

**Figure S4.** The promoter region sequence alignment of *BnaA05g08870D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh* (as a reference), the gene sequence of L780 and MI, the consensus line. Spaces indicate insertion or deletion and common bases are in black.

```

      *          20          *          40          *          60          *          80          *          100
Darmor-bzh : GGTGCAGCCAATACTGCAGTCTCTCAAGAGCTCT--AAAAAGGCTGAGATTGTGGGCACAAAATGTCATGAAGTGAAGAATCTCATGGAATAGCTA :
L780       : GGTGCAGCCAATACTGCAGTCTCTCAAGAGCTCT--AAAAAGGCTGAGATTGTGGGCACAAAATGTCATGAAGTGAAGAATCTCATGGAATAGCTA :
MI         : GGTGCAGCCAATACTGCAGTCTCTCAAGAGCTCT--AAAAAGGCTGAGATTGTGGGCACAAAATGTCATGAAGTGAAGAATCTCATGGAATAGCTA :
          GGTGCAGCCAATACTGCAGTCTCTCAAGAGGCTCgAAAAAGGCTGAGATTGTGGGCACAAAATGTCATGAAGTGAAGAATCTCATGGAATAGCTA

      *          120          *          140          *          160          *          180          *          200
Darmor-bzh : CAAGTGAACACAAATCTTGAATAGTTGCAACTTGAAGCCGTAGTTTAAACAAATCCAGCTTCGATAAAACAAATGCCAA--GCATCTGTTCTTCGC :
L780       : CAAGTGAACACAAATCTTGAATAGTTGCAACTTGAAGCCGTAGTTTAAACAAATCCAGCTTCGATAAAACAAATGCCAA--GCATCTGTTCTTCGC :
MI         : CAAGTGAACACAAATCTTGAATAGTTGCAACTTGAAGCCGTAGTTTAAACAAATCCAGCTTCGATAAAACAAATGCCAA--GCATCTGTTCTTCGC :
          CAAGTGAACACAAATCTTGAATAGTTGCAACTTGAAGCCGTAGTTTAAACAAATCCAGCTTCGATAAAACAAATGCCAA--GCATCTGTTCTTCGC

      *          220          *          240          *          260          *          280          *          300
Darmor-bzh : TTGTTTCACAATCTGCCAGTGATATTAAACAGAGTGCCTGACCTCTGCTGCTCTTATAGCTTTAAGGACTTTTGGTTTGGTTGGCGAGGTAGCTG :
L780       : TTGTTTCACAATCTGCCAGTGATATTAAACAGAGTGCCTGACCTCTGCTGCTCTTATAGCTTTAAGGACTTTTGGTTTGGTTGGCGAGGTAGCTG :
MI         : TTGTTTCACAATCTGCCAGTGATATTAAACAGAGTGCCTGACCTCTGCTGCTCTTATAGCTTTAAGGACTTTTGGTTTGGTTGGCGAGGTAGCTG :
          TTGTTTCACAATCTGCCAGTGATATTAAACAGAGTGCCTGACCTCTGCTGCTCTTATAGCTTTAAGGactgttctgttgggttggcgaggttaccgc

      *          320          *          340          *          360          *          380          *          400
