

WILD WHEAT FRAGMENT LINES

All modern bread wheats have developed from a wheat that arose 10,000 years ago by a chance crossing between an early primitive wheat, wild emmer – *Triticum dicoccoides*, and the related weed, goatgrass – *Aegilops tauschii*. By recreating this ancient event, plant breeders can find new genetic diversity for a range of important traits.

Focus on NIAB research

NIAB has created two independent chromosome segment substitution line (CSSL) populations to support the characterisation and use of ancestral genetic variation in wheat. The AB genome of wild emmer and the D genome of goatgrass have been captured as small, overlapping introgressions in the genetic background of spring wheat variety Paragon.

When both the NIAB_AB and NIAB_D series were compared with Paragon, variation was seen for many traits. Lines were identified with phenotypes that could be associated with the location of the introgressed segments.

These CSSL populations are a resource to aid trait validation and development of fine mapping resources in wheat pre-breeding.

Figure 3. Graphical genotype of 109 CSSL lines; the wild wheat fragments in each line are shown in orange (TTD-140, A and B genomes) and mid-blue (*Ae. tauschii* Ent-336, D genome)

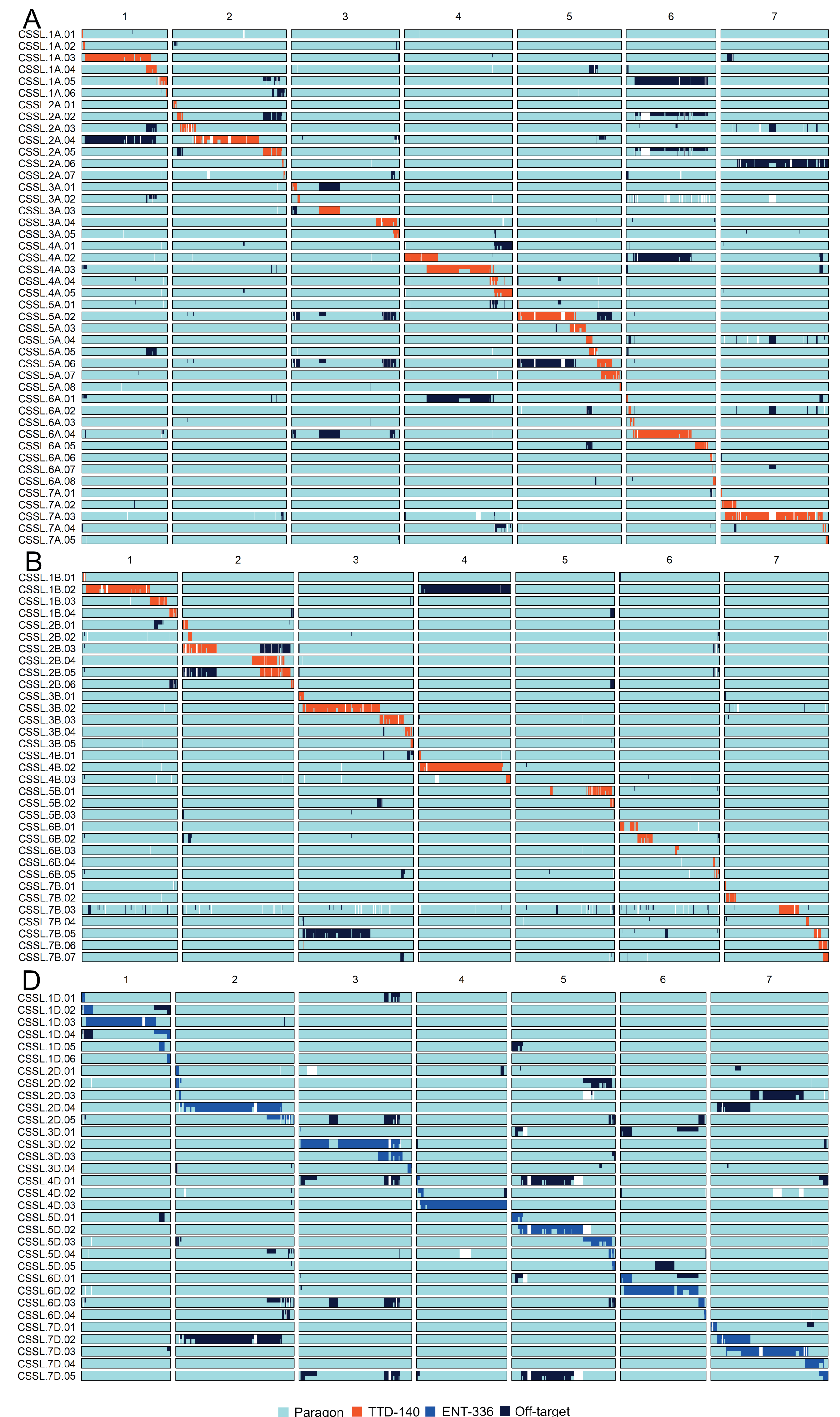


Figure 1. Identification of a *T. dicoccoides* wild fragment that includes a gene (called B1 awn inhibitor) allowing awn development

