

Primers used in this study

Primer`	Sequence (5'- 3')
Mg-MAT1-1-F	TCAGCTCGCCCAAATCAACAAT
Mg-MAT1-1-R	ACTCAAGACCCGGCACGAACAT
Mg-MAT1-2-F	GAGTTGCCTGCCCGCTTCTG
Mg-MAT1-2-R	GGCTTGGTCGTTGGGGATTGT
5'FAR1-F	TAAGGAATTTGGTGGCAGATT
5'FAR1-K-R	GGGGTACCCAGGAGCAGGCAACTCCTC
HY-K-F	GGGGTACCGCCGCGACGTTAACTGATATT
HY800-R	TATTGACCGATTCTTGCG
YG-F	TGTCGAGAAGTTTCTGATCGA
YG-R	GG-GGTACCGCTGGTGACGGAATTTTCAT
3'FAR1-F	GG-GGTACCGGGGAGAAACCCATTCA
3'FAR1-R	TTCTGGTGCCATGATCAGAGT
FAR1-XhoI-F	GAGAGACTCGAGATGTTTGCTCGGTCCAAGA
FAR1-PstI-R	GAGAGACTGCAGTTAGGATTCTTCCATGATGCC
FAR1-XbaI-R	GGTCTAGATTAGGATTCTTCCATGATGCC
FAR1-SN-F	TTTTTACTAGTCATATGATGTTTGCTCGGTCCAAGA
FP1.5-SpeI-F	GAGAGAACTAGTCTCGTAGGTGCGAAGCAGA
FAR1-Prom-R	GGGGTACCCTTTTCAGGAAACGAAGGAGC
GFP-KpnI-F	TTTTTGGTACCATGGTGAGCAAGGGCGAGG
GFP-NSC-X-R	GAGAGACTCGAGCTTGTACAGCTCGTCCATGC
FAR1-Real-F	ATGTTTGCTCGGTCCAAGA
FAR1-Real-R	GCGTCTAAAGATGGGGCGTT
PMK1-SN-F	TTTTTACTAGTCATATGATGTCTCGCGCCAATCCA
PMK1-XP-R	TTTTTCTCGAGCTGCAGTTACCGCATAATTCCTGG
Pmk1-Real-F	ATGTCTCGCGCCAATCCA
Pmk1-Real-R	AACATAGAATGATCGAACGGG
MoTub-F	GAGTCCAACATGAACGATCT
MoTub-R	GTACTCCTCTTCTCCTCGT
nqActin Sc F	ATGGATTCTGAGGTTGCTGC
nqActin Sc R	TGATACCTTGGTGTCTTGGTC
MoSTE2-RT-F	ATGGACCAGACACTATCAGCA
MoSTE2-RT-R	ATGGCAGTGTTGAAGGCGA
MoCyB2-RT-F	ACAGTTGGTCTCGAACGAGAA
MoCyB2-RT-R	TTACGTGTGGTTCTTGTCGTC
M-CycB1-RT-F	ATGGCTTATCACCACCACA
M-CycB1-RT-F	ACTTCCATGTGTCTCATGTGT

DNA sequence of MFAR1 (MGG_00134)

