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Supplemental Information

Type 1 Interferon Responses Underlie

Tumor-Selective Replication of Oncolytic

Measles Virus

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Supplemental Figures:

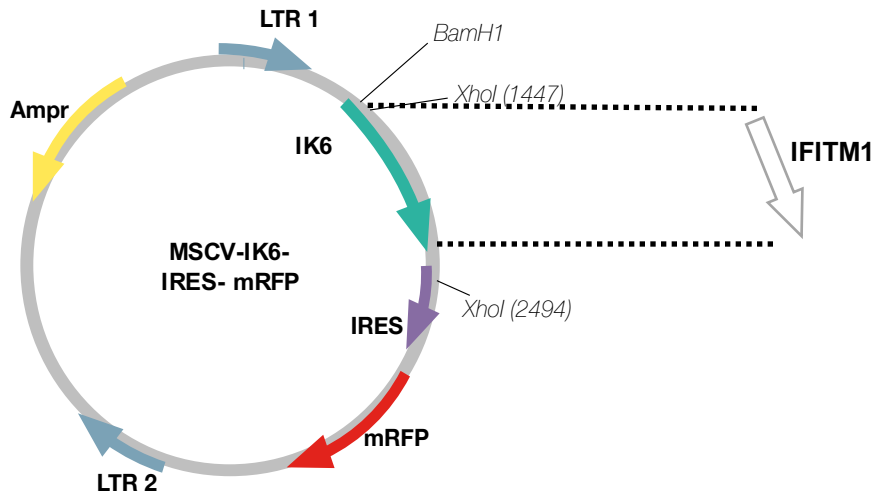
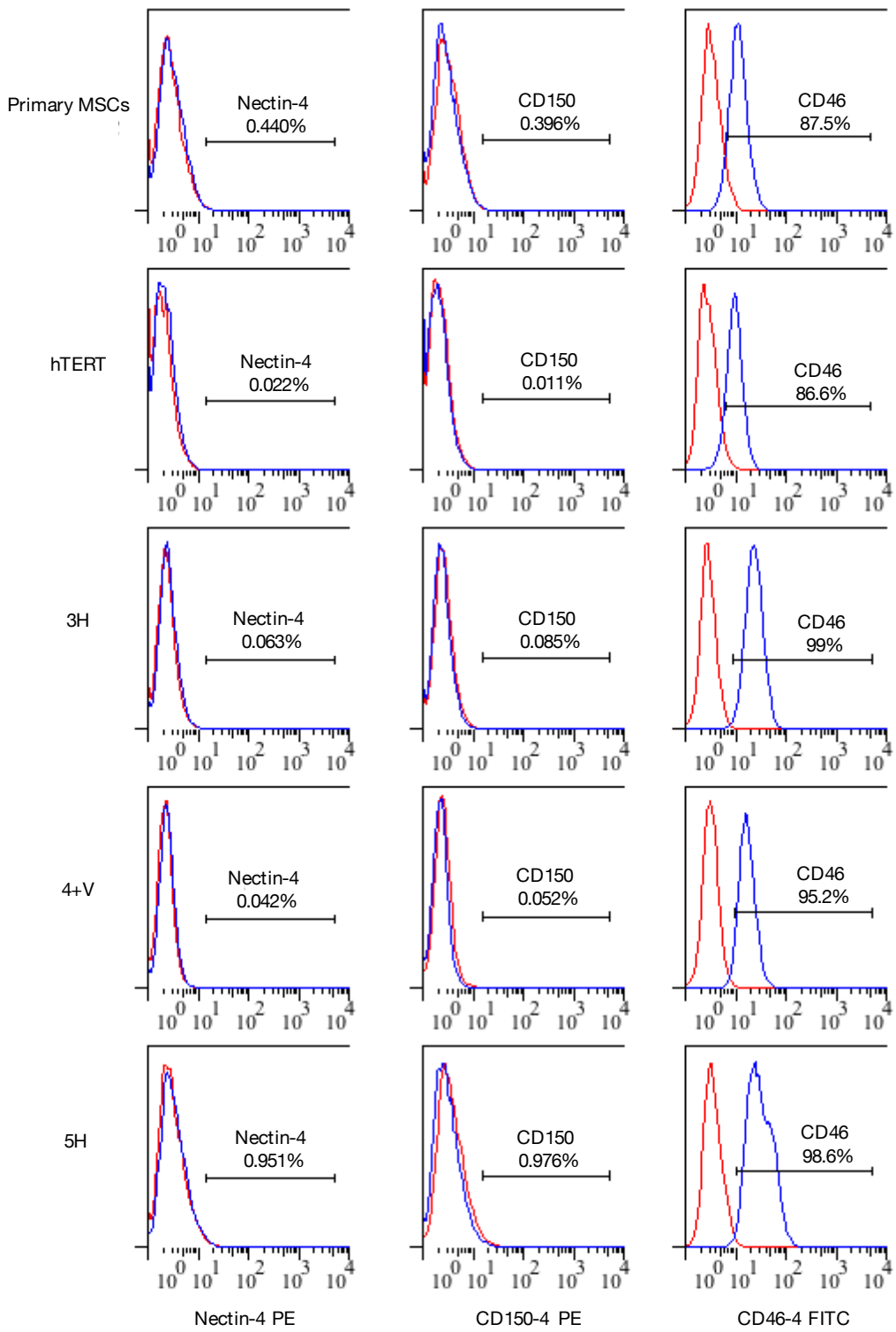


