

Transcriptome and Co-expression Network Analyses Identify Key Genes Regulating Nitrogen Use Efficiency in *Brassica juncea* L.

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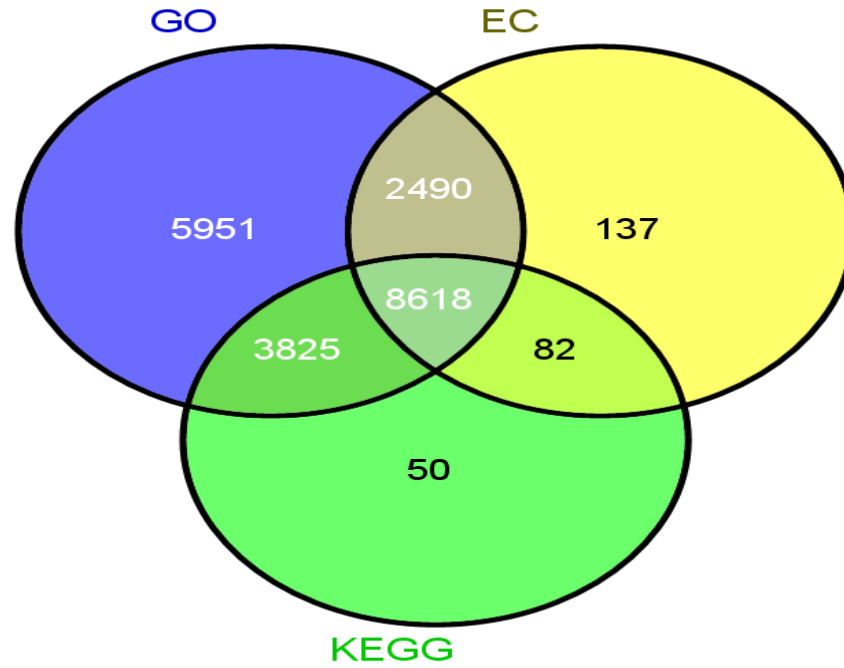
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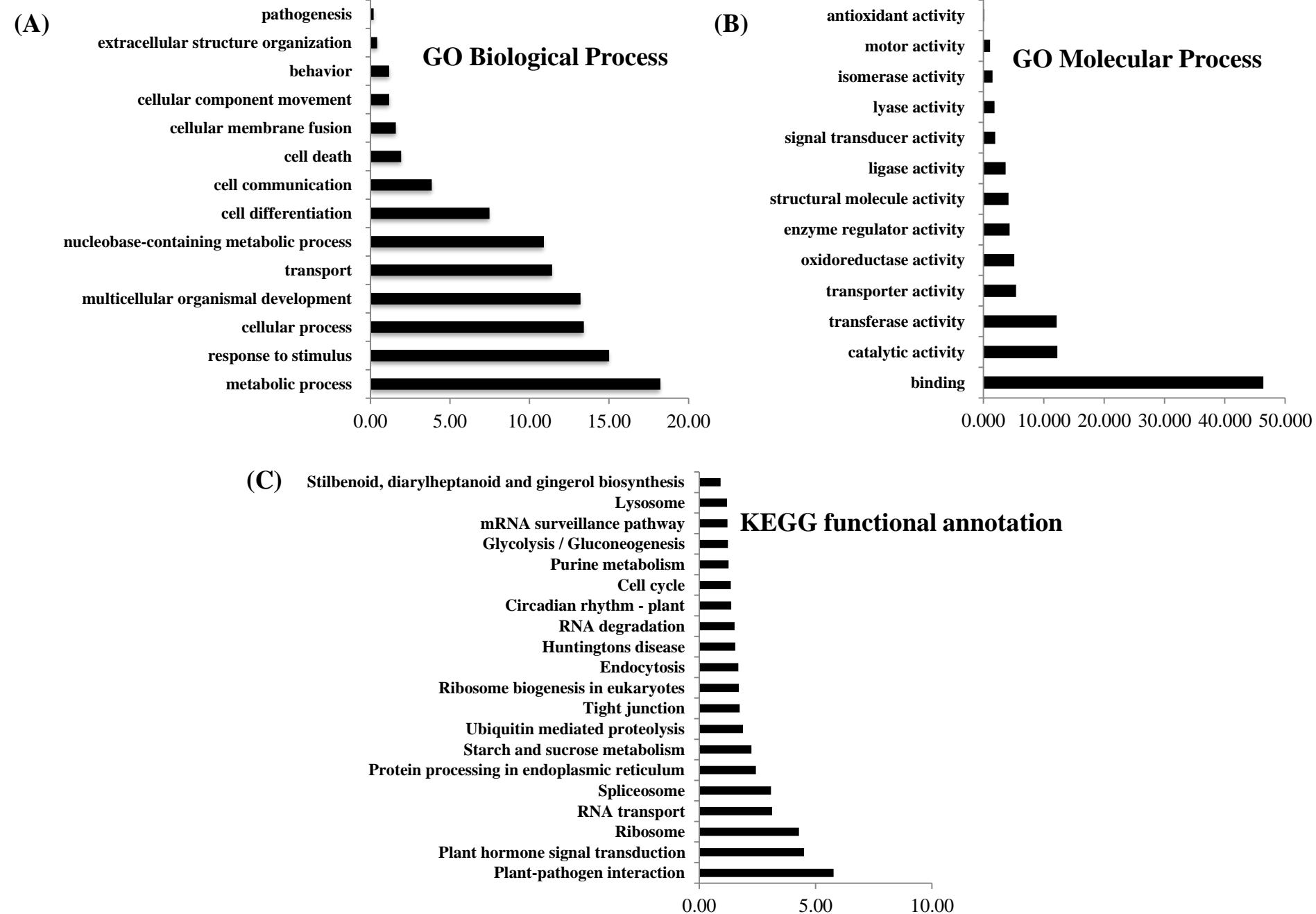
