

SISTEMA: A large and standardized collection of transcriptome data sets for human pluripotent stem cell research

Margot Jarrige, Hélène Polvèche, Alexandre Carteron, Stéphane Janczarski, Marc Peschanski, Didier Auboeuf, Cécile Martinat

▶ To cite this version:

Margot Jarrige, Hélène Polvèche, Alexandre Carteron, Stéphane Janczarski, Marc Peschanski, et al.. SISTEMA: A large and standardized collection of transcriptome data sets for human pluripotent stem cell research. iScience, 2021, 24 (7), pp.102767. 10.1016/j.isci.2021.102767. inserm-04385458

HAL Id: inserm-04385458 https://inserm.hal.science/inserm-04385458

Submitted on 22 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



SISTEMA: a large and standardized collection of transcriptome datasets for human pluripotent stem cell research

Margot Jarrige^{1#}, Hélène Polvèche^{1#}, Alexandre Carteron¹, Stéphane Janczarski³, Marc Peschanski¹, Didier Auboeuf³, Cécile Martinat^{2*}

¹CECS/AFM, I-STEM, 91100 Corbeil-Essonnes, France

²INSERM/ UEVE UMR 861, Paris Saclay Univ I-STEM 91100 Corbeil-Essonnes, France

³LBMC, Univ Lyon, ENS de Lyon, Univ Claude Bernard, CNRS UMR 5239, INSERM U1210, 46 Allée d'Italie Site Jacques Monod, F-69007, Lyon, France

[#] Contributed equally

^{*} Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Cécile Martinat (cmartinat@istem.fr).

SUMMARY

Human pluripotent stem cells have ushered in an exciting new era for disease modelling, drug discovery and cell therapy development. Continued progress toward realizing the potential of human pluripotent stem cells will be facilitated by robust datasets and complementary resources that are easily accessed and interrogated by the stem cell community.

In this context, we present SISTEMA, a quality-controlled curated gene expression database, built on a valuable catalogue of human pluripotent stem cell lines and their derivatives for which transcriptomic analyses have been generated using a single experimental pipeline. SISTEMA functions as a one-step resource that will assist the stem cell community to easily evaluate the expression level for genes of interest, while comparing them across different hPSC lines, cell types, pathological conditions or after pharmacological treatments.

INTRODUCTION

In the last decades, the isolation of human pluripotent stem cells, first from human embryos (Thomson et al., 1998), and more recently from the genetic conversion of somatic cells (Takahashi et al., 2007), represents a major breakthrough to study lineage-specific mechanisms underlying development or pathological condition and to broaden our capacity for biological therapeutics. Based on their unique capacities for self-renewal and differentiation into specialized cell types, human pluripotent stem cells have become the subject of intense research not only for developmental studies but also in the field of cell therapy, modeling of human diseases and drug discovery and testing (Bassez et al., 2018; Ben M'Barek et al., 2020; Ben M'Barek et al., 2017; Rowe & Daley, 2019).

Genome-wide expression profiling has been a common endpoint for these studies for analyzing pluripotency, differentiation and the function of genetic variants associated with monogenic diseases. A growing body of transcriptomic datasets for various hPSC lines and their specific differentiated counterparts has been deposited in public data repositories (Assou et al., 2007; Au & Sebastiano, 2014; Ghosh & Som, 2020; Godoy et al., 2018; Mair et al., 2019; Mallon et al., 2013; Streeter et al., 2017). Despite this wealth of data, exploring gene expression profiles from different experiments is not trivial. Different challenges still remain such as the integration and interpretation of massive amount of available data, the heterogeneity in original data processing as well as the quality datasets (Pinto et al., 2018). To overcome these challenges, we provide here a large well-characterized collection of human pluripotent stem cell lines and their derivatives for which transcriptomic analysis has been generated using a single experimental pipeline. Moreover, we have developed a user-friendly search engine to facilitate comparisons of gene expression data between these different biological samples. This open resource presented in SISTEMA web portal is designed for the community to examine individual or multiple genes for expression under

different states from pluripotency to differentiated conditions and under normal or pathological conditions, with 8 different monogenic diseases already represented in this growing database.

RESULTS

Data collection and dataset curation

All the biological samples were collected from the same laboratory and included 45 hPSC samples from 11 hPSC lines (2 hESCs and 9 hiPSC) at either undifferentiated state or one of eight differentiated states representing the different germ layers (Guenou et al., 2009; Maury et al., 2015; Mournetas et al., 2019; Nicoleau et al., 2013) (Figure 1A). This collection included 23 healthy and 24 clones from donors with a rare genetic disease which represented a total of 8 different pathological conditions comprising neuromuscular, neurodegenerative and skin disorders, as well as some isogenic lines generated either using CRISPR/ Cas 9 technology or lentiviral transduction (Figure 1B and 1C). Samples treated with different chemical compounds have also been included (Figure 1D). These small molecules were evaluated in the context of different pathologies such as lithium for the autism spectrum disorder caused by SHANK3 haplo-insufficiency, MG132 for Hutchinson-Gilford progeria syndrome, Thiostrepton and Bortezomib for Limb-girdle muscular dystrophy type 2D, VPA for Wolfram syndrome or Kenpaullone for Spinal muscular atrophy (Darville et al., 2016; Harhouri et al., 2017; Hoch et al., 2019). All the transcriptomic data were generated in comparison to DMSO treated controls. Of interest, some of the data provided by the database have not been published yet all the scientific community to have access to a larger spectrum of data. All the cell lines used for the creation of this database as well as the metadata files are also available upon request and following the French legal policy.

The processing of all these biological samples were performed using a unique platform following a standardized protocol from RNA extraction to biological analysis. To overcome the current limitations associated with traditional whole-transcriptome sequencing technology, e.g., the requirements of a significant amount of input RNA, we chose to process the samples by using the Ion Ampliseq technology (Li et al., 2015). This technology has been designed for targeted amplification of over 20,000 distinct human RNA targets simultaneously and is

described to present the advantage of amplifying a short amplicon (~ 150 bp) for each targeted gene allowing a much smaller amount of raw reads (only 10 Million reads sequenced by sample) required for accurate gene expression quantification (Li et al., 2015). To evaluate the reproducibility of the Ampliseq technology, one RNA sample was sequenced twice independently leading to a percentage of correlation of 97.8, which indicated a consistent performance between technical replicates (Figure S1A). This experiment also confirms the robustness of this technology allowing us to study and compare the gene expression of several samples sequenced at different times on the platform. Then we validated the sequencing coverage offered by the Ampliseq technology. For this purpose, each amplicon sequence was BLASTed against a transcriptome of reference (GRCh38.92). This analysis revealed that 99.89% of the amplicons panel were correctly identified and represented 21,080 genes. (Figure S1B). Based on this technology, a total of 443 transcriptomes were generated by following a unique and standardized protocol which led to the consistent deep sequencing coverage and percentage of alignment (Figure S2A and S2B). The sequencing process was followed by a standardized data analyzing pipeline as described in Supplementary Figure 2A. For each sample, reads were aligned to the Amplicons sequence reference using bowtie2 local (v2.3.4.1). Reads below a mapping score of 10 or multi-mapped were filtered using samtools (v0.1.19). Samples were normalized by RPM (reads per Million) and the expression values were converted into logarithm scale (log10(x+1)) using R (v3.6.0).

Web interface and graphical visualization

All expression profiles from the 443 experimental datasets have been implemented in the form of a web-resource called SISTEMA (http://sistema.ens-lyon.fr). It was designed as a user-friendly interface in which a set of tools has been integrated for providing a rapid overview of the data and for querying, analyzing and displaying data online. With the purpose of continuously updating this resource with new datasets, SISTEMA enables to compare the

expression levels of particular genes of interest or a combination of genes across different lineages and conditions.

The query can be specified by first selecting the datasets pertaining to the cell lineage(s) of interest, the genotype(s), the cell line(s), the time of differentiation, the effect of a chemical treatment (Figure 2A). Then, the users can define the gene(s) of interest (Figure 2A). As an example of querying for a single gene, the expression profile of NANOG, one of the key pluripotent markers (Chambers et al., 2007; Silva et al., 2009), has been analyzed in different samples of undifferentiated hESC samples or hiPSC-derived Keratinocytes. Once the queried data is processed, detailed information regarding the chromosomic localization, the gene structure, its interacting partners are first displayed as SISTEMA interface is linked to other databases such as Genecards, NCBI, MIM, HGNC, Ensembl, Vega and STRINGDB (Figure 2B). For better visualization, the results are presented as a histogram and a downloadable table in which data are expressed as the normalized counts in logarithmic scale observed in each sample. As expected, NANOG was found to be highly expressed in pluripotent cells whereas its expression is absent in the hiPSC-derived keratinocytes (Figure 2C-2D). For each sample, a list of different characteristics such as the cell type, genotype, the phenotype, the time and condition in culture, is provided (Table1) and the user can customize the graph and the table in function of the cell types, genotypes, cell lines or time of differentiation (Figure 2D).

SISTEMA also allows a multi-gene analysis. An option is proposed to visualize the expression profile of up to 10 genes on a selected set of samples. As an example, the expression profiles of *NANOG*, *OCT4* and *SOX2*, the triad of transcription factors known to be critical for self-renewal and pluripotency (Chambers & Tomlinson, 2009), has been analyzed in hESC and hiPSC-derived keratinocytes (Figure 3A). As for the single gene analysis, detailed information regarding each gene is provided and their expression profile is

presented as a histogram and a downloadable table (Figure 3B-3D). In addition, results are also presented as a heatmap in which the retrieved expression data for the selected genes and cell types are indicated and the samples are hierarchically clustered (Figure 3C).

Example applications

To illustrate the utility and the potential applications of SISTEMA, we first sought to evaluate the assignments of the samples from clustering the entire database in function of the expression of selected markers. For that purpose, the expression of a set of 10 genes of pluripotency, extracted from the database KEGG pathway, were analyzed across all the biological samples. Hierarchical clustering allowed the correct distinction between pluripotent stem cells and differentiated cells (Figure 4A). Conversely, the expression profile of a set of 10 genes associated with the GO term "spinal cord motoneuron differentiation" led to the distinction between pluripotent stem cells and their motoneuronal derivatives, comfirming the relevance of the SISTEMA Database (Figure 4B).

We also evaluated the possibility to define the temporal expression profile of 10 genes known to be associated with the development of the melanocyte lineage (from GO) at different time points of the differentiation protocol from human pluripotent stem cells. As expected, the expression profile of this set of markers allowed to accurately make the distinction between hPSCs and hPSC-derived melanocytes. In addition, it revealed profiles of gene expression that evolved over time along with the differentiation (Figure 4C). Thus, *CITED1* and *ENDRB*, previously described as two important regulators of melanogenesis (Howlin et al., 2015; Nair et al., 2001; Park et al., 2015), appeared progressively expressed during the differentiation process (Figure 4C). The expression of *GLI3* was in contrast more pronounced in the early specification of the melanocyte lineage, as previously described in a mouse model (Matera et al., 2008). As a control, we also chose GNAQ which appears to be the only one with no modification of its expression with the differentiation. Concordant with our observations, this

gene has been previously shown to be involved in the regulation of pigmentation rather than differentiation (Kusters-Vandevelde et al., 2010; Van Raamsdonk et al., 2004). Altogether, these analyses validated the relevance of the SISTEMA database both to evaluate the expression profiles of different gene sets across a large battery of biological samples and to visualize the expression profiles of gene sets along lineage specification.

Since their first isolation, human pluripotent stem cells have sparked widespread enthusiasm for the development of new models of human disease and have enhanced platforms for drug discovery. To evaluate the potential of SISTEMA database for these applications, we focused on the expression profile of the survival motor neuron 1 (SMN1) gene, the homozygous deletions/mutations of which causes spinal muscular atrophy (SMA), a severe genetic neuromuscular disease (Lefebvre et al., 1995). As expected, SMN1 expression was significantly decreased only in the biological samples derived from SMA patients (Figure 5A). Next, we sought to explore SISTEMA database to identify a potential small molecule capable to increase the level of SMN1, which therefore would present a therapeutic interest. Thanks to an unbiased analysis including all the pharmacologically-treated biological samples present in SISTEMA database, we identified three proteasome inhibitors, Bortezomib, Thiostrepton and MG132 that lead to an increased expression of SMN1 compared to mocktreated controls. The results were concordant with previous studies that showed at least for two of these proteasome inhibitors, Bortezomib and MG132, a beneficial effect on SMN1 expression both in vitro and in vivo (Kwon et al., 2011; Locatelli et al., 2015). In contrast, and in agreement with previous studies (Brichta et al., 2003; Dachs et al., 2013; Elshafay et al., 2019; Piepers et al., 2011), neither VPA nor lithium treatment showed a significant effect (Figure 5B).

DISCUSSION

Here we present the data access and presentation services that SISTEMA database provides, which enable the community to both discover and to reuse the cell lines and data included in this project.

SISTEMA further complements and outspreads the two gene expression databases dedicated to pluripotent stem cells, StemCellDB for human embryonic stem cells (Mallon et al., 2013) and HipSci for human induced pluripotent stem cells (Streeter et al., 2017). Whereas these online resources are based on either microarrays or whole transcriptome RNA sequencing technologies, the main strength of SISTEMA lies on the use of a unique pipeline to generate transcriptomic analysis providing a collection of quality-controlled curated data. Most of the other data resources from public repository, i.e. EBI expression atlas or NCBI short read archive, are also useful tools to explore gene expression dataset but cover a large set of biological field from microbiology to stem cells biology which makes difficult to easily and rapidly analyze a specific research. One of the objectives of Sistema is to provide a rapid overview of the gene expressing by providing a comprehensive and limited number of hESC and hIPSCs cells and their derivatives. Additionally, SISTEMA relies on the use of a recent technology, named AmpliSeq, designed for targeted amplification of over 20,000 distinct human RNA targets simultaneously using a highly multiplexed amplification method (Li et al., 2015). Because of this targeted nature and small amplicon size, the amount of raw data required for accurate gene expression quantification is much smaller with the AmpliSeq technology than classical RNA sequencing. This clearly represents an advantage since for large scale of RNA sequencing experiments involving hundreds or even thousands of samples the bioinformatics analysis as well as the data storage needs can rapidly become strenuous (Schmidt & Hildebrandt, 2017). All the data included in SISTEMA have thus been generated through this unique experimental workflow and on the same platform, giving rise to standardized operative procedures and the production of homogenous samples in term of quality and coverage depth.

Since the derivation of the first human embryonic stem cell line more than two decades ago (Thomson et al., 1998), human pluripotent stem cells have ushered in an exciting new era for the fields of stem cell biology and biomedical research. Nowadays, human pluripotent stem cells are widely used for disease modelling, drug discovery and cell therapy development. In this context, SISTEMA provides a valuable catalogue of human pluripotent stem cell lines with a representative snapshot of these cells in their undifferentiated state as well as in a wide range of differentiated cell types. SISTEMA functions as a one-step resource that will assist the stem cell community to easily evaluate the expression level for their genes of interest, while comparing them across different hPSC lines, cell types, pathological conditions or after pharmacological treatments (Figure 6). It therefore opens up a wide spectrum of applications (Figure 6), such as validating the co-expression of different genes along a differentiation process or under a pathological condition, assessing their cell-type or temporal specificities of expression, evaluating the effect of a drug treatment on a set a genes of interest. Most of the data presented on Sistema are already integrated on largest databases such as Gene Expression Omnibus. Of interest, our database also includes none published results which provide an opportunity for the scientific community to access to larger not yet published datasets.

LIMITATIONS OF THE STUDY

Currently, SISTEMA contains data generated from the amplised technology and does not include other omics. Our objective for the future is to continuously feed SISTEMA with new data generated on our platform without ruling out the possibility of including expression profiles generated by whole transcriptome RNA sequencing or single cell RNA sequencing,

also generated by the same platform as these approaches provide complementary snapshots (Li et al., 2015).

ACKNOWLEDGEMENTS

I-Stem is part of the Biotherapies Institute for Rare Diseases (BIRD) supported by the Association Française contre les Myopathies (AFM-Téléthon). This project was supported by grants from Laboratoire d'Excellence Revive (Investissement d'Avenir; ANR-10-LABX-73) and the program "investissement d'avenir" INGESTEM. We thank the groups of Anselme Perrier, Laetitia Aubry, Christine Baldeschi, Xavier Nissan, Alexandra Benchoua, Christelle Monville, Christian Pinset, for providing biological resources and Lina El-Kassar for karyotyping the cell lines. We gratefully acknowledge support from the PSMN (Pôle Scientifique de Modélisation Numérique) of the ENS de Lyon for computing resource. The authors would like to thank Jean-Baptiste Claude and Laurent Modolo for the useful discussions on the analysis protocols and the development of the web interface.

AUTHOR CONTRIBUTIONS

Conceptualization: M.J., H.P., D.A., C.M. and M.P.; Methodology: M.J., H.P., D.A. and C.M.; Investigation: M.J., H.P., A.C.; Data Curation: M.J., H.P., A.C.; Software H.P. and S.J.; Resources: M.J., H.P., A.C.; Writing – Original Draft & Review & Editing: M.J., H.P., D.A., and C.M. Funding Acquisition: C.M., M.P and D.A

DISCLOSURE OF POTENTIAL CONFLICTS OF INTEREST: The authors declare no conflicts of interest.

INCLUSION AND DIVERSITY: While citing references scientifically relevant for this work, we actively worked to promote gender balance in our reference list.

FIGURE LEGENDS

Figure 1. Representation of the phenotype and genotype diversity currently described in the database. (A). Graphical representation in percentage distribution of the 10 principal cell types that are present in SISTEMA database. Reference cells means RNA from commercial cell lines (primary cells) or total RNAextracted from human tissues; i.e. human Brain or Human foetal Brain. (B). Graphical repartition between biological samples that carry a causal mutation associated with a rare disease and healthy non affected (WT) biological samples. (C). Detailed representation of the different monogenic diseases presented in SISTEMA (EB: Epidermolysis bullosa, HD: Huntington, LND: Lesch Nyhan, SMA: Spinal Muscular Atrophy, WFS: Wolfram Syndrome, DMD: Duchenne Muscular Dystrophy, DM1: Myotonic Dystrophy type 1 and Progeria). (E). Graphical representation of pharmacological treatments performed on some biological samples. See also Figure S1 and S2.

Figure 2. Visualization of the Web Interface for single gene analysis. (A). View of the query page with the different filters that can be used for analysis such as cell type, pharmacological treatments, time of differentiation as well as the visualization of the results obtained for NANOG as the gene of interest. (B). Visualization of the general information provided for each gene as well as the different web links. (C). Level of expression of NANOG in hES cells and hES-derived keratinocytes (normalized counts: log10(cpm + 1)). (D). Visualization of the expression table gathering the different information concerning each cellular sample. This table is downloadable as an excel file. Figures C-D represent the results obtained with 9 different hESC lines. See also Table 1.

Figure 3. Visualization of the Web Interface for analysis of multiple genes. (A). for each gene analyzed, a link to NCBI database is associated as well as the possible relation between the different genes analyzed (by using STRING). (B) Histogram representing the comparative expression value for each gene analyzed in hES cells and hES-derived keratinocytes. (C). Hierarchical clustering of the genes SOX2, NANOG and POU5F1B expressed in undifferentiated hESC and in hPSC-derived keratinocytes (normalized counts: log10(cpm + 1), (D) Downloadable expression table and detailed

information about individual biological sample. Figures 3C-D correspond to the representative results obtained with 9 independent hPSC lines.

