Exploring the fluid gene space of plants using the Gramene comparative genomics and pathways resource

The project is supported by NSF IOS-1127112 and USDA-ARS 001-8062-505 002

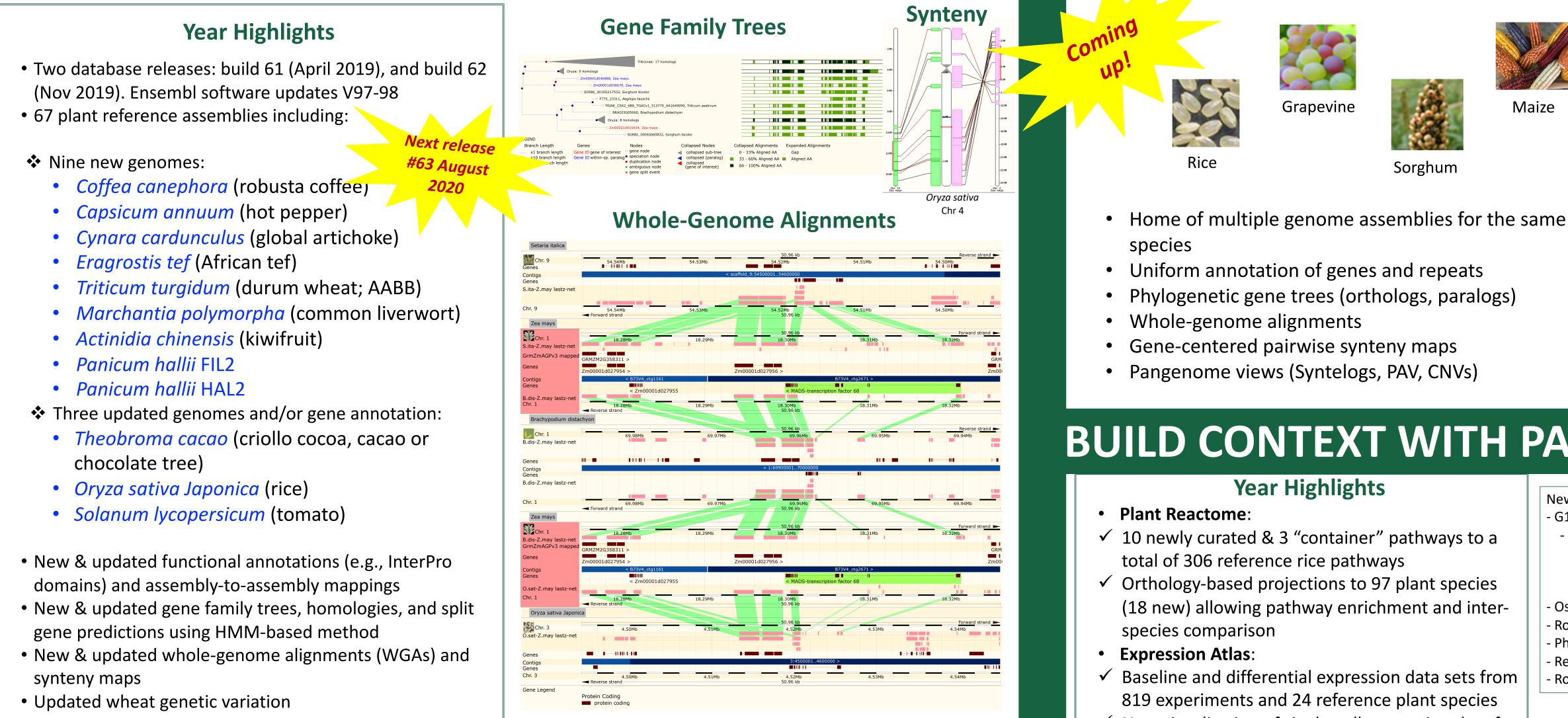
Marcela Karey Tello-Ruiz¹, Andrew Olson¹, Sharon Wei¹, Justin Preece², Parul Gupta², Sushma Naithani², Yinping Jiao¹, Bo Wang¹, Kapeel Chougule¹, Sunita Kumari¹, Vivek Kumar¹, Peter D'Eustachio³, Bruno Contreras⁴, Irene Papatheodorou⁴, Pankaj Jaiswal², Doreen Ware^{1,5}

