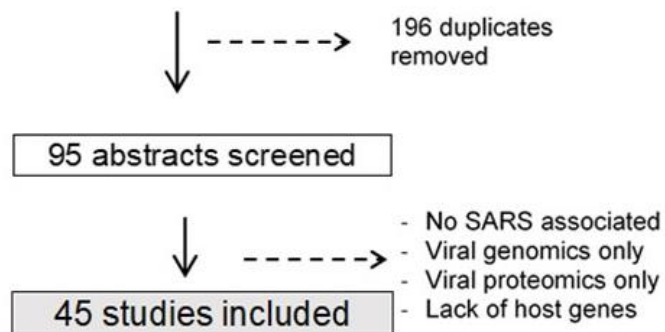
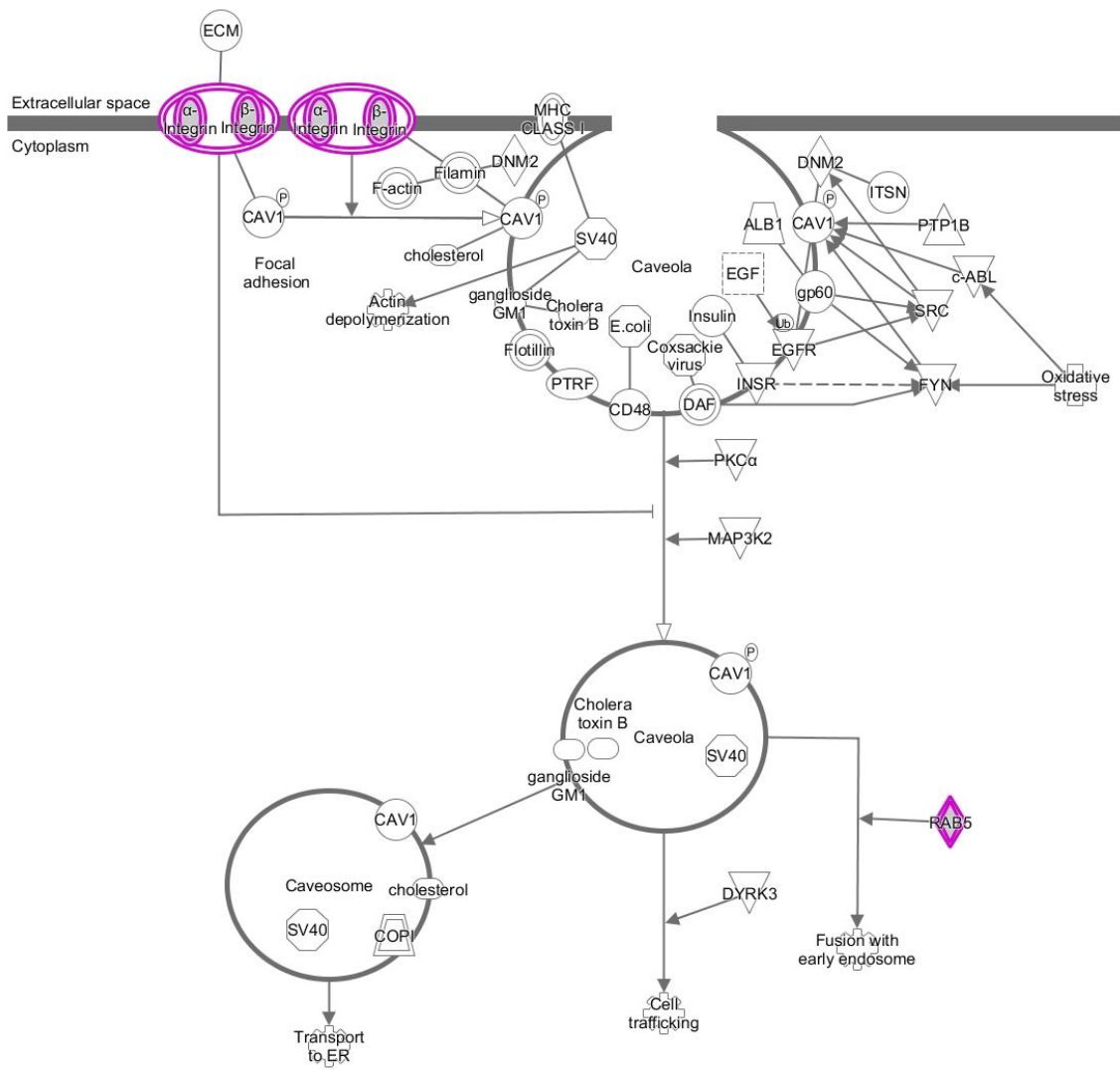


