CACTTGAGAC**CAGG**TGAGTGGGCTGGCTGCACAGTCCCGTCCAGTGCAGAGGGAGGAG

SEQUENCE BEFORE SPLICED EXONS: 154 bp, 68 bp, and 88 bp

Intron 19 - 20

GATCTCTGTGCCGGCCACAGGGGCTGCTGCAGCTGCTGCAGATGCCAGCCTTCTTGCTGG
CCCCAGCATTAGTGTCTCGGGGACAGCCCACCCAGTTCCCTGTTTCATTTTCAGAATTCT
CCTTTCCCTCTGCTACTGCACCTCACCTCCGAATCACACTTGAACCTGGTTGCTCCATGG
AGTCCCTTACCTTCCCGAAACCTGGACTCTAACCACAGCCCAGAGGGGTGCCAGGCCCTC
TTCTTGCTCTTCAAGCTCCCAGGCCACTGGCCTTCTGGTCCCCCAGGAATGTGGCACCA
GCCTGTAGCTCGGCCTCTCAGGGGCTACTGGGTGTCCTTTTTCATTTTTTAACCTTGTTTCA
TTACAAAGATAAAAACATGTTCAAGAGAAAAACGAAAAGAAGGGAATCTCTGTGAACCAGT
CCTCAAGTCCCCTCCTGGCCATGTTTCGACAAAATACACTGGCATAGACACACAAGACAGAC
GAGACGTCTTGCTCTAGAACTCCAGATGCCCATCATCCCTTTCTGTGGCTTCCCTGCGT
CCTTCTAGACTGTTCCTCCACTTCCAGTGGCCTACAATATGCGAAGCCATGCCCTCTC
TTTACTCCTGCCAGGCTCCTTATCCAGTCACCCTTTCCAGCTGTCACCCTCCTTGTCACC
TCCCACCCTCTCTAGCCCCAATGCACAGGTCTTCTCTAGGCTGGTGTTCCTCCAGGAGA
TGCCCTCTCCAGGAGAGACTAGGCCAGAGCTCCAGCTGTCTCTCCAGGGGAGTTGCGC
AAACAGCGCCTGTGTCTCCAGCAACGGTGTGGAGCGACATGCAGGGAGTATTGTCAACC
AGGGCAGCTCACCCAGGCCCGGTGTCCAGGGCTTTTCTTGCGGTGGTTTACAGAGCCAT
GCTGTGGTCACGTGGCTGGCCTCCATCTCCAGCCCTCTGGAGGTCCAGCTGTTAGTGTAG
CCTACGGGGCACGGTCCCCAGCCCCCTGCCCACTGAGCCATGCTGCTCTCAAGCAGGAT
GTTCCAGGGGCTTAGCGATCCCTCCCAGGAGCCCTTGTGCACCGCGTTTCCACTCGGGCC
ACTCCCTGGGCCCTTTGGCTGAATGGAGCTCCATGGAGGATCCGCTTATCTCTGTCTTCA
TCAGCTCTGACTGCCATAGCAAAAATACCATAGACTGGGAGGCTTAGACAACAGACACTTA
CTTTCTCGAAGTCCCGGAGGCTGGCCCAGAGCTCCACGTACTCCTGAAAATGCATCTCAG
CCCCCGGGGGAACACTACGCCAGTTCTCCAAGGGCTGCCAGTTCCCGGGGGGACTGCTC
TAGCTTTACTCCCTTTGCTTAGTCACAAAAACAAATGACATCCTTTGGAAGAAGGAGGCC
GGCGTCTCCCTCTGGAGAGGGACCTTACACCAGGCAGATGCTGCTCAGCCTGGCTCTCAC
GGCCACTTCCGTGTGGCTCCCCAAGGTMATTGCCACCATCCCCACCAGCCAGCTCAAGTG
CCTGAAGGAAGCCGGGCACGGGCCCCGGGAAGGACGAGATGACCGACGAGGAGCTGGCCGA
AGGCGAGGAAGAGATCGACCATGCCGAGCGGGAGCTCCGCAGGGGCCAGATCCTCTGGTT
CCGGGGCCTGAACCGGATTCAGACGCAGGTAAGCCCCGACTCGCTCTCGCCCTGGCACTT
CCACCCCAAGAGGGTAGAGGCAAGCTGGCCAGCAGCAGCCGAGAGCCGGCCGTCTGCACC
CGACACCCACAAGGAAACCCCTTTGGTCTTGCTGCCAAGGTCACAAAAGCAGCTGCCAGTG
TCCCCTTTGCCATTCCGGGCTGTGCCCGCTGATGGCTGTGGCACTGAGATCGCCTCTCCC
TGACAGCTCCTTCAGAGCCCAGGCATCCCCTGTAGCTAAAGGTGTGTGTGGGTGACTAAT
GGCTCTCTCAGAGGCACAGGCCAGCACCGTCCCTCATCACTGCTGGGGCTCCCTTCACTTG
GTGGGAACGGCCCCAGGTCATAGGCAAGTGACAGTATCGGGAAGAGAGGCCCATTTCAA
CAGCCACCAGCGAGCTCAAGGTTCACTGGTTGACACTGTAAATGCGATGGGGAGACTTCA
TTTGGGAAGTGGACTCTGGCCACCGAGTTGGTCTTTCTGGTTCATCCAAATCACCAGGG
TTAGGGCCGGCCAAGACCAAGGGCGTCAGCTGTGTTCCCTCTCTGAAGTCAGATGGCCACC
ACTGCCACCAGTATCAGGCGCTTGCCAGAGCTACCATGCTCCCTTGTTCCTATCTCCTCC
CGGCCAACAGTTTTGCCAGAATGCTCCAGACTCGCTGTGTCTCCACACCCCTCCCTGGAA
CTCTCTTGTGATCCCCTACAGCCTGGCCTCTGCCACCACTCCCCAGAAACGGCGCTCG
CCTAGGCCTGCGAGGCTCCCTTCCGGCTCGTGGGGTCCGGCTGTCCCTGCATCGTTCCCTG
CCTGCTGTGGGCACTGCCTGGAGACTTGCTGTCTCACC CGCCTGGCACCCCCACCTCCT
GCTCAGCCCTCGCCCCACCCTGCTGTGGCCCTTGAGTGTGAAAATCCTGGCCGGGGAGG

