A roadmap for gene functional characterisation in wheat

Cristobal Uauy (cristobal.uauy@jic.ac.uk)

@CristobalUauy

John Innes Centre
Unlocking Nature's Diversity

Genotype

```
>Sequence_1
GAGCATCGCACGATCGACGACTAGC
AGCAGCATCAGCAGCATCAGCAGCA
GCATACGAGGGACACACGCAGCTTA
GCATCAGCATCGACGATCGACTACG
CAGTACGACGACTACGCAGCATCAG
GGCAGCATCGACTACGCATCAGCAT
CGACTAGACTACGCATCAGCATCGA
```

Phenotype

In the past 4 years

Jordan et al. 2015 *Genome Biology*
He et al 2019 *Nature Genetics*
Pont et al 2019 *Nature Genetics*
Zhou et al 2020 *bioRxiv*

Gardiner et al 2015 *Genome Biology*
Gardiner et al 2018 *Genome Research*
Li et al 2019 *Genome Biology*

Pearce et al 2015 *BMC Plant Biol*
Borrill et al 2016 *Plant Physiol*
Ramirez-Gonzalez et al 2018 *Science*

Alonge et al 2020 *bioRxiv*
Walkowiak et al 2020 under review

Krasileva et al 2017 *PNAS*

IWGSC et al 2014 *Science*
Clavijo et al 2017 *Genome Research*
Avni et al 2017 *Science*
Luo et al 2017 *Nature*
Zimin et al 2017 *GigaScience*
Ling et al 2018 *Nature*
IWGSC et al 2018 *Science*
Maccaferri et al 2019 *Nature Genetics*
Alonge et al 2020 *bioRxiv*
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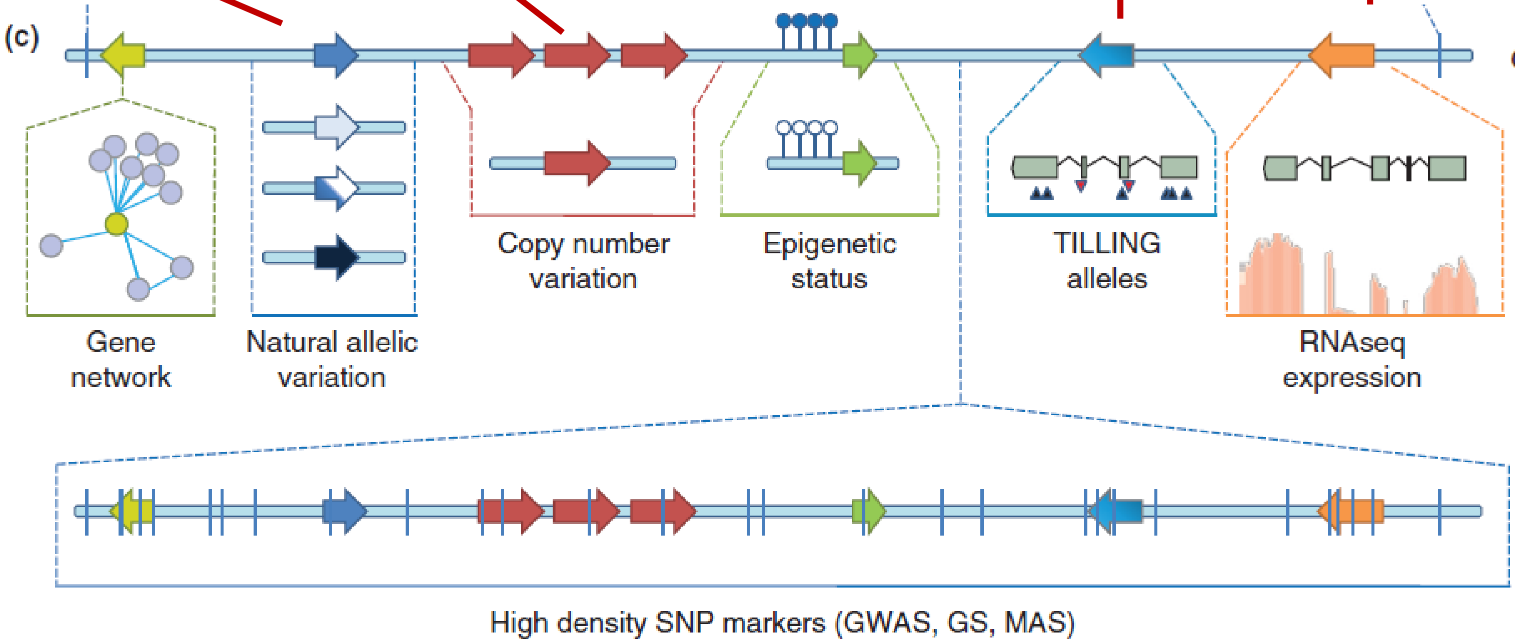


knetminer

Ramirez-Gonzalez et al 2018 *Science*
Hassani-Pak et al 2020 *bioRxiv*

CerealsDB
Tools for the analysis of the wheat genome

Wilkinson et al 2012/2016
BMC Bioinformatics

Howe et al 2020
NAR

Blake et al 2019
Database

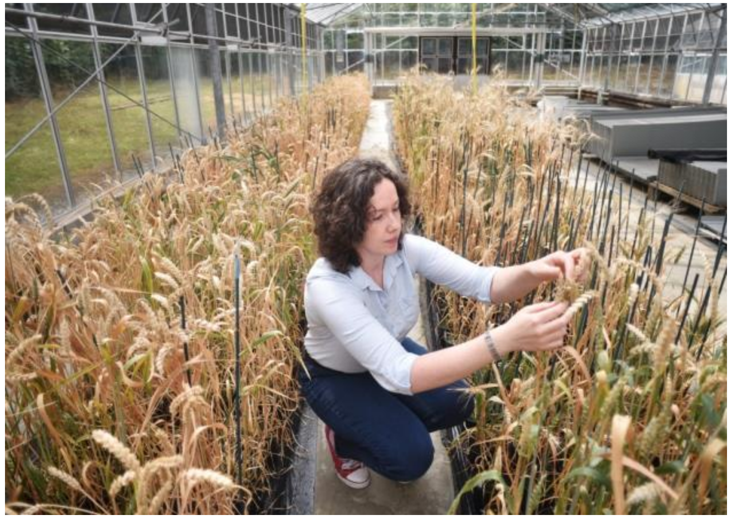
URGI

Alaux et al 2018
Genome Biology

polymarker

Ramirez-Gonzalez et al 2015 *Bioinformatics*

Bevan and Uauy 2013 *Genome Biology*



Philippa Borrill
(JIC)
University of Birmingham

Clemence Marchal
(JIC)

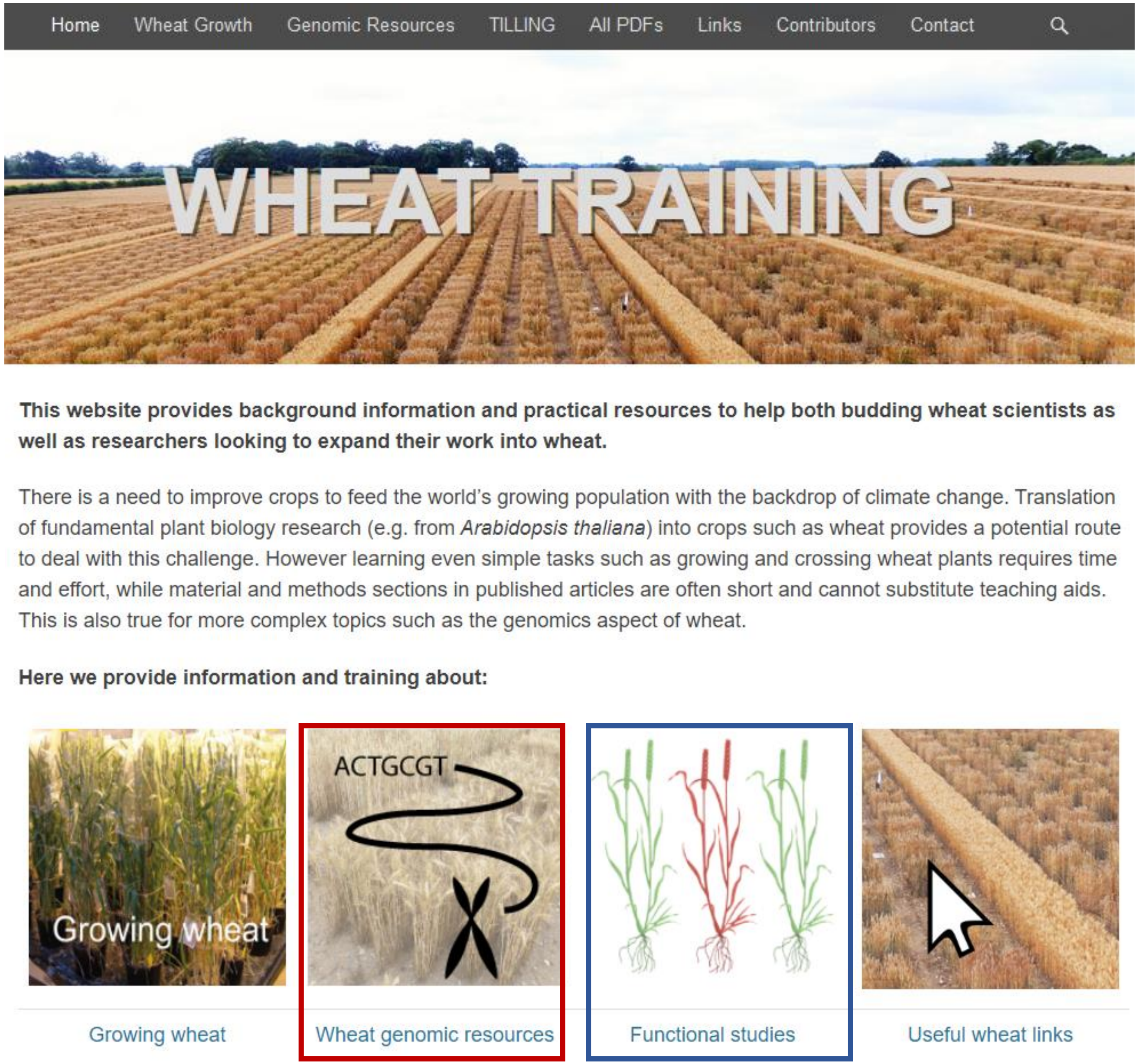
Nikolai Adamski
(JIC)

Sophie Harrington
(JIC)

Jemima Brinton
(JIC)

Plus countless additional contribuors !

www.wheat-training.com



This website provides background information and practical resources to help both budding wheat scientists as well as researchers looking to expand their work into wheat.

