



भारतीय विज्ञान शिक्षा एवं अनुसंधान संस्थान मोहाली

शिक्षा मंत्रालय, भारत सरकार द्वारा स्थापित

सैक्टर 81, नॉलेज सिटी, प० ओ० मनोली, एस० ए० एस० नगर, मोहाली, पंजाब - 140306

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH MOHALI

(Estd. By Ministry of Education, Govt of India)

Sector-81, Knowledge city, PO-Manauli, SAS Nagar Mohali-140306, Punjab

PAN No. - AAAAI1781K GST No. 03AAAAI1781K2ZS

• Phone : +91-172-2240086 & 2240121 • Fax : +91-172-2240124, 2240266 • <http://www.iisermohali.ac.in> • Email: stores@iisermohali.ac.in

Cppp/Institute Website

IISERM (1411)20/21-Pur

Dated: 20th November 2020

NOTICE INVITING E-TENDER

Online tenders are invited on behalf of Director, IISER Mohali in **TWO BID SYSTEM** for the **Supply of Custom Gene Synthesis of 19 different Custom DNA Fragments** as per technical specification and details given below and BOQ list from the original manufacturer/supplier at CPPP i. e. <https://eprocure.gov.in/eprocure/app>. Tender documents may please be downloaded from the E-procurement portal website <https://eprocure.gov.in/eprocure/app> & Institute website www.iisermohali.ac.in.

-sd-

(Mukesh Kumar)

Assistant Registrar (P&S)



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E-TENDER NOTICE

Tender Ref.- IISERM(1411)20/21-Pur

Dated :- 20th November 2020

Critical Date Sections

Sr.	Description	Date	Time
1.	Tender Publishing Date and time	20 th Nov 2020	6:00pm
2.	Tender Document download start Date & Time	20 th Nov 2020	6:00pm
3.	Bid Submission start Date & Time	20 th Nov 2020	6:00pm
4.	Bid Submission End date and Time	30 th Nov 2020	Upto 11:00am
5.	Tender opening Date and Time	1 st Dec 2020	At 11:30am

Online tenders are invited on behalf of the Director, IISER Mohali in **TWO BID SYSTEM** for following item(s) from the original manufacturer/supplier at CPPP i.e. <https://eprocure.gov.in/eprocure/app>. Tender documents may please be downloaded from the E-procurement portal website <https://eprocure.gov.in/eprocure/app> & Institute website www.iisermohali.ac.in. Tender fee in shape of DD/Banker Cheque of Rs 590/- (Non-refundable) and EMD of Rs. 16,000/- should be submitted by DD /Banker Cheque/FDR/ Bank Guarantee in favour of the Registrar, IISER Mohali payable at Mohali or through Online mode in Institute Account (Canara Bank Saving Account Number 4790101001912 and IFSC Code CNRB0004790). However, scanned copy of the both tender fee and EMD should be upload on website along with technical bid part. The hard copy of the same in original to be send to the address mentioned below duly superscribing the supply/work name and reference/ tender ID on the envelope and same must reach before opening the bid and if not received within due date the bid will be rejected summarily.

The Original EMD and Tender Fee should be sent to:

Assistant Registrar (P&S)
Indian Institute of Science Education and Research Mohali
Sector-81, Knowledge City, SAS Nagar, Mohali, Punjab, India,
Pin: 140306

Non-receipt of original EMD and Tender Fee will lead to rejection of tender.

ITEM DETAILS

Sr.	Description	Qty. (in units)
1.	<u>Supply of Custom Gene Synthesis of 19 different Custom DNA Fragments</u> <u>Technical Specifications:</u> 1) As per Annexure I and 2) Sequence Summary: Annexure-II <u>NOTE:</u> 1. Custom synthesised DNA to be provided as plasmids in pUC57 or any equivalent plasmids 2. Custom synthesis should be sequence verified and sequence to be supplied 3. Time of delivery should be 6 weeks from placing of order.	1 each Total no of bases approx. 4000)

(A) IMPORTANT NOTES:-

- I. **The online updated Price BOO is in INR format. If bidder want to quote other than INR please specify the quoted currency in the technical bid/part and fill the amount in same updated BOO.**
- II. **Please bifurcate the price on shipping terms i.e. Ex-works -> FCA/FOB -> CIP/CIF in price BOO and specify the same in technical bid without price.**
- III. **If quoted in foreign currency, kindly clearly specify the terms of delivery/country of origin/bank details with swift code/weight/size/dimension of shipment.**
- IV. **The Online bids should be submitted directly by the original manufacturer/supplier. If quotation is submitted/filled by any representative/agent/dealer then they must upload a authority certificate from the principal company.**
- V. **Kindly specify the weight of the product including weight of packing for assessment of Freight charges, if quoted in foreign currency. Also mention in Technical Bid/Compliance sheet the currency in which quoted.**
- VI. **Kindly do not quote end of life model. Spares should be available minimum period of 5 years for quoted models.**
- VII. **All MSME/NSIC/Startup Units shall be considered as per provisions/rules prescribed by Govt of India.**
- VIII. **WARRANTY: MIN ONE YEAR, IF NOT SPECIFIED ABOVE.**
- IX. **Auto-extension of last date for E-Tenders has been activated by CPP Portal which has participation 2 bids or less.**

B) SUBMISSION OF TENDER

- 1) All bid/ tender documents are to be uploaded online at Central Public Procurement portal i.e. <https://eprocure.gov.in/eprocure/app> only and in the designated cover/ part on the website against tender

ID. Tenders/ bids shall be accepted only through online mode and no manual submission of the same shall be entertained except tender fee and EMD. Late tenders will not be accepted.

- 2) The online bids shall be opened at the office of the Assistant Registrar (P&S), IISER Mohali, on above given date and time. If the tender opening date happens to be on a holiday or non-working day due to any other valid reason, the tender opening process will be attended on the next working day at same time and place. IISER Mohali will not be responsible for any error like missing of schedule data while downloading by the Bidder.
- 3) The bidder shall upload the tender documents duly filled in and stamped by the authorized signatory on each and every page. Tender not submitted/uploaded in the prescribed form and as per the tender terms and conditions shall be liable for rejection.
- 4) The bidder shall upload scanned copy of the PAN Card, GST number duly signed and stamped. **Also bidders applying against ‘MSME/NSIC Certificate’ issued by appropriate Authority, should ensure that the certificate attached is relevant to the area of service/supply. For example, If the tender is for “supply & installation of Desktop” the certificate should be issued for activity/area of “Computer supply and services activities etc” otherwise bid will be REJECTED without notice.**
- 5) E-procurement system ensures locking on the scheduled date and time. The system will not accept any bid after the scheduled date and time of submission of bid.

C) INSTRUCTIONS

1. The Online bids should be submitted directly by the original manufacturer/supplier, If quotation is submitted/filled by any representative/agent/dealer then they must upload a authority certificate from the principal company for quoting the price otherwise such quotation will be rejected.
2. The quantity mentioned in this inquiry is and shall be deemed to be only approximate and will not in any manner be binding on the Institute. Before the deadline for submission of the online bid, IISER Mohali reserves the right to modify the tender document terms and conditions. Such amendment/modification will be notified on website against said tender ID.
3. The rates offered should be FOR Chandigarh/Mohali in case of firms situated outside Chandigarh/Mohali, and free delivery at the Institute premises in case of local firms. Supplier from outside India should mention the Ex-works/FOB/FCA/CIF/CIP price clearly. Conditional tenders will be summarily rejected.
4. In case of Ex-godown terms the amount of packaging forwarding freight etc. should clearly be indicated by percentage or lump sum amount. Institute has policy not to make any advance payments towards any purchase, Letter of credit can be opened if required.
5. THE INSTITUTE IS EXEMPTED FROM CUSTOM DUTY under notification no- TU/V/RG/- CDE(1062)/201 CUSTOM DT.30.08.2016.
6. Tax: This Institute is not exempted from the payment of GST. The current rate (i.e. percentage of GST should be clearly indicated included or excluded) wherever chargeable. Please also provide/upload the copy of PAN card, GST number duly self-attested.
7. Concessional GST is applicable for all the items purchased for Research labs vide Ministry of Finance, notification no. 45/22017 dated 14.11.2017 and 47/2017 dated 14.11.2017.
8. Bidder/s quoting in currency other than **Indian Rupee (INR)** should explicitly mention the currency in which tender quoted wherever applicable in Technical Bid along the tender documents.
9. The delivery period should be specifically stated. Earlier delivery will be preferred.
10. The firms are requested to provide/upload detailed description and specifications together with the detailed drawings, printed leaflets and literature of the article quoted. The name of the

manufactures and country of manufacture should also invariably be stated. In the absence of these particulars, the quotation is liable for rejection.

11. Validity of offer: 90 days. The warranty period after satisfactory installation should be mentioned and firm should replace all manufacturing defect parts/ whole item under warranty without any extra cost including clearance, freight, taxes. Security deposit/ Bank Performance Guarantee @ 10 % of the value of supply order as per norms may be sought from the firms.
12. The right to reject all or any of the quotation and to split up the requirements for itemized L-1 or relax any or all the above conditions without assigning any reason is reserved by the IISER Mohali. For any corrigendum and addendum please be checked the website <https://eprocure.gov.in/eprocure/app> and <http://www.iisermohali.ac.in>
13. Disputes, if any, shall be subject to jurisdiction in the court of Mohali only.

