

Figure S9. The nucleotide 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. Orange represents SNP, red represents insertion, and blue represents deletion; exons are in black and introns in darkgray.

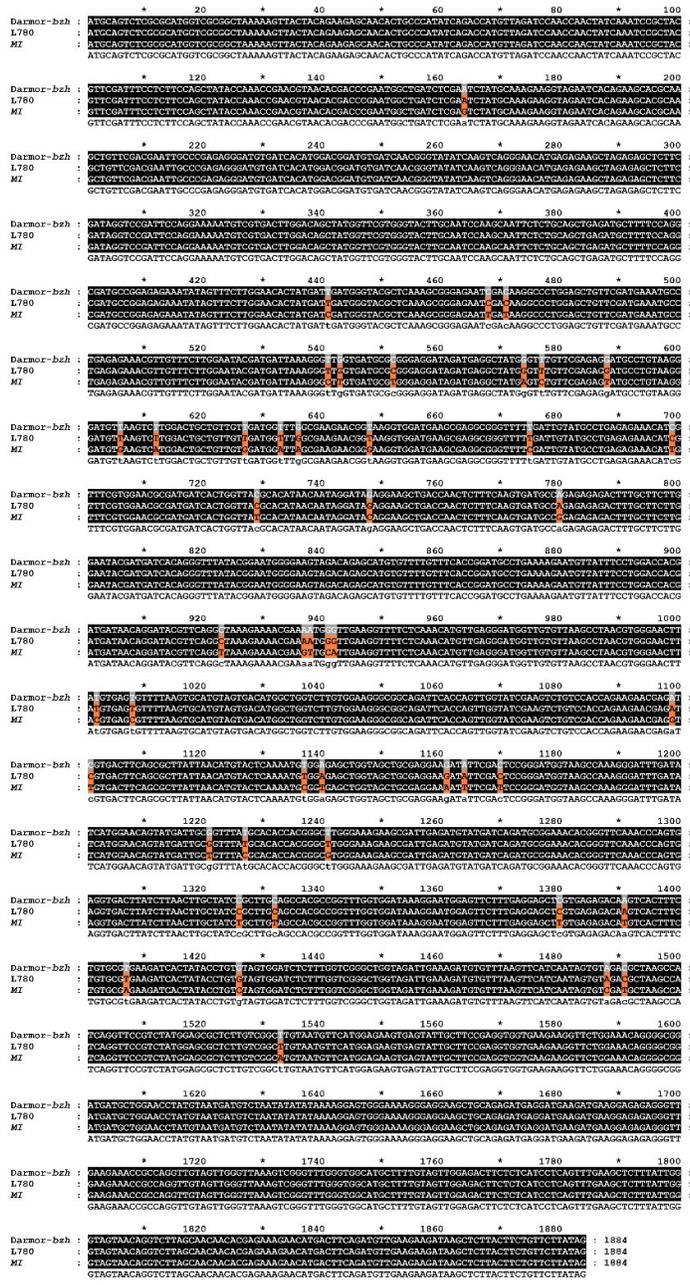


Figure S10. The nucleotide sequence alignment of *BnaA05g08880D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh* (as a reference), the gene sequence of L780 and *MI*, the consensus line. Orange represents SNP; exons are in black.