Figure 4. Pairwise dissimilarities of markers identified from specific differentiation status ("complete" method and Euclidean distance) Hierarchical clustering for 10 genes extracted from (A) KEEG "Signaling pathways regulating pluripotency of stem cells" (hsa04550) on all the biological samples included in SISTEMA database. These genes were selected on the basis of the different quality controls performed in the laboratory to validate the pluripotency of the different hiPSC and hES lines. Other genes have been selected based on the literature such as the example of ID1 gene that belongs to a family called "inhibitors of the differentiation" and previously described to be specific of human pluripotent stem cell lines (Aloia et al., 2015; Hong et al., 2011). (B) Level of expression of 10 genes selected from GO term "Spinal Cord Motor Neuron differentiation (GO 0021522) in hPS cells and hPS-derived spinal motoneurons. The genes ISL1/2 and MNX1 (also known as HB9) are two genes well known to be expressed in spinal motoneurons (Maury et al., 2015). We also used the genes referenced in the GO 0021522 and selected the ones that appear the most relevant. As two examples, Pax6 and Olig2 are two factors we routinely used to control the differentiation of human pluripotent stem cells into spinal motoneurons (Maury et al., 2015). (C). Level of expression of 10 genes selected from GO melanocyte differentiation (GO 0030318) in hPS cells and hPS-derived melanocytes.

Figure 5. Application examples of SISTEMA (A). SMN1 gene expression in different biological samples clustered in function of their phenotypes or genotypes. Each bar indicates a unique sample. (B). SMN1 expression in fibroblasts (Hoch et al., 2019) and hESC-derived neurons after treatment with different small compounds. Data have been extracted from SISTEMA and are represented as the mean of normalized count ± SEM and were statistically analyzed with DESeq2 R package using Negative binomial generalized linear model and Wald's test; *p < 0.05, **p < 0.01. Chart generated from GraphPad Prism.

Figure 6. Large spectrum of applications offered by SISTEMA

Table 1: Metadata concerning samples experiments (Related to Figure 2 and STAR Methods).

THE STAR METHODS TEXT

RESOURCE AVAILABILITY

Lead contact

Further information and requests for biological resources or metafiles should be addressed to the Lead Contact, Cécile Martinat (cmartinat@istem.fr) or Margot Jarrige (mjarrige@istem.fr).

Materials availability

This study did generate new web site available at http://sistema.ens-lyon.fr/
This study did not generate new reagents

Data and Code Availability

- Some data sets used in this work are available from publicly available sources and have been deposited at GEO (GSE 104091 and GSE119841). Accession numbers are listed in the key resources table. RNAseq data are publicity available on a user friendly interface and freely available at http://sistema.ens-lyon.fr
- All original code in this paper is available from the lead contact upon request.
- Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

*Please omit this section if your study does not use experimental models typical in the life sciences (e.g., if your study is computational or physical science research). This section should also include information related to cell lines/strains used for in vitro experiments.

RNA collection from biological samples.

RNA samples were extracted from human embryonic stem cell lines and human induced pluripotent stem cell lines collected from Institut for Stem cell Therapy and Exploration of Monogenic diseases (I-STEM). All the Human embryonic stem cell lines indicated in SISTEMA database are referenced on hPSCreg and listed here:

-SA001 (hPSCreg Name: CEBe033-A, alternative name SA00), sex Male (XY), https://hpscreg.eu/cell-line/CEBe033-A

-RC9 (hPSCreg Name: RCe013-A, alternative name RC9), sex Male (XY), https://hpscreg.eu/cell-line/RCe013-A

-RC17 (hPSCreg Name: RCe021-A , alternative name RC17), sex Female(XX), https://hpscreg.eu/cell-line/RCe021-A

The collected information regarding the cell culture conditions can be found at http://sistema.ens-lyon.fr/Echantillons.php. For the Human induced pluripotent stem cell lines not all are referenced yet but will be integrated when the program of research they are involved in will be published. The cell lines used on the study are listed on Key ressources table.

METHOD DETAILS

Data collection.

Except for the RNA reference sample, all the samples have been generated at ISTEM. Human embryonic cell (hESC) lines were used following the recommendation of the French Law of Bioethics and declared at the French Agency of Biomedicine (Number SASB1020178S). For Human induced pluripotent stem cells (hiPSC), tissue samples were collected under specific participant consents. The SISTEMA portal provides all information regarding the generation, the culture conditions of human pluripotent stem cells (hPSC) as well as their differentiation. Such information is also provided in Table 1. A unique standardized name for each sample was generated by combining "cell type"—"Phenotype"

RNA extraction.

Total RNA was extracted using the Qiacube instrument and the RNeasy micro or mini kit depending of the quantity of cells. The quality of the RNA was evaluated using the Bio-

analyseur 2100 Agilent[TM] following the protocol of the manufacturer (Qiagen®). Only samples with a RNA integrity number higher than 7 were processed.

Library generation and sequencing.

For each sample, 50 ng of total RNA was reverse transcribed using the Ion AmpliSeq Transcriptome Human Gene Expression kit following the protocol of the manufacturer (Thermofisher Scientific®). Briefly, the cDNA libraries were amplified and barcoded using Ion AmpliSeq Transcriptome Human Gene Expression core panel and Ion Xpress Barcode Adapter, named Amplicons (Thermofisher Scientific®). The amplicons were quantified using Agilent High Sensitivity DNA kit before the samples were pooled in sets of eight. Emulsion PCR and Enrichment was performed on the Ion OT2 system Instrument using the Ion PI Hi-Q OT2 200 kit (Thermofisher Scientific). Samples were loaded on an Ion PI v3 Chip and sequenced on the Ion Proton System using Ion PI Hi-Q sequencing 200 kit chemistry to generated around 10.156.774 reads per sample (200 bp read length; Thermofisher Scientific). The fastQ file was generated on the Ion Torrent server and transfer to the PSMN (for scientific pole for numerical modelling at ENS Lyon; www.ens-lyon.fr/PSMN).

Amplicon annotation.

The quality control of the sequencing data was evaluated using FastQC. The reads were trimmed using Prinseq (v0.20.4) (--trim-right 20) and filtered by average quality score (--trim-qual 20). Reads were mapped to the Amplicons sequence reference using bowtie2 local (v2.3.4.1). Reads below a mapping score of 10 or multi-mapped were filtered using samtools (v0.1.19). The level of gene expression was quantified with the specific annotation described above. Each sample was normalized by RPM (reads per Million) and the expression values were converted in logarithm scale (log10(x+1)) using R (v3.6.0).

Data implementation and web interface.

SISTEMA database was implemented using MySQL (www.mysql.com) and organized on three main tables. Briefly the first table combines all the information extracted from NCBI such as the chromosome coordinate, the gene type and the gene name (present in the seven main genetic databases: NCBI, EnsEMBL, HGNC IMGT/GENE-DB, MIM et Vega (Ashurst et al., 2005; Yates et al., 2017). The second table contains all the data curated for the sample sequence on the platform such as the library and sequencing number, the sequencing barcode, NGS user, sequencing date, FASTQ_name, sample_name, replicate, cell line, cell matrix, the team and the project). The last table corresponds to the expression value counting table transform in logarithm scale. For presentation and interpretation of the data, we chose to provide only reads per million for each gene analyzed rather than a presentation based on fold change analysis.

The web interface was developed using the programming language Php and JavaScript. Highcharts (© 2020 www.highcharts.com) and StringDB (Jeanquartier et al., 2015) APIs (application programming interface) were used. For NCBI viewer, a direct URL link in an embedded window is used. To facilitate the comprehension of the figures 2C, 3B-C and 4 on the manuscript we used color coding to label the cell type using R. The figure 5B was generated using Graphpad Prism 5.

QUANTIFICATION AND STATISTICAL ANALYSIS

For RNAseq quantification, reads were mapped to the Amplicons sequence reference using bowtie2 local (v2.3.4.1). Reads below a mapping score of 10 or multi-mapped were filtered using samtools (v0.1.19). The level of gene expression was quantified with the specific annotation described above. Each sample was normalized by RPM (reads per Million) and the expression values were converted in logarithm scale (log10(x+1)) using R (v3.6.0). For Figure 5, data have been extracted from SISTEMA and are represented as the mean of normalized count \pm SEM and were statistically analyzed with DESeq2 R package using Negative binomial generalized linear model and Wald's test; *p < 0.05, **p < 0.01.

ADDITIONAL RESOURCES

Further information relevant to the study can be found on http://sistema.ens-lyon.fr/index.php or on http://sistema.ens-lyon.fr/MatAndMeth.php

REFERENCES

Aloia L, Gutierrez A, Caballero JM, Di Croce L (2015). Direct interaction between Id1 and Zrf1 controls neural differentiation of embryonic stem cells. EMBO Rep **16**: 63-70. 10.15252/embr.201439560

Ashurst JL, Chen CK, Gilbert JG, Jekosch K, Keenan S, Meidl P, Searle SM, Stalker J, Storey R, Trevanion S, Wilming L, Hubbard T (2005). The Vertebrate Genome Annotation (Vega) database. Nucleic Acids Res **33**: D459-465. 10.1093/nar/gki135

Assou S, Le Carrour T, Tondeur S, Strom S, Gabelle A, Marty S, Nadal L, Pantesco V, Reme T, Hugnot JP, Gasca S, Hovatta O, Hamamah S, Klein B, De Vos J (2007). A meta-analysis of human embryonic stem cells transcriptome integrated into a web-based expression atlas. Stem Cells **25**: 961-973. 10.1634/stemcells.2006-0352

Au KF, Sebastiano V (2014). The transcriptome of human pluripotent stem cells. Curr Opin Genet Dev **28:** 71-77. 10.1016/j.gde.2014.09.012

Bassez G, Audureau E, Hogrel JY, Arrouasse R, Baghdoyan S, Bhugaloo H, Gourlay-Chu ML, Le Corvoisier P, Peschanski M (2018). Improved mobility with metformin in patients with myotonic dystrophy type 1: a randomized controlled trial. Brain **141**: 2855-2865. 10.1093/brain/awy231

Ben M'Barek K, Bertin S, Brazhnikova E, Jaillard C, Habeler W, Plancheron A, Fovet CM, Demilly J, Jarraya M, Bejanariu A, Sahel JA, Peschanski M, Goureau O, Monville C (2020). Clinical-grade production and safe delivery of human ESC derived RPE sheets in primates and rodents. Biomaterials **230**: 119603. 10.1016/j.biomaterials.2019.119603

Ben M'Barek K, Habeler W, Plancheron A, Jarraya M, Regent F, Terray A, Yang Y, Chatrousse L, Domingues S, Masson Y, Sahel JA, Peschanski M, Goureau O, Monville C (2017). Human ESC-derived retinal epithelial cell sheets potentiate rescue of photoreceptor cell loss in rats with retinal degeneration. Sci Transl Med **9**10.1126/scitranslmed.aai7471

Brichta L, Hofmann Y, Hahnen E, Siebzehnrubl FA, Raschke H, Blumcke I, Eyupoglu IY, Wirth B (2003). Valproic acid increases the SMN2 protein level: a well-known drug as a potential therapy for spinal muscular atrophy. Hum Mol Genet **12**: 2481-2489. 10.1093/hmg/ddg256

Chambers I, Silva J, Colby D, Nichols J, Nijmeijer B, Robertson M, Vrana J, Jones K, Grotewold L, Smith A (2007). Nanog safeguards pluripotency and mediates germline development. Nature **450**: 1230-1234. 10.1038/nature06403

Chambers I, Tomlinson SR (2009). The transcriptional foundation of pluripotency. Development **136**: 2311-2322. 10.1242/dev.024398

Dachs E, Piedrafita L, Hereu M, Esquerda JE, Caldero J (2013). Chronic treatment with lithium does not improve neuromuscular phenotype in a mouse model of severe spinal muscular atrophy. Neuroscience **250**: 417-433. 10.1016/j.neuroscience.2013.07.026

Darville H, Poulet A, Rodet-Amsellem F, Chatrousse L, Pernelle J, Boissart C, Heron D, Nava C, Perrier A, Jarrige M, Coge F, Millan MJ, Bourgeron T, Peschanski M, Delorme R, Benchoua A (2016). Human Pluripotent Stem Cell-derived Cortical Neurons for High Throughput Medication Screening in Autism: A Proof of Concept Study in SHANK3 Haploinsufficiency Syndrome. EBioMedicine **9:** 293-305. 10.1016/j.ebiom.2016.05.032

Elshafay A, Hieu TH, Doheim MF, Kassem MAM, MF EL, Holloway SK, Abo-Elghar H, Hirayama K, Huy NT (2019). Efficacy and Safety of Valproic Acid for Spinal Muscular Atrophy: A Systematic Review and Meta-Analysis. CNS drugs **33**: 239-250. 10.1007/s40263-019-00606-6

Galvan L, Francelle L, Gaillard MC, de Longprez L, Carrillo-de Sauvage MA, Liot G, Cambon K, Stimmer L, Luccantoni S, Flament J, Valette J, de Chaldee M, Auregan G, Guillermier M, Josephine C, Petit F, Jan C, Jarrige M, Dufour N, Bonvento G, Humbert S, Saudou F, Hantraye P, Merienne K, Bemelmans AP, Perrier AL, Deglon N, Brouillet E (2018). The striatal kinase DCLK3 produces neuroprotection against mutant huntingtin. Brain **141**: 1434-1454. 10.1093/brain/awy057

Ghosh A, Som A (2020). RNA-Seq analysis reveals pluripotency-associated genes and their interaction networks in human embryonic stem cells. computational biology and chemistry **85**: 1476-9271. https://doi.org/10.1016/j.compbiolchem.2020.107239

Godoy P, Schmidt-Heck W, Hellwig B, Nell P, Feuerborn D, Rahnenfuhrer J, Kattler K, Walter J, Bluthgen N, Hengstler JG (2018). Assessment of stem cell differentiation based on genome-wide expression profiles. Philosophical transactions of the Royal Society of London Series B, Biological sciences **373**10.1098/rstb.2017.0221

Guenou H, Nissan X, Larcher F, Feteira J, Lemaitre G, Saidani M, Del Rio M, Barrault CC, Bernard FX, Peschanski M, Baldeschi C, Waksman G (2009). Human embryonic stem-cell derivatives for full reconstruction of the pluristratified epidermis: a preclinical study. Lancet **374**: 1745-1753.

Harhouri K, Navarro C, Depetris D, Mattei MG, Nissan X, Cau P, De Sandre-Giovannoli A, Levy N (2017). MG132-induced progerin clearance is mediated by autophagy activation and splicing regulation. EMBO molecular medicine **9:** 1294-1313. 10.15252/emmm.201607315

Hoch L, Henriques SF, Bruge C, Marsolier J, Benabides M, Bourg N, Tournois J, Mahe G, Morizur L, Jarrige M, Bigot A, Richard I, Nissan X (2019). Identification of thiostrepton as a pharmacological approach to rescue misfolded alpha-sarcoglycan mutant proteins from degradation. Scientific reports 9: 6915. 10.1038/s41598-019-43399-w

Hong SH, Lee JH, Lee JB, Ji J, Bhatia M (2011). ID1 and ID3 represent conserved negative regulators of human embryonic and induced pluripotent stem cell hematopoiesis. J Cell Sci **124**: 1445-1452. 10.1242/jcs.077511

Howlin J, Cirenajwis H, Lettiero B, Staaf J, Lauss M, Saal L, Borg A, Gruvberger-Saal S, Jonsson G (2015). Loss of CITED1, an MITF regulator, drives a phenotype switch in vitro and can predict clinical outcome in primary melanoma tumours. PeerJ **3:** e788. 10.7717/peerj.788

Jeanquartier F, Jean-Quartier C, Holzinger A (2015). Integrated web visualizations for protein-protein interaction databases. BMC bioinformatics **16**: 195. 10.1186/s12859-015-0615-z

Kusters-Vandevelde HV, Klaasen A, Kusters B, Groenen PJ, van Engen-van Grunsven IA, van Dijk MR, Reifenberger G, Wesseling P, Blokx WA (2010). Activating mutations of the GNAQ gene: a frequent event in primary melanocytic neoplasms of the central nervous system. Acta neuropathologica **119**: 317-323. 10.1007/s00401-009-0611-3

Kwon DY, Motley WW, Fischbeck KH, Burnett BG (2011). Increasing expression and decreasing degradation of SMN ameliorate the spinal muscular atrophy phenotype in mice. Hum Mol Genet **20**: 3667-3677. 10.1093/hmg/ddr288

Lefebvre S, Burglen L, Reboullet S, Clermont O, Burlet P, Viollet L, Benichou B, Cruaud C, Millasseau P, Zeviani M, et al. (1995). Identification and characterization of a spinal muscular atrophy-determining gene. Cell **80**: 155-165.

Li W, Turner A, Aggarwal P, Matter A, Storvick E, Arnett DK, Broeckel U (2015). Comprehensive evaluation of AmpliSeq transcriptome, a novel targeted whole transcriptome RNA sequencing methodology for global gene expression analysis. BMC genomics **16:** 1069. 10.1186/s12864-015-2270-1

Locatelli D, Terao M, Kurosaki M, Zanellati MC, Pletto DR, Finardi A, Colciaghi F, Garattini E, Battaglia GS (2015). Different Stability and Proteasome-Mediated Degradation Rate of SMN Protein Isoforms. PLoS One **10**: e0134163. 10.1371/journal.pone.0134163

Mair B, Tomic J, Masud SN, Tonge P, Weiss A, Usaj M, Tong AHY, Kwan JJ, Brown KR, Titus E, Atkins M, Chan KSK, Munsie L, Habsid A, Han H, Kennedy M, Cohen B, Keller G, Moffat J (2019). Essential Gene Profiles for Human Pluripotent Stem Cells Identify Uncharacterized Genes and Substrate Dependencies. Cell Rep **27**: 599-615 e512. 10.1016/j.celrep.2019.02.041

Mallon BS, Chenoweth JG, Johnson KR, Hamilton RS, Tesar PJ, Yavatkar AS, Tyson LJ, Park K, Chen KG, Fann YC, McKay RD (2013). StemCellDB: the human pluripotent stem cell database at the National Institutes of Health. Stem Cell Res **10**: 57-66. 10.1016/j.scr.2012.09.002

Matera I, Watkins-Chow DE, Loftus SK, Hou L, Incao A, Silver DL, Rivas C, Elliott EC, Baxter LL, Pavan WJ (2008). A sensitized mutagenesis screen identifies Gli3 as a modifier of Sox10 neurocristopathy. Hum Mol Genet **17**: 2118-2131. 10.1093/hmg/ddn110

Maury Y, Come J, Piskorowski RA, Salah-Mohellibi N, Chevaleyre V, Peschanski M, Martinat C, Nedelec S (2015). Combinatorial analysis of developmental cues efficiently converts human pluripotent stem cells into multiple neuronal subtypes. Nat Biotechnol **33**: 89-96.