-sd-
(Mukesh Kumar)
Assistant Registrar (P&S)

ANNEXURE-I

SEQUENCE A (No. of Bases = 3287)

CCCggggcctcttcgctattacgccagctggcgaaggggggatgtgctgcaaggcgattaagttgggtaacgccaggggtttccag
tcacgacgttgtaaaacgacggccagtgaattgcatgcgctccatagtccttccgTAATACGACTCACTATAGATTAA
AGGTTTATACCTTCCCAGGTAACAAACCAACCACTTTTCGATCTCTTGTAGATCT
GTTCTCTAAACGAACTTTAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGT
GCACTCACGCAGTATAATTAATAACTAATTACTGTCGTTGACAGGACACGAGTAA
CTCGTCTATCTTCTGCAGGCTGCTTACGGTTTCGTCCGTGTTGCAGCCGATCATC
AGCACATCTAGGTTTTGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGT
CCCTGGTTTCAACGAGAAAACACACGTCCAACCTCAGTTTGCCTGTTTTACAGGTT
CGCGACGTGCTCGTACGTGGCTTTGGAGACTCCGTGGAGGAG
GTCTTATCAGAGGCACGTCAACATCTTAAAGATGGCACTTGTGGCTTAGTAGAA
GTTGAAAAAGGCGTTTTGCCTCAACTTGAACAGCCCTATGTGTTTCATCAA
CGTTCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGCA
GAACTCGAAGGCATTACGTACGGTCGTAGTGGTGAGACACTTGGTGTCCTTGTC
CCTCATGTGGGCGAAATACCAGTGGCTTACCGCAAGGTTCTTCTTCGTAAGAAC
GGTAATAAAGGAGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTTGAC
TTAGGCGACGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAACCTGGAAC
ACTAAACATAGCAGTGGTGTTACCCGTGAACCTCATGCGTGAGCTTAAACGGAGGG
GCATACACTCGCTATGTCGATAACAACCTTCTGTGGCCCTGATGGCTACCCTCTTG
AGTGCATTAAAGACCTTCTAGCACGTGCTGGTAAAGCTTCATGCACTTTGTCCGA
ACAACCTGGACTTTATTGACACTAAGAGGGGTGTATACTGCTGCCGTGAACATGA
GCATGAAATTGCTTGGTACACGGAACGTTCTGAAAAGAGCTATGAATTGCAGAC
ACCTTTTGAAATTAAATTGGCAAAGAAATTTGACACCTTCAATGGGGAATGTCCA
AATTTTGTATTTCCCTTAAATTCCATAATCAAGACTATTCAACCAAGGGTTGAAA
AGAAAAAGCTTGATGGCTTTATGGGTAGAATTCGATCTGTCTATCCAGTTGCGTC
ACCAAATGAATGCAACCAAATGTGCCCTTCAACTCTCATGAAGTGTGATCATTGT
GGTGAAACTTCATGGCAGACGGGCGATTTTGTAAAGCCACTTGCGAATTTTGT
GGCACTGAGAATTTGACTAAAGAAGGTGCCACTACTTGTGGTTACTTACCCCAA
ATGCTGTTGTTAAATTTATTGTCCAGCATGTCACAATTCAGAAGTAGGACCTGA
GCATAGTCTTGCCGAATACCATAATGAATCTGGCTTGAAAACCATTCTTCGTAAG
GGTGGTCGCACTATTGCCTTTGGAGGCTGTGTGTTCTTATGTTGGTTGCCATA
ACAAGTGTGCCTATTGGGTTCCACGTGCTAGCGCTAACATAGGTTGTAACCATAC
AGGTGTTGTTGGAGAAGGTTCCGAAGGTCTTAATGACAACCTTCTTGAAATACTC
CAAAAAGAGAAAGTCAACATCAATATTGTTGGTGACTTTAAACTTAATGAAGAGA
TCGCCATTATTTGGCATCTTTTCTGCTTCCACAAGTGCTTTTGTGGAAACTGT
GAAAGGTTTGGATTATAAAGCATTCAAACAAATTGTTGAATCCTGTGGTAATTTT
AAAGTTACAAAAGGAAAAGCTAAAAAAGGTGCCTGGAATATTGGTGAACAGAAA
TCAATACTGAGTCCTCTTTATGCATTTGCATCAGAGGCTGCTCGTGTTGTACGAT
CAATTTTCTCCCGCACTCTTGAAACTGCTCAAAATTCTGTGCGTGTTTTACAGAA
GGCCGCTATAACAATACTAGATGGAATTTACAGTATTCCTGAGACTCATTGAT
GCTATGATGTTACATCTGATTTGGCTACTAACAATCTAGTTGTAATGGCCTACA
TTACAGGTGGTGTGTTGAGTTGACTTCGCAGTGGCTAACTAACATCTTTGGCAC
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GGTGTAGAGTTTCTTAGAGACGGTTGGGAAATTGTTAAATTTATCTCAACCTGTG
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GTGTTTCAGACATTCTTTAAGCTTGTAATAAATTTTGGCTTTGTGTGCTGACTC
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ACGCACTCAAAGGGATTGTACAGAAAGTGTGTTAAATCCAGAGAAGAACTGGC
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TTCCACAGAAAGTGTTAACAGAGGAAGTTGTCTTGAAAACCTGGTGATTTACAACC
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TGTATTAACGGGCTTATGTTGCTCGAAATCAAAGACACAGAAAAGTACTGTGCCC
TTGCACCTAATATGATGGTAACAACAATACCTTCACACTCAAAGGCGGTGCACC

AACAAAGGTTACTTTTGGTGATGACACTGTGATAGAAGTGCAAGGTTACAAGAG
TGTGAATATCACTTTTGAAGTTGATGAAAGGATTGATAAAGTACTTAATGAGAAG
TGCTCTGCCTATACAGTTGAAGTCGGTACAGAAGTAAATGAGTTCGCCTGTGTTG
TGGCAGATGCTGTCATAAAAACTTTGCAACCAGTATCTGAATTACTTACACCACT
GGGCATTGATTTAGATGAGTGGAGTATGGCTACATACTACTTATTTGATGAGTCT
GGTGAGTTTAAATTGGCTTCACATATGTATTGTTCTTTTACCCTCCAGATGAGGA
TGAAGAAGAAGGTGATTGTGAAGAAGAAGAGTTTGAGCCATCAACTCAATATGAGTA
TGGTACTGAAGATGATTACCAAGGTAAACCTTTGCCCGG

Sequence B (Flanking EcoRV sites for cloning) (No. of Bases = 3126)

GATATCTGGCTTCACATATGTATTGTTCTTTTACCCTCCAGATGAGGATGAAGA
AGAAGGTGATTGTGAAGAAGAAGAGTTTGAGCCATCAACTCAATATGAGTATGG
TACTGAAGATGATTACCAAGGTAAACCTTTGGAATTTGGTGCCACTTCTGCTGCT
CTTCAACCTGAAGAAGAGCAAGAAGAAGATTGGTTAGATGATGATAGTCAACAA
ACTGTTGGTCAACAAGACGGCAGTGAGGACAATCAGACAACCTACTATTCAAACA
ATTGTTGAGGTTCAACCTCAATTAGAGATGGAACCTTACACCAGTTGTTTCAGACTA
TTGAAGTGAATAGTTTTAGTGGTTATTTAAACTTACTGACAATGTATACATTAA
AAATGCAGACATTGTGGAAGAAGCTAAAAAGGTAAACCAACAGTGGTTGTTAA
TGCAGCCAATGTTTACCTTAAACATGGAGGAGGTGTTGCAGGAGCCTTAAATAA
GGCTACTAACAATGCCATGCAAGTTGAATCTGATGATTACATAGCTACTAATGGA
CCACTTAAAGTGGGTGGTAGTTGTGTTTTAAGCGGACACAATCTTGCTAAACACT
GTCTTCATGTTGTCGGCCCAAATGTTAACAAGGTGAAGACATTCAACTTCTTAA
GAGTGCTTATGAAAATTTAATCAGCACGAAGTTCTACTTGCACCATTATTATCA
GCTGGTATTTTTGGTGCTGACCTATACATTCTTTAAGAGTTTGTGTAGATACTG
TTCGCACAAATGTCTACTTAGCTGTCTTTGATAAAAATCTCTATGACAACTTGT
TTCAAGCTTTTTGGAAATGAAGAGTGAAAAGCAAGTTGAACAAAAGATCGCTGA
GATTCCTAAAGAGGAAGTTAAGCCATTTATAACTGAAAGTAAACCTTCAGTTGAA
CAGAGAAAACAAGATGATAAGAAAATCAAAGCTTGTGTTGAAGAAGTTACAACA
ACTCTGGAAGAACTAAGTTCCTCACAGAAAACCTTGTTACTTTATATTGACATTA
ATGGCAATCTTCATCCAGATTCTGCCACTCTTGTTAGTGACATTGACATCACTTT
CTTAAAGAAAGATGCTCCATATATAGTGGGTGATGTTGTTCAAGAGGGTGTTTTA
ACTGCTGTGGTTATACCTACTAAAAAGGCTGGTGGCACTACTGAAATGCTAGCG
AAAGCTTTGAGAAAAGTGCCAACAGACAATTATATAACCACTTACCCGGGTCAG
GGTTTAAATGGTTACACTGTAGAGGAGGCAAAGACAGTGCTTAAAAAGTGTA
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GAACTGTTTCTTGGAATTTGCGAGAAATGCTTGCACATGCAGAAGAAACACGCA
AATTAATGCCTGTCTGTGTGGAACTAAAGCCATAGTTTCAACTATACAGCGTAA
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AGAAGCTGCTCGGTATATGAGATCTCTCAAAGTGCCAGCTACAGTTTCTGTTTCT
TCACCTGATGCTGTTACAGCGTATAATGGTTATCTTACTTCTTCTTAAACAC
CTGAAGAACATTTTATTGAAACCATCTCACTTGCTGGTTCCTATAAAGATTGGTC
CTATTCTGGACAATCTACACAACCTAGGTATAGAATTTCTTAAGAGAGGTGATAAA
AGTGTATATTACACTAGTAATCCTACCACATTCCACCTAGATGGTGAAGTTATCA
CCTTTGACAATCTTAAGACACTTCTTTCTTTGAGAGAAGTGAGGACTATTAAGGT
GTTTACAACAGTAGACAACATTAACCTCCACACGCAAGTTGTGGACATGTCAATG
ACATATGGACAACAGTTTGGTCCAACCTATTTGGATGGAGCTGATGTTACTAAAA
TAAACCTCATAATTCACATGAAGGTAAACATTTTATGTTTTACCTAATGATGA
CACTCTACGTGTTGAGGCTTTTGAGTACTACCACACAACCTGATCCTAGTTTTCTG
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ATGGTTTAACTTCTATTAAATGGGCAGATAACAACCTGTTATCTTGCCACTGCATT
GTTAACTCCAACAAATAGAGTTGAAGTTTAAATCCACCTGCTCTACAAGATGCT
TATTACAGAGCAAGGGCTGGTGAAGCTGCTAACTTTTGTGCACTTATCTTAGCCT

