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Supplementary Material

To identify ACE2 and TMPRSS2 expression in human single cell and composite tissue gene expression datasets, we used publicly available, deidentified data sources. This analysis was approved by the IRB at our institution. We downloaded single cell and bulk RNAseq datasets in the form of gene expression matrices from published sources of human airway, bone, cartilage, meniscus, skeletal muscle, and synovium tissue listed in Table 1. For scRNAseq datasets, we normalized the raw count matrices (number of hits from aligned sequencing reads) using a regularized negative binomial regression as part of R package *sctransform* [1]. We kept the cell type labels as defined by the studies. For each cell type we calculated the percentage of cells expressing either ACE2 or TMPRSS2 at a normalized gene expression value greater than zero. For each cell type we also calculated the average ACE2 and TMPRSS2 expression from normalized data. Since each dataset was normalized independently, the average expression values can only be compared between cell types within the same dataset. For bulk RNAseq datasets of human bone, we normalized the gene expression data as transcripts per kilobase million (TPM) to account for differences in gene length and sequencing depth. Data processing and visualization was done with R version 3.6.2 (2019-12-12) using the Seurat 3.1.4 package [2].

Tissue	Reference	Dataset	Data modality
Airway	Braga et al. 2019 [7]	GEO: GSE130148	scRNAseq
Bone	Weivoda et al. 2019 [8]	GEO: GSE141595, GSE141610	Bulk RNAseq
Cartilage	Ji et al. 2018 [4]	GEO: GSE104782	scRNAseq
Meniscus	Sun et al. 2019 [5]	GEO: GSE133449	scRNAseq
Skeletal muscle	De Micheli et al. 2020 [3]	GEO: GSE143704	scRNAseq
Synovium	Zhang et al. 2019 [6]	ImmPort: SDY998	scRNAseq

Supplemental Table 1. List of RNA-seq datasets analyzed in this report.

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