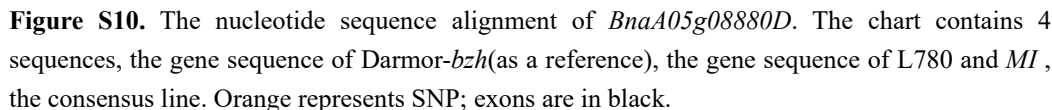


Figure S9. The nucleotide sequence alignment of *BnaA05g08870D*. The chart contains 4 sequences, the gene sequence of Darmor-bzh(as a reference), the gene sequence of L780 and *MI*, the consensus line. Orange represents SNP, red represents insertion, and blue represents deletion; exons are in black and introns in darkgray.



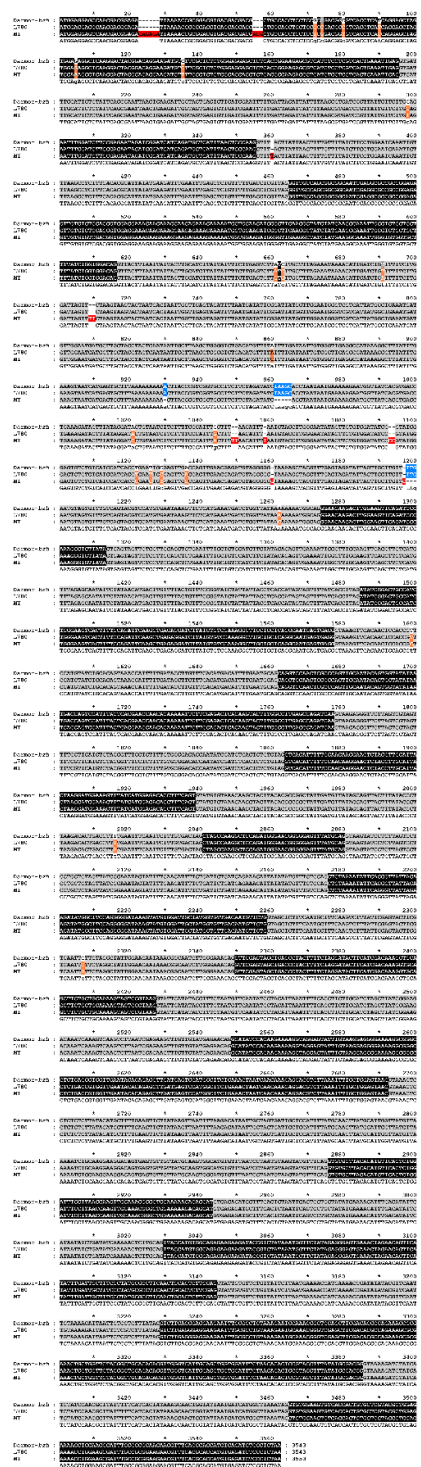


Figure S11. The nucleotide sequence alignment of *BnaA05g08890D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI* , the consensus line. Orange represents SNP, red represents insertion, and blue represents deletion; exons are in black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