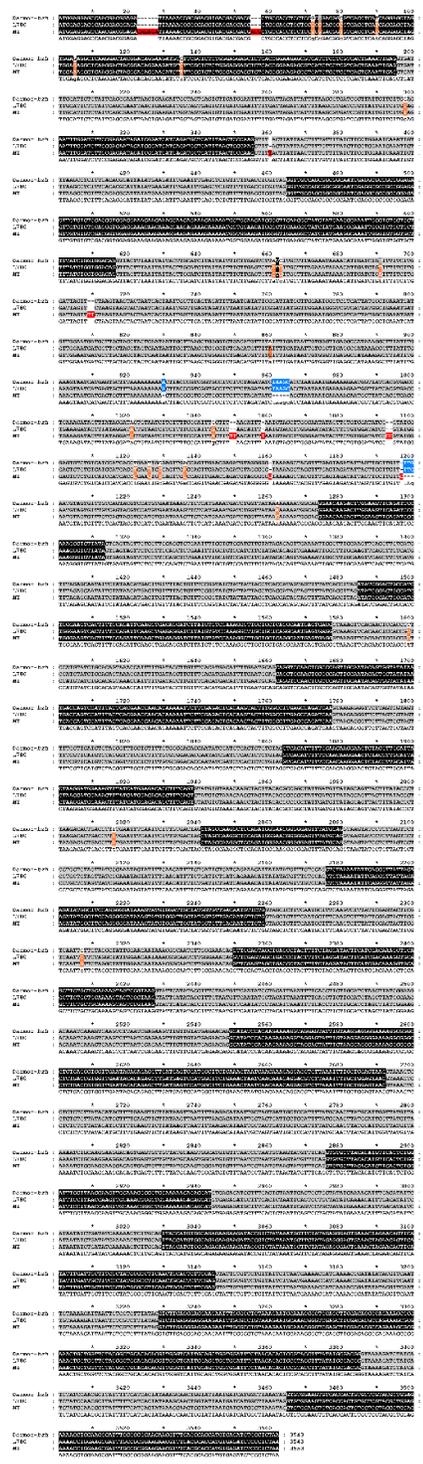


Figure S11. The nucleotide sequence alignment of *BnaA05g08890D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI* , the consensus line. Orange represents SNP, red represents insertion, and blue represents deletion; exons are in black and introns in darkgray.

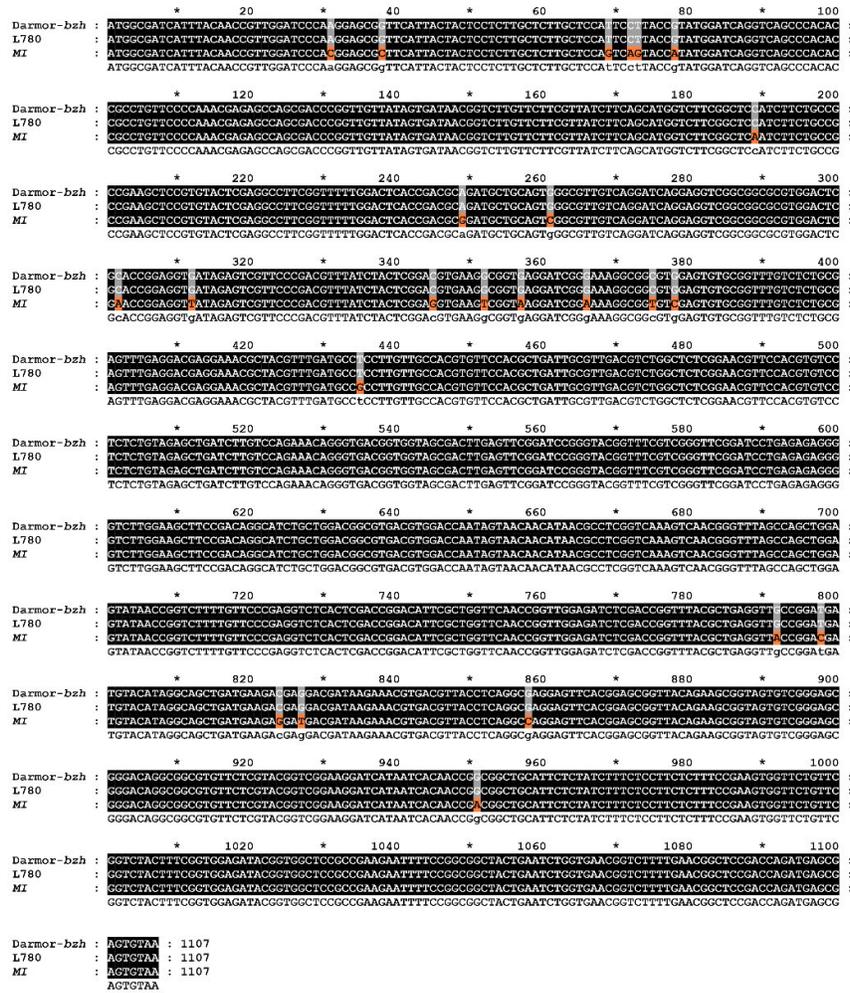


Figure S12. The nucleotide sequence alignment of *BnaA05g08900D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh* (as a reference), the gene sequence of L780 and *MI*, the consensus line. Orange represents SNP and exons are in black.

