

RNA seq based transcriptomics study to investigate the genes governing nitrogen use efficiency in Indian wheat cultivars

Sarabjit Kaur^{1†}, M. Shamshad^{2†}, Suruchi Jindal¹, Amandeep Kaur¹, Satinder Singh², Achla sharma^{2*} and Satinder Kaur^{1*}

1. School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana, India

2. Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India

†Sarabjit Kaur, M. Shamshad contributed equally to this work.

*Corresponding author email: satinder.biotech@pau.edu, achla@pau.edu

[SK: 0000-0003-0672-9268](tel:0000-0003-0672-9268)

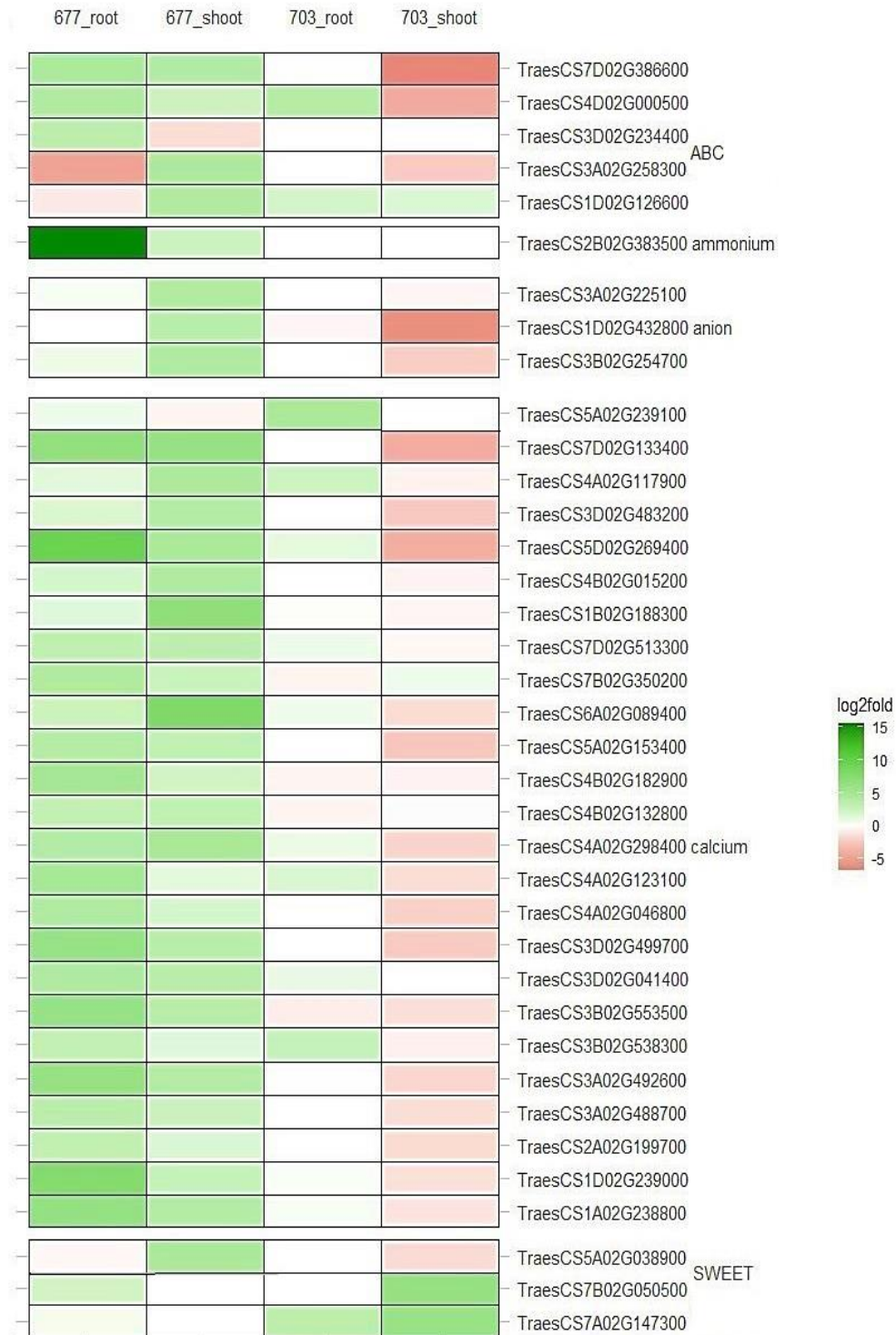
[AK: 0000-0002-9140-3424](tel:0000-0002-9140-3424)

[SK: 0000-0003-3704-3074](tel:0000-0003-3704-3074)



Supplementary Figure 1. Heatmap showing the expression patterns of genes involved as transcription factors response in between tissues and also in both genotypes.