Darmor-bzh : GGCAGCGGCAGCGTTTACATTCTGTGCTCACTCTTGTCTGTTTGGTTGATGCGAGGAGCTGGCTCTGACGCCGGGTGCGAAGCCCAATAAAGCTCGCGG :
L780       : GGCAGCGGCAGCGTTTACATTCTGTGCTCACTCTTGTCTGTTTGGTTGATGCGAGGAGCTGGCTCTGACGCCGGGTGCGAAGCCCAATAAAGCTCGCGG :
MI         : GGCAGCGGCAGCGTTTACATTCTGTGCTCACTCTTGTCTGTTTGGTTGATGCGAGGAGCTGGCTCTGACGCCGGGTGCGAAGCCCAATAAAGCTCGCGG :
          ggcagcggcagcggttaacattctgtgtcaactcttggtttggttgatgcaggaagctgogtgcagcgcgctgcgaagcccaataaagctcgcg

      *          420          *          440          *          460          *          480          *          500
Darmor-bzh : CGTGACATAAAACCTCGCGGCAATAACGTAATTTACTATTTTACCCTTAACCTAATTCATTATTTACAAAAATATGCTTCTCGCGGAGCGCTCGGTGTCG :
L780       : CGTGACATAAAACCTCGCGGCAATAACGTAATTTACTATTTTACCCTTAACCTAATTCATTATTTACAAAAATATGCTTCTCGCGGAGCGCTCGGTGTCG :
MI         : CGTGACATAAAACCTCGCGGCAATAACGTAATTTACTATTTTACCCTTAACCTAATTCATTATTTACAAAAATATGCTTCTCGCGGAGCGCTCGGTGTCG :
          cgtgcataaaacctcgcgccaataacgttaattactatttacccttaacctaatctatttacaataatgcttctcgcgagcgctcggtgtcg

      *          520          *          540          *          560          *          580          *          600
Darmor-bzh : ACCTCAACTTCCCTGCTCTCTTAAACGAATAATAATCTCTGCGAGCGTCAAGCTCTGCGAACAACAACAATTTGCTCTCATTTGACGCTTCGCGCGCGCGG :
L780       : ACCTCAACTTCCCTGCTCTCTTAAACGAATAATAATCTCTGCGAGCGTCAAGCTCTGCGAACAACAACAATTTGCTCTCATTTGACGCTTCGCGCGCGCGG :
MI         : ACCTCAACTTCCCTGCTCTCTTAAACGAATAATAATCTCTGCGAGCGTCAAGCTCTGCGAACAACAACAATTTGCTCTCATTTGACGCTTCGCGCGCGCGG :
          acctcaacttctctgctcttctaaacgaataatactgtgcagcgctcagcgctcgcgaaacaacaacaattgtctctatgacgctgcgcgcgcgc

      *          620          *          640          *          660          *          680          *          700
Darmor-bzh : CGACGAGAGCGCTGACGCGGAATCTCGGCAACCAAGCAACATGACTTTTCTGGAATTCOCATGTGCTCTTCTCCAAATCATGAGTACATTGGATG :
L780       : CGACGAGAGCGCTGACGCGGAATCTCGGCAACCAAGCAACATGACTTTTCTGGAATTCOCATGTGCTCTTCTCCAAATCATGAGTACATTGGATG :
MI         : CGACGAGAGCGCTGACGCGGAATCTCGGCAACCAAGCAACATGACTTTTCTGGAATTCOCATGTGCTCTTCTCCAAATCATGAGTACATTGGATG :
          cgacgcagcgcgtgacgcgcgaatctcgcgcaaccaacgaacatgacttttagctgaaattcccaatgtggtcttctccaaatgcatgagtagattggatc

