

S4 Fig. Subcutaneous and intramuscular BNT162b vaccination resulted on upregulated inflammatory and immune genes.

- (A) Principle-component analysis (PCA) of inflammatory and immune gene expression following vaccination with PBS or BNT162b via the subcutaneous (SC) or intramuscular (IM) route.
- **(B)** Volcano plots of SC versus IM BNT162b vaccinated gene fold changes (x-axis) and  $log_{10}p$  value (y-axis).

- (C-F) Inflammatory pathway genes TNFα (C), IL6 (D), MAP2K1 (E) and NOS2 (F) normalized
  to their respective PBS controls expressed in whole blood of s.c. and i.m. BNT162b vaccinated
  K18-hACE2 animals.
- (G-J) Complement pathway genes C1RA (G), C2 (H), C7 (I) and CFD (J) normalized to their respective PBS controls expressed in whole blood of s.c. and i.m. BNT162b vaccinated K18-hACE2 animals.
- (K-N) Interferon pathway genes IFN $\alpha$  (K), TLR7 (L), IRF7 (M) and IFIT1 (N) normalized to their respective PBS controls expressed in whole blood of s.c. and i.m. BNT162b vaccinated K18-hACE2 animals.
- Data presented as means  $\pm$  SD. Unpaired student's T test were used for experiments comparing 2 groups. \*P < 0.05, \*\*P < 0.01, \*\*\*\*P<0.0001
- Data underlying this Figure can be found in S2\_Data.

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