¹Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA; ²Oregon State University, Corvallis, OR, USA; ³NYU School of Medicine, New York, NY, USA; ⁴EMBL-EBI, Hinxton, UK, ⁵USDA ARS NAE Robert W. Holley Center for Agriculture and Health, Ithaca, NY, USA

Gramene is developed in collaboration with Ensembl Plants, and leverages the Ensembl & Reactome platforms

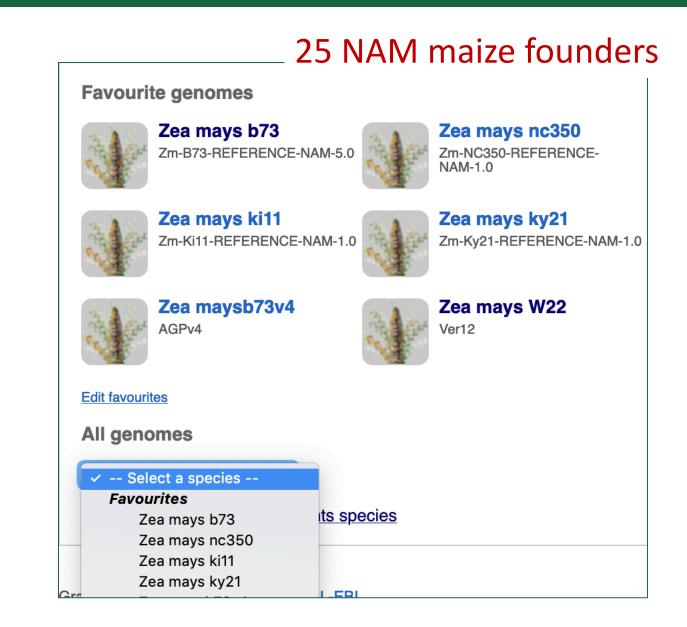
A BOUNTY OF GENOMES

(www.gramene.org)



PAN-GENOMICS: NAVIGATE MORE LINES

Maize

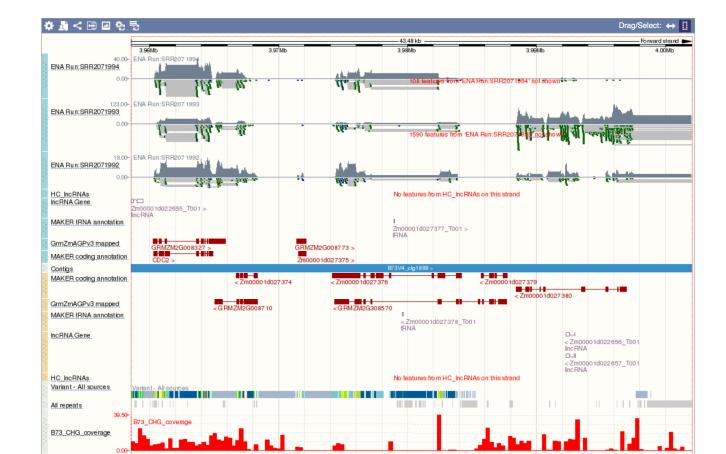


What's New in the Upcoming Release #63

- 19 new genomes including apple, clementine, cherry, pineapple, watermelon, cantaloupe, pistachio, almond, olive tree, and cannabis.
- Over 35 million new genetic variants:
 - Bread wheat (Axiom 35K and 820K arrays from CerealsDB)
 - Durum wheat (35K, 90K, 820K and TaBW280K arrays)
 - Apple (10.6M SNPs)
 - Sunflower (11.8M SNPs)

Do you want to see other plant genomes or datasets added? Take our survey! https://bit.ly/gramene

RNA-Seq Data from Public Track Hub Registry



- Uniform annotation of genes and repeats
- Phylogenetic gene trees (orthologs, paralogs)
- Gene-centered pairwise synteny maps
- Pangenome views (Syntelogs, PAV, CNVs)

