Supplementary Materials

for

ACE2 and *TMPRSS2* expression by clinical, HLA, immune, and microbial correlates across 34 human cancers and matched normal tissues: implications for SARS-COV-2 COVID-19

Running Title: Multi-dimensional correlates of *ACE2* and *TMPRSS2* expression

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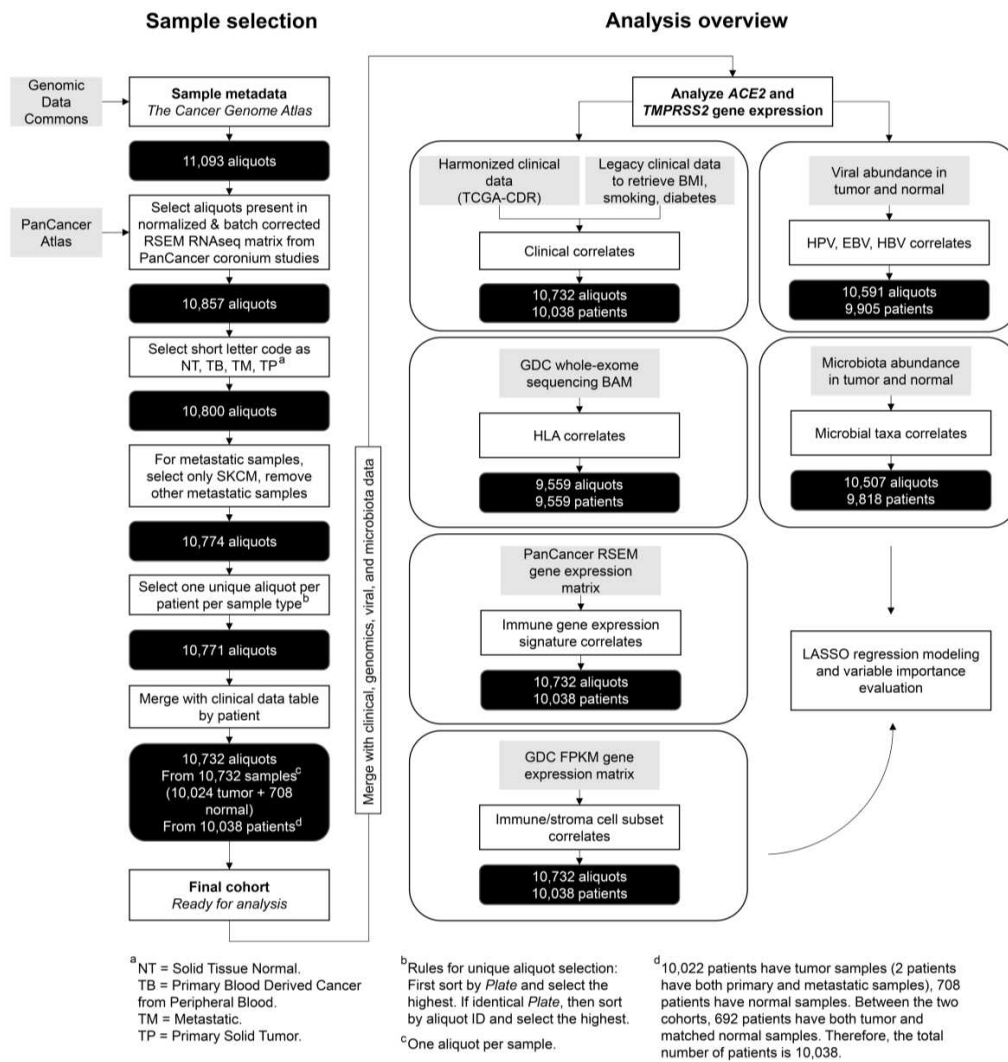5150 Centre Ave. Room 564

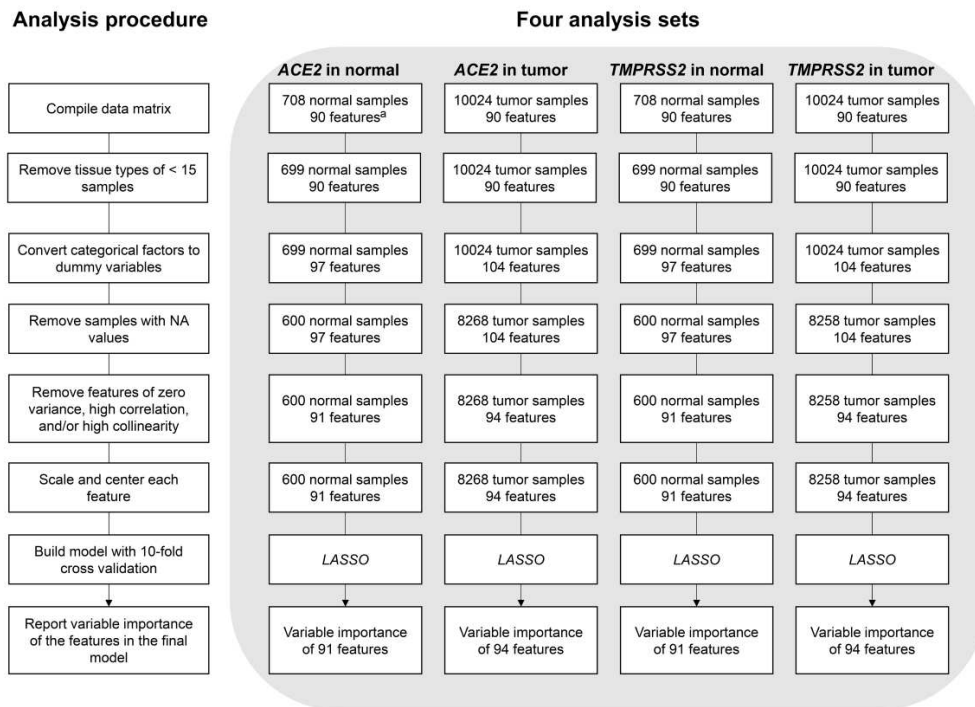Pittsburgh PA 15232

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This document contains **Supplementary Figures 1** and **2**. **Supplementary Tables 1** to **12** are

provided separately as an Excel Spreadsheet file.

Supplementary Figures

Supplementary Figure 1. Sample selection workflow.

Analysis procedure

Four analysis sets

a 90 features consist of: tissue type, clinical (age, gender, race), immune expression signatures (ISG, T cell-inflamed, myeloid, angiogenesis, and TGF-β), immune cell subsets (macrophage M1, macrophage M2, CD8 T cells, CD4 T cells), non-immune cell subsets (epithelial cell), HPV status, and 75 microbiota taxa identified from microbiota correlation analysis.

Supplementary Figure 2. Analytical workflow for variable importance evaluation using LASSO regression.