Soil represents a massive reservoir of active carbon and climate models vary dramatically in predicting how this carbon will respond to climate change over the coming century. A major cause of uncertainty is that we really still don’t understand the microorganisms that dominate the soil carbon cycle. The vast majority of soil microbes remain uncultivated and the diversity of organisms and enzymes that participate in the carbon cycle is staggeringly complex. We are developing a new toolbox for exploring the carbon cycle and the metabolic and ecological characteristics of uncultivated microorganisms. We have employed high-resolution nucleic acid stable isotope probing to characterize carbon cycling dynamics in soil. The approach allows us to track multiple 13C-labeled substrates into thousands of microbial taxa over time. We identify several major lineages of uncultivated microorganisms (including Verrucomicrobia and Chloroflexi) that participate in cellulose metabolism and are found widely in soils. Furthermore, isotopic labeling of nucleic acids enables community genomics and permits genome binning for a majority of these cellulolytic microorganisms. We also describe unexpected dynamics of carbon metabolism with different microbial taxa exhibiting characteristic patterns of substrate incorporation indicative of distinct ecological strategies. The data we describe allows us to characterize the in situ activity of novel microorganisms and they provide a basis for beginning to understand how the physiological traits of discrete microorganisms sum to govern the complex responses of the soil carbon cycle.