# Science Advances

## Supplementary Materials for

## PD-1/PD-L1 blockade abrogates a dysfunctional innate-adaptive immune axis in critical β-coronavirus disease

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Figure S1. Western blot study of TMEM176B/GAPDH ratios in peripheral blood CD14<sup>+</sup> monocytes from healthy donors (HDs), non-ICU and ICU patients.
(A) Representative western blot. \* Sample not considered for the analysis due to low GAPDH.
(B) Graphic depicting all the studied patients.





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Figure S2. Study on inflammasome activation in human THP-1 monocytes transfected with plasmids coding for GFP, E Protein-GFP, mcherry and TMEM176Bmcherry.

(A) Study of FLICA-1<sup> $\dagger$ </sup> cells. A pool of two experiments is shown. \* p< 0.05. One sample *t* test. (B) Gating strategy. One experiment representative of three is shown.

Fig. S3



#### Figure S3. Viral load and Tmem176b expression in the liver of MHV-A59-infected mice.

(A) Viral load was analyzed by RT-qPCR in the liver of WT mice at different days post-infection.
(B) *Tmem176b* expression was studied by RT-qPCR in the liver of WT mice at different days post-infection.
(C) Mouse liver cryosections from MHV-A59-infected or naive animals were stained with anti MHC class II and TMEM176B antibodies, then the nucleus was stained with DAPI and analyzed by confocal microscopy. Animals were sacrificed at 5 dpi. The arrows show MHC class II+ Tmem176b+ cells. Images are representative of 4 naive and 4 infected animals.

Fig. S4



Figure S4. Gating strategy to study conventional DCs infiltrating the liver of WT and Tmem176b<sup>-/-</sup> mice.

Analysis of FLICA-1 staining shown in Fig. 1 K-L was done in  $CD11b^{-}$  and  $CD11b^{+}$  conventional DCs as defined here. One experiment representative of three is shown.

Α 🗖 WT \*\*\*\* 1500 NIrp3-/ IL-1B (pg/ml) 1000 500 MOI=0 MOI=1 С \*\* wt 2000 -Tmem176b-/ IL-1B (pg/ml) 1500 1000 500 0 MOI=0 MOI=1 MOI=5 Е WT Tmem176b<sup>-/-</sup>ns 1010 MHV-A59 copies 10<sup>8</sup> 10<sup>e</sup> 10' 10 10 MOI=0 MOI=1 MOI=5 G \*\*\*\* \*\*\*\* 1200 WT Tmem176b-/-Ттет176b<sup>-/-</sup> т 900 IL-1β (pg/ml) Casp1 600 300 0 MOI=0 MOI=1 MOI=5

Fig. S5



### Figure S5. Tmem176b controls MHV-A59-triggered NLRP3 inflammasomes in bone marrow-derived dendritic cells (BMDCs)

(A) WT and *NIrp3*<sup> $^{\circ}$ </sup> BMDCs were left untreated or infected with MHV-A59. IL-1 $\beta$  was assessed by ELISA in the culture supernatant. One experiment representative of three is shown. \* p<0.05; \*\*\*\* p<0.0001. Two-way ANOVA test.

**(B)** WT and *Casp1/11*<sup> $\checkmark$ </sup> BMDCs (both in C57BL/6JN background) were infected with MHV-A59 and IL-1 $\beta$  was assessed by ELISA in the culture supernatant. One experiment representative of three is shown. \*\*\*\*p<0.0001. Two-way ANOVA test.

(C) WT (issued from littermate controls) and *Tmem176b*<sup> $\checkmark$ </sup> BMDCs were infected with MHV-A59 at the indicated multiplicities of infection (MOIs). IL-1 $\beta$  was assessed by ELISA in the culture supernatant. One experiment representative of four is shown. \*\* p<0.01. Two-way ANOVA test.

(D) Caspase-1 activity was studied by staining WT and  $Tmem176b^{\sim}$  BMDCs with FLICA-1 followed by flow cytometry analysis. One experiment representative of three is shown. \*\*\*\* p<0.0001. Two-way ANOVA test. (E) WT and  $Tmem176b^{\sim}$  BMDCs were infected with MHV-A59 at the indicated MOIs. MHV-A59 copies were assessed by RT-qPCR. A pool of two experiments is shown. ns: not significant. Two-way ANOVA test.

(F) WT and *Tmem176b*<sup> $\sim$ </sup> BMDCs were infected with MHV-A59 in the presence of DMSO (vehicle control) or the Caspase-1 inhibitor Z-WEDH. IL-1 $\beta$  was assessed by ELISA in the culture supernatant. One experiment representative of three is shown. \*\* p<0.01; \*\*\* p<0.001. Two-way ANOVA test. (G) WT, *Tmem176b*<sup> $\sim$ </sup> and *Tmem176b*<sup> $\sim$ </sup> Casp1<sup> $\sim$ </sup> BMDCs were infected with MHV-A59 at the indicated MOIs.