ACTGTAATAAGACAGTAGGTGAGTTAGGTGATGTTAGAGAAACAATGAGTTACT
TGTTTCAACATGCCAATTTAGATTCTTGCAAAAGAGTCTTGAACGTGGTGTGTAA
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GGTAAACAAGCTACAAAATATCTAGTACAACAGGAGTCACCTTTTGTATGATGT
C
AGCACCACCTGCTCAGTATGAACTTAAGCATGGTACATTTACTTGTGCTAGTGAG
TACACTGGTAATTACCAGTGTGGTCACTATAAACATATAACTTCTAAAGAACTT
TGTATTGCATAGACGGTGTCTTTACTTACAAAGTCCTCAGAATACAAAGGTCTTAT
TACGGATGTTTTCTACAAAGAAAACAGTTACACAACAACCATAAAACCAGTTACT
TATAAATTGGATGGTGTGTTGTTTGTACAGAAATTGACCCTAAGTTGGACAATTATT
ATAAGAAAGACAATTCTTATTTTACAGAGCAACCAATTG
ATCTTGTACCAAACCAACCATATCCAAACGCAAGCTTCGATAATTTTAAAGTTTGT
ATGTGATAATATCAAATTTGCTGATGATTTAAACCAGTTAACTGGTTATAAGAAA
CCTGCTTCAAGAG GATATC

Sequence C (Flanking EcoRV sites for Cloning) (No. of Bases = 2835)

GATATCTTGTACCAAACCAACCATATCCAAACGCAAGCTTCGATAATTTTAAAGTT
TGATGTGATAATATCAAATTTGCTGATGATTTAAACCAGTTAACTGGTTATAAG
AAACCTGCTTCAAGAGAGCTTAAAGTTACATTTTTCCCTGACTTAAATGGTGATG
TGGTGGCTATTGATTATAAACACTACACACCCTCTTTTAAAGAAAGGAGCTAAATT
GTTACATAAACCTATTGTTTGGCATGTTAACAATGCAACTAATAAAGCCACGTAT
AAACCAAATACCTGGTGTATACGTTGTCTTTGGAGCACAAA
ACCAGTTGAAACATCAAATTCGTTTGATGTACTGAAGTCAGAGGACGCGCAGGG
AATGGATAATCTTGCCTGCGAAGATCTAAAACCAGTCTCTGAAGAAGTAGTGGA
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GTAGGAGACATTATACTTAAACCAGCAAATAATAGTTTAAAAATTACAGAAGAGG
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TCATCTTTTAAATGGGATTTAACTGCTTTTGGCTTAGTTGCAGAGTGGTTTTTGG
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TTGTTTTTTCAGCTATTTTGCAGTACATTTTATTAGTAATTCCTTGGCTTATGTGGTT
AATAATTAATCTTGTACAAATGGCCCCGATTTTCAGCTATGGTTAGAATGTACATC
TTCTTTGCATCATTTTATTATGTATGGAAAAGTTATGTGCATGTTGTAGACGGTT
GTAATTCATCAACTTGTATGATGTGTTACAAACGTAATAGAGCAACAAGAGTCGA
ATGTACAACCTATTGTTAATGGTGTTAGAAGGTCCTTTTATGTCTATGCTAATGGA
GGTAAAGGCTTTTGCAAACTACACAATTGGAATTGTGTTAATTGTGATACATTCT
GTGCTGGTAGTACATTTATTAGTGATGAAGTTGCGAGAGACTTGTCCTACAGTT
TAAAAGACCAATAAATCCTACTGACCAGTCTTCTTACATCGTTGATAGTGTTACA
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TAAAGGTTTATTGCCTATTAATGTTATAGTTTTTGTATGGTAAATCAAATGTGAA
GAATCATCTGCAAAATCAGCGTCTGTTTACTACAGTCAGCTTATGTGTCAACCTA
TACTGTTACTAGATCAGGCATTAGTGTCTGATGTTGGTGATAGTGCGGAAGTTGC

AGTTAAAATGTTTGATGCTTACGTTAATACGTTTTTCATCAACTTTTAAACGTACCAA
TGGA AAAA ACTCAA AACACTAGTTGCAACTGCAGAAGCTGAACTTGCAAAGAATG
TGTCCTTAGACAATGTCTTATCTACTTTTATTTTCAGCAGCTCGGCAAGGGTTTGT
TGATT CAGATGTAGAAACTAAAGATGTTGTTGAATGTCTTAAATTGTCACATCAA
TCTGACATAGAAGTTACTGGCGATAGTTGTAATAACTATATGCTCACCTATAACA
AAGTTGAAAACATGACACCCCGTGACCTTGGTGCTTGTATTGACTGTAGTGCGC
GTCATATTAATGCGCAGGTAGCAAAAAGTCACAACATTGCTTTGATATGGAACGT
TAAAGATTTTCATGTCATTGTCTGAACAACTACGAAAACAAATACGTAGTGCTGCT
AAAAAGAATAACTTACCTTTTAAGTTGACATGTGCAACTACTAGACAAGTTGTTA
ATGTTGTAACAACAAAGATAGCACTTAAGGGTGGTAAAATTGTTAATAATTGGTT
GAAGCAGTTAATTAAAGTTACACTTGTGTTCTTTTGTGCTGCTATTTTCTATT
TAATAACACCTGTTTCATGTCATGTCTAAACATACTGACTTTTCAAGTGAAATCAT
AGGATACA
AGGCTATTGATGGTGGTGTCACTCGTGACATAGCATCTACAGATACTTGTTTTGC
TAACAAACATGCTGATTTTGACACATGGTTTAGCCAGCGTGGTGGTAGTTATACT
AATGACAAAGCTTGCCCATTGATTG CATATG

Sequence D (Sal I and Sma I cloning sites) (No. of Bases = 1887)

CCCGgggcctcttcgctattacgccagctggcgaaggggggatgtgctgcaaggcgattaagttgggtaacgccagggtttccc
agtcacgacgttgtaaaacgacggccagtgaattgtcgac
GTGACATAGCATCTACAGATACTTGTTTTGCTAACAACATGCTGATTTTGACAC
ATGGTTTAGCCAGCGTGGTGGTAGTTATACTAATGACAAAGCTTGCCCATTGATT
GCTG CAGTCATAACAAGAGAAGTGGGTTTTGTCGTGCCTGGTTTTGCCTGGCAGC
ATATTACGCACA ACTAATGGTGACTTTTTGCATTTCTTACCTAGAGTTTTTAGTG
CAGTTGGTAACATCTGTTACACACCATCAAACTTATAGAGTACACTGACTTTGC
AACATCAGCTTGTGTTTTGGCTGCTGAATGTACAATTTTTAAAGATGCTTCTGGT
AAGCCAGTACCATATTGTTATGATACCAATGTACTAGAAGGTTCTGTTGCTTATG
AAAGTTTACGCCCTGACACACGTTATGTGCTCATGGATGGCTCTATTATTCAATT
TCCTAACACCTACCTTGAAGGTTCTGTTAGAGTGGTAACAAC TTTTGATTCTGAG
TACTGTAGGCACGGCACTTGTGAAAGATCAGAAGCTGGTGTGTTGTGTATCTACTA
GTGGTAGATGGGTACTTAACAATGATTATTACAGATCTTTACCAGGAGTTTTCTG
TGGTGTAGATGCTGTAAATTTACTTACTAATATGTTTACACCACTAATTCAACCT
ATTGGTGCTTTGGACATATCAGCATCTATAGTAGCTGGTGGTATTGTAGCTATCG
TAGTAACATGCCTTGCC TACTATTTTATGAGGTTTAGAAGAGCTTTTGGTGAATA
CAGTCATGTAGTTGCC TTAATACTTTACTATTCCTTATGTCATTCACTGTACTCT
GTTTAACACCAGTTTACTCATTCTTACCTGGTGTGTTATTCTGTTATTTACTTGTAC
TTGACATTTTATCTTACTAATGATGTTTCTTTTTTAGCACATATTCAGTGGATGGT
TATGTT CACACCTTTAGTACCTTTCTGGATAACAATTGCTTATATCATTGTATTT
CCACAAAGCATTCTATTGGTCTTTAGTAATTACCTAAAGAGACGTGTAGTCTT
TAATGGTGTTCCTTTAGTACTTTTGAAGAAGCTGCGCTGTGCACCTTTTTGTTA
AATAAAGAAATGTATCTAAAGTTGCGTAGTGATGTGCTATTACCTCTTACGCAAT
ATAATAGATACTTAGCTCTTTATAATAAGTACAAGTATTTTAGTGAGCAATGGA
TACA ACTAGCTACAGAGAAGCTGCTTGTTGTCATCTCGCAAAGGCTCTCAATGAC
TTCAGTAACTCAGGTTCTGATGTTCTTTACCAACCACCACAAACCTCTATCACCT
CAGCTGTTTTGCAGAGTGGTTTTAGAAAAATGGCATTCCCATCTGGTAAAGTTGA
GGGTTGTATGGTACAAGTAACTTGTGGTACA ACTACACTTAACGGTCTTTGGCTT
GATGACGTAGTTTACTGTCCAAGACATGTGATCTGCACCTCTGAAGACATGCTTA
ACCCTAATTATGAAGATTTACTCATTCGTAAGTCTAATCATAATTTCTTGGTACA
GGCTGGTAATGTTCAACTCAGGGTTATTGGACATTCTATGCAAAATTGTGTACTT
AAGCTTAAGGTTGATACAGCCAATCCTAAGACACCTAAGTATAAGTTTGTTCGCA
TTCAACCAGGACAGACTTTTTTCAGTGTTAGCTTGTTACAATGGTTCACCATCTGG
TGTTTACCAATGTGCTATGAGGCCCAATTTCACTATTAAGGGTTCATTCCCGGG

