S01-01 Therapeutic targeting of TMPRSS2 and ACE2 as a potential strategy to combat COVID-19. Qu Deng[1], Reyaz Ur Rasool[1], Ramakrishnan Natesan[1], Irfan A. Asangani[2]. [1]Department of Cancer Biology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, [2]Department of Cancer Biology, Abramson Family Cancer Research Institute, Epigenetics Institute, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA.

The novel SARS-CoV-2 infection responsible for the COVID-19 pandemic is expected to have an adverse effect on the progression of multiple cancers, including prostate cancer, due to the ensuing cytokine storm associated oncogenic signaling. A better understanding of the host cell factors and their regulators will help identify potential therapies to block SARS-CoV-2 infection at an early stage and thereby prevent cancer progression. Host cell infection by SARS-CoV-2 requires the binding of the viral spike S protein to ACE2 receptor and priming by the serine protease TMPRSS2—encoded by a well-known androgen response gene and highly expressed in patients diagnosed with prostate cancer. Epidemiologic data showing increased severity and mortality of SARS-CoV-2 disease in men suggest a possible role for androgen in the transcriptional activation of ACE2 and TMPRSS2 in the lungs and other primary infection sites. Here, by performing in vivo castration in mice, RT-PCR, immunoblotting, Co-IP, and pseudovirus infection assays in multiple cell lines, we present evidence for the transcriptional regulation of TMPRSS2 and ACE2 by androgen, their endogenous interaction, as well as a novel combination of drugs in blocking viral infection. In adult male mice, castration led to a significant loss in the expression of ACE2 and TMPRSS2 at the transcript and protein levels in the lung, heart, and small intestine. Intriguingly, castrated mice displayed a substantial increase in ACE2 in the kidney, which could potentially be due to the low blood pressure resulting from androgen deprivation. Endogenous TMPRSS2 and ACE2 were found to be physically interacting, as observed by reciprocal immunoprecipitation followed by immunoblotting. Importantly, along with full-length zymogen form, a prominent novel small isoform of TMPRSS2 was found to be associated with ACE2 in lung and prostate cells. In an overexpression system, camostat—a serine protease inhibitor specific to TMPRSS2—inhibited the cleavage of spike S, suggesting a direct role of this serine protease in priming the viral spike S protein, a prerequisite for an active infection. Furthermore, a combination of camostat, antiandrogen, and epigenetic drugs at sublethal concentrations blocked SARS-CoV-2 pseudovirus infection in multiple cell types. Together, our preclinical data provide a strong rationale for clinical evaluation of TMRPSS2 inhibitors, antiandrogens, and epigenetic drug combinations along with antiviral drug remdesivir as early as clinically possible to prevent progression to pneumonia and multiorgan failure as a result of hyperinflammatory responses in COVID-19 patients.

S01-02 Optimizing treatment for COVID-19 using computational modeling: Implications for cancer patients. Chrysovalantis Voutouri[1], Mohammadreza Nikmaneshi[2], Melin Khandekar[2], Ankit B. Patel[2], Ashish Verma[2], Sayon Dutta[2], Triantafyllos Stylianopoulos[1], Lance L. Munn[2], Rakesh K. Jain[2]. [1]University of Cyprus, Nicosia, Cyprus, [2]Massachusetts General Hospital and Harvard Medical School, Boston, MA.

Emerging retrospective analyses show that cancer patients are more likely to develop severe COVID-19. The causes for these worse outcomes are unclear, but data suggest that cancer therapies, which can suppress the immune system, are not responsible for increased COVID-19 severity. An alternative hypothesis is that common molecular pathways are altered in cancer and COVID-19, resulting in worsened disease outcomes. Our previous work demonstrated that activated renin angiotensin signaling (RAS) modulates the tumor microenvironment, resulting in worse outcomes and therapy resistance. Inhibition of this pathway using angiotensin receptor blockers (ARBs) or angiotensin converting enzyme inhibitors (ACEIs) can improve the outcomes of cancer therapies. Similarly, there is great interest in understanding the implications of RAS in COVID-19 progression because a key component of this system, ACE2, is also the docking site for the SARS-CoV-2 virus. Indeed, multiple clinical trials are currently evaluating whether ARBs/ACEIs benefit or harm COVID-19 patients. To help guide administration of these drugs, we adapted our existing computational modeling framework of the cancer microenvironment using available data to simulate COVID-19 progression in patients. Using a systems biology approach, we mechanistically modeled the interaction of the RAS and coagulation pathways with COVID-19 infection. We further explored the efficacy of various antiviral, antithrombotic, and RAS-targeted treatment regimens to identify synergistic combinations as well as optimal schedules for therapy. The system is complex, given that viral binding of ACE2 interferes with its antiinflammatory signaling. When ACE2 is bound by the virus, its local activity decreases, leading to immune dysregulation and risk of coagulopathy, predictors of COVID-19 severity and mortality. To optimize combination treatments for cancer patients who contract COVID-19, multiple simulations were run by combining different therapeutics currently in clinical trials to predict their effects on viral load, thrombosis, oxygen saturation, and cytokine levels. These include ARBs, ACEIs, antiviral drugs, antithrombotic agents, and anti-inflammatory drugs (e.g., anti-IL6/6R). Our simulations predict that i) there is an optimal timing for treatment with antiviral drugs such as remdesivir, related to immune activation; ii) combinations of antiviral and antithrombotic drugs are able to prevent lung damage, increase blood oxygen levels, and inhibit thromboembolic events; and iii) RAS modulators can have a positive effect when added to the treatment regimen. Effective strategies for COVID-

19 treatment identified by this in silico analysis will be further analyzed in combination with cancer therapeutics (e.g., immune checkpoint blockers, chemotherapy) to provide guidelines for optimal clinical management of both cancer and COVID-19.

S01-03 A prediction of prostate cancer deaths spiking by SARS-CoV-2 infection. Alakesh Bera, Eric Russ, Digonto Chatterjee, John Karaian, Madhan Subramanian, Sreejato Chatterjee, Surya Radhakrishnan, Michael Eklund, Harvey Pollard, Meera Srivastava. Uniformed Services University, Bethesda, MD.
COVID-19 is a global issue, with over 6.25 million cases in 213 countries and territories on June 1, 2020. Although this virus infects all groups, data indicate that the risk for severe disease and death is much higher in older men, which coincides with the same group of patients at risk for prostate cancer. A recent Italian study investigated the prevalence and severity of COVID-19 in men with prostate cancer. This study indicated that of a total of 4,532 men with COVID-19, from the Veneto region of Italy, 9.5% (n=430) had cancer and out of those around 30% (n=118) had prostate cancer. Data also indicated that male cancer patients had a 1.8-fold increased risk of COVID-19 infection and developed a more severe disease. Interestingly, they observed that the prostate cancer patients (n=4) treated with androgen-deprivation therapy (ADT) were less likely to develop COVID-19, and in those who were infected, the disease was less severe. In this current study, we focused on determining the genetic basis of the higher COVID-19 prevalence and severity in male patients and particularly for prostate cancer patients. Researchers found two genes that are essential for severe acute respiratory syndrome Coronavirus 2 (SARS-CoV-2). ACE2 is a SARS-CoV-2 receptor, whereas the serine protease, TMPRSS2, primes the virus for cell entry through cleavage of the viral spike protein (S). The expression of TMPRSS2 is significantly high in normal prostate tissue and is regulated in large part by an androgen response element in the promoter region. Therefore, we decided to investigate the status of these two genes in various tumors from The Cancer Genome Atlas (TCGA) database using the cBioportal platform. We analyzed over 46,000 tumor samples from 176 studies and found that aggressive metastatic prostate cancer, including neuroendocrine prostate cancer (NEPC), has significantly higher amplification (copy number alteration) of the ACE2 and TMPRSS2 genes compared to other cancers. Next, we focused on drugs that could simultaneously target ACE2 or TMPRSS2 and oncogenic pathways and would be beneficial for prostate cancer patients infected with SARS-CoV-2. Although several inhibitors are validated in literature for both ACE2 and TMPRSS2, very limited studies were performed to see the effect on cancer cells. Therefore, we analyzed a cytotoxic effect database of over 130,000 drugs on NCI-60 cell lines with COMPARE algorithm and found two relevant compounds, NSC-148958 (FT-701) and NSC-280594 (triciribine phosphate), which target ACE2 and TMPRSS2, respectively. Computational data are currently validating different prostate cancer cell-lines and their response to these drugs. In summary, our findings provide the premise that men who are at risk for or diagnosed with prostate cancer may be more susceptible

to severe infection and death in response to SARS-CoV-2 due to the high expression of ACE2 and TMPRSS2, and triciribine phosphate and FT-701 could be a therapeutic intervention to target co-occurrence of COVID-19 and prostate cancer.

S02-01 Clinical characteristics and outcomes of coronavirus 2019 disease (COVID-19) in cancer patients treated with immune checkpoint inhibitors (ICI). Aljosja Rogiers[1], Carlo Tondini[2], Joe M. Grimes[3], Megan H. Trager[3], Sharon Nahm[4], Leyre Zubiri[5], Neha Papneja[6], Arielle Elkrief[6], Jessica Borgers[7], April Rose[8], Johanna Mangana[9], Michael Erdmann[10], Ines Pires da Silva[11], Christian Posch[12], Axel Hauschild[13], Lisa Zimmer[14], Paola Queirolo[15], Caroline Robert[16], Karijn Suijkerbuijk[17], Paolo A. Ascierto[18], Paul Lorigan[4], Richard Carvajal[3], Osama E Rahma[19], Mario Mandala[2], Georgina V. Long[1]. [1]Melanoma Institute Australia, Sydney, NSW, Australia, [2]Papa Giovanni XXIII Hospital, Bergamo, Italy, [3]Columbia University Irving Medical Center, New York, NY, [4]The Christie NHS Foundation Trust, Manchester, United Kingdom, [5]Massachusetts General Hospital, Boston, MA, [6]Segal Cancer Centre Jewish General Hospital, Montreal, QC, Canada, [7]Netherlands Cancer Institute, Amsterdam, The Netherlands, [8]Princess Margaret Cancer Centre, Toronto, ON, Canada, [9]University Hospital Zurich, Zurich, Switzerland, [10]University Medical Center Erlangen, Erlangen, Germany, [11]Westmead and Blacktown Hospitals, Sydney, NSW, Australia, [12]Technical University of Munich, Munich, Germany, [13]University Hospital Schleswig-Holstein, Kiel, Germany, [14]University Hospital Essen, Essen, Germany, [15]European Institute of Oncology, Milan, Italy, [16]Institut Gustave Roussy, Villejuif, France, [17]University Medical Center Utrecht, Utrecht, The Netherlands, [18]Istituto Nazionale Tumori IRCCS Fondazione Pascale, Naples, Italy, [19]Dana-Farber Cancer Institute, Boston, MA.

Background: ICI are widely used in the treatment of various cancer types. It has been hypothesized that ICI could confer an increased risk of severe acute lung injury or other complications associated with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

Methods: We analyzed data from 113 patients with laboratory-confirmed COVID-19 while on treatment with ICI without chemotherapy in 19 hospitals in North America, Europe, and Australia. Data collected included details on symptoms, comorbidities, medications, treatments and investigations for COVID-19, and outcomes (hospital admission, ICU admission, and mortality).

Results: The median age was 63 years (range 27–86); 40 (35%) patients were female. Most common malignancies were melanoma (n=64, 57%), non-small cell lung cancer (n=19, 17%), and renal cell carcinoma (n=11, 10%); 30 (27%) patients were treated for early (neoadjuvant/adjuvant) and 83 (73%) for advanced cancer. Most patients received anti-PD-1 (n=85, 75%), combination anti-PD-1 and anti-CTLA-4 (n=15, 13%), or anti-PD-L1 (n=8, 7%) ICI. Comorbidities included cardiovascular disease (n=31, 27%), diabetes (n=17, 15%), and pulmonary disease (n=14, 12%). Symptoms were

present in 68 (60%) patients; 46 (68%) had fever, 40 (59%) cough, and 23 (34%) dyspnea. Overall, ICI was interrupted in 58 (51%) patients. At data cutoff, 33 (29%) patients were admitted to hospital, 6 (5%) to ICU, and 9 (8%) patients died. COVID-19 was the primary cause of death in 7 patients, 3 of whom were admitted to ICU. Cancer types in patients who died were melanoma (2), non-small cell lung cancer (2), renal cell carcinoma (2), and others (3); all (9) patients had advanced cancer. Administered treatments were oxygen therapy (8), mechanical ventilation (2), vasopression (2), antibiotics (7), antiviral drugs (4), glucocorticoids (2), and anti-IL-6 (2). Of all hospitalized patients, 20 (61%) had been discharged and 4 (12%) were still in hospital at data cutoff.

Conclusion: The mortality rate of COVID-19 in patients on ICI is higher than rates reported for the general population without comorbidities but may not be higher than rates reported for the cancer population. Despite these preliminary findings, COVID-19 patients on ICI may not have symptoms and a proportion may continue ICI. Correlative analyses are ongoing and will be presented.

