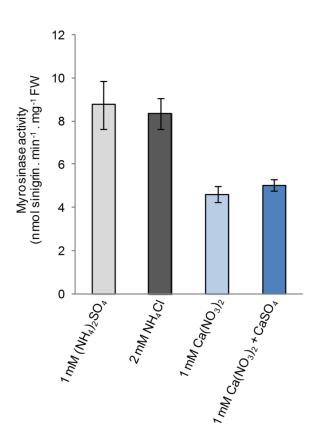
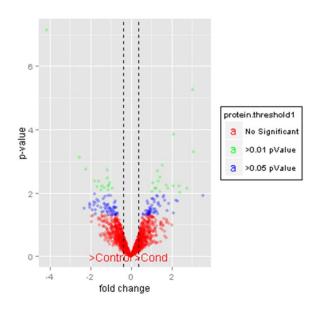
**Table S1**. Identification and quantification of glucosinolates by LC-MS in leaves of Arabidopsis plants grown under nitrate or ammonium nutrition.

Systematic name	Common name	Content (mg . g FW	
		Nitrate	Ammonium
3-methylsulfinylpropyl – GLS	Glucoiberin	n.q.	n.q.
4-methylsulfinylbutyl – GLS	Glucoraphanin	$0.107 \pm 0.01$	$0.212 \pm 0.02$
5-methylsulfinilpentyl – GLS	Glucoalyssin	n.q.	n.q.
6-methylsulfinylhexyl – GLS	Glucohesperin	n.q.	n.q.
7-methylsulfinylheptyl – GLS	Glucosibarin	n.q.	n.q.
4-methylthyobutyl – GLS	Glucoerucin	n.q.	n.q.
8-methylsulfinyloctyl – GLS	Glucohirsutin	n.q.	n.q.
3-indolylmethyl – GLS	Glucobrassicin	$0.051 \pm 0.01$	$0.039 \pm 0.00$
4-methoxy-3-indolylmethyl – GLS	Methoxyglucobrassicin	$0.013 \pm 0.00$	$0.023 \pm 0.00$
1-methoxy-3-indolylmethyl – GLS	Neoglucobrassicin	$0.020 \pm 0.00$	0.029 ± 0.00

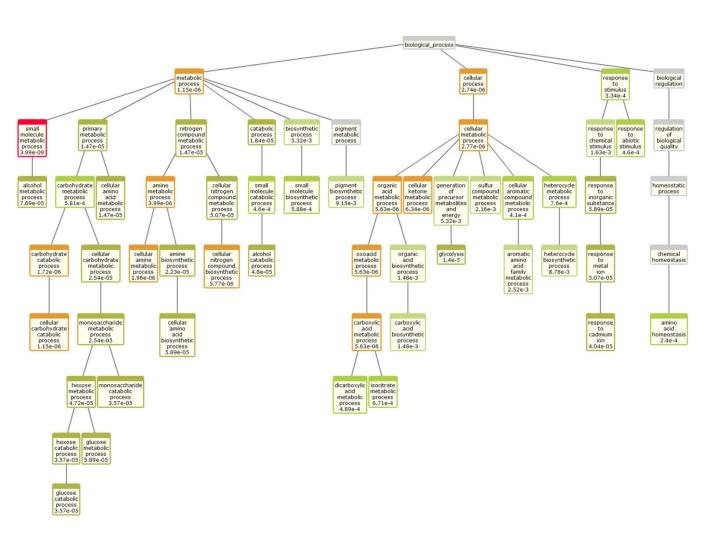
**Figures S1**. Myrosinase activity of *Arabidopsis thaliana* plants grown under different nitrogen sources: 1 mM  $(NH_4)_2SO_4$ , 1 mM  $Ca(NO_3)_2 + 1$  mM  $CaSO_4$ , and 2 mM  $NH_4Cl$ . Values represent mean  $\pm$  se (n = 3). Statistical differences according to a Student's t-test P-value  $\leq 0.05$  are indicated by an asterisk.



**Figure S2.** Volcano plot representing the fold-change of identified proteins with associated P values from the pair-wise quantitative comparisons of plants grown under nitrate or ammonium nutrition. In green, very significantly changed proteins (P < 0.01), in blue, significantly changed proteins (P < 0.05) and in red, unchanged proteins between the treatments..



**Figure S3.** Biological process GO enrichment analysis of all the differentially expressed proteins with respect to the N source. The analysis was done using the BioMaps module of VirtualPlant 1.3 software. The p-value corresponding to each term is indicated inside the diagram boxes (p<0.01).



**Figure S4.** Biological process GO enrichment analysis of the differentially expressed proteins found with higher abundance under nitrate nutrition. The analysis was done using the BioMaps module of VirtualPlant 1.3 software. The p-value corresponding to each term is indicated inside the diagram boxes (p<0.01).