Mournetas V, Massourides E, Dupont JB, Kornobis E, Polvèche H, Jarrige M, Gosselin M, Manousopoulou A, Garbis SD, Gorecki D, Pinset C (2019). Myogenesis modelled by human pluripotent stem cells uncovers Duchenne muscular dystrophy phenotypes prior to skeletal muscle commitment. BioRxivhttps://doi.org/10.1101/720920

Nair SS, Chaubal VA, Shioda T, Coser KR, Mojamdar M (2001). Over-expression of MSG1 transcriptional co-activator increases melanin in B16 melanoma cells: a possible role for MSG1 in melanogenesis. Pigment cell research **14:** 206-209. 10.1034/j.1600-0749.2001.140311.x

Nicoleau C, Varela C, Bonnefond C, Maury Y, Bugi A, Aubry L, Viegas P, Bourgois-Rocha F, Peschanski M, Perrier AL (2013). Embryonic stem cells neural differentiation qualifies the role of Wnt/beta-Catenin signals in human telencephalic specification and regionalization. Stem Cells **31**: 1763-1774.

Park PJ, Lee TR, Cho EG (2015). Substance P stimulates endothelin 1 secretion via endothelin-converting enzyme 1 and promotes melanogenesis in human melanocytes. The Journal of investigative dermatology **135**: 551-559. 10.1038/jid.2014.423

Piepers S, Cobben JM, Sodaar P, Jansen MD, Wadman RI, Meester-Delver A, Poll-The BT, Lemmink HH, Wokke JH, van der Pol WL, van den Berg LH (2011). Quantification of SMN protein in leucocytes from spinal muscular atrophy patients: effects of treatment with valproic acid. Journal of neurology, neurosurgery, and psychiatry **82**: 850-852. 10.1136/jnnp.2009.200253

Pinto JP, Machado RSR, Magno R, Oliveira DV, Machado S, Andrade RP, Braganca J, Duarte I, Futschik ME (2018). StemMapper: a curated gene expression database for stem cell lineage analysis. Nucleic Acids Res **46**: D788-D793. 10.1093/nar/gkx921

Rowe RG, Daley GQ (2019). Induced pluripotent stem cells in disease modelling and drug discovery. Nature reviews Genetics **20**: 377-388. 10.1038/s41576-019-0100-z

Schmidt B, Hildebrandt A (2017). Next-generation sequencing: big data meets high performance computing. Drug discovery today **22**: 712-717. 10.1016/j.drudis.2017.01.014

Silva J, Nichols J, Theunissen TW, Guo G, van Oosten AL, Barrandon O, Wray J, Yamanaka S, Chambers I, Smith A (2009). Nanog is the gateway to the pluripotent ground state. Cell **138**: 722-737. 10.1016/j.cell.2009.07.039

Streeter I, Harrison PW, Faulconbridge A, The HipSci C, Flicek P, Parkinson H, Clarke L (2017). The human-induced pluripotent stem cell initiative-data resources for cellular genetics. Nucleic Acids Res **45:** D691-D697. 10.1093/nar/gkw928

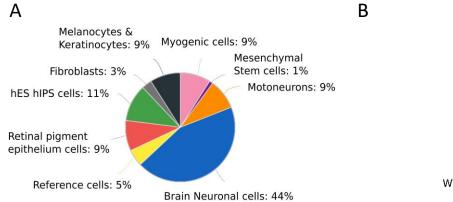
Takahashi K, Tanabe K, Ohnuki M, Narita M, Ichisaka T, Tomoda K, Yamanaka S (2007). Induction of pluripotent stem cells from adult human fibroblasts by defined factors. Cell **131**: 861-872.

Thomson JA, Itskovitz-Eldor J, Shapiro SS, Waknitz MA, Swiergiel JJ, Marshall VS, Jones JM (1998). Embryonic stem cell lines derived from human blastocysts. Science **282**: 1145-1147.

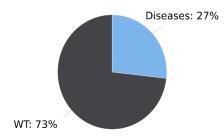
Van Raamsdonk CD, Fitch KR, Fuchs H, de Angelis MH, Barsh GS (2004). Effects of G-protein mutations on skin color. Nat Genet **36**: 961-968. 10.1038/ng1412

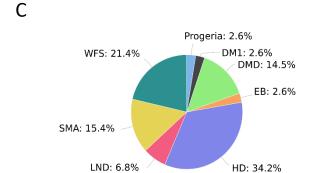
Yates B, Braschi B, Gray KA, Seal RL, Tweedie S, Bruford EA (2017). Genenames.org: the HGNC and VGNC resources in 2017. Nucleic Acids Res **45**: D619-D625. 10.1093/nar/gkw1033

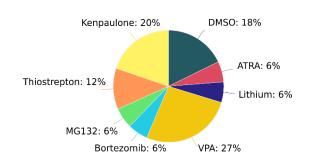
Figure 1



D

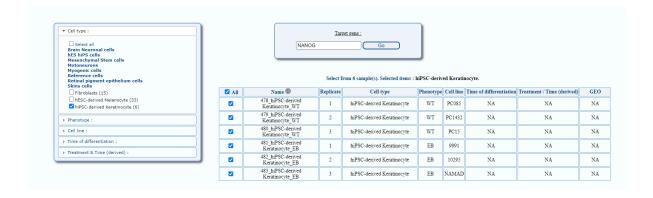


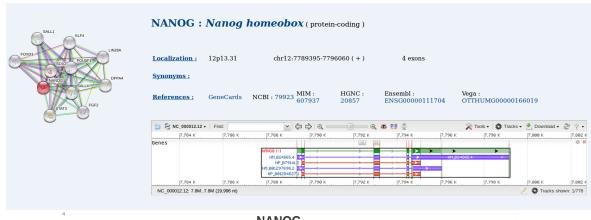


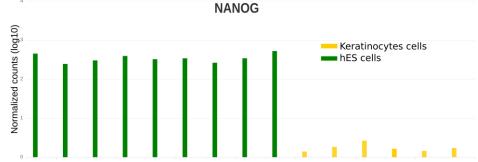




В







Count	ting scale 0	0 - 1,40	1,41 - 1,70	1,71 - 2	2 - 2,70	2,71 - 3	3 - 4	4 - 4,65		Export (.xls)		
#	NGS	Name	Counts		Replicate	Cell type	Phenotype		Cell line	Time of differentiation	Derived Treatment / Time	GEO
19	NGS13	19_hESC_WT	2.64		1 hESC		WT		SA001	NA	NA	NA
23	NGS13	23_hESC_WT	2.4		1	hESC	WT		SA001	NA	NA	NA
22	NGS13	22_hESC_WT	2.49		1	hESC	WT		SA001	NA	NA	NA
28	NGS14	28_hESC_WT	2.6		1	hESC	WT		SA001	NA	NA	NA
29	NGS14	29_hESC_WT	2.52		2	hESC	WT		SA001	NA	NA	NA
30	NGS14	30_hESC_WT	2.54		3	hESC	WT		SA001	NA	NA	NA
412	NGS29	412_hESC_WT	2.43		1	hESC	WT		SA001	NA	NA	NA
428	NGS29	428_hESC_WT	2.73		3	hESC	WT		SA001	NA	NA	NA
420	NGS29	420_hESC_WT	2.54		2	hESC	WT		SA001	NA	NA	NA
482	NGS55	482_hiPSC-derived Keratinocyte_EB	0.17		2	hiPSC-derived Keratinocyte	EB		10295	NA	NA	NA
483	NGS55	483_hiPSC-derived Keratinocyte_EB	0.24		3	hiPSC-derived Keratinocyte	EB		NAMAD	NA	NA	NA
478	NGS55	478_hiPSC-derived Keratinocyte_WT	0.15		1	hiPSC-derived Keratinocyte	WT	WT PC085		NA	NA	NA
479	NGS55	479_hiPSC-derived Keratinocyte_WT	0.27		2	hiPSC-derived Keratinocyte	WT		PC1432	NA	NA	NA
480	NGS55	480_hiPSC-derived Keratinocyte_WT	0.43		3	hiPSC-derived Keratinocyte	WT		PC15	NA	NA	NA
481	NGS55	481_hiPSC-derived Keratinocyte_EB	0.22		1	hiPSC-derived Keratinocyte	EB		9991	NA	NA	NA

479_hiPSC-derived Keratinocyte_WT

480_hiPSC-derived Keratinocyte_WT

479 10

480 11

NGS55

NGS55

hiPSC-derived Keratinocyte

hiPSC-derived Keratinocyte WT

WT

PC1432

PC15

NA

NA

NA

NA

NA

NA

0.27

0.43

0.76

0.32

0.56

2

3

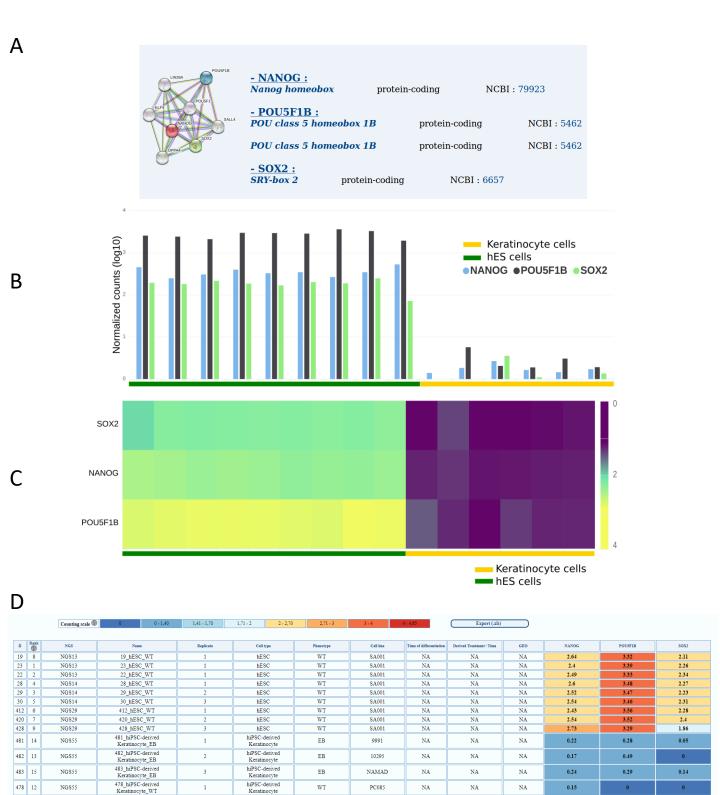
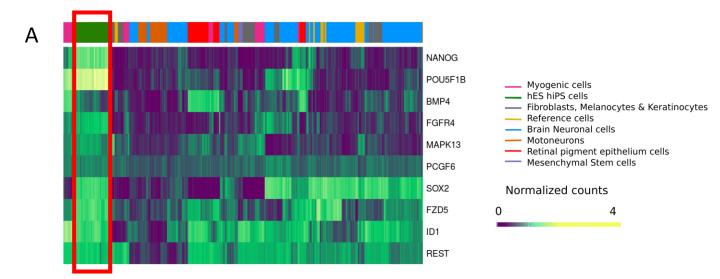
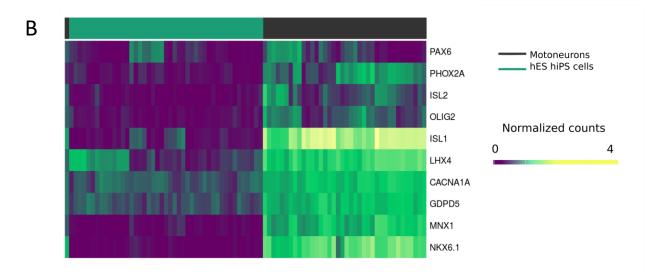


Figure 4





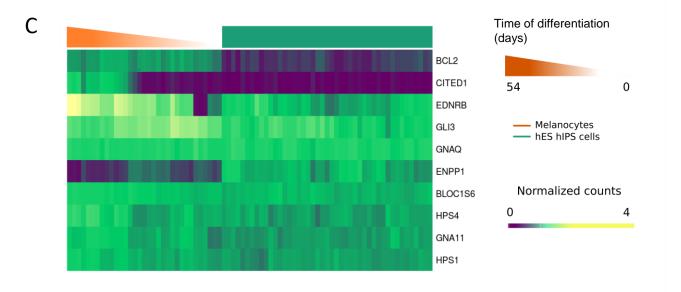
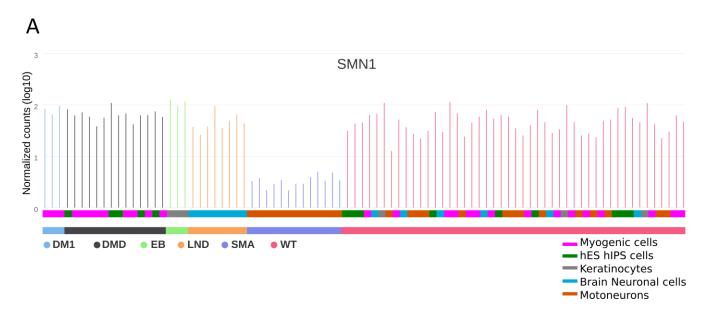


Figure 5



В

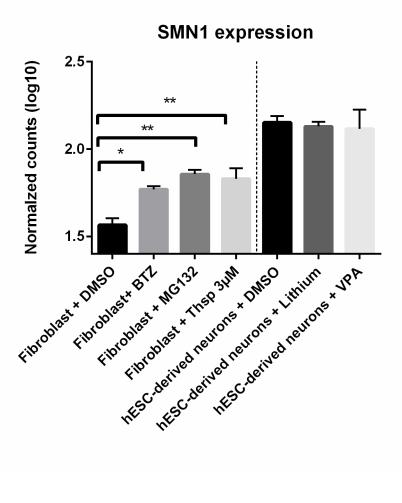
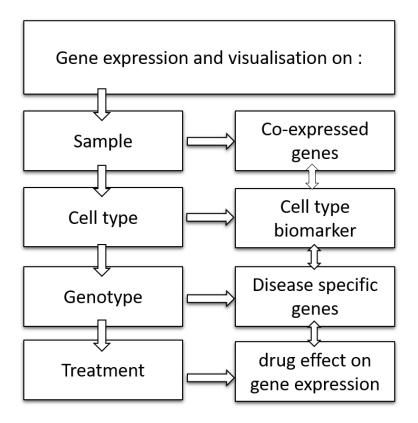