Intron 20 - 21

AAGAAAGGGCCCATGGGGACCCACCTGCGGCCTGGCCCCTCTCCCACCGCAGCCCCTGC
AGCCTCTCCTTCATGGCCTGCCCTCCCCCAGCAGCCTCCAGAGGGCCACCCAGCATGCT
TCACACTCCACCTCCTTCTGCAAGGCCCTGGGCCACCATCTCTCAGGTCACAGCCATCACT
CCCTGCCCTCCAGGCCCTGTCCAGGATCCCCAGTTGCAATGCCCTGACATGGAGCGAC
TGACCCTCCTCCCTGAGGTCCTGCCAGAGTAAGGACACCACTGCACACTTGGCTGCGGAG

CCAGGGCCCGCCTGAGCCACCAGCCCCAGCTCAAGCGGGAATAGGCGGGGCCTGAGGCCA
CACCCC**TTCCC**AGGGTCAGTCACACATCACCAAGGGCCTGTCCCAAAGAATCATCCATGC
AACTTGCACAAAGCTGTTCTTGGTGCCCTGGGTCTGTG**TTCCC**TCCCAGTGGTCTCAAG
GGCCGAGTCTCAAGGGACCCAGCCTCAGGGCAACCCCACTCCCTGGGCCTCAGCCTCCTT
TGCTTGCCCTTGGCTCAGCTCAGCCCCCTCCAAACACCACCCTCTGCAGTGGGACTGGTGGAG
CCTCTCTCCATTGTCTAAGGATGAAGTCTACGCTCCTGACCATGGCCTTCAAGCCCCTG
CCTCTTGGTGTACCCCCAACCTTCCCTGCACACCTGCACCCCTGCACCCCCGGCTGCCTTT
CCAATCATGCCCCTCTGCCCCTGTGCCACTGCACCTCCCCAACTCCCCTGCGTGCCTCCCCT
GGGCCCTCATGCTTACAAAGCCCTCTTTGACTCCTCTCACTCTCACCACGGGCTCCTTGC
AAAACCTTCCAGAGCTACAGAGTCCCCCAGAGACCACGATCACGCAGGGCTAGGTCAAGG
GGCAACAAAGAACTCCACATTTCAAGAGCCCCCAGGGGTCCAAGGGGCCTCTCCAGCTG
AGAACCGGGAGGCGAGGCTGGCATCCTAGGCACCGAACACAGCGTAGCCTGGGAAGGATG
TGTTAGGTCTGGACTCTGAACACTGTCACCTATGCCCTGGCCTGGCCAGAACACAGAGAG
CCCCGGTGAGGAAGGGGAGCAGGCTTTGTGCGCAGATGGCCTGCGTCTCCCCTCCCACGT
GCAGGGGCTACTGCCTCAAGCACAATGCTCGGACAGGCCAGGGGTGCAGCACAGATAGTC
TGTTCTCG**TTCCC**TGCAATAAATATTTCTGCGCTAAATCTTAAACACATCGAATGTTAGA
AGCAGCATTCACATCTCCCCAGTGCCCTCCTAGCGGCCCAACTGTGCCTTCTACGAGAC
CATGCCTATGGGCCCCCCAGCTGCCCCAGATGGGCTCTTATCTATCGTACCCCTGTTGT
GCTACAGAGCCCAGAGCTGCCCAAGCCTGGGGTGGGGGGTGAGGACAGCAGGACCTTGCC
CCTCGGCGGCCCACTTCACTCCTGCCGCGCAGCCGAAGGCGACGTTAGGTTTTCCAGCA
GCTGAGACAACAGCCCTGCCCTGACCTGAAGCATCAGTGGTGTGAGTGGTACCCCGGCCA
CCTGTGTGTCTCGTGTCTCTGTATGTGGGGGCCGCTGCAGCCTGGCTAGTAGAAGCGAG
TCCCATCGGTGAGAGTCTTAGAGTTCAGGCTGTTCCAATTGTCGGTGTCTCACAGAGACA
