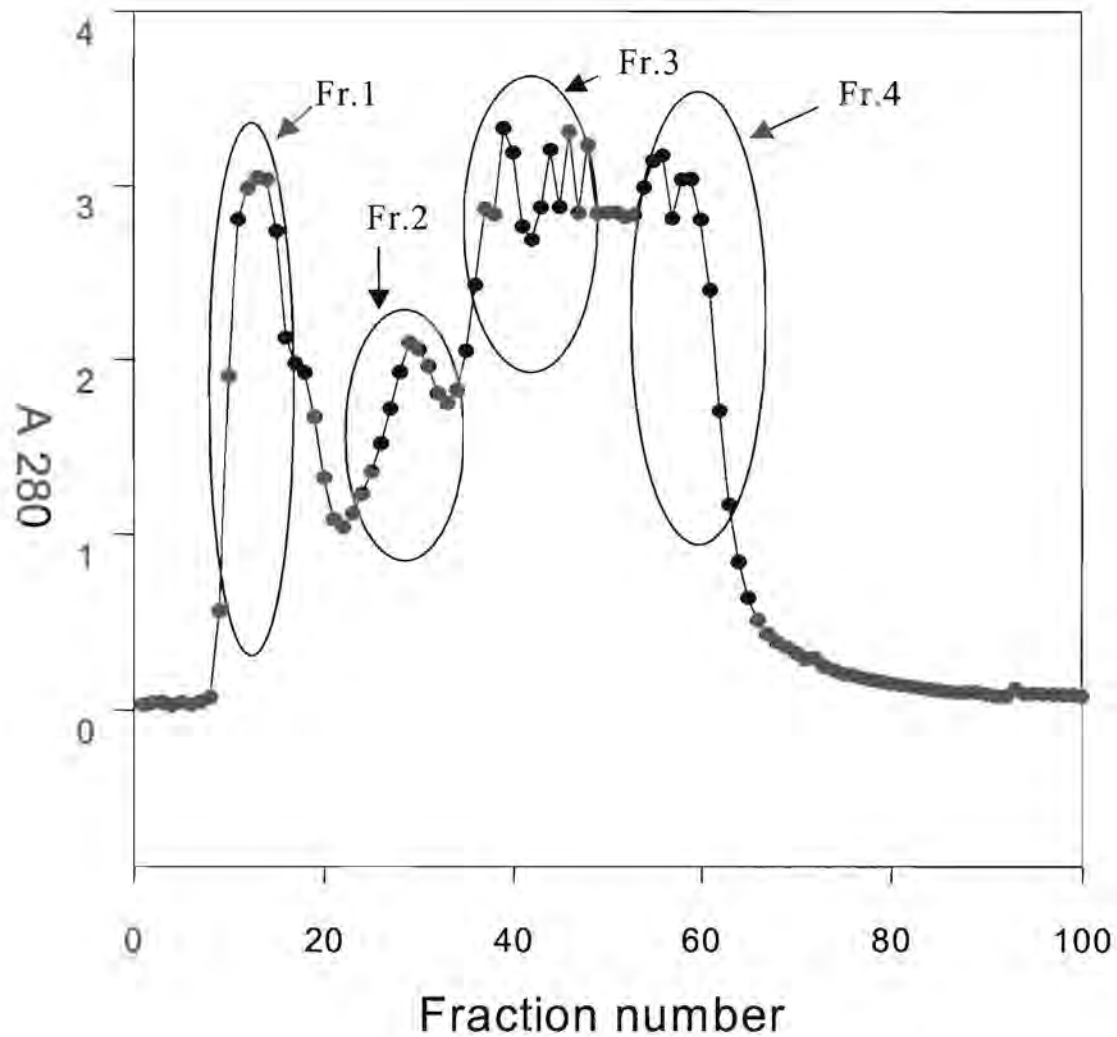




APPENDICES

Appendix I: Graph showing the elution profile of different fractions by gel-filtration chromatography.



Graph of absorbance against fraction number is shown. The fractions constituting an elution peak are circled. Four fractions represented as Fr.1 to Fr.4 were collected and assayed for caseinolytic activity by the cup-plate assay. Fractions: Fr.2, Fr.3 and Fr.4, which showed activity, were further purified by ion-exchange chromatography.

Appendix II: Multiple amino acid sequence alignment of different alkaline serine proteases.

