**Supplementary file of**

**Four potential repurposed drugs to cure COVID-19 using scRNA-seq data and a bioinformatics pipeline**

 We developed a ranking score system that prioritizes these drugs based on 3 novel scores: The connectivity score from CLUE platform (*S1*), the genetic perturbation score (*S2*) and the class score (*S3*).

Each drug has a total score which is aggregated from three different scores:

1. ***connectivity score ():***

is the potency score of drug *i* to reverse the gene expression of the DEGs.

is the connectivity score of the drug *i*  generated from the CLUE server (11).

CLUE query system require a list of up (qup) and down (qdown) regulated genes that were compared to the reference database (Touchstone, r) in LINCS using the weighted Kolmogorov-Smirnov enrichment statistic (18) as shown below:

Where is the weighted connectivity score which represent the similarity measure between a query q (qup , qdown ) and a reference signature r. is the enrichment of in r and is the enrichment of in r.

1. ***genetic perturbation score ():***

is the genetic perturbation score that represents the averaged connectivity score of knocking down the target genes (*1,…,j*) of drug *i*

is the connectivity score of knocking down target gene *j* by drug *i*

1. ***class score ():***

is the class score of drug *i* that represents the number of drugs that have negative connectivity score and belong to the same class as drug *i*.

is the ratio between number of drugs that have negative score and the total number of drugs belonging to the class of drug *i.*

is number of drugs that have negative connectivity score and belong to class *of drug i*. And is number of drugs that have positive connectivity score and belong to class *of drug i*.