S02-02 Covid-19 treatment candidate hydroxychloroquine impairs tumor response to anti-PD1. Simon Wabitsch, Jack C McVey, Chi Ma, Benjamin Ruf, Laurence Diggs, Bernd Heinrich, Tim F Greten. GI-Malignancy Section, Thoracic and GI Oncology Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD.

Background and Aims: Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) has caused a worldwide health crisis. As of now, only one treatment has been established for the coronavirus infection disease 2019 (Covid-19), which has disproportionally affected patients with comorbidities such as cancer. Hydroxychloroquine (HCQ) has been studied as a potential treatment for Covid-19. Here we studied whether HCQ treatment could influence the effect of immunotherapy against colorectal and liver cancer.

Methods: In vitro studies were conducted to assess the effect of HCQ on lymphocyte activation and proliferation as well as cell growth and antigen presentation. Mouse cell lines used included MC38, CT26, RIL-175, SB1, and LD1 while human tumor cell lines used were TFK-1 and EGI-1. Mice bearing subcutaneous MC38, CT26, and RIL-175 tumors were treated with HCQ, anti-PD1, or both. Tumor volume was measured over 19 days. Systemic and tumor-infiltrating immune cells were analyzed by flow cytometry.

Results: HCQ treatment impairs T-cell production of TNF-α and IFNγ in vitro and in vivo. Whereas cell growth was decreased in all tumor cell lines, in vitro treatment of tumor cells with HCQ revealed an upregulation of MHC-1 in CT26, SB1, LD1, TFK-1, and EGI-1 but not in MC38 and RIL-175. HCQ treatment impaired response to anti-PD1 treatment in all subcutaneous models. Compared to control, HCQ treatment led to increased tumor growth in MC38 tumors. Flow cytometry analysis revealed an impaired activation of CD4+ T cells as well as tumor-infiltrating cytotoxic antigen-specific CD8+ T cells.

Conclusion: This study shows that HCQ treatment can result in immunotherapy failure due to a systematic immunosuppressive effect that overcomes the increased MHC expression on tumor cells.

S02-03 SARS-CoV-2 induces inflammatory cytokine release, which may be exacerbated by immune checkpoint blockade. Layne Weatherford, Maria Lehn, McKenzie Crist, Chelsea Wendling, Kristin Hudock, Vinita Takiar, Trisha Wise-Draper. University of Cincinnati, Cincinnati, OH.

Cancer patients infected with the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have a higher mortality rate compared to non-cancer patients. Recent anticancer treatment, including immunotherapy, is associated with severe infection including development of acute respiratory distress syndrome (ARDS) and high levels of cytokine release resulting in cytokine storm. Immune checkpoint inhibitors (ICIs) are approved for use in multiple cancer types and function by blocking the interaction between PD-1 and its ligand PD-L1, activating antitumor cytotoxic immune cells. However, ICIs can also increase inflammatory cytokine secretion, which may predispose to the development of cytokine storm. In fact, we have shown via single-cell cytokine secretion analysis that pembrolizumab (anti-PD-1 antibody) increases cytokine secretion by polyfunctional strength index, a measure of the percentage of cells secreting multiple functional cytokines. Therefore, we hypothesize that ICIs may worsen inflammatory cytokine secretion and potentiate cytokine storm and downstream complications in COVID-19 patients. Peripheral blood mononuclear cells (PBMCs) were isolated via Ficoll density gradient centrifugation from healthy donors, head and neck cancer (HNC) patients, and COVID-19-infected cancer patients. Flow cytometry was performed on patient PBMCs, after staining for viability and immune cell markers including CD3, CD8, CD19, and CD45. PBMCs were also activated overnight with low-dose IL-2, cocultured with Cal27 or HN5 cell lines, and subjected to various treatment conditions. For non-COVID-19 patients, PBMCs were exposed to 25 nM SARS-CoV-2 recombinant spike (S) protein, a virulent protein associated with cytokine storm, or control prior to drug treatments. Preliminary flow cytometry analysis showed that a COVID-19-positive patient with thyroid cancer had an increased proportion of CD8+ cells compared with a COVID-negative ovarian cancer patient and healthy donor. Recombinant SARS-CoV-2 S protein caused increased secretion of IL-6, IL-2, perforin, and MIP-1b from PBMCs isolated from both healthy donors and HNC patients, which was measured by IsoLight Codeplex bulk cytokine analysis or ELISA. We have previously shown that metformin, a commonly prescribed antidiabetes drug, decreases the proportion of cells that secrete inflammatory cytokines such as IL-6, which is thought to be an important cytokine for cytokine storm. Interestingly, we observed that metformin treatment resulted in decreased IL-6 secretion from PBMCs isolated from a COVID-19-positive patient. Results from this project suggest that ICIs may potentiate cytokine storm, and ongoing investigation will be informative to oncologists as to whether ICI treatment should be postponed in severe COVID-19 infections. In

addition, metformin may be a novel potential treatment for COVID-19 patients to prevent and treat cytokine storm.

S03-01 Pan-HLA prediction of SARS-CoV-2 epitopes. Katie M. Campbell[1], Gabriela Steiner[2], Daniel K. Wells[1], Antoni Ribas[1], Anusha Kalbasi[1]. [1]University of California Los Angeles, Los Angeles, CA, [2]Parker Institute for Cancer Immunotherapy, San Francisco, CA.

Introduction: Delineating antiviral T-cell responses to SARS-CoV-2 may shed light on the heterogeneity of clinical outcomes and inform vaccine or therapeutic approaches. Viral antigens can be predicted using computational tools that calculate the binding affinity between viral peptides and antigen presentation machinery. However, in order to account for the role of host genetics in the diversity of responses, this analysis must be performed with consideration of the global diversity of the human leukocyte antigen (HLA) proteins responsible for antigen presentation.

Methods: We deployed binding predictions across the SARS-CoV-2 peptidome for 9,360 Class I HLA alleles (2,987 HLA-A; 3,707 HLA-B; 2,666 HLA-C; 9-mers) using a consensus approach of 7 algorithms and 3,486 Class II HLA alleles (15-mers) using a consensus approach of 4 algorithms. All pMHC predictions were filtered to include only those with consensus binding less than 500 nM.

Results: There were 368,145 unique combinations of peptides and HLA alleles (pMHCs) with a predicted binding affinity of less than 500nM, including 1,103 unique 9-mer and 2,547 15-mer peptides and 1,022 MHC Class I and 8,075 MHC Class II HLA proteins. Of these pMHCs, 82% of 9-mers overlapped with 15-mers, suggesting cross-presentation to both CD4 and CD8 T cells in a subset of individuals. We evaluated this filtered dataset with respect to the population frequency of HLA haplotypes. While the predicted susceptibility of SARS-CoV-2 antigen presentation differed greatly across countries, there was a subset of 21 Class I antigens shared by common HLA types across 30 or more countries (out of 79 countries with reported population frequency data). Our database has been made publicly available, and we have developed a user interface to explore the results based upon viral proteins, HLA alleles, or country populations of interest.

Conclusions: With the ongoing SARS-CoV-2 pandemic, there are worldwide efforts to generate a successful vaccine and to evaluate clinical samples to understand the viral pathogenesis and diverse outcomes in patients. This application can serve as a guide to identify responses of putative SARS-CoV-2-specific T cells across patients with a broad range of HLA haplotypes internationally.

S03-02 Sequence-based prediction of SARS-CoV-2 vaccine targets using a mass spectrometry-based bioinformatics predictor identifies immunogenic T-cell epitopes. Asaf Poran, Dewi Harjanto, Matt Malloy, Christina M. Arieta, Daniel A. Rothenberg, Divya Lenkala, Marit M. van Buuren, Terri A. Addona, Michael S. Rooney, Lakshmi Srinivasan, Richard B. Gaynor. BioNTech US, Cambridge, MA.

The ongoing COVID-19 pandemic has created an urgency to identify novel vaccine targets for protective immunity against SARS-CoV-2. Consistent with observations for the closely related SARS-CoV, early reports identify a protective role for both humoral and cell-mediated immunity for SARS-CoV-2. In this study, we leveraged our bioinformatics binding prediction tools for human leukocyte antigen (HLA)-I and HLA-II alleles that cover nearly the entire population and were developed using mass spectrometry-based profiling of 74 individual HLA-I and 83 individual HLA-II alleles. We applied these binding predictors, initially developed to predict tumor neoantigen presentation, to identify T-cell epitopes from SARS-CoV-2 proteins. To determine the ability of our tools to identify viral T-cell epitopes, we validated HLA-I and HLA-II predictions on *Coronaviridae* family epitopes deposited in the Virus Pathogen Database and Analysis Resource (ViPR) database. We then applied our HLA-I and HLA-II predictors to 13 open reading frames (ORFs) of SARS-CoV-2 and identified 11,897 HLA-I and 8,046 HLA-II candidate peptides that were highly ranked for binding. From our SARS-CoV-2 predicted peptide-HLA-I allele pairs, 374 pairs identically matched previously reported pairs in the ViPR database, originating from other coronaviruses with homologous sequences. Of these pairs, 333 (89 %) had a positive HLA-binding assay result, reinforcing the validity of our predictions. Furthermore, we assayed a subset of epitopes with highly predicted binding scores for their ability to be recognized by specific CD8+ T cell in human donor PBMCs. These epitopes were chosen from four structural proteins (S, N, M, E) and one nonstructural protein (ORF1ab) from SARS-CoV-2, and epitopes from all five proteins were found to be immunogenic. Finally, it was important to address the expression of SARS-CoV-2 proteins within cells since their subsequent processing is necessary for MHC presentation and the generation of specific epitopes. We utilized publicly available proteomic data to infer the relative expression of SARS-CoV-2 proteins from infected cell lines and determined that the different proteins vary significantly in their expression levels, with the nucleocapsid being the most highly expressed viral protein across these studies. Our predictions identify few epitopes from each SARS-CoV-2 protein, which are predicted to bind multiple HLA-I or HLA-II alleles, potentially covering over 99% of the USA, European, and Asian populations. Finally, using our bioinformatic platform, we identify multiple putative epitopes that are potential targets for CD4+ and CD8+ T cells whose predicted HLA binding properties cover nearly the entire population. We further propose that when considering the

protein expression levels of these epitopes and their ability to elicit a T-cell response, these epitopes may be effective when included in vaccines against SARS-CoV-2 to induce broad cellular immunity.

S03-03 A computational approach to identify a possible SARS-CoV-2 vaccine from receptor binding domain peptide sequence on spike glycoproteins. Majid Al-Zahrani. King Abdulaziz University, Jeddah, Makkah, Saudi Arabia.

The novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) is a pathogenic virus responsible for the coronavirus disease 2019 (COVID-19) outbreak. The virus has rapidly spread worldwide and caused serious global health and economic issues. The World Health Organization has declared COVID-19 a pandemic and suggested that all countries should take extreme countermeasures to stop it from spreading. SARS-CoV-2 targets the angiotensin-converting enzyme 2 (ACE2) receptor on human lung cells through receptor binding domain on the spike proteins (S-RBD) via N487, Y489, and G496 residues as previously reported. The virus uses ACE2 to inoculate mRNA and to replicate inside the cells, which results in a severe respiratory syndrome. Patients might experience serious symptoms including fever, cough, inability to taste, shortness of breath, and sometimes respiratory failure. Therefore, developing a vaccine is highly necessary to control the outbreak, which led to our goal in this study to identify antigenic peptide sequences on the S-RBD domain that may induce the immune response to provide protection from the virus. We virtually analyzed S-RBD protein structure by multiple sequence alignment (MSA) via CLUSTAL OMEGA to study the homology of the S-RBD domain in both strains (SARS-CoV and SARS-CoV-2), and the results showed 76% identical shared amino acids. Moreover, the S-RBD sequence for SARS-CoV-2 was blasted against the sequence “486-FNCYFPLQSYGFQ-498” on Drugbank database with a penalty of -1 for each indel, -3 for the mismatch, and with an expected value of 8 to screen for potential molecules that might interact with the target sequence. The blast results showed a possible alignment with complement component 4A (C4-A) protein, a protein involved in autoimmunity and antibody signaling, on the residues F490, C488, P491, Y495, G496, F497, and Q498. Lastly, a molecular docking analysis was performed by ClusPro 2.0 docking system to analyze the binding affinity of C4-A protein to the S-RBD-protein, and the results of the docking analysis showed 30 different bindings with different weighted energy coefficient scores. The top 10 binding conformations were chosen based on the coefficient score values between -856.2 to -985.4. The highest binding affinity of C4-A protein was observed on the target sequence, which might be a therapeutic approach for a possible COVID-19 vaccine. Further experiments are required to synthesize recombinant peptides for S-RBD protein and test it on animal models to check if it will induce C4-A production in response to recombinant S-RBD peptide and antibodies signaling to counter SARS-CoV-2 virus and, hopefully, competing with ACE2 binding to S-protein.