Figure 6



# NGS# Name 1 NGS13	Sample hIPSC 4603c45 Mef P49 hIPSC 4603c45 Mef P48 hIPSC 4603c45 Mef P51 hIPSC 4603c45 CS P47-4 hIPSC 4603c45 CS P47-5 n3 hIPSC 4603c45 CS P47-5 n2 hIPSC 4603c45 L7 P47-4 hIPSC 4603c45 L7 P47-5 hESC RC9 CS P35 hESC RC9 CS P40 hESC RC9 CS P41 hESC RC9 L7 P35-6 hESC RC9 L7 P35-5 hESC SA001 Mef P73 hESC SA001 Mef P76 hESC SA001 CS P71-3 hESC SA001 L7 P71-5 hESC SA001 L7 P71-5 hESC SA001 L7 P71-3 hESC SA001 L7 P71-3 hESC SA001 L7 P71-3	1 4603c45 1 RC9 1 RC9 1 RC9 1 RC9 1 RC9 1 RC9 1 SA001	Phenotype WT	Gene Edited NO	SC Cell passage P49 P48 P51 P51 P52 P52 P51 P52 P35 P40 P41 P41 P40 P73 P75 P76 P74 P75 P76 P74 P75 P76 P74	ging SC Matrix MEF MEF MEF Cellstart Cellstart L7 L7 Cellstart Cellstart Cellstart Cellstart Cellstart Cellstart Cellstart L7 L7 MEF MEF MEF Cellstart Cellstart Cellstart Cellstart Cellstart MEF	SC Medium NA NA NA StemPro StemPro StemPro NA NA StemPro StemPro StemPro StemPro StemPro NA MA NA MA	SC Treatment / Tin	NA N	Cell type hiPSC hiPSC hiPSC hiPSC hiPSC hiPSC hiPSC hiPSC hiPSC hESC hESC hESC hESC hESC hESC hESC hE	Matrix (derived) NA	Treatment / Time (derived) NA	Time of differentiate NA	Neurodegenerative	GEO NA NA NA NA NA NA NA NA NA N
26 NGS5	hESC WT SA001 hESC WT SA001 P54 hESC WT SA001 P67 hESC SA001 P60 n1 hESC SA001 P60 n2 hESC SA001 P60 n3 hESC RC9 hESC-derived Melanocyte days 32 n1 hESC-derived Melanocyte days 32 n2 hESC-derived Melanocyte days 32 n3 hIPSC derived motoneurons WT 14-5 D10 hIPSC derived motoneurons WT 1427 D10	2 SA001 2 SA001 1 SA001 1 SA001 2 SA001 1 RC9 1 SA001 2 SA001 3 SA001 1 1 14-27	WT W	NO N	P54 P67 P60 P60 P60 P60 P60 P60 NA NA	MEF MEF MEF MEF Cellstart MEF MEF MEF NA NA	medium and PLURIQ StemPro medium and PLURIQ	NO NO NO NO NO NO NO NO	NA NA NA NA NA NA NA NA	hESC hESC hESC hESC hESC hESC hESC hESC	NA NA NA NA NA Gelatin Gelatin NA NA	NA N	NA NA NA NA NA NA DIV32 DIV32 DIV32 DIV10 DIV10	Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Neurodegenerative Genodermatose Genodermatose Motoneurons Motoneurons	NA
45 NGS43 45_hiPSC-derived Motoneuron_WT 48 NGS24 48_hESC-derived Melanocyte_WT 49 NGS24 49_hESC-derived Melanocyte_WT 50 NGS24 50_hESC-derived Melanocyte_WT 51 NGS24 51_hESC-derived Melanocyte_WT 52 NGS24 52_hESC-derived Melanocyte_WT 53 NGS24 53_hESC-derived Melanocyte_WT 54 NGS24 54_hESC-derived Melanocyte_WT 55 NGS24 55_hESC-derived Melanocyte_WT 56 NGS24 56_hESC-derived Melanocyte_WT	hIPSC derived motoneurons WT 56c02 D10 hESC-derived melanocyte WT SA001 days14 n1 NGS24 hESC-derived melanocyte WT SA001 days21 n1 NGS24 hESC-derived melanocyte WT SA001 days32 n1 hESC-derived melanocyte WT SA001 days32 n2 hESC-derived melanocyte WT SA001 days32 n3 hESC-derived melanocyte WT SA001 days40 n1 hESC-derived melanocyte WT SA001 days40 n2 hESC-derived melanocyte WT SA001 days40 n3 hESC-derived melanocyte WT SA001 days40 n3	1 56c02 1 SA001 1 SA001 1 SA001 2 SA001 1 SA001 2 SA001 1 SA001 1 SA001	WT WT WT WT WT WT WT WT	NO N	NA P60 P60 P60 P60 P60 P60 P60 P60	NA MEF MEF MEF MEF MEF MEF MEF	medium and PLURIQ	NO NO NO NO NO NO NO	NA NA NA NA NA NA	hiPSC-derived Motoneuron hESC-derived Melanocyte	NA Gelatin Gelatin Gelatin Gelatin NA NA NA NA	NA NA NA NA NA NA NA NA NA	DIV10 DIV14 DIV21 DIV32 DIV32 DIV32 DIV40 DIV40 DIV40	Motoneurons Genodermatose	NA NA NA NA NA NA NA NA
57 NGS24 57_hESC-derived Melanocyte_WT 58 NGS24 58_hESC-derived Melanocyte_WT 59 NGS24 59_hESC-derived Melanocyte_WT 60 NGS24 60_hESC-derived Melanocyte_WT 61_Reference melanocyte - mel 311 P5 61 NGS24 Lonza_WT 62_Reference melanocyte - mel 311 P5 62 NGS24 Lonza_WT 63_Reference melanocyte - mel 663 P5	hESC-derived melanocyte WT SA001 days54-P4 n1 hESC-derived melanocyte WT SA001 days54-P7 n1 hESC-derived melanocyte WT SA001 days54-P7 n2 hESC-derived melanocytedaysWT SA001 54-P7 n3 Reference melanocyte - mel 311 P5 Lonza - n1 Reference melanocyte - mel 311 P5 Lonza - n2	1 SA001 1 SA001 2 SA001 3 SA001 1 NA 2 NA	WT WT WT WT WT	NO NO NO NO NO NO NO NO	P60 P60 P60 P60 NA	MEF MEF MEF NA NA	medium and PLURIQ medium and PLURIQ medium and PLURIQ medium and PLURIQ NA NA	NO NO NO NO	NA NA NA NA	hESC-derived Melanocyte hESC-derived Melanocyte hESC-derived Melanocyte hESC-derived Melanocyte Reference melanocyte - mel 311 P5 Lonza Reference melanocyte - mel 311 P5 Lonza	NA NA NA NA NA	NA NA NA NA NA	DIV54-P4 DIV54-P7 DIV54-P7 DIV54-P7 NA NA	Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose	NA NA NA NA NA
63 NGS24 Lonza_WT 64_Reference melanocyte - mel 704 P5 64 NGS24 Lonza_WT NGS31- 65 33 65_hESC-derived Melanocyte_WT NGS31- 66 33 66_hESC-derived Melanocyte_WT 70 NGS5 70_hESC-derived Melanocyte_WT 71 NGS5 71_hESC-derived Melanocyte_WT 72 NGS5 72_hESC-derived Melanocyte_WT 73 NGS5 73_hESC-derived Melanocyte_WT 74 NGS5 74_hESC-derived Melanocyte_WT	Reference melanocyte - mel 663 P5 Lonza - n3 Reference melanocyte - mel 704 P5 Lonza - n4 hESC-derived melanocyte WT SA001 days54-P4 n2 hESC-derived melanocyte WT SA001 days54-P4 n3 hESC-derived melanocyte WT SA001 days4 n1 hESC-derived melanocyte WT SA001 days4 n2 hESC-derived melanocyte WT SA001 days4 n3 hESC-derived melanocyte WT SA001 days14 n1 NGS5 hESC-derived melanocyte WT SA001 days14 n2 NGS5 hESC-derived melanocyte WT SA001 days14 n2 NGS5 hESC-derived melanocyte WT SA001 days14 n3	3 NA 4 NA 2 SA001 3 SA001 1 SA001 2 SA001 1 SA001 2 SA001 2 SA001	WT WT WT WT WT WT WT	NO	NA NA P60 P60 NA NA NA NA	NA MEF MEF MEF MEF MEF MEF	NA medium and PLURIQ	NO NO NO NO	NA NA NA NA NA	Reference melanocyte - mel 663 P5 Lonza Reference melanocyte - mel 704 P5 Lonza hESC-derived Melanocyte	NA NA NA NA Gelatin Gelatin Gelatin Gelatin	NA NA NA NA NA NA NA NA	NA NA DIV54-P4 DIV54-P4 DIV4 DIV4 DIV4 DIV4 DIV14	Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose	NA NA NA NA NA NA NA NA
75 NGS5 75_hESC-derived Melanocyte_WT 76 NGS14 76_hESC-derived Melanocyte_WT 77 NGS14 77_hESC-derived Melanocyte_WT 78 NGS14 78_hESC-derived Melanocyte_WT 79 NGS14 79_hESC-derived Melanocyte_WT 80 NGS14 80_hESC-derived Melanocyte_WT 81 NGS14 81_hESC-derived Melanocyte_WT	hESC-derived melanocyte WT SA001 days7 n1 hESC-derived melanocyte WT SA001 days7 n2 hESC-derived melanocyte WT SA001 days7 n3 hESC-derived melanocyte WT SA001 days14 n1 NGS14 hESC-derived melanocyte WT SA001 days14 n2 NGS14 hESC-derived melanocyte WT SA001 days14 n3 NGS14 hESC-derived melanocyte WT SA001 days21 n1	3 SA001 1 SA001 2 SA001 3 SA001 1 SA001 2 SA001 3 SA001	WT WT WT WT WT WT	NO NO NO NO NO NO NO NO	P60 P60 P60 P60 P60	MEF MEF MEF MEF MEF	medium and PLURIQ	NO NO NO NO	NA NA NA NA	hESC-derived Melanocyte	Gelatin Gelatin Gelatin Gelatin Gelatin Gelatin Gelatin	NA NA NA NA NA NA	DIV14 DIV7 DIV7 DIV14 DIV14 DIV14	Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose Genodermatose	NA NA NA NA NA NA
82 NGS14 82_hESC-derived Melanocyte_WT 83 NGS14 83_hESC-derived Melanocyte_WT 84 NGS14 84_hESC-derived Melanocyte_WT 85 NGS21 85_hiPSC-derived NSC_WT 86 NGS21 86_hiPSC-derived NSC_WT 87 NGS21 87_hiPSC-derived NSC_WT 88 NGS21 88_hiPSC-derived NSC_WT 89 NGS21 89_hiPSC-derived NSC_WFS 90 NGS21 90_hiPSC-derived NSC_WFS 91 NGS21 91_hiPSC-derived NSC_WFS 92 NGS21 92_hiPSC-derived NSC_WT 93 NGS21 93_hiPSC-derived NSC_WT 94 NGS21 94_hiPSC-derived NSC_WT 95 NGS21 95_hiPSC-derived NSC_WFS 96 NGS21 96_hiPSC-derived NSC_WFS 97 NGS27 97_hiPSC-derived Neuron_WT	hESC-derived melanocyte WT SA001 days21 n2 hESC-derived melanocyte WT SA001 days21 n3 hIPSC-derived NSC WT 1869 hIPSC-derived NSC WT i90c16 hIPSC-derived NSC WT PB12c13 hIPSC-derived NSC WT 4603c45 hIPSC-derived NSC WFS WS1 hIPSC-derived NSC WFS WS2 hIPSC-derived NSC WFS WS5 hIPSC-derived NSC WFS WS5 hIPSC-derived NSC WT 1869 Tg 8h hIPSC-derived NSC WT i90 Tg 8h hIPSC-derived NSC WS5 Tg 8h hIPSC-derived NSC WS5 Tg 8h hIPSC-derived NSC WFS WS2 Tg 8h hIPSC-derived Neurons WT 1869 days14	1 SA001 2 SA001 3 SA001 1 i90cl16 1 PB12c13 1 4603c45 1 WS1 1 WS2 1 WS5 1 i90cl16 1 PB12c13 1 WS5 1 WS5 1 WS5 1 WS5	WT WT WT 1869 WT WT WT WFS WFS WFS 1869 WT WT WT WT WT WT WT WT WT WT	NO N	P60 P60 NA	MEF	medium and PLURIQ medium and PLURIQ medium KSR	NO N	NA NA passed passed	hESC-derived Melanocyte hESC-derived Melanocyte hESC-derived Melanocyte hiPSC-derived NSC hiPSC-derived NSC	Gelatin Gelatin Gelatin PO-lam PO-lam	NA	DIV21 DIV21 DIV21 P10 P10 P9 P11 P10 P11 P10 P11 P11 P10 P10 P10 P9 P11 P11 DIV14	Genodermatose Genodermatose Genodermatose Motoneurons	NA N
98 NGS27 98_hiPSC-derived Neuron_WT 99 NGS27 99_hiPSC-derived Neuron_WT 100 NGS27 100_hiPSC-derived Neuron_WFS 101 NGS27 101_hiPSC-derived Neuron_WFS 102 NGS27 102_hiPSC-derived Neuron_WFS 103 NGS38 103_hiPSC-derived Neuron_WFS	hIPS-derived Neurons WT PB12 days14 hIPS-derived Neurons WT i90c16 days14 hIPS-derived Neurons WFS WS1 days14 hIPS-derived Neurons WFS WS2 days14 hIPS-derived Neurons WFS WS5 days14 hIPSC-derived Neurones WFS WS5 days18 n1 hIPSC-derived Neurones WFS WS5 days18 VPA	1 PB12c13 1 i90cl16 1 WS1 1 WS2 1 WS5	WT WFS WFS WFS WFS	NO NO NO NO NO NO	NA NA NA NA	MEF MEF MEF MEF	medium KSR medium KSR medium KSR medium KSR medium KSR	NO NO NO NO NO	NA NA NA	hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron	PO-lam PO-lam PO-lam PO-lam PO-lam	NA NA NA NA	DIV14 DIV14 DIV14 DIV14 DIV14 DIV18	Motoneurons Motoneurons Motoneurons Motoneurons Motoneurons	NA NA NA NA
104 NGS38 104_hiPSC-derived Neuron_WFS 105 NGS38 105_hiPSC-derived Neuron_WFS 106 NGS38 106_hiPSC-derived Neuron_WFS 107 NGS38 107_hiPSC-derived Neuron_WFS 108 NGS38 108_hiPSC-derived Neuron_WFS 109 NGS38 109_hiPSC-derived Neuron_WFS 110 NGS38 110_hiPSC-derived Neuron_WFS 111 NGS40 111_hiPSC-derived Neuron_WFS	1,5mM n1 hIPSC-derived Neurones WFS WS5 days18 n2 hIPSC-derived Neurones WFS WS5 days18 VPA 1,5mM n2 hIPSC-derived Neurones WFS WS5 days18 n3 hIPSC-derived Neurones WFS WS5 days18 VPA0,5mM hIPSC-derived Neurones WFS WS5 days18 VPA1mM hIPSC-derived Neurones WFS WS5 days18 VPA1,5mM n3 hIPSC-derived Neurones WFS WS2 days18 n1	 WS5 	WFS WFS WFS WFS WFS WFS WFS WFS	NO NO NO NO NO NO NO NO NO	NA NA NA NA NA NA	MEF MEF MEF MEF MEF MEF	medium KSR	NO NO NO NO NO NO NO	NA NA NA NA	hiPSC-derived Neuron	PO-lam PO-lam PO-lam PO-lam PO-lam PO-lam PO-lam PO-lam	VPA 1.5 mM VPA 1.5 mM NA VPA 0.5 mM VPA 1 mM VPA 1.5 mM	DIV18 DIV18 DIV18 DIV18 DIV18 DIV18 DIV18 DIV18	Motoneurons Motoneurons Motoneurons Motoneurons Motoneurons Motoneurons Motoneurons	NA NA NA NA NA NA NA
112 NGS40 112_hiPSC-derived Neuron_WFS 113 NGS40 113_hiPSC-derived Neuron_WFS 114 NGS40 114_hiPSC-derived Neuron_WFS 115 NGS40 115_hiPSC-derived Neuron_WFS	hIPSC-derived Neurons WFS WS2 days18 VPA 0,5mM n1 hIPSC-derived Neurons WS2 days18 VPA 1,5mM n1 hIPSC-derived Neurons WS2 days18 n2 hIPSC-derived Neurons WS2 days18 VPA 0,5mM n2 hIPSC-derived Neurons WS2 days18 VPA	1 WS2 1 WS2 2 WS2 2 WS2	WFS WFS WFS	NO NO NO	NA NA NA	MEF MEF MEF	medium KSR medium KSR medium KSR medium KSR	NO NO NO	NA NA	hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron	PO-lam PO-lam PO-lam PO-lam	VPA 0.5 mM VPA 1.5 mM NA VPA 0.5 mM	DIV18 DIV18 DIV18 DIV18	Motoneurons Motoneurons Motoneurons	NA NA NA
116 NGS40 116_hiPSC-derived Neuron_WFS 117 NGS40 117_hiPSC-derived Neuron_WFS 118 NGS40 118_hiPSC-derived Neuron_WFS 119 NGS40 119_hiPSC-derived Neuron_WFS 120 NGS1 120_hESC-hiPSC-derived MSC_WT 121 NGS1 121_hESC-hiPSC-derived MSC_WT 122 NGS1 122_hESC-hiPSC-derived MSC_WT	1,5mM n2 hIPSC-derived Neurons WS2 days18 n3 hIPSC-derived Neurons WS2 days18 VPA 0,5mM n3 hIPSC-derived Neurons WS2 days18 VPA 1,5mM n3 hESC-hiPSC-derived MSC DMSO n1 hESC-hiPSC-derived MSC DMSO n2 hESC-hiPSC-derived MSC DMSO n3	 2 WS2 3 WS2 3 WS2 1 NA 2 NA 3 NA 	WFS WFS WFS WT WT	NO NO NO NO NO NO	NA NA NA NA NA NA	MEF MEF MEF NA NA NA	medium KSR medium KSR medium KSR medium KSR MA NA NA	NO NO NO NO NO NO	NA NA NA NA NA	hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron hiPSC-derived Neuron hESC-hiPSC-derived MSC hESC-hiPSC-derived MSC hESC-hiPSC-derived MSC	PO-lam PO-lam PO-lam PO-lam Gelatin Gelatin Gelatin	VPA 1.5 mM NA VPA 0.5 mM VPA 1.5 mM DMSO 0.1 % DMSO 0.1 % DMSO 0.1 %	DIV17 DIV17 DIV17 DIV17 P10 P10 P10	Motoneurons Motoneurons Motoneurons Motoneurons Progeria - LGMD Progeria - LGMD	NA NA NA NA NA NA NA
123 NGS1 123_hESC-hiPSC-derived MSC_ATAR 124 NGS1 124_hESC-hiPSC-derived MSC_ATAR 125 NGS1 125_hESC-hiPSC-derived MSC_ATAR 373 NG28 373_hiPSC-derived RPE_HD 374 NG28 374_hiPSC-derived RPE_HD 375 NG28 375_hiPSC-derived RPE_HD	hESC-hiPSC-derived MSC ATAR n1 hESC-hiPSC-derived MSC ATAR n2 hESC-hiPSC-derived MSC ATAR n3 hIPSC-derived RPE HD Delta60 days44 LV shLuc MC37 n1 hIPSC-derived RPE HD Delta60 days44 LV shHTT â€" sh6 MC37 n1 hIPSC-derived RPE HD Delta60 days44 LV shLuc MC37 n2 hIPSC-derived RPE HD Delta60 days44 LV shHTT	 NA NA NA delta60 delta60 delta60 	ATAR ATAR ATAR HD HD	NO NO Yes: lentiviral transduction luciferase (ctrl for sample 374_376_378_387) Yes: lentiviral transduction luciferase (ctrl for sample 374_376_378_387) Yes: lentiviral transduction luciferase (ctrl for sample 195->197) Yes: lentiviral transduction luciferase (ctrl for sample 195->197)	NA NA NA P64 P64	NA NA NA L7 L7	NA NA NA StemPro StemPro StemPro	NO NO NO NO	NA NA NA	hESC-hiPSC-derived MSC hESC-hiPSC-derived MSC hESC-hiPSC-derived MSC hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE	Gelatin Gelatin Gelatin NA NA	ATRA 10ÂμΜ ATRA 10ÂμΜ ATRA 10ÂμΜ Ientivirus Ctrl (Luciferase) KO HTT gene (lentivirus) Ientivirus Ctrl (Luciferase)	P10 P10 P10 DIV44 DIV44	Progeria - LGMD Progeria - LGMD Progeria - LGMD Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA
376 NG28 376_hiPSC-derived RPE_HD 377 NG28 377_hiPSC-derived RPE_HD 378 NG28 378_hiPSC-derived RPE_HD 379 NG28 379_hiPSC-derived RPE_HD 380 NG28 380_hiPSC-derived RPE_HD	â€" sh6 MC37 n2 hIPSC-derived RPE HD Delta60 days44 LV shLuc MC37 n3 hIPSC-derived RPE HD Delta60 days44 LV shHTT â€" sh6 MC37 n3 hIPSC-derived RPE HD Delta60 days44 LV shLuc MC37 n4 hIPSC-derived RPE HD HD1 days44 LV shLuc MC10 n1 hIPSC-derived RPE HD HD1 days44 LV shHTT	2 delta603 delta603 delta604 delta601 HD1	HD HD HD HD	sample 374_376_378_387) Yes: lentiviral transduction luciferase (ctrl for sample 195->197) Yes: lentiviral transduction luciferase (ctrl for sample 374_376_378_387) Yes: lentiviral transduction luciferase (ctrl for sample 195->197) Yes: lentiviral transduction luciferase (ctrl for sample 381_383_385_386)	P64 P64 P64 P37	L7 L7 L7 L7 CellStart	StemPro StemPro StemPro StemPro StemPro	NO NO NO NO	NA NA NA	hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE	NA NA NA NA	KO HTT gene (lentivirus) lentivirus Ctrl (Luciferase) KO HTT gene (lentivirus) lentivirus Ctrl (Luciferase) lentivirus Ctrl (Luciferase)	DIV44 DIV44 DIV44 DIV44	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA
