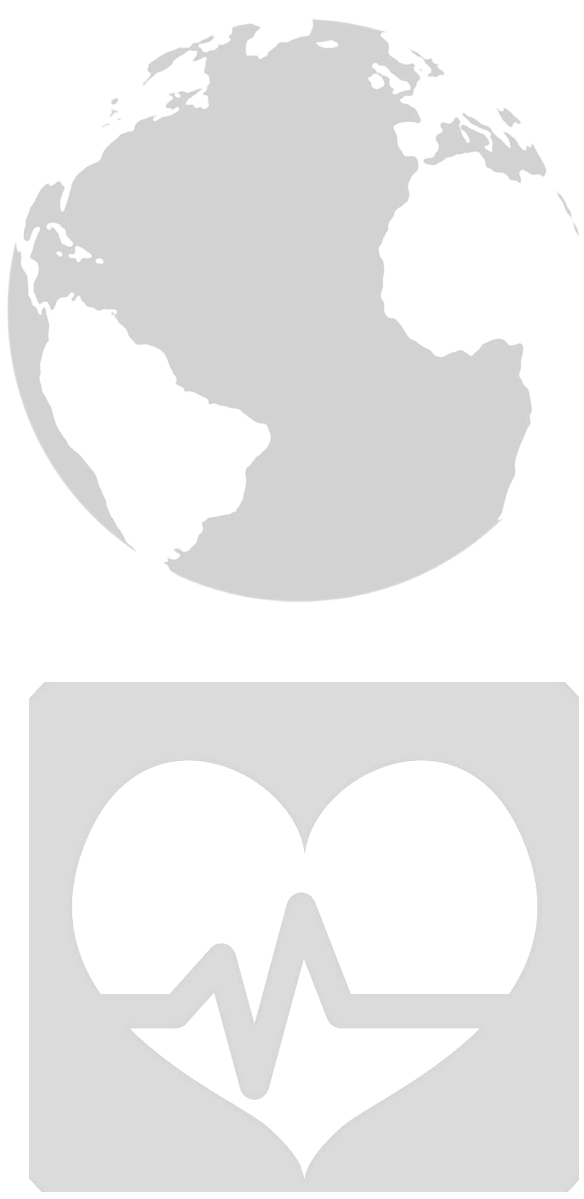


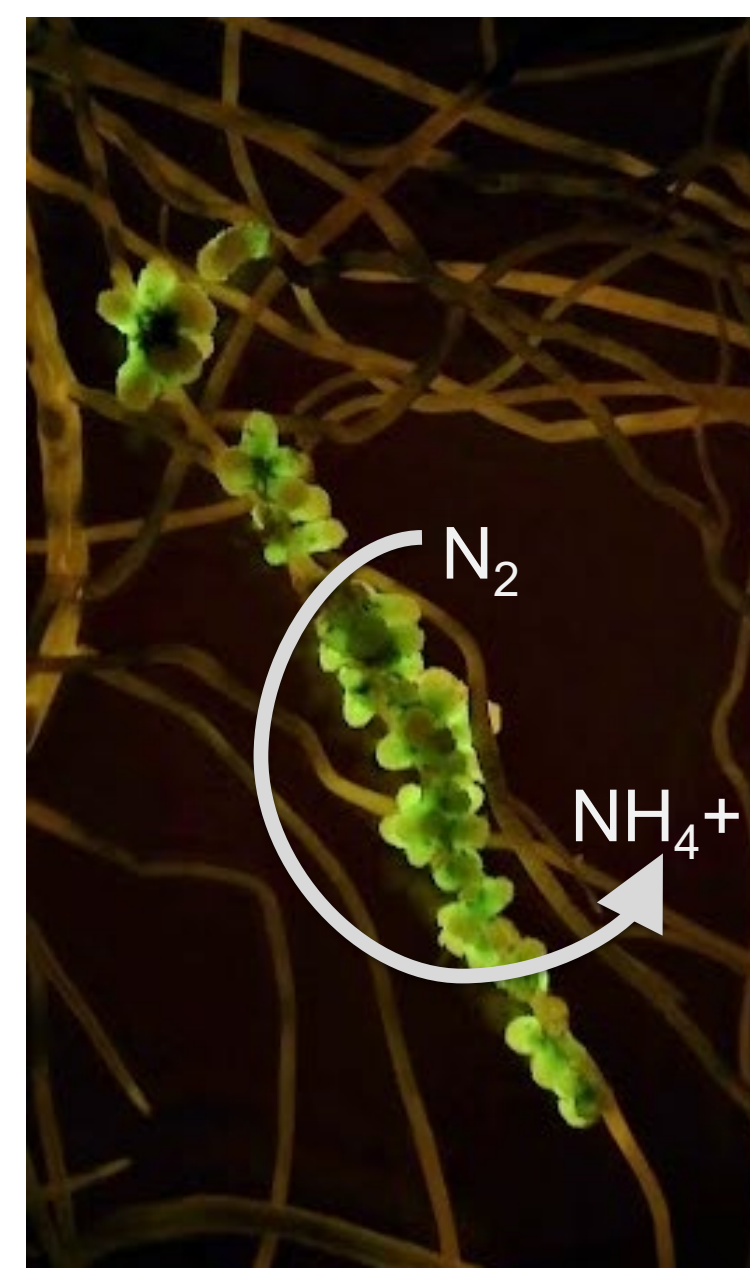
Optimizing sustainable plant-based protein for local production

