

Supplementary Information.

Identification of candidate repurposable drugs to combat COVID-19 using a signature-based approach

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Drug	Trade Names	Clinical Indication	Target	Canonical Mechanism of Action and Clusters	Anatomical Chemical Therapeutic Classification	Literature Citing Relevance to SARS-CoV-2 and Coronaviridae	Putative Effect on SARS-CoV-2
Drugs with iLINCS signature present.							
Hydroxy-chloroquine ¹	Plaquenil	Malaria; Immuno-suppressant	Toll-like receptor 9; Toll-like receptor 7	Toll-like receptor antagonist	Antiparasitic products, insecticides and repellents	2-4	Alkalinization of phagolysosome; modification of post-translation protein modifications ^{5,6}
Chloroquine ⁷	Aralen	Malaria; Amebiasis	Toll-like receptor 9 Glutathione S-transferase (A2); High mobility group protein B1; tumor necrosis factor				
Lopinavir ⁸	Kaletra / Aluvia (with Ritonavir)	HIV/AIDS Antiviral Therapy	Human immunodeficiency virus type 1 protease	Protease inhibitor	Antiinfectives for systemic use	9-12	Inhibition of CoV-polyprotein processing ^{9,13}
Ritonavir ¹⁴	Norvir; Kaletra /Aluvia (with Lopinavir)						
Fedratinib ¹⁵	Inrebic	Antineoplastic	Tyrosine-protein kinase JAK2; Receptor-type tyrosine-protein kinase FLT3	JAK Inhibitor	Antineoplastic and immunomodulating agents	16	Inhibition of clathrin-mediated viral endocytosis; mediation of inflammatory response, attenuation of cytokine storms from prolonged infection ^{16,17}
Ruxolitinib ¹⁸	Jakafi, Jakavi	Antineoplastic	Tyrosine-protein kinase JAK1 and JAK2				
Baricitinib ¹⁹	Olumiant, Baricinix	Immuno-suppressant	Tyrosine-protein kinase JAK1, JAK2, and JAK3; Protein-tyrosine kinase 2-beta				
Drugs with iLINCS signature present but not included in analysis.							
Azithromycin ²⁰	Act Azithromycin, AzaSITE, Zithromax, Zmax	Bacterial infections	23S Ribosomal RNA; Protein-arginine deaminase type-4	Inhibition of bacterial protein synthesis	Antiinfectives for systemic use	4	Adjunct therapy with hydroxychloroquine.
Losartan ²¹	Act Losartan, Cozaar	Hypertension	Type-1 angiotensin II (AGII) receptor	AGII receptor antagonist	Cardiovascular system	22	Angiotensin receptor blocker.
Drugs with iLINCS signature not present.							
Remdesivir ²³	Remdesivir	Ebola	Replicase polyprotein 1ab; RNA-directed RNA polymerase L	Nucleoside analog, inhibition of viral RNA polymerase	No record	24-27	Inhibition of RNA dependent RNA polymerase ²⁷
Rocaglate	Not found in DrugBank.				No record	28	Inhibition of viral translation ²⁸ .
Silvestrol	Not found in DrugBank.				No record	28,29	Inhibition of viral translation ²⁸ .
Umifenovir ³⁰	Arbidol	Viral prophylaxis; Broad spectrum antiviral	Cytochrome P450 3A4, 2E1, 1A2, 2D6, 2C9, 3A5; UDP-glucuronosyltransferase 2B7, 1-9; Dimethylaniline monooxygenase 1, 3	Aromatic rings interfere with viral endocytosis, exocytosis, intracellular trafficking, and destabilize membranes	Antiinfectives for systemic use	31-33	No specific purported mechanism yet published.
N10169	Not found in DrugBank.				No record	34	Inhibition of pyrimidine biosynthesis ³⁴ .

Interferon Alphacon-1 ³⁵	Infergen	Antineoplastic	Interferonalpha/beta receptor 1, 2	Interferon receptor agonist, JAK activator	Antineoplastic and immunomodulating agents	^{36,37}	Upregulation of MHC 1 to present viral antigens.
<i>Polygonaceae</i> spp.; <i>Rheum palmatum</i> L.	Not found in DrugBank				No record	^{38,39}	Inhibition of viral cell-entry by preventing interaction of CoV Spike Protein from interacting with ACE2 receptor ³⁹
Camostat mesylate ⁴⁰	N/A	Pancreatitis, Japan ^{41,42}	N/A	Serine protease inhibitor TMPRSS2	Blood and blood forming organs	⁴³⁻⁴⁵	Inhibition of viral cell-entry ⁴³

Table S1. Selected drugs implicated in the treatment of COVID-19.

