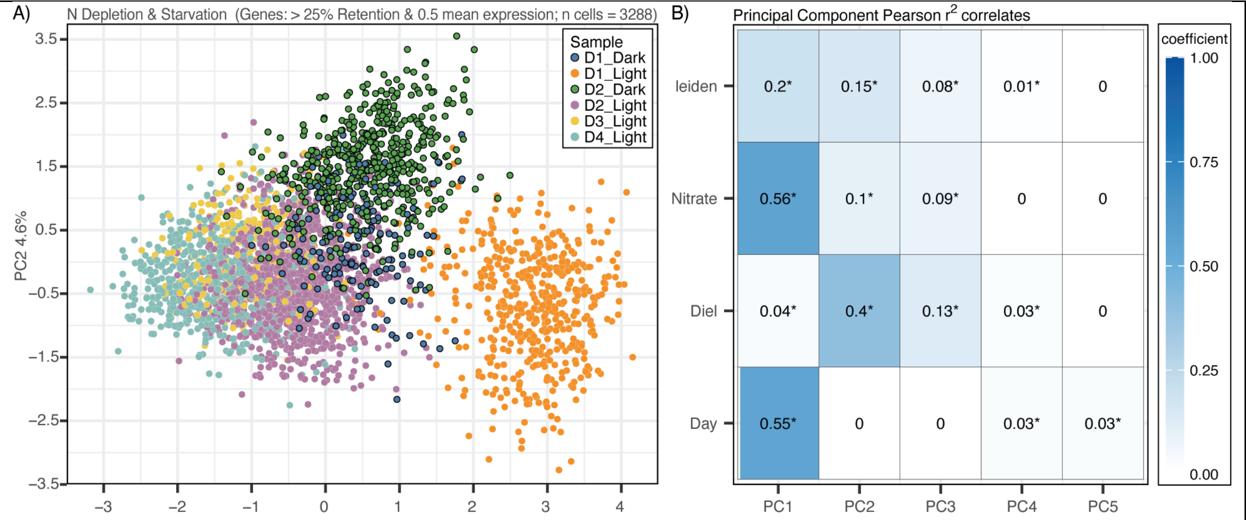
Supplementary Table 1. Summary of Leiden cluster composition per sample

