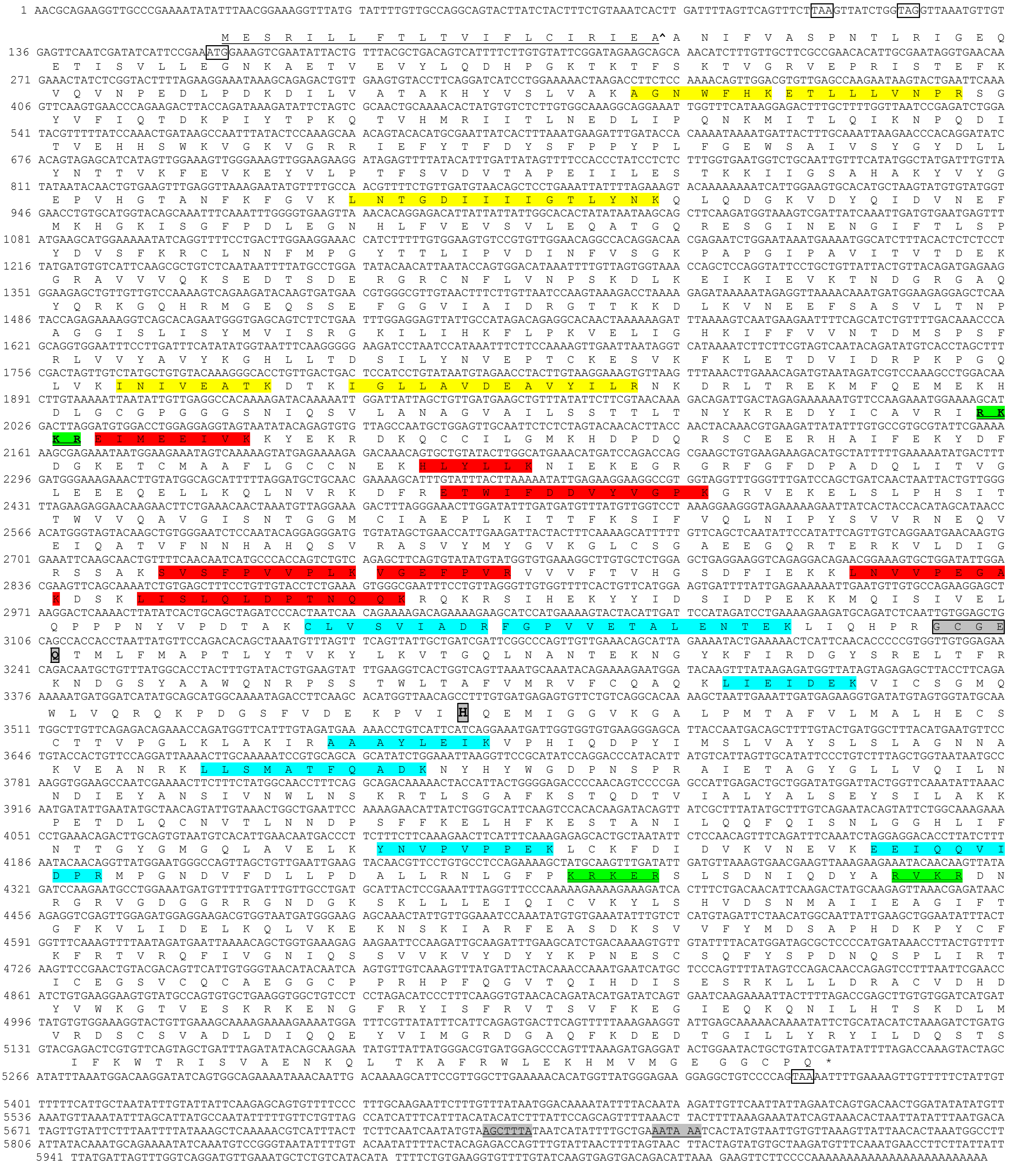
Supplementary Fig. 1. cDNA sequence and deduced amino acid sequence of CrC3. The cDNA sequence of CrC3 is shown with the translation embedded above the nucleotide sequence. The translation start and stop codons are boxed. There are two stop codons upstream and in frame with the translation start codon. The UTR functional element search was carried out in the UTRdb collections using UTRscan at http://bighost.area.ba.cnr.it/BIG/UTRScan/. The poly(A) signal, AATAAA in the 3'UTR is underlined and shaded. A Brd box (AGCTTTA at position 5734-5740 is shaded and double-underlined) in the 3'UTR and an internal ribosome entry site (IRES) in the 5'UTR (46-132) are found. The Brd Box negatively regulates gene expression, at both transcription and translation levels, but mainly represses translation. Cellular mRNAs containing IRES often encode regulatory proteins, whose expression is tightly regulated, and the current hypothesis is that IRES-mediated translation of certain mRNAs helps the cell to cope with transient stress (Vagner *et al,* 2001, *EMBO Rep* **2:** 893-898). The presence of Brd box and IRES indicates that the expression of CrC3 is tightly regulated in steady state, and may respond to an infection signal by boosting translation in a shifted mode of ribosome recruitment, instead of the usually stimulated transcription for other genes. We have indeed observed that the level of CrC3 transcript remains unchanged in response to bacteria infection. From our present analysis, we have observed that Brd box and IRES consistently occur in many other C3 sequences. The secretion leader peptide (1-21) predicted by SignalP V1.1 (Nielsen e*t al*, 1997, *Prot Engineer* **10**: 1-6) at the http://www.cbs.dtu.dk/services/SignalP, is underlined. Peptide sequences of p34, p50 and p75, identified by MS-MS (see Fig. 1 and Table 1), are highlighted in the amino acid sequence of CrC3 (p75: yellow; p34: red; p50: cyan). The thioester motif GCGEQ and conserved catalytic His are boxed and shaded grey. The predicted α/β joint process site RKKR, and potential α/γ joint process sites (KRKER, RVKR) are double-underlined and highlighted in green.



