



# Certificate of analysis

SFC271-03-06

Operator: Alison McBride

Date: 11/01/2016

Supervisor: Zam Cader

Date: 01/11/2016

Signature:

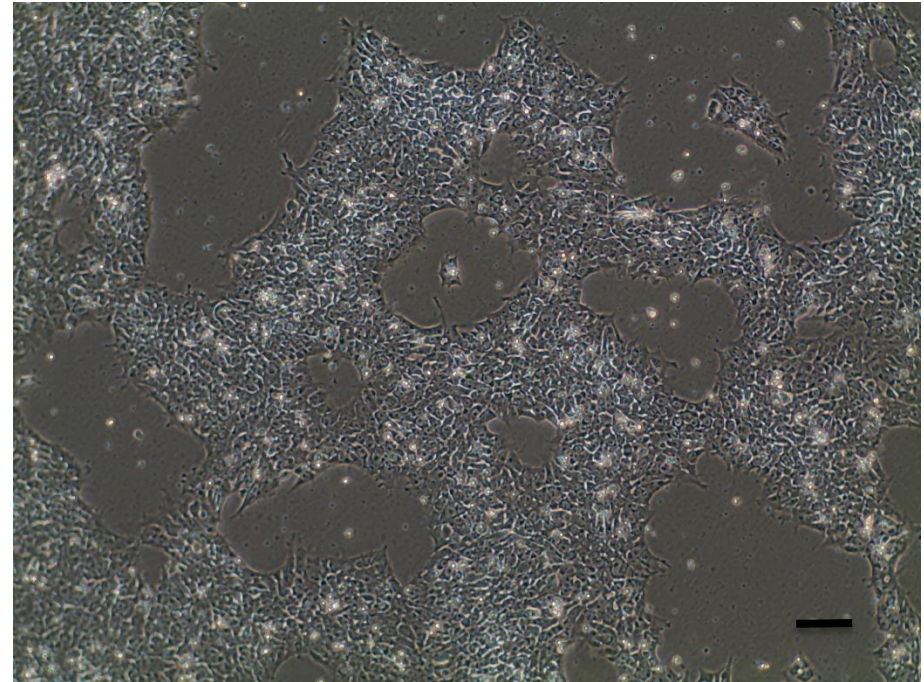
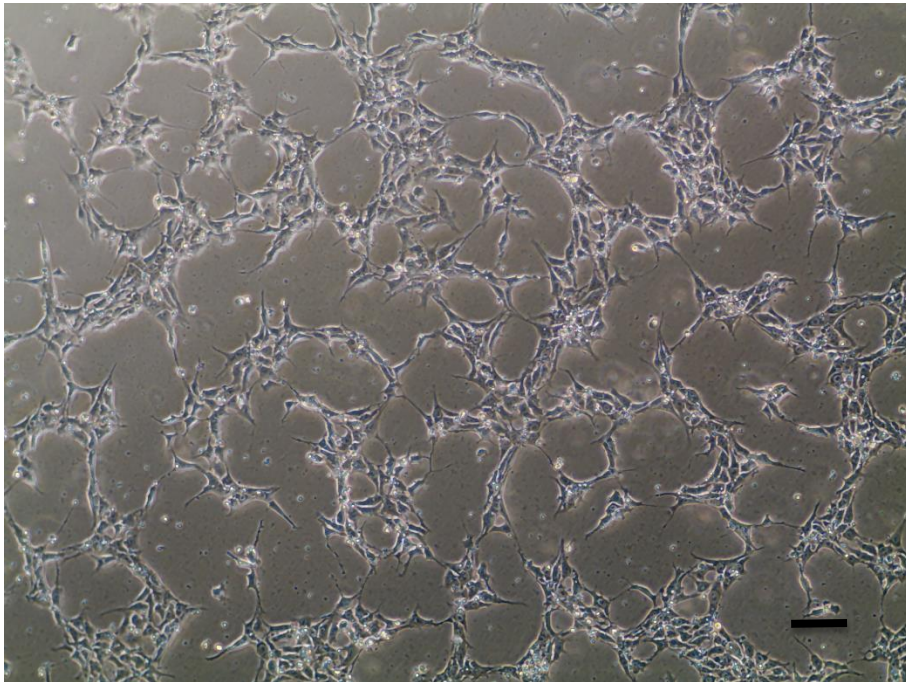
A handwritten signature in blue ink that reads "Zam Cader". The signature is written in a cursive, flowing style.