Alignment: A:\sq.136762.pir

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      .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
                10         20         30         40         50
M22407      NSSEKEVIVV YKN-KAGKET IL---DS--- -----DADVEQ
P16396      NSSEKEVIVV YKN-KAGKET IL---DS--- -----DADVEQ
D13158      SBEKKEYLIV VEPDEVSAQS VE--ES--- -----YDVEVIH
D26542      SEEKKEYLIV VEPDEVSAQS VE--ES--- -----YDVEVIH
BAA25184     EEAKEKYLIG FKEQEVMSQF VD---QIDGD EYSISSSQVE D--VEIDLLH
M65086     EEAKEKYLIG FNEQEAVSEF VE--QVEAN DEVAILSEEE E--VEIELLH
M64743     SSTEKKYIVG FKQTSAMSS AK---KKD-- -----VIS E--KGGKVQK
AAB47045     -----
BAA93474     SESEKSYIVG FK--ASATTN SS---KKQ-- -----AVT Q--NGGKLEK
M13760     -----
D10730     -----
JW0075     DYVPNQLIVK FKQNASLSNV QS---FHKSV G-----A N--VLSKDDK
JC4802     DYVPGELIVK FKGISAQST QS---IHAQY G-----A K--SIEKSKY
AY028615    AYVQGEVIVQ FKEQVNAEEK AK---ALKEV G-----A T--AVPDNDR
AAK29176    AYVQGEVIVQ FKEQVNAEEK AK---ALKEV G-----A T--AVPDNDR
Q45670     AYVQGEVIVQ FKEQVNAEEK AK---ALKEV G-----A T--AVPDNDR

      .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
                60         70         80         90        100
M22407      QYKHLPAVAV TADQETV--- -----KELKQD
P16396      QYKHLPAVAV TADQETV--- -----KELKQD
D13158      EFETIPVCHA ELPREGEL----- -----KELKQD
D26542      EFETIPVCHA ELPREGEL----- -----KELKQD
BAA25184     EPDFIPVLSV ELDPQDV--- -----EALELD
M65086     EFETIPVLSV ELSPEDV--- -----DALELD
M64743     QFKYVNAAAA TLDEKAV--- -----KELKKD
AAB47045     -----
BAA93474     QYRLINAAQV KMSEQAA--- -----KKLEHD
M13760     -----MNGE
D10730     -----MR-K

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JW0075 LGFEVVQFSK GTVKEKI--- -----KSYKNN
 JC4802 LGFEVVKFD- GSVEKMI--- -----EKYKNN
 AY028615 VKSKFNVLKV GNVEAVV--- -----KALNHN
 AAK29176 VKSKFNVLKV GNVEAVV--- -----KALNHN
 Q45670 VKSKFNVLKV GNVEAVV--- -----KALNNN

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 110 120 130 140 150

M22407 PDILYVENNV S-----FTA ADSTDFKVL S DGTDTSDNFE QWNLEP-IQV
 P16396 PDILYVENNV S-----FTA ADSTDFKVL S DGTDTSDNFE QWNLEP-IQV
 D13158 PNVKAISENA E-----VTI SQT-----V PWAISE-IST
 D26542 PNVKAISENA E-----VTI SQT-----V PWAISE-INT
 BAA25184 PAISYIEEDA E-----VTT MQT-----V PWGINR-VQA
 M65086 PAISYIEEDA E-----VTT MAQS-----V PWGISR-VQA
 M64743 PSVAYVEEDH I-----AHE YAQS-----V PYGISQ-IKA
 AAB47045 -----AQS-----V PYGISQ-IKA
 BAA93474 PSIAYVEEDH K-----AEA YAQT-----V PYGIPQ-IKA
 M13760 IRLIPYVTNE Q-----IMD VNE-----L PEGIKV-IKA
 D10730 FRLIPYKQVD K-----VSA LSE-----V PMGVEI-VEA
 JW0075 PDVEYAEPNY Y-----VHA FWTPNDPYFN -----N QYGLQK-IQA
 JC4802 PNVEYVEPNH Y-----VHI MWTPND-LTS -----R QWGPQK-VQA
 AY028615 PLVEYAEPNY L-----FNA AWTPNDTY YQ G-----Y QYGPQN-TYT
 AAK29176 PLVEYAEPNY L-----FNA AWTPNDTY YQ G-----Y QYGPQN-TYT
 Q45670 PLVEYAEPNY L-----FNA AWTPNDTY YQ G-----Y QYGPQN-TYT