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   1 AACGCAGAAGGTTGCCCGAAAATATATTTAACGGAAAGGTTTATG TATTTTGTTGCCAGGCAGTACTTATCTACTTTCTGTAAATCACTT GATTTTAGTTCAGTTTCTTAAGTTATCTGGTAGGTTAAATGTTGT

                              M  E  S  R  I  L  L   F  T  L  T  V  I  F  L  C  I  R  I  E  A^ A   N  I  F  V  A  S  P  N  T  L  R  I  G  E  Q
 136 GAGTTCAATCGATATCATTCCGAAATGGAAAGTCGAATATTACTG TTTACGCTGACAGTCATTTTCTTGTGTATTCGGATAGAAGCAGCA AACATCTTTGTTGCTTCGCCGAACACATTGCGAATAGGTGAACAA
      E  T  I  S  V  L  L  E  G  N  K  A  E  T  V   E  V  Y  L  Q  D  H  P  G  K  T  K  T  F  S   K  T  V  G  R  V  E  P  R  I  S  T  E  F  K
 271 GAAACTATCTCGGTACTTTTAGAAGGAAATAAAGCAGAGACTGTT GAAGTGTACCTTCAGGATCATCCTGGAAAAACTAAGACCTTCTCC AAAACAGTTGGACGTGTTGAGCCAAGAATAAGTACTGAATTCAAA
      V  Q  V  N  P  E  D  L  P  D  K  D  I  L  V   A  T  A  K  H  Y  V  S  L  V  A  K  A  G  N   W  F  H  K  E  T  L  L  L  V  N  P  R  S  G
 406 GTTCAAGTGAACCCAGAAGACTTACCAGATAAAGATATTCTAGTC GCAACTGCAAAACACTATGTGTCTCTTGTGGCAAAGGCAGGAAAT TGGTTTCATAAGGAGACTTTGCTTTTGGTTAATCCGAGATCTGGA
      Y  V  F  I  Q  T  D  K  P  I  Y  T  P  K  Q   T  V  H  M  R  I  I  T  L  N  E  D  L  I  P   Q  N  K  M  I  T  L  Q  I  K  N  P  Q  D  I
 541 TACGTTTTTATCCAAACTGATAAGCCAATTTATACTCCAAAGCAA ACAGTACACATGCGAATTATCACTTTAAATGAAGATTTGATACCA CAAAATAAAATGATTACTTTGCAAATTAAGAACCCACAGGATATC
      T  V  E  H  H  S  W  K  V  G  K  V  G  R  R   I  E  F  Y  T  F  D  Y  S  F  P  P  Y  P  L   F  G  E  W  S  A  I  V  S  Y  G  Y  D  L  L
 676 ACAGTAGAGCATCATAGTTGGAAAGTTGGGAAAGTTGGAAGAAGG ATAGAGTTTTATACATTTGATTATAGTTTTCCACCCTATCCTCTC TTTGGTGAATGGTCTGCAATTGTTTCATATGGCTATGATTTGTTA
      Y  N  T  T  V  K  F  E  V  K  E  Y  V  L  P   T  F  S  V  D  V  T  A  P  E  I  I  L  E  S   T  K  K  I  I  G  S  A  H  A  K  Y  V  Y  G
 811 TATAATACAACTGTGAAGTTTGAGGTTAAAGAATATGTTTTGCCA ACGTTTTCTGTTGATGTAACAGCTCCTGAAATTATTTTAGAAAGT ACAAAAAAAATCATTGGAAGTGCACATGCTAAGTATGTGTATGGT
      E  P  V  H  G  T  A  N  F  K  F  G  V  K  L   N  T  G  D  I  I  I  I  G  T  L  Y  N  K  Q   L  Q  D  G  K  V  D  Y  Q  I  D  V  N  E  F