Sequence E (flanking SmaI cloning sites) (No. of Bases = 626)

CCCGG

GGACAGACTTTTTCAGTGTTAGCTTGTTACAATGGTTCACCATCTGGTGTTTACC
AATGTGCTATGA
GGCCCAATTTCACTATTAAGGGTTCATTCCTTAATGGTTCATGTGGTAGTGTTGG
TTTAAACATAGATTATGACTGTGTCTCTTTTTGTTACATGCACCATATGGAATTAC
CAACTGGAGTTCATGCTGGCACAGACTTAGAAGGTAACTTTTATGGACCTTTTGT
TGACAGGCAAACAGCACAAAGCAGCTGGTACGGACACAACCTATTACAGTTAATGT
TTAGCTTGGTTGTACGCTGCTGTTATAAATGGAGACAGGTGGTTTCTCAATCGA
TTTACCACAACCTCTTAATGACTTTAACCTTGTGGCTATGAAGTACAATTATGAAC
CTCTAACACAAGACCATGTTGACATACTAGGACCTCTTTCTGCTCAAACCTGGAAT
TGCCGTTTTAGATATGTGTGCTTCATTAAAAGAATTACTGCAAAATGGTATGAAT
GGACGTACCATATTGGGTAGTGCTTTATTAGAAGATGAATTTACACCTTTTGATG
TTGTTAGACAATGCTCAGG TGTTACTTTCCAAAGTGCAGTGAAAAGAACAATC
AAGGGTACACACCACTGGTTGTT CCCGGG

SEQUENCE F (SmaI cloning sites) (No. of Bases = 635)

CCCGGG AGATGAATTTACACCTTTTGATGTTGTTAGACAATGCTCAGG
TGTTACTTTCCAAAGTGCAGTGAAAAGAACAATC
AAGGGTACACACCACTGGTTGTTACTCACAATTTGACTTCACTTTTAGTTTTAG
TCCAGAGTACTCAATGGTCTTTGTTCTTTTTTTGTATGAAAATGCCTTTTTACCT
TTTGCTATGGGTATTATTGCTATGTCTGCTTTTGCAATGATGTTTGTCAAACATA
AGCATGCATTTCTCTGTTTGTGTTTGTACCTTCTCTTGCCACTGTAGCTTATTTT
AATATGGTCTATATGCCTGCTAGTTGGGTGATGCGTATTATGACATGGTTGGATA
TGGTTGATACTAGTTTGTCTGGTTTTAAGCTAAAAGACTGTGTTATGTATGCATC
AGCTGTAGTGTTACTAATCCTTATGACAGCAAGAACTGTGTATGATGATGGTGCT
AGGAGAGTGTGGACACTTATGAATGTCTTGACACTCGTTTATAAAGTTTATTATG
GTAATGCTTTAGATCAAGCCATTTCCATGTGGGCTCTTATAATCTCTGTTACTTC
TAACTACTCAGGTGTAGTTACAACCTGTCATGTTTTTGGCCAGAGGTATTG
CCCGGG

SEQUENCE G (SmaI cloning sites) (No. of Bases = 626)

CCCGGGAAGCCATTTCCATGTGGGCTCTTATAATCTCTGTTACTTCTAACTACTC
AGGTGTAGTTA
CAACTGTCATGTTTTTGGCCAGAGGTATTGTTTTTATGTGTGTTGAGTATTGCCC
TATTTTCTTCATAACTGGTAATACACTTCAGTGTATAATGCTAGTTTATTGTTTCT
TAGGCTATTTTTGTACTTGTACTTTGGCCTCTTTTGTGTTACTCAACCGCTACTTT
AGACTGACTCTTGGTGTTTATGATTACTTAGTTTCTACACAGGAGTTTAGATATA
TGAATTCACAGGGACTACTCCCACCCAAGAATAGCATAGATGCCTTCAAACCTCAA
CATTAAATTGTTGGGTGTTGGTGGCAAACCTTGTATCAAAGTAGCCACTGTACAG
TCTAAAATGTCAGATGTAAAGTGCACATCAGTAGTCTTACTCTCAGTTTTGCAAC
AACTCAGAGTAGAATCATCATCTAAATTGTGGGCTCAATGTGTCCAGTTACACAA
TGACATTCTCTTAGg
ctttagt gagggttaat tccgagcttg gcgtaatcat ggcatagctgtttcctgtg tgaaattgtt atccgctcac aattccacac
aacataggag CCCGGG

Fragment 6_SEQUENCE H (SmaI cloning sites) (No. of Bases = 2763)

CCCGGGAGATGTAAAGTGCACATCAGTAGTCTTACTCTCAGTTTTGCAACAACCTC
AGAGTAGAATCATCATCTAAATTGTGGGCTCAATGTGTCCAGTTACACAATGACA
TTCTCTTAGCTAAAGATACTACTGAAGCCTTTGAAAAAATGGTTTCACTACTTTC
TGTTTTGCTTTCCATGCAGGGTGCTGTAGACATAAACAAGCTTTGTGAAGAAATG
CTGGACAACAGGGCAACCTTACAAGCTATAGCCTCAGAGTTTAGTTCCCTTCCAT

CATATGCAGCTTTTGCTACTGCTCAAGAAGCTTATGAGCAGGCTGTTGCTAATGG
TGATTCTGAAGTTGTTCTTAAAAAGTTGAAGAAGTCTTTGAATGTGGCTAAATCT
GAATTTGACCGTGATGCAGCCATGCAACGTAAGTTGGAAAAGATGGCTGATCAA
GCTATGACCCAAATGTATAAACAGGCTAGATCTGAGGACAAGAGGGGCAAAAGTT
ACTAGTGCTATGCAGACAATGCTTTTCACTATGCTTAGAAAGTTGGATAATGATG
CACTCAACAACATTATCAACAATGCAAGAGATGGTTGTGTTCCCTTGAACATAAT
ACCTCTTACAACAGCAGCCAACTAATGGTTGTCATACCAGACTATAACACATAT
AAAAATACGTGTGATGGTACAACATTTACTTATGCATCAGCATTGTGGGAAATCC
AACAGGTTGTAGATGCAGATAGTAAAATTGTTCAACTTAGTGAAATTAGTATGGA
CAATTCACCTAATTTAGCATGGCCTCTTATTGTAACAGCTTTAAGGGCCAATTCT
GCTGTCAAATTACAGAATAATGAGCTTAGTCCTGTTGCACTACGACAGATGTCTT
GTGCTGCCGGTACTACACAACTGCTTGCACTGATGACAATGCGTTAGCTTACTA
CAACACAACAAAGGGAGGTAGGTTTGTACTTGCACTGTTATCCGATTTACAGGAT
TTGAAATGGGCTAGATTCCCTAAGAGTGATGGAAGTGGTACTATCTATACAGAAC
TGGAACCACCTTGTAGGTTTGTACAGACACACCTAAAGGTCCTAAAGTGAAGTA
TTTATACTTTATTAAAGGATTAAACAACCTAAATAGAGGTATGGTACTTGGTAGT
TTAGCTGCCACAGTACGTCTACAAGCTGGTAATGCAACAGAAGTGCCTGCCAAT
TCAACTGTATTATCTTTCTGTGCTTTTGTGCTAGATGCTGCTAAAGCTTACAAAG
ATTATCTAGCTAGTGGGGGACAACCAATCACTAATTGTGTTAAGATGTTGTGTAC
ACACACTGGTACTGGTCAGGCAATAACAGTTACACCGGAAGCCAATATGGATCA
AGAATCCTTTGGTGGTGCATCGTGTTGTCTGTACTGCCGTTGCCACATAGATCAT
CCAAATCCTAAAGGATTTTGTGACTTAAAAGGTAAGTATGTACAAATACCTACAA
CTTGTGCTAATGACCCTGTGGGTTTTACACTTAAAAACACAGTCTGTACCGTCTG
CGGTATGTGGAAAGGTTATGGCTGTAGTTGTGATCAACTCCGCGAACCCATGCT
TCAGTCAGCTGATGCACAATCGTTTTTAAACGGGTTTGCGGTGTAAGTGCAGCC
CGTCTTACACCGTGCGGCACAGGCACTAGTACTGATGTCGTATACAGGGCTTTT
GACATCTACAATGATAAAGTAGCTGGTTTTGCTAAATTCCTAAAACTAATTGTT
GTCGCTTCCAAGAAAAGGACGAAGATGACAATTTAATTGATTCTTACTTTGTAGT
TAAGAGACACACTTTCTCTAACTACCAACATGAAGAAACAATTTATAATTTACTT
AAGGATTGTCCAGCTGTTGCTAAACATGACTTCTTTAAGTTTAGAATAGACGGTG
ACATGGTACCACATATATCACGTCAACGTCTTACTAAATACACAATGGCAGACCT
CGTCTATGCTTTAAGGCATTTTGATGAAGGTAATTGTGACACATTAAAAGAAATA
CTTGTACATACAATTGTTGTGATGATGATTATTTCAATAAAAAGGACTGGTATG
ATTTTGTAGAAAACCCAGATATATTACGCGTATACGCCAACTTAGGTGAACGTGT
ACGCCAAGCTTTGTTAAAAACAGTACAATTCTGTGATGCCATGCGAAATGCTGGT
ATTGTTGGTGTACTGACATTAGATAATCAAGATCTCAATGGTAACTGGTATGATT
TCGGTGATTTCATACAAACCACGCCAGGTAGTGAGGTTCTGTTGTAGATTCTTA
TTATTCATTGTTAATGCCTATATTAACCTTGACCAGGGCTTTAACTGCAGAGTCA
CATGTTGACACTGACTTAACAAAGCCTTACATTAAGTGGGATTTGTTAAATATG
ACTTCACGGAAGAGAGGTTAAAACTCTTTGACCGTTATTTTAAATATTGGGATCA
GACATACCACCCAAATTGTGTTA
ACTGTTTGGATGACAGATGCATTCTGCATTGTGCAAACCTTTAATGTTTTATTCTC
TACAGTGTTCCCACTTACAAGTTTTGGACCAGTACTGAGAAAAATATTTGTTGAT
GGTGTTCATTTGTAGTTTCAACTGGATACCACTTCAGAGAGCTAGGTGTTGTAC
ATAATCAGGATGTAACTTACATAGCTCTAGACTTAGTTTTAAGGAATTACTTGT
GTATGCTGCTGACCCTGCTATGCACGCTGCTTCTGGTAATCTATTACCCGGG

