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Bioinformatic Approaches for Identification of Potential Repurposable Drugs in COVID-19

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Abstract

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Introduction: Repurposing existing drugs approved for other conditions is crucial to identifying specific therapeutics against SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) causing COVID-19 (coronavirus disease 2019) pandemic. Towards this attempt, it is important to understand how this virus hijacks the host system during the course of infection and determine potential virus- and host-targeted inhibitors.

Methods: This study elucidates the underlying virus-host interaction based on differentially expressed gene profiling, functional enrichment and pathway analysis, protein-protein and protein-drug interactions utilizing the information on transcriptional response to SARS-CoV-2 infection from GSE147507 dataset containing COVID-19 case relative to healthy control and infected cell culture compared to uninfected one.

Results: Low IFN signaling, chemokines level elevation, and proinflammatory cytokines release were observed markedly. We identified MYC-rapamycin and ABCG2-rapamycin interactions, and unique gene signatures in case (regulation of protein modification and MAPK signaling) as well as in cell (metabolic dysregulation and interferon signaling) different from known COVID-19 genes.

Conclusion: Among a plethora of repurposable drugs those appearing here with unique gene signatures might be helpful in COVID-19

Keywords: COVID-19, SARS-CoV-2, GSE 147507 dataset, protein-protein interaction, gene-drug interaction, repurposable drugs.

INTRODUCTION

As of December 17, 2020, the ongoing COVID-19 (coronavirus disease-2019) pandemic caused 72,851,747 confirmed infections globally including 1,643,339 deaths[1], because of the lack of specific treatments or vaccines. Repurposing drugs may possibly curtail the time and costs compared to de novo drug discovery, in addition to providing principal information on pharmacology and toxicology, as well as ascertaining novel indications for prompt clinical trials and regulatory assessment[2-5]. The present study address this by mapping the interaction between viral proteins and human proteins in SARS-CoV-2 infected case compared to healthy control, in SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) infected-compared to uninfected cell culture. This was achieved by downloading the GSE147507 dataset from the Gene Expression Omnibus (GEO) database (www.ncbi.nlm.nih.gov/geo/) related to transcriptional response to SARS-CoV-2 infection[6]. The underlying virus-host interactions was elucidated based on differentially expressed genes (DEGs) profiling, functional enrichment and pathway analysis, protein-protein interaction (PPI) network,

and protein-drug interaction (PDI) in context to COVID-19. Herein we explore the major regulatory genes as potential biomarkers of COVID-19, transcriptional response to SARS-CoV-2 infection in cell culture as well as in case, comparison of the known gene signatures in COVID-19 with that in case and culture, and identification of potential repurposable drugs for COVID-19 treatment.

METHODS

COVID-19 disease associated genes and network

The top 100 COVID-19 associated human genes were retrieved from disease query of the STRING (Search Tool for the Retrieval of Interacting Genes) (http://string-db.org/cgi/input.pl; version 1.5.0) App[6] of the Cytoscape software, version 3.7.2 (https://cytoscape.org/), according to Shannon et al.[8]. A STRING network was created with top 44 COVID-19 related genes ranked in order of disease scores and degree connectivity; the set of top 44 genes were named as group A with their disease scores and degree connectivity ranging from 1.043351 to 3.922025 and from 1 to 29, respectively.

SARS-CoV-2 gene expression data acquisition and PPI network analysis

The gene expression dataset GSE5147507 was obtained from the gene expression omnibus database (www.ncbi.nlm.nih.gov/geo/) related to transcriptional response to SARS-CoV-2 infection[6], from where 10 samples were selected and divided into group B and group C. Group B contained technical replicates of human lung biopsy samples from a single COVID-19 deceased male patient of >60 years with no treatment (GSM4462415: Series15_COVID19Lung_1 and GSM4462416: Series15_COVID19Lung_2) and biological replicates of human lung biopsy samples derived from two uninfected male patients of >60 years with no treatment (GSM4462413: Series15_HealthyLungBiopsy_1 and GSM4462414: Series15_HealthyLungBiopsy_2). Group C contained independent biological triplicates of transformed lung alveolar cells (A549) transduced with a vector expressing human ACE2 mock treated (GSM4486157: Series16_A549-ACE2_Mock_1, GSM4486158: Series16_A549-ACE2_Mock_2, and GSM4486159: Series16_A549-ACE2_Mock_3) or infected with USA-WA1/2020 SARS-CoV-2 strain (GSM4486160: Series16_A549-ACE2_SARS-CoV-2_1, GSM4486161: Series16_A549-ACE2_SARS-CoV-2_2, and GSM4486162: Series16_A549-ACE2_SARS-CoV-2_3).

The DEGs were identified in COVID-19 case relative to the uninfected control (group B), and in ACE2-induced A549 cell line with SARS-CoV-2 infection compared to the uninfected cell line (group C); the threshold for DEGs were set as $|log2FoldChange|$ ($|log_2FC|$) >10, and $|log_2FC|$ >3 respectively, for the two groups. A PPI network was constructed with the DEGs in group B and group C using STRING App of the Cytoscape software, version 3.7.2 (https://cytoscape.org/), as per Shannon et al.[8]. The significant DEGs were expressed as heatmaps using R programming (https://www.r-project.org/; version 3.6.1 [2019-07-05]) gplots tools from the Biobase packages (https://CRAN.R-project.org/package=gplots) of the Bioconductor project[9].

GO and KEGG pathway enrichment analyses

The DEGs $|log_2FC|$ were analyzed at the functional level for GO (Gene Ontology) and KEGG pathway enrichment using the STRING Enrichment App of the Cytoscape software (https://cytoscape.org/), following Shannon et al.[8], with P value<0.05 as the cut-off criterion. The enrichment analyses were depicted using R programming (https://www.r-project.org/; version 3.6.1 [2019-07-05]) ggplot tools from the Biobase packages (https://CRAN.R-project.org/package=ggplot2) of the Bioconductor project[9].

SARS-CoV-2 protein and drug interaction (PDI) network analysis

The PDI network was constructed with STITCH: protein/compound query for the three groups A, B, and C comprising top 44 COVID-19 related genes, 255 DEGs among COVID-19 case compared to uninfected control, and 363 DEGs among ACE2 induced cell line treated with and without SARS-CoV-2, using STRING App of the Cytoscape software, version 3.7.2 (https://cytoscape.org/), according to Shannon et al.[8]; the approved and experimental repurposable drugs against COVID-19 were included to create the PDI network[4,10].

