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The Global Phosphorylation Landscape of SARS-CoV-2 Infection

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SUMMARY

The causative agent of the coronavirus disease 2019 (COVID-19) pandemic, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has infected millions and killed hundreds of thousands of people worldwide, highlighting an urgent need to develop antiviral therapies. Here, we present a quantitative mass spectrometry-based phosphoproteomics survey of SARS-CoV-2 infection in Vero E6 cells, revealing dramatic rewiring of phosphorylation on host and viral proteins. SARS-CoV-2 infection promoted casein kinase II (CK2) and p38 MAP kinase activation, production of diverse cytokines, and shutdown of mitotic kinases resulting in cell cycle arrest. Infection also stimulated a marked induction of CK2-containing filopodia protrusions possessing budding viral particles. Eighty-seven drugs and compounds were identified by mapping global phosphorylation profiles to dysregulated kinases and pathways. We found pharmacologic inhibition of p38, CK2, CDKs, AXL and PIKFYVE kinases to possess antiviral efficacy, representing potential COVID-19 therapies.

Keywords

SARS-CoV-2; phosphoproteomics; p38; MAPK; casein kinase II; AXL; CDK; PIKFYVE

INTRODUCTION

SARS-CoV-2 is an enveloped positive-sense RNA virus that belongs to the lineage B *Betacoronavirus* family. It is closely related to SARS-CoV, the causative agent of SARS which emerged in the human population in 2002 (79% genetic similarity), and several SARS-related coronaviruses that circulate in bats (up to 98% genetic similarity) (Lai et al. 2020; Zhou et al. 2020). The pathophysiology of severe COVID-19 is similar to that of severe disease caused by SARS-CoV and is characterized by acute respiratory distress and excessive inflammation capable of inducing respiratory failure, multi-organ failure, and death (Wong et al. 2004; Zhang et al. 2020).

To enter host cells, the SARS-CoV-2 spike (S) protein binds to an ACE2 receptor on the target cell, and is subsequently primed by a serine protease, TMPRSS2, that cleaves the S protein and allows fusion of viral and lysosomal membranes (Hoffmann et al. 2020). Following entry, viral genomic RNA is translated to produce polyproteins ORF1a and ORF1ab, which are subsequently cleaved by viral proteases into non-structural proteins that form the viral replication/transcription complex (RTC). Extensive remodeling of the host endoplasmic reticulum leads to the formation of double-membrane vesicles within which viral RNA synthesis occurs. The viral RNA genome is replicated by transcription of the negative-strand genomic RNA template, while subgenomic mRNAs are transcribed and translated to produce structural and accessory proteins. Structural proteins and viral genomes assemble at the endoplasmic reticulum-Golgi intermediate compartment (ERGIC) (Haan, de Haan, and Rottier 2005), followed by transport to the cell surface for release by exocytosis (Fehr and Perlman 2015).

While much about SARS-CoV-2 biology can be inferred based on similarity to SARS-CoV, SARS-CoV-2 is a novel coronavirus with unique properties which contribute to its pandemic-scale spread. Unlike SARS-CoV, SARS-CoV-2 infection is commonly asymptomatic, particularly in the younger population (Guan et al. 2020), and contagious prior to symptom onset (Rothe et al. 2020; Peiris et al. 2003; Bai et al. 2020). These characteristics contribute to the difficulty of containing SARS-CoV-2 spread through public health strategies and amplify the need to develop vaccines and therapies to protect against and treat COVID-19. Largely, clinical management of COVID-19 is limited to infection prevention and supportive care. Thus far, remdesivir, a broad-spectrum antiviral, is the only medication approved for emergency use to treat COVID-19 by the food and drug administration (FDA) in the United States (Grein et al. 2020). While the evidence supporting remdesivir use in patients with advanced COVID-19 is promising, there remains an urgent need for potent SARS-CoV-2 therapeutics, especially those that could be given in the outpatient setting, in order to effectively combat the COVID-19 pandemic.

Proteomics approaches that globally quantify changes in protein abundance and phosphorylation represent a powerful tool to elucidate mechanisms of viral pathogenesis by providing a snapshot of how cellular pathways and processes are rewired upon infection (Johnson et al. 2020). Importantly, the functional outcomes of many phosphorylation events are well annotated, especially for kinases where phosphorylation directly regulates their activity. State-of-the-art bioinformatics approaches can then be employed to readily identify regulated kinases from phosphorylation profiles, many of which are likely to be established drug targets with therapeutic potential (Ochoa et al. 2020, 2016). Here, we present a quantitative survey of the global phosphorylation and protein abundance landscape of SARS-CoV-2 infection, map phosphorylation changes to disrupted kinases and pathways, and use these profiles to rapidly prioritize drugs and compounds with the potential to treat SARS-CoV-2 infection.

RESULTS

Phosphorylation signaling represents a primary host response to SARS-CoV-2 infection

To determine how SARS-CoV-2 hijacks host-protein signaling, a global phosphoproteomics experiment was performed in Vero E6 cells, a cell line originating from the kidney of a female African green monkey (*Chlorocebus sabaeus*) (Osada et al. 2014). This cell line was selected due to its high susceptibility to SARS-CoV-2 infection (Harcourt et al. 2020). Cells were harvested in biological triplicate at 6 timepoints after SARS-CoV-2 infection (0, 2, 4, 8, 12, or 24 hours) or after mock infection at 0 or 24 hours (**Figure 1A**). Using a data-independent acquisition (DIA) proteomics approach, each sample was then analyzed for changes in global protein abundance or phosphorylation (data available in **Table S1**). *Chlorocebus sabaeus* and human protein sequences were aligned and both phosphorylation sites and protein identifiers were mapped to their respective human protein orthologs. Phosphorylation fold changes calculated using either the 0- or 24-hour mock control were highly comparable (correlation coefficient r=0.77); therefore, the 0-hour mock was used for all subsequent comparisons.

Quality control filtering of the data was performed and two samples from each of the phosphorylation and protein abundance datasets were removed due to poor correlation with their respective replicates (**Figure S1A, S1B**). Principal component analysis (PCA) of the remaining samples revealed good separation of mock and infected samples as well as high quantitative reproducibility between biological replicates (**Figures 1B, 1C, S1C**). In total, high-quality quantification of 4,624 human-orthologous phosphorylation sites and 3,036 human-orthologous proteins were collected (**Figure S1D**). Successful infection was confirmed by the observation of a dramatic increase in viral protein abundance over the course of a 24 hour infection period (**Figure 1D, S1E**).

As expected, an increase was observed in the number of significantly regulated phosphorylation sites and proteins over the infection time course, with the majority of regulation occurring at the level of phosphorylation (**Figure 1E, 1F**), as opposed to protein abundance (**Figure 1G, 1H**). Of the few proteins that significantly increased in abundance upon infection, the vast majority were SARS-CoV-2 viral proteins (**Figure 1H**). In contrast, the majority of host proteins decreased in abundance. This finding is consistent with mechanisms of host mRNA nuclear export and/or host mRNA translation inhibition that are common in viral infections (Kuss et al. 2013; Walsh and Mohr 2011). Gene ontology enrichment analysis of significantly downregulated proteins revealed several terms related to platelet regulation (**Figure 1I, S1F**). Several downregulated host proteins are known to be involved in platelet regulation, thrombosis, and in preventing blood coagulation, including APOH, CD9, TSPAN14, AHSG, SERPINA1, and A2M (Mather et al. 2016; Mangin et al. 2009; Taggart et al. 2000). The downregulation of these proteins suggests they may mechanistically contribute to symptoms of blood coagulation and stroke in COVID-19 patients (Han et al. 2020).

Lastly, the contribution of protein abundance to phosphorylation level changes was evaluated. For nearly all cases of a significantly changed phosphorylation site, no corresponding significant change in protein abundance was observed (**Figure 1J**), further suggesting that phosphorylation signaling represents a primary host response over this time course of infection, as opposed to transcriptional regulation that would influence protein abundance.

Phosphorylation of SARS-CoV-2 viral proteins by the host proteome

Viral protein phosphorylation within the host cell may play a role in sensing and responding to cell state. We detected 25 phosphorylation sites in SARS-CoV-2 viral proteins that we combined with another proteomics

dataset (Davidson et al. 2020) to amass a total of 49 sites detected across seven viral proteins (**Table S2**). Of note, this analysis does not distinguish cleaved from uncleaved viral proteins in the assignment of viral phosphorylation sites. The degree of conservation, indicative of functional constraint, was estimated for each residue position (**Figure 2A**) (Ng and Henikoff 2003) and the sites were mapped to positions within structured regions for five proteins, with the majority observed in accessible positions (i.e. loops) (**Figure 2B**). The top kinase families predicted by sequence to regulate these sites included casein kinase II (CK2), CDK, and PKC, among others (**Figure 2C**), suggesting these kinases may contribute to the regulation of viral replication.

While it is unlikely that all phosphorylation sites on viral proteins play important functional roles, several sites in membrane (M) protein, Nsp9, and nucleocapsid (N) protein (**Figures 2D-F**) suggest potential functionality. Five phosphorylation sites were detected in the M protein cluster within a short C-terminal region of the protein (207 to 215; **Figure 2D**). Although these acceptor residues are not predicted to be conserved, several are negatively charged residues in M proteins of other related viruses (**Figure 2E**). This evolutionary pattern suggests that negative charge in this region may play a functional role, reminiscent of other multi-site phosphorylation events (Serber and Ferrell 2007).

To identify phosphorylation sites that may regulate protein-protein interactions, all sites were mapped to 3-dimensional structures and SPPIDER was used to assess whether sites resided within interface regions (Porollo and Meller 2007) (**Figure 2A**, **Table S2**). The single phosphorylation site in Nsp9 was predicted to be at an interface region (“True”), which was supported by inspection of the homodimer structure (PDB ID 6W4B). Additional phosphorylation sites were predicted to be at interface residues within the S protein (**Figure 2A**). However, inspection of spike in complex with ACE2 receptor (Shang et al. 2020; Lan et al. 2020) reveals some of these phosphorylation sites to be near to, but not at, the interface region.

Finally, phosphorylation sites in N protein, a structural protein that binds to and assists in packaging viral RNA were investigated. Most sites occurred within the N-terminal portion of the protein, at or near the RNA binding region, but avoided the C-terminal dimerization domain. The cluster of phosphorylation sites within an arginine/serine (RS)□dipeptide rich region, C-terminal to the RNA binding region (**Figure 2A**), is conserved in other coronavirus N proteins. This region is phosphorylated in SARS-CoV by serine-arginine (SR) protein kinases, modulating the role of SARS-CoV N in host translation inhibition (Peng, Lee, and Tarn 2008). It is likely that the phosphorylation of this same region in SARS-CoV-2 plays a similar role. Interestingly, *in vitro* inhibition of SARS-CoV N protein phosphorylation at the RS-rich region results in reduced viral load and cytopathic effect (Wu et al. 2009), highlighting its importance for viral fitness. In addition, sites spanning the sequence of the RNA binding domain, which forms a claw-like structure, were observed (Kang et al. 2020). Several phosphorylation sites cluster in the structural model, predicted to impact the surface charge of the so-called acidic wrist region (**Figure 2F**) but not the positive surface charge of the RNA binding pocket. We hypothesize that this surface charge difference may modulate N protein function, potentially via allosteric regulation of RNA binding capacity.

Phosphorylation of SARS-CoV-2 host interacting proteins during infection

The recently published SARS-CoV-2 virus-human protein-protein interaction map detected 332 human proteins interacting with 27 (26 wild-type and 1 mutant) viral proteins (Gordon et al. 2020). Here, we found some of these host proteins (40/332) to be significantly differentially phosphorylated upon infection (**Figure 3**). Virus-host protein-protein interactions could drive changes in phosphorylation by affecting host protein subcellular localization or by sterically blocking kinase access. Furthermore, the phosphorylation of these proteins upon

infection may signify an additional mode of functional control over these putative dependency and restriction factors.

SARS-CoV-2 N protein is known to interact with several RNA processing proteins that are differentially phosphorylated during infection, including LARP1 and RRP9. Here, LARP1 phosphorylation decreases on several sites, which is consequently known to increase LARP1 affinity for 3' untranslated regions (UTRs) of mRNAs encoding ribosomal proteins, thus driving inhibition of protein synthesis (Hong et al. 2017). This mechanism may be utilized by SARS-CoV-2 to prioritize the synthesis of viral proteins over host proteins. In addition, ORF6 interacts with the NUP98/RAE complex and NUP98 phosphorylation was found to increase at S888, a site within its peptidase domain. NUP98 autocatalytic cleavage is required for localization to the nuclear pore, and thus it is possible that NUP98 interaction with ORF6 and/or its virus-induced phosphorylation prevents host mRNA export through the nuclear pore (Krull et al. 2010; Hodel et al. 2002). A similar mechanism is employed by vesicular stomatitis virus (VSV) matrix protein to block host mRNA export by targeting NUP98/RAE complex, leading to the exclusive translation of cytoplasmic VSV mRNAs (Quan et al. 2014).

For Nsp12, the majority of its protein interactors displayed decreased phosphorylation during infection. Since Nsp12 is known to encode the RNA-dependent RNA polymerase, responsible for replicating the viral genome, and several of these interacting proteins are related to RNA processing (LARP4B, CRTC3), their regulation may possess functional implications for Nsp12 in viral RNA replication. In addition, Nsp8 interacts with several proteins whose phosphorylation increases (LARP7, MPHOSPH10) and decreases (CCDC86) on several sites. Notably, LARP7 and MEPCE are important regulators of RNA polymerase II-mediated transcription elongation as part of the 7SK snRNP complex. Regulation of these phosphorylation sites may contribute to the regulation of P-TEFb (CDK9) and transcriptional regulation of the virus, similarly to how these proteins are regulated during HIV infection (Mbonye et al. 2015).

SARS-CoV-2 infection regulates host kinase signaling

To study global changes in kinase signaling and their effect on host protein phosphorylation, regulated phosphorylation sites were grouped in five clusters based on their dynamics using a data-driven clustering approach (**Figure 4A**, **STAR Methods**). For each of the groups, enrichment analysis was performed for functions and pathways (**Figures 4A**, **Table S3**). The dynamics of these changes can be linked to the viral life cycle: entry (0-2 hours), replication (4-12 hours) and egress (24 hours). Cluster 1 and 2 include phosphorylation sites that, on average, are upregulated during infection. Cluster 1 sites tend to be upregulated within 2 hours (i.e. linked to viral entry) and are enriched in mRNA processing, cell cycle, apoptosis, and proteins involved in HIV infection; cluster 2 includes apoptosis proteins with a later onset of phosphorylation, associated with replication and/or egress. Phosphorylation sites in clusters 3 and 4 are downregulated and are enriched in RNA processing functions. Sites within cluster 5 possess a dynamical response to infection with an immediate downregulation followed by a rise during the middle and a renewed downregulation at late timepoints. This cluster was enriched for DNA replication and cell cycle, among others. These observations are corroborated by standard gene ontology enrichment analyses of biological processes regulated by phosphorylation (**Figure S1G, Table S3, STAR Methods**).

We estimated activity regulation for 97 kinases based on the regulation of their known substrates (Ochoa et al. 2016; Hernandez-Armenta et al. 2017) (**Table S4**), with the strongest regulation linked to viral entry (0-2 hours) and late replication/egress (24 hours). The kinases predicted to be most strongly activated (**Figure 4B, S2A**) include several members of the p38 pathway, including p38ɣ (MAPK12), as well as CK2 (CSNK2A1/2),

Ca(2+)/calmodulin-dependent protein kinase (CAMK2G), and GMP-dependent protein kinases PRKG1/2, which can inhibit Rho signaling. Kinases predicted to be downregulated include several cell cycle kinases (CDK1/2/5, AURKA), cell growth related signaling pathway kinases (PRKACA, AKT1/2, MAPK1/3, PIM1), and cytoskeleton (PAK1), among others. Some of the changes in kinase activity can be linked directly to host-viral protein interactions (**Figure 4C**). Kinase activity estimates based on the 24-hour mock control gave highly correlated results (r=0.81), identifying the same set of highly regulated kinases (**Figure S2D**). Among the 10 interacting kinases detected in a virus-host protein-protein interaction map (Gordon et al. 2020), an increase in activity for CK2, and a decrease for MARK2 and PRKACA was observed (**Figure 4C**). Of note, although we predict decreased activity for PRKACA based on the phosphorylation of its substrates, we simultaneously detected a significant increase in T198 phosphorylation (at 8, 12, and 24 hours post infection) within the activation loop, suggesting an increase in PRKACA activity. It is possible that Nsp13 is sequestering active PRKACA away from its typical substrates.