S04-01 Famotidine use and quantitative symptom tracking for COVID-19 in nonhospitalized patients: A case series. Tobias Janowitz[1], Eva C. Gablenz[1], David J. Pattinson[2], Timothy C. Wang[3], Joseph Conigliaro[4], Kevin J. Tracey[5], David A. Tuveson[1]. [1]Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, [2]University of Cambridge, Cambridge, United Kingdom, [3]Columbia University, New York, NY, [4]Northwell Health, New Hyde Park, NY, [5]The Feinstein Institute for Medical Research, Manhasset, NY.

Objective: Treatment options for nonhospitalized patients with coronavirus disease 2019 (COVID-19) to reduce morbidity, mortality, and spread of the disease are an urgent global need. The over-the-counter histamine-2 receptor antagonist famotidine is a putative therapy for COVID-19. We quantitively assessed longitudinal changes in patient-reported outcome measures in nonhospitalized patients with COVID-19 who self-administered high-dose famotidine orally.
Design: Patients were enrolled consecutively after signing written informed consent. Data on demographics, COVID-19 diagnosis, famotidine use, drug related side-effects, temperature measurements, oxygen saturations, and symptom scores were obtained using questionnaires and telephone interviews. Based on an NIH-endorsed Protocol to research Patient Experience of COVID-19, we collected longitudinal severity scores of five symptoms (cough, shortness of breath, fatigue, headaches, and anosmia) and general unwellness on a 4-point ordinal scale modeled on performance status scoring. All data are reported at the patient level. Longitudinal combined normalized symptom scores were statistically compared.

Results: Ten consecutive patients with COVID-19 who self-administered high-dose oral famotidine were identified. The most frequently used famotidine regimen was 80mg three times daily (n=6) for a median of 11 days (range: 5 to 21 days). Famotidine was well tolerated. All patients reported marked improvements of disease-related symptoms after starting famotidine. The combined symptom score improved significantly within 24 hours of starting famotidine and peripheral oxygen saturation (n=2), and device recorded activity (n=1) increased.

Conclusions: The results of this case series suggest that high-dose oral famotidine is well tolerated and associated with improved patient reported outcomes in nonhospitalized patients with COVID-19. A blinded outpatient trial is planned. The findings may be transferable and relevant to the treatment of patients with cancer and COVID-19.

S04-02 Treatment with tocilizumab does not inhibit induction of anti-COVID-19 antibodies in patients with severe SARS-CoV-2 infection. Alexandra Cabanov, Blake A. Flood, Jeffrey Bloodworth, Emily F. Higgs, Jessica Fessler, Michael Y.K. Leung, Kyle R. Cron, Jonathan Trujillo, Athalia R. Pyzer, Sherin Rouhani, Garth Strohbehn, Brian Heiss, Mark Ratain, Pankti Reid, Kiang-Teck J. Yeo, Randy F. Sweis, Yuanyuan Zha, Thomas F. Gajewski. University of Chicago, Chicago, IL.

Tocilizumab (TCZ), an interleukin-6 (IL-6) receptor-blocking monoclonal antibody, is used to treat various rheumatologic conditions and cytokine release syndrome in CAR-T cell therapy and has been repurposed to treat COVID-19-related hyperinflammation. There are limited data available reporting how TCZ affects the immune response in the context of COVID-19. To investigate this question, we recruited patients treated with TCZ as part of a COVID-19 biobanking protocol (A-28063295) to study immune parameters that might be affected. We enrolled 19 patients who were treated with a range of 40-200mg TCZ as part of a low-dose TCZ trial (COVIDOSE, reported separately as abstract A-94803796), and 11 patients who received 400mg TCZ on a standard-of-care expanded-access basis. As IL-6 acts as a stimulant of B-cell proliferation, plasma cell maturation, and antibody responses, we evaluated whether blocking the IL-6 receptor with TCZ therapy impairs antibody generation to SARS-CoV-2. To evaluate antibody levels in these patients, we performed ELISAs against the SARS-CoV-2 spike glycoprotein and its receptor-binding domain (RBD). The spike glycoprotein, a structural protein of SARS-CoV-2, is a crucial component in the recognition, attachment, and entry of the virus into host cells. Specifically, the RBD is responsible for binding the ACE2 receptor on human cells, and likely serves as a major target for neutralizing antibodies. To establish if the formation and persistence of antibodies was affected by TCZ treatment, we analyzed serum and plasma samples longitudinally from 29 patients treated with TCZ and 26 control patients. To account for potential variability between plates, the measured optical density (OD) values were normalized to the OD for COVID-19-negative control serum at 1:50 dilution, and the same negative control was tested on each plate. Titers were calculated as the linear interpolation of the inverse dilution at which the normalized OD value crossed a threshold of 1, representing the maximum OD measured for the negative control. Anti-spike and anti-RBD antibodies increased significantly over time in both TCZ-treated patients and controls ($p < 0.005$ for both). Increasing antibody titers throughout the disease course followed a similar trajectory in TCZ-treated patients compared to control patients, suggesting that TCZ treatment does not impede the generation of antibodies to SARS-CoV-2. Additionally, TCZ-treated patients achieved comparable maximal observed antibody titers to control patients (average maximal log10 (titer) of 5.42 and 4.96 for spike and of 4.39 and

4.44 for RBD, respectively). These data suggest that TCZ does not impair the induction of anti-SARS-CoV-2 antibodies.

S05-01 Profound CD8 T-cell responses towards SARS-CoV-2 OFR1ab in COVID-19 patients. Anastasia Gangaev[1], Steven L. Ketelaars[1], Sanne Patiwael[1], Anna Dopler[1], Olga I. Isaeva[1], Kelly Hoefakker[1], Sara De Biasi[2], Cristina Mussini[2], Giovanni Guaraldi[2], Massimo Girardis[2], Cami M.P. Talavera Ormeno[3], Paul J.M. Hekking[3], Neubury M. Lardy[4], Mireille Toebes[1], Robert Balderas[5], Ton N. Schumacher[1], Huib Ovaa[3], Andrea Cossarizza[2], Pia Kvistborg[1]. [1]Netherlands Cancer Institute, Amsterdam, The Netherlands, [2]University of Modena and Reggio Emilia School of Medicine, Modena, Italy, [3]Leiden University Medical Center, Leiden, Italy, [4]Sanquin Diagnostics B.V., Amsterdam, The Netherlands, [5]BD Biosciences, San Diego, CA.
While there is accumulating evidence on the antibody response against SARS-CoV-2, we are only beginning to acquire knowledge regarding the SARS-CoV-2 specific CD8 T-cell response. Therefore, it is an urgent matter to gain a deeper insight into the virus specific CD8 T-cell response to both assist vaccine design and provide tools to evaluate the vaccine-induced T-cell responses. To address this issue, we have analyzed samples from 20 COVID-19 patients for CD8 T-cell recognition of 500 predicted SARS-CoV-2-derived epitopes restricted to 10 of the most common HLA-A and HLA-B alleles. For each HLA allele, the top 50 epitopes were selected based on predicted binding affinity and likelihood of successful proteasomal processing. In addition, SARS-CoV-2 epitope predictions shared by the science community were considered. To probe for CD8 T-cell recognition of the selected epitopes, we made use of our in-house technology based on multiplexing of peptide HLA (pHLA) multimers conjugated to fluorescent dyes. Our data demonstrated that CD8 T-cell reactivity against SARS-CoV-2 was common. Remarkably, a substantial fraction of the observed CD8 T-cell responses were directed towards the ORF1ab polyprotein 1ab. These CD8 T-cell responses were frequently of a profound magnitude. In particular, a CD8 T-cell response towards a potentially immunodominant epitope (TTDPSFLGRY) restricted to the HLA-A*01:01 allele was found in all patients positive for this allele. Interestingly, the fraction of SARS-CoV-2 specific CD8 T cells expressing the inhibitory receptor NKG2A was higher as compared to bulk CD8 T cells. In conclusion, the fact that a major part of the identified SARS-CoV-2 specific CD8 T-cell response is directed against a part of the viral genome that is not included in the majority of vaccine candidates currently in development may potentially influence their clinical activity and toxicity profile.

S05-02 COVIDOSE: Low-dose tocilizumab in the treatment of COVID-19 pneumonitis. Garth W. Strohbehn, Brian L. Heiss, Sherin J. Rouhani, Jonathan A. Trujillo, Athalia R. Pyzer, Jovian Yu, Alec J. Kacew, Alexandra Weiss, Spring Maleckar, Rachel Wright, Adriana Koziol, Bethany Martell, Keith Danahey, Theodore G. Karrison, Cuoghi Edens, Iazsmin Bauer Ventura, Natasha Pettit, Bakhti Patel, Jennifer Pisano, Mary Strek, Thomas F. Gajewski, Mark J. Ratain, Pankti D. Reid. University of Chicago, Chicago, IL.

Background: Morbidity and mortality due to coronavirus disease 2019 (COVID-19) may in part be due to interleukin-6 (IL-6)-mediated hyperinflammation. The IL-6 receptor-targeted monoclonal antibody tocilizumab (TCZ) has been repurposed to treat COVID-19-related hyperinflammation, but prospective data are lacking. Given TCZ's risks of secondary infection and potential blunting of the adaptive immune response and its finite supply, study of the efficacy, safety, and dose response of TCZ for the treatment of COVID-19-related hyperinflammation is needed.

Methods: We conducted an adaptive phase 2 study of low-dose (LD) TCZ in hospitalized, non-mechanically ventilated adult patients with COVID-19 pneumonitis and evidence of hyperinflammatory syndrome, with C-reactive protein (CRP) ≥ 40 micrograms per milliliter. Dose cohorts were determined by a trial Operations Committee, with the initial doses of 80 or 200 milligrams, depending on the magnitude of CRP elevation and epidemiologic risk factors. Doses were decreased to 40 mg and 120 mg after interim assessment. The primary objective was to assess the relationship of dose to clinical improvement in temperature and oxygen requirement and biochemical response by CRP.

Results: 32 patients received LD TCZ. 25 of 32 (78%) patients receiving LD TCZ at any dose achieved fever resolution. In terms of dose-response, fever resolution in 24 hours was observed in 6 of 8 (75%) who received 200 milligrams, 3 of 4 (75%) who received 120 milligrams, 11 of 15 (73%) who received 80 milligrams, and 5 of 5 (100%) who received 40 milligrams (p = 0.80 for response rate difference). Biochemical response consistent with interleukin-6 pathway inhibition, corresponding to a ≥ 25% CRP decline, after a single dose of LD TCZ was observed in 5 of 8 (63%) who received 200 milligrams, 4 of 4 (100%) who received 120 milligrams, 10 of 15 (67%) who received 80 milligrams, and 5 of 5 (100%) who received 40 milligrams (p = 0.34 for response rate difference). 100% of patients achieved CRP response within two doses of LD TCZ. Within the 28-day follow-up period, 5 (16%) patients died. For patients who recovered, median time to clinical recovery was 4 days (interquartile range, 2-5). Clinically presumed and/or cultured bacterial superinfections were reported in 4 (12.5%) patients. Correlative biologic

studies examining anti-SARS-CoV-2 antibody production across a range of TCZ doses are presented separately (abstract A-22514927).

Conclusions: LD TCZ, in addition to standard of care, was associated with improvement of clinical hyperinflammation parameters in hospitalized adult patients with COVID-19 pneumonitis. No relationship between TCZ dose and clinical or biochemical response relationship was identified. Results of the COVIDOSE trial provide a rationale for a randomized, controlled trial of LD TCZ versus standard of care in those patients with COVID-19 pneumonitis who have evidence of hyperinflammation. (COVIDOSE, ClinicalTrials.gov number, NCT04331795.)

S05-03 Preserving innate memory to overcome SARS-CoV-2 infection through the mevalonate pathway. Juan Luis Gomez, Adam Brufsky. University of Pittsburgh, Pittsburgh, PA.

Background: Easily accessible therapies have been proposed to treat SARS-CoV-2 infection. Given that the mevalonate pathway is critical in preventing nonspecific inflammation, events that interfere in this pathway in mononuclear or epithelial lung cells might determine the outcome of infected patients. Based on its mechanism of action, we hypothesize that in patients with metastatic cancer (MC), zoledronic acid (ZA) may influence the severity of COVID-19 disease.

Methods: In silico analysis compared normalized expression levels of prenylation-related genes in mononuclear and epithelial cells, between infected and noninfected SARS-CoV and SARS-CoV-2 samples, from available GEO datasets. RNA analysis was done using R v3.6.3. Counts were normalized with EdgeR, and ggpubr package and was used to compute t-tests. For analyzing samples from GSE150728, Partek Flow was used to align and normalize reads from single-cell RNA.

