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Supplementary information

Two types of bHLH transcription factor determine the competence of the pericycle for lateral root initiation

In the format provided by the authors and unedited

Plasmid sequences used in this study

Information of plasmids used in this study

To open with a commonly-used DNA viewer / editor (ApE, Snapgene, etc.), copy each gene of interest (starting with LOCUS, ending with //) and save as a simple text (.txt).

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pDOE_TMO5-NmVen210 x LHW-CVen210 248

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Plasmids for overexpression

pER8::PFA1 (gateway)

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VERSION

SOURCE

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COMMENT
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DEFINITION

ACCESSION

VERSION

SOURCE

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COMMENT

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DEFINITION

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VERSION

SOURCE

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DEFINITION

ACCESSION

VERSION

SOURCE

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COMMENT

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COMMENT
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Plasmids for SRDX fusion

pER8 (35Spro)::PFA1-SRDX

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DEFINITION

ACCESSION

VERSION

SOURCE

  ORGANISM

COMMENT

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DEFINITION

ACCESSION

VERSION

SOURCE

  ORGANISM

COMMENT

COMMENT

COMMENT    ApEinfo:methylated:1

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Plasmids for fluorescent protein markers

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PFA2pro::H2B-TdTomato

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LOCUS       proPFA2_H2B-tdTom      15750 bp    DNA       circular    18-MAR-2020

DEFINITION  pNOS_Sul_tNOS inserted into pGreenII (bases 626 to 3070) inserted

            into Digestion of pBar_A_circle (modified) - Fragment 1 2 (bases 2

            to 5).

ACCESSION   urn.local...1355456929956.1049

VERSION     urn.local...1355456929956.1049

KEYWORDS    .
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PFA4pro::H2B-TdTomato

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LOCUS       proPFA4_H2B-tdTom      15517 bp    DNA       circular    18-MAR-2020
DEFINITION  pNOS_Sul_tNOS inserted into pGreenII (bases 626 to 3070) inserted
            into Digestion of pBar_A_circle (modified) - Fragment 1 2 (bases 2
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          to 5).
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VERSION     urn.local...1355456929956.1049
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  ORGANISM   .
COMMENT
COMMENT
COMMENT     ApEinfo:methylated:1
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11581 cttccggaga ctgtcatacg cgtaaaacag ccagcgctgg cgcgatttag ccccgacata

11641 gccccactgt tcgtccattt ccgcgcagac gatgacgtca ctgcccggct gtatgcgcga

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11881 gagcagagat agcgctgatg tccggcggtg cttttgccgt tacgcaccac cccgtcagta

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12181 tggggtatct ttaaatactg tagaaaagag gaaggaaata ataaatggct aaaatgagaa

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PFA1pro::PFA1-GFP (partial)

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LOCUS       proPFA1_PFA1-GFP_partial      7568 bp    DNA       linear      18-MAR-2020
DEFINITION  .
ACCESSION
VERSION
SOURCE      .
  ORGANISM  .
COMMENT
COMMENT
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      121 atttaggtgt ccggttccta aataatagct ggaccaagtt attcacccca cccttactgt
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      241 accaagttcg gctgttttga accgttgcta aattgtgttg ttctaataga tcgtttggtt
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      421 accgtttaac aaaatatgtg atgtgcaaat tttaaacttc ctcgcacaac gaacctgaac
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      661 tttcattcat gtaatttaac taaactataa tcactaattg aatattttca attaaacttt
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     1861 agctctataa tggtattgat acaacatgca agtagaaagc aatcaactat atgtgaataa
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2101 acctaatgta gcaagggaat cagccaaata attggcttct ctcgataaac caaaaataaa

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2221 catcataaaa gattagctag tgactattga ctccgagtcc gattctactc cttatgcact

2281 tatgattgat gaagcgtgga gcttctagta tcgtcatgcc ttctcccacc aatgcttgta

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2401 acacgtgtgg cggaggcata tcttggtaac acaggttggc caaatggtaa ataccaagtc

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2521 cagtaacttt ctggaaataa aagtgatatt taaaatcttt gaaacttaga ttaatctcca

2581 aaatctataa tgttatctag aatatcatgg ttgaaaagga aataattatt actaataaaa

2641 agattaacca tttttattat tgtcgatcaa ttagttagta tatgatatat atgctgttta

2701 gggaaactca agttttgagt tagttgtgtg actctgcatg ttgtcctgtc caaagattaa

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2881 cgcagaccgc atataacaca tccttcggtg gcttatatat aactatatgt aatttaaatg

2941 taacgtagtg gacgtacccc actagcatat aatattgtca ccaccaccga tcgtatcata

3001 tatacacttt atattctcta atgcacatat cctagactct taaccaacaa aataaaagaa

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3181 ACGTCTTTCT ACCATAAGAG TAGTAATAAT AACTCACACG CCAACGCTAG CTGTGAAGAA

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3301 TCCAATCATC ACTCTCTCTC GGCTTCGAAT CAGCCTGCCT CCTCCTCCGA TGAGTTGCTT

3361 CGCGACCATG TAGTATCTTC TCATAATCAT CTATGGAGTC TTGCCTTCTT gtaagcatct

3421 atcaaaacac ttaaatttta tttatctttt cgaaccatta acaaatcttc tttagtatcg

3481 tgttcttact tacaattcac ataacggtta ttgtggattc aaagtttagt ttaaggtttt

3541 aggttctacg ctccactcca taaagaaatc atctagttct cactattaat actttcgttt

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4261 GATGGATCAT CATCATCACA TAGCATCAAG AAATTCATCA ACAACATCAG AATTACCATC

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6361 CAGAGAAGAT CACAACAAAA GGGGACCGAA GCATCTTGAT CTAAGGAGTA GAGGGCTTTG

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6481 GAATCCCACG TATAGAGGTT CTTTGTATCG TGGCGCGCCA GCTGCTGCCG CTGCTGCTGC

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PFA2pro::PFA2-GFP (partial)

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LOCUS       proPFA2_PFA2-GFP_partial       7836 bp    DNA       linear      18-MAR-2020
DEFINITION  .
ACCESSION
VERSION
SOURCE      .
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COMMENT
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DEFINITION  .

ACCESSION

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SOURCE     .

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COMMENT

COMMENT

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4681 atctctctct ctctcattgt ctgcaaattt ttgctttacc tttcagaaag atgatgagtg

4741 tgtattagta tatttgtata ctgtcattat tacttatcat gttattgtta ttatatcttt

4801 atggatttat tttatatgta aggtctattt caatagatat ttatgttgga gatgaatgaa

4861 tgatatacca tttcttagat tttgttttac tgaatctcat gtgcttttgt gtcagACTGA

4921 TGCAGCCTCA GTGCTCTCTG AAGCCATTGA ATACATTAAG TTCTTACACC AACAAGTTTC

4981 Tgtaagttag cccactcctt cgtattttta gtacacaaac attttctgct acagtttagt

5041 tagttattgt atttcttcta ctgatgtaca acaaacctgc aaatgattat aactcagGCT

5101 CTGAGCAACC CATACATGAA AAGTGGAGCT TCTTTACAAC ATCAACAGgt aatattttaa

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    5281 catctttaag attggacaat aaagcattat tccaagaaac aatgtagcga gacggttttt