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*          20          *          40          *          60          *          80          *          100
Darmor-bzh : ATGCCAGCGGACGATATGCCACAGCCAGGATTCGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTTAGCCTTCCTCATCTTCATCGTGG :
L780       : ATGCCAGCGGACGATATGCCACAGCCAGGATTCGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTTAGCCTTCCTCATCTTCATCGTGG :
MI        : ATGCCAGCGGACGATATGCCACAGCCAGGATTCGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTTAGCCTTCCTCATCTTCATCGTGG :
ATGCCAGCGGACGATATGCCACAGCCAGGATTCGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTTAGCCTTCCTCATCTTCATCGTGG

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

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

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

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

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

*          620         *          640         *          660         *          680         *          700
Darmor-bzh : ATATCATTATCGAGATCCATTCGACCGGACACCTGTGGCTGAAACCGGTGGAGAAATTTGGACCGGTTTACACCGGTTACAGATGGGTACGGAGG :
L780       : ATATCATTATCGAGATCCATTCGACCGGACACCTGTGGCTGAAACCGGTGGAGAAATTTGGACCGGTTTACACCGGTTACAGATGGGTACGGAGG :
MI        : ATATCATTATCGAGATCCATTCGACCGGACACCTGTGGCTGAAACCGGTGGAGAAATTTGGACCGGTTTACACCGGTTTACAGATGGGTACGGAGG :
ATATCATTATCGAGATCCATTCGACCGGACACCTGTGGCTGAAACCGGTGGAGAAATTTGGACCGGTTTACACCGGTTTACAGATGGGTACGGAGG

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

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

*          920         *          940
Darmor-bzh : GAGCAGACATCTAGAGAATCCGACACGATGATCTAGTCTAA : 942
L780       : GAGCAGACATCTAGAGAATCCGACACGATGATCTAGTCTAA : 942
MI        : GAGCAGACATCTAGAGAATCCGACACGATGATCTAGTCTAA : 942
GAGCAGACATCTAGAGAATCCGACACGATGATCTAGTCTAA

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Figure S13. The nucleotide sequence alignment of *Bna.A05g08910D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI*, the consensus line. Orange represents SNP and exons are in black.

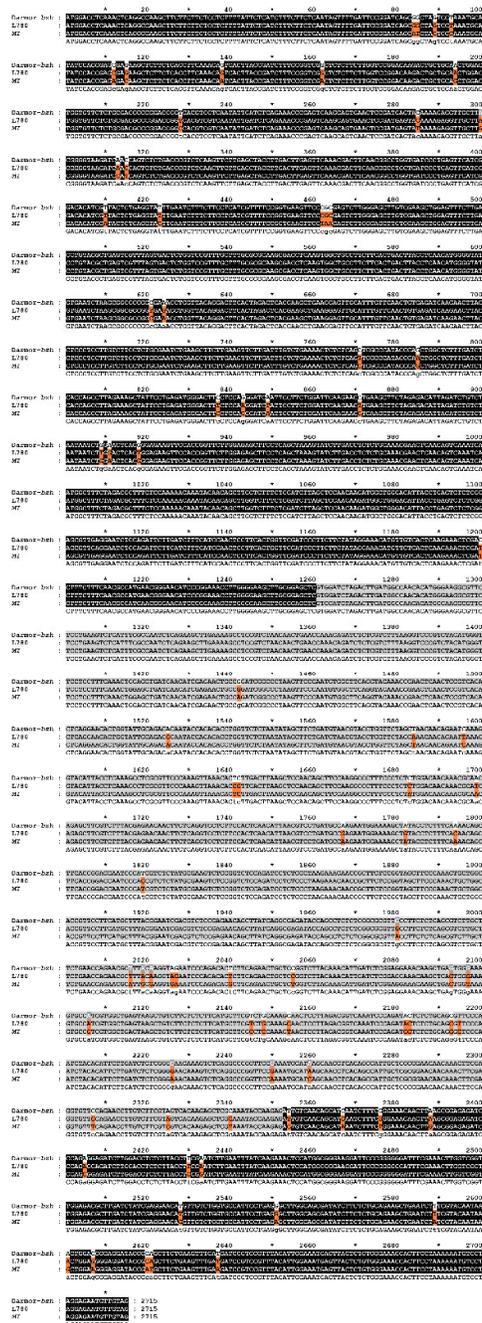


Figure S14. The nucleotide sequence alignment of *Bna.A05g08950D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI*, the consensus line. Orange represents SNP; exons are in black and introns in darkgray.