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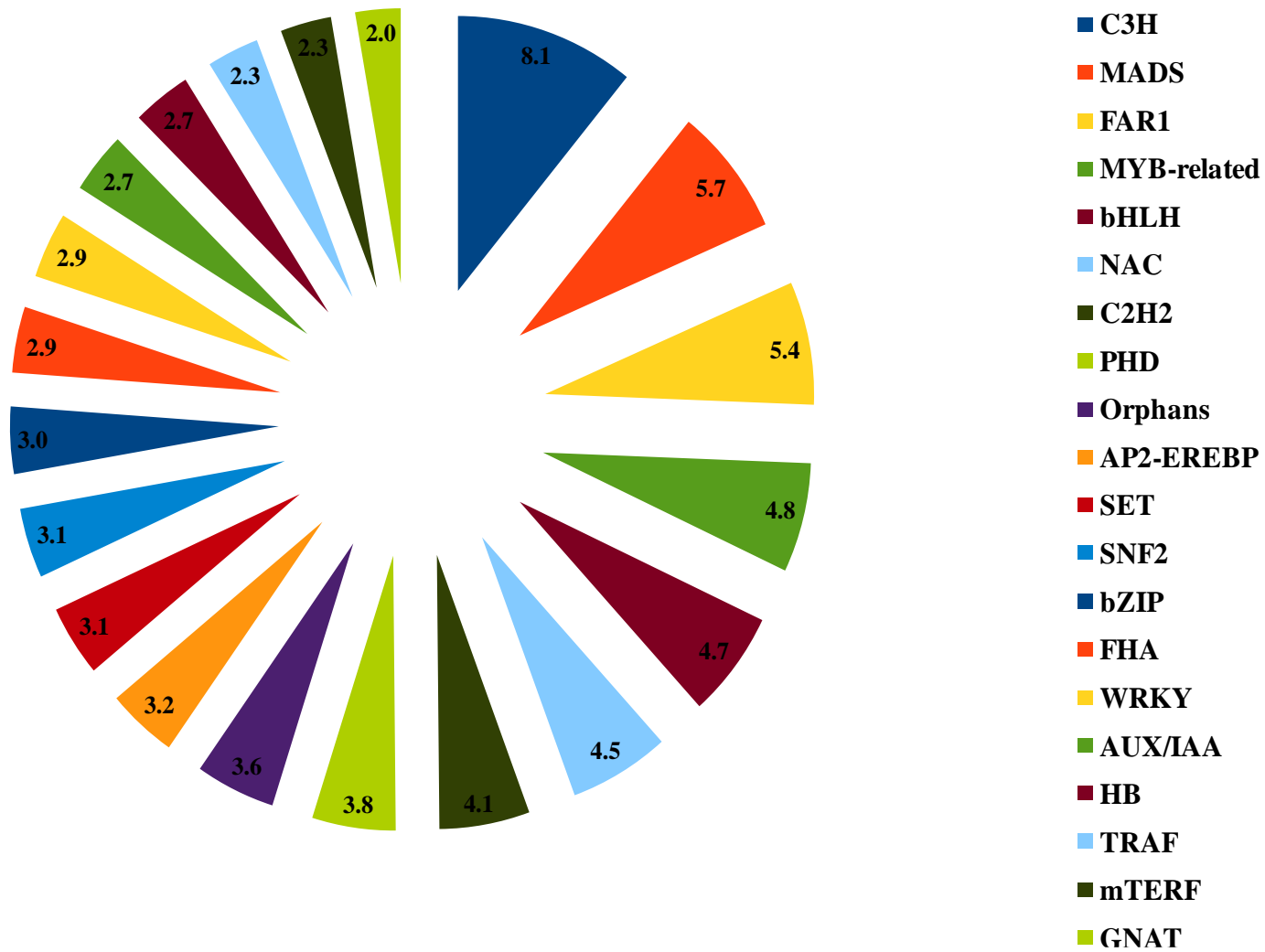
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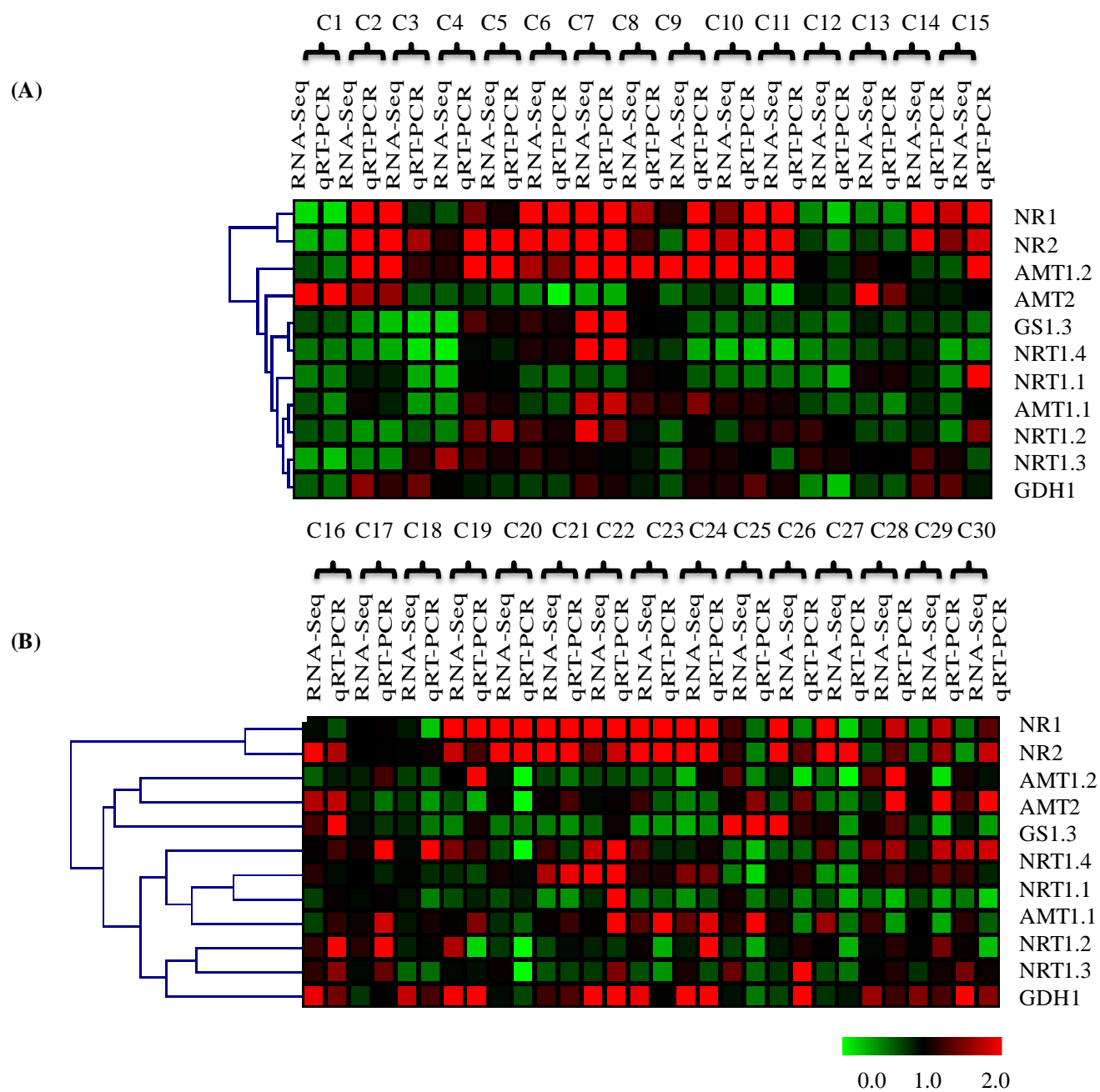
Supplementary Fig S1: Venn diagram showing transcripts annotated under GO, EC and KEGG



