

Brief research report

## **Effects of GS-CA1 on nuclear envelope-associated early HIV-1 infection steps**

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### Supplementary Figures

S1. Western blot analysis of nuclear envelope-enriched fractions, using the Mab414 antibody specific for FG repeats and the GAPDH as a cytoplasmic control.

S2. Principal component analysis (PCA) The graph shows variability between samples. PC1 (x-axis) explained 32% of data variability, whereas PC2 (y-axis) explained 18%. The color code is as follows: Control, green; GS-CA1 treatment, orange; HIV-1-infected, light blue; HIV1 infection + GS-CA1 treatment, gray. PCA was performed using the z-scores of all proteins in all samples. The distance between dots indicates the level of dissimilarity between replicates.

S3. (A) Identified, quantifiable, and quantified proteins in comparison analyses. Identified proteins are total proteins identified in this analysis based on the presence of unique peptides; quantifiable proteins (orange) are proteins identified in all replicates of at least one of the two groups (4300 proteins were quantifiable on average for the whole analysis); quantified proteins (gray) are quantifiable proteins with at least two peptides. (B) Number of proteins found to be

dysregulated. Blue bars show the total modulated proteins in each condition, orange bars indicate upregulated proteins, and gray bars represents downregulated proteins.

S4. MS analysis of nuclear envelope-enriched fractions from HIV-1 (NL43<sub>GFP</sub>)-infected and GS-CA1-treated THP-1 cells, compared to HIV-1-infected cells (A) and compared to GS-CA1-treated cells (B). Colored dots indicate the upregulated (red) or downregulated (blue) proteins whereas gray dots indicate non-modulated proteins. The threshold parameters used are the same as in Fig. 2.

S5. Volcano plot showing proteins significantly modulated in an MS analysis of nuclear envelope-enriched fractions from THP-1 cells treated with IFN- $\beta$ , compared with the untreated control. Colored dots indicate upregulated (red) or downregulated (blue) proteins whereas gray dots indicate non-modulated proteins. The plot at the bottom shows an enlargement for the highly upregulated proteins. The parameters used are the same as before.