    5341 gcaacgaaaa aagaaatcat ttgcaactta tatttttct ttgttttcta atgatgatgc

    5401 agAGTGATCA TTCCACAGAG CTAGAAGTAT CAGAAGAACC AGATCTTAGA AGTCGAGGTT

    5461 TATGCTTAGT GCCAGTTTCA AGCACATTTC CAGTGACACA CGATACTACA GTAGATTTCT

    5521 GGACTCCTAC ATTTGGTGGG ACTTTTAGAG GCGCGCCAGC TGCTGCCGCT GCTGCTGCCG

    5581 CTGCTGGGGG TGGAGGTATG GTGAGCAAGG GCGAGGAGCT GTTCACCGGG GTGGTGCCCA

    5641 TCCTGGTCGA GCTGGACGGC GACGTAAACG GCCACAAGTT CAGCGTGTCC GGCGAGGGCG

    5701 AGGGCGATGC CACCTACGGC AAGCTGACCC TGAAGTTCAT CTGCACCACC GGCAAGCTGC

    5761 CCGTGCCCTG GCCCACCCTC GTGACCACCC TGACCTACGG CGTGCAGTGC TTCAGCCGCT

    5821 ACCCCGACCA CATGAAGCAG CACGACTTCT TCAAGTCCGC CATGCCCGAA GGCTACGTCC

    5881 AGGAGCGCAC CATCTTCTTC AAGGACGACG GCAACTACAA GACCCGCGCC GAGGTGAAGT

    5941 TCGAGGGCGA CACCCTGGTG AACCGCATCG AGCTGAAGGG CATCGACTTC AAGGAGGACG

    6001 GCAACATCCT GGGGCACAAG CTGGAGTACA ACTACAACAG CCACAACGTC TATATCATGG

    6061 CCGACAAGCA GAAGAACGGC ATCAAGGTGA ACTTCAAGAT CCGCCACAAC ATCGAGGACG

    6121 GCAGCGTGCA GCTCGCCGAC CACTACCAGC AGAACACCCC CATCGGCGAC GGCCCCGTGC

    6181 TGCTGCCCGA CAACCACTAC CTGAGCACCC AGTCCGCCCT GAGCAAAGAC CCCAACGAGA

    6241 AGCGCGATCA CATGGTCCTG CTGGAGTTCG TGACCGCCGC CGGGATCACT CTCGGCATGG

    6301 ACGAGCTGTA CAAGTAACTT AATTAAGACT AGTGGGGTAC CGTCGACCTG CAGGCATGCC

    6361 CGCTGAAATC ACCAGTCTCT CTCTACAAAT CTATCTCTCT CTATAATAAT GTGTGAGTAG

    6421 TTCCCAGATA AGGGAATTAG GGTTCTTATA GGGTTTCGCT CATGTGTTGA GCATATAAGA

    6481 AAACCCCTTA GTATGTATTT TGTATTTTGT AAAAATACTT CTATCAATAA AAATTTTCTA

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PFB1pro::PFB1-GFP (partial)

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DEFINITION  .
ACCESSION
VERSION
SOURCE      .
  ORGANISM  .
COMMENT
COMMENT
COMMENT     ApEinfo:methylated:1
FEATURES             Location/Qualifiers
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      121 ttgatgatgc tcgaacaatc aaaaggctac aaaggaagta ttttttttt tttttagaat
      181 agatcggttt atctcgtttg gttcggttga acttaatttg gttttagttt gtatttgtgt
      241 ctttaaaatt gatacggtta gaacgaatgt atatgtgttg tattctttat aaattaataa
      301 aatgtattta taaatagaat aagatttatc atttttatct tattatataa agtttggttt
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      541 aaataatatt tgtttgtata ttaaaataag ggagatttat aaaattacac ttttttttact
      601 actcttttgc aacaataccc ttttatgttg tccattttta aaaatacccc ttctcttgaa
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     1981 ctgaattgtg atagaagaga gaaaacattt tctaggaaac taaattgtct cttttgaatt
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2221 taattagaat taggagggat acaataatag ataactacaa ttcattcgtc atgttctaaa

2281 aatagagagc aataagtacg acggacagta ccgtcactac ttggcgtcat ggtagatagg

2341 tagtggatct gctagatata tgagaacgga aagaaccaga agctattaga ggcgggagga

2401 gatatgtggg gatgatttca gtgcaattcc acgacgcacc atttccactt tcgtaacacc

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2521 ttccaaatac atcaattcaa attatataat atctagtggc aattataagt atatcatata

2581 ttttcaaaat taattaaaaa gattactaaa ttatgtttga ctacaactat tataatagtt

2641 aaaaacataa acaaaaacaa agaaactatt ttaataaaaa aatcaagtaa acattaaaac

2701 ataagcaaaa aataatgtta aagaaattat taattattaa tttactaata attaatacct

2761 ctataaatta attgttagag gtttaacgta atttataagg aaaactaaag aagactttaa

2821 cccataaaga aaaaaacaaa gactgaattg aaggcccata tttagaagaa gagaaagaag

2881 acccaaatat gatataaaat ccagcccatt tatatatttt tattttgttt ctggaaggaa

2941 aataagaaaa tggcaaaaac gaaataatct gaaaaagtaa ggtcttttac caaaaaggat

3001 atttttttta taaacagagc ataaagtttt cacttttctt ctgctccttt ctcgtctctg

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3181 ctcacagtga ctcgttcgag tcaaagtctc tgtctttagc tcaaaccATG GCTAGTAACA

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3301 GCCTTCCTAA CTTCTCAGCC TCTTCTGCCG CCGGTTTATC TGGAGTTGAC GGAGGATTAG

3361 GTGGTGGAGC ACCGCCTATG ATGCTGCAGT TGGGTTCCGG AGAAGAAGGA AGTCACATGG

3421 GTGGCTTAGG AGGAAGTGGA CCAACTGGGT TTCACAATCA GATGTTTCCT TTGGGGTTAA

3481 GTCTTGATCA AGGGAAAGGA CCTGGGTTTC TTAGACCTGA AGGAGGACAT GGAAGTGGGA

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4021 GCCACCTCCA TCGGCCCCAC ATCAGCCTAC TTCAATCCGT CCCAGGGTTC GAGCTAGGCG

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5281 aaaaacttta gtaatggggt tttgattcag attttgctta aaatgtcaat agGATGAAAC

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6601 AGGAATCCGG GCCTGTGAGA

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PFB2pro::PFB2-GFP (partial)

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LOCUS      1                   6150 bp    DNA       linear      29-OCT-2020
DEFINITION  .
ACCESSION
VERSION
SOURCE     .
  ORGANISM  .
COMMENT
COMMENT    ApEinfo:methylated:1
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3061 TGGTCTCTCT GGAATCGGCG GCGTGGGTCC ACCTCCGATG ATGCTTCAGC TTGGTTCAGG

