New norovirus classified as a recombinant GII.g/GII.1 causes an extended foodborne outbreak at a university hospital in Munich.

Noroviruses are among the most prevalent causative agents for gastroenteritis worldwide. The low infectious dose, its stability in the environment, and its genetic variability enable the virus to cause outbreaks, especially in health care facilities and other similar settings. Genotype II.4 has been most prevalent over the last years. To characterize an extended norovirus outbreak at a university hospital in Munich, Germany, molecularly and epidemiologically. The outbreak affecting more than 100 persons within 3 days was monitored by real time PCR. The rapid onset indicated a food-borne outbreak. Rigorous hygienic measures, including disinfection procedures and closure of wards helped contain the outbreak within 6 days. A 2193 nt sequence covering polymerase (825 nt) and capsid gene (1388 nt) was characterized from 4 specimens derived from different wards and the catering facility. Our polymerase sequences were classified GII.g, whereas the capsid belonged to GII.1. Recombination analysis revealed a putative breakpoint at a typical location. Our sequenced region clustered with GIIg/GII.1 sequences first detected in Hungary, Belgium, and the US in 2010. p-Distances on nucleic acid level were 0.18 and 0.21, respectively. Our data establish a novel strain classified as GII.g/GII.1 as the causative agent for an extended outbreak.