.....|.....||.....||.....||.....||.....|
 160 170 180 190 200

M22407 KQAWKAGLTG KNIKIAVIDS GISP-----HD -----
 P16396 KQAWKAGLTG KNIKIAVIDS GISP-----HD -----
 D13158 QQAHNRRGIFG NGARVAVLDT GIAS-----HP -----
 D26542 QQAHNRRGIFG NGARVAVLDT GIAS-----HP -----
 BAA25184 PIAQSRGFTG TGVRAVLDT GISN-----HA -----
 M65086 PAAHNRRGLTG SGVKVAVLDT GIST-----HP -----
 M64743 PALHSQGYTG SNVKVAVIDS GIDSS-----HP -----
 AAB47045 PALHSQGYTG SNVKVAVIDS GIDSS-----HP -----
 BAA93474 PAVHAQGYKG ANVKVAVLDT GIHAA-----HP -----
 M13760 PEMWAKGVKG KNIKVAVLDT GCDTS-----HP -----
 D10730 PAVWKASAKG AGQIIGVIDT GCQVD-----HP -----

JW0075 PQAWDSQRSD PGVKVAIIDT GVQGS-----HP -----
 JC4802 PQAWDVTRSS SSTVIAIVDT GVQTN-----HP -----
 AY028615 AYAWDVTKGS SGQEIAVIDT GVDYT-----HP -----
 AAK29176 AYAWDVTKGS SGQEIAVIDT GVDYT-----HP -----
 Q45670 DYAWDVTKGS SGQEIAVIDT GVDYT-----HP -----

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 210 220 230 240 250

M22407 --DLS--IAG GYSAVSYTSS -----YKDD NGH-----THVAG
 P16396 --DLS--IAG GYSAVSYTSS -----YKDD NGH-----THVAG
 D13158 --DLR--IAG GASFISSEPS -----YHDN NGH-----THVAG
 D26542 --DLR--IAG GASFISSEPS -----YHDN NGH-----THVAG
 BAA25184 --DLR--IRG GASFVPGEPN -----ISDG NGH-----THVAG
 M65086 --DLN--IRG GASFVPGEPS -----TQDG NGH-----THVAG
 M64743 --DLN--VRG GASFVPSETN P-----YQDG SSH-----THVAG
 AAB47045 --DLN--VRG GASFVPSETN P-----YQDG SSH-----THVAG
 BAA93474 --DLN--VAG GASFVPSEPN A-----TQDF QSH-----THVAG
 M13760 --DLKNQIIG GKNFSDDDGG KEDA--ISDY NGH-----THVAG
 D10730 --DLAERIIG GVNLTDDYGG VETN--FSDN NGH-----THVAG
 JW0075 --DLASKVIY GHDYVDNDNT -----SDDG NGH-----THCAG
 JC4802 --DLQKIVQ GYDFVDNDSN -----PQDG NGH-----THCAG
 AY028615 --DLDGKVIK GYDFVDNDYD -----PMDL NNH-----THVAG
 AAK29176 --DLDGKVIK GYDFVDNDYD -----PMDL NNH-----THVAG
 Q45670 --DLDGKVIK GYDFVDNDYD -----PMDL NNH-----THVAG

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 260 270 280 290 300

M22407 IIGAK-HN-- GYGIDGIAPE AQIYAVKALD QN----GSGD LQSLQIDW
 P16396 IIGAK-HN-- GYGIDGIAPE AQIYAVKALD QN----GSGD LQSLQIDW
 D13158 TIAAL-NN-- SIGVLGVAPN AELYAVKVLG AS----GSGS VSSIAQGLEW
 D26542 TIAAL-NN-- SIGVLGVAPN AELYAVKVLG AS----GSGS VSSIAQGLEW
 BAA25184 TIAAL-NN-- SIGVLGVAPN VDLYGKVLG AS----GSGS ISGIAQGLQW
 M65086 TIAAL-NN-- SIGVLGVAPN AELYAVKVLG AS----GSGS VSSIAQGLEW
 M64743 TIAAL-NN-- SIGVLGVSPS ASLYAVKVLG ST----GSGQ YSWIINGIEW
 AAB47045 TIAAL-NN-- SIGVLGVSPS ASLYAVKVLG ST----GSGQ YSWIINGIEW
 BAA93474 TIAAL-DN-- TIGVLGVAPS ASLYAVKVLG RY----GDGQ YSWIISGIEW
 M13760 TIAAN-DS-- NNGIAGVAPE ASLLIVKVLG GEN---GSGQ YEWIINGINY
 D10730 TVAAA-ET-- GSGVGVAPK ADLFIKALS GD----GSGE MGWIAKAIRY

