



S I R W I L L I A M  
**DUNN SCHOOL**  
O F P A T H O L O G Y

# Certificate of analysis

DRICUi026-A

Operator: SH Ellwood Date: 19/06/2023

Supervisor: SA Cowley Date: 19/06/2023

Signature: *SA Cowley*

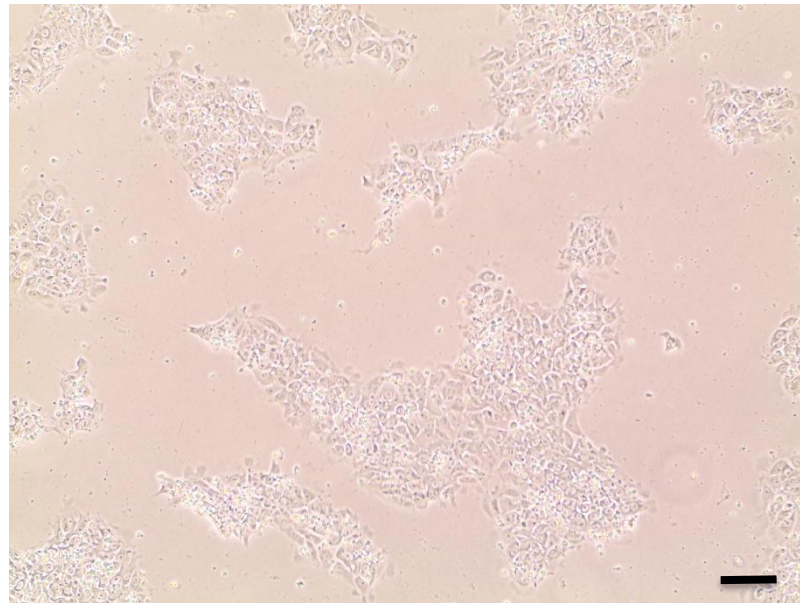
# Source of cells and reprogramming information

- ADCAR24745UC T cells from Cardiff 10/05/2022
- Reprogrammed at UOXF AKA IPMAR28
- Reprogrammed on 06/2022 SC/SE
- Reprogramming system Cytotune v2
- Clone DRICUi026-A = IPMAR28A6
- Banked at p13 06/2023 SE

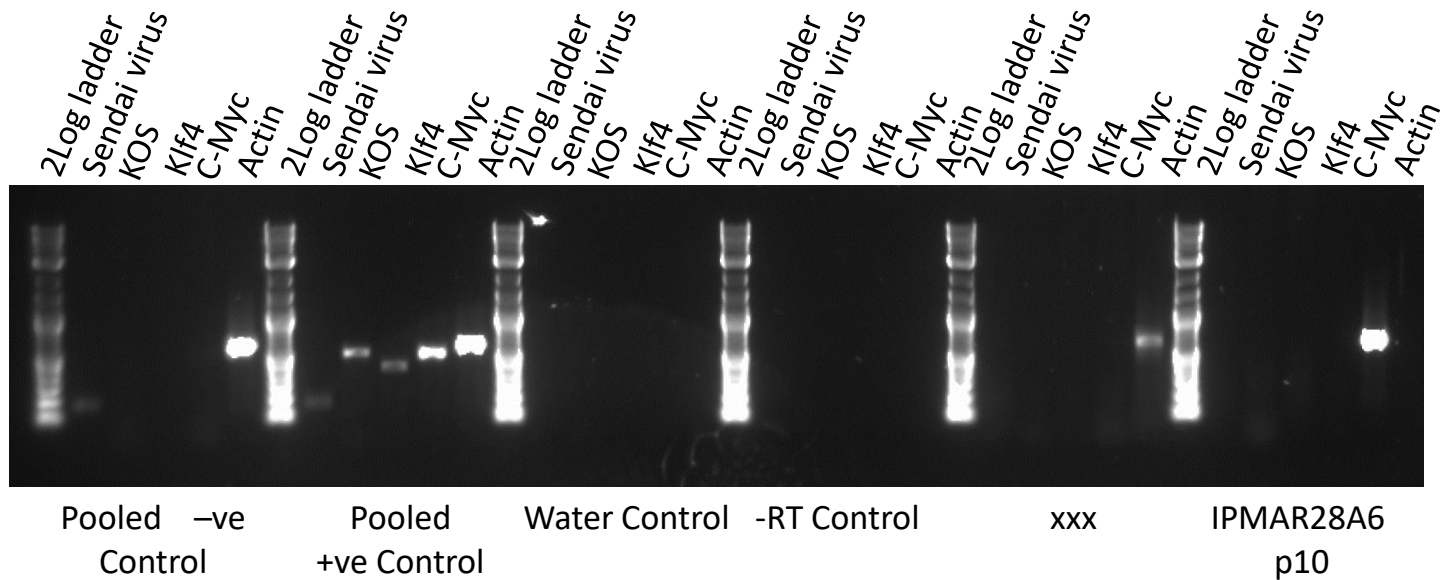
# Viability post-thaw and Morphology according to JMSCFSOP19 passage 13

