

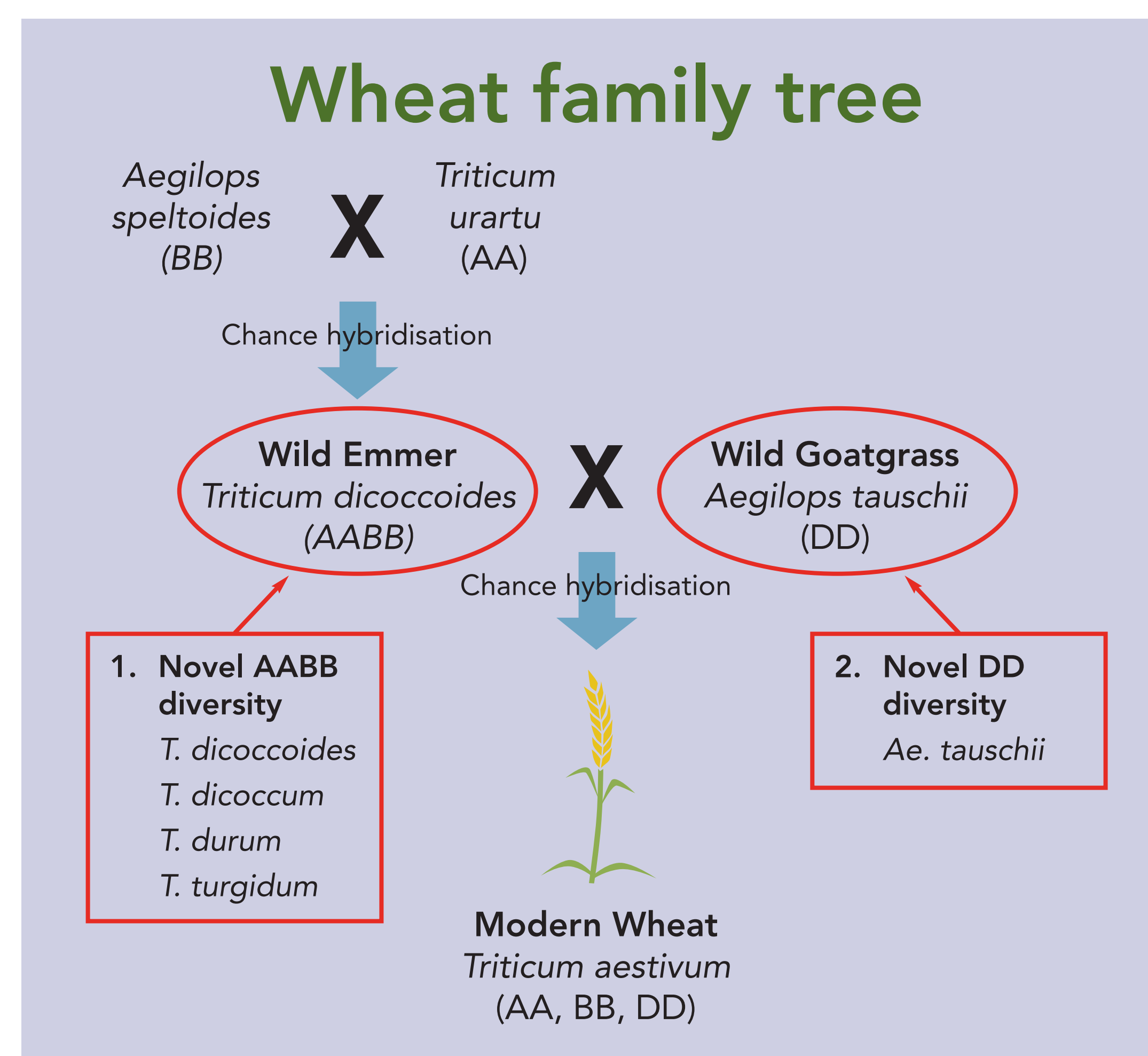
# INCREASING GENETIC DIVERSITY IN WHEAT

Wheat is a hexaploid (42 chromosomes, ABD genomes). Its ancestors include tetraploids (28, AB genomes) and diploids (14, D genome).

