

**ABSTRACT** The U.S. Department of Energy (DOE) Joint Genome Institute's (JGI) Sequencing Technologies group is committed to the generation of high-quality genomic DNA sequence to support the DOE mission areas of renewable energy generation, global carbon management, and environmental characterization and clean-up. The U.S. DOE JGI was established in 1997 in Walnut Creek, CA, to unite the expertise and resources of five national laboratories— Lawrence Berkeley, Lawrence Livermore, Los Alamos, Oak Ridge, and Pacific Northwest – along with HudsonAlpha Institute for Biotechnology. JGI is operated by the University of California for the U.S. DOE.

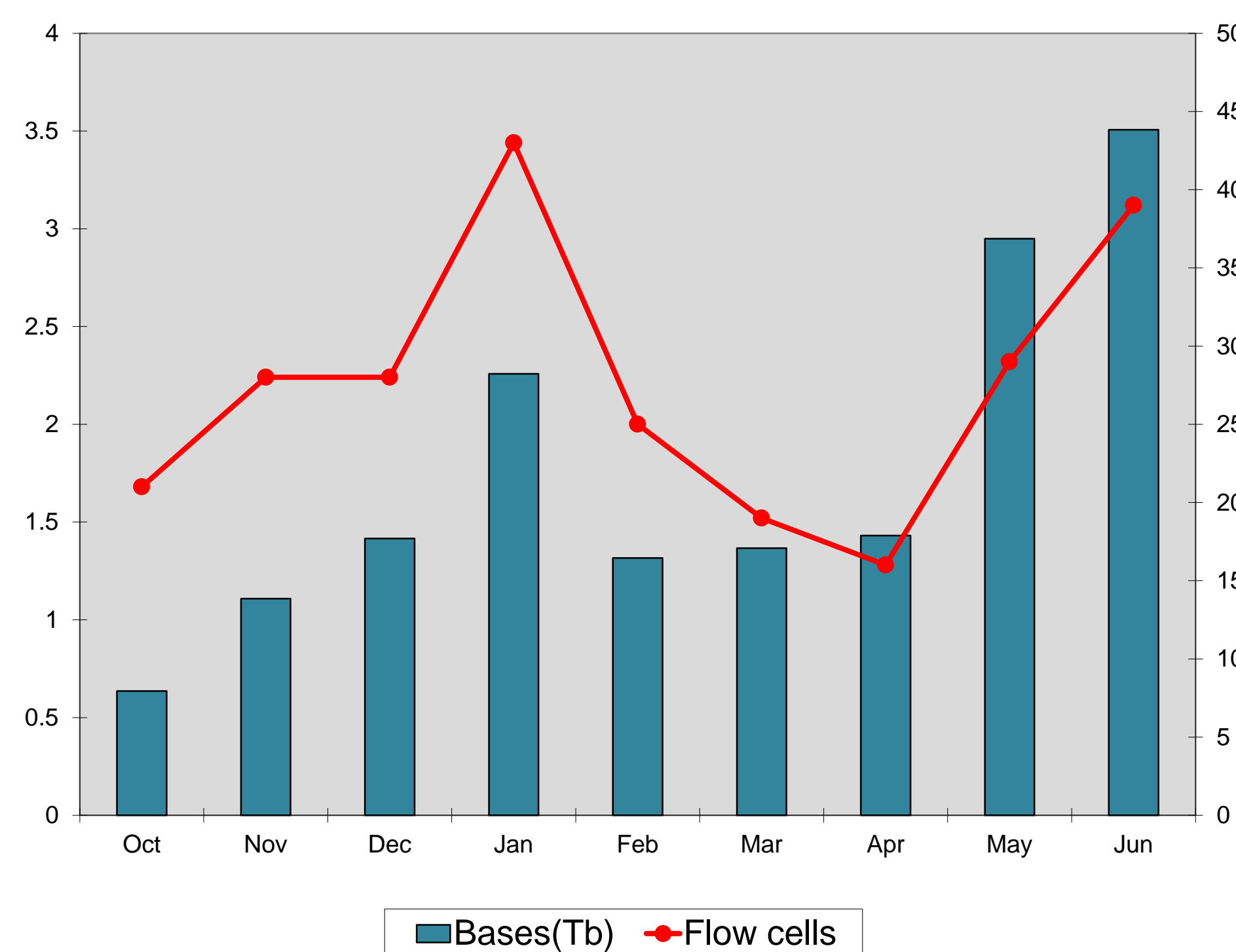
## Production

In FY11, the Illumina Sequencing Platform team has undergone many changes. We have been in the process of transferring our projects from GAIIx runs to HiSeq2000 runs. We began the year with 12 GAIIx's and 2 HiSeq2000's. We now have 5 GAIIx's and 8 HiSeq2000's at our disposal. The recent launch of the HiSeq v3 reagents and updated software has increased our throughput per run, and improved coverage per lane. This has led to the increased demand for pooled libraries and multiplex runs.

