

Fine Mapping of Tissue Specific Albino Gene (*Bntsa1*) in *Brassica napus*



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Introductions

Chlorophyll is the most important pigment involved in plant photosynthesis, playing curial role in plant growth and crop yield formation. Albino is one kind of mutant which completely lack of chlorophyll. Therefore, these mutants are usually regarded as valuable materials for identifying genes of chlorophyll biosynthesis or degradation, chloroplast differentiation and organelles transplantation, and for revealing how the albino phenotype is regulated as well. Previously, we have identified a mutant in *Brassica napus* (named as *Bntsa1*) which completely lacked of chlorophyll in reproductive tissues such as buds, flowers, siliques and developing seeds but vegetative tissues including leaves and stems are all in green as wild type plants in the whole life cycle. To investigate the formation of this interesting trait, genetic analysis and gene mapping were performed accordingly.

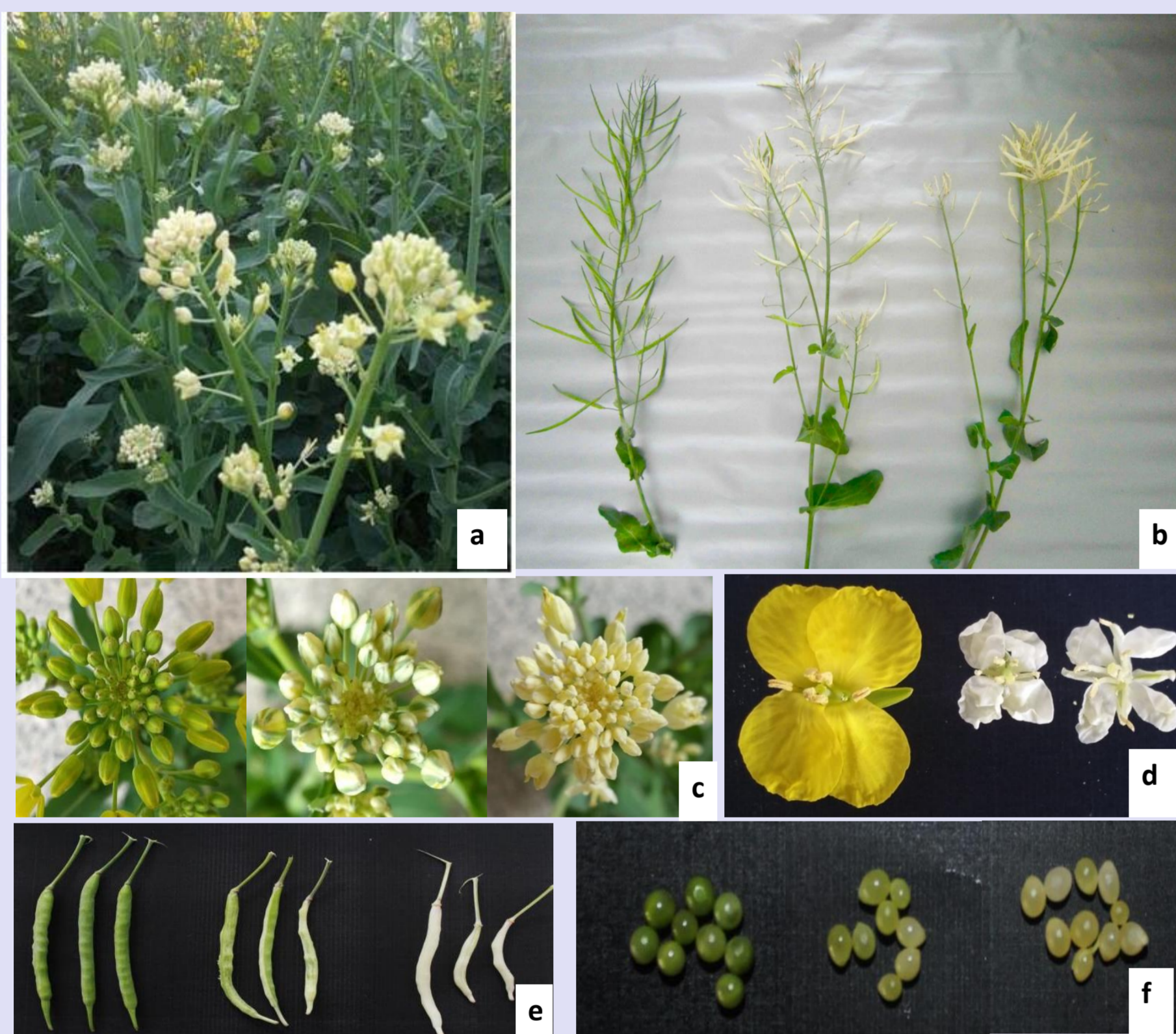


Fig. 1 The mutant *Bntsa1* in the field, which completely lacked of chlorophyll in reproductive tissues but vegetative tissues are normal in whole life cycle(a); Phenotypic segregation in a F_2 population: from left to right are branches (b), buds (c), flowers (d), siliques (e), seeds (f) of normal wild type plant and heterozygous, homozygous albino mutant, respectively.