      *          720          *          740          *          760          *          780          *          800
Darmor-bzh : ATATGATTTAACAGGAATCAAGGTGTGGAATGTATGTAATACCACTGGAATGAAATAGGATCTCAAAATATATGCGTTAAAATTTCAGACAAAT :
L780       : ATATGATTTAACAGGAATCAAGGTGTGGAATGTATGTAATACCACTGGAATGAAATAGGATCTCAAAATATATGCGTTAAAATTTCAGACAAAT :
MI         : ATATGATTTAACAGGAATCAAGGTGTGGAATGTATGTAATACCACTGGAATGAAATAGGATCTCAAAATATATGCGTTAAAATTTCAGACAAAT :
          ATATGATTTAACAGGAATCAAGGTGTGGAATGTATGTAATACCACTGGAATGAAATAGGATCTCAAAATATATGCGTTAAAATTTCAGACAAAT

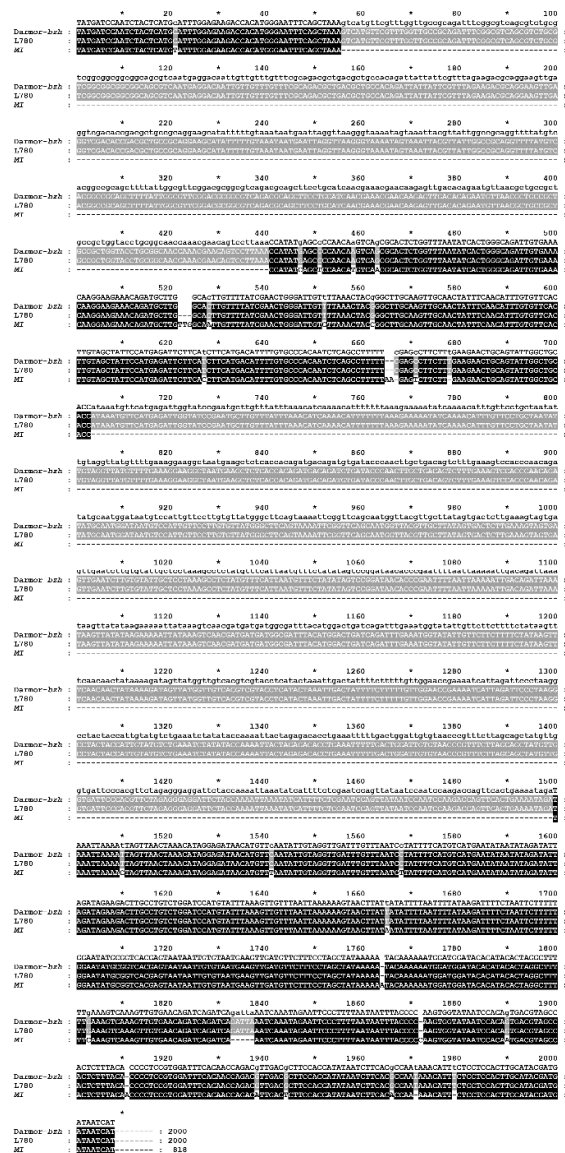
      *          820          *          840          *          860          *          880          *          900
Darmor-bzh : ACATGAAAGCTTGATATTTATCAAAAGGATATATGCAAGTTAATTTTAAATGGGCGCGGAACTCGCGGAGCCAAAAGGAGGGTTAGGCCAACAAATTTG :
L780       : ACATGAAAGCTTGATATTTATCAAAAGGATATATGCAAGTTAATTTTAAATGGGCGCGGAACTCGCGGAGCCAAAAGGAGGGTTAGGCCAACAAATTTG :
MI         : ACATGAAAGCTTGATATTTATCAAAAGGATATATGCAAGTTAATTTTAAATGGGCGCGGAACTCGCGGAGCCAAAAGGAGGGTTAGGCCAACAAATTTG :
          ACATGAAAGCTTGATATTTATCAAAAGGATATATGCAAGTTAATTTTAAATGGGCGCGGAACTCGCGGAGCCAAAAGGAGGGTTAGGCCAACAAATTTG

      *          920          *          940          *          960          *          980          *          1000
Darmor-bzh : CGGAGGACTTTGACTTTTGACTTTGAGGAGGGTATTATGGTCATTTACGAATACCTTAACACGTTGATTAATTTTATTCTCTGCTCTCTCTCTCT :
L780       : CGGAGGACTTTGACTTTTGACTTTGAGGAGGGTATTATGGTCATTTACGAATACCTTAACACGTTGATTAATTTTATTCTCTGCTCTCTCTCTCTCT :
MI         : CGGAGGACTTTGACTTTTGACTTTGAGGAGGGTATTATGGTCATTTACGAATACCTTAACACGTTGATTAATTTTATTCTCTGCTCTCTCTCTCTCT :
          CGGAGGACTTTGACTTTTGACTTTGAGGAGGGTATTATGGTCATTTACGAATACCTTAACACGTTGATTAATTTTATTCTCTGCTCTCTCTCTCTCT

      *          1020          *          1040          *
Darmor-bzh : TTGTACTATAAAATCCTCTAGACTGTGATTGACGTTGATAGACGACGACG : 1043
L780       : TTGTACTATAAAATCCTCTAGACTGTGATTGACGTTGATAGACGACGACG : 1043
MI         : TTGTACTATAAAATCCTCTAGACTGTGATTGACGTTGATAGACGACGACG : 655
          TTGTACTATAAAATCCTCTAGACTGTGATTGACGTTGATAGACGACGACG

