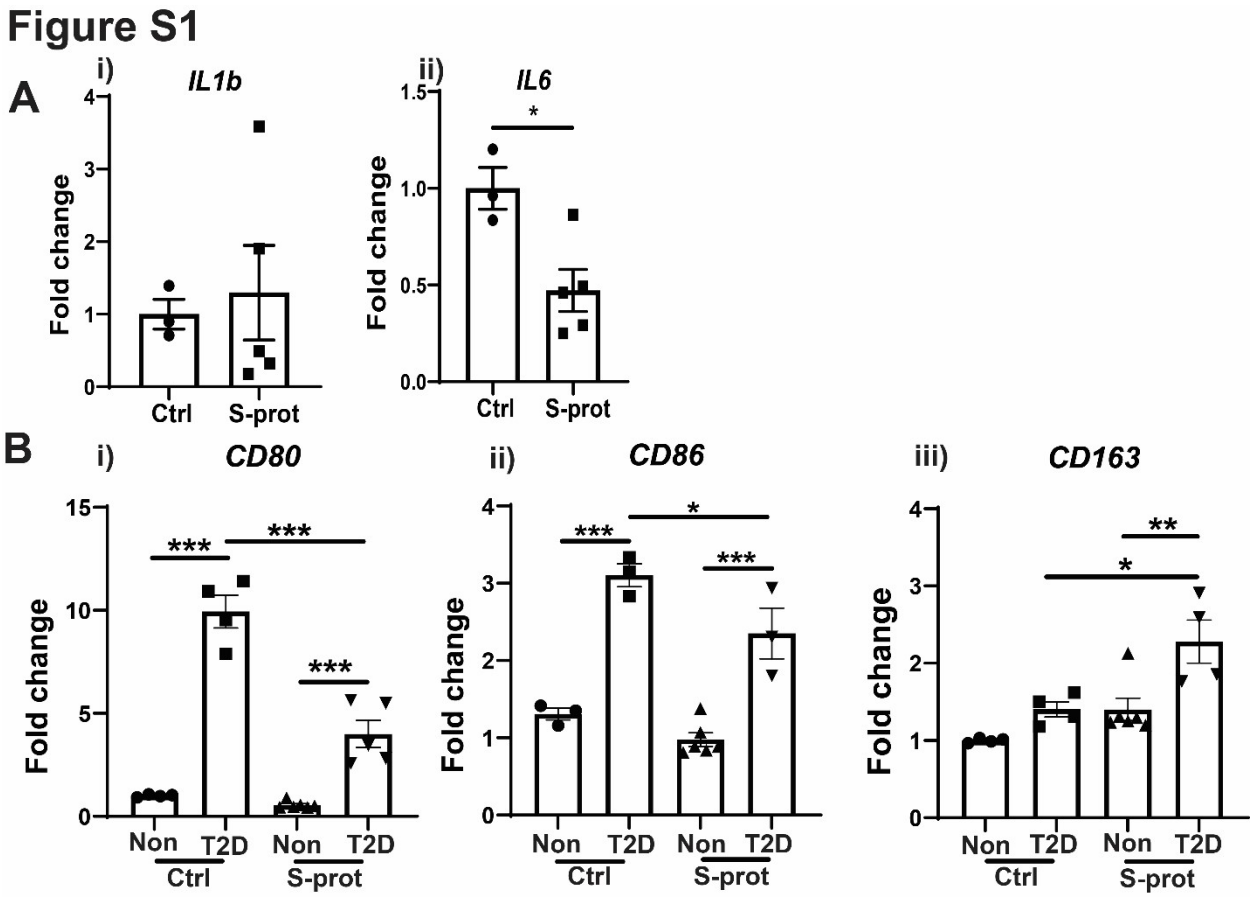


**Figure S1. S-protein over-expression in macrophages altered cytokine expressions. A**. THP-1 were differentiated into macrophages and the gene expression of i) *IL10* and ii) *IL6* was measured using qRT-PCR at 72h post over-expression of S-protein (S-prot) with respect to control (Ctrl) empty lentivirus. **B**. Primary macrophages obtained from peripheral blood monocytes were overexpressed with S-protein (S-prot) and cultured in non-diabetic (Non) or T2D media. 72h post-transduction, cells were collected for RNA analysis. Bar graph representing macrophage marker M1-i) *CD80*, ii) *CD86*, and M2- *CD163* as measured by qRT-PCR. Statistical significance was assessed using Student's two-tailed t-test and one-way ANOVA (*p≤0.05, **p≤0.01, ***p≤0.001).