Strategies

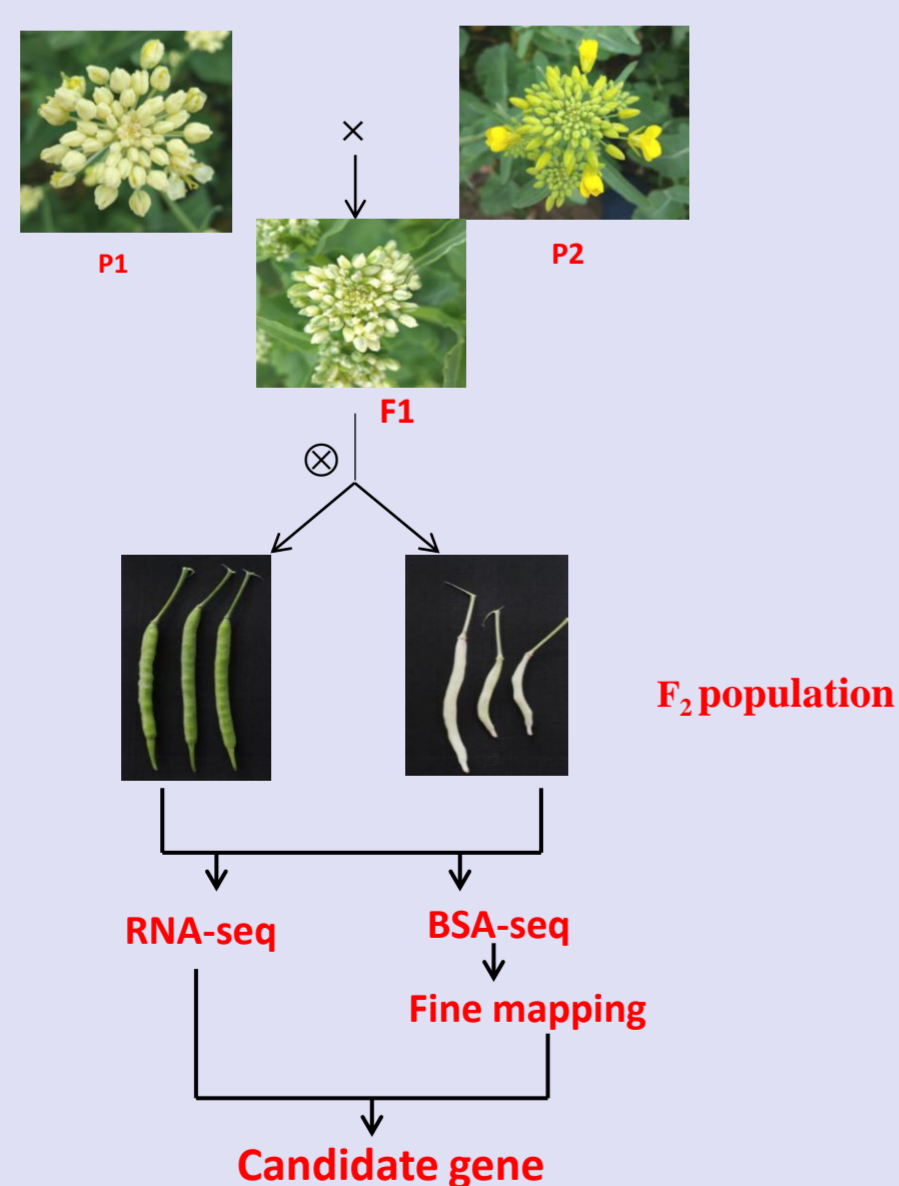


Fig. 2 A strategy of BSA-seq and RNA-seq have been employed on two DNA/RNA bulks of normal green siliques and homozygous albino siliques, respectively, for identifying candidate genes.

Results

- 1. F_1 plants presented an incomplete albino phenotype in reproductive tissues, and segregation ratio of 1:2:1 was observed in F_2 generation.
