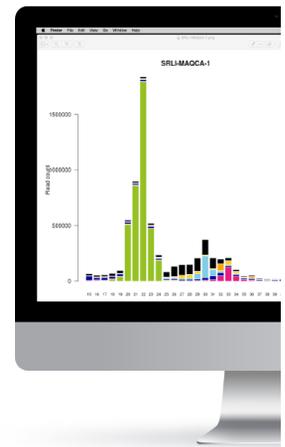


# Comprehensive RNA seq data quality control and reliable data processing using Cobra

At Biogazelle we take gene expression data analysis seriously. Our qbase+ end-user software for Mac and Windows supports researchers since 2008 in their quantitative PCR data management, quality control and statistical analyses. To handle massively parallel RNA sequencing data, we developed a cloud-based pipeline for RNA seq data management and analysis, using established tools like TopHat-Cufflinks when available and developing our own tools when needed.

## Reliable: Validated workflows and quality control checks. Full control over your data.

- ✓ All data processing and quality control pipelines in Cobra are fully ISO 17025:2005 validated prior to release, using publically available benchmark datasets with extensive data quality control. The resulting 90-page validation report is your ultimate guarantee.
- ✓ The quality of your RNA sequencing data is controlled at multiple points during processing and analysis. Any deviations are automatically reported by Cobra and investigated by a PhD-level data analysis expert assigned to your project.
- ✓ Cobra incorporates additional quality control checks relevant to your RNA sequencing data, such as ribosomal RNA content following a total RNA library prep or globin content for whole blood-derived data.



## Traceable: Full insight in every single data manipulation. For years after completion.

We keep detailed records of both computational and manually performed tasks, including tool and database versions. You can request these detailed records, months or years after completion of your project, to get full insight in every single data manipulation.

## Secure: Worry-free through controlled data access and data loss prevention.

- ✓ Your RNA sequencing data is protected from unwanted eyes by limited IP access range, user authentication and secure data transfer.
- ✓ Data backup – from raw sequencing data to final report – using multi-site redundancy guarantees that no piece of data will ever get lost.



## Flexible. Meeting your custom data processing needs.

- ✓ Cobra is a versatile platform with on demand incorporation of custom reference data allowing reliable processing of your custom project.
- ✓ Your custom project still benefits from the validated pipelines, quality controls and standard reporting in Cobra.

## High performance: Immediate data processing. No delay.

No more queuing of your data. Cobra can analyze very large scale projects within a day. Multiple projects are independently analyzed in parallel.

## The software

Cobra is the software we use internally to manage data and perform analyses in RNA sequencing studies, both for small RNAs like microRNAs, piRNAs or tRNA-fragments as well as long RNAs including both messenger RNA (mRNA) and long non-coding RNA (lncRNA). It can process local data or fetch new project files from Illumina's BaseSpace. Small RNA sequencing data are processed using our own Ant code\* whereas poly+ RNA or total RNA seq data are processed by Sailfish/Salmon (quick expression analysis of known transcripts) or the TopHat-Cufflinks/HTSeq tools (for novel transcripts or if mapping results need to be visualized). For both types of data analysis, reporting of quality control and results is being integrated.

\* Ant, its small size definitely refers to small RNA sequencing, but its Dutch translation "mier" ('ie' sounds like 'ee' in beer) is an even better match for the miRs that are the primary focus of small RNA seq.

## What's in a name?

Cobra has a lengthy disambiguation list in Wikipedia but was selected because it combines a reference to biology and animals, much like the company name, with a link to (gene) expression via the avant-garde movement CoBrA. CoBrA was the name coined in 1948 for a group of expressionist artists from Copenhagen, Brussels and Amsterdam. As such, it not only refers to expression, albeit in an artistic rather than scientific way, but also to the Belgian roots of Biogazelle.

Would you like to learn more about our capabilities? Check out other tech notes in our Knowledge Center at [www.biogazelle.com/knowledge-center/technotes](http://www.biogazelle.com/knowledge-center/technotes)