JW0075 ITGALTNN-- SVGIAGVAPQ TSIYAVRVLN NQ----GSG- TDAVAQGIRE
 JC4802 IAAAVTNN-- GTGIAGMAPN ASIMPVRVLN NS----GSGT MAAVANGIAY
 AY028615 IAAAETNN-- ATGIAGMAPN TRILAVRALD RN----GSGT LSDIADAIY
 AAK29176 IAAAETNN-- ATGIAGMAPN TRILAVRALD RN----GSGT LSDIADAIY
 Q45670 IAAAETNN-- ATGIAGMAPN TRILAVRALD RN----GSGT LSDIADAIY

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 310 320 330 340 350

M22407 SIANR----- -MDIVNMSLG TTSDSKILHD AVNKAYEQGV LLVAASGN DG
 P16396 SIANR----- -MDIVNMSLG TTSDSKILHD AVNKAYEQGV LLVAASGN DG
 D13158 AINNN----- -MHIINMSLG STSGSSTLEL AVNRANNAGI LLVGAAGNTG
 D26542 AINNN----- -MHIINMSLG STSGSSTLEL AVNRANNAGI LLVGAAGNTG
 BAA25184 AANNG----- -MHIANMSLG SSAGSATMEQ AVNQATASGV LVVAASGN SG
 M65086 AGNNG----- -MHVANLSLG SPSPSATLEQ AVNSATSRGV LVVAASGN SG
 M64743 AISNN----- -MDVINMSLG GPSGSTALKT VVDKAVSSGI VVAAAAGNEG
 AAB47045 AISNN----- -MDVINMSLG GPTGSTALKT VVDKAVSSGI VVAAAAGNEG
 BAA93474 AVANN----- -MDVINMSLG GPNGSTALKK AVDTANNRGV VVAAAAGNSG
 M13760 AVEQK----- -VDIISMSLG GPSDVPELEE AVKNAVKNGV LVVCAAGNEG
 D10730 AVDWRGPKGE QMRIITMSLG GPTDSEELHD AVKYAVSNNV SVVCAAGNEG
 JW0075 AADSG----- -AKVISLSLG APNGGTALQQ AVQYAWNKG S VIVAAAAGNAG
 JC4802 AAQNG----- -ADVISLSLG GTSGSSALQS AVQQAWNSGA VVAAAAGNSS
 AY028615 AADSG----- -AEVINLSLG CDCHTTTLEN AVNYAWNKG S VVAAAAGNNG
 AAK29176 AADSG----- -AEVINLSLG CDCHTTTLEN AVNYAWNKG S VVAAAAGNNG
 Q45670 AADSG----- -AEVINLSLG CDCHTTTLEN AVNYAWNKG S VVAAAAGNNG

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 360 370 380 390 400

M22407 NGK----PVN YPAAYSSVVA VSATNEKNQL ASFSTTGD-- --EVEFSAPG
 P16396 NGK----PVN YPAAYSSVVA VSATNEKNQL ASFSTTGD-- --EVEFSAPG
 D13158 RQG----VN YPARYSGVMA VAAVDQNGQR ASFSTYGP-- --EVEFSAPG
 D26542 RQG----VN YPARYSGVMA VAAVDQNGQR ASFSTYGP-- --EVEFSAPG
 BAA25184 AGN----VG FPARYANAMA VGATDQNNNR ASFSQYGA-- --GLDIVAPG
 M65086 AGS----IS YPARYANAMA VGATDQNNNR ASFSQYGA-- --GLDIVAPG
 M64743 SSGS-SSTVG YPAKYPSTIA VGAVNSSNQR ASFSSAGS-- --ELDVMAPG
 AAB47045 SSGS-TSTVG YPAKYPSTIA VGAVNSSNQR ASFSSAGS-- --ELDVMAPG
 BAA93474 STGS-TSTVG YPAKYDSTIA VANVNSNNVR NSSSSAGP-- --ELDV SAPG
 M13760 DGDERTTEELS YPAAYNEVIA VGSVSVAREL SEFSNANK-- --EIDL VAPG
 D10730 DGREDTNEFA YPAAYNEVIA VGAVDFDLRL SDFPNTNE-- --EIDIVAPG

AAB47045 VSIQSTLPGG IYGAYNGISM ATPHVAGAAA LILSKHP-- --IWINAQVR
 BAA93474 TSILSTVPSS GYTSYTGTSM ASPHVAGAAA LILSKYP-- --NLSTSQVR
 M13760 ENILSTLPNK KYGKLTGTSM AAPHVSGALA LIKSYEESF QRKLSESEVF
 D10730 VGIKSTYLD S GYAELSGTSM AAPHVAGALA LIINLAKDAF KRTLSETEIC
 JW0075 SNIYSTYKGS TYQSLSGTSM ATPHVAGVAV LLANQGY-- ----SNTQIR
 JC4802 SNIYSTYLN S SYASLSGTSM ATPHVAGLAA LLASQGR-- ----SNSQIR
 AY028615 VDIVSTITGN RYAYMSGTSM ASPHVAGLAA LLASQGR-- ----NNIEIR
 AAK29176 VDIVSTITGN RYAYMSGTSM ASPHVAGLAA LLS-QGR-- ----NNIEIR
 Q45670 VDIVSTITGN RYAYMSGTSM ASPHVAGLAA LLASQGR-- ----NNIEIR