ATGTTTGCTCGGTCCAAGAGCAAATTCACGGCTTCGGCGCAGACAAGCGCCAGCAAGAGTCAGGATTCTTGGGTTCAGACTCAAGA
 TCTAGGACAACCTCTGAGCGACCTTACACGGCAACCTCCTTCAACGCCCATCTTTAGACGCACCATCATACGCTCCTTCGTTCTTGAA
 AAGA**GTAGGTTCCAAGTTCGGCCACCCACCGTGTTCCTACCTTTAATTCCTGATCTTTCGTCAACTCTGGCCTAGTCCAAACCTAG**
CCGCTGGATGACCATTGGGTGCGACTCTTCCATCGTTGCACTCTCTACGCTTCCAGGTCTTCTGCGCTCATCACCCCAAATCC
ATGGCGCACATAGCTGACTTGACGGCTTTTTCTCGCCACTTGAATTCAGACAGCTCCATATCAAGTGGTACAATTAAGCCACCCC
 AGTCCACCGTTCGTGGCATCGGTTTCTCCAACCACTCTGTTGACAGCTACGGGAGATCAATCGACCAACATGAGTTCAGAACG
 TGGCGCACGCGCAGGGAGCGTACCTTTGTGGGCTCCGAGTGTCCGTCTGTGAGGAGCCATTAGAACACACTCTCCGTGGAGAGAG
 GATACTTCAGTTCTCTGTGGTCATGTGTCCACGAGGCCTGCTTTATGAGTACATCAAGGAGATAGAGTCACAGTATTGCCCGTCT
 GCAATGCGCTCTGCACCTGGACACAAGTCGGGGTGGAACGTGCTCGATATAG**GTAGGCTCCCAAGTAAAGCCAGCTACGTTGTGC**
CTCCCCGTGACGGTCAATGGCCTACCAAAAAATCAGCAACCTCGTCAGGTCGGTGAACCTCAGATTGAGGTCGAATGGGAACCA
 ACACCGACCCCTCAACAATGGGATGATCATGGGCGTCCGCAAAGCCGGGGTTCGAATGCACGTTCTGGTTCGGAGTTGGCTTAAGC
 CATCTAGCAGCCACAATGGCAGGGACAACGCCATGCCGCGGAGCAACCGAGACACACGAGACAGCGGGCACAGCAACCCCATTC
 GGAACGATATATGAGACATGGGCGTAGTGACAGCGAAGCGACGGGAGTGGCGTCTTCGACAGGTTACCTGAGACAACACAGAGC
 GGAGGCCCGAGCGCGCCACGACTACGACTTGCAAGCCATGGAGACGTCGCTCGCAAGCCCTCGGAGCATTGCACGAAACCCGATC
 CCTCTCCCGACCGTGACCGTTCGCTCAGAGTTCACACGATCAACAGGTCTCGACAACAACAACTTTGACATGTCTTATTACCATCGA
 GGTACCCGACTGCAATGGCGACCAAGCCGAGGACTTGCCAATGGGAAATATCCACTCCCGCAACAAATGCACCACAGGCCCC
 TCAACAGGTACCATCACGGATGGACGCTCGCGTCGCCGAAGATCCGTATGGTCCACATCACCTACACAGTCGGTGCCTCGCTCTTTT
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 TTCGGAAGCTTCGTCTGTATGGCACGCTGAGGGTGGGCAAGGATAAAATATCGTGGCAGGAGCTTGAGTGCTACCTTTTCGCCGAG
 ATGCTCATTTCGTCAAGGAGAAGAAGACACCGGCTGGCGCCAGCAGCAATGGGACGAGAATGGCTTGCTCGCAAGCCGCGCTG
 CACCCTCAAGGGTTCATCCTCATCAAGAAGCACTTGAACGAGGTTTCTGAAACGGGGAGTATCGACGAGAATGTGCTCACCTTAAC
 CTTTCGGTGGCAGAGCTTCGCAATTCACCTGCGATTCCAAAACCGCAACCACTCAAGCTGTGGCAACAGGCTCTCATGGATCTTAA
 TGCTGTTGAAACCTCCCACTACGAGGCCAGACTATGAGCGTGGCGAATTTCCGAGGCCGAAGAGGATGAGTGGCAACGCAGCC
 AACAACAAGGACAGAGAACGTCGTCCTTGGCTCCTCACTTGGAACGGACCGAAATCCACGACGACCGCCCCACCGAGTACACCA
 GCGTTGCAAAGAGCCCGCTGTTCCCTCCCGTGCACGTCCCAATCGACGTCGTGGTGTGGTGCTATATCGAGCTCCATGCAAGGTGTC
 AAGATCAACTTGGTCCGAGATGCCCTCAGGTTTCATGGTCCATCAGCTCGCGACCGTGACCGGATGGGTCTCGTGACCTTTGGATCTG
 GTGGAGGTGGTGTACCAATCGTGGCATGACGACTAAGTCTTGGCACGGCTGGGGAGGTGCTCTGAACCTATCAAGCCGGTGGGA
 CAAAAGAGCCACCGGCAGATGTTGTGAGGGTGCCAATGTTGCCATGGACCTGCTGATGCAGAGGAAGTACAACAACCAATTGC
 CACCATCATGCTCATCAGTGACGCTTCAACCTCGGATGCCGACAGCGTGGACTTTGTCGTGTCAAGAGCAGAGGCTGCCAA**GTAGCT**
GGATCTGCGTATGACTTTAACTGTTGGAACATCATACTAATAACTCACTTTAGGATCTCGATCCACTCATTGGCTCGGAATGAC
 GCACAAGCCCGACACCATGATTGAGCTTTCAACCAGAACAAAGGCCTCATACCTATGTCAAGGACTGGATGATGTTGAGGGAATG
 CCTTGCCGGCTGCCTTGATCTGCCAAACATTGTCTCACCAGAACGTGAACTCAAGTTGAAATTGCCGAAGGATGCCAGCAAAG
 TTCCACAAGATCAGTGGTGACTCCAAATCACCAAGCGCGCAACGGGTGGGACGCCGAGGCTTCTCTGGGAGACCTGCGGTTTGGC
 GACAAGAGGGATATATTGGTGCAACTGGTGATCTTCCAGACACCGCTCAGAAGACAGCTGCCACAAGATCCATGGGAGACCATC
 GTATCTGGCTCGAAGCGCTGGGTGGACCAATGGACCTGAAGAGCAGCGCACAGTCTCTGTGAGGAAGTCCCGCTTATCCAGGCG
 GATCTTAAGTGGGGCGACATACTCCGTGACGGCACCTTGATGCACATGCCTCGTCCGTCACTCCTCGCCATCACAATGCTGCCTGCGAC
 AAACCACAAAAGTCCAAGTCGTGGCAAAACACCCCTCAATCCCGCTCACCCGCACATCGTGACGACGAGGATGGAGCTTTTGACA
 TCAGACATGCTGACAAGGGCATTGACGCTCGTGTCAAGAGGCCAGCAGACCGTGGCCACACACTTTGAACGAGACACGTTCAATTC
 TCAAGGGGTGGGCAAGGGAGGTCTACCCCTGTCCGCGGCTGCGTCCAGGTCGCAACCGTCGACGCTCACCCGAACCATGAAG
 GATCCCTACCTCGCTCACTCCAGAACGCAACATTCTCCCTCGCCACTGCATCAGCAACGTCGATTATCCGCCACACATGACCCAG
 GCAATGATGCGCAGACCTTCAACGGACGCTCTCAGCGATTGCACGGTGGGCCGGGATCCAGCGGCAATTGATGTGCAGACCGTTTCA
 GCGCTGGACTCGGAGCTCATGTACGCTCGAATGGATCGGCCATCCCGCGTCTTTGGGCGCGACAGCCGAAGGCTGTGTTGCAG
 GCCATTGGTGTGATCAGCTCTCAGCGCGCTTTACGTTCCGACGCGGATCGAGGCTTTGTGGGCGGGAAGGATCTCGGGCGTCAAGA
 AACTTACCGAGCACTCGCGTGAAGTGGAGAGAAGAGGGTGGTGGCGAGGGTGGCATCATGGAAGAATCTAA.