- Vial cell count immediately post-thaw  $2.32 \times 10^6$
- Viability immediately post-thaw 61%
- Photo at day 3 post-thaw (scale bar =  $100\mu\text{m}$ ):

Day 3 post-thaw, 20% plated to 1w.6wp



# Sendai Cytotune 2 clearance: according to Cytotune manual Virus undetectable at passage 10



Product sizes: SeV 181bp; KOS 528bp; SeV-Klf 410bp; SeV-Myc 532bp; Actin 623bp

# Sterility:

Mycoplasma Test: According to MycoAlert Lonza LT07-318 undetectable at passage 14.

Visual inspection of thawed cells cultured without antibiotic/antimycotic for 4 days:  
no evidence of bacteria, yeast or fungus.

| Sample      | Clone                 | Passage number | Initial | Reading 1 | Reading 2 | Ratio/Status  |
|-------------|-----------------------|----------------|---------|-----------|-----------|---------------|
| +ve control |                       |                |         | 0.888     | 114.2     | <b>128.60</b> |
| -ve control |                       |                |         | 3.476     | 0.816     | <b>0.23</b>   |
|             | IPMAR28A6 DRICUi026-A | p14            | SE      | 1.818     | 1.12      | <b>0.62</b>   |

Results mean:

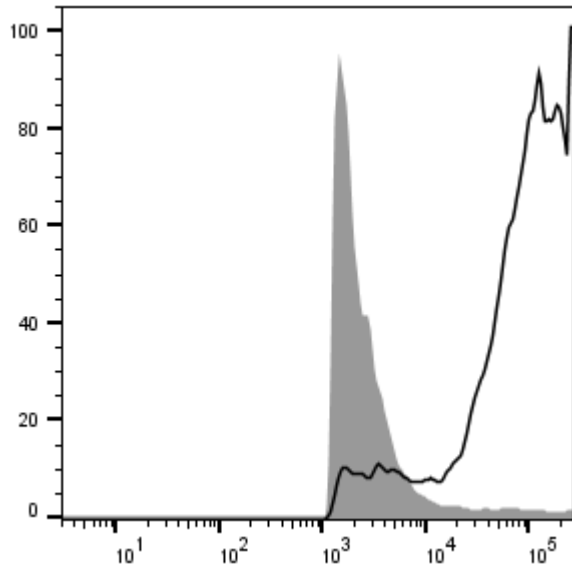
Ratio **0 - 0.999** negative for mycoplasma

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

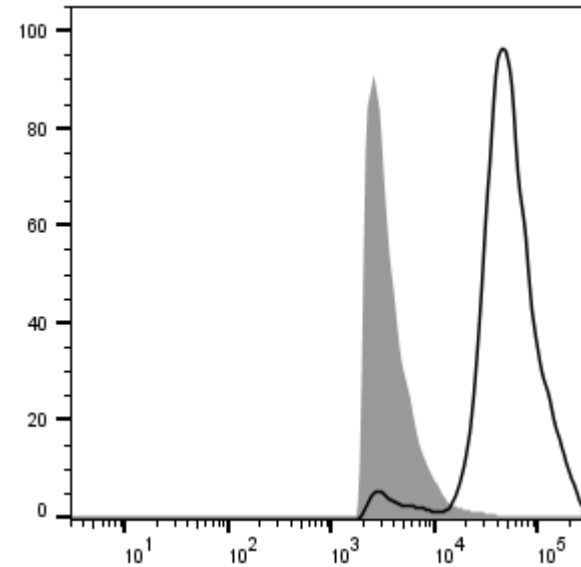
Ratio above **1.3** positive for mycoplasma

