



Quarterly Newsletter: Fall 2021

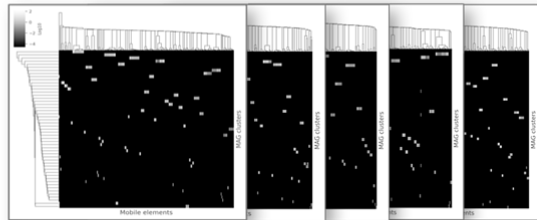


A NEW DIMENSION OF THE METAGENOME



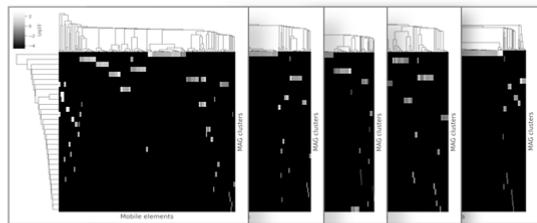
Make the most of your data with the latest product features from Phase Genomics

PHAGE



MICROBIAL
HOSTS

PLASMIDS



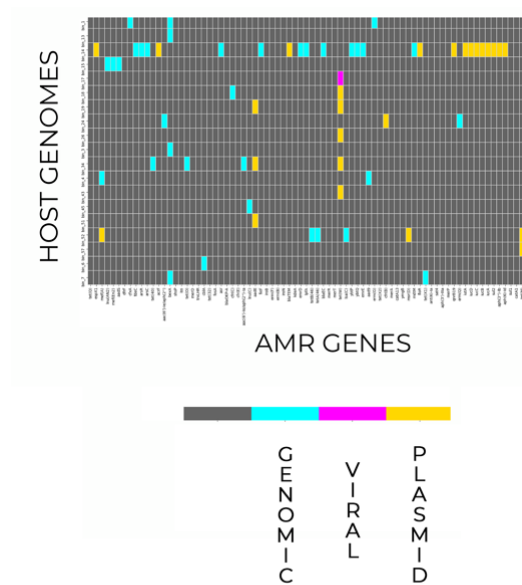
MICROBIAL
HOSTS

D0 D1 D2 D3 D4

ADD A NEW DIMENSION TO MOBILE ELEMENT ANALYSIS
WITH THE PROXIMETA™ PLATFORM

Unlock a new dimension in the study of antibiotic resistance genes, reservoirs and mechanisms

Our ProxiMeta™ Metagenome Deconvolution Platform provides a powerful tool for studying AMR. The proximity ligation library prep captures fragments of DNA that are co-located in cells *in vivo*. Computational integration with metagenomics enables accurate, strain-level assignments of MGEs and ARGs with their hosts which can be tracked over time.



Dive deeper into your data

Identify and distinguish genomic, viral, and plasmid AMR genes within metagenomic samples and assign them to their hosts.

MORE ON OUR SITE

Catch us at a Conference

- [American Society of Human Genetics](#) (October 18-22)
 - [Genome Startup Day: Inside the Microbiome Industry](#) (October 27)
 - [Microbiome and Cancer Symposium](#) – Univ. of Minnesota (November 19)
 - [International Plant and Animal Genome XXIX](#) – San Diego, CA (January 8-12)
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Research Highlights



Phase Genomics Included in Over 100 Publications

Below are some of the publications that were released this quarter.

WATCH THE VIDEO

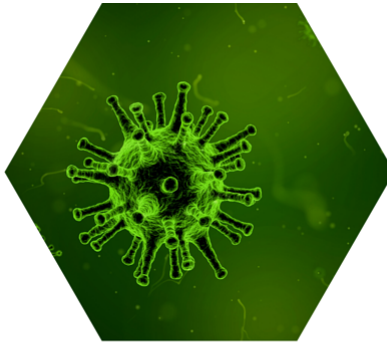
Metagenomics & Microbiology



Danofloxacin Treatment Alters the Diversity and Resistome Profile of Gut Microbiota in Calves



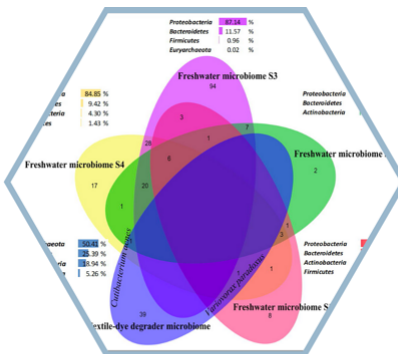
The stem rust fungus *Puccinia graminis* f. *sp. tritici* induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation



Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants



Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with *Salmonella enterica* Serovar Heidelberg

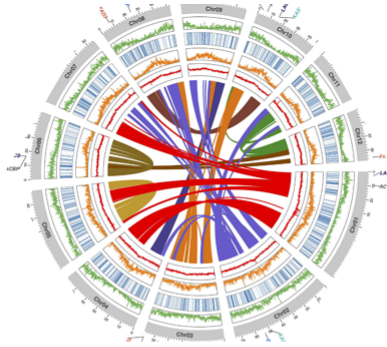


Hi-C deconvolution of a textile dye-related microbiome reveals novel taxonomic landscapes and links phenotypic potential to individual genomes



Novel canine high-quality metagenome-assembled genomes, prophages, and host-associated plasmids by long-read metagenomics together with Hi-C proximity ligation

Plant & Animal Genomics



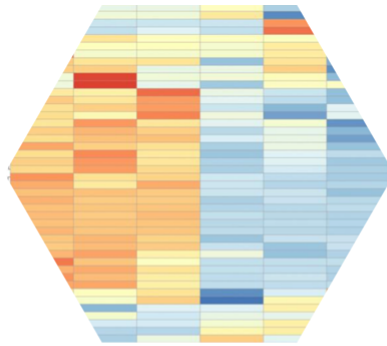
Genomic Resources to Guide Improvement of the Shea Tree



The *Gossypium anomalum* genome as a resource for cotton improvement and evolutionary analysis of hybrid incompatibility



Chromosome-scale assembly and evolution of the tetraploid *Salvia splendens* (Lamiaceae) genome



Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*



Genome assembly of two nematode-resistant cotton lines (*Gossypium hirsutum* L.)



Chromosome-level *Thlaspi arvense* genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates



A Chromosome-Scale Assembly of the Wheat Leaf Rust Pathogen *Puccinia triticina* Provides Insights Into Structural Variations and Genetic Relationships With Haplotype Resolution

MORE PAPERS

Have a project in mind?

Contact Us

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