

# Pairwise Differential Expression Results

Name: L1\_vs\_C1

## Dataset Overview

- Number of total features: **23,937**
- Number of filtered features: **12,393**
- Number of features after filtering: **11,544**
- Number of analyzed samples: **2**

## Results

Number of differentially expressed (DE) features (Probability > 0.9): **5,363**

- Up-regulated ( $M > 0$ ): **2,655**
- Down-regulated ( $M < 0$ ): **2,708**

## Experimental Design

Sample	Raw lib. size	Normalized lib. size	Condition
C1	19,241,190	24,332,773.402	Reference
L1	35,242,306	30,454,310.168	Contrast

## Analysis Parameters

Parameter	Value
CPM Filter	1.0
Normalization Method	TMM (Trimmed mean of M values)
Number of Simulated Replicates	5
Size of the Simulated Replicates	0.2
Variability	0.02
Contrast Condition	L1
Reference Condition	C1

## References

- Tarazona S., Furio-Tari P., Turra D., Pietro AD., Nueda MJ., Ferrer A. and Conesa A. (2015). Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. *Nucleic acids research*, 43(21), e140.
- Tarazona S., Garcia-Alcalde F., Dopazo J., Ferrer A. and Conesa A. (2011). Differential expression in RNA-seq: a matter of depth. *Genome research*, 21(12), 2213-23.
- OmicsBox - Bioinformatics made easy. BioBam Bioinformatics (Version 3.2.2). March 3, 2019. [www.biobam.com/omicsbox](http://www.biobam.com/omicsbox).

## Pairwise Differential Expression Results

Name: S1\_vs\_C1

### Dataset Overview

- Number of total features: **23,937**
- Number of filtered features: **12,435**
- Number of features after filtering: **11,502**
- Number of analyzed samples: **2**

### Results

Number of differentially expressed (DE) features (Probability > 0.9): **6,815**

- Up-regulated (M > 0): **2,969**
- Down-regulated (M < 0): **3,846**

### Experimental Design

Sample	Raw lib. size	Normalized lib. size	Condition
C1	19,241,190	15,257,786.876	Reference
S1	17,282,404	21,832,888.499	Contrast

### Analysis Parameters

Parameter	Value
CPM Filter	1.0
Normalization Method	TMM (Trimmed mean of M values)
Number of Simulated Replicates	5
Size of the Simulated Replicates	0.2
Variability	0.02
Contrast Condition	S1
Reference Condition	C1

### References

- Tarazona S., Furio-Tari P., Turra D., Pietro AD., Nueda MJ., Ferrer A. and Conesa A. (2015). Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. *Nucleic acids research*, 43(21), e140.
- Tarazona S., Garcia-Alcalde F., Dopazo J., Ferrer A. and Conesa A. (2011). Differential expression in RNA-seq: a matter of depth. *Genome research*, 21(12), 2213-23.
- OmicsBox - Bioinformatics made easy. BioBam Bioinformatics (Version 3.2.2). March 3, 2019. [www.biobam.com/omicsbox](http://www.biobam.com/omicsbox).