3121 CAACGAAGGG AATCATAATC ATATGGGTGC CATTGGAGGA GGTGGACCTG TAGGGTTTCA

3181 TAATCAGATG TTTCCGTTGG GATTAAGTCT CGATCAAGGG AAAGGACATG GCTTTCTTAA

3241 ACCTGATGAA ACTGGTAAAC GTTTCCAAGA CGATGTTCTT GATAATCGAT GTTCCTCTAT

3301 GAAACCTgta agtttctctt cagaatcttc actttgtctt tttcttttgt gttctcgaga

3361 aaataaagtg aaattcaaat ctttagggtt tcaaaatggt gtcgtttttg agaaaaccca

3421 gcttaggtct aaatttgata gttaccgaga gtttttggct cagattggtg agatttgatg

3481 tttttgaaga aacccaagtt gaagattttg atgtgtttta aagtcataac actaaaatta

3541 gttttgcaag aaactttagt ataaaagagt gttcttttat gtccaaatta tattgtaaga

3601 aaatttgctc tttagtttct tttctcatgt ggataattcc gtcatagttt gaattgttgc

3661 tataactact ctagtggcga ccgttcttgt gagaagcggt ttttaagctt ttcttaatgt

3721 tattacggca ttgttttgtg ttttgttgaa gATTTTCCAT GGGCAGCCAA TGTCACAGCC

3781 AGCTCCACCA ATGCCGCATC AACAGTCTAC TATTCGGCCT AGAGTTAGGG CTAGGCGAGG

3841 TCAAGCTACC GATCCACATA GCATCGCTGA GAGGgtaaga tgtttgatac actttttta

3901 tcttctggtc tctttttcg atttttatgt gataatgttt gatcaaagct ttaattatag

3961 cttttggttg agaaagttcg attagttctt acttactaag aacggtaaga cctaacctga

4021 atgtatttgc tttgcaacag CTCCGAAGGG AAAGAATAGC AGAACGGATC AGGTCGTTGC

4081 AGGAACTTGT ACCTACCGTT AACAAGgttg gtatcttttt ctctagagct tcagctactg

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4141 ttttcatgtc gcgaagagag cttgaaagag attttaaaag tagggagaaa actagagttg
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4261 tttgctttcc ttttgcagAC AGATAGGGCT GCTATGATCG ACGAGATTGT CGATTATGTA
4321 AAGTTTCTCA GGCTCCAAGT TAAGgtaaac acccaagtca ttttcagttt tctattctct
4381 ggtttttgaa aatgctatca ttaaaagttt gtagaaagat tatttaaaac agccagaagg
4441 atttagtggt gtaaatcctt ggtccccacc accacctact ctcttaaacc aaacttccaa
4501 tcttaataaa agattataat tgtttaatct ggcaataaag agtaatcaaa gagtacatga
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4621 catcacaatt gaggactatt gtaataaagc taatgagaac attgaagaat attttatgca
4681 atgatgggct ttgataatat ttttccttca taagctttat ctctggtcaa ctatggcagG
4741 TCCTGAGCAT GAGCCGTCTT GGTGGAGCCG GTGCTGTCGC ACCACTAGTC ACTGAAATGC
4801 CATTATCTTC ATCAGTTGAG gttagactag agagagatac ttcattaaaa aaagaacaga
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4981 TGGAAGAAAA CGTTGGAGCA GCGATGCAAC TTTTGCAATC AAAGGCTCTT TGCATAATGC
5041 CGATCTCATT GGCAATGGCG ATTTACCATT CTCAGCCACC AGACACATCT TCTTCAATCG
5101 TCAAACCAGA GATGAATCCT CCACCGCCCG GGGGTGGAGG TATGGTGAGC AAGGGCGAGG
5161 AGCTGTTCAC CGGGGTGGTG CCCATCCTGG TCGAGCTGGA CGGCGACGTA AACGGCCACA
5221 AGTTCAGCGT GTCCGGCGAG GGCGAGGGCG ATGCCACCTA CGGCAAGCTG ACCCTGAAGT
5281 TCATCTGCAC CACCGGCAAG CTGCCCGTGC CCTGGCCCAC CCTCGTGACC ACCCTGACCT
5341 ACGGCGTGCA GTGCTTCAGC CGCTACCCCG ACCACATGAA GCAGCACGAC TTCTTCAAGT
5401 CCGCCATGCC CGAAGGCTAC GTCCAGGAGC GCACCATCTT CTTCAAGGAC GACGGCAACT
5461 ACAAGACCCG CGCCGAGGTG AAGTTCGAGG GCGACACCCT GGTGAACCGC ATCGAGCTGA
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5581 ACAGCCACAA CGTCTATATC ATGGCCGACA AGCAGAAGAA CGGCATCAAG GTGAACTTCA
5641 AGATCCGCCA CAACATCGAG GACGGCAGCG TGCAGCTCGC CGACCACTAC CAGCAGAACA
5701 CCCCCATCGG CGACGGCCCC GTGCTGCTGC CCGACAACCA CTACCTGAGC ACCCAGTCCG
5761 CCCTGAGCAA AGACCCCAAC GAGAAGCGCG ATCACATGGT CCTGCTGGAG TTCGTGACCG
5821 CCGCCGGGAT CACTCTCGGC ATGGACGAGC TGTACAAGTA ACTTAATTAA GACTAGTGGG
5881 GTACCGTCGA CCTGCAGGCA TGCCCGCTGA AATCACCAGT CTCTCTCTAC AAATCTATCT
5941 CTCTCTATAA TAATGTGTGA GTAGTTCCCA GATAAGGGAA TTAGGGTTCT TATAGGGTTT
6001 CGCTCATGTG TTGAGCATAT AAGAAAACCC CTTAGTATGT ATTTTGTATT TTGTAAAAAT
6061 ACTTCTATCA ATAAAAATTT TCTAATTCCT TAAAACCAAA AATCCAGGGG GTTGCCCGAA
6121 CTCGGAATTC AGGAATCCGG GCCTGTGAGA
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//

Plasmids for complementation

pLH5000_*PFA1pro*::PFA1

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LOCUS      PFA1_complementat      16503 bp    DNA       circular    18-MAR-2020
DEFINITION  Binary vector pLH5000, complete sequence.
ACCESSION   AY234327
VERSION     AY234327.1  GI:29569706
KEYWORDS    .
SOURCE      Binary vector pLH5000
  ORGANISM  Binary vector pLH5000 other sequences; artificial sequences;
            vectors.
REFERENCE   1  (bases 1 to 8958)
  AUTHORS   Hausmann,L. and Toepfer,R.
  TITLE     Development of Plasmid Vectors
  JOURNAL   (in) Brauer,D., Roebbelen,G. and Toepfer,R. (Eds.); BIOENGINEERING
            OF CUSTOM-TAILORED RAPE VARIETIES: 155-172; GPZ e. V., Von
            Sieboldstr. 8, Goettingen, Germany (1999)
REFERENCE   2  (bases 1 to 8958)
  AUTHORS   Hausmann,L. and Toepfer,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2003) Institute for Grapevine Breeding
            Geilweilerhof, Siebeldingen 76833, Germany
COMMENT
COMMENT     ApEinfo:methylated:1
FEATURES             Location/Qualifiers
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                /experiment="experimental evidence, no additional details
                recorded"
                /note="original nucleotide changed to destroy a SfiI
                restriction site"
                /replace="c"
                /locus_tag="original nucleotide changed to destroy a SfiI
                restriction site"
                /label="original nucleotide changed to destroy a SfiI
                restriction site"
                /ApEinfo_label="original nucleotide changed to destroy a
                SfiI restriction site"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     stem_loop      11739..11771
                /note="palindromic sequence"
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                /label="palindromic sequence"
                /ApEinfo_label="palindromic sequence"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_difference 11747..11747
                /experiment="experimental evidence, no additional details
                recorded"
                /note="nucleotide changed to conserve palindromic sequence
                following SfiI restriction site-destruction"
                /replace="g"
                /locus_tag="nucleotide changed to conserve palindromic
                sequence following SfiI restriction site-destruction"
                /label="nucleotide changed to conserve palindromic
                sequence following SfiI restriction site-destruction"
                /ApEinfo_label="nucleotide changed to conserve palindromic
                sequence following SfiI restriction site-destruction"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_difference 11762..11762
                /experiment="experimental evidence, no additional details
                recorded"
                /note="original nucleotide changed to destroy two SfiI
                restriction sites"
                /replace="c"
                /locus_tag="original nucleotide changed to destroy two
                SfiI restriction sites"
                /label="original nucleotide changed to destroy two SfiI
                restriction sites"
                /ApEinfo_label="original nucleotide changed to destroy two
                SfiI restriction sites"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
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                width 5 offset 0"
regulatory      11829..11834
                /regulatory_class="minus_35_signal"
                /locus_tag="regulatory(6)"
                /label="regulatory(6)"
                /ApEinfo_label="regulatory"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
regulatory      11850..11855
                /regulatory_class="minus_10_signal"
                /locus_tag="regulatory(7)"
                /label="regulatory(7)"
                /ApEinfo_label="regulatory"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
regulatory      11883..11890
                /regulatory_class="ribosome_binding_site"
                /locus_tag="regulatory(8)"
                /label="regulatory(8)"
                /ApEinfo_label="regulatory"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
CDS             11894..12523
                /note="partitioning protein ParA encoded by parA of
                plasmid pVS1; similar to F plasmid SopA in GenBank
                Accession Number X04619, RK2 IncC in GenBank Accession
                Number L27758, and P1 ParA in GenBank Accession Number
                X02954"
                /codon_start=1
                /transl_table=11
                /product="ParA"
                /protein_id="AAO85347.1"
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/db_xref="GI:29569709"

/translation="MKVIAVLNQKGGSGKTTIATHLARALQLAGADVLLVDSDPQGSA

RDWAAVREDQPLTVVGIDRPTIDRDVKAIGRRDFVVIDGAPQAADLAVSAIKAADFVL

IPVQPSPYDIWATADLVELVKQRIEVTDGRLQAAFVVSRAIKGTRIGGEVAEALAGYE

LPILESRITQRVSYPGTAAAGTTVLESEPEGDAAREVQALAAEIKSKLI"

/locus_tag="ParA"

/label="ParA"

/ApEinfo_label="ParA"

/ApEinfo_fwdcolor="pink"

/ApEinfo_revcolor="pink"

/ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}

width 5 offset 0"

misc_feature 12790..12802

/note="identical to the korB operator binding site of

plasmid RK2 in GenBank Accession Number L27758.1"

/locus_tag="identical to the korB operator binding site of

plasmid RK2 in GenBank Accession Number L27758.1"

/label="identical to the korB operator binding site of

plasmid RK2 in GenBank Accession Number L27758.1"

/ApEinfo_label="identical to the korB operator binding

site of plasmid RK2 in GenBank Accession Number L27758.1"

/ApEinfo_fwdcolor="pink"

/ApEinfo_revcolor="pink"

/ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}

width 5 offset 0"

CDS 12850..14025

/note="partitioning protein ParB encoded by parB of

plasmid pVS1; similar to F plasmid SopB in GenBank

Accession Number X04619, RK2 KorB in GenBank Accession

Number L27758, and P1 ParB in GenBank Accession Number

X02954"

/codon_start=1

/transl_table=11

/product="ParB"

/protein_id="AAO85348.1"

/db_xref="GI:29569710"

/translation="MPHVWRNGRLARRKRLGCLPALQWHWNPQARGIGVSGRKPSGPV

QIGAALGDDLVEKLKAAQAAQRQRIEAEARPGESWQAAADRIRKESRQPPAAGAPSIR

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                KPPKGDEQPDFFVPMLYDVGTRDSRSIMDVAVFRLSKRDRRAGEVIRYELPDGHVEVS
                AGPAGMASVWDYDLVLMAVSHLTESMNRYREGKGDKPGRVFRPHVADVLKFCRRADGG
                KQKDDLVETCIRLNTTHVAMQRTKKAKNGRLVTVSEGEALISRYKIVKSETGRPEYIE
                IELADWMYREITEGKNPDVLTVHPDYFLIDPGIGRFLYRLARRAAGKAEARWLFKTIY
                ERSGSAGEFKKFCFTVRKLIGSNDLPEYDLKEEAGQAGPILVMRYRNLIEGEASAGS"
                /locus_tag="ParB"
                /label="ParB"
                /ApEinfo_label="ParB"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
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                /experiment="experimental evidence, no additional details
                recorded"
                /note="compared to GenBank Accession Number U10487"
                /replace=""
                /locus_tag="compared to GenBank Accession Number U10487"
                /label="compared to GenBank Accession Number U10487"
                /ApEinfo_label="compared to GenBank Accession Number
                U10487"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_difference 13029..13029
                /experiment="experimental evidence, no additional details
                recorded"
                /note="original nucleotide changed to destroy a SfiI
                restriction site"
                /replace="c"
                /locus_tag="original nucleotide changed to destroy a SfiI
                restriction site(1)"
                /label="original nucleotide changed to destroy a SfiI
                restriction site(1)"
                /ApEinfo_label="original nucleotide changed to destroy a
                SfiI restriction site"
                /ApEinfo_fwdcolor="pink"
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                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_difference 13350..13350
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                recorded"
                /note="original nucleotide changed to destroy a SfiI
                restriction site"
                /replace="c"
                /locus_tag="original nucleotide changed to destroy a SfiI
                restriction site(2)"
                /label="original nucleotide changed to destroy a SfiI
                restriction site(2)"
                /ApEinfo_label="original nucleotide changed to destroy a
                SfiI restriction site"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     repeat_region   complement(14017..14031)
                /note="repeat D'"
                /rpt_type=inverted
                /locus_tag="repeat D'"
                /label="repeat D'"
                /ApEinfo_label="repeat D'"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     stem_loop      14039..14061
                /note="palindromic sequence"
                /locus_tag="palindromic sequence(1)"
                /label="palindromic sequence(1)"
                /ApEinfo_label="palindromic sequence"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
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misc_feature    14068..14487
                /note="parC region; contains putative cis-acting sites for
                replication, partition and incompatibility"
                /locus_tag="parC region; contains putative cis-acting
                sites for replication, partition and incompatibility"
                /label="parC region; contains putative cis-acting sites
                for replication, partition and incompatibility"
                /ApEinfo_label="parC region; contains putative cis-acting
                sites for replication, partition and incompatibility"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
protein_bind    14091..14099
                /note="putative DnaA box"
                /bound_moiety="DnaA"
                /locus_tag="putative DnaA box"
                /label="putative DnaA box"
                /ApEinfo_label="putative DnaA box"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
repeat_region   14102..14116
                /note="repeat D"
                /rpt_type=direct
                /locus_tag="repeat D"
                /label="repeat D"
                /ApEinfo_label="repeat D"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
repeat_region   14123..14137
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                /rpt_type=direct
                /locus_tag="repeat D(1)"
                /label="repeat D(1)"
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                /ApEinfo_label="repeat D"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     repeat_region   14144..14158
                /note="repeat D"
                /rpt_type=direct
                /locus_tag="repeat D(2)"
                /label="repeat D(2)"
                /ApEinfo_label="repeat D"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     repeat_region   14165..14179
                /note="repeat D"
                /rpt_type=direct
                /locus_tag="repeat D(3)"
                /label="repeat D(3)"
                /ApEinfo_label="repeat D"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_feature    14188..14266
                /note="AT-rich region"
                /locus_tag="AT-rich region"
                /label="AT-rich region"
                /ApEinfo_label="AT-rich region"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     protein_bind    14278..14286
                /note="putative DnaA box"
                /bound_moiety="DnaA"
                /locus_tag="putative DnaA box(1)"
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                /label="putative DnaA box(1)"
                /ApEinfo_label="putative DnaA box"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
repeat_region   14382..14395
                /note="repeat E"
                /rpt_type=direct
                /rpt_unit_range=6837..6843
                /locus_tag="repeat E"
                /label="repeat E"
                /ApEinfo_label="repeat E"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
misc_feature    14495..15899
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                /locus_tag="similar to GenBank Accession Number M35007"
                /label="similar to GenBank Accession Number M35007"
                /ApEinfo_label="similar to GenBank Accession Number
                M35007"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
regulatory      14626..14631
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                /locus_tag="regulatory(9)"
                /label="regulatory(9)"
                /ApEinfo_label="regulatory"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
regulatory      14649..14654
                /regulatory_class="minus_10_signal"
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/locus_tag="regulatory(10)"

/label="regulatory(10)"

/ApEinfo_label="regulatory"

/ApEinfo_fwdcolor="pink"

/ApEinfo_revcolor="pink"

/ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}

width 5 offset 0"

gene 14671..15681

/gene="aadA"

/note="different start codons are described in the

literature"

/locus_tag="aadA"

/label="aadA"

/ApEinfo_label="aadA"

/ApEinfo_fwdcolor="pink"

/ApEinfo_revcolor="pink"

/ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}

width 5 offset 0"

CDS 14671..15681

/gene="aadA"

/note="confers resistance to streptomycin and

spectinomycin"

/codon_start=1

/transl_table=11

/product="streptomycin/spectinomycin adenyltransferase"

/protein_id="AAO85349.1"

/db_xref="GI:29569711"

/translation="MRSRNWSRTLTERSGGNGAVAVFMACYDCFFGVQSMPRASKQQA

RYAVGRCLMLWSSNDVTQQGSRPKTKLNIMREAVIAEVSTQLSEVVGVIERHLEPTLL

AVHLYGSAVDGGLKPHSDIDLLVTVTVRLDETTRRALINDLLETSASPGESEILRAVE

VTIVVHDDIIPWRYPAKRELQFGEWQRNDILAGIFEPATIDIDLAILLTKAREHSVAL

VGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWAGDERNVVLTLSRIWYSAVTGKIA

PKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRLASRADQLEEFVHYVKGEITKVV

GK"

/locus_tag="streptomycin/spectinomycin adenyltransferase"

/label="streptomycin/spectinomycin adenyltransferase"

/ApEinfo_label="streptomycin/spectinomycin

adenyltransferase"