# Source of fibroblasts and reprogramming information

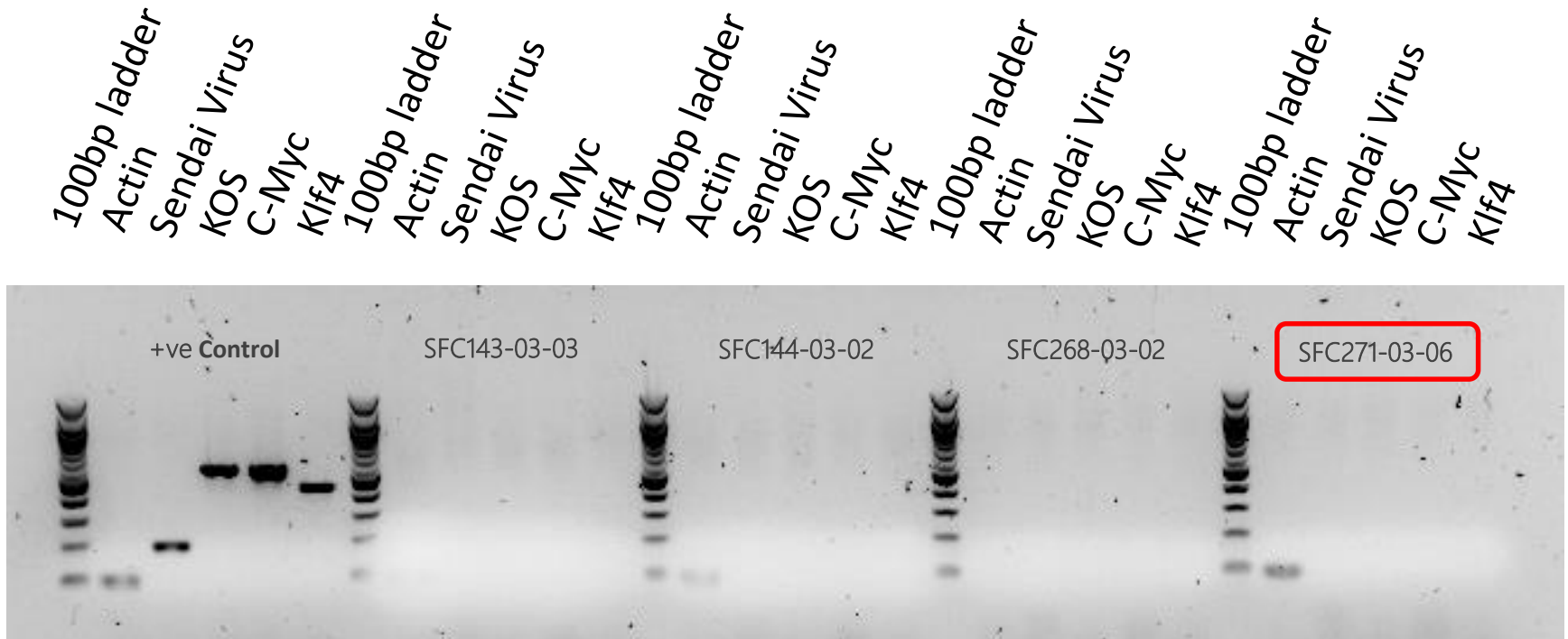
- SF271 from Glostrup Hospital, Denmark  
18/05/2015
- Reprogrammed at UOXF Z
- Reprogrammed on 20/08/2015 at passage 4
- Cytotune v2 WP3 SOP10