Supplementary Fig S2: Functional Annotation detail of transcriptome data: (A): Occurrence of different biological processes and molecular processes (B) based on GO slim categories with their corresponding percentage, (C): Top-20 KEGG pathways on the basis of their transcript abundance.

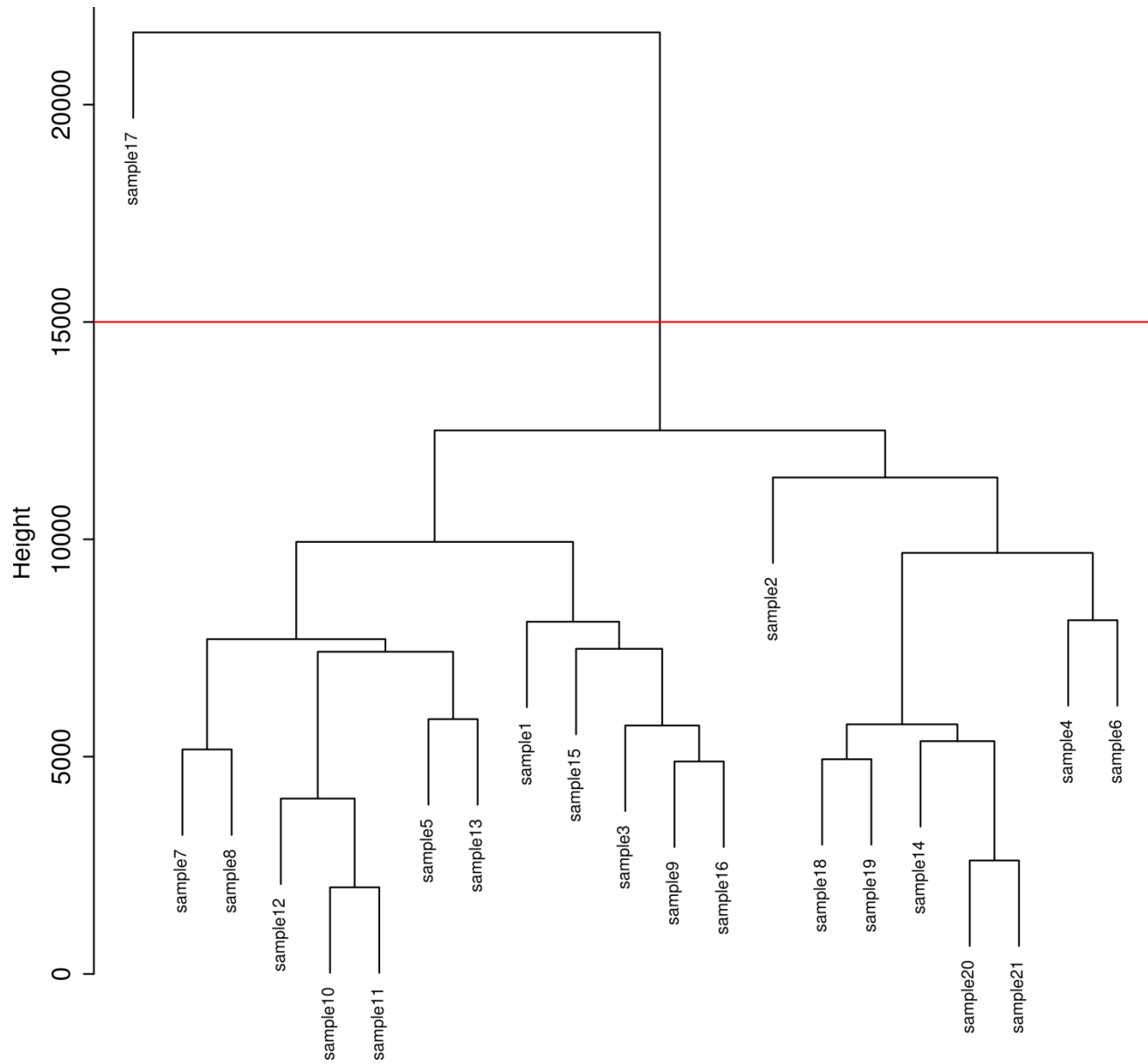


Supplementary Fig S3: Top-20 transcription factor (TF) families on the basis of transcript abundance.

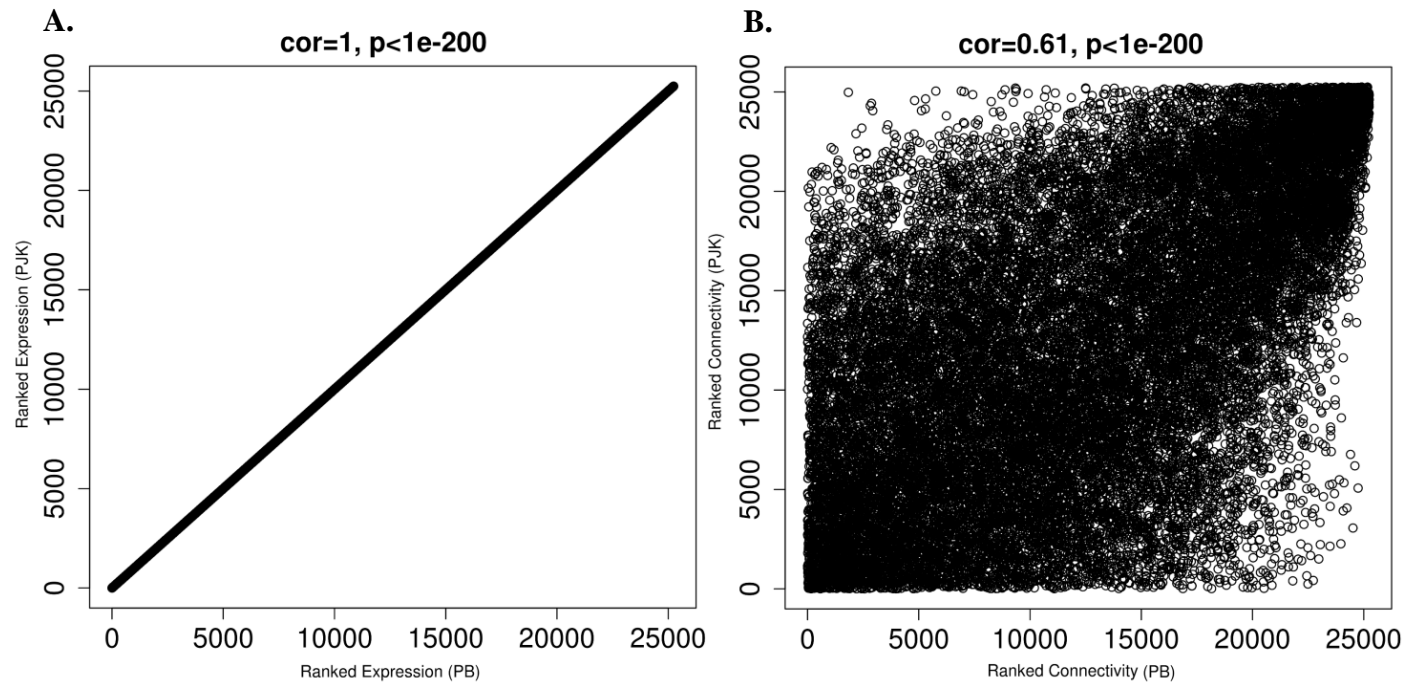


(B)

Supplementary Fig S4: Validation of the RNA-seq data from qRT-PCR: The expression level of eleven genes is measured through qRT-PCR in all 30 comparative conditions of (A) Pusa Bold and (B) Pusa Jaikisan. *Ubq9* was used as endogenous reference. The qRT-PCR data was significantly correlated with RNA-seq data ($r=0.76$, $p<0.0001$)