 946 GAACCTGTGCATGGTACAGCAAATTTCAAATTTGGGGTGAAGTTA AACACAGGAGACATTATTATTATTGGCACACTATATAATAAGCAG CTTCAAGATGGTAAAGTCGATTATCAAATTGATGTGAATGAGTTT
      M  K  H  G  K  I  S  G  F  P  D  L  E  G  N   H  L  F  V  E  V  S  V  L  E  Q  A  T  G  Q   R  E  S  G  I  N  E  N  G  I  F  T  L  S  P
1081 ATGAAGCATGGAAAAATATCAGGTTTTCCTGACTTGGAAGGAAAC CATCTTTTTGTGGAAGTGTCCGTGTTGGAACAGGCCACAGGACAA CGAGAATCTGGAATAAATGAAAATGGCATCTTTACACTCTCTCCT
      Y  D  V  S  F  K  R  C  L  N  N  F  M  P  G   Y  T  T  L  I  P  V  D  I  N  F  V  S  G  K   P  A  P  G  I  P  A  V  I  T  V  T  D  E  K
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      G  R  A  V  V  V  Q  K  S  E  D  T  S  D  E   R  G  R  C  N  F  L  V  N  P  S  K  D  L  K   E  I  K  I  E  V  K  T  N  D  G  R  G  A  Q
1351 GGAAGAGCTGTTGTTGTCCAAAAGTCAGAAGATACAAGTGATGAA CGTGGGCGTTGTAACTTTCTTGTTAATCCAAGTAAAGACCTAAAA GAGATAAAAATAGAGGTTAAAACAAATGATGGAAGAGGAGCTCAA
      Y  Q  R  K  G  Q  H  R  M  G  E  Q  S  S  E   F  G  G  V  I  A  I  D  R  G  T  T  K  K  D   L  K  V  N  E  E  F  S  A  S  V  L  T  N  P
1486 TACCAGAGAAAAGGTCAGCACAGAATGGGTGAGCAGTCTTCTGAA TTTGGAGGAGTTATTGCCATAGACAGAGGCACAACTAAAAAAGAT TTAAAAGTCAATGAAGAATTTTCAGCATCTGTTTTGACAAACCCA
      A  G  G  I  S  L  I  S  Y  M  V  I  S  R  G   K  I  L  I  H  K  F  L  P  K  V  E  L  I  G   H  K  I  F  F  V  V  N  T  D  M  S  P  S  F
1621 GCAGGTGGAATTTCCTTGATTTCATATATGGTAATTTCAAGGGGG AAGATCCTAATCCATAAATTTCTTCCAAAAGTTGAATTAATAGGT CATAAAATCTTCTTCGTAGTCAATACAGATATGTCACCTAGCTTT
      R  L  V  V  Y  A  V  Y  K  G  H  L  L  T  D   S  I  L  Y  N  V  E  P  T  C  K  E  S  V  K   F  K  L  E  T  D  V  I  D  R  P  K  P  G  Q
1756 CGACTAGTTGTCTATGCTGTGTACAAAGGGCACCTGTTGACTGAC TCCATCCTGTATAATGTAGAACCTACTTGTAAGGAAAGTGTTAAG TTTAAACTTGAAACAGATGTAATAGATCGTCCAAAGCCTGGACAA
      L  V  K  I  N  I  V  E  A  T  K  D  T  K  I   G  L  L  A  V  D  E  A  V  Y  I  L  R  N  K   D  R  L  T  R  E  K  M  F  Q  E  M  E  K  H
1891 CTTGTAAAAATTAATATTGTTGAGGCCACAAAAGATACAAAAATT GGATTATTAGCTGTTGATGAAGCTGTTTATATTCTTCGTAACAAA GACAGATTGACTAGAGAAAAAATGTTCCAAGAAATGGAAAAGCAT
      D  L  G  C  G  P  G  G  G  S  N  I  Q  S  V   L  A  N  A  G  V  A  I  L  S  S  T  T  L  T   N  Y  K  R  E  D  Y  I  C  A  V  R  I  R  K