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Background



CLIMATE & HEALTH considerations drive increased interest in plant-based, local, and sustainable protein production. Cultivation of legumes is central for achieving the global goals, promising reduction in chemical fertilizer usage.



LEGUMES

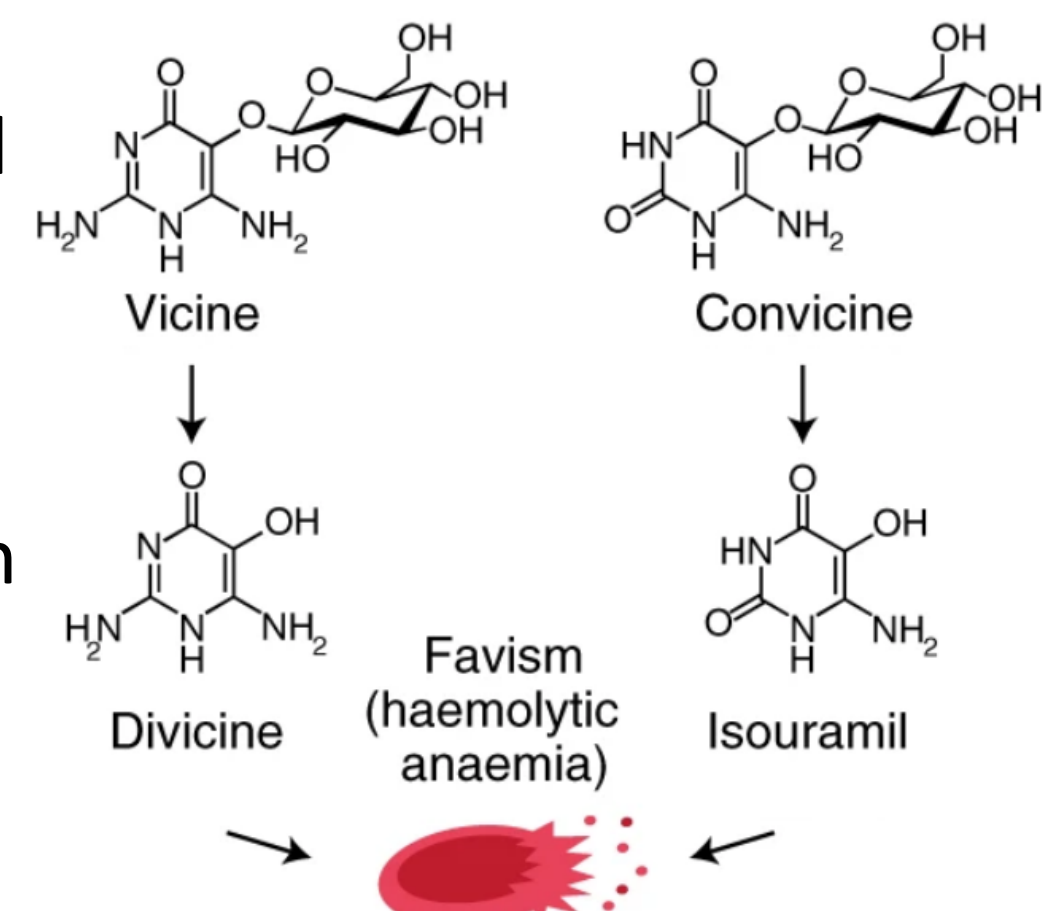
engage in root nodule symbiosis with soil bacteria called rhizobia. Rhizobia capture nitrogen from the air supporting growth of the host.



