Supplementary file

**Gene sequences used**

**Cloned sequence of Forkhead for dsRNA**

>FKH

ATGTCGGGCAACTGTCTCACCTCGACGCCGATCGGGTACAGCTCGATGGGGTCGCCGATCAGCAACATGGGCTCGTGCATGGGCGGCAACGGCATGAGCACGATGGCGGCCATGTCCGGGTACTCGAGCGTGGCCGGCAGCCGGGAGGTGCTGGGCGATCCGAGCTCGCCAAACTCGGTCGCGCTGCAGCGGGCCCGCACGGAGAAGCCGGCCGCGACGTACCGGCGGAACTACACGCACGCCAAGCCGCCCTACTCGTACATCAGCCTGATCACGATGGCGATCCAGAACAAAA

AGAP001671     ATGCAAAAGCTCTACCCGGAAAGCTCGATCAATACGAGCAGTAGCATGGCGGTGGGCGGT 60

FKH2      ------------------------------------------------------------ 0

AGAP001671     GGAGGCGGAGGCGGCGGCGGCGGCGGTGGCGGCAACATGAGCCCGATGGCCACCACGTAC 120

FKH2      ------------------------------------------------------------ 0

AGAP001671     AGCAGCATGAACAGTATGGGGATGGCGGTCGGCGGCATGACGTCCGTGTCGCCCCAGGGC 180

FKH2      ------------------------------------------------------------ 0

AGAP001671     GGCGGGTTCGGCGCGACCGTGCTCGGCAGCCCGGGCATGGGCGGGATGGGCGCCGCCATG 240

FKH2      ------------------------------------------------------------ 0

AGAP001671     AACAGCATGTCGGGCAACTGTCTCACCTCGACGCCGATCGGGTACAGCTCGATGGGGTCG 300

FKH2      ------ATGTCGGGCAACTGTCTCACCTCGACGCCGATCGGGTACAGCTCGATGGGGTCG 54

                 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

AGAP001671     CCGATCAGCAACATGGGCTCGTGCATGGGCGGCAACGGCATGAGCACGATGGCGGCCATG 360

FKH2      CCGATCAGCAACATGGGCTCGTGCATGGGCGGCAACGGCATGAGCACGATGGCGGCCATG 114

           \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

AGAP001671     TCCGGGTACTCGAGCGTGGCCGGCAGCCGGGAGGTGCTGGGCGATCCGAGCTCGCCCAAC 420

FKH2      TCCGGGTACTCGAGCGTGGCCGGCAGCCGGGAGGTGCTGGGCGATCCGAGCTCGCCAAAC 174

           \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*

AGAP001671     TCGGTCGCGCTGCAGCGGGCCCGCACGGAGAAGCCGGCCGCGACGTACCGGCGGAACTAC 480

FKH2      TCGGTCGCGCTGCAGCGGGCCCGCACGGAGAAGCCGGCCGCGACGTACCGGCGGAACTAC 234

           \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

AGAP001671     ACGCACGCCAAGCCGCCCTACTCGTACATCAGCCTGATCACGATGGCGATCCAGAACAAC 540

FKH2      ACGCACGCCAAGCCGCCCTACTCGTACATCAGCCTGATCACGATGGCGATCCAGAACAAA 294

           \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

AGAP001671     CCGCACAAGATGCTGACGCTGGCCGAGATCTACCAGTTCATCATGGATCTGTTCCCGTTC 600

FKH2      A----------------------------------------------------------- 295

AGAP001671     TACCGGCAGAACCAGCAGCGGTGGCAGAACTCGATCCGGCACTCGCTCAGCTTCAACGAC 660

FKH2      ------------------------------------------------------------ 295

AGAP001671     TGCTTCGTGAAGGTGCCCCGCACGCCGGACAAGCCGGGCAAGGGGTCGTTCTGGACGCTC 720

FKH2      ------------------------------------------------------------ 295

AGAP001671     CATCCCGACTCGGGCAACATGTTCGAGAACGGGTGCTACCTGCGGCGCCAGAAGCGGTTC 780

FKH2      ------------------------------------------------------------ 295

AGAP001671     AAGGACGAGAAGAAGGAGGTGCTCCGGTCGCTGCACAAGAGCCCGGCGCACGGCGGCAGC 840

FKH2      ------------------------------------------------------------ 295