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      *      20      *      40      *      60      *      80      *      100
Darmor-bzh : ATGCCAGCGGACGATATGCCACAGCCAGGATTCTGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTCTAGCCTTCTCCATCTTCATCGTGG ;
L780 : ATGCCAGCGGACGATATGCCACAGCCAGGATTCTGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTCTAGCCTTCTCCATCTTCATCGTGG ;
MI : ATGCCAGCGGACGATATGCCACAGCCAGGATTCTGTGAAAAATGAAAGCGACCTAGCCATCATGGTGGCAACGGCTCTAGCCTTCTCCATCTTCATCGTGG ;
      *      120      *      140      *      160      *      180      *      200
Darmor-bzh : GTTTGGCTTCGGTTTGCATATCGCTGGGCGCTGCGCAGGTTTACGCGGACGAGCAATCGGTAAACCTGTCTACACACCCCCAACATGAATCCAGACCGG ;
L780 : GTTTGGCTTCGGTTTGCATATCGCTGGGCGCTGCGCAGGTTTACGCGGACGAGCAATCGGTAAACCTGTCTACACACCCCCAACATGAATCCAGACCGG ;
MI : GTTTGGCTTCGGTTTGCATATCGCTGGGCGCTGCGCAGGTTTACGCGGACGAGCAATCGGTAAACCTGTCTACACACCCCCAACATGAATCCAGACCGG ;
      *      220      *      240      *      260      *      280      *      300
Darmor-bzh : GAGGAGGGGTACGACAGCGCGTGGGATCGACGACGCGATCGTGGAATCGTTTCAGAGCTTCTATACTCTGAGGTGAGGACAGCGATTGGTAAAGG ;
L780 : GAGGAGGGGTACGACAGCGCGTGGGATCGACGACGCGATCGTGGAATCGTTTCAGAGCTTCTATACTCTGAGGTGAGGACAGCGATTGGTAAAGG ;
MI : GAGGAGGGGTACGACAGCGCGTGGGATCGACGACGCGATCGTGGAATCGTTTCAGAGCTTCTATACTCTGAGGTGAGGACAGCGATTGGTAAAGG ;
      *      320      *      340      *      360      *      380      *      400
Darmor-bzh : GGGGTCGAGTGTGTGGTGTGTCTTTGTGAGTCCAGACAAATGATAGGCTGAGTTTGTAGCCTAATTGTTGCAAGTGATATCATGCTGATTGCGTAAGT ;
L780 : GGGGTCGAGTGTGTGGTGTGTCTTTGTGAGTCCAGACAAATGATAGGCTGAGTTTGTAGCCTAATTGTTGCAAGTGATATCATGCTGATTGCGTAAGT ;
MI : GGGGTCGAGTGTGTGGTGTGTCTTTGTGAGTCCAGACAAATGATAGGCTGAGTTTGTAGCCTAATTGTTGCAAGTGATATCATGCTGATTGCGTAAGT ;
      *      420      *      440      *      460      *      480      *      500
Darmor-bzh : TCTGGCTCTCTGATCACTCCACGTGTCCGCTCTGCCGTGTGGATCTTGTCTTCCAACAGGGTCAGGGGAGCGACCCGGATCTTGAATAGGAGTTTGTGA ;
L780 : TCTGGCTCTCTGATCACTCCACGTGTCCGCTCTGCCGTGTGGATCTTGTCTTCCAACAGGGTCAGGGGAGCGACCCGGATCTTGAATAGGAGTTTGTGA ;
MI : TCTGGCTCTCTGATCACTCCACGTGTCCGCTCTGCCGTGTGGATCTTGTCTTCCAACAGGGTCAGGGGAGCGACCCGGATCTTGAATAGGAGTTTGTGA ;
      *      520      *      540      *      560      *      580      *      600
Darmor-bzh : TACTACAGAAGCGCGTTTGTCTGAAAGTATGACGTGGACTAATAGGAGCAGACCGCCTCGGTCTAGGTGATGAGATTGCCCAATTTCGAGTCTCTGGT ;
L780 : TACTACAGAAGCGCGTTTGTCTGAAAGTATGACGTGGACTAATAGGAGCAGACCGCCTCGGTCTAGGTGATGAGATTGCCCAATTTCGAGTCTCTGGT ;
MI : TACTACAGAAGCGCGTTTGTCTGAAAGTATGACGTGGACTAATAGGAGCAGACCGCCTCGGTCTAGGTGATGAGATTGCCCAATTTCGAGTCTCTGGT ;
      *      620      *      640      *      660      *      680      *      700
Darmor-bzh : ATATCATTATCGAGATCTCATTCGACCGGACACCTGTGTGGCTGAACCGGTGGAGAATTTGACACCGGTTTACCAGATGGGTACGGACGA ;
L780 : ATATCATTATCGAGATCTCATTCGACCGGACACCTGTGTGGCTGAACCGGTGGAGAATTTGACACCGGTTTACCAGATGGGTACGGACGA ;
MI : ATATCATTATCGAGATCTCATTCGACCGGACACCTGTGTGGCTGAACCGGTGGAGAATTTGACACCGGTTTACCAGATGGGTACGGACGA ;
      *      720      *      740      *      760      *      780      *      800
Darmor-bzh : GACTGATAAAGAAGAGCGTGGTGAGAAGCTCGCAGGTTTGTACAGAAGCAGAAGTGTGGAAGCAGAAGCGCGAGGAGTGTCTTCTCAGAACAAATGGT ;
L780 : GACTGATAAAGAAGAGCGTGGTGAGAAGCTCGCAGGTTTGTACAGAAGCAGAAGTGTGGAAGCAGAAGCGCGAGGAGTGTCTTCTCAGAACAAATGGT ;
MI : GACTGATAAAGAAGAGCGTGGTGAGAAGCTCGCAGGTTTGTACAGAAGCAGAAGTGTGGAAGCAGAAGCGCGAGGAGTGTCTTCTCAGAACAAATGGT ;
      *      820      *      840      *      860      *      880      *      900
Darmor-bzh : TAACTATAAGAACCATCGGCGGTACATTGATGACTCTCTCCTTCACTGATCATCTTCGCGTATGGTTGGCAGGAGATGTGGTGGCTCCGCCGAATAGT ;
L780 : TAACTATAAGAACCATCGGCGGTACATTGATGACTCTCTCCTTCACTGATCATCTTCGCGTATGGTTGGCAGGAGATGTGGTGGCTCCGCCGAATAGT ;
MI : TAACTATAAGAACCATCGGCGGTACATTGATGACTCTCTCCTTCACTGATCATCTTCGCGTATGGTTGGCAGGAGATGTGGTGGCTCCGCCGAATAGT ;
      *      920      *      940
Darmor-bzh : GAGCAGACATCTAGAGAATTCGACACGATGATCTAGTGTAA : 942
L780 : GAGCAGACATCTAGAGAATTCGACACGATGATCTAGTGTAA : 942
MI : GAGCAGACATCTAGAGAATTCGACACGATGATCTAGTGTAA : 942
GAGCAGACATCTAGAGAATTCGACACGATGATCTAGTGTAA

