



PHASEBOOK

Quarterly Newsletter: Spring 2022



Expanding Possibilities in Precision Medicine



New Insights with Ultra-long-range Sequencing

Phase Genomics is expanding into the clinical research and oncology space, featuring ultra-long-range sequencing technology that opens doors into precision oncology and reproductive genomics. Check out the brochures recently added to our site for details on the technology that is unlocking the wealth of genomic structure information stored in FFPE samples via a cost-effective and scalable NGS-based assay.

ONCOTERRA™ REPORT

PATIENT INFORMATION		SPECIMEN INFORMATION		PROVIDER INFORMATION	
Accession ID	657836	Specimen ID	309110	Ordering Physician	Jenna Johnson, MD
Name	Loren Smith	Type	FFPE	Organization	Comprehensive Cancer Center University of Medicine
Date of Birth	07/20/69	Collection Date	03/22/2022		

RESULT SUMMARY

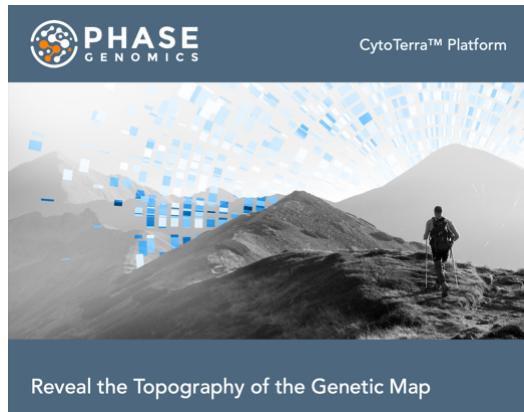
CHROMOSOME NUMBER	SEX CHROMOSOME COMPLEMENT	DETECTED ABNORMALITY
46	XY	de(11)q(24.2),de(11)q(24.3q5)

DETAILED RESULTS

FIGURE	CHANGE	ISCN	GENOMIC COORDINATES	GENE
Figure 1A	deletion	de(11) (q4.2)	chr11:124100000-127250000	ACRV1, CCDC15, CIOH, CHIK1, DOPS, DDX25, ED4, ESAM, FAM118B, FEZ1, FOXRED1, HEPACAM, HEPN1, HYL531, KIRREL, MSAINT2, NGRN, OR10D3, OR10D5, OR10D6, OR10D7, OR10D8, OR10D9, OR10D10, PANK3, PATE1, PATE2, PATE1, PATE4, PNOX2, PUSS, ROBO3, ROBO4, RPL34, SIAE, SLC37A2, SPAT1, SPPA, STAGA1, STTJA, TBRG1, TIRAP, TMEM12B, USGR2, VNR2, YWAL
Figure 1B	deletion	de(11) (q24.3q5)	chr11:128550000-133600000	ADAMTS15, ADAMTS6, APLP2, ARID1A, ARID5, ETS1, ELL, KCNQ1, SCN1A, SPRR1, NTM, OFC1, PIPR1, PRKDC, SNTA1, STTJA, TMEM149, TP53BP1, ZBTB44

ANALYSIS

This section contains several panels of genomic data. At the top left is a track viewer showing multiple chromosomes with various genetic features. To the right of this are two main plots: a scatter plot of genomic coordinates with a red diagonal line and a smaller scatter plot below it. Below these are two line graphs showing numerical values across a range of positions.



Learn more about the [OncoTerra](#) and [CytoTerra](#) platforms.

Catch us at a Conference

We are looking forward to a safe return to in-person events to celebrate the achievements researchers have been making around the globe. Phase Genomics is dedicated to making our presence at these events as safe as possible and will be adapting to the most recent safety guidelines and regulations.

[Life Science Innovation Northwest](#) – Seattle, WA (April 20-21)

[Digestive Disease Week](#) – San Diego, CA (May 21-24)

[Advances in Genome Biology & Technology](#) – Orlando, FL (June 6-9)

[American Society for Microbiology: Microbe](#) – Washington, DC (June 9-13)

[Sequencing to Function: Analysis & Applications for the Future](#) – Santa Fe, NM
(June 21-23)

Stand with Ukraine

We are supporting the humanitarian effort in Ukraine because it is the right thing &

because it is personal - several team members have family residing in the country. Phase Genomics matched our team's contributions to support those suffering. We encourage other biotech companies to do the same.



Charities we support

[Razom for Ukraine](#)

[Voices of Children](#)

[UN Humanitarian Crisis Fund](#)

Recent Research



Physical separation of haplotypes in dikaryons allows benchmarking of phasing accuracy in Nanopore and HiFi assemblies with Hi-C data



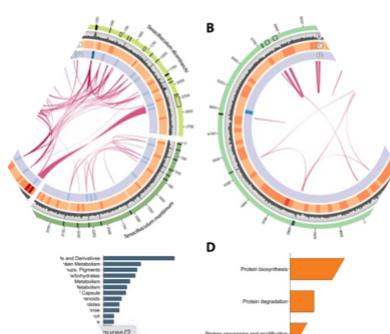
Novel canine high-quality metagenome-assembled genomes, prophages and host-associated plasmids provided by long-read metagenomics together with Hi-C proximity ligation



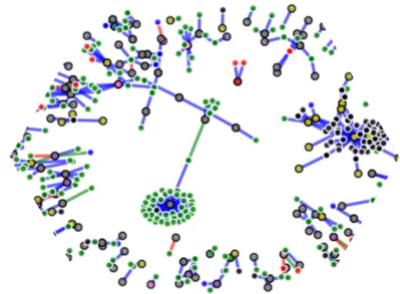
A Chromosome Scale Assembly of
an Australian *Puccinia striiformis* f.
sp. *tritici* Isolate of the PstS1 Lineage



A chromosome-level, fully phased genome
assembly of the oat crown rust fungus *Puccinia*
coronata f. sp. *avenae*: a resource to enable
comparative genomics in the cereal rusts



Proximity ligation strategy for the
genomic reconstruction of microbial
communities associated with the
ectoparasite *Caligus rogercresseyi*



Generating lineage-resolved,
complete metagenome-assembled
genomes from complex microbial
communities



Genomic signatures of high-altitude
adaptation and chromosomal
polymorphism in geladas



Phylogenomics of the genus *Glycine*
sheds light on polyploid evolution
and life-strategy transition



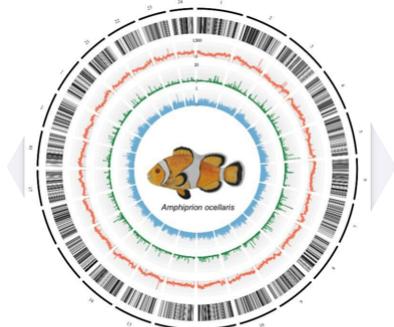
Temporal matches and mismatches
between monarch butterfly and
milkweed population changes over
the past 12,000 years



Aphidinae comparative genomics
resource



Buxus and Tetracentron genomes
help resolve eudicot genome history



A chromosome-scale genome assembly of the false clownfish,
Amphiprion ocellaris



Chromosome-level de novo genome assembly of *Telopea speciosissima* (New South Wales waratah) using long-reads, linked-reads and Hi-C

MORE PAPERS

Have a project in mind?

Contact Us

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