Information relating to these drugs (trade name, clinical indication, targets, and canonical mechanism of action) were referenced from DrugBank (<https://www.drugbank.ca/>). Anatomical Therapeutic Chemical (ATC) classification was referenced from (https://www.whocc.no/atc_ddd_index/). The first-level of ATC classification is indicated.

Table S2.

No. chemical perturbagens identified						
Log fold change						
Cell line	Drug grouping	0	0.26	0.5	0.85	1
A549-10uM-24h	1	174	382	934	3528	5587
A549-10uM-24h	2	810	268	751	2449	3780
A549-10uM-24h	3	2002	2200	2474	3516	3799
A549-10uM-24h	4	701	961	1648	3743	4786
A549-10uM-24h	5	434	527	1455	4512	4612
A549-10uM-6h	1	997	1651	3134	4824	5090
A549-10uM-6h	2	505	655	1170	3455	4864
A549-10uM-6h	3	490	876	1313	2110	3009
A549-10uM-6h	4	378	558	859	2026	2465
A549-10uM-6h	5	1078	327	429	1422	3074
HA1E-10uM-24h	1	539	1860	4299	5477	5749
HA1E-10uM-24h	2	344	784	1724	3791	4078
HA1E-10uM-24h	3	662	953	1434	2804	3390
HA1E-10uM-24h	4	1054	1159	1468	1731	1890
HA1E-10uM-24h	5	314	600	1370	3713	4989
HT29-10uM-24h	1	539	1701	4286	5422	5557
HT29-10uM-24h	2	817	1113	2619	4173	4449
HT29-10uM-24h	3	2107	1660	1442	1963	2267
HT29-10uM-24h	5	713	1945	4633	6124	6170
MCF7-10uM-24h	1	452	1030	2923	5674	5783
MCF7-10uM-24h	2	378	729	1376	4493	5636
MCF7-10uM-24h	3	1890	2122	2119	3110	3420
PC3-10uM-24h	1	551	2394	6470	6567	6050
PC3-10uM-24h	2	1218	2114	3751	6381	6012
PC3-10uM-24h	3	1743	1875	1966	3172	4234
PC3-10uM-24h	4	880	380	822	3590	4879
VCAP-10uM-24h	1	2009	1175	1739	4745	5077
VCAP-10uM-24h	2	957	1742	3773	6912	6475
VCAP-10uM-24h	3	1630	1170	1865	3563	4568
VCAP-10uM-24h	4	1374	2314	3099	4148	4383
VCAP-10uM-24h	5	218	582	2073	5518	5532
VCAP-10uM-6h	1	2188	858	1210	4543	6498
VCAP-10uM-6h	2	1200	2315	3905	4855	4879
VCAP-10uM-6h	3	400	474	551	1562	2207
VCAP-10uM-6h	4	1065	841	955	1044	1612
VCAP-10uM-6h	5	3508	1151	1151	2552	4509

Table S2. L1000 genes with expression change at log fold change (LFC) threshold 0.85 were selected to generate drug cluster gene signatures. At this threshold, following connectivity analysis, a large number of candidate drug signatures were identified as concordant to the drug cluster signatures which represent drugs that are used or are being explored for the treatment of coronavirus or COVID-19. Higher thresholds (LFC 1) were found to be too permissive for chemical perturbagen identification, introducing excess noise, while lower thresholds (LFC 0.5- all LINCS signature) were more restrictive, limiting the number of chemical perturbagens identified.

Table S3.

Cell line	Concentration	Time	No. of drug signatures	No. of unique drug signatures
A549	10uM	24h	9	6
A549	10uM	6h	7	6
HA1E	10uM	24h	9	6
HT29	10uM	24h	9	7
MCF7	10uM	24h	15	6
PC3	10uM	24h	10	6
VCAP	10uM	24h	9	7
VCAP	10uM	6h	8	7

Table S3. iLINCS cell lines and conditions used to generate signatures for 9 drugs used for drug clustering analysis.

