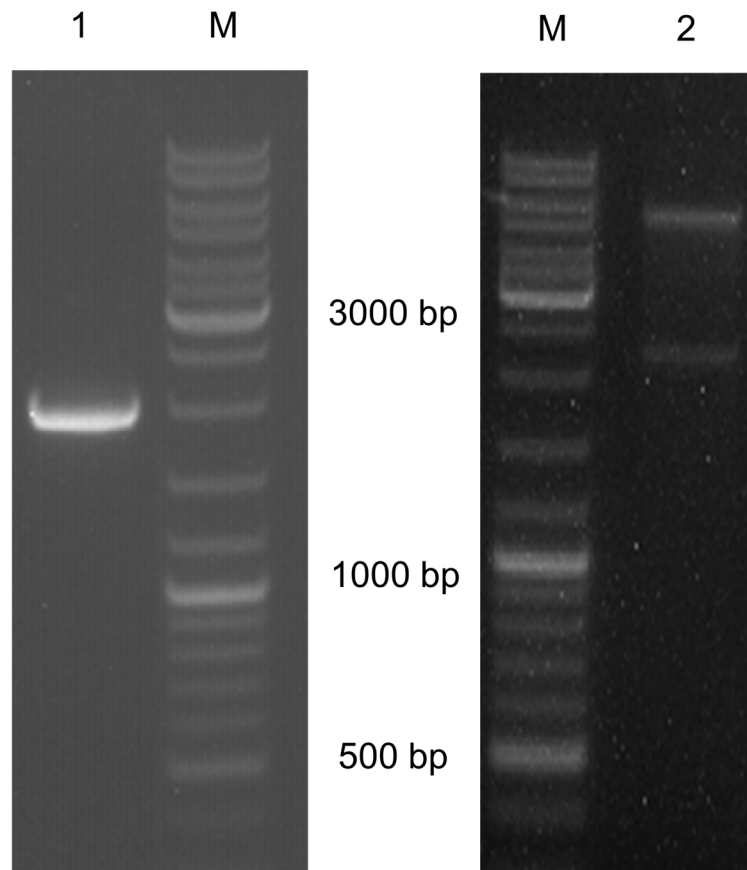(a)

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1     gataccaggacagaacccagtcgaggttgtcaatatacaggattgtggtattgaaaacctcgaaaATG
1                                                                       M

69    TTGCAAATACAGTCCGTGATGCCACATACGGGTGGCCAGGAACGTTCACAGGACTTGGATCTAATTGAG
2     L  Q  I  Q  S  V  M  P  H  T  G  G  Q  E  R  S  Q  D  L  D  L  I  E

138   GTATTATGGCGACAAGACATAGACCTGGGTGTTGGGAAGGAGGTTTTTGACATCAATCTCCGACGAGAA
25    V  L  W  R  Q  D  I  D  L  G  V  G  K  E  V  F  D  I  N  L  R  R  E

207   CTTGAGCGGGACAGAGAGATAGAACTACAGAAAAAGAGAGAAAAGCAAAAGGAACTTGAGCTACTCAGA
48    L  E  R  D  R  E  I  E  L  Q  K  K  R  E  K  Q  K  E  L  E  L  L  R

276   CTAAAGGCAGATGAAGAGAAGCGACAGCAGCAGCAATGGCTAAGCCAGAATTTCATGCAGGATGGA
71    L  K  A  D  E  E  K  R  Q  Q  Q  Q  W  L  S  Q  N  F  M  Q  D  G

345   GAAACTGGCGAATGGGTTCCCTTGAATGGCTCGGTGTCTCTCCAGTCCTCGCCCCCACAGATGCCTCCA
94    E  T  G  E  W  V  P  L  N  G  S  V  S  L  Q  S  S  P  P  Q  M  P  P

414   GATGTCCTCACCAACTCCCAGCTGCTAAACAGTGCCTTATCCTTGGAGGAGGCACTGGACATCTTGCAT
117   D  V  L  T  N  S  Q  L  L  N  S  A  L  S  L  E  E  A  L  D  I  L  H

483   GCCGAGACTGGCACATTTGTTGACCCCGGCTACACTGTGCCCGACGACAACACACAACTGCCCATGCCA
140   A  E  T  G  T  F  V  D  P  G  Y  T  V  P  D  D  N  T  Q  L  P  M  P

552   CCCCAGTCACACATCAGCCCCACAGTGCCAGCTGTGGGAGAATTTTCTGCTGGAAACAGAGAACTACCCC
163   P  Q  S  H  I  S  P  T  V  P  A  V  E  N  F  L  L  E  T  E  N  Y  P

621   ACACAGGCTGTGCAGCAGCCTCCACAACACCTCTCAGCAAATCTGAACCGACAGGAGAGTCTGGACCAG
186   T  Q  A  V  Q  Q  P  P  Q  H  L  S  A  N  L  N  R  Q  E  S  L  D  Q

690   CACTGGGACGACCTCGTCAGCCTGCTGGATCTGGCTGGAGTGAACAGTTCCCAGCTGAACATGACCAAC
209   H  W  D  D  L  V  S  L  L  D  L  A  G  V  N  S  S  Q  L  N  M  T  N

759   ATGAACCCCACACAGCTGAATATGAGCCAGTTGAATACCGCCAGTACTGGGCCACAGATGAATGTCACA
232   M  N  P  T  Q  L  N  M  S  Q  L  N  T  A  S  T  G  P  Q  M  N  V  T

828   AACATAAACACTCCATCAATGAATATCACCACATTGAACAGCATGGCATTGAACATGAGCAACGAGGCA
255   N  I  N  T  P  S  M  N  I  T  T  L  N  S  M  A  L  N  M  S  N  E  A