2026 GACTTAGGATGTGGACCTGGAGGAGGTAGTAATATACAGAGTGTG TTAGCCAATGCTGGAGTTGCAATTCTCTCTAGTACAACACTTACC AACTACAAACGTGAAGATTATATTTGTGCCGTGCGTATTCGAAAA
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2161 AAGCGAGAAATAATGGAAGAAATAGTCAAAAAGTATGAGAAAAGA GACAAACAGTGCTGTATACTTGGCATGAAACATGATCCAGACCAG CGAAGCTGTGAAGAAAGACATGCTATTTTTGAAAAATATGACTTT
      D  G  K  E  T  C  M  A  A  F  L  G  C  C  N   E  K  H  L  Y  L  L  K  N  I  E  K  E  G  R   G  R  F  G  F  D  P  A  D  Q  L  I  T  V  G
2296 GATGGGAAAGAAACTTGTATGGCAGCATTTTTAGGATGCTGCAAC GAAAAGCATTTGTATTTACTTAAAAATATTGAGAAGGAAGGCCGT GGTAGGTTTGGGTTTGATCCAGCTGATCAACTAATTACTGTTGGG
      L  E  E  E  Q  E  L  L  K  Q  L  N  V  R  K   D  F  R  E  T  W  I  F  D  D  V  Y  V  G  P   K  G  R  V  E  K  E  L  S  L  P  H  S  I  T
2431 TTAGAAGAGGAACAAGAACTTCTGAAACAACTAAATGTTAGGAAA GACTTTAGGGAAACTTGGATATTTGATGATGTTTATGTTGGTCCT AAAGGAAGGGTAGAAAAAGAATTATCACTACCACATAGCATAACC
      T  W  V  V  Q  A  V  G  I  S  N  T  G  G  M   C  I  A  E  P  L  K  I  T  T  F  K  S  I  F   V  Q  L  N  I  P  Y  S  V  V  R  N  E  Q  V
2566 ACATGGGTAGTACAAGCTGTGGGAATCTCCAATACAGGAGGGATG TGTATAGCTGAACCATTGAAGATTACTACTTTCAAAAGCATTTTT GTTCAGCTCAATATTCCATATTCAGTTGTCAGGAATGAACAAGTG
      E  I  Q  A  T  V  F  N  N  H  A  H  Q  S  V   R  A  S  V  Y  M  Y  G  V  K  G  L  C  S  G   A  E  E  G  Q  R  T  E  R  K  V  L  D  I  G
2701 GAAATTCAAGCAACTGTTTTCAACAATCATGCCCACCAGTCTGTC AGAGCTTCAGTGTATATGTATGGTGTGAAAGGCTTGTGCTCTGGA GCTGAGGAAGGTCAGAGGACAGAACGGAAAGTGCTGGATATTGGA
      R  S  S  A  K  S  V  S  F  P  V  V  P  L  K   V  G  E  F  P  V  R  V  V  V  F  T  V  H  G   S  D  F  I  E  K  K  L  N  V  V  P  E  G  A
2836 CGAAGTTCAGCAAAATCTGTGAGCTTTCCTGTTGTACCTCTGAAA GTGGGCGAATTTCCTGTTAGGGTTGTGGTTTTCACTGTTCATGGA AGTGATTTTATTGAGAAAAAATTGAATGTTGTGCCAGAAGGAGCT
      K  D  S  K  L  I  S  L  Q  L  D  P  T  N  Q   Q  K  R  Q  K  R  S  I  H  E  K  Y  Y  I  D   S  I  D  P  E  K  K  M  Q  I  S  I  V  E  L
2971 AAGGACTCAAAACTTATATCACTGCAGCTAGATCCCACTAATCAA CAGAAAAGACAGAAAAGAAGCATCCATGAAAAGTACTACATTGAT TCCATAGATCCTGAAAAGAAGATGCAGATCTCAATTGTGGAGCTG