Table S4.

		No. chemical perturbagens identified				
		log fold change (LFC)				
Cell line	Disease	0	0.26	0.5	0.85	1
A549-10uM-24h	GSE145926	310	457	846	3544	3472
A549-10uM-24h	GSE147507 PS	16	32	83	293	394
A549-10uM-24h	GSE147507 CL	68	168	387	2371	4596
A549-10uM-6h	GSE145926	310	457	846	3544	3472
A549-10uM-6h	GSE147507 PS	16	32	83	293	394
A549-10uM-6h	GSE147507 CL	68	168	387	2371	4596
HA1E-10uM-24h	GSE145926	310	457	846	3544	3472
HA1E-10uM-24h	GSE147507 PS	16	32	83	293	394
HA1E-10uM-24h	GSE147507 CL	68	168	387	2371	4596
HT29-10uM-24h	GSE145926	310	457	846	3544	3472
HT29-10uM-24h	GSE147507 PS	16	32	83	293	394
HT29-10uM-24h	GSE147507 CL	68	168	387	2371	4596
MCF7-10uM-24h	GSE145926	310	457	846	3544	3472
MCF7-10uM-24h	GSE147507 PS	16	32	83	293	394
MCF7-10uM-24h	GSE147507 CL	68	168	387	2371	4596
PC3-10uM-24h	GSE145926	310	457	846	3544	3472
PC3-10uM-24h	GSE147507 PS	16	32	83	293	394
PC3-10uM-24h	GSE147507 CL	68	168	387	2371	4596
VCAP-10uM-24h	GSE145926	310	457	846	3544	3472
VCAP-10uM-24h	GSE147507 PS	16	32	83	293	394
VCAP-10uM-24h	GSE147507 CL	68	168	387	2371	4596
VCAP-10uM-6h	GSE145926	310	457	846	3544	3472
VCAP-10uM-6h	GSE147507 PS	16	32	83	293	394
VCAP-10uM-6h	GSE147507 CL	68	168	387	2371	4596

Table S4. L1000 genes with expression change at log fold change (LFC) threshold 0.5 were selected to generate severe acute respiratory syndrome coronavirus 2020 (SARS-CoV-2) gene signatures. At this threshold, following connectivity analysis, a large number of candidate drug signatures were identified as discordant to the SARS-CoV-2 signatures (discordance ≤ -0.321). GSE145926: COVID-19 patient samples described in Liao et al.⁴⁶ GSE147507 PS: COVID-19 patient samples (lung tissue) described in Blanco-Melo et al.⁴⁷. GSE147507 CL: SARS-CoV-2 infected A549_ ACE2 cell line sample described in Blanco-Melo et al.⁴⁷.

Table S5

Drug	Trade name	Drug Class	Target	Canonical MOA	ATC classification	Antiviral properties
Trametinib	Mekinist	Antineoplastic; Kinase inhibitor	Mitogen-activated extracellular signal regulated kinase (MEK) 1, 2	MEK inhibitor	Antineoplastic and immunomodulating agents	MERS-CoV ⁴⁸ , SARS-CoV-2 ⁴⁹
Withaferin A	N/A	Antineoplastic; Steroidal lactone	Unknown	N/A	N/A	SARS-CoV-2 ⁵⁰⁻⁵³
Parthenolide	N/A	Anti- inflammatory; Sesquiterpene lactone	Unknown	N/A	N/A	SARS ⁵⁴
Lapatinib	Tykerb, Tyverb	Antineoplastic; Kinase inhibitor	Epidermal growth factor receptor; Receptor tyrosine-protein kinase erbB-2	EGFR, ERBB1 inhibitor	Antineoplastic and immunomodulating agents	SARS-CoV-2 ⁵⁵
Sorafenib	Nexavar	Antineoplastic; Kinase inhibitor	Raf kinase, Platelet-derived growth factor, Vascular endothelial growth factor receptor	Raf/Mek/Erk inhibitor	Antineoplastic and immunomodulating agents	SARS-CoV-2 ⁵⁶
Auranofin	Ridaura	Anti- inflammatory; Gold salt	Peroxiredoxin-5, mitochondrial; Inhibitor of nuclear factor kappa-B kinase subunit beta	Not fully elucidated.	Anti-inflammatory and antirheumatic products	SARS-CoV-2 ⁵⁷
Selumetinib	N/A	Anti-neoplastic; Kinase inhibitor	Mitogen-activated extracellular signal regulated kinase (MEK) 1, 2	MEK inhibitor	Antineoplastic and immunomodulating agents	SARS-CoV-2 ⁴⁹
Erlotinib	Tarceva	Antineoplastic; tyrosine kinase inhibitor	Epidermal growth factor receptor	EGFR receptor	Antineoplastic and immunomodulating agents	HCV, RNA viruses, dengue, Ebola ⁵⁸⁻⁶⁰
Alvocidib	N/A	Antineoplastic	Cyclin dependent kinases	Cdk inhibitor	N/A	HSV, HIV, Flu ⁶¹⁻⁶⁶
Quinacrine	Atabrine	Antiparasitic; Antimalarial	DNA	DNA intercalator; full MOA not elucidated	N/A	EMCV, poliovirus
Vandetanib	Zactima/Zictifa	Antineoplastic; Kinase inhibitor	Vascular endothelial growth factor receptor; Epidermal growth factor	VEGF, EGFR, RET inhibitor	Antineoplastic and immunomodulating agents	Andes virus ⁶⁷