There is a need to improve crops to feed the world's growing population with the backdrop of climate change. Translation of fundamental plant biology research (e.g. from *Arabidopsis thaliana*) into crops such as wheat provides a potential route to deal with this challenge. However learning even simple tasks such as growing and crossing wheat plants requires time and effort, while material and methods sections in published articles are often short and cannot substitute teaching aids. This is also true for more complex topics such as the genomics aspect of wheat.

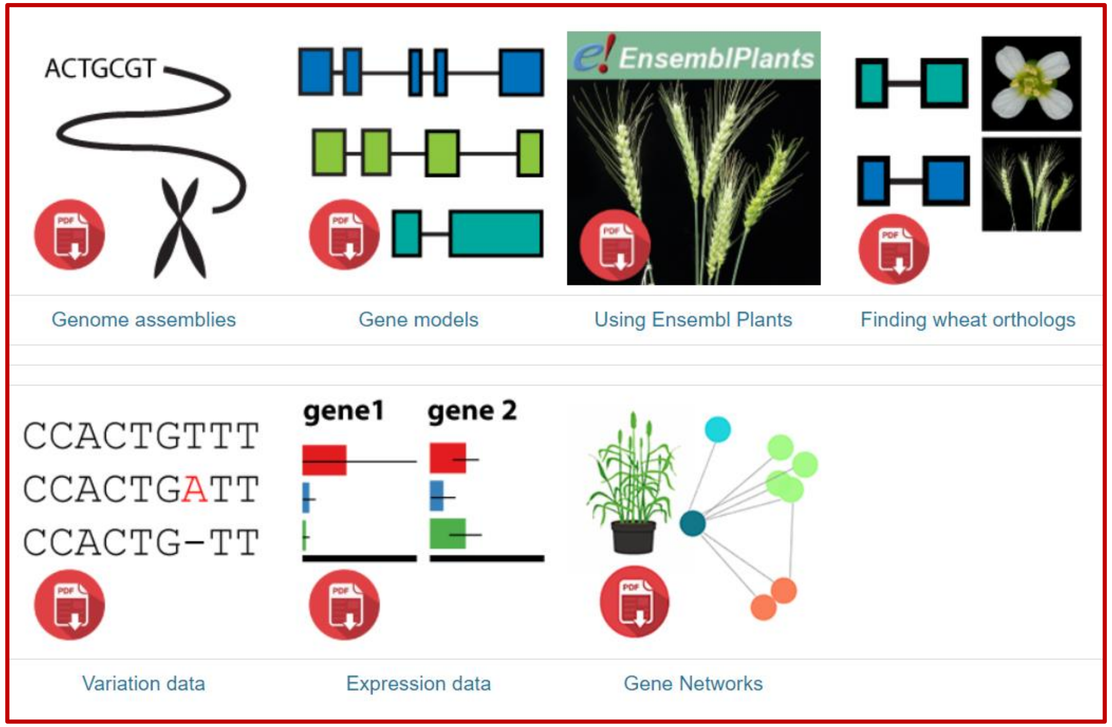
Here we provide information and training about:

