ภาคผนวก

1. สารเคมี

Acrylamide (Amersham Bioscience, Sweden)

Agarose (Gibco/BRL, USA)

Ammnonium peroxydisulfate (USB corporation, USA)

Bisacrylamide (Amersham Bioscience, Sweden)

Boric acid (Merck, Germany)

Chloroform (Lab Scan, Ireland)

dNTP mix (Invitrogen, USA)

EDTA (Fisher Scientific, USA)

Ethanol (Merck, USA)

Ethidium bromide (Bio Basic Inc, Canada)

Isopropanol (Merck, Germany)

Oligonucleotide primer (Bio Basic Inc, Canada)

Silver nitrate (Merck, Germany)

Sodium chloride (Merck, Germany)

Sodium carbonate (Merck, Germany)

TEMED (USB corporation, USA)

Tris (USB corporation, USA)

Taq DNA polymerase (Invitrogen, USA)

2. ชุดน้ำยาสำเร็จรูป

Trizol^{TM} reagent (Invitrogen, USA)

SuperScript^{TM} III First-Strand Synthesis for RT-PCR (Invitrogen, USA)

3. อุปกรณ์และเครื่องมือ

Electrophoresis for agarose gel, Gel-Mate 2000 (Toyobo, Japan)

Electrophoresis, vertical apparatus, Hoefer SQ3 (Amersham pharmacia biotech, U.S.A.)

Power Supply, Model E833 (Consort, Belgium)

Gel documentation (Model Gene Genius & gene Tools, U.S.A.)

Gel dryer, Model GD 2000 (Amersham Bioscience, U.S.A.)

Hot Air Oven, Model ULE 400 (Memmert, Germany)

PCR Thermocycler, PTC-100™ (MJ research, U.S.A.)

Spectrophotometer UV/visible light (UV-VIS Biowave S2100, Gemmany)

ThermoShaker, Model DKSI001a (Daiki, Korea)

Magnetic Stirrer, Model HS115 (HL Instrument, Thailand)

Microcentrifuge tube 1.5 ml (Sorenson, Bioscience. Inc., U.S.A.)

PCR tube (Sorenson, Bioscience. Inc., USA)

pH meter (Model CG 842, Inc., U.S.A.)

Pipette, 0.2 µl (CappAero,Denmark)

Pipette, 20, 200, 1000 µl (Gilson, France)

Refrigerated Bench Top Centrifuge, Model Universal 32R (Hettich, Germany)

Vortex mixer, Genie II Model G560E (Scientific Industries, U.S.A.)

4. สารละลาย

Acetic acid solution (10%)

Glacial acetic	250	ml
ddH_2O added to	2500	ml

Acrylamide (19:1) (40%)

Acrylamide	152	g
Bis-acrylamide	8	g
ddH_2O added to	400	ml

$AgNO_3$ solution (0.1%)

$AgNO_3$	2.5	g
ddH_2O added to	2500	ml

EDTA (0.5 M) (pH 8)

EDTA ($Na_2.2H_2O$)	186.1	g
ddH_2O added to	1000	ml

Nitric acid solution (1%)

65%Nitric acid	35.5	ml
ddH_2O added to	2500	ml

Polyacrylamide-urea gel (6%)

Urea (ultrapure)	29.4	g
40% acrylamide	10	ml
10X TBE	7	ml
ddH_2O	30	ml
APS	400	µl
TEMED	30	µl

TBE (10X) buffer (pH 8)

Tris	108	g
Boric acid	55	g
EDTA (0.5M)	40	ml
ddH_2O added to	1000	ml

ลำดับนิวคลีโอไทด์ที่ได้จากบริษัท 1st Base ประเทศมาเลเซีย

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 1

>1st_BASE_497734_1F_Forward_OPD03 ขนาด 510 bp
GTGCAGTACTTAGGCATTGATTGTGTTGCTGCCTTCCTCATACCAAGAACTTGAGTCCTATTTCAGCATACTTGTGCAAAGCAAGG
TAGCAAAGACCAAAGCTTCGATCCTCTCGCTGCCTTCGATGAAAATTGTTTTGGTAGCCTTAGGAGGGAGAAACGTGTATCCCTGC
AACAAAGATTTGCATGAAGCTAGTGTCCACCCACAAGTCGGGCGACAAGACCCAAAAATTTTCATGAGGCAAGAAAGTTTGTCTTA
CTATTTTTCAAAAAAATGTGATCCACCCGGAAAAAGGGGAGGCGCCCCCGCCCCAGCAAAGGGGAAAACCTTTTTTACGACAGGGG
GCAGAAAAAAATGCCCCCCCCCCCCCCGTCCCCAAAAACCTGGTCTGAGAAAAAAAAAACCCCTTTTTTTTAATAAGCTTCCGATC
AACGCCGGGAAGCCTGCAATTTTTTCCCAACATTTTCTTTTGGATAAAAACAAACCTGGTCTCACCTTCCGCCCCCCCGC

>1st_BASE_497735_1R_Reverse_Oligo_VA ขนาด 646 bp
GNTGAATAACAACAGAATTAAGAAAATACGGCACAAAAACCGAGGGGATATTCTCGTGAAGCAGCAACTCCCCTTTAAAAAAAGGG
TAGGTGTTAAACTGTGCCCATCCCCCCCCCCACCCACAAAAGGTAGCACCAATTGGGTGAAAACCAACTGGGTCAGGGGGAAAAAA
AAGGACATGTCCATTCCCAATTTAGCCTTTTCCTCTTTTCCCACTCCCCCCCCCCGCTGGGGTTGGGACCCAAAAAAAAAAAGGAG
CAGTTGAAAAAAAAAGAAAAGATTTTTTCCCCCCTGCCACCGCCACAAAAAAAAAAAACAAAACAAAAAAAAAAAAAAAAAAGTCT
GGGTGGGGACCCCTTCCCCCCCCCCAACCGGAGAAAAAAAAAAAAGAGCCCCAAAAATTCAGAGAGAAAAAAAAAAAAAAATTTCCC
CCCTCCCCTTTAAAAAAACCAACAGGCGAGGGAAGAAAGAGGCCACCCCCCCCCCCTAATTTTTCCCCAAACGCACCCAAGGGGGG
GAAGTTCCCAATTATTTTCTCCCCATCAAAAAACCCCATTTTGGGGGGAAAAAAAAAAAAAAAAAAAAAAAAGGGTCCCTGCACGTC
GCGTCCCCACGACTGCACAACAACCAAGCGGGGAGCCCCGAACG

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 2

>1st_BASE_497736_2F_Forward_OPD03 ขนาด 230 bp
NNNNNTTNNNTCCAACCTTTGCCATGTANAAACCCAANNNTTAAGTCTGTTAATTACCAAACTCCCTCCATTTAATGGGGGTGTAG
TATTGTTTATAATAACCCACCTTTGCAAAATCAGACAGCCTTTGAGGGGAAGATATTTTTTGGGATCAATCTTTTTAAAAATGGGT
AGCCTTTGTTGCGCTATTCCATTATTTGTCTTTTCTTTATTACCAAATATTTCCTGGG

>1st_BASE_497737_2R_Reverse_Oligo_VA ขนาด 249 bp
GNNNNNNNANNNNNNNNNNNNNNNNCANNNNNGNNNNTGCCGTTCTTCTACNTACTTCTTAAAAATTCCACATAAAAAAAAAAAAA
AGAGCGATTTTAGACATAAAGTGTTAAATTGTCATTATTTTTTACTTTTGATGAATTCTTTAGAATGAATATTAGTTGTTTGATTT
TTTGTGAGAAAGGGCCATAACATTTTGAATTAATTAACCAACTTTTTTTTTTGTACCAAATTTCCTTATAAAATTAC

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 3

>1st_BASE_497738_3F_Forward_OPD03.ab1 ขนาด 267 bp
NNNNNNNNNNNNGNNNGNGNNGNGGANTACAGNAAANCAAATTTCATGGCTGGGANAAGCAGAGGATAACTCNNNAANTGATGGCN
TTTATGGCACCTGCTGCCCTACACCCACCACGCCTGNNNAANCTNAGNGCGNNCGGGAGCNGACNCANNTNNTTTNNTCCCGTGTT
TTTTTTTAAAAAAGCCCCGGGNNAGACCGGANGAGCTCTCTATTCCGGGGGTTAAATTTTGTGGGGTTTTTCCCCCGGGGGGGGGG
AAAAAAAAA

>1st_BASE_497739_3R_Reverse_Oligo_VA ขนาด 164 bp
GNNNNNNNNGGGCGAGTGAGCGTCCTCGGGCCGTTTAGGCCTTTTTTTGCAAACTTTTAAAAATCTCTACATAAAATTTCTTAAAA
GGCGATTTTGACATAGAGTAGTAATTCTTTTCATTCAACTCTTTGCATCGTGTGTATTGTTGTGGTCTCGACTTGATC

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 4

>1st_BASE_497740_4F_Forward_OPD03.ab1 ขนาด 344 bp
NNNNNNNNNNNNNNNNNTGAGNTGNGCNANGNNGGAACCAAATTTCTTGTGANTTGNNCAATAAGANNATCNCNNTTCCCNTTAATG
NGGCTGTAGCATTGCTGTTCTACTCCGCNNNCCCTANNANACTCCNANTTGCTGTGCCAACNAANNANTTTAGTAGCAAGTTGTTT
ATNNCNTTTTTTAGATTTTTTTTAGGCGAGTGTCCAACCACTCCTCTTATTTTNCCCCCATATTTTTTTTTCGGGCAAAAAAAAAA
AATAGCCTTGACGATGTTTCCAAGAGTCTTGGTCGAACCGCGTTATNNGTTTTTCTTTTTCTCTTTTTCGATCCAATTGTAGTATN

>1st_BASE_497741_4R_Reverse_Oligo_VA.ab1 ขนาด 156 bp
NNNNGGCCCCNACANNNGNTTGGGNNACTGCCGCTANTGCCATGTTTTATATTAATTNAAGTNATTCGTTTTACTNGNNTTNAAAG
NTTNATTTTGGTATANTGGNAATTNNTATGATTATATTAAGCTGAGATTTAAAAACGATGTCGAGTAACA

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 5

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>1st_BASE_497742_5F_Forward_OPD03.ab1 ขนาด 383 bp
NNNNNNNNNNNNANNGNNTGTGGATAGANGNAACCAAATTTCATGGNTTTGNACAATAAGAGNAAACCTCTTCAATATAANGNGTT
GTTGAAAGTGCTGTTCGACTCCGCNAANNCTAGNTATCTNNNNCGNNCNCGGCGNGTNNTANNTATTTTTATAGGAGGTTTTTTTT
TTTCAAGCCCCCGAGATATGCGGAGGGGAGTGTCCAAAAAGGGGTAAAATTTTTAGAACCTTTTTTTTTCCCGGGGGGGAAAAAAA
AAAANATCCTTAACAAGGTTTCCAAGATCCTGTGCCAGACCGGAAAAATGTCTTGCCACCTCCTTGATTCCAGCAGCCAGCACGCC
CTTCTTCGCTGCTTGAGTATTNTTTTTTCTTTCTANNCT
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>1st_BASE_497743_5R_Reverse_Oligo_VA ขนาด 451 bp
TCGTGCAGTGGAAGGGGAGGAAGGGGCCGGGAGGGCCATTGGACATCAATGTCTTTAAAAGACCTCCACCTTAAACCGAGCATGGG
AGGGGCCACAGGCGGGAGAGGCGAACCTTTTCCCCTGCGACACAGCGAAATCTGCGACCGTTGGCAAGCGACTTCGAAAAGAAAAT
CGCCTTCGCCCCAGGTTTAAAAAAAACCAAAGGCCGGGGGTATTTCCTGGGGAGGGGGGTTTCCGTTGAGGGGGGGGGGGGGACCAA
ACCCCAAAGGCCGGTGGGTCCCCAAAACCCCTTTTGGGTGGTTAACACAAAGCCACAATAAAAGGGGGACTCCCCTAAAAAAAGGA
TAACCCAAAAAGGTTTTTTGGGAGGAAAAACCCGGGGGGGGAGAGGGGGGGGTCCCCAGCCCCAAAAAAGACCCCGAGAAAAAATG
GTAAAAGATCCTACCTGACGC
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 6

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>1st_BASE_497744_6F_Forward_OPD03.ab1 ขนาด 649 bp
NNNNNNTTNGNCTCANNCNGNNGCNANANANNAAANCNNATTTCTTAGGATGGGAAANGAAAGAAAAAATNCTCGCAAAACAAAGG
AGNTTATGGTACGTGCTGCTAGATGTCGTNANCNGGNTNACNNAGNANGNGTGGGGANGNNCNANNCTCNTTTTAGTTGGNTNTAT
CCTTTTTCGNGCACCNGGANCAAGAGCCGTTGNTGTTAAAGGGCTTTATCATTAATGGCANTANTTTNCCNGGCCCGCACNAAGAN
TGTCTATGNAGGGTCCCTTCCGCCCCTTCAAACGCTAAAGAAGGGCCAAANNAAAATATCCATAACCGCTAATTGCATGTTCTCTG
AGGGTTTTCAATGTTCCTTTCTTTGATTTCATACCCAATTATTTATTTGTTTCTGATCTAGTCCAGTTGAGTCTGCCCGTGCTTTC
TTATCAATTCAGTTGGACACGGTCATTTGTAGTGAACATTCCACCACTCAAGCTGGGTATGCCTTGCTTTCTTGGGTAGCTTTCCT
TTCTTTTTCTTCCTGGAAAACACCTTCTTCCACGTACTTATGNGACTTCCATCCTTGCGAAGTAGTTTATCTTTAACATCTTTGTC
TTCACTGCTTGGTTGCCCTTCATGTGCCTCACATTCTCGCCCTCTCC
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>1st_BASE_497745_6R_Reverse_Oligo_VA ขนาด 720 bp
NNNNAGATAGACGTAAACGTCCTTCCTTTTGCCGCGGCCCTCTCAGCAGGAGAGATTCCCGTGAGAAAACCACCCCCCTTATAAAA
CGCAGGGGGGCAGGGGATCATTTCAGACCAATTGTCATCCGCAAAATGGTTACCCGCATCCGTCTGCAGGGCGGCGACATAGGGAC
GGACAGGCAATCCCGCCTCACACCTGAAGGCGGAGTCCCCCCTTCTCTCCTTGGCGGCACTCCTAGGTAAGGGCCCTGGAACCCAA
ACCGGGGCGAATTTTTTAATCGGAGACCGCAGTGCCTGCTGACCGCTGGGGGGCACAAAAGGGAAGAAATGGTCCCATTCTGGTTA
GCGCTCGGGGGGGGGGACATTTGGACACGTCGGGAGGGAAGGGGAAGACACCCGTTTTGCCTCTACTGGGGAGGAAAGAAACTCGGG
GCGCGGTGAACAATAACATTGTCTCCCACCCATCACAACTCAATATAAGATTGTAGCGAACAGCACGCAAAGCGAGAAAATACACC
ACAGCATTCATCGGAGCGAGACAGAGACGCGGTATAATAGGTATAAATAGCCTCTTGTTTTTGGTAGGTCTGCGAGCCAGACACTA
CCTCTCTCATGGGGCTGTATCTATTGCTAGATCGGATCTAACCCGACAACATGGGGCCCGTAAGTTGTGCGCGCGAACCCAAAGGG
ACCACGACAACGGATCAACCAGGACGACCAAA
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 7

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>1st_BASE_497746_7F_Forward_OPD08.ab1 ขนาด 390 bp
NNNNNNNGGATNNNGNNNNNNNTGACTATNTATAAAATCTTTCTTGTCTCATAGAAGTAATGCATTGAAGATCTTTTACTTGGAGA
GCTTGCATATCCTCATTTGAACTNNNAGTTGAGNNTTCGNCNGNNGGTGGGCTANNAANCAGCTAGTTGTGTNNCTCCCGTGGCAG
TCNCTTGAAAACCAAATTGGGGGATCNNCCCGGGGGTACTTTAGNNNTTTTTTTTTTTTANGAANGGGTNTTGNAAAAANTCNTTT
TTTTCCCNNAAAAACNCCATAAAAAAAANNNNNACNTGGGCGGTTTTNTNNGGGAAAGGGGGGGTGGGTTTCTGTAAAGAAATGCN
GATGNNNTTTTTNATGTTNCTTTNTTTGGGGCTCNNCCNNTNTTTN
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>1st_BASE_497747_7R_Reverse_Oligo_VA.ab1 ขนาด 374 bp
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAACNNNNNNNNNNNNNNNNNNNNANNNNGANNNAANNNCNNNNNNNNNNN
NNNGNNNNTTNATTTTTTTTTNNNCAANNAAAAAATTTTTTNNAAAAACNTNNTTANAGTNTTCTNNTGNNNNTNTTANGAGGCCA
ACCCGGGNAGGCTATGGGGGCCTCTTTTGGGNNTTTTTTTGCGGTNGGTCTTTCGGCGAAGGGGGTGGGGGGGCTTTCAANNCAAC
TTCACCCCAAAAAAGGCCNTCCCCCCGNTANTTTTTTTTTTTNGGGAGGGAGAGATGNTTATCCCNGGGGGGCGNCNCGGGGCATT
TNGTTTNNTTTTTTGTTNNAAAAAAAAANT
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 8

```
>1st_BASE_497748_8F_Forward_OPD08.ab1 ขนาด 519 bp
NNNNNNNNNTNNGNNNNNNTTGAANACAGCACAAATTTGTCTTGTCGNTACAACTACTGCTGCGAAGATCTTTTACTTGGACCTTT
TCCATCTGCCTTTTTGATCTTGAAGATTAACGAGTTGGTNCCNCTCGGGTGNNGNATAGCTAGCTTTGTCNCCGCTGTTGNGGATT
CTCTGCAGACAAAACNGTATGACACCACNGNNGGGTANATNAGAANTCNTTTNNTTTCAAGAAAATGTNNTATAANCNTTNTCCNC
NCCANAACCCCNAAAAAACNNCCCCCCCCTTGNGGGNGGGTTTTNGNNAGNNGGGNNGGGNNTGCNAATACCNCCCCCCGAAGNTT
TCANTGTCCCTTTTGTTGGNAATCNCANNATNNGTCNTTGCTTCTGATCTGGTCCTTTTGAGTCTGCTTTGCTTTCTTATCNATTC
ATTTGGATAAGGCCTTTTGTAGTGAACATTCCACCNCTCAGGCTNGGTATGCCTTGCTTCCTTTGTTTGTTTTCCTTTCTTTTTCT
TCT
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>1st_BASE_497749_8R_Reverse_Oligo_VA.ab1 ขนาด 409 bp
CNNNNNNNNNGGGNNGGNGGGGCTCATAGGACCGANCGCTCTCTGGACATAAGAGGGCTCTACGGGAATTTGGAGGGGTGACCTTA
TTGGAGCTTTCTGGCCGGTTCCAATATGGATATTAAGCAAAATGTACCCAGAGAAGAAGTGGATCCCGCTCATCAACATTCCTGTC
ATATCTTATGGTTTTGCCGGTATGCCGCCTGCAACACCGACCAACATAGCTAGCTGGCTCATCACCGGAACGATCTTCAACTTCTT
TGTTTTCCGNNATCGAAAGANCTGGTAAAAAAAAAACAACTATGTGCTATCTGCTGTTTTGGATGAGGGCACGGGATTCATGGGGG
TGCTGTTGCCCCCCAGCCCGGGGAGAATCCGGGTTTTGGGGGGGGCNNCCNNNNNNNNACACANN
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 9

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>1st_BASE_497750_9F_Forward_OPD08.ab1 ขนาด 374 bp
NNNNNNANNNGGNANGNNNTGANCATCNATCACATCTATTCTTGTCTCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGC
TGGCATATCCATAACTGAACTTCGAGATTNGGAGTACCTCNCNNCCGGTNCCCGNAGTTATTGNGTGGTGCGTTGGTCCGNNATNT
GGGGANANACACAAAANGNNNGACANTTGNTAAAGGNGGGCCTTCCTTTNTNCTCCACANTTTTTAATNNTNNCTTTTGGCCGGG
AGAAAACCNCGANAAAAAAAANNCNCCNTATTNGTGGGGGTCTCCTTNNGGAAANNGGGGCGGGGGTNTATAAAANATCCNTNCAAA
AAGGNAAAACNCTTTGGGGGAANNACAANN
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```
>1st_BASE_497751_9R_Reverse_Oligo_VA.ab1 ขนาด 407 bp
NNNNNNNNNANGTGNAGNTCAGGNGNTCTGATANGCAACGCGCTNCAGCTTTGGACCTGCAGGGCTCTACTGGAATTTGATGTGAA
TTTACTTGATTGACGCTTTCTTGCCGGTTCCAAAATGGATATTAAGCAAAATGTACCCCGAGAAGAAGTGGATCCCACTCATCAAC
ATTCCTGTCATATCTTATGGTTTTGCCGGTATGCCGCCTGCAACACCGACCAACATAGCTAGCTGGCTCATCACCGGAACAATCTT
CAACTTCTTTGTTTTCCGGTATCGAAAGGGCTGGTGGCAAAGAAACAACTATGTGCTATCTGCAGCTTTGGATGCTGGCACGGCGT
TCGTGGGGGTCCTGTTGTTCTTTGCCCTCGAGAAACAGGTTTTTGGGGGGGACAAAAAAAAAN
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 10

