

## Project Title

9th August 2023

Redmine issue:	#9999
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*(As copy and pasted from Redmine issue.)*

## **Project history**

*A brief summary of the project's key points.*

**2018-12-19** Meeting with the group to plan data analyses

### Data responsibilities

Unfortunately, NBIS does not have resources to keep any files associated with the support request; we kindly suggest that you safely store the results delivered by us. In addition, we kindly ask that you remove the files from UPPMAX/UPPNEX. The main storage at UPPNEX is optimized for high-speed and parallel access, which makes it expensive and not the right place for long-term archiving. Please be considerate of your fellow researchers by not taking up this expensive space.

The responsibility for data archiving lies with universities and we recommend asking your local IT for support with long-term data storage. The [Data Center](#) at SciLifeLab may also be of help with discussing other options.

Please note that special considerations may apply to human-derived, sensitive personal data. This should be handled according to specific laws and regulations as outlined at the [SciLifeLab website](#).

### Acknowledgments

If you are presenting the results in a paper, at a workshop or at a conference, we kindly remind you to acknowledge us according to the signed [NBIS User Agreement](#):

Please acknowledge NBIS like so: *Support by NBIS (National Bioinformatics Infrastructure Sweden) is gratefully acknowledged.*

NBIS staff should be included as co-authors if the support work leads to a publication and when this is merited in accordance to the ethical recommendations for authorship, *i.e.* the [ICMJE recommendations](#). If applicable, please include *Supp Ortstaff, National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Stockholm University* as co-author.

In addition, Uppmax kindly asks you to [acknowledge UPPMAX and NAISS](#). If applicable, please add: *The computations/data handling/ [SIMILAR] were/was enabled by resources in project /b2000000 provided by the National Academic Infrastructure for Supercomputing in Sweden (NAISS) at UPPMAX, funded by the Swedish Research Council through grant agreement no. 2022-06725.*

In any and all publications based on data from NGI Sweden, the authors must [acknowledge SciLifeLab, NGI, VR and UPPMAX](#).





Results 1

You should soon be contacted by one of our managers with a request to close down the project in our internal system and for invoicing matters. If we do not hear from you within **30 days** the project will be automatically closed and invoice sent.

Again, we would like to remind you about data responsibility and acknowledgements, see [Data responsibilities](#) and [Acknowledgments](#).

You are naturally more than welcome to come back to us with further data analysis request at any time via <https://nbis.se/services/bioinformatics>. Thank you for using NBIS, we wish you the best of luck with your future research!

## R session info

- R version 3.5.1 (2018-07-02), x86\_64-conda\_cos6-linux-gnu
- Running under: Ubuntu 20.04.6 LTS
- Matrix products: default
- BLAS/LAPACK: /home/julie/miniconda3/envs/sweavenf/lib/R/lib/libRlapack.so
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: knitr 1.23
- Loaded via a namespace (and not attached): compiler 3.5.1, evaluate 0.14, magrittr 1.5, stringi 1.4.6, stringr 1.4.0, tools 3.5.1, xfun 0.13