....|....||....||....||....||....|



JW0075 QIIESTTDKI SGTG---TYW KNGRVNAYKA VQYAKQLQEN KAS-----
 JC4802 AAIENTADKI SGTG---TYF QHGRINAYKA VNY-----
 AY028615 QAIEQTADKI SGTG---TYF KYGRINSYNA VTY-----
 AAK29176 QAIEQTADKI SGTG---TYF KYGRINSYNA VTY-----
 Q45670 QAIEQTADKI SGTG---TYF KYGRINSYNA VTY-----

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 510 520 530 540 550

M22407 AQIDINKARE LISQLPNSDA KTALHKRLDK VQSYRNVKDA KDKVAKAEKY
 P16396 AQIDINKARE LISQLPNSDA KTALHKRLDK VQSYRNVKDA KDKVAKAEKY

APPENDIX III: Nucleotide sequence of hybridisation-positive clones from genomic DNA library of *Geobacillus* sp. PA-9

1. Blot 15 sequence, 634 nucleotides (forward)

AACCGGGCCCGTCGACTCTAGAGCTCTGCAGGCATGCGATATCCCACTGGAAGCTTCCGTTCTTTAAAT
CCGTCTACAAGAATAACAGGAAGCTGATGATATATCGCAACCTCTTCCACCGTTTCGATCGCCCGCGC
ATACGGACTGGAATGACGACATCGATTGTTCTTTGTTCAAGATTTGCGCGACGCGCTTAGCATCTTG
TTTTCCCGCTCCGATAACGGCCGGTGCCGTTTCATCAGGCGTAAAAATCGAGTGGGCGTGCCTCACCA
AATATACGTTTGTGTTTCATCTTGCCCTATTCTTTTAAACAGTCTAACGTAAAATCGACCAACTCCCGT
TGTTTCATCAGGCGGCATTCCGCATTGCCAACATAGCCGATGTGTCTTTCAAAGTGCTTGCCAAATTTG
CACAAAACGCTCTTCATCGGTTTCGACATCGATAAATGTCTTCCACACCCGCGCCATTTCATTAT
GGCAGCTCCTTGCAAAAATGTTTTCTGCCTAACAGCGGATTTCCCGACTCCATCGAAAATCCGCGCC
CCCAAACGCGATGATTTGCCGCATTCTCCCCCTCATGCCAGCCGTTTCACGAGTTTCGTAATAAAATC
CCTTCTGGCATCCC

2. Blot 1 sequence, 618 nucleotides (forward)

AATTCGGGGATCCACGCGTCTTAAGGcGGCCGCGGTACCGGGCCCGTCGACTCTAGAGCTCTGCAGG
CATGCGATATCCCATGGAAGCTTcCGTTCITTTAAATCCGTCTACAAGAATAACAGGAAGCTGATGATAT
ATCGCAcACCTCTTCCACCGTTTCGATCGCCCGCGCATACGGACTGGAATGACGACATCGATTGTTCT
TTGTTCAAGATTTGCGCGACGCGCTTAGCATCTTTGTTTTCCCGCTCGATAAcCGGCCGGTGCCGTTAAT
CAGGCGTAAAAATCGAGTGGGCGTGCCTCACAAAATATAAGcTTTGTGTTcATCTTGCCTCAcTTcTTT
TTAACAGTCTAACGTAAAATcCGACCAAcCTCCCGTTGTTTCAcTCAaGGCGGCATTCCGGCAaTTGCC
AACATAGCCGATGTGTCTTTTCAAAGTGCTTgCaATTtGCACcAAAACCGCTCTTcTCGGTTTCcGAC
ATCGATAAAcTGTCcTTCCACcACCCGCGGcCcATTTCaATTATGGCAGCTCTTgAAAAATGTTTTcTTG
cCCTAACnAGCGGGATTTTcCCgACTCCAttCgAAAAATCCGCCCCCCCCCaAACCGA