Growing wheat

Wheat genomic resources

Functional studies

Useful wheat links



Genome assemblies

Gene models

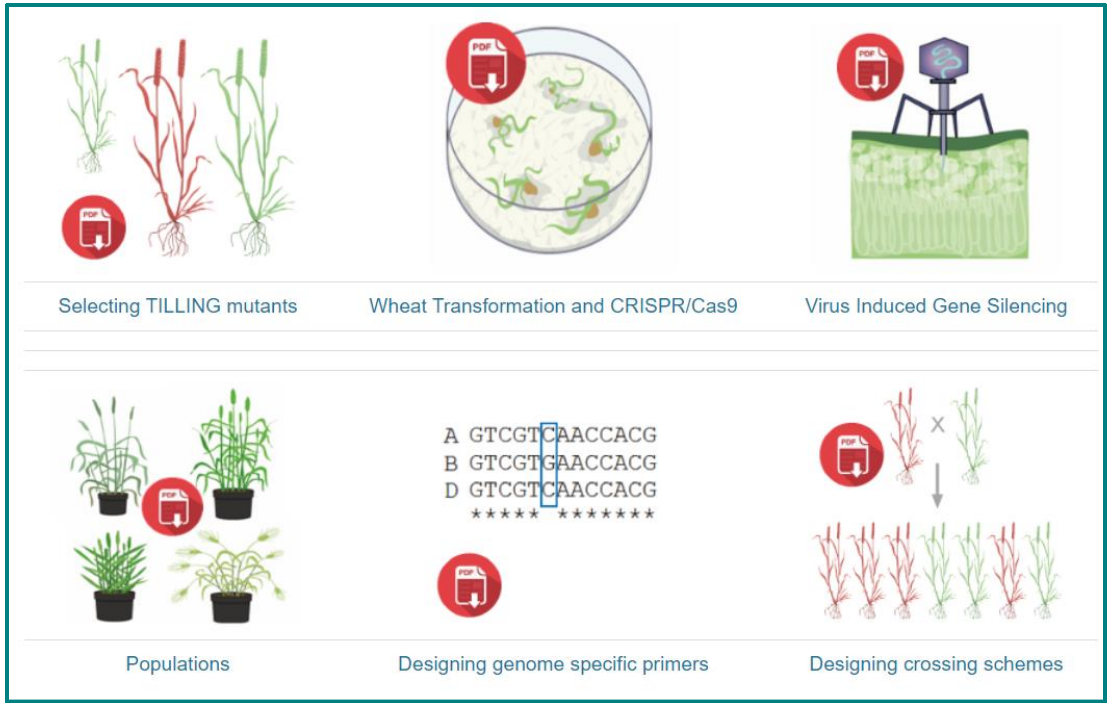
Using Ensembl Plants

Finding wheat orthologs

Variation data

Expression data

Gene Networks



Selecting TILLING mutants

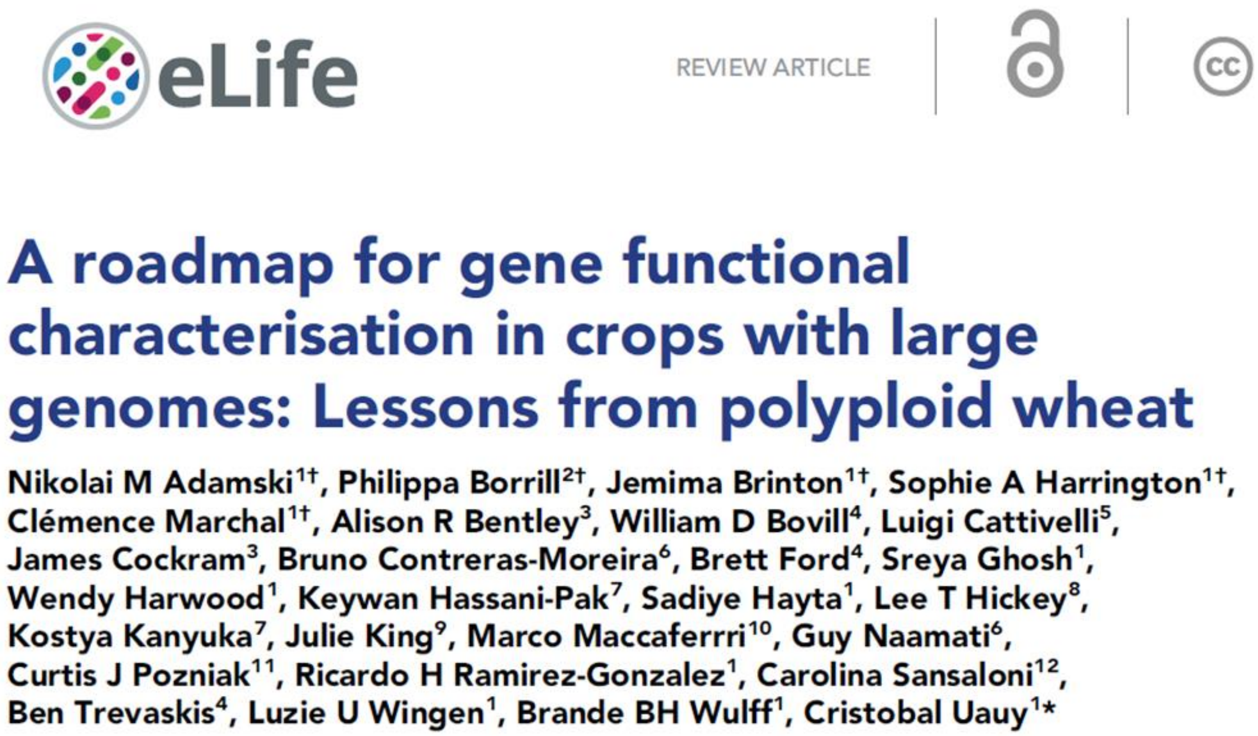
Wheat Transformation and CRISPR/Cas9

Virus Induced Gene Silencing

Populations

Designing genome specific primers

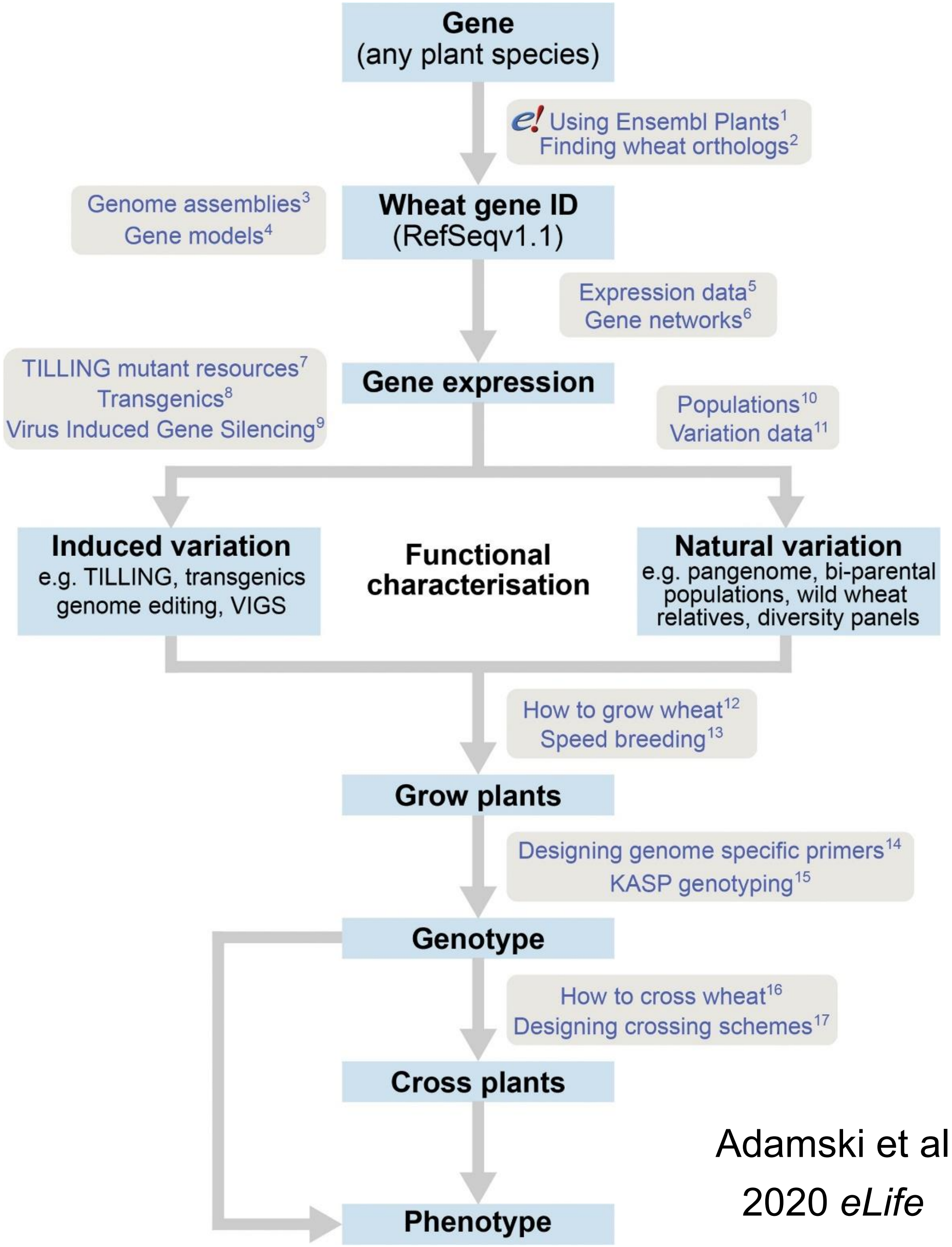
Designing crossing schemes



eLife REVIEW ARTICLE

A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat

Nikolai M Adamski[1†], Philippa Borrill[2†], Jemima Brinton[1†], Sophie A Harrington[1†], Clémence Marchal[1†], Alison R Bentley[3], William D Bovill[4], Luigi Cattivelli[5], James Cockram[3], Bruno Contreras-Moreira[6], Brett Ford[4], Sreya Ghosh[1], Wendy Harwood[1], Keywan Hassani-Pak[7], Sadiye Hayta[1], Lee T Hickey[8], Kostya Kanyuka[7], Julie King[9], Marco Maccaferrri[10], Guy Naamati[6], Curtis J Pozniak[11], Ricardo H Ramirez-Gonzalez[1], Carolina Sansaloni[12], Ben Trevaskis[4], Luzie U Wingen[1], Brande BH Wulff[1], Cristobal Uauy[1]*



Gene
(any plant species)

e! Using Ensembl Plants[1]
Finding wheat orthologs[2]

Genome assemblies[3]
Gene models[4]

Wheat gene ID
(RefSeqv1.1)

Expression data[5]
Gene networks[6]

TILLING mutant resources[7]
Transgenics[8]
Virus Induced Gene Silencing[9]

Gene expression

Populations[10]
Variation data[11]

Induced variation
e.g. TILLING, transgenics genome editing, VIGS

Functional characterisation

Natural variation
e.g. pangenome, bi-parental populations, wild wheat relatives, diversity panels

How to grow wheat[12]
Speed breeding[13]

Grow plants

Designing genome specific primers[14]
KASP genotyping[15]

Genotype

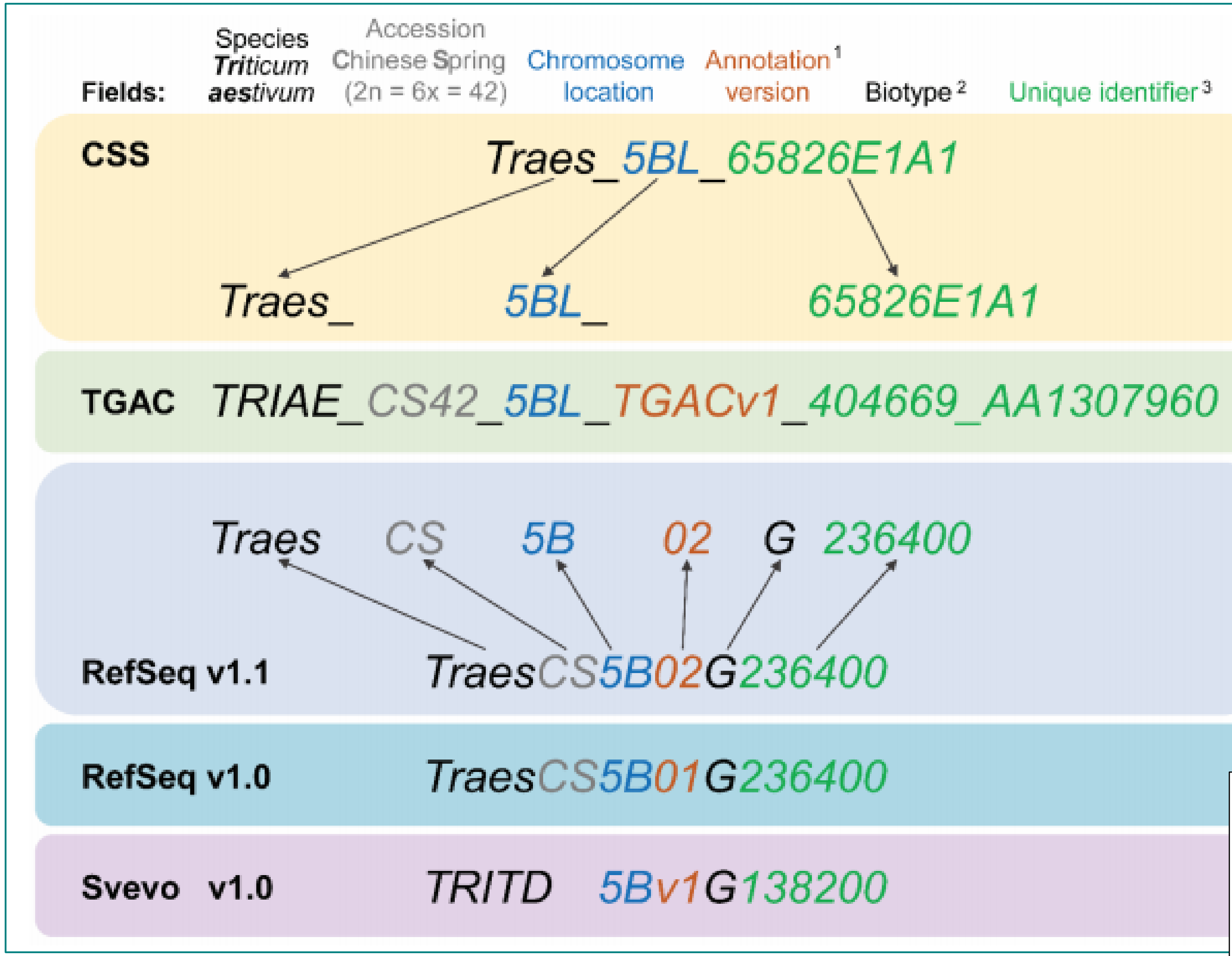
How to cross wheat[16]
Designing crossing schemes[17]

Cross plants

Phenotype

Adamski et al
2020 *eLife*

The importance of good gene models (and clear nomenclature)



Fields: Species *Triticum aestivum* | Accession Chinese Spring (2n = 6x = 42) | Chromosome location | Annotation[1] version | Biotype[2] | Unique identifier[3]

CSS *Traes_5BL_65826E1A1*

*Traes_* *5BL_* *65826E1A1*

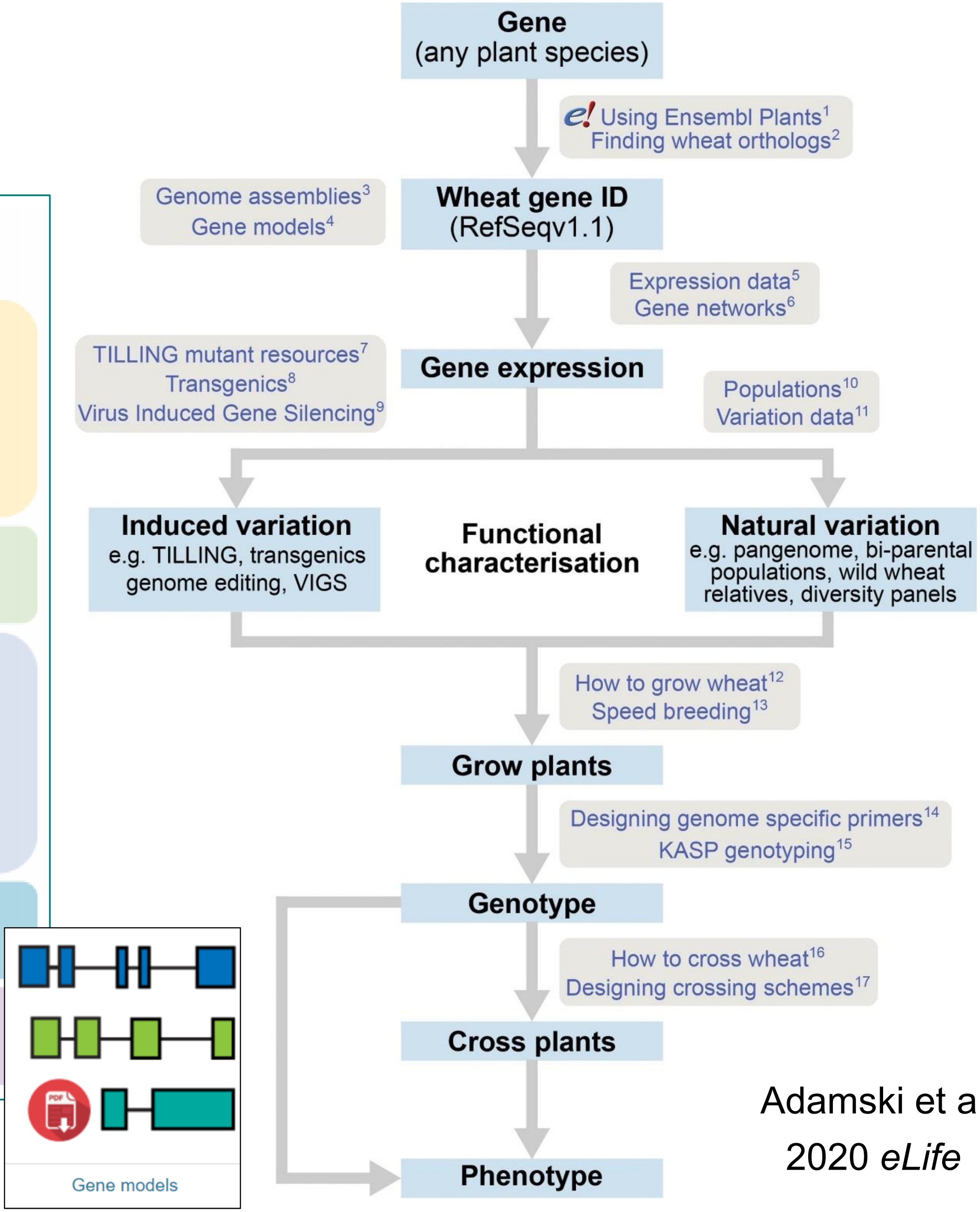
TGAC *TRIAE_CS42_5BL_TGACv1_404669_AA1307960*