CGGGCAGCTGAGTCCCCTGTTTTGCGTATGAG**GGAAA**CAGGGTGCCTCT**TTCCC**CCTGGC
ACCAGCCGATCCGACTCTTCCACGGGCTCCTGACCCCATGGCTTTTTCGCTTTGACTTTG
TCACATCCAACCTACCATGTTTTCTCAGGAATGCTGAACCAGTCGGTCTTTTTAGCCAGCT
ATGTAAGAGCATCTGCTCTCTTTGATTGAAACACCTGCTTGAAAAATGGAGCTAAAGCT
TGGGAGAAGCCCGTCAGGTTGTACGTATGCCCAAGCCAAGAAAAACATTTCCCTAGGCAG
CTGGCCCCAGGTTTTCTGCTTTTTGGGAACCACAAAATCGCTCCCCAGATTTTGGAGGCCG
GCACAAGCTTTTTCTGTTGCTAAGTGAAGGCATTTTGTAACTGCTCGCACCATGGTTCCA
TACTAACATATCAACGCACCAGATGGACAGGGTGTCAATCCAGAATAAAAGAGTCCTTCA
AACCAGAACATGTAGCTTTCTGAAGCGCTCATGACTCGGTCTGTCTTTTTTGCATCCCA
TTATAATGCAAAGAGAAGCTTCGTGAGCAACTGGGCCCTGCTCCCGGCTCAGCTCTTGGG
CTTCCAGGTGTGGGGTGGTGGCGACTGTGGTATTGTCACTGATGTGGCTCTCCCACTGGG
ACACCATCTGTAGCCAGGCCAGACCAATGCAAATCTGAGGCAG**GGAAA**GGCATCTTTCCTA
TCCCTCATCACTTTTGGCGCAGCGAGAGTCCCTCTCCTGAATCTAGACAGGAGACCCCCCA
CCCCGCAAGCCACCGCGACGCCATCACATCAACCATCCTCCTTCCGTGCGCTGACACACT
CAGTATGCATTCCTCACGGTCGCAGCAAGTGCCATGAGG**TTCCC**CCTGTGACAAGCAAGC
GAGTGGGATGTGCTGGGCGGAAGGGGACTGGGCAGGCTGAGAAGAAGGAGGAGTCTTTTC
CACAGCGGTCAAAGGCTGAAGTGGCGTACATCCTCATTTTTGGCCGGTGCAGGGGGAGTC
TGAACACTCAAGCTGCCTTCTTCCACGAAGCCCTGGCCCCGTTTCAAGACACCAGGTGAA
CCTGGTGGCCACCACATAGCACTGCAGGGCTCGGGCTGGAGCAGGTAGCTTTGGGCTCCA
GATGCGCACACTGGCTTTGCTGTTACATCATCTCCAGTGAAGACGGACATGAGTCCCCAT
CCCAGCCAAGGGCAGGTCA**GGAAA**TCCAAAGACACTGGGTCAAGGCCCTCCTGCAGGCCT
CAGT**TTCCC**CAGCCTTGCT**TTCCC**CCTCAATTTGCAGGAAGCTGTAAGAGTGGGGACAAAG
CGAAGCCACGGCTGCCAGTCCGTGG**GGAAA**ACCCCTCCTCCGCTAGGTCCATTCTTCTGC
TGAAGTTTCGAGGGGGCGCCCCCTGCCAGTCACTCAGATGAGCCACAGAAGCTGGCGGA
GACGGGCAGGCGGATGGAGCATGGGGCATAAGTCTCCGGGTTTAGAGGAAGCAGGGCGG
GTTCTAATAGGAGCGTGTGATGTCCTCAGGTGTGTTGGAGAG**GGAAA**AACAAGGTTGAGA
ACTATGAAGTACTTCCCTGATAAGTGGCTTGCAAGGGGCATTTCTGACATGTTTGCAGTGT
GCCCTGACTTGTGACCCCC**TTCCCTTCCA**ATCTCATGACCACTAACCATCTGCTCAGCA