- 2. *Bntsa1* was mapped onto chromosome A03 within 145kb region between 5363001 and 5508604 (Fig 3).

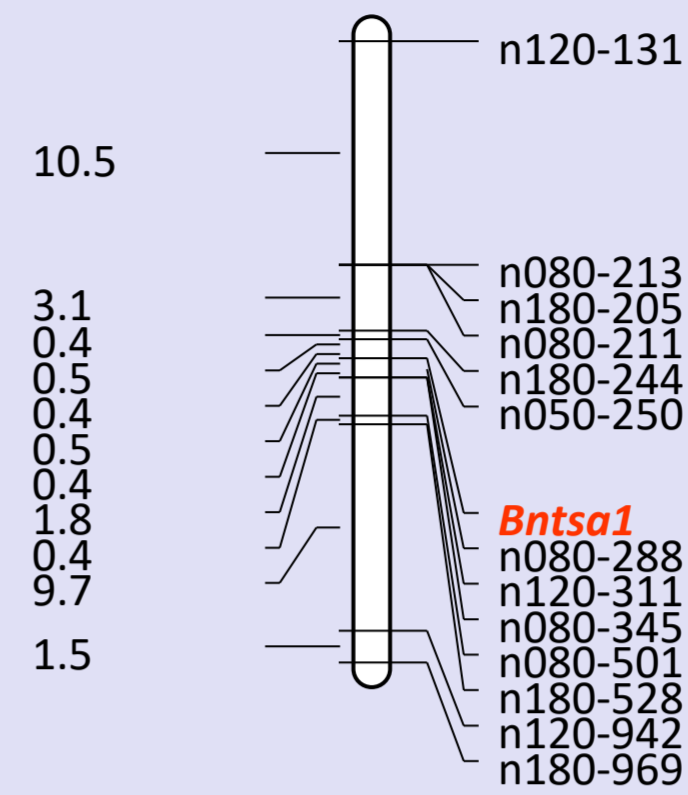


Fig. 3 *Bntsa1* was mapped onto A3 chromosome within 145kb region.

- 3. Totally, 39 ORFs within this region were predicted, of which 38 have homologous genes in *Arabidopsis thaliana*.
- 4. Of 39 ORFs, 6 genes have differences between bulks at DNA or expression level.