* Colours indicate the differential gene expression in nitrogen stressed tissue; upregulated, green, downregulated, red, white: not differentially expressed.



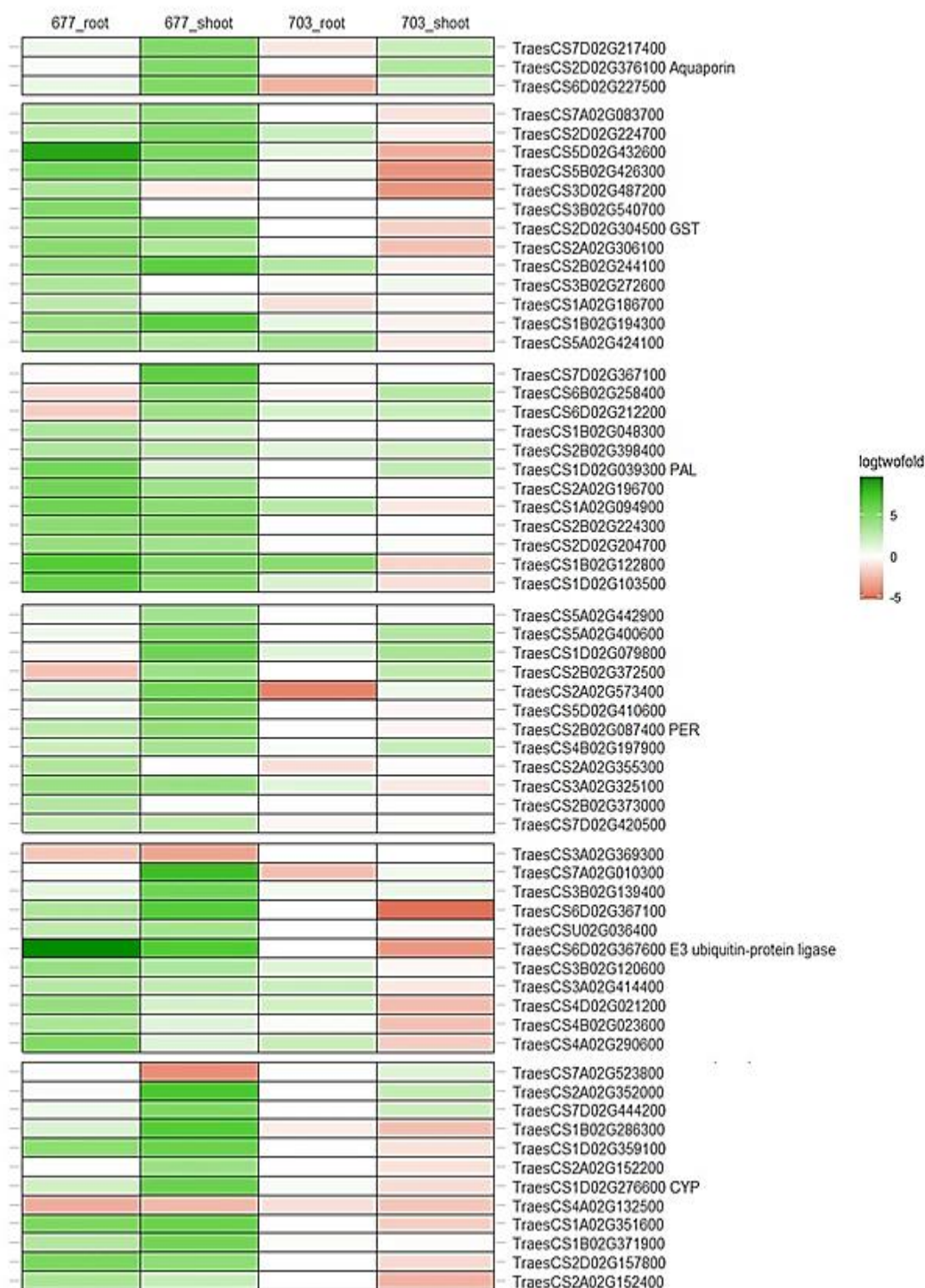
Supplementary Figure 2. Heatmap showing the expression patterns of genes involved as transporter in between tissues and also in both genotypes.

* Colours indicate the differential gene expression in nitrogen stressed tissue; upregulated, green, downregulated, red, white: not differentially expressed.



Supplementary Figure 3. Heatmap showing the expression patterns of genes involved as protein kinases in between tissues and also in both genotypes.

* Colours indicate the differential gene expression in nitrogen stressed tissue; upregulated, green, downregulated, red, white: not differentially expressed.



Supplementary Figure 4. Heatmap showing the expression patterns of other genes in between tissues and also in both genotypes

* Colours indicate the differential gene expression in nitrogen stressed tissue; upregulated, green, downregulated, red, white: not differentially expressed.