BUILD CONTEXT WITH PATHWAYS & EXPRESSION

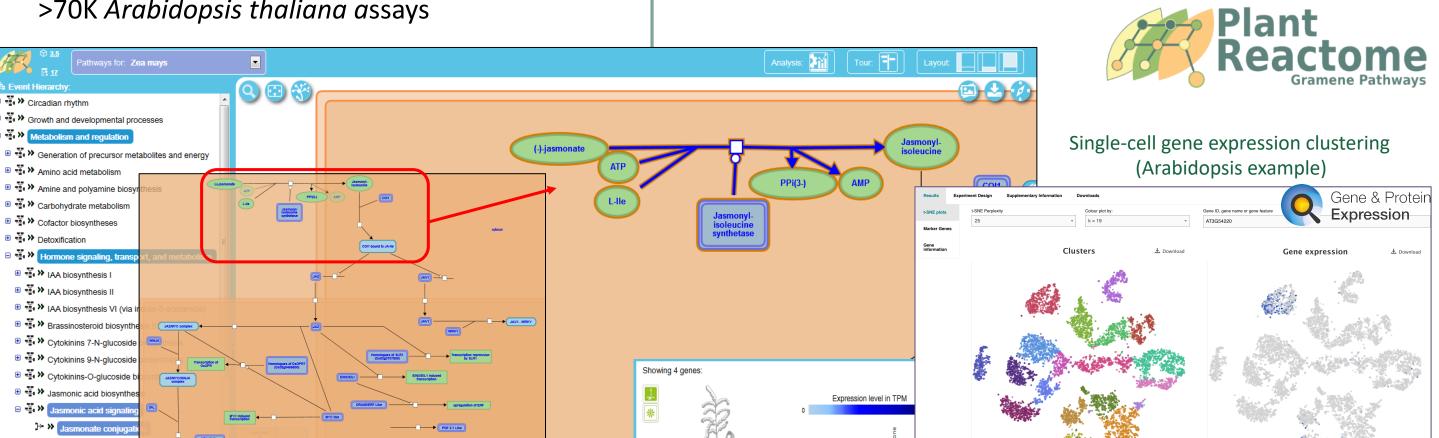
- ✓ 10 newly curated & 3 "container" pathways to a
- ✓ Orthology-based projections to 97 plant species (18 new) allowing pathway enrichment and inter-

nis is the gene tree containing **Zm00001d001941**. Gene name: invertase cell wa

ark genes as okay or flag genes that you think might have issues and choose a reason from the drop down menu. When finished, enter your email

- ✓ Baseline and differential expression data sets from 819 experiments and 24 reference plant species
- ✓ New visualization of single-cell expression data for >70K Arabidopsis thaliana assays
- Newly curated pathways:
- G1 Phase
- G1/S Transition
- Assembly of pre-replication complex
- Activation of pre-replication complex
- G1/S-specific transcription
- OsNAC5 transcription network involved in drought and high salinity tolerance
- Root hair development
- Phytic Acid biosynthesis (lipid independent)
- Response to aluminum stress
- Root-specific gene-network of NAC10_TF induced by drought, salinity, and ABA