To better understand the signalling states of cells over the course of infection, we compared our data to a compilation of public phosphoproteomic datasets of other conditions (Ochoa et al. 2016) (**Figure 4D**, **S2B**). The first and last time point of infection resembled a kinase activation state induced by inhibition of mTOR, ERK, AKT, and EGFR, consistent with the estimated kinase activities of these growth related pathways. Between 2 to 12 hours post infection, kinase activity states resembling inhibition of PI3K, p70S6K, and ROCK kinases were observed. Finally, several of the timepoints resembled S/G2 cell cycle state, suggestive of a cell cycle block. Conversely, some conditions were anticorrelated with kinase activity profiles (**Figure 4D, S2B**). In line with a S/G2 cell-cycle block, infection signaling appeared opposite to that of a mitotic cell. In addition, inhibitors of HDACs (scriptaid, trichostatin A), the proteasome (bortezomib), Hsp90 (geldanamycin) and voltage-gated sodium channels (valproic acid) were also anti-correlated. These drugs, or drugs targeting these protein activities, could induce a signalling state that inhibits viral replication.

To further link kinase activities to downstream protein complexes, enrichment of up- or down-regulated phosphorylation sites was determined within a curated set of human protein complexes defined by CORUM (Giurgiu et al. 2019) (**Figure 4E and S2C**). This analysis revealed significant changes in phosphorylation of splicing related complexes (Spliceosome), the proteasome (PA700−20S−PA28), and chromatin remodelling complexes (HuCHRAC and MLL2). In addition, a subset of regulated phosphorylation sites were detected that have known regulatory functions or high predicted functional scores (Ochoa et al. 2020) that are linked to the regulation of protein activities (**Table S5**). Consistent with the observed signaling changes described above, these regulatory phosphosites are involved in the activation of chaperones (including HSP90), proteasome activity, inhibition of the APC, regulation of HDACs and cytoskeleton proteins, among others.

CK2 and N co-localize at virus-induced filopodial protrusions

Phosphoproteomics data indicate regulation of several kinases and effector proteins related to cytoskeleton organization upon SARS-CoV-2 infection. Kinases downstream of Rho/Rac/Cdc42 GTPases (PAK1/2 and ROCK1/2) and several well characterized phosphorylation site targets of PAK1/2 kinase in vimentin (VIM S39 and S56) and stathmin (STMN1 S16 and S25) were found to be downregulated during infection (**Figure 5A-B**). The interaction of Nsp7 with RhoA (Gordon et al. 2020) may contribute to this downregulation. In contrast, signaling via CK2 is strongly upregulated, as determined by the increase in phosphorylation of well characterized target sites (**Figure 5A-B**). Among the many roles of this kinase, we noted increased phosphorylation of cytoskeleton protein targets such as α-Catenin (CTNNA1 S641) and the heavy chain of the motor protein Myosin IIa (MYH9 S1943). In addition to these kinase-mediated effects, the Nsp2 protein of

SARS-CoV-2 also interacts directly with strumpellin (WASHC5), a subunit of the actin assembly-inducing WASH complex (Gordon et al. 2020), further implicating cytoskeleton regulation during infection. To study the relevance of these observations in a human infection model, high-resolution immunofluorescence imaging of fixed Caco-2 human colon epithelial cells was performed 24 hours post infection (**STAR Methods**).

SARS-CoV-2 infected Caco-2 cells were imaged for filamentous actin and the SARS-CoV-2 M protein, revealing prominent M protein clusters, possibly marking assembled SARS-CoV-2 viral particles, localized along the shafts and at the tips of actin-rich filopodia (**Figures 5B**, **S3B**). SARS-CoV-2 infection induced a dramatic increase in filopodial protrusions, which were significantly longer and more branched than in uninfected cells (**Figure 5D**). Uninfected cells also exhibited filopodial protrusions, but their frequency and shape were dramatically different (**Figure S3A**). Reorganization of the actin cytoskeleton is a common feature of many viral infections and it is associated with different stages of the viral life cycle (Taylor, Koyuncu, and Enquist 2011).

We hypothesize that induction of virus-containing filopodia could be important for SARS-CoV-2 egress and/or cell-to-cell spread within epithelial monolayers. Given that RHO/PAK/ROCK signaling is downregulated, we next asked if CK2 could play a role in this process. At 24 hours, infected cells showed CK2 expression along the thin filopodia protrusions (**Figures 5E**), partially co-localized with SARS-CoV-2 N protein (**Figure 5F**). Scanning and transmission electron microscopy were used (**Figure 5G, 5H, S3C, S3D**) to image the cellular protrusions at higher resolution. Assembled viral particles are clearly visible along these filopodia (**Figure 5G**) with instances where the viral particles appear to be budding from the protrusions (**Figure 5H**). Finally, we performed global phosphoproteomics analysis upon N protein over-expression and observed CK2 activity to be significantly upregulated (**Figure S3E, Table S1, Table S4**). As CK2 activity can promote actin polymerization (D'Amore et al. 2019), we hypothesize that N-protein may allosterically control CK2 activity and regulate cytoskeleton organization.

SARS-CoV-2 infection promotes p38/MAPK signaling activity and cell cycle arrest

Kinase activity analysis of SARS-CoV-2 phosphorylation profiles predicted an upregulation of several components of the p38/MAPK signaling pathway, including MAP2K3, MAP2K6, MAPK12, MAPKAPK2 (MK2), and MAPKAPK3 (**Figure 6A, 6B**). Immunoblotting for activated phospho-p38 (T180/Y182), phospho-MK2 (T334), and phospho-CREB and phospho-ATF-1 at their respective MAPKAPK2 sites (S133 in both) confirmed activation of the p38/MAPK pathway during SARS-CoV-2 infection in ACE2-expressing A549 human lung carcinoma cells (ACE2-A549) (**Figure 6C**). Furthermore, phosphoproteomics data depict increased phosphorylation of p38 pathway substrates such as negative elongation factor E (NELFE), heat shock protein beta-1 (HSPB1), and signal transducer and activator of transcription 1-alpha/beta (STAT1), among others (**Figure 6D)**. The regulation of these sites occurs late in the time course (24 hours post infection), likely reflecting a more advanced stage of viral infection, replication, and egress.

The p38/MAPK pathway mediates the cellular response to environmental stress, pathogenic infection, and pro-inflammatory cytokine stimulation, while downstream effectors of the pathway include transcription factors and RNA-binding proteins that promote inflammatory cytokine production (Cuadrado and Nebreda 2010; Wen, Sakamoto, and Miller 2010). Analysis of estimated transcription factor activity from gene expression data (**STAR Methods, Table S6**) derived from the infection of a human adenocarcinoma alveolar basal epithelial cell line (A549), a human epithelial lung cancer cell line (Calu3), and primary human bronchial/tracheal epithelial (NHBE) cells, demonstrated that transcription factors regulated by the p38/MAPK pathway were among the most highly activated upon infection (**Figure 6E**) (Blanco-Melo et al. 2020).

To investigate the contribution of the p38/MAPK pathway to cytokine production, SARS-CoV-2 infected ACE2-A549 cells were treated with the p38 inhibitor SB203580. The mRNA of inflammatory cytokines IL-6, TNFα, and others, increased during infection and was inhibited by p38 inhibition in a dose-dependent manner (**Figure 6F right, S4A**). Interestingly, p38 inhibition also reduced SARS-CoV-2 subgenomic mRNA (**Figure 6F left**) in the absence of major cellular toxicity (**Figure S5**), indicative of reduced viral replication. The SB203580-induced decrease in virus production was further confirmed using an anti-NP antibody-based assay (**Figure S5**, NY Vero E6). Multiplexed ELISA analysis on supernatants of cells from the same experiment demonstrated strong upregulation of inflammatory cytokines at the protein level, including IL-6, CXCL8, CCL20, and CCL2, which were decreased upon p38 inhibition (**Figure S4B, Table S7**). However, as SARS-CoV-2 replication is also inhibited by SB203580, we cannot deconvolve the contributions of p38/MAPK pathway activity and SARS-CoV-2 virus presence on cytokine production.

Comparing phosphoproteomics profiles of SARS-CoV-2 infected cells to a database of phosphorylation profiles collected at specific cell cycle stages, viral infection was most highly correlated with cells arrested at the S/G2 transition and was negatively correlated with profiles of cells in mitosis (**Figure 6G**). We also observed SARS-CoV-2-dependent regulation of CDK2 T14/Y15 phosphorylation, initially increased in response to SARS-CoV-2 infection at 2 hours followed by a decrease over the remainder infection time course (**Figure 6H left**). CDK2 activity promotes the transition from the G2 phase of the cell cycle into mitosis and is inhibited by phosphorylation at positions T14 and Y15 by kinases WEE1 and MYT1, preventing premature entry into mitosis (Parker and Piwnica-Worms 1992; Mueller et al. 1995). CDK2 can also become phosphorylated when the cell cycle is arrested due to checkpoint failures or DNA damage. In addition, H2AX S140 phosphorylation (i.e., γ-H2AX), a hallmark of the DNA damage response, exhibited a profile similar to CDK2, suggesting that the DNA damage response may become activated early during infection (Rogakou et al. 1998) (**Figure 6H right**).

To more directly test whether SARS-CoV-2 infection affects cell cycle progression, cells were infected with SARS-CoV-2 for 24 hours and their DNA content was measured using DAPI DNA staining and flow cytometry. A significant increase in the fraction of cells in S phase and at the G2/M transition, and a decrease in the fraction of cells in G0/G1 phase, was observed (**Figure 6I, S4C**). This observation is consistent with an arrest between S and G2 phases of the cell cycle. A relationship between p38 activity and cell cycle arrest has been previously described and the two could be mechanistically linked during SARS-CoV-2 infection (Lee et al. 2002; Yee et al. 2004).

Mapping kinase activities to pharmacological modulators identifies SARS-CoV-2 therapies

In order to identify effective therapies for SARS-CoV-2 infection, kinase inhibitors were mapped to the most differentially regulated kinase activities (**Figure 7A**) and to specific phosphorylation sites **(Table S8, STAR Methods)**. This resulted in a list of 87 drugs and compounds: 10 FDA-approved, 53 investigational new drugs (INDs, undergoing clinical testing), and 24 pre-clinical. Many of the drugs and compounds identified were reported to target several host kinases in cell-free assays at a minimum, though many have been observed to hit targets in cellular assays as well (**Figure 7A**). We reasoned that testing molecules with both overlapping and unique targets would help specify the molecular targets of greatest importance for SARS-CoV-2. Here, 68 total drugs and compounds were tested for antiviral efficacy (via RT-qPCR, anti-NP antibody, plaque assay, and/or TCID50) and cellular toxicity at two different institutions, in New York (Mount Sinai; 25 drugs/compounds) and Paris (Institut Pasteur; 62), and in two cell lines, Vero E6 (68) and A549-ACE2 (61). All pharmacological profiling results can be found in **Figure S5** and **Table S8**.

We found pharmacological inhibitors of CK2, p38 MAP kinase signaling, PIKFYVE, and cyclin dependent kinases (CDKs) to possess strong antiviral efficacy. Cells were pre-treated with inhibitor molecules followed by SARS-CoV-2 infection (**STAR Methods**) and both virus quantity (anti-NP antibody against SARS-CoV-2) and cell viability were quantified 48 hours post infection. As a positive control and for comparison, remdesivir was tested and the expected favorable antiviral activity was observed (IC_{50} = 1.28 μM; **Figure 7B**). Silmitasertib, an inhibitor of CSNK2A1 and CSNK2A2, was found to possess antiviral activity (IC_{50} = 2.34 μM; **Figure 7C, S5**). In conjunction with data supporting physical interaction (Gordon et al. 2020) and co-localization with N protein (**Figure 5F**), as well as a potential role in remodeling extracellular matrix upon infection (**Figure 5, S3**), CK2 signaling appears to be an important pathway hijacked by SARS-CoV-2. Furthermore, silmitasertib is currently being considered for human testing as a potential treatment for COVID-19.

To probe SARS-CoV-2 dependence on MAP kinase signaling, SARS-CoV-2 replication was measured in response to pharmacological and genetic perturbation of MAP kinase components that were upregulated during infection (**Figure 7D**). Potent antiviral activity was observed for gilteritinib (**Figure 7E**; IC_{50} = 0.807 μM), an inhibitor of AXL kinase, upstream of p38; ralimetinib (**Figure 7F**; IC_{50} = 0.873 μM), an inhibitor of MAPK11 (p38α) and MAPK14 (p38□); MAPK13-IN-1 (**Figure 7G**; IC_{50} = 4.63 μM), an inhibitor of MAPK13 (p38-□); and ARRY-797 (**Figure 7H**; IC_{50} = 0.913 μM) in A549-ACE2 cells, a MAPK14 inhibitor. To further probe the dependence of SARS-CoV-2 on p38 pathway members, siRNA-mediated knockdown of MAP2K3, p38-□ (MAPK13), and p38-ɣ (MAPK12) was performed in A549-ACE2 cells and a significant decrease in SARS-CoV-2 replication was observed for all three, with little-to-no effect on cell viability (**Figure 7I**).

In addition, we noted the marked regulation of phosphatidylinositol enzyme activities for PIK3CA, PLCB3, and PIKFYVE, suggesting a potential role for the appropriate balance of phosphatidylinositol species. To target this process, apilimod, a small molecule inhibitor of PIKFYVE, was tested and found to possess strong antiviral activity in two cell lines (Vero E6:IC_{50} < 0.08 μM; A549-ACE2:IC_{50} = 0.007 μM), corroborated by a recent study (Ou et al. 2020) (**Figure 7J**). Lastly, we noted the pronounced regulation of CDK signaling pathways (**Figure 4B**) and cell cycle stage (**Figure 6I**) during viral infection, suggesting the virus may regulate the cell cycle to enhance viral replication. Accordingly, strong antiviral activity for the CDK inhibitor dinaciclib was observed across two cell lines (Vero E6:IC_{50} = 0.127 μM; A549-ACE2:IC_{50} = 0.032 μM) (**Figure 7K**).

DISCUSSION

We used a mass spectrometry-based approach to study perturbations in protein abundance and phosphorylation during SARS-CoV-2 infection. Viral proteins increased starting at 8 hours post infection, indicative of viral replication, while only small changes in host protein abundance were observed within 24 hours. In contrast, large changes were observed in protein phosphorylation, highlighting the degree by which the virus makes use of the host post-translational regulatory systems to promote rapid changes in cellular signaling.

Changes in phosphorylation reflect altered activities of kinases that are hijacked during the infection. Based on changes in phosphorylation of their annotated substrates, we estimated changes in activity of 97 of the 518 human kinases. The changes in kinase activity offer insights into the biology of viral infection. Kinases represent ideal drug targets; here, we identified kinases and pathways altered by SARS-CoV-2 infection that can be targeted by 87 FDA approved drugs and compounds in clinical trials or in preclinical development (**Table S8**).

The most strongly regulated kinases fall into a set of signaling pathways that include p38/MAPK signaling, AKT and ERK signaling, Rho GTPase cytoskeleton signaling, and cell cycle regulation. The downregulation of ROCK and PAK kinase activity and upregulation of CK2 cytoskeleton related targets suggests virus-induced changes in cytoskeleton organization. Imaging of infected cells revealed the formation of actin-rich filopodia containing viral proteins. Higher resolution electron microscopy data confirms the presence of assembled viral particles in these structures. Many viruses, including vaccinia, ebola, and Marburg, hijack the host cell cytoskeleton to promote egress and rapid cell-to-cell spread across epithelial monolayers. Vaccinia promotes Arp2/3-dependent actin assembly, producing a filopodial protrusion with a virus at the tip (Leite and Way 2015). In contrast, Marburg virus hijacks the unconventional motor protein Myosin X, which promotes filopodia formation and trafficks the virus along the filopodia shaft. The SARS-CoV-2 protein clusters peppered throughout the length of filopodial protrusions more closely resemble Marburg than vaccinia, but additional work is required to understand whether SARS-CoV-2 makes use of either Myosin X motor activity or actin filament assembly to move along filopodia. CK2 is known to phosphorylate myosin proteins at endocytic sites to drive actin polymerization (Fernández-Golbano et al. 2014). Furthermore, CK2 was found to regulate actin tail formation during vaccinia virus infection, enabling efficient cell-to-cell spread of the virus (D. E. Alvarez and Agaisse 2012; Smith and Law 2004). Here, the CK2 inhibitor silmitasertib displayed robust antiviral activity, suggesting a role for this kinase in regulating the SARS-CoV-2 life cycle.

In addition, kinase activity profiling analysis shows CDK1/2 activities are significantly reduced by SARS-CoV-2 infection, leading to a S/G2 phase arrest that is similar to infectious bronchitis virus (IBV), a prototypical coronavirus (Dove et al. 2006; Li, Tam, and Liu 2007), and other RNA viruses (Lilley, Schwartz, and Weitzman 2007; Ariumi et al. 2008). Arresting cells in S/G2 phase may provide benefits for viral replication and progeny production by ensuring an abundant supply of nucleotides and other essential host DNA repair/replication proteins (Chaurushiya and Weitzman 2009).