```
>1st_BASE_497752_10F_Forward_OPD08.ab1 ขนาด 408 bp
NNNNANNNNGNGNAGNGNAGGGGNATGATATNACGGATTCNCTCTACTTTANAAAAGAAGTTCTGTTGGTTTTTCTTTTTTCCCAC
TTAAAATGGCCGTTCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTAATTACATCACCAAGGAAGGACTCTACT
CAGCTAGAAAGGAGAAGCTTGGATTAAAAGAATGGAAGAAGGGGATTTTAATGCCTTTCTAAGGAGACTGAAGGCTCTTAATATTC
TAGGATCCTGGGNNGGGAGGGTGNGGGGAAAAAAAAAAAACCCCCCCCCCTGGGGTTTTTTTTTTTCTTCTTTAAAAAACCCCCCT
TTTCCCCCCCGNACNTTTTCTTTTCCAAAANTTNNNNGGGNNNGNGGNNNAAANAAACAAAAAA
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>1st_BASE_497753_10R_Reverse_Oligo_VA.ab1 ขนาด 423 bp
NNNNNNNNNNNANNAAAAANGGGGCTCNNACNNAANNNCACCCTCTTTGGANTTAAAAAGTCTACGGCAANNNAAGGANTGNTCCT
TTTTTAACTATCNTCCTNCGTTATAGAGATTNACAGCCTTAGGNNCCTNNAAAGGCATTNACTTNCCCTTCTTCCTTCTTNTATGT
NATCTGCGTCTATCTAGCTGAGTCAAAAATGTACCTAGGGGATGGTAATGCTGTACTAAGCTATCCAGAATTATCTAAATTTTCTA
TTTTTCTTGCCGGNNAGTGTAAGGGGGAAAAAAAAAAAAACCCCTCTCGGCGGGGTCTTTTTTTCTCTCCCTTCCAAGATNCTCCNT
TCCCTCCTTCCCCCCCACTTGCCCCCTTACATTTTTTTGGGGGGGGGGGGGGGAGGCCCGGGGAGCAACACAAAAAAATT
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 11

```
>1st_BASE_497754_11F_Forward_OPD08.ab1 ขนาด 393 bp
NNNNNNNNGTNGCGNGGTTATTGNNCATGAGATCACATTTTTCCCTGCGCTAGAATCCAAGGTCCGAAGANTTTTAGCTGGNGAGC
TTGATATCTTNATTGAACTCCAAGTTNNGNTGTGGACATCCGCGNANNACNNATTCCTGCNNGTTCNGGTTTCTGGGGGANAATTG
GGAAATTGCCCTTTTTTTCCCCTGTTCCCCGGANAGGGGGACCCTTCTTCTTTTCCCAGAGAATTTTTAATAACCCCCTTTTTGGG
GGGGGGGGGTGNTNCCCCGAAAAAAAAAAAAAACCCCCCTTTTTTTTGGGGGACCTCTTTGGGNGGAAAAAAACACGNNTTTTTAA
AAAACANTCCCCCCAATTTTTTGGTTTTTGGGGGGGGGAANANCAAAAA
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```
>1st_BASE_497755_11R_Reverse_Oligo_VA.ab1 ขนาด 401 bp
NNNNNNANNANNGNANNCANTGNTCTGATGNNCATGGTCTTCCTCTTTGGTCCTGGAGGGCTCTACCGGAATTAGGTCGCTTNTAC
TTTATTGGCGCTTTCTGGCCCTTTCCAGTATGGATATTAANNAAATGGACCCAGAGAAGAAGTGGATCCCGCTCATCAACATTCCT
GTCATATCTTATGGTTTTGCCGGTATGCCGCCTGCAACACCGACCAACATAGCTAGCTGGCTCATCACCGGAACGATCTTCAACTA
CTTTGTTTTCCGGTATCGAAAGGACTGGTAAAAAAAAAACAACTATATTCTATCGGCAGCTTTGGAAAAAAAAAAAAANNGGTCATG
AAAACCCCAACCCCCCCCCAACTTTTGGGGAATTTTTTTTTTGGGGGCNCAAAAAAA
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ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 12

```
>1st_BASE_497756_12F_Forward_OPD08.ab1 ขนาด 394 bp
NNNNNNNNNNNNNTACNNTTTGGTCATCTATAAATCAATTCTTGTCTCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCT
TGTTATCCATAACTGAACTTCNNNTTTTGTCTGNNNCCNCCNCCNNNGNCCCANNNGGNACANNNTGGNNNNACNNGGGCCCCCAN
NGGGGCCCCCNNTGGGGCCCCCANTGGGGNCCCCCTGGGCCCAANTGGGGNCCNATTGGGGCCCCATTGGGCNNACGGGGGGCACA
NNGGGNNNNTNGGGNNNNNANGGGNNTANNNGCGNNCNNTNNNNNNNNNNNNNNNGNANNNNNTNNNNNNNNTGTGNNGNNTNNNGT
GNGCGTNNNTNNATANNNNNNNNNNNNNNNNNCTNNNNNNTNNNNNNNNN
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```
>1st_BASE_497757_12R_Reverse_Oligo_VA.ab1 ขนาด 564 bp
NNNNNNNNNNNNNNTACNNATTTGNTCATCTATAAAATCAATTCTTGTCTCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGA
GCTTTTATATCAATAACTAATNCTNNNNTNNNTGNNNNNNNNCNCGNGGNNGNNNNNNNNNNNNTNNNNNCCNCNNGGCCCCCAAC
TGGGGCACAAAATNGGGCACCACTNGGGGNACCCACTGGGGGCAAAAACTGGGGGGCACACAATTGGGGCCAACAATTGGGGGNNN
CCATTGGGGCACCAACTGGGGCACCCCCTGGGGGCCCACAACGGGGGGACCAAAATGGGGGAAACCCCTGGGGGCACAAACTGGGG
GCACACAANGGGGCACCAAACTGGGGCACACACTTGGGGCACAACACTGGGGNNAAACAANGGGGGCCAAAAATGGGGCCCAAAAA
TGGGGCANAAATTGGGGCNAACACTTGGGCCCCNANTGGGGNAAACAATGGGGCCCCTNTTGGGCNCACACTTNNNAAATANTNNN
TCCAATNTNGNNNNNTNTTTTTTTTTTNNTNNGNNNNNNNTNTTNNTT
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ผลการทำ alignment ระหว่างเส้นที่ได้จาก forwerd primer และ reverse primer ด้วยโปรแกรม DNAMAN

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 1

```
>1st_BASE_497734_1F_Forward_OPD03 ขนาด 510 bp
GTGCAGTACTTAGGCATTGATTGTGTTGCTGCCTTCCTCATACCAAGAACTTGAGTCCTATTTCAGCATACTTGTGCAAAGCAAGG
TAGCAAAGACCAAAGCTTCGATCCTCTCGCTGCCTTCGATGAAAATTGTTTTGGTAGCCTTAGGAGGGAGAAACGTGTATCCCTGC
AACAAAGATTTGCATGAAGCTAGTGTCCACCCACAAGTCGGGCGACAAGACCCAAAAATTTTCATGAGGCAAGAAAGTTTGTCTTA
CTATTTTTCAAAAAAATGTGATCCACCCGGAAAAAGGGGAGGCGCCCCCGCCCCAGCAAAGGGGAAAACCTTTTTTACGACAGGGG
GCAGAAAAAAATGCCCCCCCCCCCCCCGTCCCCAAAAACCTGGTCTGAGAAAAAAAAAAACCCCTTTTTTTTAATAAGCTTCCGATC
AACGCCGGGAAGCCTGCAATTTTTTCCCAACATTTTCTTTTGGATAAAAACAAACCTGGTCTCACCTTCCGCCCCCCCGC
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Revers complementary
>1st_BASE_497735_1R_Reverse_Oligo_VA ขนาด 646 bp
CGTTCGGGGCTCCCCGCTTGGTTGTTGTGCAGTCGTGGGGACGCGACGTGCAGGGACCCTTTTTTTTTTTTTTTTTTTTTTTCCCC
CCAAAATGGGGTTTTTTGATGGGGAGAAAATAATTGGGAACTTCCCCCCCTTGGGTGCGTTTGGGGAAAAATTAGGGGGGGGGGGT
GGCCTCTTTCTTCCCTCGCCTGTTGGTTTTTTTAAAGGGGAGGGGGGAAATTTTTTTTTTTTTTTCTCTCTGAATTTTTGGGGCTC
TTTTTTTTTTTCTCCGGTTGGGGGGGGGGAAGGGGTCCCCACCCAGACTTTTTTTTTTTTTTTTTTGTTTTGTTTTTTTTTTTTTGT
GGCGGTGGCAGGGGGGAAAAAATCTTTTCTTTTTTTTTCAACTGCTCCTTTTTTTTTTTGGGTCCCAACCCCAGCGGGGGGGGGGA
GTGGGAAAAGAGGAAAAGGCTAAATTGGGAATGGACATGTCCTTTTTTTTCCCCCTGACCCAGTTGGTTTTCACCCAATTGGTGCT
ACCTTTTGTGGGTGGGGGGGGGGATGGGCACAGTTTAACACCTACCCTTTTTTTAAAGGGGAGTTGCTGCTTCACGAGAATATCCC
CTCGGTTTTTGTGCCGTATTTTCTTAATTCTGTTGTTATTCANC
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Fast alignment of DNA sequences DNAMAN1 and DNAMAN2

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN1, from 3 to 480
Lower line: DNAMAN2, from 135 to 612

DNAMAN1:DNAMAN2 identity= 28%

3     BASEFFORWARDOPDGTGCAGTACTTAGGCATTGATTGTGTTGCTGCCTTCCTCATACCA
       |                |     |  |    |    |      |
135   AAATAATTGGGAACTTCCCCCCCTTGGGTGCGTTTGGGGAAAAATTAGGGGGGGGGGGTG

63    AGAACTTGAGTCCTATTTCAGCATACTTGTGCAAAGCAAGGTAGCAAAGACCAAAGCTTC
          |||   |||     | |     || |  ||||    |  |  ||         ||
195   GCCTCTTTCTTCCCTCGCCTGTTGGTTTTTTAAAGGGGAGGGGGAAATTTTTTTTTTT

123   GATCCTCTCGCTGCCTTCGATGAAAATTGTTTTGGTAGCCTTAGGAGGGAGAAACGTGTA
        | |||||      || |  |    || ||||  |  ||    | ||| |      |
255   TTTTCTCTCTGAATTTTTGGGGCTCTTTTTTTTTTTCTCCGGTTGGGGGGGGGGAAGGGG
```

```
183     TCCCTGCAACAAAGATTTGCATGAAGCTAGTGTCCACCCACAAGTCGGGCGACAAGACCC
        ||||  |    |   |||   |     |  |||           |          |   |
315     TCCCCACCCAGACTTTTTTTTTTTTTTTTTTGTTTTGTTTTTTTTTTTTGTGGCGGTGGC
243     AAAAATTTTCATGAGGCAAGAAAGTTTGTCTTACTATTTTCAAAAAAATGTGATCCACC
        |         |             ||| ||      |  ||        || |  ||| |
375     AGGGGGGAAAAAATCTTTTCTTTTTTTTTCAACTGCTCCTTTTTTTTTTTTGGGTCCCAAC

303     CGGAAAAAGGGGAGGCGCCCCCGCCCCAGCAAAGGGGAAAACCTTTTTTACGACAGGGGG
        |  |    |||| ||            || ||| ||  |||       |      |
435     CCCAGCGGGGGGGGGGAGTGGGAAAAGAGGAAAAGGCTAAATTGGGAATGGACATGTCCT

363     CAGAAAAAAATGCCCCCCCCCCCCCCGTCCCCAAAAACCTGGTCTGAGAAAAAAAAAACC
                       |||         || || ||    || |
495     TTTTTTTCCCCCTGACCCAGTTGGTTTTCACCCAATTGGTGCTACCTTTTGTGGGTGGGG

423     CCTTTTTTTTAATAAGCTTCCGATCAACGCCGGGAAGCCTGCAATTTTTTCCCAACAT
               |      || ||   | | || |          |     ||    |  ||
555     GGGGGGATGGGCACAGTTTAACACCTACCCTTTTTTTAAAGGGGAGTTGCTGCTTCAC
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 2

```
>1st_BASE_497736_2F_Forward_OPD03 ขนาด 230 bp
NNNNNTTNNNTCCAACCTTTGCCATGTANAAACCCAANNNTTAAGTCTGTTAATTACCAAACTCCCTCCATTTAATGGGGGTGTAG
TATTGTTTATAATAACCCACCTTTGCAAAATCAGACAGCCTTTGAGGGGAAGATATTTTTTGGGATCAATCTTTTTAAAAATGGGT
AGCCTTTGTTGCGCTATTCCATTATTTGTCTTTTCTTTATTACCAAATATTTCCTGGG

Revers complementary
>1st_BASE_497737_2R_Reverse_Oligo_VA ขนาด 249 bp
GTAATTTTATAAGGAAATTTGGTACAAAAAAAAAAGTTGGTTAATTAATTCAAAATGTTATGGCCCTTTCTCACAAAAAATCAAAC
AACTAATATTCATTCTAAAGAATTCATCAAAAGTAAAAAATAATGACAATTTAACACTTTATGTCTAAAATCGCTCTTTTTTTTTT
TTTTATGTGGAATTTTTAAGAAGTANGTAGAAGAACGGCANNNNCNNNNNTGNNNNNNNNNNNNNNNNTNNNNNNNC

Fast alignment of DNA sequences DNAMAN5 and DNAMAN6

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN5, from 2 to 242
Lower line: DNAMAN6, from 23 to 270

DNAMAN5:DNAMAN6 identity= 31%

2       TBASEFFORWARDOPDNNNNNTTNNNTCCAACCTTTGCCATGTANAAACCCAANNNTTAA
        | |       |          |       ||    |    |    ||  | ||   |||
23      TAATTTTATAAGGAAATTTGGTACAAAAAAAAAAGTTGGTTAATTAATTCAAAATGTTAT

62      GTCTGTTAATTACCAAACTCCCTCCATTTAATGGGGGTGTAGTATTGTTTATAATAACCC
        | |  ||  | || |||   |   ||  ||||     |     |   || || | ||
83      GGCCCTTTCTCACAAAAAATCAAACAACTAATATTCATTCTAAAGAATTCATCAAAAGTA

122     ACCTTTGCAAAATCAGACAGCCTTTGAGGGGAAGATA.......TTTTTTGGGATCAATC
        |    |    |       |  ||||  |   || ||        ||||||    |   |
143     AAAAATAATGACAATTTAACACTTTATGTCTAAAATCGCTCTTTTTTTTTTTTTTTATGTG

175     TTTTTAAAAATGGGTAGCCTTTGTTGCGCTATTCCATTATTTGTCTTTTCTTTATTACCA
           ||   ||   |||          ||  |          ||
203     GAATTTTTAAGAAGTANGTAGAAGAACGGCANNNNCNNNNNTGNNNNNNNNNNNNNNNNT

235     AATATTTC
               |
263     NNNNNNNC
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 3

```
>1st_BASE_497738_3F_Forward_OPD03.ab1 ขนาด 267 bp
NNNNNNNNNNNNGNNNGNGNNGNGGANTACAGNAAANCAAATTTCATGGCTGGGANAAGCAGAGGATAACTCNNNAANTGATGGCN
TTTATGGCACCTGCTGCCCTACACCCACCACGCCTGNNNAANCTNAGNGCGNNCGGGAGCNGACNCANNTNNTTTNNTCCCGTGTT
TTTTTTTAAAAAAGCCCCGGGNNAGACCGGANGAGCTCTCTATTCCGGGGGTTAAATTTTGTGGGGTTTTTCCCCCGGGGGGGGGG
AAAAAAAAA

Revers complementary
>1st_BASE_497739_3R_Reverse_Oligo_VA ขนาด 164 bp
GATCAAGTCGAGACCACAACAATACACACGATGCAAAGAGTTGAATGAAAAGAATTACTACTCTATGTCAAAATCGCCTTTTAAGA
AATTTTATGTAGAGATTTTTAAAAGTTTGCAAAAAAAGGCCTAAACGGCCCGAGGACGCTCACTCGCCCNNNNNNNNC

Fast alignment of DNA sequences DNAMAN8 and DNAMAN9

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN8, from 29 to 199
Lower line: DNAMAN9, from 26 to 185

DNAMAN8:DNAMAN9 identity= 21%

29    NNNGNNNGNGNNGNGGANTACAGNAAANCAAATTTCATGGCTGGGANAAGCAGAGGATAA
             |        | ||||    |   ||     ||  ||  |  |        |
26    AAGTCGAGACCACAACAATACACACGATGCAAAGAGTTGAATGAAAAGAATTACTACTCT
89    CTCNNNAANTGATGGCNTTTATGGCACCTGCTGCCCTACACCCACCACGCCTGNNNAANC
       |    || |       |             |           |            ||
86    ATGTCAAAATCGCCTTTTAAGAAATTTTATGTAGAGATTTTTAAAAGTTTGCAAAAAAAG

149   TNAGNGCGNNCGGGAGCNGACNCANNTNNTTTNNTCCCGTGTTTTTTTTTA
                |  |||    | ||             ||
146   GCCTAAACGGCCCGAGGACGCTCACT...........CGCCCNNNNNNNNC
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 4

```
>1st_BASE_497740_4F_Forward_OPD03.ab1 ขนาด 344 bp
NNNNNNNNNNNNNNNNNTGAGNTGNGCNANGNNGGAACCAAATTTCTTGTGANTTGNNCAATAAGANNATCNCNNTTCCCNTTAATG
NGGCTGTAGCATTGCTGTTCTACTCCGCNNNCCCTANNANACTCCNANTTGCTGTGCCAACNAANNANTTTAGTAGCAAGTTGTTT
ATNNCNTTTTTTAGATTTTTTTTAGGCGAGTGTCCAACCACTCCTCTTATTTTNCCCCCATATTTTTTTTTCGGGCAAAAAAAAAA
AATAGCCTTGACGATGTTTCCAAGAGTCTTGGTCGAACCGCGTTATNNGTTTTTCTTTTTCTCTTTTTCGATCCAATTGTAGTATN

Revers complementary
>1st_BASE_497741_4R_Reverse_Oligo_VA.ab1 ขนาด 156 bp
TGTTACTCGACATCGTTTTTAAATCTCAGCTTAATATAATCATANNAATTNCCANTATACCAAAATNAANCTTTNAANNCNAGTAA
AACGAATNACTTNAATTAATATAAAACATGGCANTAGCGGCAGTNNCCCAANCNNNTGTNGGGGCCNNNN

Fast alignment of DNA sequences DNAMAN11 and DNAMAN12

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN11, from 55 to 201
Lower line: DNAMAN12, from 33 to 179

DNAMAN11:DNAMAN12 identity= 25%

55    ACCAAATTTCTTGTGANTTGNNCAATAAGANNATCNCNNTTCCCNTTAATGNGGCTGTAG
      ||    ||| |        |   ||||  |  || |   || ||  ||          |
33    ACATCGTTTTTAAATCTCAGCTTAATATAATCATANNAATTNCCANTATACCAAAATNAA

115   CATTGCTGTTCTACTCCGCNNNCCCTANNANACTCCNANTTGCTGTGCCAACNAANNANT
        ||      | | |                | |   |       || ||
93    NCTTTNAANNCNAGTAAAACGAATNACTTNAATTAATATAAAACATGGCANTAGCGGCAG

