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

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Supplementary Figure 1. Heatmap showing the expression patters of genes involved as trancription 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 patters 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.

|  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  | TraesCS1A02G359100 <br> CDK <br> TraesCS1D02G363800 |  |
|  |  |  |  | TraesCS2D02G107100 |  |
|  |  |  |  | TraesCS2B02G124100 |  |
|  |  |  |  | TraesCS1B02G454100 |  |
|  |  |  |  | TraesCS4D02G089200 |  |
|  |  |  |  | TraesCS1A02G031100 |  |
|  |  |  |  | TraesCS7D02G525000 |  |
|  |  |  |  | TraesCS4D02G089600 |  |
|  |  |  |  | TraesCS4B02G092200 cysteine-rich |  |
|  |  |  |  | TraesCS7B02G262800 |  |
|  |  |  |  | TraesCS7D02G357500 |  |
|  |  |  |  | TraesCS7D02G357400 |  |
|  |  |  |  | TraesCS7D02G358000 |  |
|  |  |  |  | TraesCS7B02G262300 |  |
|  |  |  |  | TraesCS2B02G232500 |  |
|  |  |  |  | TraesCS2D02G211000 |  |
|  |  |  |  | TraesCS5A02G355600 |  |
|  |  |  |  | TraesCS5D02G112200 |  |
|  |  |  |  | - TraesCS2D02G175100 F-box domain |  |
|  |  |  |  | TraesCS4A02G127600 |  |
|  |  |  |  | TraesCSU02G250100 |  |
|  |  |  |  | TraesCS2A02G205100 |  |
|  |  |  |  | TraesCS2B02G208900 |  |
|  |  |  |  | TraesCS5B02G183000 |  |
|  |  |  |  | TraesCS2D02G462000 |  |
|  |  |  |  | TraesCS5D02G417400 LRR |  |
|  |  |  |  | TraesCS7A02G321600 |  |
|  |  |  |  | TraesCS7B02G260600 |  |
|  |  |  |  | TraesCS2D02G190200 |  |
|  |  |  |  | TraesCS1D02G410100 | log2fold |
|  |  |  |  | TraesCS1B02G431400 | - 10 |
|  |  |  |  | TraesCS1B02G385100 |  |
|  |  |  |  | TraesCS3A02G255700 |  |
|  |  |  |  | TraesCS1D02G370100 | 0 |
|  |  |  |  | TraesCS1B02G384900 |  |
|  |  |  |  | TraesCS1B02G385300 |  |
|  |  |  |  | TraesCS1D02G372700 |  |
|  |  |  |  | TraesCS3D02G256400 MAPK |  |
|  |  |  |  | TraesCS4A02G062600 |  |
|  |  |  |  | - TraesCS4B02G239400 |  |
|  |  |  |  | TraesCS3A02G256300 |  |
|  |  |  |  | TraesCS3D02G256500 |  |
|  |  |  |  | TraesCS4A02G106400 |  |
|  |  |  |  | TraesCS3B02G288100 |  |
|  |  |  |  | TraesCS4B02G197800 |  |
|  |  |  |  | TraesCS3A02G256200 |  |
|  |  |  |  | TraesCS7A02G410700 |  |
|  |  |  |  | TraesCS2D02G401500 |  |
|  |  |  |  | TraesCS2A02G081400 |  |
|  |  |  |  | TraesCS5D02G329100 |  |
|  |  |  |  | - TraesCS1A02G320900 |  |
|  |  |  |  | - TraesCS2A02G190200 |  |
|  |  |  |  | TraesCS7B02G069100 |  |
|  |  |  |  | TraesCS1D02G073100 |  |
|  |  |  |  | - TraesCS6D02G280700 probable serine/threonine |  |
|  |  |  |  | TraesCS2D02G197600 |  |
|  |  |  |  | - TraesCS6B02G367100 |  |
|  |  |  |  | TraesCS3B02G547600 |  |
|  |  |  |  | TraesCS4D02G274400 |  |
|  |  |  |  | TraesCS2B02G096000 |  |
|  |  |  |  | TraesCS5D02G456100 |  |
|  |  |  |  | TraesCS2B02G216800 |  |
|  |  |  |  | TraesCS1B02G404000 |  |
|  |  |  |  | TraesCS2D02G079200 |  |
|  |  |  |  | TraesCS7A02G266200 serine/arginine |  |
|  |  |  |  | TraesCS1D02G299400 |  |
|  |  |  |  | TraesCS2A02G422900 |  |
|  |  |  |  | TraesCS5B02G197400 U-box domain |  |
|  |  |  |  | TraesCS7D02G201600 |  |
|  |  |  |  | TraesCS7B02G105600 |  |

Supplementary Figure 3. Heatmap showing the expression patters 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 patters 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.