SEQUENCE I (SmaI Cloning site) (No. of Bases = 1254)

CCCGgggcctcttcgtattacgccagctggcgaaggggggatgtgctgcaaggcgattaagttgggtaacgccagggtttccc
agtcacgacgttgtaaaacgacggccagtgaattc
TTCAACTGGATACCACTTCAGAGAGCTAGGTGTTGTACATAATCAGGATGTAAAC
TTACATAGCTCTAGACTTAGTTTTAAGGAATTACTTGTGTATGCTGCTGACCCTG
CTATGCACGCTGCTTCTGGTAATCTATTACTAGATAAACGCACTACGTGCTTTTC

AGTAGCTGCACTTACTAACAATGTTGCTTTTCAAACGTGCAAAACCCGGTAATTTT
AACAAAGACTTCTATGACTTTGCTGTGTCTAAGGGTTTCTTTAAGGAAGGAAGTT
CTGTTGAATTAACAACTTCTTCTTTGCTCAGGATGGTAATGCTGCTATCAGCGA
TTATGACTACTATCGTTATAATCTACCAACAATGTGTGATATCAGACAACTACTA
TTTGTAGTTGAAGTTGTTGATAAGTACTTTGATTGTTACGATGGTGGCTGTATTA
ATGCTAACCAAGTCATCGTCAACAACCTAGACAAATCAGCTGGTTTTCCATTTAA
TAAATGGGGTAAGGCTAGACTTTATTATGATTCAATGAGTTATGAGGATCAAGAT
GCACTTTTTCGCATATACAAAACGTAATGTCATCCCTACTATAACTCAAATGAATC
TTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTAT
CTGTAGTACTATGACCAATAGACAGTTTCATCAAAAATTATTGAAATCAATAGCC
GCCACTAGAGGAGCTACTGTAGTAATTGGAACAAGCAAATTCTATGGTGGTTGG
CACAACATGTTAAAAACTGTTTATAGTGATGTAGAAAACCCCTCACCTTATGGGTT
GGGATTATCCTAAATGTGATAGAGCCATGCCTAACATGCTTAGAATTATGGCCTC
ACTTGTTCTTGCTCGCAAACATACAACGTGTTGTAGCTTGTACACCGTTTCTAT
AGATTAGCTAATGAGTGTGCTCAAGTATTGAGTGAAATGGTCATGT CCCGGG

SEQUENCE J (SmaI cloning sites) (No. of Bases = 711)

CCCGGGAGAATTATGGCCTCACTTGTTCTTGCTCGCAAACATACAACGTGTTGTA
GCTTGTACACCGTTTCTATAGATTAGCTAATGAGT
GTGCTCAAGTATTGAGTGAAATGGTCATGTGTGGCGGTTCACTATATGTTAAACC
AGGTGGAACCTCATCAGGAGATGCCACAACCTGCTTATGCTAATAGTGTTTTAAC
ATTTGTCAAGCTGTCACGGCCAATGTTAATGCACTTTTATCTACTGATGGTAACA
AAATTGCCGATAAGTATGTCCGCAATTTACAACACAGACTTTATGAGTGTCTCTA
TAGAAATAGAGATGTTGACACAGACTTTGTGAATGAGTTTTACGCATATTTGCGT
AAACATTTCTCAATGATGATACTCTCTGACGATGCTGTTGTGTGTTTCAATAGCA
CTTATGCATCTCAAGGTCTAGTGGCTAGCATAAAGAACTTTAAGTCAGTTCTTTA
TTATCAAAACAATGTTTTTATGTCTGAAGCAAAATGTTGGACTGAGACTGACCTT
ACTAAAGGACCTCATGAATTTTGCTCTCAACATACAATGCTAGTTAAACAGGGTG
ATGATTATGTGTACCTTCCTTACCCAGATCCATCAAGAATCCTAGGGGCGCGCTG
TTTTGTAGATGATATCGTAAAAACAGATGGTACA
CTTATGATTGAACGGTTCGTGTCTTTAGCT CCCGGG

SEQUENCE K (No. of Bases = 1870)

CCCGGGATCCATCAAGAATCCTAGGGGCGGCTGTTTTGTAGATGATATCGTAA
AAACAGATGGTACACTTATGATTGAACGGTTCGTGTCTTTAGCTATAGATGCTTA
CCCACTTACTAAACATCCTAATCAGGAGTATGCTGATGTCTTTCATTTGTACTTA
CAATACATAAGAAAGCTACATGATGAGTTAACAGGACACATGTTAGACATGTATT
CTGTTATGCTTACTAATGATA
ACACTTCAAGGTATTGGGAACCTGAGTTTTTATGAGGCTATGTACACACCGCATA
AGTCTTACAGGCTGTTGGGGCTTGTGTTCTTTGCAATTCACAGACTTCATTAAGA
TGTGGTGCTTGCATACGTAGACCATTCTTATGTTGTAAATGCTGTTACGACCATG
TCATATCAACATCACATAAATTAGTCTTGTCTGTTAATCCGTATGTTTGCAATGCT
CCAGGTTGTGATGTCACAGATGTGACTCAACTTTACTTAGGAGGTATGAGCTATT
ATTGTAAATCACATAAACCACCCATTAGTTTTCCATTGTGTGCTAATGGACAAGT
TTTTGGTTTATATAAAAATACATGTGTTGGTAGCGATAATGTTACTGACTTTAAT
GCAATTGCAACATGTGACTGGACAAATGCTGGTGATTACATTTTAGCTAACACCT
GTACTGAAAGACTCAAGCTTTTTGCAAGCAAAACGCTCAAAGCTACTGAGGAGA
CATTTAACTGTCTTATGGTATTGCTACTGTACGTGAAGTGCTGTCTGACAGAGA
ATTACATCTTTCATGGGAAGTTGGTAAACCTAGACCACCACTTAACCGAAATTAT
GTCTTTACTGGTTATCGTGTAATAAAACAGTAAAGTACAAATAGGAGAGTACA
CCTTTGAAAAAGGTGACTATGGTGATGCTGTTGTTTACCGAGGTACAACAACCTTA
CAAATTAAATGTTGGTGATTATTTTGTGCTGACATCACATACAGTAATGCCATTA
AGTGCACCTACACTAGTGCCACAAGAGCACTATGTTAGAATTACTGGCTTATACC

CAACACTCAATATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAAGGT
TGGTATGCAAAAGTATTCTACACTCCAGGGACCACCTGGTACTGGTAAGAGTCA
TTTTGCTATTGGCCTAGCTCTCTACTACCCTTCTGCTCGCATAGTGTATACAGCT
TGCTCTCATGCCGCTGTTGATGCACTATGTGAGAAGGCATTAAAAATATTTGCCTA
TAGATAAATGTAGTAGAATTATACCTGCACGTGCTCGTGTAGAGTGTTTTGATAA
ATTCAAAGTGAATTCAACATTAGAACAGTATGTCTTTTGTACTGTAAATGCATTG
CCTGAGACGACAGCAGATATAGTTGTCTTTGATGAAATTTCAATGGCCACAAATT
ATGATTTGAGTGTTGTCAATGCCAGATTACGTGCTAAGCACTATGTGTACATTGG
CGACCCTGCTCAATTACCTGCACCACGCACATTGCTAACTAAGGGGCACACTAGA
ACCAGAATATTTCAATTCAGTGTGTAGACTTATGAAAACCTATAGGTCCAGACATG
TTCCTCGGAACCTTGTCGGCGTTGTCCTGCTGAAATTGTTGACACTGTGAGTGCTT
TGGTTTATGATAATAAGCTTAAAGCACATAAAGACAAATCAGCTCAATGCTTTAA
AATGTTTTATAAGGGTGTTATCACGCATGATGTTTCATCTGCAAgctttagt gagggttaat
tccgagcttg gcgtaatcat ggtcatagctgtttctgtg tgaattgtt atccgctcac aattccacac aacataggag
CCCCGGG

SEQUENCE L (SmaI Cloning sites) (No. of Bases = 2795)

CCCCGGGCTGCTGAAATTGTTGACACTGTGAGTGCTTTGGTTTATGATAATAAGCT
TAAAGCACATAAAGACAAATCAGCTCAATGCTTTAAAATGTTTTATAAGGGTGTT
ATCACGCATGATGTTTCATCTGCAATTAACAGGCCACAAATAGGCGTGGTAAGA
GAATTCCTTACACGTAACCCTGCTTGGAGAAAAGCTGTCTTTATTTACCTTATA
ATTCACAGAATGCTGTAGCCTCAAAGATTTTGGGACTACCAACTCAAACCTGTTGA
TTCATCACAGGGCTCAGAATATGACTATGTCATATTCACTCAAACCACTGAAACA
GCTCACTCTTGTAATGTAAACAGATTTAATGTTGCTATTACCAGAGCAAAAGTAG
GCATACTTTGCATAATGTCTGATAGAGACCTTTATGACAAGTTGCAATTTACAAG
TCTTGAAATTCCACGTAGGAATGTGGCAACTTTACAAGCTGAAAATGTAAACAGGA
CTCTTTAAAGATTGTAGTAAGGTAATCACTGGGTTACATCCTACACAGGCACCTA
CACACCTCAGTGTTGACACTAAATTCAAAACCTGAAGGTTTATGTGTTGACATACC
TGGCATACTAAGGACATGACCTATAGAAGACTCATCTCTATGATGGGTTTTAAA
ATGAATTATCAAGTTAATGGTTACCCTAACATGTTTATCACCCGCGAAGAAGCTA
TAAGACATGTACGTGCATGGATTGGCTTCGATGTGCGAGGGGTGTCATGCTACTA
GAGAAGCTGTTGGTACCAATTTACCTTTACAGCTAGGTTTTTCTACAGGTGTTAA
CCTAGTTGCTGTACCTACAGGTTATGTTGATACACCTAATAATACAGATTTTTTCC
AGAGTTAGTGCTAAACCACCGCCTGGAGATCAATTTAAACACCTCATACCACTTA
TGTAACAAAGGACTTCCTTGGAATGTAGTGCGTATAAAGATTGTACAAATGTTAAG
TGACACACTTAAAAATCTCTCTGACAGAGTCGTATTTGTCTTATGGGCACATGGC
TTTGAGTTGACATCTATGAAGTATTTTGTGAAAATAGGACCTGAGCGCACCTGTT
GTCTATGTGATAGACGTGCCACATGCTTTTCCACTGCTTCAGACACTTATGCCTG
TTGGCATCATTCTATTGGATTTGATTACGTCTATAATCCGTTTATGATTGATGTTT
AACAAATGGGGTTTTTACAGGTAACCTACAAAGCAACCATGATCTGTATTGTCAAGT
CCATGGTAATGCACATGTAGCTAGTTGTGATGCAATCATGACTAGGTGTCTAGCT
GTCCACGAGTGCTTTGTTAAGCGTGTTGACTGGACTATTGAATATCCTATAATTG
GTGATGAACTGAAGATTAATGCGGCTTGTAGAAAGGTTCAACACATGGTTGTTA
AAGCTGCATTATTAGCAGACAAATTCAGTTCTTCACGACATTGGTAACCCTAA
AGCTATTAAGTGTGTACCTCAAGCTGATGTAGAATGGAAGTTCTATGATGCACAG
CCTTGTAGTGACAAAGCTTATAAAATAGAAGAATTATTCTATTCTTATGCCACAC
ATTCTGACAAATTCACAGATGGTGTATGCCTATTTTGGAAATTGCAATGTCGATAG
ATATCCTGCTAATTCATTGTTTGTAGATTTGACACTAGAGTGCTATCTAACCTT
AACTTGCTGTTGTGATGGTGGCAGTTTGTATGTAAATAAACATGCATTCCACA
CACCAGCTTTTGATAAAAGTGCTTTTGTAAATTTAAAACAATTACCATTTTTTCTAT
TACTCTGACAGTCCATGTGAGTCTCATGGAAAACAAGTAGTGTCAGATATAGATT
ATGTACCACTAAAGTCTGCTACGTGTATAACACGTTGCAATTTAGGTGGTGCTGT
CTGTAGACATCATGCTAATGAGTACAGATTGTATCTCGATGCTTATAACATGATG
ATCTCAGCTGGCTTTAGCTTGTGGGTTTACAAACAATTTGATACTTATAACCTCT

GGAACACTTTTACAAGACTTCAGAGTTTAGAAAAATGTGGCTTTTAATGTTGTAAA
TAAGGGACACTTTGATGGACAACAGGGTGAAGTACCAGTTTCTATCATTAAATAAC
ACTGTTTACACAAAAGTTGATGGTGTGATGTAGAATTGTTTGAAAATAAAACAA
CATTACCTGTTAATGTAGCATTTGAGCTTTGGGCTAAGCGCAACATTAAACCAGT
ACCAGAGGTGAAAATACTCAATAATTTGGGTGTGGACATTGCTGCTAATACTGTG
ATCTGGGACTACAAAAGAGATGCTCCAGCACATATATCTACTATTGGTGTGTTGTT
CTATGACTGACATAGCCAAGAAACCAACTGAAACGATTTGTGCACCACTCACTGT
CTTTTTTGGATGGTAGAGTTGATGGTCAAGTAGACTTATTTAGAAATGCCCCGTAAT
GGTGTCTTATTACAGAAGGTAGTGTTAAAGGTTTACA
ACCATCTGTAGGTCCCAAACAAGCTAGTCTTAATGGAGTCACATTAATTGGAGAA
GCCGTAAAAACACAGTTCAATTATTATAAGAAAGTTGATGGTGTGTTGCCAACAAT
TACCTGAACTTACTTTACTCAGAGTAGAAATTTACAAGAATTTAAACCCAGGAG
TCAAATGGAAATTGATTTCTTAGAATTAGCTATGGATGAATTCATTGAACGGTAT
AAATTAGAAGGCTATGCCTTCGAACATATCGTTTATGGAGATTTTAGTCATAGTC
AGTTAGGTCCCGGG

Fragment 9_SEQUENCE M (No. of Bases = 3074)

CCCGGGGAATTTAAACCCAGGAGTCAAATGGAAATTGATTTCTTAGAATTAGCTA
TGGATGAATTCATTGAACGGTATAAATTAGAAGGCTATGCCTTCGAACATATCGT
TTATGGAGATTTTAGTCATAGTCAGTTAGGTGGTTTACATCTACTGATTGGACTA
GCTAAACGTTTTAAGGAATCACCTTTTGAATTAGAAGATTTTATTCCTATGGACA
GTACAGTTAAAAACTATTTTCATAACAGATGCGCAAACAGGTTTCATCTAAGTGTGT
GTGTTCTGTTATTGATTTATTACTTGATGATTTTGTGAAATAATAAAATCCCAAG
ATTTATCTGTAGTTTCTAAGGTTGTCAAAGTGACTATTGACTATACAGAAATTTT
ATTTATGCTTTGGTGTAAGATGGCCATGTAGAAACATTTTACCCAAAATTACAA
TCTAGTCAAGCGTGGCAACCGGGTGTGCTATGCCTAATCTTTACAAAATGCAAA
GAATGCTATTAGAAAAGTGTGACCTTCAAATTATGGTGATAGTGCAACATTACC
TAAAGGCATAATGATGAATGTCGCAAAATATACTCAACTGTGTCAATATTTAAAC
ACATTAACATTAGCTGTACCCTATAATATGAGAGTTATACATTTTGGTGCTGGTT
CTGATAAAGGAGTTGCACCAGGTACAGCTGTTTTAAGACAGTGGTTGCCTACGG
GTACGCTGCTTGTCGATTTCAGATCTTAATGACTTTGTCTCTGATGCAGATTCAAC
TTTGATTGGTGATTGTGCAACTGTACATACAGCTAATAAATGGGATCTCATTATT
AGTGATATGTACGACCCTAAGACTAAAAATGTTACAAAAGAAAATGACTCTAAAG
AGGGTTTTTTCATTACATTTGTGGGTTTATACAAACAAAAGCTAGCTCTTGGAGG
TTCCGTGGCTATAAAGATAACAGAACATTCTTGAATGCTGATCTTTATAAGCTC
ATGGGACACTTCGCATGGTGGACAGCCTTTGTTACTAATGTGAATGCGTCATCAT
CTGAAGCATTTTTAATTGGATGTAATTATCTTGGCAAACCACGCGAACAAATAGA
TGGTTATGTCATGCATGCAAATTACATATTTTGGAGGAATACAAATCCAATTCAG
TTGTCTTCCTATTCTTTATTTGACATGAGTAAATTTCCCCTTAAATTAAGGGGTAC
TGCTGTTATGTCTTTAAAAGAAGGTCAAATCAATGATATGATTTTATCTCTTCTTA
GTAAAGGTAGACTTATAATTAGAGAAAACAACAGAGTTGTTATTTCTAGTGATGT
TCTTGTTAACAACATAACGAACAATGTTTGTGTTTTCTTGTTTTATTGCCACTAGTC
TCTAGTCAGTGTGTTAATCTTACAACCAGAACTCAATTACCCCTGCATACACTA
ATTCTTTCACACGTGGTGTGTTATTACCCTGACAAAGTTTTTCAGATCCTCAGTTTTA
CATTCAACTCAGGACTTGTTCTTACCTTTCTTTTCCAATGTTACTTGGTTCCATGC
TATACATGTCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCA
TTTAATGATGGTGTGTTATTTTGCTTCCACTGAGAAGTCTAACATAATAAGAGGCT
GGATTTTTTGGTACTACTTTAGATTTCGAAGACCCAGTCCCTACTTATTGTTAATAA
CGCTACTAATGTTGTTATTAAAGTCTGTGAATTTCAATTTTGAATGATCCATTTT
TGGGTGTTTATTACCACAAAAACAACAAAAGTTGGATGGAAAGTGAGTTCAGAG
TTTATTCTAGTGCGAATAATTGCACTTTTGAATATGTCTCTCAGCCTTTTCTTATG
GACCTTGAAGGAAAACAGGGTAATTTCAAAAATCTTAGGGAATTTGTGTTAAGA
ATATTGATGGTTATTTTAAATATATTCTAAGCACACGCCTATTAATTTAGTGCGT