175   TTAGTAGCAAGTTGTTTATNNCNTTTT
      |              |     |
153   TNNCCCAANCNNNTGTNGGGGCCNNNN
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 5

```
>1st_BASE_497742_5F_Forward_OPD03.ab1 ขนาด 383 bp
NNNNNNNNNNNNANNGNNTGTGGATAGANGNAACCAAATTTCATGGNTTTGNACAATAAGAGNAAACCTCTTCAATATAANGNGTT
GTTGAAAGTGCTGTTCGACTCCGCNAANNCTAGNTATCTNNNNCGNNCNCGGCGNGTNNTANNTATTTTTATAGGAGGTTTTTTTT
TTTCAAGCCCCCGAGATATGCGGAGGGGAGTGTCCAAAAAGGGGTAAAATTTTTAGAACCTTTTTTTTTCCCGGGGGGGAAAAAAA
AAAANATCCTTAACAAGGTTTCCAAGATCCTGTGCCAGACCGGAAAAATGTCTTGCCACCTCCTTGATTCCAGCAGCCAGCACGCC
CTTCTTCGCTGCTTGAGTATTNTTTTTTCTTTCTANNCT

Revers complementary
>1st_BASE_497743_5R_Reverse_Oligo_VA ขนาด 451 bp
GCGTCAGGTAGGATCTTTTACCATTTTTTCTCGGGGTCTTTTTTGGGGCTGGGGACCCCCCCCTCTCCCCCCCCGGGTTTTTCCTC
CCAAAAAACCTTTTTGGGTTATCCTTTTTTTAGGGGAGTCCCCCTTTTATTGTGGCTTTGTGTTAACCACCCAAAAGGGGTTTTGG
GGACCCACCGGCCTTTGGGGTTTGGTCCCCCCCCCCCCTCAACGGAAACCCCCCTCCCCAGGAAATACCCCCGGCCTTTGGTTTTT
TTTAAACCTGGGGCGAAGGCGATTTTCTTTTCGAAGTCGCTTGCCAACGGTCGCAGATTTCGCTGTGTCGCAGGGGAAAAGGTTCG
CCTCTCCCGCCTGTGGCCCCTCCCATGCTCGGTTTAAGGTGGAGGTCTTTTAAAGACATTGATGTCCAATGGCCCTCCCGGCCCCT
TCCTCCCCTTCCACTGCACGA

Fast alignment of DNA sequences DNAMAN14 and DNAMAN15

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN14, from 38 to 392
Lower line: DNAMAN15, from 65 to 416

DNAMAN14:DNAMAN15 identity= 30%

38    TGTGGATAGANGNAACCAAATTTCATGGNTTTGNACAATAAGAGNAAACCTCTTCAATAT
      || || | |      ||   | ||        |     |      |||   | |   |
65    TGGGGCTGGGGACCCCCCCCTCTCCCCCCCCGGGTTTTTCCTCCCAAAAAACCTTTTTGG

98    AANGNGTTGTTGAAAGTGCTGTTCGACTCCGCNAANNCTAGNTATCTNNNNCGNNCNCGG
             | ||   || |  || |  ||                  |        | |
125   GTTATCCTTTTTTTAGGGGAGTCCCCCTTTTATTGTGGCTTTGTGTTAACC...ACCCAA

158   CGNGTNNTANNTATTTTTATAGGAGGTTTTTTTTTTTCAAGCCCCCGAGATATGCGGAGG
         |   |          |  ||   ||    |||      |||||    |   ||||
182   AAGGGGTTTTGGGGACCCACCGGCCTTTGGGGTTTGGTCCCCCCCCCCCCTCAACGGAAA

218   GGAGTGTCCAAAAAGGGGTAAAATTTTTAGAACCTTTTTTTTTCCCGGGGGGGAAAAAAA
            |||  |                      |||||||   || |||| |||    |
242   CCCCCCTCCCCAGGAAATACCCCCGGCCTTTGGTTTTTTTTAAACCTGGGGCGAAGGCGA

278   AAAANATCCTTAACAAGGTTTCCAAGATCCTGTGCCAGACCGGAAAAATGTCTTGCCACC
            |    ||   | || ||||    |   |      | |              |
302   TTTTCTTTTCGAAGTCGCTTGCCAACGGTCGCAGATTTCGCTGTGTCGCAGGGGAAAAGG

338   TCCTTGATTCCAGCAGCCAGCACGCCCTTCTTCGCTGCTTGAGTATTNTTTTTTC
      | |     ||| ||     || |  ||           |   ||     | |||
362   TTCGCCTCTCCCGCCTGTGGCCCCTCCCATGCTCGGTTTAAGGTGGAGGTCTTTT
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 6

```
>1st_BASE_497744_6F_Forward_OPD03.ab1 ขนาด 649 bp
NNNNNNTTNGNCTCANNCNGNNGCNANANANNAAANCNNATTTCTTAGGATGGGAAANGAAAGAAAAAATNCTCGCAAAACAAAGG
AGNTTATGGTACGTGCTGCTAGATGTCGTNANCNGGNTNACNNAGNANGNGTGGGGANGNNCNANNCTCNTTTTAGTTGGNTNTAT
CCTTTTTCGNGCACCNGGANCAAGAGCCGTTGNTGTTAAAGGGCTTTATCATTAATGGCANTANTTTNCCNGGCCCGCACNAAGAN
TGTCTATGNAGGGTCCCTTCCGCCCCTTCAAACGCTAAAGAAGGGCCAAANNAAAATATCCATAACCGCTAATTGCATGTTCTCTG
AGGGTTTTCAATGTTCCTTTCTTTGATTTCATACCCAATTATTTATTTGTTTCTGATCTAGTCCAGTTGAGTCTGCCCGTGCTTTC
TTATCAATTCAGTTGGACACGGTCATTTGTAGTGAACATTCCACCACTCAAGCTGGGTATGCCTTGCTTTCTTGGGTAGCTTTCCT
TTCTTTTTCTTCCTGGAAAACACCTTCTTCCACGTACTTATGNGACTTCCATCCTTGCGAAGTAGTTTATCTTTAACATCTTTGTC
TTCACTGCTTGGTTGCCCTTCATGTGCCTCACATTCTCGCCCTCTCC

Revers complementary
>1st_BASE_497745_6R_Reverse_Oligo_VA ขนาด 720 bp
TTTGGTCGTCCTGGTTGATCCGTTGTCGTGGTCCCTTTGGGTTCGCGCGCACAACTTACGGCCCCATGTTGTCGGGTTAGATCCG
ATCTAGCAATAGATACAGCCCCATGAGAGAGGTAGTGTCTGGCTCGCAGACCTACCAAAAACAAGAGGCTATTTATACCTATTATA
CCGCGTCTCTGTCTCGCTCCGATGAATGCTGTGGTGTATTTTCTCGCTTTGCGTGCTGTTCGCTACAATCTTATATTGAGTTGTGA
TGGGTGGGAGACAATGTTATTGTTCACCGCGCCCCGAGTTTCTTTCCTCCCCAGTAGAGGCAAAACGGGTGTCTTCCCCTTCCCTC
CCGACGTGTCCAAATGTCCCCCCCCCGAGCGCTAACCAGAATGGGACCATTTCTTCCCTTTTGTGCCCCCCAGCGGTCAGCAGGCA
CTGCGGTCTCCGATTAAAAAATTCGCCCCGGTTTGGGTTCCAGGGCCCTTACCTAGGAGTGCCGCCAAGGAGAGAAGGGGGGACTC
CGCCTTCAGGTGTGAGGCGGGATTGCCTGTCCGTCCCTATGTCGCCGCCCTGCAGACGGATGCGGGTAACCATTTTGCGGATGACA
ATTGGTCTGAAATGATCCCCTGCCCCCCTGCGTTTTATAAGGGGGGTGGTTTTCTCACGGGAATCTCTCCTGCTGAGAGGGCCGCG
GCAAAAGGAAGGACGTTTACGTCTATCTNNNN

Fast alignment of DNA sequences DNAMAN1 and DNAMAN2

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN1, from 6 to 667
Lower line: DNAMAN2, from 74 to 734

DNAMAN1:DNAMAN2 identity= 31%

6     EFFORWARDOPDABNNNNNNTTNGNCTCANNCNGNNGCNANANANNAAANCNNATTTCTT
                          |  |  |    | |       |    | |
74    AACTTACGGGCCCCATGTTGTCGGGTTAGATCCGATCTAGCAATAGATACAGCCCCATGA

66    AGGATGGGAAANGAAAGAAAAAATNCTCGCAAAACAAAGGAGNTTATGGTACGTGCTGCT
        || |               |   ||  |||||  |||  | |  |  ||| |  |
134   GAGAGGTAGTGTCTGGCTCGCAGACCTACCAAAAACAAGAGGCTATTTATACCTATTATA

126   AGATGTCGTNANCNGGNTNACNNAGNANGNGTGGGGANGNNCNANNCTCNTTTTAGTTGG
          |||     |  | |            |||| |          ||     |  |
194   CCGCGTCTCTGTCTCGCTCCGATGAATGCTGTGGTGTATTTTCTCGCTTTGCGTGCTGTT

186   NTNTATCCT.TTTTCGNGCACCNGGANCAAGAGCCGTTGNTGTTAAAGGGCTTTATCATT
         ||   | || |   |      ||      |  |    |||||  |  |
254   CGCTACAATCTTATATTGAGTTGTGATGGGTGGGAGACAATGTTATTGTTCACCGCGCCC

245   AATGGCANTANTTTNCCNGGCCCGCACNAAGANTGTCTATGNAGGGTCCCTTCCGCCCCT
         |    |    | ||  |      | ||    || | |      ||||| ||| |
314   CGAGTTTCTTTCCTCCCCAGTAGAGGCAAAACGGGTGTCTTCCCCTTCCCTCCCGACGTG

305   TCAAACGCTAAAGA.....AGGGCCAAANNAAAATATCCATAACCGCTAATTGCATGTTC
      || ||   |          || || ||    ||     |     |     ||   ||  |
374   TCCAAATGTCCCCCCCCCGAGCGCTAACCAGAATGGGACCATTTCTTCCCTTTTGTGCCC

360   TCTGAGGGTTTTCAATGTTCCTTTCTTTGATTTCATACCCAATTATTTATTTGTTTCTGA
       |    |||   ||          ||  | | ||  |   ||  |||        | ||
434   CCCAGCGGTCAGCAGGCA......CTGCGGTCTCCGATTAAAAAATTCGCCCCGGTTTGG

420   TCTAGTCCAGTTGAGTCTGCCCGTGCTTTCTTATCAATTCAGTTGGACACGGTCATTTGT
        |             ||    ||||   |      |    |  |||| | | | |  |
488   GTTCCAGGGCCCTTACCTAGGAGTGCCGCCAAGGAGAGAAGGGGGGACTCCGCCTTCAGG

480   AGTGAACATTCCACCACTCAAGCTGGGTAT...GCCTTGCTTTCTTGGGTAGCTTTCCTT
       ||||           ||     |   |||   |||   ||      ||  ||
548   TGTGAGGCGGGATTGCCTGTCCGTCCCTATGTCGCCGCCCTGCAGACGGATGCGGGTAAC

537   TCTTTTTCTTCCTGGAAAACACCTTCTTCCACGTACTTATGNGACTTCCATCCTTGCGAA
        |||| |       ||     ||      |    ||                ||   ||
608   CATTTTGCGGATGACAATTGGTCTGAAATGATCCCCTGCCCCCCTGCGT....TTTATAA
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597  GTAGTTTATCTTTAACATCTTTGTCTTCACTGCTTGGTTGCCCTTCATGTGCCTCACATT
     |  |  |   |||  ||      |||   |||||  |  | ||            |
664  GGGGGGTGGTTTTCTCACGGGAATCTCTCCTGCTGAGAGGGCCGCGGCAAAAGGAAGGAC

657  CTCGCCCTCTC
      |   | |||
724  GTTTACGTCTA
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 7

```
>1st_BASE_497746_7F_Forward_OPD08.ab1ขนาด 390 bp
NNNNNNNGGATNNNGNNNNNNNTGACTATNTATAAAATCTTTCTTGTCTCATAGAAGTAATGCATTGAAGATCTTTTACTTGGAGA
GCTTGCATATCCTCATTTGAACTNNNAGTTGAGNNTTCGNCNGNNGGTGGGCTANNAANCAGCTAGTTGTGTNNCTCCCGTGGCAG
TCNCTTGAAAACCAAATTGGGGGATCNNCCCGGGGGTACTTTAGNNNTTTTTTTTTTTTANGAANGGGTNTTGNAAAAANTCNTTT
TTTTCCCNNAAAAACNCCATAAAAAAAANNNNNACNTGGGCGGTTTTNTNNGGGAAAGGGGGGGTGGGTTTCTGTAAAGAAATGCN
GATGNNNTTTTTNATGTTNCTTTNTTTGGGGCTCNNCCNNTNTTTN

Revers complementary
>1st_BASE_497747_7R_Reverse_Oligo_VA.ab1 ขนาด374 bp
ANTTTTTTTTTNNAACAAAAAANNAAACNAAATGCCCCGNGNCGCCCCCCNGGGATAANCATCTCTCCCTCCCNAAAAAAAAAAAN
TANCGGGGGGANGGCCTTTTTTGGGGTGAAGTTGNNTTGAAAGCCCCCCCACCCCCTTCGCCGAAAGACCNACCGCAAAAAAANNC
CCAAAAGAGGCCCCCATAGCCTNCCCGGGTTGGCCTCNTAANANNNNCANNAGAANACTNTAANNANGTTTTTNNAAAAAATTTTT
TNNTTGNNNAAAAAAAAATNAANNNNCNNNNNNNNNNNNNNGNNNTTNNNTCNNNNTNNNNNNNNNNNNNNNNNNNGTTNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

Fast alignment of DNA sequences DNAMAN4 and DNAMAN5

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN4, from 15 to 391
Lower line: DNAMAN5, from 21 to 397

DNAMAN4:DNAMAN5 identity= 27%

15   OPDABNNNNNNNGGATNNNGNNNNNNNTGACTATNTATAAAATCTTTCTTGTCTCATAGA
        |                     ||  || |  |           |    |    | |
21   AABANTTTTTTTTTNNAACAAAAAANNAAACNAAATGCCCCGNGNCGCCCCCCNGGGATA

75   AGTAATGCATTGAAGATCTTTTACTTGGAGAGCTTGCATATCCTCATTTGAACTNNNAGT
     |              |||| |  ||     |      | |    |    | |       |
81   ANC............ATCTCTCCCTCCCNAAAAAAAAAAANTANCGGGGGGANGGCCTTT

135  TGAGNNTTCGNCNGNNGGTGGGCTANNAANCAGCTAGTTGTGTNN.....CTCCCGTGGC
     |  |   |       |  ||          || |   ||           |  |||
129  TTTGGGGTGAAGTTGNNTTGAAAGCCCCCCCACCCCCTTCGCCGAAAGACCNACCGCAAA

190  AGTCNCTTGAAAACCAAATTGGGGGATCNNCCCGGGGGTACTTTAGNNNTTTTTTTTT..
     |   |    ||||              | |||||||    | |     |
189  AAAANNCCCAAAAGAGGCCCCCATAGCCTNCCCGGGTTGGCCTCNTAANANNNNCANNAG

248  .....TTTANGAANGGGTNTTGNAAAAANTCNTTTTTTTCCCNNAAAAACNCCATAAAAA
          | ||   |||  | |   ||||| |  ||  ||      |||||    |
249  AANACTNTAANNANGTTTTTNNAAAAAATTTTTTNNTTGNNNAAAAAAAAATNAANNNNC

303  AAANNNNNACNTGGGCGGTTTTNTNNGGGAAAGGGGGGGTGGGTTTCTGTAAAGAAATGC
        |||||  |   |   ||  || |
309  NNNNNNNNNNNNNNGNNNTTNNNTCNNNNTNNNNNNNNNNNNNNNNNNNGTTNNNNNNNN

363  NGATGNNNTTTTTNATGTTNCTTTNTTTG
     |    |||     |     |    |
369  NNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 8

```
>1st_BASE_497748_8F_Forward_OPD08.ab1 ขนาด 519 bp
NNNNNNNNNTNNGNNNNNNTTGAANACAGCACAAATTTGTCTTGTCGNTACAACTACTGCTGCGAAGATCTTTTACTTGGACCTTT
TCCATCTGCCTTTTTGATCTTGAAGATTAACGAGTTGGTNCCNCTCGGGTGNNGNATAGCTAGCTTTGTCNCCGCTGTTGNGGATT
CTCTGCAGACAAAACNGTATGACACCACNGNNGGGTANATNAGAANTCNTTTNNTTTCAAGAAAATGTNNTATAANCNTTNTCCNC
NCCANAACCCCNAAAAAACNNCCCCCCCCTTGNGGGNGGGTTTTNGNNAGNNGGGNNGGGNNTGCNAATACCNCCCCCCGAAGNTT
TCANTGTCCCTTTTGTTGGNAATCNCANNATNNGTCNTTGCTTCTGATCTGGTCCTTTTGAGTCTGCTTTGCTTTCTTATCNATTC
ATTTGGATAAGGCCTTTTGTAGTGAACATTCCACCNCTCAGGCTNGGTATGCCTTGCTTCCTTTGTTTGTTTTCCTTTCTTTTTCT
TCT

Revers complementary
>1st_BASE_497749_8R_Reverse_Oligo_VA.ab1 ขนาด 409 bp
NNTGTGTNNNNNNNNGGNNGCCCCCCCCAAAACCCGGATTCTCCCCGGGCTGGGGGGCAACAGCACCCCCATGAATCCCGTGCCCT
CATCCAAAACAGCAGATAGCACATAGTTGTTTTTTTTTTACCAGNTCTTTCGATNNCGGAAAACAAAGAAGTTGAAGATCGTTCCG
GTGATGAGCCAGCTAGCTATGTTGGTCGGTGTTGCAGGCGGCATACCGGCAAAACCATAAGATATGACAGGAATGTTGATGAGCGG
GATCCACTTCTTCTCTGGGTACATTTTGCTTAATATCCATATTGGAACCGGCCAGAAAGCTCCAATAAGGTCACCCCTCCAAATTC
CCGTAGAGCCCTCTTATGTCCAGAGAGCGNTCGGTCCTATGAGCCCCNCCNNCCCNNNNNNNNNG

Fast alignment of DNA sequences DNAMAN7 and DNAMAN8

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN7, from 90 to 517
Lower line: DNAMAN8, from 8 to 432

DNAMAN7:DNAMAN8 identity= 25%

90    TTTTACTTGGACCTTTTCCATCTGCCTTTTTGATCTTGAAGATTAACGAGTTGGTNCCNC
                          | |        |            ||      | | |  |
8     REVERSEOLIGOVAABNNTGTGTNNNNNNNNGGNNGCCCCCCCCAAAACCCGGATTCTCC

150   TCGGGTGNNGNATAGCTAGCTTTGTCNCCGCTGTTGNGGATTCTCTGCAGACAAAACNGT
       ||||    |       |||     |     |   | |   ||     | |||  |   |
68    CCGGGCTGGGGGGCAACAGCACCCCCATGAATCCCGTGCCCTCATCCAAAACAGCAGA.T

210   ATGACACCACNGNNGGGTANATNAGAANTCNTTTNNTTTCAAGAAAATGTNNTATAANCN
      |  |||     |     |   |   | ||| ||   |  |   |||        |
127   AGCACATAGTTGTTTTTTTTTTACCAGNTCTTTCGATNNCGGAAAACAAAGAAGTTGAAG

270   TTNTCCNCNCCANAACCCCNAAAAAACNNCCCCCCCCTTGNGGGNGGGTTTTNGNNAGNN
       |     |         ||    |           |  ||  |  ||          |
187   ATCGTTCCGGTGATGAGCCAGCTAGCTATGTTGGTCGGTGTTGCAGGCGGCATACCGGCA

330   GGGNNGGGNNTGCNAATACCNCCCCCCGAAGNTTTCANTGTCCCTTTTGTTGGNAATCNC
                     ||  |               |    |||  ||  |         |
247   ...AAACCATAAGATATGACAGGAATGTTGATGAGCGGGATCCACTTCTTCTCTGGGTAC

390   ANNATNNGTCNTTGCTTCTGATCTGGTCCTTTTGAGTCTGCTTTGCTTTCTTATCNATTC
      |   |   |  |  |                   |  || |  |    ||    |
304   ATTTTGCTTAATATCCATATTGGAACCGGCCAGAAAGCTCCAATAAGGTCACCCCTCCAA

450   ATTTGGATA.AGGCCTTTTGTAGTGAACATTCCACCNCTCAGGCTNGGTATGCCTTGCTT
      |||    || || ||| || |    |     |   |  ||      |     ||   |
364   ATTCCCGTAGAGCCCTCTTATGTCCAGAGAGCGNTCGGTCCTATGAGCCCCNCCNNCCCN

