Fluids contained in the basalt-hosted deep subsurface of the world’s oceans represent one of the most inaccessible and understudied biospheres on earth. Recent improvements in sampling infrastructure have allowed us to collect large volumes of crustal fluids (~$10^4$ L) from Circulation Obviation Retrofit Kits (CORKs) placed in boreholes located on the eastern flank of the Juan de Fuca Ridge. We detected viruses within these fluids by TEM and epifluorescence microscopy in samples collected from 2010 to 2014. Viral abundance, determined by epifluorescence counts, indicated that concentrations of viruses in subsurface basement fluids (~$10^5$ ml$^{-1}$) are lower than the overlying seawater, but are higher in abundance than microbial cells in the same samples. Analysis of TEM images revealed distinct viral morphologies (rod and spindle-shaped) that resemble the morphologies of viral families infecting archaea. There are very few, if any, direct observations of these viral morphologies in marine samples, although they have been observed in enrichment cultures and their signature genes detected in metagenomic studies from hydrothermal vents and marine sediments. Analysis of metagenomes from the JdFR crustal fluids revealed sequences with homology to bacterial viruses from families podoviridae, myoviridae and siphoviridae; and archaeal viruses from the rudiviridae, bicaudaviridae and fuselloviridae. Prokaryotic communities in fluids percolating through the basaltic basement rock of the JdFR flank are distinct from those inhabiting the overlying sediments and seawater. Likewise, our data support the idea that the viral assemblage in these fluids is distinct from viral assemblages in other marine and terrestrial aquatic environments. Our data also suggest that viruses contribute to the mortality of deep subsurface prokaryotes through cell lysis, and viruses may alter the genetic potential of their hosts through the processes of lysogenic conversion and horizontal gene transfer.