```

**Figure S5.** The promoter region sequence alignment of *BnaA05g08890D*. The chart contains 4 sequences, the gene sequence of Darmor-bzh(as a reference), the gene sequence of L780 and MI , the consensus line. Spaces indicate insertion or deletion and common bases are in black.



**Figure S6.** The promoter region sequence alignment of *BnaA05g08900D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI* , the consensus line. Spaces indicate insertion or deletion and common bases are in black. The complete sequence of large fragment insertion was not acquired due to the Poly structure and the obtained sequence is listed as below.

>large fragment insertion

```

CCCAATTTCTCACAATAAAGCTCTCTAGAAATCATAAACATGATCAACATAAAGCTTTCCCTCAACGATATAATAGACCTTTTAAGTAGGGGATGATGGTTCAAAGCTATACCTGATGACGAAATAGTAGTGGGGAAGATGGTCGGAGCTTGCTC

CAGTGATTACACAATGTTTACTTTAAACCTAGTGTAAACAGAGAGGTTGATGACAACTATATGGAGTCTATGTTCTTACCTACTAAGAAGGATGGTATGGCTCCACGGGAACAGGAAAGCATGTGCGACATGTTATATACAGGAAA

TAATGTGACGCCCTCATCTGTGTCACAATTAGTAAATGATGACCTGGTTACCATATAGTTTATTGGAACCATCCGATATATGAAGAACATATATTATAACGGCTAACGTGGAACCCAAATACATATGTTAAAGCAGCTGCTATGATGACTT

TTTTTTTGTGCAACCCAGCATATTAGCTTAATTACAAATGTAACATAACCTAAATTAATAGATATCTAGCTAAATACCCAAATGAACATAAGCTATTTTTTTTTTAAAGCAATCAATAGCTATAATATACAGAATTTACCAATTAAGT

TCCTCACTTATAGGATATATTTAAGGAACAAAAGGTTAAACATGAGAGAGATAGGATGACAAATACATTACCCAAAGTTAAAAATATTGTTTTTCTCCACCGCTTATTTCCGAAGCTTCGATGACGTACATCTTTGTTCCACCCAGCTGCTATT

ATGGATTACTATCCAGATATTACTAAGCTTAGCTTACAAAAGAGACTATAGATGATGAATTTATAGACAGTGACAGAAATAATAAATAACAATGACCTGTTTGTGATGTCAGAGAAAGTCGATCATGATGGTTAACTAGCCCTATATA

GGCTGGCGATTAAAGCTAAGATATAGAGAGATTGGTCAATAACCTCCAACTGGAGGTGAACCGGTTTCTACAGCATGTTGAAGTCTTTATAGATGCTTCCCTTATTAAGCTTTTACACACAACTTACTTTACTGAGACCGGATAGGC

TCTGAGAAGACGATATACTTCAGTTAACTGGTAGTCCGAGGAGTTTCATAGAGTCGAAAAGGTGATCTCTTATATCTTGAAGACATAACTATTTCTTACTTACGATGGGACCCAAATAGCTATCATCTCGGACTAATGTTCTTCTTT

```

TATATGGACAGATGGCACGTTTGGTTCTGTTTAAAGGGACAGTGGTTCAAGTCGCAGGATGGTGTGTGGAGGTTGCACCAAGATCCTACCATGACAGGGCGTGACATACTATTGCAAAACCCGAGCACCTTGAAACACTTAAAGACCTTGT

CAGGGCTGTCTTCTGTCTTCGTACAGAAACCCGATGGTAGTTACTTTCAGCTCCCACAGTGGATGCTCGAGCTGATGGCGGGACGTGGCTCCACATAACCTAAACAGTAACGCAGACGTGCATATGATGATGACGTACATGACGTGAAT

GTAGAACAAGGCTTTGCGTCATATTGGTGCTCAGGATGTGGCTACATACAGTTCAAGTGCAGAGACCTTTTACATCGGATCTCCACATTCCTAGCCCAAGGTGTGACGGAGGAGCAACACATGGCGCGTGTGTAGGTATATTACGTA