NIAB is using two approaches to increase the genetic diversity of wheat:

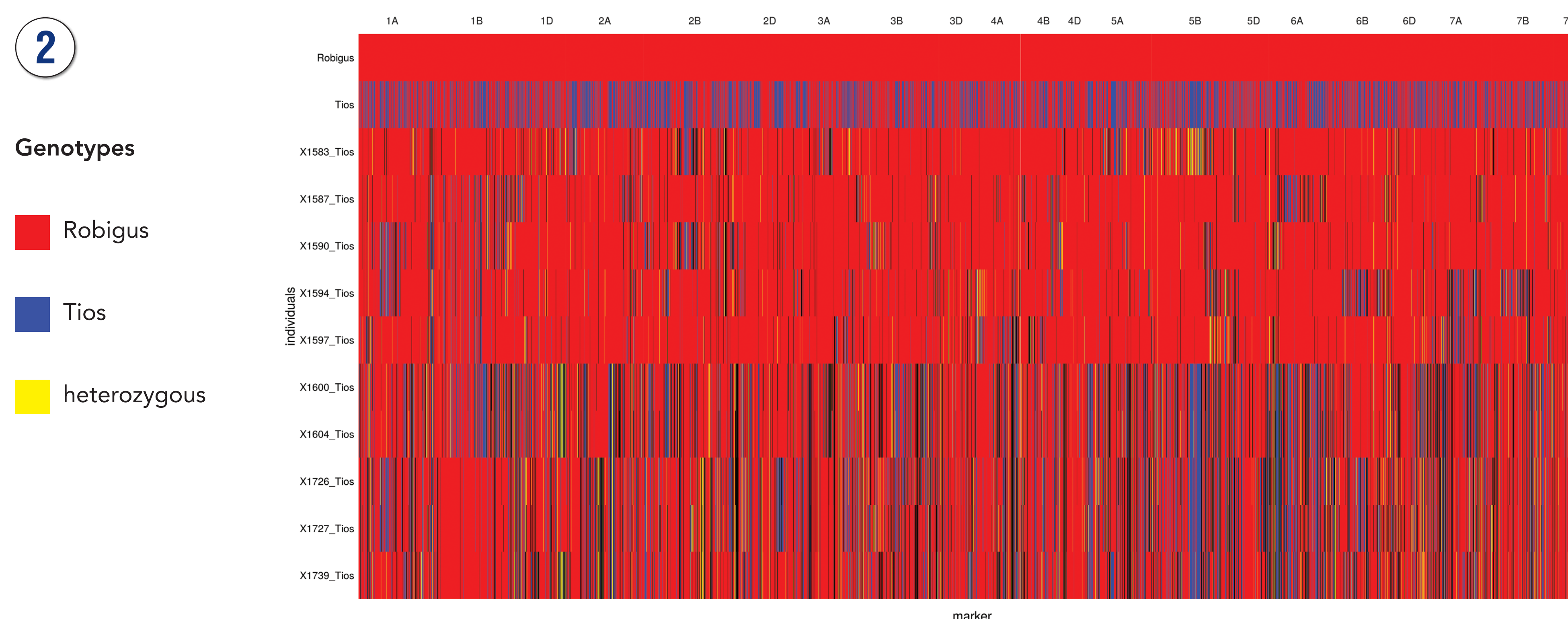
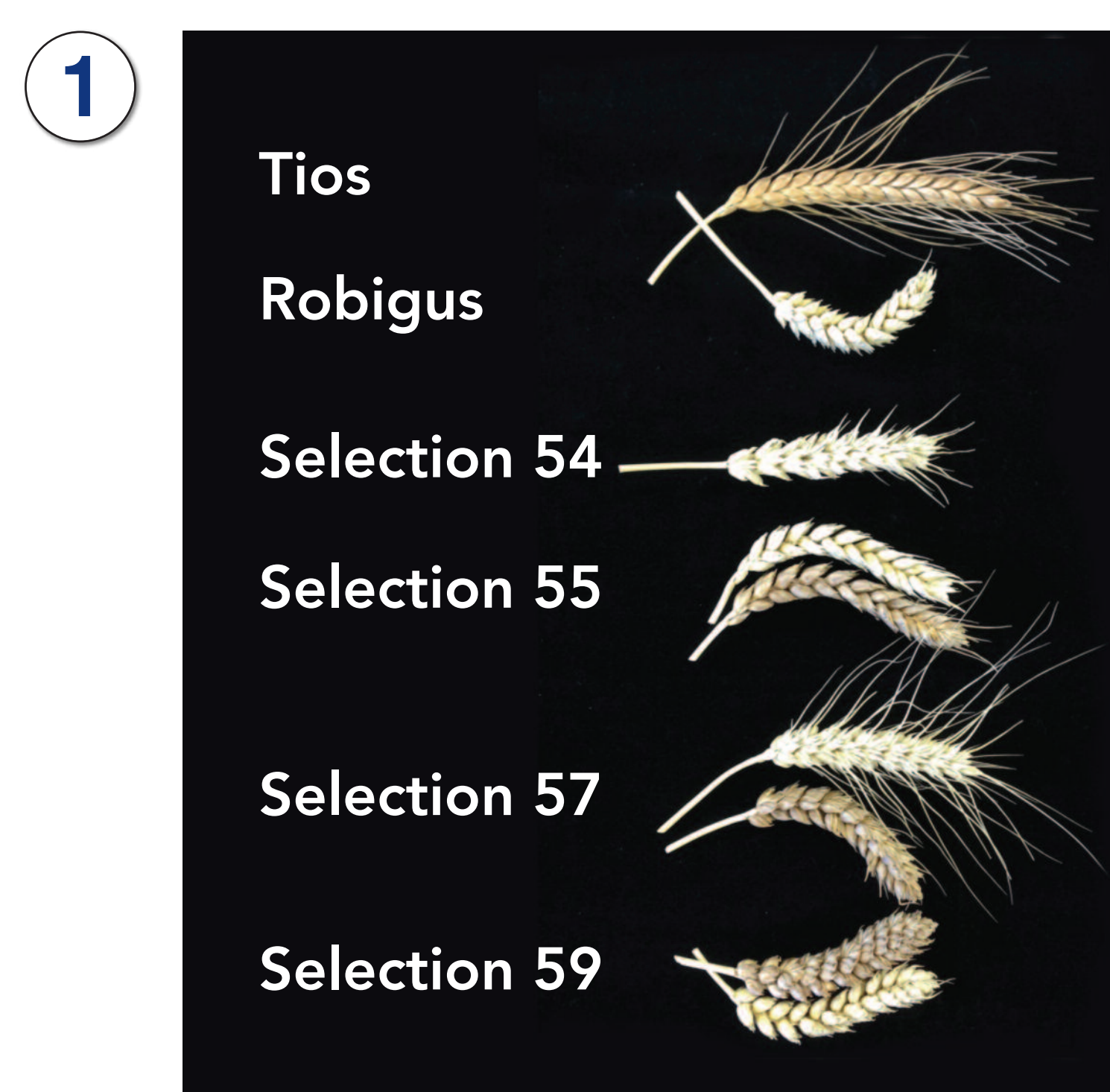
1. Crossing directly with tetraploid wheat to import variation into the A and B genomes.
2. Crossing with novel re-synthesised wheat (SHW) to import D genome diversity.

Traits observed include higher grain micronutrient content, different photosynthetic capacity and water-use efficiency, variation in pest and disease resistance and different leaf and ear morphologies.