AACCCTCTCTCGGTGGGTGGCACAGAGGCTGGCCTCAGTCAGGGCCCTGTCCAAACATCG
CCAGCTCCCAGTGAGCGGGGTGACCCGATGAGGCTTTGCTGTCACCCTATGTGCCAGTG
GTGGCCCCATCCTCGCCAGCCCTCCCCTCCGTGATAGCCTGGACAACAGTGCAAGCCA
AACTTTATCTCATTTTCTCTCCACAG**ATGGAGGTAGTGAGTACCTTCAAGAGAAGCGGT**
TCAGTTCAGGGTGCTGTGCGCCGGCGGTCTTCGGTCTCAGCCAGCTTCATGAYGTAACC
AATCTTTCTACCCCTACTCAGCAATTCTCTCTGCTGCCAATCCTACCAGTGCTGCTGGG
AGTGAGTCYTGACTTCCCTTTTCTCTCATAAAATGGCATCTCTGGGGAAGAATAAGCCTCC
CCAGCTCGGCCTTCTCTCTTTTGCAGTCTTGCATTCCGCTCACCGTGGCTTTTCTGTTCT
TTCTTTACCGCCCTGTCCAGTCTTCCCGCCAGACGGTGTCTCTCGAAAGCCATATTCT
TTTATGAAACGTATTCAACCCATGGCACTTCCGGACCTCCCGTTCTTTGCTTTGTTGGT
TTTTCGGTTTGTGTTTAGTGCTCCTTGTGCCATTGGTTCTCTTTTCTTGAACCTTGTCTGC
CTTTGCCGATGGTTCTTCATGAACTTGGGCCGCTTCTGGGGGTGTCTGGTGTGAGGCTAG
GGCCTTGCTCAGTGTTTGTGAGTGGTGCAGCATCAGGGCAGCACGCGGGCTCAGGGCCGCCTT
CCCGGGGCTGGAGGGGTGGCGGGTGCC**TTTCCC**ACACTGTTTGCCACAGAAGAATCTAGC
CCACGTACCCAGGAACCTGGAGCGGCGCTTCCAGCATCCTCCTTGAAGTGGTTTCCTAAGG
ATGCCGCTGTCACCTGTCCCCAGGTGGGCTCAGTGCTGACCAATCACTACTGCACAGGTG
GTGCCTGCCCTGTAGGCCTTGCCCCAAGCCACCGGGTGTAGAGG**TTTCCC**CAGAAGTGG
CACTCAGAGGCCTTCAAGACGTTGCCA**GGAAATTTCCC**ACCATGTTGGTACAGTTT
AAAGAGAACCCAGGGGCTGTCTAAGGAGGTAGAACTTCCAGAATTGCTCACATCTTTT