CACATGAATATCGTTTGAATACATAATAAAAAATGATCTAAACCATTACCAACATCTTTGTTGATAGATATGATACGTGGTAACGAGCTACTGTGCAGTGAGCAAGTGCTTAACGAAATCTTTGACGAAGAAAAATGGTCTTACTCTATCGTTT

CTCTTTGGAGATTCAAAAAGCCAAAAACAGTCTCGACCTCAATTAGGACCCATGGTGGAACGTATGACCACATTGTACCTAATATCGGTGGTGAGGGGGGGACACATGTTACGATGGAGGTGGAGTTCCCAACACTGAGGTTCACCCAGA

CGTAGCAAGGGGTGAGCTTCCAACCCGGTGACGTTCCCTTAAATACTCTCCACATTTGGTATGTTCTCTACTTACATTTTGTATTTAACAATAAATAATAATAATATAACGATATATATAGATAAACGGTTGCCTATAGCTTATTTGTTAGATA

CTTAACATATATTACAACCTAATAGTTCAACGGCTTCCATTTGTAGGATATCTACCAATCAACACAGCTGCATCCATGACGACCCTCCTCGTCAGAGCATGTATGGGCCACACTATTATACGCCGATATGGGAAGCATGGCTGTGTAGAGGAAGC

TATTTGGGAACCTGTATGCTACCAAGGTATGCAGTTGATGTGCAGAGAATTTATGGATACCAGGATCTGAATACGTTGGATATCCCCCAATGACCTCAATATCGGTAAACCTACTGGTCCACCTATGCTTTGGGTCCCCAATGGTCCACCTATGC

ATGGGTACGGGGTTCCTATTGAAGTTCTTCTACGGCTTCATACGGAGGTGCATAACGTTCTGTGACATTGGAGTAACAGTCAATACATCCAAAGAACCCGGTATCAGAGATGGCATCTGTGTTGAGAAGGTATGATGAGACTATTTCAAAA

TTATGGAATTTACATCCCAATACTCTGTAACAGAGCATGCACTAAAGTCAATTACTTATATCTGAACATACATTTCTTATTTTTCCTACTGAAAGGGGAGTCCATCCATCGGCCAGAGCTGCAACTATGCGGACTTGGACGTTA

ACTTCAGATTGGAGACACAACCCGGCAGCCGATGTTGGTTGATGCTGGAGAGGGTCGGGACGCTGAAGAATCTGCCAAACAGATGAAAATAAATAGGGACAACCTTTATGTAATGTCTAAACCTTTTGGCGTGTGAAATAGC

TCGTAGACTTGGTAGCATGTGAAATATGGGAGTTCGTTTACTATGATGACGTTTCTCGAGCCTCCAGTCGGTGAATAGTTTGTCTCTATGAAGATGTATGTGTGATTAATTTAGTATGTGCCTTTGTAATACTTTTGTCTCAATGATT

ATATAACGTAAACGTAAACCGCAATTATATCTTATTTGGTTATCAACAAAATAACCCATAAACTTAAACCGGCTTATAGGTAAAAAATGTTGTCTAAAATTACTCCATCACTAAATGATGTGTGTTATGCCACCTTTTGAACCTAGTTTTT

CCAGTTAGTAACGATAGGAAGGAATCTTAACAACATTTGCTTTCATAAGTTGAGTCTTCATCGTTACATTAAGACAATGTTGTTAAAGTTAGCCGTAAACCTATTGTCTCTCTCATAATAATAGTACAACAACATGAGAAAGAACCTAAA

TTACATAGTTCCCATGAAATGAACCTCTCATATTTGTACCTGTATGCTTCCAACCTCTCATCTAATAAATAAATCAACACAAAGAGCCATATGCAACAAGAGGGGAAAAAAGAGTTTAAACAGCGAATCTTATAATATGACACATGTTCTCTCAA