Possible repurposable drugs in SARS-CoV-2 and human protein interaction

The host-virus gene interaction in COVID-19 case and SARS-CoV-2 infected cell line were combined with PDI network to demonstrate potential repurposable therapeutics in the treatment of COVID-19, using all possible combinations of DEGs significance level: case significant and cell line insignificant, case insignificant and cell line significant, both case and cell line significant (case less than cell line), both case and cell line significant (case greater than cell line), and both case and cell line insignificant.

RESULTS AND DISCUSSION

The putative physiological response to SARS-CoV-2 infection from virus entry to release from the host, in the present study, as expressed from COVID-19 case and SARS-CoV-2 infected cell line is depicted in Figure 1. Briefly, the RBD of FURIN preactivated SARS-CoV-2 spike protein binds with human ACE2 receptor in association with TMPRSS2 to facilitate viral entry by endocytosis[4], and thereafter the virus release genome into the cytosol by autophogosome-lysosomal pathway involving ULK, PI3K, ATG5-ATG12-ATG, and LC3-PE genes. The genomic RNA containing ORF1a and ORF1b is translated to pp1a and pp1ab replicase polyproteins that auto-cleave into 16 nsps, to constitute the RTC (replication and transcription complex), which synthesizes minus-stranded RNA[3,4,11]; both full-length and subgenome-length strands are synthesized. The structural and accessory proteins are encoded by subgenomic mRNAs positioned at one-fourth of the genome near 3′ end[12,13]. The genomes are then packaged into nucleocapsids and enveloped by budding from smooth intracellular membranes to release virions by exocytosis. The SARS-CoV-2 has evolved strategies including inhibition of host IFN signaling (by nsp1 to decrease p-STAT1 in infected cells)[14], PKR-mediated apoptosis (NendoU by evading dsRNA sensors in host cell)[15,16], NKRF repression by nsp9 and nsp10 as well as hijacking of ubiquitination by nsp10 with DUB activity[15], to evade the host immune response against viral infection. The current dataset GSE5147507 contain the expression of CDK; N protein mediated restriction of cell cycle by CDK4/6 protein[17], which was significantly decreased in both COVID-19 case and SARS-CoV-2 infected cell line, and nsp14 mediated upregulation of viral replication and transcription by DDX1 gene[18], which was decreased in both COVID-19 case and SARS-CoV2 infected cell line in the current study. The virus counteract IL6 by inducing DUSP1 (decreased in COVID-19 case, elevated in SARS-CoV-2 infected cell line), a negative regulator of p38 MAPK (decreased in both case and cell line), also reported by Liao et al.[19]. The viroporin E protein activate NLRP3 inflammasome (decreased in case, elevated in cell line) to trigger production of TNF, IL6, and IL1B proinflammatory cytokines causing host-immunopathological conditions: hypercytokinemia, ARDS and multi-organ failure[20].

Herein, the DEGs of COVID-19 retrieved from STRING disease query of Cytoscape (https://cytoscape.org/) were designated as group A, whereas the dataset GSE5147507 was analyzed to identify DEGs in COVID-19 case versus uninfected healthy control categorized into group B, and ACE2-induced A549 cell line infected with SARS-CoV-2 versus uninfected A549 cell line recognized as group C (Figure 2). The PPI network constructed with top genes from group A, B, and C are depicted in Figure 2(a-d). The three study groups, A, B, and C displayed 255, 363, and 98 number of DEGs (Figure 2e) with common expression of CSF2 among all the three groups; TMPRSS2 expression was overlapping between group A and group B, while CYP1A1, PLEKHA4, and MXT4 expression were common between group B and group C; group A and group C shared ALB, APOH, BATF2, ENPEP, IFNB1, TNF, and TNNI3 gene expression. There were 18 genes in two clusters: CSF3, IL1B, IL2RA, and IL6 in group A, FOS, MFN2, MYC, PDGFRB, PPP3R1, TSC1 in group B, and

ALDH3A1, ACDH3A2, CAT, CES1, CTSD, EGR1, TNF, and TNFSF10 in group C (Figure 3a).

Apart from the genes involved in SARS-CoV-2 infection from virus entry to release from the host (Figure 1), it elicits host innate immune response against the virus through IFN and chemokine signaling (Figure 3b-d). The cells respond to viral PRRs by downstream expression of IRFs (particularly, IRF3 downregulated in case and cell line, IRF9 downregulated in case, and IRF7 upregulated in cell line) and NFKB (downregulated in case; upregulated in cell line) to induce IFN-I and IFN-II signaling. The COVID-19 case study depicted failure to express significant IFN-I transcriptional response due to the absence of IFNA, IFNB, and ISRE, although other genes related to type I and type II IFN signaling were significantly induced in the case (Figure 3c); SARS-CoV-2 infection in cell line too showed significant induction of only few genes related to type I and type II IFN signaling. Within the IFN signaling, the IRF9-STAT2 pathway was expressed in both case (mostly down-regulated) and cell line (mostly upregulated) eliciting genes responsible for restricting viral replication (IFI6, IFIT1, IFIT2, IFIT3, IFITM1, IFITM3, OAS1, OAS3, OAS2, MX1, MX2, RSAD2, OASL) and activating apoptosis (XAF1, IRF2, IRF7) (Figure 3d). The SARS-CoV-2 viral replication restricted the expression of ISG15 (both case and cell line in the GSE5147507 dataset analyzed), that play a role in the induction of myriad of antiviral interferon-stimulated genes[21]. The ISG20 (in the current dataset GSE5147507), downregulated in COVID-19 case, acts as IFN-mediated ssRNA antiviral exoribonuclease, is related to IFNG signaling. Despite virus replication (strong expression in case compared to cell line), the host response to SARS-CoV-2 was ineffective to instigate a strong IFN-I and -II pathways whereas concurrently inducing elevated levels of chemokines required to engage effector cells. The differentially decreased genes that are involved in inflammasome activation and activity include NLRP3, CASP5, IL1A, IL1B, IL18RAP, and IL1R2, and those involved in chemokine signaling for recruiting innate immune cells to the epithelium include CCL2, CCL3, and CCL4, while the most significant ISGs in SARS-CoV-2 infection include IFI6, IFI44L, IFI27 and OAS2 genes[22].