509   CCTTTGTTT

424   NNNNNNNNG
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 9

```
>1st_BASE_497750_9F_Forward_OPD08.ab1 ขนาด 374 bp
NNNNNNANNNGGNANGNNNTGANCATCNATCACATCTATTCTTGTCTCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGC
TGGCATATCCATAACTGAACTTCGAGATTNGGAGTACCTCNCNNCCGGTNCCCGNAGTTATTGNGTGGTGCGTTGGTCCGNNATNT
GGGGANANACACAAAANGNNNGACANTTGNTAAAGGNGGGCCTTCCTTTNTNCTCCACANTTTTTTAATNNTNNCTTTTGGCCGGG
AGAAAACCNCGANAAAAAAAANNCNCCNTATTNGTGGGGGTCTCCTTNNGGAAANNGGGGCGGGGGTNTATAAAANATCCNTNCAAA
AAGGNAAAACNCTTTGGGGGAANNACAANN

Revers complementary
>1st_BASE_497751_9R_Reverse_Oligo_VA.ab1 ขนาด 407 bp
NTTTTTTTTTGTCCCCCCCAAAAACCTGTTTCTCGAGGGCAAAGAACAACAGGACCCCCACGAACGCCGTGCCAGCATCCAAAGCT
GCAGATAGCACATAGTTGTTTCTTTGCCACCAGCCCTTTCGATACCGGAAAACAAAGAAGTTGAAGATTGTTCCGGTGATGAGCCA
GCTAGCTATGTTGGTCGGTGTTGCAGGCGGCATACCGGCAAAACCATAAGATATGACAGGAATGTTGATGAGTGGGATCCACTTCT
TCTCGGGGTACATTTTGCTTAATATCCATTTTGGAACCGGCAAGAAAGCGTCAATCAAGTAAATTCACATCAAATTCCAGTAGAGC
CCTGCAGGTCCAAAGCTGNAGCGCGTTGCNTATCAGANCNCCTGANCTNCACNTNNNNNNNNN
```

```
Fast alignment of DNA sequences DNAMAN10 and DNAMAN11

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN10, from 33 to 393
Lower line: DNAMAN11, from 21 to 382

DNAMAN10:DNAMAN11 identity= 31%

33    ANGNNNTGANCATCNATCACATCTATTCTTGTCTCATAGAAGTCCTCCATTGAAGATCTT
      |  |  |     |    | |    |  | ||| ||      |      |    ||  |
21    AABNTTTTTTTTTGTCCCCCCCAAAAACCTGTTTCTCGAGGGCAAAGAACAACAGGACCC

93    TTACCTGGAGAGCTGGCATATCCATAACTGAACTTCGAGATTNGGAGTACCTCNCNNC..
        ||       |       ||||| | ||| |  | |    | |  ||  ||
81    CCACGAACGCCGTGCCAGCATCCAAAGCTGCAGATAGCACATAGTTGTTTCTTTGCCACC

151   ........CGGTNCCCGNAGTTATTGNGTGGTGCGTTGGTCCGNNATNTGGGGANANACA
              || | || | |   |  |        | | || |      || |
141   AGCCCTTTCGATACCGGAAAACAAAGAAGTTGAAGATTGTTCCGGTGATGAGCCAGCTAG

203   CAAAANGNNNGACANTTGNTAAAGGNGGGCCTTCCTTTNTNCTCCACANTTTTTTAATNN
      | |            |||     ||    ||  |           | |       |||
201   CTATGTTGGTCGGTGTTGCAGGCGGCATACCGGCAAAACCATAAGATATGACAGGAATGT

263   TNNCTTTTGGCCGGGAGAAAACCNCGANAAAAAAAANNCNCCNTATTNGTGGGGGTCTCCT
      |      |||     |      | ||    |         | | ||  |     ||   |
261   TGATGAGTGGGATCCACTTCTTCTCGGGGTA.........CATTTTGCTTAATATCCATT

323   TNNGGAAANNGGGGCGGGGGTNTATAAAANATCCNTNCAAAAAGGNAAAACNCTTTGGGG
      |  | |       |   | ||  || ||  |      ||  ||     |          |
312   TTGGAACCGGCAAGAAAGCGTCAATCAAGTAAATTCACATCAAATTCCAGTAGAGCCCTG

383   GAANNACAANN
       |    |||
372   CAGGTCCAAAG
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 10

```
>1st_BASE_497752_10F_Forward_OPD08.ab1 ขนาด 408 bp
NNNNANNNNGNGNAGNGNAGGGGNATGATATNACGGATTCNCTCTACTTTANAAAAGAAGTTCTGTTGGTTTTTCTTTTTTCCCAC
TTAAAATGGCCGTTCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTAATTACATCACCAAGGAAGGACTCTACT
CAGCTAGAAAGGAGAAGCTTGGATTAAAAGAATGGAAGAAGGGGATTTTAATGCCTTTCTAAGGAGACTGAAGGCTCTTAATATTC
TAGGATCCTGGGNNGGGAGGGTGNGGGGAAAAAAAAAAAACCCCCCCCCCTGGGGTTTTTTTTTTTCTTCTTTAAAAAACCCCCCT
TTTCCCCCCCGNACNTTTTCTTTTCCAAAANTTNNNNGGGNNNGNGGNNNAAANAAACAAAAAA

Revers complementary
>1st_BASE_497753_10R_Reverse_Oligo_VA.ab1 ขนาด 423 bp
AATTTTTTTGTGTTGCTCCCCGGGCCTCCCCCCCCCCCCCCAAAAAAATGTAAGGGGGCAAGTGGGGGGGAAGGAGGGAANGGAGN
ATCTTGGAAGGGAGAGAAAAAAAGACCCCGCCGAGAGGGGTTTTTTTTTTTCCCCCTTACACTNNCCGGCAAGAAAAATAGAAAA
TTTAGATAATTCTGGATAGCTTAGTACAGCATTACCATCCCCTAGGTACATTTTTGACTCAGCTAGATAGACGCAGATNACATANA
AGAAGGAAGAAGGGNAAGTNAATGCCTTTNNAGGNNCCTAAGGCTGTNAATCTCTATAACGNAGGANGATAGTTAAAAAAGGANCA
NTCCTTNNNTTGCCGTAGACTTTTTAANTCCAAAGAGGGTGNNNTTNNGTNNGAGCCCCNTTTTTNNTNNNNNNNNNNN

Fast alignment of DNA sequences DNAMAN13 and DNAMAN14

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN13, from 4 to 397
Lower line: DNAMAN14, from 65 to 446

DNAMAN13:DNAMAN14 identity= 44%

4     ASEFFORWARDOPDABNNNNANNNNGNGNAGNGNAGGGGNATGATATNACGGATTCNCTC
      |                        | | |  |  ||  |     ||   |||
65    AAAAAAATGTAAGGGGGCAAGTGGGGGGGAAGGAGGGAANGGAGNATCTTGGAAGGGAGA

64    TACTTTANAAAAGAAGTTCTGTTGGTTTTTCTTTTTTCCCACTTAAAATGGCCGTTCAAA
       |    |  |             ||||||| ||||||||| |||| | |  |||   | |
125   GAAAAAAAGACCCCGCCGAGAGGGGTTTTTTTTTTTCCCCCTTACACTNNCCGGCAAGA

124   GTATTGTGAATATGTTGTAAAACTTCTTA.CTCTGTACACTAATTACATCACCAAGGAAG
        | |   ||  |    |||  ||   || ||  |||||  | |  |||| || ||| |
185   AAAATAGAAAATTTAGATAATTCTGGATAGCTTAGTACAGCATTACCATCCCCTAGGTAC

183   GACTCT.ACTCAGCTAGAAAGGAGAAGCTTGGATTAAAAGAATGGAAGAAGGGGATTTTA
         | | ||||||||||| ||  | || |   ||  ||  |  |||||||||| |  | |
245   ATTTTTGACTCAGCTAGATAGACGCAGATNACATANAAGAA..GGAAGAAGGGNAAGTNA

242   ATGCCTTTCTAAGGAGACTGAAGGCTCTTAATATTCTAGGATCCTGGGNNGGGAGGGTGN
      ||||||||  | |       |||||| | |          |||        | |||  |
303   ATGCCTTTNNAGGNNCCT..AAGGCTGTNA..........ATCTCTATAACGNAGGANGA

302   GGGGAAAAAAAAAAAACCCCCCCCCCTGGGGTTTTTTTTTTTCTTCTTTAAAAAACCCCC
        |  ||||||  |     ||     | |   |    |||||       || |
351   TAGTTAAAAAAGGANCANTCCTTNNNTTGCCGTAGACTTTTTAANTCCAAAGAGGGTGNN

362   CTTTTCCCCCCCGNACNTTTTCTTTTCCAAAANTTN
       ||            ||||||   |       |  |
411   NTTNNGTNNGAGCCCCNTTTTTNNTNNNNNNNNNNN
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 11

```
>1st_BASE_497754_11F_Forward_OPD08.ab1 ขนาด 393 bp
NNNNNNNNGTNGCGNGGTTATTGNNCATGAGATCACATTTTTCCCTGCGCTAGAATCCAAGGTCCGAAGANTTTTAGCTGGNGAGC
TTGATATCTTNATTGAACTCCAAGTTNNGNTGTGGACATCCGCGNANNACNNATTCCTGCNNGTTCNGGTTTCTGGGGGANAATTG
GGAAATTGCCCTTTTTTTCCCCTGTTCCCCGGANAGGGGGACCCTTCTTCTTTTCCCAGAGAATTTTTAATAACCCCCTTTTTGGG
GGGGGGGGGTGNTNCCCCGAAAAAAAAAAAAAACCCCCCTTTTTTTTGGGGGACCTCTTTGGGNGGAAAAAAACACGNNTTTTTAA
AAAACANTCCCCCCAATTTTTTGGTTTTTGGGGGGGGGAANANCAAAAA
```

```
Revers complementary
>1st_BASE_497755_11R_Reverse_Oligo_VA.ab1 ขนาด 401 bp
TTTTTTTTGNGCCCCCAAAAAAAAAATTCCCCAAAAGTTGGGGGGGGTTGGGGTTTTCATGACCNNTTTTTTTTTTTTCCAAAGCT
GCCGATAGAATATAGTTGTTTTTTTTTTACCAGTCCTTTCGATACCGGAAAACAAAGTAGTTGAAGATCGTTCCGGTGATGAGCCA
GCTAGCTATGTTGGTCGGTGTTGCAGGCGGCATACCGGCAAAACCATAAGATATGACAGGAATGTTGATGAGCGGGATCCACTTCT
TCTCTGGGTCCATTTNNTTAATATCCATACTGGAAAGGGCCAGAAAGCGCCAATAAAGTANAAGCGACCTAATTCCGGTAGAGCCC
TCCAGGACCAAAGAGGAAGACCATGNNCATCAGANCANTGNNTNCNNTNNTNNNNNN
```

```
Fast alignment of DNA sequences DNAMAN1 and DNAMAN2

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN1, from 3 to 386
Lower line: DNAMAN2, from 43 to 424

DNAMAN1:DNAMAN2 identity= 34%

3       BASEFFORWARDOPDABNNNNNNNNGTNGCGNGGTTATTGNNCATGAGATCACATTTTTC
         |             |         |    | |||| |           |    ||||||
43      AAAAAAATTCCCCAAAAGTTGGGGGGGGTTGGGGTTTTCATGACCNNTTTTTTTTTTTTC

63      CCTGCGCTAGAATCCAAGGTCCGAAGANTTTTAGCTGGNGAGCTTGATATCTTNATTGAA
        |          ||  ||  |        ||||       |  |||   ||        |
103     CAAAGCTGCCGATAGAATATAGTTGTTTTTTTTTTACCAGTCCTTTCGATACCGGAAAAC

123     CTCCAAGTT.NNGNTGTGGACATCCGCGNANNACNNATTCCTGCNNGTTCNGGTTTCTGG
             ||||   | |     |      |    |   |    ||   ||    ||| | ||
163     AAAGTAGTTGAAGATCGTTCCGGTGATGAGCCAGCTAGCTATGTTGGTCGGTGTTGCAGG

182     GGGANAATTGGGAAATTGCCCTTTTTTTCCCCTGTTCCCCGGANAGGGGGACCCTTCTTC
         ||   |  || |||   || |     |   | |       ||   | ||   |  ||||
223     CGGCATACCGGCAAAA..CCATAAGATATGACAGGAATGTTGATGAGCGGGATCCACTTC

242     TTTTCCCAGAGAATTTTTAATAACCCCCTTTTTGGGGGGGGGGGGTGNTNCCCCGAAAAA
        || ||   |   ||||    |||   || |  |||   |||   |      ||   |||
281     TTCTCTGGGTCCATTTNNT.TAATATCCATACTGGAAAGGGCCAGAAAGCGCCAATAAAG

302     AAAAAAAAACCCCCCTTTTTTTTGGGGGACCTCTTTGGGNGGAAAAAAACACGNNTTTTT
         | ||   |||    |    |   |    ||         |   || | || |||  |
340     TANAAGCGACCTAATTCCGGTAGAGCCCTCCAGGACCAAAGAGGAAGACCATGNNCATCA

362     AAAAAACANTCCCCCCAATTTTTG
         |  |   |   |     |
400     GANCANTGNNTNCNNTNNTNNNNNN
```

