**Supplemental Table 1 |** Summary of TFs previously linked to N.

**Supplemental Table 2 | a,** Promoters screened in yeast one-hybrid analysis. **b**, TFs added to the yeast one-hybrid TF library from *de novo* cloning or Arabidopsis Biological Resource Center clones.

**Supplemental Table 3 |** **a,** TF-promoter interactions as obtained using yeast one hybrid analysis. **b**, TF-promoter interactions for nitrate assimilation subnetwork. **c**, TF-promoter interactions for the TFs ANR1, LBD37, NLP6, NLP7, and TGA1. **d**, Processes bound by TFs in the YNM.

**Supplemental Table 4 |** CPK-NLP7-dependent genes in network

**Supplemental Table 5** **|** Hormone-regulated genes25 present within the YNM. a, abscisic acid-regulated genes. **b**, ethylene-regulated genes. **c**, methyl jasmonate-regulated genes. **d**, auxin-regulated genes. **e**, cytokinin-regulated genes. **f**, brassinosteroid-regulated genes. **g**, gibberellic acid-regulated genes.

**Supplemental Table 6 | a,** Publically available gene expression datasets profiling transcriptome changes in response to nitrogen availability/treatment. **b,** Re-normalized cell type resolution gene expression dataset profiling transcriptome changes in response to nitrogen availability9. Genes with extremely low or absent expression in all microarray conditions were removed from the datasets or not analyzed when a corresponding unique probe was not available for a gene.

**Supplemental Table 7 |** **a,** Pearson and Spearman Rank Correlation of transcription factor and target interactions across publically available nitrogen availability microarray experiments. Gene expression correlations were calculated across 49 datasets for the N treatment dataset and 14 datasets for the cell type-specific dataset. **b,** TF–promoter gene interactions with a Pearson or Spearman rank correlation greater than >±0.5 for the N treatment dataset; and >±0.8 for the cell type-specific dataset from table in **a**. **c,** TF–promoter gene interactions with significant correlations from table from **a** for TFs tested for root phenotypes

**Supplemental Table 8 |** NeCORR transcription factor ranking analysis.

**a**, Significant nodes (Significant nodes represent TFs or target genes with more highly correlated (or anti-correlated) edges than expected by chance) in the YNM in various N treatment categories. n = 95 promoters and 332 TFs. **b**, one-sided gini correlations for all interactions in the YNM. **c**, significant interactions based on gini correlations based on cell type transcriptomic data, root transcriptomic data, shoot transcriptomic data, nitrate transcriptomic data, nitrate-glutamine transcriptomic data, nitrate-carbon transcriptomic data, nitrate continuous treatment transcriptomic data and nitrate time course transcriptomic data (7-72 samples per dataset). Genes with extremely low or absent expression in all microarray conditions were removed from the datasets or not analyzed when a corresponding unique probe was not available for a gene. p-value was calculated based on 10000 random permutations. (see **Methods**).

**Supplemental Table 9 |** Transcription factor outgoing connectivity.

**Supplemental Table 10 | a,** Transcription factors weighting based on the total number and percentage of targets that are classical N metabolism genes. **b**, Genes with mutant lines characterized and their associated ranking. **c**, Data used for TF rankings. **d**, Core target genes used in rankings

**Supplemental Table 11 |** T-DNA mutants and primers used for genotyping

**Supplemental Table 12 |** Novel N-Associated Transcription Factors and their Respective Root and Shoot Mutant Phenotypes.

**Supplemental Table 13 |** Root and Shoot Phenotyping Statistical Summary. List of all genotypes tested for root and shoot phenotyping, the number for biological replicates (n) per experiment, and the p-value significance from the ANOVA tests (see Methods).

**Supplemental Table 14** **|** Principal Component Traits and Loading Vector for Principal Axes. RSA measurements from Col-0 roots (n = 209 1mM KNO3, n = 201 10mM KNO3) were used as input data.

**Supplemental Table 15 |** Curated Genes Critical for Regulation of Root Length and Lateral Root Initiation and their presence in the YNM

**a**. Genes critical for regulation of root length. **b**, Genes critical for regulation of root length in the YNM. **c**, Genes associated with lateral root development in the YNM.

**Supplemental Table 16 |** Correlation of Transcription Factor Mutant Shoot and Root Phenotypes Relative to Ranking Datasets

Spearman rank correlation values, p-value significance from the Spearman rank correlations, and number of correlations tested per category (n).

**Supplemental Table 17 |** Normalized Expression Data for Wild Type and Mutants at 1 and 10mM KNO3. **a**, All expressed genes. **b**, Expressed genes in the YNM.

**Supplemental Table 18 |** Genotype and Genotype by Nitrate Condition-Dependent Gene Expression in Wild Type (Col-0) Arabidopsis Roots and in Transcription Factor Mutant Alleles. **a**, All expressed genes. **b**, Expressed genes in the YNM.

**Supplemental Table 19 |** **a**, Number of mapped reads per biological replicate for RNAseq experiment (n = 4 biological replicates per genotype per condition. **b**, Pearson correlation values between replicates.

**Supplemental Table 20 |** Significantly Differentially Expressed Genes in Nitrogen Metabolism Mutants and in Nitrogen Transcriptional Regulator Mutants microarray analysis. **a**, all differentially expressed genes in the mutants. **b**, Differentially expressed genes in the YNM.