AGAP001671     CTCGATGCGGTCGGCAGCCCGGACAAGAAGGACCCGAACGAGGAGCACCACCATCACCAT 900

FKH2      ------------------------------------------------------------ 295

AGAP001671     CACCATCACAGCCACAGCCACCACAGCCACCGGACGGAGCACGTGTCCAAGCTGAGCGCG 960

FKH2      ------------------------------------------------------------ 295

AGAP001671     GCAGTCGACACGCACGGCATGCTGAACAGTGCGCACGGTAAAGACGCGGACGCGCTCGCG 1020

FKH2      ------------------------------------------------------------ 295

AGAP001671     ATGCTGCACGCGACGGCCGACTTATGCTTAGCCCAACAATCTCATTCACAGCATGGTGGT 1080

FKH2      ------------------------------------------------------------ 295

AGAP001671     TCGCACCACCCTACGCACCACCACCACCACCATCCGGCCCACCAGCAGCTGCAGCAGGAG 1140

FKH2      ------------------------------------------------------------ 295

AGAP001671     GAATTGACGGCTATGGTAAATCGCTGCCACCCTTCGCTGCTTGGTGAATATCACTCGATG 1200

FKH2      ------------------------------------------------------------ 295

AGAP001671     CACCTGAAGCAGGAACCGGCGGGCTACACGCCCTCTAGTCACCCGTTCTCGATCACCCGG 1260

FKH2      ------------------------------------------------------------ 295

AGAP001671     CTGCTGCCGACCGAGTCGAAGGCGGACATCAAGATGTACGAGATGAGCCAGTACGCCGGC 1320

FKH2      ------------------------------------------------------------ 295

AGAP001671     TACAACGGGCTCAGCCCGCTGCCGAACTCGCACGCGGCCGCGGCCGCCCTCGGGCAGGAC 1380

FKH2      ------------------------------------------------------------ 295

AGAP001671     TCGTACTATCACCAGAGCCTCGGCTACCACCATGCGTCCACGGGCACGACCAGCTTGTGA 1440

FKH2      ------------------------------------------------------------ 295

**Cloned sequence of Doublesex for dsRNA**

>DSX

CAAGCGGTGGTCAACGAATACTCACGATTGCATAATCTGAACATGTTTGATGGCGTGGAGTTGCGCAATACCACCCGTCAGAGTGGATGATAAACTTTCCGCACCACTGTAACTGTCCGTATCTTTGTATGTGGGTGTGTGTATGTGTGTTTGGTGAAACGAATTCAATAGTTCTGTGCTATTTTAAATCAAGCCGCGTGCGCAACTGATGCCGATAAGTTCAAACTAGTGTTTAAGGAGTGGAGCGAGAGAGCCGCACC

DSX --CAAGCGGTGGTCAACGAATACTCACGATTGCATAATCTGAACATGTTTGATGGCGTGG 58

AGAP004050-RB GTCAAGCGGTGGTCAACGAATACTCACGATTGCATAATCTGAACATGTTTGATGGCGTGG 60

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DSX AGTTGCGCAATACCACCCGTCAGAGTGGATGATAAACTTTCCGCACCACTGTAACTGTCC 118

AGAP004050-RB AGTTGCGCAATACCACCCGTCAGAGTGGATGATAAACTTTCCGCACCACTGTAACTGTCC 120

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

DSX GTATCTTTGTATGTGGGTGTGTGTATGTGTGTTTGGTGAAACGAATTCAATAGTTCTGTG 178

AGAP004050-RB GTATCTTTGTATGTGGGTGTGTGTATGTGTGTTTGGTGAAACGAATTCAATAGTTCTGTG 180

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

DSX CTATTTTAAATCAAGCCGCGTGCGCAACTGATGCCGATAAGTTCAAACTAGTGTTTAAGG 238

AGAP004050-RB CTATTTTAAATCAAGCCGCGTGCGCAACTGATGCCGATAAGTTCAAACTAGTGTTTAAGG 240

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

DSX AGTGGAGCGAGAGAGCCGCACC-------------------------------------- 260

AGAP004050-RB AGTGGAGCGAGAGAGCCGCACCACGGTACAGAAGGGCAGCAGAATGGGTCGGCAGCCTAG 300

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DSX ------------------------------------------------------------ 260

