**Lab Resource: Single Cell Line – supplementary file**

**Title:** Generation of an induced pluripotent stem cell line from a Huntington’s Disease patient with a long HTT-PolyQ sequence

**Authors:**

Duncan C. Miller1,2, Pawel Lisowski3,4,5, Carolin Genehr1, Erich E. Wanker1, Josef Priller5,6, Alessandro Prigione1,7\*, Sebastian Diecke1,2\*

**Affiliations:**

1Max Delbrück Center for Molecular Medicine (MDC), Berlin, Germany

2DZHK (German Centre for Cardiovascular Research), partner site Berlin, Berlin, Germany

3Berlin Institute for Medical Systems Biology (BIMSB), Max Delbrück Center for Molecular Medicine (MDC), Berlin, Germany

4Institute of Genetics and Animal Biotechnology, Polish Academy of Sciences, Magdalenka n/ Warsaw, Poland

5Department of Psychiatry and Neurosciences, Charité − Universitätsmedizin, Berlin, Germany

6University of Edinburgh and UK DRI, Edinburgh, UK

7Department of General Pediatrics, Neonatology and Pediatric Cardiology, Medical Faculty, Heinrich Heine University, Düsseldorf, Germany

\* Corresponding authors

**Supplementary figure S1**

1. Summary of CNVs from SNP microarray karyotyping. Threshold for automatic reporting by KaryoStudio software was >4.5x104, however further manual assessment in case of false positives is recommended, especially in cases of loss of heterozygosity. Red highlighed values are over 3.0x105 cut-off.

Value 1 = heterozygous loss, 2 = loss of heterozygosity, 3 = heterozygous gain.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Index | Chr | Start | Stop | Length | Value | Conf | CNV Index | Cytobands | # Markers | Genes |
| 334 | 3 | 4943652 | 5026898 | 83246 | 1 | 52.03315 | 0 | p26.2 | 34 | BHLHE40; |
| 336 | 4 | 133671899 | 134065224 | 393325 | 3 | 143.2203 | 2 | q28.3 | 56 |  |
| 337 | 4 | 134074058 | 134553039 | 478981 | 3 | 407.4032 | 3 | q28.3 | 80 | PCDH10; |
| 338 | 7 | 15852195 | 16076502 | 224307 | 1 | 244.5385 | 4 | p21.1 | 79 |  |
| 339 | 10 | 68423358 | 68764791 | 341433 | 1 | 303.4593 | 5 | q21.3 | 132 | CTNNA3; LRRTM3; |
| 341 | 15 | 24521050 | 24649604 | 128554 | 1 | 50.28538 | 7 | q12 | 13 | GABRB3; |
| 342 | 22 | 33482112 | 33697034 | 214922 | 3 | 285.471 | 8 | q12.3 | 64 |  |
| 343 | X | 2700157 | 3265143 | 564986 | 2 | 357.5465 | 9 | p22.33 | 246 | XG; XGPY2; GYG2; ARSD; ARSD; ARSE; ARSH; ARSF; MXRA5; |
| 344 | X | 114788545 | 114890055 | 101510 | 2 | 51.88255 | 10 | q23 | 22 | PLS3; PLS3; |

1. Clearance of sendai virus in BIHi035-A analysed by reverse transcription PCR (RT-PCR). Absence of sendai viral genome (SeV) and transcript derived from the three separate viruses was confirmed by agarose gel electrophoresis. The positive control was an unrelated transduced fibroblast/hiPSC sample taken at very early passage (p2), and 18S was used as housekeeping gene.



Primer

1. SeV

2. cMyc

3. KOS

4. Klf4

5. Hu18SRNA

1. Mycoplasma contamination tested by the qPCR-based Venor*®*GeM qOneStep Kit:

|  |  |  |
| --- | --- | --- |
| **Mycoplasma****520 nm** | **Internal amplification control****560 nm** | **Interpretation** |
| Ct<40 | Irrelevant | Sample is Mycoplasma contaminated |
| Ct≥40 | Ct≥40 | qPCR inhibition |
| Ct≥40 | Ct<40 | Sample is Mycoplasma free |

*Results*

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample** | **Ct** **of Mycoplasma DNA**  | **Ct of Internal amplification DNA**  | **Result** |
| 1 (neg. control) | >45 | 28,9 | Passed |
| 2 (pos. control) | 25,4 | 25,2 | Passed |
| 3 | >45 | 25,6 | **Negative** |