ACAAATAGATAGACAAGGTTGACATAAGACATGACGTAATAACAGGTACGCTTCGAGGAGAACCAGTACCGTCTTCTACCAAAGGACTTTATTAACCCGGGTAAAAAGCGGTTTCTACAGCTTCTGTAGAAATCATACACCAATATCGTGC

CTTTGTGCTTCCACTGGAATGACAGTTGGAGTATAGACCTACAGCCGTCAAATCCAACAGCGCATGTGCTGGATCAAAAGACAGGCGGTCAACGCCGATCTGCGGGATTAGTGTTTGGAGCAACCTTTGATTTCTTCAACCCGAAGT

TTGTTGCCGATAGTAGGAACACCATTAACCTAACGCTCTCACTATATAAGGAAACATGTCAGAGATTGGTAGCAGCTCTTTTACCAACGCTTCATCCGTAATAAGACCTTGGTGCAGTCCAGAACATATATCTTCGACGAAGGGATATCTACACAA

AGGCCAACCCAATGTCTCGATGGAGCGTTGAATGAATATACCACTCGCCACAGCAATGTGTCTCGGGAACCTTTCTAACACAATCTACCACTCCCTTACTGAAACATATTTTCCCTCTGCTTTGACTTTTAAACCTTGGAAATCTCTTC

CAAGCAAAATCTGCACACGATGTCAAGGAACACTGGAATGGTATCTATCCCAACGCTTCGTGTTAAGCTGTAAGTGAACAAACCTTGTAAGTATATCTATGACCTGAGTAATAATAAAGCATCGTGAGGATACAAATAGACGGT

AATAAATAGTCAATTAACGCTAACGTAACGCTACGCCAGGAAGAATCTGTCTCTCTCGATGTGACCATGTCTTCCGATCTACTGACAAGCCGCAACATTGATAACACTGGAAAGAAATAACAAAGTATAGTAAGTAGAGTCCCTACCTCG

GTAAATTTCAAGAAAGAAACAATCAATATATATTTCAAAATATGAATAGATTTTGTAAAATACCACCTTTCTTAAGTAAGAGCTTCAGACGCAAGTACTTATCAGGAATCCAGAACATGACATACCCAATCATCCCTAGAAGTTGTCTT

CACGAGCCCTATTAACAATTTGGGTACCGACTGTAGTCGGTGATAAGTTGCGGTGAACATGCCGCTCCGCTGCTTTACGGCAAGTCAGAGTTTCTCATTATCGCAAAACACTGCTTCAATAGGTTCTTGAACGGAGATATGTTATTAT

GTCCCATGTGCCAGCTTCTGTGCCGTTCAATTCGAAGCTCTGAGTTCAGGCCAAGTGAAGAAAGGAATCTCATGTCCAAAGAACACGTGACCGCTACACACATTTAAACATCTTTGGCTTTCTGAAATAAGCGTACATAGTGAACAA

TCAAGAATTTTAAAAAATTTGTACATTTACTCTCCCTGTGGGCCGTCTGGGTGACACCACACAAGATGCATGCTGATTATACACCCTCAGCGTTCCAGCGGAACGGACCTTCGGAGGAAGGAGATAAGTAGGTCGACATGCCAT

AATTTGAAAAAAATTTGAAGACGGAAAGATTAATAATGCCTATTTTAAACTTGCTTCTCATTTTACAAAGCTTCAGAAAGTGGTATGGAGGGAAACATTAACCGAATACTAATAGGTAACAAAGTAGTGTGAATTTGAAAAATATAT

GAAACAGAGAGCTTACTTCGGATAGTCTTTGAAAGCTGTTTCGGGACATACGCTCTTTGATGAATACTGGATGTTCAATTTTCCGTTGACTATCTTCAGGATGCCCGCGGAGATAAGGGGATCGTGCCTATGGGACTCCGCTCAG

ATCCCTGACACAATCACTAACTATAAGGAGTTCTCTCATACTTAAATAACAAAAATTTCTTCAAAATATATGACCAAAAGGACGCTACTTTGAAGGAAGATGAAGTTGGTGCAAAATCATATCTGAAGTTGTATCTTAACCAATTTAA