Figure S1

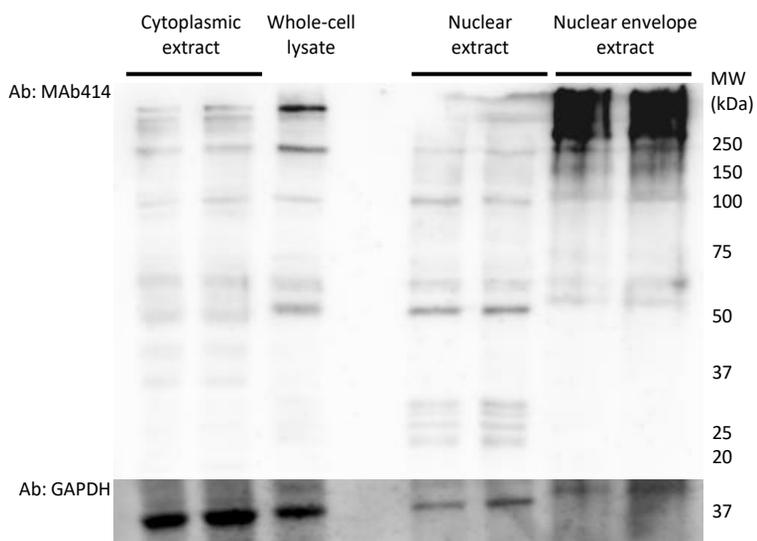


Figure S2

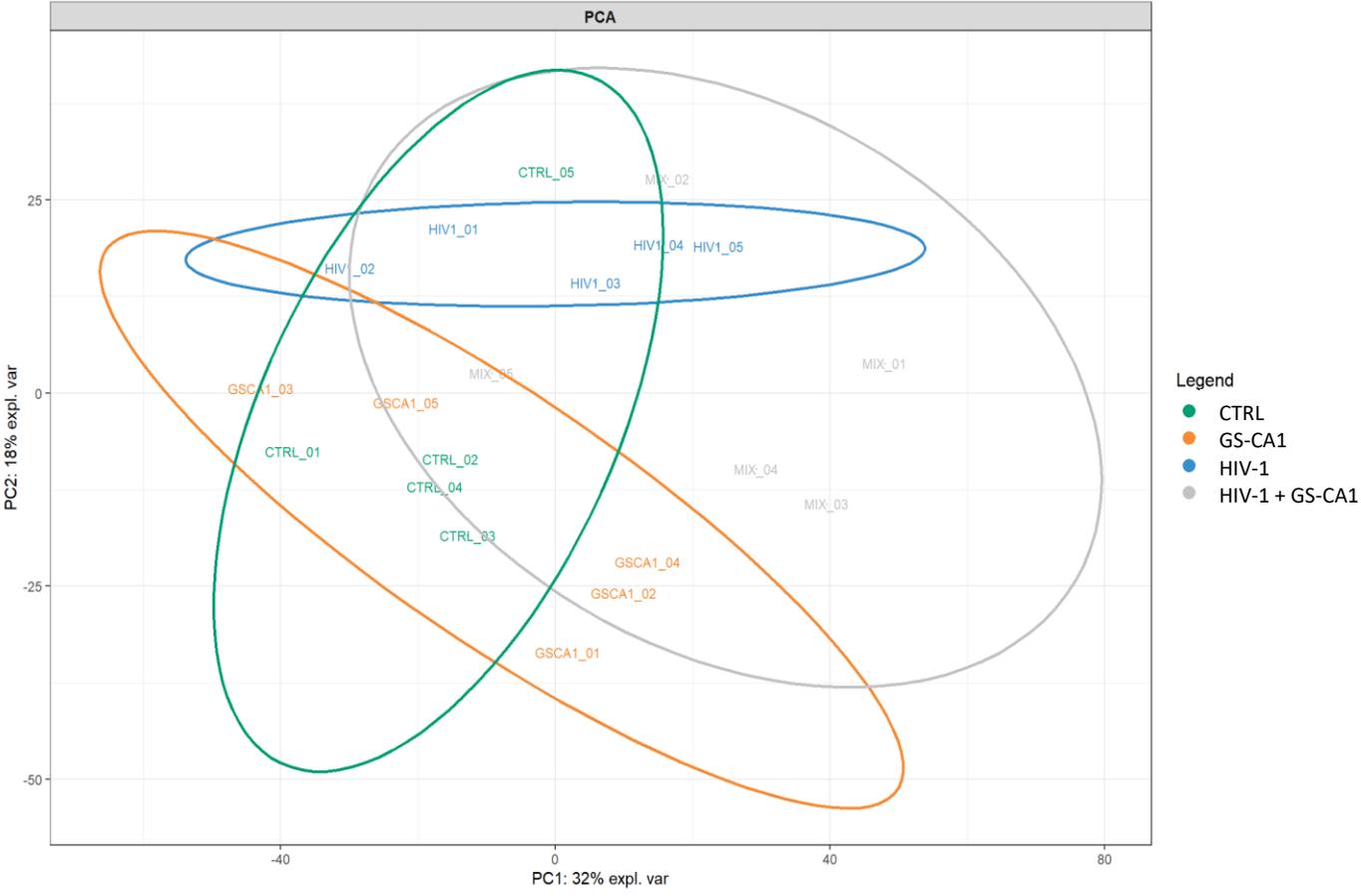
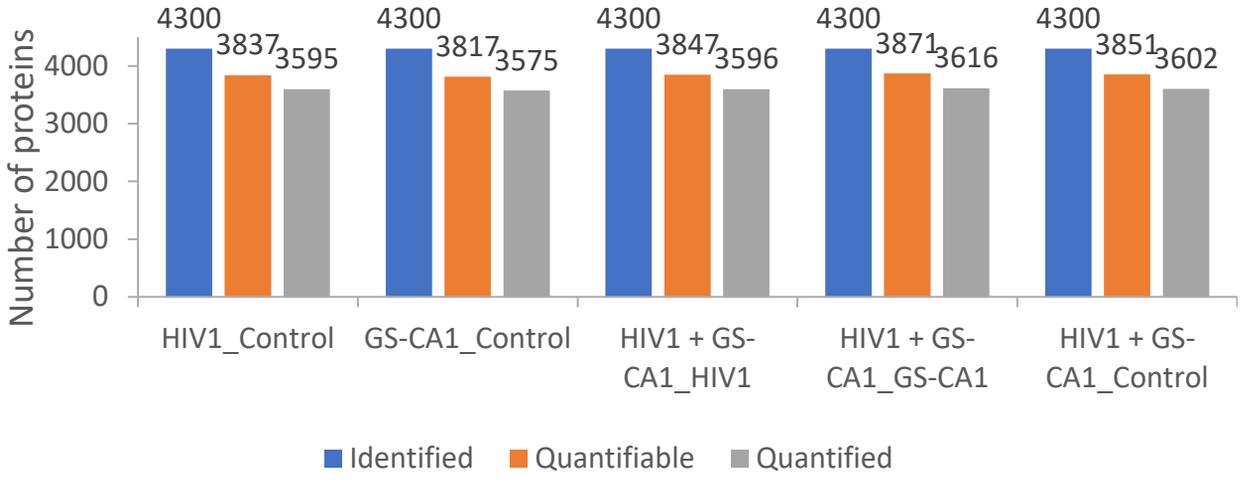