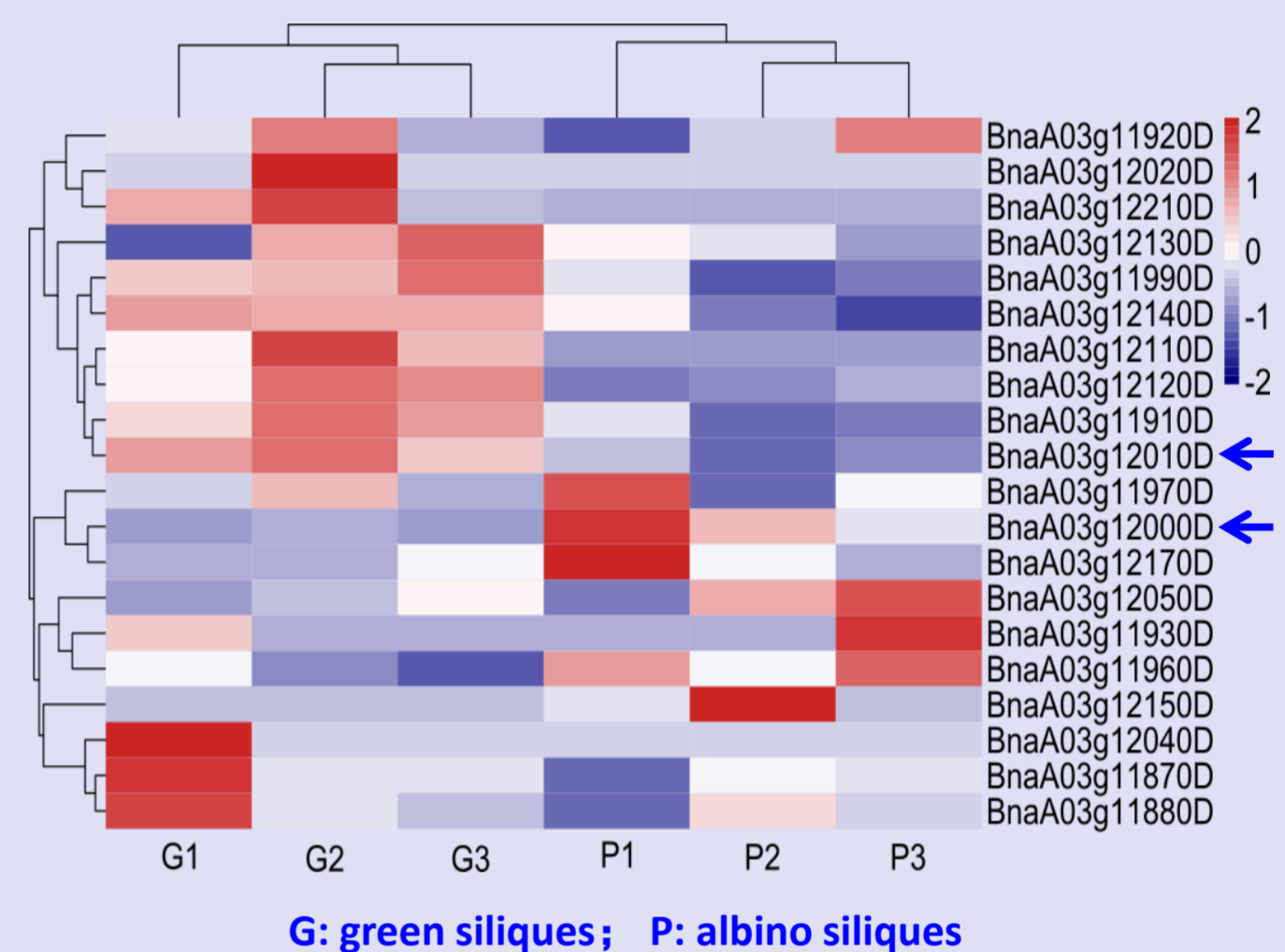


Fig. 4 Transcriptomic analysis shows 3 genes have significant differences at expression levels between two bulks within the mapped region.