Results: Analysis of data from the 2003 SARS outbreak (GSE1739) showed that PBMCs isolated from infected patients expressed lower levels of HMGCR, FNTA, COX10, and PGGT1B (<0.05). In vitro results from SARS-CoV-infected Calu-3 cells (GSE17400) showed a trend of downregulation of MVK, RABGGTA, FDFT1, FNTA, and RAB27A (n=3/group). Next, we analyzed the transcriptional response to SARS-CoV-2 in Calu-3 and A549-infected cells in vitro (GSE147507). Differential downregulation of FNTA, MVK, HMGCR, and FDPS ($p<0.05$), and only upregulation of FNTA and PGGT1B ($p<0.05$), was observed in Calu-3 cells. The same dataset offered expression data from autopsy-derived, COVID-19-infected bronchial tissue from 2 patients. Here, we found that FDFT1, FNTA, HMGCR, RABGGTA, and FDPS were downregulated >1.5-fold as compared to their healthy controls. Infected A549 cells showed decreased levels of MVK and RABGGTA ($p<0.05$). In SARS-CoV-2-infected A549 cells, ACE2 transduction upregulated RABGGTA, HMGCR, COX10, and RAB27B when compared to non-transduced infected cells. This suggested that downregulation of prenylation might occur upon binding of the viral spike protein to the ACE2 receptor. Finally, we analyzed single-cell RNA-seq transcripts from uninfected PBMCs (no SARS reads) isolated from acutely ill SARS-CoV-2 patients (GSE150728). Here, we found no differences in the expression of any of these genes. This suggests that disruption of the mevalonate pathway may only account to infected cells.

Conclusion: In light of these findings, coronaviruses may hijack the mevalonate pathway and induce autoimmunity. Response to coronavirus infection may differ in

patients with MC under treatment with ZA, statins, or other substances that interfere with prenylation-mediated small vesicle trafficking (i.e., hydroxychloroquine, nicotine). Hence, studies that investigate SARS-CoV-2 disease severity in patients under treatment with ZA are strongly needed.

S06-01 Changes implemented by U.S. oncology practices in response to COVID-19 pandemic: Initial report from the ASCO Registry on COVID-19 and cancer. Suanna S. Bruinooge, Elizabeth Garrett-Mayer, Stephen Meersman, Patricia Hurley, Brian Bourbeau, Allyn Moushey, Sybil Green, Deborah Kamin, Stephen Grubbs, Richard L. Schilsky. American Society of Clinical Oncology, Alexandria, VA.

Background: In April 2020, ASCO initiated a registry to capture and analyze status and outcomes of patients with cancer and COVID-19, and to describe effects of the pandemic on U.S. cancer practices. Initial findings of changes to care delivery are included.

Methods: Practices provide data on changes to care delivery due to COVID-19 and longitudinal data on patients with cancer and confirmed COVID-19. At present, 26 cancer practices have enrolled in the Registry—5 academic, 15 hospital/health-system (H/HS) owned, and 6 physician-owned (P-O) located in 19 states. Enrollment of practices and data collection is ongoing.

Results: Twenty sites, from 17 practices (3 academic, 9 H/HS owned, and 5 P-O in 15 states) responded (April 20-June 4). All incorporated telemedicine visits; 90% reported use of telemedicine was new. 30% reported "declining some but not all" new patient requests. For patients with cancer not on active therapy, 15% of sites postponed some routine visits, 35% conducted virtually all routine visits by telemedicine, and 50% used telemedicine for some routine visits. Most sites (95%) reported following clinical guidelines for visit postponement; 90% reported following local health authorities on when to resume routine visits. 90% screened patients prior to in-office visits for COVID-19 symptoms by phone and at clinic entrance; 10% screened patients using only one method. 30% modified intravenous (IV) drug infusions, including halting some or all (10%), shortening some or all (20%), or switching from IV to oral drugs (15%). While no sites conducted home-based, anticancer drug infusions, 30% are considering this option if COVID19 conditions change. Most sites modified laboratory specimen collection, including allowing a collection site closer to home (60%) and collection in a patient's home (1 site). Two sites only allowed patients on oral anticancer drugs to use alternate collection sites. Only 1 site reported specimen collection in patients' homes. All reported making the following changes to clinic arrangements: requiring use of masks, eliminating accompaniment by a support person (with exceptions), and reducing the visit numbers or increasing time between visits. No sites reported shortages of anticancer or supportive care drugs. 45% experienced shortages of nasopharyngeal swabs, 45% of medical hand sanitizer, and 75% of personal protective equipment. 40% of sites

have experienced staffing reductions or changes due to reduced patient visits (30%), transfer to other clinical areas (20%), availability (15%), and COVID-19 illness (15%).

Conclusions: The COVID-19 pandemic has had a substantial impact on most aspects of cancer care delivery in U.S. oncology practices. All practices incorporated telemedicine, which is new to most. Adjustments were made to patient visits and scheduled IV drug infusions. Sites reported shortages of equipment related to COVID-19, not cancer or supportive care drug shortages. At the time of the AACR meeting we expect to have data from more practices.

S06-03 Cancer care telehealth utilization rates and provider attitudes in the wake of the novel coronavirus pandemic: The Kaiser Permanente Northern California experience. Elad Neeman[1], Tatjana Kolevska[2], Mary Reed[3], Tilak Sundaresan[1], Amit Arora[4], Yan Li[5], Samantha Seaward[5], Gillian Kuehner[6], Sharon Likely[7], Julia Trossman[8], Christine Weldon[8], Raymond Liu[1]. [1]San Francisco Medical Center, Kaiser Permanente Northern California, San Francisco, CA, [2]Napa/Solano Medical Center, Kaiser Permanente Northern California, Napa, CA, [3]Kaiser Permanente Division of Research, Oakland, CA, [4]San Leandro Medical Center, Kaiser Permanente Northern California, San Leandro, CA, [5]Oakland Medical Center, Kaiser Permanente Northern California, Oakland, CA, [6]Vallejo Medical Center, Kaiser Permanente Northern California, Vallejo, CA, [7]Modesto Medical Center, Kaiser Permanente Northern California, Modesto, CA, [8]The Center for Business Models in Healthcare, Chicago, IL.
Background: In response to the SARS-CoV-2 pandemic, the multidisciplinary care of cancer patients has rapidly evolved. This study aims to determine utilization trends of in-person, telephone, and video visits, before and after the California shelter-in-place (SIP) orders on 3/19/20, and assess perspectives of cancer care providers on telehealth.

Methods: This study was conducted in 22 medical centers of a large integrated health care system. Utilization of different visit types in medical oncology (excluding infusion visits) was collected between 12/1/2019–5/24/2020, for a total of 104,588 visits. Chi-square with Yates correction was used for p-values. Voluntary, anonymous electronic surveys were sent to 276 cancer care providers measuring attitudes and experiences with telehealth. Overall, 68.8% responded: 101/128 medical oncologists (MedOnc), 34/37 radiation oncologists (RadOnc), 16/62 breast surgeons (Brst Surg), 18/28 breast oncology nurse navigators (OncNav), and 21/21 cancer survivorship advanced practitioners (SurvOnc).

Results: Comparing visit types prior to and after SIP, in-person visits went from 55.3% to 3.3%, telephone visits went from 44.2% to 79%, and video visits went from 0.5% to 17.8% (p<.0001). Between 12/2019 and 05/2020, video visits increased from 0.42% to 31.3%. Telephone visits increased from 39.3 to a peak of 86.6% in 04/2020 and then decreased to 63.7%. In-person visits dropped from 60.3% to 2.3% in 04/2020 and then increased to 5.0% (p<.0001). Satisfaction with telehealth was high: 87.1% of MedOnc, 91.2% of RadOnc, 68.6% of BrstSurg, 72.2% of OncNav, and 90.4% SurvOnc providers were very or somewhat satisfied. Most providers preferred to increase or maintain telehealth utilization after the pandemic: 84% of MedOnc, 85% of RadOnc, 81% of BrstSurg, 51% of OncNav, and 90% of SurvOnc. Among most providers, highest cited benefits of telehealth included work from home, reduced

commute, staying on time, flexible hours, and shorter visits. Commonly cited challenges included connection/equipment problems, need for physical exam, difficulty evaluating performance status, and in-person visit required anyway. Of MedOnc, 11.8% responded that a patient suffered an adverse effect that could have been prevented with in-person visit. In-person visits were thought to promote the strongest provider-patient connection, followed by video, telephone visits, and emails. MedOnc providers deemed in-person visits were needed for end-of-life discussion (49%), discussing a new diagnosis (47.1%), palliative care discussion (34.3%), and clinical trial enrollment (34.3%). Activities for which email or phone visits were most accepted included check-in pretreatment, survivorship planning/follow-up, and patient navigation.

Conclusion: Overall, telehealth utilization has rapidly increased and is well accepted by various cancer care providers. Addressing technical issues and tailoring visit type to specific activities may further promote telehealth adoption and satisfaction.

S07-01 Examining COVID-19 preventive behaviors among cancer survivors in the United States: An analysis of the COVID-19 Impact Survey. Jessica Y. Islam[1], Marlene Camacho-Rivera[2], Denise C. Vidot[3]. [1]UNC Lineberger Comprehensive Cancer Center, Chapel Hill, NC, [2]SUNY Downstate Health Sciences University , New York, NY, [3]University of Miami Sylvester Comprehensive Cancer Center, Miami, FL.
Background: Cancer survivors are at high risk of contracting severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the infection that leads to COVID-19, as they are generally older and cancer therapies frequently lead to immunosuppression. Recently, to mitigate exposure the CDC recommended avoiding nonessential doctor appointments, which may lead to barriers in effective continuity of care and surveillance of cancer survivors during the COVID-19 pandemic. The patterns of COVID-19 preventive behaviors practiced by cancer survivors are unknown, including practices related to canceling doctors' appointments.

Objective: Our objective was to evaluate COVID-19-related preventive behaviors among cancer survivors in the United States (US). We further examined behaviors related to canceling or postponing activities, specifically doctors' appointments.

Methods: We utilized nationally representative weighted data from a sample of 4,428 US adults from the COVID-19 Impact Survey collected during Week 1 (April 20-26, 2020) and Week (May 4-10, 2020). We defined cancer survivors as those with a self-reported prior diagnosis of cancer. We presented frequencies and used $\chi 2$ tests to compare COVID-19-related preventive behaviors among cancer survivors to other adults. We calculated prevalence ratios with 95% confidence intervals using Poisson regression and robust estimation of standard errors to estimate determinants of canceling doctors' appointments among cancer survivors.

Results: Cancer survivors were mostly over the age of 60 years (62%), female (53%), non-Hispanic White (62%), and resided in urban areas (72%). Cancer survivors adhered to most recommended COVID-19-related preventive behaviors and were more likely to maintain social distancing (92%, $\chi 2$ p-value=0.005), wear a face mask (89%, $\chi 2$ p-value=0.001), and avoid crowded areas (84%, $\chi 2$ p-value=0.048) compared to other adults. Additionally, we found that cancer survivors are more likely to cancel their doctors' appointments (44%, $\chi 2$ p-value=0.001) whereas they were less likely to cancel other social activities such as work (20%, $\chi 2$ p-value=0.001) and school-related (12%, $\chi 2$ p-value=0.002) activities, even among those below the age of 60. However, cancer survivors were more likely to report symptoms in the last 7 days, including muscle or body aches ($\chi 2$ p-value=0.003). The proportion of cancer patients who have canceled doctors' appointments due to COVID-19 rose from the

month of April (35%) to May (52%). Younger adults aged 18-29 years, females, and rural cancer survivors were more likely to cancel their doctors' appointments, whereas NH-Blacks are less likely to cancel a doctor's appointment when compared to NH-Whites.

Conclusion: Cancer survivors are adhering to recommended preventive behaviors. Cancer survivors' continuity of care may be impacted by COVID-19, specifically young adults, females, and rural residents.

S07-02 Patient-reported outcomes of breast cancer patients during the COVID-19 outbreak in the epicenter of China: A cross-sectional survey study. Juanjuan Li[1], Cesar Augusto Santa-Maria[2], Hongfang Feng[3], Lingcheng Wang[4], Pengcheng Zhang[5], Yuangbing Xu[6], Yuyan Tan[7], Zhongchun Liu[1], Bo Du[8], Meng Lan[8], Qingfeng Yang[1], Feng Yao[1], Yi Tu[1], Shengrong Sun[1], Xingrui Li[9], Chuang Chen[1]. [1]Renmin Hospital of Wuhan University, Wuhan, China, [2]Johns Hopkins School of Medicine, Baltimore, MD, [3]Huangshi Central Hospital of Edong Healthcare Group, Huangshi, China, [4]Renmin Hospital, Hubei University of Medicine, Shiyan, China, [5]Xiangyang No. 1 People's Hospital of Hubei University of Medicine, Xiangyang, China, [6]Xiaogan Hospital Affiliated to Wuhan University of Science and Technology, Xiaogan, China, [7]Yichang Central People's Hospital, Yichang, China, [8]Wuhan University, Wuhan, China, [9]Tongji Hospital, Wuhan, China.

