Zenodo Dataset for the publication

Neurothreads: development of supportive carriers for mature dopaminergic neuron differentiation and implantation

by

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This dataset contains the raw data used to produce all the main and supplementary figures of the publication mentioned above. It also includes the statistical analysis and graphing.

History

This is version v3 of this dataset. It has been updated through the peer review process to v2, with further minor completion to v3. The changes associated with each version are documented in detail in the change log file (i.e. __CHANGE LOG.pdf in this repository).

Qualitative figures (images)

For the qualitative subfigures (images), this dataset provides high resolution images corresponding to the figures in the paper.

Quantitative figures (analysis)

For the quantitative analysis, this dataset provides an extensive documentation of the data used, and also of the analysis and aggregation.

General approach to quantitative analysis

In general, the approach is based on a two-step analysis:

1) The raw data is stored, tabulated, and aggregated per condition as appropriate in Excel files (.xlsx)
2) The relevant overview data is then transferred to Graphpad Prism files (.pzfx) for graphing and statistical analysis

For this reason, there is generally both a .xlsx and a .pzfx file per subfigure. For example, Fig. 4c provides gene expression analysis for different conditions of LUHMES cells (undifferentiated, differentiated on 2D TC plates, and differentiated on 3D cryogels). So according to the above scheme:

1) Fig_4c.xlsx contains the raw Ct values obtained by RT-PCR. This data involves technical triplates per sample, as well as multiple wells and gels per experiment and condition. Fig_4c.xlsx provides aggregation of this data to the relevant per-experiment level as well as the details on normalization to house-keeping genes. Fig_4c provides the aggregated and normalized data in its first sheet.

2) We then copied this high-level data to a Graphpad file, provided as Fig_4c.pzfx. This file provides graphing and statistical analysis of the summary data.

Additional files

In addition to the .xlsx and .pzfx files indicated above, we also provide other files as appropriate. For example, for Fig. 4c, we also provided the main graphical output separately as a pdf file, for users not having access to graphpad, for example. In Fig. 4c, we additionally provided the direct output of conversion of the RT-PCR .sds files to Excel files as a zip. These files are even more detailed, as they show exact well loading. Such deeper raw data files serve mostly documentation purposes, as they have only very marginally been documented for readability.

The file "clustering_analysis.pdf" globally describes our analysis of clustering effects present in the data in the framework of the Moulton factor analysis[1]. This provides the data-driven rationale for aggregation to biological replicates for experiments concerning primarily biological readout such as cell differentiation and morphology, as given in the manuscript. The file "clustering_analysis_R_scripts.zip" provides the detailed R scripts used in the clustering analysis. These scripts use a custom R-library, which for the purpose of versioning is hosted on Github (https://github.com/tbgitoo/moultonTools).

Bibliography

1. Angrist, J. & Pischke, J.-S. *Mostly harmless econometrics: An empiricist's companion*.

   (Princeton University Press, 2009).