

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.

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*          20          *          40          *          60          *          80          *          100
Darmor-bzh : GGTGCAGCAAACTGCGAGTCTTCAAAGAGCTC-----AAAAAGGCTGAGATTGGGGCACAAAATGTCATGAGTGAAGAATCTCATGGAATAGCTA
L780       : GGTGCAGCAAACTGCGAGTCTTCAAAGAGCTC-----AAAAAGGCTGAGATTGGGGCACAAAATGTCATGAGTGAAGAATCTCATGGAATAGCTA
MI        : GGTGCAGCAAACTGCGAGTCTTCAAAGAGAGCTTT-----AAAAAGGCTGAGATTGGGGCACAAAATGTCATGAGTGAAGAATCTCATGGAATAGCTA
          GGTGCAGCAAACTGCGAGTCTTCAAAGAGGCTC          gAAAAAGGCTGAGATTGGGGCACAAAATGTCATGAGaTGAAGAATCTCATGGAATAGCTA

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

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

*          320         *          340         *          360         *          380         *          400
Darmor-bzh : GGCAGCGGCAGCGTTAACATTCTGTGCACTCTTGTCTGTTTCCCTGATGAGGAAAGCTGGCTGACGGCCGGTTCGGAAACCCCAATAAAAGCTGGCG
L780       : GGCAGCGGCAGCGTTAACATTCTGTGCACTCTTGTCTGTTTCCCTGATGAGGAAAGCTGGCTGACGGCCGGTTCGGAAACCCCAATAAAAGCTGGCG
MI        : -----
          ggagcggcagcgttaacattctgtgtaactcttctggttctggttggatgaggaagctggtgctgacgcccgtccgaaacccaaataaaagctgggc

*          420         *          440         *          460         *          480         *          500
Darmor-bzh : CGTGACATAAAACCTGGCGCCAAATAAGCTAATTTACTAATTTACCCTTAACCTAATTCATTAATTAACAAAATATGCTTCTCGGGCAGCGTGGCTGCG
L780       : CGTGACATAAAACCTGGCGCCAAATAAGCTAATTTACTAATTTACCCTTAACCTAATTCATTAATTAACAAAATATGCTTCTCGGGCAGCGTGGCTGCG
MI        : -----
          cgtgacataaaacctggcgccaaataagcttaattactatcttaacccttaacctaattcattattacaaaaatagcttctcgggcagcgtcggtgctg

*          520         *          540         *          560         *          580         *          600
Darmor-bzh : ACCTCAACTTCCCGCTCTCTAAACGAAATTAATCTCTGGCAGGCTCAGCGTCTCCGAAACAAACAAATTCCTCTATTCAGCTCCCGCCCGCGG
L780       : ACCTCAACTTCCCGCTCTCTAAACGAAATTAATCTCTGGCAGGCTCAGCGTCTCCGAAACAAACAAATTCCTCTATTCAGCTCCCGCCCGCGG
MI        : -----
          acctcaacttctcgctctcttaaacgaaataaactctgtgagcgtcagcgtctcgaaacaaacaaactgtctctatgagcgtcggcggcggc

*          620         *          640         *          660         *          680         *          700
Darmor-bzh : CGAGCGAGCCCTGAGCGCGAAATCTGGSCAACCAAGAGAGATGACTTTAGTGAATTCOCATGTGCTCTTCTCCAAATCATGAGTACATTGGATC
L780       : CGAGCGAGCCCTGAGCGCGAAATCTGGSCAACCAAGAGAGATGACTTTAGTGAATTCOCATGTGCTCTTCTCCAAATCATGAGTACATTGGATC
MI        : -----
          cgagcagacgtgagccgaaactctgaggcaaccaacgaatgactttagctgaaattcccatgtggtcttctccaaatcatgagtagattggatc

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

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

*          920         *          940         *          960         *          980         *          1000
Darmor-bzh : CGGAGGACTTTGACTTTGACTTTGAGAGGAGGTTATTGATCATTACGAATACTTAACACGTTGATTAATTT---ATTCTCGCTCTCTCTCTCTCT
L780       : CGGAGGACTTTGACTTTGACTTTGAGAGGAGGTTATTGATCATTACGAATACTTAACACGTTGATTAATTT---ATTCTCGCTCTCTCTCTCTCTCT
MI        : CGGAGGACTTTGACTTTGACTTTGAGAGGAGGTTATTGATCATTACGAATACTTAACACGTTGATTAATTT---ATTCTCGCTCTCTCTCTCTCTCT
          CGGAGGACTTTGACTTTGACTTTGAGAGGAGGTTATTGATCATTACGAATACTTAACACGTTGATTAATTTaATTCTCGCTCTCTCTCTCTCTCT

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

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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.