FABA BEAN (*Vicia faba*) is a legume crop cultivated for its high-protein seeds. It is adapted to a wide variety of climates, thus offering an opportunity to reduce the import of soy from overseas, and boost local protein production for food and feed in Europe.

Challenges we address

Faba beans produce vicine and convicine (V&C). V&C can cause favism, a haemolytic anaemia, in people with G6PD deficiency - a genetic condition affecting 400 million people worldwide.



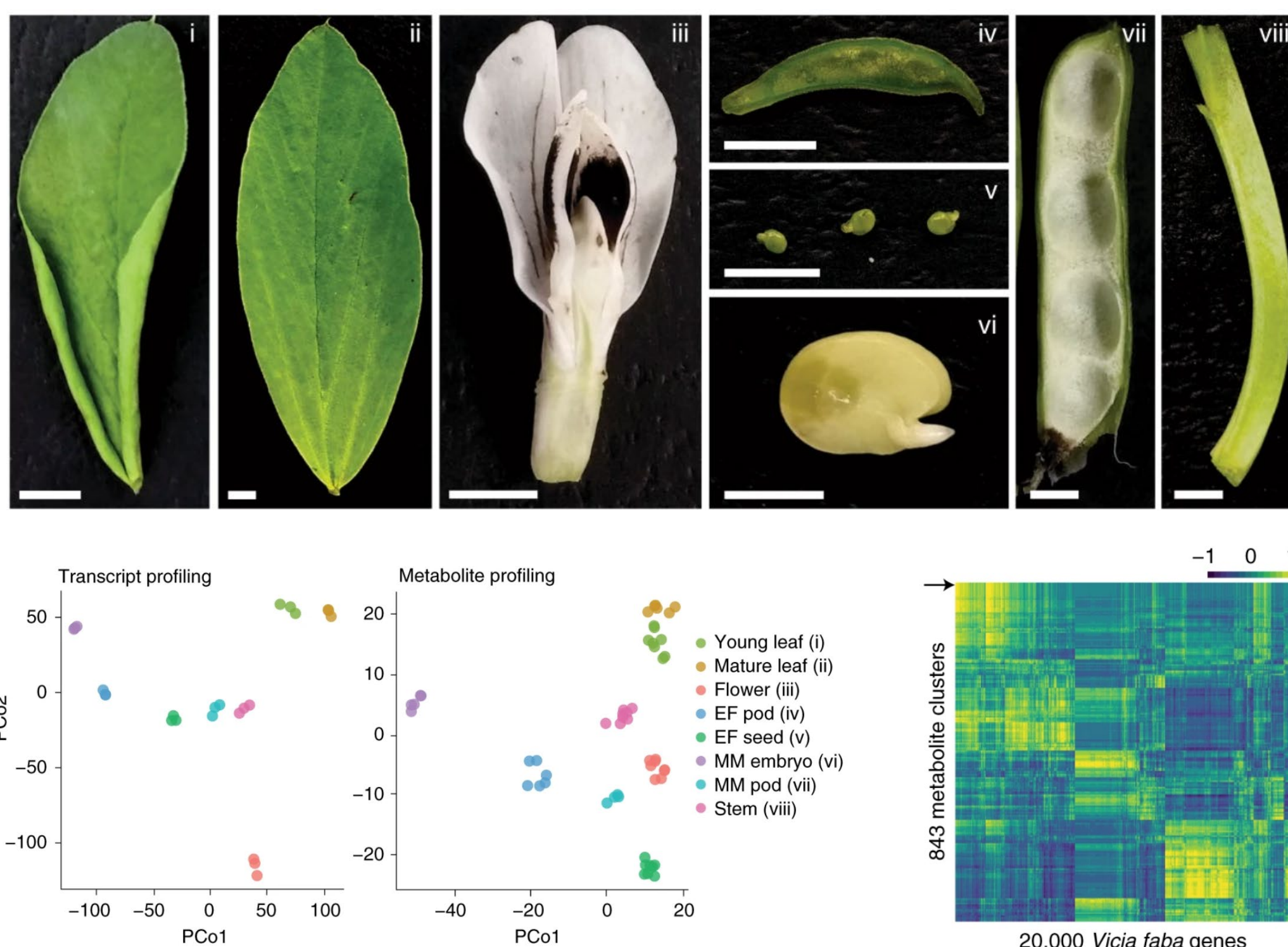
Faba beans suffer from yield instability due to stresses. Grain protein composition could be improved ensuring better nutritional composition.