GATCTCCCTCAGGGTTTTTCGGCTTTAGAACCATTTGGTAGATTTGCCAATAGGTA
TTAACATCACTAGGTTTCAAACCTTTACTTGCTTTACATAGAAGTTATTTGACTCCT
GGTGATTCTTCTTCAGGTTGGACAGCTGGTGCTGCAGCTTATTATGTGGGTATC
TTCAACCTAGGACTTTTTCTATTAATAAATAATGAAAATGGAACCATACAGATGC
TGTAAGACTGTGCACTTGACCCTCTCTCAGAAACAAAGTGACGTTGAAATCCTTC
ACTGTAGAAAAAGGAATCTATCAAACCTTCTAACTTTAGAGTCCAACCAACAGAAT
CTATTGTTAGATTTTCTAATATTACAACTTGTGCCCTTTTGGTGAAGTTTTTAAC
GCCACCAGATTTGCATCTGTTTATGCTTGGAACAGGAAGAGAATCAGCAACTGT
GTTGCTGATTATTCTGTCTATATAATTCCGCATCATTTTCCACTTTTAAGTGTTA
TGGAGTGTCTCCTACTAAATTAATGATCTCTGCTTTACTAATGTCTATGCAGAT
TCATTTGTAATTAGAGGTGATGAAGTCAGACAAATCGCTCCAGG
GCAAACCTGGAAAGATTGCTGATTATAATTATAAATTACCAGATGATTTTACAGGC
TGCGTTATAGCTTGGAAATTCTAACAATCTTGATTCTAAGGTTGGTGGTAATTATA
ATTACCTGTATAGATTGTTTAGGAAGTCTAATCTCAAACCTTTTGAGAGAGATAT
TTCAACTGAAATCTATCAGGCCGGTAGCACACCTTGTAATGGTGTGGAAGGTTTT
AATTGTTACTTTTCTTTACAATCATATGGTTTCCAACCCACTAATGGTGTGTTA
CCAACCATAACAGAGTAGTAGTACTTTCTTTTGAAGTTCTACATGCACCAGCAACT
GTTTGTGGACCTAAAAAGTCTACTAATTTGGTTAAAAACAAATGTGTCAATTTCA
ACTTCAATGGTTTAACAGGCACAGGTGTTCTTACTGAGTCTAACAAAAAGTTTCT
GCCTTTCCAACAATTTGGCAGAGACATTGCTGACACTACTGATGCCCGGG

SEQUENCE N (SmaI cloning sites) (No of bases =2787)

CCCGGGAAAACAAATGTGTCAATTTCAACTTCAATGGTTTAAACAGGCACAGGTGT
TCTTACTGAGTCTAACAAAAAGTTTCTGCCTTTCCAACAATTTGGCAGAGACATT
GCTGACACTACTGATGCTGTCCGTGATCCACAGACACTTGAGATTCTTGACATTA
CACCATGTTCTTTTGGTGGTGTGAGTGTATAACACCAGGAACAAATACTTCTAA
CCAGGTTGCTGTTCTTTATCAGGGTGTTAACTGCACAGAAGTCCCTGTTGCTATT
CATGCAGATCAACTTACTCCTACTTGGCGTGTTTATTCTACAGGTTCTAATGTTT
TTCAAACACGTGCAGGCTGTTTAATAGGGGCTGAACATGTCAACAACCTCATATGA
GTGTGACATACCCATTGGTGCAGGTATATGCGCTAGTTATCAGACTCAGACTAAT
TCTCCTCGGCGGGCACGTAGTGTAGCTAGTCAATCCATCATTGCCTACACTATGT
CACTTGGTGCAGAAAATTCAGTTGCTTACTCTAATAACTCTATTGCCATACCCAC
AAATTTTACTATTAGTGTACCACAGAAATTCTACCAGTGTCTATGACCAAGACA
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TGTTGCAATATGGCAGTTTTTGTACACAATTAAACCGTGCTTTAACTGGAATAGC
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AAAACACCACCAATTAAGATTTTGGTGGTTTTAATTTTTACAAATATTACCAG
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GCTGCTAGAGACCTCATTTGTGCACAAAAGTTTAAACGGCCTTACTGTTTTGCCAC
CTTTGCTCACAGATGAAATGATTGCTCAATACACTTCTGCACTGTTAGCGGGTAC
AATCACTTCTGGTTGGACCTTTGGTGCAGGTGCTGCATTACAAATACCATTGCT
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AGAACCAAAAATTGATTGCCAACCAATTTAATAGTGCTATTGGCAAAATTCAGA
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CTCTATCTTTATGCTTTAGTCTACTTCTTGCGAGAGTATAAACTTTGTAAGAATAAT
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SEQUENCE O (No of bases =3044)

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ATAAAATTGTTGATGAGCCTGAAGAACATGTCCAAATTCACACAATCGACGGTTC
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ACTAGCGTGCCTTTGTAAGCACAAGCTGATGAGTACGAACCTTATGTACTCATTCTG
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CGTGGTATTCTTGCTAGTTACACTAGCCATCCTTACTGCGCTTCGATTGTGTGCG
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TCGTGTTAAAAATCTGAATTCTTCTAGAGTTCCTGATCTTCTGGTCTAAACGAAC
TAAATATTATATTAGTTTTTCTGTTTGGAACTTTAATTTTAGCCATGGCAGATTCC
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 GGATGAGGCTGGTTCTAAATCACCCATTCAGTACATCGATATCGGTAATTATACA
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 TTTAGATTTTCATCTAAACGAACAACTAAA
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 TCGAGTGTACAGTGAAC
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 aaaaaaaaaaaaaaaCGGCCGggccggcatgggtccagcctcctcgctggcgccggctgggcaacattccgaggggaccg
 tcccctcggaatggcgaatgggacgggcccctgcgatatcgcgacgaggatcta
 ctttagt gagggttaat tccgagcttg gcgtaatcat ggcatagctgtttcctgtg tgaaattgtt atccgctcac aattccacac
 aacataggag CCCGGG

Sequence P (5' end: XbaI, 3' end: EcoRI, Size: 2436bp)

TCTAGACAAACTCAAATCTCTATCAAGGCCGTTTCGTCTGTACATCTACAAGCACA
 CCCCATTCACAACAGTCCAAAGTCTCATAAGATGTTGGTCATTACTTCTAACTA
 TAGATTGTCTTGTACATCCATAGACTCAAGTCTCCAAACTTTTTGCTAACCCAA
 CAAGCTGAATTCAAGAGACACGGTTCAGAAACTGGTTATTCCAAACTGAAGGT
 TTGCCACCATTGTCTTTGAACTGTGCTCCAAACGACGCTTCTTACTTCGGTAACG
 TGTCCGACTTGAAGTCTGACCACTCTAACAAGTACGAAGAAAAAGACATCCAAAT
 GAGAAATTTGCGTGAAGAAATTAAGAACATGTTGTCCTCCATGGGTGACGGTAG
 ATCTTCTGTTTCCCCTTACGATACTGCTTGGGTTTTCTTCATTGAAGACACCAAT
 ACTAACATCAACGGCACTTCTAAGAGACCATTGTTCCCATCTTGCTTGCAATGGA
 TAATTGACAACCAATTGGATGACGGTCTTGGGGTGAAGAATTGGTCTTCTGTAT
 CTACGATAGATTGCTAAATACTTTGGCCTGTGTCGTTGCATTGACTTTGTGGAAC
 ACCTGTTTGCATAAGAGAAACAAGGGTGTGTCATGTTTCATCAAGGAAAACCTAAGA
 AAGTTGGAAGGTGGTGAAGTTGTAAACATGACTTCCGGTTTTGCAATTCGTCTTCC
 CATCTTTGTTGGACAAGGCTCAACAACCTTCACATTGATAACATCCCATACGATGC
 TCCCGTTTTTCAGAGATATTTACGCCAGAAGAGAAGTCAAGTTTACCAGATTCCCT
 AAGGATTTGATTTCATACAATTCCAACCATTGTCTTATTCTCCTTGGAAGGCTTAA
 GGGATTTGGACTGGCAAAGATTGTTGAAGTTACAAATGGAAGATGGTTCCTTCTT
 GACCTCTCCATCCTCTACCGCCATTGTTTTTCATGAATACCAACGATGATAAATGT
 TTCACCTTCTTGCAAAACGCTGTTCAAAAGTTCAACGGTGGTGTTCATGTTCTT
 ACCCAGCTGACATCCAAGCTAGATTATGGGCTATTGACAGATTGCAAAGATTGG
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 TGCACCAATATTTGGCTAACAACCAATCTAAGGATAAGTGGGTATTGCTAAGGA
 TATTCAGGTGAAATTAGATACGCTTTGGAGTTCCAATGGTACGCTTCATTGCCA