**(G)** WT, *Tmem176b*<sup> $\checkmark$ </sup> and *Tmem176b*<sup> $\checkmark$ </sup> *Casp1*<sup> $\checkmark$ </sup> BMDCs were infected with MHV-A59 at the indicated MOIs. IL-1 $\beta$  was assessed by ELISA in the culture supernatant. One experiment representative of three is shown. \*\*\*\* p<0.0001. Two-way ANOVA test.

Fig. S6



## Figure S6. Depletion of the CD8 compartment increases viral load in Tmem176b<sup> $\checkmark$ </sup> mice treated with anti-IL-1 $\beta$ antibodies.

*Tmem176b*<sup>-/-</sup> mice were infected with MHV-A59 at day 0 through i.p. injection. One  $\mu$ g anti-IL-1 $\beta$  was injected i.p every 5 days since day -2. One hundred  $\mu$ g anti-CD8 antibody was injected i.p every 3 days since day -2. Viral load was assessed by RT-PCR in livers at 5 dpi. Mann-Whitney test. \* p< 0.05.



Figure S7. Casp1/11 deficiency is associated with reinforced CD8<sup>+</sup> T cell responses and improved outcome of MHV-A59 infection.

(A) WT and  $Casp1/11^{--}$  mice were infected with MHV-A59 (1200 PFU). Total CD8<sup>+</sup> T cells were studied by flow cytometry in the spleen. The left panel shows representative dot plots whereas the right graphic shows the absolute number of CD8<sup>+</sup> T cells for 8 WT and 8  $Casp1/11^{--}$  mice. \*\* p<0.01. Student's *t* test.

**(B)** MHV-specific CD8<sup>+</sup> T cells in the spleen were studied in the animals used in A. \* p<0.05. Student's *t* test. **(C)** *In vivo* MHV-sp cytotoxic (CTL) activity assay was performed on 8 WT and 11 Casp1/11<sup>-/-</sup> infected mice at 5 dpi. Representative histograms are shown in the left panel. The percentage of specific lysis was calculated with the formula showed in the materials and methods section. \*\* p<0.01. Student's *t* test.

**(D)** Mouse survival was studied in MHV-A59-infected WT (C57BL/6JN) and  $Casp1/11^{-4}$  animals treated with depleting anti-CD8 antibody. One hundred µg anti-CD8 antibody was injected i.p every 3 days since day -2. CD8 depletion was confirmed by flow cytometry. \*\*\* p< 0,001. Log-rank (Mantel-Cox) test.

(E) Viral load was analyzed by RT-qPCR in the liver of 5 WT and 3 Casp1/11<sup>-/-</sup> as well as 4 Casp1/11<sup>-/-</sup> animals treated with depleting anti-CD8 antibody. ns One-way ANOVA test.

Fig. S8



### Figure S8. Impact of cell culture media from infected monocytes on the functionality of alloreactive CD4+ T cells

(A) Study of PD-1 expression by CD4<sup> $^+$ </sup> TCR- $\beta^{^+}$  cells co-cultured with allogeneic monocytes ± cell culture media (CCM) from SARS-CoV-2-infected monocytes ± 5µM ISQ. One experiment representative of three is shown.

**(B-C)** Flow cytometry study of IFN- $\gamma$  expression by CD4<sup>+</sup> T cells co-cultured with allogeneic monocytes ± CCM from uninfected monocytes (Mock) or SARS-CoV-2-infected cells ± anti-PD-1 or control antibody (20

 $\mu$ g/ml). The percentage of IFN- $\gamma^{^{+}}$  cells is shown in B and the mean fluorescence intensity (MFI) of positive cells in C. The graphics show one expreriment representative of three. \* p<0.05; \*\* p < 0.01. One-way ANOVA test.

Fig. S9



Figure S9. Flow cytometry study of HLA-DR/CD38 within peripheral blood  $CD8^{\dagger}$  T cells and TOX/PD-1 within HLA-DR<sup> $\dagger$ </sup> CD38<sup> $\dagger$ </sup> CD8<sup> $\dagger$ </sup> T cells from healthy donors.





*Figure S10. Flow cytometry study of HLA-DR/CD38 in CD8<sup>+</sup> T cells from non-UCI and UCI patients.* (A) Representative dot plots.

**(B)** The graphic shows the individual percentages of CD38<sup>+</sup> HLA-DR<sup>+</sup> cells within CD8<sup>+</sup> TCR- $\beta^+$  for each studied patient. p= 0.07. Student's *t* test.



Figure S11. Correlation of the indicated genes in moderate and severe COVID-19 patients from McClain et al. (46).

Fig. S12



Figure S12. Correlation of the indicated genes in moderate and severe COVID-19 patients from McClain et al. (46).



Fig. S13

Figure S13. Correlation of the indicated parameters in non-ICU and ICU patients.

ICU

1500

15000

30

300

•

40

Fig. S14



#### Figure S14. Correlation of anti-SARS-CoV-2 spike IgG with the indicated parameters. Plasmatic anti-SARS-CoV-2 spike IgG were measured by ELISA.

(A) Anti-SARS-CoV-2 spike IgG levels in healthy donors (HDs), non-ICU and ICU patients. (B, D, F and H) non-ICU patients.