3. Blot 13 sequence, 635 nucleotides (forward)

TAACAGGAATTCGGGGATCCACGCGTCTTAAGGCGGCCGCGGTACCGGGCCCGTCGACTCTAGAGC
TCTGCAGGCATGCGATATCCATGGAAGCTTCCGTGAAGCCGCTGCCGCATGGGCTGCAGAAATTTTCC
ATACGCTTAAAAGCTGTGTTAAAAGCGAAAGGCTACAACACGGCTGTCCGGTACGAAGGCGGATTTG
CCTCCGAACCTAAAATCGAACGAAGAAGCGCTGCACACACGATCCACTTGAAGCGATCGAAAAAGCC
GGCCTACAAACCAGGCCGAACAACGTGATGCCTCGCTACTGGACGTTGCTTCGTCCGAGCTGTACACA
CAAAGAAGATGGCAAAATATCATTTGGAAGGCGAAGGCGTCGTCAAAACATCACGAAGAAATGGTTGC
TTCGGTATGAAGAGCTTGTGTCGAAATATCCCGATCATCTCGATCGAAGACGGACTTGACGAAAAATGA
CTGGGAAGGCCATAAACTGTTACTGACGCCGCTTGGCACAAAGTGCAGCTCCGTCCGGTGACCGAC
TTTGTTTTGTAACGAACCACCAAAAAACTGGCCCCGAAGGCATTGAAAAAAGGCGTCCGGCAACCTC
GAATTTTAAATTAAGTGAACCCAAA

4. **Blot 3 sequence, 640 nucleotides (forward)**

TTTTTATAACACGAATTCCTCGGGGATCCACGCGTCTTAAGGCGGCGCGGTACCGGGCCCGCTCGACTC
TAGAGCTCTGCACGGCATGCGATATCCCATGGAAGCTTCGTTCTTTAAATCCGTCTACAAGAATAACA
GGAAGCTGATGATATATCGCAACCTCTTCCACCGTTTCGATCGCCCGCGCATAACGGACTGGAAATGAC
GACTCGATTGTTCTTTGTTCAAGATTGCGCGACGCGCTTAGCATCTTGTTTTCCCGCTCCGATAAC
GGCCGGTGCCGTTTCATCAGGCGTAAAAATCGAGTGGGCGTGCCTCACCAAATATCGTTTGTGTTTCATCT
TGCTCATTCTTTTTAACCAGTCTAACGTAAAATCGACCAACCTCCCGTTGTTTCATCAGGCGGCATT
CGCATTGCCCAACATAGCCGATGTGTCTTTTCCAAAGTGCTTGCCAAATTTGCACAAAACCGCTCTTCA
TCCGGTTTCCGACAATCGATAAATGTCCTTCCACACCCCGCCGGCATTTCATTATGGCAGCCTCCTT
GCCAAAAATGTTTTCTTTGCCTAACACGCGGATTTCCCCGACTCCATCGAAAATCCGCGGCCCAAA
ACGCGATGATTTGCCGCAATTC

APPENDIX IV: Nucleotide sequence of PCR clones

1. 9I1-amplicon, 679 nucleotides (forward/reverse consensus)

TCCTTGTGGAAGCAGCCTCCGTTCCAAGCGAATCCCCTCGAGCGGGGGCTCGTTCGGCGCGAGCGGAT
GGGTCCGCGCGTTTCTTTATAGCGCGCACCAGCGTCGAATCTTGCGCATCCAAAAACAAAATTTGC
GGAACAATCGCCGCTTGTTAGACAGCTCATCGAGCGCCGAAACAAAATGGTCGAAAAAATCGCGGC
TGCGCAAGTCCATCACAAGAGCGACTTtGTtCATTtGTtCCCcGATtCcTTCaCaAaGCTCcAAAAaCTTtGgCA
AtAGCGTCCgCGcAAATtGTCAaCGCAAAAAaCCGAGgTCTtCAaAaGCTTtGAaTGgCCACCGTTtCCCcG
CCCcGGACATGCcGGTGATAaTGACGAGCTGAATCGGCGGCGCTCCCCcGTTTtGCCCCATCTCCGCACC
TCcTCTCcGTCAGCTCGGGTCAaGCCGATAGGAAAGCAACTCAAATCTTCCGTATACACAAAACGTTCC
ATACAATATCCCATCGCCTTTGACCGCATACTCGACAATATGATAATCGCCCGGAGCCATCGGAAGCG
ACGGGAGCGCTTCGAGTTCATGCCAAGCGAGCGTTCTTCTTCGGATGAGGCGACGTTTTCCCCGATG
AACTCATCGGCAAAAAACGTAAACATCATCCACTCTGACACCGTCTCGCTC

2. 9I11-amplicon, 601 nucleotides (reverse)