ลำดับนิวคลีโอไทด์ของ cDNA คู่ที่ 12

```
>1st_BASE_497756_12F_Forward_OPD08.ab1 ขนาด 394 bp
NNNNNNNNNNNNTACNNTTTGGTCATCTATAAATCAATTCTTGTCTCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCT
TGTTATCCATAACTGAACTTCNNNTTTTGTCTGNNNCCNCCNCCNNNGNCCCANNNGGNACANNNTGGNNNNACNNGGGCCCCCAN
NGGGGCCCCCNNTGGGGCCCCCANTGGGGNCCCCCTGGGCCCAANTGGGGNCCNATTGGGGCCCCATTGGGCNNACGGGGGGCACA
NNGGGNNNNTNGGGNNNNNANGGGNNTANNNGCGNNCNNTNNNNNNNNNNNNNNGNANNNNNTNNNNNNNNTGTGNNGNNTNNNGT
GNGCGTNNNTNNATANNNNNNNNNNNNNNNNNNNNCTNNNNNNNTNNNNNNNNN

Revers complementary
>1st_BASE_497757_12R_Reverse_Oligo_VA.ab1 ขนาด 564 bp
AANNAANANNNNNNNCNNANNAAAAAAAAAANANNNNNCNANATTGGANNNANTATTTNNNAAGTGTGNGCCCAANAGGGGCCCCA
TTGTTTNCCCCANTNGGGGCCCAAGTGTTNGCCCCAATTTNTGCCCCATTTTTGGGCCCCATTTTTGGCCCCCNTTGTTTNNCCCC
AGTGTTGTGCCCCAAGTGTGTGCCCCAGTTTGGTGCCCCNTTGTGTGCCCCCAGTTTGTGCCCCCAGGGGTTTCCCCCATTTTGGT
CCCCCCGTTGTGGGCCCCCAGGGGGTGCCCCAGTTGGTGCCCCAATGGNNNCCCCCAATTGTTGGCCCCAATTGTGTGCCCCCCAG
TTTTTGCCCCCAGTGGGTNCCCCNAGTGGTGCCCNATTTTGTGCCCCAGTTGGGGGCCNNGNGGNNNNNANNNNNNNNNNNNCNNC
CNCGNGNNNNNNNNCANNNANNNNAGNATTAGTTATTGATATAAAAGCTCTCCAGGTAAAAGATCTTCAATGGAGGACTTCTATGA
GACAAGAATTGATTTTATAGATGANCAAATNNGTANNNNNNNNNNNNN

Fast alignment of DNA sequences DNAMAN4 and DNAMAN5

Ktuple=2  Gap_penalty=7

Upper line: DNAMAN4, from 2 to 371
Lower line: DNAMAN5, from 44 to 404

DNAMAN4:DNAMAN5 identity= 27%

2     TBASEFFORWARDOPDABNNNNNNNNNNNNTACNNTTTGGTCATCTATAAATCAATTCTT
        |       |        | |      || |   |||    |         |||
44    NAAAAAAAAAANANNNNNCNANATTGGANNNANTATTTNNNAAGTGTGNGCCCAANAGGG

62    GTCTCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTTGTTATCCATAACTGA
      | | ||| |    || |  | |  |  |   |    |      ||  |  ||     |
104   GCCCCATTGTTTNCCCCANTNGGGGCCCAAGTGTTNGCCCCAATTTNTGCCCCATTTTTG

122   ACTTCNNNTTTTGTCTGNNNCCNCCNCCNNNGNCCCANNNGGNACANNNTGGNNNNACNN
          |   |||||          || |||  |
164   GGCCCCATTTTTGG.........CCCCCNTTGTTTNNCCCCAGTGTTGTGCCCCAAGTGT

182   GGGCCCCCANNGGGGCCCCCNNTGGGGCCCCCANTGGGGNCCCCCTGGGCCCAANTGGGG
      | |||||     ||  ||||| || |  ||||      |  ||||  ||
215   GTGCCCCAGTTTGGTGCCCCNTTGTGTGCCCCCAGTTTGTGCCCCCAGGGGTTTCCCCCA

242   NCCNATTGGGGCCCCATTGGGCNNACGGGGGGCACANNGGGNNNNTNGGGNNNNNANGGG
            |    ||    |||||   | |||||  |    |                |
275   TTTTGGTCCCCCCGTTGTGGGCCCCCAGGGGGTGCCCCAGTTGGTGCCCCAATGGNNNCC

302   NNTANNNGCGNNCNNTNNNNNNNNNNNNNNGNANNNNNTNNNNNNNNTGTGNNGNNTNNN
         |   |    |                                   |  |
335   CCCAATTGTTGGCCCCAATTGTGTGCCCCCCAGTTTTTGCCCCCAGTGGGTNCCCCNAGT

362   GTGNGCGTNN
      |    |
395   GGTGCCCNAT
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD03 เส้นที่ได้จาก forward primer เปรียบเทียบความเหมือนกันภายในกลุ่มด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497734_1F_Forward_OPD03       510 bp
Sequence 2: 1st_BASE_497736_2F_Forward_OPD03       230 bp
Sequence 3: 1st_BASE_497738_3F_Forward_OPD03.ab1   267 bp
Sequence 4: 1st_BASE_497740_4F_Forward_OPD03.ab1   344 bp
Sequence 5: 1st_BASE_497742_5F_Forward_OPD03.ab1   383 bp
Sequence 6: 1st_BASE_497744_6F_Forward_OPD03.ab1   649 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 28.2609
Sequences (1:3) Aligned. Score: 20.2247
Sequences (1:4) Aligned. Score: 20.9302
Sequences (1:5) Aligned. Score: 24.0209
Sequences (1:6) Aligned. Score: 19.2157
Sequences (2:3) Aligned. Score: 18.2609
Sequences (2:4) Aligned. Score: 23.0435
Sequences (2:5) Aligned. Score: 22.6087
Sequences (2:6) Aligned. Score: 24.3478
Sequences (3:4) Aligned. Score: 18.3521
Sequences (3:5) Aligned. Score: 30.3371
Sequences (3:6) Aligned. Score: 22.8464
Sequences (4:5) Aligned. Score: 34.3023
Sequences (4:6) Aligned. Score: 20.0581
Sequences (5:6) Aligned. Score: 20.8877
Guide tree file created:   [clustalw.dnd]

There are 5 groups
Start of Multiple Alignment

Aligning...
Group 1:                     Delayed
Group 2:                     Delayed
Group 3: Sequences:   2      Score:4641
Group 4:                     Delayed
Group 5:                     Delayed
Alignment Score 6399

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment

1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      --------------------------------------------------
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      GTGCAGTACTTAGGCATTGATTGTGTTGCTGCCTTCCTCATACCAAGAAC
1st_BASE_497744_6F_Forward_OPD      --------------------------------------------------

1st_BASE_497740_4F_Forward_OPD      -------------------------------------------NNNNNNN
1st_BASE_497742_5F_Forward_OPD      ----------------------------------------------NNNN
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------NNNNNN
1st_BASE_497736_2F_Forward_OPD      -----------------------------------------------NNN
1st_BASE_497734_1F_Forward_OPD      TTGAGTCCTATTTCAGCATACTTGTGCAAAGCAAGGTAGCAAAGACCAAA
1st_BASE_497744_6F_Forward_OPD      ---------------------------------------------NNNNN
```

```
1st_BASE_497740_4F_Forward_OPD      NNNNNNNNNTGAGNTGNGCNA-NGNNGGAACCAAATTTCTTGTGANTTGN
1st_BASE_497742_5F_Forward_OPD      NNNNNNNNANNGNNTGTGGAT-AGANGNAACCAAATTTCATG-GNTTTGN
1st_BASE_497738_3F_Forward_OPD      NNNNNNGNNNGNGNNGNGGANTACAGNAAANCAAATTTCATG--GCTGGG
1st_BASE_497736_2F_Forward_OPD      NNTTNNNTCCAACCTTTGCCATGTANAAACCCAANNNTTAAG----TCTG
1st_BASE_497734_1F_Forward_OPD      GCTTCGATCCTCTCGCTGCCTTCGATGAAAATTGTTTTGGTAGCCTTAGG
1st_BASE_497744_6F_Forward_OPD      NTTNGNCTCANNCNGNNGCNANANANNAAANCNNATTTCTTAGGATGGGA
                                                     *          *        *

1st_BASE_497740_4F_Forward_OPD      NCAATAAGANNATC-NCNNTTCCCNTTAATGNGGCTGTAGCAT-TGCTGT
1st_BASE_497742_5F_Forward_OPD      ACAATAAGAGNAAA-CCTCTTCAATATAANGNGTTGTTGAAAG-TGCTGT
1st_BASE_497738_3F_Forward_OPD      ANAAGCAGAGGATA-ACTCNNNAANTGATGGCNTTTATGGCACCTGCTGC
1st_BASE_497736_2F_Forward_OPD      TTAATTA--CCAAA-CTCCCTCCATTTAATGGGGGTGTAGTAT----TGT
1st_BASE_497734_1F_Forward_OPD      AGGGAGAAACGTGT-ATCCCTGCAACAAAGATTTGCATGAAGC-TAGTGT
1st_BASE_497744_6F_Forward_OPD      AANGAAAGAAAAAATNCTCGCAAAACAAAGGAGNTTATGGTACGTGCTGC
                                          *                    *         *         **

1st_BASE_497740_4F_Forward_OPD      TCTAC-TC--CGCNNNCCCTANNANACTCCNANTTGCT---GTGCCAACN
1st_BASE_497742_5F_Forward_OPD      TCGAC-TC--CGCNAANNCTAGNTATCTNNNNCGNNCNCG-GCGNGTNNT
1st_BASE_497738_3F_Forward_OPD      CCTACACC--CACCACGCCTGNNNAANCTNAGNGCGNNCGGGAGCNGACN
1st_BASE_497736_2F_Forward_OPD      T-TATAAT--AACCCACCTTTGCAAAATCAGACAGCCTTT-GAGGGGAAG
1st_BASE_497734_1F_Forward_OPD      CCACCCAC--AAGTCGGGCGACAAGACCCAAAAATTTTCATGAGGCAAGA
1st_BASE_497744_6F_Forward_OPD      TAGATGTCGTNANCNGGNTNACNNAGNANGNGTGGGGANG-NNCNANNCT

1st_BASE_497740_4F_Forward_OPD      -AANNANTTTAGTAGCAAGTTGTTTATNNCN--T--TTTTTAGATTTTTT
1st_BASE_497742_5F_Forward_OPD      -ANNTATTTTTATAGGAGGTTTTTTTTTTTC--AAGCCCCCGAGATATGC
1st_BASE_497738_3F_Forward_OPD      CANNTNNTTTNNTCCCGTGTTTTTTTTTAAA--AAAGCCCCGGGNNAGAC
1st_BASE_497736_2F_Forward_OPD      -ATATTTTTTGGGATCAA--TCTTTTTAAAA--A------TGGGTAGCCT
1st_BASE_497734_1F_Forward_OPD      AAGTTTGTCTTACTA-----TTTTTCAAAAA--AATGTGATCCACCCGGA
1st_BASE_497744_6F_Forward_OPD      CNTTTTAGTTGGNTNTATCCTTTTTCGNGCACCNGGANCAAGAGCCGTTG
                                             *          * ***

1st_BASE_497740_4F_Forward_OPD      TTAGGCGAGTGTCCAACCACTCCTCTTATTTTNCCCCCATATTTTTTTTT
1st_BASE_497742_5F_Forward_OPD      GGAGGGGAGTGTCCAAAAAGGGGTAAAATTTTAGAACCTTTTTTTTTTCC
1st_BASE_497738_3F_Forward_OPD      CGGANGAGCTCTCTATTCCGGGGGTTAAATTTTGTGGGGTTTTTCCCCCG
1st_BASE_497736_2F_Forward_OPD      TTGTTGCGCTATTCCATTATTTGTCTTTTCTTTATTACCAAATATTTCCT
1st_BASE_497734_1F_Forward_OPD      AAAAGGGGAGGCGCCCCCGCCCCAGCAAAGGGGAAAACCTTTTTTACGAC
1st_BASE_497744_6F_Forward_OPD      NTGTTAAAGGGCTTTATCATTAATGGCANTANTTTNCCNGGCCCGCACNA

1st_BASE_497740_4F_Forward_OPD      CGGGCA--AAAAAAAAAAATAGCCTTGACGATGTTTCCAAGAGTCTTGGT
1st_BASE_497742_5F_Forward_OPD      CGGGGGGGAAAAAAAAAAANATCCTTAACAAGGTTTCCAAGATCCTGTGC
1st_BASE_497738_3F_Forward_OPD      GGGGGGGGGAAAAAAAAA--------------------------------
1st_BASE_497736_2F_Forward_OPD      GGG-----------------------------------------------
1st_BASE_497734_1F_Forward_OPD      AGGGGGCAGAAAAAAATGCCCCCCCCCCCCCCGTCCCCAAAAACCTGGTC
1st_BASE_497744_6F_Forward_OPD      AGANTGTCTATGNAGGGTCCCTTCCGCCCCTTCAAACGCTAAAGAAGGGC
                                     *

1st_BASE_497740_4F_Forward_OPD      CGAACCGCGTTATNNGT--TTTTCTTTTTCTCTTTTTCGATCCAATTGTA
1st_BASE_497742_5F_Forward_OPD      CAGACCG-GAAAAATGT--CTTGCCACCTCCTTGATTCCAGCAGCCAGCA
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      TGAGAAAAAAAAAACCC--CTTTTTTTTAATAAGCTTCCGATCAACGCCG
1st_BASE_497744_6F_Forward_OPD      CAAANNAAAATATCCATAACCGCTAATTGCATGTTCTCTGAGGGTTTTCA

1st_BASE_497740_4F_Forward_OPD      GTATN---------------------------------------------
1st_BASE_497742_5F_Forward_OPD      CGCCCTTCTTCGCTGCTTGAGTATTNTTTTTTCTTTCTANNCT-------
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      GGAAGCCTGCAATTTTTTCCCAACATTTTCTTTTGGATAAAAACAAACCT
1st_BASE_497744_6F_Forward_OPD      ATGTTCCTTTCTTTGATTTCATACCCAATTATTTATTTGTTTCTGATCTA

1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      --------------------------------------------------
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      GGTCTCACCTTCCGCCCCCCCGC---------------------------
1st_BASE_497744_6F_Forward_OPD      GTCCAGTTGAGTCTGCCCGTGCTTTCTTATCAATTCAGTTGGACACGGTC
```

```
1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      --------------------------------------------------
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      ATTTGTAGTGAACATTCCACCACTCAAGCTGGGTATGCCTTGCTTTCTTG

1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      --------------------------------------------------
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      GGTAGCTTTCCTTTCTTTTTCTTCCTGGAAAACACCTTCTTCCACGTACT

1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      --------------------------------------------------
1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      TATGNGACTTCCATCCTTGCGAAGTAGTTTATCTTTAACATCTTTGTCTT

1st_BASE_497740_4F_Forward_OPD      ---------------------------------------------
1st_BASE_497742_5F_Forward_OPD      ---------------------------------------------
1st_BASE_497738_3F_Forward_OPD      ---------------------------------------------
1st_BASE_497736_2F_Forward_OPD      ---------------------------------------------
1st_BASE_497734_1F_Forward_OPD      ---------------------------------------------
1st_BASE_497744_6F_Forward_OPD      CACTGCTTGGTTGCCCTTCATGTGCCTCACATTCTCGCCCTCTCC
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD03 เส้นที่ได้จาก reverse primer เปรียบเทียบความเหมือนกันภายในกลุ่มด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497735_1R_Reverse_Oligo_VA       646 bp
Sequence 2: 1st_BASE_497737_2R_Reverse_Oligo_VA       248 bp
Sequence 3: 1st_BASE_497739_3R_Reverse_Oligo_VA       164 bp
Sequence 4: 1st_BASE_497741_4R_Reverse_Oligo_VA.ab1   156 bp
Sequence 5: 1st_BASE_497743_5R_Reverse_Oligo_VA       451 bp
Sequence 6: 1st_BASE_497745_6R_Reverse_Oligo_VA       720 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 22.1774
Sequences (1:3) Aligned. Score: 20.122
Sequences (1:4) Aligned. Score: 20.5128
Sequences (1:5) Aligned. Score: 26.8293
Sequences (1:6) Aligned. Score: 24.7678
Sequences (2:3) Aligned. Score: 31.0976
Sequences (2:4) Aligned. Score: 21.1538
Sequences (2:5) Aligned. Score: 18.9516
Sequences (2:6) Aligned. Score: 18.9516
Sequences (3:4) Aligned. Score: 23.7179
Sequences (3:5) Aligned. Score: 25
Sequences (3:6) Aligned. Score: 23.7805
Sequences (4:5) Aligned. Score: 21.1538
Sequences (4:6) Aligned. Score: 19.2308
Sequences (5:6) Aligned. Score: 24.1685
Guide tree file created:   [clustalw.dnd]

There are 5 groups
Start of Multiple Alignment
```

```
Aligning...
Group 1:                     Delayed
Group 2:                     Delayed
Group 3: Sequences:   2      Score:2163
Group 4:                     Delayed
Group 5:                     Delayed
Alignment Score 4329

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      -----GNTGAATAACAACAGAATTAAGAAAATACGGCACAAAAACCGAGG
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      NNNNAGATAGACGTAAACGTCCTTCCTTTTGCCGCGGCCCTCTCAGCAGG
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------


1st_BASE_497737_2R_Reverse_Oli      ------------------GNNNNNNNANNNNNNNNNNNNNNNNNCANNNNN
1st_BASE_497739_3R_Reverse_Oli      ------------------GNNNNNNNNGGGCGAGTGAGCGTCCTCGGGCC
1st_BASE_497735_1R_Reverse_Oli      GGATATTCTCGTGAAGCAGCAACTCCCCTTTAAAAAAAGGGTAGGTGTTA
1st_BASE_497743_5R_Reverse_Oli      ----------------------TCGTGCAGTGGAAGGGGAGGAAGGGGCC
1st_BASE_497745_6R_Reverse_Oli      AGAGATTCCCGTGAGAAAACCACCCCCCTTATAAAACGCAGGGGGGCAGG
1st_BASE_497741_4R_Reverse_Oli      ------------------NNNNGGCCCCNACANNNGNTTGGGNNACTGCC


1st_BASE_497737_2R_Reverse_Oli      GNNNNTGCCG-TTCTTCTACNTACTTCTTAAAAAT-TCCACATAAAAAAA
1st_BASE_497739_3R_Reverse_Oli      GTTTAGGCC--TTTTTTTGCAAACTTTTAAAAATC-TCTACATAAAATTT
1st_BASE_497735_1R_Reverse_Oli      AACTGTGCCCATCCCCCCCCCCACCCACAAAAGGT-AGCACCAATTGGGT
1st_BASE_497743_5R_Reverse_Oli      GGGAGGGCCATTGGACATCAATGTCTTTAAAAGACCTCCACCTTAAACCG
1st_BASE_497745_6R_Reverse_Oli      GGATCATTTCAGACCAATTGTCATCCGCAAAATGGTTACCCGCATCCGTC
1st_BASE_497741_4R_Reverse_Oli      GCTANTGCCA----TGTTTTATATTAATTNAAGTNATTCGTTTTACTNGN
                                                                  **

1st_BASE_497737_2R_Reverse_Oli      AAAAAAAGAGCGATTTTA---GACATAAAGTGTTAAATTG-TCATTATTT
1st_BASE_497739_3R_Reverse_Oli      CTTAAAAG-GCGATTTT----GACATAGAGTAGTAA-TTC-TTTTCATTC
1st_BASE_497735_1R_Reverse_Oli      GAAAACCAACTGGGTCAGGGGGAAAAAAAAGGACATGTCCATTCCCAATT
1st_BASE_497743_5R_Reverse_Oli      AGCATGGGAGGGGCCACAGGCGGGAGAGGCGAACCTTTTCCCCTGCGACA
1st_BASE_497745_6R_Reverse_Oli      TGCAGGGCGGCGACATAGGGACGGACAGGCAATCCCGCCTCACACCTGAA
1st_BASE_497741_4R_Reverse_Oli      NTTNAAAGNTTNATTTTGG--TATANTGGNAATTNN-TATGATTATATTA
                                                            *

1st_BASE_497737_2R_Reverse_Oli      TTTACTTTTGAT-GAATTCTTTAGAATGAATATTAGTTGTTTGATTTTTT
1st_BASE_497739_3R_Reverse_Oli      AACTCTTTGCATCGTGTGTATTGTTGTGGTCTCGACTTGATC--------
1st_BASE_497735_1R_Reverse_Oli      TAGCCTTTTCCTCTTTTCCCACTCCCCCCCCCCGCTGGGGTTGGGACCCA
1st_BASE_497743_5R_Reverse_Oli      CAGCGAAATCTGCGACCGTTGGCAAGCGACTTCGAAAAGAAAATCGCCTT
1st_BASE_497745_6R_Reverse_Oli      GGCGGAGTCCCCCCTTCTCTCCTTGGCGGCACTCCTAGGTAAGGGCCCTG
1st_BASE_497741_4R_Reverse_Oli      AGCTGAGATTTAAAAACGATGTCGAGTAACA-------------------


1st_BASE_497737_2R_Reverse_Oli      GTGAGAAAGG-GCCATAACATTTTGAATTAATTAACCAACTTTTTTTTTT
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      AAAAAAAAAA-GGAGCAG--TTGAAAAAAAAAGAAAAGATTTTTTCCCCC
1st_BASE_497743_5R_Reverse_Oli      CGCCCCAGGT-TTAAAAA-----AAACCAAAGGCCGGGGGTATTTCCTGG
1st_BASE_497745_6R_Reverse_Oli      GAACCCAAACCGGGGCGAATTTTTTAATCGGAGACCGCAGTGCCTGCTGA
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------


1st_BASE_497737_2R_Reverse_Oli      GTACCAAATTTCCTTATAAAATTA--------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      CTGCCACCGCCACAAAAAAAAAAAACAAAACAAAAAAAAAAAAAAAAAAG
1st_BASE_497743_5R_Reverse_Oli      GGAGGGGGGTTTCCGTTGAGGGGGGGGGGGGACCAAACCCCAAAGGCCGG
1st_BASE_497745_6R_Reverse_Oli      CCGCTGGGGGGCACAAAAGGGAAGAAATGGTCCCATTCTGGTTAGCGCTC
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------
```

```
1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      TCTGGGTGGGGACCCCTTCCCCCCCCCCAACCGGAGAAAAAAAAAAAGAG
1st_BASE_497743_5R_Reverse_Oli      TGGGTCCCCAAAACCCCTTTTGGGTGGTTAACACAAAGCCACAATAAAAG
1st_BASE_497745_6R_Reverse_Oli      GGGGGGGGGACATTTGGACACGTCGGGAGGGAAGGGGAAGACACCCGTTT
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      CCCCAAAAATTCAGAGAGAAAAAAAAAAAAAAATTTCCCCCCTCCCCTTT
1st_BASE_497743_5R_Reverse_Oli      GGGGACTCCCCTAAAAAAAGGATAACCCAAAAAGGTTT---------TTT
1st_BASE_497745_6R_Reverse_Oli      TGCCTCTACTGGGGAGGAAAGAAACTCGGGGCGCGGTGAACAATAACATT
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      AA-----AAAAACCAACAGGCGAGGGAAGAAAGAGGCCACCCCCCCCCCC
1st_BASE_497743_5R_Reverse_Oli      GG-----GAGGAAAAACCCGGGGGGGGAGAGGGGGGGGTCCCCAGCCCCA
1st_BASE_497745_6R_Reverse_Oli      GTCTCCCACCCATCACAACTCAATATAAGATTGTAGCGAACAGCACGCAA
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      TAATTTTTCCCCAAACGCACCCAAGGGGGGGAAGTTCCCAATTATTTTCT
1st_BASE_497743_5R_Reverse_Oli      AAAAAGACCCCGAGAAAAAATGGTAAAAGATCCTACCTGACGC-------
1st_BASE_497745_6R_Reverse_Oli      AGCGAGAAAATACACCACAGCATTCATCGGAGCGAGACAGAGACGCGGTA
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      CCCCATCAAAAAACCCCATTTTGGGGGGAAAAAAAAAAAAAAAAAAAAAA
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      TAATAGGTATAAATAGCCTCTTGTTTTTGGTAGGTCTGCGAGCCAGACAC
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      AGGGTCCCTGCACGTCGCGTCCCCACGACTGCACAACAACCAAGCGGGGA
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      TACCTCTCTCATGGGGCTGTATCTATTGCTAGATCGGATCTAACCCGACA
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497735_1R_Reverse_Oli      GCCCCGAACG----------------------------------------
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      ACATGGGGCCCGTAAGTTGTGCGCGCGAACCCAAAGGGACCACGACAACG
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------

1st_BASE_497737_2R_Reverse_Oli      --------------------
1st_BASE_497739_3R_Reverse_Oli      --------------------
1st_BASE_497735_1R_Reverse_Oli      --------------------
1st_BASE_497743_5R_Reverse_Oli      --------------------
1st_BASE_497745_6R_Reverse_Oli      GATCAACCAGGACGACCAAA
1st_BASE_497741_4R_Reverse_Oli      --------------------
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD03 เส้นที่ได้จาก forward primer เปรียบเทียบความเหมือนกันของส่วน bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497734_1F_Forward_OPD03       510 bp
Sequence 2: 1st_BASE_497738_3F_Forward_OPD03.ab1   267 bp
Sequence 3: 1st_BASE_497742_5F_Forward_OPD03.ab1   383 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 20.2247
Sequences (1:3) Aligned. Score: 24.0209
Sequences (2:3) Aligned. Score: 30.3371
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1:                     Delayed
Group 2:                     Delayed
Alignment Score 1673

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      --------------------------------------------------
1st_BASE_497734_1F_Forward_OPD      GTGCAGTACTTAGGCATTGATTGTGTTGCTGCCTTCCTCATACCAAGAAC


1st_BASE_497738_3F_Forward_OPD      --------------------------------------------NNNNNN
1st_BASE_497742_5F_Forward_OPD      ----------------------------------------------NNNN
1st_BASE_497734_1F_Forward_OPD      TTGAGTCCTATTTCAGCATACTTGTGCAAAGCAAGGTAGCAAAGACCAAA


1st_BASE_497738_3F_Forward_OPD      NNNNNNGNNNGNGNNGNGGANTACAGNAAANCAAATTTCATGGCTG-GGA
1st_BASE_497742_5F_Forward_OPD      NNNNNNNNANNGNNTGTGGAT-AGANGNAACCAAATTTCATGGNTTTGNA
1st_BASE_497734_1F_Forward_OPD      GCTTCGATCCTCTCGCTGCCTTCGATGAAAATTGTTTTGGTAGCCTTAGG
                                                     *      *   **     ***  * *

1st_BASE_497738_3F_Forward_OPD      NAAGCAGAGGATAACTCNNNAANTGATGGCNTTTATGGCACCTGCTGCCC
1st_BASE_497742_5F_Forward_OPD      CAATAAGAGNAAACCTCTTCAATATAANGNGTT-GTTGAAAGTGCTGTTC
1st_BASE_497734_1F_Forward_OPD      AGGGAGAAACGTGTATCCCTGCAACAAAGATTTGCATGAAGCTAGTGTCC
                                           *       **        *  *  **    * *  *  **  *

1st_BASE_497738_3F_Forward_OPD      TACACCCACCACGCCTGNNNAANCTNAGNGCGNNCGGGAGCNGACNCANN
1st_BASE_497742_5F_Forward_OPD      GAC-TCCGCNAANNCTAGNTATCTNNNNCGNNCNCGGCGNGTNNTANNTA
1st_BASE_497734_1F_Forward_OPD      ACCCACAAGTCGGGCGACAAGACCCAAAAATTTTCATGAGGCAAGAAAGT
                                      *  *        *                   *

1st_BASE_497738_3F_Forward_OPD      TNNTTTNNTCCCGTGTTTTTTTTTAAAAAAGCCCCGGGNNAGACCGGANG
1st_BASE_497742_5F_Forward_OPD      TTTTTATAGGAGGTTTTTTTTTTTCAAG--CCCCCGAGATATGCGGAGGG
1st_BASE_497734_1F_Forward_OPD      TTGTCTTACTATTTTTCAAAAAAATGTGATCCACCCGGAAAAAGGGGAGG
                                    *  *         * *               * **  *  *    *   *

1st_BASE_497738_3F_Forward_OPD      AGCT---CTCTATTCCGGGGGTTAAATTTTGTGGGG---TTTTTCCCCCG
1st_BASE_497742_5F_Forward_OPD      GAGT---GTCCAAAA-AGGGGTAAAATTTTAGAACCTTTTTTTTTCCCG