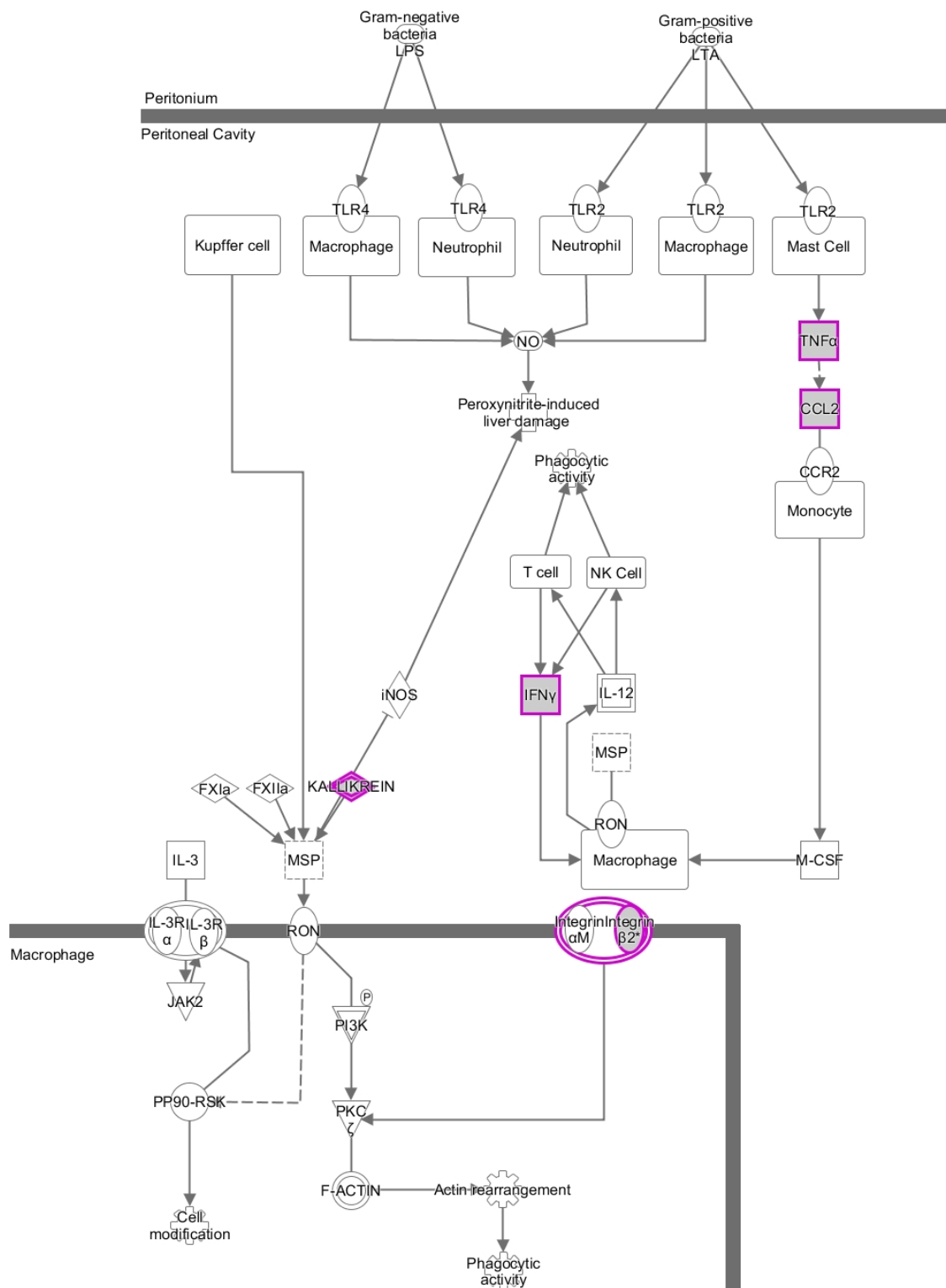
PubMed searched terms		Number publications
COVID-19	+ genes	28
	+ protein interaction	40
	+ protein receptor	85
SARS-CoV-2	+ gene	66
	+ interactome	4
	+ protein interaction	31
SARS-CoV	+ interactome	7
	+ nsp protein	30
Total		291



**Supplementary Figure S1: PubMed search between the 31st of March and 25th of May 2020.** Several searching terms were entered in the database to identify all reported SARS-CoV host interactome reported genes.