### JGI Production Instruments

5 GAIIx Analyzers + PEM | 8 HiSeq2000 Sequencers | 6 cBot Cluster Stations

#### FY11 Production Throughput - GA and HiSeq



#### FY11 Throughput Events:

##### Oct 2010:

2 HiSeq2000's added

##### Nov 2010:

Multiplex runs introduced;  
3 GAIIx's removed and  
3 HiSeq2000's added

##### Jan 2011:

HiSeq v2 TruSeq reagents  
launched

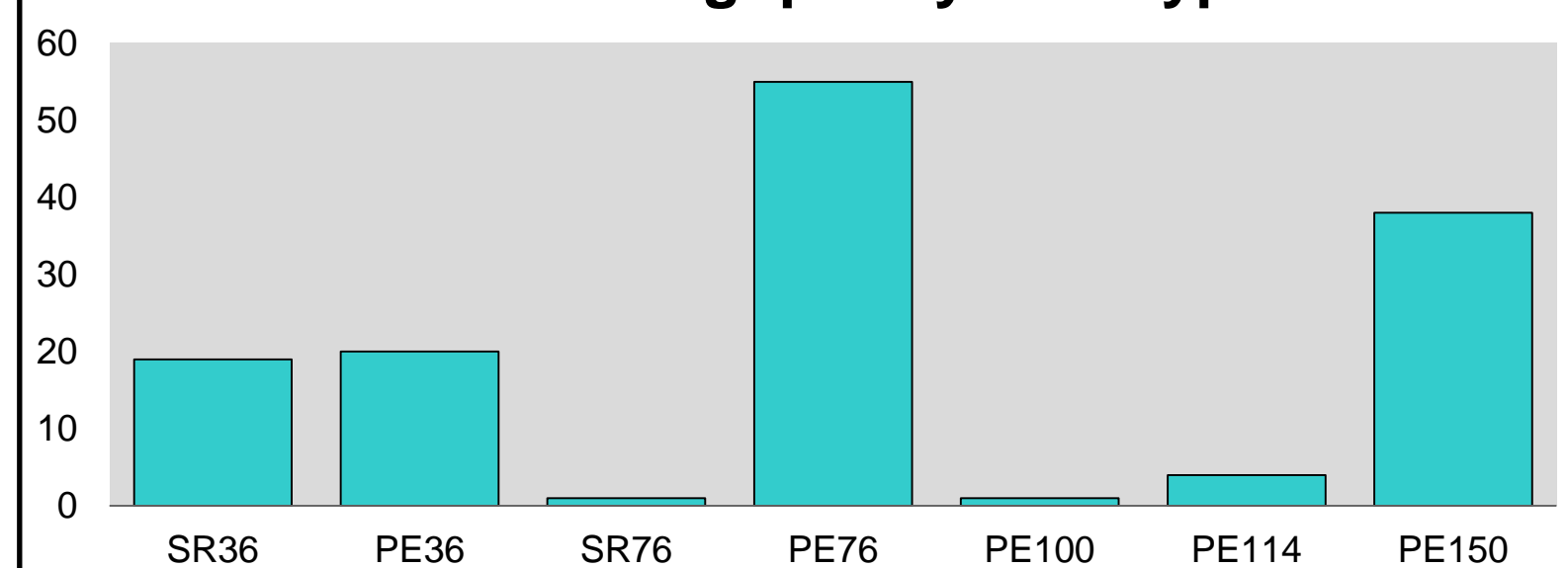
##### Mar 2011:

4 GAIIx's removed and  
3 HiSeq2000 added

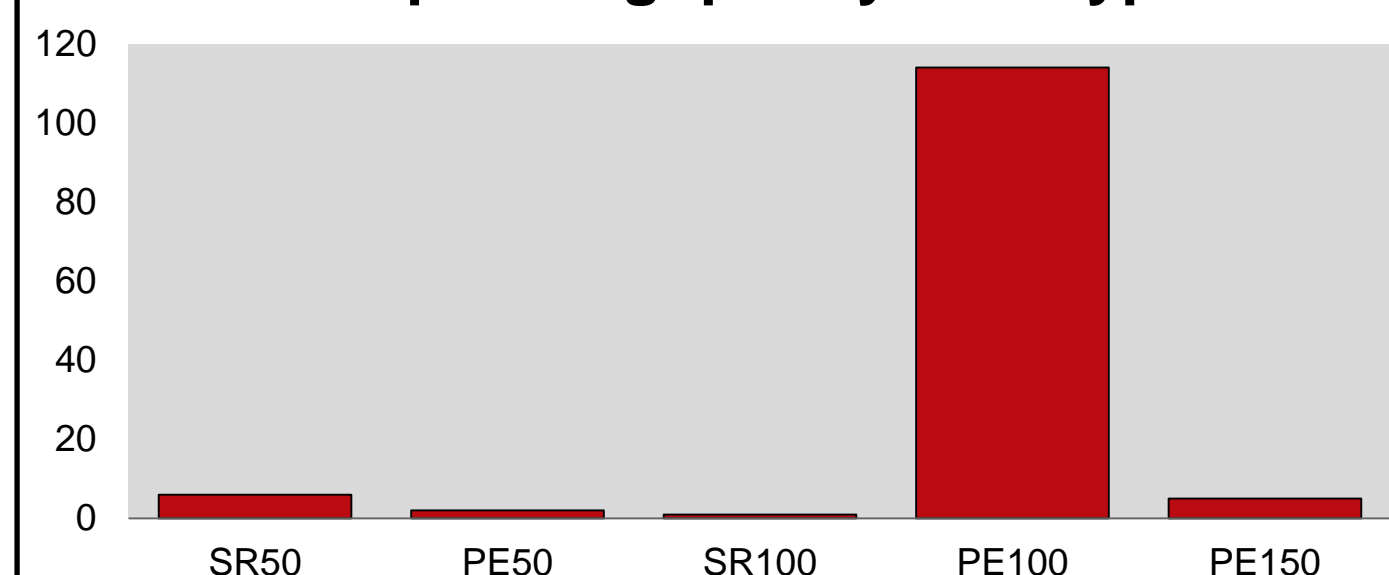
##### July 2011:

HiSeq v3 reagents introduced

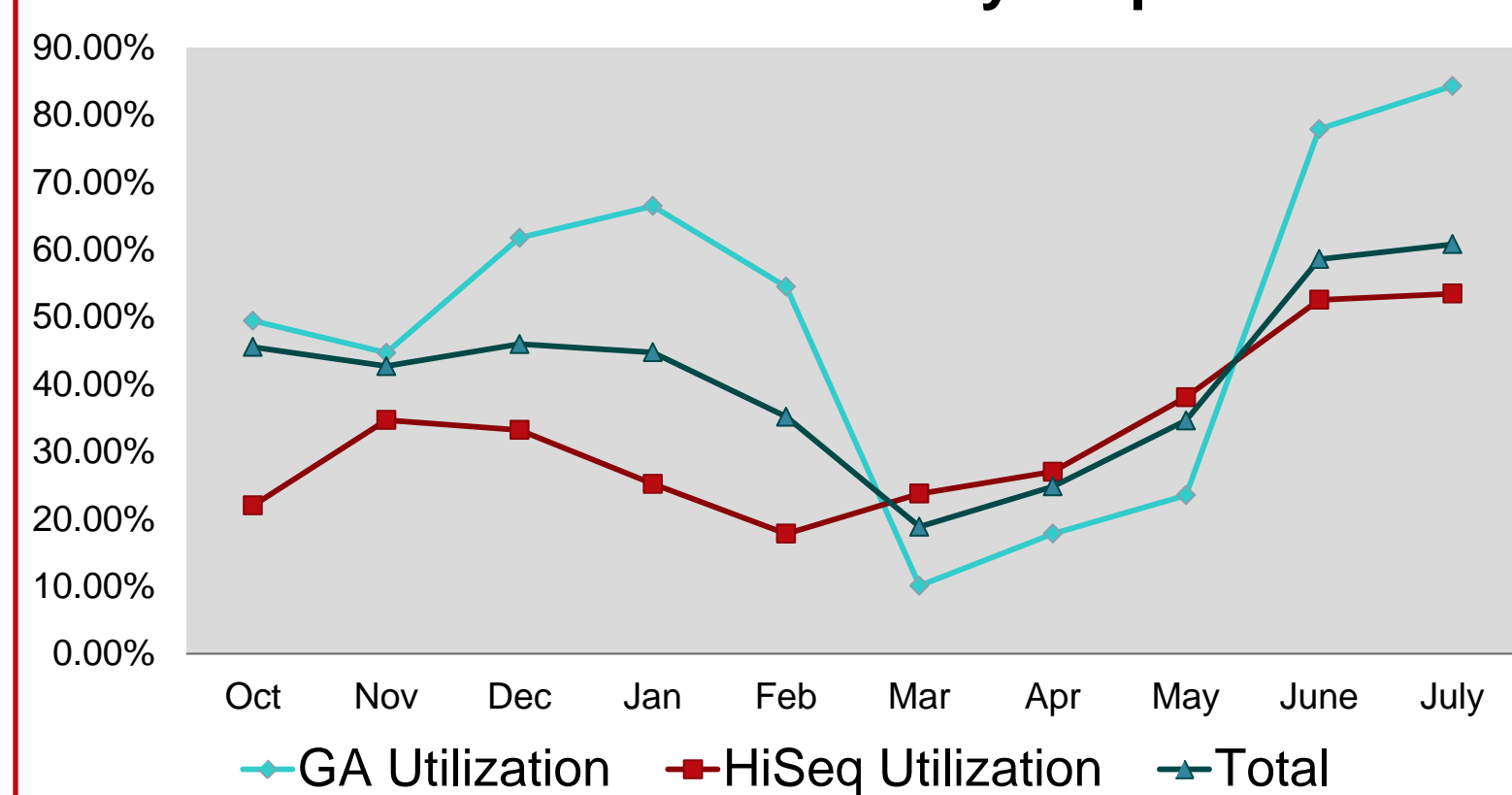
#### GA Throughput by Run Type



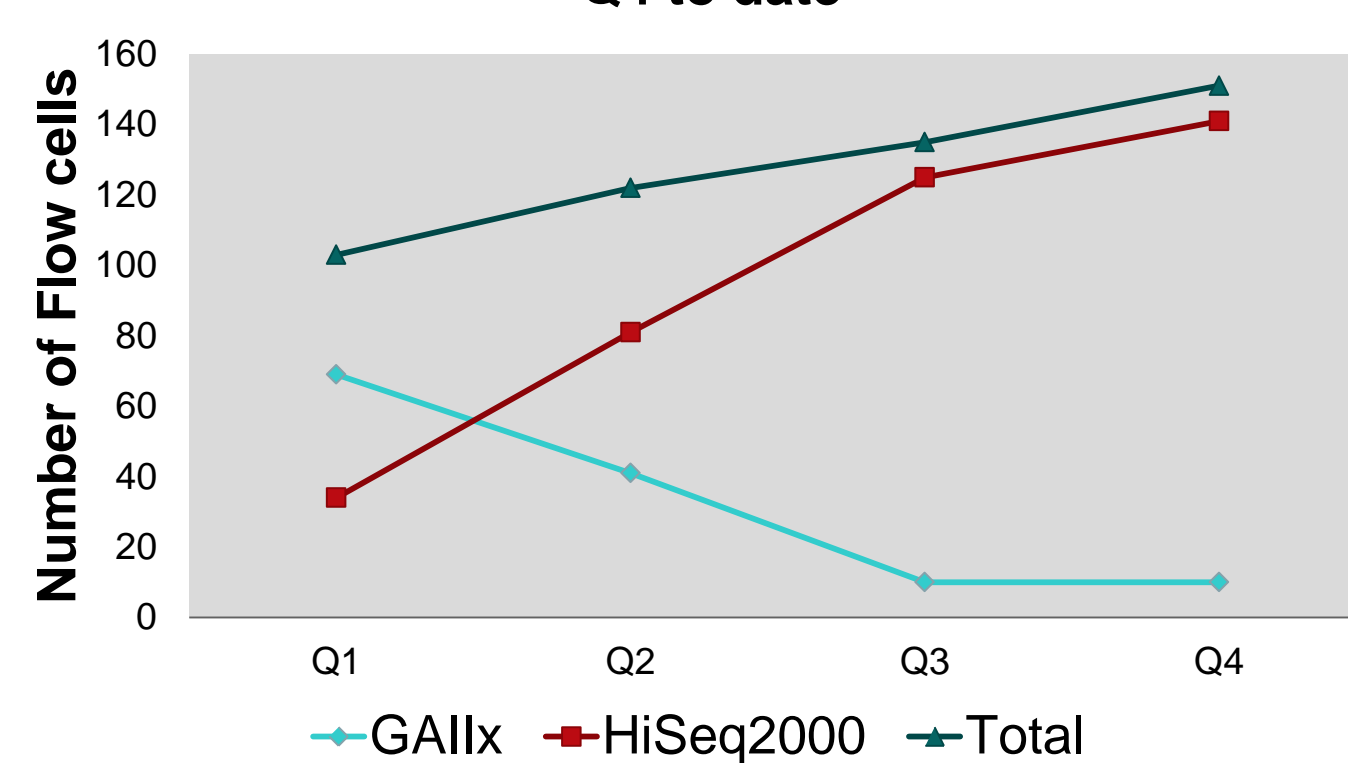
#### HiSeq Throughput by Run Type



#### FY11 Illumina Utilization by Sequencer



#### FY11: Transition from GA to HiSeq \* Q4 to date



## What types of DNA do we sequence and why?

JGI engages users from the National Laboratory system, academic institutions, and private industry to perform sequencing projects that directly relate to the DOE Office of Biological and Environmental Research's missions in alternative energy, global carbon cycling, and bioremediation. JGI's sequencing portfolio is drawn from its user programs, including the Community Sequencing Program and the new Bioenergy Research Centers, as well as targets chosen by DOE to meet programmatic objectives.

### PLANT



One of the world's leading grain crops, sorghum is also an important model for tropical grasses of worldwide importance with a collective minimum economic impact of \$69 billion U.S. per year. Sorghum is representative of the tropical grasses in that it has "C4" photosynthesis, using a complex combination of biochemical and morphological specializations resulting in more efficient carbon assimilation at high temperatures.

Photo: Daniel George Döhne

### FUNGAL



*Trichoderma reesei* is an industrially important cellulolytic filamentous fungus. In light of *T. reesei*'s capacity to secrete large amounts of cellulases and hemicellulases, the DOE is funding research into developing *T. reesei* as a host to produce low-cost enzymes for the conversion of plant biomass materials into industrially useful bioproducts such as sugars and bioethanol.