The present dataset featured a wide array of gene expression of chemokine subfamilies (Figure 3b). The most significantly expressed CCL chemokines were CCL4 and CCL23 with log_2FC values 2.28 and -8.9, respectively in COVID-19 case compared to healthy control group. CCL4 and CCL26 were expressed most significantly with log_2FC 2.96 and -2.76, respectively along with CCL3 (disease score = 1.8; log_2FC 1.1) in SARS-CoV-2 infected- compared to uninfected cell line. In addition to the expression of monocyte associated CCL8 in COVID-19 case, CCL2 (disease score = 1.66) was also expressed significantly in both case and cell line. CCR7 in COVID-19 case (log_2FC -11.08), and CCR6 in both case (log_2FC -6.74) and cell line (log_2FC 3.22) were the most significantly expressed chemokine receptors. Among CXC subfamily, CXCR4 (disease score = 1.85; log_2FC -6.8 in case and 2.42 in cell line, CXCL10 (disease score = 1.79; log_2FC 2.07 in cell line), CXCL11 (log_2FC -1.62 in case and 5.25 in cell line) and CXCL2 (log_2FC -7.7 in case and 4.24 in cell line) were significant. CXCR4 is involved with the binding of CD4 to support HIV entry into cells and highly expressed in cancer; CXCL11 is dominant ligand for CXCR3 (CXCL3 log_2FC -7.15 in case and 2.98 in cell line) and is induced by IFNG while CXCL2 is expressed at the inflammatory site and may inhibit hematopoietic progenitor cell proliferation [23]. The current dataset expressed CX3CL1 (log_2FC -5.73) in COVID-19 case and CX3CR1 (log_2FC -1.32) in cell line. The CX3CL1 plays role in cancer,

atherosclerosis, AIDS, and inflammatory diseases; CX3CR1 gene is involved in adhesion, migration of leucocytes, and acts as a co-receptor for HIV1[23].

The present study alongside the other reports[24] indicate SARS-CoV-2 infection, marked by low IFN-I and IFN-II signaling, induce profuse release of proinflammatory cytokines (TNF, IL1B, IL6, IL8, CSF2, CSF3), chemokines (CCL2, CXCL10, CCL3) and T cell-derived IL17 triggering immunopathogenicity with multi-organ damage, even while the immune response seeks to suppress and eradicate the virus. The COVID-19 severity dependent gene expression is depicted in Figure 3e. Among the plasma cytokines (IL2, IL4, IL6, IL10, IL17, TNFA and IFNG) related to COVID-19 severity and progress, the IL10 level was higher in severe compared to mild patients, IL10 was positively correlated with IL6 level, leucocyte count and neutrophil count, but not with lymphocytes and monocytes count[25].

Functional analyses of statistically enriched genes are represented in Figure 4 and 5. The most enriched GO and KEGG pathway among known COVID-19 genes were regulation of signaling receptor activity (FDR 3.64×10^{-22}) and cytokine-cytokine receptor interaction (FDR 6.01×10^{-22}), respectively (Figure 4a and 5a), while among genes downregulated in COVID-19 case were regulation of protein modification (FDR 2.03×10^{-5}) and MAPK signaling (FDR 1.23×10^{-5}) (Figure 4b and 5b), respectively. The top GO and KEGG pathway in downregulated DEGs of SARS-CoV-2 infected cell line were secretion by cell (FDR 1.67×10^{-6}) and metabolism of drugs (FDR 4.66×10^{-8}) (Figure 4c and 5c), respectively, while those among upregulated DEGs were IFN signaling pathway (FDR 1.69×10^{-13}) and NOD-like receptor signaling (FDR of 3.82×10^{-6}) (Figure 4d and 5d), respectively.

The major candidate genes in group A were ACE2 (highest disease score 2.55, significantly downregulated in case) and IL6 (highest degree connectivity 29, significantly downregulated in case and upregulated in cell line) with cytokine-cytokine receptor interaction as the top enriched pathway. The enriched pathway (Figure 5a), and ACE2 under expression along with IL6 activation are related to angiogenesis and cancer[26,27]. The DEGs in group B exhibited major candidate genes to be MYC (with highest degree connectivity) and SFN (with highest log_2FC) both related to cancer along with FOS, PPP3R1, TSC1, PDGFRB, and MFN2 in PPI network (Figure 2b). The enriched MAPK and PI3K-AKT pathways are important mediators of cellular processes, dysregulation of which is associated with cancer pathogenesis[28,29]. The key candidate genes in group C DEGs (downregulated) were ALB (highest degree connectivity) and EPHX1 (highest log_2FC) (Figure 2c), and upregulated DEGs were TNF with highest degree connectivity and IFNB1 with highest log_2FC (Figure 2d). The gene families for ALB and TNF are plasma proteins, intracellular and secreted proteins, in addition to cancer-related and candidate cardiovascular disease genes. Similarly, EPHX1 is related to intracellular proteins, cancer-related genes along with potential drug targets, whereas IFNB1 belongs to cancer-related and secreted proteins related gene families[30]. Several of the other cancer associated genes (GSTA1, ABCG2, CAT, CTSD, TF, EGR1, TNFSF10) appeared in the network (Figure 2c-d) were linked with transcriptional response to SARS-CoV-2 infected cell lines affecting innate immunity (CHRNB4, CAT, CTSD, IFNB1), and endothelial and vascular inflammation (TNF, ICAM) in COVID-19.

These DEGs altogether displayed association with old and new drugs potentially useful in COVID-19 therapy and tested or used in the oncological settings as well[31], including

rapamycin, chloroquine, lopinavir, ritonavir, ribavirin as appeared in PDI network in our study (Figure 6), remdesivir, tocilizumab and sarilumab as shown in virus-human protein interaction (Figure 1). The PDI network of group A genes showed top scores of 0.985 and 0.923 for rapamycin (degree of interaction: 5) with IL10, IL2A, CD8A, CD40LG, and CSF3 (Figure 6a). Cyclosporine possessed the highest degree of interaction (=7) with CD40LG, IL1B, IFNG, CD8A, IL6, CSF3, and IL2RA, with score ranging from 0.453 to 0.897) (Figure 6a). The IL6 gene had highest degree of interaction (=4) with azithromycin, oseltamivir, cyclosporine, and prednisone]. The PDI network of group B genes showed top scores of 0.926 and 0.876 respectively, in PPP3R1-cyclosporine and MYC-doxycycline interactions; rapamycin had highest degree of interaction (=5) with TSC1, MYC, PDGFRB, MFN2, and PPP3R1; MYC was commonly interacting gene for doxycycline, rapamycin and cyclosporine (Figure 6b). In group C, TNF-chloroquine and ABCG2-cyclosporine had top interaction scores of 0.969 and 0.955. The highest degree of interaction (=5) was achieved for rapamycin (scores: 0.683-0.884), with ABCG2, GSTA1, TF, ALDH3A1 and ALDH3A2, while the gene with highest degree (=6) was ABCG2 having interaction with cyclosporine, rapamycin, ivermectin, ritonavir, CHQ, and macrolides (scores: 0.466-0.955) (Figure 6c). In general, The PDI network showed rapamycin as top interactor with IL6, MYC and ABCG2 genes in group A, B and C, respectively (Figure 6a-c).