CACTAGTGATTGCAGCAGAAAGAAGGAAGCACGAAAGGAAAAGTGATTTTGGCGACGGTGAAGGGCG
ATGTGCATGACATGGCAAAAACCTTGGTCGACATTATTTTAAGCAACAACGGCTATGAAGTGATCGACC
TTGGCATCAAAGTCGCCCCCAGCAGCTCATCGAAGCGGTGCGCGAGCATAAACCGGACATCATCGGC
CTGTCCGGCCTGCTCGTCAAATCGGCGCAACAAATGGTCGTCACCGCCAAAGACTTGCGGCAAGCCG
TGTTTCGACCCCGATTTTAGTCGGCGGCGCCGCTTGACGCGTAAAGTTTACGGAAAACAAAATCGCGC
CCGAATACGACGGCATCGTCTGTACGCGAAGGACGCCATGGATGGGCTCGCCCTTGCCAACCAAATT
CGCCAGCGTAATCGAATTTCCGCGGCCGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCAATTCGC
CCTATAGTGAGTCGTATTACAATCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCG
TTACCCAACCTAATCGCCTTGACGACATCCCCCTTTCCGACGCTGGCGTAATAGCG

3. 9I12-Amplicon, 677 nucleotides (reverse)

GGAACGTTCCGCCACCATCGATGAAATCGCCGACCATCTAGGCTTATCAGCGGAGGAGACGATTGAA
ATTTTGGCCGGCCGCGACCATACCAGCCTGTTTCGATCGACGCCCCCGTGAAGACAGCGAAAAGGA
CGGAACGACCATCGGAGAATTTATCGCTGATCAGACAAATGAGGTTGAAGCGCTGATCGAACGTTTGG
ATTTGCAGCAGGCGATCGACAAGCTGAGCGAGCAGGAACGGCTCGTCATTGACGCCGTTTTCCGCCG
GGAGAAACGCAGCGCTCGCTCGCCGAACGGCTCGGCGTCTCAAAATGACGATCAGCCGCATCCAAA
AGCGAGCGATCGACAAACTGAAACGGCAGCTTGCCGCCATCCGTCCTGATCTTACACCGTCAAGCC
AAACGAAGGAAGAAAGAGGGATCATGCTGTTTGGCGAAGAAAAGACGGCGGCTGCGCGTTGCTCCGC
ATTCGAACCATCGCTCGCCGAACCAAAAACGGCGCCGCCGAGTGCGGACAGGCACTAACGGCGGGCG
AGCAGCAGCAATGTCTGATCATCTTTTGTTCGTATCGGTGATATGCCCGAATTTGCTCATATAGCTCG
TGAACGATTTGCGCAGCGGGCTGATCAAGATTGACCGGGCGAGCATCGAAGCAAGAACGGAAAACC
G

4. 9I13-Amplicon, 808 nucleotides (forward)

TCGACTNCTATAGGGCGAATTGGGCCNCGACGTCGCATGCTCCCAGCCGCGCATGGCTTGGCCcGCGGG
AATTCGATTGCAGCAGAAAGAAGGAAGCACCGTCTTCCGGGGGAAGAGGCGTTTCGTTGTATGATA
CGTACGGCTTCCCCTCGAGCTGACGGAAGAGTACGCCGCCGAGGCAGGAATGACGGTCGATCACGC
CGGTTTTGAGCGCGAGATGGAGCGCCAGCGCGAACGGGGCCCGCGCCGCTCGCCAAGACGTCGATTCC
ATGCAAGTGCAAGGCGGCGTGTCTCGCGATTTGAAAGACGAAAGCCGGTTTGTTCGGCTACGATGAGCT
TGTTGCCTCGTCAGCGTCTCGCCATCGTTAAAGACGGACGGCTTGTTCGAGGAAGTGAAAGCCGGTG
AAGAGGCGCAAAATCATCGTCGACGTCACGCCGTTTTACGCCGAAAGCGGCGGTCAAGTCGCCGACCA

AGGCGTATTTGAAAGCGAGACCGGGAGAGCGGTTCGTCAAAGATGTGCAAAAAGCGCCGAACGGCCAG
CACCTTCACTCGATTGTCGTCGAGCGCGCGCGGCGGCAAAAAAGGAGCCCGCTATACGGCGCGCGTTGA
TGAGGCGAAGCGGGCGCGCATCGTGAAAAACCATACGGCGACCCATTTGCTTCATCAAGCGTAAAA
GACGTGCTCGGCCGCCATGTCACcAAGCGGGGTCGCTCGTCGCTCCGGATCGGCTGCGCTTTGACTTCA
CCCATTTGGCCAAGTGAAGCCGGACGAGCTCGAGCGCATCGAGGGGATCGTCATGACAATTTGG