# Figure S2

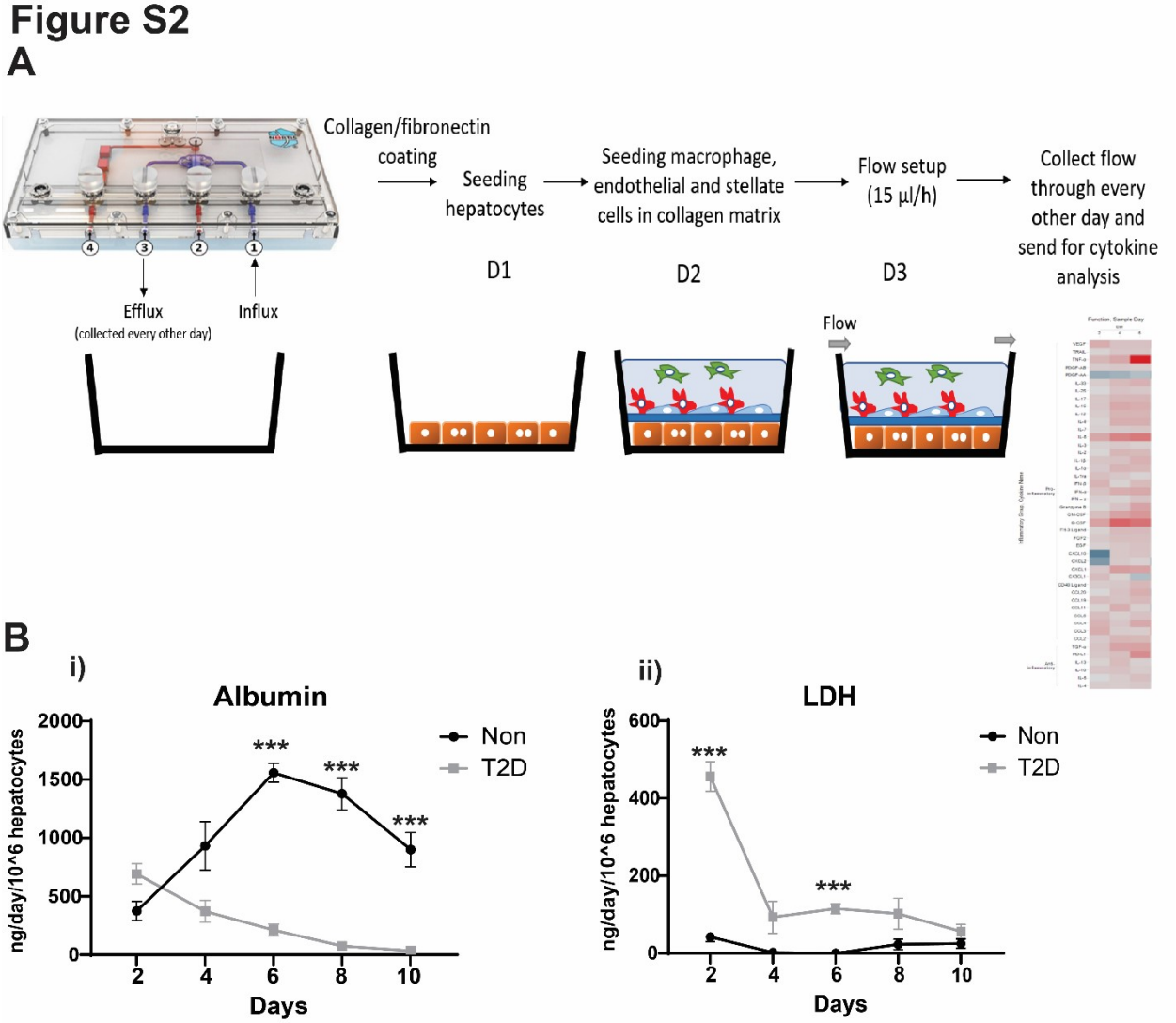


**Figure S2. Schematic and validation of LAMPS model**. **A**. Schematic showing setup of liver MPS model, briefly collegen and fibronectin is first coated on Nortis single-channel device from inlet 1, next hepatocytes were seeded, followed by endothelial-macrophage mix in collagen matrix and stellate-LX-2 cells. Next day, flow was started using non-diabetic (non) and type 2 diabetic (T2D) media with rate 15 µl/h, collecting efflux from outlet 4 every alternate days. **B.** Line graph assesing the levels of albumin and and lactate dehydrogenase (LDH) in the efflux of non and T2D media across 10 days. Statistical significance was assessed using multiple Student's two-tailed t-test (*p≤0.05, **p≤0.01, ***p≤0.001).