(C, E, G and I) ICU patients.

(B-C) TMEM176B/GAPDH ratio was determined by western blot in samples peripheral blood CD14<sup>+</sup> (D-E) Active Caspase-1 was assessed by ELISA in plasma

(F-G) TOX<sup>\*</sup> PD-1<sup>\*</sup> in HLA-DR<sup>\*</sup> CD38<sup>\*</sup> CD8<sup>+</sup> T cells from peripheral blood were studied by flow cytometry.

**(H-I)** HLA-DR<sup>+</sup> CD38<sup>+</sup> CD8<sup>+</sup> T cells from peripheral blood were studied by flow cytometry.



Figure S15. Study of Charlson comorbidity index (A, C, E, G and I) and mortality (B, D, F, H and J) (A-B) Active Caspase-1 was assessed by ELISA in plasma

(C-D) Anti-SARS-CoV-2 spike IgG was determined by ELISA in plasma.

(E-F)  $TOX^{+}PD-1^{+}$  in HLA-DR<sup>+</sup>  $CD38^{+}CD8^{+}T$  cells from peripheral blood were studied by flow cytometry.

(G-H) HLA-DR<sup>+</sup> CD38<sup>+</sup> CD8<sup>+</sup> T cells from peripheral blood were studied by flow cytometry.

(I-J) TMEM176B/GAPDH ratio was determined by western blot in samples peripheral blood CD14<sup>+</sup> monocytes and expressed in arbitrary units (AU).





Figure S16. PD-L1 blockade triggers TNF production by CD38<sup>+</sup> HLA-DR<sup>+</sup> PD-1<sup>+</sup> TOX<sup>+</sup> CD8<sup>+</sup> T cells treated with SARS-CoV-2 peptides.

PBMCs from three lymphopenic critical patients were studied. Cells were incubated for 24 h with 20 µg/ml control IgG (human IgG1) or anti-PD-L1 antibody. Then, 6 nmol SARS-CoV-2 peptides were added to the culture for 6 h. Representative dot plots are shown.

Fig. S17



*Figure S17. Study of cytokines secreted in the culture supernatant of PBMCs form ICU patients.* Supernatants of PBMCs cultures used in Figure 4G-H were assessed for an array of 12 cytokines. Cells were incubated for 24 h with 20  $\mu$ g/ml control IgG (human IgG1) or anti-PD-L1 antibody. Then, 6 nmol SARS-CoV-2 peptides were added to the culture for 6 h. Cytokines were quantified by flow cytometry using a bead-cased multiplex kit. Absolute values were standardized in relationship to the control condition (100%). One sample *t* test. ns= not significant; \* p< 0.05.

Characteristic	
No.	30
Age, median (IQR), years	65.5 (53.0 – 76.0)
Male	22/30 (73.3 %)
Female	8/30 (26.7 %)
Length of hospital stay, median (IQR), days	18 (10 – 33)
WHO-CPS score, median (IQR)	8 (5 – 10)
Charlson co-morbidity index, median (IQR)	2 (1 – 3)
ICU	19/30 (63.3 %)
non-ICU	11/30 (36.7 %)
Temperature, median (IQR), ºC	37.8 (37.0 – 38.0)
Respiratory rate, median (IQR), bpm	25.5 (24.0 – 28.0)
SpO <sub>2</sub> , median (IQR), %	88.0 (86.0 – 89.0)
Co-existing conditions	10/30 (33.3 %)
Dementia	3/30 (10.0 %)
Diabetes mellitus	3/30 (10.0 %)
Chronic obstructive pulmonary disease	3/30 (10.0 %)
Congestive heart failure	1/30 (3.3 %)
Connective tissue diseases	1/30 (3.3 %)
Ischemic cardiomyopathy	1/30 (3.3 %)
Smoking	
No	26/30 (86.7 %)
Current	1/30 (3.3 %)
Former	3/30 (10.0 %)
Laboratory values, median (IQR)	
CRP, mg/L	158.0 (107.8 – 196.0)
D-Dimer, μg/mL	1.8 (0.7 – 4.2)
Neutrophile count, cells/µL	6100 (4500 – 9125)
Lymphocyte count, cells/µL	850 (500 -1200)
Lymphocytes to Neutrophiles ratio	0.14 (0.08 – 0.29)
Hemoglobin, g/dL	13.8 (13.4 – 15.7)
Platelet count, number x10 <sup>3</sup> /µL	211.0 (176.0 – 262.5)
AST, IU/L	59.0 (44.0 – 76.0)
ALT, IU/L	46.0 (39.0 – 74.3)
Albumin, g/dL	3.7 (3.5 – 4.1)
Creatinine, mg/dL	1.1 (0.9 – 1.4)
Azotemia, mg/dL	48.0 (35.0 – 65.0)
Ferritin, mg/L	1354.0 (581.0 – 2545.5)
LDH, IU/L	467.5 (339.0 – 683.0)
Number of deaths	12/30 (40.0 %)

#### Table S1. Characteristics of the studied patients.

IQR: Interquartile range