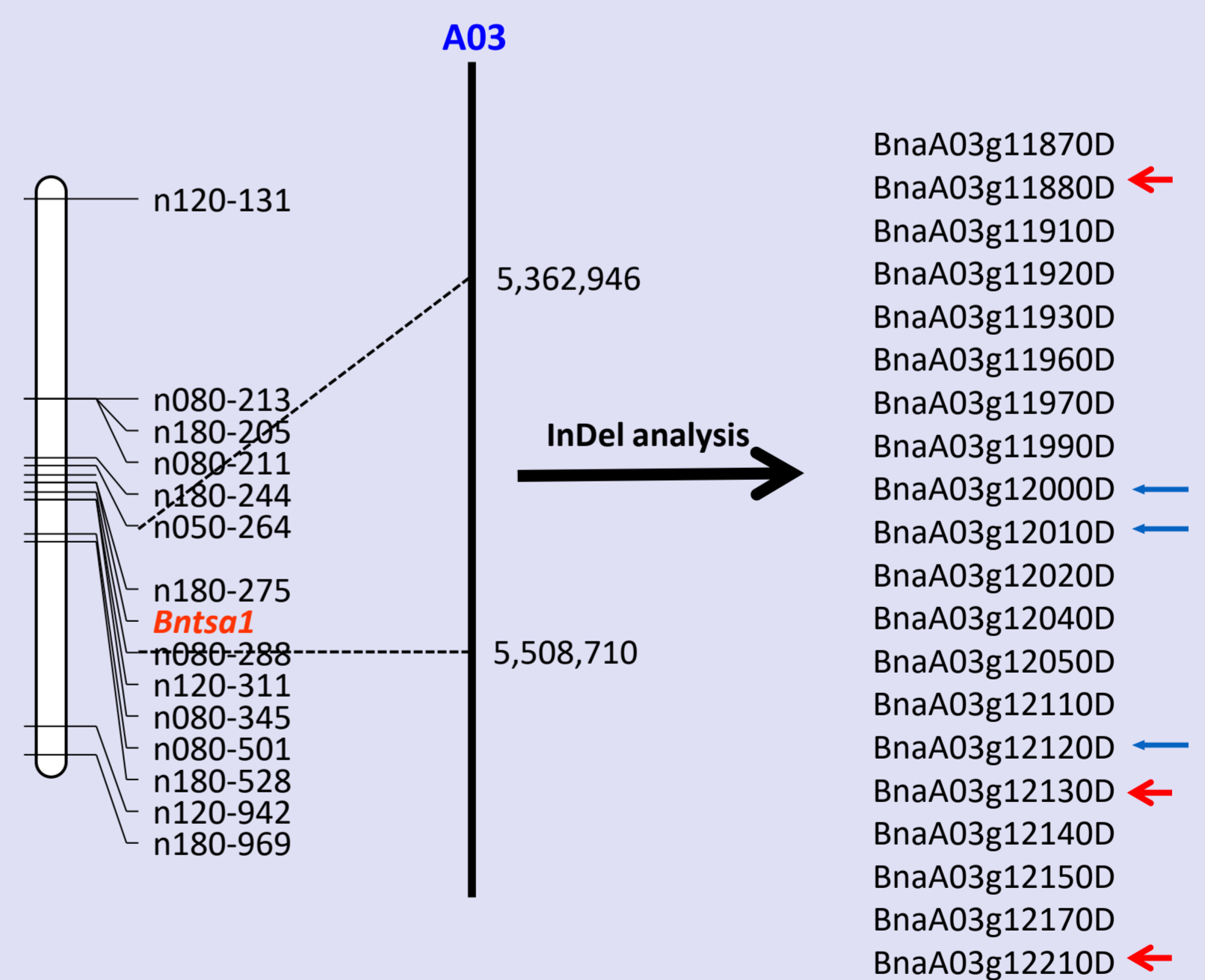


Fig.5 Totally 6 candidate genes were identified based on comparison of the differences at expression and DNA levels.

Conclutions

- A reproductive tissue albino mutant (*Bntsa1*) was indentified, and this trait was controlled by single nuclear gene in an incompletely dominant model.
- *Bntsa1* was mapped onto chromosome A03 within 145kb region between 5363001 and 5508604 by using BSA-seq and RNA-seq analysis with a small F_2 population.
- Six candidate genes were finally indentified, none of them are involved in the chlorophyll biosynthetic pathway.
- This result might provide new knowledges for further understanding the chlorophyll formation or chloroplast differentiation.