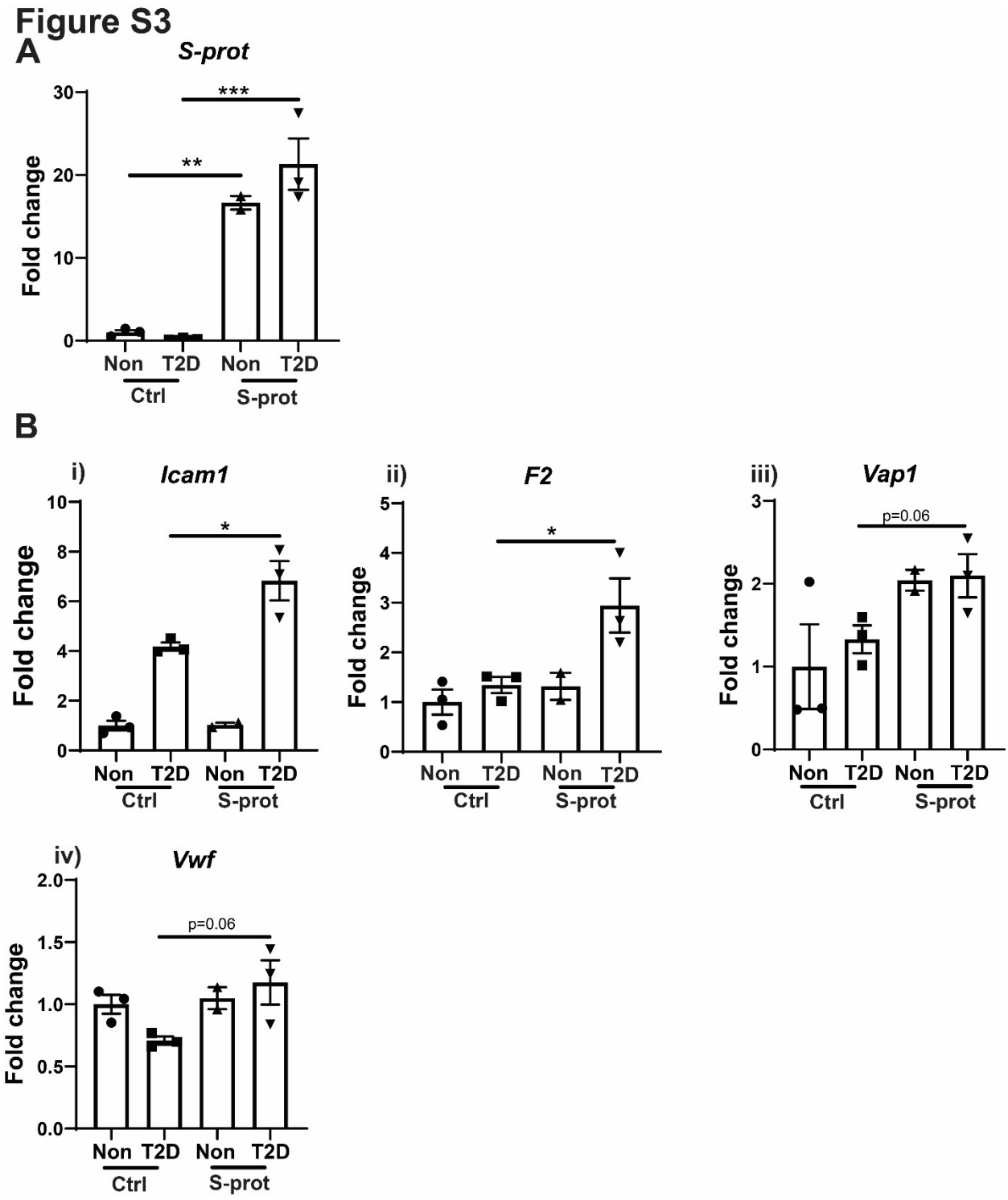


**Figure S3. S-protein over-expression in LSECs increased pro-thrombotic markers when cultured alone.** Similar to macrophages, liver sinusoidal endothelial cells (LSECs) were cultured separately both in non-diabetic (Non) or T2D media for 72h with S-protein (S-prot) overexpression. **A.** Bar graph validating the overexpression of S-protein (S-prot) with respect to control (Ctrl) by qRT-PCR. **B.** Bar graph representing pro-thrombotic genes – i) *ICMA1*, ii) *F2*, iii) *VAP1*, iv) *VWF*. Statistical significance was assessed using Student's two-tailed t-test and one-way ANOVA (*p≤0.05, **p≤0.01, ***p≤0.001).