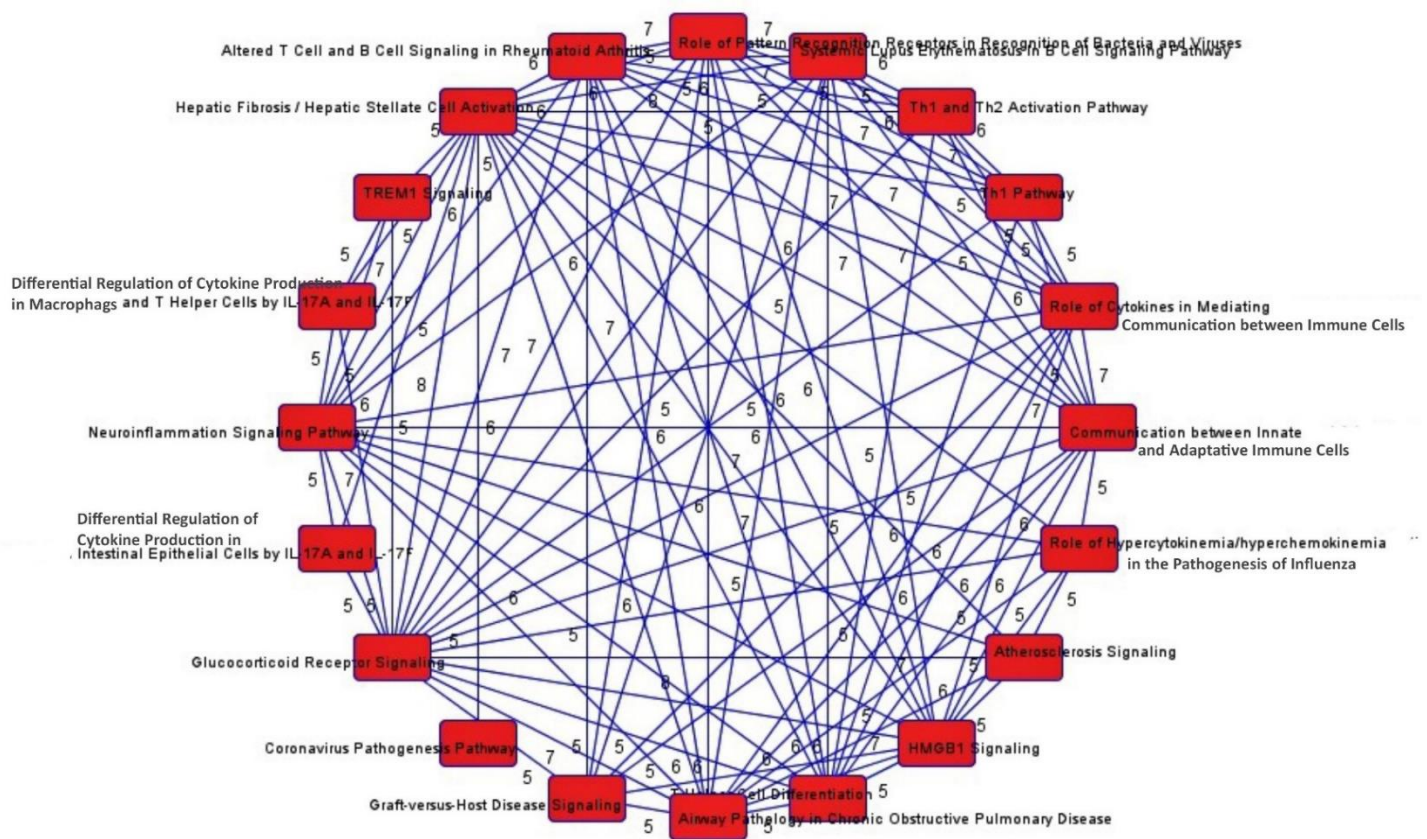
**Supplementary Figure S2: Caveolar-mediated Endocytosis signalling pathway.** Most significant canonical pathway associated with all candidate genes. Purple lines show the literature reported candidate genes in the pathway. Figure generated with IPA software.



**Supplementary Figure S3: MSP-ROn signalling pathway.** Second most significant canonical pathway associated with all candidate genes. Purple lines show the literature reported candidate genes in the pathway. Figure generated with IPA software.

