SUPPLEMENTARY DATA

Fig. S1. Legume phylogenetic tree. A phylogenetic tree illustrating the evolutionary history of the Phaseoloids. Stars denote known WGD events. The more ancient event, common to all legume species, occurred 60 MYA. A second WGD event occurred 13 MYA in the ancestral species of *G. max* and *G. soja*. *G. max* and *G. soja* diverged from a common ancestor 287 thousand years ago, followed by domestication of *G. max* (denoted by §) 6–9000 years ago.

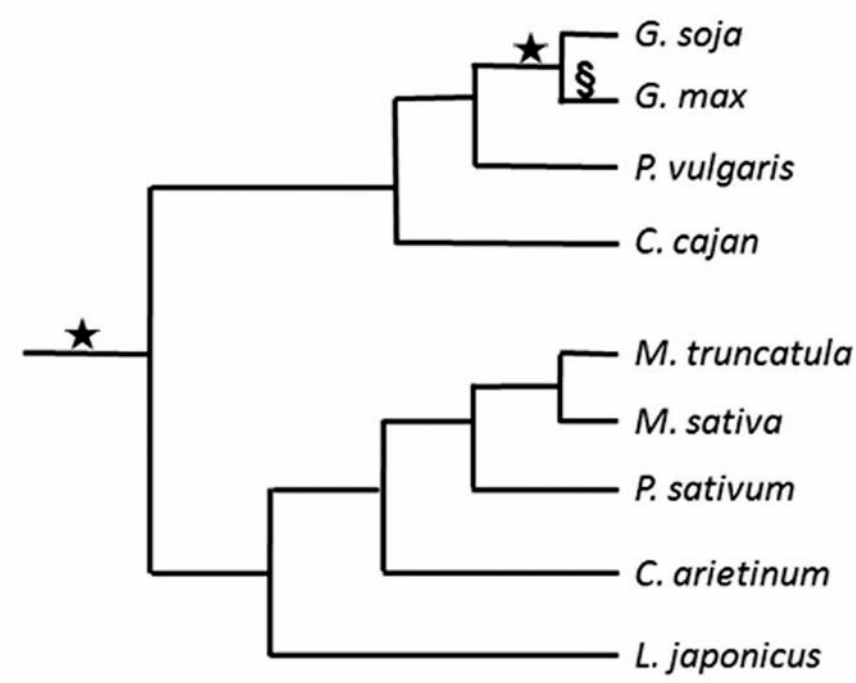

Fig. S2. Metabolism overview of P_i deficiency in leaves. Classification of transcripts differentially expressed due to P_i deficiency in leaves using MapMan (Thimm *et al*. 2004). MapMan categories in red are up regulated in P_i deficient leaves, while categories in blue are up regulated in P_i sufficient leaves. Note the increased expression of lipid metabolism, sulfur assimilation, and cell wall modification in P_i deficient leaves and the increased expression of transcripts involved in photosynthesis, ATP and flavonoid biosynthesis in P_i sufficient leaves.