https://plantreactome.gramene.org



WORKING WITH THE PLANT COMMUNITY

Virtual Maize Annotation Jamboree March 2020

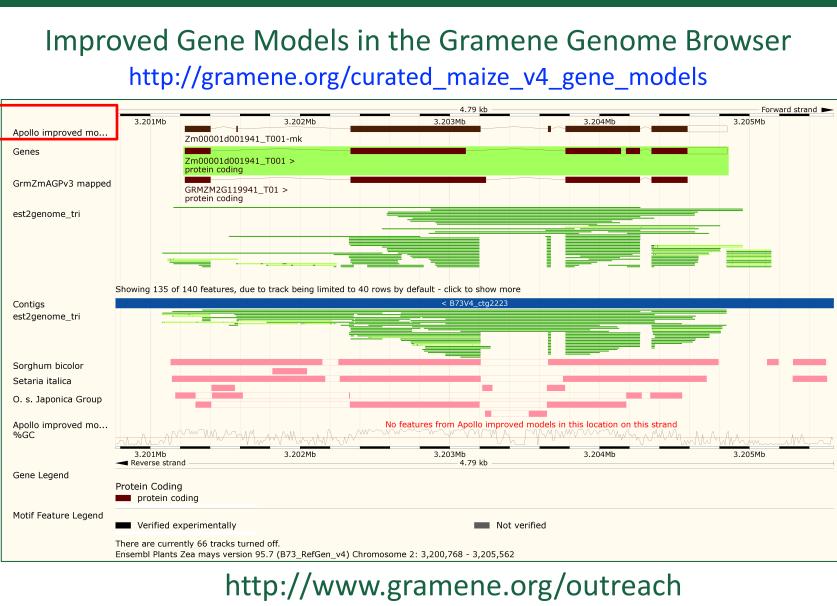


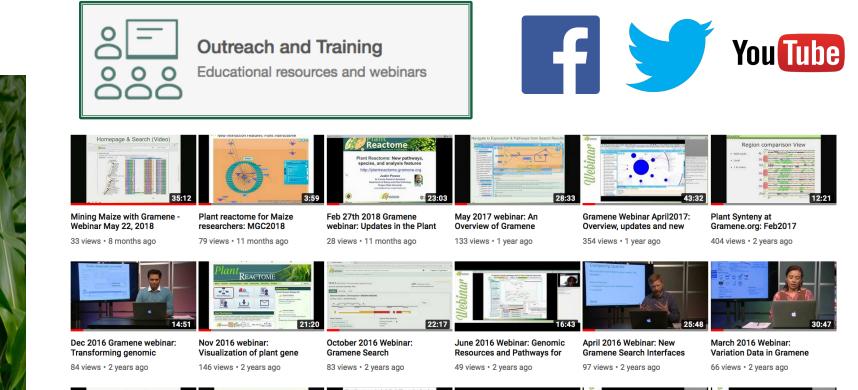
https://www.cshl.edu/teachers-make-genomes-more-useful-from-home/

Community Annotation to develop CUREs

Looking for a virtual activity with undergrads?

- Are you a plant researcher or educator who would like to see the structural annotation for your favorite maize or sorghum genes optimized using the latest available evidence?
- We are looking for researchers to work with an individual PUI faculty and her/his students on *improving genes of interest in a community curation*