Combined with the current findings, several approved or experimental drugs have been repurposed against SARS-CoV-2 including remdesivir (HIV reverse transcriptase inhibitor), anti-influenza favipiravir (RdRp inhibitor), ribavirin (RNA synthesis and capping inhibitor), anti-influenza baloxavir marboxil (cap-dependent endonuclease), HIV protease inhibitors lopinavir and ritonavir, endocytosis inhibitor antimalarial chloroquine/hydroxychloroquine, antibiotic azithromycin, immunosuppressant cyclosporine (cyclophilin inhibitor), rapamycin (FKBP/mTORC inhibitor), tocilizumab (IL6 receptor antagonist), sarilumab (tocilizumab efficacy dependent), antihelminthic ivermectin (integrase and importin α/β1 inhibitor), antiprotozoal/antiviral netazoxanide (inhibitor of viral replication by tizoxanide metabolite), nefamostat/camostat (ACE2 receptor/TMPRSS2 inhibitor), antidepressant fluvoxamine, INFβ-1a inhibitor (CD73 ecto-5/-neucleotidase) are under clinical trials for COVID-19 treatment[4,9,32-36].

CONCLUSION

Overall, the plausible repurposing drugs for COVID-19 treatment include cyclosporine, doxycycline, chloroquine and rapamycin that emerged as top scoring interactors with MYC, PPP3R1, FOS, ABCG2, and TNF in SARS-CoV-2 infection compared to drug (cyclosporine, azithromycin, rapamycin, and oseltamivir) interaction with IL6, CD8A, CD40LG, IL10, and CSF3 known COVID-19 genes. Among a plethora of available repositionable drugs, those with their targets, appearing in this investigation, might be helpful to combat the ongoing COVID-19 pandemic.

Acknowledgement

Conflict of Interest

The authors declared that they have no conflicts of interest to this work.

Authors' contribution

MM: Retrieved, processed and analyzed data, and wrote the paper; SM: designed the study, discussed and co-wrote the paper.

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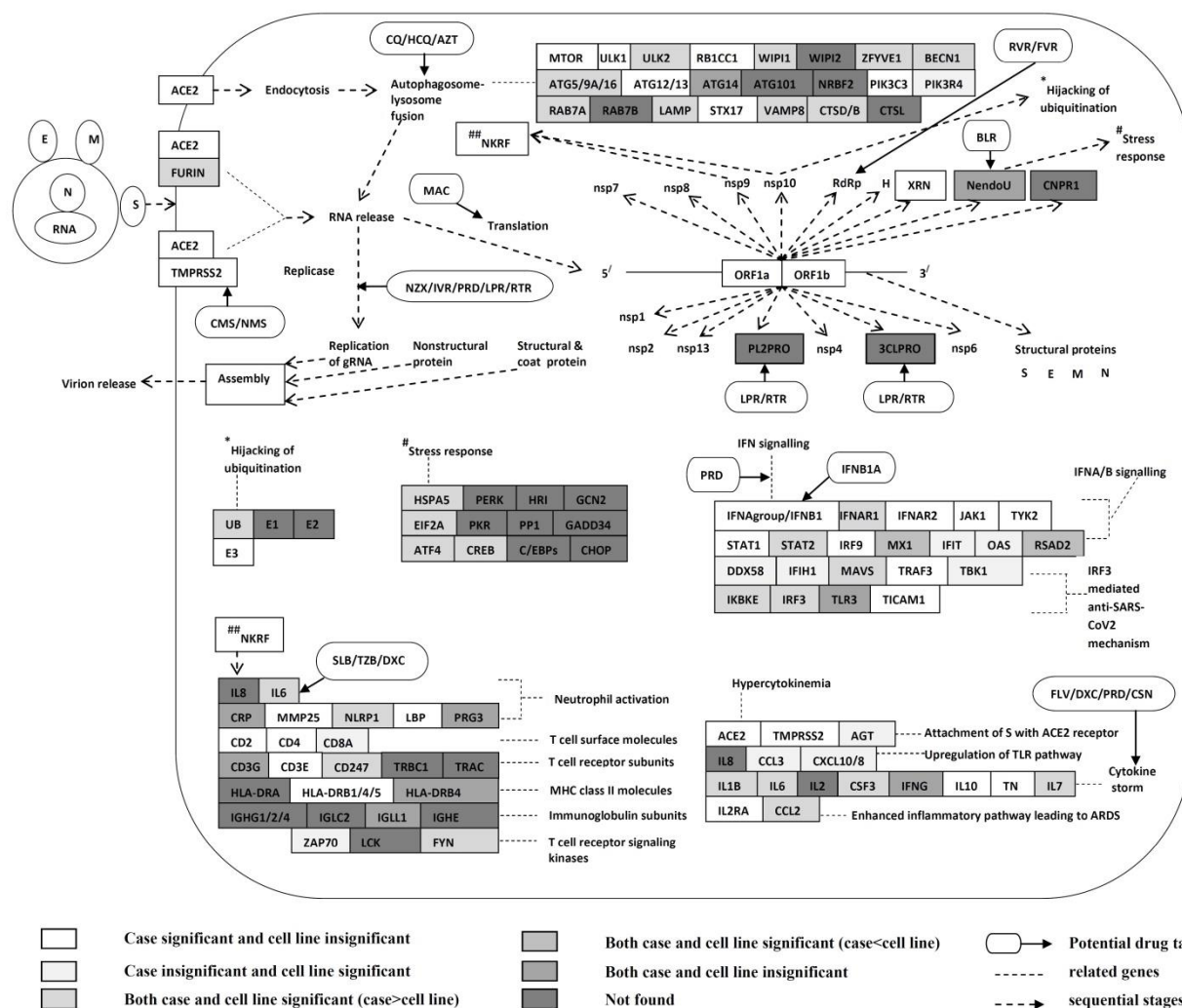36. Uno Y. Camostat mesilate therapy for COVID-19. *Intern Emerg. Med* 2020; doi: 10.1007/s11739-020-02345-9