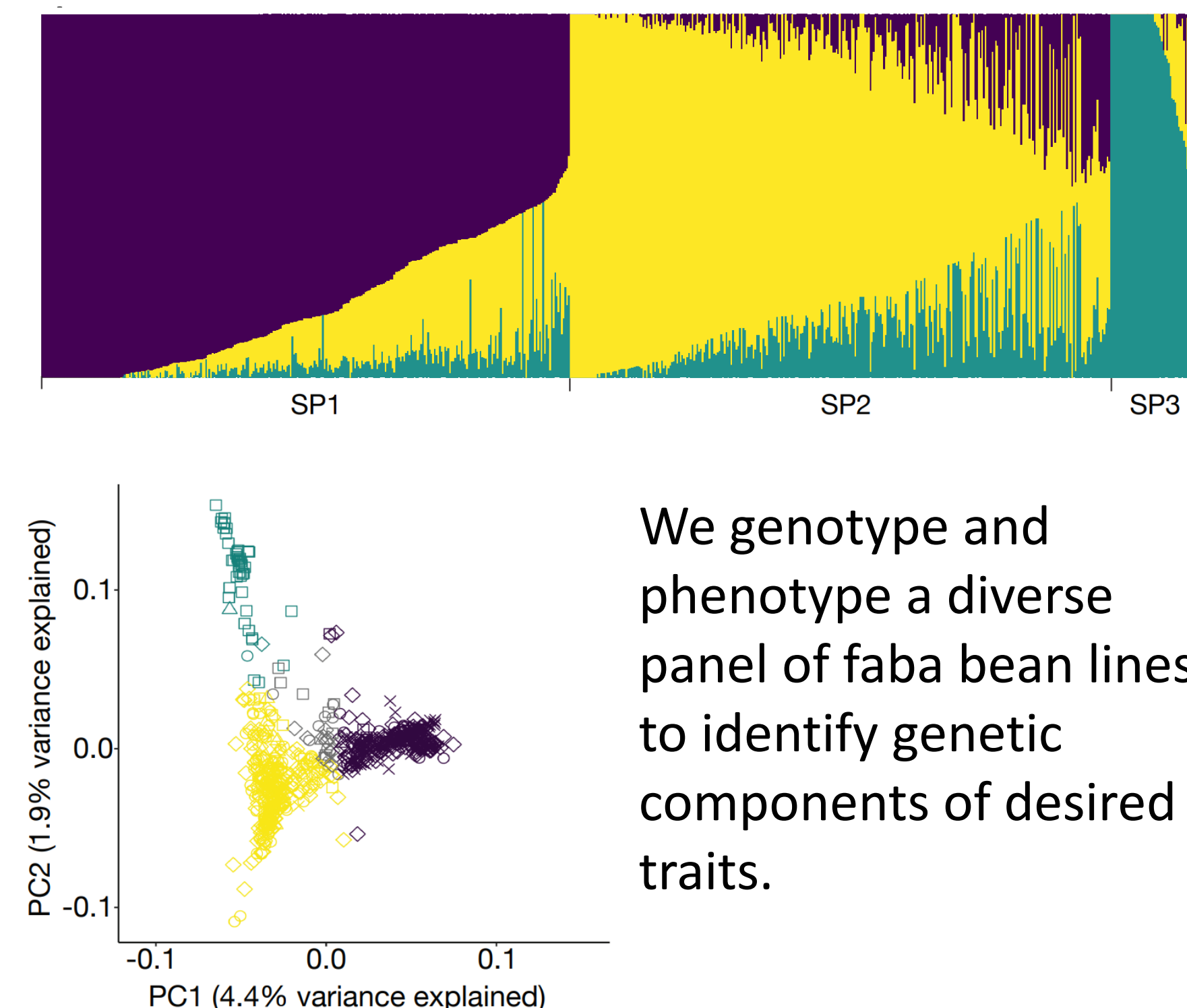
Efficient nitrogen fixation depends of both plant and bacterial genetics. Pairing faba beans with their optimal symbiotic match has not yet been explored.