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stem_loop       15684..15741
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                /locus_tag="palindromic sequence; putative termination
                signal"
                /label="palindromic sequence; putative termination signal"
                /ApEinfo_label="palindromic sequence; putative termination
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                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
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                width 5 offset 0"
misc_feature    15900..16501
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                Agrobacterium tumefaciens; similar to GenBank Accession
                Number X00493"
                /locus_tag="left border region from octopine-type Ti
                plasmid of Agrobacterium tumefaciens; similar to GenBank
                Ac"
                /label="left border region from octopine-type Ti plasmid
                of Agrobacterium tumefaciens; similar to GenBank Ac"
                /ApEinfo_label="left border region from octopine-type Ti
                plasmid of Agrobacterium tumefaciens; similar to GenBank
                Ac"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
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                width 5 offset 0"
misc_difference 15918..15919
                /note="compared to GenBank Accession Number X00493;
                removed to destroy a KpnI restriction site"
                /replace="ggtacc"
                /locus_tag="compared to GenBank Accession Number X00493;
                removed to destroy a KpnI restriction site"
                /label="compared to GenBank Accession Number X00493;
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                removed to destroy a KpnI restriction site"
                /ApEinfo_label="compared to GenBank Accession Number
                X00493; removed to destroy a KpnI restriction site"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_feature    16202..16225
                /note="left flanking T-DNA border"
                /locus_tag="left flanking T-DNA border"
                /label="left flanking T-DNA border"
                /ApEinfo_label="left flanking T-DNA border"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     source          8926..16503
                /organism="Binary vector pLH5000"
                /mol_type="other DNA"
                /db_xref="taxon:226212"
                /locus_tag="source:Binary vector pLH5000(1)"
                /label="source:Binary vector pLH5000(1)"
                /ApEinfo_label="source:Binary vector pLH5000"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_feature    8926..8932
                /note="multiple cloning site from vector pBlueSfi BA in
                GenBank Accession Number AF327875"
                /locus_tag="multiple cloning site from vector pBlueSfi BA
                in GenBank Accession Number AF327875(1)"
                /label="multiple cloning site from vector pBlueSfi BA in
                GenBank Accession Number AF327875(1)"
                /ApEinfo_label="multiple cloning site from vector pBlueSfi
                BA in GenBank Accession Number AF327875"
                /ApEinfo_fwdcolor="pink"
                /ApEinfo_revcolor="pink"
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                /ApEinfo_label="PFA1 promoter region"
                /ApEinfo_fwdcolor="cyan"
                /ApEinfo_revcolor="green"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_feature    4425..7845
                /locus_tag="PFA1-coding genomicDNA-w/stop"
                /label="PFA1-coding genomicDNA-w/stop"
                /ApEinfo_label="PFA1-coding genomicDNA-w/stop"
                /ApEinfo_fwdcolor="#ff9f0a"
                /ApEinfo_revcolor="green"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
     misc_feature    7846..8923
                /locus_tag="genomic sequence downstream of PFA1 coding
                region"
                /label="genomic sequence downstream of PFA1 coding
                region"
                /ApEinfo_label="genomic sequence downstream of PFA1
                coding region"
                /ApEinfo_fwdcolor="#ff0c55"
                /ApEinfo_revcolor="green"
                /ApEinfo_graphicformat="arrow_data {{0 1 2 0 0 -1} {} 0}
                width 5 offset 0"
ORIGIN
        1 tctagaacat ggtggagcac gacactctcg tctactccaa gaatatcaaa gatacagtct
       61 cagaagacca gagggctatt gagacttttc aacaaagggt aatatcggga aacctcctcg
      121 gattccattg cccagctatc tgtcacttca tcgaaaggac agtagaaaag gaagatggct
      181 tctacaaatg ccatcattgc gataaaggaa aggctatcgt tcaagatgcc tctaccgaca
      241 gtggtcccaa agatggaccc ccacccacga ggaacatcgt ggaaaaagaa gacgttccaa
      301 ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg gatgacgcac
      361 aatcccacta tccttcgcaa gacccttcct ctatataagg aagttcattt catttggaga
      421 ggacctcgag ggccaatttg ccatcatggt tcgaccattg aactgcatcg tcgccgtgtc
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```
 481 ccaaaatatg gggattggca agaacggaga ccgaccctgg cctccgctca ggaacgagtt
 541 caagtacttc caaagaatga ccacaacctc ttcagtggaa ggtaaacaga atctggtgat
 601 tatgggtagg aaaacctggt tctccattcc tgagaagaat cgacctttaa aggacagaat
 661 taatatagtt ctcagtagag aactcaaaga accaccacga ggagctcatt ttcttgccaa
 721 aagtttggat gatgccttaa gacttattga acaaccggaa ttggcaagta aagtagacat
 781 ggtttggata gtcggaggca gttctgttta ccaggaagcc atgaatcaac caggccacct
 841 cagactcttt gtgacaagga tcatgcagga atttgaaagt gacacgtttt tcccagaaat
 901 tgatttgggg aaatataaac ttctcccaga atacccaggc gtcctctctg aggtccagga
 961 ggaaaaaggc atcaagtata agtttgaagt ctacgagaag aaagactaac aggaagatgc
1021 tttcaagttc tctgctcccc tcctaaagct agtccgcaaa aatcaccagt ctctctctac
1081 aaatctatct ctctctattt ttctccagaa taatgtgtga gtagttccca gataagggaa
1141 ttagggttct tatagggttt cgctcatgtg ttgagcatat aagaaaccct tagtatgtat
1201 ttgtatttgt aaaatacttc tatcaataaa atttctaatt cctaaaacca aaatccagtg
1261 acctgcaggc atgcaagctg atccactaga ggccatggcg gccgcactag tggatccccc
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1381 aatacgtaat gtggcgctat acgtaatgtg gataactgga aaagagacta aaacacatca
1441 taattcatcc tatttaggtg tccggttcct aaataatagc tggaccaagt tattcacccc
1501 acccttactg ttttcatcaa ggtaaccctt agggctaaga cgacaaaact ttcttagctt
1561 ataactatat aaccaagttc ggctgttttg aaccgttgct aaattgtgtt gttctaatag
1621 atcgtttggt tggcggttgg ccaaaataaa aatccttact ttggtaaaca aattataaac
1681 gaatatatga tattggtact ctacatgaat tgtaactatt tttccttggc tttggttatt
1741 ccttagtcct taccgtttaa caaaatatgt gatgtgcaaa ttttaaactt cctcgcacaa
1801 cgaacctgaa cttgatggtt tcatgcgtta caaaaaggga aagaaaaaga acttagaaaa
1861 atattgtttc atgcatgaat catgaatggg cttatgcaga aaatccaaac accaataaat
1921 aaatgggcct agaatacttc cattacttgc ctaatcgttc tcttccacta aaagtttaca
1981 tggtttcata ctttcattca tgtaatttaa ctaaactata atcactaatt gaatattttc
2041 aattaaactt tcggccatta gaaaaacatc ttgggttatg ttgctatcga ttggttattg
2101 actattatat acagagtcaa atagaaatga taatgaaata aacaaaagtc aacctcagaa
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15901 gcttgcttgg tcgttccgcg tgaacgtcgg ctcgattgta cctgcgttca aatactttgc

15961 gatcgtgttg cgcgcctgcc cggtgcgtcg gctgatctca cggatcgact gcttctctcg

16021 caacgccatc cgacggatga tgtttaaaag tcccatgtgg atcactccgt tgccccgtcg

16081 ctcaccgtgt tgggggggaag gtgcacatgg ctcagttctc aatggaaatt atctgcctaa

16141 ccggctcagt tctgcgtaga aaccaacatg caagctccac cgggtgcaaa gcggcagcgg

16201 cggcaggata tattcaattg taaatggctt catgtccggg aaatctacat ggatcagcaa

16261 tgagtatgat ggtcaatatg gagaaaaaga aagagtaatt accaattttt tttcaattca

16321 aaaatgtaga tgtccgcagc gttattataa aatgaaagta cattttgata aaacgacaaa

16381 ttacgatccg tcgtatttat aggcgaaagc aataaacaaa ttattctaat tcggaaatct

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   16441 ttatttcgac gtgtctacat tcacgtccaa atgggggctt agatgagaaa cttcacgatc
   16501 ggc
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Plasmids for Y2H bait constructs

pBTM116_PFA1 (gateway, partial)