			receptor; REarranged during Transfection (RET) tyrosine kinases			
Dasatinib	Sprycel	Antineoplastic	Tyrosine protein kinase ABL1; Proto-oncogene tyrosine-protein kinase Src; Ephrin type-A receptor 2; Tyrosine-protein kinase Lck	BCR/ABL and Src family tyrosine kinase inhibitor	Antineoplastic and immunomodulating agents	HIV ^{68,69}
Thioridazine	Mellaril/Melleril	Antipsychotic; Phenothiazine	Dopamine D1/D2 receptors, Alpha-1A/1B adrenergic receptor	Inhibition of mesolimbic dopaminergic D1 and D2 receptors	Psycholeptics	Ebola ^{70,71} , HCV ⁷² ; CHIKV, SFV ⁷³ ; RVFV ⁷⁴
Candidate repurposable drugs currently in trial for COVID-19						
Gallocatechin Gallate	N/A (Veregen, Sinecatechin)	Antioxidant	Unknown	Not fully elucidated	Antibiotics and chemotherapeutics for dermatological use (as a Sinecatechin)	
Decitabine	Dacogen	Antineoplastic; cytosine analogue	DNA, nucleotide analog	Leads to DNA hypomethylation by trapping DNA methyltransferases	Antineoplastic and immunomodulating agents	
Fenretinide	N/A	Antineoplastic; chemopreventive synthetic retinoid	Not fully elucidated	Inhibits cell growth through retinoid receptor dependent and independent pathways	N/A	
Curcumin	N/A	Anti-inflammatory, antimicrobial, antioxidant	Not fully elucidated	Antioxidant, reactive oxygen species scavenger	N/A	
Simvastatin	Zocor	Antilipemic	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase	HMG-CoA reductase inhibitor	Lipid modifying agent	

Sirolimus	Rapamune	Immuno-suppressant; Macrolide lactams	Serine/threonine-protein kinase mTOR	mTOR inhibitor	Immunosuppressants	
Cyclosporine	Cequa	Immuno-suppressant	Calcium signal-modulating cyclophilin ligand	Calcineurin inhibitor	N/A	

Table S5.

Detailed information on the top 20 candidate drugs. Information relating to these drugs (were referenced from DrugBank (<https://www.drugbank.ca/>) and Anatomical Therapeutic Chemical (ATC) classification (https://www.whooc.no/atc_ddd_index/) databases. The first-level of ATC classification is indicated.