897   AACACTACAAGCGTTATGACTTCTCAGTCGGTACAGAGCCCCTGCATCAACAACAATGTGCTGCTGCAG
278   N  T  T  S  V  M  T  S  Q  S  V  Q  S  P  C  I  N  N  N  V  L  L  Q

996   AATGCCACTATGCCAGCTCCAGTGGCCGATGTCACAATGCCTGTTCCAGTCACCAACACAACTCAAAGC
301   N  A  T  M  P  A  P  V  A  D  V  T  M  P  V  P  V  T  N  T  T  Q  S

1035  ATGTCGCCCATCAATAGCACAGGATTCCTGCCCCCAAGCCAGGAGTTCAACTCCTCTGTGCCCAACACA
324   M  S  P  I  N  S  T  G  F  L  P  P  S  Q  E  F  N  S  S  V  P  N  T

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347   D  T  M  G  G  L  D  W  D  T  S  E  M  L  F  S  N  V  T  G  T  V  N

1173  CAGACCGAGGGTCTCGAAGACATTGATGGCATCCTGCCCAACTTCCTGCCAGAAGATGAGCTTGATCTG
370   Q  T  E  G  L  E  D  I  D  G  I  L  P  N  F  L  P  E  D  E  L  D  L

1242  GCCATCAATGAAGGACTACAGACCATGCAGATGTTGGATGAAGCCAGTAGCGATTCTGCTGTGTCGATG
393   A  I  N  E  G  L  Q  T  M  Q  M  L  D  E  A  S  S  D  S  A  V  S  M

1311  GGCAGTGCTTCTCCAATGCAGGAGTTAAGTGAGTCAAACGTCATGTCTCCATATGATGGTCTGGAGGGT
416   G  S  A  S  P  M  Q  E  L  S  E  S  N  V  M  S  P  Y  D  G  L  E  G

1380  GCAACTGGCGGCAGTGACTACGGCAGCCCTACCTACTCCAAGACTTCCAAGTATGAGCCTGATGAATAC
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1449  CATTACAGCTACTCCTGCAGCTTCGGCCACAGGGACTCCTCCCAGACAAACTATTCCACATCCTCCAAT
462   H  Y  S  Y  S  C  S  F  G  H  S  D  S  S  Q  T  N  Y  S  T  S  S  N

1518  GACACCGGATGTCAACAAGCCTCTTGGTGGCAACAACCACATCAATCACAATCATCATATCCTCTTAAG
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1587  CCCGGAGCATCTCCCAAGGAAATAAAGACAAGCATGAGGACAGACAAGCCAAAGACAAAGGGTCCCCAT
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1656  GCTCGAGATCAAAAGCGTGCCCATGAGCTGAATGTCCCCTTCACGGTTGACCAAATCATTGAGTCTCCA
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1725  GTGGAGGAATTTAACGAGATGATCACGAAGTACAAACTCACAGAGCCTCAAATACAACTCATCCGAGAT
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1794  ATCAGGAGAAGAGGAAAAAATAAAGTTGCTGCTCAGAATTGTCGGAAAAGAAAATTAGATGTTGTGGTA
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1863  ACCCTGGAGGATGAGATGGACAACCTGAAGGAGATGAAGGAACAGCTGATGAGGGAGCGGCAGCAGATT
600   T  L  E  D  E  M  D  N  L  K  E  M  K  E  Q  L  M  R  E  R  Q  Q  I

1932  GACAAGCAGACACGCGAGATGAAAGAGAAGTTCAGCCACATGTACCAGGAGATCTTCCATTCACTGCGG
623   D  K  Q  T  R  E  M  K  E  K  F  S  H  M  Y  Q  E  I  F  H  S  L  R

2001  GATGAACATGGCCGCCCATATGATCCAAATGAGTACTCTCTCCAGCAGTCCAGTGATGGCAATGTATTT
646   D  E  H  G  R  P  Y  D  P  N  E  Y  S  L  Q  Q  S  S  D  G  N  V  F

2070  CTCGTTCCCAGGAATTACAGCTCTGAAGACCAACTTGCCAATGGGAACAAGAAAAGGAAAATATCAAG
669   L  V  P  R  N  Y  S  S  E  D  Q  L  A  N  G  N  K  K  R  K  N  I  K

2139  AAAGATGATTGAagaaacagaattatatcatcattgatcatattgagtgctattgaaaggtaacccctt
692   K  D  D  *

2208  gaggtctactgtggcgttgaatttaggattcccatttgtttttcggggcttttagattcagggatgaac
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4485  gtcagactgagcttgaatgtagtattttaccttcttcaaaagaaataaaggtgaagatttttttttatata
4554  aaaaaaaaaaaaaa
```

(b)

Supplementary Figure S1. Analysis of the *Haliotis discus hannai* Nrf2 protein sequence. (a) Sequence of the full-length cDNA and deduced amino acids of HdhNrf2. The start of the ORF (ATG) is shown in bold, and a stop codon (TAA) is shown in bold and marked with an "*". The numbers on the left of the sequence give the position of the first nucleotide and amino acid on each line. The basic leucine zipper (bZIP) domain of Cap'n'Collar (CNC) transcription factor is underlined in bold. (b) The bZIP domain of Cap'n'Collar transcription factor domain (BZIP_C) of *Haliotis discus hannai* Nrf2 protein.

Supplementary Figure S2. Recombinant expression vector construction diagram. Left: Amplification of the target fragment. Right: Enzymatically digested recombinant plasmid. Marker: SM0331, Thermo; 1: Amplification of HdhNrf2 target fragment; 2: Enzymatically digested pET28a-Nrf2 recombinant plasmid.