

(a)

General Information

Number of samples:	12
Number of groups:	9
Number of genes:	20825
Dimension 1st level SOM:	20 x 20
Analysis finished:	Di Jun 03 16:26:20 2014 CEST

Results

- [Raw Data \(PDF\)](#)

1st Level SOM Analysis

These reports comprise the SOM portraits in standard and alternative color scales, as well as supporting maps and profiles which provide supplementary information about the 1st level SOM.

- [1st Level SOM Expression Portraits \(PDF\)](#)
- [Alternative Color Scales: absolute, WAD, loglogFC \(PDF\)](#)
- [Rank Portraits: FC, WAD, shrinkage-t \(PDF\)](#)

- [Supporting Maps \(PDF\)](#)

- [Entropy Profiles \(PDF\)](#)
- [Topology Profiles \(PDF\)](#)

Sample Summaries

Summary page for the individual samples.

- [Sample Reports \(HTML\)](#)

Geneset Enrichment Analysis

Functional analyses using predefined gene sets. The results are visualized in terms of heatmaps, profile plots and population maps.

- [Functional Analysis \(HTML\)](#)

2nd Level Analysis

Sample similarity analyses based on different metrics applied, using the metadata as input.

- [2nd Level SOM \(PDF\)](#)
- [Similarity Based Methods: Neighbor Joining, Hierarchical Clustering \(PDF\)](#)
- [Correlation Based Methods: Spanning Tree, Networks, Maps \(PDF\)](#)
- [Component Based Methods: 2d-ICA, 3d-ICA \(PDF\)](#)

3rd Level Analysis

Different criteria of spot module definition such as overexpression or mutual correlations between the metagenes where applied. The reports comprise integrated portraits, functional analyses.

- [Spot Reports \(HTML\)](#)

Group Analyses

Analyses based on group-wise aggregated data, including portraits, clustering and functional analyses.

- [Group Analysis Reports \(HTML\)](#)

(b)

Group Overview

Groups	Number of Samples
Homeostasis	2
Endocrine	1
Digestion	1
Exocrine	1
Epithelium	1
Reproduction	1
Muscle	1
Imune System	2
Nervous System	2

Sample Summary Sheets

For each sample a report sheet is created which summarizes the most relevant information using the global and local perspective. The global summary shows the ranked list of differentially expressed genes for the whole sample, the ranked list of over- and underexpressed gene sets after GSZ-overexpression analysis and the respective p-value distributions. The local summary sheets present the analogous information for each single spot detected. The gene and gene set list are provided as tables.

Sample Name	Group	Summary Sheet	Global Gene List	Local Gene List	Gene Set List
liver	Homeostasis	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
kidney cortex	Homeostasis	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
				CSV 4	
thyroid gland	Endocrine	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
small intestine	Digestion	PDF	CSV	CSV 1	CSV
				CSV 2	
prostate	Exocrine	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
tongue	Epithelium	PDF	CSV	CSV 1	CSV
				CSV 2	
testis	Reproduction	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
				CSV 4	
skeletal muscle	Muscle	PDF	CSV	CSV 1	CSV
				CSV 2	
bone marrow	Imune System	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
lymph node	Imune System	PDF	CSV	CSV 1	CSV
				CSV 2	
accumbens	Nervous System	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	
cerebral cortex	Nervous System	PDF	CSV	CSV 1	CSV
				CSV 2	
				CSV 3	

(c)

Spot Module Report Sheets

Reports contain the spot module expression profiles and assignments of the spots to samples and to groups.

- [Overexpression Spot Report \(PDF\)](#)
- [Underexpression Spot Report \(PDF\)](#)
- [K-Means Cluster Report \(PDF\)](#)
- [Group Overexpression Report \(PDF\)](#)

Spot Module Network Analysis

Networks of spot association are visualized as graphs. WTO, correlation networks and correlation spanning trees, are given for individual spots and spot patterns.

- [Overexpression Networks \(PDF\)](#)
- [Underexpression Networks \(PDF\)](#)
- [K-Means Cluster Networks \(PDF\)](#)
- [Group Overexpression Networks \(PDF\)](#)

Chromosomal Enrichment

For each spot, enrichment of chromosomal positions (chromosome/band) is visualized as overview heatmaps and individual chromosome plots.

- [Overexpression Chromosomal Enrichment \(PDF\)](#)

(d)

Gene Sets

Enrichment profiles of individual predefined gene sets are shown as bar plots across all samples. Additionally the log FC-expression profiles of the leading metagenes are shown. Further, members of each gene set are given as population maps and tables.

Category BP

Geneset name	Category	Profile	Population Map	Members
'de novo' posttranslational protein folding	BP	PDF	PDF	CSV
2-oxoglutarate metabolic process	BP	PDF	PDF	CSV
3'-phosphoadenosine 5'-phosphosulfate metabolic process	BP	PDF	PDF	CSV
3'-UTR-mediated mRNA stabilization	BP	PDF	PDF	CSV
7-methylguanosine mRNA capping	BP	PDF	PDF	CSV
acrosome assembly	BP	PDF	PDF	CSV
acrosome reaction	BP	PDF	PDF	CSV
actin cytoskeleton organization	BP	PDF	PDF	CSV
actin cytoskeleton reorganization	BP	PDF	PDF	CSV
actin filament-based movement	BP	PDF	PDF	CSV
actin filament bundle assembly	BP	PDF	PDF	CSV