Traes *CS* *5B* *02* *G* *236400*

RefSeq v1.1 *TraesCS5B02G236400*

RefSeq v1.0 *TraesCS5B01G236400*

Svevo v1.0 *TRITD 5Bv1G138200*



Gene models

Gene
(any plant species)

Using Ensembl Plants[1]
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How to cross wheat[16]
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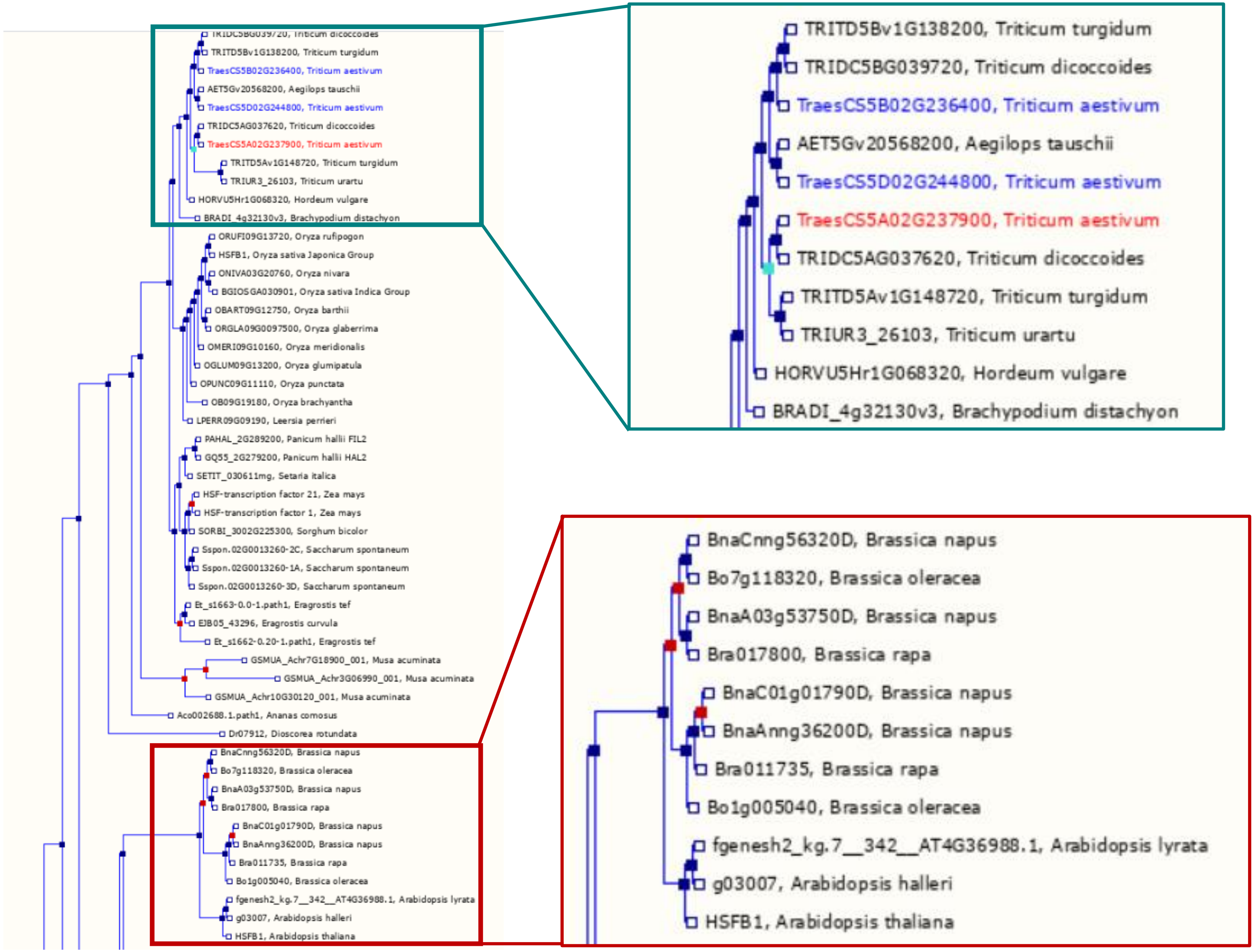
Cross plants