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LOCUS      PFA1_pBTM116_gw       7074 bp    DNA       circular    09-APR-2020
DEFINITION  .
ACCESSION
VERSION
SOURCE     .
  ORGANISM  .
COMMENT
COMMENT
COMMENT    ApEinfo:methylated:1
FEATURES           Location/Qualifiers
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                    /ApEinfo_label="TRP1 promoter"
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       61 ATATCCGCAA TGACAAAAAA ATGATGGAAG ACACTAAAGG AAAAAATTAA CGACAAAGAC
      121 AGCACCAACA GATGTCGTTG TTCCAGAGCT GATGAGGGGT ATCTCGAAGC ACACGAAACT
      181 TTTTCCTTCC TTCATTCACG CACACTACTC TCTAATGAGC AACGGTATAC GGCCTTCCTT
      241 CCAGTTACTT GAATTTGAAA TAAAAAAAAG TTTGCTGTCT TGCTATCAAG TATAAATAGA
      301 CCTGCAATTA TTAATCTTTT GTTTCCTCGT CATTGTTCTC GTTCCCTTTC TTCCTTGTTT
      361 CTTTTTCTGC ACAATATTTC AAGCTATACC AAGCATACAA TCAACTCCAA GCTTGAATTA
      421 ATTCCGGGCG GAATGAAAGC GTTAACGGCC AGGCAACAAG AGGTGTTTGA TCTCATCCGT
      481 GATCACATCA GCCAGACAGG TATGCCGCCG ACGCGTGCGG AAATCGCGCA GCGTTTGGGG
      541 TTCCGTTCCC CAAACGCGGC TGAAGAACAT CTGAAGGCGC TGGCACGCAA AGGCGTTATT
      601 GAAATTGTTT CCGGCGCATC ACGCGGGATT CGTCTGTTGC AGGAAGAGGA AGAAGGGTTG
      661 CCGCTGGTAG GTCGTGTGGC TGCCGGTGAA CCACTTCTGG CGCAACAGCA TATTGAAGGT
      721 CATTATCAGG TCGATCCTTC CTTATTCAAG CCGAATGCTG ATTTCCTGCT GCGCGTCAGC
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      841 CAGGATGTAC GTAACGGTCA GGTCGTTGTC GCACGTATTG ATGACGAGGT TACCGTTAAG
      901 CGCCTGAAAA AACAGGGCAA TAAAGTCGAA CTGTTGCCAG AAAATAGCGA GTTTAAACCA
      961 ATTGTCGTAG ATCTTCGTCA GCAGAGCTTC ACCATTGAAG GGCTGGCGGT TGGGGTTATT
     1021 CGCAACGGCG ACTGGCTGGA ATTCCCGATC ACAAGTTTGT ACAAAAAAGC AGGCTTCATG
     1081 TTAAGGGAAG AATGTACTCC AAGTTCATCA TGGTGGGAAG ATGTTCAACA TCATCATAAT
     1141 GATCATGCAA ACTCGATTAG TTCGACGTCT TTCTACCATA AGAGTAGTAA TAATAACTCA
     1201 CACGCCAACG CTAGCTGTGA AGAAGACAAT CTCTCCGTCT CTACCGTACG CGCTTCGAAT
     1261 CGTTTGGACC TAACCGCTGA ATCCTCCAAT CATCACTCTC TCTCGGCTTC GAATCAGCCT
     1321 GCCTCCTCCT CCGATGAGTT GCTTCGCGAC CATGTAGTAT CTTCTCATAA TCATCTATGG
     1381 AGTCTTGCCT TCTTGCCTGG TAGAAGCTTA GGAGATCAAA TGATGGATCA TCATCATCAC
     1441 ATAGCATCAA GAAATTCATC AACAACATCA GAATTACCAT CATTCGAGCC AGCGTGCCAT
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1501 AACGGTAATG GTAACGGTTG GATCTATGAC CCAAATCAAG TTAGGTACGA TCAAAGTAGT

1561 GACCAACGGC TGTCAAAGTT GACGGATCTT GTAGGCAAGC ACTGGTCAAT TGCACCACCG

1621 AATAATCCCG ACATGAACCA TAACCTTCAT CATCACTTCG ATCATGATCA TTCTCAAAAC

1681 GACGACATTT CTATGTACAG ACAAGCCTTG GAGGTGAAAA ATGAGGAAGA TCTTTGTTAC

1741 AATAATGGCT CAAGTGGTGG TGGTTCCTTG TTCCATGATC CTATAGAAAG TTCTAGAAGT

1801 TTCCTTGATA TAAGGTTAAG TAGGCCATTA ACGGATATTA ATCCGTCATT TAAGCCATGC

1861 TTTAAGGCCT TAAACGTATC CGAGTTTAAC AAGAAAGAAC ATCAAACGGC ATCTCTGGCA

1921 GCAGTGAGAC TGGGAACAAC AAACGCTGGA AAAAAGAAGA GATGTGAAGA AATTTCCGAT

1981 GAGGTTTCAA AGAAGGCCAA GTGCAGTGAG GGCTCTACAC TTTCGCCAGA GAAGGAACTA

2041 CCCAAAGCCA AACTTCGAGA CAAGATCACG ACTCTACAGC AAATTGTGTC TCCCTTTGGA

2101 AAGACTGATA CTGCTTCTGT GCTTCAAGAG GCCATCACTT ACATAAATTT TTATCAAGAG

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2221 GGATGGGACA GAGAAGATCA CAACAAAAGG GGACCGAAGC ATCTTGATCT AAGGAGTAGA

2281 GGGCTTTGTT TGGTTCCTAT TTCATATACC CCAATCGCAT ACCGCGATAA CAGTGCAACT

2341 GACTACTGGA ATCCCACGTA TAGAGGTTCT TTGTATCGTA ACCCAGCTTT CTTGTACAAA

2401 GTGGTGATGT AACTAATTGA GGGGATCCGT CGACCTGCAG CCAAGCTAAT TCCGGGCGAA

2461 TTTCTTATGA TTTATGATTT TTATTATTAA ATAAGTTATA AAAAAAATAA GTGTATACAA

2521 ATTTTAAAGT GACTCTTAGG TTTTAAAACG AAAATTCTTA TTCTTGAGTA ACTCTTTCCT

2581 GTAGGTCAGG TTGCTTTCTC AGGTATAGCA TGAGGTCGCT CTTATTGACC ACACCTCTAC

2641 CGGCATGCCG GCAAGTGCAC AAACAATACT TAAATAAATA CTACTCAGTA ATAACCTATT

2701 TCTTAGCATT TTTGACGAAA TTTGCTATTT TGTTAGAGTC TTTTACACCA TTTGTCTCCA

2761 CACCTCCGCT TACATCAACA CCAATAACGC CATTTAATCT AAGCGCATCA CCAACATTTT

2821 CTGGCGTCAG TCCACCAGCT AACATAAAAT GTAAGCTTTC GGGGCTCTCT TGCCTTCCAA

2881 CCCAGTCAGA AATCGAGTTC CAATCCAAAA GTTCACCTGT CCCACCTGCT TCTGAATCAA

2941 ACAAGGGAAT AAACGAATGA GGTTTCTGTG AAGCTGCACT GAGTAGTATG TTGCAGTCTT

3001 TTGGAAATAC GAGTCTTTTA ATAACTGGCA AACCGAGGAA CTCTTGGTAT TCTTGCCACG

3061 ACTCATCTCC ATGCAGTTGG ACGATATCAA TGCCGTAATC ATTGACCAGA GCCAAAACAT

3121 CCTCCTTAGG TTGATTACGA AACACGCCAA CCAAGTATTT CGGAGTGCCT GAACTATTTT

3181 TATATGCTTT TACAAGACTT GAAATTTTCC TTGCAATAAC CGGGTCAATT GTTCTCTTTC

3241 TATTGGGCAC ACATATAATA CCCAGCAAGT CAGCATCGGA ATCTAGAGCA CATTCTGCGG

3301 CCTCTGTGCT CTGCAAGCCG CAAACTTTCA CCAATGGACC AGAACTACCT GTGAAATTAA

3361 TAACAGACAT ACTCCAAGCT GCCTTTGTGT GCTTAATCAC GTATACTCAC GTGCTCAATA

3421 GTCACCAATG CCCTCCCTCT TGGCCCTCTC CTTTTCTTTT TTCGACCGAA TTAATTCGTA

3481 ATCATGTCAT AGCTGTTTCC TGTGTGAAAT TGTTATCCGC TCACAATTCC ACACAACATA

3541 CGAGCCGGAA GCATAAAGTG TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA ACTCACATTA

3601 ATTGCGTTGC GCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATTAA

3661 TGAATCGGCC AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGCGCTCTTC CGCTTCCTCG

3721 CTCACTGACT CGCTGCGCTC GGTCGTTCGG CTGCGGCGAG CGGTATCAGC TCACTCAAAG

3781 GCGGTAATAC GGTTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA

3841 GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT CCATAGGCTC

3901 CGCCCCCCTG ACGAGCATCA CAAAAATCGA CGCTCAAGTC AGAGGTGGCG AAACCCGACA

3961 GGACTATAAA GATACCAGGC GTTTCCCCCT GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG

4021 ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT GGCGCTTTCT

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4201 TCCAACCCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA CAGGATTAGC