The predicted increase in p38/MAPK activity led us to investigate the effects of p38/MAPK inhibition on pro-inflammatory cytokine production and viral replication in SARS-CoV-2 infected cells. Recent immunological studies have indicated that increased IL-6, IL-10, TNF-α and lymphopenia are associated with severe COVID-19 cases (Pedersen and Ho 2020). The p38/MAPK pathway responds to and controls the production of potentially harmful pro-inflammatory cytokines. Several pathogenic viral infections induce a p38/MAPK signaling state that exhibits uncontrolled positive feedback regulation, leading to excessive inflammation that is associated with severe disease. Inhibition of p38/MAPK signaling suppressed the overproduction of inflammatory cytokines induced by several viral infections, including SARS-CoV, Dengue virus, and influenza A virus, improving survival in mice (Fu et al. 2014; Growcott et al. 2018; Jimenez-Guardeño et al. 2014). However, p38/MAPK inhibition did not directly impair the virus in these cases but instead the host's immune response to the infection. In contrast, during SARS-CoV-2 infection, p38/MAPK inhibition both suppressed cytokine production and impaired viral replication by an as yet unknown mechanism, suggesting that p38/MAPK inhibition may target multiple mechanisms related to COVID-19 pathogenesis.

We tested 68 drugs and compounds and found antiviral activity for several that are either FDA approved, in clinical testing, or under preclinical development for various diseases, including silmitasertib (CK2; phase 2), gilteritinib (AXL; FDA approved), ARRY-797 (p38; phase2/3), MAPK13-IN-1 (p38; preclinical), SB203580 (p38; preclinical), ralimetinib (p38; phase 2), apilimod (PIKFYVE; phase 1), and dinaciclib (CDK; phase 3), among others (**Figure S5, Table S8**). Silmitasertib, a small molecule undergoing clinical trials for various cancers, is now being considered for testing in humans to combat COVID-19. Although the effectiveness of CK2 inhibition may be attributed to its regulation of stress granules (Gordon et al. 2020), viral egress and dissemination could be facilitated by CK2-mediated remodeling of the extracellular matrix (**Figure 5**).

Ralimetinib is currently in phase 2 clinical trials for the treatment of ovarian cancer (Patnaik et al. 2016) and ARRY-797 is in phase 3 clinical trials for the treatment of cardiomyopathy. The antiviral activity observed for gilteritinib, an FDA-approved drug for the treatment of acute myeloid leukemia, is supported by the involvement of another AXL inhibitor, bencentinib, in the RECOVERY COVID-19 clinical trial in the United Kingdom. AXL is known to regulate various intracellular signaling pathways (Allen et al. 2002; Hafizi and Dahlbäck 2006), including Ras/ERK, PI3K, and p38 (Allen et al. 2002); AXL inhibition here may contribute to the downregulation of p38 signaling. Apilimod, a PIKFYVE inhibitor, has been described by a recent study for its antiviral capacity (Ou et al. 2020). Here, we expand upon this into a mechanism of regulation by phosphorylation of PIKFYVE upon SARS-CoV-2 infection.

Similar to successful antiretroviral therapy for HIV, a combinatorial drug cocktail may constitute a viable treatment option for SARS-CoV-2 infection. Specifically, combining remdesivir with the kinase inhibitors identified in this study as well as with translation inhibitors and/or modulators of sigma-1 receptor (Gordon et al. 2020) warrants further testing. Furthermore, pairing genetic and pharmacological perturbations in a systematic fashion could identify new combination therapy approaches and illuminate disease mechanisms.

The unbiased, global phosphoproteomics approaches used here highlight cellular processes hijacked during SARS-CoV-2 infection. To address the need for improved therapeutic strategies to fight COVID-19, we employed a data-driven approach by mapping phosphorylation profiles of dysregulated signaling pathways to drugs and compounds targeting those signaling pathways. We hope this paradigm can be employed in the future to find additional therapies for COVID-19 and other infectious diseases.

Limitations of Study

A limitation of the current study is the use of a non-human cell line for proteomics analysis upon SARS-CoV-2 infection; here, an African green monkey cell line (Vero E6) was used because it was previously shown to be highly permissible to SARS-CoV-2 infection (Harcourt et al., 2020). However, pharmacological inhibition of SARS-CoV-2 was assessed in human lung A549-ACE2 cells in addition to Vero E6. The majority of drug effects were found to be replicated between cell lines.

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AUTHOR CONTRIBUTIONS

Conceptualization by M.B., D.L.S., N.J.K.; Infection experiments by B.M., V.V.R., B.N., L.M., C.K., Q.D.T., A.H., T.V., K.M.W., E.M.; Proteomics sample coordination and preparation by E.S., M.S., J.M.F., J.Z.G., J.X.; Proteomics data acquisition by A.L.R., D.L.S.; Data analysis by M.C.M., B.J.P., D.M., C.H.A., Ai.D., Ma.M., D.Q., Y.Z., J.R.J., D.L.S., P.B., J.K.L., M.G., M.B., C.J.P.M.; Figure generation by M.C.M., B.J.P., D.M., C.H.A., Ai.D., Ma.M., D.Q., J.R.J., D.L.S., P.B., M.B.; Cell cycle experiments by R.R., B.M.; Infection imaging by S.W., J.K., S.U., G.K., R.G.; Manuscript prepared by M.B., D.E.G., K.O., J.R.J., D.L.S., P.B., N.J.K., R.D.M.; Literature review by R.M.K., Ma.M., J.B., A.R., T.P., Q.L., R.H., M.C., Mo.M., M.K., G.J., B.T., J.H., D.L.S., M.B.; RNAseq analysis by Au.D., A.V., J.S.R.; Drug curation by Y.S., J.E.M., K.M.S., A.R.L., E.J.M., E.F., S.B.; Interactive map by T.M., M.C.O., Y.C., J.C.J.C., D.J.B, S.K., M.B., R.M.K.; Electron microscopy by E.R.F, E.D.W.; Work supervised by T.K., J.K.L., A.G., B.S., M.O., J.S.R., G.K., R.G., B.R.T., K.M.S., J.R.J., D.L.S., A.G.S., M.V., P.B., and N.J.K.

DECLARATION OF INTERESTS

The **Krogan** Laboratory has received research support from Vir Biotechnology and F. Hoffmann-La Roche. **Kevan Shokat** has consulting agreements for the following companies involving cash and/or stock compensation: Black Diamond Therapeutics, BridGene Biosciences, Denali Therapeutics, Dice Molecules, eFFECTOR Therapeutics (zotatifin & tomivosertib), Erasca, Genentech/Roche, Janssen Pharmaceuticals, Kumquat Biosciences, Kura Oncology, Merck, Mitokinin, Petra Pharma, Qulab Inc. Revolution Medicines (WDB002), Type6 Therapeutics, Venthera, Wellspring Biosciences (Araxes Pharma).

MAIN FIGURE LEGENDS

Figure 1. Global Proteomics of Phosphorylation and Abundance Changes upon SARS-CoV-2 Infection. (**A**) Vero E6 cells were infected with SARS-CoV-2 (MOI 1.0). After 1 hour of viral uptake, cells were harvested (0 h) or subsequently after 2, 4, 8, 12, or 24 hours. As a control, Vero E6 cells were also mock infected for 1 hour, and either harvested immediately thereafter (0 h), or after 24 hours of mock infection. All conditions were performed in biological triplicate. Following cell harvest, cells were lysed and proteins digested into peptides. Aliquots of all samples were analyzed by mass spectrometry (MS) to measure changes in protein abundance

upon infection, while the remaining sample was enriched for phosphorylated peptides and subsequently analyzed to measure changes in phosphorylation signaling. A DIA approach was used for all MS acquisitions. Lastly, all phosphorylation sites and protein identifiers were mapped to their respective human protein orthologs. (**B**) Principal component analysis (PCA) of phosphorylation replicates after removing outliers. See also Figure S1. (**C**) Correlation of protein abundance (AB) and phosphorylation sites (PH) between replicates within a biological condition (red), and across biological conditions (black). (**D**) Median abundance of individual SARS-CoV-2 proteins in the protein abundance analysis. (**E**) The number of significantly regulated phosphorylation site groups across the infection time course. (**F**) Volcano plot of phosphorylation site group quantification at 24 hours postl infection. (**G**) The number of significantly regulated proteins across the infection time course. (**H**) Volcano plot of protein quantification at 24 hours post infection. For **E-H**, all infection timepoints are compared to the mock infection at 0 hours, and significantly regulated proteins are defined as (absolute value of log2(inf/mock) > 1 and adjusted p-value < 0.05; or when only detected in infected or mock based on replicate and MS feature counts, see **STAR Methods**). (**I**) Gene Ontology enrichment analysis of all significantly changing proteins in terms of abundance divided into two sets, downregulated (blue) and upregulated (red). (**J**) Proportion of significantly regulated phosphorylation site groups with a correlated (i.e. same direction; AB match) or anti-correlated (i.e. opposite direction; AB mismatch) significant or insignificant (grey) change in protein abundance. See also Figure S1.

Figure 2. Overview of SARS-CoV-2 Viral Protein Phosphorylation Sites in the Host Cell. (A) Localization of phosphorylation sites across viral protein sequences from this study and a previous study (Davidson et al. 2020). Stem height indicates predicted deleteriousness of alanine substitutions. Dot color indicates whether the residue is (true), or is not (false), predicted to form part of an interaction interface based on SPPIDER analysis. Positions with no structural coverage are excluded from interface prediction. **(B)** Distribution of secondary structure elements in which viral phosphorylation sites were found, as classified by DSSP. **(C)** Distribution of top matching host kinases to viral phosphorylation sites according to NetPhorest (Horn et al. 2014). **(D)** Phosphorylation cluster in the C-terminal tail of the M protein (red residues) structure (Heo and Feig 2020) and associated sequence motif. Asterisks indicate phosphorylation sites. **(E)** Alignment of M protein phosphorylation cluster across different coronaviruses. Asterisks indicate phosphorylation sites. **(F)** Surface electrostatic potential of non-phosphorylated (left) and phosphorylated (right) RNA-binding domain of the N protein (PDB ID: 6M3M). Position of phosphorylation sites indicated with arrows. Blue denotes positive charge potential; red indicates negative charge potential. Electrostatic potential was computed with APBS after preparation with PDB2PQR.

Figure 3. Phosphorylation on SARS-CoV-2 Host Factors. The SARS-CoV-2 virus-host protein-protein interaction map (Gordon et al. 2020) found 332 human proteins interacting with 27 (26 wildtype, 1 mutant) viral proteins. Here, we find 40/332 proteins significantly differentially phosphorylated across at least two timepoints (adjusted p-value < 0.05 and abs(log2FC) > 1). Viral proteins are shown as red diamonds. Interacting host proteins are shown as grey circles. Phosphorylation sites emanate from host proteins, colored by their log2 fold change compared to uninfected control samples (red, increase; blue, decrease) at each timepoint (0, 2, 4, 8, 12, and 24 hours post infection) in clockwise fashion. An interactive version of phosphorylation data can be found at kroganlab.ucsf.edu/network-maps.

Figure 4. Signaling Changes in Host Cells in Response to SARS-CoV-2 Infection. (A) Clusters of significantly changing phosphorylation sites (abs(log2FC) > 1 and adjusted p-value < 0.05) across the time course of infection with non-redundant enriched Reactome pathway terms (q-value < 0.01) shown for each cluster. Horizontal red lines below each pathway term correspond to phosphorylated proteins belonging to the pathway and black-bordered rectangle is indicative of a significantly enriched term. **(B)** Kinases depicting a

strong change in activity upon infection (abs. log10(p-value) > 2.5) in at least one time point, with predicted activity in at least 5 out of 6 timepoints, are shown. **(C)** Schematic representation of interaction between host kinases and SARS-CoV-2 viral proteins from Gordon et al. (2020). Substrate phosphorylation sites for each kinase are color-coded as blue (up) and red (down) based on the direction of change during infection. Only phosphorylation sites corresponding to the kinase activity direction are shown. **(D)** Correlation of kinase activity profiles of each time point with other biological conditions with at least one significantly changing kinase (abs(log10(P-value)) > 2.5) and having significant correlation with at least one time-point (FDR < 5%). **(E)** Overall phosphorylation change (-log10(p-value)) of a protein complex, estimated as the change in phosphorylation on member proteins. Only non-redundant protein complexes with significant change in phosphorylation (abs(log10(P-value)) > 2.5) in at least one time-point are shown. See also Figure S2.

Figure 5. Colocalization of CK2 and Viral Proteins at Actin Protrusions. (**A**) Pathway of regulated phosphorylation sites and SARS-CoV-2 interaction partners involved in cytoskeletal reorganization. (**B**) Regulation of individual kinase activity or phosphorylation sites depicted in (A). (**C**) Caco-2 cells infected with SARS-CoV-2 at an MOI of 0.1 for 24 hours prior to immunostaining for F-actin and M-protein, as indicated. Shown is a confocal section revealing M protein localization along and to the tip of filopodia (left) and magnification of dashed box (right). (**D**) Dot plot quantification of the number and length of filopodia in either untreated (MOCK) or infected Caco-2 cells for 24 hours with SARS-CoV-2. Filopodia length was measured from the cortical actin to the tip of the filopodium. Error bars represent SD. Statistical testing by Mann-Whitney test. (**E**) Caco-2 cells infected with SARS-CoV-2 at an MOI of 0.01 for 24 hours prior to immunostaining for F-actin, N-protein, and casein kinase II (CK2) as indicated (left). Magnification of the dashed box as single channels (right). (**F**) Magnification of dashed box from panel **E** with quantification of colocalization between CK2 and N protein throughout infected Caco-2 cells. Displayed is the proportion of N-protein positive particles colocalizing with CK2. Error bars represent SD. (**G**) Scanning electron microscopy and (**H**) transmission electron microscopy images of SARS-CoV-2 budding from Vero E6 cell filopodia (black arrow). See also Figure S3.

Figure 6. SARS-CoV-2 Activates the p38/MAPK Signaling Pathway and Causes Cell Cycle Arrest. (A) Diagram of p38/MAPK signaling pathway. (**B**) Kinase activity analysis for kinases in the p38/MAPK pathway. (**C**) Western blot analysis of phosphorylated p38/MAPK signaling components in mock and SARS-CoV-2-infected ACE2-A549 cells at 24 hours post infection. (**D**) Log2 fold change profiles of indicated p38/MAPK substrates during SARS-CoV-2 infection in Vero E6 cells. (**E**) Transcription factor activity analysis of SARS-CoV-2-infected A549, Calu-3, and NHBE cells comparing p38/MAPK transcription factors to transcription factors not associated with the p38/MAPK pathway. Statistical test is Mann-Whitney. (**F**) RT-qPCR analysis of indicated mRNA from ACE2-A549 cells pre-treated with p38 inhibitor SB203580 at indicated concentrations for 1 hour prior to infection with SARS-CoV-2 for 24 hours. Statistical test by Student's t-test. See also Figure S4 and S5. (**G**) Heatmap of Pearson's correlation coefficients comparing SARS-CoV-2-infected Vero E6 phosphorylation profiles to profiles of cells with induced DNA damage and cells arrested at indicated cell cycle stages. (**H**) Log2 fold change profiles of indicated cell cycle and DNA damage substrates during SARS-CoV-2 infection in Vero E6 cells. (**I**) DNA content analysis of cells infected with SARS-CoV-2 for 24 hours compared to mock-infected cells.

Figure 7. Mapping Regulated Kinases to Kinase Inhibitors Identifies SARS-CoV-2 Therapies. (A) Kinase inhibitors (left) mapped to kinases (right) whose activity was regulated by SARS-CoV-2 infection. Lines connecting them indicate known kinase targets for each drug/compound. **(B)** Vero E6 cells pre-treated with remdesivir at indicated doses followed by SARS-CoV-2 infection for 48 hours. Percent viral titer compared to mock drug treatment (anti-NP antibody; red line, dots, and text) and cell viability (black) depicted. Error bars

represent SD. **(C)** As in **B**, Vero E6 cells treated with CK2 inhibitor silmitasertib. Physical interactions between N protein and CSNK2A2 and CSNK2B, CK2 subunits, were observed in a prior study (Gordon et al. 2020). **(D)** Predicted increased kinase activity for p38 signaling pathway and drugs/compounds targeting pathway members (Ralimetinib, MAPK13-IN-1, and ARRY-797) and upstream drivers (Gilteritinib). **(E-G)** As in **B**, Vero E6 cells treated with AXL inhibitor, Gilteritinib **(E)**, MAPK11/14 inhibitor, Ralimetinib **(F)**, or the MAPK13 inhibitor, MAPK13-IN-1 **(G)** prior to SARS-CoV-2 infection. (**H**) A549-ACE2 lung epithelial cells treated with the MAPK14 inhibitor, ARRY-797, prior to SARS-CoV-2 infection. **(I)** Small-interfering RNA (siRNA) knockdown of p38 pathway genes in A549-ACE2 leads to significant decrease of SARS-CoV-2 viral replication (red) as assessed by RT-qPCR in the absence of effects on cell viability (black). ACE2 and non-targeting siRNAs are included as positive and negative controls, respectively. **(J-K)** Vero E6 or A549-ACE2 cells treated with PIKFYVE inhibitor Apilimod **(J)**, or CDK inhibitor Dinaciclib **(K)** prior to SARS-CoV-2 infection. See also Figure S6.