CATAACATTTTACAACGTTTCCAAATTTTCCCTACGAATTAACCTCTGCATTTCTAAATTTTATATATCTATAAATATAGACTTACAAGATGTGAGTGACTTATGGCACCGGTTCTCCGCCCTAGGTGGAGTTAGTAGTTACTCAGATTTT

CCAACATATATCAATAATCTGGCTATTGCTTACGCGTTGGAGAGAGAAATTTTCAAGGAGAACCTACTTTGACAAACACTATCACTTGCCCAAGCGTTGATTACCCAATCATCTACTTCCACCCCATGGCGAAATCGCGCGG

TATTAATTTGACAGACTTCTTATGTACCATTATAGTAAGTGGATGGCGTCTGGATCTCAACTGCTGCTTGGTACTAGCTTTGGAAATGTACGAAAGGATTTCGGTCTTAAACTCTGAGAAATGTATCCACACTACCAACAACCTGAAGC

CTGATACGAGAGAGCATTTGAAGACACCTCTTACGGACGCTACAGCAAAATCGATTTTGTCTCCAGTCTATGAATCTCAGGTGCCAAAATGAGTGAACAAGAGCTTGATTTTGTATCTGACTGAGGTCTATAGGTGCCTAATTCGTCT

TCGTGTAACCTTTTCTTCTTCCCTCTCTTCAACTCTCACGCACTCTCTCTACATCCACTTTAGTCAGACACCTCTAAACATCTCTTTACGGATAACAACGTTATCTAAAATAAGATTGACCAAGTTATCAACCTTGACATCAACAATCA

TCTGACCAATTAACAAAGAGTCGACGTCACGCCCTTGGAGGATCAACTGGAAGAATGCTGGTCACCAATGCCTACGATACACAGTAAAAAAAAGTTATAGTGCAATATGGGTGCCGTACTTTATTTACTGATTACGAACATATACGTTAATAA

AAACACCTCAGCTTCTCTCAATTTTCGCGAGCATGTCCCGGACTTAATGCTGCTTCTTGTCTTCCGGGTAAACGATACCCGCTCTCTCATCGCTCTCAGACTCTGATGAAGAATCAGCTTCTGTACGACTCTGTGAGTGAAGAACTGC

TTCAACGATAACAAGCTGGAGGGCAGGGCAATCTTTCAAGGCTATTGTGTTTTCGACAGTGAAATCTCATCTCTTTTAAATACTGTTCATCAACATATCAAAAGCTAGTCTCCCCAAGGGAAGGAAAAAATCGTCCATATCCACCA

GCAGCTACGCGTGTCTCTCAACATCTTACATACGAGATTGTGACAGCAAAAATGAAGACACAATGCAAGGCAAGCCAGTTTATCCCGGAGATCTTTGTGCGTAACGGTTTCTCCCGCAGCATTTTACCGCTCTAGATACTCGCAATTTCT

TCATACCTTCGGAATAACTCCGGCAATACGGTTTCTCTCTCATATTTTCTCTCTCTGCAATTTGATGTCTTTGGAAATCACCAAGGAAGACCGGTACTATGGCAAACTCCGTAGCGAGAATCAATAGTTTACCAGGAATCGAAAC

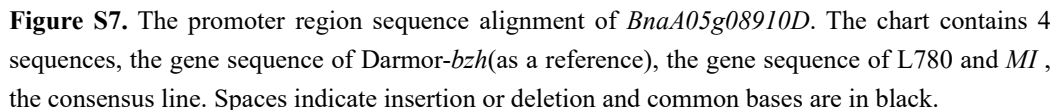
CAAGCCCTGTGCTTTTATCAATTTAAGTTGCCTGACAATAGATATCTAGCAAACTACCAGAAAAGCTGGTTTTCGAAATTCGACCAACTTCCGATGAAGTCCCTTCAGCGCTCGATCTCGTCCGATCTAGAGCTTCAAGAAT

