

## Supplementary file of

### Repurposing didanosine as a potential treatment for COVID-19 using scRNA-seq data

We developed a ranking score system that prioritizes these drugs based on 3 scores: The connectivity score from CLUE platform ( $S_1$ ), the genetic perturbation score ( $S_2$ ) and the class score ( $S_3$ ).

$$S_{t_{di}} = S_{1_{di}} + S_{2_{di}} + S_{3_{di}}$$

Each drug has a total score  $S_{t_{di}}$  which is aggregated from three different scores:

- 1- Drug's connectivity score: which is calculated from LINCS cloud server (CLUE.IO). It was based on the weighted Kolmogorov-Smirnov enrichment statistic.
- 2- Genetic perturbation score: which is the average of the connectivity score of drug's target genes.
- 3- Class score: which represents the number of drugs per each class that have negative connectivity score ( $<-90$ ).