SUPPLEMENTAL FIGURES

Figure S1. Related to Figure 1; Proteomics: Quality Control (QC), orthology, enrichments, viral proteins. (**A**) Principal component analysis computed on intensities summarized by MSstats at the level of phosphorylation site groups within (from left to right) all runs, with one outlier run removed, and with two outlier runs removed. Outlier runs are labeled 00Hr.2 and 02.Hr.2. (**B**) Principal components analysis computed on protein intensities as summarized by MSstats (from left to right) within all runs, with one outlier run removed, and with two outlier runs removed. Outlier runs are both labeled 00Hr.2; one is mock and the other is infected. (**C**) Coefficient of variance box plot for each condition. Black lines depict the median and their values are indicated above each box plot. (**D**) Mapping detected and quantifiable proteins and phosphorylation sites from the green monkey (Chlorocebus sabaeus) protein sequences to human genes. Proteins and sites were considered quantifiable if MSstats computed a non-infinite fold change for any time point or if an infinite log2 fold change passes criteria for inclusion in any time point. (**E**) Intensities of viral proteins as summarized over all peptide ion fragments by MSstats, averaged across replicates. The MSstats summarization is based on the median intensity of all fragments after data- pre-processing (STAR methods). (**F**) Gene Ontology enrichment analysis for proteins significantly regulated in terms of abundance upon infection, separated by time point and direction of phosphorylation regulation. All terms with significant over-representation (adjusted p-value < 0.01) in the regulated gene set are kept, and redundant terms are removed (see STAR Methods). Numbers in cells indicate the number of genes that match the term for a given time point and direction. (**G**) Gene Ontology enrichment analysis for significantly phosphorylated proteins upon infection, separated by time point and direction of protein regulation. Details same as for (**F**).

Figure S2. Related to Figure 4; Full kinase activities, correlated conditions, and regulated complexes. (**A**) Changes in predicted kinase activities across different timepoints post-infection. (**B**) Correlation of kinase activity profiles of each time-point with other biological conditions. Kinase activities were estimated for a wide-range of biological conditions obtained from previously published phosphoproteomics datasets (Ochoa et al., 2016). (**C**) Changes in phosphorylation in protein complexes. Overall Phosphorylation change (-log10 P-value) of a protein complex was derived from change in phosphorylation of sites in member proteins. (**D**) Kinase activity estimates when using either the 0-hour or 24-hour mock controls for those top regulated kinase activities from the 0-hour control comparison.

Figure S3. Related to Figure 5; Microscopy images in response to SARS-CoV-2 infection. (**A**) Non-infected Caco2 cells co-stained for F-actin, CK2 and nuclei (DAPI). Magnification of the indicated area is displayed as a single channel and merged images on the right panels. (**B**) Caco2 cells infected with SARS-

CoV-2 at an MOI of 0.1 for 24 h prior to immunostaining for F-actin and M-protein, as indicated. See lower (1) and right (2) panel for magnification of regions indicated by dashed boxes. (**C**) Scanning electron microscopy and (**D**) transmission electron microscopy image of SARS-CoV-2 budding from Vero E6 cell filopodia. (**E**) N protein was found to physically interact with Casein Kinase II subunits (cartoon, left), CSNK2B and CSNK2A2 (Gordon et al., 2020). To test whether N protein could directly control CK2 activity, N protein was transduced via lentivirus in Vero E6 cells and stably induced via doxycycline for 48 hours followed by phosphoproteomics analysis. Kinase activities were calculated as before (STAR methods) and top up- (>1.5, red) and down-regulated (<1.5, blue) kinases are shown. See Table S1 for full phosphoproteomics data and Table S4 for full list of predicted kinase activities.

Figure S4. Related to Figure 6; Cytokine profiling upon infection, p38 inhibition, and cell cycle analysis. (**A**) RT-qPCR analysis of indicated mRNA from A549-ACE2 cells pre-treated with p38 inhibitor SB203580 at indicated concentrations for one hour prior to infection with SARS-CoV-2 for 24 hours. Statistical test is Student's t-test. Errors bars are SD. (**B**) Same as in (**A**) but a Luminex-based quantification of indicated cytokines. Error bars are SD. (**C**) Cell cycle analysis of Vero E6 cells (same as in Figure 6I) upon SARS-CoV-2 infection at an MOI of 1. Cell stained with DAPI DNA stain prior to flow cytometry analysis. Statistical test is Mann-Whitney test. Error bars are SD.

Figure S5. Related to Figure 7; Pharmacological profiling. Dose response of phosphoproteomics-informed drugs and compounds. Assays performed in New York (red, anti-NP; blue TCID50) and Paris (red, RT-qPCR; purple, plaque assays) across two cell lines (A549-ACE2 and Vero E6). Cell viability shown in black. Mean of three biological replicates is shown. Error bars are SEM.

STAR METHODS

RESOURCE AVAILABILITY

Lead Contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by Nevan J. Krogan (Nevan.Krogan@ucsf.edu).

Materials Availability

Plasmid pLVX-TetOne-Puro-SARS-CoV-2-N-2xStrep is available upon request from the Lead Contact.

Data and Code Availability

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD019113 (Perez-Riverol et al. 2019). An interactive version of phosphorylation data can be found at kroganlab.ucsf.edu/network-maps. Supplemental Tables are available from Mendeley Data at http://dx.doi.org/10.17632/dpkbh2g9hy.1.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Cells. African green monkey kidney epithelial Vero E6 (Vero 76, clone E6, Vero E6, ATCC® CRL-1586™) authenticated by ATCC and tested negative for mycoplasma contamination prior to commencement were maintained in a humidified atmosphere at 37°C with 5% CO_2, in Dulbecco's modified Eagle's medium (DMEM) containing 10% (v/v) fetal bovine serum (FBS, Invitrogen). ACE2-expressing A549 cells, a human lung epithelial cell line, were a kind gift from Brad Rosenberg. A549-ACE2 cells were cultured in DMEM supplemented with 10% FBS and maintained at 37°C with 5% CO_2. Caco-2 (ATCC® HTB-37™) human colon

epithelial cells were maintained in a humidified atmosphere at 37°C with 5% CO_2 in DMEM-containing 20% (v/v) FBS.

Viruses (Institut Pasteur, Paris)**.** The SARS-CoV-2 isolate BetaCoV/France/IDF0372/2020 was supplied by the National Reference Centre for Respiratory Viruses hosted by Institut Pasteur (Paris, France) and headed by Pr. Sylvie van der Werf. The isolate originated from a human sample provided by Dr. X. Lescure and Pr. Y. Yazdanpanah from the Bichat Hospital, Paris, France. The isolate was supplied through the European Virus Archive goes Global (EVAg) platform. Viral stocks were prepared by propagation in Vero E6 cells in DMEM supplemented with 2% FBS. Viral titers were determined by plaque assay in Minimum Essential Media (MEM) supplemented with 2% (v/v) FBS (Invitrogen) and 0.05% agarose. All experiments involving live SARS-CoV-2 were performed in compliance with Institut Pasteur Paris's guidelines for Biosafety Level 3 (BSL-3) containment procedures in approved laboratories. All experiments were performed in at least three biologically independent samples.

Viruses (Mount Sinai, New York). For infection experiments in ACE2-A549 cells, SARS-CoV-2, isolate USA-WA1/2020 (NR-52281), which shares 99.983% sequence identity with the BetaCoV/France/IDF0372/2020 isolate, was deposited by the Center for Disease Control and Prevention and obtained through BEI Resources, NIAID, NIH. SARS-CoV-2 was propagated in Vero E6 cells in DMEM supplemented with 2% FBS, 4.5 g/L D-glucose, 4 mM L-glutamine, 10 mM Non-Essential Amino Acids, 1 mM Sodium Pyruvate and 10 mM HEPES as described previously (Blanco-Melo et al. 2020). All work involving live SARS-CoV-2 was performed in the CDC/USDA-approved BSL-3 facility of the Global Health and Emerging Pathogens Institute at the Icahn School of Medicine at Mount Sinai in accordance with institutional biosafety requirements.

Viruses (University of Freiburg, Germany). For infection experiments in Caco-2 cells, SARS-CoV-2 isolate Muc-IMB-1/2020, kindly provided by the Bundeswehr Institute of Microbiology, Munich, Germany, was used. SARS-CoV-2 was propagated in Vero E6 cells in DMEM supplemented with 2% FBS. All work involving live SARS-CoV-2 was performed in the BSL-3 facility of the Institute of Virology, University Hospital Freiburg, and was approved according to the German Act of Genetic Engineering by the local authority (Regierungspraesidium Tuebingen, permit UNI.FRK.05.16/05).

METHODS DETAILS

Vero E6 cell infection for proteomic analysis. Vero E6 cells were seeded using $2x10^6$ cells in T25 flasks. The following day cells were either mock infected or infected with SARS-CoV-2 at a MOI of 1 in serum-free DMEM at 37°C for 1 hour. After absorption the 0 hour samples were lysed immediately, while the media for other samples was replaced with 2% FBS / DMEM (Invitrogen) and incubated at 37°C for times indicated before lysis.

Cell lysis and digestion. Cells were lysed using 1% IGEPAL (Sigma) in PBS (Invitrogen) for 20 minutes at room temperature (RT) to inactivate the virus. These specific lysis conditions were used as this was the approved virus inactivation protocol. Proteins contained in the cell lysate were then immediately precipitated using 90% methanol (v/v) (Sigma) by centrifugation at 20,000x g for 10 min. The protein pellets were frozen at -80°C. Precipitated proteins were resuspended in lysis buffer (8 M urea, 100 mM ammonium bicarbonate (ABC), 150 mM NaCl, protease inhibitor (mini-cOmplete, Roche) and phosphatase inhibitors (phosSTOP, Roche). Tris-(2-carboxyethyl)phosphine (TCEP) was added to a final concentration of 4 mM. Lysis was performed via probe sonication, on ice, at 20% amplitude for 20 s., followed by 10 seconds of rest. This process was performed a total of three times. Following lysis, protein concentration was determined using Bradford assay. Iodoacetamide (IAA) was added to each sample to a final concentration of 10 mM, and

samples were incubated in the dark at room temperature for 30 minutes. Excess IAA was quenched by the addition of dithiothreitol (DTT) to 10 mM, followed by incubation in the dark at RT for 30 minutes. Samples were then diluted with 0.1 M ABC (pH = 8.0) to a final urea concentration of 2 M. Trypsin (Promega) was added at a 1:100 (enzyme:protein w:w) ratio and digested overnight at 37°C with rotation. Following digestion, 10% trifluoroacetic acid (TFA) was added to each sample to a final pH ~2. Samples were desalted under vacuum using Sep Pak tC18 cartridges (Waters). Each cartridge was activated with 1 mL 80% acetonitrile (ACN)/0.1% TFA, then equilibrated with 3 x 1 mL of 0.1% TFA. Following sample loading, cartridges were washed with 4 x 1 mL of 0.1% TFA, and samples were eluted with 4 x 0.5 mL 50% ACN/0.25% formic acid (FA). 20 µg of each sample was kept for protein abundance measurements, and the remainder was used for phosphopeptide enrichment. Samples were dried by vacuum centrifugation.

Phosphopeptide enrichment. For each sample batch, 400 µL (30 µL per sample) of 50% Superflow bead slurry (Qiagen) was added to a 2 mL bio-spin column. Beads were incubated with 4 x 500 µL of 100 mM EDTA for 30 seconds, washed with 2 x 500 µL H_2O, incubated 4 x 500 µL with 15 mM $FeCl_3$ for 1 minute and washed 3 x 500 µL H_2O and once with 500 µL of 0.5% FA to remove residual Fe. Beads are resuspended in 600 µL of H_2O and 60 µL is aliquoted into a C18 NEST column that had been equilibrated with 150 µL of 80% ACN, 0.1% TFA. 1 mg of digested peptides were resuspended in 75% ACN/0.15% TFA and incubated with beads for 2 minutes, mixed by pipetting and incubated again for 2 minutes. Beads were washed 4 x 200 µL with 80% ACN, 0.1% TFA, then washed 3 x 200 uL with 0.5% FA, incubated 2 x 200 µL with 500 mM potassium phosphate buffer pH 7 and incubated 2 x 200 µL with 0.5% FA for 15 s. Phosphopeptides were eluted by centrifugation at 3000 RPM for 30s with 2 x 75 uL of 50% ACN, 0.1% FA.

Mass spectrometry data acquisition. Digested samples were analyzed on an Orbitrap Exploris 480 mass spectrometry system (Thermo Fisher Scientific) equipped with an Easy nLC 1200 ultra-high pressure liquid chromatography system (Thermo Fisher Scientific) interfaced via a Nanospray Flex nanoelectrospray source. For all analyses, samples were injected on a C18 reverse phase column (25 cm x 75 µm packed with ReprosilPur 1.9 µm particles). Mobile phase A consisted of 0.1% FA, and mobile phase B consisted of 0.1% FA/80% ACN. Peptides were separated by an organic gradient from 5% to 30% mobile phase B over 112 minutes followed by an increase to 58% B over 12 min, then held at 90% B for 16 minutes at a flow rate of 350 nL/minute. Analytical columns were equilibrated with 6 µL of mobile phase A. To build a spectral library, one sample from each set of biological replicates was acquired in a data dependent manner. Data dependent analysis (DDA) was performed by acquiring a full scan over a m/z range of 400-1000 in the Orbitrap at 60,000 resolving power (@200 m/z) with a normalized AGC target of 300%, an RF lens setting of 40%, and a maximum ion injection time of 60 ms. Dynamic exclusion was set to 60 seconds, with a 10 ppm exclusion width setting. Peptides with charge states 2-6 were selected for MS/MS interrogation using higher energy collisional dissociation (HCD), with 20 MS/MS scans per cycle. For phosphopeptide enriched samples, MS/MS scans were analyzed in the Orbitrap using isolation width of 1.3 m/z, normalized HCD collision energy of 30%, normalized AGC of 200% at a resolving power of 30,000 with a 54 millisecond maximum ion injection time. Similar settings were used for data dependent analysis of samples used to determine protein abundance, with an MS/MS resolving power of 15,000 and a 22 millisecond maximum ion injection time. Data-independent analysis (DIA) was performed on all samples. An MS scan at 60,000 resolving power over a scan range of 390-1010 m/z, a normalized AGC target of 300%, an RF lens setting of 40%, and a maximum injection time of 60 ms was acquired, followed by DIA scans using 8 m/z isolation windows over 400-1000 m/z at a normalized HCD collision energy of 27%. Loop control was set to All. For phosphopeptide enriched samples, data were collected using a resolving power of 30,000 and a maximum ion injection time of 54 ms. Protein abundance samples were collected using a resolving power of 15,000 and a maximum ion injection time of 22 milliseconds.

Spectral library generation and raw data processing. Raw mass spectrometry data from each DDA dataset were used to build separate libraries for DIA searches using the Pulsar search engine integrated into Spectronaut version 13.12.200217.43655 (Bruderer et al. 2015) by searching against a database of Uniprot *Chlorocebus* sequences (19,136 proteins, downloaded April 3, 2020) and 29 Sars-CoV-2 protein sequences translated from genomic sequence downloaded from GISAID (accession EPI_ISL_406596, downloaded April 7, 2020) with two mutations (G22661T Spike V367F and G26144T ORF3a G251V) detected by RNASeq analysis of virus stocks. For protein abundance samples, data were searched using the default BSG settings, variable modification of methionine oxidation, static modification of carbamidomethyl cysteine, and filtering to a final 1% false discovery rate (FDR) at the peptide, peptide spectrum match (PSM), and protein level (Elias and Gygi 2007). For phosphopeptide enriched samples, BSG settings were modified to include phosphorylation of S, T, and Y as a variable modification. The generated search libraries were used to perform directDIA searches of the DIA data. For protein abundance samples, default BSG settings were used, with no data normalization performed. For phosphopeptide enriched samples, the Significant PTM default settings were used, with no data normalization performed, and the DIA-specific PTM site localization score in Spectronaut was applied.

