

Supplemental Table 1. T_{DS} assay for immuno-monitoring

A) Vaccinated mice

| | gag-specific CD8 (1 epitope) vaccinated mice | | total CD8 untreated mice | |
|--------|---|--|-----------------------------|--|
| | % in G ₁ | % in S-G ₂ /M (T _{DS}) | % in G ₁ | % in S-G ₂ /M (T _{DS}) |
| day 3 | 22.36 | 4.98 (** vs day 44) | 3.82 | 0.18 |
| day 7 | 76.28 (** vs day 44) | 0.61 | 5.05 | 0.20 |
| day 44 | 1.56 | 0.02 | 6.67 | 0.17 |

B) T1D patients

| | islet-specific CD8 (5 epitopes) | | total CD8 | |
|---|---------------------------------|---|---------------------|--|
| | % in G ₁ | % in S-G ₂ /M (T _{DS}) | % in G ₁ | % in S-G ₂ /M (T _{DS}) |
| T1D patients, T _{DS} positive (T1D T _{DS} ⁺) | 15.25 | 1.79 (** vs HD; *** vs T1D T _{DS} ⁻) | 2.14 | 0.11 |
| T1D patients, T _{DS} negative (T1D T _{DS} ⁻) | 2.09 | 0.00 | 1.04 | 0.02 |
| Healthy donors (HD) | 2.63 | 0.05 | 1.41 | 0.04 |

C) COVID-19 patients

| | CD4 T _{EM} | | CD8 T _{EM} | | γδ T cells | |
|-------------------------------|--------------------------------------|--|-----------------------|--|-------------------------------------|--|
| | % in G ₁ | % in S-G ₂ /M (T _{DS}) | % in G ₁ | % in S-G ₂ /M (T _{DS}) | % in G ₁ | % in S-G ₂ /M (T _{DS}) |
| Severe COVID-19 | 12.89 (**** vs HD) (** vs Mod) | 1.25 (**** vs HD) (**** vs Mod) | 20.78 (**** vs HD) | 1.43 (**** vs HD) (* vs Mod) | 9.87 (**** vs HD) (** vs Mod) | 0.33 |
| Moderate COVID-19 (Mod) | 8.08 (*** vs HD) | 0.50 (** vs HD) | 12.88 (**** vs HD) | 1.02 (* vs HD) | 7.49 (** vs HD) | 0.18 (* vs HD) |
| Healthy Donors (HD) | 3.45 | 0.12 | 2.27 | 0.04 | 1.67 | 0.02 |

Dual Ki-67/DNA staining was combined with peripheral blood T cell multi-color flow cytometric analysis, for a refined immuno-monitoring evaluation including cell cycle. **(A)** BALB/c mice were vaccinated by prime with the viral vector ChAd3 carrying the model antigen HIV-1 gag (gag), and boost with Modified Vaccine Ankara carrying gag, both administered intramuscularly in the quadriceps. Analysis of gag₁₉₇₋₂₀₅-specific and total CD8 T cells was performed at the indicated times after boost in vaccinated and untreated mice, respectively (15). **(B)** Peripheral Blood Mononuclear Cells (PBMCs) from Type 1 Diabetes (T1D) patients, all within 1 year from diagnosis, and healthy donors (HD) were analyzed, using a pool of the following tetramers to identify islet-specific CD8 T cells: PPI₁₅₋₂₄, InsB₁₀₋₁₈, GAD₁₁₄₋₁₂₃, IGRP₂₆₅₋₂₇₃, and IA-2₇₉₇₋₈₀₅ HLA-A*02 tetramers. T_{DS}⁺ and T_{DS}⁻ T1D patients were defined as those having > and < 0.248% T_{DS} (i.e. HD mean + 3xSD) among islet-specific CD8 T cells, respectively (16). **(C)** PBMCs were obtained from HD and hospitalized COVID-19 patients, classified according to a World Health Organization's (WHO) eight-point scale as moderate (scores 3-4) and severe (scores 5-8). Patient classification reflected peak severity. CD4 T_{EM}, CD8 T_{EM}, and γδ T cells were analyzed (17). Numbers represent mean percentages of cells in G₁, and in S-G₂/M (T_{DS}) from a total of 45 mice in (A), and of 21 and 104 donors in (B) and (C), respectively. Statistical analysis was performed by Kruskal-Wallis with Dunn's multiple comparison test (A and B) (15, 16), and by a linear mixed model grouped by severity, with patient as random variable, corrected for age- and sex-dependency (C) (17). Differences were considered statistically significant when * P=.05, ** P=.01, *** P=.001, **** P=.0001, ***** P=.00001. See original references for more details (15-17).