**Results.** Thirty seven of 70 (53%) of patients received vancomycin over 61 courses with a mean duration of 8 days; 14 (23%) of these courses were with neutropenic fever. No indication was documented by the provider for 21 (34%) vancomycin courses (Figure 1). Almost half of all courses given for neutropenic fever did not meet guideline indications (Figure 2). Adverse events occurred in 19 (31%) of vancomycin courses, including 11 (18%) associated with acute kidney injury.

Vancomycin was associated with reduced relative abundance of organisms correlated with reduced risk of subsequent severe acute graft vs. host disease and *Clostridium scindens*, an organism protective against *C. difficile* infection (CDI) (Figure 3, in bold). Adverse events occurred in 1 in 3 courses of vancomycin. Vancomycin correlated with microbiome changes which have been associated with increased risk for aGVHD and CDI.

**Background.** There is little known about the dynamics of the infant virome and how it relates to healthy growth and development. This study will establish the baseline gut virome and observe dynamic changes in a cohort of infants from birth to 3 years old. We hypothesize that changes in the gut virome will impact growth and immune development.

**Methods.** One hundred and twenty-eight infants were enrolled in the Stanford’s Outcome Research in Kids (STORK) cohort prior to 36 weeks gestation. Stool samples were collected at an average of 90, 134, 162 days old/infant. Baseline data were collected at birth (height, weight, length, Apgar’s score, antibiotic use) and health surveys were collected weekly. Stool samples (n = 477) were extracted using the EZ1 Viral Kit (Qiagen). Libraries were prepared using the Nextera XT Kit (Ilumina) and sequenced on an Illumina HiSeq 2500 on rapid mode (150/150 bp paired-end sequencing). Datasets were analyzed using SURPI; a bioinformatic pipeline for pathogen detection.

**Results.** A subset of the infants were tested (n = 27), 54% of which were male. The infants were 62% white, Hispanic 26% white, non-Hispanic, 8% Asian, and 4% other. Seventy-five stool samples—sequenced at an average depth of 22 million reads—were analyzed from the 27 infants. Vertebrate viruses (42.8%) and phages (45.2%) represented the majority of the viral reads, while the other reads were invertebrates, plants, or protozoa (12%). Virome abundance, richness, and diversity were 5.5e+04 species reads per million, 55.5 on the Chaos Richness scale, and 1.45 on the Shannon Diversity Index respectively, with values increasing as the infants aged. The phage families most commonly identified were Myoviridae, Podoviridae, and Siphoviridae. There were seven different human viral families observed: Adenoviridae, Astroviridae, Caliciviridae, Parvoviridae, Picornaviridae, Reoviridae, and Anelloviridae. Five infants were documented to have cold symptoms within 7 days of sampling, they were found to have mas- tandenovirus C (1), marmastovirus 1 (1), bocavirus (3). Three infants were documented to have caliciviruses (2) and adenovirus (1); however, no symptoms were reported.

**Conclusion.** This study will comprehensively characterize the development of the human virome and monitor its effect on growth and immune development.

**Disclosures.** All authors: No reported disclosures.