381 NG28 381_hiPSC-derived RPE_HD 382 NG28 382_hiPSC-derived RPE_HD 383 NG28 383_hiPSC-derived RPE_HD 384 NG28 384_hiPSC-derived RPE_HD 385 NG28 385_hiPSC-derived RPE_HD 386 NG28 386_hiPSC-derived RPE_HD	â€" sh6 MC10 n1 hIPSC-derived RPE HD HD1 days44 LV shLuc MC10 n2 hIPSC-derived RPE HD HD1 days44 LV shHTT â€" sh6 MC10 n2 hIPSC-derived RPE HD HD1 days44 LV shLuc MC10 n3 hIPSC-derived RPE HD HD1 days44 LV shHTT â€" sh6 MC10 n3 hIPSC-derived RPE HD HD1 days44 LV shHTT â€" sh6 MC10 n4	1 HD1 2 HD1 2 HD1 3 HD1 4 HD1	HD HD HD HD HD	Yes: lentiviral transduction KO HTT Yes: lentiviral transduction luciferase (ctrl for sample 381_383_385_386) Yes: lentiviral transduction KO HTT Yes: lentiviral transduction luciferase (ctrl for sample 381_383_385_386) Yes: lentiviral transduction KO HTT Yes: lentiviral transduction KO HTT	P37 P37 P37 P37 P37	CellStart CellStart CellStart CellStart CellStart CellStart	StemPro StemPro StemPro StemPro StemPro StemPro	NO NO NO NO NO	NA NA NA	hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE hiPSC-derived RPE	NA NA NA NA NA	KO HTT gene (lentivirus) lentivirus Ctrl (Luciferase) KO HTT gene (lentivirus) lentivirus Ctrl (Luciferase) KO HTT gene (lentivirus) KO HTT gene (lentivirus)	DIV44 DIV44 DIV44 DIV44 DIV44	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA NA
387 NG28 387_hiPSC-derived RPE_HD 141 NGS25 141_hiPSC_WT 142 NGS25 142_hiPSC-derived Mesoderm precursor_WT 143 NGS25 143_hiPSC_DMD 144 NGS25 144_hiPSC-derived Mesoderm precursor_DMD 145 NGS25 145_Primary Myoblast_WT	hIPSC-derived RPE HD Delta60 days44 LV shLuc MC37 n5 hiPSC WT M398 n2 hiPSC-derived Mesoderm precursor M398 WT hiPSC DMD M418 hiPSC-derived Mesoderm precursor DMD M418 Primary myoblast WT M398	5 delta601 M3981 M3981 M4181 M4181 M398	HD WT WT DMD DMD WT	Yes: lentiviral transduction luciferase (ctrl for sample 195->197) NO NO NO NO NO	P64 P16 P16 P17 P17 NA	L7 Matrigel Matrigel Matrigel Matrigel NA	StemPro mTes R mTes R mTes R mTes R NA	NO NO 3 days BMP4 NO 3 days BMP4 NO	not passed not passed not passed not passed	hiPSC-derived RPE hiPSC hiPSC-derived Mesoderm precursor hiPSC hiPSC-derived Mesoderm precursor Primary Myoblast	NA NA NA NA	lentivirus Ctrl (Luciferase) NA NA NA NA	DIV44 NA NA NA NA	Neurodegenerative Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases	NA NA NA NA
146 NGS25 146_Primary Myoblast-derived Myotube_WT 147 NGS25 147_Primary Myoblast_DMD 148 NGS25 148_Primary Myoblast_DMD 149 NGS25 149_hiPSC-derived Mesoderm precursor_WT 150 NGS25 150_hiPSC-derived Mesoderm precursor_WT 151 NGS25 151_hiPSC_WT	Primary myoblast WT M194 Primary Myoblast DMD M197 Primary Myoblast DMD M418 hiPSC-derived Mesoderm precursor WT M180 n1 hiPSC-derived Mesoderm precursor WT M180 n2 hiPSC WT M194 n1	1 M194 1 M197 1 M418 1 M180 1 M180 1 M194	WT DMD DMD WT WT WT	NO NO NO NO	NA NA NA P34 P34 P24	NA NA NA Matrigel Matrigel	NA NA NA mTes R mTes R mTes R	NO NO NO 3 days BMP4 NO	not passed	Primary Myoblast-derived Myotube Primary Myoblast Primary Myoblast hiPSC-derived Mesoderm precursor hiPSC-derived Mesoderm precursor hiPSC	NA NA NA NA	NA NA NA NA	NA NA NA NA	Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases	NA NA NA NA NA
155 NGS25 155_Primary Myoblast_WT 156 NGS25 156_Primary Myoblast-derived Myotube_DMD 157 NGS19 157_hiPSC_WT	hiPSC-derived Mesoderm precursor WT M194 hiPSC DMD M197 hiPSC-derived Mesoderm precursor DMD M197 Primary Myoblast WT M180 Primary myoblast-derived Myotube M313 DMD hiPSC WT V1024 n1	1 M194 1 M197 1 M197 1 M180 1 M313 1 V1024	WT DMD DMD WT DMD WT	NO NO NO NO	P24 P23 P23 NA NA P27	Matrigel Matrigel Matrigel Matrigel Matrigel Matrigel	mTes R mTes R mTes R NA NA mTes R	3 days BMP4 NO 3 days BMP4 NO NO	not passed	hiPSC-derived Mesoderm precursor hiPSC hiPSC-derived Mesoderm precursor Primary Myoblast Primary Myoblast-derived Myotube hiPSC	NA NA NA NA	NA NA NA NA	NA NA NA NA	Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases	NA NA NA NA
158 NGS19 158_hiPSC_DMD 159 NGS19 159_hiPSC-derived Mesoderm precursor_WT 160 NGS19 160_hiPSC-derived Mesoderm precursor_DMD 161 NGS19 161_hiPSC_WT 162 NGS19 162_hiPSC_DMD 163 NGS19 163_hiPSC-derived Mesoderm precursor_WT	hiPSC DMD M202 n1 hiPSC-derived Mesoderm precursor WT V1024 n1 hiPSC-derived Mesoderm precursor DMD M202	1 M202 1 V1024 1 M202 1 V1024 1 M202 1 V1024	DMD WT DMD WT DMD WT DMD	NO NO NO NO NO NO NO	P14 P27 P14 P27 P14 P27	Matrigel Matrigel Matrigel Matrigel Matrigel Matrigel	mTes R	NO 3 days BMP4 3 days BMP4 NO NO 3 days BMP4	not passed passed not passed passed not passed	hiPSC-derived Mesoderm precursor hiPSC-derived Mesoderm precursor hiPSC hiPSC hiPSC	NA NA NA NA NA	NA NA NA NA NA NA	NA NA NA NA NA	Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases	NA NA NA NA NA NA
164 NGS19 164_hiPSC-derived Mesoderm precursor_DMD 165 NGS19 165_hiPSC_WT 166 NGS19 166_hiPSC_DMD 167 NGS19 167_hiPSC-derived Mesoderm precursor_WT 168 NGS19 168_hiPSC-derived Mesoderm precursor_DMD	hiPSC WT V1024 n3 hiPSC DMD M202 n3 hiPSC-derived Mesoderm precursor WT V1024 n3 hiPSC-derived Mesoderm precursor DMD M202 n3	1 M202 1 V1024 1 M202 1 V1024 1 M202	DMD WT DMD WT	NO NO NO NO NO	P14 P27 P14 P27	Matrigel Matrigel Matrigel Matrigel	mTes R mTes R mTes R mTes R	3 days BMP4 NO NO 3 days BMP4 3 days BMP4	not passed passed not passed passed	hiPSC-derived Mesoderm precursor hiPSC hiPSC hiPSC-derived Mesoderm precursor hiPSC-derived Mesoderm precursor	NA NA NA	NA NA NA NA	NA NA NA NA	Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases	NA NA NA NA
169 NGS19 169_hiPSC_WT 170 NGS19 170_Primary Myoblast-derived Myotube_WT 171 NGS19 171_Primary Myoblast_DMD 172 NGS19 172_Primary Myoblast_WT 173 NGS32 173_Primary Myoblast-derived Myotube_WT 174 NGS32 174_Primary Myoblast-derived Myotube_WT	hiPSC WT V1024 n4 Primary Myoblast-derived Myotube WT V1024 NGS19 Primary Myoblast DMD M202 Primary Myoblast WT V1024 Primary Myoblast-derived Myotube WT M180 Primary Myoblast-derived Myotube WT M194	1 V1024 1 V1024 1 M202 1 V1024 1 M180 1 M194	WT WT DMD WT WT	NO NO NO NO NO NO	P27 NA NA NA NA	Matrigel NA NA NA NA	mTes R NA NA NA NA	NO NO NO NO NO	passed NA NA NA NA	hiPSC Primary Myoblast-derived Myotube Primary Myoblast Primary Myoblast Primary Myoblast-derived Myotube Primary Myoblast-derived Myotube	NA NA NA NA	NA NA NA NA	NA NA NA NA	Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases	NA NA NA NA
176 NGS32 176_Primary Myoblast-derived Myotube_DMD 177 NGS32 177_Primary Myoblast-derived Myotube_WT	Primary Myoblast-derived Myotube DMD M197 Primary Myoblast-derived Myotube DMD M202 Primary Myoblast-derived Myotube WT M398 Primary Myoblast-derived Myotube DMD M418 Primary Myoblast-derived Myotube WT V1024 NGS32 hESC-derived RPE WT RC9 days44 LV 19Q n1	1 M197 1 M202 1 M398 1 M418 1 V1024 1 RC9	DMD WT DMD WT WT	NO NO NO NO Ves: lentiviral transduction HTT (ctrl for sample 389_391_393)	NA NA NA NA P37	NA NA NA NA CellStart	NA NA NA NA StemPro	NO NO NO NO NO	NA NA NA NA	Primary Myoblast-derived Myotube hESC-derived RPE	NA NA NA NA NA	NA NA NA NA Overexpression HTT (lentivirus)	NA NA NA NA DIV44	Muscular diseases Muscular diseases Muscular diseases Muscular diseases Muscular diseases Neurodegenerative	NA NA NA NA NA
389 NG28 389_hESC-derived RPE_WT 390 NG28 390_hESC-derived RPE_WT 391 NG28 391_hESC-derived RPE_WT 392 NG28 392_hESC-derived RPE_WT 393 NG28 393_hESC-derived RPE_WT 394 NG28 394_hiPSC-derived RPE_WT	hESC-derived RPE WT RC9 days44 LV 82Q n1 hESC-derived RPE WT RC9 days44 LV 19Q n2 hESC-derived RPE WT RC9 days44 LV 82Q n2 hESC-derived RPE WT RC9 days44 LV 19Q n3 hESC-derived RPE WT RC9 days44 LV 82Q n3 hIPSC-derived RPE i90cl17 days44 LV shLuc MC20 n1 hIPSC-derived RPE i90cl17 days44 LV shHTT –	1 RC9 2 RC9 2 RC9 3 RC9 3 RC9 1 i90cl17	WT WT WT WT WT	Yes: lentiviral transduction mutated HTT Yes: lentiviral transduction HTT (ctrl for sample 389_391_393) Yes: lentiviral transduction mutated HTT Yes: lentiviral transduction HTT (ctrl for sample 389_391_393) Yes: lentiviral transduction mutated HTT Yes: lentiviral transduction luciferase (ctrl for sample 395)	P37 P37 P37 P37 P37 P69	CellStart CellStart CellStart CellStart CellStart	StemPro StemPro StemPro StemPro StemPro StemPro	NO NO NO NO NO	NA NA NA	hESC-derived RPE hESC-derived RPE hESC-derived RPE hESC-derived RPE hESC-derived RPE hESC-derived RPE	NA NA NA NA NA	overexpression mutated HTT (lentivirus) overexpression HTT (lentivirus) overexpression mutated HTT (lentivirus) overexpression HTT (lentivirus) overexpression mutated HTT (lentivirus) lentivirus Ctrl (Luciferase)	DIV44 DIV44 DIV44 DIV44 DIV44	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA NA
395 NG28 395_hiPSC-derived RPE_WT 216 NGS11 216_hiPSC-derived Cortical Neurons_HD 217 NGS11 217_hiPSC-derived Cortical Neurons_HD 218 NGS11 218_hiPSC-derived Cortical Neurons_HD 219 NGS11 219_hiPSC-derived Cortical Neurons_HD	sh6 i90cl17 hIPSC-derived Cortical Neurons HD Delta60 LV shHTT, sh6 n1 hIPSC-derived Cortical Neurons HD Delta60 LV shHTT, sh6 n2 hIPSC-derived Cortical Neurons HD Delta60 LV shHTT, sh6 n3 hIPSC-derived Cortical Neurons HD Delta60 LV	 i90cl17 delta60 delta60 delta60 delta60 	WT HD HD	Yes: lentiviral transduction KO HTT Yes: lentiviral transduction luciferase (ctrl for sample 216->218)	P69 P56 P56 P56	L7 Cellstart Cellstart Cellstart Cellstart	StemPro StemPro StemPro StemPro StemPro	NO NO NO NO	NA NA NA	hiPSC-derived RPE hiPSC-derived Cortical Neurons hiPSC-derived Cortical Neurons hiPSC-derived Cortical Neurons hiPSC-derived Cortical Neurons	NA PO-lam PO-lam PO-lam	KO HTT gene (lentivirus) KO HTT gene (lentivirus) KO HTT gene (lentivirus) KO HTT gene (lentivirus)	DIV44 DIV35 DIV35 DIV35	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA
219 NGS11 219_hiPSC-derived Cortical Neurons_HD 220 NGS11 220_hiPSC-derived Cortical Neurons_WT 221 NGS11 221_hiPSC-derived Cortical Neurons_WT 222 NGS11 222_hiPSC-derived Cortical Neurons_WT 223 NGS11 223_hiPSC-derived Cortical Neurons_WT	shLuc n1 hIPSC-derived Cortical Neurons WT I90 LV shHTT, sh6 n1 hIPSC-derived Cortical Neurons WT I90 LV shHTT, sh6 n2 hIPSC-derived Cortical Neurons WT I90 LV shHTT, sh6 n3 hIPSC-derived Cortical Neurons WT I90 LV shLuc n1	1 delta60 1 l90cl17 2 l90cl17 3 l90cl17 1 l90cl17	HD WT WT WT	yes: lentiviral transduction KO HTT Yes: lentiviral transduction luciferase (ctrl for sample 220->222)	p34 p34 p34 p34	Cellstart Cellstart Cellstart Cellstart Cellstart	StemPro StemPro StemPro StemPro StemPro	NO NO NO NO	not passed not passed not passed	hiPSC-derived Cortical Neurons	PO-lam PO-lam PO-lam PO-lam PO-lam	lentivirus Ctrl (Luciferase) KO HTT gene (lentivirus) KO HTT gene (lentivirus) KO HTT gene (lentivirus) lentivirus Ctrl (Luciferase)	DIV35 DIV35 DIV35 DIV35	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA
224 NGS11 224_hiPSC-derived Cortical Neurons_HD 225 NGS11 225_hiPSC-derived Cortical Neurons_WT 226 NGS11 226_hiPSC-derived Cortical Neurons_HD 227 NGS11 227_hiPSC-derived Cortical Neurons_WT 180 NGS2 180_hESC-derived striatal neurons_WT	hIPSC-derived Cortical Neurons HD Delta60 LV shLuc n2 hIPSC-derived Cortical Neurons WT I90 LV shLuc n2 hIPSC-derived Cortical Neurons HD Delta60 LV shLuc n3 hIPSC-derived Cortical Neurons WT I90 LV shLuc n3 hESC-derived striatal neurons WT RC9 days49 LV GFP n1	 2 delta60 2 l90cl17 3 delta60 3 l90cl17 1 RC9 	HD WT HD WT	Yes: lentiviral transduction luciferase (ctrl for sample 216->218) Yes: lentiviral transduction luciferase (ctrl for sample 220->222) Yes: lentiviral transduction luciferase (ctrl for sample 216->218) Yes: lentiviral transduction luciferase (ctrl for sample 220->222) Yes: lentiviral transduction GFP (ctrl for sample (184->191)	P56 p34 P56 p34 P38	Cellstart Cellstart Cellstart Cellstart Cellstart	StemPro StemPro StemPro StemPro stemPro	NO NO NO NO	not passed NA not passed	hiPSC-derived Cortical Neurons hiPSC-derived Cortical Neurons hiPSC-derived Cortical Neurons hiPSC-derived Cortical Neurons hESC-derived striatal neurons	PO-lam PO-lam PO-lam PO-lam	lentivirus Ctrl (Luciferase) lentivirus Ctrl (Luciferase) lentivirus Ctrl (Luciferase) lentivirus Ctrl (Luciferase)	DIV35 DIV35 DIV35 DIV35	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA GSE104091_GSM27896
181 NGS2 181_hESC-derived striatal neurons_WT 182 NGS2 182_hESC-derived striatal neurons_WT 183 NGS2 183_hESC-derived striatal neurons_WT 184 NGS2 184_hESC-derived striatal neurons_WT 185 NGS2 185_hESC-derived striatal neurons_WT 186 NGS2 186_hESC-derived striatal neurons_WT 187 NGS2 187_hESC-derived striatal neurons_WT	hESC-derived striatal neurons WT RC9 days49 LV GFP n2 hESC-derived striatal neurons WT RC9 days49 LV GFP n3 hESC-derived striatal neurons WT RC9 days49 LV GFP n4 hESC-derived striatal neurons WT RC9 days49 LV DKIN n1 hESC-derived striatal neurons WT RC9 days49 LV DKIN n2 hESC-derived striatal neurons WT RC9 days49 LV DKIN n3 hESC-derived striatal neurons WT RC9 days49 LV DKIN n3	2 RC9 3 RC9 4 RC9 1 RC9 2 RC9 3 RC9 4 RC9	WT WT WT WT WT WT	Yes: lentiviral transduction GFP (ctrl for sample (184->191) Yes: lentiviral transduction GFP (ctrl for sample (184->191) Yes: lentiviral transduction GFP (ctrl for sample (184->191) Yes: lentiviral transduction DKIN Yes: lentiviral transduction DKIN Yes: lentiviral transduction DKIN Yes: lentiviral transduction DKIN	P38 P38 P38 P38 P38 P38	Cellstart Cellstart Cellstart Cellstart Cellstart Cellstart Cellstart	stemPro stemPro stemPro stemPro stemPro stemPro stemPro	NO NO NO NO NO NO	NA NA NA NA	hESC-derived striatal neurons	PO-lam PO-lam PO-lam PO-lam PO-lam PO-lam	lentivirus Ctrl (GFP) DIV35 lentivirus Ctrl (GFP) DIV35 lentivirus Ctrl (GFP) DIV35 overexpression DKIN gene DIV35 (lentivirus)	DIV49 DIV49 DIV49 DIV49 DIV49 DIV49	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	GSE104091_GSM278966 GSE104091_GSM278966 GSE104091_GSM278966 GSE104091_GSM278966 GSE104091_GSM2789666 GSE104091_GSM27896666
188 NGS2 188_hESC-derived striatal neurons_WT 189 NGS2 189_hESC-derived striatal neurons_WT 190 NGS2 190_hESC-derived striatal neurons_WT 191 NGS2 191_hESC-derived striatal neurons_WT 192 NGS3 192_hESC-derived RPE_WT	hESC-derived striatal neurons WT RC9 days49 LV DKIN-K543M n1 hESC-derived striatal neurons WT RC9 days49 LV DKIN-K543M n2 hESC-derived striatal neurons WT RC9 days49 LV DKIN-K543M n3 hESC-derived striatal neurons WT RC9 days49 LV DKIN-K543M n4 hESC-derived RPE WT RC9 LV shL n1	1 RC9 2 RC9 3 RC9 4 RC9 1 RC9	WT WT WT WT	Yes: lentiviral transduction DKIN-K543 Yes: lentiviral transduction DKIN-K543 Yes: lentiviral transduction DKIN-K543 Yes: lentiviral transduction DKIN-K543 Yes: lentiviral transduction luciferase (ctrl for sample 195->197)	P38 P38 P38 P38	Cellstart Cellstart Cellstart Cellstart Cellstart	stemPro stemPro stemPro StemPro	NO NO NO NO	NA NA	hESC-derived striatal neurons hESC-derived striatal neurons hESC-derived striatal neurons hESC-derived striatal neurons hESC-derived RPE	PO-lam PO-lam PO-lam PO-lam CellStart-Fibro	overexpression mutatedDKIN mutated DIV35 (lentivirus) lentivirus Ctrl (Luciferase) DIV29	DIV49 DIV49 DIV49 DIV49 DIV34	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	GSE104091_GSM27896 GSE104091_GSM27896 GSE104091_GSM27896 GSE104091_GSM27896