1st_BASE_497734_1F_Forward_OPD      CGCCCCCGCCCCAGCAAAGGGGAAAACCTT---------TTTTACGACAG
                                             *        ***  ***  **         ****    * *
```

```
1st_BASE_497738_3F_Forward_OPD      GGGGGGGGGAAAAAAAAA--------------------------------
1st_BASE_497742_5F_Forward_OPD      GGGGGGAAAAAAAAAAANATCCTTAACAAGGTTTCCAAGATCCTGTGCCA
1st_BASE_497734_1F_Forward_OPD      GGGGCAGAAAAAAATGCCCCCCCCCCCCCCGTCCCCAAAAACCTGGTCTG
                                    ****     *****

1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      GACCGGAAAAATGTCTTGCCACCTCCTTGATTCCAGCAGCCAGCACGCCC
1st_BASE_497734_1F_Forward_OPD      AGAAAAAAAAAACCCCTTTTTTTTAATAAGCTTCCGATCAACGCCGGGAA


1st_BASE_497738_3F_Forward_OPD      --------------------------------------------------
1st_BASE_497742_5F_Forward_OPD      TTCTTCGCTGCTTGAGTATTNTTTTTTCTTTCTANNCT------------
1st_BASE_497734_1F_Forward_OPD      GCCTGCAATTTTTTCCCAACATTTTCTTTTGGATAAAAACAAACCTGGTC


1st_BASE_497738_3F_Forward_OPD      -------------------
1st_BASE_497742_5F_Forward_OPD      -------------------
1st_BASE_497734_1F_Forward_OPD      TCACCTTCCGCCCCCCCGC
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD03 เส้นที่ได้จาก reverse primer เปรียบเทียบความเหมือนกันของส่วน bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497735_1R_Reverse_Oligo_VA   646 bp
Sequence 2: 1st_BASE_497739_3R_Reverse_Oligo_VA   451 bp
Sequence 3: 1st_BASE_497743_5R_Reverse_Oligo_VA   164 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 26.8293
Sequences (1:3) Aligned. Score: 20.122
Sequences (2:3) Aligned. Score: 25
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1:                     Delayed
Group 2:                     Delayed
Alignment Score 1302

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497735_1R_Reverse_Oli      GNTGAATAACAACAGAATTAAGAAAATACGGCACAAAAACCGAGGGGATA
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------


1st_BASE_497735_1R_Reverse_Oli      TTCTCGTGAAGCAGCAACTCCCCTTTAAAAAAAGGGTAGGTGTTAAACTG
1st_BASE_497739_3R_Reverse_Oli      -----------------TCGTGCAGTGGAAGGGGAGGAAGGGGCCGGGAG
1st_BASE_497743_5R_Reverse_Oli      --------------------GNNNNNNNNGGGCGAGTGAGCGTCCTCGGG
                                                                     * *   * *       *

1st_BASE_497735_1R_Reverse_Oli      T-GCCCATCCCCCCCCCCAC---CCACAAAAGGTAGCACCAATTGGGTGA
1st_BASE_497739_3R_Reverse_Oli      G-GCCATTGGACATCAATGT---CTTTAAAAGACCTCCACCTTAAACCGA
1st_BASE_497743_5R_Reverse_Oli      CCGTTTAGGCCTTTTTTTGCAAACTTTTAAAAATCTCTACATAAAATTTC
                                      *                    *    ***     *  *
```

```
1st_BASE_497735_1R_Reverse_Oli      AAACCAACTGGGTCAGGGG-GAAAAAAAAGGACATGTCCATTCCCAATTT
1st_BASE_497739_3R_Reverse_Oli      GCATGGGAGGGGCCACAGGCGGGAGAGGCGAACCTTTTCCCCTGCGACAC
1st_BASE_497743_5R_Reverse_Oli      TTAAAAGGCGATTTTGACA-TAGAGTAGTAATTCTTTTCATTCAACTCTT
                                      *      *             *          * * *

1st_BASE_497735_1R_Reverse_Oli      AGCCTTTTCCTCTTTTCCCACTCCCCCCCCCCGCTGGGGTTGGGACCCAA
1st_BASE_497739_3R_Reverse_Oli      AGCGAAATCTGCGACCGTTGGCAAGCGACTTCGAAAAGAAAATCGCCTTC
1st_BASE_497743_5R_Reverse_Oli      TGCATCGTGTGTATTGTTGTGGTCTCGACTTGATC---------------
                                     **    *                 *  *

1st_BASE_497735_1R_Reverse_Oli      AAAAAAAAAGGAGCAGTTGAAAAAAAAAGAAAAGATTTTTTCCCCCCTGC
1st_BASE_497739_3R_Reverse_Oli      GCCCCAGGTTTAAAAAAAACCAAAGGCCGGGGGTATTTCCTGGGGAGGGG
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      CACCGCCACAAAAAAAAAAAACAAAACAAAAAAAAAAAAAAAAAAGTCTG
1st_BASE_497739_3R_Reverse_Oli      GGTTTCCGTTGAGGGGGGGGGGGGACCAAACCCCAAAGGCCGGTGGGTCC
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      GGTGGGGACCCCTTCCCCCCCCCAAC-CGGAGAAAAAAAAAAAAGAGCCC
1st_BASE_497739_3R_Reverse_Oli      --CCAAAACCCCTTTTGGGTGGTTAACACAAAGCCACAATAAAAGGGGGA
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      CAAAAATTCAGAGAGAAAAAAAAAAAAAAATTTCCCCCCTCCCCTTTAAA
1st_BASE_497739_3R_Reverse_Oli      CTCCCCTAAAAAAAGGATAACCCAAAAAGGTTT-----------TTTGGG
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      AAAACCAACAGGCGAGGGAAGAAAGAGGCCACCCCCCCCCCCTAATTTTT
1st_BASE_497739_3R_Reverse_Oli      AGGAAAAACCCGGGGGGGGAGAGGGGGGGGTCCCCAGCCCCAAAAAAGAC
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      CCCCAAACGCACCCAAGGGGGGGAAGTTCCCAATTATTTTCTCCCCATCA
1st_BASE_497739_3R_Reverse_Oli      CCCGAGAAA-----AAATGGTAAAAGATCCTACCTGACGC----------
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      AAAAACCCCATTTTGGGGGGAAAAAAAAAAAAAAAAAAAAAAAGGGTCCC
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      TGCACGTCGCGTCCCCACGACTGCACAACAACCAAGCGGGGAGCCCCGAA
1st_BASE_497739_3R_Reverse_Oli      --------------------------------------------------
1st_BASE_497743_5R_Reverse_Oli      --------------------------------------------------

1st_BASE_497735_1R_Reverse_Oli      CG
1st_BASE_497739_3R_Reverse_Oli      --
1st_BASE_497743_5R_Reverse_Oli      --
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD03 เส้นที่ได้จาก forward primer เปรียบเทียบความเหมือนกันของส่วน coma bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497736_2F_Forward_OPD03       230 bp
Sequence 2: 1st_BASE_497744_6F_Forward_OPD03.ab1   649 bp
Sequence 3: 1st_BASE_497740_4F_Forward_OPD03.ab1   344 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 24.3478
Sequences (1:3) Aligned. Score: 23.0435
Sequences (2:3) Aligned. Score: 20.0581
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1:                    Delayed
Group 2:                    Delayed
Alignment Score 1202

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497736_2F_Forward_OPD      ----NNNNNTTNNNTCCAACCTTTGCCATGTANAAA-CCCAANNNTTAAG
1st_BASE_497744_6F_Forward_OPD      --NNNNNNTTNGNCTCANNCNGNNGCNANANANNAAANCNNATTTCTTAG
1st_BASE_497740_4F_Forward_OPD      NNNNNNNNNNNNNNNNNTGAGNTGNGCNANGNNGGAA-CCAAATTTCTTGT
                                        ****    *           ** *      **  *  *    *

1st_BASE_497736_2F_Forward_OPD      TCTGTTAATT-----ACCAAACTCCCTCCATTTAATGGGGGT-GTAGTAT
1st_BASE_497744_6F_Forward_OPD      GATGGGAAANGAAAGAAAAAAATNCTCGCAAAACAAAGGAGNTTATGGTAC
1st_BASE_497740_4F_Forward_OPD      GANTTGNNCAATAAGANNATCNCNNTTCCCNTTAATGNGGCT-GTAGCAT
                                                   *  *        *     ** *  * *  * * *

1st_BASE_497736_2F_Forward_OPD      -TGTTTATA-ATAACCCACCTTTGCAAAATCAGACAGCCTTTGAGGGGAA
1st_BASE_497744_6F_Forward_OPD      GTGCTGCTAGATGTCGTNANCNGGNTNACNNAGNANGNGTGGGGANGNNC
1st_BASE_497740_4F_Forward_OPD      -TGCTGTTCTACTCCGCNNNCCCTANNANACTCCNANTTGCTGTGCCAAC
                                     ** *  *  *   *            *              *

1st_BASE_497736_2F_Forward_OPD      GATATTTTTTG-----GGATCAATCTTTTTAAAAATGGGTAGCCTTTGTT
1st_BASE_497744_6F_Forward_OPD      NANNCTCNTTTTAGTTGGNTNTATCCTTTTTCGNGCACCNGGANCAAGAG
1st_BASE_497740_4F_Forward_OPD      NAANNANTTTA--GTAGCAAGTTGTTTATNNCNTTTTTTAGATTTTTTTT
                                     *      **      *         * *

1st_BASE_497736_2F_Forward_OPD      GCGCTATTCCATTATTTGTCTTTTCTTTATTACCAAATATTTCCTGGG--
1st_BASE_497744_6F_Forward_OPD      CCGTTGNTGT-TAAAGGGCTTTATCATTAATGGCANTANTTTNCCNGGCC
1st_BASE_497740_4F_Forward_OPD      AGGCGAGTGTCCAACCACTCCTCTTATTTTNCCCCCATATTTTTTTTTCG
                                      *    *     *       * *  **     *     ***

1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      CGCACNAAGANTGTCTATGNAGGGTCCCTTCCGCCCCTTCAAACGCTAAA
1st_BASE_497740_4F_Forward_OPD      GGCAAAAAAAAAA------AATAGCCTTGACGATGTTTCCAAGAGTCTTG


1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      GAAGGGCCAAANNAAAATATCCATAACCGCTAATTGCATGTTCTCTGAGG
1st_BASE_497740_4F_Forward_OPD      GTCGAACCGCGTTATNNGTTTTTCTTTTTCTCTTTTTCGATCCAATTGTA


1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      GTTTTCAATGTTCCTTTCTTTGATTTCATACCCAATTATTTATTTGTTTC
1st_BASE_497740_4F_Forward_OPD      GTATN---------------------------------------------



1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      TGATCTAGTCCAGTTGAGTCTGCCCGTGCTTTCTTATCAATTCAGTTGGA
1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------
```

```
1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      CACGGTCATTTGTAGTGAACATTCCACCACTCAAGCTGGGTATGCCTTGC
1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------

1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      TTTCTTGGGTAGCTTTCCTTTCTTTTTCTTCCTGGAAAACACCTTCTTCC
1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------

1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      ACGTACTTATGNGACTTCCATCCTTGCGAAGTAGTTTATCTTTAACATCT
1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------

1st_BASE_497736_2F_Forward_OPD      --------------------------------------------------
1st_BASE_497744_6F_Forward_OPD      TTGTCTTCACTGCTTGGTTGCCCTTCATGTGCCTCACATTCTCGCCCTCT
1st_BASE_497740_4F_Forward_OPD      --------------------------------------------------

1st_BASE_497736_2F_Forward_OPD      --
1st_BASE_497744_6F_Forward_OPD      CC
1st_BASE_497740_4F_Forward_OPD      --
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD03 เส้นที่ได้จาก reverse primer เปรียบเทียบความเหมือนกันของส่วน coma bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497737_2R_Reverse_Oligo_VA        249 bp
Sequence 2: 1st_BASE_497741_4R_Reverse_Oligo_VA.ab1    156 bp
Sequence 3: 1st_BASE_497745_6R_Reverse_Oligo_VA        720 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 22.4359
Sequences (1:3) Aligned. Score: 19.2771
Sequences (2:3) Aligned. Score: 19.2308
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1:                        Delayed
Group 2:                        Delayed
Alignment Score 644

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      NNNNAGATAGACGTAAACGTCCTTCCTTTTGCCGCGGCCCTCTCAGCAGG

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      AGAGATTCCCGTGAGAAAACCACCCCCCTTATAAAACGCAGGGGGGCAGG

1st_BASE_497737_2R_Reverse_Oli      --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli      --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli      GGATCATTTCAGACCAATTGTCATCCGCAAAATGGTTACCCGCATCCGTC
```

```
1st_BASE_497737_2R_Reverse_Oli        --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        TGCAGGGCGGCGACATAGGGACGGACAGGCAATCCCGCCTCACACCTGAA

1st_BASE_497737_2R_Reverse_Oli        --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        GGCGGAGTCCCCCCTTCTCTCCTTGGCGGCACTCCTAGGTAAGGGCCCTG

1st_BASE_497737_2R_Reverse_Oli        --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        GAACCCAAACCGGGGCGAATTTTTTAATCGGAGACCGCAGTGCCTGCTGA

1st_BASE_497737_2R_Reverse_Oli        --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        CCGCTGGGGGGCACAAAAGGGAAGAAATGGTCCCATTCTGGTTAGCGCTC

1st_BASE_497737_2R_Reverse_Oli        --------------------------------------------------
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        GGGGGGGGGACATTTGGACACGTCGGGAGGGAAGGGGAAGACACCCGTTT

1st_BASE_497737_2R_Reverse_Oli        ------GNNNNNNNANNNNNNNNNNNNNNNNCANNNNNGNNNNTGCCGTT
1st_BASE_497741_4R_Reverse_Oli        ------NNNNGGCCCCNACANNNGNTTGGGNNACTGCCGCTANTGCCATG
1st_BASE_497745_6R_Reverse_Oli        TGCCTCTACTGGGGAGGAAAGAAACTCGGGGCGCGGTGAACAATAACATT
                                                                                 *  * * 

1st_BASE_497737_2R_Reverse_Oli        CTTCTACNTACTTCTTAAAAATTCCACATAAAAAAAAAAAAAAAGAGCGAT
1st_BASE_497741_4R_Reverse_Oli        TTTTATATTAATTN--AAGTNATTCGTTTTACTNGNNTTNAAAGNTTNAT
1st_BASE_497745_6R_Reverse_Oli        GTCTCCCACCCATC---ACAACTCAATATAAGATTGTAGCGAACAGCACG
                                       *          *    *    *     * *          **       

1st_BASE_497737_2R_Reverse_Oli        TTTAGACATAAAGTGTTAAATTGTCATTATTTTT-TACTTTTGATGAATT
1st_BASE_497741_4R_Reverse_Oli        TTTGG---TATANTGGNAA-TTNNTATGATTATA-TTAAGCTGAGA----
1st_BASE_497745_6R_Reverse_Oli        CAAAGCGAGAAAATACACCACAGCATTCATCGGAGCGAGACAGAGACGCG
                                          *    * *             * **           **      

1st_BASE_497737_2R_Reverse_Oli        CTTTAGAATGAATATTAGTTGTTTGATTTTTTGTGAGA--AAGGGCCATA
1st_BASE_497741_4R_Reverse_Oli        -TTTAAAAACGATGTCGAGTAACA--------------------------
1st_BASE_497745_6R_Reverse_Oli        GTATAATAGGTATAAATAGCCTCTTGTTTTTGGTAGGTCTGCGAGCCAGA
                                       * **   *   **                                     

1st_BASE_497737_2R_Reverse_Oli        ACATTTTGAATTAATTAACCAACTTTTTTTTTTGTACCAAATTTCCTTAT
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        CACTACCTCTCTCATGGGGCTGTATCTATTGCTAGATCGGATCTAACCCG

1st_BASE_497737_2R_Reverse_Oli        AAAATTAC------------------------------------------
1st_BASE_497741_4R_Reverse_Oli        --------------------------------------------------
1st_BASE_497745_6R_Reverse_Oli        ACAACATGGGGCCCGTAAGTTGTGCGCGCGAACCCAAAGGGACCACGACA

1st_BASE_497737_2R_Reverse_Oli        -----------------------
1st_BASE_497741_4R_Reverse_Oli        -----------------------
1st_BASE_497745_6R_Reverse_Oli        ACGGATCAACCAGGACGACCAAA
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD08 เส้นที่ได้จาก forward primer เปรียบเทียบความเหมือนกันภายในกลุ่มด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497746_7F_Forward_OPD08.abl     390 bp
Sequence 2: 1st_BASE_497748_8F_Forward_OPD08.abl     519 bp
Sequence 3: 1st_BASE_497750_9F_Forward_OPD08.abl     374 bp
Sequence 4: 1st_BASE_497752_10F_Forward_OPD08.abl    408 bp
Sequence 5: 1st_BASE_497754_11F_Forward_OPD08.abl    393 bp
Sequence 6: 1st_BASE_497756_12F_Forward_OPD08.abl    394 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 27.6923
Sequences (1:3) Aligned. Score: 31.5508
Sequences (1:4) Aligned. Score: 19.2308
Sequences (1:5) Aligned. Score: 22.0513
Sequences (1:6) Aligned. Score: 21.7949
Sequences (2:3) Aligned. Score: 22.1925
Sequences (2:4) Aligned. Score: 16.4216
Sequences (2:5) Aligned. Score: 21.883
Sequences (2:6) Aligned. Score: 14.2132
Sequences (3:4) Aligned. Score: 17.9144
Sequences (3:5) Aligned. Score: 23.262
Sequences (3:6) Aligned. Score: 23.5294
Sequences (4:5) Aligned. Score: 23.6641
Sequences (4:6) Aligned. Score: 13.198
Sequences (5:6) Aligned. Score: 15.7761
Guide tree file created:   [clustalw.dnd]

There are 5 groups
Start of Multiple Alignment

Aligning...
Group 1:                     Delayed
Group 2:                     Delayed
Group 3:                     Delayed
Group 4:                     Delayed
Group 5:                     Delayed
Alignment Score 8139

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497746_7F_Forward_OPD      NNNNNNNGGATNNNGNNNNNNNTGACTAT-NTATAAAATCT-TTCTTGTC
1st_BASE_497750_9F_Forward_OPD      ---NNNNNNANNNGGNANGNNNTGANCAT-CNATCACATCTATTCTTGTC
1st_BASE_497748_8F_Forward_OPD      --NNNNNNNNTNNGNNNNNNTTGAANAC-AGCACAAATTT-GTCTTGTC
1st_BASE_497754_11F_Forward_OP      -NNNNNNNNGTNGCGNGGTTATTGNNCATGAGATCACATTTTTCCCTG-C
1st_BASE_497752_10F_Forward_OP      ---NNNNANNNNGNGNAGNGNAGGGGNATGATATNACGGATTCNCTCTAC
1st_BASE_497756_12F_Forward_OP      ---NNNNNNNNNNNTACNNTTTGGTCAT-CTAT-AAATCAATTCTTGTC
                                       ****                *   *       *        *    *

1st_BASE_497746_7F_Forward_OPD      TCATAGAAGTAATGCATTGAAGATCTTTTACTTGGAGAGCTTGCATATCC
1st_BASE_497750_9F_Forward_OPD      TCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTGGCATATCC
1st_BASE_497748_8F_Forward_OPD      GN-TACAACTACTGCTGCGAAGATCTTTTACTTGGACCTTTTCCATCTGC
1st_BASE_497754_11F_Forward_OP      GC-TAGAATCCAAGGTCCGAAGAN-TTTTAGCTGGNGAGCTTG-ATAT-C
1st_BASE_497752_10F_Forward_OP      TT-TANAAAAGAAGTTCTGTTGGTTTTTCTTTTTTCCCACTTA-AAATGG
1st_BASE_497756_12F_Forward_OP      TCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTTG-TTATCC
                                       ** **          *  *   ***    *       *      *


1st_BASE_497746_7F_Forward_OPD      TCATTTGAACTNNNAGTTGAGNNTTCGNCNGNNGGTGGGCTANNAANCAG
1st_BASE_497750_9F_Forward_OPD      ATAACTGAACTTCGAGATTNGGAGTACCTCNCNNCCGGTNCCCGNAG---
1st_BASE_497748_8F_Forward_OPD      CTTTTTGATCTTGAAGATTAACGAGTTGGTNCCNCTCGGGTGNNGNATAG
1st_BASE_497754_11F_Forward_OP      TTNATTGAACTCCAAGTTNNGNTGTGGACATCCGC--GNANNACNNATTC
1st_BASE_497752_10F_Forward_OP      CCGTTCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTA
1st_BASE_497756_12F_Forward_OP      ATAACTGAACTTCNNNTTTTGTCTGNNNCCNCCNCCNNNGNCCCANN---
                                           *  *
```

```
1st_BASE_497746_7F_Forward_OPD       CTAGTTGTGTNNC-TCCCGTGGCAGTCNCTTGAAAACCAAATTGGGGGAT
1st_BASE_497750_9F_Forward_OPD       -TTATTGNGTGGT-GCGTTGGTCCGNNATNTGGGGANANACACAAAANGN
1st_BASE_497748_8F_Forward_OPD       CTAGCTTTGTCNCCGCTGTTGNGGATTCTCTGCAGACAAAACNGTATGAC
1st_BASE_497754_11F_Forward_OP       CTGCNNGTTCNGG-TTTCTGGGGGANAATTGGGAAATTGCCCTTTTTTTC
1st_BASE_497752_10F_Forward_OP       ATTACATCACCAAGGAAGGACTCTACTCAGCTAGAAAGGAGAAGCTTGGA
1st_BASE_497756_12F_Forward_OP       --NGGNACANNNTGGNNNNACNNGGGCCCCCANNGGGGCCCCCNNTGGGG

1st_BASE_497746_7F_Forward_OPD       CNNCCCGGGGG-TACTTTAGNNNTTTTTTTTTTTTANGAANGGGTN----
1st_BASE_497750_9F_Forward_OPD       NNGACANTTGN-TAAAGGNGGGCCTTCCTTTNTNCTCCACAN--TT----
1st_BASE_497748_8F_Forward_OPD       ACCACNGNNGGGTANATNAGAANTCNTTTNNTTTCAAGAAAATGTN----
1st_BASE_497754_11F_Forward_OP       CCCTGTTCCCCGGANAGGGGGACCCTTCTTCTTTTCCCAGAGAATT----
1st_BASE_497752_10F_Forward_OP       TTAAAAGAATGGAAGAAGGGGATTTTAATGCCTTTCTAAGGAGACTGAAG
1st_BASE_497756_12F_Forward_OP       CCCCCANTGGGGNCCCCCTGGGCCCAANTGGGGNCCNATTGGGGCCCCA-
                                                        *        *

1st_BASE_497746_7F_Forward_OPD       -TTGNAAAAANTCNTTTTTTTCCCNNAAAA-----ACNCC-ATAAAAAAA
1st_BASE_497750_9F_Forward_OPD       -TTTTAATNNTNNCTTTTGGCCGGGAGAAA-----ACCNCGANAAAAAAA
1st_BASE_497748_8F_Forward_OPD       -NTATAANCNTTNT------CCNCNCCANA-----ACCCCNAAAAAACNN
1st_BASE_497754_11F_Forward_OP       -TTTAATAACCCCCTTTTTGGCGGGGGGGGGTGNTNCCCCGAAAAAAAAA
1st_BASE_497752_10F_Forward_OP       GCTCTTAATATTCTAGGATCCTGGGNNGGGAGGGTGNGGGGAAAAAAAAA
1st_BASE_497756_12F_Forward_OP       -TTGGGCNNACGGGGGGCACANNGGGNNNNTNGGGNNNNNANGGGNNTAN
                                       *

1st_BASE_497746_7F_Forward_OPD       A------NNNNNACNTGGGCGGT--TTTNTNNGGGAAAGGGGGGGTGGGT
1st_BASE_497750_9F_Forward_OPD       N------NCNCCNTATTNGTGGGGGTCTCCTTNNGGAAANNGGGGCGGGG
1st_BASE_497748_8F_Forward_OPD       C------CCCCCCCTTGNGGGNGGGTTTTNGNNAGNNGGGNNGGGNNTGC
1st_BASE_497754_11F_Forward_OP       AAAAACCCCCCTTTTTTTGGGGGACCTCTTTGGGNGGAAAAAAACACGN
1st_BASE_497752_10F_Forward_OP       AAA--CCCCCCCCCCTGGGTTTTTTTTTTCTTCTTTAAAAAACCCCCC
1st_BASE_497756_12F_Forward_OP       NNG---CGNNCNNTNNNNNNNNNNNNNNGNANNNNNTNNNNNNNNNTGTGN

1st_BASE_497746_7F_Forward_OPD       TTCTGTAAAGAAATGCNGATGNNNTTTTTNATGTTNCTTTNTTTGGGGCT
1st_BASE_497750_9F_Forward_OPD       GTNTATAAA-------ANATCCNTNCAAAAAGGNAAAACNCTTTGGGGGA
1st_BASE_497748_8F_Forward_OPD       NAATACCNC------CCCCCGAAGNTTTCANTGTCCCTTTTGTTGGNAAT
1st_BASE_497754_11F_Forward_OP       NTTTTTAAA-------AAACANTCCCCCCAATTTTTTGGTTTTTGGGGGG
1st_BASE_497752_10F_Forward_OP       TTTTCCCCCCCGNACNTTTTCTTTTCCAAAANTTNNNNGGGNNNGNGGNN
1st_BASE_497756_12F_Forward_OP       NGNNTNNNGTGNGCGTNNNTNNATANNNNNNNNNNNNNNNNNNCTNNNNNN

1st_BASE_497746_7F_Forward_OPD       CNNCCNNTNTTTN-------------------------------------
1st_BASE_497750_9F_Forward_OPD       ANNACAANN-----------------------------------------
1st_BASE_497748_8F_Forward_OPD       CNCANNATNNGTCNTTGCTTCTGATCTGGTCCTTTTGAGTCTGCTTTGCT
1st_BASE_497754_11F_Forward_OP       GGGAANANCAAAAA------------------------------------
1st_BASE_497752_10F_Forward_OP       NAAANAAACAAAAAA-----------------------------------
1st_BASE_497756_12F_Forward_OP       TNNNNNNNNN----------------------------------------

1st_BASE_497746_7F_Forward_OPD       --------------------------------------------------
1st_BASE_497750_9F_Forward_OPD       --------------------------------------------------
1st_BASE_497748_8F_Forward_OPD       TTCTTATCNATTCATTTGGATAAGGCCTTTTGTAGTGAACATTCCACCNC
1st_BASE_497754_11F_Forward_OP       --------------------------------------------------
1st_BASE_497752_10F_Forward_OP       --------------------------------------------------
1st_BASE_497756_12F_Forward_OP       --------------------------------------------------

1st_BASE_497746_7F_Forward_OPD       --------------------------------------------------
