Viruses are the most abundant life-like entities on the planet Earth. However, there is not currently an effective approach that sufficiently detects ‘unknown’ viruses in any given environment. It is estimated that as little as 0.1% of the Earth’s microorganisms have been cultured, and that as little as 0.1-0.01% of viruses have been discovered. Recently, the discovery of CRISPRs (Clusters of Regularly Interspaced Short Palindromic Repeats) has led us to believe they may be an effective way to discover new viruses. It has been proposed that the spacer sequences between the direct repeat units of the CRISPR loci are derived from viruses and function as guide sequences to protect the cell from viral infection. A very limited number of CRISPR-spacer sequences match to known viral genomes while others have no matches to other sequences in the public databases. We hypothesize these non-matching CRISPR spacer sequences are to novel viruses that we have not yet isolated. Therefore, we believe that the cellular CRISPR loci serve as a record of the viruses that have replicated within the cell. We have designed a microarray utilizing CRISPR-spacer sequences as probes to search for new archaeal viruses present within the high temperature (>80°C) acidic (pH<4) environments of Yellowstone thermal features. We have been able to show this microarray approach can detect viral sequences directly from environmental samples, and this technology may be extremely useful for samples in which culturing may not be possible. We have further demonstrated that this microarray approach can be used to examine temporal changes in viral populations in the environment. We have concluded that the CRISPR microarray platform provides a high-throughput approach to screen environments for new viruses.