# Figure S4

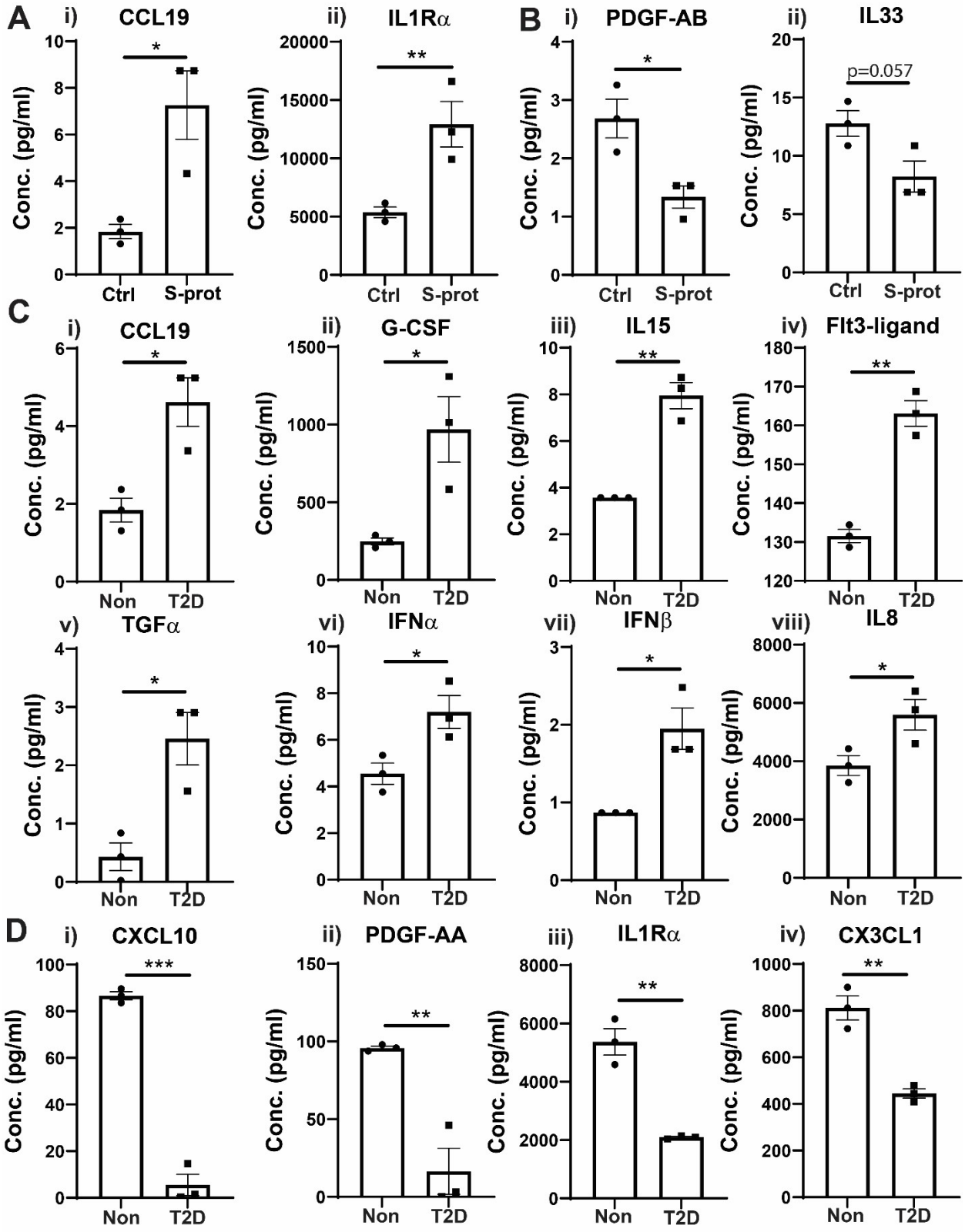
A
i) CCL19
ii) IL1Rα
B
i) PDGF-AB
ii) IL33
p=0.057
C
i) CCL19
ii) G-CSF
iii) IL15
iv) Flt3-ligand
v) TGFα
vi) IFNα
vii) IFNβ
viii) IL8
D
i) CXCL10
ii) PDGF-AA
iii) IL1Rα
iv) CX3CL1
Conc. (pg/ml)
Ctrl
S-prot
Non
T2D

**Figure S4. Cytokines altered by S-protein and T2D condition alone in LAMPS.** Cytokines were measured in the efflux from LAMPS where S-protein was over-expressed both in macrophages and endothelial cells obtained from non-diabetic patients (non-diabetic-COVID-19-LAMPS). **A.** Bar graph representing i) CCL19 and ii) IL1Rα that were increased and, **B**. i) PDGF-AB and ii) IL33 that were reduced by S-protein, measured using Luminex assay. Similarly, macrophages and endothelial cells from T2D patients were cultured in T2D media, called T2D-LAMPS. Bar graph representing **C**. cytokines (i) CCL19, ii) G-CSF, iii) IL15, iv) Flt-3-ligand, v) TGF-α, vi) IFN-α, vii) IFN-β, viii) IL8) that were increased and **D**. cytokines (i) CXCL10, ii) PDGF-AA, iii) IL1Rα, and iv) CXC3CL1) that were decreased in T2D conditions with respect to non-diabetic condition (Non). Statistical significance was assessed using Student's two-tailed t-test (*$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$).