193 NGS3 193_hESC-derived RPE_WT 194 NGS3 194_hESC-derived RPE_WT 195 NGS3 195_hESC-derived RPE_WT 196 NGS3 196_hESC-derived RPE_WT 197 NGS3 197_hESC-derived RPE_WT	hESC-derived RPE WT RC9 LV shL n3 hESC-derived RPE WT RC9 LV shL n4 hESC-derived RPE WT RC9 LV shHTT, sh6 n1 hESC-derived RPE WT RC9 LV shHTT, sh6 n3 hESC-derived RPE WT RC9 LV shHTT, sh6 n4	3 RC9 4 RC9 1 RC9 3 RC9 4 RC9	WT WT WT WT	Yes: lentiviral transduction luciferase (ctrl for sample 195->197) Yes: lentiviral transduction luciferase (ctrl for sample 195->197) Yes: lentiviral transduction KO HTT Yes: lentiviral transduction KO HTT	P37 P37 P37 P37	Cellstart Cellstart Cellstart Cellstart Cellstart	StemPro StemPro StemPro StemPro StemPro	NO NO NO NO	NA NA NA	hESC-derived RPE hESC-derived RPE hESC-derived RPE hESC-derived RPE hESC-derived RPE	CellStart-Fibro CellStart-Fibro CellStart-Fibro CellStart-Fibro	lentivirus Ctrl (Luciferase) DIV29 lentivirus Ctrl (Luciferase) DIV29 KO HTT gene DIV29 (lentivirus) KO HTT gene DIV29 (lentivirus)	DIV34 DIV34 DIV34 DIV34	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA NA
126 NGS41 126_Fibroblasts_WT 127 NGS41 127_Fibroblasts_WT 128 NGS41 128_Fibroblasts_WT 129 NGS41 129_Fibroblasts_WT	Fibroblasts lenti R77C mCherry DMSO 0,1% n1 Fibroblasts lenti R77C mCherry DMSO 0,1% n2 Fibroblasts lenti R77C mCherry DMSO 0,1% n3 Fibroblasts lenti R77C mCherry Btz 30 nM n1	1 NA 2 NA 3 NA 1 NA	WT WT WT	Yes: lentiviral transduction α -SGmutated (R77C) mCherry	NA - NA - NA - NA	NA NA NA	NA NA NA	NO NO NO	NA NA NA	Fibroblasts Fibroblasts Fibroblasts	Collagen Collagen Collagen	α-SGmutated (R77C) overexpression DMSO 0.1 % - 24h α-SGmutated (R77C) overexpression DMSO 0.6 % - 24h α-SGmutated (R77C) overexpression DMSO 0.6 % - 24h α-SGmutated (R77C) overexpression bortezomib 30 nM - 24h α-SGmutated (R77C) overexpression	NA .1 NA NA	LGMD LGMD LGMD	GSE119841_GSM338499 GSE119841_GSM338499 GSE119841_GSM338499
130 NGS41 130_Fibroblasts_WT 131 NGS41 131_Fibroblasts_WT 132 NGS41 132_Fibroblasts_WT 133 NGS41 133_Fibroblasts_WT 134 NGS41 134_Fibroblasts_WT 135 NGS41 135_Fibroblasts_WT 228 NG22 228_hESC-derived striatal neurons_WT	Fibroblasts lenti R77C mCherry Btz 30 nM n2 Fibroblasts lenti R77C mCherry Btz 30 nM n3 Fibroblasts lenti R77C mCherry Thsp 3 ÂμM n1 Fibroblasts lenti R77C mCherry Thsp 3 ÂμM n2 Fibroblasts lenti R77C mCherry Thsp 3 ÂμM n3 Fibroblasts lenti R77C mCherry Thsp 5 ÂμM n1 hESC-derived striatal neurons WT RC9 on microfluidic chip connected to hESC-derived Cortical Neurons RC9 n1	2 NA 3 NA 1 NA 2 NA 3 NA 1 NA 1 RC9	WT WT WT WT WT	mCherry Yes: lentiviral transduction α -SGmutated (R77C) mCherry	NA - NA - NA - NA	NA NA NA NA NA	NA NA NA NA NA Stempro	NO NO NO NO NO NO	NA NA NA NA	Fibroblasts Fibroblasts Fibroblasts Fibroblasts Fibroblasts Fibroblasts Fibroblasts	Collagen Collagen Collagen Collagen Collagen Collagen PO-lam	bortezomib 30 nM - 24h α-SGmutated (R77C) overexpression bortezomib 30 nM - 24h α-SGmutated (R77C) overexpression Thiostrepton 3 ÂμM - 24h α-SGmutated (R77C) overexpression Thiostrepton 5 ÂμM - 24h	NA NA NA NA NA DIV46	LGMD LGMD LGMD LGMD LGMD Neurodegenerative	GSE119841_GSM338493 GSE119841_GSM338493 GSE119841_GSM338493 GSE119841_GSM338493 NA
229 NG22 229_hESC-derived striatal neurons_WT 230 NG22 230_hESC-derived striatal neurons_WT 231 NG22 231_hESC-derived striatal neurons_WT	hESC-derived striatal neurons WT RC9 on microfluidic chip connected to hESC-derived Cortical Neurons RC9 n2 hESC-derived striatal neurons WT RC9 on microfluidic chip connected to hESC-derived Cortical Neurons RC9 n3 hESC-derived striatal neurons WT RC9 on microfluidic chip connected to hESC-derived Cortical Neurons RC9 n4	2 RC9 3 RC9 4 RC9	WT WT	NO NO	P40 P40	L7 L7	Stempro Stempro	NO NO	NA	hESC-derived striatal neurons hESC-derived striatal neurons hESC-derived striatal neurons	PO-lam PO-lam PO-lam	Microfluidic chip Microfluidic chip Microfluidic chip	DIV46 DIV46	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
232 NG22 232_hESC-derived striatal neurons_WT 233 NG22 233_hESC-derived striatal neurons_WT 234 NG22 234_hESC-derived striatal neurons_WT 235 NG22 235_hESC-derived striatal neurons_WT	hESC-derived striatal neurons WT RC9 n1 hESC-derived striatal neurons WT RC9 n2 hESC-derived striatal neurons WT RC9 n3 hESC-derived striatal neurons WT RC9 n4 hESC-derived Cortical Neurons WT RC9 on microfluidic chip connected to hESC-derived	1 RC9 2 RC9 3 RC9 4 RC9	WT WT WT	NO NO NO	P40 P40 P40 P40	L7 L7 L7 L7	Stempro Stempro Stempro Stempro	NO NO NO	NA NA	hESC-derived striatal neurons hESC-derived striatal neurons hESC-derived striatal neurons hESC-derived striatal neurons	PO-lam PO-lam PO-lam	Microfluidic chip Microfluidic chip Microfluidic chip Microfluidic chip	DIV46 DIV46 DIV46	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA
236 NG22 236_hESC-derived Cortical Neuron_WT 237 NG22 237_hESC-derived Cortical Neuron_WT 238 NG22 238_hESC-derived Cortical Neuron_WT	striatal neurons WT RC9 n1 hESC-derived Cortical Neurons WT RC9 on microfluidic chip connected to hESC-derived striatal neurons WT RC9 n2 hESC-derived Cortical Neurons WT RC9 on microfluidic chip connected to hESC-derived striatal neurons WT RC9 n3 hESC-derived Cortical Neurons WT RC9 on	1 RC9 2 RC9 3 RC9	WT WT	NO NO	P38 P38	vitronectine vitronectine vitronectine	na	NO NO	NA	hESC-derived Cortical Neuron hESC-derived Cortical Neuron hESC-derived Cortical Neuron	PO-lam PO-lam	Microfluidic chip Microfluidic chip Microfluidic chip	DIV46 DIV46	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
239 NG22 239_hESC-derived Cortical Neuron_WT 240 NGS46 240_hiPSC-derived Cortical Neurons_WT 241 NGS46 241_hiPSC-derived striatal neurons_WT	microfluidic chip connected to hESC-derived striatal neurons RC9 n4 hiPSC-derived Cortical Neurons WT i90 on microfluidic chip conne and C226:C260cted to hIPSC-derived MSN WT i90 n1 hiPSC-derived MSN WT i90 on microfluidic chip n1 hiPSC-derived Cortical Neurons WT i90 on	4 RC9 1 i90cl16 1 i90cl16	WT WT	NO NO	P38 P47 P47	vitronectine vitronectine vitronectine	Stem Max	NO NO	NA	hESC-derived Cortical Neuron hiPSC-derived Cortical Neurons hiPSC-derived striatal neurons	PO-lam PO-lam PO-lam	Microfluidic chip hIPSC-derived Cortical Neurons on microfluidi chip connected to hIPSC-derived MSN Microfluidic chip	DIV44	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
242 NGS46 242_hiPSC-derived Cortical Neurons_WT 243 NGS46 243_hiPSC-derived striatal neurons_WT 244 NGS46 244_hiPSC-derived striatal neurons_WT 245 NGS46 245_hiPSC-derived Cortical Neurons_WT	microfluidic chip connected to hIPSC-derived MSN WT i90 n2 hiPSC-derived MSN WT i90 on microfluidic chip n2 hiPSC-derived MSN WT i90 on microfluidic chip n3 hiPSC-derived Cortical Neurons WT i90 on microfluidic chip connected to hIPSC-derived MSN WT i90 n3	2 i90cl162 i90cl163 i90cl163 i90cl16	WT WT WT	NO NO NO	P47 P47 P47	vitronectine vitronectine vitronectine vitronectine	Stem Max Stem Max	NO NO NO	NA	hiPSC-derived Cortical Neurons hiPSC-derived striatal neurons hiPSC-derived striatal neurons hiPSC-derived Cortical Neurons	PO-lam PO-lam PO-lam	hIPSC-derived Cortical Neurons on microfluidichip connected to hIPSC-derived MSN Microfluidic chip Microfluidic chip hIPSC-derived Cortical Neurons on microfluidichip connected to hIPSC-derived MSN	DIV44 DIV44	Neurodegenerative Neurodegenerative Neurodegenerative Neurodegenerative	NA NA NA
246 NGS46 246_hiPSC-derived striatal neurons_WT 247 NGS46 247_hiPSC-derived Cortical Neurons_WT 248 NGS46 248_hiPSC-derived striatal neurons_WT	hiPSC-derived MSN WT i90 on microfluidic chip n4 hiPSC-derived Cortical Neurons WT i90 on microfluidic chip connected to hIPSC-derived MSN WT i90 n4 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 n1	4 i90cl16 4 i90cl16 1 i90cl16	WT WT	NO NO	P47 P47	vitronectine vitronectine vitronectine	Stem Max Stem Max	NO NO	NA NA	hiPSC-derived striatal neurons hiPSC-derived Cortical Neurons hiPSC-derived striatal neurons	PO-lam PO-lam PO-lam	Microfluidic chip hIPSC-derived Cortical Neurons on microfluidi chip connected to hIPSC-derived MSN hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons	DIV44 C DIV44	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
249 NGS46 249_hiPSC-derived striatal neurons_WT 250 NGS46 250_hiPSC-derived striatal neurons_WT 251 NGS46 251_hiPSC-derived striatal neurons_WT	hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 n2 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 n3 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 n4	2 i90cl163 i90cl164 i90cl16	WT WT	NO NO	P47 P47	vitronectine vitronectine vitronectine	Stem Max	NO NO	NA	hiPSC-derived striatal neurons hiPSC-derived striatal neurons	PO-lam PO-lam PO-lam	hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons	DIV44	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
252 NGS46 252_hiPSC-derived striatal neurons_WT 253 NGS46 253_hiPSC-derived striatal neurons_WT	hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D2 n1 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D2 n2 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons	1 i90cl16 2 i90cl16	WT	NO NO	P47	vitronectine	Stem Max	NO NO	NA	hiPSC-derived striatal neurons hiPSC-derived striatal neurons	PO-lam	hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2 hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2 hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical	DIV44	Neurodegenerative Neurodegenerative	NA NA
254 NGS46 254_hiPSC-derived striatal neurons_WT 255 NGS46 255_hiPSC-derived striatal neurons_WT 256 NGS46 256_hiPSC-derived striatal neurons_WT	hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D2 n4 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D1-D2 n1	3 i90cl164 i90cl161 i90cl16	WT WT	NO NO	P47 P47	vitronectine vitronectine vitronectine	Stem Max	NO NO	NA	hiPSC-derived striatal neurons hiPSC-derived striatal neurons	PO-lam PO-lam PO-lam	Neurons and dopaminergique antagonist D2 hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2 hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2	DIV44	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
257 NGS46 257_hiPSC-derived striatal neurons_WT 258 NGS46 258_hiPSC-derived striatal neurons_WT 259 NGS46 259 hiPSC-derived striatal neurons WT	hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D1-D2 n2 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D1-D2 n3 hiPSC-derived MSN WT i90 on microfluidic chip connected to hIPSC-derived Cortical Neurons WT i90 with dopaminergique antagonist D1-D2 n4	2 i90cl163 i90cl164 i90cl16	WT WT	NO NO	P47 P47	vitronectine vitronectine vitronectine	Stem Max	NO NO	NA	hiPSC-derived striatal neurons hiPSC-derived striatal neurons	PO-lam PO-lam PO-lam	hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2 hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2 hIPSC-derived striatal neurons on microfluidic chip connected to hIPSC-derived Cortical Neurons and dopaminergique antagonist D2	DIV44	Neurodegenerative Neurodegenerative Neurodegenerative	NA NA
259 NGS46 259_hiPSC-derived striatal neurons_WT 260 NGS17 260_hESC-derived Neuron_WT 261 NGS17 261_hESC-derived Neuron_WT 262 NGS17 262_hESC-derived Neuron_WT 263 NGS17 263_hESC-derived Neuron_WT 264 NGS17 264 hESC-derived Neuron WT	n4 hESC-derived neurones WT SA001 days28 VPA 3mM n1 hESC-derived neurones WT SA001 days28 VPA 3mM n2 hESC-derived neurones WT SA001 days28 VPA 3mM n3 hESC-derived neurones WT SA001 days28 Lithium 0,5mM n1 hESC-derived neurones WT SA001 days28	4 i90cl16 1 SA001 2 SA001 1 SA001 2 SA001	WT WT WT WT WT	NO NO NO NO NO NO	P47 P24 P24 P24 P24	vitronectine MEF MEF MEF MEF	medium KSR medium KSR medium KSR medium KSR	NO NO NO NO NO	passed passed passed passed	hiPSC-derived striatal neurons hESC-derived Neuron hESC-derived Neuron hESC-derived Neuron hESC-derived Neuron	PO-lam Po-Lam Po-Lam Po-Lam Po-Lam	Neurons and dopaminergique antagonist D2 VPA 3mM 24h VPA 3mM 24h VPA 3mM 24h Lithium 0.5 mM 24h	DIV44 DIV28 DIV28 DIV28 DIV28 DIV28	Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity	NA NA NA NA NA
264 NGS17 264_hESC-derived Neuron_WT 265 NGS17 265_hESC-derived Neuron_WT 266 NGS17 266_hESC-derived Neuron_WT 267 NGS17 267_hESC-derived Neuron_WT 268 NGS17 268_hESC-derived Neuron_WT 269 NGS23 269_hiPSC_WT	Lithium 0,5mM n2 hESC-derived neurones WT SA001 days28 Lithium 0,5mM n3 hESC-derived neurones WT SA001 days28 DMSO n1 hESC-derived neurones WT SA001 days28 DMSO n2 hESC-derived neurones WT SA001 days28 DMSO n3 hiPSC WT 1869c07	2 SA001 3 SA001 1 SA001 2 SA001 3 SA001 1 1869c07	WT WT WT WT WT	NO NO NO NO NO NO	P24 P24 P24 P24 P24 P49	MEF MEF MEF MEF vitronectine	medium KSR medium KSR medium KSR medium KSR medium KSR	NO NO NO NO NO NO	passed passed	hESC-derived Neuron hESC-derived Neuron hESC-derived Neuron hESC-derived Neuron hESC-derived Neuron hiPSC	Po-Lam Po-Lam Po-Lam Po-Lam Po-Lam NA	Lithium 0.5 mM 24h Lithium 0.5 mM 24h DMSO mM 24h DMSO mM 24h DMSO mM 24h NA	DIV28 DIV28 DIV28 DIV28 DIV28 NA	Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity	NA NA NA NA NA
269 NGS23 269_hiPSC_WT 270 NGS23 270_hiPSC_WT 271 NGS23 271_hESC-derived dopaminergic Neuron_WT 272 NGS23 272_hESC-derived dopaminergic Neuron_WT 273 NGS23 273_hiPSC-derived dopaminergic Neuron_WT 274 NGS23 274_hiPSC-derived dopaminergic Neuron_LND 275 NGS23 275_hiPSC-derived dopaminergic Neuron_LND	hiPSC WT PB12c03 hIPSC-derived dopaminergic neurons WT 1869c07 hESC-derived dopaminergic neurons WT SA001 hIPSC-derived dopaminergic neurons WT P12c03 hIPSC-derived dopaminergic neurons LND 23784c05 hIPSC-derived dopaminergic neurons LND	1 1869c07 1 PB12c03 1 1869c07 1 SA001 1 PB12c03 1 23784c05	WT WT WT WT LND LND	NO NO NO NO NO NO NO NO	P49 P40 P35 P64 P40 P27	vitronectine vitronectine vitronectine	iPS brew iPS brew iPS brew iPS brew	NO NO NO NO NO NO	NA NA NA NA	hiPSC hiPSC hESC-derived dopaminergic Neuron hESC-derived dopaminergic Neuron hiPSC-derived dopaminergic Neuron hiPSC-derived dopaminergic Neuron hiPSC-derived dopaminergic Neuron	NA NA PO-lam-fibro PO-lam-fibro PO-lam-fibro PO-lam-fibro	NA NA NA NA NA	NA NA DIV25 DIV25 DIV25 DIV25	Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity Neuroplasticity	NA NA NA NA NA NA