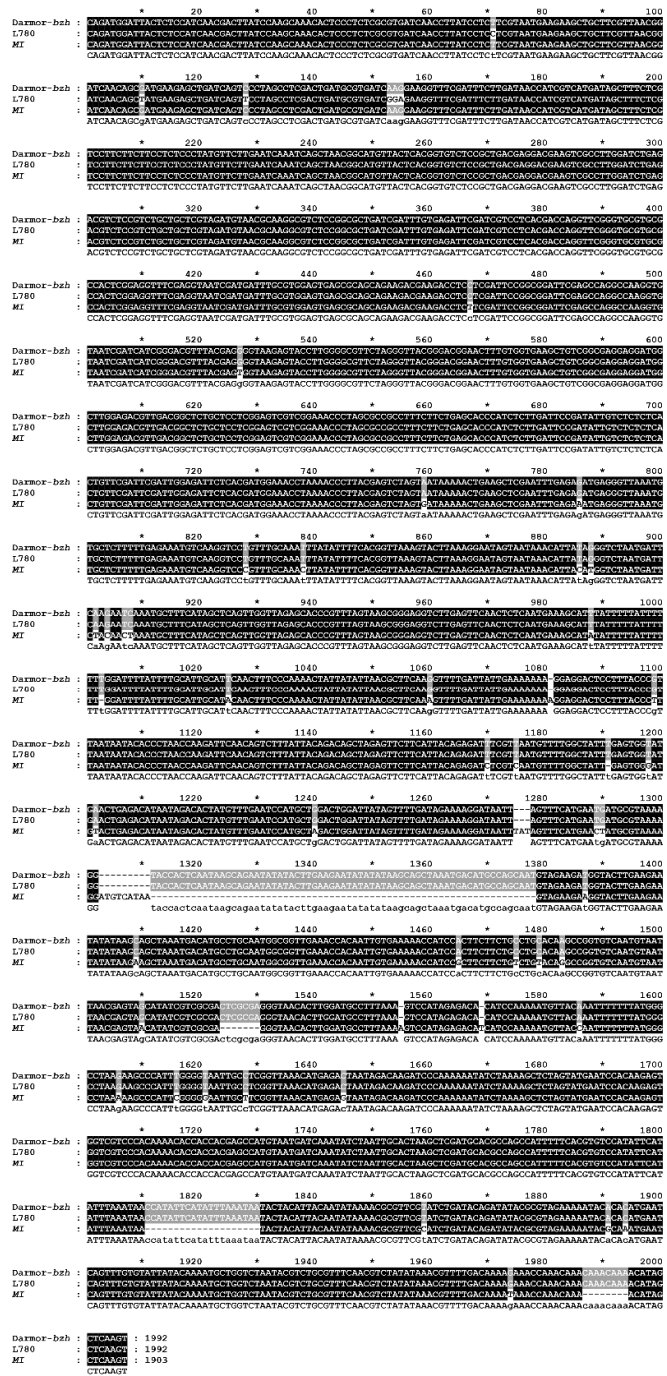
GTGTTTAGCGCCCGACGACTGGTATGTCAGAACCTAACACGACGGGTCTCTCTCTCGCGAACAATTCGGTAAGGATACGGTGGTTCTCTCCATTTCTCTTCGCGAAATCACGACTCCGTGAAGAGGCCATCTCGATTACGAA

AACTGTGTGCTGTATAGAGAGGTGAAAAATAAACGCCGATGAGAGATGAAGAAAAATGAAAGCGTATAATACAAGGAATCGACTAATATACATAAAAAAGGATAGATATAAGGCAAGATAGGTTTTTTCAGACCTTTGAAGTACATTTG

CATACTGTACCAAGATATTTCTACTACAGTACAAGCGTGTCTACCGCTTCTCCCGTTGTCTGCACAAGCGCCATCTAGTTTGGGGACTACATCTCCGTTCTCTCTCATAGTGAGGGTACTGTGCGTATACCGGAAACTCAACAG

TACGATGCCCATCCACCTAATTTACATCTCTTCCATGTATATCTAGTGCAAAAACCC





**Figure S8.** The promoter region sequence alignment of *BnaA05g08950D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI* , the consensus line. Spaces indicate insertion or deletion and common bases are in black.