Immunofluorescence microscopy. Caco-2 cells seeded on glass coverslips were infected with SARS-CoV-2 Isolate Muc-IMB-1/2020, second passage on Vero E6 cells ($2x10^6$ PFU/mL) at an MOI of 0.1 or 0.01. At 24 hours post-infection cells were washed with PBS and fixed in 4% paraformaldehyde in PBS for 20 minutes at room temperature (RT), followed by permeabilization with 0.3% Triton X-100 in PBS for 10 minutes at RT and blocking in 5% fetal calf serum in PBS for 1 hour at RT. Incubation with primary antibodies against CK2α (Abcam, ab70774, 1:500), SARS-CoV membrane (M) protein (Rockland, #100-401-A55, 1:500) and SARS-CoV nucleocapsid (N) protein (Rockland, #200-401-A50, 1:1000) was performed for 1 hour at RT. After washing with PBS, cells were incubated with AF568-labeled goat-anti-rabbit (Invitrogen, #A11011) and AF647-labeled goat-anti-mouse (Invitrogen, #A21235) secondary antibodies (1:200) as well as AF488-labeled Phalloidin (Hypermol, #8813-01, 1:250) for 2 hours at RT. Fluorescence images were generated using a LSM800 confocal laser-scanning microscope (Zeiss) equipped with a 63X, 1.4 NA oil objective and Airyscan detector and the Zen blue software (Zeiss) and processed with Zen blue software and ImageJ/Fiji. For 3D-reconstruction, cells were fixed and stained as indicated and imaged as z-stack with 0.15 µm sections. Z-stack was processed using Imaris software 64x 9.5.1 and displayed as MIP. To quantify colocalization between Casein-Kinase-2 and N-protein colocalization events in filopodia of SARS-CoV-2 infected Caco-2 cells were counted. 42 +/- 19 % of the N-protein particles detected in filopodia colocalize with CK2. Length of filopodia was measured using Metamorph (Version 7.8). Distance was measured starting at cortical actin to the tip of Filopodia.

Electron microscopy. Vero E6 cells were seeded overnight and then infected for 24 hours with SARS-CoV-2 isolate nCoV-WA1-2020 on silicon chips for scanning electron microscopy or Thermanox™ for transmission electron microscopy. For *scanning electron microscopy (SEM)***,** cells were fixed with Karnovsky's formulation of 2% paraformaldehyde/2.5% glutaraldehyde in 0.1 M Sorenson's phosphate buffer, and then post-fixed with 1.0% osmium tetroxide/0.8% potassium ferrocyanide in 0.1 M sodium cacodylate buffer washed with 0.1 M sodium cacodylate buffer then stained with 1% tannic acid in dH_2O. After additional buffer washes, the samples were further osmicated with 2% osmium tetroxide in 0.1M sodium cacodylate, then washed with dH_2O. Specimens were dehydrated with a graded ethanol series from 50%, 75%, 100% x 3 for 5 minutes each, critical point dried under CO_2 in a Bal-Tec model CPD 030 Drier (Balzers, Liechtenstein), mounted with double sided carbon tape on aluminum specimen mounts (Ted Pella), and sputter coated with 35 Å of iridium in a Quorum EMS300T D sputter coater (Electron Microscopy Sciences, Hatfield, PA) prior to viewing at 5 kV in a Hitachi SU-8000 field emission scanning electron microscope (Hitachi, Tokyo, Japan). For *transmission*

electron microscopy (TEM), specimens were fixed as described above for scanning electron microscopy and additionally stained overnight with 1% uranyl acetate at 4°C after the second osmium staining and then dehydrated with the same graded ethanol series, and embedded in Spurr's resin. Thin sections were cut with a Leica UC7 ultramicrotome (Buffalo Grove, IL) prior to viewing at 120 kV on a FEI BT Tecnai transmission electron microscope (Thermofisher/FEI, Hillsboro, OR). Digital images were acquired with a Gatan Rio camera (Gatan, Pleasanton, CA).

N overexpression in Vero E6 cells. The N-protein cassette was subcloned from pLVX-EF1a-SARS-CoV-2-N-2xStrep-IRES-Puro (Gordon et al. 2020) into pLVX-TetOne-Puro (Takara) using the restriction enzymes EcoRI and BamHI to create pLVX-TetOne-Puro-SARS-CoV-2-N-2xStrep. Sequence integrity was confirmed by Sanger sequencing (GeneWiz). To produce lentiviruses, HEK293T cells (50% confluent in a T175 flask) were transfected with 5 µg of each of the pLVX-TetOne-Puro lentiviral plasmids, 3.33 µg Gag-Pol packaging construct, and 1.66 µg VSV-G envelope (pMD2.G, Addgene) using PolyJet (SignaGen). Culture supernatant was precipitated with a final concentration of 8.5% PEG-6000 and 0.3M sodium chloride (NaCl), incubated at 4°C for 2-4 hours. Virions were pelleted at 3500 rpm for 20 minutes in a spin bucket rotor, suspended in 0.5 mL 1xPBS, and aliquoted for storage at 80°C. Vero E6 cells were seeded in T75 flasks at 50% confluence and transduced with 200 µL precipitated lentivirus derived from pLVX-TetOne-Puro-SARS-CoV-2-N-2xStrep or pLVX-TetOne-Puro empty vector. 48 hours post transduction 10 µg/mL Puromycin was added to cultures to select transduced cells. Polyclonal stable cell lines were seeded into 15 cm dishes in triplicate and treated with 1 µg/mL doxycycline for 48 hours. Cells were washed in ice cold PBS and harvested by scraping in cold PBS. Cell pellets were lysed directly (8 M urea, 100 mM ammonium bicarbonate (ABC), 150 mM NaCl, protease inhibitor (mini-cOmplete, Roche) and phosphatase inhibitors (phosSTOP, Roche), and protein digestion and phosphopeptide enrichment was performed as described above for SARS-CoV-2 infected Vero E6 cells. During the analysis, one of three replicates of the N-overexpressed samples was found to be an outlier based on principal component analysis (as in Figure S1A-B) and was removed. N-overexpression (n=2) was compared to empty vector (EV) controls (n=3) during analysis (full data available in Table S1). Kinase activity predictions were also performed the same as for viral infection phosphoproteomics (full data available in Table S4).

Cell cycle analysis. $1x10^5$ Vero E6 cells were seeded per sample. The following day cells were either mock infected or infected with SARS-CoV-2 (isolate BetaCoV/France/IDF0372/2020) at an MOI of 1. The samples were incubated for 24 hours before detaching cells using Trypsin 0.05% (Thermo). Cells were pelleted at 500x g for 2 minutes, followed by fixation using 4% Formalin (Thermo) for 30 minutes. Cells were washed 2x with PBS (Thermo) before permeabilizing using 0.1% Triton X-100 (Thermo) for 20 minutes. Finally, cells were pelleted again and incubated with 1 mg/mL 4′,6-diamidino-2-phenylindole (DAPI; Thermo) in PBS for 30 minutes before analysing cell cycle using fluorescence by flow cytometry using the BD FACSymphony with a violet laser (405 nm) and 450/50 nm filter. Gating was performed by first selecting singlets by gating highly correlated cells in an SSC-A vs SSC-H plot. Next, typical cellular morphology was gated using a FSC-A vs SSC-A plot. These singles were then used to draw histograms which were gated for G0/G1, S, and G2/M phases.

SARS-CoV-2 infections in ACE2-A549 cells and lysis for cytokine analysis. Approximately 5×10^5 A549-ACE2 cells were pre-treated with either DMSO or SB203580 (0.01, 0.1, 1, 10 µM final concentration). After 1 hour of pre-treatment, cells were infected with SARS-CoV-2 (isolate USA-WA1/2020) at an MOI of 0.1 while maintaining inhibitor concentrations in the media for 30 hours post infection. The supernatants from infected cells were analysed by multiplexed ELISA for the presence of secreted cytokines and chemokines. For RNA analysis, cells were lysed in TRIzol and total RNA was extracted and DNase treated using the Direct-zol RNA

Miniprep Plus kit (Zymo Research) according to the manufacturer's instructions. For protein analysis, whole cell lysates were obtained by lysis in RIPA buffer and analysed by SDS-PAGE and Western blot.

Cytokine RT-qPCR analysis. Gene expression of selected cytokines as well as SARS-CoV-2 replication was quantified by RT-qPCR. Reverse transcription of extracted total RNA samples was performed using oligo (dT) primers and SuperScript IV Reverse Transcriptase according to the manufacturer's instructions. Quantitative real-time PCR analysis of cDNA samples was performed using KAPA SYBR FAST qPCR Master Mix (2X) Universal on a LightCycler 480 Instrument II (Roche). For viral quantification, primers specifically targeting the subgenomic viral N RNA were used. ΔCT values were determined relative to the ACTB and ΔΔCT values were normalized to the average of mock infected samples (for host genes) or to infected DMSO treated samples (for viral replication). Error bars indicate the standard deviation of the mean from three independent biological replicates.

Multiplexed cytokine ELISA. Supernatants from infected cells were evaluated for 34 cytokines/chemokines by multiplex ELISA for the following analytes: CCL2/MCP-1, CCL3/MIP-1α, CCL4/MIP-1β, CCL5/RANTES, CCL7/MCP-3, CCL8/MCP-2, CCL11/Eotaxin, CCL13/MCP-4, CCL20/MIP-3α, CXCL1/GROα, CXCL2/GROβ, CXCL5/ENA-78, CXCL8/IL-8, CXCL9/MIG, CXCL10/IP-10, CXCL16, IL-1α, IL-1β, IL-1RA, IL-4, IL-6, IL-7, IL-10, IL-12p70, IL-15, IL-16, IL-17A, IL-22, GM-CSF, MMP-9, S100A8, TNFα, TGFβ, and Trappin-2/Elafin. All antibodies and cytokine standards were purchased as antibody pairs from R&D Systems (Minneapolis, MN) or Peprotech (Rocky Hill, NJ). Individual magnetic Luminex bead sets (Luminex Corp, CA) were coupled to cytokine-specific capture antibodies according to the manufacturer's recommendations. Samples were analyzed on a Luminex MAGPIX platform and quantified using a standard curve. For each bead region, >50 beads were collected per analyte. The median fluorescence intensity of these beads was recorded for each bead and was used for analysis using a custom R script and a 5P regression algorithm.

SARS-CoV-2 viral quantification via antibody staining in presence of inhibitors. (Mount Sinai, New York)**.** 2,000 Vero E6 cells were seeded into 96-well plates and incubated for 24 hours. Two hours before infection, the medium was replaced with 100 µL of DMEM (2% FBS) containing the compound of interest at concentrations 50% greater than those indicated, including a DMSO control. Plates were then transferred into the BSL-3 facility and 100 PFU (MOI 0.025) was added in 50 µL of DMEM (2% FBS), bringing the final compound concentration to those indicated. Plates were then incubated for 48 hours at 37°C. After infection, supernatants were removed and cells were fixed with 4% formaldehyde for 24 hours prior to being removed from the BSL-3 facility. The cells were then immunostained for the viral NP protein (anti-sera produced in the Garcia-Sastre lab; 1:10,000) with a DAPI counterstain. Infected cells (488 nM) and total cells (DAPI) were quantified using the Celigo (Nexcelcom) imaging cytometer. Infectivity was measured by the accumulation of viral NP protein in the nucleus of the Vero E6 cells (fluorescence accumulation). Percent infection was quantified as ((Infected cells/Total cells) - Background) *100 and the DMSO control was then set to 100% infection for analysis. The IC_{50} for each experiment was determined using the Prism software (GraphPad). For select inhibitors, infected supernatants were assayed for infectious viral titer using the Median Tissue Culture Infectious Dose $TCID_{50}$ method. For this, infectious supernatants were collected at 48 hours post infection and frozen at −80°C until later use. Infectious titers were quantified by limiting dilution titration on Vero E6 cells. Briefly, Vero E6 cells were seeded in 96-well plates at 20,000 cells/well. The next day, SARS-CoV-2-containing supernatant was applied at serial 10-fold dilutions ranging from 10^{-1} to 10^{-6} and, after 5 days, viral CPE was detected by staining cell monolayers with crystal violet. $TCID_{50}$/mL was calculated using the method of Reed and Muench.

Cytotoxicity cell viability assays. (Mount Sinai, New York). Cytotoxicity was also performed using the MTT assay (Roche), according to the manufacturer's instructions. Cytotoxicity was performed in uninfected Vero E6 cells with same compound dilutions and concurrent with viral replication assay. All assays were performed in biologically independent triplicates.

siRNA-based knockdown of host kinases. (Institut Pasteur, Paris)**.** Host kinases were knocked-down in A549 cells stably expressing ACE2 cells using OnTargetPlus siRNA SMARTpools (Horizon Discovery). Briefly, A549-ACE2 cells seeded at $2x10^4$ cells/well in 96-well plates 18 hours prior to the experiment. The next day, each well was transfected with 6 pmoles of siRNA SMARTpool, using Lipofectamine RNAiMAX (Thermo Fisher Scientific) according to the manufacturer's instructions. 24 hours post transfection, the cell culture supernatant was removed and replaced with virus inoculum (MOI of 0.1 PFU/cell). Following a 1 hour adsorption at 37°C, the virus inoculum was removed and replaced with fresh Opti-MEM media (Thermo Fisher Scientific) containing 2% FBS (v/v). 72 hours post-infection (p.i.), the cell culture supernatant was heat-inactivated at 95°C for 5 minutes, and detection of viral genomes performed by RT-qPCR.

SARS-CoV-2 viral quantification via RT-qPCR in presence of inhibitors. (Institut Pasteur, Paris)**.** Detection of viral genomes was performed by RT-qPCR, directly from the inactivated supernatant (Lista et al. 2020). SARS-CoV-2 specific primers targeting the N gene region: 5′-TAATCAGACAAGGAACTGATTA-3′ (Forward) and 5′-CGAAGGTGTGACTTCCATG-3′ (Reverse) (Chu et al. 2020) were used with the Luna Universal One-Step RT-qPCR Kit (NEB) in an *Applied Biosystems* QuantStudio 7 thermocycler, with the following cycling conditions: 55°C for 10 minutes, 95°C for 1 minute, and 40 cycles of 95°C for 10 seconds, followed by 60°C for 1 minute. The number of viral genomes is expressed as PFU equivalents/mL, and was calculated by performing a standard curve with RNA derived from a viral stock with a known viral titer.

SARS-CoV-2 titration by plaque assay. (Institut Pasteur, Paris)**.** Vero E6 cells were seeded in 24-well plates at a concentration of $7.5x10^4$ cells/well. The following day, serial dilutions were performed in serum-free MEM media. After 1 hour absorption at 37°C, 2x overlay media was added to the inoculum to give a final concentration of 2% (v/v) FBS / MEM media and 0.05% (w/v) Agarose (all Thermo Fisher Scientific) to achieve a semi-solid overlay. Plaque assays were incubated at 37° C for 3 days. Samples were fixed using 4% Formalin (Sigma Aldrich) and plaques were visualized using crystal Violet solution (Sigma Aldrich) (Gordon et al., 2020).

siRNA Cell viability assays. (Institut Pasteur, Paris)**.** Cell viability in siRNA knocked-down cells was measured using the CellTiter Glo luminescent cell viability assay (Promega) following the manufacturer's instructions, and luminescence measured in a Tecan Infinity 2000 plate reader. Percent viability was calculated relative to untreated cells (100% viability) and cells lysed with 20% ethanol (0% viability), included in each experiment.

QUANTIFICATION AND STATISTICAL ANALYSIS

Mass spectrometry data pre-processing. Quantitative analysis was performed in the R statistical programming language (version 3.6.1, 2019-07-05). Initial quality control analyses, including inter-run clusterings, correlations, principal components analysis, peptide and protein counts and intensities were completed with the R package artMS (version 1.5.3). Based on obvious outliers in intensities, correlations, and clusterings, 2 runs were discarded from the protein abundance data and 2 runs were discarded from the phosphopeptide data (Figure S1). Additionally, the phosphopeptide data were filtered based on feature (i.e. peptide ion) intensity, removing any single feature with intensity less than 2^{14}—this decision was made based

on apparent lack of correlation between runs of feature intensities below this intensity. Thus for both phosphopeptides and protein abundance we had 2 control timepoints and 6 infected timepoints, each with 3 biologically distinct replicates, except for infected at 0 and 2 hours in the phosphopeptide data and control at 0 hours and infected at 0 hours in the protein abundance data which only had 2 replicates each.

Statistical analysis of protein abundance changes between control and infected runs were computed using peptide ion fragment data output from Spectronaut and processed using a pipeline of three functions from the R package MSstats (version 3.19.5) (Choi et al. 2014): function MSstats::SpectronauttoMSstatsFormat with default settings other than setting "removeProtein_with1Feature = TRUE"; function MSstats::dataProcess with default settings other than setting "censoredInt = 0", "featureSubset = highQuality", "remove_uninformative_feature_outlier = TRUE", "clusters=7"; and function MSstats::groupComparison with all default settings.

Phosphopeptide intensity data were summarized at the peptide ion level along with confident localization of phosphorylation as described in the previous section. Quantification of phosphorylations based on peptide ions were processed using artMS as a wrapper around MSstats, via functions artMS::doSiteConversion and artMS::artmsQuantification with default settings. All peptides containing the same set of phosphorylated sites were grouped and quantified together into phosphorylation site groups. For both phosphopeptide and protein abundance MSstats pipelines, MSstats performs normalization by median equalization, imputation of missing values and median smoothing to combine intensities for multiple peptide ions or fragments into a single intensity for their protein or phosphorylation site group, and statistical tests of differences in intensity between infected and control timepoints.