Purpose: We aimed to analyze the psychological status of breast cancer (BC) patients in the epicenter of the COVID-19 pandemic.

Patients and Methods: A total of 658 individuals were recruited from multiple breast cancer centers in Hubei Province. Online questionnaires were conducted and included demographic information, clinical features, and four patient-reported outcomes (PROs) scales (GAP-7, PHQ-9, ISI, and IES-R). Multivariable logistic regression analysis was designed to identify potential factors on mental health outcomes.

Results: Questionnaires were collected from February 16 to 19, 2020, the peak time point of COVID-19 outbreak in China. 46.2% of BC patients had to modify planned necessary anticancer treatment during the outbreak. 8.9% and 9.3% of patients reported severe anxiety and severe depression, respectively. 20.8% and 4.0% of patients showed severe distress and insomnia, respectively. Multivariable logistic regression analysis demonstrated poor general condition, shorter duration after BC diagnosis, aggressive BC molecular subtypes, and close contact with COVID-19 patients as independent factors associated with anxiety. Poor general condition and CVC (central venous catheter) flushing delay were factors independently associated with depression. In terms of insomnia, poor general condition was the only associated independent factor. Poor physical condition and treatment discontinuation were underlying risk factors for distress based on multivariable analysis.

Conclusion: High rates of anxiety, depression, distress, and insomnia were observed in patients with breast cancer during the COVID-19 outbreak. Special attention should be paid to the psychological status of breast cancer patients, especially those

with poor general condition, treatment discontinuation, aggressive molecular subtypes, and metastatic breast cancer.

S07-03 Scientia potentia est: How the Italian world of oncology changes in the COVID19 pandemic. Zelmira Ballatore, Lucia Bastianelli, Filippo Merloni, Nicoletta Ranallo, Luca Cantini, Lorenzo Mariotti, Claudia Catani, Michela Burattini, Alessandra Lucarelli, Rossana Berardi. Department of Oncology, AOU Riuniti, Università Politecnica delle Marche, Ancona, Italy.

Background: After COVID-19 was declared a pandemic by the World Health Organization, a response from the Italian Health System to react to an unprecedented condition became necessary and sudden. COVID- 19 pandemic required oncologists to redefine clinical organization and management of cancer patients. The aim of our study was to take a picture of the situation of Italian oncologies and to evaluate the difficulties in patients' management.

Methods: Between 18th March and 9th April 2020 we conducted an online survey (Google Forms). It consisted of 45 questions ranging from individual perception of pandemic management by oncologic centers to physicians' and nurses' psychological distress and patient care. The survey was anonymous and broadcast to oncology health workers by mailing contacts, word of mouth, and social networks.

Results: A total of 383 oncology health workers participated in the survey. The majority was female (72%) and from central Italy (46%). Impressively, a total of 357 (93%) participants declared the Oncologic Department reorganized routine clinical activity, but only 41% were adequately trained about the required procedures. 20% of the survey attendees thought they had not received adequate and timely protective devices with respect to clinical needs, and according to 58% the supply of these devices was only partial. 34% of professionals declared that they did not have or know a defined common guideline to reschedule patients' treatments. More than 80% of interviewees declared feeling worried about being at greater risk of contagion than the general population, and 92% feared to transmit virus to family members. Deferring treatments has caused fear/anxiety in 228 of the interviewed (60%). Symptoms of stressful situations emerged with a deterioration in sleep quality in 62% of professionals, worsening of mood (69%), and lower concentration ability (49%).

Conclusions: Our survey demonstrated the flexibility of oncologic teams. However, the emergency response quality has been heterogeneous, and several drawbacks emerged from this first analysis. Information, protection, testing, and training of health care professionals are keywords that should be kept in mind to encourage recovery after this tragedy and to be ready to face a similar emergency in the near future.

S07-04 Impact of COVID-19-related psychosocial distress on health-related quality of life in rural cancer survivors. Scherezade K. Mama[1], Michelle Cardel[2], Kathryn H. Schmitz[3]. [1]The Pennsylvania State University, University Park, PA, [2]University of Florida, Gainesville, FL, [3]Penn State College of Medicine, Hershey, PA.
Purpose: Rural cancer survivors report poorer health-related quality of life (QOL) than those residing in urban areas and have been disproportionately impacted by COVID-19. This study explored associations between the perceived threat of COVID-19 and psychosocial distress due to COVID-19 on health-related QOL in rural cancer survivors residing in central Pennsylvania.

Method: Previous participants (n=195) in the Partnering to Prevent and Control Cancer (PPCC) study who had a working email address were sent an email invitation to complete an online questionnaire. Of the 195 cancer survivors contacted, 90 (46.2%) have responded to the email invitation and completed the questionnaire to date. The questionnaire assessed sociodemographics, perceived threat of COVID-19, psychosocial distress related to COVID-19, and QOL (physical and social functioning, role limitations due to physical health and emotional problems, fatigue, emotional well-being, pain, and general health). Linear regression models were used to explore associations between COVID-19 perceived threat and psychosocial distress and QOL; all models were adjusted for age, body mass index (BMI), and education.

Results: Rural cancer survivors who completed the online questionnaire were mostly women (70%), non-Hispanic white (97.8%), in their 60s (M age=60.4±13.9 years), with overweight (M BMI=29.0±7.6 kg/m^2), and college graduates (67.8%). Most participants were breast (37.8%) or prostate (23.3%) cancer survivors, not currently receiving treatment (93.3%), and were more than 12 weeks but less than 5 years post-treatment (93.7%). Nearly half (41.1%) of participants rated their health as excellent or very good, and 17.8% rated their health as fair or poor. Generally, participants felt that COVID-19 was a threat to them, their city, school, community, or household (M score=17.2±3.4, scale: 5-20), but did not feel anxious, worried, or depressed due to the COVID-19 outbreak (M score=6.8±3.1, scale: 5-20). Although perceived threat was not associated with QOL, psychosocial distress related to COVID-19 was significantly associated with role limitations due to emotional problems (B=-3.958, SE=.993, p<.001), energy/fatigue (B=-2.730, SE=.606, p<.001), emotional well-being (B=-3.733, SE=.435, p<.001), and social functioning (B=-2.987, SE=.730, p<.001) in adjusted models.

Conclusions: Although the perceived threat of COVID-19 was low among rural cancer survivors, participants reported elevated psychosocial distress related to COVID-19,

which negatively impacted their mental but not physical health. These findings highlight the potential of the COVID-19 outbreak to exacerbate the persistent long-term adverse effects of cancer treatment on health-related QOL among rural cancer survivors. Psychosocial and behavioral interventions are critically needed to reduce COVID-19-related psychosocial distress among rural cancer survivors and to improve QOL and promote health equity among this vulnerable, underserved population.

S08-01 Highly sensitive and full-genome interrogation of SARS-CoV-2 using multiplexed PCR enrichment followed by next-generation sequencing. Chenyu Li[1], David N. Debruyne[1], Julia Spencer[1], Vidushi Kapoor[1], Lily Y. Liu[1], Bo Zhou[2], Utsav Pandey[3], Moiz Bootwalla[3], Dejerianne Ostrow[3], Dennis T. Maglinte[3], David Ruble[3], Alex Ryutov[3], Lishuang Shen[3], Lucie Lee[1], Rounak Feigelman[1], Grayson Burdon[1], Jeffrey Liu[1], Alejandra Oliva[1], Adam Borcherding[4], Hongdong Tan[4], Alexander E. Urban[2], Xiaowu Gai[3], Jennifer Dien Bard[3], Guoying Liu[1], Zhitong Liu[1]. [1]Paragon Genomics, Hayward, CA, [2]Stanford University, Palo Alto, CA, [3]Children's Hospital Los Angeles, Los Angeles, CA, [4]MGI, BGI-Shenzhen, Shenzhen, China.
Many detection methods have been used or reported for the diagnosis and/or surveillance of COVID-19. Among them, reverse transcription polymerase chain reaction (RT-PCR) is the most commonly used because of its high sensitivity, typically claiming detection of about 5 copies of viruses. However, it has been reported that only 47-59% of the positive cases were identified by some RT-PCR methods, probably due to low viral load, timing of sampling, degradation of virus RNA in the sampling process, or possible mutations spanning the primer binding sites. Therefore, alternative and highly sensitive methods are imperative. With the goal of improving sensitivity and accommodating various application settings, we developed a multiplex-PCR-based method comprising 343 pairs of specific primers and demonstrated its efficiency at detecting SARS-CoV-2 at low copy numbers. The assay produced clean characteristic target peaks of defined sizes, which allowed for direct identification of positives by electrophoresis. We further amplified the entire SARS-CoV-2 genome from 8 to half a million viral copies purified from 13 COVID-19 positive specimens and detected mutations through next-generation sequencing. Finally, we developed a multiplex-PCR-based metagenomic method in parallel that required modest sequencing depth for uncovering SARS-CoV-2 mutational diversity and potentially novel or emerging isolates.

S09-01 Cancer and race: Two important risk factors for COVID-19 incidence as captured by the COVID Symptom Study real-time epidemiology tool. David A. Drew[1], Long H. Nguyen[1], Wenjie Ma[1], Chun-Han Lo[1], Amit D. Joshi[1], Daniel Sikavi[2], Christina M. Astley[3], Karla Lee[4], Mary Ni Lochlainn[4], Maria Gomez[5], Sebastien Ourselin[4], Andrew T. Chan[1]. [1]Massachusetts General Hospital and Harvard Medical School, Boston, MA, [2]Massachusetts General Hospital, Boston, MA, [3]Boston Children's Hospital, Harvard Medical School, Broad Institute of Harvard and MIT, Boston, MA, [4]King's College London, London, United Kingdom, [5]Lund University, Malmo, Sweden.

Background: The COVID-19 pandemic and response underscore the urgent need for real-time population-level data, especially for vulnerable populations (e.g., cancer patients, racial and ethnic minorities). Smartphone applications ("apps") facilitate the collection of self-reported data at scale, the results of which can then be rapidly redeployed to inform the public health response. The COVID Symptom Study is an app that was launched March 24, 2020, and is now used by nearly 4 million people in the U.S., U.K., and Sweden.

Methods: COVID Symptom Study app users self-report health status (e.g., symptoms, COVID-19 testing, health care utilization), comorbidities, demographics, and key risk factors for infection on a daily basis. Multivariable adjusted logistic regression models were used to determine the association of cancer and race with COVID-19 prevalence, adjusting for age, sex, comorbidities, and risk factors for infection, from app launch through May 25, 2020.

Results: Among 23,266 individuals with cancer and 1,784,293 without cancer, we documented 155 and 10,249 self-reports of COVID-19, respectively. Compared to individuals without cancer, those with cancer had an increased risk of COVID-19 (adjusted odds ratio (aOR): 1.60; 95% confidence interval (CI): 1.36-1.88). The association was stronger among older participants >65 compared to younger participants (Pinteraction<0.001) and among males (aOR: 1.71; 95%CI: 1.36-2.15) compared to females (aOR: 1.43; 95%CI: 1.14-1.79; Pinteraction=0.02). Chemotherapy/immunotherapy was associated with a 2-fold increased risk of COVID-19 (aOR: 2.22; 95% CI: 1.68-2.94) and risk of COVID-related hospitalization (aOR:2.47; 95% CI: 2.22-2.76). In a separate analysis, we documented 8,990 self-reported cases of positive COVID-19 testing among 2,304,472 non-Hispanic white participants (93.6% of cohort); 93 among 19,498 Hispanic participants; 204 among 19,498 Black participants; 608 among 64,429 Asian participants; and 352 among 65,046 mixed race/other racial minorities. Compared with non-Hispanic white participants, the ORs for reporting a positive COVID-19 test for racial minorities

ranged from 1.44 (mixed race/other races) to 2.59 (Black). After accounting for risk factors for infection, comorbidities, and sociodemographic characteristics, the aORs were 1.37 (95% CI 1.09-1.72) for Hispanic participants, 1.42 (95% CI 1.23-1.64) for Black participants, 1.44 (95% CI 1.33-1.57) for Asian participants, and 1.18 (95% CI 1.06-1.32) for mixed race/other minorities.

Conclusion: Our results demonstrate an increase in COVID-19 risk among ethnic minorities and individuals with cancer, particularly those on treatment with chemotherapy/immunotherapy. The association with minorities was not completely explained by other known risk factors for COVID-19 or sociodemographic characteristics. These findings highlight the utility of app-based syndromic surveillance for quantifying the impact of the COVID-19 pandemic on at-risk populations.

S09-02 Outcomes by race for cancer patients hospitalized with SARS-CoV-2 infection. Steven S. Chang, Clara Hwang, Mohamed A. Elshaikh, Amy Tang, Christine M. Neslund-Dudas, Albert M. Levin, Laila M. Poisson, Benjamin A. Rybicki. Henry Ford Cancer Institute, Detroit, MI.

