

SUPPLEMENTARY MATERIAL

Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis

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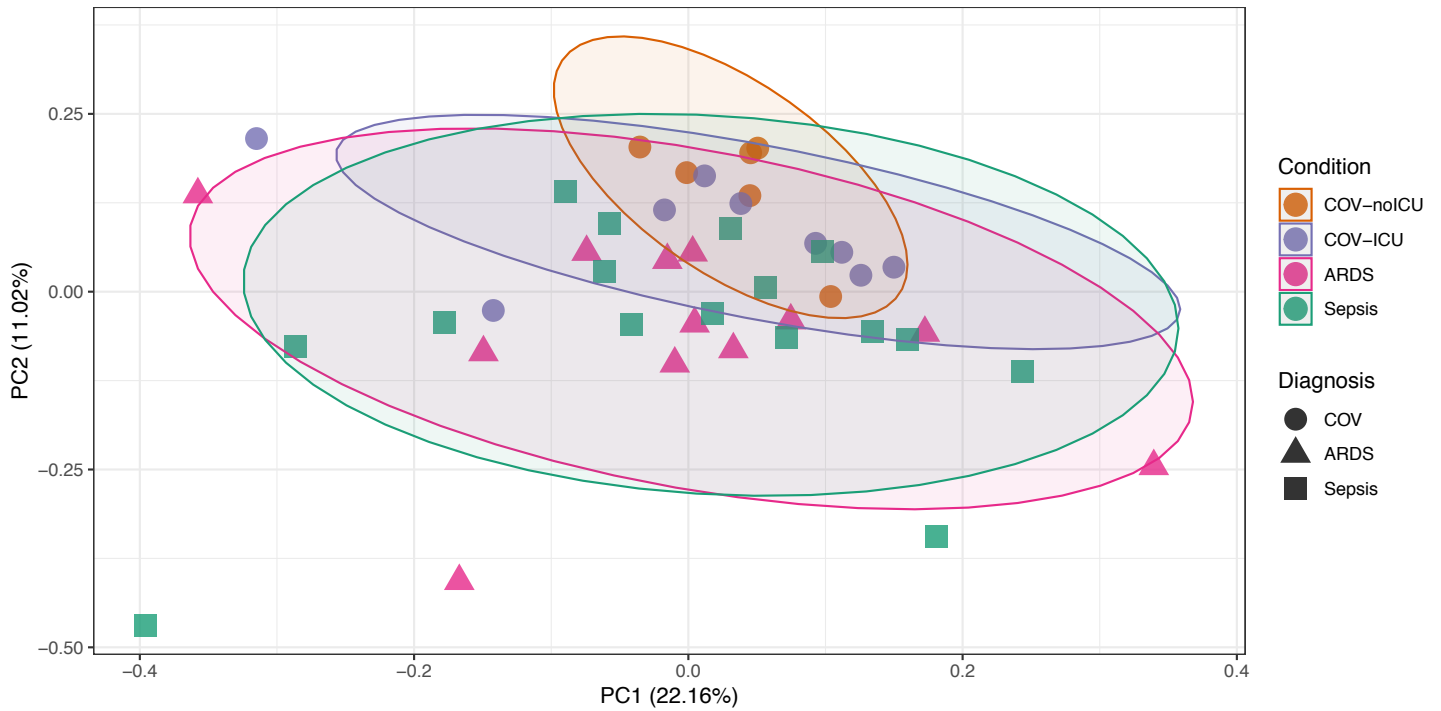
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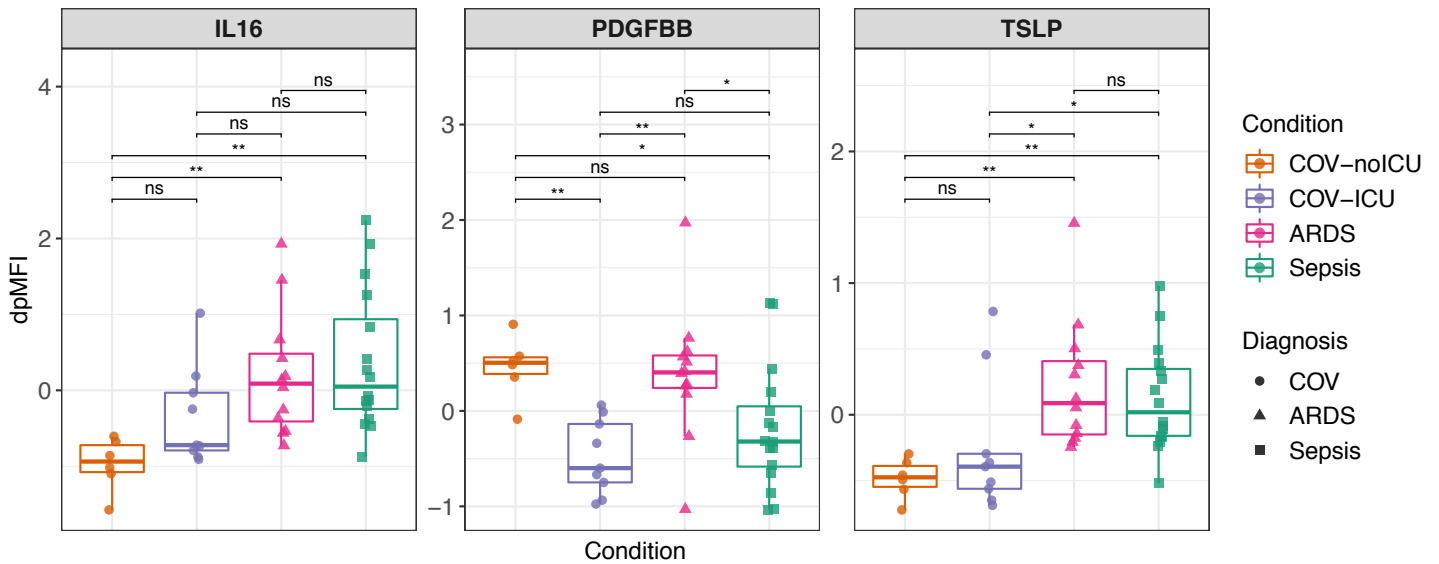
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Supplemental Figure S1. Principal component analysis (PCA) of 70 additional cytokines in moderate COVID-19, severe COVID-19, ARDS and sepsis. Moderate COVID-19 (COV-noICU, orange), $n = 6$. Severe COVID-19 (COV-ICU, purple), $n = 9$. ARDS (pink), $n = 12$. Sepsis (green), $n = 16$. PCA computed by singular value decomposition of the dpMFI values of the 70 cytokines, colored by condition. The first principal component (PC) explains 22.16% of the variability; the second PC explains 11.02% of the variability. The data ellipses were computed assuming a multivariate t-distribution with the ggfortify R package.