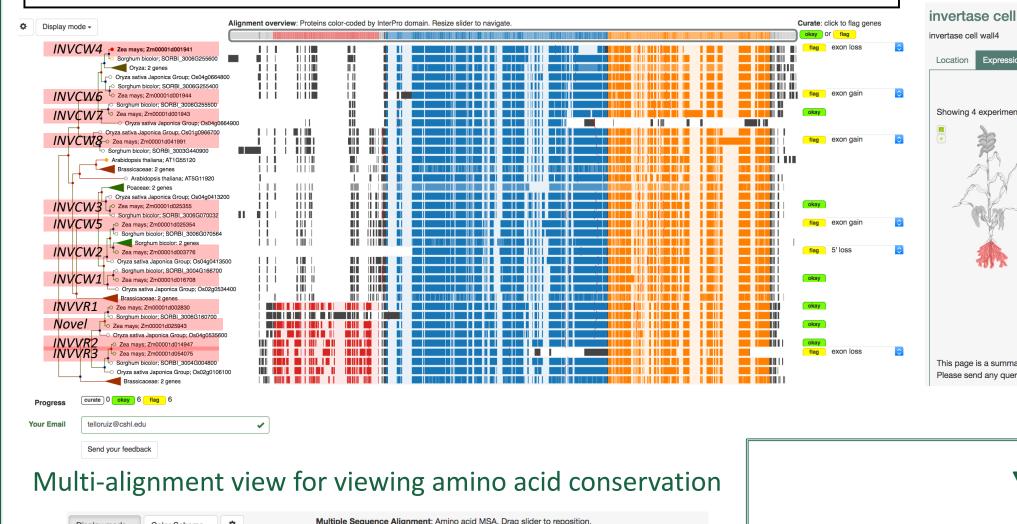


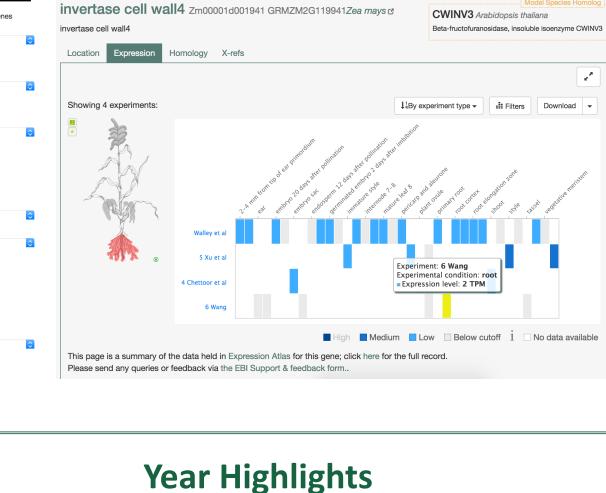
H→ → COI1 bi H→ → Nuclear H→ → Ubiquiti H→ → Nuclear H→ → Nuclear H→ → Ubiquiti J→ → JAZ/MY H→ → JAZ/MY H→ → JAZ/MY H→ → Transcr	Inde conjugati inds JA-Ile conjugati r uptake of JAV ination and proteosomal degra ination and proteosomal degra inds MYC like YC binds NINJA iduced transcription of JA indu YC/NINJA binds TPL ription of OsOPR avs EIN3/EIL1 induced transcr	adation c adation c adation c uced gen	ion ♣ Molecules 1995 : acid signaling Species: 2 9) 01d008957 ☑ Ens 01d009714 ☑ Ens		Expression 11 Ana		 3 days after sowing, root 3 days after sowing, meristematic zone and elongation zone 3 days after sowing, cortical parenchyma of root 6 days after sowing, roinary roo 7 days after sowing, taproot zon 7 days after sowing, taproot zon 2 days after sowing, taproot zon 	- LP.01 one leaf visible stage, prim - LP.03 three leaves visible stage, i - LP.05 five leaves visible stage, ii - Constant, 13 - Constant, 13 - Constant, 14 - Constant,	 Attended and a second a secon	 - LP.18 eighteen leaves visible stat - anthesis, leaf - Graster anthesis, leaf - Graster anthesis, leaf - 12 days after anthesis, leaf - 18 days after anthesis, leaf 	- 24 days after anthesis, leaf - 30 days after anthesis, leaf - 30 days after anthesis, leaf - 0 Claster 15 - 2 days after pollination, seed - 2 days after pollination, leaf - 6 days for pollination, leaf	-18 days after pollination, leaf 18 days after pollination, seed -18 days after pollination, endosp -20 days after pollination, seed	- 20 days after pollination, endosp - 22 days after pollination, plant e - 24 days after pollination, leaf - 24 days after pollination, seed	- 24 days after pollination, endosp - 30 days after pollination, interno - whole plant flowering stage, thin whole plant flowering stage, anth
						Zm00001d03934 Zm00001d03934	1 D				Ш	Ł	I,	
Species	Pathways	Reactions	Genes	Sequence source	Homology method	Browse and search								
Oryza sativa	306	1810	1939	UniProt	Curated Reference	 Pathways Reactions Small molecules 								
Zea mays	253	678	1466	Ensembl Gramene	Compara	Known gene expressionData analysis	rec	cord.						
						OMICs Species comparison						 		

DIG DEEP WHEN YOU SEARCH & ANALYZE GENES

Gramene Gene Tree Triage Tool

Gramene Search Results: Location, Expression, Homology, Pathway & X-Refs Views





effort.

Researchers are invited to take ownership of a set of genes of her/his interest and be the expert consultant for the PUI professor and his students. Join this effort and be among the first to gain access to unpublished gene annotations.

