

Fig. S4

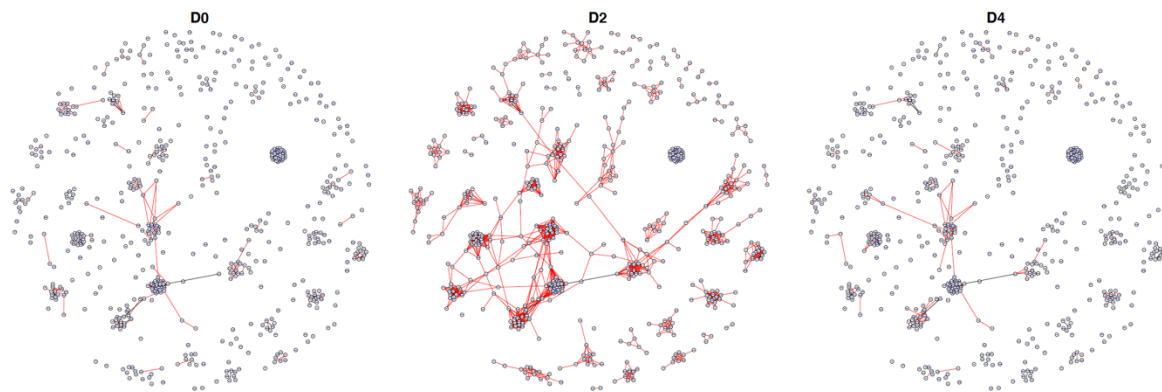


Fig. S4 Differential Co-Expression Networks in Monocytes of Patients with Good Prognosis on Days 0, 2 and 4. The black edges show co-expression pairs at three time points, and red edges show the changes in co-expression with time. For each cell type, we enriched the top 500 most highly expressed genes to yield 332 genes that interact with SARS-CoV-2 using the hypergeometric test. To identify the pathways most affected by MSC treatment, we performed differential co-expression analyses using R package DiffCorr and found that the network on day 2 was significantly rewired, with many activated interactions, and the network on day 4 was largely restored to that of day 0. Related to Fig. 2.