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4321 ACTAGAAGAA CAGTATTTGG TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA

4381 GTTGGTAGCT CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT TTTTGTTTGC

4441 AAGCAGCAGA TTACGCGCAG AAAAAAAGGA TCTCAAGAAA GGATTCGTTG AATCTTTTCT

4501 ACCGGGGGTC TGACGCTTCA GTGGAACGAA AAACTTCACG TTAAGGGATT TTTGGGTCAT

4561 GAGATTATCA AAAAAGGGAT CTTCACCTAG ATCCCTTTTA AATTAAAAAA TGAAGTTTTA

4621 AATCAATCTA AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG CTTAATCAGT

4681 GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA TAGTTGCCTG ACTCCCCGTC

4741 GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG

4801 CGAGACCCAC GCTCACCGGC TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC

4861 GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG

4921 GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTACA

4981 GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG TTCCCAACGA

5041 TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT

5101 CCGATCGTTG TCAGAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG

5161 CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA

5221 ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC GGCGTCAATA

5281 CGGGATAATA CCGCGCCACA TAGCAGAACT TTAAAAGTGC TCATCATTGG AAAACGTTCT

5341 TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT CCAGTTCGAT GTAACCCACT

5401 CGTGCACCCA ACTGATCTTC AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA

5461 ACAGGAAGGC AAAATGCCGC AAAAAAGGGA TTGGGGGGCG ACACGGAAAT GTTGAATACT

5521 CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG GGTTATTGTC TCATGAGCGG

5581 ATACATATTT GAATGTATTT AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG

5641 AAAAGTGCCA CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG

5701 GCGTATCACG AGGCCCTTTC GTCTCGCGCG TTTCGGTGAT GACGGTGAAA ACCTCTGACA

5761 CATGCAGCTC CCGGAGACGG TCACAGCTTG TCTGTAAGCG GATGCCGGGA GCAGACAAGC

5821 CCGTCAGGGC GCGTCAGCGG GTGTTGGCGG GTGTCGGGGC TGGCTTAACT ATGCGGCATC

5881 AGAGCAGATT GTACTGAGAG TGCACCATAA CGCATTTAAG CATAAACACG CACTATGCCG

5941 TTCTTCTCAT GTATATATAT ATACAGGCAA CACGCAGATA TAGGTGCGAC GTGAACAGTG

6001 AGCTGTATGT GCGCAGCTCG CGTTGCATTT TCGGAAGCGC TCGTTTTCGG AAACGCTTTG

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    6121 TTGAAAACCA AAAGCGCTCT GAAGACGCAC TTTCAAAAAA CCAAAAACGC ACCGGACTGT

    6181 AACGAGCTAC TAAAATATTG CGAATACCGC TTCCACAAAC ATTGCTCAAA AGTATCTCTT

    6241 TGCTATATAT CTCTGTGCTA TATCCCTATA TAACCTACCC ATCCACCTTT CGCTCCTTGA

    6301 ACTTGCATCT AAACTCGACC TCTACATTTT TTATGTTTAT CTCTAGTATT ACTCTTTAGA

    6361 CAAAAAAATT GTAGTAAGAA CTATTCATAG AGTGAATCGA AAACAATACG AAAATGTAAA

    6421 CATTTCCTAT ACGTAGTATA TAGAGACAAA ATAGAAGAAA CCGTTCATAA TTTTCTGACC

    6481 AATGAAGAAT CATCAACGCT ATCACTTTCT GTTCACAAAG TATGCGCAAT CCACATCGGT

    6541 ATAGAATATA ATCGGGGATG CCTTTATCTT GAAAAAATGC ACCCGCAGCT TCGCTAGTAA

    6601 TCAGTAAACG CGGGAAGTGG AGTCAGGCTT TTTTTATGGA AGAGAAAATA GACACCAAAG

    6661 TAGCCTTCTT CTAACCTTAA CGGACCTACA GTGCAAAAAG TTATCAAGAG ACTGCATTAT

    6721 AGAGCGCACA AAGGAGAAAA AAAGTAATCT AAGATGCTTT GTTAGAAAAA TAGCGCTCTC

    6781 GGGATGCATT TTTGTAGAAC AAAAAAGAAG TATAGATTCT TTGTTGGTAA AATAGCGCTC

    6841 TCGCGTTGCA TTTCTGTTCT GTAAAAATGC AGCTCAGATT CTTTGTTTGA AAAATTAGCG

    6901 CTCTCGCGTT GCATTTTTGT TTTACAAAAA TGAAGCACAG ATTCTTCGTT GGTAAAATAG

    6961 CGCTTTCGCG TTGCATTTCT GTTCTGTAAA AATGCAGCTC AGATTCTTTG TTTGAAAAAT

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pBTM116_PFA2 (gateway, partial)

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DEFINITION  .
ACCESSION
VERSION
SOURCE     .
  ORGANISM  .
COMMENT
COMMENT
COMMENT    ApEinfo:methylated:1
FEATURES           Location/Qualifiers
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ORIGIN
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      121 AGCACCAACA GATGTCGTTG TTCCAGAGCT GATGAGGGGT ATCTCGAAGC ACACGAAACT
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      241 CCAGTTACTT GAATTTGAAA TAAAAAAAAG TTTGCTGTCT TGCTATCAAG TATAAATAGA
      301 CCTGCAATTA TTAATCTTTT GTTTCCTCGT CATTGTTCTC GTTCCCTTTC TTCCTTGTTT
      361 CTTTTTCTGC ACAATATTTC AAGCTATACC AAGCATACAA TCAACTCCAA GCTTGAATTA
      421 ATTCCGGGCG GAATGAAAGC GTTAACGGCC AGGCAACAAG AGGTGTTTGA TCTCATCCGT
      481 GATCACATCA GCCAGACAGG TATGCCGCCG ACGCGTGCGG AAATCGCGCA GCGTTTGGGG
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      601 GAAATTGTTT CCGGCGCATC ACGCGGGATT CGTCTGTTGC AGGAAGAGGA AGAAGGGTTG
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721 CATTATCAGG TCGATCCTTC CTTATTCAAG CCGAATGCTG ATTTCCTGCT GCGCGTCAGC

781 GGGATGTCGA TGAAAGATAT CGGCATTATG GATGGTGACT TGCTGGCAGT GCATAAAACT

841 CAGGATGTAC GTAACGGTCA GGTCGTTGTC GCACGTATTG ATGACGAGGT TACCGTTAAG

901 CGCCTGAAAA AACAGGGCAA TAAAGTCGAA CTGTTGCCAG AAAATAGCGA GTTTAAACCA

961 ATTGTCGTAG ATCTTCGTCA GCAGAGCTTC ACCATTGAAG GGCTGGCGGT TGGGGTTATT

1021 CGCAACGGCG ACTGGCTGGA ATTCCCGATC ACAAGTTTGT ACAAAAAAGC AGGCTTCATG

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1441 CAACACCAAA GTTACCAAGC GAAGAGGATA CAAAATTGGG AAGAACAAGT TTTGAGGCAC