Interested? Contact us! feedback@gramene.org

Gramene's Plant Reactome: resources for maize research	Gramene Webinars, Dec, 2015: Plant Data Minining	Gramene Webinars: Updates on Plant Reactome 16 Feb,	Gramene Webinar Nov 2015: Variant Effect Prediction	Gramene webinar Aug2015 : Plant Reactome	Gramene Webinar July 2015 by Dr. Pankaj Jaiswal:
54 views • 2 years ago	49 views • 3 years ago	54 views • 3 years ago	185 views • 3 years ago	323 views • 3 years ago	90 views • 3 years ago
PertAPE - Seture shares our and execution payments and re- constraints our and sequents - Marcia - Marcia		 Caston of my data? 9.2 9.2	Polypiold View for Hexaploid Wheat	Lasselsoerd (ts1) encodes LOX8	
Programatic Acess to Ensembl Genome by Dr. Paul	Exploring Gene Trees by Dr. Joshua Stein - Gramene	Gramene Webinar June 2015: Upload and anlyze your data	Browsing & Comparing Genomes using the Gramene	Maize Data and Resources by Dr. Marcela Karey Tello-Ruiz	Rice Data and Resources in Gramene Database
48 views • 3 years ago	69 views • 3 years ago	52 views • 3 years ago	191 views • 3 years ago	112 views • 3 years ago	239 views • 3 years ago
				•	

