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Supplemental information

Immune system cells from COVID-19 patients display compromised mitochondrial-nuclear expression co-regulation and rewiring toward glycolysis

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Supplemental information

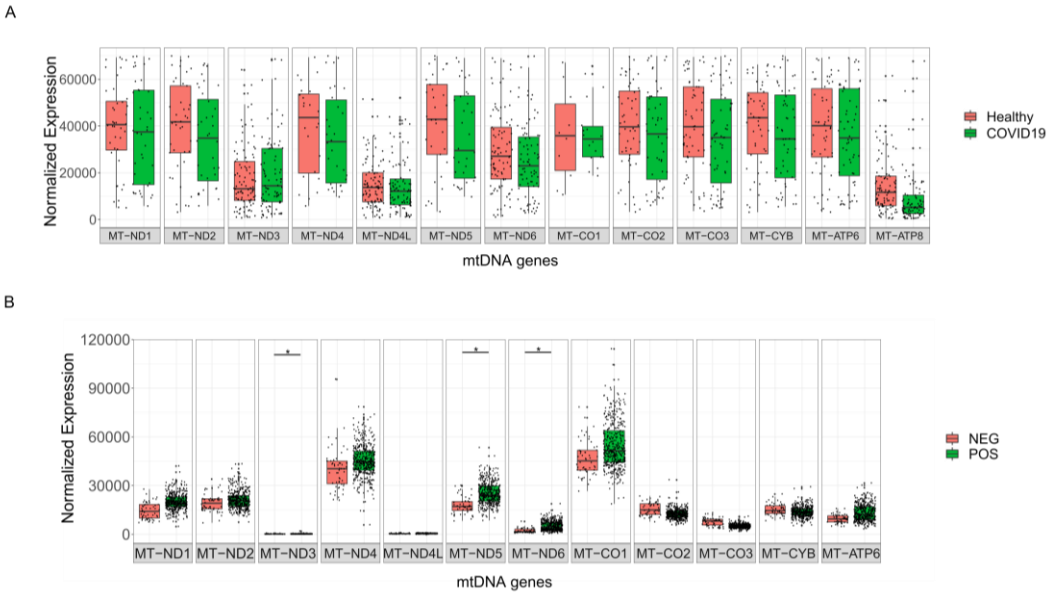

Figure S1. Expression of mtDNA-encoded genes did not significantly differ between healthy and COVID-19 patients in Nasopharyngeal (upper airway) samples, related to Figure 2, Table S1. Box plots representing mtDNA-encoded gene expression of (A) healthy (N=103), COVID-19 patients (N=94) from Dataset I, (B) negative controls (NEG) (N=54), SARS-CoV-2 positive individuals (POS) (N=430) from Dataset IV. X-axes – gene names; Y-axes – normalized read counts, which reflects expression levels.

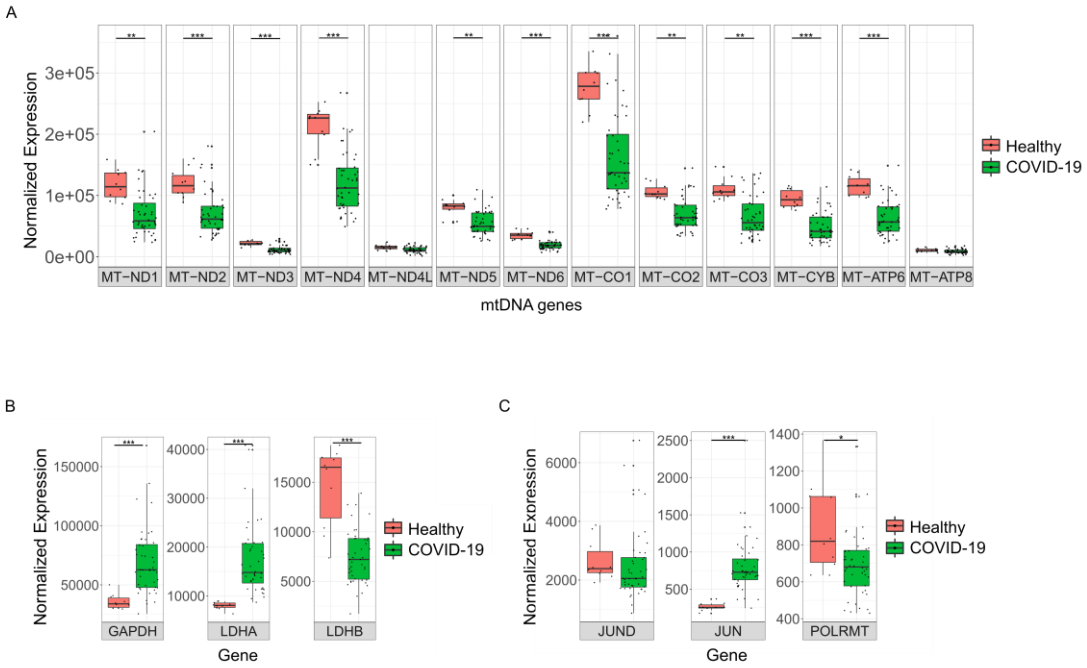

Figure S2. Decreased mtDNA gene expression levels as a feature of COVID-19 in whole blood (Dataset V), related to Figures 2,3, Tables S1-S3. (A) Box plot of Bulk RNA-seq analysis in whole blood display lower mtDNA gene expression in COVID-19 patients as compared to healthy controls. (B) Box plots of GAPDH, LDHA and LDHB and (C) JUND, JUN, POLRMT expression levels. Significance: * - p<0.05, ** - p<0.005, *** - p<0.0005. X, Y axes – as in Fig. 2.