274 NGS23 274_hiPSC-derived dopaminergic Neuron_LND 23784c05 1 23784c05 LND NO
hIPSC-derived dopaminergic neurons LND
275 NGS23 275_hiPSC-derived dopaminergic Neuron_LND 2227c02 1 2227c02 LND NO

hIPSC-derived dopaminergic neurons LND 276 NGS23 276_hiPSC-derived dopaminergic Neuron_LND 2852c03 277_hiPSC-derived dopaminergic Neuron hIPSC-derived dopaminergic neurons progenitor 277 NGS23 progenitor_WT WT 1869c07 278_hiPSC-derived dopaminergic Neuron hESC-derived dopaminergic neurons progenitor 278 NGS23 progenitor_WT SA001 279_hiPSC-derived dopaminergic Neuron hIPSC-derived dopaminergic neurons progenitor 279 NGS23 progenitor_WT WT PB12c03 280_hiPSC-derived dopaminergic Neuron hIPSC-derived dopaminergic neurons progenitor 280 NGS23 progenitor_LND LND 23784c05	1 2852c03 LND 1 1869c07 WT 1 SA001 WT 1 PB12c03 WT 1 23784c05 LND	NO P2 NO P3 NO P6 NO P3 NO P2	vitronectine iPS brew NO vitronectine iPS brew NO vitronectine iPS brew NO vitronectine iPS brew NO	NA hiPSC-derived dopaminergic Neuror NA hiPSC-derived dopaminergic Neuror NA hiPSC-derived dopaminergic Neuror	n progenitor PO-lam-fibro NA n progenitor PO-lam-fibro NA n progenitor PO-lam-fibro NA	DIV25 Neuroplasticity DIV10 Neuroplasticity DIV10 Neuroplasticity DIV10 Neuroplasticity DIV10 Neuroplasticity DIV10 Neuroplasticity	NA NA NA NA
281_hiPSC-derived dopaminergic Neuron hIPSC-derived dopaminergic neurons progenitor 281 NGS23 progenitor_LND LND 2227c02 282_hiPSC-derived dopaminergic Neuron hIPSC-derived dopaminergic neurons progenitor 282 NGS23 progenitor_LND LND 2852c03 284_hiPSC-derived dopaminergic Neuron hIPSC-derived dopaminergic neurons progenitor 284 NGS23 progenitor_LND LND 2851c15 hIPSC-derived dopaminergic neurons 285 NGS23 285_hiPSC-derived dopaminergic Neuron_LND LND 2851c15 hESC-derived LGE-like progenitors WT AB267	1 2227c02 LND 1 2852c03 LND 1 2851c15 LND 1 2851c15 LND	NO P2 NO P2 NO P2 NO P2	vitronectine iPS brew NO vitronectine iPS brew NO vitronectine iPS brew NO vitronectine iPS brew NO	NA hiPSC-derived dopaminergic Neuror NA hiPSC-derived dopaminergic Neuror NA hiPSC-derived dopaminergic Neuror	n progenitor PO-lam-fibro NA n progenitor PO-lam-fibro NA n PO-lam-fibro NA	DIV10 Neuroplasticity DIV10 Neuroplasticity DIV10 Neuroplasticity DIV25 Neuroplasticity	NA NA NA
286 NGS8 286_hESC-derived LGE-like progenitors_WT P1D21 hESC-derived striatal neurons WT AB267 P1D55 287 NGS8 287_hESC-derived striatal neurons_WT n1 hESC-derived LGE-like progenitors WT AB267 288 NGS8 288_hESC-derived LGE-like progenitors_WT P2D21 hESC-derived striatal neurons WT AB267 P2D55 289 NGS8 289_hESC-derived striatal neurons_WT n1 hESC-derived LGE-like progenitors WT AB268 290 NGS8 290_hESC-derived LGE-like progenitors_WT P1D21	RC9 WT 1 RC9 WT RC9 WT 1 RC9 WT RC9 WT	NO P4 NO P4 NO P4 NO P4 NO P4	40 L7 StemPro NO 40 L7 StemPro NO	NA hESC-derived striatal neurons NA hESC-derived LGE-like progenitors NA hESC-derived striatal neurons	PO-lam NA PO-lam NA L7 NA PO-lam NA L7-Fibro NA	DIV21 Neurodegenerative DIV55 Neurodegenerative DIV21 Neurodegenerative DIV55 Neurodegenerative DIV21 Neurodegenerative	NA NA NA
hESC-derived striatal neurons WT AB268 P1D55 291 NGS8 291_hESC-derived striatal neurons_WT n1 hESC-derived striatal neurons WT AB268 P1D55 292 NGS8 292_hESC-derived striatal neurons_WT n2 hESC-derived striatal neurons WT AB268 P1D55 293 NGS8 293_hESC-derived striatal neurons_WT n3 hESC-derived LGE-like progenitors WT AB268 294 NGS8 294_hESC-derived LGE-like progenitors_WT P2D21	1 RC9 WT 2 RC9 WT 3 RC9 WT RC9 WT	NO P4 NO P4 NO P4 NO P4	L7 StemPro NO L7 StemPro NO L7 StemPro NO L7 StemPro NO	NA hESC-derived striatal neurons NA hESC-derived striatal neurons NA hESC-derived striatal neurons	PO-lam NA PO-lam NA PO-lam NA L7-Fibro NA	DIV55 Neurodegenerative DIV55 Neurodegenerative DIV55 Neurodegenerative DIV21 Neurodegenerative	NA NA NA
hESC-derived striatal neurons WT AB268 P2D55 295 NGS8 295_hESC-derived striatal neurons_WT n1 hESC-derived striatal neurons WT AB268 P2D55 296 NGS8 296_hESC-derived striatal neurons_WT n2 hESC-derived striatal neurons WT AB268 P2D55 297 NGS8 297_hESC-derived striatal neurons_WT n3 298 NGS8 298_hESC-derived MGE-like progenitors_WT hESC-derived MGE-like progenitors WT AB266	1 RC9 WT 2 RC9 WT 3 RC9 WT	NO P4 NO P4 NO P4 NO P3	L7 StemPro NO L7 StemPro NO L7 StemPro NO L7 StemPro NO	NA hESC-derived striatal neurons NA hESC-derived striatal neurons NA hESC-derived striatal neurons	L7-Fibro-PO-lam NA L7-Fibro-PO-lam NA L7-Fibro-PO-lam NA	DIV55 Neurodegenerative DIV55 Neurodegenerative DIV55 Neurodegenerative DIV21 Neurodegenerative	NA NA NA
299 NGS8 299_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT AB277-1 300 NGS8 300_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT AB277-2 301 NGS8 301_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT AB236 2 302 NGS8 302_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT AB256 1	RC9 WT RC9 WT RC9 WT RC9 WT	NO P4 NO P2 NO P2	L7 StemPro NO CellStart StemPro NO	NA hESC-derived LGE-like progenitors NA hESC-derived LGE-like progenitors	L7 NA L7-L7 NA CellStart NA L7 NA	DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative	NA NA NA
hESC-derived LGE-like progenitors WT AB263 303 NGS8 303_hESC-derived LGE-like progenitors_WT P1D21 n2 hESC-derived LGE-like progenitors WT AB264 304 NGS8 304_hESC-derived LGE-like progenitors_WT P1D21 n2 hESC-derived LGE-like progenitors WT AB265 305 NGS8 305_hESC-derived LGE-like progenitors_WT P1D21 n3 306 NGS8 306_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT fresh	RC9 WT RC9 WT RC17 WT H9 WT	NO P3 NO P3 NO P2 NO NA	StemPro NO NO L7 StemPro NO	NA hESC-derived LGE-like progenitors NA hESC-derived LGE-like progenitors	L7 NA L7 NA L7 NA PO-Fibro NA	DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative	NA NA NA
307 NGS8 307_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT frozen 308 NGS8 308_Human Fœtal tissus Cortex_WT Human Fœtal tissus Cortex WT CX1 2097 309 NGS8 309_Human Fœtal tissus Cortex_WT Human Fœtal tissus Cortex WT CX2 2102 310 NGS8 310_Human Fœtal tissus Cortex_WT Human Fœtal tissus Cortex WT CX3 2107 311 NGS8 311_Human Fœtal tissus LGE_WT Human Fœtal tissus LGE WT LGE 4 2121	RC9 WT 1 NA WT 2 NA WT 3 NA WT 4 NA WT	NO NA NO NA NO NA NO NA NO NA NO NA	A NA NA NO A NA NA NO	NA Human Fœtal tissus Cortex NA Human Fœtal tissus Cortex	PO-Fibro NA NA NA NA NA NA NA NA NA	NA Neurodegenerative	NA NA NA NA
312 NGS8 312_Human Fœtal tissus LGE_WT Human Fœtal tissus LGE WT LGE1 2097 313 NGS8 313_Human Fœtal tissus LGE_WT Human Fœtal tissus LGE WT LGE2 2102 314 NGS8 314_Human Fœtal tissus LGE_WT Human Fœtal tissus LGE WT LGE3 2107 315 NGS8 315_Human Fœtal tissus LGE_WT Human Fœtal tissus LGE WT LGE5 2132 316 NGS8 316_Human Fœtal tissus LGE_WT Human Fœtal tissus LGE WT LGE6 2134 317 NGS8 317_Human Fœtal tissus MGE_WT Human Fœtal tissus MGE WT MGE1 2097	1 NA WT 2 NA WT 3 NA WT 5 NA WT 6 NA WT	NO NA NO NA NO NA NO NA NO NA NO NA	A NA NA NO	NA Human Fœtal tissus LGE	NA	NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative	NA NA NA NA
318 NGS8 318_Human Fœtal tissus MGE_WT Human Fœtal tissus MGE WT MGE2 2102 319 NGS8 319_Human Fœtal tissus MGE_WT Human Fœtal tissus MGE WT MGE3 2107 320_hESC-derived Telencephalic hESC-derived Telencephalic Rosette NSC WT 320 NGS8 Rosette_NSC_WT MM30 hESC-derived LGE-like progenitors WT MM30-2 321 NGS8 321_hESC-derived LGE-like progenitors_WT 1 hESC-derived LGE-like progenitors WT MM30-2	2 NA WT 3 NA WT RC9 WT RC9 WT	NO NA NO NA NO P4 NO P4	A NA NA NO 40 L7 StemPro NO 40 L7 StemPro NO	NA Human Fœtal tissus MGE NA hESC-derived Telencephalic Rosette NA hESC-derived LGE-like progenitors	L7 NA	NA Neurodegenerative NA Neurodegenerative DIV10 Neurodegenerative DIV20 Neurodegenerative	NA NA NA
322 NGS8 322_hESC-derived LGE-like progenitors_WT 323_hESC-derived Telencephalic 323_hESC-derived Telencephalic 324 NGS8 324_hESC-derived LGE-like progenitors_WT 325_hESC-derived Telencephalic 325_hESC-derived Telencephalic 325_hESC-derived Telencephalic 326_NGS8 326_hESC derived LGE-like progenitors_WT 327_hESC derived LGE-like progenitors_WT 328_hESC derived LGE-like progenitors_WT 329_hESC derived LGE-like progenitors_WT 320_hESC derived LGE-like progenitors_WT	RC9 WT RC9 WT RC9 WT RC9 WT		L7 StemPro NO L7 StemPro NO L7 StemPro NO L7 StemPro NO	NA hESC-derived Telencephalic Rosette NA hESC-derived LGE-like progenitors NA hESC-derived Telencephalic Rosette	L7 NA _NSC L7 NA	DIV20 Neurodegenerative DIV10 Neurodegenerative DIV20 Neurodegenerative DIV10 Neurodegenerative	NA NA NA
326 NGS8 326_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT MM33 327_hESC-derived Telencephalic hESC-derived Telencephalic Rosette NSC WT MM28 328 NGS8 328_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT MM28 hESC-derived LGE-like progenitors WT MM28 329 NGS8 329_hESC-derived LGE-like progenitors_WT RHDUSC01 hESC-derived LGE-like progenitors WT MM28 330 NGS8 330_hESC-derived LGE-like progenitors_WT RHDUSC02	RC9 WT RC9 WT RC9 WT 1 RC9 WT 2 RC9 WT	NO P4 NO P4 NO NO NA	L7 StemPro NO L7 StemPro NO NO NO NO NO NO NO NO	NA hESC-derived Telencephalic Rosette NA hESC-derived LGE-like progenitors NA hESC-derived LGE-like progenitors	L7 NA _NSC L7 NA L7 NA L7 NA L7 NA	DIV20 Neurodegenerative DIV10 Neurodegenerative DIV20 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative	NA NA NA NA
hESC-derived LGE-like progenitors WT 331 NGS8 331_hESC-derived LGE-like progenitors_WT RHQQD01 hESC-derived LGE-like progenitors WT 332 NGS8 332_hESC-derived LGE-like progenitors_WT RHQQD02 333 NGS8 333_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT RH1 334 NGS8 334_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT RH2	1 RC9 WT 2 RC9 WT RC17 WT 2 RC9 WT	NO NA NO NA NO NA	A NA StemPro NO A NA StemPro NO A CellStart StemPro NO	NA hESC-derived LGE-like progenitors NA hESC-derived LGE-like progenitors NA hESC-derived LGE-like progenitors	L7 NA L7 NA CellStart NA CellStart NA	DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative DIV21 Neurodegenerative	NA NA NA
335 NGS8 335_hESC-derived Cortical Neuron_WT hESC-derived Cortical Neurons WT SG46 336 NGS8 336_hESC-derived Cortex progenitors_WT hESC-derived Cortex progenitors WT SG73 n2 337 NGS8 337_hESC-derived Cortex progenitors_WT hESC-derived Cortex progenitors WT SG73 n3 338 NGS8 338_hESC-derived Cortex progenitors_WT hESC-derived Cortex progenitors WT SG73 n1	1 i90cl17 WT 2 RC9 WT 3 RC9 WT 1 RC9 WT	NO P3 NO P3 NO P3 NO P3	CellStart StemPro NO StemPro NO StemPro NO StemPro NO	NA hESC-derived Cortical Neuron NA hESC-derived Cortex progenitors NA hESC-derived Cortex progenitors	PO-lam NA PO-lam NA PO-lam NA PO-lam NA	DIV46 Neurodegenerative DIV20 Neurodegenerative DIV20 Neurodegenerative DIV20 Neurodegenerative	NA NA NA
339 NGS8 339_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT MM38 340 NGS8 340_hESC-derived LGE-like progenitors_WT hESC-derived LGE-like progenitors WT MM39 Adult Human Brain total tissus clonetech 341 NGS8 341_Human Adult Brain total tissus_WT 636530 342 NGS8 342_Human Adult striatum tissus_WT Adult Human striatum tissus T15 343 NGS8 343_Human Adult Caudate tissus_WT Adult Human Caudate tissus T13	RC9 WT RC9 WT 1 NA WT 1 NA WT 1 NA WT	NO P4 NO P4 NO NA NO NA NO NA	A NA NA NO	NA Human Adult Brain total tissus NA Human Adult striatum tissus	L7 NA L7 NA NA NA NA NA NA NA NA	DIV20 Neurodegenerative DIV20 Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative	NA NA NA NA
344_Human Adult Brain cerebral cortex Adult Human Brain cerebral cortex tissus clonetech 636561 345_NGS8 345_Human Fœtal tissus_WT Fœtal Human tissus clonetech 636106 346_NGS8 346_Human Adult Cortex tissus_WT Adult Human Cortex tissus clonetech 636164 347_NGS8 347_Human Adult Caudate tissus_WT Adult Human Caudate tissus clonetech 636132 348_NGS8 348_Adult Human Whole Brain tissus_WT Adult Human Whole Brain tissus	1 NA WT	NO NA NO NA NO NA NO NA	A NA NA NO A NA NA NO	NA Human Adult Cortex tissus NA Human Adult Caudate tissus	NA NA NA NA	NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative NA Neurodegenerative	NA NA NA
136 NGS41 136_Fibroblasts_WT Fibroblasts lenti R77C mCherry Thsp 5 ÂμM n2 137 NGS41 137_Fibroblasts_WT Fibroblasts lenti R77C mCherry Thsp 5 ÂμM n3 Fibroblasts lenti R77C mCherry MG132 1 ÂμM 138 NGS41 138_Fibroblasts_WT n1 Fibroblasts lenti R77C mCherry MG132 1 ÂμM 139 NGS41 139_Fibroblasts_WT n2	2 NA WT 3 NA WT 1 NA WT 2 NA WT	Yes: lentiviral transduction α -SGmutated (R77C)-mCherry NAYes: lentiviral transduction α -SGmutated (R77C)-mCherry NAY	A NA NA NO A NA NA NO A NA NA NO A NA NA NO	NA Fibroblasts NA Fibroblasts	α-SGmutated (R77C) overexpression Collagen Thiostrepton 5 ÂμM - 24h α-SGmutated (R77C) overexpression Collagen Thiostrepton 5 ÂμM - 24h α-SGmutated (R77C) overexpression MG Collagen ÂμM - 24h α-SGmutated (R77C) overexpression MG Collagen ÂμM - 24h	NA LGMD NA LGMD 132 1 NA LGMD	NA NA GSE119841_GSM3384942 GSE119841_GSM3384943
Fibroblasts lenti R77C mCherry MG132 1 ÂμM 140 NGS41 140_Fibroblasts_WT n3 472_hiPSC-derived Myotube_WT_CRISPR 472 NGS54 MBNL1 hiPSC-derived Myotube_E3_56c2_n1 473_hiPSC-derived Myotube_WT_CRISPR 473 NGS54 MBNL1 hiPSC-derived Myotube_E3_56c2_n2 474_hiPSC-derived Myotube_WT_CRISPR 474 NGS54 MBNL1 hiPSC-derived Myotube_E3_56c2_n3 475_hiPSC-derived Myotube_WT_CRISPR	3 NA WT 1 56c02_CRISPR MBNL1 WT_CRISPR MBNL1 2 56c02_CRISPR MBNL1 WT_CRISPR MBNL1 3 56c02_CRISPR MBNL1 WT_CRISPR MBNL1	Yes: lentiviral transduction α-SGmutated (R77C)- mCherry Yes: CRISPR gene editing KO MBNL1 Yes: CRISPR gene editing KO MBNL1 NA Yes: CRISPR gene editing KO MBNL1	A NA NA NO	NA hiPSC-derived Myotube NA hiPSC-derived Myotube	α-SGmutated (R77C) overexpression MG Collagen ÂμM - 24h NA Yes: CRISPR gene editing KO MBNL1 NA Yes: CRISPR gene editing KO MBNL1 NA Yes: CRISPR gene editing KO MBNL1	NA LGMD NA Motoneurons NA Motoneurons NA Motoneurons	GSE119841_GSM3384944 NA NA
475 NGS54 MBNL1/2 hiPSC-derived Myotube_H4_56c2_n1 476_hiPSC-derived Myotube_WT_CRISPR 476 NGS54 MBNL1/2 hiPSC-derived Myotube_H4_56c2_n2 477_hiPSC-derived Myotube_WT_CRISPR 477 NGS54 MBNL1/2 hiPSC-derived Myotube_H4_56c2_n3 198 NGS6 198_hiPSC-derived RPE_HD hiPSC-derived RPE HD HD1 LV -DOX n2 hiPSC-derived RPE HD HD1 LV LV DOXi HTT,	1 56c02_CRISPR MBNL1/2 WT_CRISPR MBNL1/ 2 56c02_CRISPR MBNL1/2 WT_CRISPR MBNL1/ 3 56c02_CRISPR MBNL1/2 WT_CRISPR MBNL1/ 2 HD1 HD	Yes: CRISPR gene editing KO MBNL1/2 Yes: CRISPR gene editing KO MBNL1/2 Yes: lentiviral transduction Ctrl (ctrl for sample 199- >201 & 203->208 Yes: lentiviral transduction KO HTT	A NA NA NO 27 Cellstart StemPro NO	NA hiPSC-derived Myotube NA hiPSC-derived RPE	NA Yes: CRISPR gene editing KO MBNL1/2 Yes: CRISPR gene editing KO MBNL1/2 NA Yes: CRISPR gene editing KO MBNL1/2 NA Ientivirus Ctrl	NA Motoneurons NA Motoneurons NA Motoneurons DIV45 Neurodegenerative	NA NA NA
199 NGS6 199_hiPSC-derived RPE_HD sh4 n1 hiPSC-derived RPE HD HD1 LV LV DOXi HTT, sh4 n2 hiPSC-derived RPE HD HD1 LV LV DOXi HTT, sh4 n3 201 NGS6 201_hiPSC-derived RPE_HD sh4 n3 hiPSC-derived RPE HD HD1 LV LV DOX n3 hiPSC-derived RPE HD HD1 LV LV DOX n3 hiPSC-derived RPE HD HD1 LV LV DOX i HTT,	1 HD1 HD 2 HD1 HD 3 HD1 HD HD	Yes: lentiviral transduction KO HTT Yes: lentiviral transduction KO HTT Yes: lentiviral transduction Ctrl (ctrl for sample 199- >201 & 203->208 Yes: lentiviral transduction KO HTT	Cellstart StemPro NO Cellstart StemPro NO Cellstart StemPro NO Cellstart StemPro NO	NA hiPSC-derived RPE NA hiPSC-derived RPE NA hiPSC-derived RPE	NA KO HTT gene (lentivirus) NA KO HTT gene (lentivirus) NA KO HTT gene (lentivirus) NA lentivirus Ctrl	DIV45 Neurodegenerative DIV45 Neurodegenerative DIV45 Neurodegenerative DIV45 Neurodegenerative	NA NA NA