ignment overview				
ignifient overview	n00001d044330	VPKORWTPEEEAALK		VAKHGPGKWRTILRDSDFSALLRLRSNVDLK
ultiple Sequence Alignmer		APKORWTPEEEAALK		VAKHGPGKWRTILRDSDFSALLRLRSNVDLK
eighborhood conservation	RBI_3003G202600	APKORWTPEEEAALK		VAKHGPGKWRTILRDSDFSELLRLRSNVDLK
eighborhood conservation	2403m.g	APKORWTPEEEAALK		VAKHGPCKWRTILROPDFSTLLRLRSNVDLK
	Triticinae: 3 genes	AP <mark>KQR</mark> WTSBEBAALK		VAKHGPGKWRTILRDTDFSAVLRLRSNVDLKVGRGDHC
	TRIAE_CS42_3AL_TGACv1_196916_/	AA0663740AP <mark>KOR</mark> WTSEBEAAL <mark>K</mark>	A <mark>G</mark>	-VAKHGPCKWRTILRDTDFSAVLRLRSNVDLK
	TRIUR3_08672	AP <mark>KOR</mark> WTSEEEAAL <mark>K</mark>		-VA <mark>KHGPCK</mark> W <mark>RTILRDTDF</mark> SAVL <mark>RLRSNVDLK</mark>
1 1	Lo HORVU3Hr1G051190	AP <mark>K</mark> QR <mark>WTSEEE</mark> AAL <mark>K</mark>	A <mark>G</mark>	-VA <mark>KHGPCK</mark> W <mark>RTILRDTDFS</mark> AVLHL <mark>RSNVDLK</mark>
	BRADI2G42240	AP <mark>KOR</mark> WTSEEEAALK	A <mark>G</mark>	VAKHGPGKWRTILRDPDFSAVLCLRSNVDLK
"	Oryzinae: 12 genes	APKORWTABEEAALK	A <mark>G</mark>	VAKHGTCKWRTILRDPEFTALLRLRSNVDLK
₽	oaceae: 33 genes, 2 paralogs	RLAPKOKWTABEEAALK	AGGGGGG <mark>AQ</mark> G <mark>R</mark>	IAKHGAGKWRTILKDPEF <mark>SNILR</mark> YRSNVDLKVR
Musa	a acuminata subsp. malaccensis: 4 genes	APKOKWTPEEEAALK	A <mark>G</mark>	VL <mark>KHGAGK</mark> WRTILKDPEF <mark>SG</mark> VLCM <mark>RSNVDLK</mark>
Diosco	orea rotundata: 2 genes	APKOKWTSEEESALK	A <mark>G</mark>	VV <mark>K</mark> HGAGKWRTILKDPEF <mark>S</mark> GILCL <mark>RSN</mark> VDLK
AMTR_s	00007p00193000	APK <mark>OK</mark> WTSEEEAAL <mark>R</mark>	A <mark>G</mark>	VDK <mark>YGPGKWRTILKDP</mark> VF <mark>S</mark> VILAL <mark>RSNVDLK</mark>
	bids: 12 genes	APKOKWTABEEAALK	A <mark>G</mark>	VI <mark>KHGVGKWRTILKDPEF</mark> SGVLYL <mark>RSNVDLK</mark>
	Malvaceae: 2 genes	APKOKWTPEEEAALK	<mark>5G</mark>	VI <mark>KHGAGKWRTILKDPEF</mark> SGVLYL <mark>RSNVDLK</mark>
📑 🕞	AT1G49950	APKOKWTQEEESALK	<mark>3G</mark>	VI <mark>KHGPGK</mark> WRTILKDPEF <mark>SG</mark> VLYL <mark>RSNVDLK</mark>
	fgenesh2_kg.14077AT1G49950.2	APKOKWTQBEESALK	3 <mark>6</mark>	VI <mark>KHGPGK</mark> W <mark>RTILKDPEF<mark>SG</mark>VLYL<mark>RSNVDLK</mark></mark>
	Brassica: 13 genes	APKOKWTQBEESALR	3 <mark>6</mark>	VV <mark>KHGPGK</mark> W <mark>RTILKDPDF<mark>SG</mark>VLFL<mark>RSNVDLK</mark></mark>
VIT_03s	0091g01030	AP <mark>KO</mark> KWTPBEEAALK	A <mark>G</mark>	-VV <mark>KHGAGK</mark> W <mark>RTILKDPEFSG</mark> VLFL <mark>RSNVDLK</mark>
So So	anaceae: 6 genes	AP <mark>KO</mark> KWTPBEEAALK	A <mark>G</mark>	-VL <mark>KHGPGK</mark> W <mark>RTILKDPEFSG</mark> VLYL <mark>RSNVDLK</mark>
Pentap	etalae: 2 genes	APK <mark>OK</mark> WTSBEBAALK	A <mark>G</mark>	-VV <mark>KHGAGK</mark> W <mark>RTILKDPEFSS</mark> VLYL <mark>RSNVDLK</mark>
BVRB_3	060630	APK <mark>OK</mark> WTABEBAALK	A <mark>G</mark>	-VL <mark>KHGAGK</mark> W <mark>RTILKDPE</mark> Y <mark>NG</mark> VLYL <mark>RSNVDLK</mark>
Pentapetala	e: 58 genes	AP <mark>KOK</mark> WTABEBAAL <mark>K</mark>	A <mark>G</mark>	VL <mark>KHGTGK</mark> W <mark>RTILSDPE</mark> FSSIL <mark>KSR</mark> SNVDLK
Magnoliophy	ta: 81 genes, 2 paralogs	TSVQDLI <mark>KLCCKK</mark> LNLNPK <mark>OK</mark> WTSEEEEALL.	A <mark>GRR</mark> IMF <mark>G</mark> VA <mark>GETEQ</mark> VEM	EVL <mark>KHGPGK</mark> WKNIQKDPEFAPVL <mark>SSR</mark> SNIDLK
Embryophyta: 9 g	enes	APK <mark>OK</mark> WTABEBAAL <mark>R</mark>	A <mark>G</mark>	VEK <mark>YGPGKWRAIOKDPK</mark> FGPCLV <mark>SRSN</mark> VDLK
	- OSTLU_27049	TAKYKWTRABEDALR	D <mark>G</mark>	-V <mark>RKHGPGK</mark> W <mark>RTIOKDPELGDILR</mark> A <mark>RSN</mark> VDLK

- Gene, genomic location, gene expression, phylogeny, cross-references, and pathway data available via Gramene search
- Plant Reactome landing using Joomla
- Improved Gramene Gene Tree Triage Tool to flag canonical gene transcripts for potential annotation errors based on protein homology