      Q  P  P  P  N  Y  V  P  D  T  A  K  C  L  V   S  V  I  A  D  R  F  G  P  V  V  E  T  A  L   E  N  T  E  K  L  I  Q  H  P  R  G  C  G  E
3106 CAGCCACCACCTAATTATGTTCCAGACACAGCTAAATGTTTAGTT TCAGTTATTGCTGATCGATTCGGCCCAGTTGTTGAAACAGCATTA GAAAATACTGAAAAACTCATTCAACACCCCCGTGGTTGTGGAGAA
      Q  T  M  L  F  M  A  P  T  L  Y  T  V  K  Y   L  K  V  T  G  Q  L  N  A  N  T  E  K  N  G   Y  K  F  I  R  D  G  Y  S  R  E  L  T  F  R
3241 CAGACAATGCTGTTTATGGCACCTACTTTGTATACTGTGAAGTAT TTGAAGGTCACTGGTCAGTTAAATGCAAATACAGAAAAGAATGGA TACAAGTTTATAAGAGATGGTTATAGTAGAGAGCTTACCTTCAGA
      K  N  D  G  S  Y  A  A  W  Q  N  R  P  S  S   T  W  L  T  A  F  V  M  R  V  F  C  Q  A  Q   K  L  I  E  I  D  E  K  V  I  C  S  G  M  Q
3376 AAAAATGATGGATCATATGCAGCATGGCAAAATAGACCTTCAAGC ACATGGTTAACAGCCTTTGTGATGAGAGTGTTCTGTCAGGCACAA AAGCTAATTGAAATTGATGAGAAGGTGATATGTAGTGGTATGCAA
      W  L  V  Q  R  Q  K  P  D  G  S  F  V  D  E   K  P  V  I  H  Q  E  M  I  G  G  V  K  G  A   L  P  M  T  A  F  V  L  M  A  L  H  E  C  S
3511 TGGCTTGTTCAGAGACAGAAACCAGATGGTTCATTTGTAGATGAA AAACCTGTCATTCATCAGGAAATGATTGGTGGTGTGAAGGGAGCA TTACCAATGACAGCTTTTGTACTGATGGCTTTACATGAATGTTCC
      C  T  T  V  P  G  L  K  L  A  K  I  R  A  A   A  Y  L  E  I  K  V  P  H  I  Q  D  P  Y  I   M  S  L  V  A  Y  S  L  S  L  A  G  N  N  A
3646 TGTACCACTGTTCCAGGATTAAAACTTGCAAAAATCCGTGCAGCA GCATATCTGGAAATTAAGGTTCCGCATATCCAGGACCCATACATT ATGTCATTAGTTGCATATTCCCTGTCTTTAGCTGGTAATAATGCC
      K  V  E  A  N  R  K  L  L  S  M  A  T  F  Q   A  D  K  N  Y  H  Y  W  G  D  P  N  S  P  R   A  I  E  T  A  G  Y  G  L  L  V  Q  I  L  N
3781 AAGGTGGAAGCCAATCGAAAACTTCTTTCTATGGCAACCTTTCAG GCAGACAAAAACTACCATTACTGGGGAGACCCCAACAGTCCCCGA GCCATTGAGACTGCTGGATATGGATTACTGGTTCAAATATTAAAC
      N  D  I  E  Y  A  N  S  I  V  N  W  L  N  S   K  R  T  L  S  G  A  F  K  S  T  Q  D  T  V   I  A  L  Y  A  L  S  E  Y  S  I  L  A  K  K
3916 AATGATATTGAATATGCTAACAGTATTGTAAACTGGCTGAATTCC AAAAGAACATTATCTGGTGCATTCAAGTCCACACAAGATACAGTT ATCGCTTTATATGCTTTGTCAGAATACAGTATTCTGGCAAAGAAA
      P  E  T  D  L  Q  C  N  V  T  L  N  N  D  P   S  F  F  K  E  L  H  F  K  E  S  T  A  N  I   L  Q  Q  F  Q  I  S  N  L  G  G  H  L  I  F