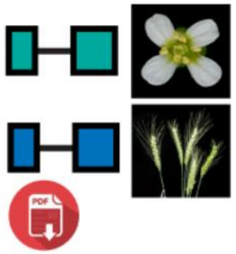
Phenotype

Adamski et al
2020 *eLife*

Pre-computed gene trees in *e!* to identify wheat orthologs

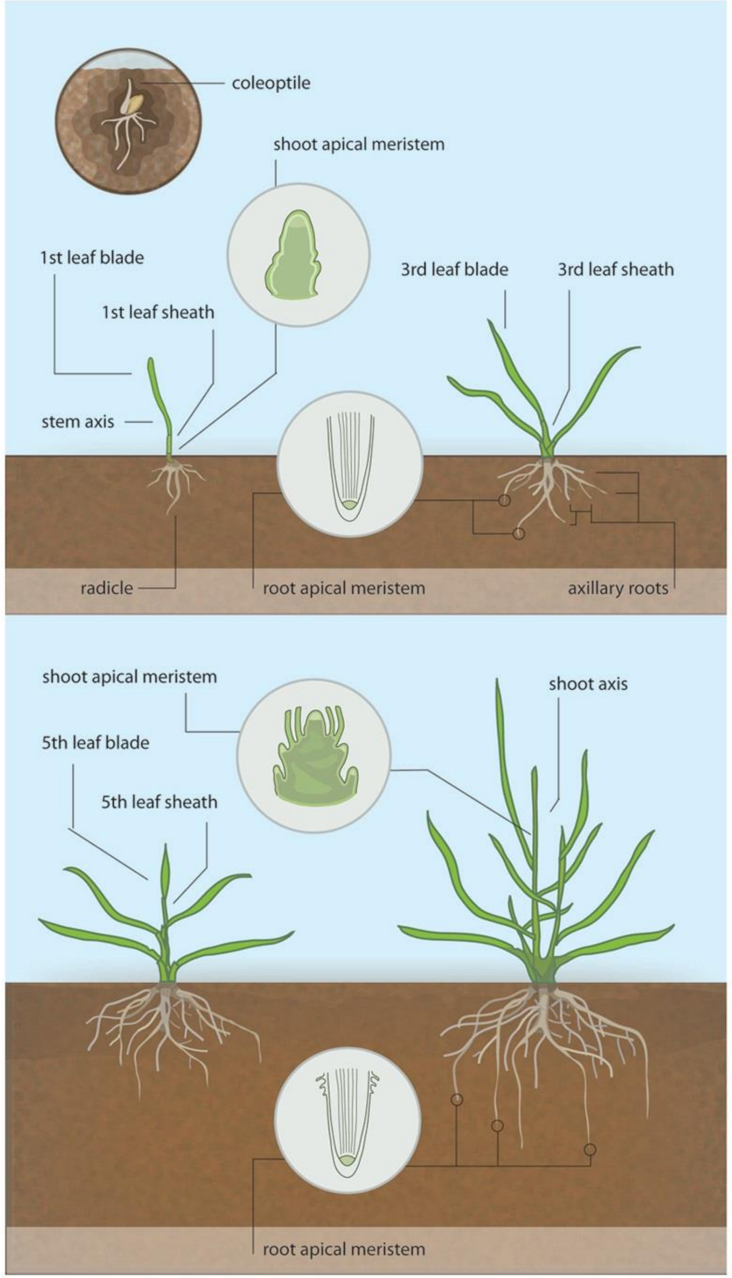


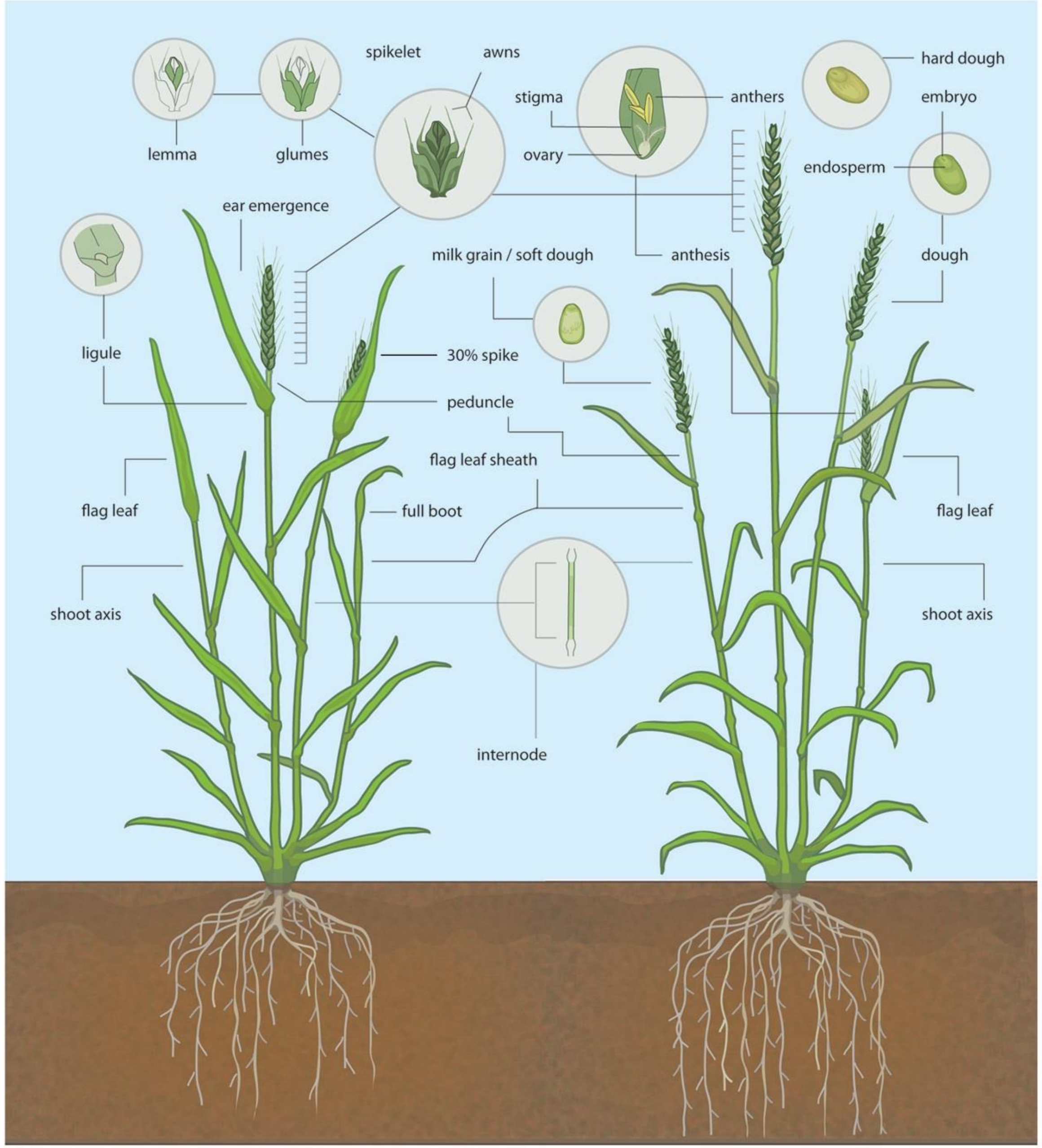
Using Ensembl Plants



Finding wheat orthologs

Where is my gene expressed?



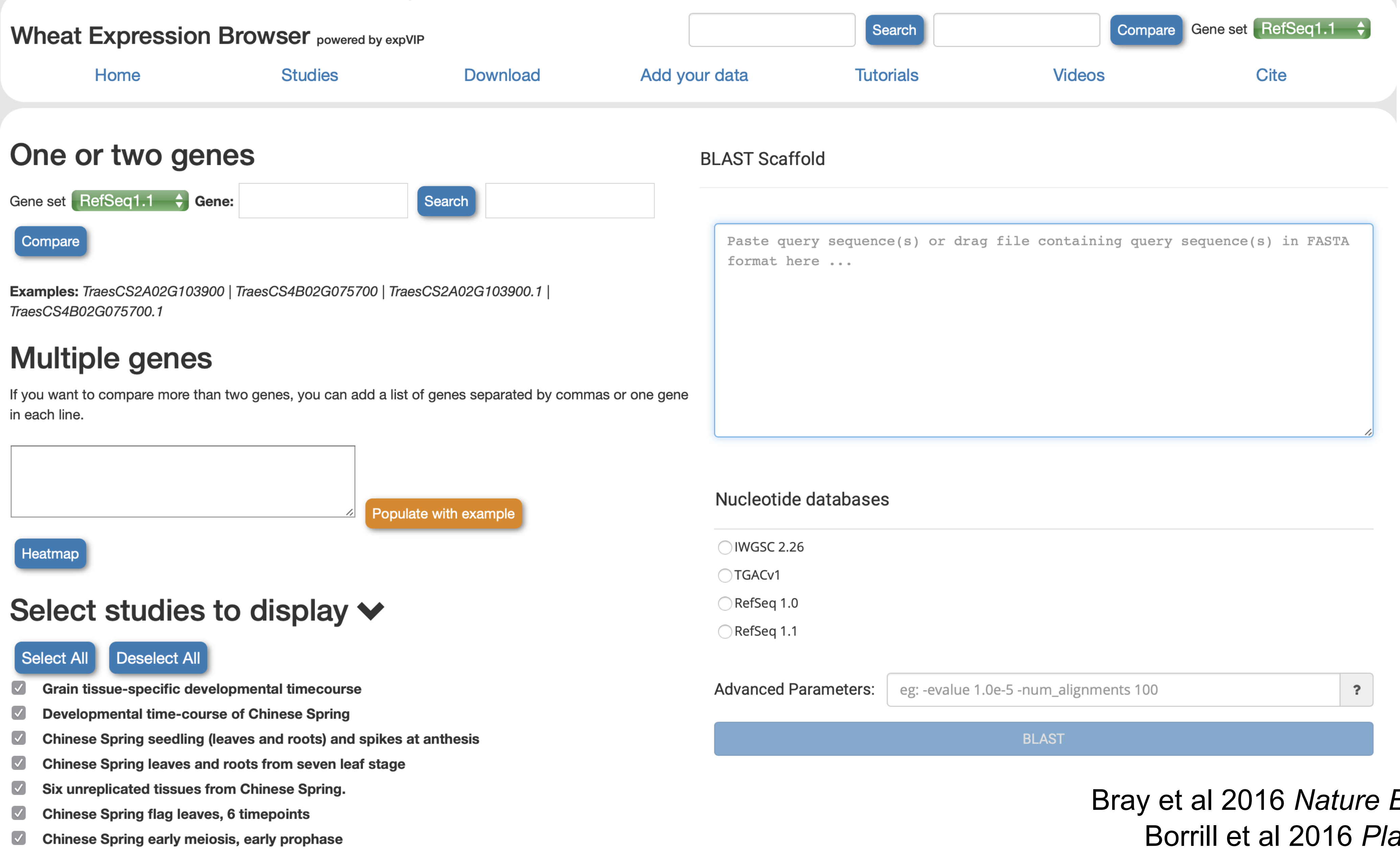


Philippa Borrill
(JIC)
University of Birmingham

Ricardo Ramirez-Gonzalez (JIC)

expVIP (>1,000 samples)

http://wheat-expression.com



Wheat Expression Browser powered by expVIP

Search | Compare | Gene set RefSeq1.1

Home | Studies | Download | Add your data | Tutorials | Videos | Cite

One or two genes

Gene set RefSeq1.1 **Gene:** Search

Compare

Examples: *TraesCS2A02G103900* | *TraesCS4B02G075700* | *TraesCS2A02G103900.1* | *TraesCS4B02G075700.1*

Multiple genes

If you want to compare more than two genes, you can add a list of genes separated by commas or one gene in each line.

Populate with example

Heatmap

Select studies to display

Select All | Deselect All

- ☑ **Grain tissue-specific developmental timecourse**
- ☑ **Developmental time-course of Chinese Spring**
- ☑ **Chinese Spring seedling (leaves and roots) and spikes at anthesis**
- ☑ **Chinese Spring leaves and roots from seven leaf stage**
- ☑ **Six unreplicated tissues from Chinese Spring.**
- ☑ **Chinese Spring flag leaves, 6 timepoints**
- ☑ **Chinese Spring early meiosis, early prophase**

BLAST Scaffold

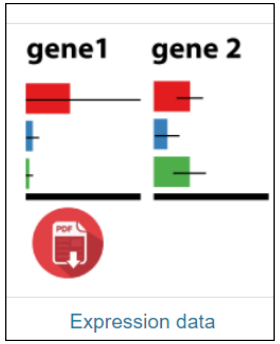
```
Paste query sequence(s) or drag file containing query sequence(s) in FASTA
format here ...
```

Nucleotide databases

- ○ IWGSC 2.26
- ○ TGACv1
- ○ RefSeq 1.0
- ○ RefSeq 1.1

Advanced Parameters: eg: -evalue 1.0e-5 -num_alignments 100 ?