Purpose: Disparities in COVID-19 outcomes have been widely reported, with disproportionate negative impacts on the African American (AA) population. The purpose of this study was to evaluate the impact of race on COVID-19 outcomes for cancer patients hospitalized in a large Michigan health care system.

Methods: A cohort of hospitalized, laboratory-confirmed SARS-CoV-2 positive patients was identified through the Henry Ford Health System Institutional COVID prospective patient registry between March 1st–May 2020. Those with a diagnosis of cancer were identified using our institutional tumor registry and electronic health record (EHR). Patient self-reported race/ethnicity data were extracted from the system's centralized EHR, as were other demographic and clinical covariates. Racial differences in cumulative incidence of mortality and hospital discharge were tested. To further evaluate the effect of race on the mortality, Fine-Gray competing-risks model was performed with discharge alive as a competing event. A $P<0.05$ was considered statistically significant.

Results: Out of the 204 COVID+ cancer patients hospitalized in our health care system, 69.6% were AA (N=142). AA patients were slightly younger than non-AA patients (70.35 v. 74.58, p=0.023). No difference in mean BMI was detected (30.33 AA v. 29.87 non-AA, p = 0.68). A smaller proportion of AA patients had active cancer (36.6% v. 40.3%, p = 0.73). Outcomes were generally inferior in the AA cohort, although these differences were not statistically significant. The rate of ICU admission was 41.5% in AA and 37.1% in non-AA (p=0.659). 34.5% of AA patients required intubation compared to 25.8% of non-AA patients (p=0.288). In our model, older age was the only variable that significantly increased the risk of death (standard hazard ratio SHR 1.05, p = 0.002). The risk of death was higher for AA patients (SHR 1.92, p=0.068) and males (SHR 1.62, p = 0.078) but did not meet statistical significance.

Discussion: COVID-19 outcomes were worse in the AA cancer population, but these differences did not meet statistical significance. Inferior outcomes for AA cancer patients were seen despite younger age and a smaller proportion of patients with active cancer. Our analysis focused on hospitalized patients, which would tend to select patients with similar disease severity. Notably, AA patients were significantly over-represented in our cohort (70% of hospitalizations compared to 14% of

Michigan population). Our results suggest that racial disparities in outcomes for cancer patients with a SARS-CoV-2 infection may exist, but further study of larger, less selected populations is needed.

S09-03 Factors affecting COVID-19 outcomes in cancer patients: A first report from Guy's Cancer Centre in London. Beth Russell[1], Charlotte Moss[1], Sophie Papa[1], Sheeba Irshad[1], Paul Ross[2], James Spicer[1], Shahram Kordasti[1], Danielle Crawley[1], Harriet Wylie[1], Fidelma Cahill[1], Anna Haire[1], Kamarul Zaki[2], Fareen Rahman[2], Ailsa Sita-Lumsden[2], Debra Josephs[1], Deborah Enting[1], Mary Lei[2], Sharmista Ghosh[2], Claire Harrison[2], Angela Swampillai[2], Richard Sullivan[1], Anne Rigg[2], Saoirse Dolly[2], Mieke Van Hemelrijck[1], Guy's Cancer Real World Evidence Programme[2]. [1]King's College London, London, United Kingdom, [2]Guy's and St. Thomas' NHS Foundation Trust, London, United Kingdom.

Background: Current precautionary management decisions being made for cancer patients are based on assumptions supported by limited evidence, based on small case series from China and Italy and larger series from New York and a recent consortium of 900 patients from over 85 hospitals in the USA, Canada, and Spain. Hence, there is insufficient evidence to support clinical decision-making for cancer patients diagnosed with COVID-19 due to the lack of large studies.

Methods: We used data from a single large UK Cancer Centre to assess demographic/clinical characteristics of 156 cancer patients with a confirmed COVID-19 diagnosis between 29 February-12 May 2020. Logistic/Cox proportional hazards models were used to identify which demographic and/or clinical characteristics were associated with COVID-19 severity/death.

Results: 128 (82%) presented with mild/moderate COVID-19 and 28 (18%) with severe disease. Initial diagnosis of cancer >24m before COVID-19 (OR:1.74 (95%CI: 0.71-4.26)), presenting with fever (6.21 (1.76-21.99)), dyspnea (2.60 (1.00-6.76)), gastrointestinal symptoms (7.38 (2.71-20.16)), or higher levels of CRP (9.43 (0.73-121.12)) were linked with greater COVID-19 severity. During median follow-up of 47d, 34 patients had died of COVID-19 (22%). Asian ethnicity (3.73 (1.28-10.91), palliative treatment (5.74 (1.15-28.79), initial diagnosis of cancer >24m before (2.14 (1.04-4.44), dyspnea (4.94 (1.99-12.25), and increased CRP levels (10.35 (1.05-52.21)) were positively associated with COVID-19 death. An inverse association was observed with increased levels of albumin (0.04 (0.01-0.04).

Conclusions: Our analysis of one of the largest single-center series of COVID-19-positive cancer patients to date confirms a similar distribution of age, sex, and comorbidities as reported for other populations. With respect to cancer-specific observations, patients who have lived longer with their cancer were found to be more susceptible to a greater infection severity, possibly reflecting the effect of more advanced malignant disease, as almost half of the severe cohort were on third-

line metastatic treatment, or the impact of this infection. The latter was also found to be associated with COVID-19 death in cancer patients, as were Asian ethnicity and palliative treatment. Further validation will be provided from other large case series, as well as from those including longer follow-up, to provide more definite guidance for oncologic care.

S09-04 Unemployment and cancer screening: Baseline estimates to inform health care provision in the context of COVID-19 economic distress. Stacey A. Fedewa, K. Robin Yabroff, Zhiyuan Zheng, Priti Bandi, Ann Goding Sauer, Robert A. Smith, Nigar Nargis, Jeffrey Drope, Ahmedin Jemal. Office of the Chief Medical and Scientific Officer, American Cancer Society, Atlanta, GA.

Introduction: During the COVID-19 pandemic, the unemployment rate has sharply risen from 3.5% in February 2020 to 13.3% in May 2020, a level not seen since the Great Depression. There are an estimated 21.0 million unemployed adults in the United States. Employers are the most common source of health insurance among working-aged adults and their families. Thus, job loss may lead to loss of insurance and reduce access to cancer screening, which can detect cancer at earlier, more treatable stages, and reduce cancer mortality. In this study, we examined sequential associations between unemployment, health insurance, and cancer screening to inform COVID's potential longer-lasting impacts on early cancer detection.

Methods: Up-to-date (UTD) and recent (past-year) breast (BC) and colorectal cancer (CRC) screening prevalence were computed among respondents aged 50-64 years in 2000-2018 National Health Interview Survey data. Respondents were grouped as unemployed (not working but looking BC n=852; CRC n=1,747) and employed (currently working BC n=19,013; CRC n= 36,566). A series of logistic regression models with predicted marginal probabilities were used to estimate unemployed vs. employed unadjusted (PR) and adjusted prevalence ratios (aPR) and corresponding 95% Confidence Intervals (CI).

Results: Unemployed adults were four times as likely to be uninsured as employed adults (41.4% v 10.0%, p-value <0.001). Unemployment was associated with lower UTD breast (67.8% vs 77.5%, p-value<0.001, PR=0.82, 95%CI 0.77,0.87) and colorectal (49.4% and 60.1%, p-value<0.001, PR=0.86, 95%CI 0.80, 0.92) cancer screening prevalence. These differences remained after adjusting for race/ethnicity, age, and sex, but were eliminated after accounting for health insurance. Patterns and magnitudes of PR and aPRs were similar for past-year CRC and BC screening prevalence.

Conclusion: Unemployment was adversely associated with guideline-recommended and potentially life-saving breast and colorectal cancer screening. Compared to the employed, the unemployed disproportionately lacked health insurance, which accounted for their lower cancer screening utilization. Expanding and ensuring health insurance coverage after job loss may mitigate COVID-19's economic impacts on cancer screening.

S10-01 COVID-19 severity and outcomes in hospitalized patients with cancer at a New York City tertiary medical center: A matched cohort study. Gagandeep Brar, Laura C. Pinheiro, Michael Shusterman, Brandon Swed, Evgeniya Reshentnyak, Orysya Soroka, Frank Chen, Samuel Yamshon, John Vaughn, Peter Martin, Doru Paul, Manuel Hidalgo, Manish A. Shah. New York-Presbyterian Hospital/Weill Cornell Medical Center, New York, NY.

Background: New York City has been at the epicenter of the SARS-CoV-2 (COVID-19) pandemic. Immunocompromised cancer patients may be more vulnerable to COVID-related morbidity and mortality. The objectives of this study were to determine if patients with cancer have worse outcomes compared to their noncancer counterparts and to identify potential demographic and clinical predictors of morbidity and mortality among cancer patients.

Methods: We used data from a retrospective observational cohort of adult patients who tested positive for COVID-19 at New York-Presbyterian hospitals between March 3 and April 25, 2020. Patients with active cancer were matched 1:4 to noncancer controls on age, gender, and diabetes status. Using Kaplan-Meier curves and the log-rank test, we compared morbidity (intensive care unit admission and intubation) and mortality outcomes between cancer patients and controls. We identified demographic and clinical predictors of worse outcomes using Cox Proportional Hazard models. Hazard ratios and 95% confidence intervals were calculated for all estimates.

Results: We included 445 COVID-19 positive adult patients of whom 89 had active malignancy. Among cancer patients, the median age was 72 years, 54% were male, and 52% were non-white. Presenting symptoms were similar between cancer and noncancer groups. Nearly half of cancer patients were on active treatment including cytotoxic and immunosuppressive therapy, and 40.9% of patients received cytotoxic treatment within 90 days of admission. Both patients with and without cancer received hydroxychloroquine in similar proportions (64% vs. 65.5%), and more cancer patients received remdesivir (7.9% vs. 3.7%). Overall, age (HR 1.14; 95% CI 1.00-1.29; p=0.049), male sex (HR 1.43; 95% CI 1.04-1.96, p=0.07), dyspnea on presentation (HR 1.81, 95% CI 1.3-2.58; p=0.0005), and bilateral lung infiltrates (HR 1.94; 95% CI 1.30-2.89; p=0.001) were associated with worse outcomes. Observed complications were similar for cancer and noncancer patients, including myocardial infarction (3.4% vs. 4.2%), vasopressor requirements (24.7% vs. 26.2%), bacteremia (9% vs. 10.4%), and venous thromboembolic events (7.9% vs. 7.3%), respectively. There were no statistically significant differences in morbidity or mortality between cancer and noncancer patients (p=0.287).

Conclusion: We demonstrate that COVID-19 hospitalized patients with active malignancies have comparable morbidity and mortality to patients without cancer. In contrast to previous findings, we observed no differences in risk of ICU admission, intubation, or death between cancer and noncancer patients. Our findings suggest that active malignancy may not be a contributive risk factor in comparison to other significant comorbidities that may be more responsible for the unfavorable prognosis of COVID-19 in cancer patients. We should consider the consequences of limiting care for cancer patients on cancer-specific outcomes and mortality in the context of COVID-19.

S10-02 Using real-world data (RWD) from an integrated platform for rapid analysis of patients with cancer with and without COVID-19 across distinct health systems. Shirish M. Gadgeel[1], Michael A. Thompson[2], Monika A. Izano[3], Clara Hwang[1], Tom Mikkelsen[1], James L. Weese[2], Frank M. Wolf[3], Andrew Schrag[3], Sheetal Walters[3], Harpreet Singh[4], Jonathan Hirsch[3], Thomas D. Brown[3], Paul G. Kluetz[4]. [1]Henry Ford Health System, Detroit, MI, [2]Aurora Cancer Care, Advocate Aurora Health, Milwaukee, WI, [3]Syapse, San Francisco, CA, [4]Oncology Center of Excellence, FDA, Silver Spring, MD.

Introduction: Reports suggest worsened outcomes in patients with cancer (pts) and COVID-19 (Cov), varying by geography and local peak dynamics. We describe characteristics and clinical outcomes of pts with and without Cov.

Methods: RWD at 2 Midwestern health systems from the Syapse Learning Health Network were used to identify adults with active cancer (AC) or past history of cancer (PHC). AC pts were identified by encounters with ICD-10 code for malignant neoplasm or receipt of an anticancer agent within 12 months prior to February 15, 2020; PHC pts were identified by encounters with an active cancer code from May 15, 2015 to February 15, 2019 and no receipt of anticancer therapy within the prior 12 months. Cov was defined by diagnostic codes and laboratory results from February 15 to May 13, 2020. Comorbidities were assessed prior to February 15, 2020; hospitalizations (hosp), invasive mechanical ventilation (IMV), and all-cause mortality (M) were assessed from February 15 to May 27, 2020.