Our approach

Develop detailed omics

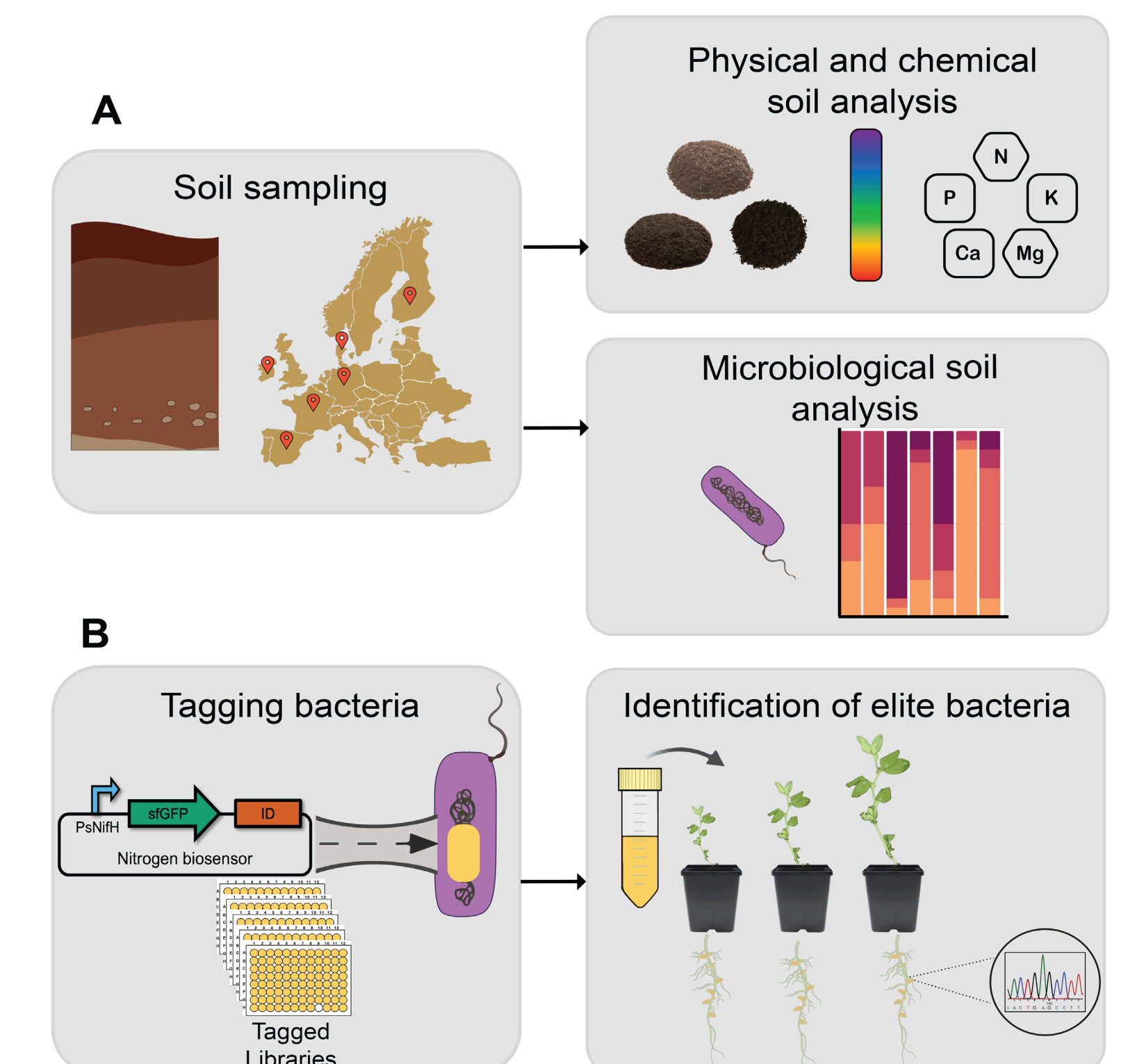


Explore genetic variation in faba