AGAP004050-RB CTGCACTGGTGCGGTGCGTCCGGCGTCTCGGGGGGAGGGCGAGGAAATTCTAGTGTTAAA 360

DSX ------------------------------------------------------------ 260

AGAP004050-RB TCGGAGCAGCAAAAACAAAACAGTGGTCGTCCCGTTCAAGAAACGGCCTGTACACACACA 420

DSX ------------------------------------------------------------ 260

AGAP004050-RB CAGAAAACACTGCAGCATGTTTGTACATAGTAGATCCTAGAGCAGGTGGTCGTTGCTCCT 480

DSX ------------------------------------------------------------ 260

AGAP004050-RB CGAACGCTCTGGACGCACGGCTTCGCGCGTATTTGCGTAGCGTTCCGCCGATCGTGGGTA 540

DSX ------------------------------------------------------------ 260

AGAP004050-RB TTCGTACTGCCACAAGCCCGCTTTCTCCCATGCAATCTCTGCAACCAAACCAACAAACAA 600

DSX ------------------------------------------------------------ 260

AGAP004050-RB CAACAAAAAACCAATCGACAAAATGAATCACACCCCTTTTGTATCATCTGTATATTCTTG 660

DSX ------------------------------------------------------------ 260

AGAP004050-RB TTCTTTGCGTTCTTTTCTATGTGGCCCACGCCCCGGCGGGTACGTAATTGCGTCGAAAAC 720

DSX ------------------------------------------------------------ 260

AGAP004050-RB CCCGAAAACCCCGGCACATACAGTGTACATACGGTTTGAGGACAACTTTGACCTGCAGCC 780

DSX ------------------------------------------------------------ 260

AGAP004050-RB CTTCTGGGGTTGCCACGTGTAGCTATACTTGTGAGATCGGGCGCCGACGGTGTAAAGCGC 840

DSX ------------------------------------------------------------ 260

AGAP004050-RB GAATGGCCGCCACACAGTGTGTCCACTCCAACACTACCCCTCTGGAACTACCCCGTCCAG 900

DSX ------------------------------------------------------------ 260

AGAP004050-RB GGATGCACCGGCTCGGCTCATGCCCCTGCAAAACAGTCCGGGCTCCACTGTAGTAGCTCC 960

DSX ------------------------------------------------------------ 260

AGAP004050-RB GGCGTTGCTCTGAGAGAAGGATGCCCTTCGAAGTGTCGAAAGCGTGCATTGGGCGTTCAA 1020

DSX ------------------------------------------------------------ 260

AGAP004050-RB GTGTGTGTGTGTGTGTTAGGTTTAGCGAGAAACAGCAGCAGTTGCGTGTGCTGAAAAGCG 1080

DSX ------------------------------------------------------------ 260

AGAP004050-RB AAGGAGTAATAGAGTGCATAATGAAAATGAAAATGAAAATGAAGCAAAAGTAGAAGGCGG 1140

DSX ------------------------------------------------------------ 260

AGAP004050-RB AGGAGAGCAACCTGTGTTCCACTAGTAGCGAATAGTTTAGTCTAGTTTCGTCACCAATCA 1200

DSX ------------------------------------------------------------ 260

AGAP004050-RB ACCTTCCAACCATCGTTCAACCAATACCTGAGTCAACATCGTCATCGTTATCGTGCCACA 1260

DSX ------------------------------------------------------------ 260

AGAP004050-RB ACTTTATTAAAAATGAACCTTGTCCGCGCCACCGTAGGGTGATCTAAGGCGACCTTTCTT 1320

DSX ------------------------------------------------------------ 260

AGAP004050-RB ACGGGCGCGACCCACATGCCATCGTCACCTTCTCCAATCAAAACCAACAGCCTGTACCGA 1380

DSX ------------------------------------------------------------ 260

AGAP004050-RB TGGTGTGCAATTGTGCGTGCGTGTGTGTTATTAGCAAAAAAAGAGAAAGAGTCGACGAGA 1440

DSX ------------------------------------------------------------ 260

AGAP004050-RB GAGAGATAGATCGAGATCGAGAGTACAAAAGAGCAGTAGAAATGTTCGTTGTTTGTTTTT 1500

DSX ------------------------------------------------------------ 260

AGAP004050-RB CGTAACACAGTTGTTTAGCCAAAATGGGAATTTCCAATAATCCCGGGGGCGGGGAAATGC 1560

DSX ------------------------------------------------------------ 260

AGAP004050-RB GGGAATACTGCGTACACACATACATCAATCAAAAAGAAAAATCCTTGCGCTACATCACTA 1620

DSX ------------------------------------------------------------ 260

AGAP004050-RB CCGTTTGCGCGGTGCTGATCTAGAGCAGACCACTTTCCACTCCACTCTACAATCAATCAA 1680

DSX ------------ 260

AGAP004050-RB TCTGTGCAGAAG 1692

**Plasmids**

>pGEM-T vector

GGGCGAATTGGGCCCGACGTCGCATGCTCCCGGCCGCCATGGCCGCGGGATATCACTAGTGCGGCCGCCTGCAGGTCGAC

CATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATG

GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAG

CCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCAC

TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT

CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG

TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT

ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGT

CCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC

TCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA

CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA

CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT

ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA

GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAA

ACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT

AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGAT

CTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCC

CCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCC

GAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTC

GCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCAT

TCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCT

CCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCAT

GCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTT

GCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCT

TCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC

AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGA

CACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGA

TACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGATGCGGT

GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT

TAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACC

GAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAA

AACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCAC

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AAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAA

TGCGCCGCTACAGGGCGCGTCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCT

ATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT

GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATA

**Promoters**

T7 Promoter TAATACGACTCACTATAGGG