# Viability post-thaw and Morphology according to SOP19 passage 16

- Cell count immediately post-thaw  $1.94 \times 10^6$
- Viability immediately post-thaw 92%
- Photo at 24h and low density day 4 post-thaw (scale bar =  $100\mu\text{m}$ ):



# Sendai clearance: according to WP3 SOP15 undetectable at passage 16



Product sizes: Actin 92bp; SeV 181bp; SeV KOS 528bp; SeV-Myc 532bp; SeV-Klf 410bp;

# Mycoplasma Test:

## According to MycoAlert Lonza LT07-318 undetectable at passage 16

| Sample       | Passage Number | Initials | Reading 1 | Reading 2 | Ratio/Status |
|--------------|----------------|----------|-----------|-----------|--------------|
| + ve control |                |          | 46        | 1691      | 36.76        |
| - ve control |                |          | 61        | 16        | 0.26         |
| SFC271-03-06 | p16            | AM       | 34        | 15        | 0.44         |

Results:

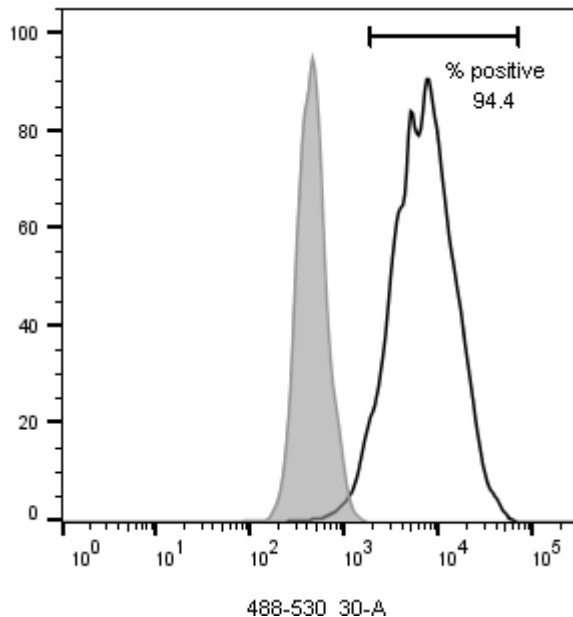
Ratio **0 - 0.999** negative for mycoplasma

Ratio **1 – 1.3** Borderline Result (retest required)

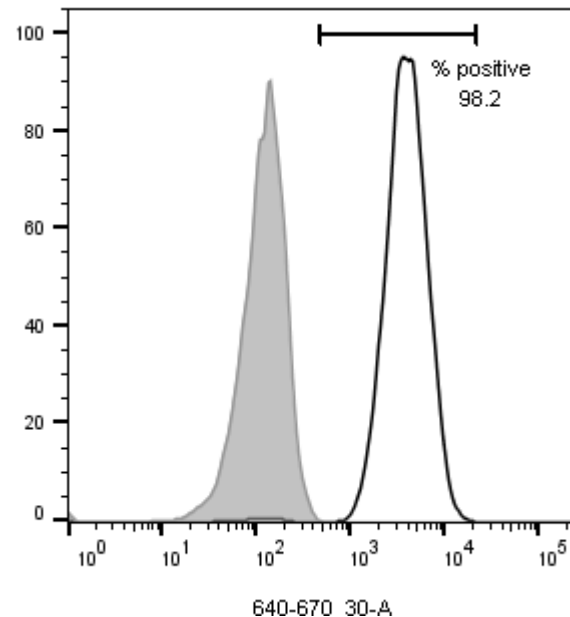
Ratio above **1.3** positive for mycoplasma

# Flow cytometric analysis according to WP3 SOP 20 and 21 passage 16

Tra-1-60:



NANOG:



# SNP analysis

according to WP3 SOP Preparation of DNA and RNA samples for Illumina arrays

- Passage 16
- Identity to parent fibroblasts confirmed
- **Karyotype abnormalities:** Approx. 3Mbp patient-related region detected on Chromosome 6; position 26194113-29272012 and 26231608-29323259 for Fibroblasts and iPSCs respectively.
- For details and raw data see StemDB