Figure 1: Host-virus gene interaction in COVID-19 case and SARS-CoV-2 infected cell line. The SARS-CoV-2 utilizes different strategies (inhibition of host IFN signaling, PKR-mediated apoptosis, NKRF repression, and hijacking of ubiquitination) to evade the host immune response while host counteract the SARS-CoV-2 infection through immune response by IFN and chemokine signaling. The repurposable approved and experimental drugs (AZT: azithromycin; BLR: baloxavir; CMS: camostat; CQ: chloroquine; CSN: cyclosporine A; DXC: doxycycline; FLV: fluvoxamine; FVR: favipiravir; HCQ: hydroxychloroquine; IFNB1A: interferon beta 1a; IVR: ivermectin; LPR: lopinavir; MAC: macrolides; NMS: nafamostat; NZX: nitazoxanide; PRD: prednisone; RPN: rapamycin; RTR: ritonavir; RVR: remdesivir; SLB: sarilumab; TZB: tocilizumab) act at several host-virus interaction sites exerting anti-SARS-CoV-2 activity.
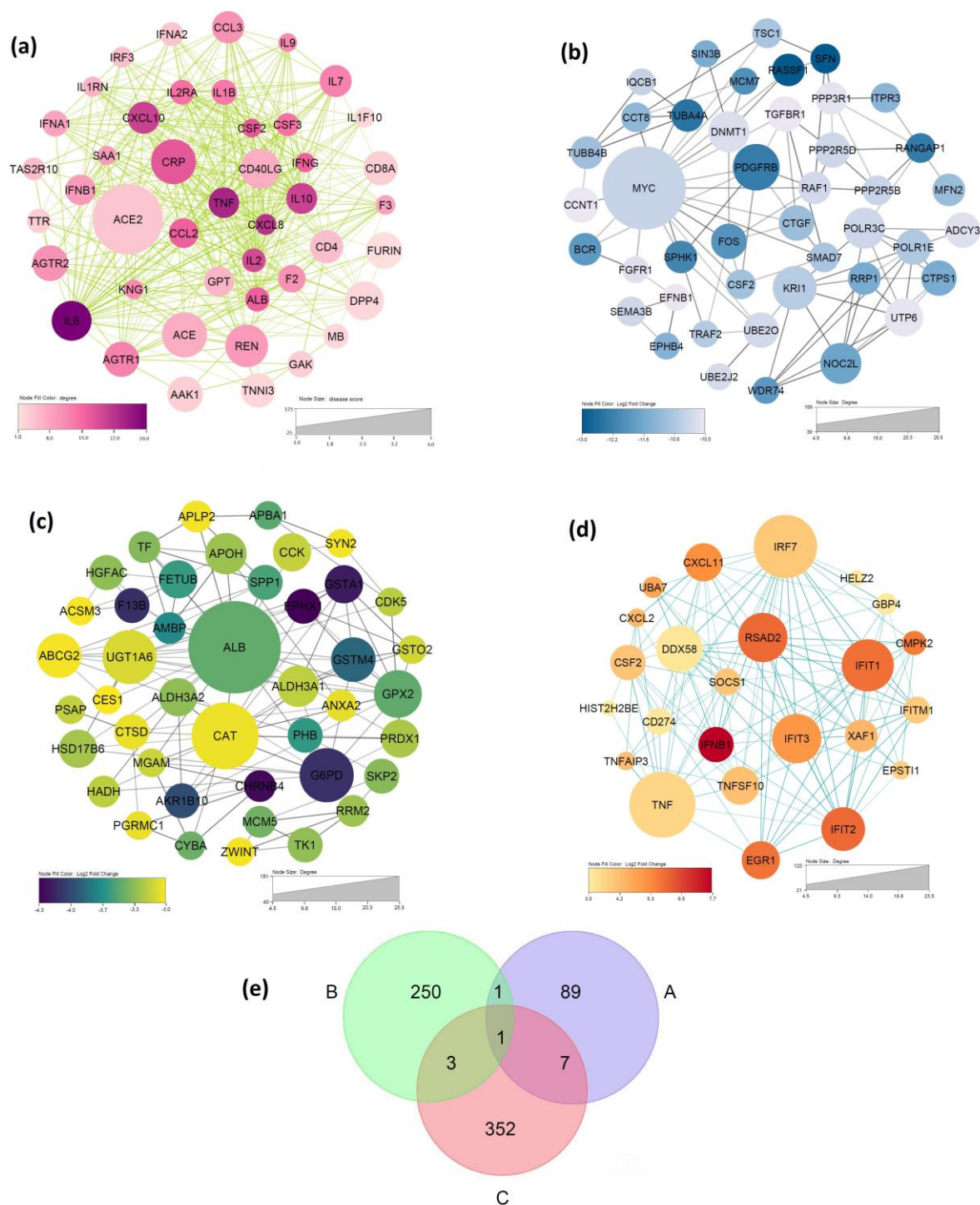
Figure 2: The DEGs (differentially expressed genes) in group A (COVID-19 associated human genes), group B (COVID-19 case versus uninfected healthy control) and group C (ACE2-induced A549 cell line infected with SARS-CoV-2 versus uninfected A549 cell line). PPI (protein-protein interaction) network of top genes: (a) group A displaying 44 genes with disease scores (1.043351-3.922025) and degree connectivity (1-29), (b) group B (DEG threshold |log$_2$FC|)>10) showing 100% downregulation (n=44) with log$_2$FC (-13.0 to -10.0) and degree connectivity (5.0 to 25.0), (c) group C (DEG threshold |log$_2$FC|)>3) with 64.74% gene downregulation (n=46), log$_2$FC (-4.3 to -3.0) and degree connectivity (5.0 to 25.0), (d) group C (DEG threshold |log$_2$FC|)>3) with 35.26% gene upregulation (n=24), log$_2$FC (3.0-7.7) and degree connectivity (5.0-23.0). (e) Venn diagram consisting of 255, 363, and 98 DEGs in group A, B and C, respectively.
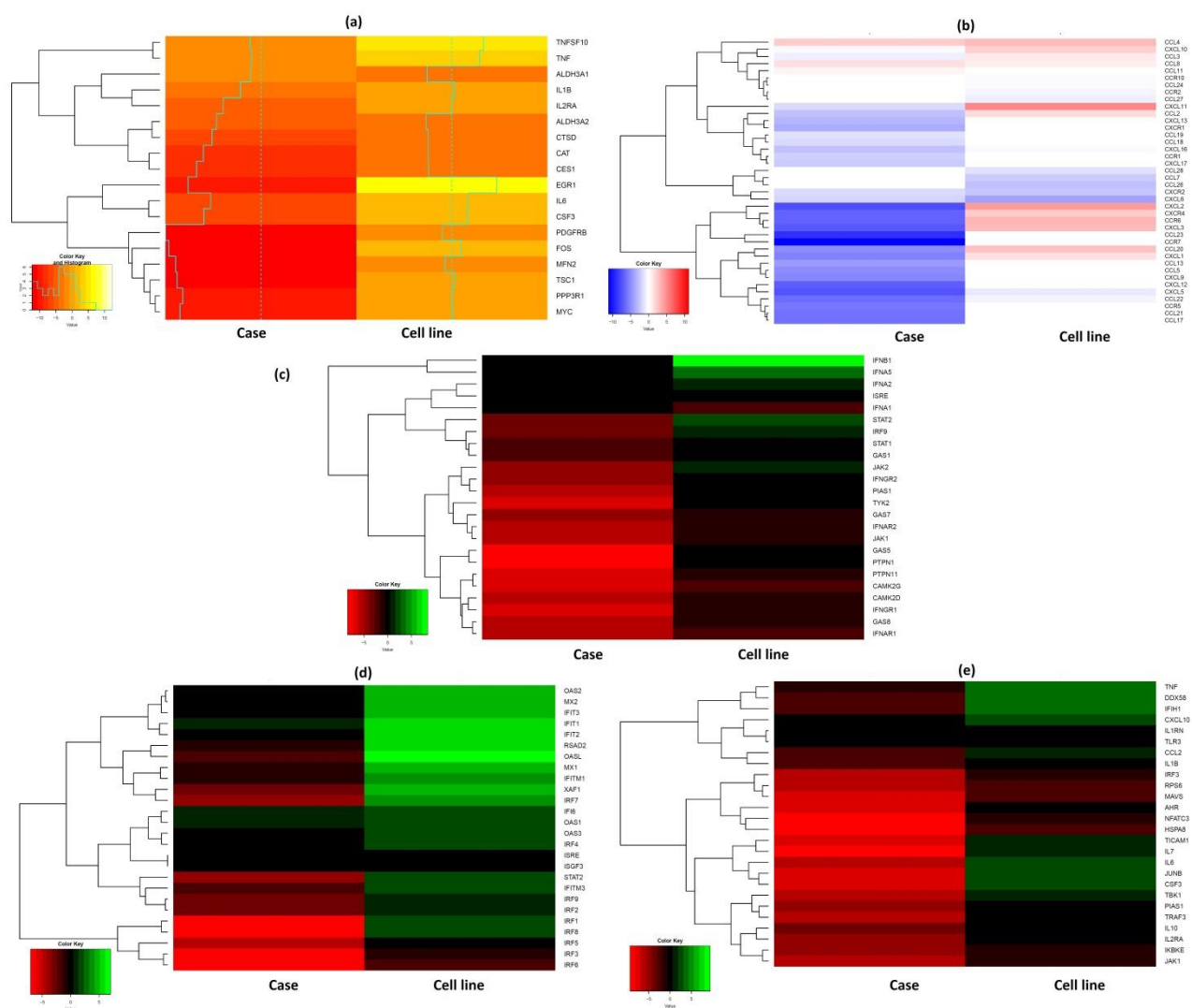
Figure 3: Heat maps of DEGs (differentially expressed genes) in COVID-19 case and SARS-CoV-2 infected cell line. (a) Key genes of group A, B and C displaying 18 DEGs between lung biopsy sample of COVID-19 case compared to uninfected control and ACE2 transduced lung alveolar A549 cell line infected with or without SARS-CoV-2. The host innate immune response through (b) chemokine signaling, (c) IFN signaling, (d) IRF9-STAT2 pathway. (e) COVID-19 severity dependent gene expression. The interleukin-based COVID-19 disease mechanism centered on highly downregulated ILs (IL7, IL6, IL10, IL1B, and IL2RA) in case, and less significantly upregulated ILs (IL7 and IL6) in cell line. The COVID-19 severity related downregulated genes in case were