ABSTRACT

Disclosed herein are methods of extracting genetic material from a diverse population of one or more types of microbes in a sample. Microbes can be prokaryotes or eukaryotes and may include bacteria, archaea, fungi, protozoa, helminths, parasites, viruses, phages, and others. Extraction may be from a single sample and subsequent identification may be through a molecular method such as qPCR, PCR, RFLP, SSCP, allele specific PCR, targeted sequencing, pull down sequencing, whole shotgun sequencing, or other methods. Also provided are methods that include extracting nucleic acid molecules from a variety of organisms such as fungi (*i.e.*, Saccharomyces spp.), animal cells (Bos taurus), plants (*e.g.*, Hordeum vulgare) from the gut of a human subject, performing a metagenomics analysis therefrom, and determining a probiotic treatment or dietary guidance for the subject based on the metagenomics analysis.

Figure 1