BLAST

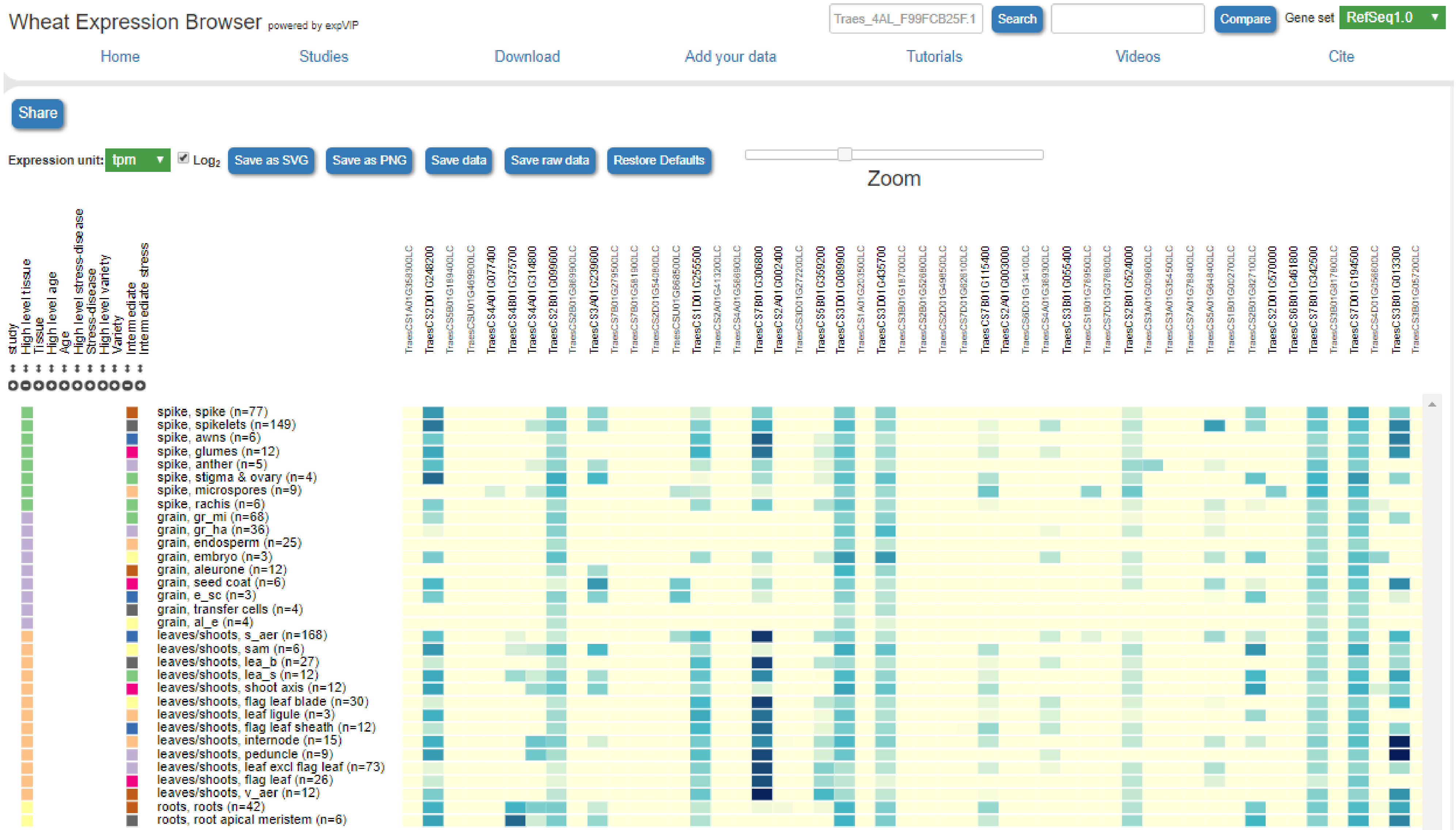


Bray et al 2016 *Nature Biotechnology*

Borrill et al 2016 *Plant Physiology*

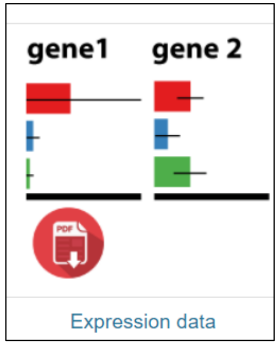
Ramirez-Gonzalez et al 2018 *Science*

Visual interface (>1,000 samples)



Wheat Expression Browser powered by expVIP

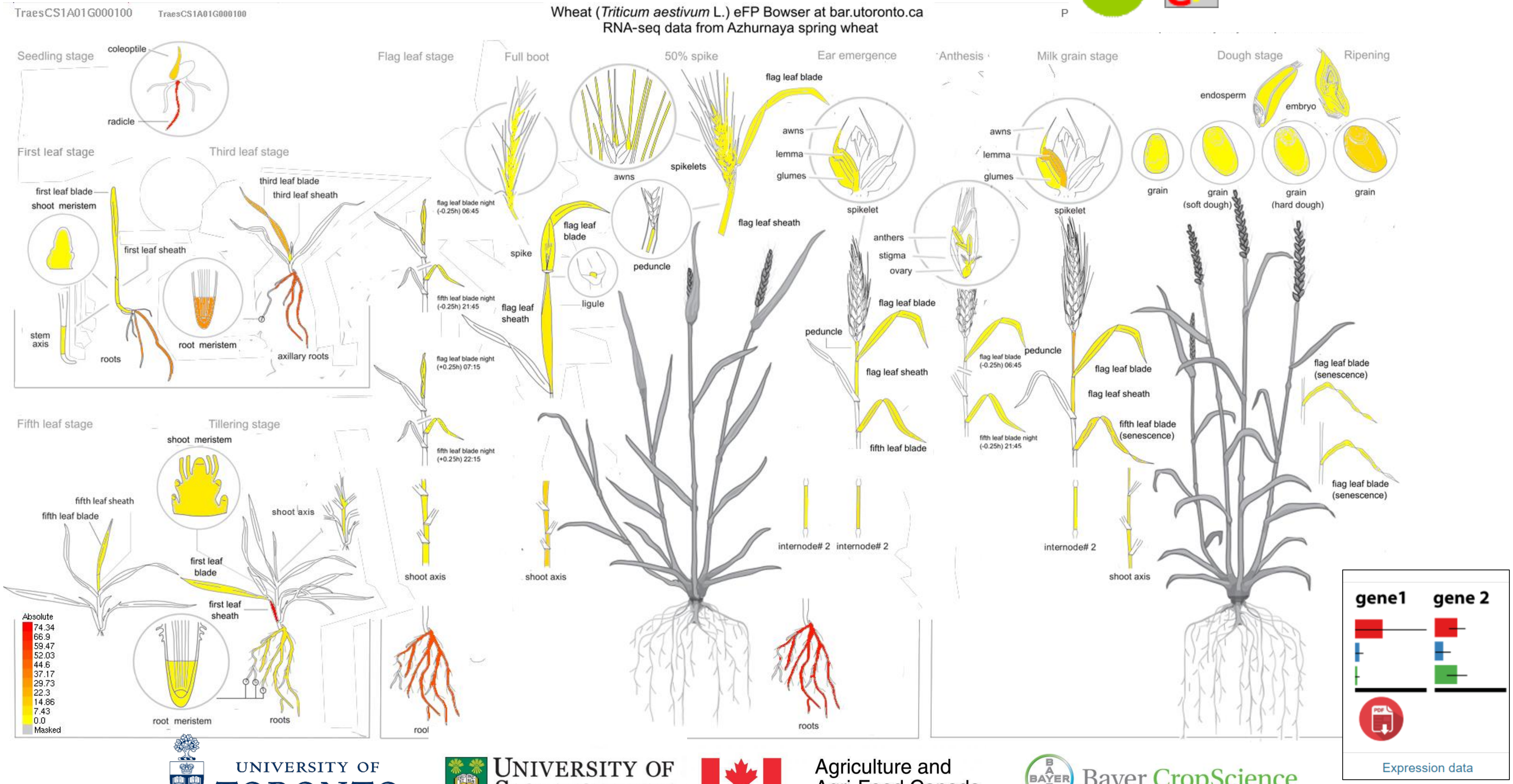
spike, spike (n=77)
spike, spikelets (n=149)
spike, awns (n=6)
spike, glumes (n=12)
spike, anther (n=5)
spike, stigma & ovary (n=4)
spike, microspores (n=9)
spike, rachis (n=6)
grain, gr_mi (n=68)
grain, gr_ha (n=36)
grain, endosperm (n=25)
grain, embryo (n=3)
grain, aleurone (n=12)
grain, seed coat (n=6)
grain, e_sc (n=3)
grain, transfer cells (n=4)
grain, al_e (n=4)
leaves/shoots, s_aer (n=168)
leaves/shoots, sam (n=6)
leaves/shoots, lea_b (n=27)
leaves/shoots, lea_s (n=12)
leaves/shoots, shoot axis (n=12)
leaves/shoots, flag leaf blade (n=30)
leaves/shoots, leaf ligule (n=3)
leaves/shoots, flag leaf sheath (n=12)
leaves/shoots, internode (n=15)
leaves/shoots, peduncle (n=9)
leaves/shoots, leaf excl flag leaf (n=73)
leaves/shoots, flag leaf (n=26)
leaves/shoots, v_aer (n=12)
roots, roots (n=42)
roots, root apical meristem (n=6)



Borrill et al 2016 *Plant Physiology*
Ramirez-Gonzalez et al 2018 *Science*

Wheat eFP (70 tissue*development stage)