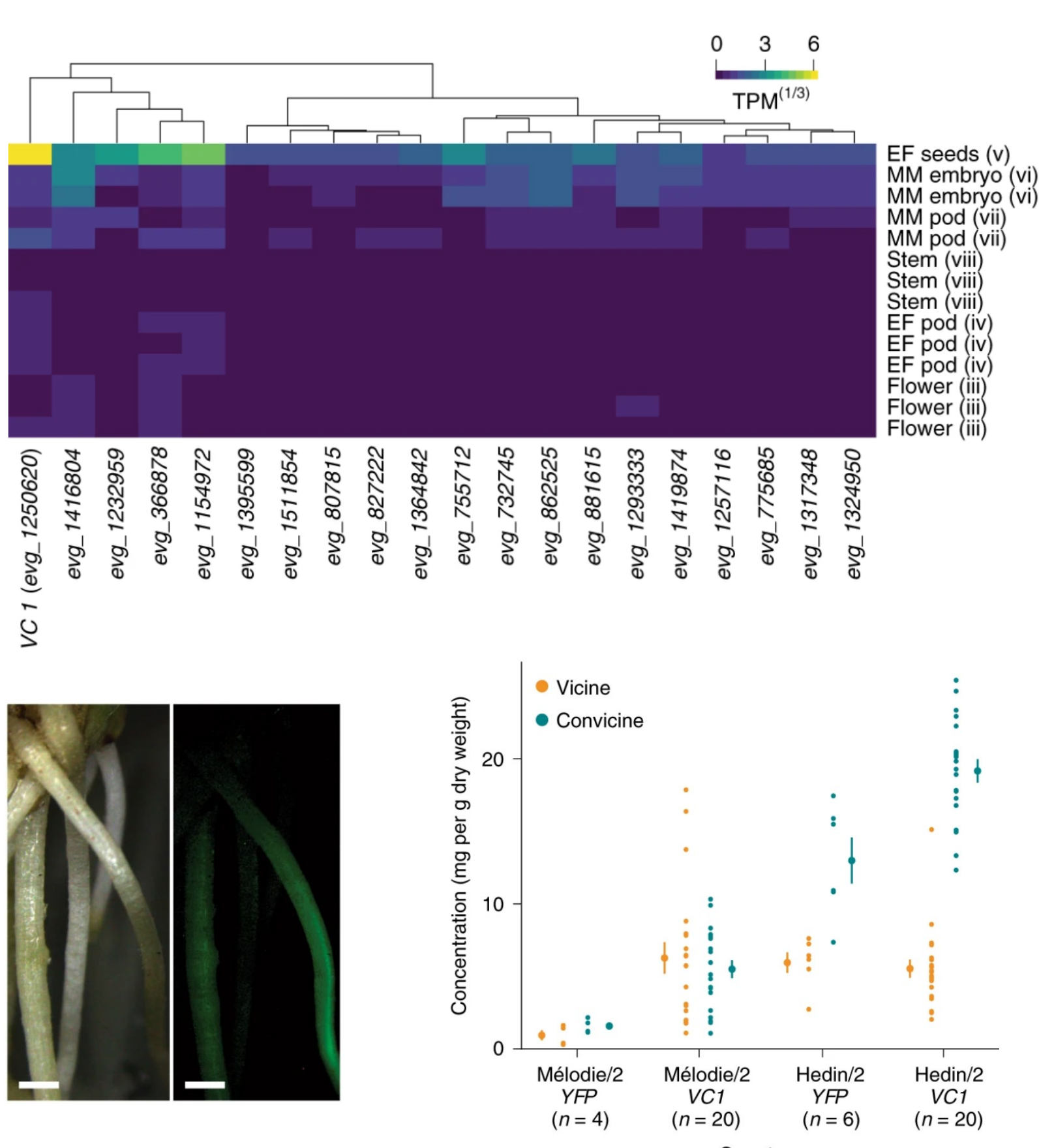
We genotype and phenotype a diverse panel of faba bean lines to identify genetic components of desired traits.