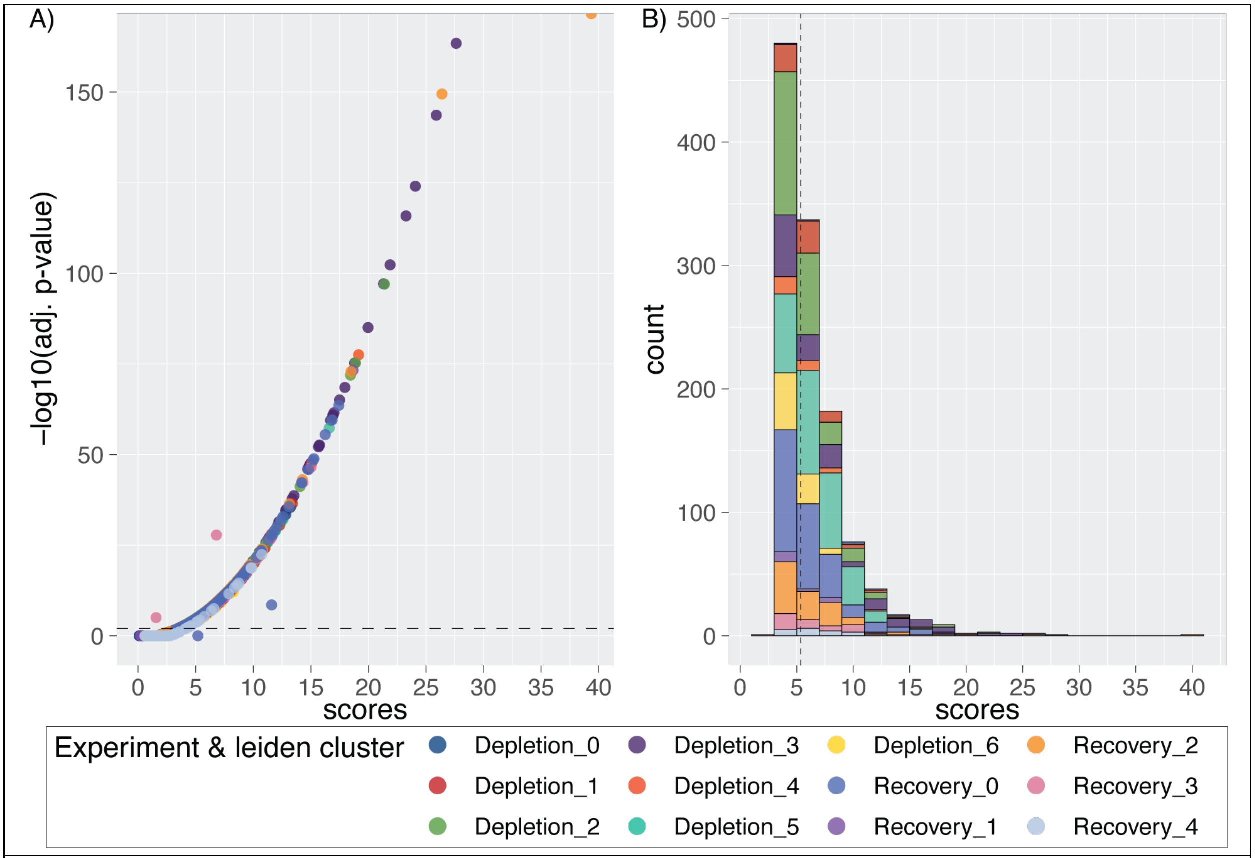
N-condition	Samples	Total cells (n = 7303) per sample	Leiden Cluster	n cells per cluster	(%) cells per cluster
Depletion	D1_Dark	161	Nitrogen Assimilation	7	4.35
			Nitrogen Starvation	3	1.86
			Protein Synthesis (aqua blue)	147	91.30
			Protein Synthesis (dark blue)	4	2.48
	D1_Light	485	Multifunctional State	26	5.36
			C & N Redistribution	1	0.21
			Photosynthesis	456	94.02
			Protein Synthesis (dark blue)	2	0.41
	D2_Dark	527	Multifunctional State	75	14.23
			C & N Redistribution	8	1.52
			Nitrogen Assimilation	347	65.84
			Nitrogen Starvation	4	0.76
			Photosynthesis	1	0.19
			Protein Synthesis (aqua blue)	54	10.25
			Protein Synthesis (dark blue)	38	7.21
Starvation	D2_Light	1260	Multifunctional State	11	0.87
			C & N Redistribution	532	42.22
			Nitrogen Assimilation	11	0.87
			Nitrogen Starvation	25	1.98
			Protein Synthesis (aqua blue)	3	0.24
			Protein Synthesis (dark blue)	678	53.81
	D3_Light	276	Multifunctional State	6	2.17
			C & N Redistribution	95	34.42
			Nitrogen Assimilation	11	3.99
			Nitrogen Starvation	6	2.17
			Protein Synthesis (aqua blue)	1	0.36
			Protein Synthesis (dark blue)	157	56.88
	D4_Light	579	Multifunctional State	7	1.21
			C & N Redistribution	14	2.42
			Nitrogen Assimilation	2	0.35
			Nitrogen Starvation	501	86.53
			Protein Synthesis (dark blue)	55	9.50
	D5_Dark	30	Nitrogen Starvation	25	83.33
			Photosynthesis & Nitrogen Assimilation (blue)	1	3.33
			Photosynthesis & Nitrogen Assimilation (purple)	2	6.67
			Protein Turnover Inhibition	2	6.67
Recovery	H02	540	Nitrogen Starvation	503	93.15
			Photosynthesis & Nitrogen Assimilation (blue)	2	0.37
			Photosynthesis & Nitrogen Assimilation (purple)	8	1.48
			Protein Turnover Inhibition	27	5.00
	H06	554	Nitrogen Starvation	526	94.95
			Photosynthesis & Nitrogen Assimilation (blue)	3	0.54
			Photosynthesis & Nitrogen Assimilation (purple)	12	2.17
			Protein Turnover Inhibition	11	1.99
			Silicon Import	2	0.36
	H12	2891	Nitrogen Starvation	72	2.49
			Photosynthesis & Nitrogen Assimilation (blue)	1257	43.48
			Photosynthesis & Nitrogen Assimilation (purple)	1214	41.99
			Protein Turnover Inhibition	214	7.40
			Silicon Import	134	4.64