IL6, IL7, IL10, IL1B, IL2RE, TNF, CCL2, CSF3, PIAS1, RPS6, HSPA8, JUNB, NFATC3, JAK1, and AHR. In cell line the mostly expressed upregulated genes related to COVID-19 severity were JUNB, IL6, TNF, CXCL10, IL7, and CCL2, and the downregulated genes were RPS6, HSPA8, and NFATC3.
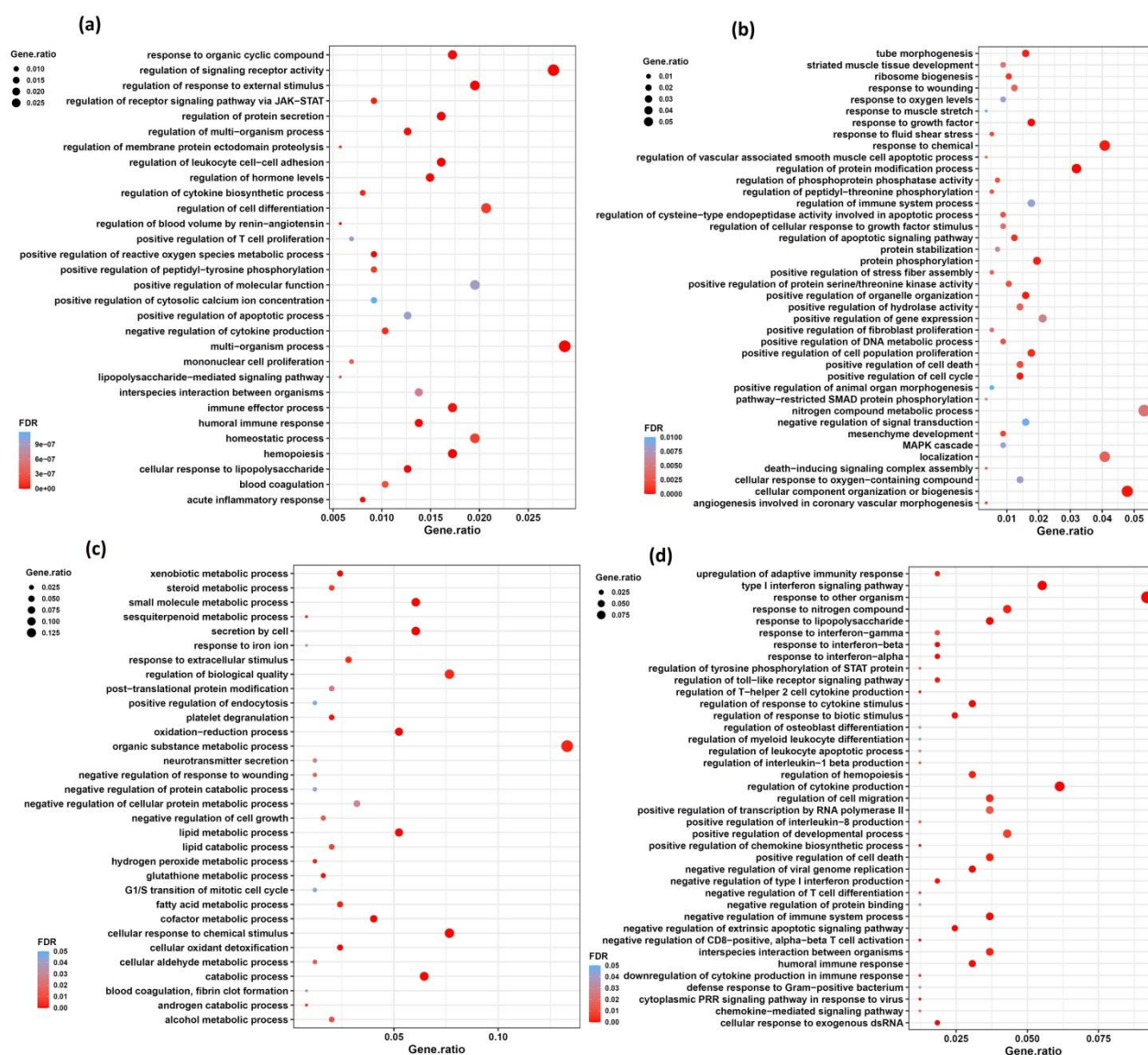
Figure 4: Gene Ontology of enriched DEGs (differentially expressed genes). (a) Group A: known COVID-19 genes. The top two enriched biological processes were regulation of signaling receptor activity (FDR 3.64 × 10⁻²²) and leukocyte cell-cell adhesion (FDR 1.44 × 10⁻¹³) among known COVID-19 genes. (b) Group B: COVID-19 case compared to uninfected healthy control. Regulation of protein modification process (FDR 2.03 × 10⁻⁵) and response to growth factor (FDR 5.01 × 10⁻⁵) among DEGs downregulated in COVID-19 case. (c) Group C: SARS-CoV-2 infected versus uninfected cell line downregulated genes. Regulation of secretion by cell (FDR 1.67 × 10⁻⁶) and cellular oxidant detoxification (FDR 1.57 × 10⁻⁵) among downregulated DEGs of SARS-CoV-2 infected cell line in group C. (d) Group C: SARS-CoV-2 infected versus uninfected cell line upregulated genes. Type I interferon signaling pathway (FDR 1.69 × 10⁻¹³) and response to other organism (FDR 6.96 × 10⁻¹³) among upregulated DEGs of SARS-CoV2 infected cell line in group C.