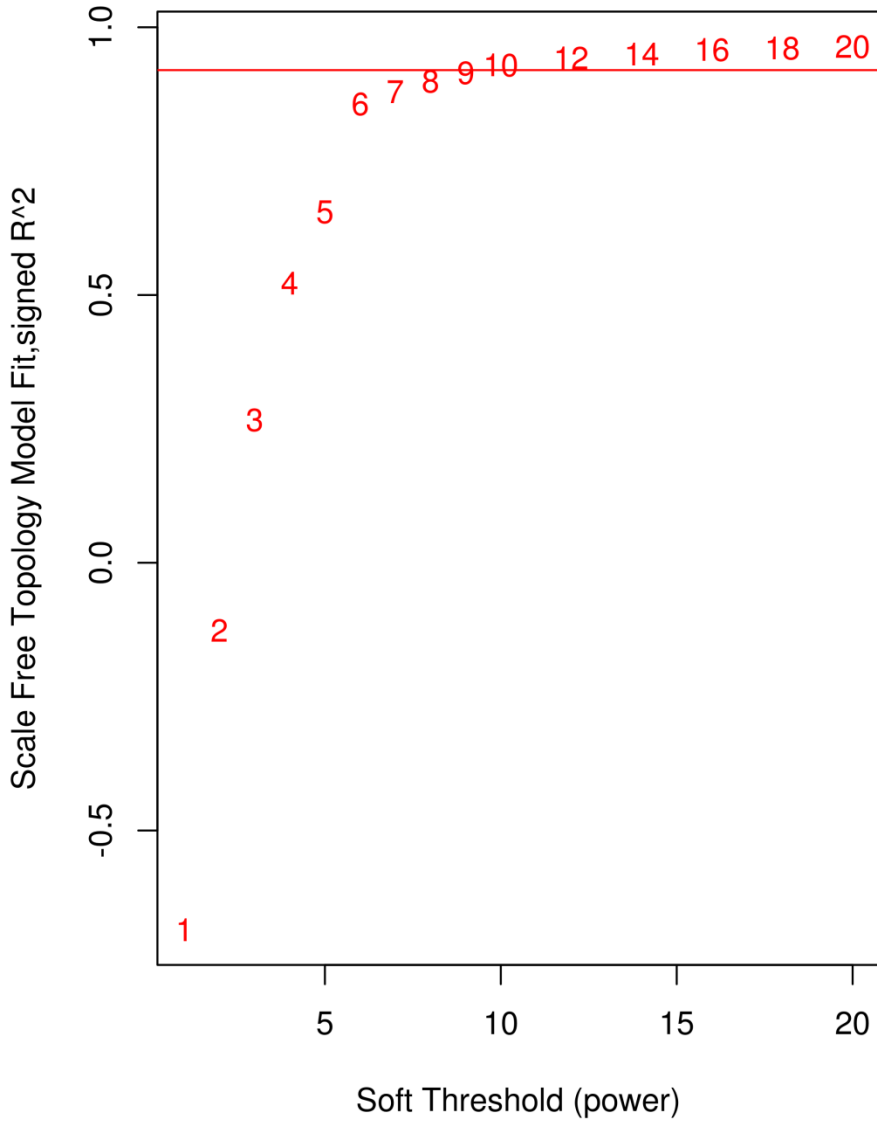


Supplementary Fig S5: Filtering and pre-processing of data: Sample 17 was eliminated as outlier from Pusa Bold.

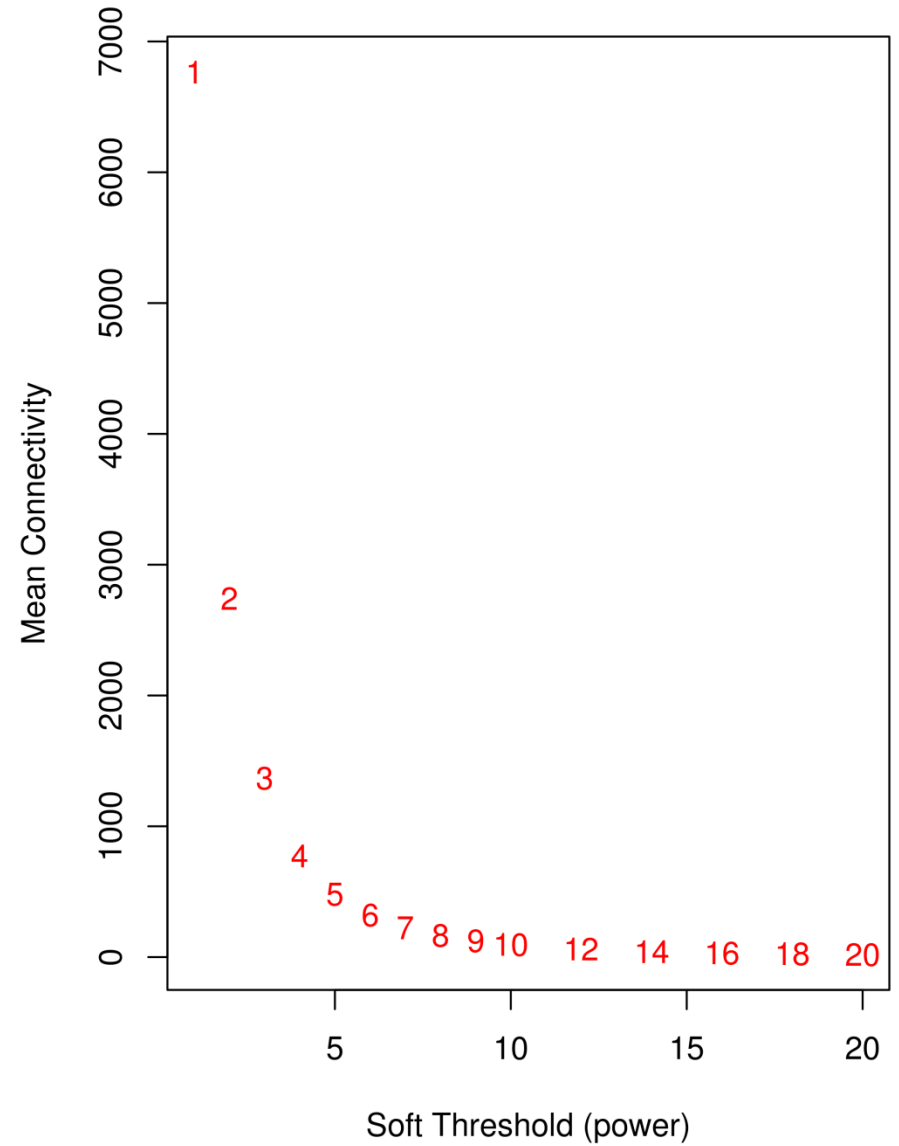


Supplementary Fig S6: Positive correlation and significant p-values of average gene expression ($\text{cor}=1, p \leq 1\text{e-}200$) (a) and overall connectivity ($\text{cor}=0.61, p \leq 1\text{e-}200$) (b).