Figure S1

Figure S1

Correlation between DEG for COVID-19 patient sample datasets

Pearson's r : 0.032, p -value: 0.335

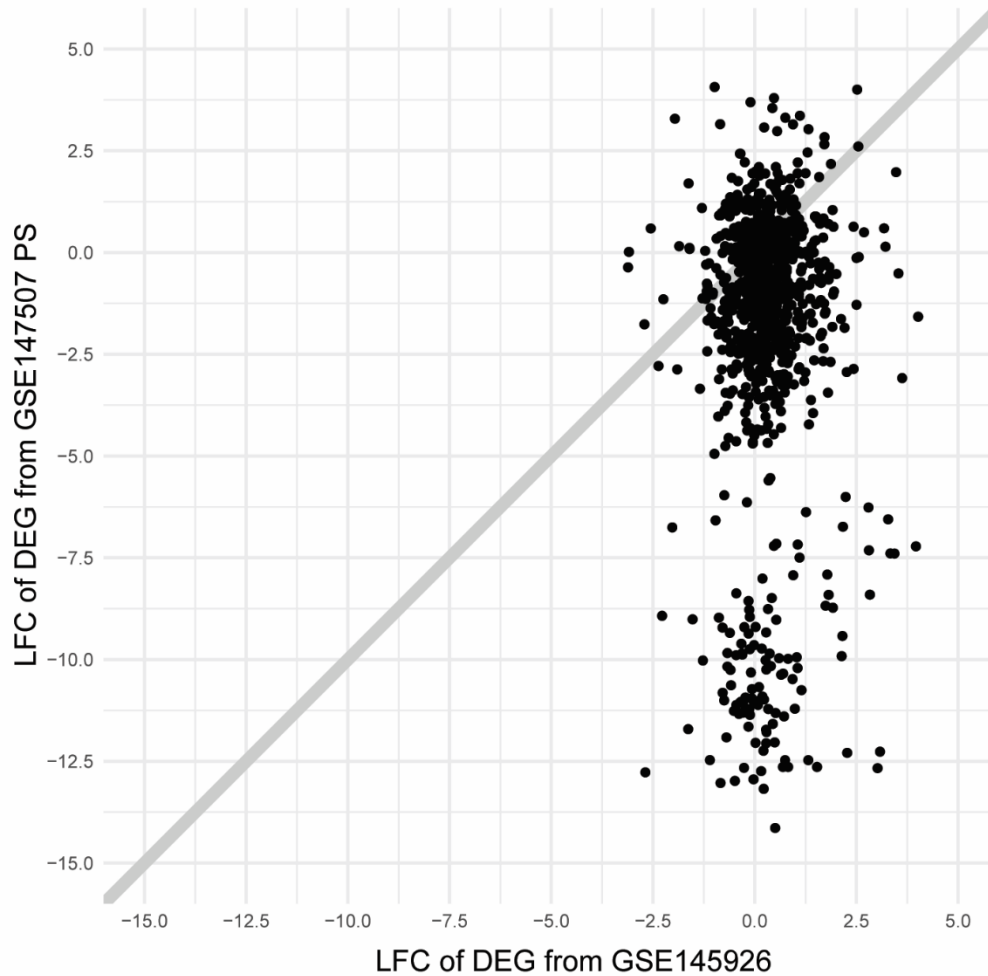


Figure S1. Correlation between COVID-19 patient sample datasets GSE147507 PS and GSE145926. There was no significant correlation between the log fold change (LFC) differential gene expression (DEG) values for GSE147507 PS²⁴ and GSE145926²⁵ COVID-19 patient samples, derived from lung tissue and bronchoalveolar fluid immune cells, respectively.

Figure S2

A

GSE147507 CL		
Pathway name	# Genes found	FDR
Signaling by Interleukins	64	6.30E-09
Interleukin-4 and Interleukin-13 signaling	32	9.16E-08
Cytokine Signaling in Immune system	85	2.17E-07
Signaling by Receptor Tyrosine Kinases	57	6.31E-07
Generic Transcription Pathway	96	3.09E-04
Extra-nuclear estrogen signaling	17	4.02E-04
Estrogen-dependent nuclear events downstream of ESR-membrane signaling	9	4.22E-04
Response of EIF2AK1 (HRI) to heme deficiency	9	4.22E-04
MyD88-independent TLR4 cascade	16	7.32E-04
TRIF(TICAM1)-mediated TLR4 signaling	16	7.32E-04
Immune System	144	9.37E-04
ESR-mediated signaling	26	9.37E-04
Signaling by NTRKs	20	9.37E-04
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	15	9.54E-04
Toll Like Receptor 3 (TLR3) Cascade	15	9.54E-04