BAR Wheat eFP Browser



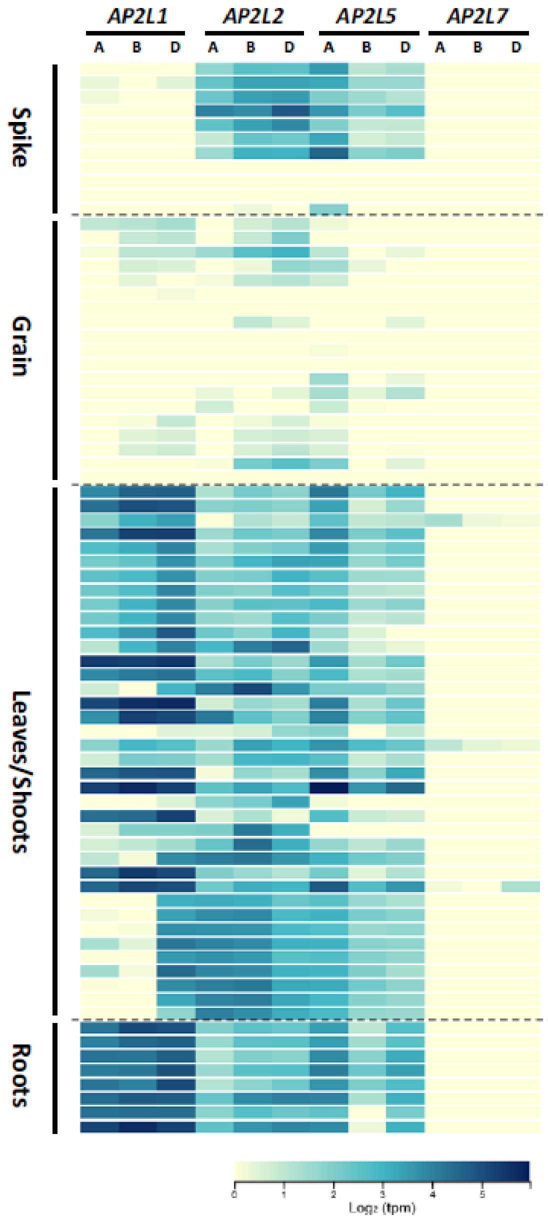
Expression data

UNIVERSITY OF TORONTO

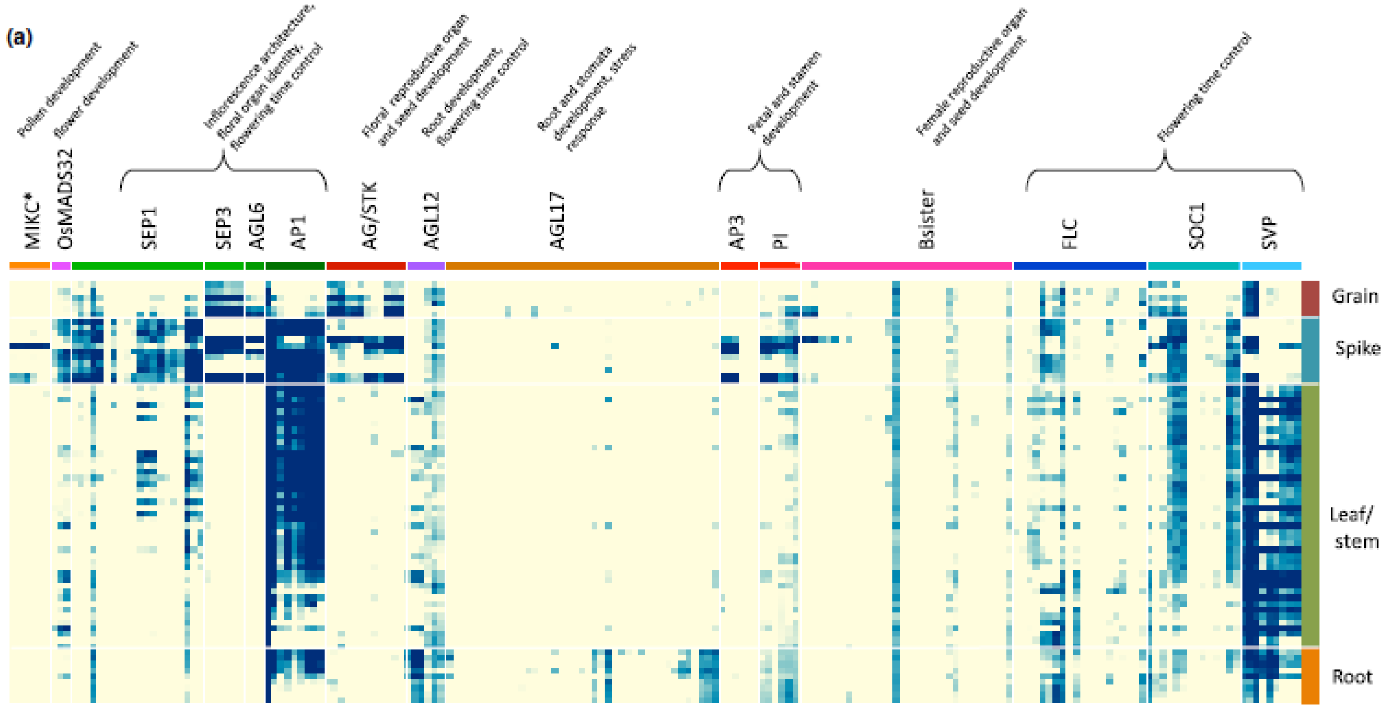
UNIVERSITY OF SASKATCHEWAN

Agriculture and Agri-Food Canada

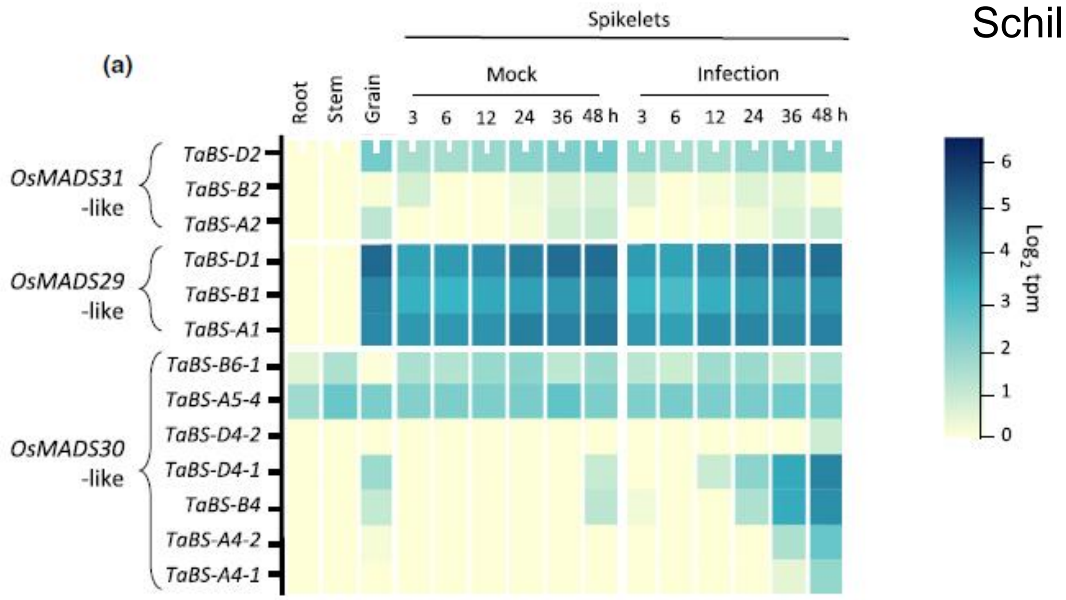
Bayer CropScience



Debernardi et al 2020
Plant Journal



Schilling et al 2020 *New Phytologist*



Susanne Schilling

Rainer Melzer

Univ. College Dublin

Data Availability

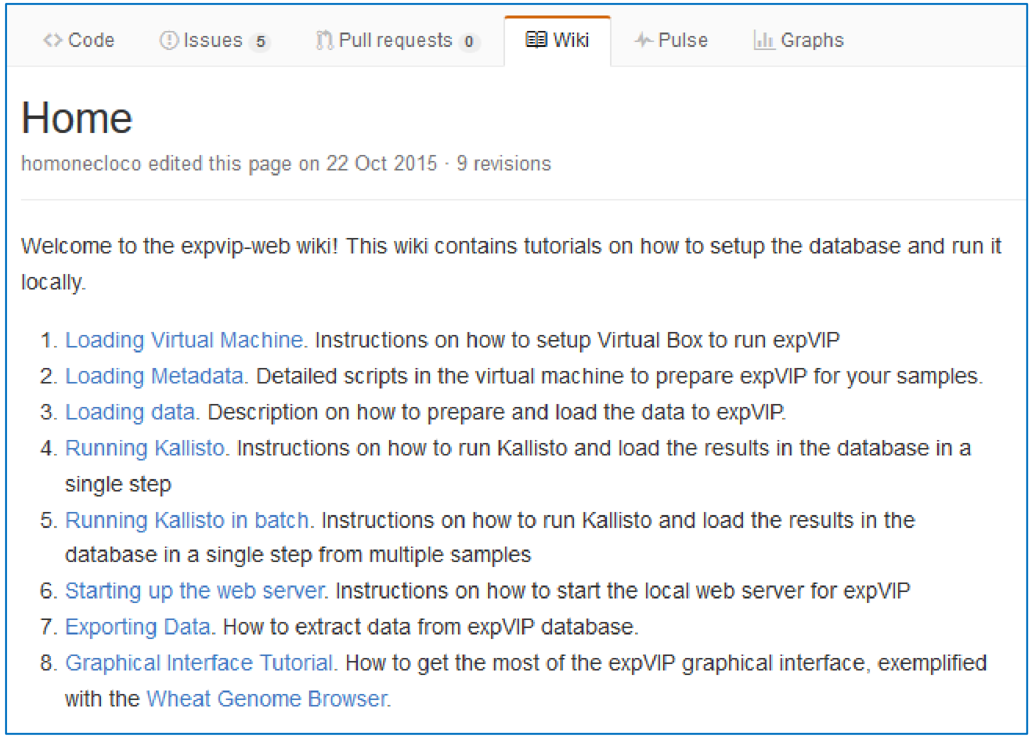
http://www.wheat-expression.com

Ricardo Ramirez-Gonzalez (JIC)

Source code

Database and interface setup:
https://github.com/Uauy-Lab/expvip-web

BioJS visualisation component:
http://biojs.io/d/bio-vis-expression-bar



Home

homonecloco edited this page on 22 Oct 2015 · 9 revisions

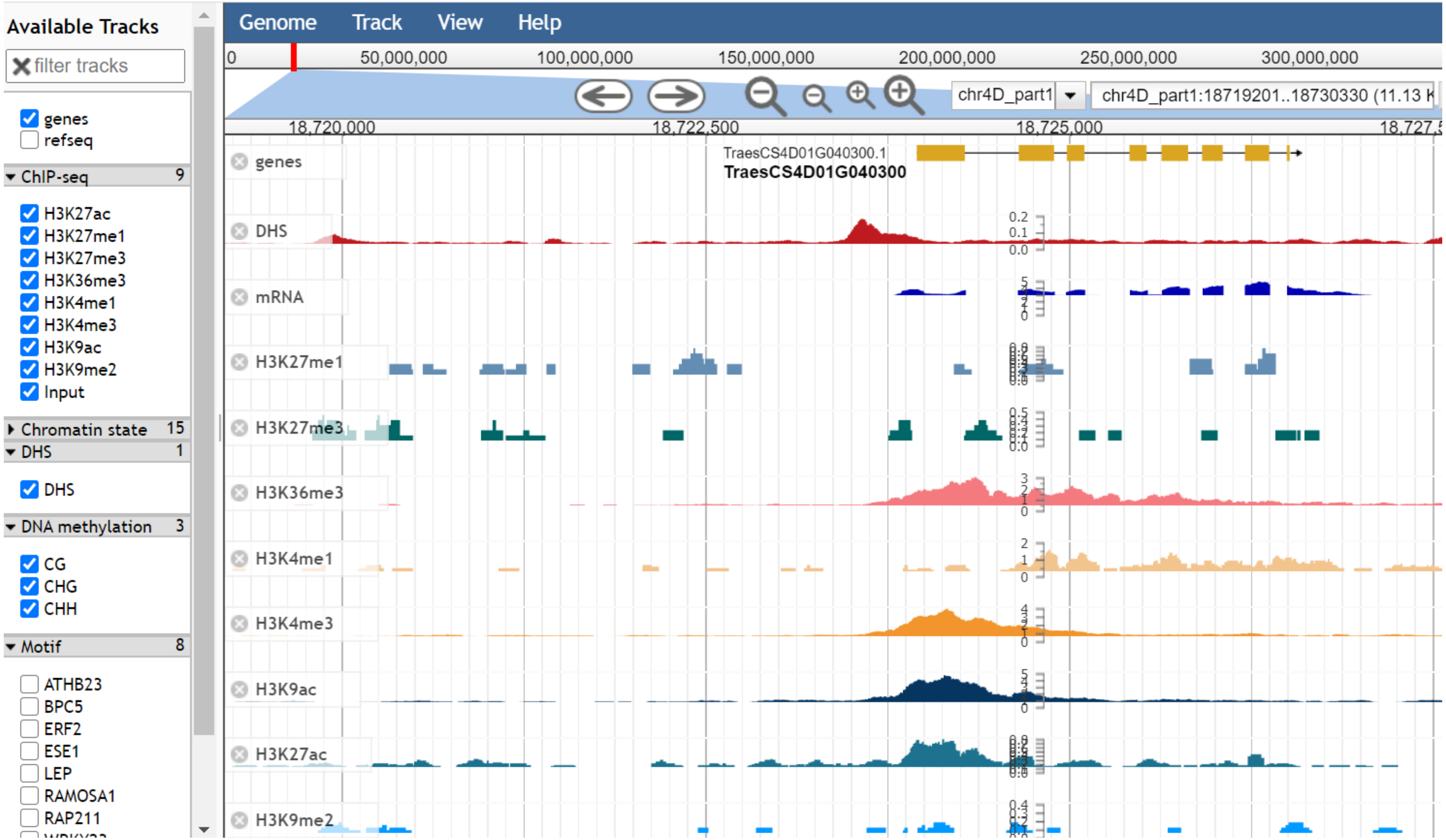
Welcome to the expvip-web wiki! This wiki contains tutorials on how to setup the database and run it locally.