Scale independence

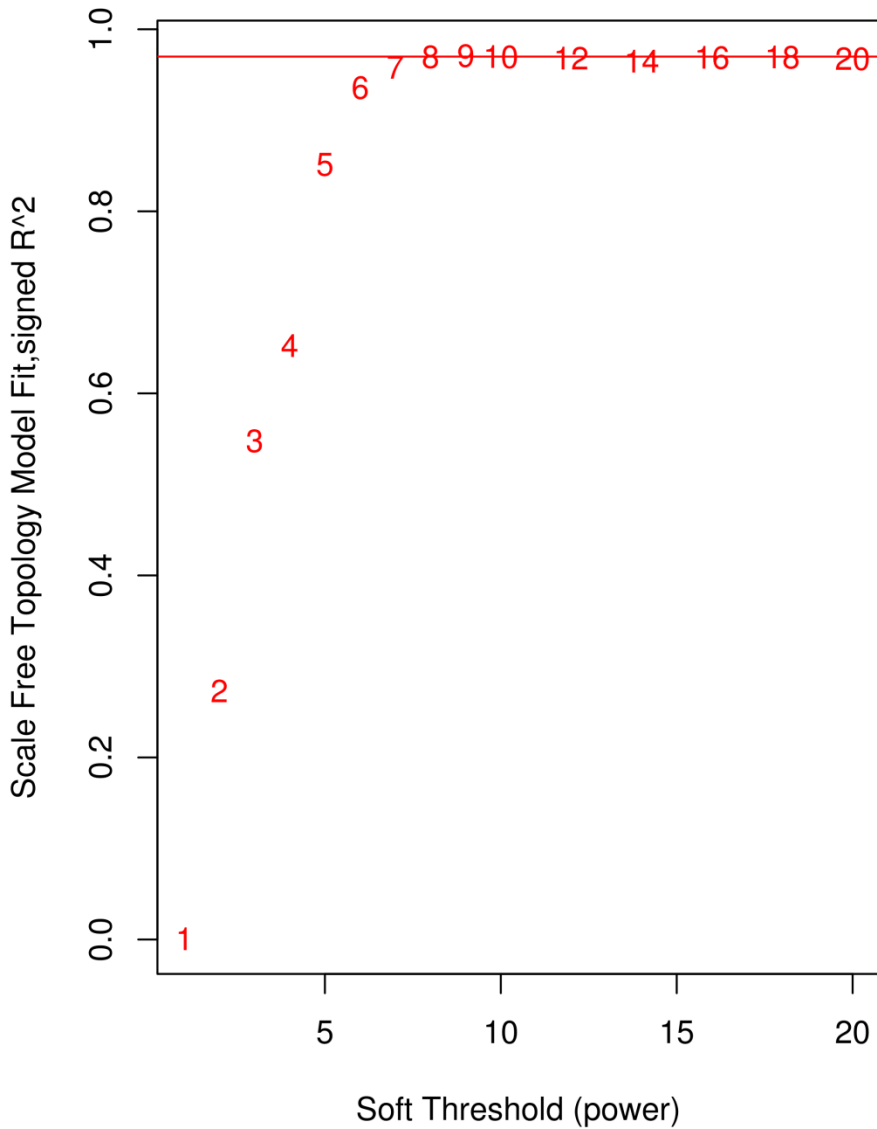


Mean connectivity

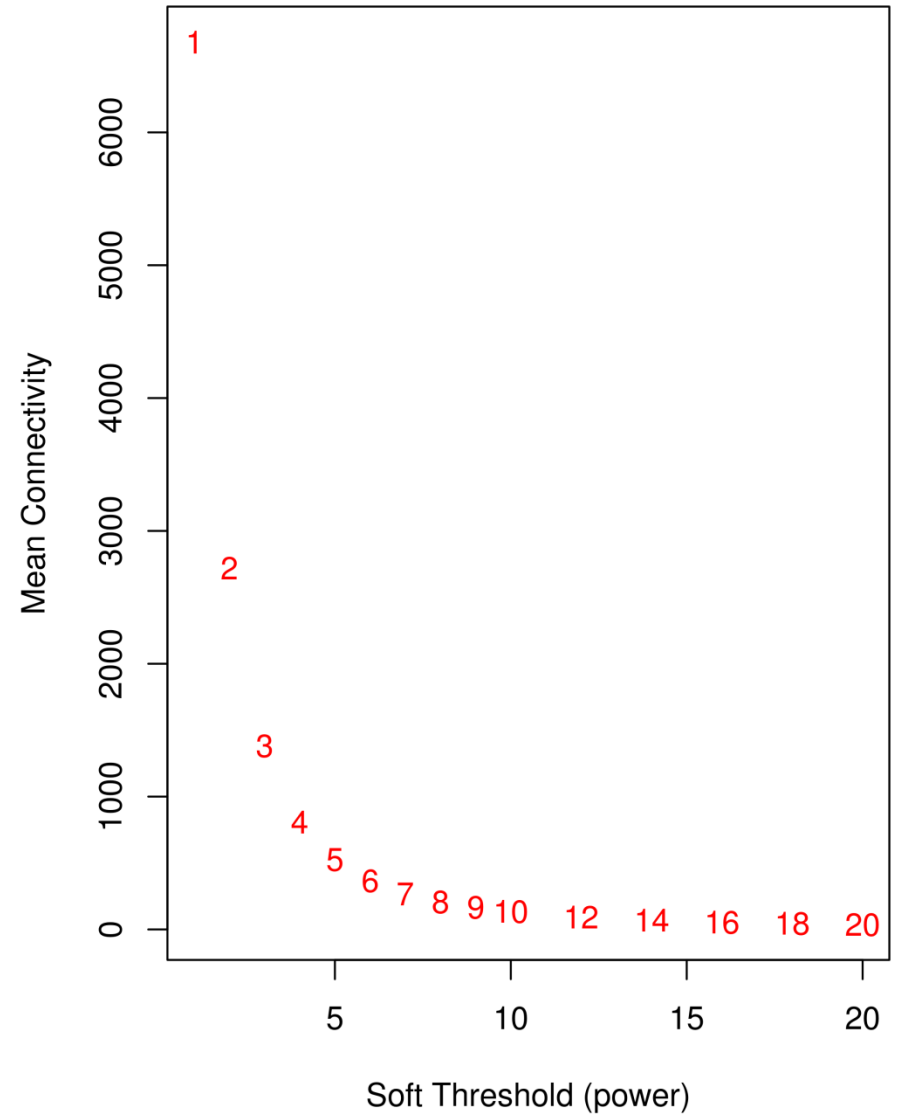


Supplementary Fig S7: Evaluation of network topology of Pusa Bold for various soft thresholding powers using pickSoftThreshold function and appropriate power.