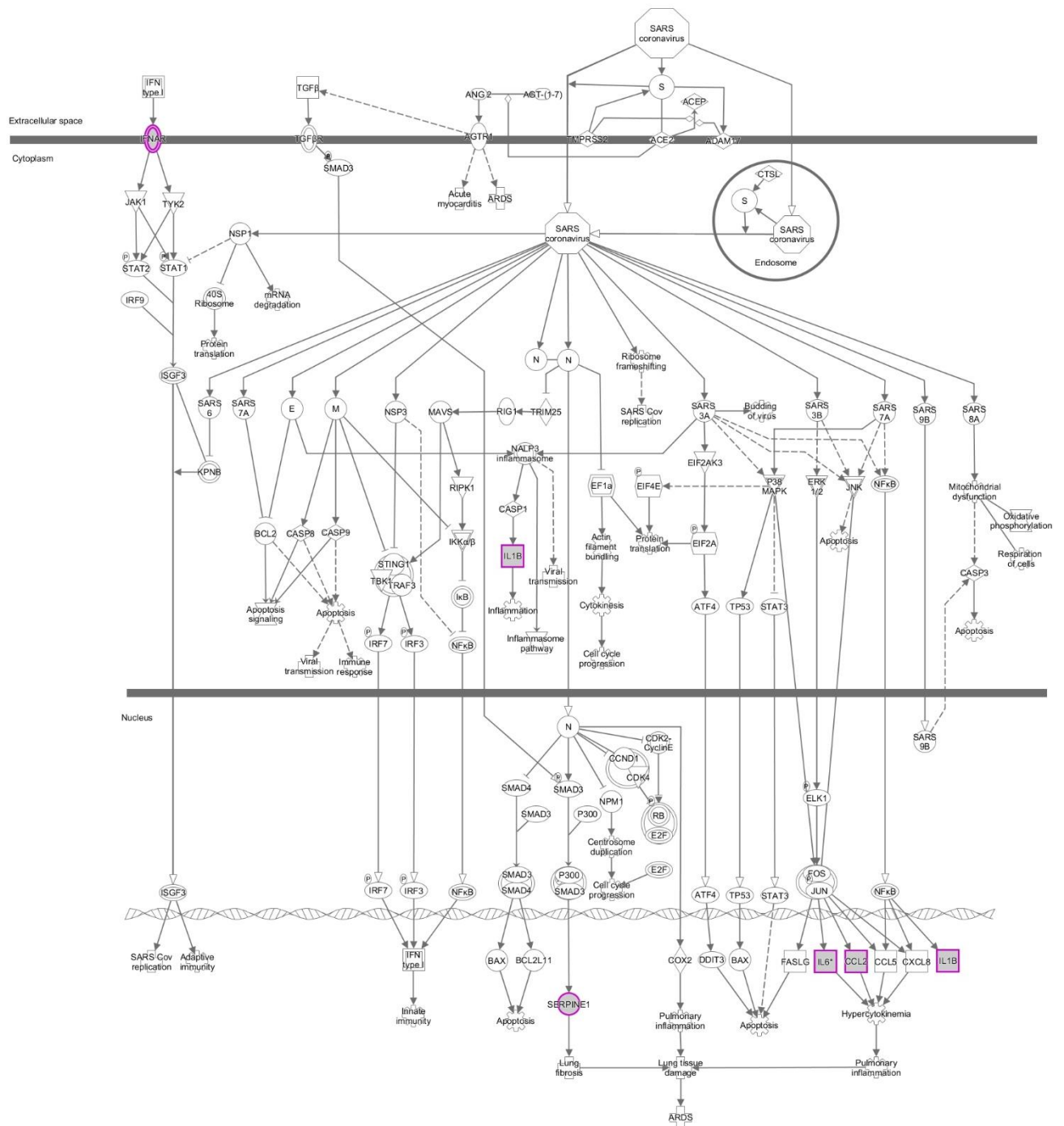






**Supplementary Figure S6: Overlapping of those canonical pathways with common candidate genes.** The 20 most significant pathways with a minimum of five common candidate genes associated with COVID-19 aggressive phenotype are shown. The bright red colour square reflects the high level of significance ( $2.5 \times 10^{-18} < P < 1 \times 10^{-8}$ ). Figure generated by IPA generated software (Qiagen Inc.). P values calculated by Fisher's Exact Test.





**Supplementary Figure S7: Coronavirus Pathogenesis signalling pathway.** Showing the host-coronavirus pathway. Purple lines show the location of the candidate genes associated with aggressive COVID-19 symptoms in the pathway. Figure generated with IPA software.