5. Consensus sequence of PRC amplicon 9II4 (ca. 1.2 kb in size)

AAGCAGCACGATTGATGATTGGGAAGCGGTGCATGAGGAATATTATTTATTTCCCATCCGATGAAGCGG
AAGAAAACCACCGCGACGATTGGCTAAAATTCAACAACCTTTAAATCGGACGTGGAAGATTTCTTTCCG
AACTACACTGGCATTGTGGGTGAGGATTGTACGTCAATGACCAACTTCAGAAGCTGACGATCAACAT
AACGATGCCATTTTACGGCAAGGCGGAAGTGATTGGCTCACCCAATATGTGACCGGTTTGGTGATGG
AAAAATTTCCGGATTACATCACCGTCAACGTCTACATCTCTTCAGCCGGCCAACCCGAAAGCCTCATC
GTGCGCCAAGCGCAAGCAGATGAGCCGTTTGTGCATATTTATCAATAAGTTAGCAGGCCACAACCGTG
GGGCAGCATGAGGGTGTCCCAAAGGACCGGGATGCCCTCTCTCAACGCTATAATATAGACTAACC
TCGCCTCCATACTGCTGTGTCTTTCTTGAGGGGAGATCGTCTTTTGGGTTCATCCCATGCTTTGTTGGT
AGGAACCATTGCCAAGCGAAGCACcGTCCTGCTCTGACTTGCATCAGCGATGGgATGGTTTGTtGATAG
AACCGGTTGGAAAAGGTGGTGA AAAACCGCTGTTTGCCTTgATCGGTGATGGAACGCGTGAACATAG
AGGCTGATGCAGCAAGCTTTTtCTACTTGAGAAaCGATCCTAaGAaGTGGTGGCGGAGTAAATCACACC
CCTCCTAGAGGGTTGGTGA AAAACCGTTGTTTCTTTGAGCAATGGGGGAGCGTTTGAAGACGATCC
CGATGCGACAAGGCTTTTCTATTTGAGAAACAGGCTTGATAAGCGACTTGCTCCCTTAAATCACCGGC
CTCCTAGAGGGTTGGTGACAAACGGCTGCCAAGAGCAAATCTGCGGCATTTCCGCAAAAAAGAAAGGC
TGATTTACCCCGCTTTTCTAACGGAGAAGCAGATGGAATCGCAGGATGTTGTACGAAATCACCGCTC
CTCTAGTGAAGAATCGGCACAGGGGCTCGGAGCGTTTTTCCCGCTGCGGCATTGTGCGCATTTACG
GCGGCGCGCTCGCTGTTTACGCACTGACAAAAGAGGTGGGGCTGCCGCGCATATCAGGCTGGCCTTTC
ATTCACACGCCGCTGGCCAAATGGACGGTGCCATAGCGATTTCGTCAAGCCGGTGCTTCTCTTCTGCTG
TGC

6. Consensus sequence of PCR amplicon 9II5 (ca. 1.35 kb in size)

GCAGCAGAAAGAAGGAAGCAAGCTACACCGTCAACACGCCATGGACACAACCGAAATCAAAGGCA
CGCCCAAACGGGTCGTTGTATTGACAAACGAAGGAACAGAAGCCCTGCTTGCCTAGGTGTGAAACC
GGTCGGCGCCGTC AATCGTGGACGGGCGATCCGTGGTATGACCACATTAAGACAAAAATGGACGGCG
TCAAAGAGCTCGGGTTGGAATCGGAGCCGAACGTTGAAGCGATCGCTGCTTTAAAACCGGACTTGATC
ATCGGCAACAAAAATGCGCCATGAAAAAATTTATGAACAGTTGAAACAAATCGCTCCAACCGTTTTCGC
TGAAACGCTGCGTGGCAACTGGAAAGACAACCTTACGCTCTATGCGAAAGCGGTGAATCAAGAAGAG
AAAGGAAAACAAGTCATTGCCGAATACGATCAGCACATTGAAGACTTAAAAGCGAAACTCGGCGACA
AGCTGAAAATGAAAGTGTCCGGTCGTCGCTTCATGGCTGGTGACGTCCGCATCTACCATAAAGACTCG
TTCTCCGGCGTCATCTTGGACCAGCTCGGCTTCGCCCCTCCGGAATCGCAACGTC AACGACTTCGCGG
AACCGGCGTGACGAAGAACGCATCCGGCCATGGACGGCGACATCCTGTTCTCTTTACGTATGAACAGG
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