1st_BASE_497750_9F_Forward_OPD       --------------------------------------------------
1st_BASE_497748_8F_Forward_OPD       TCAGGCTNGGTATGCCTTGCTTCCTTTGTTTGTTTTCCTTTCTTTTTCTT
1st_BASE_497754_11F_Forward_OP       --------------------------------------------------
1st_BASE_497752_10F_Forward_OP       --------------------------------------------------
1st_BASE_497756_12F_Forward_OP       --------------------------------------------------

1st_BASE_497746_7F_Forward_OPD       --
1st_BASE_497750_9F_Forward_OPD       --
1st_BASE_497748_8F_Forward_OPD       CT
1st_BASE_497754_11F_Forward_OP       --
1st_BASE_497752_10F_Forward_OP       --
1st_BASE_497756_12F_Forward_OP       --
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD08 เส้นที่ได้จาก reverse primer เปรียบเทียบความเหมือนกันภายในกลุ่มด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497747_7R_Reverse_Oligo_VA.ab1     374 bp
Sequence 2: 1st_BASE_497749_8R_Reverse_Oligo_VA.ab1     409 bp
Sequence 3: 1st_BASE_497751_9R_Reverse_Oligo_VA.ab1     407 bp
Sequence 4: 1st_BASE_497753_10R_Reverse_Oligo_VA.ab1    423 bp
Sequence 5: 1st_BASE_497755_11R_Reverse_Oligo_VA.ab1    401 bp
Sequence 6: 1st_BASE_497757_12R_Reverse_Oligo_VA.ab1    564 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 13.1016
Sequences (1:3) Aligned. Score: 15.508
Sequences (1:4) Aligned. Score: 14.1711
Sequences (1:5) Aligned. Score: 14.4385
Sequences (1:6) Aligned. Score: 16.0428
Sequences (2:3) Aligned. Score: 68.059
Sequences (2:4) Aligned. Score: 24.2054
Sequences (2:5) Aligned. Score: 63.3416
Sequences (2:6) Aligned. Score: 18.3374
Sequences (3:4) Aligned. Score: 18.9189
Sequences (3:5) Aligned. Score: 64.5885
Sequences (3:6) Aligned. Score: 15.9705
Sequences (4:5) Aligned. Score: 23.4414
Sequences (4:6) Aligned. Score: 17.0213
Sequences (5:6) Aligned. Score: 16.4589
Guide tree file created:   [clustalw.dnd]

There are 5 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences:   2      Score:6541
Group 2: Sequences:   3      Score:6248
Group 3:                     Delayed
Group 4:                     Delayed
Group 5:                     Delayed
Alignment Score 10599

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497749_8R_Reverse_Oli      --------------------------------------------------
1st_BASE_497751_9R_Reverse_Oli      --------------------------------------------------
1st_BASE_497755_11R_Reverse_Ol      --------------------------------------------------
1st_BASE_497753_10R_Reverse_Ol      --------------------------------------------------
1st_BASE_497757_12R_Reverse_Ol      NNNNNNNNNNNNNTACNNATTTGNTCATCTATAAAATCAATTCTTGTCTC
1st_BASE_497747_7R_Reverse_Oli      --------------------------------------------------


1st_BASE_497749_8R_Reverse_Oli      --------------------------------------------------
1st_BASE_497751_9R_Reverse_Oli      --------------------------------------------------
1st_BASE_497755_11R_Reverse_Ol      --------------------------------------------------
1st_BASE_497753_10R_Reverse_Ol      --------------------------------------------------
1st_BASE_497757_12R_Reverse_Ol      ATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTTTTATATCAAT
1st_BASE_497747_7R_Reverse_Oli      --------------------------------------------------
```

```
1st_BASE_497749_8R_Reverse_Oli      ------CNNNNNNNNNGGGNNGGNGGGGCTCATAGG-ACCGANCGCT--C
1st_BASE_497751_9R_Reverse_Oli      -NNNNNNNNNANGTGNAGNTCAGGNGNTCTGATANGCAACGCGCTNCAGC
1st_BASE_497755_11R_Reverse_Ol      ----NNNNNNANNANNGNANNCANTGNTCTGATGNNCATGGTCTTCCT-C
1st_BASE_497753_10R_Reverse_Ol      ----NNNNNNNNNNNANNAAAAANGGGGCTCNNACNNAANNNCACCCT-C
1st_BASE_497757_12R_Reverse_Ol      AACTAATNCTNNNNTNNNTGNNNNNNNNCNCGNGGNNGNNNNNNNNNNNN
1st_BASE_497747_7R_Reverse_Oli      --------------------------------NNNNNNNNNNNNNNNNNN

1st_BASE_497749_8R_Reverse_Oli      TCTGGACATAAGAGGGCTCTACGGGAATTTGGAGGGG--TGACCTTATTG
1st_BASE_497751_9R_Reverse_Oli      TTTGGACCTGC-AGGGCTCTACTGGAATTTGATGTGAATTTACTTGATTG
1st_BASE_497755_11R_Reverse_Ol      TTTGGTCCTGG-AGGGCTCTACCGGAATTAGGT-CGCTTNTACTTTATTG
1st_BASE_497753_10R_Reverse_Ol      TTTGGANTTAAAAAG--TCTACGGCAANNNAAG-GANTGNTCCTTTTTTA
1st_BASE_497757_12R_Reverse_Ol      TNNNNNCCNCNNGGCCCCCAACTGGGGCACAAAATNGGGCACCACTNGGG
1st_BASE_497747_7R_Reverse_Oli      NNNNNNNNNNNNNNNNNNNAACNNNNNNNNNNNNNNNNNNNANNNNGANN
                                                        **

1st_BASE_497749_8R_Reverse_Oli      GAGCTTTCTGGCCGGT--------------TCCAATATGGATATTAAGCA
1st_BASE_497751_9R_Reverse_Oli      ACGCTTTCTTGCCGGT--------------TCCAAAATGGATATTAAGCA
1st_BASE_497755_11R_Reverse_Ol      GCGCTTTCTGGCCCTT--------------TCCAGTATGGATATTAANNA
1st_BASE_497753_10R_Reverse_Ol      ACTATCNTCCTNCGTT------------------ATAGAGATTNACAGCC
1st_BASE_497757_12R_Reverse_Ol      GNACCCACTGGGGGCAAAAACTGGGGGGCACACAATTGGGGCCAACAATT
1st_BASE_497747_7R_Reverse_Oli      NAANNNCNNNNNNNNN-----------------NNNNNGNNNNTTNATTT
                                                                                  *

1st_BASE_497749_8R_Reverse_Oli      AAATGTACCCAGAGAAGAAGTGGATCCCGC-TCATCAACATTCCTGTCAT
1st_BASE_497751_9R_Reverse_Oli      AAATGTACCCCGAGAAGAAGTGGATCCCAC-TCATCAACATTCCTGTCAT
1st_BASE_497755_11R_Reverse_Ol      AA-TGGACCCAGAGAAGAAGTGGATCCCGC-TCATCAACATTCCTGTCAT
1st_BASE_497753_10R_Reverse_Ol      TTAGGNNCCTNNAAAGGCATTNACTTNCCC-TTCTTCCTTCTTNTATGTN
1st_BASE_497757_12R_Reverse_Ol      GGGGGNNNCCATTGGGGCACCAACTGGGGCACCCCCTGGGGGCCCACAAC
1st_BASE_497747_7R_Reverse_Oli      TTTTTTNNNCAANNAAAAAATTTTTNNAA------AAACNTNNTTANAGT
                                                      *     *

1st_BASE_497749_8R_Reverse_Oli      ATCT-TATGGTTTTGCCGGTA-----TGCCGCCTGCAAC-ACCGACCAAC
1st_BASE_497751_9R_Reverse_Oli      ATCT-TATGGTTTTGCCGGTA-----TGCCGCCTGCAAC-ACCGACCAAC
1st_BASE_497755_11R_Reverse_Ol      ATCT-TATGGTTTTGCCGGTA-----TGCCGCCTGCAAC-ACCGACCAAC
1st_BASE_497753_10R_Reverse_Ol      ATCTGCGTCTATCTAGCTGAG-----TCAAAAATGTACCTAGGGGATGGT
1st_BASE_497757_12R_Reverse_Ol      GGGGGGACCAAAATGGGGGAAACCCCTGGGGGCACAAACTGGGGGCACAC
1st_BASE_497747_7R_Reverse_Oli      NTTCTNNTGNNNNTNTTANGA---------GGCCAACCCGGGNAGGCTAT
                                                 *                        *

1st_BASE_497749_8R_Reverse_Oli      ATAG-----CTA-GCTGGCTCATCACCGGAACGATCTTCAACTT-CTTTG
1st_BASE_497751_9R_Reverse_Oli      ATAG-----CTA-GCTGGCTCATCACCGGAACAATCTTCAACTT-CTTTG
1st_BASE_497755_11R_Reverse_Ol      ATAG-----CTA-GCTGGCTCATCACCGGAACGATCTTCAACTA-CTTTG
1st_BASE_497753_10R_Reverse_Ol      AATG-----CTGTACTAAGCTATC--CAGAATTATCTAAATTTT-CTATT
1st_BASE_497757_12R_Reverse_Ol      AANGGGGCACCAAACTGGGGCACACACTTGGGGCACAACACTGG-GGNNA
1st_BASE_497747_7R_Reverse_Oli      GGGGGCCTCTTTTGGGNNTTTTTTGCGGTNGGTCTTTCGGCGAAGGGGG
                                       *                      *

1st_BASE_497749_8R_Reverse_Oli      TTTTCCGNNATCGAAAGANCTGGTAAAAAAAAAACAACTATGTGCTATCT
1st_BASE_497751_9R_Reverse_Oli      TTTTCCGGTATCGAAAGGGCTGGTGGCAAAGAAACAACTATGTGCTATCT
1st_BASE_497755_11R_Reverse_Ol      TTTTCCGGTATCGAAAGGACTGGTAAAAAAAAAACAACTATATTCTATCG
1st_BASE_497753_10R_Reverse_Ol      TTTCTTGCCGGNNAGTGTAAGGGGGAAAAAAAAAAAACCCCTCTCGGCGG
1st_BASE_497757_12R_Reverse_Ol      AACAANGGGGGCCAAAAATGGGGCCCAAAAATGGGGCANAAATTGGGGCN
1st_BASE_497747_7R_Reverse_Oli      TGGGGGGGCTTTCAANNCAACTTCACCCCAAAAAAGGCCNTCCCCCCGNT
                                          *      *               *

1st_BASE_497749_8R_Reverse_Oli      GCTGTTTTGGATGAGGGCACG-GGATTCATGGGGGTGCTGTTGCCCCCCA
1st_BASE_497751_9R_Reverse_Oli      GCAGCTTTGGATGCTGGCACG-GCGTTCGTGGGGGTCCTGTTGTTCTTTG
1st_BASE_497755_11R_Reverse_Ol      GCAGCTTTGGAAAAAAAAAAAANNGGTCATGAAAACCCCAACCCCCCCCA
1st_BASE_497753_10R_Reverse_Ol      GGTCTTTTTTTCTCTCCCTTCCAAGATNCTCCNTTCCCTCCTTCCCCCCC
1st_BASE_497757_12R_Reverse_Ol      AACACTTGGGCCCCNANTGGGGNAAACAATGGGGCCCCTNTTGGGCNCAC
1st_BASE_497747_7R_Reverse_Oli      ANTTTTTTTTTTTNGGGAGGGAGAGATGNTTATCCCNGGGGGGCGNCNCG
                                         **                      *

1st_BASE_497749_8R_Reverse_Oli      GCCCGGGGAGAATCCGGGTT--TTGGGGGGGGCNNCCNNNNNNNNACACA
1st_BASE_497751_9R_Reverse_Oli      CCCTCGAGAAA--CAGGTTT--TTGGGGGGGACAAAAAAAAAN-------
1st_BASE_497755_11R_Reverse_Ol      ACTTTTGGGGAA-TTTTTTT--TTTGGGGGCNCAAAAAAAA---------
1st_BASE_497753_10R_Reverse_Ol      ACTTGCCCCCTTACATTTTT--TTGGGGGGGGGGGGGGAGGCCCGGGGAG
1st_BASE_497757_12R_Reverse_Ol      ACTTNNNAAATANTNNNTCCAATNTNGNNNNNTNTTTTTTTTTTNNTNNG
1st_BASE_497747_7R_Reverse_Oli      GGGCATTTNGTTTNNTTTTTTGTTNNAAAAAAAAANT-------------
                                                          *
```

```
1st_BASE_497749_8R_Reverse_Oli      NN-------------
1st_BASE_497751_9R_Reverse_Oli      ---------------
1st_BASE_497755_11R_Reverse_Ol      ---------------
1st_BASE_497753_10R_Reverse_Ol      CAACACAAAAAAATT
1st_BASE_497757_12R_Reverse_Ol      NNNNNNNTNTTNNTT
1st_BASE_497747_7R_Reverse_Oli      ---------------
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD08 เส้นที่ได้จาก forward primer เปรียบเทียบความเหมือนกันของส่วน bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497746_7F_Forward_OPD08.abl    390 bp
Sequence 2: 1st_BASE_497750_9F_Forward_OPD08.abl    374 bp
Sequence 3: 1st_BASE_497754_11F_Forward_OPD08.abl   393 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 31.5508
Sequences (1:3) Aligned. Score: 22.0513
Sequences (2:3) Aligned. Score: 23.262
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences:   2      Score:5273
Group 2:                     Delayed
Alignment Score 2207

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497746_7F_Forward_OPD      NNNNNNNGGATNNNGNNNNNNNTGACTATNT-ATAAAATCT-TTCTTGTC
1st_BASE_497750_9F_Forward_OPD      ---NNNNNNANNNGGNANGNNNTGANCATCN-ATCACATCTATTCTTGTC
1st_BASE_497754_11F_Forward_OP      -NNNNNNNNGTNGCGNGGTTATTGNNCATGAGATCACATTTTTCCCTGCG
                                       ****    *  **      **   **   ** * ** * * * **

1st_BASE_497746_7F_Forward_OPD      TCATAGAAGTAATGCATTGAAGATCTTTTACTTGGAGAGCTTGCATATCC
1st_BASE_497750_9F_Forward_OPD      TCATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTGGCATATCC
1st_BASE_497754_11F_Forward_OP      C--TAGAATCCAAGGTCCGAAGAN-TTTTAGCTGGNGAGCTTG-ATATCT
                                       *****          *****  *****  *** ***** * *****

1st_BASE_497746_7F_Forward_OPD      TCATTTGAACTNNNAGTTGAGNNTTCGNCNGNNGGTGGGCTANNAANCAG
1st_BASE_497750_9F_Forward_OPD      ATAACTGAACTTCGAGATTNGGAGTACCTCNCNNCCGGTNCCCGNAG---
1st_BASE_497754_11F_Forward_OP      TNA-TTGAACTCCAAGTTNNGNTGTGGACATCCG-CGNANNACNNATTCC
                                      *  ******   ** *  *   *           *        *

1st_BASE_497746_7F_Forward_OPD      CTAGTTGTGTNNCTCCCGTGGCAGTCNCTTGAAAACCAAATTGGGGGATC
1st_BASE_497750_9F_Forward_OPD      -TTATTGNGTGGTGCGTTGGTCCGNNATNTGGGGANANACACAAAANGNN
1st_BASE_497754_11F_Forward_OP      TGCNNGTTCNGGTTTCTGGGGGANAATTGGGAAATTGCCCTTTTTTTCCC
                                                       *          *

1st_BASE_497746_7F_Forward_OPD      NNCCCGGGGGTACTTTAGNNNTTTTTTTTTTTTANGAANGGGTNTTGNAA
1st_BASE_497750_9F_Forward_OPD      NGACANTTGNTAAAGGNGGGCCTTCCTTTNTNCTCCACAN--TTTTTTAA
1st_BASE_497754_11F_Forward_OP      CTGTTCCCCGGANAGGGGGACCCTTCTTCTTTTCCCAGAGAATTTTTAAT
                                               *     *     *  **  *     *     * **  *

1st_BASE_497746_7F_Forward_OPD      AAANTCNTTTTTTTCCCNNAAAA-----ACNCC-ATAAAAAAAAN-----
1st_BASE_497750_9F_Forward_OPD      TNNTNNCTTTTGGCCGGGAGAAA-----ACCNCGANAAAAAAANN-----
1st_BASE_497754_11F_Forward_OP      AACCCCCTTTTGGGGGGGGGGGGGTGNTNCCCCGAAAAAAAAAAAAAACC
                                           ****                  *  * * *******

1st_BASE_497746_7F_Forward_OPD      -NNNNACNTGGGCGGT--TTTNTNNGGGAAAGGGGGGGTGGGTTTCTGTA
1st_BASE_497750_9F_Forward_OPD      -CNCCNTATTNGTGGGGGTCTCCTTNNGGAAANNGGGGCGGGGGTNTATA
1st_BASE_497754_11F_Forward_OP      CCCCTTTTTTTTGGGGGACCTCTTTGGGNGGAAAAAAACACGNNTTTTTA
                                            *    **     *      *             *  * * **
```

```
1st_BASE_497746_7F_Forward_OPD      AAGAAATGCNGATGNNNTTTTNATGTTNCTTTNTTTGGGGCTCNNCCNN
1st_BASE_497750_9F_Forward_OPD      AA-------ANATCCNTNCAAAAAGGNAAAACNCTTTGGGGGAANNACAA
1st_BASE_497754_11F_Forward_OP      AA-------AAACANTCCCCCCAATTTTTTGGTTTTTGGGGGGGGGAANA
                                    **         *           *          *******

1st_BASE_497746_7F_Forward_OPD      TNTTTN-
1st_BASE_497750_9F_Forward_OPD      NN-----
1st_BASE_497754_11F_Forward_OP      NCAAAAA
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD08 เส้นที่ได้จาก reverse primer เปรียบเทียบความเหมือนกันของส่วน bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497747_7R_Reverse_Oligo_VA.ab1    374 bp
Sequence 2: 1st_BASE_497751_9R_Reverse_Oligo_VA.ab1    407 bp
Sequence 3: 1st_BASE_497755_11R_Reverse_Oligo_VA.ab1   401 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 15.508
Sequences (1:3) Aligned. Score: 14.4385
Sequences (2:3) Aligned. Score: 64.5885
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences:   2      Score:6344
Group 2:                     Delayed
Alignment Score 2550

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment

1st_BASE_497751_9R_Reverse_Oli      NNNNNNNNNANGTGNAGNTCAGGNGNTCTGATANGCAACGCGCTNCAGCT
1st_BASE_497755_11R_Reverse_Ol      --NNNNNNANNANNGNANNCAN-TGNTCTGATGNNCATGGT-CTTCCTCT
1st_BASE_497747_7R_Reverse_Oli      -------------------------------NNNNNNNNNNNNNNNNNNN
                                                                     *

1st_BASE_497751_9R_Reverse_Oli      TTGGACCTGCAGGGCTCTACTGGAATTTGATGTGAATTTACTTGATTGAC
1st_BASE_497755_11R_Reverse_Ol      TTGGTCCTGGAGGGCTCTACCGGAATTAGGT-CGCTTNTACTTTATTGGC
1st_BASE_497747_7R_Reverse_Oli      NNNNNNNNNNNNNNNNNNNAACNNNNNNNNNN--NNNNNNNNNANNNNGAN
                                                      *                            *

1st_BASE_497751_9R_Reverse_Oli      GCTTTCTTGCCGGTTCCAAAATGGATATTAAGCAAAATGTACCCCGAGAA
1st_BASE_497755_11R_Reverse_Ol      GCTTTCTGGCCCTTTCCAGTATGGATATTAANNAAA-TGGACCCAGAGAA
1st_BASE_497747_7R_Reverse_Oli      NNAANNNCNNNNNNNNNNNNNNGNNNNTTNATTTTTTTTNNNCAANNAA
                                                          *    ** *      *     *    **

1st_BASE_497751_9R_Reverse_Oli      GAAGTGGATCCCACTCATCAACATTCCTGTCATAT-CTTATGGTTTTGCC
1st_BASE_497755_11R_Reverse_Ol      GAAGTGGATCCCGCTCATCAACATTCCTGTCATAT-CTTATGGTTTTGCC
1st_BASE_497747_7R_Reverse_Oli      AAA----ATTTTTTNNAAAAACNTNNTTANAGTNTTCTNNTGNNNNTNTT
                                     **    **       *  *** *   *    * * **  **    *

1st_BASE_497751_9R_Reverse_Oli      GGTATGCCG-CCTGCAACACCGACCAACATAGCTAGCTGGCTCATCACCG
1st_BASE_497755_11R_Reverse_Ol      GGTATGCCG-CCTGCAACACCGACCAACATAGCTAGCTGGCTCATCACCG
1st_BASE_497747_7R_Reverse_Oli      ANGAGGCCAACCCGGGNAGGCTATGGGGGCCTCTTTTGGGNNTTTTTTG
                                       * ***  ** *      * *         **    **    *    *
```

```
1st_BASE_497751_9R_Reverse_Oli        -GAACAATCTTCAACTTCTTTGTTTTCCGGTATCGAAAGGGCTGGTGGCA
1st_BASE_497755_11R_Reverse_Ol        -GAACGATCTTCAACTACTTTGTTTTCCGGTATCGAAAGGACTGGTAAAA
1st_BASE_497747_7R_Reverse_Oli        CGGTNGGTCTTTCGGCGAAGGGGGTGGGGGGGCTTTCAANNCAACTTCAC
                                       *     ****          *  *   **       *   *   *

1st_BASE_497751_9R_Reverse_Oli        AAGAAACAACTATGTGCTATCTGCAGCTTTGGATGCTGGCACG-GCGTTC
1st_BASE_497755_11R_Reverse_Ol        AAAAAACAACTATATTCTATCGGCAGCTTTGGAAAAAAAAAAAAANNGGTC
1st_BASE_497747_7R_Reverse_Oli        CCCAAAAAAGGCCNTCCCCCCGNTANTTTTTTTTTTNGGGAGGGAGAGA
                                         *** **     * *   *   *  ***                *

1st_BASE_497751_9R_Reverse_Oli        GTGGGGGTCCTGTTGTTCTTTG-CCCTCGAGAAACAGGTTTTGGGGGGG
1st_BASE_497755_11R_Reverse_Ol        ATGAAAACCCCAACCCCCCCCAACTTTTGGGGAATTTTTTTTTGGGGGC
1st_BASE_497747_7R_Reverse_Oli        TGNTTATCCCNGGGGGGCGNCNCGGGGCATTTNGTTTNNTTTTTTGTTNN
                                              **       *                     ****  *

1st_BASE_497751_9R_Reverse_Oli        ACAAAAAAAAAN
1st_BASE_497755_11R_Reverse_Ol        NCAAAAAAAA--
1st_BASE_497747_7R_Reverse_Oli        AAAAAAAAANT-
                                        *******
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD08 เส้นที่ได้จาก forward primer เปรียบเทียบความเหมือนกันของส่วน coma bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497748_8F_Forward_OPD08.ab1    519 bp
Sequence 2: 1st_BASE_497752_10F_Forward_OPD08.ab1   408 bp
Sequence 3: 1st_BASE_497756_12F_Forward_OPD08.ab1   394 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 16.4216
Sequences (1:3) Aligned. Score: 14.2132
Sequences (2:3) Aligned. Score: 13.198
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1:                    Delayed
Group 2:                    Delayed
Alignment Score 1222

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497748_8F_Forward_OPD      --NNNNNNNNNTNNGNNNNNNNTTGAANACAGCACAAATTTGTCTTGTCGN
1st_BASE_497752_10F_Forward_OP      NNNNANNNNGNGNAGNGNAGGGGNATGATATNACGGATTCNCTCTACT-T
1st_BASE_497756_12F_Forward_OP      ---NNNNNNNNNNNNTACNNTTTGGTCAT-CTATAAATCAATTCTTGTCT
                                       * **** * *              *    *   **      *

1st_BASE_497748_8F_Forward_OPD      TACAACTACTGCTG--CGAAGATCTTTTACTTGGACCTTTTCCATCTGCC
1st_BASE_497752_10F_Forward_OP      TANAAAAGAAGTTC--TGTTGGTTTTTCTTTTTTCCCACTTAAAATGGCC
1st_BASE_497756_12F_Forward_OP      CATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTTGTTATCCAT
                                     * *             *  * * ***    *       **

1st_BASE_497748_8F_Forward_OPD      TTTTTGATCTTGAAGATTAACGAGTTGGTNCCNCTCGGGTGNNGNATAGC
1st_BASE_497752_10F_Forward_OP      GTTCAAAGTATTGTGAATAT---GTTGTAAAACTTCTTACTCTGTACA-C
1st_BASE_497756_12F_Forward_OP      AACTGAACTTCNNNTTTTGTCT-GNNNCCNCCNCCNNNGNCCCANNNGGN
                                          *          *     *


1st_BASE_497748_8F_Forward_OPD      TAGCTTTGTCNCCGCTGTTGNGGATTCTCTGCAGACAAAACNGTATGACA
1st_BASE_497752_10F_Forward_OP      TAATTACATCACCAAGG--AAGGACTCTACTCAGCTAGAAAGG-------
1st_BASE_497756_12F_Forward_OP      ACANNNTGGNNNNACNN--GGGCCCCCANNGGGGCCCCCNNTG-------
                                                         *    *      *        *
```

```
1st_BASE_497748_8F_Forward_OPD      CCACNGNNGGGTANATNAGAANTCNTTTNNTTTCAAGAAAATGTNNTATA
1st_BASE_497752_10F_Forward_OP      ----AGAAGCTTGGATTAAAAG------AAT---GGAAGAAGGGGATTTT
1st_BASE_497756_12F_Forward_OP      -----GGGCCCCCANTGGGGNCCCCCTGGGC--CCAANTGGGGNCCNATT
                                         *         *                          *     *

1st_BASE_497748_8F_Forward_OPD      ANCNTTNTCCNCNCCANAACCCCNAAAAAACNNCCCCCCCCTTGNGGGNG
1st_BASE_497752_10F_Forward_OP      AATGCCTTTCTAAGGAGA----CTGAAGGCTCTTAATATTCTAGGATCCT
1st_BASE_497756_12F_Forward_OP      GGGGCCCCATTGGGCNNA----CGGGGGGCACANNG-------GGNNNNT
                                                     *    *                    *

1st_BASE_497748_8F_Forward_OPD      GGTTTTNGNNAGNNGGGNNGGGNNTGCNAATACCNCCCCCCGAAGNTTTC
1st_BASE_497752_10F_Forward_OP      GGGNNGGGAGGGTGNGGGGAAAAAAAAAAAACCCCCCCCCCTGGGGTTTT
1st_BASE_497756_12F_Forward_OP      NGGGNNNNNANGGGNNTANNNGCGNNCNNTNNNNNNNNNNNNNNGNANNN
                                     *         *                                *

1st_BASE_497748_8F_Forward_OPD      ANTGTCCCTTTTGTTGGNAATCNCANNATNNGTCNTTGCTTCTGATCTGG
1st_BASE_497752_10F_Forward_OP      TTTTTTTCTTCTTTAAAAAACCCCCCTTTTCCCCCCCGNACNTTTTCT--
1st_BASE_497756_12F_Forward_OP      NNTNNNNNNNNTGT-GNNGNNTNNNGTGNGCGTNNNTNNATANNNNNN--
                                      *        * *

1st_BASE_497748_8F_Forward_OPD      TCCTTTTGAGTCTGCTTTGCTTTCTTATCNATTCATTTGGATAAGGCCTT
1st_BASE_497752_10F_Forward_OP      -TTTCCAAAANTTNNNNGGGNNNGNGGNNNAAANAAACAAAAAA------
1st_BASE_497756_12F_Forward_OP      ---NNNNNNNNNNNCTNNNNNNTNNNNNNNNN------------------
                                                                 *

1st_BASE_497748_8F_Forward_OPD      TTGTAGTGAACATTCCACCNCTCAGGCTNGGTATGCCTTGCTTCCTTTGT
1st_BASE_497752_10F_Forward_OP      --------------------------------------------------
1st_BASE_497756_12F_Forward_OP      --------------------------------------------------

1st_BASE_497748_8F_Forward_OPD      TTGTTTTCCTTTCTTTTTCTTCT
1st_BASE_497752_10F_Forward_OP      -----------------------
1st_BASE_497756_12F_Forward_OP      -----------------------
```