Photo: Irma Salovuori, VTT Biotechnology

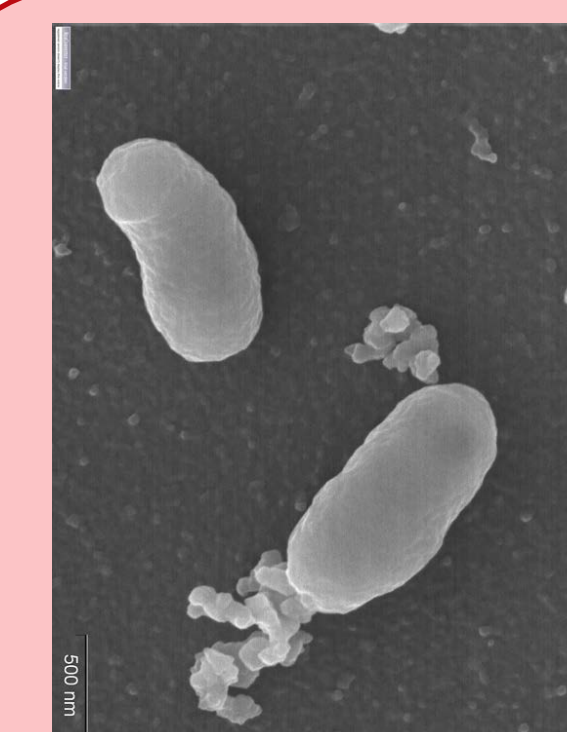
### METAGENOME



Microorganisms in permafrost soil are largely responsible for cycling the carbon that is currently trapped. As the permafrost thaws, the trapped organic matter becomes accessible for microbes to degrade, releasing greenhouse gases, namely methane, as a byproduct. Therefore, knowledge of microbial carbon cycling processes is crucial for understanding and eventually reducing negative global impacts due to thawing of permafrost soils. Little is currently known about the identities or functions of microorganisms in permafrost soils. Sequencing will provide a metagenomic analysis of permafrost soil communities that are undergoing change. As this data is tied to a large global change research effort, it could be one of the first studies of its kind to link genomes to large scale climate change in northern ecosystems.

Photo: USGS Soil Carbon Research

### MICROBIAL



*Burkholderia* strains are involved in carbon cycling and contribute to a healthy, carbon dioxide-fixing environment by fixing atmospheric nitrogen and helping to counter plant pathogens. The bacteria are also known for their ability to break down pollutants in soil and water such as the organic chemical trichloroethene. The abundance of these bacteria in nature suggests they have a larger role in maintaining the biogeochemistry of the planet than is currently unknown.

Photo: US DOE-Office of Science