# Flow cytometric analysis according to JMSCFSOP05 passage 14

DRICUi026 Tra-1-60 88.8%



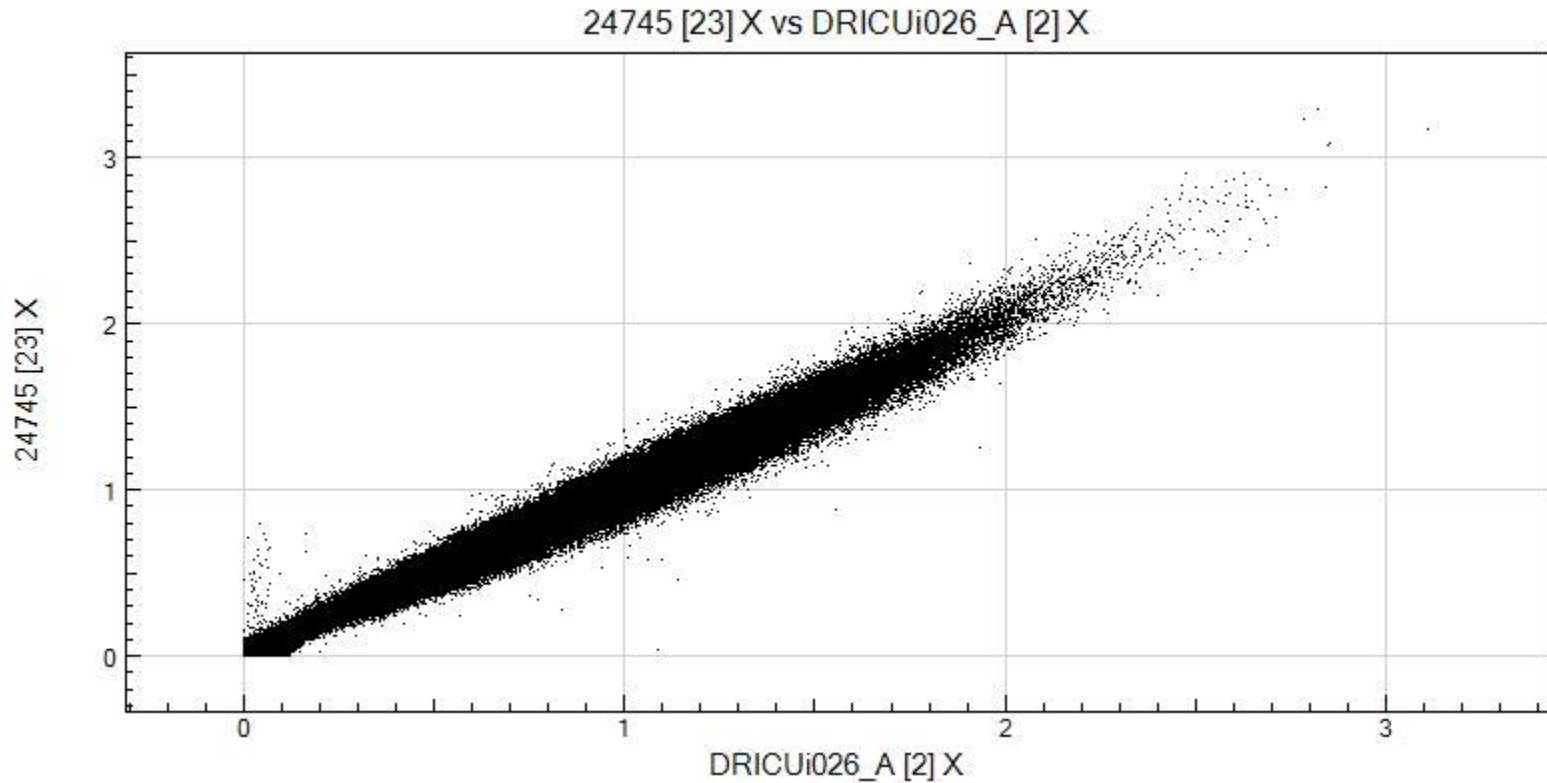
DRICUi026 Nanog 78.2%



# Illumina GSA SNP analysis according to JMSCFSOP16

- Passage 13
- Identity to parent PBMC confirmed
- Karyotype abnormalities:
  - No gross abnormalities detected vs PBMC