203 NGS6 203_hiPSC-derived RPE_HD sh5 n1 hiPSC-derived RPE HD HD1 LV LV DOXi HTT, 204 NGS6 204_hiPSC-derived RPE_HD sh5 n2 hiPSC-derived RPE HD HD1 LV LV DOXi HTT, 205 NGS6 205_hiPSC-derived RPE_HD sh5 n3 hiPSC-derived RPE HD HD1 LV LV DOXi HTT, 206 NGS6 206_hiPSC-derived RPE_HD sh6 n1 hiPSC-derived RPE HD HD1 LV LV DOXi HTT, 207 NGS6 207_hiPSC-derived RPE_HD sh6 n2	1 HD1 HD 2 HD1 HD 3 HD1 HD 1 HD1 HD 2 HD1 HD	Yes: lentiviral transduction KO HTT P2	Cellstart StemPro NO Cellstart StemPro NO Cellstart StemPro NO Cellstart StemPro NO	NA hiPSC-derived RPE NA hiPSC-derived RPE NA hiPSC-derived RPE	NA KO HTT gene (lentivirus)	DIV45 Neurodegenerative DIV45 Neurodegenerative DIV45 Neurodegenerative DIV45 Neurodegenerative DIV45 Neurodegenerative	NA NA NA
hiPSC-derived RPE HD HD1 LV LV DOXi HTT, sh6 n3 209 NGS6 209_hiPSC-derived RPE_HD hiPSC-derived RPE HD HD1 LV -DOX n1 396 NGS12 396_hESC-derived neural progenitor_WT hESC-derived neural progenitor day3 chir 0 mM 397 NGS12 397_hESC-derived neural progenitor_WT hESC-derived neural progenitor day3 chir 1 mM	3 HD1 HD 1 HD1 WT 1 SA001 WT	Yes: lentiviral transduction KO HTT Yes: lentiviral transduction Ctrl (ctrl for sample 199- >201 & 203->208 NO NO NA NO NA	27 Cellstart StemPro NO 27 Cellstart StemPro NO	NA hiPSC-derived RPE NA hiPSC-derived RPE NA hESC-derived neural progenitor	NA KO HTT gene (lentivirus) NA lentivirus Ctrl NA NA NA	DIV45 Neurodegenerative DIV45 Neurodegenerative DIV3 Motoneurons DIV3 Motoneurons	NA NA NA
398 NGS12 398_hESC-derived neural progenitor_WT hESC-derived neural progenitor day3 chir 3 mM 399 NGS12 399_hESC-derived neural progenitor_WT hESC-derived neural progenitor day4 chir 0 mM 400 NGS12 400_hESC-derived neural progenitor_WT hESC-derived neural progenitor day4 chir 3 mM 401 NGS12 401_hESC-derived neural progenitor_WT hESC-derived neural progenitor day4 chir 1 mM	1 SA001 WT 1 SA001 WT 1 SA001 WT 1 SA001 WT	NO NA NO NA NO NA NO NA	A NA NA NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor	NA NA NA NA NA	DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons	NA NA NA
402 NGS12 402_hESC-derived neural progenitor_WT hESC-derived neural progenitor day7 chir 3 mM hESC-derived neural progenitor day14 - chir 3 mM RA 100 day2 hESC-derived neural progenitor day14 - chir 3 mM RA 100 day4 hESC-derived neural progenitor_WT 3 mM RA 100 day4 hESC-derived neural progenitor day14 - chir 405 NGS12 405_hESC-derived neural progenitor_WT 3 mM RA 100 day7 hESC-derived neural progenitor WT SA001 EB	1 SA001 WT 1 SA001 WT 1 SA001 WT 1 SA001 WT	NO NA NO NA NO NA NO NA	A NA NA NO A NA NA NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor NA hESC-derived neural progenitor	NA NA NA NA NA NA NA NA	DIV14 Motoneurons DIV14 Motoneurons DIV14 Motoneurons DIV14 Motoneurons	NA NA NA
406 NGS29 406_hESC-derived neural progenitor_WT days 2 n1 hESC-derived neural progenitor WT SA001 EB 407 NGS29 407_hESC-derived neural progenitor_WT days 3 n1 hESC-derived neural progenitor WT SA001 EB 408 NGS29 408_hESC-derived neural progenitor_WT days 4 n1 409 NGS29 409_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T1 n1 410 NGS29 410_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T2 n1	1 SA001 WT 1 SA001 WT 1 SA001 WT 1 SA001 WT	NO P5 NO P5 NO P5 NO P5 NO P5	Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor NA hESC-derived neural progenitor	en suspension NA	DIV2 Motoneurons DIV3 Motoneurons DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons	NA NA NA NA
411 NGS29 411_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T3 n1 hESC WT SA001 n1 413 NGS29 413_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T4 n1 hESC-derived neural progenitor WT SA001 EB 414 NGS29 414_hESC-derived neural progenitor_WT days 2 n2 hESC-derived neural progenitor WT SA001 EB	1 SA001 WT 1 SA001 WT 1 SA001 WT 2 SA001 WT	NO P5	Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor	en suspension NA en suspension NA en suspension NA en suspension NA	DIV4 Motoneurons NA Motoneurons DIV4 Motoneurons DIV2 Motoneurons	NA NA NA
415 NGS29 415_hESC-derived neural progenitor_WT days 3 n2 hESC-derived neural progenitor WT SA001 EB 416 NGS29 416_hESC-derived neural progenitor_WT days 4 n2 417 NGS29 417_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T1 n2 418 NGS29 418_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T2 n2 419 NGS29 419_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T3 n2	2 SA001 WT	NO P5 NO P5 NO P5 NO P5 NO P5	Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor NA hESC-derived neural progenitor	en suspension NA	DIV3 Motoneurons DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons	NA NA NA NA
420 NGS29 420_hESC_WT hESC WT SA001 n2 421 NGS29 421_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T4 n2 hESC-derived neural progenitor WT SA001 EB 422 NGS29 422_hESC-derived neural progenitor_WT days 2 n3 hESC-derived neural progenitor WT SA001 EB 423 NGS29 423_hESC-derived neural progenitor_WT days 3 n3 hESC-derived neural progenitor WT SA001 EB	2 SA001 WT 2 SA001 WT 3 SA001 WT WT	NO P5 NO P5 NO P5 NO P5	Matrigel mTeSR NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor NA hESC-derived neural progenitor	en suspension NA en suspension NA en suspension NA en suspension NA	NA Motoneurons DIV4 Motoneurons DIV2 Motoneurons DIV3 Motoneurons	NA NA NA
424 NGS29 424_hESC-derived neural progenitor_WT days 4 n3 425 NGS29 425_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T1 n3 426 NGS29 426_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T2 n3 427 NGS29 427_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T3 n3 428 NGS29 428_hESC_WT hESC-WT hESC-WT SA001 n3	3 SA001 WT	NO P5 NO P5 NO P5 NO P5 NO P5 NO P5	Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO Matrigel mTeSR NO	NA hESC-derived neural progenitor NA hESC-derived neural progenitor NA hESC-derived neural progenitor	en suspension NA	DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons DIV4 Motoneurons NA Motoneurons Motoneurons	NA NA NA NA
429 NGS29 429_hESC-derived neural progenitor_WT hESC-derived neural progenitor WT SA001 T4 n3 430 NGS26 430_hiPSC-derived Motoneuron_WT hiPSC-derived Motoneurons WT 1427 day1 hiPSC-derived Motoneurons WT VUB01 day1 431 NGS26 431_hiPSC-derived Motoneuron_WT NGS26 432 NGS26 432_hiPSC-derived Motoneuron_WT hiPSC-derived Motoneurons WT 14-5 day1	3 SA001 WT 1 14-27 WT 1 VUB01 WT 1 14-May WT	NO P5 NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	en suspension NA	DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons	NA NA NA
433 NGS26 433_hiPSC-derived Motoneuron_SMA hiPSC-derived Motoneurons SMA 232-7 day1 hiPSC-derived Motoneurons SMA 13-2 day1 434 NGS26 434_hiPSC-derived Motoneuron_SMA NGS26 435 NGS26 435_hiPSC-derived Motoneuron_SMA hiPSC-derived Motoneurons SMA 13-1 day1 hiPSC-derived Motoneurons WT VUB01 day1 436 NGS33 436_hiPSC-derived Motoneuron_WT NGS33 hiPSC-derived Motoneurons SMA 13-2 day1 437 NGS33 437_hiPSC-derived Motoneuron_SMA NGS33	1 232-7 SMA 1 13-Feb SMA 1 13-Jan SMA 1 VUB01 WT 1 13-Feb SMA	NO NA NO NA NO NA NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	NA	DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons	NA NA NA
438 NGS33 438_hiPSC-derived Motoneuron_SMA hiPSC-derived Motoneurons SMA 13-11 day1 439 NGS33 439_hiPSC-derived Motoneuron_WT hiPSC-derived Motoneurons WT 232-11 day1 440 NGS33 440_hiPSC-derived Motoneuron_WT hiPSC-derived Motoneurons WT VUB01 day10 441 NGS33 441_hiPSC-derived Motoneuron_SMA hiPSC-derived Motoneurons SMA 13-2 day10	1 13-Nov SMA 1 232-1114-27 WT 1 VUB01 WT 1 13-Feb SMA	NO NA NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	NA NA NA NA NA NA NA	DIV1 Motoneurons DIV1 Motoneurons DIV10 Motoneurons DIV10 Motoneurons	NA NA NA
442 NGS33 442_hiPSC-derived Motoneuron_SMA hiPSC-derived Motoneurons SMA 13-11 day10 443 NGS33 443_hiPSC-derived Motoneuron_WT hiPSC-derived Motoneurons WT 232-11 day10 hiPSC-derived Motoneurons WT VUB01 day10 444 NGS33 444_hiPSC-derived Motoneuron_WT KEN hiPSC-derived Motoneurons SMA 13-2 day10 445 NGS33 445_hiPSC-derived Motoneuron_SMA KEN hiPSC-derived Motoneurons SMA 13-11 day10	1 13-Nov SMA 1 232-11 14-27 WT 1 VUB01 WT 1 13-Feb SMA	NO NA NO NA NO NA	A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron	NA NA NA NA NA Kenpaulone – 10 microM NA Kenpaulone – 10 microM	DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons	NA NA NA
446 NGS33 446_hiPSC-derived Motoneuron_SMA KEN hiPSC-derived Motoneurons WT 232-11 day10 447 NGS33 447_hiPSC-derived Motoneuron_WT KEN 448 NGS43 448_hiPSC-derived Motoneuron_WT hiPSC-derived motoneurons WT 14,5 day1 449 NGS43 449_hiPSC-derived Motoneuron_WT hiPSC-derived motoneurons WT 14-27 day1	1 13-Nov SMA 1 232-11 14-27 WT 1 14-May WT 1 14-27 WT	NO NA NO NA NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	NA Kenpaulone – 10 microM NA Kenpaulone – 10 microM NA NA NA NA	DIV10 Motoneurons DIV10 Motoneurons DIV1 Motoneurons DIV1 Motoneurons	NA NA NA
450 NGS43 450_hiPSC-derived Motoneuron_WT hiPSC-derived motoneurons WT 56c02 day1 451 NGS43 451_hiPSC-derived Motoneuron_SMA hiPSC-derived motoneurons SMA 13,1 day1 452 NGS43 452_hiPSC-derived Motoneuron_SMA hiPSC-derived motoneurons SMA 13,11 day1 453 NGS43 453_hiPSC-derived Motoneuron_SMA hiPSC-derived motoneurons SMA 232,11 day1 454 NGS43 454_hiPSC-derived Motoneuron_WT hiPSC-derived motoneurons WT 14-5 day10	1 56c02 WT 1 13-Jan SMA 1 13-Nov SMA 1 232-11 SMA 1 14-May WT	NO NA NO NA NO NA NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	NA	DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons DIV1 Motoneurons	NA NA NA NA
455 NGS43 455_hiPSC-derived Motoneuron_WT hiPSC-derived motoneurons WT 14,27 day10 456 NGS43 456_hiPSC-derived Motoneuron_WT hiPSC-derived motoneurons WT 56c02 day10 457 NGS43 457_hiPSC-derived Motoneuron_SMA hiPSC-derived motoneurons SMA 13,1 day10 458 NGS43 458_hiPSC-derived Motoneuron_SMA hiPSC-derived motoneurons SMA 13,11 day10	1 14-27 WT 1 56c02 WT 1 13-Jan SMA 1 13-Nov SMA	NO NA NO NA NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	NA NA NA NA NA NA NA NA	DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons	NA NA NA
459 NGS43 459_hiPSC-derived Motoneuron_SMA hiPSC-derived motoneurons SMA 232,11 day10 hiPSC-derived motoneurons WT 14-5 day10 460 NGS43 460_hiPSC-derived Motoneuron_WT KEN hiPSC-derived motoneurons WT 14-27 day10 461 NGS43 461_hiPSC-derived Motoneuron_WT KEN hiPSC-derived motoneurons WT 56c02 day10 462 NGS43 462_hiPSC-derived Motoneuron_WT KEN hiPSC-derived motoneurons SMA 13-1 day10	1 232-11 SMA 1 14-May WT 1 14-27 WT 1 56c02 WT	NO NA NO NA NO NA NO NA	A Matrigel iPS brew NO A Matrigel iPS brew NO A Matrigel iPS brew NO	NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron NA hiPSC-derived Motoneuron	NA NA Kenpaulone – 10 microM NA Kenpaulone – 10 microM NA Kenpaulone – 10 microM	DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons	NA NA NA
463 NGS43 463_hiPSC-derived Motoneuron_SMA KEN hiPSC-derived motoneurons SMA 13-11 day10 464 NGS43 464_hiPSC-derived Motoneuron_SMA KEN hiPSC-derived motoneurons SMA 232-11 day10 465 NGS43 465_hiPSC-derived Motoneuron_SMA KEN 466 NGS54 466_hiPSC-derived Myotube_DM1 hiPSC-derived Myotube DM1 61c7_n1 467 NGS54 467_hiPSC-derived Myotube_DM1 hiPSC-derived Myotube DM1 61c7_n2 468 NGS54 468_hiPSC-derived Myotube_DM1 hiPSC-derived Myotube DM1 61c7_n3 469 NGS54 469_hiPSC-derived Myotube_WT hiPSC-derived Myotube WT_56c2_n1	1 13-Jan SMA 1 13-Nov SMA 1 232-11 SMA 1 61c7 DM1 2 61c7 DM1 3 61c7 DM1 1 56c02 WT	NO NA NO NA NO NA NO NA NO NO	A Matrigel iPS brew NO A Matrigel iPS brew NO A NA NA NO A NA NA NO A NA NA NO	NA hiPSC-derived Motoneuron	NA Kenpaulone – 10 microM NA Kenpaulone – 10 microM NA Kenpaulone – 10 microM NA NA NA NA NA NA NA NA NA	DIV10 Motoneurons DIV10 Motoneurons DIV10 Motoneurons NA Motoneurons	NA NA NA NA NA NA NA
470 NGS54 470_hiPSC-derived Myotube_WT hiPSC-derived Myotube WT_56c2_n2 471 NGS54 471_hiPSC-derived Myotube_WT hiPSC-derived Myotube WT_56c2_n3 hiPSC-derived striatal neurons HD Delta60 210 NGS7 210_hiPSC-derived striatal neurons_HD days43 LV HTT, sh4 n1 hiPSC-derived striatal neurons HD Delta60 211 NGS7 211_hiPSC-derived striatal neurons_HD days43 LV HTT, sh4 n2 hiPSC-derived striatal neurons HD Delta60 212 NGS7 212_hiPSC-derived striatal neurons_HD days43 LV HTT, sh4 n3	1 56c02 WT 2 56c02 WT 3 56c02 WT 1 delta60 HD 2 delta60 HD 3 delta60 HD	NO ctrl line for sample 472->476 Yes: lentiviral transduction KO HTT Yes: lentiviral transduction KO HTT Yes: lentiviral transduction KO HTT P5	A NA NA NO NO NO NO NO StemPro NO	NA hiPSC-derived Myotube NA hiPSC-derived Myotube NA hiPSC-derived striatal neurons NA hiPSC-derived striatal neurons	NA NA NA NA NA NA NA PO-lam KO HTT gene (lentivirus) PO-lam KO HTT gene (lentivirus) PO-lam KO HTT gene (lentivirus)	NA Motoneurons NA Motoneurons NA Motoneurons DIV43 Neurodegenerative DIV43 Neurodegenerative DIV43 Neurodegenerative	NA NA NA NA NA
hiPSC-derived striatal neurons HD Delta60 213 NGS7 213_hiPSC-derived striatal neurons_HD days43 LV HTT, sh5 n1 hiPSC-derived striatal neurons HD Delta60 214 NGS7 214_hiPSC-derived striatal neurons_HD days43 LV HTT, sh5 n2 hiPSC-derived striatal neurons HD Delta60 215 NGS7 215_hiPSC-derived striatal neurons_HD days43 LV HTT, sh5 n3 478 NGS55 478_hiPSC-derived Keratinocyte_WT hiPSC-derived Keratinocyte WT_PC085 479_NGS55 479_hiPSC-derived Keratinocyte_WT hiPSC-derived Keratinocyte WT_PC1432	1 delta60 HD 2 delta60 HD 3 delta60 HD 1 PC085 WT 2 PC1432 WT	Yes: lentiviral transduction KO HTT Yes: lentiviral transduction KO HTT P5 Yes: lentiviral transduction KO HTT NO NO NO NA	54 L7 StemPro NO 54 L7 StemPro NO A NA NA NO A NA NA	NA hiPSC-derived striatal neurons NA hiPSC-derived striatal neurons NA hiPSC-derived Keratinocyte NA hiPSC-derived Keratinocyte	PO-lam KO HTT gene (lentivirus) PO-lam KO HTT gene (lentivirus) PO-lam KO HTT gene (lentivirus) NA NA NA	DIV43 Neurodegenerative DIV43 Neurodegenerative DIV43 Neurodegenerative NA Genodermatose NA Genodermatose	NA NA NA NA
480 NGS55 480_hiPSC-derived Keratinocyte_WT 481 NGS55 481_hiPSC-derived Keratinocyte_EB 482 NGS55 482_hiPSC-derived Keratinocyte_EB 483 NGS55 483_hiPSC-derived Keratinocyte_EB 484 NGS55 483_hiPSC-derived Keratinocyte_EB 485 hiPSC-derived Keratinocyte_EB 486 hiPSC-derived Keratinocyte_EB 487 NGS55 483_hiPSC-derived Keratinocyte_EB 488 NGS55 483_hiPSC-derived Keratinocyte_EB 489 hiPSC-derived Keratinocyte_EB3_NAMAD 480 NGSD3 600_metaSample hiPSC median_WT 481 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 482 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 483 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 484 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 485 MiPSC-derived Keratinocyte_EB3_NAMAD 486 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 487 MetaSample hiPSC WT median 488 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 489 NGS55 MiPSC-derived Keratinocyte_EB3_NAMAD 480 NGS55 Mi	3 PC15 WT 1 9991 EB 2 10295 EB 3 NAMAD EB 21 metaSample WT 24 metaSample WT	NO NA NA	A NA NA NO A NA NA NO A NA NA NO	NA hiPSC-derived Keratinocyte NA hiPSC-derived Keratinocyte NA hiPSC-derived Keratinocyte NA hiPSC-derived Keratinocyte NA metaSample hiPSC median	NA	NA Genodermatose NA Genodermatose NA Genodermatose NA Genodermatose NA NGS plateform NA NGS Plateform	NA NA NA NA