Identifying significantly regulated proteins. When not explicitly indicated, we used defaults for MSstats for adjusted p-values, even in cases of N=2. By default, MSstats uses Student's t-test for p-value calculation and Benjamini-Hochberg method of FDR estimation to adjust p-values. Phosphorylation fold change data were filtered for quality based on consistency of observations between treatment and controls by requiring the MSstats reported value missingPercentage < 0.60. This value is the proportion of features, i.e. peptide ions, that are missing across the treatment and control replicates for a specific fold change computation. MSstats phosphorylation results had to be further simplified to effects at single sites. The results of artMS/MSstats are fold changes of specific phosphorylation site groups detected within peptides, so one phosphorylation site can have multiple measurements if it occurs in different phosphorylation site groups (see Table S1 for examples). This complex dataset was reduced to a single fold change per site and time point by choosing (per time point) the fold change with the lowest p-value, favoring those detected in both treatment and control, i.e. non-infinite log2 fold change values. This single-site dataset, further reduced to those with human orthology (Table S1), was used as the input for kinase activity analysis.

Significance filters of adjusted p-value < 0.05 and absolute log2 fold change (infected/mock) > 1 were applied to both phosphorylation and abundance data sets. Additionally, for protein abundance data, if a protein was detected in only infected but not mock, or vice versa, we required detection in 3 replicates or by 3 peptide ion fragments in at least 2 replicates. These significance-filtered data were used for enrichment analyses and counts of significant effects (Figure 1).

Mapping *C. sabaeus* and *H. sapiens* proteins. Orthologous pairs of gene identifiers between *C.sabaeus* and *H.sapiens* were downloaded from Ensembl using the BioMart web interface (http://uswest.ensembl.org/biomart/martview) on April 6, 2020. Ensembl gene identifiers were mapped to UniProt identifiers and protein sequences using a table of ID mappings and reference proteome sequences for

H.sapiens downloaded from Uniprot on April 6, 2020. Orthologous pairs of sequences were aligned using the Needleman-Wunsch global alignment algorithm implemented in the R package Biostrings (v. 2.52) function pairwiseAlignment with default parameters. The resulting alignments were used to convert the sequence positions of detected phosphorylations in *C.sabaeus* to positions in *H.sapiens* protein sequences.

GO enrichment analysis. Sets of genes with significant up and down effects were tested for enrichment of Gene Ontology (GO Biological Process, Molecular Function and Cellular Component) terms. Sets of genes were either combined across timepoints (Figure 1I) or collected separately per time point (Figure S1F-G). The over-representation analysis (ORA) was performed using the enricher function of clusterProfiler package (version 3.12.0) in R with default parameters. The gene ontology terms were obtained from the c5 category of Molecular Signature Database (MSigDBv7.1) (Subramanian et al. 2005). Significant GO terms (adjusted p.value < 0.01) were identified and further refined to select non-redundant terms. In order to select non-redundant gene sets, we first constructed a GO term tree based on distances (1-Jaccard Similarity Coefficients of shared genes in MSigDB) between the significant terms. The GO term tree was cut at a specific level (h=0.99) to identify clusters of non-redundant gene sets. For results with multiple significant terms belonging to the same cluster, we selected the most significant term (i.e., lowest adjusted p.value).

Clustering of phosphorylation changes. Phosphorylation sites with one-to-one mapping to human S, T or Y amino acids and showing significant change in phosphorylation (abs log2FC > 1 and Adj. p-value < 0.05) in one or more conditions were selected and clustered using hierarchical clustering (complete-linkage) with pearson correlation (1-r) as the distance measure. The cluster tree was cut into 5 clusters using a dynamic tree cutting method, cutreeHybrid function in dynamicTreeCut (Langfelder, Zhang, and Horvath 2008) package in R, with a minimum cluster size of 130 sites. Phosphorylated proteins in each cluster were tested for enrichment of Reactome pathways (Jassal et al. 2020). The over-representation analysis (ORA) was based on the hypergeometric distribution and performed using the enricher function of clusterProfiler package in R (Yu et al. 2012). The pathway terms were obtained from the c2 category (Reactome) of Molecular Signature Database (MSigDBv6.1).

Estimation of kinase activities in the time-course experiment. Kinase activities were estimated using known kinase-substrate relationships in literature (Bachman, Gyori, and Sorger 2019). The resource comprises of a comprehensive collection of phosphosite annotations of direct substrates of kinases obtained from six databases, PhosphoSitePlus, SIGNOR, HPRD, NCI-PID, Reactome, and the BEL Large Corpus, and using three text-mining tools, REACH, Sparser, and RLIMS-P. Kinase activities were inferred as a -log10(p-value) of Z-test from the comparison of fold changes in phosphosite measurements of the known substrates against the overall distribution of fold changes across the sample. This statistical approach has been previously shown to perform well at estimating kinase activities (Hernandez-Armenta et al. 2017; Casado et al. 2013). We collected substrate annotations for 400 kinases with available data. Kinase activities for kinases with 3 or more measured substrates were considered leaving us with 97 kinases with activity estimates in at least one or more infection timepoints.

Comparison of phosphorylation profiles with other conditions. In addition to the time-course experiment, we also estimated kinase activities of cell line perturbation in a range of biological conditions using the K-test based approach, from a large resource of previously published phosphoproteomics datasets comprising of 435 biological conditions which include several drug treatments (chlorzoxazone, paclitaxel), inhibitors (EGFRi, AKTi) and cell cycle states (Ochoa et al. 2016). After selecting for kinase activities derived from 3 or more substrates, a total of 214 kinases had activity estimates for at least one biological condition including all 97 kinases which were estimated in the time-course experiment. Of the 435 conditions, 309 conditions with at

least one kinase with significantly changing activity (-log10(P-value) from Z-test > 2.5) were selected. Individual timepoints of the infection experiment were correlated with each selected biological condition based on Pearson correlation of their kinase activity profiles. Conditions with significant correlation (5% FDR) with one or more timepoints were identified. Several conditions corresponded to the same biological treatment (such as drug perturbation) in different concentrations. In such cases, the conditions are represented together with strongest correlation.

Phosphorylation of protein complexes. Annotations for protein complexes were obtained from CORUM v3.0 database (Giurgiu et al. 2019). Overall significance of changes of phosphosites of a protein complex was inferred from the log2 fold change of individual phosphosites of protein members of the complex using the same Z-test based approach described for estimation of kinase activities. Among the 3512 complexes, 1070 complexes with phosphorylation changes obtained from 4 or more phosphosites were considered. Of these, 67 complexes had significant phosphorylation change (-log10(P-value) from Z-test > 2.5) in at least one time point. In order to select non-redundant complexes, we first constructed a complex term tree based on distances (1-Jaccard Similarity Coefficients of shared genes) between the significant complexes. The term tree was cut at a specific level (h=0.99) to identify clusters of non-redundant complexes. The largest complex was selected from each cluster.

Transcription factor activity after SARS-CoV-2 infection. To evaluate the effect of SARS-CoV-2 infection at the Transcription Factor (TF) level, we applied DoRothEA (Garcia-Alonso et al. 2019) to RNA-seq datasets of different human lung cell lines from a recent study (GSE147507) (Blanco-Melo et al. 2020). DoRothEA is a comprehensive resource containing a curated collection of TF-target interactions. Each TF-target interaction is associated with a confidence level based on the number of supporting evidence. Here we selected the most reliable interactions (A,B and C levels) and computed TF activities based on the normalized expression of their targets using the VIPER algorithm (M. J. Alvarez et al. 2016). For the TF activity enrichment analysis, VIPER was executed with the Wald statistic resulting from the differential expression analysis at the gene level between controls and SARS-CoV-2 infected cells using the DESeq2 package (Love, Huber, and Anders 2014). In VIPER, we set the eset.filter parameter to FALSE and consider five as the minimum number of targets allowed per regulon.

Pharmacological profiling dose response analysis. A hill function was fit to each dose response curve using the `lsqcurvefit` function in MATLAB (R2018a). IC_{50} (virus) and CC_{50} (cell viability) values were defined as the concentration at which the percent measure (virus or cell viability quantification) crossed the 50% mark. If the fit curve did not begin above 50% and cross to below 50% throughout the dose response, an IC_{50} or CC_{50} value was marked as greater than the maximum tested concentration. For $TCID_{50}$ and plaque assay results, which are not depicted in a percent scale, the IC_{50} values were extracted directly from the parameterized hill equation (see Figure S5 and Table S8).