Results: We identified 800 pts with Cov (0.5%) out of a total of 154,585 pts with AC or PHC. Compared to AC pts without Cov (AC WO, 39,402), AC pts with Cov (AC Cov, 388) were more likely to be non-Hispanic Black (NHB, 39% vs. 9%), have renal failure (RF, 24% vs. 12%), cardiac arrhythmias (33% vs. 19%), congestive heart failure (CHF, 16% vs. 8%), obesity (19% vs. 14%), pulmonary circulation disorder (PCD, 9% vs. 4%), and a zip code with median annual household income (ZMI) <$30k (18% vs. 5%). Comorbidity and income were similarly distributed for PHC pts with Cov (PHC Cov, 412). Compared to PHC pts without Cov (PHC WO, 114,383), coagulopathy (coag) was more common in PHC Cov pts (10% vs. 5%). Hosp for AC Cov pts was higher than for AC WO pts (81% vs. 15%). Hosp for PHC Cov pts was also higher than for PHC WO pts (68% vs. 6%). Hosp was highest for NHB pts in both AC Cov and PHC Cov groups (88% and 72%) and for AC Cov pts in low ZMI (94% in <$30K). Pts <50 years old had hosp rates of 79% (AC Cov) and 49% (PHC Cov). IMV rate for AC Cov pts was higher than for PHC Cov pts (21% vs. 14%). Rates of IMV for AC Cov pts were highest in low ZMI (27%) and in pts with coag (36%). M by group was: AC Cov 16%; AC WO 1%; PHC Cov 11%; PHC WO 1%. Among AC Cov pts, M was higher for men (19% vs. 13%) and

pts with PCD (31%), RF (25%), or diabetes (DM, 24%); among PHC Cov pts, M was also higher for men (14% vs. 8%) and pts with coag (30%), valvular disease (27%), or PCD (24%). Increasing age, DM, RF, and PCD were associated with increased risk of M for AC Cov pts in age, race/ethnicity, and comorbidity-adjusted logistic regression; increasing age and coag were associated with M in PHC Cov pts.

Conclusion: In this rapid characterization from RWD, pts with Cov have higher rates of pre-existing cardiopulmonary/vascular and renal conditions and increased risk of hospitalization, IMV, and mortality than pts without Cov. Higher Cov risk and worse outcomes in NHB and lower-income pts suggest health care disparities. Whether these outcomes are due to comorbidities or acute sequelae merits further study, as does investigation of alternative definitions for real-world populations and outcomes.

S10-03 Increased risk of COVID-19-related death among cancer survivors. Jie Shen, Hua Zhao. Virginia Commonwealth University, Richmond, VA.

Significant variations in experience of the COVID-19 pandemic have been observed in the United States. Increased risk of COVID-19-related death has been reported among cancer survivors, but due to limited sample size in those studies, to what extent the previous cancer diagnosis may play a role in the determination of COVID-19-related death is still unclear. In this study, using aggregated real-world data extracted from TriNetx electronic medical record data from 34 hospitals around United States, we assessed the relationship between prior cancer diagnosis in the past 5 years and COVID-19-related death within one month after the diagnosis of virus contraction. A total of 24,534 patients aged 18-80 years old who contracted COVID-19 were identified from January 20th to May 4th, 2020. Among them, 3,619 were cancer survivors. In the univariate analysis, we found that cancer patients had 2.55-fold increased risk ratio (RR) of death than those without cancer (RR=2.55, 95% Confidence Interval (CI): 2.25, 2.88), although the risk was decreased but still significant (RR=1.42, 95% CI: 1.21, 1.67) after adjustment for demographics (e.g., age, gender, and race) and other pre-existing chronic diseases, including obesity, diabetes, hypertension, chronic ischemic heart disease, chronic kidney disease, asthma, and COPD. When stratified by cancer sites, significant associations were observed between respiratory and intrathoracic, oral, digestive, breast, male genital, urinary, blood, and skin cancers with COVID-19-related death in the univariate analysis. As expected, the most significant cancer site was respiratory and intrathoracic cancer with an RR of 6.49 (95% CI: 5.21, 8.07). However, after adjustment for demographics and other pre-existing chronic diseases, the significant associations remained for respiratory and intrathoracic, digestive, and blood cancers (RR=1.89, 95% CI: 1.31, 2.73; RR=1.59, 95% CI: 1.06, 2.38; RR=2.08, 95% CI: 1.51, 2.86, respectively). In addition, among cancer survivors, men were found to have higher RR of death than women (RR=1.41, 95% CI: 1.12, 1.78), but the RR did not differ between Blacks and Whites. In summary, our data show significant increased COVID-19-related death among cancer survivors. The elevated risk was particularly evident among those who had respiratory and intrathoracic, digestive, and blood cancers.

S11-01 Assessing the impact of the COVID-19 pandemic on cancer patients, survivors, and caregivers. Amy Leader, Preethi Selvan, Lisa Capparella, Rebecca Cammy, Janene Palidora, Ayako Shimada, Benjamin Leiby, Gregory Garber, Brooke Worster. Sidney Kimmel Cancer Center, Thomas Jefferson University, Philadelphia, PA.

Background: The COVID-19 global pandemic created significant and unprecedented disruptions in in medical care and social services. Cancer patients are at increased risk of COVID-19 infection due to their immunosuppressive state and may fare worse than others who are COVID-19 positive because of their aggressive underlying disease. While presumed to be substantial, the extent of the impact of the pandemic on cancer patients, survivors, and caregivers was unknown.

Methods: Between April 23, 2020 and May 19, 2020, our urban, NCI-designated cancer center launched a "COVID and Cancer" survey for cancer patients, survivors, and caregivers. The purpose of the survey was to assess disruptions to cancer care, use and perceptions of telemedicine, access to social services and cancer support programs, and psychosocial well-being. The online survey was distributed through our cancer center's email list for patient and survivor programming, via the electronic patient portal to patients in active treatment, and across our cancer center's social media platforms. Descriptive statistics reported mean scores and frequencies while bivariate statistics reported differences in outcomes by respondent characteristics. The protocol and survey were approved by our Institutional Review Board.

Results: In less than one month and in the height of the pandemic, 1,107 people completed the survey. After removing duplicate and incomplete responses, the final sample of 985 respondents included 377 (38%) patients in active treatment, 576 (56%) survivors, and 18 (2%) caregivers. Fifty-six percent (n=555) were female; the mean age of respondents was 63 years old (SD= 11.9). Seventy-two percent (n=705) of respondents had solid tumor cancers while some had either a heme malignancy (22%) or both (4%). Among the 688 respondents who needed cancer care during the pandemic, 294 (43%) reported disruptions in appointments, labs, or scans. Fewer (<5%) reported disruptions in surgery, chemotherapy, or radiation. Almost half (n=335, 49%) reported a telehealth visit during this time. Most respondents (n=612, 62%) were worried about contracting COVID-19. Cancer patients who were in active treatment were significantly more likely to be worried about contracting COVID-19, as well as accessing medication, transportation, or caregiver support, than those who were not in active treatment.

Conclusions: Disruptions in cancer care were observed during the pandemic. Cancer patients in active treatment were more worried that resources needed for their care such as medication, transportation, and caregiver support would be impacted by the pandemic. At our cancer center, we tried to mitigate some of the survey observations by developing COVID-specific patient and caregiver support programs, partnering with local agencies to provide groceries and transportation to patients, and enhancing infrastructure to assist with telehealth appointments. Cancer center support services can overcome these barriers and ensure patient care, even in a pandemic.

S11-02 Patient-reported impact of the COVID-19 pandemic on breast cancer screening, diagnosis, and treatment: A national survey. Erica T. Warner[1], Emily Restrepo[1], Christine Benjamin[2], Ricki Fairley[3], Laura Roudebush[4], Leah Eshraghi[4], Crystal Hertz[4], Simo Du[5], Laura Carfang[5]. [1]Massachusetts General Hospital, Boston, MA, [2]SHARE Cancer Support, New York, NY, [3]Sisters Network Inc., Houston, TX, [4]Dr. Susan Love Foundation for Breast Cancer Research, Encino, CA, [5]Survivingbreastcancer.org, Boston, MA.

Introduction: The COVID-19 pandemic has altered the health care delivery system. The purpose of this study was to determine the impact of the COVID-19 pandemic on breast cancer screening, diagnosis, and treatment.

Methods: Potential survey respondents were identified through partnerships with breast cancer organizations including Dr. Susan Love Foundation for Breast Cancer Research, SHARE, Survivingbreastcancer.org, Sisters Network Inc., the African American Breast Cancer Alliance, and through ResearchMatch.org. Study information was shared via social media, websites, or email. Individuals were eligible for this study if they: 1) receive routine breast cancer screening, *or* 2) are undergoing diagnostic evaluation for breast cancer, *or* 3) had ever been diagnosed with breast cancer. Participants accessed and completed the 10-15-minute REDCap survey either by emailing the research team and receiving a private survey link or by clicking a public link. The survey collected information on respondent demographics; breast cancer screening and diagnosis; the extent to which screening, diagnosis, or treatment had been changed, delayed, or canceled because of COVID-19; personal protective practices; extent of worry about financial and health implications of COVID-19; and use of telemedicine. We used descriptive statistical analyses to better understand the impact of the COVID-19 pandemic on respondents.

Results: There are currently 415 survey respondents, 404 of whom agreed to participate in the study. 46.8% (N=189) of respondents were white, 26.7% (N=108) Black, 6.7% (N=27) Asian, and 5.5% Hispanic or Latino (N=22). Most respondents were between the ages of 50 and 69 years (52.2%, N=211). 43.3% (N=175) of respondents had been diagnosed with breast cancer and, of those, 36% (N=63) were in active treatment. More than a quarter of participants (26.5%, N=107) reported delayed or canceled breast cancer care due to COVID-19; the most frequently affected care was screening mammogram, ultrasound, or MRI (97.2%, N=104). 20.6% (N=13) of women in active treatment reported delayed or canceled surgery, chemotherapy, or radiation visits. 22.3% (N=90) of respondents reported that an in-person visit was changed to a phone call or videoconference, and 39.1% (N=158) said they had discussed COVID-19 with a health care provider. 29.1% (N=51) of those with

breast cancer were worried or very worried that the COVID-19 pandemic would make it harder for them to get cancer care; among those without breast cancer, 34.9% (N=80) were worried that COVID-19 would make it harder to obtain health care, including breast cancer screening and diagnosis.

Conclusions: The COVID-19 pandemic continues to disrupt breast cancer-related care, primarily screening. Planning and coordination are necessary to ensure the timely return of these patients to care. Most participants agreed to be contacted for follow-up, allowing us to investigate the long-term effects of delayed breast cancer screening, diagnostic evaluation, and treatment on health outcomes.

S11-03 Impact of COVID-19 on breast and prostate cancer screening and early detection in a large health care provider group. Mara M. Epstein[1], Devi Sundaresan[2], Meagan Fair[2], Lawrence Garber[2], Mary Charpentier[2], Jerry H. Gurwitz[1], Terry S. Field[1]. [1]The Meyers Primary Care Institute; University of Massachusetts Medical School, Worcester, MA, [2]Reliant Medical Group, Worcester, MA.

Purpose: Massachusetts has been heavily impacted by the COVID-19 pandemic with new cases rising from 6,621 in March to 55,584 in April and 34,760 in May 2020. Most clinics and hospitals stopped performing elective procedures and reduced the volume of patients seeking in-person care starting in mid-March. This abstract quantifies the rates of mammography and PSA testing, both for screening and diagnostic purposes, as well as breast and prostate biopsies performed during the first five months of 2020 as compared to the same months in 2019 for a large health care provider group in central Massachusetts.

Methods: Men and women aged 30-85 without a history of breast or prostate cancer who were active patients of the provider group between January 2019 and May 2020 were included in this analysis. We compared the monthly rates per 1,000 people of mammography, total PSA, and breast and prostate biopsy for the period of January-May 2019 and January-May 2020 overall and by age and race/ethnicity. Procedures were identified by CPT codes in the group's electronic health record.

Results: In total, 65,312 men and 80,629 women were included in the analysis of 2019 data and 66,396 men and 82,695 women in 2020. About 70% of the population was non-Hispanic white, 3% non-Hispanic Black, 4% Hispanic, 4% Asian, and 18% other/unknown. The median age was 53 for men and 52 for women. The monthly number of mammograms declined significantly between January-May 2019 and the same months in 2020 from an average of 13.6 mammograms per 1,000 women per month in 2019 to 6.1 in March, 0.25 in April and 1.1 per 1,000 women in May 2020. Digital tomosynthesis also declined from an average of 34.7 per 1,000 women in 2019 to 14.6, 1.4, and 1.5 across March through May of 2020. The level of decline increased with age and was greatest among the oldest women, aged 75-85. Parallel declines occurred among all racial/ethnic groups. Breast biopsies declined steadily from an average of 0.9 per 1,000 women per month in 2019 to 0.8 in March, 0.4 in April and 0.1 per 1,000 women in May 2020. PSA testing was conducted in 2019 with an average of 34.4 men tested per 1,000 per month. Declines in PSA were slightly less than mammography with 17.6 tests completed per 1,000 men in March, 6.1 in April, and 11.3 in May 2020. Prostate biopsies were infrequent in 2019 with an average of 0.15 per 1,000 men per month and did not decline in 2020. Declines were slightly greater in younger men aged 30-54 and similar across racial/ethnic groups.