Figure S3

**A**



**B**

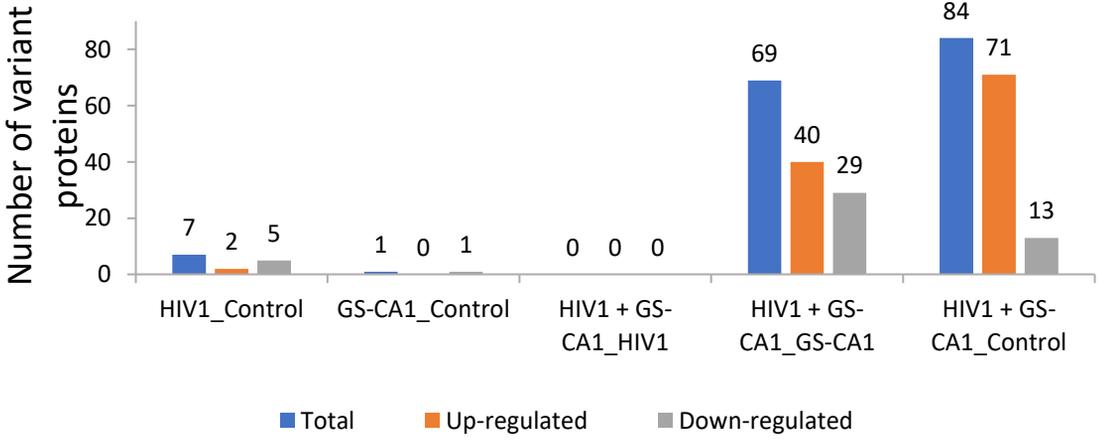


Figure S4

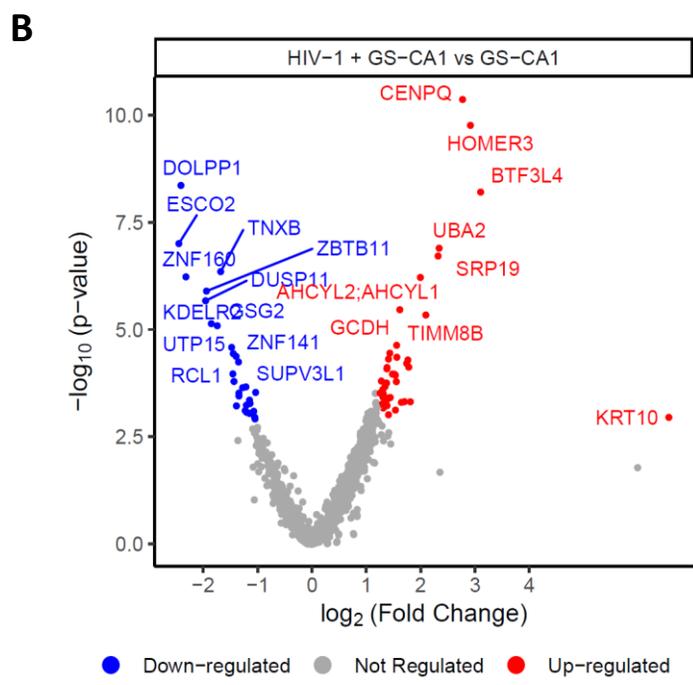
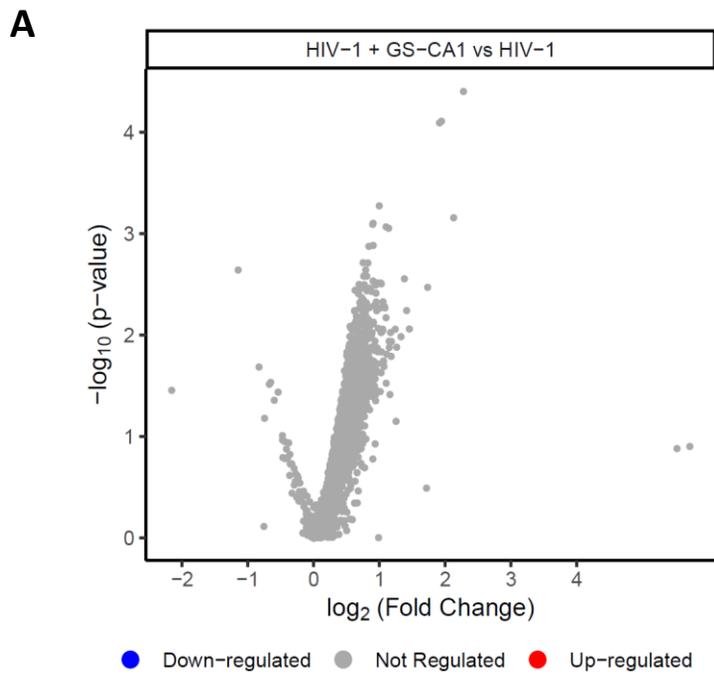


Figure S5