4051 CCTGAAACAGACTTGCAGTGTAATGTCACATTGAACAATGACCCT TCTTTCTTCAAAGAACTTCATTTCAAAGAGAGCACTGCTAATATT CTCCAACAGTTTCAGATTTCAAATCTAGGAGGACACCTTATCTTT
      N  T  T  G  Y  G  M  G  Q  L  A  V  E  L  K   Y  N  V  P  V  P  P  E  K  L  C  K  F  D  I   D  V  K  V  N  E  V  K  E  E  I  Q  Q  V  I
4186 AATACAACAGGTTATGGAATGGGCCAGTTAGCTGTTGAATTGAAG TACAACGTTCCTGTGCCTCCAGAAAAGCTATGCAAGTTTGATATT GATGTTAAAGTGAACGAAGTTAAAGAAGAAATACAACAAGTTATA
      D  P  R  M  P  G  N  D  V  F  D  L  L  P  D   A  L  L  R  N  L  G  F  P  K  R  K  E  R  S   L  S  D  N  I  Q  D  Y  A  R  V  K  R  D  N
4321 GATCCAAGAATGCCTGGAAATGATGTTTTTGATTTGTTGCCTGAT GCATTACTCCGAAATTTAGGTTTCCCAAAAAGAAAAGAAAGATCA CTTTCTGACAACATTCAAGACTATGCAAGAGTTAAACGAGATAAC
      R  G  R  V  G  D  G  G  R  R  G  N  D  G  K   S  K  L  L  L  E  I  Q  I  C  V  K  Y  L  S   H  V  D  S  N  M  A  I  I  E  A  G  I  F  T
4456 AGAGGTCGAGTTGGAGATGGAGGAAGACGTGGTAATGATGGGAAG AGCAAACTATTGTTGGAAATCCAAATATGTGTGAAATATTTGTCT CATGTAGATTCTAACATGGCAATTATTGAAGCTGGAATATTTACT
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4591 GGTTTCAAAGTTTTAATAGATGAATTAAAACAGCTGGTGAAAGAG AAGAATTCCAAGATTGCAAGATTTGAAGCATCTGACAAAAGTGTT GTATTTTACATGGATAGCGCTCCCCATGATAAACCTTACTGTTTT
      K  F  R  T  V  R  Q  F  I  V  G  N  I  Q  S   S  V  V  K  V  Y  D  Y  Y  K  P  N  E  S  C   S  Q  F  Y  S  P  D  N  Q  S  P  L  I  R  T
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4861 ATCTGTGAAGGAAGTGTATGCCAGTGTGCTGAAGGTGGCTGTCCT CCTAGACATCCCTTTCAAGGTGTAACACAGATACATGATATCAGT GAATCAAGAAAATTACTTTTAGACCGAGCTTGTGTGGATCATGAT
      Y  V  W  K  G  T  V  E  S  K  R  K  E  N  G   F  R  Y  I  S  F  R  V  T  S  V  F  K  E  G   I  E  Q  K  Q  N  I  L  H  T  S  K  D  L  M
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5401 TTTTTCATTGCTAATATTTGTATTATTCAAGAGCAGTGTTTTCCC TTTGCAAGAATTCTTTGTTTATAATGGACAAAATATTTTACAATA AGATTGTTCAATTATTAGAATCAGTGACAACTGGATATATATGTT
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  5941 TTATGATTAGTTTGGTCAGGATGTTGAAATGCTCTGTCATACATA TTTTCTGTGAAGGTGTTTTGTATCAAGTGAGTGACAGACATTAAA GAAGTTCTTCCCCAAAAAAAAAAAAAAAAAAAAAAAA
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Supplementary Fig. 1