Supplementary Table 2. Summary of total cells in each Leiden cluster

N-condition	Sample	Leiden Cluster	n cells per sample	Total cells (n = 7303) per cluster
Depletion	D1_Light	C & N Redistribution	1	650
Depletion	D2_Dark		8	
Starvation	D2_Light		532	
Starvation	D3_Light		95	
Starvation	D4_Light		14	
Depletion	D1_Light	Multifunctional State	26	125
Depletion	D2_Dark		75	
Starvation	D2_Light		11	
Starvation	D3_Light		6	
Starvation	D4_Light		7	
Depletion	D1_Dark	Nitrogen Assimilation	7	378
Depletion	D2_Dark		347	
Starvation	D2_Light		11	
Starvation	D3_Light		11	
Starvation	D4_Light		2	
Depletion	D1_Dark	Nitrogen Starvation	3	539
Depletion	D2_Dark		4	
Starvation	D2_Light		25	
Starvation	D3_Light		6	
Starvation	D4_Light		501	
Starvation	D5_Dark	Nitrogen Starvation	25	1126
Recovery	H02		503	
Recovery	H06		526	
Recovery	H12		72	
Depletion	D1_Light	Photosynthesis	456	457
Depletion	D2_Dark		1	
Starvation	D5_Dark	Photosynthesis & Nitrogen Assimilation (blue)	1	1263
Recovery	H02		2	
Recovery	H06		3	
Recovery	H12		1257	
Starvation	D5_Dark	Photosynthesis & Nitrogen Assimilation (purple)	2	1236
Recovery	H02		8	
Recovery	H06		12	
Recovery	H12		1214	
Depletion	D1_Dark	Protein Synthesis (aqua blue)	147	205
Depletion	D2_Dark		54	
Starvation	D2_Light		3	
Starvation	D3_Light		1	
Depletion	D1_Dark	Protein Synthesis (dark blue)	4	934
Depletion	D1_Light		2	
Depletion	D2_Dark		38	
Starvation	D2_Light		678	
Starvation	D3_Light		157	
Starvation	D4_Light		55	
Starvation	D5_Dark	Protein Turnover Inhibition	2	254
Recovery	H02		27	
Recovery	H06		11	
Recovery	H12		214	
Recovery	H06	Silicon Import	2	136
Recovery	H12		134	



Supplementary Figure 1. Correlation of principal components with environmental factors. A) PCA of 53 genes that were consistently observed across >25% of 3,288 cells across the N-depletion and N-starvation phases (same as Fig 4A). **B**) Pearson correlation between principal components and shared factors.



Supplementary Figure 2. Distribution of Wilcoxon rank-sum statistical scores and adjusted p-values. A) Each gene in a cluster was statistically scored to determine the most relevant marker genes. A threshold of less than or equal to 0.01for the adjusted p-value (horizontal dashed line) and a score greater than the median score of all genes in all clusters **B**) The distribution (bin width of 2) of scores per leiden cluster (vertical dashed line: Median = 5.18).

Supplementary Data File 1. [Functional_Enriched_Genes_Ranked.csv] Significantly differentially expressed genes (i.e., adjusted p-value less than or equal to 0.01 and a score greater than the median score of all genes in all clusters) ranked per cluster that had a significant enrichment for a pathway or process sourced from Gene Ontology (MF, BP, and CC) and/or KEGG. Genes that did not have a functional enrichment were also added if their cluster rank was less than 20 to allow for manual curation and annotation.

- **gene_symbol**: refers to the transcript id or gene symbol for a particular gene.
- **scores**: Wilcoxon rank-sum statistical score per cluster. Some genes appear in multiple clusters.
- **pval_adj**: adjusted p-value from the Wilcoxon rank-sum statistical score (correction method: Benjamini-Hochberg).
- **Cluster_Rank**: The ranking of each marker gene in a cluster (e.g., 1 = highest score).
- **Experiment_leiden_cluster**: Numerical designation for the cluster in each experiment (7 clusters for depletion, 5 clusters for recovery).
- **Exp_Cluster_ngenes**: Number of significantly differentially expressed genes per cluster that was searched for functional enrichment using gProfiler2.
- source: Databases for which functional enrichment's were sourced Gene Ontology[1] (MF, BP, and CC) and KEGG[2].
- **p_value**: the p-value refers to statistically significant result, which indicates the likelihood that the observed overlap between a list of genes and an enriched pathway, processes, or biological function is a true biological relationship[3]
- **term_name**: the given name referenced from the source database
- **Leiden_Cluster_Name**: The name given to a leiden cluster, based on gene annotations, supporting biological information, and functional enrichment analysis.
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References

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3 Kolberg L *et al.* "gprofiler2– an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler.". *F1000Research, 9 (ELIXIR)(709). R package version 0.2.3.* **9 (ELIXIR)(709). R package version 0.2.3.** (2020).

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