Figure S1 Schematic diagram of construction of MSV-IFITM1-IRES-mRFP. LTR= long terminal repeat; Ampr= ampicillin resistance; MSCV= murine stem cell virus; IRES=internal ribosome entry site; mRFP= monomeric red fluorescent protein; IK6= ikarus gene. BamH1 and XhoI are restriction sites.

A

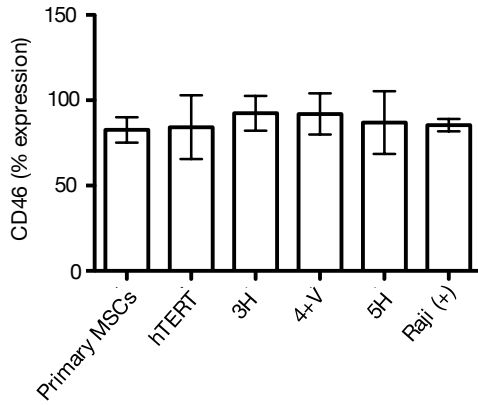
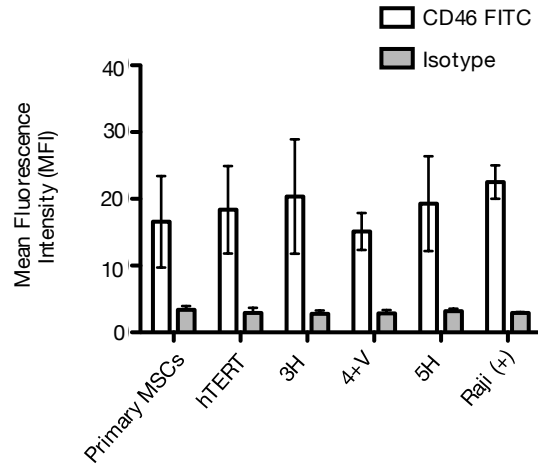
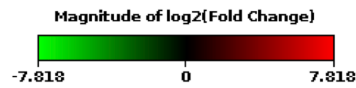
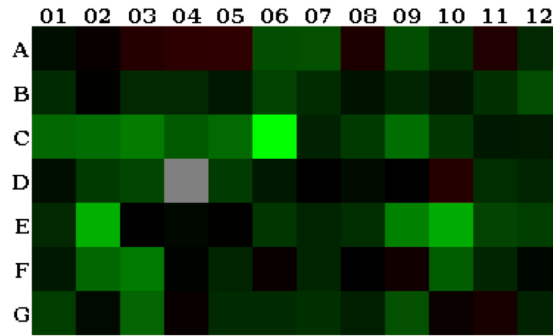
B**C**

Figure S2 MSC MV receptor expression profiles. (A) Representative flow cytometry histograms showing the percent age of cell surface expression of MV receptors CD46, CD150/SLAM and nectin-4 in transformed MSCs. Isotype-stained cells were used as negative controls. (B) Cumulative CD46 expression data and (C) corresponding mean fluorescent intensities (MFIs) for MSCs. Raji cells were used as a positive control for CD46 expression. Data shown is the mean SEM for 5 independent experiments.