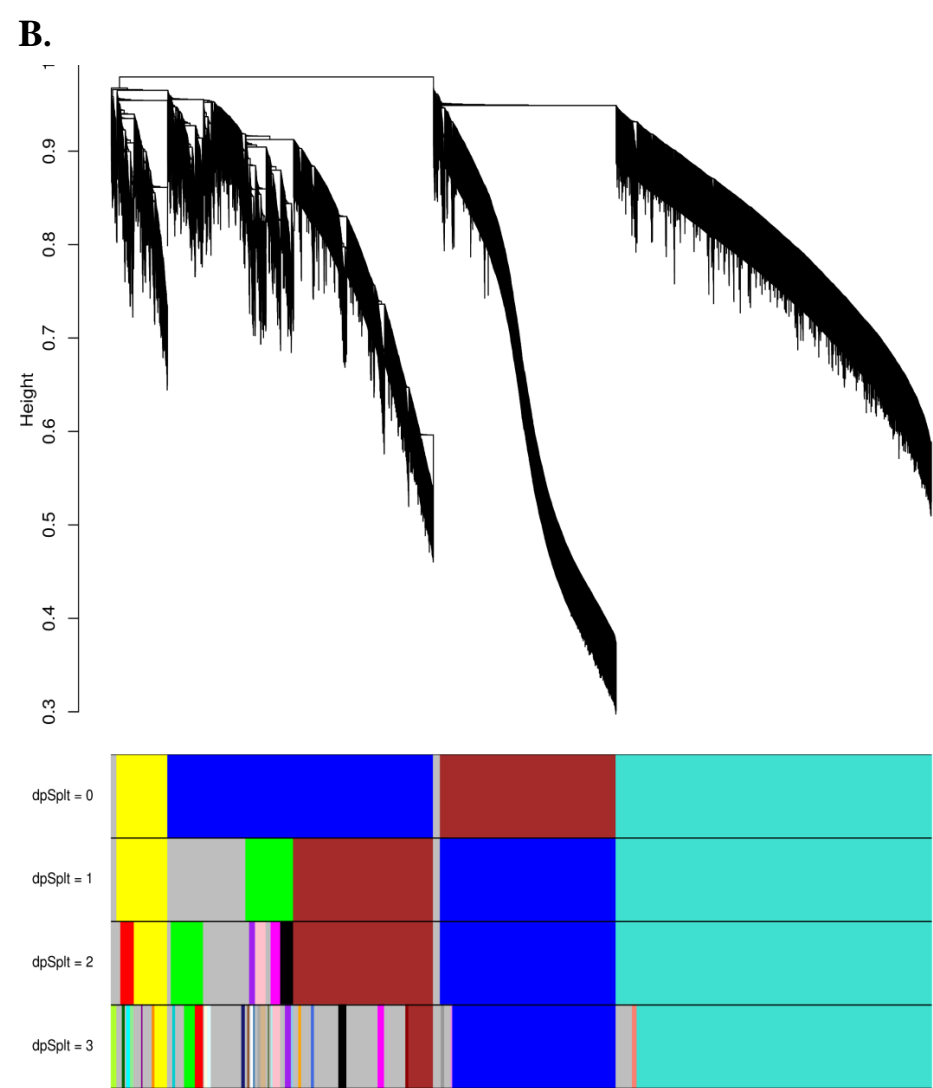
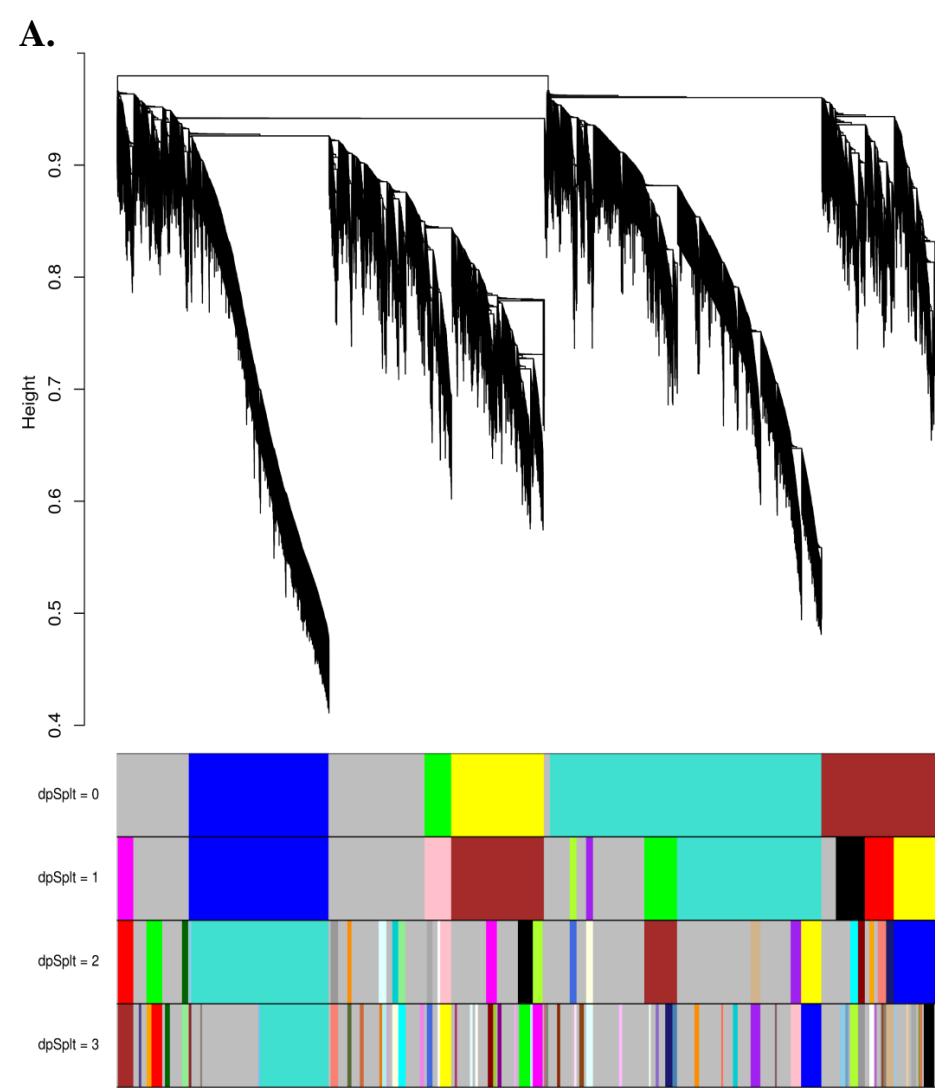
Scale independence