PMCA3: 21 NFAT motifs

Splice region in PMCA4 gene (ID: ENSG00000058668)

Legend:

GGCGTGTGGGTGTGG - exon

TTTCCC - NFAT binding motif

GGAAA - NFAT binding motif

TATAAA - TATA box

alternative splicing region

R - Altered nucleotides recognized during splicing

SEQUENCE BEFORE SPLICED EXON 36 bp

Intron 1 - 2

GTAGGATATTTGTATATTTGCTTTTTTTCAATCATTCAATTTTATGAACATGGGGTCTAA
GCAGATTTCAAACAAAGACCATT**TATAAA**ACTGGACCATTTTAATGTTTACAATGTAAT
AAATCTCTTGATTGCAGACATATATGGCTGTTGGTAGAAACATTACAGTAATGGCAGTT
TTTTCAGTTGGTGTGTAGTCCCCAATAATTATATATGAAATTGCTGTCAAACCAGTAAGA
CTGCATTTATGCAGCCATCATTTT**CAGG**ACTGTTGGTAACCTGAGCATATTTTCTCCAAA
TAACTTTGCCTCCTTGTGTCACAAGGCCAATTCGCTCACATTTACCTCAATGACAATAT
CTTTGGTAATAACACCCACAGTTGTATACGGTGGGGATGAGGGATTCTTCTTTACACCAA
GTATTGGTGGGCAAAGGTGGCTTT**CAG**TTCAAGATGTAATACATGGGCTTTCTTGAAAT
GCATATTGGCCTGATCAGTCTTCTTATTTAGGTGGTTTTCTTGTAAGCCATCTCCGAC
AAAGCAGAGTTTAGTAACCACCCTCTCCATGCCTTCTTCTTCTC**TTTCC**TGTTCAAAC
AACTTTTAATACGTCTGTTTCTCCCTGGGCATGACTTTAGTCAGAGGGAC**TTCCCG**TTT
TCCCACCTTCTCTTTTCAATTTCTGTTTAATCATATT**GGAAA**GTAAGTTGGCTCGAGATTG
TCCCTCTCTGTCCAGCAGATAAG**CAGG**TACTGCTCCCTGTGGAGTCTTTTCATCCTTCTT
TTGTTTGGTGTCTCTTTTCAATGCATCTTGATAGTCTTTTTCATTTGTATTTTCTCAGC
ATGACACTGTTTAAGGTAAAGCTTAGCCCTCAGACCAATCATTTGCTTTGCCTTCTTTGA
ACGTTTCATGAGCCTCTCGTTCATAAGCCTCTCAGC**TTTCC**TTCTTTCTTTTCTTCTCATG
GTAATCCAAACGGTATCCATAGTGTATGTTATGGTGTAAATCAATATATTCGTTCTGTGGCAT
GGTGACAGGCGCAGAACCACCAGGAGTAGCCCCTGAGGTGCGAAAACACTCTCAATTTTA
AGGTCTCAGAGACTCCACGCAGGCCGGGACAGGAAAGGGTCACCCTTTTTTAAAAATATT

Intron 4 - 5

AGTCTCCATGTAAGTCTCGGCCATTGCTGTCTAGATAGGGCCCATGGGAACAGCCATGAGA
TAGGGTTGAAGGAGTTGGAGGACCCTACCCTCAGCCAGTCTCTTACTATCTCCTTCACTG
TCCCTCC**TTCCC**CTTTGTG**Y**CTAG**GTGATCTGCTGCCTGCAGATGGAATCCTGATCCAA**
GGGAATGATCTGAAGATTGATGAGAGCTCTCTGACAGGGGAATCTGACCATGTCAAGAAG
TCCCTGGACAAAGACCCCATGTTGCTCTCAGGTA**Y**AGGCCCTGGCTGCCCAAG**TTCCC**AT
TTACCTCCCTGCAAACACCTAGGCCACAGGATCCAGACCCTGTTCTCTCCTCTGACTCTG
TCCCATCTCC**TTCCC**TGGGGTTCAGCTGGGGCAACAGCATTTTGGTGGGTGGAATACAAG
GATATCAGGCAGCCTAAATGAAGTTTTCCATGAAACAAGTGTATAAGGGCCTTGAAGGG