Layout	01	02	03	04	05	06	07	08	09	10	11	12
A	ADAR -1.34	BAG3 1.21	BST2 2.11	CASP1 2.54 A	CAV1 2.66	CCL2 -5.34 B	CCL5 -5.39	CD70 1.79 A	CD80 -5.35 A	CD86 -2.65 B	CDKN1B 1.95	CIITA -2.34
B	CRP -2.43 B	CXCL10 -1.02 B	DDX58 -2.36	EIF2AK2 -2.33	GBP1 -1.70	HLA-A -4.09	HLA-B -2.56	HLA-E -1.45	HLA-G -2.23	IFI16 -1.54	IFI27 -2.79	IFI30 -5.10
C	IFI6 -9.24	IFIH1 -10.23	IFIT1 -13.80	IFIT2 -6.90	IFIT3 -9.65	IFITM1 -225.62	IFITM2 -2.06	IFITM3 -3.41	IFNA1 -10.35	IFNA2 -3.14 B	IFNA4 -1.56 B	IFNAR1 -1.71
D	IFNAR2 -1.34	IFNB1 -3.36 B	IFNE -4.49	IFNW1 -1.86 C	IL10 -3.62 B	IL15 -1.63	IL6 1.01	IRF1 -1.28	IRF2 1.02	IRF3 2.24	IRF5 -2.61 B	IRF7 -2.16 B
E	IRF9 -2.32	ISG15 -43.19	ISG20 1.04	JAK1 -1.19	JAK2 -1.05	MAL -3.11 B	MET -2.19	MNDA -2.62	MX1 -15.76 A	MX2 -38.09 A	MYD88 -4.17	NMI -3.68
F	NOS2 -1.66 B	OAS1 -8.92	OAS2 -13.46 A	PML -1.07	PRKCZ -2.18 B	PSME2 1.18	SH2D1A -2.22 B	SHB -1.00	SOCS1 1.40	STAT1 -7.46	STAT2 -2.24	STAT3 -1.14
G	TAP1 -3.80	TICAM1 -1.22	TIMP1 -8.29	TLR3 1.17 B	TLR7 -2.42 B	TLR8 -2.39 B	TLR9 -2.77 B	TMEM173 -1.92	TNFSF10 -5.57 A	TRAF3 1.25	TYK2 1.76 A	VEGFA -2.02

Figure S3 Heat map of genes differentially expressed between hTERT and 5H MSCs. After being normalized against house-keeping genes, the average delta Ct values of target genes were compared between hTERT and 5H cells at baseline ($n=3$) and presented as fold regulation. This heat map shows the range of the fold regulations. Data were analysed using RT² profiler PCR array data analysis.

Position	Gene Symbol	Fold Regulation	p-Value
C06	IFITM1	-225.62	0.044523
E10	MX2	-38.09	0.002336
E09	MX1	-15.76	0.049148
F03	OAS2	-13.46	0.036223
C09	IFNA1	-10.35	0.014486
C05	IFIT3	-9.65	0.038361
F02	OAS1	-8.92	0.004198
G03	TIMP1	-8.29	0.005028
F10	STAT1	-7.46	0.006393
C04	IFIT2	-6.90	0.036567
G09	TNFSF10	-5.57	0.001976
D03	IFNE	-4.49	0.017604
H02	B2M	-4.11	0.009224
C08	IFITM3	-3.41	0.029079
E08	MNDA	-2.62	0.036293
A12	CIITA	-2.34	0.031149
B04	EIF2AK2	-2.33	0.039561
B09	HLA-G	-2.23	0.036003

Table S1 Genes significantly downregulated in 5H MSC compared to hTERT MSCs. List of genes significantly downregulated in 5H cells compared to hTERT cells ($p < 0.05$). Data were analysed using RT² profiler PCR array data analysis.