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Figure S13. The nucleotide 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. Orange represents SNP and exons are in black.

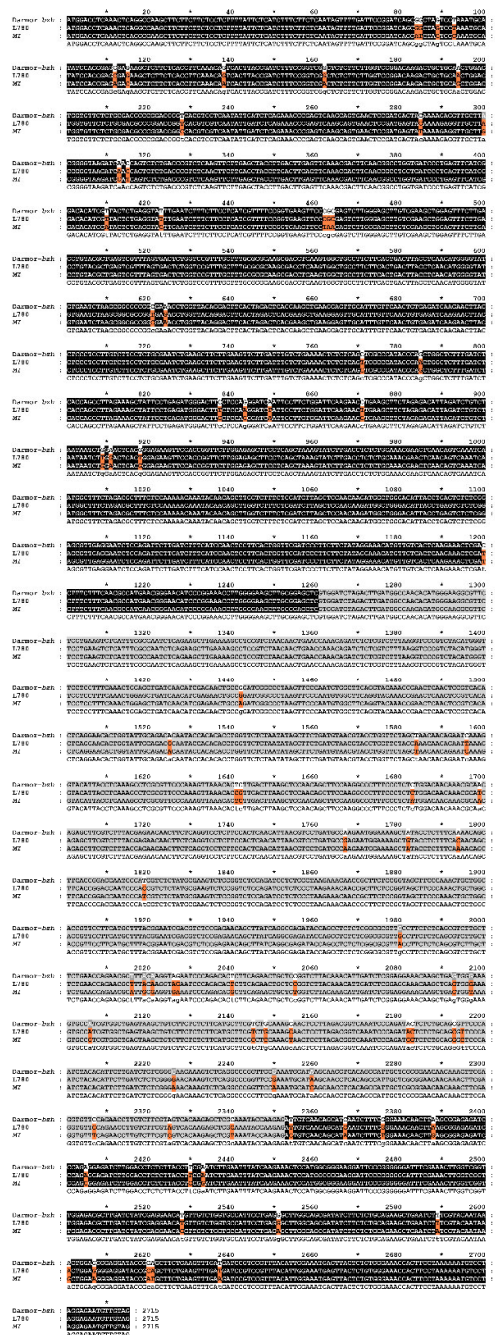


Figure S14. The nucleotide sequence alignment of *BnaA05g08950D*. The chart contains 4 sequences, the gene sequence of Darmor-*bzh*(as a reference), the gene sequence of L780 and *MI*, the consensus line. Orange represents SNP; exons are in black and introns in darkgray.