**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

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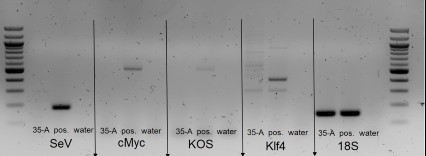
**Supplementary figure S1**

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** |