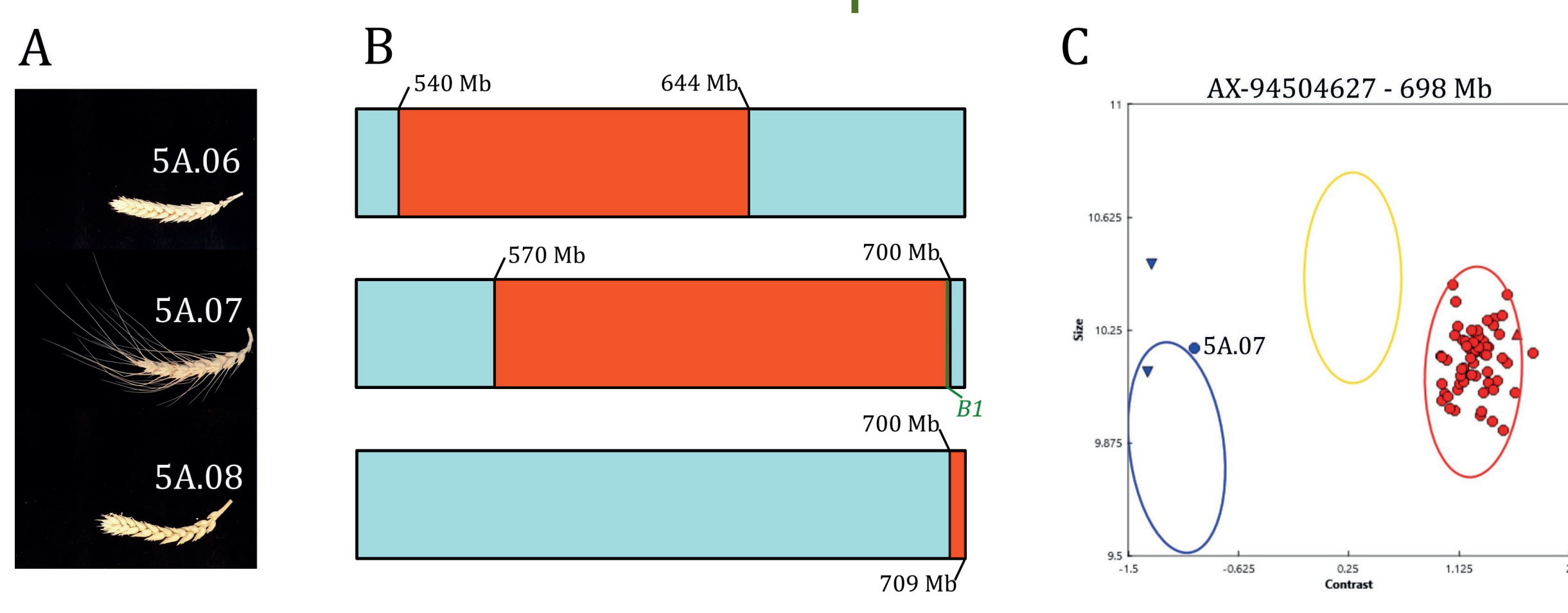
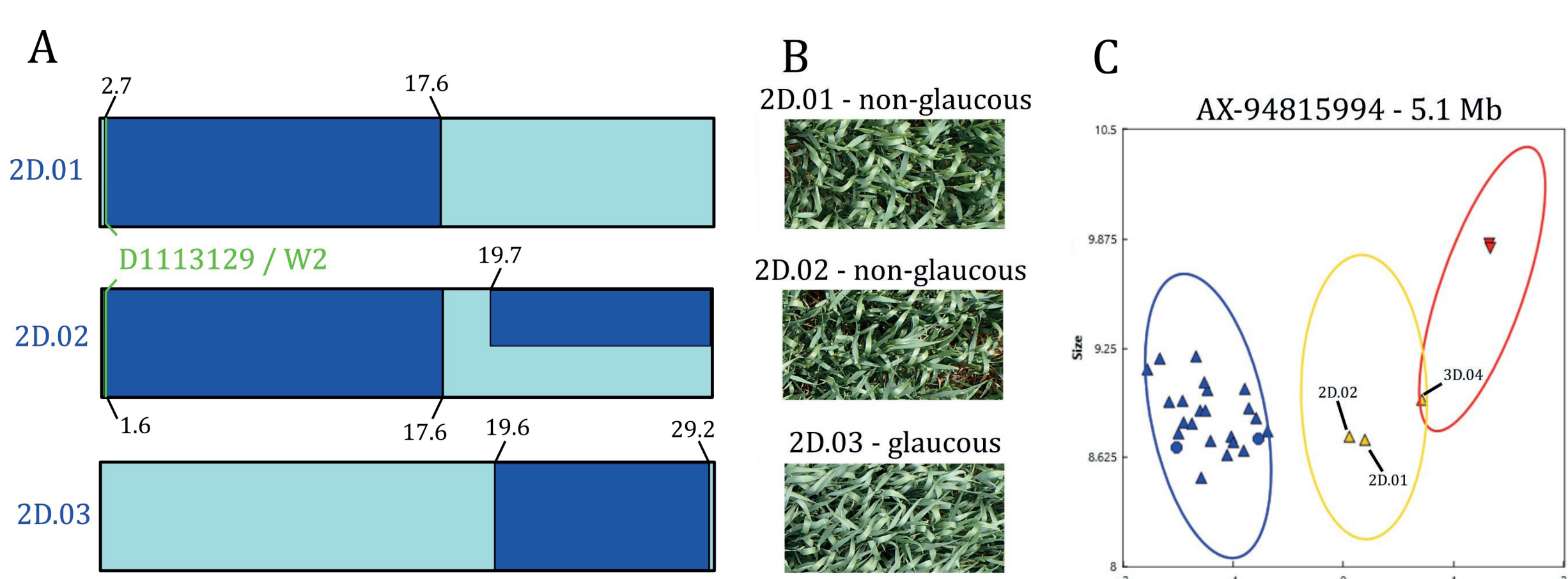


Figure 2. identification of an *Ae. tauschii* wild fragment that includes a gene that alters the waxy appearance of leaves and ears



Genome – a plant's complete set of genetic information

Introgression – the transfer of genetic material from one line into another by repeatedly crossing with one of the parents

Phenotype – the observable characteristics of a plant, resulting from the interaction of its genes with the growing environment

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