AGAGTTGAATCCCGTTTATACATTGATCAATACGGTGGTGCTGACGAAATCTGGA
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CGCTAAGTTGGACTACAACAGATGCCAATCCCAACACAGATTTGAATGGTTGATC
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TACCGTGACATGTCTATCAAGAAGTCCAACGAAACGAAGGAAATCATTGTTTTGA
ACAACTTGTGTCAATTCTTGCATCAATTGACTAAGGAAACTTACCAAGATTTAGG
TAAGGACATTCACCACCAATTGCACAACGTCTGGGAAGAATGGTTGGAAGAAAA
CAACACCACCTGTCAAGAAGCTGCTGTCTTATTGGTCCAAACCATCAACTTGTCT
AGTGGTCACATGACTCACGATGAAATCTTGTCCAAGTACACCAACAAAGTCTGTC
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TATTGAATTGCACATGCAAGCCTTAGTCAAGTTGGTTTTCTCTAACACTTCATCC
AACAATATTAACCAAGGAATCGAAGATACCTACTTCAAGGTTGTCAAGACTTTCT
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GTTCCAGAAGGCTTGAGAATTC

Sequence Q (Cloning sites NcoI, EcoRV) 1544 bases

CCATGGCTCTCAACGGCGCACCGTCCTCGTCGACCCTTACCGTCCCTTCGACCG
ACGAGGTCACCGCCCCGCGAGCTCAAGCTCTCGCCTTCGACCGTCGCCCTCGTCT
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TCAACGGCGGTGAGGGAGCGATGCTCCTCAACGACGAGGAGATCATCACCTCG
TCCAGAAGGGCAAGCTCGCCGCTATGCGCTCGAGAAGCTTCTCAAGGACTACG
TCCGCGCCGTCTCGATCCGCGCTGCTCTCATCTCGCGCGCCTCGGCTCGCAAAA
CCCTCGAGGCGTCCGACCTGCCGTTCTTCCACTTCGACTACTCGCGCGTCATGG
GCCAGTGCTGTGAGAACGTCGTCGGCTACATGCCCATCCCCGTCGGTATCGCGG
GACCGCTCCGAATCGACGGCAACGTCCTCCCCATCCCGATGGCTACGACCGAAG
GCGCGCTCGTCGCCTCTACCTCGCGTGGTTGCAAGGCCCTTAACGTCTCGGGCG
GCGTCACGACCGTCGTCACGCAGGACGCGATGACCCGTGGCCCGGCTCTCGACT
TCCCGAGCGTCATCATGTGCGCCGCGCCCAAGCGCTGGGTCGACTCGGACGAGG
GCAGCAACATCCTCAAGGCCGCGTTCAACTCGACTTCGAGATTCGCCAGGCTCA
AGAGCCTCAAGACTGCGATGGCTGGTCGCACGCTCTTTGTCCGCTTCGCCACCC
AGACTGGCGACGCGATGGGCATGAACATGATCTCCAAGGGCTGCGAGCGCGCTC
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GGGAAGAGTGTCGTCGCCGAGGGCATCATCCCTGGCGAGGCGGTCAAGTCGAT
CCTCAAGACGACCGTCAGCGACCTCGTCCGCTCAACATCACCAAGAACCTCAT
CGGCTCGGCGATGGCCGGCTCCGTGCGGCGCAACAACGCCACGCGTCCAACAT
CCTCACGGCCATCTACCTCGCGACCGGCCAGGACCCCGCCAGAACGTCGAGTC
GAGCAACTGCATGACGCTCATGGAGGCCATCAACGACGGAAAGGACCTCTTGAT
CACCTGCTCGATGCCGTCGATCGAGGTTGGCACCGTCGGAGGCGGCACCATCCT
CCTCCCGCAGGCCGCCATGCTGGACATGCTCGGCGTCAAAGGTCCGCACCCGAC
CTCGCCCGGCCAGAACGCGCAGCAGCTCGCTCGCGTCGTCTGCGCCGCCGTCAT
GGCCGGCGAGCTCTCGCTCATGTGCGGCCCTCGCGGCCGGCTCGCTCGTTCAAG
CCACTTGGCGCACAACCGCTCGGCACCTGCGACGCTGCCGCCAGACACCCCA
GATCGGCTCGCGCGCCGCGACGCTGTCTTGAACGGCACGCAGCGCCTCGCGCC
GTTGACGGTGACCAAGGGCAAGGACTAGGATATC

SEQUENCE R Hind III SacI (Bases 1092)

AAGCTTATGTCGCTGGACTGGTACGACAACTTTATCGACAAGGTGCAGGGCACG
CCGTCGTGGCAGCCCGCGCAGGAGCAGGTCTTGACAGAGCCGTACACCTACCTC
GCCTCGATCCCTGGCAAGGAGGTGCGCTCGGCGCTCATCGCGGCGTTCAACCAG

TGGATGGGTGTCGCAGACGTCGATCTCGAGATTGTCAAGAGAGTCGTCGGGATG
CTGCACACGGCCAGCCTGCTGATGGACGACGTCGAGGACGACTCGCACCTCCGT
CGAGGCATGCCTGTCGCACACAAGATCTACGGGATCCCCCAGACGATCAACTCG
GCCAACTATGTCTACTTTCTCGCGTTTCAAGAACTCCAGCGGATACACCCCCGGC
CGGGCATCAAGGTCTGAAGAGATGGTCACCGAGGAGCTGCTGAACCTGCATCGCG
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AGTACATCGACATGGTCAACAACAAGACGGGAGGACTGTTCCGCATCGCGATCA
AGTTGATGATGGCCGCTTCGCCTGCAGCACCACGAGATTACGTCCCGCTCGCCA
ACCTGATCGGCATCATCTTCCAGATTTCGCGACGACTACGTGAACCTGCAATCGG
TCGAGTACGCAAACAACAAGGGCTTCTGCGAAGACTTCTCCGAAGGCAAATTCT
CCTTCCCCATCGTCCACTCGATCCGCTCCGACACCTCGAACCGCCAAATCCTCAA
CATCCTCCGCGAGCGGCCCTCTTCTCCCGGTCCGAAAGAGTACGCTGTCAGCTA
CATGGAGACGCGGACGGGCTCCTTCGCGTACACGCGCGAGGTGTTGCGCAAGTT
GACGCAGCAGGCGAGGGATGAGGTTGCGCGGCTGGGAGGGAACAGAGGCGTCG
AGGCGATTCTCGACAAGCTGGTGTGAGGGAACCGCAGGCGAGGGCGACTGGC
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GGTCAAGGCGGTGACGAACGGCGTCAATGGCGTCCATGCGCACGAGCTTCCCAA
AGTCTGAGAGCTC

Sequence S Hind III SpeI (4047)

AAGCTTTAGTTTTACAGCTGACTGAAGGCGGGAAACGACAATCTGATCCAAGCT
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TCCTAGGATCCCACGGCTGCGCATCCGGATCCTCCCCGCGCTGCTGGCGCCTCG
CCCGCTCCCGCTCGTACTCCGCCATGACCGTCAACCCCTGGCAGAGCAGGCGGT
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ACTACCCGCGCCTTCACACCACCCTCACAACCTACCAACCCTCTCCTACAGAACC
CAATTGATAGTTTAAACTTACCCATGGACGACGACAAGGTAGATGATCAACTCCC
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TCCGCAGCAACAAAGGAGCGACGGAAGGGTGCGGGCGATCTTCCCGTGGCCTG
CGGTCTTCTCAGCGGATGCAGGGTTCTCGCTGCGTGTCAAGCCAGCGAGGTGAG
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ACTGCTCGCGAGTTGCATGCCGCCGGTACGTCATCGCGGGTCGATCAAGACAGT
CCGCACTTCGTATAGCATACATTATACGAAGTTATTTATTGAATTCAATTCGGCC
CGCGGCCGCGGGTTAATTCAGTACATTGACTAGT

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ANNEXURE-II

Fragment Name	Restriction site	Restriction site	size of fragment
A	Sma I	Sma I	3312
B	EcoRV	EcoRV	3126
C	EcoRV	NdeI	2835
D	Sma I	Sma I	1882
E	Sma I	Sma I	649
F	Sma I	Sma I	635
G	Sma I	Sma I	626
H	Sma I	Sma I	2763
I	Sma I	Sma I	1106
J	Sma I	Sma I	711
K	Sma I	Sma I	1871
L	Sma I	Sma I	2801
M	Sma I	Sma I	3074
N	Sma I	Sma I	2787
O	Sma I	SmaI	3044
P	XbaI	EcoRI	2436
Q	NcoI	EcoRV	1544
R	HindIII	SacI	1092
S	HindIII	SpeI	4047
TOTAL			40341