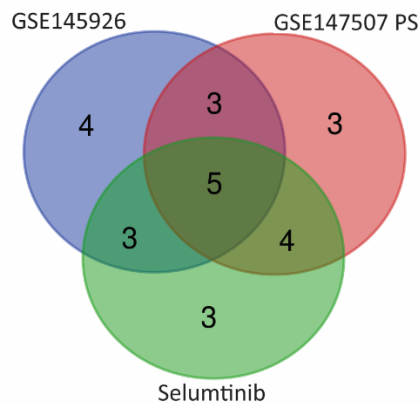
B

GSE147507 PS		
Pathway name	# Genes found	FDR
Mitotic G1 phase and G1/S transition	49	5.97E-13
Cell Cycle	107	3.25E-10
Cell Cycle, Mitotic	90	3.06E-09
Signaling by Interleukins	94	5.93E-09
G1/S Transition	37	2.14E-08
Transcriptional Regulation by TP53	75	3.87E-08
Signaling by Receptor Tyrosine Kinases	89	4.56E-08
Interleukin-4 and Interleukin-13 signaling	44	8.43E-08
Apoptosis	39	5.28E-07
S Phase	37	1.33E-06
Signaling by NTRKs	35	1.65E-06
Cell Cycle Checkpoints	48	2.05E-06
Cyclin A:Cdk2-associated events at S phase entry	24	4.50E-06
Programmed Cell Death	40	4.92E-06
Gene expression (Transcription)	186	6.07E-06

C

GSE145926		
Pathway name	# Genes found	FDR
Mitotic G1 phase and G1/S transition	32	2.26E-09
Signaling by Receptor Tyrosine Kinases	66	2.26E-09
Interleukin-4 and Interleukin-13 signaling	33	7.41E-08
Signaling by Interleukins	63	7.41E-08
Cell Cycle	67	2.10E-07
G0 and Early G1	14	2.41E-07
Generic Transcription Pathway	111	4.82E-07
Cell Cycle, Mitotic	57	5.43E-07
TP53 Regulates Transcription of Cell Cycle Genes	16	2.94E-06
G1/S Transition	24	3.11E-06
TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest	10	3.11E-06
Estrogen-dependent nuclear events downstream of ESR-membrane signaling	11	5.37E-06
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	14	5.37E-06
Transcriptional Regulation by TP53	47	5.93E-06
RNA Polymerase II Transcription	113	6.06E-06

D



E

Selumetinib		
Pathway name	# Genes found	FDR
Mitotic G1 phase and G1/S transition	38	5.31E-14
Cell Cycle, Mitotic	72	5.31E-14
Cell Cycle	84	5.31E-14
G1/S Transition	31	2.66E-11
Transcriptional Regulation by TP53	56	1.23E-10
S Phase	32	3.60E-10
G0 and Early G1	16	7.46E-10
Cell Cycle Checkpoints	39	1.52E-09
Gene expression (Transcription)	125	1.68E-08
Generic Transcription Pathway	110	1.93E-08
RNA Polymerase II Transcription	114	1.38E-07
Cyclin E associated events during G1/S transition	19	3.03E-07
Cyclin A:Cdk2-associated events at S phase entry	19	4.00E-07
Resolution of AP sites via the multiple-nucleotide patch replacement pathway	12	6.56E-07
DNA Replication	23	1.11E-06

F

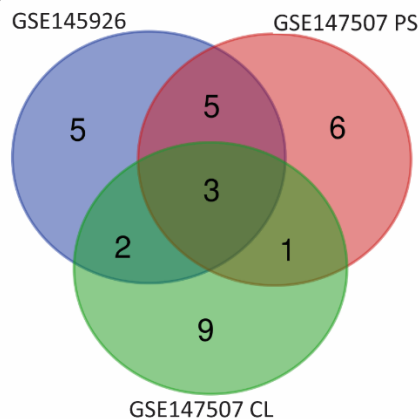


Figure S2. Biological pathway analysis of datasets GSE147507 CL (A), GSE147507 PS (B), and GSE145926 (C). Venn diagram shows common (in bold) and unique pathways (D). Biological pathway analysis of the candidate drug selumetinib (E) and venn diagram (F) showing common pathways (red) between COVID-19 patient sample datasets (GSE147507 PS and GSE145926) and selumetinib.

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