ลำดับนิวคลีโอไทด์ที่ได้จากไพรเมอร์ OPD08 เส้นที่ได้จาก reverse primer เปรียบเทียบความเหมือนกันของส่วน coma bract ที่ระยะการเจริญเติบโตต่างๆ ด้วยโปรแกรม CLUSTAL W

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: 1st_BASE_497749_8R_Reverse_Oligo_VA.ab1    409 bp
Sequence 2: 1st_BASE_497753_10R_Reverse_Oligo_VA.ab1   423 bp
Sequence 3: 1st_BASE_497757_12R_Reverse_Oligo_VA.ab1   564 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 24.2054
Sequences (1:3) Aligned. Score: 18.3374
Sequences (2:3) Aligned. Score: 17.0213
Guide tree file created:   [clustalw.dnd]

There are 2 groups
Start of Multiple Alignment

Aligning...
Group 1:                     Delayed
Group 2:                     Delayed
Alignment Score 1691

CLUSTAL-Alignment file created  [clustalw.aln]

CLUSTAL 2.1 multiple sequence alignment


1st_BASE_497749_8R_Reverse_Oli      --------------------------------------------------
1st_BASE_497753_10R_Reverse_Ol      --------------------------------------------------
1st_BASE_497757_12R_Reverse_Ol      NNNNNNNNNNNNNTACNNATTTGNTCATCTATAAAATCAATTCTTGTCTC
```

```
1st_BASE_497749_8R_Reverse_Oli      --------------------------------------------------
1st_BASE_497753_10R_Reverse_Ol      --------------------------------------------------
1st_BASE_497757_12R_Reverse_Ol      ATAGAAGTCCTCCATTGAAGATCTTTTACCTGGAGAGCTTTTATATCAAT

1st_BASE_497749_8R_Reverse_Oli      ------CNNNNNNNNNGGGNNGGNGGGGCTCATA--GGACCGANCGCTCT
1st_BASE_497753_10R_Reverse_Ol      ----NNNNNNNNNNNANNAAAAANGGGGCTCNNACNNAANNNCACCCTCT
1st_BASE_497757_12R_Reverse_Ol      AACTAATNCTNNNNTNNNTGNNNNNNNNCNCGNGGNNGNNNNNNNNNNNN
                                           *  ****         *    * *

1st_BASE_497749_8R_Reverse_Oli      CTGGACATAAGAGGGCTCTA-CGGGAATTTGGAGGGGTGACCTTATTGGA
1st_BASE_497753_10R_Reverse_Ol      TTGGANTTAAAAAG--TCTA-CGGCAANNNA-AGGANTGNTCCTTTTTTA
1st_BASE_497757_12R_Reverse_Ol      TNNNNNCCNCNNGGCCCCCAACTGGGGCACAAAATNGGGCACCACTNGGG
                                                 *   * * * *        *     *  *   *

1st_BASE_497749_8R_Reverse_Oli      GCTTTCTGGCCGGTTCCAATATGGATATTAAGCAAAATGTACCCA-----
1st_BASE_497753_10R_Reverse_Ol      ACTATCNTCCTNCGTT--ATAGAGATTNACAGCCTTAGGNNCCTN-----
1st_BASE_497757_12R_Reverse_Ol      GNACCCACTGGGGGCAAAAACTGGGGGGCACACAATTGGGGCCAACAATT
                                         *            *    *        *     *  **

1st_BASE_497749_8R_Reverse_Oli      ---GAGAAGAAGTGGATCCCGCTCATCAACATTCCTGTCATATCT-TA-T
1st_BASE_497753_10R_Reverse_Ol      ---NAAAGGCATTNACTTNCCCTTCTTCCTTCTTNTATGTNATCTGCG-T
1st_BASE_497757_12R_Reverse_Ol      GGGGGNNNCCATTGGGGCACCAACTGGGGCACCCCCTGGGGGCCCACAAC
                                              * *      *                       *

1st_BASE_497749_8R_Reverse_Oli      GGTTTTGCCGGTATGCCGCCTGCAAC-ACCGAC-CAACATAGCTA-GC-T
1st_BASE_497753_10R_Reverse_Ol      CTATCTAGCTGAGTCAAAAATGTACCTAGGGGA-TGGTAATGCTGTAC-T
1st_BASE_497757_12R_Reverse_Ol      GGGGGGACCAAAATGGGGGAAACCCCTGGGGGCACAAACTGGGGGCACAC
                                            *    *           *    *          *     *

1st_BASE_497749_8R_Reverse_Oli      GGCTCATCACCGGAACGATCTTCAACTTCTTTGTTTTCCGNNATCGAAAG
1st_BASE_497753_10R_Reverse_Ol      AAGCTATC--CAGAATTATCTAAATTTTCTATTTTTCTTGCCGGNNAGTG
1st_BASE_497757_12R_Reverse_Ol      AANGGGGCACCAAACTGGGGCACACACTTGGGGCACAACACTGGGGNNAA
                                           *  *  *         *   *

1st_BASE_497749_8R_Reverse_Oli      A--NCTGGTAAAAAAAA--------AACAACTATGTGCTA--TCTG--CT
1st_BASE_497753_10R_Reverse_Ol      T--AAGGGGGAAAAAAA--------AAAAACCCCTCTCGG--CGGGGTCT
1st_BASE_497757_12R_Reverse_Ol      ACAANGGGGGCCAAAAATGGGGCCCAAAAATGGGGCANAAATTGGGGCNA
                                          **    *****        ** **               *

1st_BASE_497749_8R_Reverse_Oli      GTTTTGGATGAGGGCACGGGATTCATGGGGGTGCTGTTGCCCCCCA---G
1st_BASE_497753_10R_Reverse_Ol      TTTTTTCTCTCCCTTCCAAGATNCTCCNTTCCCTCCTTCCCCCCCACTTG
1st_BASE_497757_12R_Reverse_Ol      ACACTTGGGCCCCNANTGGGGNAAACAATGGGGCCCCTNTTGGGCNCACA
                                        *              *                 *      *

1st_BASE_497749_8R_Reverse_Oli      CCCGGGGAG-AATCC---GGGTTTTGGGGGGGGCNNCCNNNNNNNNACAC
1st_BASE_497753_10R_Reverse_Ol      CCCCCTTAC-ATTTTTTTGGGGGGGGGGGGGGAGGCCCGGGGAGCAACAC
1st_BASE_497757_12R_Reverse_Ol      CTTNNNAAATANTNNNTCCAATNTNGNNNNNTNTTTTTTTTTTNNTNNGN
                                    *      *  * *            *

1st_BASE_497749_8R_Reverse_Oli      ANN-----------
1st_BASE_497753_10R_Reverse_Ol      AAAAAAATT-----
1st_BASE_497757_12R_Reverse_Ol      NNNNNNTNTTNNTT
```

ผลการเปรียบเทียบลำดับนิวคลีโอไทด์ที่ได้จากเส้น forward primer ของ cDNA แถบที่ 10 กับลำดับเบสบนฐานข้อมูลใน NCBI

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gb|AC132808.2|  Homo sapiens chromosome 3 clone RP11-794P9, complete sequence
Length=195741

 Score =  340 bits (184),  Expect = 3e-90
 Identities = 217/233 (93%), Gaps = 4/233 (2%)
 Strand=Plus/Plus

Query  38      TTCNCTCTACTTTA-NAAAAGA-AGTTCTGTT-GGtttttcttttttCCCACTTAAAATG  94
               ||| || |||||||  |||||| | ||||||| ||||| |||||||||||||||||||||
Sbjct  152181  TTC-CTATACTTTACAAAAAGACAATTCTGTTGGGTTTGTCTTTTTTCCCACTTAAAATG  152239

Query  95      GCCGTTCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTAATTACATCA  154
               || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  152240  GCTGTGCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTAATTACATCA  152299

Query  155     CCAAGGAAGGACTCTACTCAGCTAGAAAGGAGAAGCTTGGATTAAAAGAATGGAAGAAGG  214
               |||| ||||| ||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  152300  CCAAAGAAGGGCTCTACTCAGCTAGAAAGGAGAAGCTTGGATTAGAAGAATGGAAGAAGG  152359

Query  215     GGATTTTAATGCCTTTCTAAGGAGACTGAAGGCTCTTAATATTCTAGGATCCT  267
               ||||||||||||||||||||||  |||||||||||| ||||||||||||||||
Sbjct  152360  GGATTTTAATGCCTTTCTAAGGTTACTGAAGGCTCTGAATATTCTAGGATCCT  152412


gb|AC093418.2|  Homo sapiens chromosome 3 clone RP11-1035L22, complete sequence
Length=206320

 Score =  335 bits (181),  Expect = 2e-88
 Identities = 216/233 (93%), Gaps = 4/233 (2%)
 Strand=Plus/Minus

Query  38      TTCNCTCTACTTTA-NAAAAGA-AGTTCTGTT-GGtttttcttttttCCCACTTAAAATG  94
               ||| || |||||||  |||||| | ||||||| ||||| |||||||||||||||||||||
Sbjct  173872  TTC-CTATACTTTACAAAAAGACAATTCTGTTGGGTTTGTCTTTTTTCCCACTTAAAATG  173814

Query  95      GCCGTTCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTAATTACATCA  154
               || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173813  GCTGTGCAAAGTATTGTGAATATGTTGTAAAACTTCTTACTCTGTACACTAATTACATCA  173754

Query  155     CCAAGGAAGGACTCTACTCAGCTAGAAAGGAGAAGCTTGGATTAAAAGAATGGAAGAAGG  214
               |||| ||||| ||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  173753  CCAAAGAAGGGCTCTACTCAGCTAGAAAGGAGAAGCTTGGATTAGAAGAATGGAAGAAGG  173694

Query  215     GGATTTTAATGCCTTTCTAAGGAGACTGAAGGCTCTTAATATTCTAGGATCCT  267
               ||||||||||||||||||||||  |||||||||| | ||||||||||||||||
Sbjct  173693  GGATTTTAATGCCTTTCTAAGGTTACTGAAGGCTATGAATATTCTAGGATCCT  173641
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ประวัติผู้เขียน

ชื่อ-สกุล	นางสาว ทิพย์วรรณ ใจภา
วันเดือนปีเกิด	20 กรกฎาคม 2528
ประวัติการศึกษา	- สำเร็จการศึกษาระดับมัธยมศึกษา โรงเรียนไชยปราการ จังหวัดเชียงใหม่ ปีการศึกษา 2546 - สำเร็จการศึกษาระดับปริญญาตรีวิทยาศาสตรบัณฑิต สาขาพืชสวน จากมหาวิทยาลัยเกษตรศาสตร์ วิทยาเขตกำแพงแสน ปีการศึกษา 2551