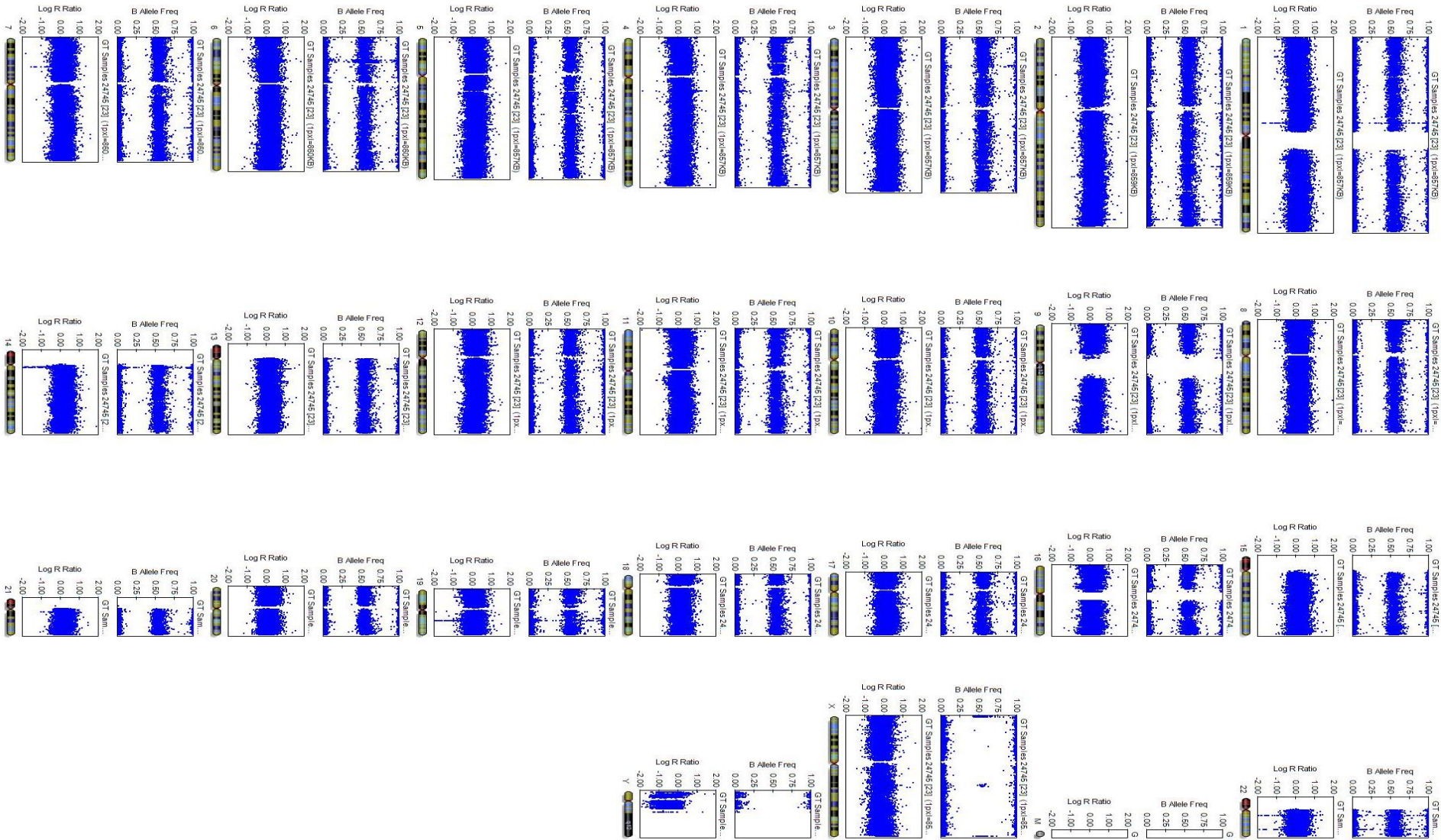
# Alignment of ADCAR24745UC PBMC SNPs with DRICUi026-A



Regression  
Coefficient  
 $R^2 = 0.9909$



# Karyogram ADCAR24745UC PBMC



# Karyogram DRICUi026-A