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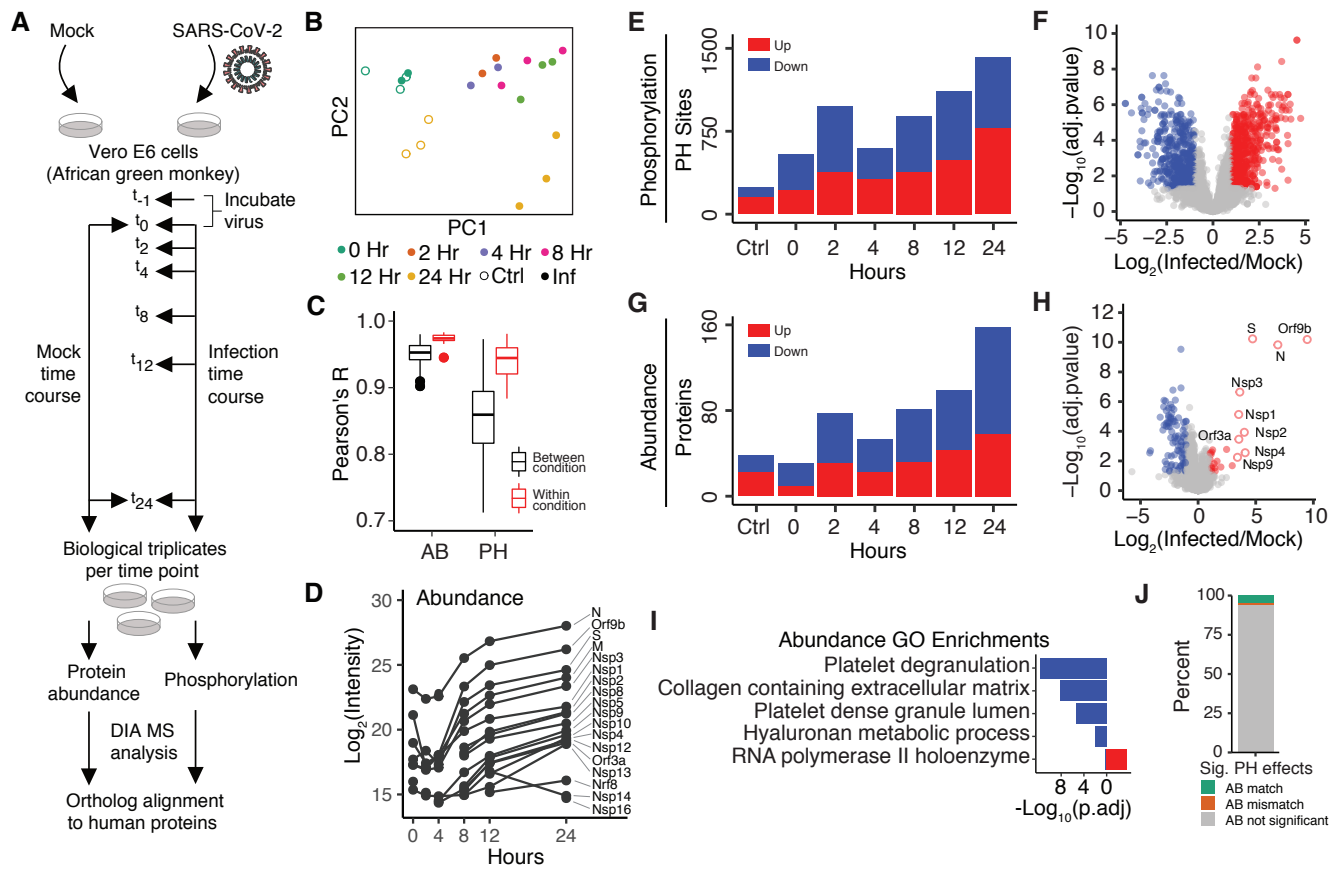
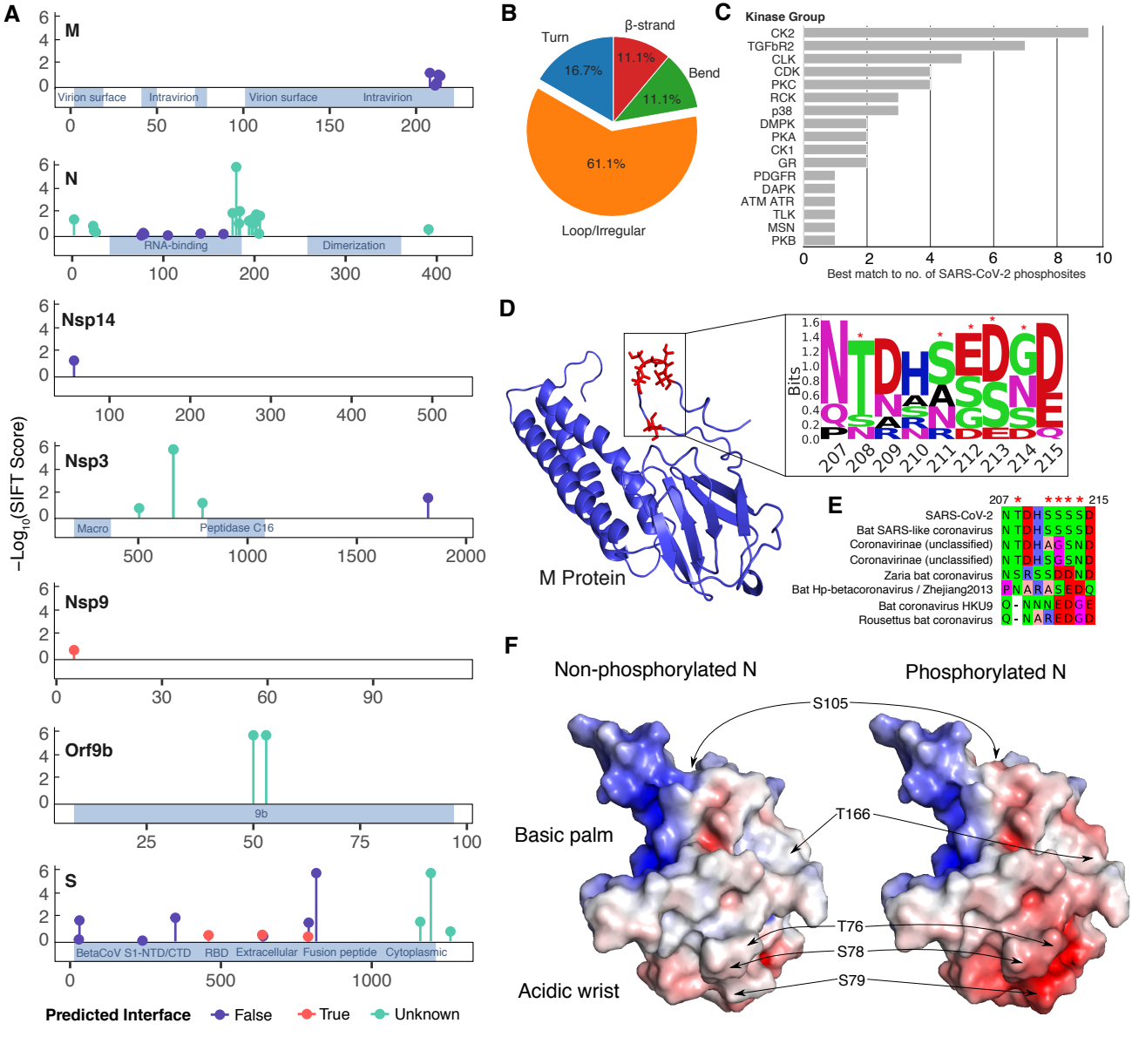
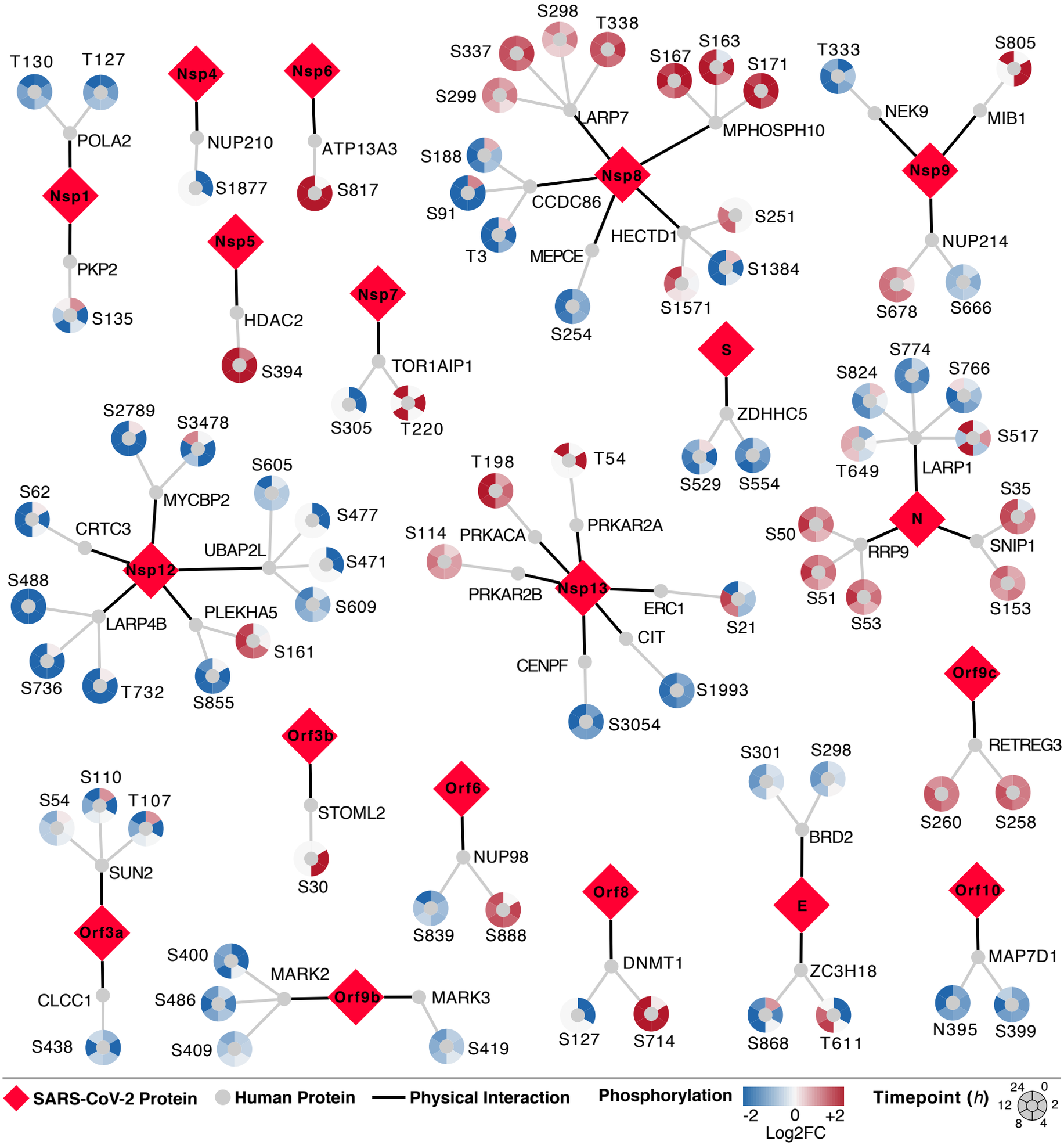
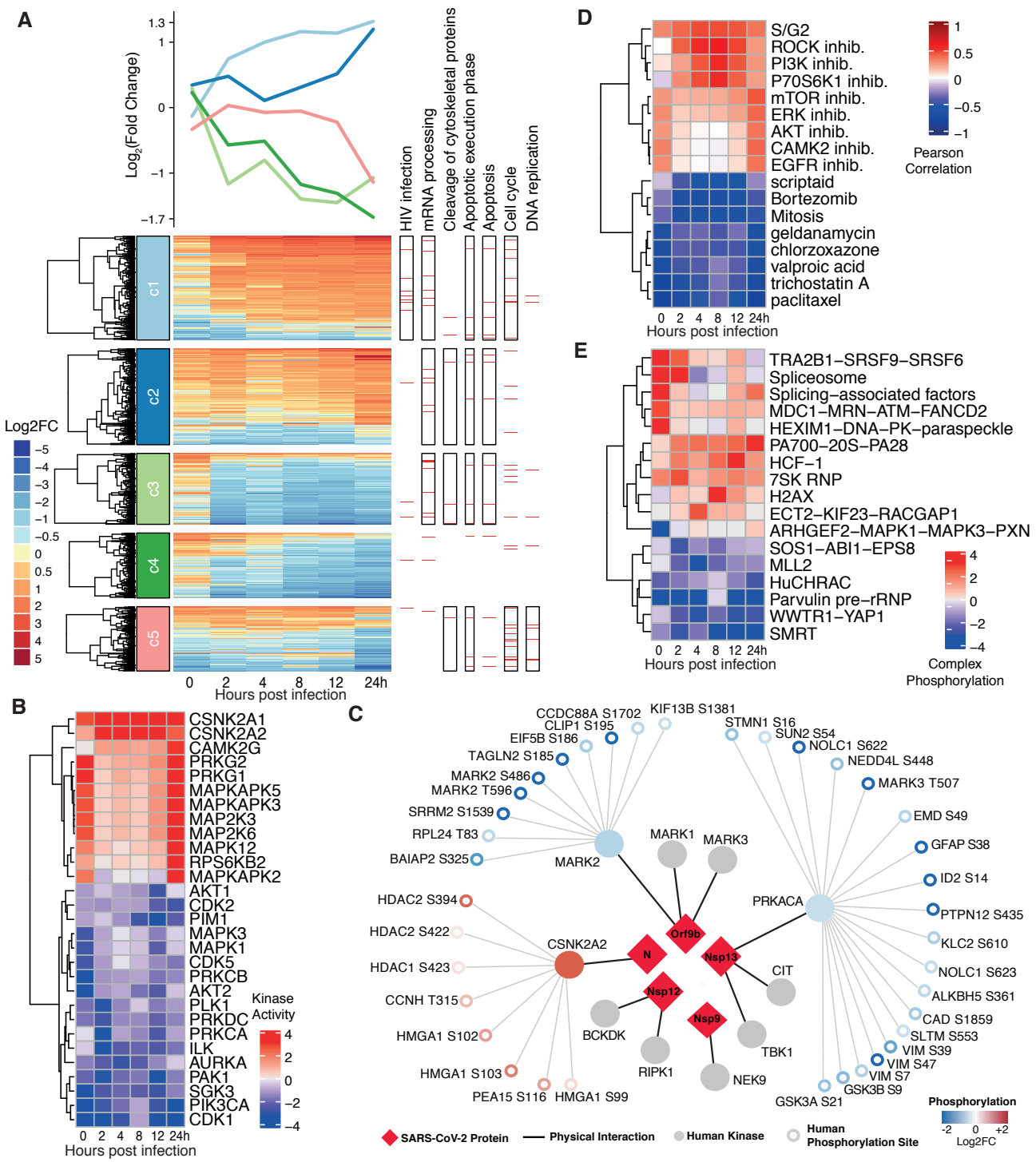
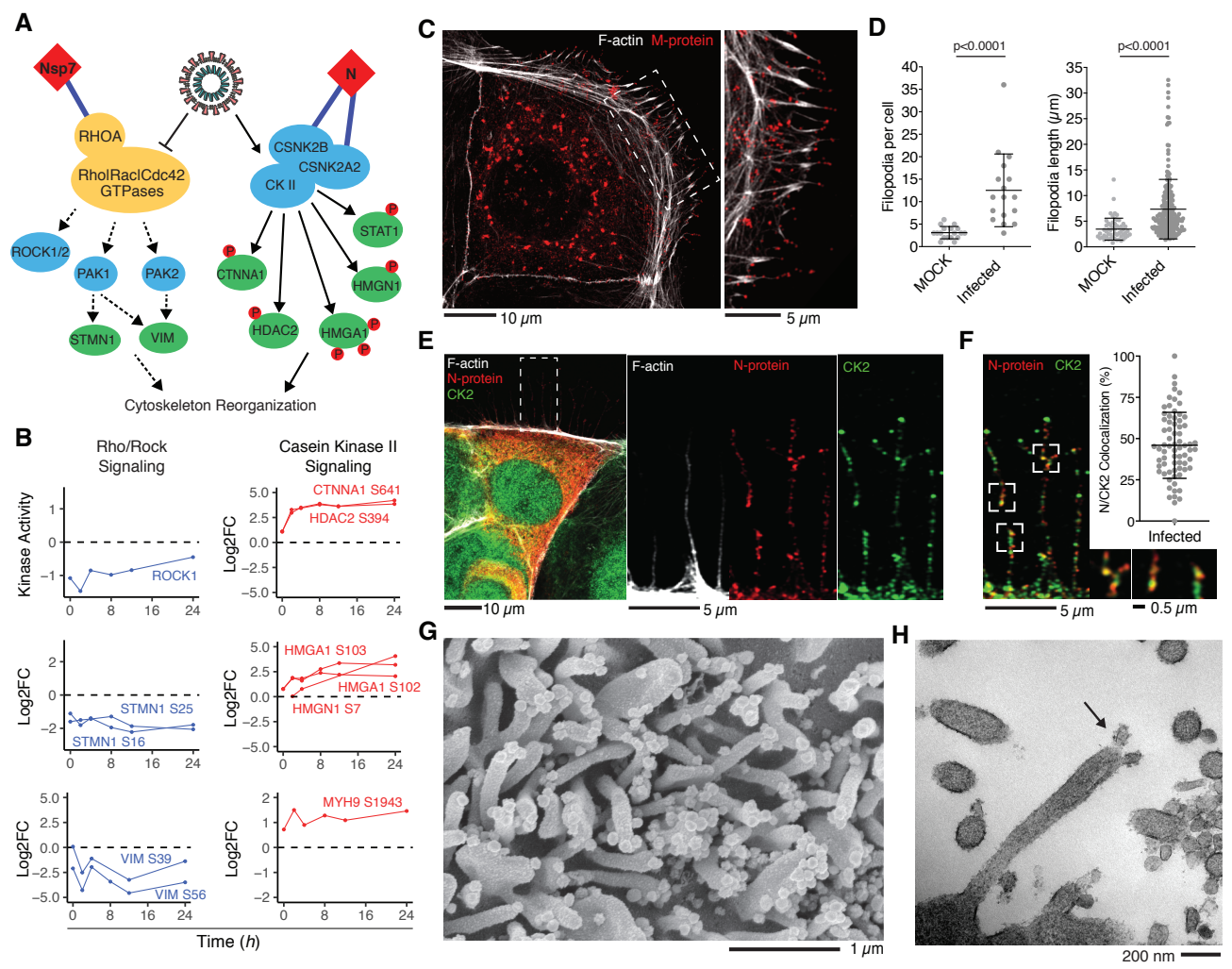
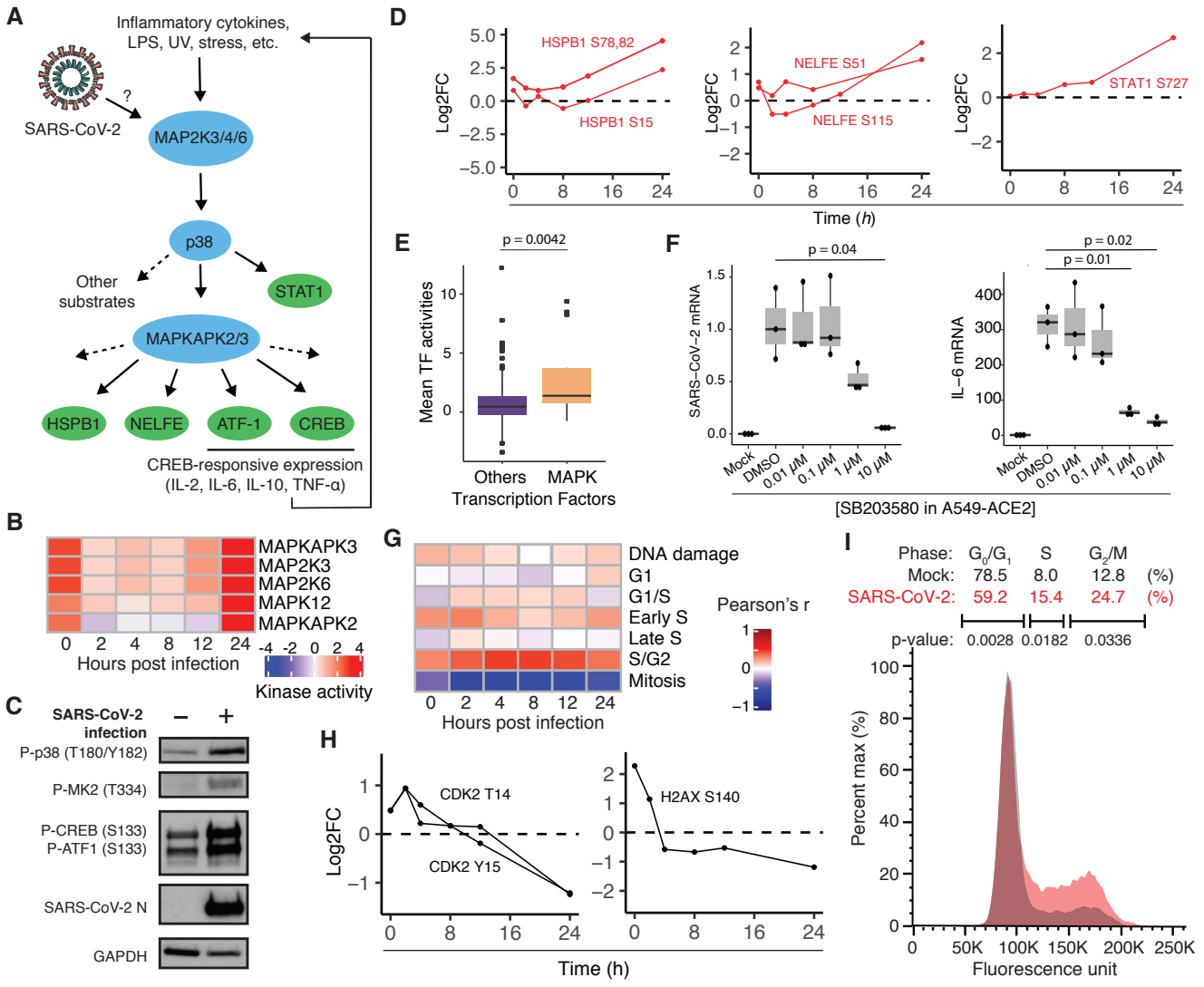

A
Mock
SARS-CoV-2
Vero E6 cells
(African green monkey)
Incubate virus
Mock time course
Infection time course
Biological triplicates per time point
Protein abundance
Phosphorylation
DIA MS analysis
Ortholog alignment to human proteins
B
PC2
PC1
0 Hr
2 Hr
4 Hr
8 Hr
12 Hr
24 Hr
Ctrl
Inf
C
Pearson's R
Between condition
Within condition
AB
PH
D
Abundance
Log2(Intensity)
Hours
E
Phosphorylation
PH Sites
Up
Down
Hours
F
−Log10(adj.pvalue)
Log2(Infected/Mock)
G
Abundance
Proteins
H
S
Orf9b
N
Nsp3
Nsp1
Nsp2
Orf3a
Nsp4
Nsp9
I
Abundance GO Enrichments
Platelet degranulation
Collagen containing extracellular matrix
Platelet dense granule lumen
Hyaluronan metabolic process
RNA polymerase II holoenzyme
-Log10(p.adj)
J
Percent
Sig. PH effects
AB match
AB mismatch
AB not significant