TATATGGACAGATGGCCAGCTTTGGTTCGTGTTTTAAGGGACAGTGGTCAAGTCGAGGATGGTGTGGAGGTTCCGACCAAGATCTACATGACAGGGCGTGACATACTATTGCAAAACACCGAGCACCTTGAACACTAAAGACCTGT
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CTCTTTGGAGATCAAAAAGCCAAAAACAGTCTCGACCTCAATTAGGACCCATGGTGGAACTGATGACCACTTGTACCTAATCGTGGTGGAGGGGGGACACATGTTACGATGGAGGTGGATTTCCCAACTGAGGTTCAACCGA
CGTAGCAAGGGGTGAGCTCCACCCGGTACGTTCCCTTAATACTCTCCACATTTGGTATGTTCTCTACTACATTTTGTATTAACAATAAATAATAATAACGATATATATAGATAAACCGTTGCTATAGCTTATTTGTTAGATA
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TATGGGAAACTGTATGCTACAGGATGAGTGTGACAGAAATTTATGGATACCAGGATCTGAACTGTGATTTCCCAATGACCTCAATATCGGTAACCTACTGGTCCACCTATGCTGGTCCCCAAATGGTCCACCTATGC
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ACTCTAGATGGAGACACAAACCCGGACGCGATGTTGGTGTGATGCTGGAGGGTGGGACGCTTGAAGAATCTGCCAAACAGATGTAATAATAAGGACAACTTTATGATAAGTCTCAAACTTTGGCGTGTGAAATGAC
TCGTAGACTGGTATGATGTAATAATGGAGTTCGTTACTATGATGACGTTTTCTCGAGCCTCAGTCGGTGAATAGTTGTCTCTATGAAAGATGATGTGTGATATAATTTATGATGTGCCTTTGTAATACTTTGTTCAATGATT
ATATAAGTAAACGTAACCGCAATTAATCTTATTTGGTAACTAAACAAAATAACCCATAAACTAAACCGGCTTATAGGTAATAAAATGTTGTCTAAAATTAATCCACTAAATGATGTGTATGCCCACCTTTTGAACCTAGTTTT
CCAGTAGTAAACGATGATGAAAGAACTTAACAACATTTGCTTCAATCAAGTTGAGTCTTCCATGCTTACATAAAGCAATGTTGTTAAGTTAGCCGTAACCTATGTCTCTCTCATAATAATAGTACAAACACTATGAGAAAGTCAA
TTACATAGTCCCAATGAAATGAACTCTCATATTTGTACCTGTATGCTTCAACTCTCACTAATAACTAACTACACAAAGAGCCATGACAAAGAGGGGAAAAAGAGTTAACAGCGAATCTTATAATGATGACATGTTCTCTCAA
ACAAATAGATAAGCAAGGTGACATAAGACATGACGTAATAACAGGTACGCTTCGAGGAGAACCGGTACGCTTCTACCAAAGGACTTTATTAACCCGGTAAAAAGCGTTTCTACAGCTTCTGTGAATTCATACCAATAATCGTGC
CTTTGTGCTCCACTGGAATGACAGTTGGATGATAGACCTACAGCGCTCAATCCAAACAGCAGCTGTGTTGATCAAAAGACAGCGGTCAACCGCGCATCTGCGGGATGATGTTTGGACCAACCTTTGATTTCAACCCGAAT
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ATCCCTGACAACTAATACTATAAGGATCTCTCATACTAAATAACAAAAATTTCTCAAAATATATGTCACAAAGGACGCTACTTTGAAGGAAGATGAAAGTTGGTGAACATATCTGAAATGTTATCTAAACCAATTA