Mean connectivity

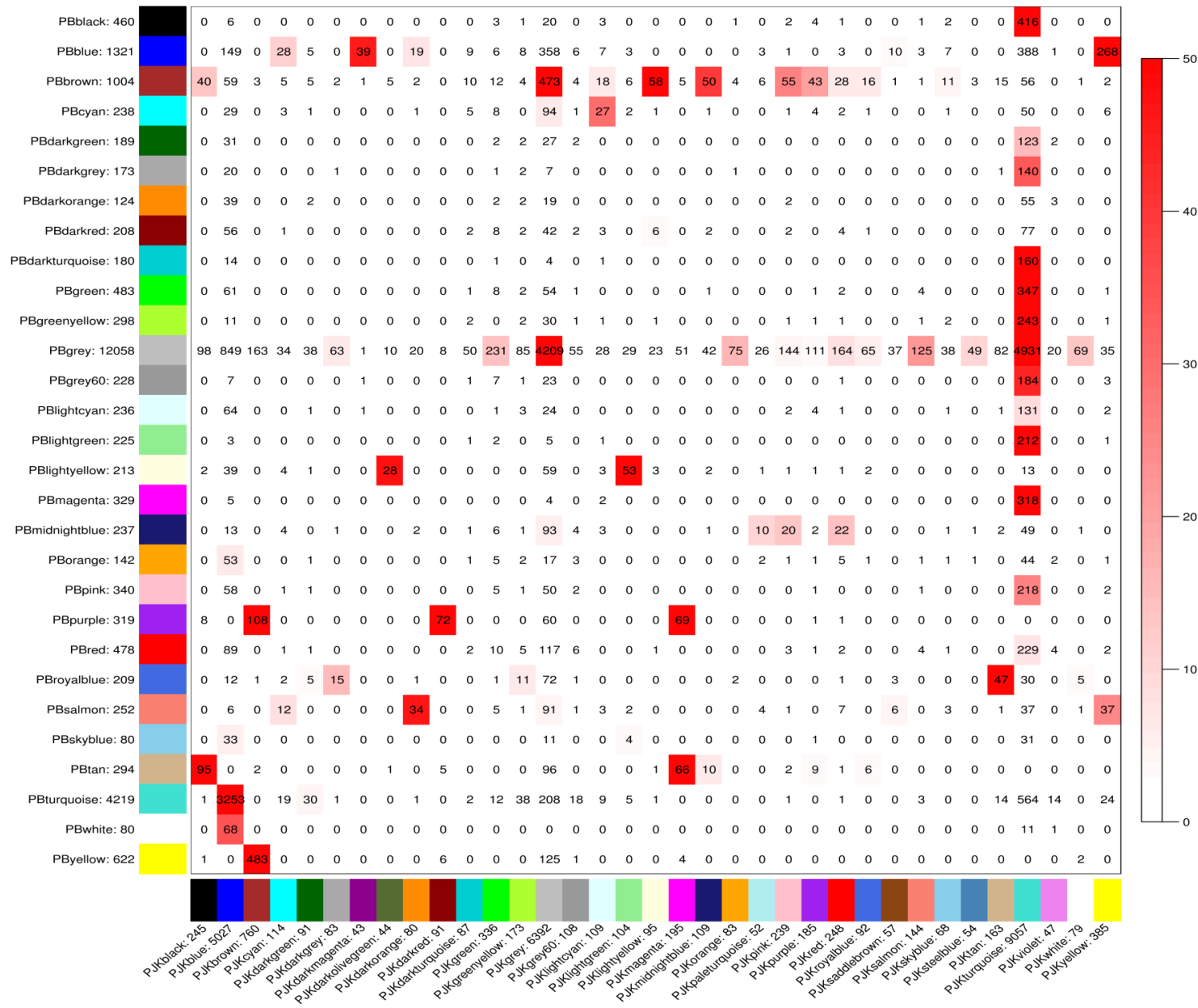


Supplementary Fig S8: Evaluation of network topology of Pusa Jaikisan for various soft thresholding powers using pickSoftThreshold function and appropriate power.



Supplementary Fig S9: Hierarchical clustering based on DistOM: 29 modules in (A) Pusa Bold and 35 modules in (B) Pusa Jaikisan were obtained by deepslit 2 and 3.

Correspondence of PJK and PB consensus modules



Supplementary Fig S10: Consensus match of Pusa Bold and Pusa Jaikisan modules: Modules identifier in the Pusa Bold were compared with most similar module in the Pusa Jaikisan based on significant overlap genes using overlap Table function of WGCNA

Pusa Bold

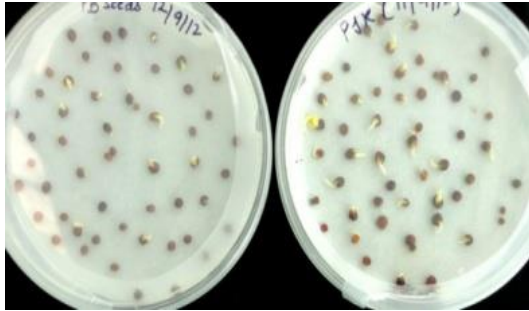
Pusa Jai Kisan

Pusa Bold

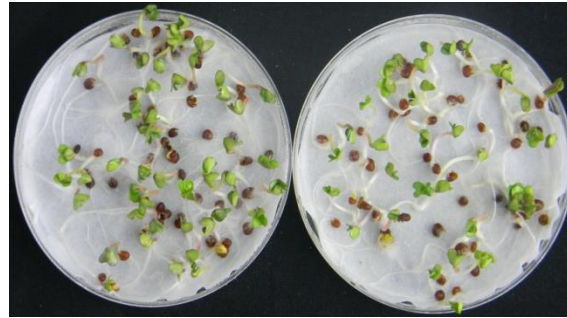
Pusa Jai Kisan

Pusa Bold

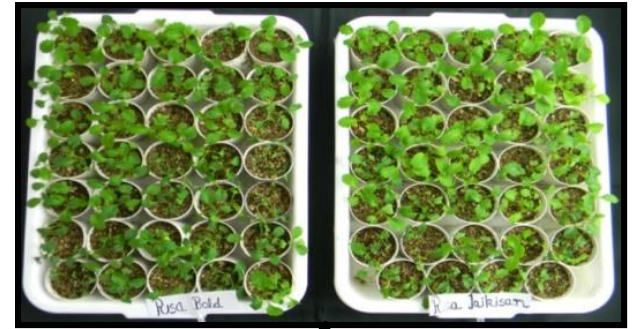
Pusa Jai Kisan



Surface sterilized seeds were germinated in petriplates



1 week old seedling in petriplates



Plantlets were transferred to pots

Close up view



Pusa Bold

Pusa Jai Kisan

After emergence of true leaves, various nitrate treatments were given

Time points

20 m, 2 h, 12 h, 24 h, 3d, 7d

20 m, 2 h, 12 h, 24 h, 3d, 7d

2 h, 12 h, 24 h, 3d, 7d

2 h, 12 h, 24 h, 3d, 7d

0 mM KNO₃ (Control)

0.25 mM KNO₃ (Low)

2.0 mM KNO₃ (Medium)