Assess nitrogen fixing capabilities



Advances we make

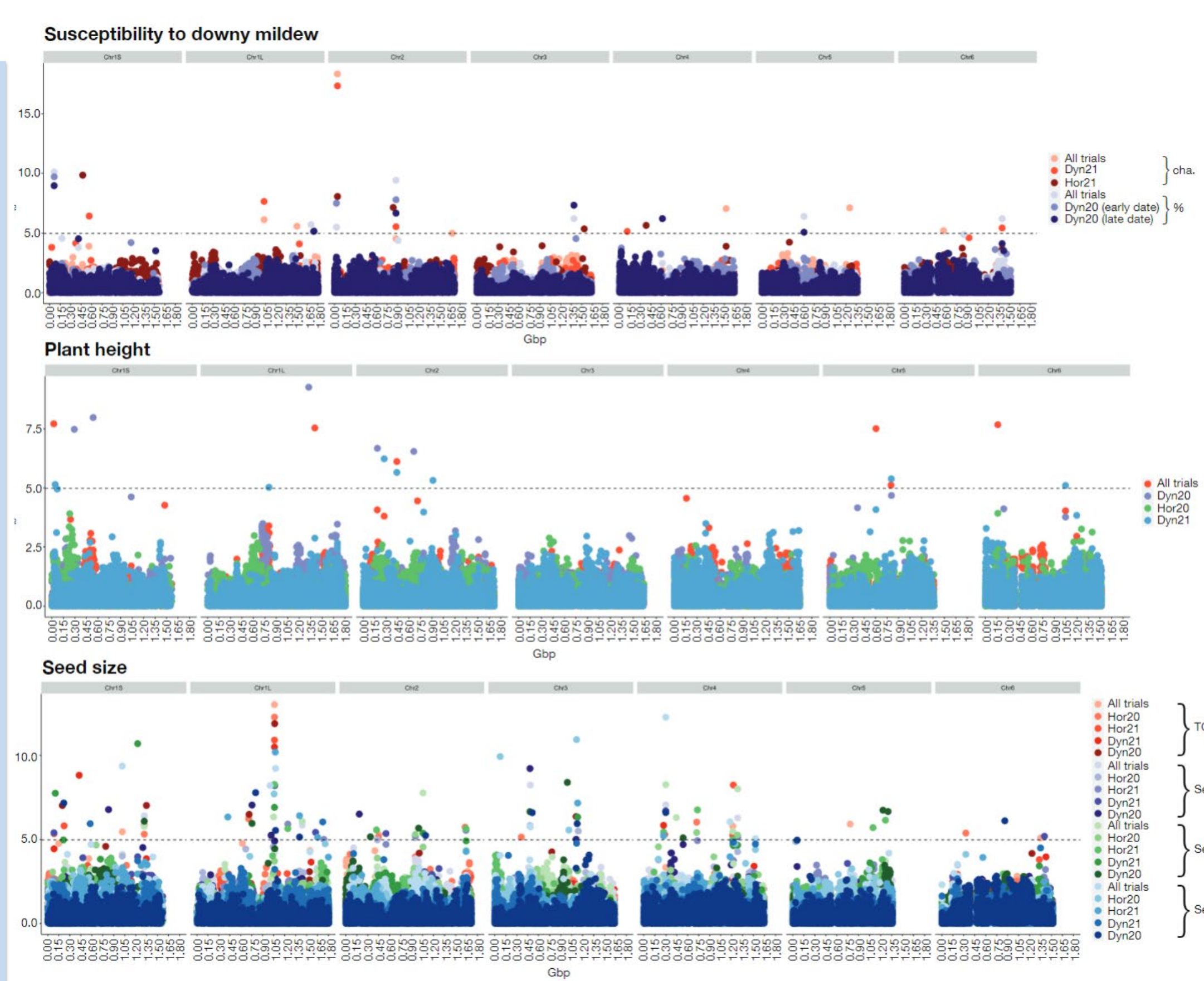
V&C biosynthesis – novel insights



We identified **VC1** – crucial gene involved in biosynthesis of V&C. This will aid in removing V&C from faba bean for improved food safety.