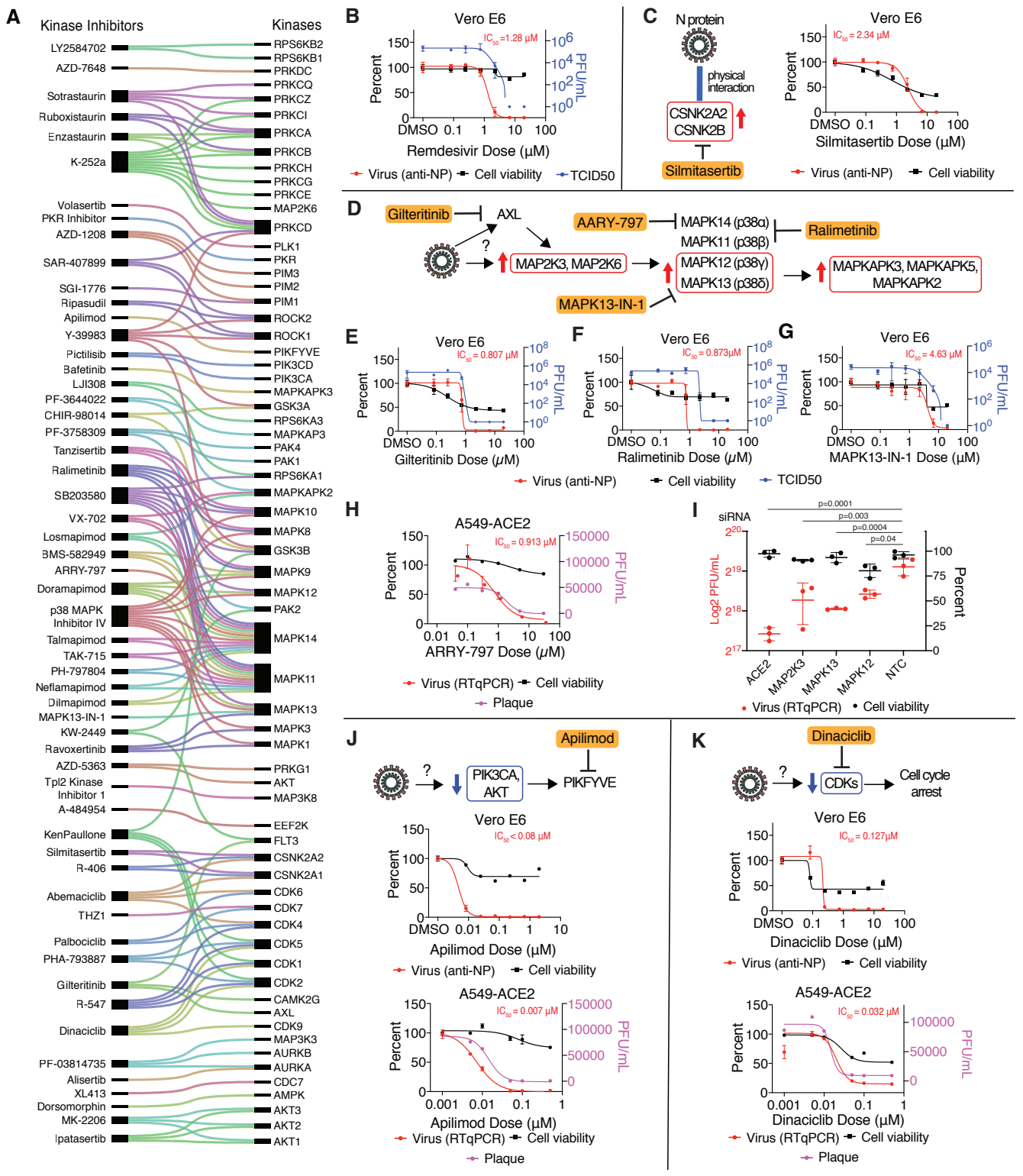

A
M
Virion surface
Intravirion
Virion surface
Intravirion
N
RNA-binding
Dimerization
Nsp14
Nsp3
Macro
Peptidase C16
Nsp9
Orf9b
9b
S
BetaCoV S1-NTD/CTD
RBD
Extracellular
Fusion peptide
Cytoplasmic
−Log10(SIFT Score)
Predicted Interface
False
True
Unknown
B
Turn
β-strand
Bend
Loop/Irregular
16.7%
11.1%
11.1%
61.1%
C
Kinase Group
CK2
TGFbR2
CLK
CDK
PKC
RCK
p38
DMPK
PKA
CK1
GR
PDGFR
DAPK
ATM ATR
TLK
MSN
PKB
Best match to no. of SARS-CoV-2 phosphosites
D
M Protein
Bits
E
SARS-CoV-2
Bat SARS-like coronavirus
Coronavirinae (unclassified)
Coronavirinae (unclassified)
Zaria bat coronavirus
Bat Hp-betacoronavirus / Zhejiang2013
Bat coronavirus HKU9
Rousettus bat coronavirus
F
Non-phosphorylated N
Phosphorylated N
S105
T166
Basic palm
T76
S78
S79
Acidic wrist

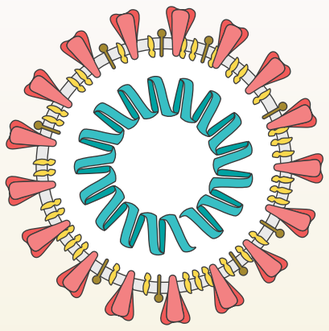

T130
T127
POLA2
Nsp1
PKP2
S135
Nsp4
NUP210
S1877
Nsp6
ATP13A3
S817
Nsp5
HDAC2
S394
Nsp7
TOR1AIP1
S305
T220
S298
T338
S337
S299
LARP7
S163
S167
S171
MPHOSPH10
S188
S91
T3
CCDC86
Nsp8
HECTD1
S251
S1384
MEPCE
S254
S1571
T333
S805
NEK9
MIB1
Nsp9
NUP214
S678
S666
S
ZDHHC5
S529
S554
S774
S824
S766
S517
T649
LARP1
S35
N
S50
RRP9
SNIP1
S51
S53
S153
S2789
S3478
MYCBP2
S605
S62
CRTC3
S477
UBAP2L
Nsp12
S471
S488
S609
LARP4B
PLEKHA5
S161
S736
T732
S855
T198
T54
PRKACA
PRKAR2A
S114
PRKAR2B
Nsp13
ERC1
S21
CIT
CENPF
S1993
S3054
Orf9c
RETREG3
S260
S258
S301
S298
BRD2
E
ZC3H18
S868
T611
Orf10
MAP7D1
N395
S399
Orf3b
STOML2
S30
Orf6
NUP98
S839
S888
Orf8
DNMT1
S127
S714
S110
S54
T107
SUN2
Orf3a
CLCC1
S438
S400
MARK2
S486
Orf9b
MARK3
S409
S419
SARS-CoV-2 Protein
Human Protein
Physical Interaction
Phosphorylation
-2
0
+2
Log2FC
Timepoint (h)
24
0
12
2
8
4


A
Log2(Fold Change)
1.3
1
0
−1
−1.7
HIV infection
mRNA processing
Cleavage of cytoskeletal proteins
Apoptotic execution phase
Apoptosis
Cell cycle
DNA replication
c1
c2
c3
c4
c5
Log2FC
−5
−4
−3
−2
−1
−0.5
0
0.5
1
2
3
4
5
0 2 4 8 12 24h
Hours post infection
B
CSNK2A1
CSNK2A2
CAMK2G
PRKG2
PRKG1
MAPKAPK5
MAPKAPK3
MAP2K3
MAP2K6
MAPK12
RPS6KB2
MAPKAPK2
AKT1
CDK2
PIM1
MAPK3
MAPK1
CDK5
PRKCB
AKT2
PLK1
PRKDC
PRKCA
ILK
AURKA
PAK1
SGK3
PIK3CA
CDK1
Kinase Activity
4
2
0
−2
−4
0 2 4 8 12 24h
Hours post infection
C
CCDC88A S1702
CLIP1 S195
KIF13B S1381
EIF5B S186
TAGLN2 S185
MARK2 S486
MARK2 T596
SRRM2 S1539
RPL24 T83
BAIAP2 S325
MARK2
MARK1
MARK3
HDAC2 S394
HDAC2 S422
HDAC1 S423
CCNH T315
HMGA1 S102
HMGA1 S103
PEA15 S116
HMGA1 S99
CSNK2A2
BCKDK
RIPK1
NEK9
TBK1
CIT
Orf9b
N
Nsp13
Nsp12
Nsp9
STMN1 S16
SUN2 S54
NOLC1 S622
NEDD4L S448
MARK3 T507
EMD S49
GFAP S38
ID2 S14
PRKACA
PTPN12 S435
KLC2 S610
NOLC1 S623
ALKBH5 S361
CAD S1859
SLTM S553
VIM S39
VIM S47
VIM S7
GSK3B S9
GSK3A S21
SARS-CoV-2 Protein
Physical Interaction
Human Kinase
Human Phosphorylation Site
Phosphorylation
−2 0 +2
Log2FC
D
S/G2
ROCK inhib.
PI3K inhib.
P70S6K1 inhib.
mTOR inhib.
ERK inhib.
AKT inhib.
CAMK2 inhib.
EGFR inhib.
scriptaid
Bortezomib
Mitosis
geldanamycin
chlorzoxazone
valproic acid
trichostatin A
paclitaxel
1
0.5
0
−0.5
−1
Pearson Correlation
0 2 4 8 12 24h
Hours post infection
E
TRA2B1−SRSF9−SRSF6
Spliceosome
Splicing−associated factors
MDC1−MRN−ATM−FANCD2
HEXIM1−DNA−PK−paraspeckle
PA700−20S−PA28
HCF−1
7SK RNP
H2AX
ECT2−KIF23−RACGAP1
ARHGEF2−MAPK1−MAPK3−PXN
SOS1−ABI1−EPS8
MLL2
HuCHRAC
Parvulin pre−rRNP
WWTR1−YAP1
SMRT
4
2
0
−2
−4
Complex Phosphorylation
0 2 4 8 12 24h
Hours post infection


A
Nsp7
N
RHOA
RhoIRacICdc42
GTPases
CSNK2B
CSNK2A2
CK II
ROCK1/2
PAK1
PAK2
STMN1
VIM
CTNNA1
HDAC2
HMGA1
STAT1
HMGN1
Cytoskeleton Reorganization
B
Rho/Rock
Signaling
Casein Kinase II
Signaling
Kinase Activity
ROCK1
Log2FC
CTNNA1 S641
HDAC2 S394
STMN1 S25
STMN1 S16
HMGA1 S103
HMGA1 S102
HMGN1 S7
VIM S39
VIM S56
MYH9 S1943
Time (h)
C
F-actin M-protein
10 μm
5 μm
D
p<0.0001
p<0.0001
Filopodia per cell
Filopodia length (μm)
MOCK
Infected
E
F-actin
N-protein
CK2
10 μm
5 μm
F
N-protein CK2
N/CK2 Colocalization (%)
Infected
5 μm
0.5 μm
G
1 μm
H
200 nm

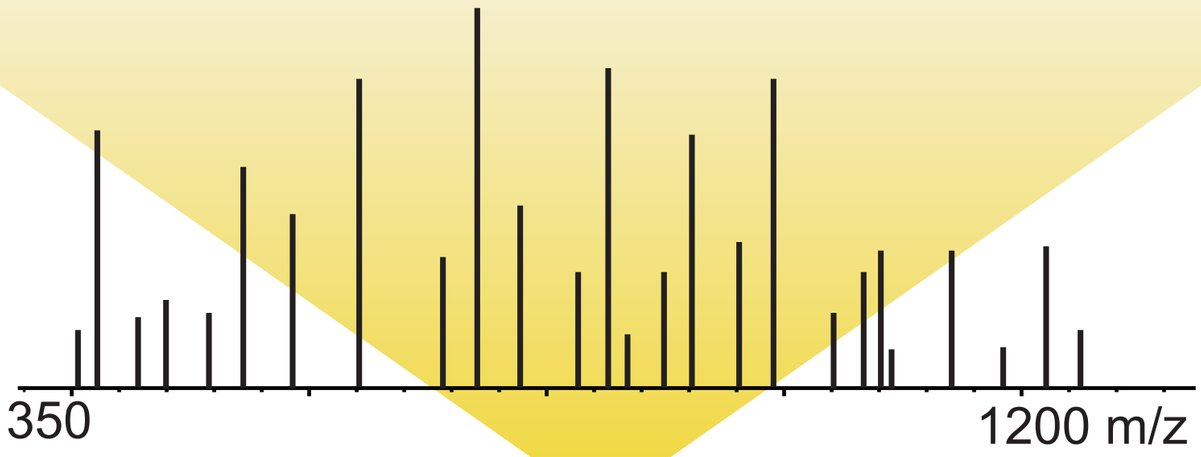

A
Inflammatory cytokines,
LPS, UV, stress, etc.
SARS-CoV-2
?
MAP2K3/4/6
p38
Other
substrates
STAT1
MAPKAPK2/3
HSPB1
NELFE
ATF-1
CREB
CREB-responsive expression
(IL-2, IL-6, IL-10, TNF-α)
B
MAPKAPK3
MAP2K3
MAP2K6
MAPK12
MAPKAPK2
0 2 4 8 12 24
Hours post infection
-4 -2 0 2 4
Kinase activity
C
SARS-CoV-2 infection
– +
P-p38 (T180/Y182)
P-MK2 (T334)
P-CREB (S133)
P-ATF1 (S133)
SARS-CoV-2 N
GAPDH
D
HSPB1 S78,82
HSPB1 S15
NELFE S51
NELFE S115
STAT1 S727
Log2FC
Time (h)
E
p = 0.0042
Mean TF activities
Others
MAPK
Transcription Factors
F
p = 0.04
p = 0.02
p = 0.01
SARS–CoV–2 mRNA
IL–6 mRNA
Mock
DMSO
0.01 μM
0.1 μM
1 μM
10 μM
[SB203580 in A549-ACE2]
G
DNA damage
G1
G1/S
Early S
Late S
S/G2
Mitosis
Pearson's r
Hours post infection
H
CDK2 T14
CDK2 Y15
H2AX S140
Log2FC
Time (h)
I
Phase: G0/G1 S G2/M
Mock: 78.5 8.0 12.8 (%)
SARS-CoV-2: 59.2 15.4 24.7 (%)
p-value: 0.0028 0.0182 0.0336
Percent max (%)
Fluorescence unit


A
Kinase Inhibitors
Kinases
LY2584702
AZD-7648
Sotrastaurin
Ruboxistaurin
Enzastaurin
K-252a
Volasertib
PKR Inhibitor
AZD-1208
SAR-407899
SGI-1776
Ripasudil
Apilimod
Y-39983
Pictilisib
Bafetinib
LJI308
PF-3644022
CHIR-98014
PF-3758309
Tanzisertib
Ralimetinib
SB203580
VX-702
Losmapimod
BMS-582949
ARRY-797
Doramapimod
p38 MAPK Inhibitor IV
Talmapimod
TAK-715
PH-797804
Neflamapimod
Dilmapimod
MAPK13-IN-1
KW-2449
Ravoxertinib
AZD-5363
Tpl2 Kinase Inhibitor 1
A-484954
KenPaullone
Silmitasertib
R-406
Abemaciclib
THZ1
Palbociclib
PHA-793887
Gilteritinib
R-547
Dinaciclib
PF-03814735
Alisertib
XL413
Dorsomorphin
MK-2206
Ipatasertib
RPS6KB2
RPS6KB1
PRKDC
PRKCQ
PRKCZ
PRKCI
PRKCA
PRKCB
PRKCH
PRKCG
PRKCE
MAP2K6
PRKCD
PLK1
PKR
PIM3
PIM2
PIM1
ROCK2
ROCK1
PIKFYVE
PIK3CD
PIK3CA
MAPKAPK3
GSK3A
RPS6KA3
MAPKAP3
PAK4
PAK1
RPS6KA1
MAPKAPK2
MAPK10
MAPK8
GSK3B
MAPK9
MAPK12
PAK2
MAPK14
MAPK11
MAPK13
MAPK3
MAPK1
PRKG1
AKT
MAP3K8
EEF2K
FLT3
CSNK2A2
CSNK2A1
CDK6
CDK7
CDK4
CDK5
CDK1
CDK2
CAMK2G
AXL
CDK9
MAP3K3
AURKB
AURKA
CDC7
AMPK
AKT3
AKT2
AKT1
B
Vero E6
IC50=1.28 μM
Percent
PFU/mL
DMSO 0.1 1 10 100
Remdesivir Dose (μM)
Virus (anti-NP)
Cell viability
TCID50
C
N protein
physical interaction
CSNK2A2
CSNK2B
Silmitasertib
Vero E6
IC50 = 2.34 μM
Percent
DMSO 0.1 1 10 100
Silmitasertib Dose (μM)
Virus (anti-NP)
Cell viability
D
Gilteritinib
AXL
?
MAP2K3, MAP2K6
AARY-797
MAPK14 (p38α)
MAPK11 (p38β)
Ralimetinib
MAPK12 (p38γ)
MAPK13 (p38δ)
MAPK13-IN-1
MAPKAPK3, MAPKAPK5, MAPKAPK2
E
Vero E6
IC50 = 0.807 μM
Percent
PFU/mL
DMSO 0.1 1 10 100
Gilteritinib Dose (μM)
F
Vero E6
IC50 = 0.873μM
Ralimetinib Dose (μM)
G
Vero E6
IC50 = 4.63 μM
MAPK13-IN-1 Dose (μM)
Virus (anti-NP)
Cell viability
TCID50
H
A549-ACE2
IC50 = 0.913 μM
Percent
PFU/mL
0.01 0.1 1 10 100
ARRY-797 Dose (μM)
Virus (RTqPCR)
Cell viability
Plaque
I
siRNA
p=0.0001
p=0.003
p=0.0004
p=0.04
Log2 PFU/mL
Percent
ACE2
MAP2K3
MAPK13
MAPK12
NTC
Virus (RTqPCR)
Cell viability
J
Apilimod
?
PIK3CA, AKT
PIKFYVE
Vero E6
IC50 < 0.08 μM
Percent
DMSO 0.01 0.1 1 10
Apilimod Dose (μM)
Virus (anti-NP)
Cell viability
A549-ACE2
IC50 = 0.007 μM
PFU/mL
0.001 0.01 0.1 1
Apilimod Dose (μM)
Virus (RTqPCR)
Cell viability
Plaque
K
Dinaciclib
?
CDKs
Cell cycle arrest
Vero E6
IC50 = 0.127μM
Percent
DMSO 0.1 1 10 100
Dinaciclib Dose (μM)
Virus (anti-NP)
Cell viability
A549-ACE2
IC50 = 0.032 μM
PFU/mL
0.001 0.01 0.1 1
Dinaciclib Dose (μM)
Virus (RTqPCR)
Cell viability
Plaque



SARS-CoV-2 infection timecourse

Phosphoproteomics



Kinase activity