

## Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

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### COVID-19 Genomics and Precision Public Health Weekly Update Content

- Pathogen and Human Genomics Studies
- Non-Genomics Precision Health Studies
- News, Reviews and Commentaries

#### Pathogen and Human Genomics Studies

- Variants in SARS-CoV-2 Associated with Mild or Severe ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=433](#))  
JD Voss et al, MEDRXIV, December 3, 2020

In 155,958 SARS-CoV-2 genomes, we found that models that included viral genomic variants outperformed other models (AUC=0.91 as compared with 0.68 for age and gender alone;  $p<0.001$ ). Among individual variants, we found 17 single nucleotide variants in SARS-CoV-2 have more than two-fold greater odds of being associated with higher severity and 67 variants associated with =0.5 times the odds of severity.

- Cold-chain transportation in the frozen food industry may have caused a recurrence of COVID-19 cases in destination: Successful isolation of SARS-CoV-2 virus from the imported frozen cod package surface. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=435](#))  
Liu Peipei et al. Biosafety and health 2020 Nov

After two stevedores in Qingdao, China, developed COVID-19, packages of imported frozen cod in a shipment they had handled were found to be contaminated with closely related SARS-CoV-2 of apparent European origin. The authors postulate that transport at freezing temperatures maintained virus viability during transport.

- Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=436](#))  
DE Gordon et al, Science, December 4, 2020

This study mapped the interactions between viral and human proteins for SARS-CoV-2, SARS-CoV-1, and MERS-CoV; analyzed the localization of viral proteins in human cells; and used genetic screening to identify host factors that enhance or inhibit viral infection. For a subset of interactions essential for the virus life cycle, the authors determined the cryo-electron microscopy structures and mined patient data to understand how targeting host factors may be relevant to clinical outcomes.

- A 6-mRNA host response whole-blood classifier trained using patients with non-COVID-19 viral infections accurately predicts severity of COVID-19 ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=450](#))  
L Buturovic et al, MEDRXIV, December 8, 2020

We developed a blood-based generalizable host-gene-expression-based classifier for the severity of viral infections and validated it in multiple viral infection settings including COVID-19. We selected 6 host mRNAs and trained a logistic regression classifier with a training AUROC of 0.90 for predicting 30-day mortality in viral illnesses. In validation cohorts the locked 6-mRNA classifier had an AUROC of 0.91.

#### Non-Genomics Precision Health Studies

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