

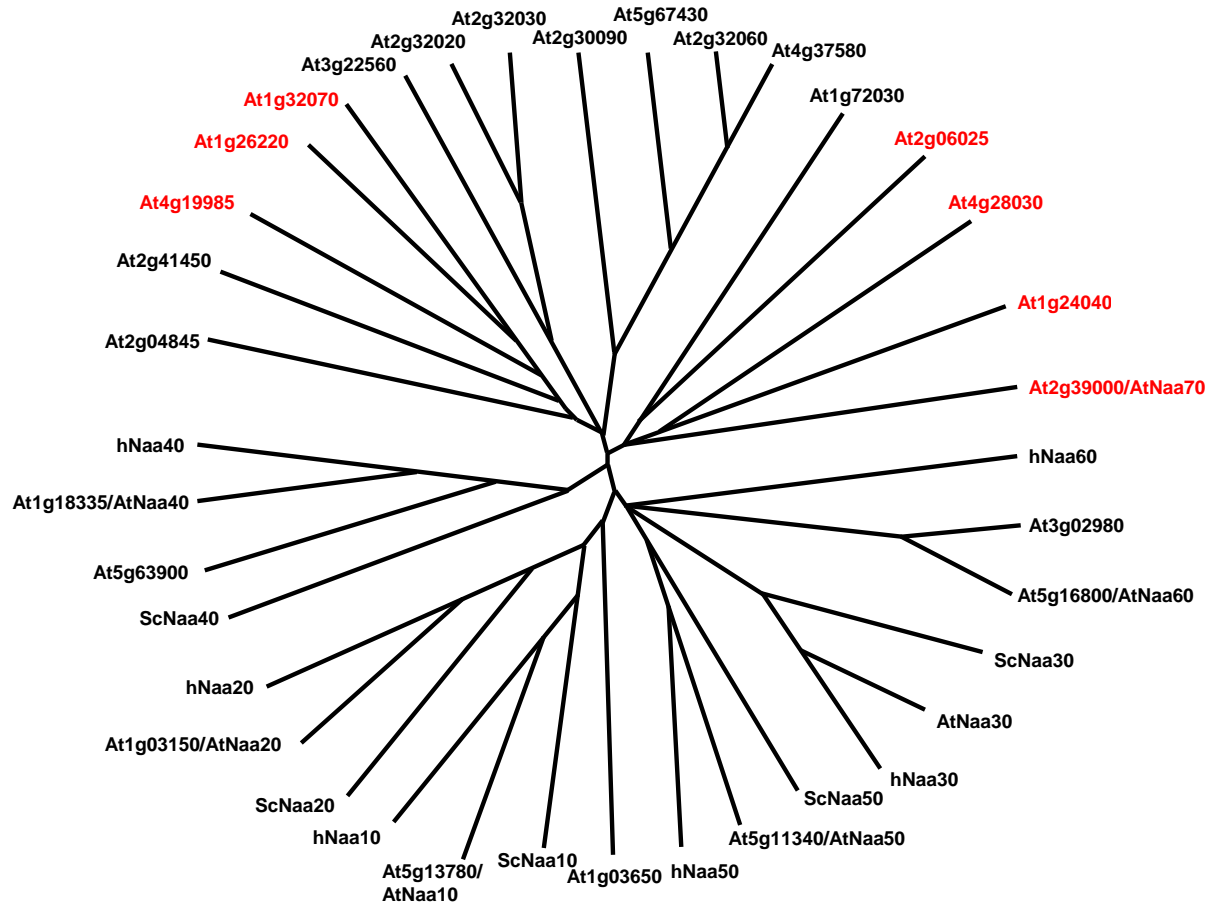
PROTEOMICS

Supporting Information for Proteomics

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**Molecular identification and functional characterization of the first
N α -acetyltransferase in plastids by global acetylome profiling**



Supplemental Figure 1. Phylogenetic tree of 25 putative Nats present in Arabidopsis

Protein sequences of 12 *bona fide* Nats from eukaryotes have been used to identify potential Nat candidates (25) encoded by the Arabidopsis genome. The phylogenetic tree of known metazoan putative Arabidopsis Nats was created with Clustal Omega [1] and visualized by using the Treeview open software source [2]. Proteins labelled in red are predicted to localize in plastids. Please note that the plant cytosolic Nats cluster with their corresponding Nat from metazoan and that these Nats form a separate branch of the tree (lower part).

References

- [1] McWilliam, H., Li, W., Uludag, M., Squizzato, S., *et al.*, Analysis Tool Web Services from the EMBL-EBI. *Nucleic acids research* 2013, 41, W597-600.
- [2] Page, R. D., TreeView: an application to display phylogenetic trees on personal computers. *Computer applications in the biosciences: CABIOS* 1996, 12, 357-358.