CATAACTTTTACAACTTTCCAAATTTTCCCTACGAATAACTCTGCATTTCTAAATTTTATATCTATAAATATAGACTTACAAGATGTGAGTACTTACTGGACCGGTTCTCGCCCTAGGTGGAGTTAGTATGATCTCAGATTT
CCAACACTATCAATAATGCTGCTATGCTTACCGGTTGGAGAGAAATTTTCAAGGAGAACTTACTTTCGACAAACACTATCACTTCCCAAGCGGTTGATTACCAATCATCTACTTCCACCCATGGGAAATCGCCGGC
TATATTTGACAGACTTCTTATGACTCTATTAGTAACTGGATGGCGTCTGATCTTCAACTGCTGCTGGTACTAGCTTTGGAAATGACGAAAGGATTTCCGCTTAAACTCTGCAAGATGATCCACTACCAACACTGAAAGC
CTGATACGAGAGAGCATGGAAGACACCTCTACGGACGCTACAGCAAAATCGATTTTGTCTCAGTCTATGAAATCTCAGGTGCCAAAATGAGTGAACAAGAGCTTTGATTTTGTATCTGACTGAGGTCTATAGTGCCTCATCTCT
TCTGTACTACTTTCTTTCTCTCTCTTCAACTCTCAGCATCTCTCTACATCACTTATGTCAGACCACTTAAACATCTCTTACGGATAACACGTTATCAAAATAAGATGACCAAGATATCAACTTGCATCAACACATCA
TCTGACCAATTAACAAAGAGTGCAGCTACGGCTTGGAGGATCAACTGGAAGAATGCTGTACCAATGCTCAGTACACAGTAAACAAAGTTATGATGATATGGGTGCGGTTACTTATTTACTGATACGAACATATACGGTAATA
AAACACCTCAGCTTCTCTATCAATTTCCGAGCATGTCGGGACTTAATGCTGCTTCTTGTCTTCCGGTAAACGATCAGCTCTCTCATGCTCTCAGACTGTATGAAAGATCAGCTTCTGTGACGACTCTGTGAGTGAAGAACTGC
TTCAACGATAACAAAGTGGAGGGGAGGGCAATCTTTCAAGGCTATGTTGTTTGGCAGTGAAGTCTCATCTCTTTTAAATCTGTGATCAACATATAAAAGTAGTCTCCCAAGGGGAAAGAAAAAATCGTCCATATCCACCA
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TCTACCTCCGAAATAACCGCCCAATACGGTTCTCTCTCATATTTTCTCTCTCTGACTTGTGATGCTTTGGAAATCACCACAAGGAAGACCGGTCATGTCGAACTCCCGTAGCGGAATCAATGGTTTACCGAAATCGAAAC
CAAGCCTGCTTTTATCAATTTAAGTGCCTGACAAATGATATCTAGCAAACTTACCAGAAAAAGTGGTTTTCCGAAATTCGACCACTTCCGAAATGAAAGTCCCTTACGCGCTCGATCTGCTCCGATCTAGAGCTCAAGAAAT
GTGTTAGCGCCGACGACTGATGTCAGAACCTAACCGACGGTCTCTCTCCGCGAACATTTCCGGTAAGGATACGGTGGTTCTCCATTTCTCTCTCGGAAATCAGACTCCGTAAGAGGCCATCTCGATACGAA
AACTGTGTGCTGATAGAGAGGTAATAAATAACCCGATGAGAGATGAAAGAAAAAGGCGTATAACAAAGGAATCGACTAATACTATAAAAAGGATAGATAAGGCAAGATAGGTTTTTTCAGCCTTTGAAGTACATTTG
CATACTGACCAAGATATTTCTACTACAGTAAAGCGTGTCTACCGCTTCTCCGGTGTCTGACAAAGGCCACTTAGTTTGGGGACTACTACTCCGTTCTCTCTCATACTAGGGGATCTGCTGGTATCCGAAACTCAACG
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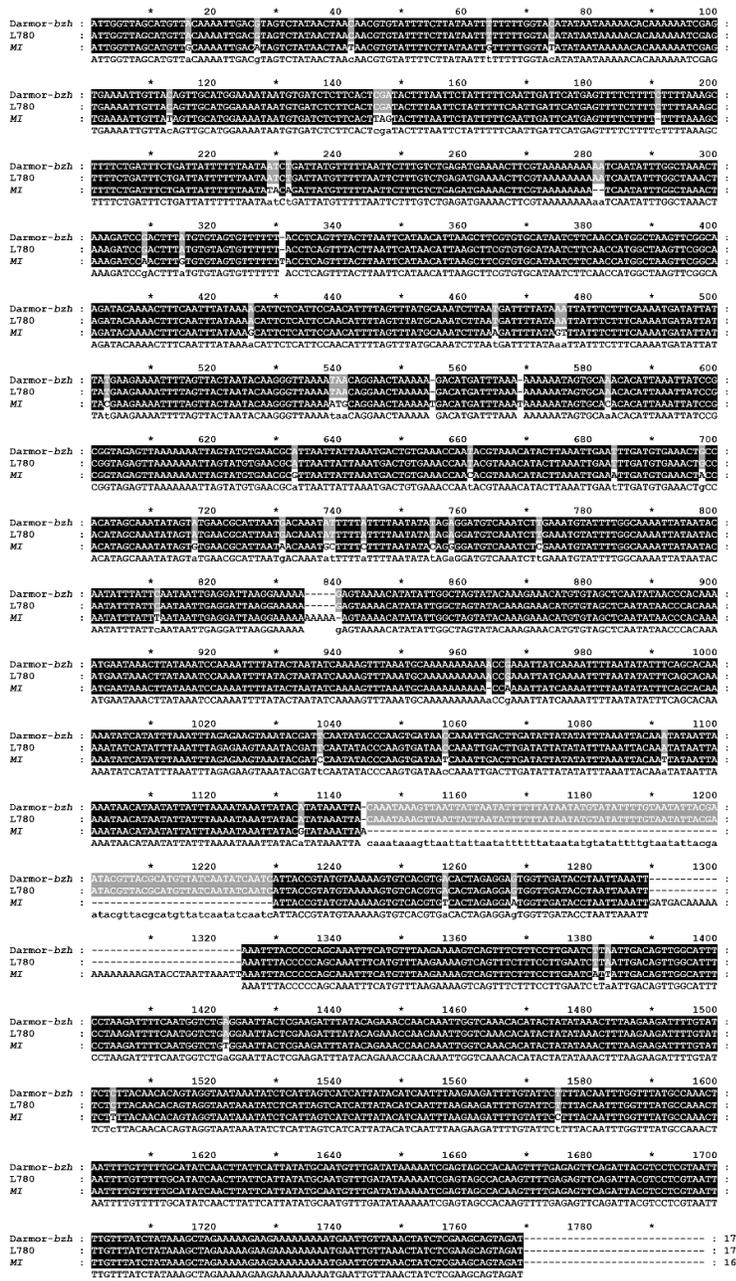