Supplemental Figure S2. Differentially expressed cytokines: IL-16, PDGF-BB, and TSLP.

Box plots are shown for IL-16, PDGF-BB, and TSLP, which were the only 3 cytokines that had adjusted p-values < 0.05 by Kruskal-Wallis test with correction for multiple testing with the Benjamini-Hochberg method. Moderate COVID-19 (COV-noICU, orange), n = 6. Severe COVID-19 (COV-ICU, purple), n = 9. ARDS (pink), n = 12. Sepsis (green), n = 16. Adjusted p-values for specific comparisons shown in the plots were calculated by Wilcoxon rank sum tests with correction by the Benjamini-Hochberg correction method. The box plot visualizes the following summary statistics: the middle line represents the median; the lower hinge corresponds to the first quartile (25th); the upper hinge corresponds to the third quartile (75th); upper and lower whiskers extend from the hinge respectively to the largest value and smallest value or no further than 1.5 * interquartile range; data points beyond the whiskers are outliers.



Supplemental Figure S3. Boxplots for the remaining 67 cytokines measured.

Moderate COVID-19 (COV-noICU, orange), n = 6. Severe COVID-19 (COV-ICU, purple), n = 9. ARDS (pink), n = 12. Sepsis (green), n = 16. Adjusted p-values (shown in the top right of the plot for each cytokine) were all > 0.05 by Kruskal-Wallis test with correction for multiple testing with the Benjamini-Hochberg method. The box plot visualizes the following summary statistics: the middle line represents the median; the lower hinge corresponds to the first quartile (25th); the upper hinge corresponds to the third quartile (75th); upper and lower whiskers extend from the hinge respectively to the largest value and smallest value or no further than 1.5 * interquartile range; data points beyond the whiskers are outliers.

Cytokine	Group 1	Group 2	Significance	Adj p-value
PDGFBB	COV-noICU	COV-ICU	**	0.005
PDGFBB	COV-noICU	ARDS	ns	0.694
PDGFBB	COV-noICU	Sepsis	*	0.038
PDGFBB	COV-ICU	ARDS	**	0.005
PDGFBB	COV-ICU	Sepsis	ns	0.423
PDGFBB	ARDS	Sepsis	*	0.039
IL16	COV-noICU	COV-ICU	ns	0.122
IL16	COV-noICU	ARDS	**	0.002
IL16	COV-noICU	Sepsis	**	0.002
IL16	COV-ICU	ARDS	ns	0.122
IL16	COV-ICU	Sepsis	ns	0.070
IL16	ARDS	Sepsis	ns	0.703
TSLP	COV-noICU	COV-ICU	ns	0.634
TSLP	COV-noICU	ARDS	**	0.002
TSLP	COV-noICU	Sepsis	**	0.002
TSLP	COV-ICU	ARDS	*	0.038
TSLP	COV-ICU	Sepsis	*	0.042
TSLP	ARDS	Sepsis	ns	0.767

Supplemental Table S1. Adjusted p-values for comparisons in PDGF-BB, IL-16, and TSLP. Moderate COVID-19 (COV-noICU), n = 6. Severe COVID-19 (COV-ICU), n = 9. ARDS, n = 12. Sepsis, n = 16. Adjusted p-values for specific comparisons shown in the plots in Figure S2 were calculated by Wilcoxon rank sum tests with correction by the Benjamini-Hochberg correction method.