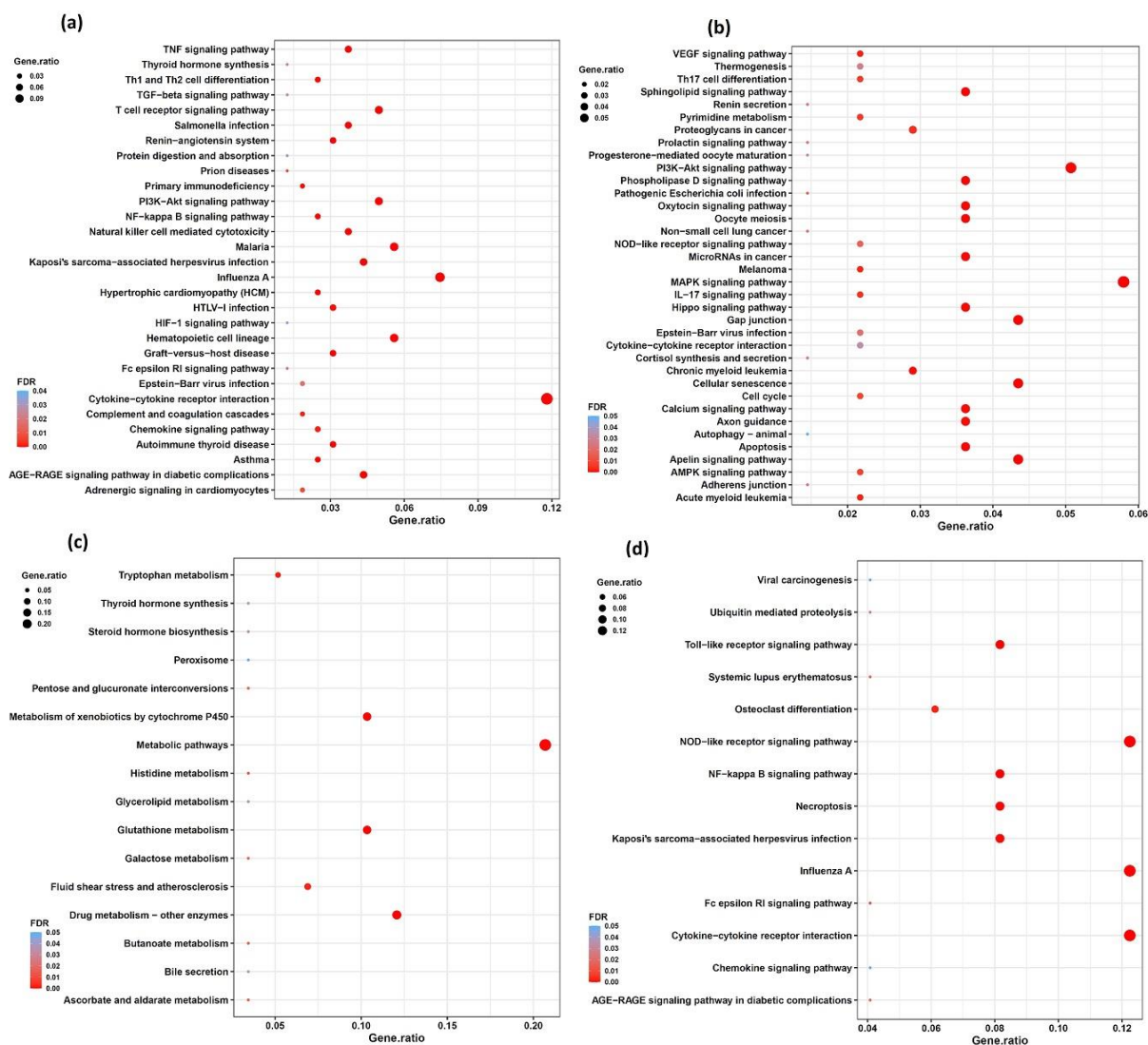
Figure 5: KEGG pathway analysis of enriched DEGs (differentially expressed genes). (a) Group A: known COVID-19 genes. The group A genes were enriched with top two KEGG pathways in cytokine-cytokine receptor interaction (FDR 6.01×10^{-22}) and malaria (FDR 1.1×10^{-13}). (b) Group B: COVID-19 case compared to uninfected healthy control. Group B genes exhibited mostly enriched pathways including MAPK signaling (FDR 1.23×10^{-5}) and PI3K-AKT signaling (FDR 1.8×10^{-4}). (c) Group C: SARS-CoV-2 infected versus uninfected cell line downregulated genes. Among downregulated DEGs in group C, pathways enriched were metabolism of drugs, glutathione, xenobiotics, tryptophan, and histidine. (d) Group C: SARS-CoV-2 infected versus uninfected cell line upregulated genes. Among upregulated DEGs in group C, the majorly enriched pathways were NOD-like receptor signaling, influenza A (both with FDR of 3.82×10^{-6}) and cytokine-cytokine receptor interaction (FDR 1.47×10^{-5}).
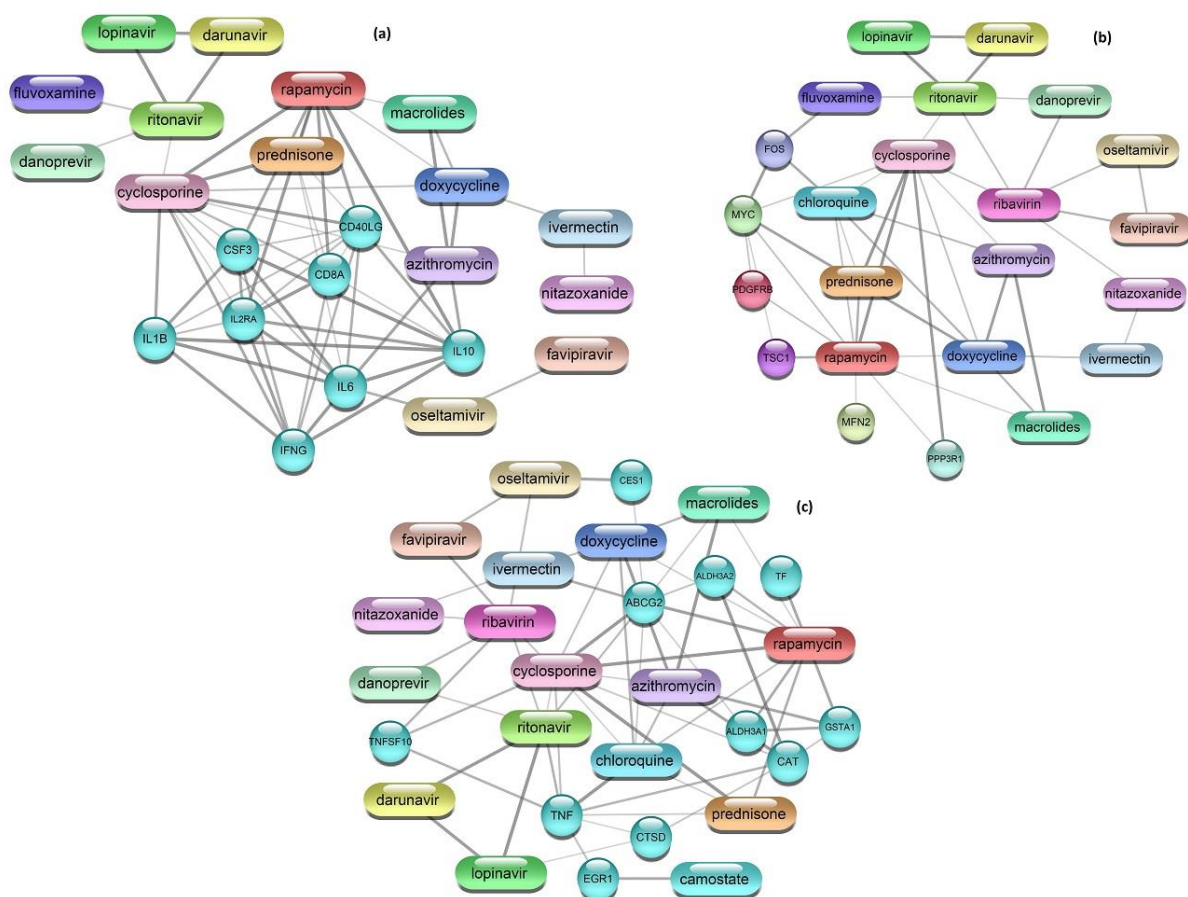
Figure 6: PDI (protein-drug interaction) network of repurposable drugs versus top genes. (a) Group A: known COVID-19 genes. (b) Group B: COVID-19 case compared to uninfected healthy control. (c) Group C: SARS-CoV-2 infected versus uninfected cell line (upregulated and downregulated) genes.