

Validation data for 293-SARS2-S cells

<https://www.invivogen.com/293-sars2-spike>

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Version 21E07-ED

293-SARS2-S cells were generated from the human embryonic kidney (HEK)-293 cell line, by transfection of the original Wuhan-Hu-1 SARS-CoV-2 Spike (D614) gene. SARS-CoV-2 Spike (S) overexpression in 293-SARS2-S cells has been verified by qRT-PCR (Figure 1). Notably, 293-SARS2-S cells can be used in fusion assays utilizing cells expressing SARS-CoV-2 host receptors (i.e. HEK-Blue™ hACE2 cells) (Figure 2).

Validation of SARS-CoV-2 Spike overexpression by qRT-PCR

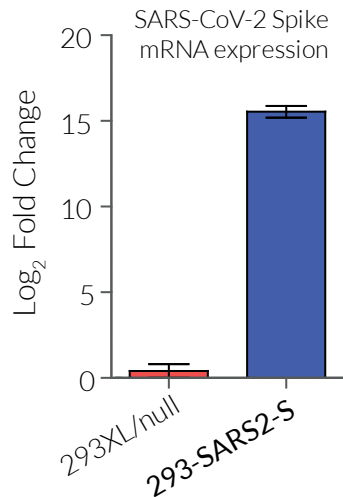


Figure 1: SARS-CoV-2 Spike mRNA expression in 293-SARS2-S cells. Total mRNA was extracted from ~5x10⁵ HEK-293 (parental) and 293-SARS2-S cells and SARS-CoV-2 Spike mRNA was amplified using quantitative (q)RT-PCR. Data are represented as the log₂ fold change comparing hACE2 expression to a house keeping gene.

Assessing cell fusion with InvivoGen's COVID-19 cell lines

To measure cell fusion, 293-SARS2-S cells were transiently transfected with a hMyD88-expression plasmid. Upon co-culture with InvivoGen's SARS-CoV-2 permissive reporter cells, fusion occurred and the expression of MyD88 in the 293-SARS2-S cells triggered a signaling cascade activating the NF-κB-dependent SEAP reporter in the ACE2-expressing cells.

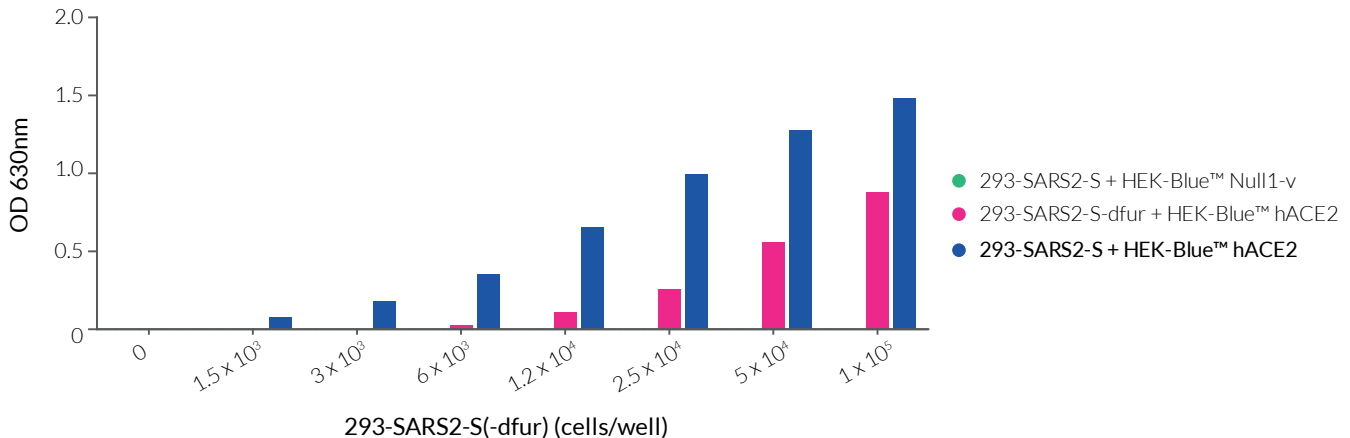


Figure 2: Assessing cell fusion with 293-SARS2-S cells. 293-SARS2-S-dfur and 293-SARS2-S cells were transiently transfected with a MyD88 expression plasmid (pUNO1-hMyD88) using LyoVec™. After 24 hours, the cells were washed, and a dilution series was co-cultured with either 2.5x10⁴ HEK-Blue™ Null1-v or HEK-Blue™ hACE2 cells. After overnight incubation, cell fusion was assessed by measuring the activity of SEAP in the supernatant using QUANTI-Blue™ Solution, a SEAP detection reagent. Data are presented as OD630nm.

TECHNICAL SUPPORT

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