Intron 5 - 6

GCTTTGCTGGTTGCAGGGGTGGCGGGGGCAGGAGGGAGGGCTTACCCTAAAGCGGTTAGA
CACATTTTCTCCTTACTCCCAATTTGTCTGGTCTGTTTTAAATGCGCCAGCTCTTGAC
CTTTTCTTACTGTGCTAAGCACATCATATCCATGGGGTAGGGAGGAGTATTTTTTCTTC
TAAGTTTGTGTTTCATACCAATCATGTCTAGGTATTAATAAACCATTCC**TTCCC**ATCT
TCTCCTTTCC**Y**GTGTAG**GGACCCATGTCATGGAAGGTTCTGGCCGGATGGTGGTGACAGC**
TGTTGGTGTCAACTCTCAGACTGGAATCATCCTTACTCTCTTGGGGTCAATGAGGATGA
CGAAGGGGAGAAAAGAAGAAAGGTAAGGGGCATCTGGAATGAGATTCTCTTCTCTCA

TCCCCATGGACAAACAAGGAAGCGAGGGAGCAGATCTGGATAGAAAGCATGGTTGGAAGA
ATCTGCTGCCATGAAGAAAGCAGATATCCAAACTCCTTGCTGAGATAAAGATGTAAATCC
TTGGCTCCAGGGAGCTCTGATGAAAACCAGATCCTGGCTCTAGGCTCCCAAATCAGGTTG

SEQUENCE AFTER SPLICED EXON 175 bp

CTTATCCCCTATAGGCAAGACAACAAATAGAAAAGT**GGAAA**AGAGGCCGGGTGCGGTGGC
TCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCTGGCAGATCATAAAGTCAGGAGT
TCGAGACCAGCCTGGCCAACATAGTGAAACCTTGGCTCTGCCAAAAATACAAAAATTAGC
TGGACGTGGTGGTGGGCGCCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAGAATCG
CTTGAACCCGGAAGGCTGAGGTTGCAGTGAGCTGAGATCGCGCCATTACACACCAGCCTG
GGCAACAAGGCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGAAGAAGAAAAGTGGATT
GCAGACTCACTATGCACCTGACTGTACTTCCAGGCAGGTGCTTTTTCTGTCTGCCAGAGA
AACATTCCAGGGTGTGTGGCTGCCTCACCTATCCAGGGCGATGCAGCTCCCTGGGGACA
CAGGTGCTTCCCTGGGGAGCCCTGAGCACTTCTCCGTGTTGCTGGCCTCACATCCAATTGG
GCAGGCATTGGAGTCCGGGCACTGCCTGGAGCTCACCAGAAGGTGCTTTACAGTGGTCCT
TGGTTTGTCTCTCAGAGGGCTTGGTCCCCTCTGCTGTGAGGCTGGACTGCAGCTGTGGTG
GCAAGTGACCAGATGTCAGTACTGAGCAGCCTGACCATGGTCTAGGTGGTGCTTGGATGCATC
CACTTGGCTTCCCTTGGTCATTGAGTTTCAAGAAGAGAACTCCAGGAGACGGCTTGGCC

AATGCAGCTTTCAAACGTCCTAGTTGCCGTCCTCACCCAGCCACCCCACTGCTTGA
AAGTTGAGCCATGTGATGTTTCTAGTGCCCCATGATCTCTTCTGATGTGTGTTTGGTTTT
GATGCTGAGCAGTCATGTTTTATAGTCTGGGTTTTGTTTCTCTCCTAAATCCACCATCTC
CTTGTCTGCCGGCCAATTCTCACCTCTCTATTTTCTCATCCTCCTTTTCC**TTCCC**CTGG
TAYAG**ATCAAAGTGGTCAAAGCGTTCCATAGTTCCCTCCACGAAAGCATT**CAGAAACCCT
ACAACCAAAGTCCATCCACAGCTTCATGACCACCTGAATTYGCCATAR**AGGAGGAGT**
TGCCACGAACACCCTCCTGGATGAGGAAGAGGAGGAAAATCCTGACAAGGCTTCTAAGT
TTGGGACTAGGGTGTCTGTTGGATGGTGGAGGTCATYCATATGCCAATACAAACAACA

PMCA4: 10 NFAT motifs