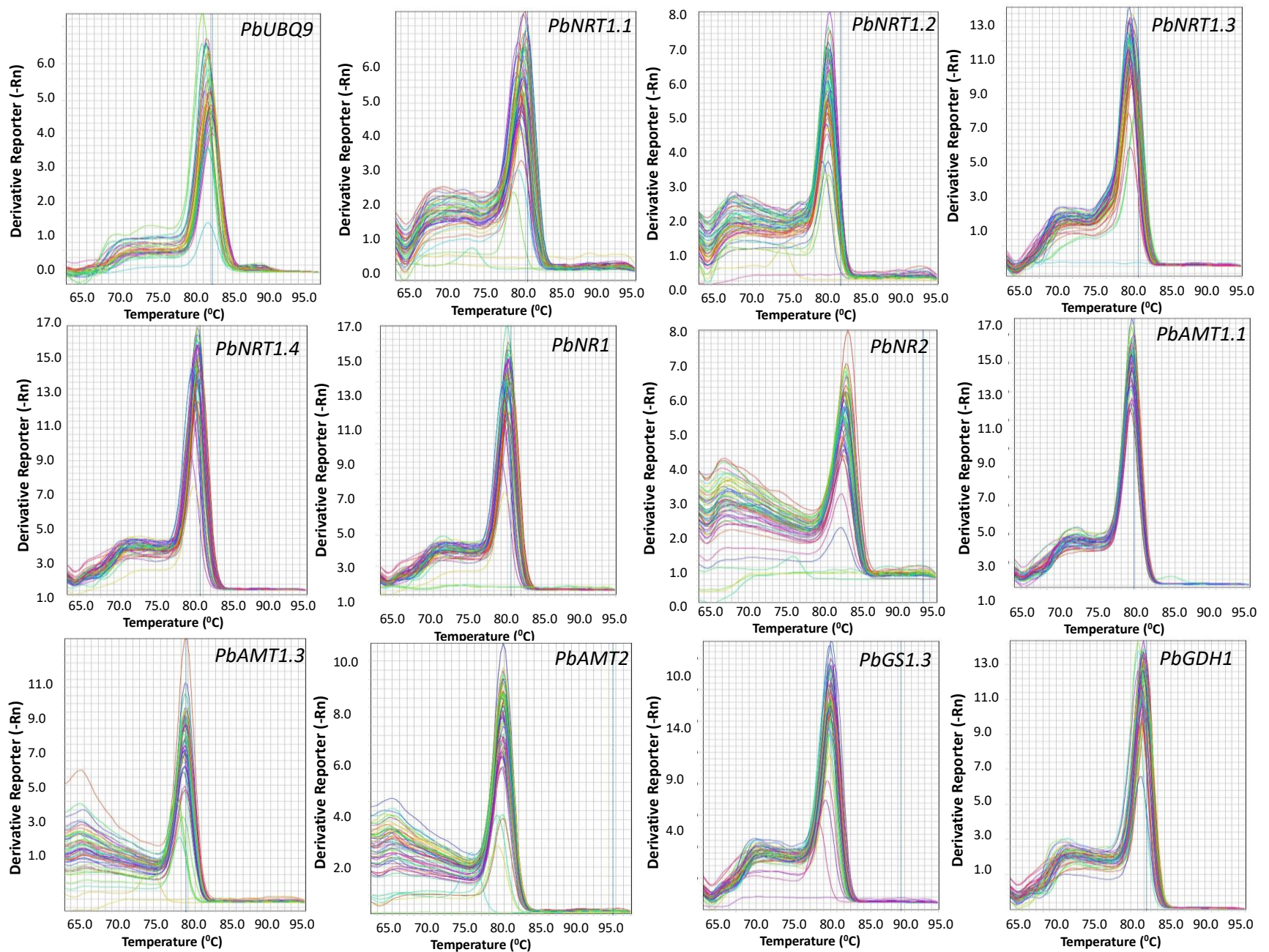
4.0 mM KNO₃ (High)

Growth parameters were studied after 21 days of treatment



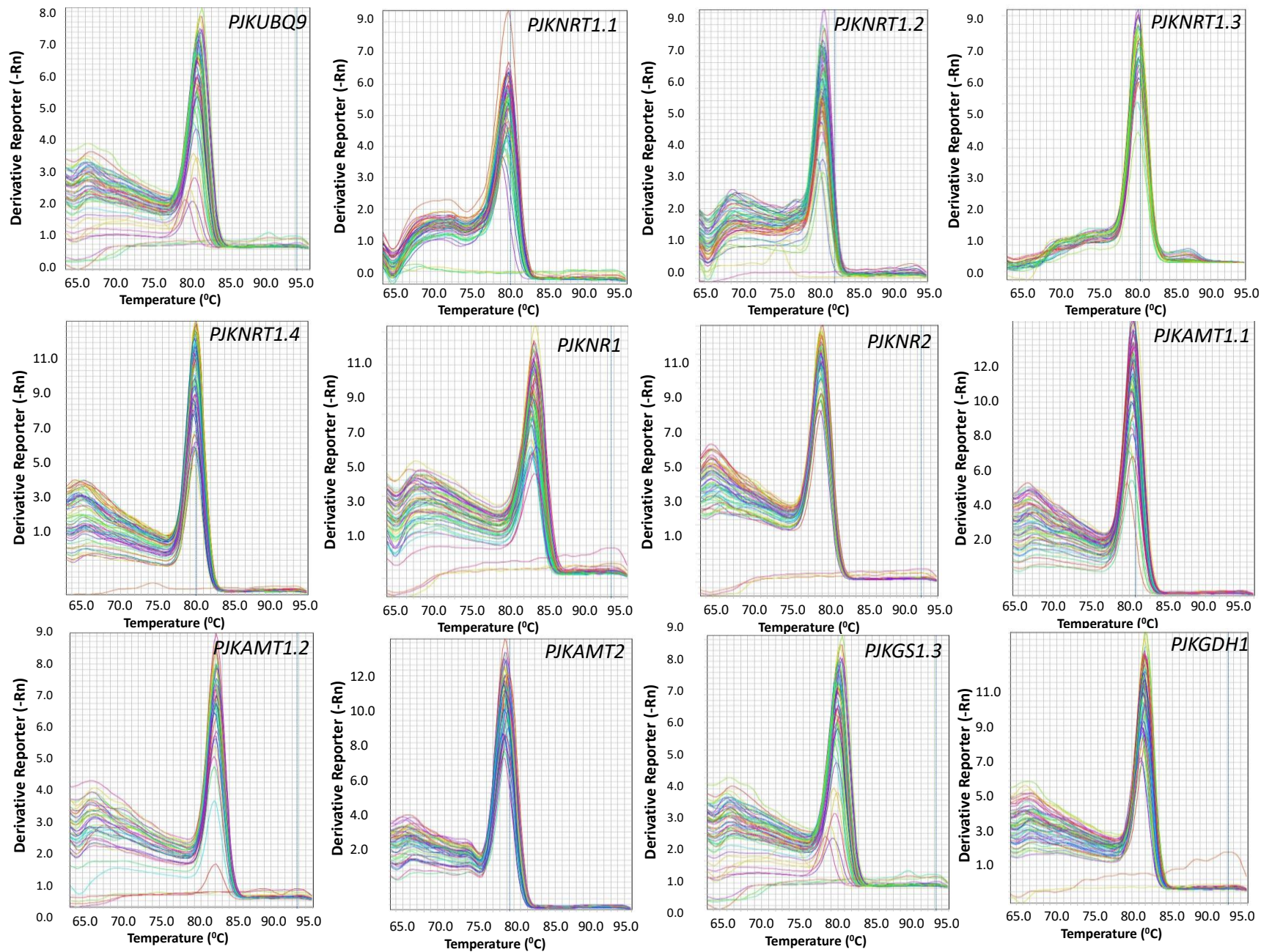
Transcriptome analysis

Supplementary Fig S11: Experimental design to study growth parameters and transcriptome analysis of Pusa Bold and Pusa Jaikisan in response to various nitrate treatments.



Continued

Supplementary Fig S12: Melt curves results of all the genes used for qRT-PCR analysis.



Supplementary Fig S12: Melt curves results of all the genes used for qRT-PCR analysis.