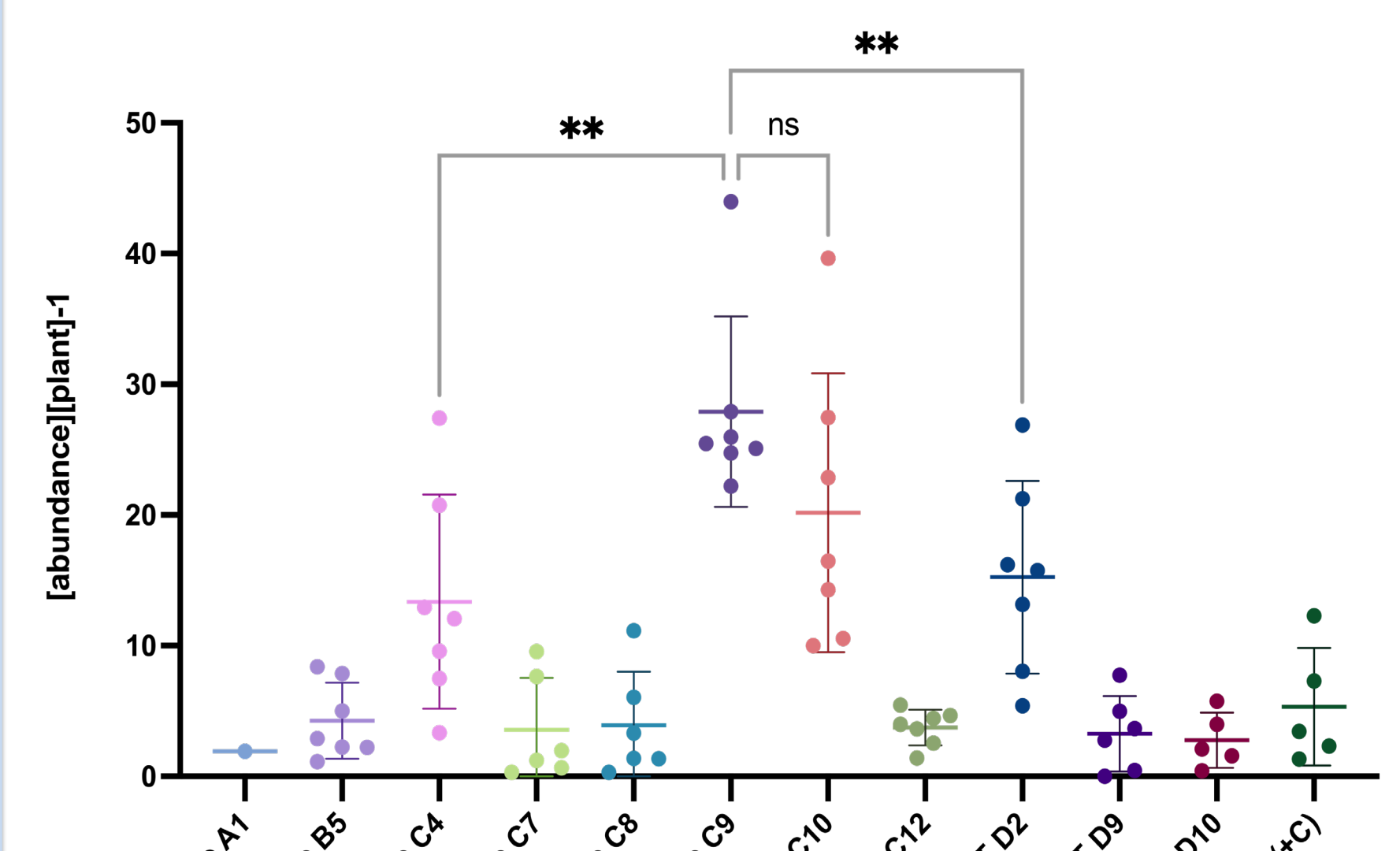
Trait genetics



We use Genome Wide Association Studies to find genetic markers for agronomy-relevant traits. These markers will be used in breeding programmes to obtain improved faba bean varieties.

Rhizobial competition

We created a collection of approx. 1000 rhizobial isolates and tagged them with nitrogen biosensor, giving us the opportunity to simultaneously test up to 475 different rhizobia across 200+ faba bean genotypes.



The setup enabled us to identify strains that increase the plant biomass by 26% when they are introduced to soils with suboptimal native rhizobia composition.