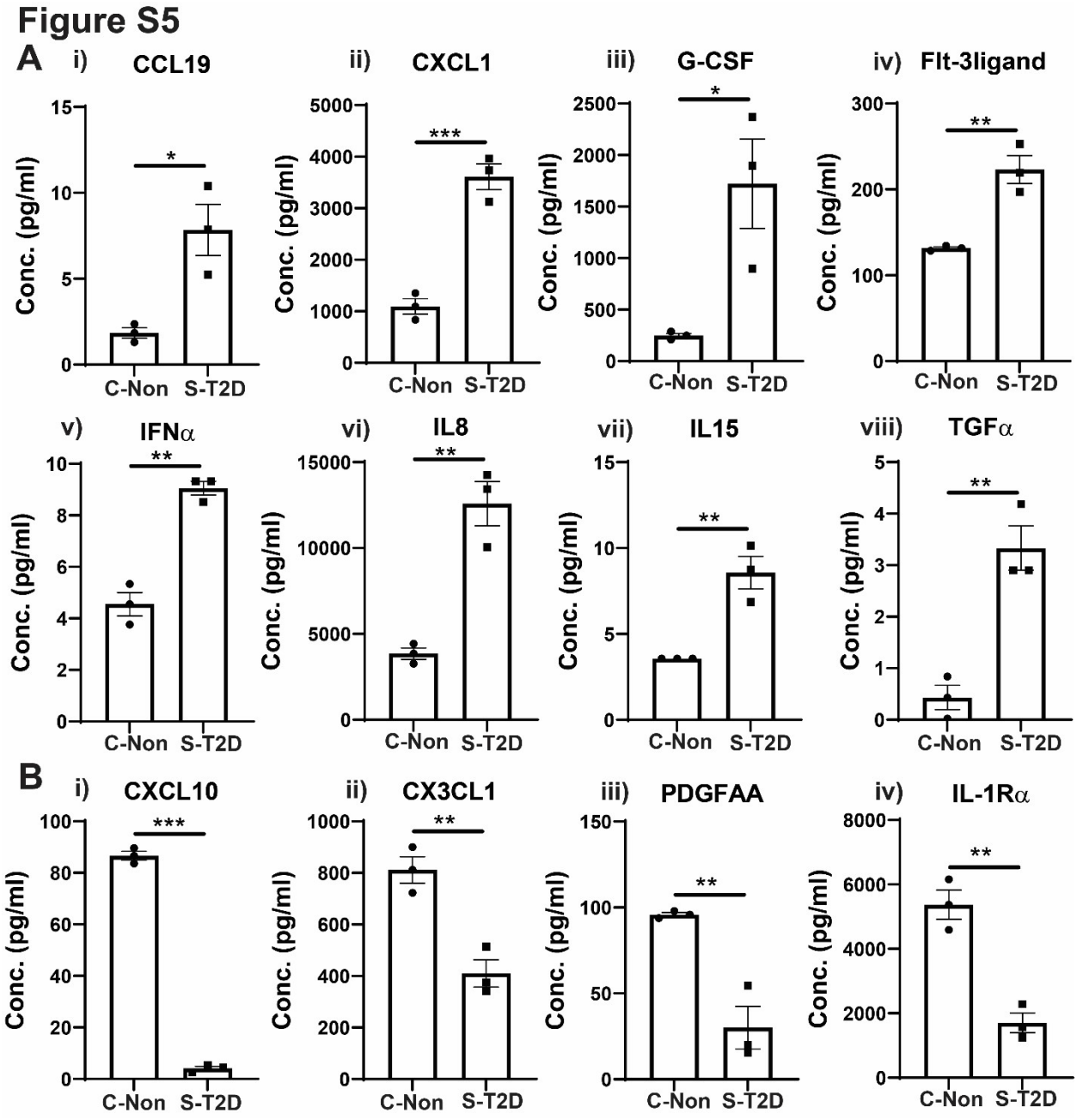


**Figure S5. Cytokines altered by both S-protein and T2D conditions in T2D-COVID-19 LAMPS.** Bar graph representing **A**. cytokines (i) CCL19, ii) CXCL1, iii) G-CSF, iv) Flt-3-ligand, v) IFN-α, vi) IL8, vii) IL15, viii) TGF-α) that were increased and **B**. cytokines (i) CXCL10, ii) CXC3CL1, iii) PDGF-AA, and iv) IL1Rα) that were decreased by combination of S-protein and T2D media in T2D-COVID-19-LAMPS (S-T2D) with respect to non-diabetic-non-COVID-19-LAMPS (C-non). Statistical significance was assessed using Student's two-tailed t-test (*p≤0.05, **p≤0.01, ***p≤0.001).