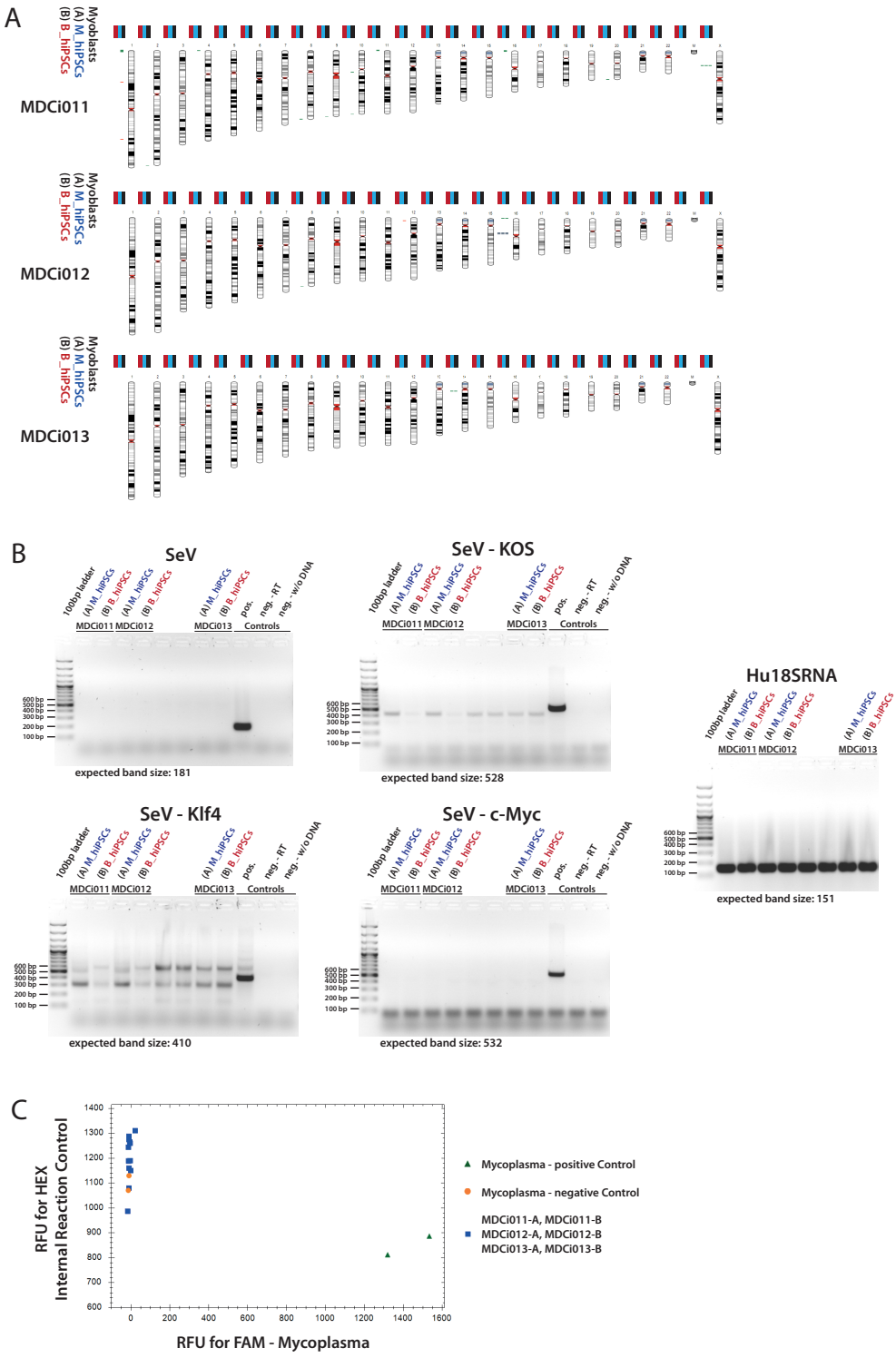

Supplementary figure S1:

(A) Virtual karyotypes of donor myoblasts and all generated hiPSC clones in passages 13-15 with typical karyotypes. Insertions (green), deletions (red) and loss of heterozygosity (grey) compared to the human reference genome are shown next to each chromosome for each individual sample. Reportable copy number changes are gains and losses greater than 0.4Mb and regions of loss of heterozygosity above 3 Mb (in accordance with WiCell criteria). Legend shows myoblasts (black), M_hiPSCs (blue) and B_hiPSCs (red) for each donor). **(B)** RT-PCR showing the absence of Sendai-virus RNA for all generated hiPSC clones in passages 13-15. SeV: total Sendai-virus; SeV-KOS: Sendai-virus Klf4/OCT4/SOX2, SeV-Klf4 and SeV-c-Myc. Human 18sRNA was used to verify the presence of cDNA in all samples. Two negative controls (water / no enzyme) and one positive control from freshly Sendai-virus infected myoblasts were used. **(C)** All hiPSC lines were tested negative for Mycoplasma. HEX dye was detected positive for all tests confirming functional RTqPCR reactions as internal reaction control. FAM dye detection was used for Mycoplasma detection and was only detected positive for positive controls.