1501 CAAGCTTCCA TGAAACAAGA GAGTAGTAAT AATAATAGTT ATGGAATAAT GTCCTCACCA

1561 AACTCACCTC CAAACAAATC TTGTGCTACA ATTATCAACA CCAATGAAGA CAACAACAAT

1621 AACATTCACA GTGGTCTTAA CTTGTCCGAG TGTAATAGCT CAGAGATGAT TGGGTCTTCT

1681 TTTGCTAATA AGAAACCAAA ACTTCAAGTT CCTTCATCAC AATCAACTCT CAAGGTGAGA

1741 AAGGAGAAAC TTGGAGGCAG AATAGCATCT CTTCACCAGC TAGTATCTCC CTTTGGCAAG

1801 ACTGACACAG CCTCTGTCTT GTCGGAGGCT ATTGGATACA TTAGATTCCT CCACAGTCAA

1861 ATTGAGGCTT TAAGTCTACC ATACTTTGGT ACTCCCTCGA GGAACAATAT GATGCACCAA

1921 CATGCACAAA GAAATATGAA TGGTATATTT CCTGAGGACC CTGGTCAGCT TGTGAATGAG

1981 TATTGCATGA AAAGAGGAGT TTCATTGTCA TCGACGGACA ATCAAAAATC AAATCCTAAC

2041 GAAGAACCGA TGAAAGATTT GAGAAGTAGA GGGCTTTGTC TTGTTCCCAT CTCATGCACA

2101 CTACAAGTTG GCAGCGACAA TGGTGCCGAC TATTGGGCTC CGGCGTTCGG AACCACTCTC

2161 CAGAACCCAG CTTTCTTGTA CAAAGTGGTG ATGTAACTAA TTGAGGGGAT CCGTCGACCT

2221 GCAGCCAAGC TAATTCCGGG CGAATTTCTT ATGATTTATG ATTTTTATTA TTAAATAAGT

2281 TATAAAAAAA ATAAGTGTAT ACAAATTTTA AAGTGACTCT TAGGTTTTAA AACGAAAATT

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2401 CGCTCTTATT GACCACACCT CTACCGGCAT GCCGGCAAGT GCACAAACAA TACTTAAATA

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pBTM116_PFB1 (gateway, partial)

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ACCESSION
VERSION
SOURCE      .
  ORGANISM  .
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2461 CACCAGCTAA CATAAAATGT AAGCTTTCGG GGCTCTCTTG CCTTCCAACC CAGTCAGAAA

2521 TCGAGTTCCA ATCCAAAAGT TCACCTGTCC CACCTGCTTC TGAATCAAAC AAGGGAATAA

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Plasmids for single-vector BiFC

pDOE_PFA2-NmVen210 x LHW-CVen210

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DEFINITION  .
ACCESSION
VERSION
SOURCE      .
  ORGANISM  .
COMMENT
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pDOE_PFA1-NmVen210 x LHW-CVen210

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LOCUS      PFA1XLHW_in_pDOE      17932 bp    DNA       linear      03-DEC-2019

DEFINITION  .

ACCESSION

VERSION

SOURCE     .

  ORGANISM  .

COMMENT

COMMENT    ApEinfo:methylated:1

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pDOE_TMO5-NmVen210 x LHW-CVen210

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DEFINITION  .

ACCESSION

VERSION

SOURCE     .

  ORGANISM  .

COMMENT

COMMENT    ApEinfo:methylated:1

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pDOE_PFA2-NmVen210 x PFB1-CVen210

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COMMENT

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DEFINITION  .

ACCESSION

VERSION

SOURCE      .

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COMMENT

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13621 CCGTCGATTA GGAAGCCGCC CAAGGGCGAC GAGCAACCAG ATTTTTTCGT TCCGATGCTC

13681 TATGACGTGG GCACCCGCGA TAGTCGCAGC ATCATGGACG TGGCCGTTTT CCGTCTGTCG

13741 AAGCGTGACC GACGAGCTGG CGAGGTGATC CGCTACGAGC TTCCAGACGG GCACGTAGAG

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13861 GTTTCCCATC TAACCGAATC CATGAACCGA TACCGGGAAG GGAAGGGAGA CAAGCCCGGC

13921 CGCGTGTTCC GTCCACACGT TGCGGACGTA CTCAAGTTCT GCCGGCGAGC CGATGGCGGA

13981 AAGCAGAAAG ACGACCTGGT AGAAACCTGC ATTCGGTTAA ACACCACGCA CGTTGCCATG

14041 CAGCGTACGA AGAAGGCCAA GAACGGCCGC CTGGTGACGG TATCCGAGGG TGAAGCCTTG

14101 ATTAGCCGCT ACAAGATCGT AAAGAGCGAA ACCGGGCGGC CGGAGTACAT CGAGATCGAG

14161 CTAGCTGATT GGATGTACCG CGAGATCACA GAAGGCAAGA ACCCGGACGT GCTGACGGTT

14221 CACCCCGATT ACTTTTTGAT CGATCCCGGC ATCGGCCGTT TTCTCTACCG CCTGGCACGC

14281 CGCGCCGCAG GCAAGGCAGA AGCCAGATGG TTGTTCAAGA CGATCTACGA ACGCAGTGGC

14341 AGCGCCGGAG AGTTCAAGAA GTTCTGTTTC ACCGTGCGCA AGCTGATCGG GTCAAATGAC

14401 CTGCCGGAGT ACGATTTGAA GGAGGAGGCG GGGCAGGCTG GCCCGATCCT AGTCATGCGC

14461 TACCGCAACC TGATCGAGGG CGAAGCATCC GCCGGTTCCT AATGTACGGA GCAGATGCTA

14521 GGGCAAATTG CCCTAGCAGG GGAAAAAGGT CGAAAAGGTC TCTTTCCTGT GGATAGCACG

14581 TACATTGGGA ACCCAAAGCC GTACATTGGG AACCGGAACC CGTACATTGG GAACCCAAAG

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14941 CGCCGGCGCC CACATCAAGG CACCCTGCCT CGCGCGTTTC GGTGATGACG GTGAAAACCT

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15061 ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCGCAG CCATGACCCA

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15361 GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG

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15481 AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC

15541 TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC

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16021 GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA

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16201 TCCCCGATAT CCTCCCTGAT CGACCGGACG CAGAAGGCAA TGTCATACCA CTTGTCCGCC

16261 CTGCCGCTTC TCCCAAGATC AATAAAGCCA CTTACTTTGC CATCTTTCAC AAAGATGTTG

16321 CTGTCTCCCA GGTCGCCGTG GGAAAAGACA AGTTCCTCTT CGGGCTTTTC CGTCTTTAAA

16381 AAATCATACA GCTCGCGCGG ATCTTTAAAT GGAGTGTCTT CTTCCCAGTT TTCGCAATCC

16441 ACATCGGCCA GATCGTTATT CAGTAAGTAA TCCAATTCGG CTAAGCGGCT GTCTAAGCTA

16501 TTCGTATAGG GACAATCCGA TATGTCGATG GAGTGAAAGA GCCTGATGCA CTCCGCATAC

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   16741 GTGGTCCCTT TATACCGGCT GTCCGTCATT TTTAAATATA GGTTTTCATT TTCTCCCACC

   16801 AGCTTATATA CCTTAGCAGG AGACATTCCT TCCGTATCTT TTACGCAGCG GTATTTTTCG

   16861 ATCAGTTTTT TCAATTCCGG TGATATTCTC ATTTTAGCCA TTTATTATTT CCTTCCTCTT

   16921 TTCTACAGTA TTTAAAGATA CCCCAAGAAG CTAATTATAA CAAGACGAAC TCCAATTCAC

   16981 TGTTCCTTGC ATTCTAAAAC CTTAAATACC AGAAAACAGC TTTTTCAAAG TTGTTTTCAA

   17041 AGTTGGCGTA TAACATAGTA TCGACGGAGC CGATTTTGAA ACCGCGGTGA TCACAGGCAG

   17101 CAACGCTCTG TCATCGTTAC AATCAACATG CTACCCTCCG CGAGATCATC CGTGTTTCAA

   17161 ACCCGGCAGC TTAGTTGCCG TTCTTCCGAA TAGCATCGGT AACATGAGCA AAGTCTGCCG

   17221 CCTTACAACG GCTCTCCCGC TGACGCCGTC CCGGACTGAT GGGCTGCCTG TATCGAGTGG

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