The greatest single-month change in test rates occurred between April 2019 and April 2020 in both women (screening mammogram rate declined 98%, tomosynthesis 96%) and men (PSA testing rate declined 83%), reflecting the peak of the COVID-19 surge in Massachusetts.

Conclusions: The observed decline in these common screening and diagnostic procedures reflects the impact of the COVID-19 pandemic on cancer prevention and early detection, signaling possible downstream effects on the timing and staging of future cancer diagnoses.

S12-01 High mortality among hospital-acquired COVID-19 infection in patients with cancer: An observational cohort study from Quebec and British Columbia. Arielle Elkrief[1], Antoine Desilets[1], Neha Papneja[2], Lena Cvetkovic[1], Catherine Groleau[2], Yahia Abdelali Lakehal[1], Layla Shbat[2], Corentin Richard[2], Julie Malo[1], Wiam Belkaid[1], Erin Cook[2], Stephane Doucet[3], Thai Hoa Tran[4], Patrice Savard[3], Kevin Jao[5], Nathalie Daaboul[6], Eric Bhang[7], Jonathan Loree[7], Wilson Miller[2], Donald Vinh[8], Nathaniel Bouganim[9], Gerald Batist[2], Caroline Letendre[10], Bertrand Routy[1]. [1]Centre de recherche de l'Université de Montréal, Montreal, QC, Canada, [2]Segal Cancer Centre, Montreal, QC, Canada, [3]Centre hospitalier de l'Université de Montréal, Montreal, QC, Canada, [4]St. Justine Hospital, Montreal, QC, Canada, [5]Sacre Coeur Hospital, Montreal, QC, Canada, [6]Charles Le Moyne Hospital, Montreal, QC, Canada, [7]BC Cancer Centre, Montreal, QC, Canada, [8]McGill University Healthcare Centre, Montreal, QC, Canada, [9]Cedar Cancer Centre, Montreal, QC, Canada, [10]Hopital Maisonneuve Rosemont, Montreal, QC, Canada.

Background: Studies suggest that patients with cancer are more likely to experience severe outcomes from COVID-19. Therefore, cancer centers have undertaken efforts to care for patients with cancer in COVID-free zones. Nevertheless, nosocomial transmission of COVID-19 in patients with cancer likely occurs, but the frequency and relevance of these events remain unknown. The goal of this study was to determine the incidence and impact of hospital-acquired COVID-19 in this population and identify prognostic factors for COVID-19 severity in patients with cancer.

Methods: Patients with cancer and a laboratory-confirmed or presumed diagnosis of COVID-19 were prospectively identified using provincial registries and hospital databases between March 3rd and May 23rd, 2020, in the provinces of Quebec and British Columbia. Patients' baseline characteristics including age, sex, comorbidities, cancer type, and type of anticancer treatment were collected. The primary outcome was incidence of hospital-acquired infection defined by diagnosis of SARS-CoV-2 5 days after hospital admission for COVID-unrelated cause. Co-primary outcomes were death or composite outcomes of severe illness from COVID-19 such as hospitalization, supplemental oxygen, intensive-care unit (ICU) admission, and/or mechanical ventilation.

Results: A total of 253 patients (N=250 adult and N=3 pediatric) with COVID-19 and cancer were identified, and the majority were residents of Quebec (N=236). Ninety patients (35.6%) received active anticancer treatment in the last 3 months prior to COVID-19 diagnosis. During a median follow-up of 23 days, 209 (82.6%) required hospitalization, 38 (15%) required admission to ICU, and 71 (28%) died. Forty-seven (19%) had a diagnosis of hospital-acquired COVID-19. Median overall survival was

shorter in those with hospital-acquired infection, compared to a contemporary community-acquired population (27 days vs. 71 days, HR 2.2, 95% CI 1.2-4.0, p=0.002). Multivariate analysis demonstrated that hospital-acquired COVID-19, age, ECOG status, and advanced stage of cancer were independently associated with death.

Conclusion: Our study demonstrates a high rate of nosocomial transmission of COVID-19, associated with increased mortality in both univariate and multivariate analysis in the cancer population, reinforcing the importance of treating patients with cancer in COVID-free zones. We also validated that age, poor ECOG, and advanced cancer were negative prognostic factors for COVID-19 in patients with cancer.

S12-02 Risk of morbidity and mortality in COVID-19 patients with cancer. Naomi Alpert, Bridget Marcellino, Joseph Rapp, Wil Lieberman-Cribbin, Emanuela Taioli. Icahn School of Medicine at Mount Sinai, New York, NY.

Introduction: Morbidity and mortality of cancer patients with COVID-19 have not been examined. The goal of this analysis was to compare the demographics and clinical characteristics of COVID-19 cancer patients to the rest of COVID-19 patients and assess whether cancer is associated with morbidity or mortality.

Methods: COVID-19-positive patients with an inpatient or emergency encounter at the Mount Sinai Health System between 03/01/20-05/27/20 were included in the analysis. Patients were compared across cancer status (noncancer, non-solid cancers, and solid cancers) on demographics and clinical characteristics. Multivariable logistic regressions were used to model the associations of cancer status with sepsis, acute venous thromboembolism, and mortality.

Results: There were 5,516 COVID-19 positive patients included, 96 (1.7%) with non-solid cancers and 325 (5.8%) with solid cancers. Those with solid cancers were significantly older (mean: 70.9 vs. 63.8 and 63.2 years) and more likely to be non-Hispanic Black (26.5% vs. 23.9% and 22.9%) than noncancer and non-solid cancers patients. Those with cancer had significantly more additional comorbid conditions (42.7% and 49.8% ≥2 comorbidities for non-solid and solid cancers, vs. 30.4% for noncancer). Platelets (mean [noncancer]: 223.8, mean [non-solid cancer]: 182.6, mean [solid cancer]: 218.3 $x10^3/\mu L$), white blood cell count (mean [noncancer]: 8.4, mean [non-solid cancer]: 6.7, mean [solid cancer]: 8.0 $x10^3/\mu L$), hemoglobin (mean [noncancer]: 13.1, mean [non-solid cancer]: 11.2, mean [solid cancer]: 12.0 g/dL), and red blood cell count (mean [non-cancer]: 4.5, mean [non-solid cancer]: 3.7, mean [solid cancer]: 4.1 $x10^6/\mu L$) were significantly lower in cancer patients, and lowest in those with non-solid cancers. After adjustment and compared to noncancer patients, those with cancer had significantly higher risk of acute venous thromboembolism (OR_{adj}: 1.77, 95% CI: 1.01-3.09) and sepsis (OR_{adj}: 1.34, 95% CI: 1.09-1.64). There was no significant difference in mortality (OR_{adj}: 1.02, 95% CI: 0.81-1.29). There was no significant difference in all outcomes for solid and non-solid cancer types.

Conclusion: COVID-19 patients with cancer, particularly solid tumors, are significantly older, with more comorbidities than those without cancer. There was no statistically significant difference in mortality for COVID-19 patients with cancer, but a significantly higher risk of thromboembolism and sepsis. Further research into the

effect that cancer treatments may have in inflammatory and immune responses to COVID is warranted.

S12-03 Thoracic cancers international COVID-19 collaboration (TERAVOLT): Small-cell lung cancer and other rare thoracic malignancies. Alessio Cortellini[1], Anne-Marie C. Dingemans[2], Oscar Arrieta[3], Javier Baena[4], Matteo Brighenti[5], Enriqueta Felip[6], Marina Chiara Garassino[7], Pilar Garrido[8], Carlo Genova[9], Federica Grosso[10], Leora Horn[11], Li-Ching Huang[12], Jan Van Meerbeeck[13], Solange Peters[14], Ernest Nadal[15], Jacobo Rogado[16], Yu Shyr[11], Marcello Tiseo[17], Valter Torri[18], Annalisa Trama[7], Heather Wakelee[19], Jennifer G Whisenant[11], Giuseppe Viscardi[7], Fabrice Barlesi[20], Sanjay Popat[21]. [1]Department of Biotechnology and Applied Clinical Sciences, University of L'Aquila, L'Aquila, AQ, Italy, [2]Erasmus University Medical Center, Rotterdam, University Maastricht, Maastricht, Rotterdam, The Netherlands, [3]Thoracic Oncology Unit and Laboratory of Personalized Medicine, Instituto Nacional de Cancerología, Mexico City, Mexico, [4]Hospital Universitario 12 de Octubre, Madrid, Spain, [5]ASST Cremona, Cremona, Italy, [6]Vall d'Hebron University Hospital, Vall d'Hebron Institute of Oncology (VHIO), Barcelona, Spain, [7]Fondazione IRCCS Istituto Nazionale dei Tumori, Milan, Italy, [8]Medical Oncology Department, Hospital Universitario Ramón y Cajal, IRYCIS and CIBERONC, Madrid, Spain, [9]IRCCS Ospedale Policlinico San Martino, Genova, Italy, [10]Azienda Ospedaliera Nazionale Santi Antonio e Biagio e Cesare Arrigo, Alessandria, Italy, [11]Vanderbilt Ingram Cancer Center, Vanderbilt University, Nashville, TN, [12]Center for Quantitative Sciences, Vanderbilt University Medical Center, Nashville, TN, [13]Antwerp University Hospital, Edegem, Belgium, [14]Oncology Department, Lausanne University Hospital, Lausanne University, Lausanne, Switzerland, [15]Thoracic Oncology Unit, Department of Medical Oncology, Catalan Institute of Oncology, Hospitalet, Barcelona, Spain, [16]Medical Oncology Department, Hospital Universitario Infanta Leonor, Madrid, Spain, [17]Medical Oncology Unit, University Hospital of Parma, Department of Medicine and Surgery, University of Parma, Parma, Italy, [18]Laboratory of Clinical Research Methodology, Oncology Department, "Mario Negri" Institute of Pharmacological Researches-IRCCS, Milan, Italy, [19]Stanford Cancer Institute, Stanford University, Stanford, CA, [20]Gustave Roussy Institute, Villejuif, Aix Marseille University, CNRS, INSERM, CRCM, Marseille, France, [21]Royal Marsden Hospital NHS Foundation Trust, London, United Kingdom.

Background: At the last update of the TERAVOLT registry, patients with thoracic malignancies and COVID-19 showed a high mortality rate (35.5% overall and 31% due to COVID-19) compared to the general population and to other solid tumors. Major determinants of mortality were age, Eastern Cooperative Oncology Group Performance Status (ECOG-PS), and previous administration of chemotherapy. No cancer-specific data are available with respect to small-cell lung cancer (SCLC) and other rare thoracic malignancies.

Methods: TERAVOLT is an international, multicenter observational registry launched to collect data on patients with thoracic malignancies diagnosed with COVID-19 infection. Risk factors for hospitalization and mortality were identified by Wilcoxon rank sum tests (continuous variables) or $\chi 2$ tests (categorical variables). Here we present the subgroup analyses of SCLC and other rare thoracic malignancies, including malignant pleural mesothelioma (MPM), thymic carcinoma/thymoma, and carcinoid/neuroendocrine lung tumors.

Results: As of June 4th, 2020, a total of 581 patients with COVID-19 and thoracic cancers have been entered; among them, 66 (11%) were SCLC, 22 (4%) were MPM, 18 (3%) were thymic carcinoma/thymoma, 12 (2%) were carcinoid/neuroendocrine lung tumors, and 442 (76%) NSCLC; 21 were an unknown type. Among SCLC patients, 54% were > 65 years old, 56% were males, 98% were current/former smokers, 31% had an ECOG-PS ≥ 2, 67% had stage IV disease, 82% were on current oncologic treatment at the COVID-19 diagnosis, and 58% were receiving chemotherapy alone or in combination with immune checkpoint inhibitors. Among other non-NSCLC patients, 56% were > 65 years old, 56% were males, 69% were current/former smokers, 24% had an ECOG-PS ≥ 2, 50% had stage IV disease, 52% were on current oncologic treatment at the COVID-19 diagnosis, and 37% were receiving chemotherapy alone or in combination with immune checkpoint inhibitors. Overall, 79.7% of the patients required hospitalization, 15.4% were admitted to an ICU, and 39.8% died (36.2% due to COVID-19). Among SCLC patients, 74.2% required hospitalization, 14.3% were admitted to an ICU, and 42.2% died (37.5% due to COVID-19). Among SCLC patients, age > 65 years old (p=0.81), gender (p=0.71), smoking status (p=1.0), ECOG-PS ≥ 2(p=0.17), disease stage of IV (p=0.37), and having received chemotherapy alone or with checkpoint inhibitors (p=0.84) were not associated with mortality.

Conclusions: This analysis confirmed that patients with thoracic malignancies have a high mortality and risk for hospitalization due to COVID-19 overall. SCLC patients showed the highest mortality rate among thoracic cancer patients.