*Red colour indicates intronic sequences in the gene.

Amino acid sequence of MFAR1 protein (MGG_00134)

MFARSKSKFHGFGADKRQQESGFLGSDSRRTTSEPYTATSFNAPSLDAPSYAPSFPEKNSSISSGTIKPPQSHRSSASVSSNHVSVDYGRS
 IAPNMSSERARTRRERTFVGSECAVCEEPLEHTLRGERILQFSCGHVSHEACFYEYIKEIESQYCPSCNAPLHLDTSRGGNVLDIEKISNLVRSV
 NSDSRSIGTPTPTPQQWDDHGRPQSRGSNARSGSGVGLSHPSHNGRDNAMPRSNRDTRDSGHSNPHSERYMRHGRSDSEATGVASS
 TGYPETTQSGGPRRAHDYDLQAMETSLASPRSIARNPIPLPTVTVRSEFPTINRSRQQQTTLTCLITIEVPDCKWRPDPEDLPMGNIHSPQQ
 MHHQAPQQVPSRMDARVAEDPYGPTSPTQSVPRFFPYESREVLEEMTENLRNRVDNWHGLDLSRFGKLRLYGTLRVGKDKISWQEC
 YLFAEMLICVKEKTPAGAQQQWDENGLPRKPRCTLKGSILIKHLNEVSETGSIDENVLTNLNSVAELSQFHLRFQNRNQLKLWQQALMD
 LNAVETSPVRSPDYERGEFSEAEDEWQRSQQGQRTSSLASSTWNGPKSTTTAPTEYTSVAKSPLFPPVHVPIDVVVVVPISSSMQGVKI
 NLVRDALRFMVHQLGDRDRMGLVTFGSGGGGVPIVGMTTKSWHGWGGVLNSIKPVGQKSHRADVVEGANVAMDLLMQRKYNNPIA
 TIMLISDASTSDADSVDFVVSRAEAAKISHSFGLGMTHKPD TMIELSTRTKASYTYVKDWMMLRECLAGCLGSAQTL SHQNVKLKLP
 GSPAKFHKISGALQITKRATGRDAEASLGDLRFGDKRDILVQLVILPDTASEDQLPQDPWETIVSGLEALGGPMDPEEQRTVSVEEVPLIQA
 DLNWGDILRDGTLMHMPRPSSLAITMLPATNHQKSKSWQNTPIPPHIVQRRMELLTSDMLTRALTIVSRGQH DRAHTLLNETRSILK
 GLGKGGLPPVPPAASRSQPSTPHPNHEGSPTSLTPERKHSPSPTASATSHYPPHMTQAMMRPSTDALSALHGGPGSSGIDVQTVSALDS
 ELMSALEWIGHPAVFGDRSRKAVLQAIGVISSQRAFTFRTPIEALWAGRISGVKKLTEHSREWREEGGEGGIMEES*