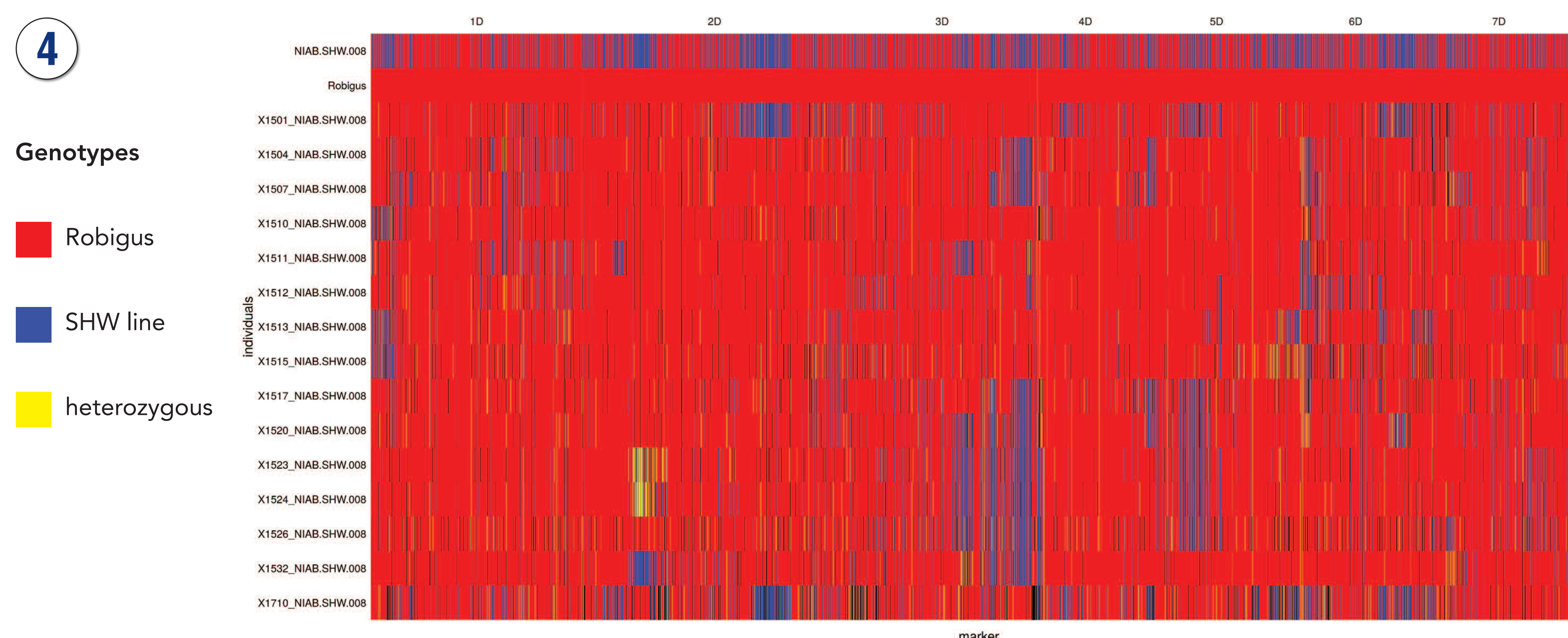
## AB genome diversity

50 tetraploids including wild emmer (*T. dicoccoides*), cultivated emmer (*T. dicoccum*) and durum wheat (*T. durum*) have been crossed to current varieties Paragon and Robigus. The resulting lines are being characterised for phenotype (1). Graphical genotypes (2) clearly show introgressions – genetic material transferred from the tetraploid parents.



## Resynthesis and D genome diversity

50 novel SHWs have been created, each containing the D genome from a different goatgrass. Each novel SHW is crossed to Paragon and Robigus (3). Introgressions from the D genome donor are identified with genetic markers (4).



Highly variable populations are being created from each cross and demonstrated at NIAB Cambridge each year. These lines, capturing novel variation, are the starting material for new collaborations with breeders and researchers.