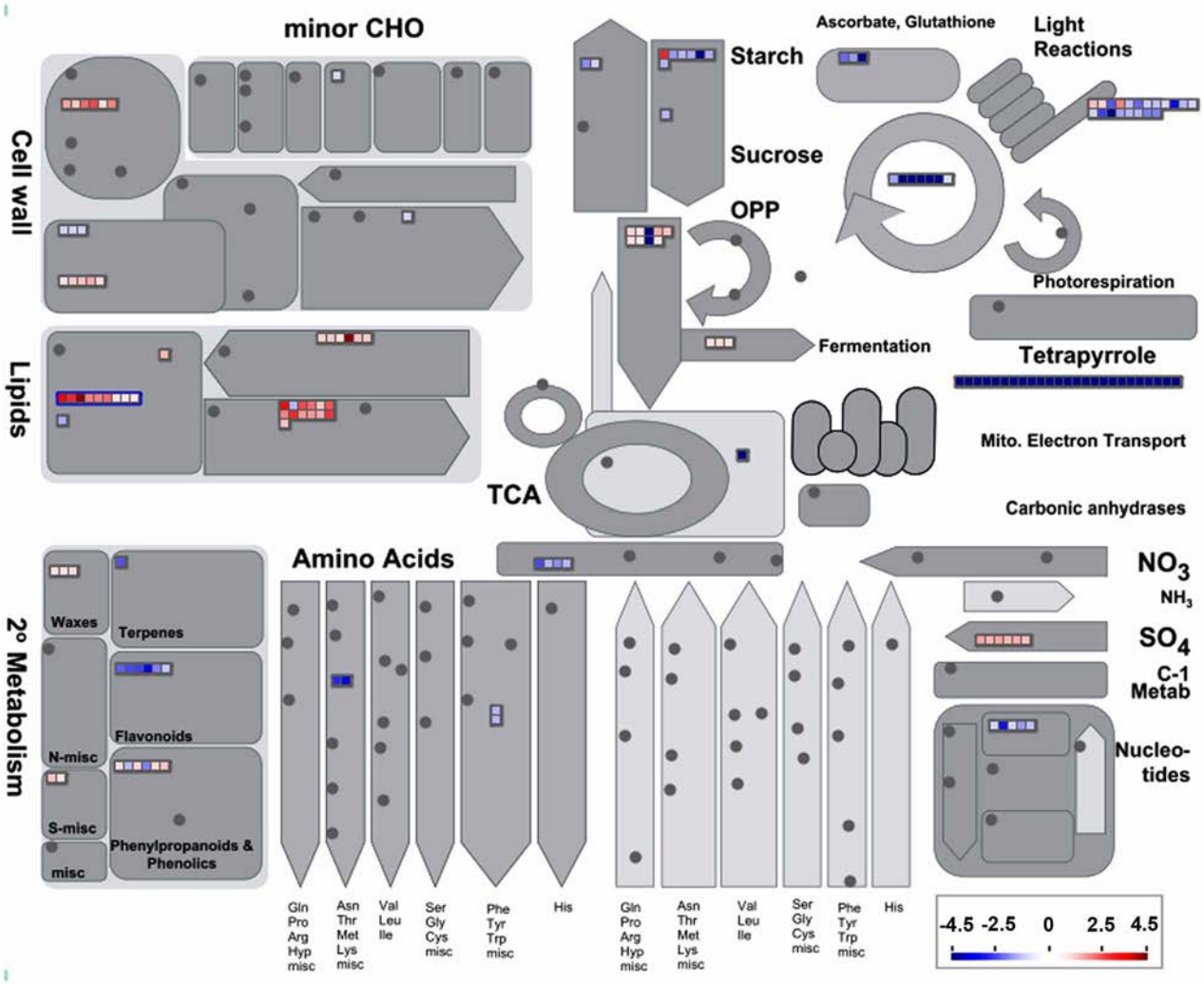

Fig. S3. Metabolism overview of P_i deficiency in root tissues. Classification of transcripts involved in metabolism differentially expressed due to P_i deficiency in roots using MapMan (Thimm *et al*. 2004). MapMan categories in red are up regulated in P_i deficient cluster roots, while categories in blue are up regulated in P_i sufficient normal roots. Note the increased expression of glycolysis, lipid metabolism, malate syntase, and cell wall modification P_i deficient cluster roots.

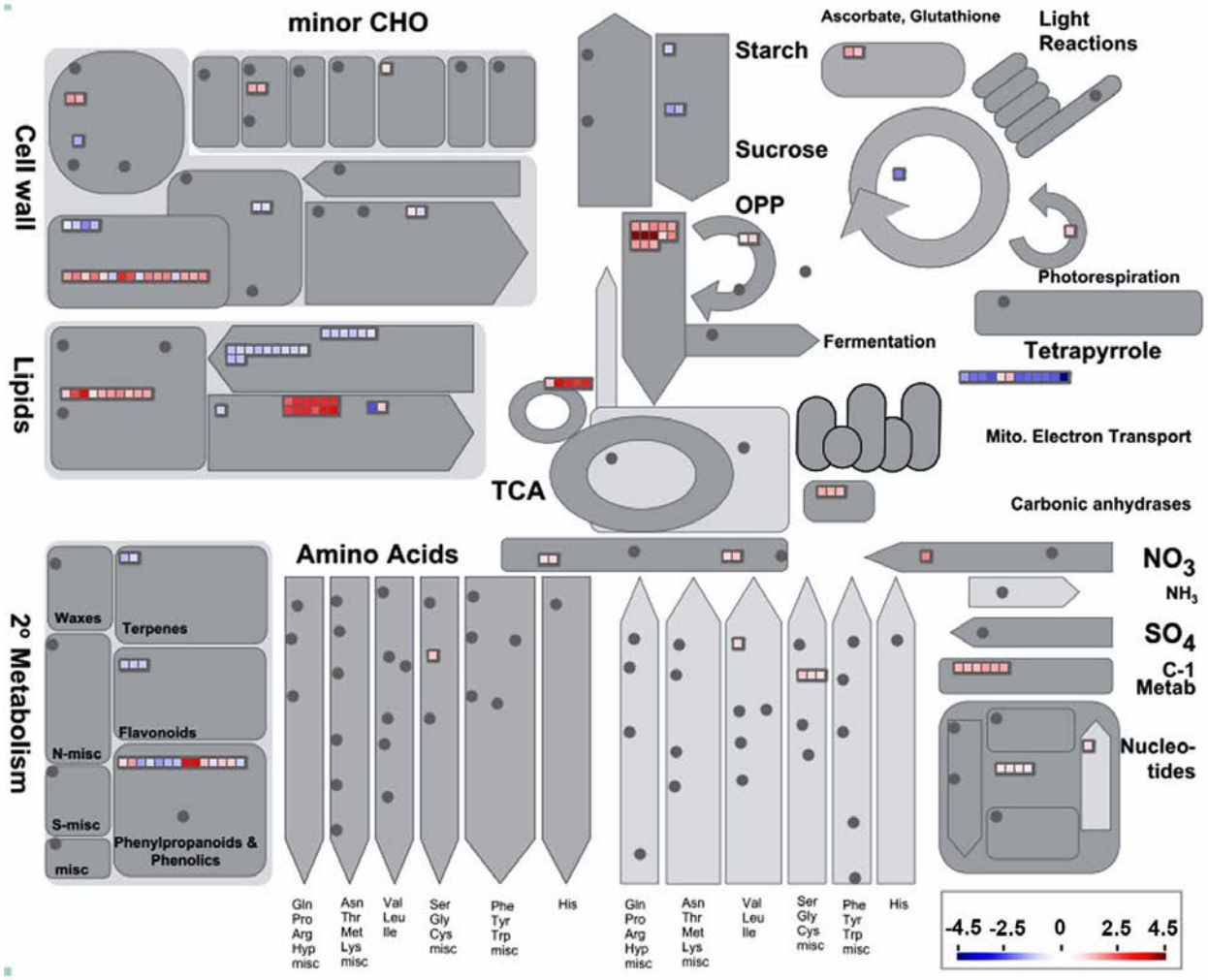

Fig. S4. The umbrella of genomics. The field of genomics is rapidly expanding. The inclusion of novel next-generation sequencing technologies with more traditional experimental approaches will provide added power and insight into many basic plant biology questions. Leveraging of information from various experimental platforms and fields of study will provide help elucidate genetic mechanisms and improve plant breeding efforts to increase legume production worldwide.