Figure S7. The promoter region sequence alignment of *BnaA05g08910D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh* (as a reference), the gene sequence of L780 and MI, the consensus line. Spaces indicate insertion or deletion and common bases are in black.

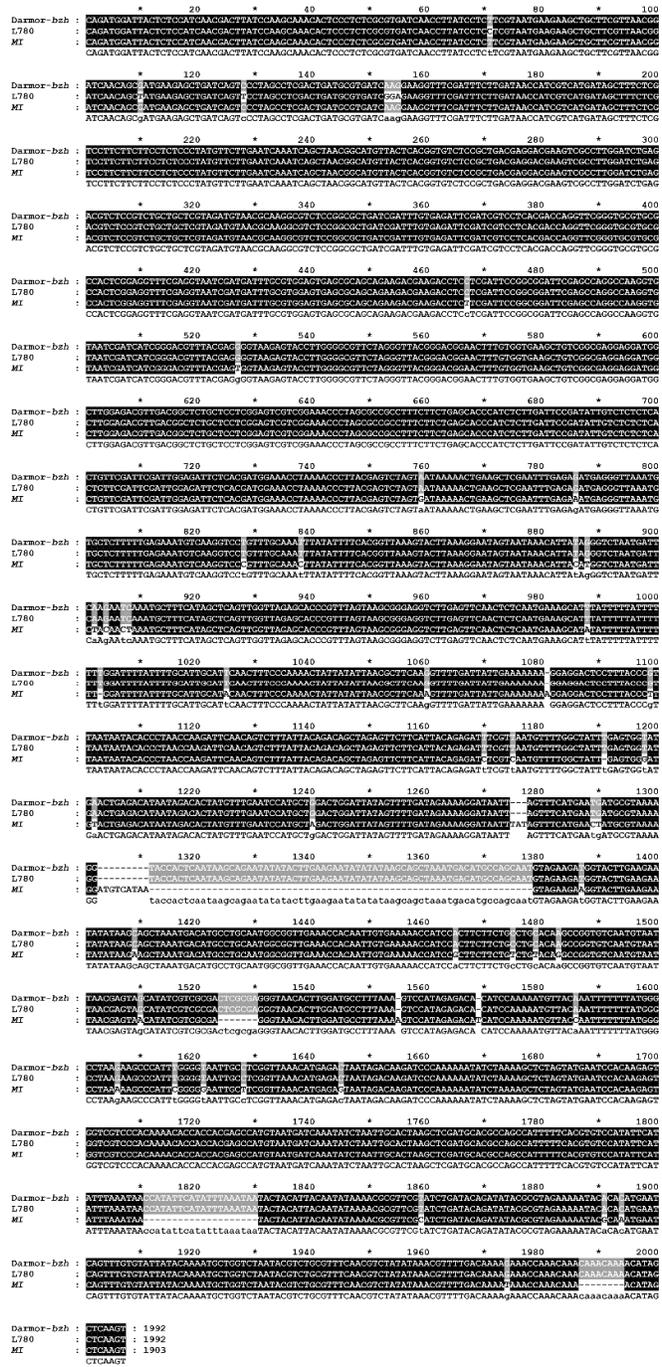


Figure S8. The promoter region sequence alignment of *BnaA05g08950D*. The chart contains 4 sequences, the gene sequence of *Darmor-bzh* (as a reference), the gene sequence of *L780* and *MI*, the consensus line. Spaces indicate insertion or deletion and common bases are in black.