1. Loading Virtual Machine. Instructions on how to setup Virtual Box to run expVIP
2. Loading Metadata. Detailed scripts in the virtual machine to prepare expVIP for your samples.
3. Loading data. Description on how to prepare and load the data to expVIP.
4. Running Kallisto. Instructions on how to run Kallisto and load the results in the database in a single step
5. Running Kallisto in batch. Instructions on how to run Kallisto and load the results in the database in a single step from multiple samples
6. Starting up the web server. Instructions on how to start the local web server for expVIP
7. Exporting Data. How to extract data from expVIP database.
8. Graphical Interface Tutorial. How to get the most of the expVIP graphical interface, exemplified with the Wheat Genome Browser.

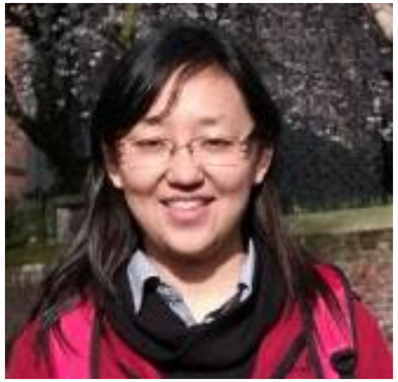
https://opendata.earlham.ac.uk/wheat/under_license/toronto/Ramirez-Gonzalez_etal_2018-06025-Transcriptome-Landscape/

Epigenetic marks

http://bioinfo.sibs.ac.cn/cs_epigenome



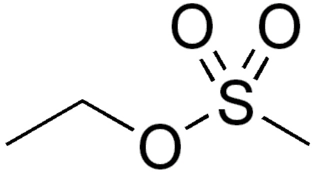
Zijuan Li
(CAS)



Yijing Zhang
(CAS)

Li et al 2019 *Genome Biology*

Mutants in every wheat gene: *in silico* TILLING



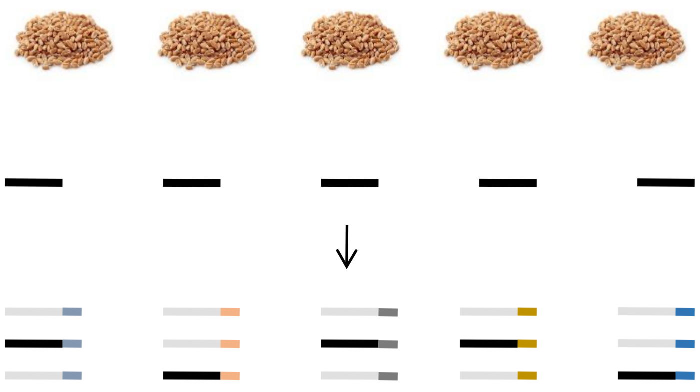
EMS

Mutant Population

Ksenia Krasileva
(Earlham)-
Berkeley

Jorge Dubcovsky
(UC Davis)

Andy Phillips
(RRes)



Seeds

DNA

Exome
capture

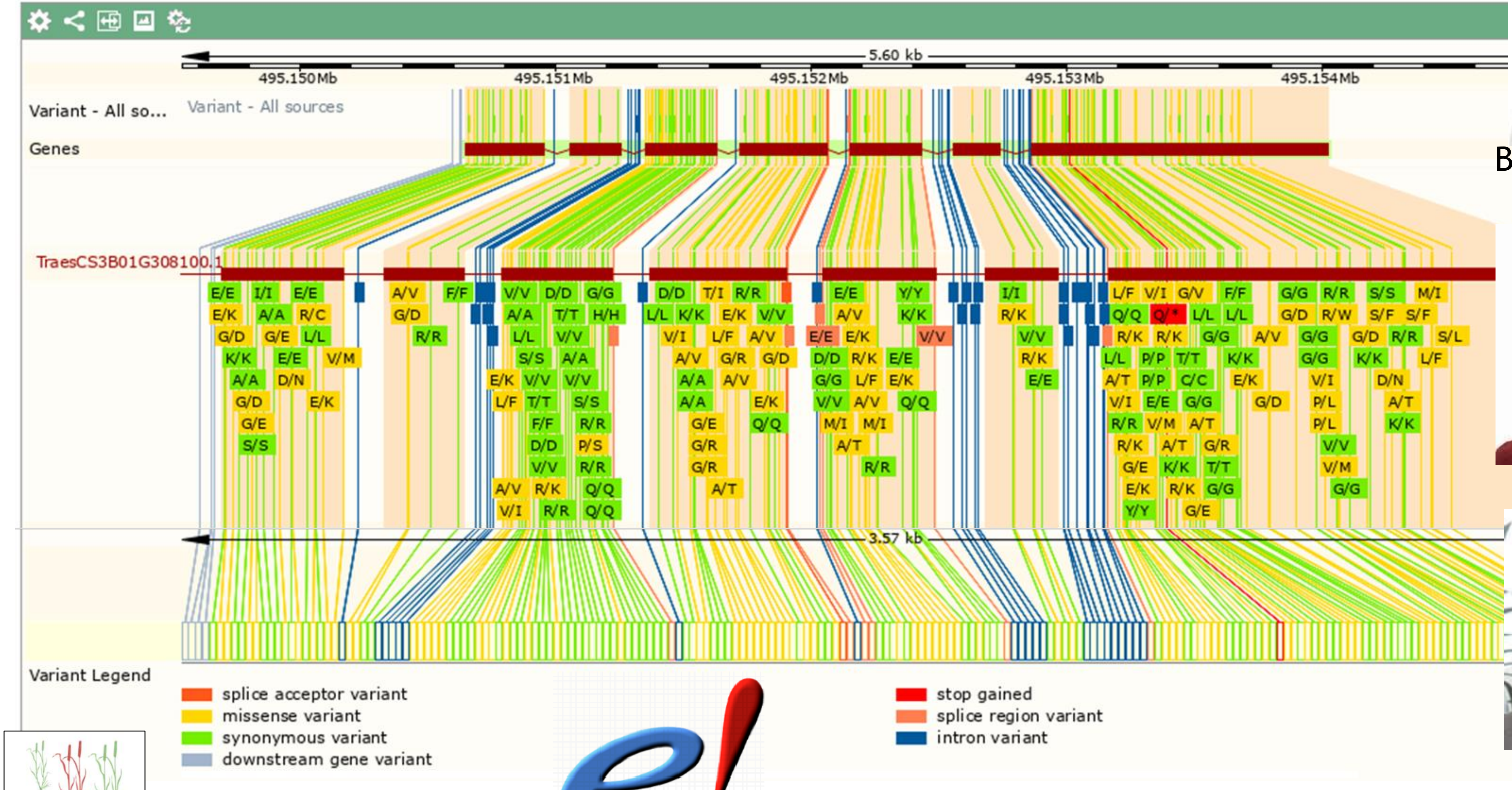
Mutant
Identification

SeedStor

ATG**T**	ATGC	AT**A**C	ATGC	ATGC
T**A**CT	TG**T**T	TGCT	TGCT	TGCT
CGTG	**A**GTG	CGTG	**T**GTG	CGT**A**

Krasileva et al 2017 *PNAS*
Uauy, Wulff, Dubcovsky 2017 *ANR Genetics*

Access to >10M wheat mutants online



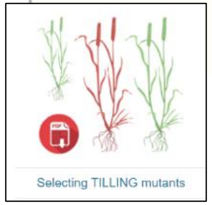
Variant Legend

🟧 splice acceptor variant
🟨 missense variant
🟩 synonymous variant
▨ downstream gene variant
🟥 stop gained
🟧 splice region variant
🟦 intron variant


Bruno Contreras Moreira

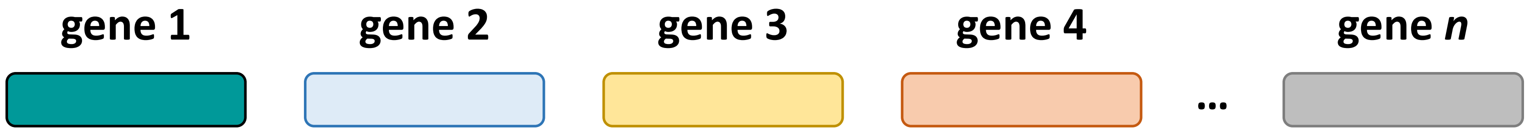

Guy Naamati


Dan Bolser



Krasileva et al 2017 *PNAS*
Uauy, Wulff, Dubcovsky 2017 *ANR Genetics*

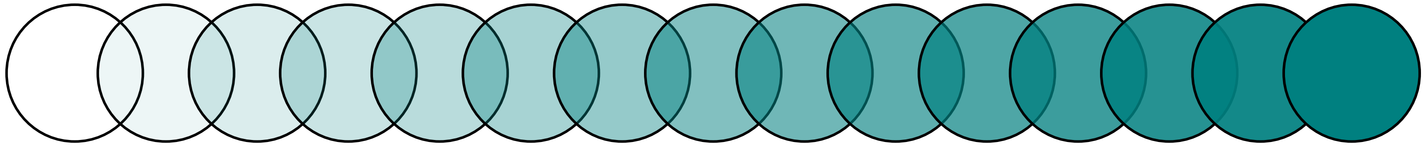
Phenotypes of agricultural importance are “complex”



e.g. Yield,
Nutritional Value

Diploids

Continuous phenotypic variation



Not Presence *Absence*

Continuous phenotypic
variation

Polyploids

Sugar cane

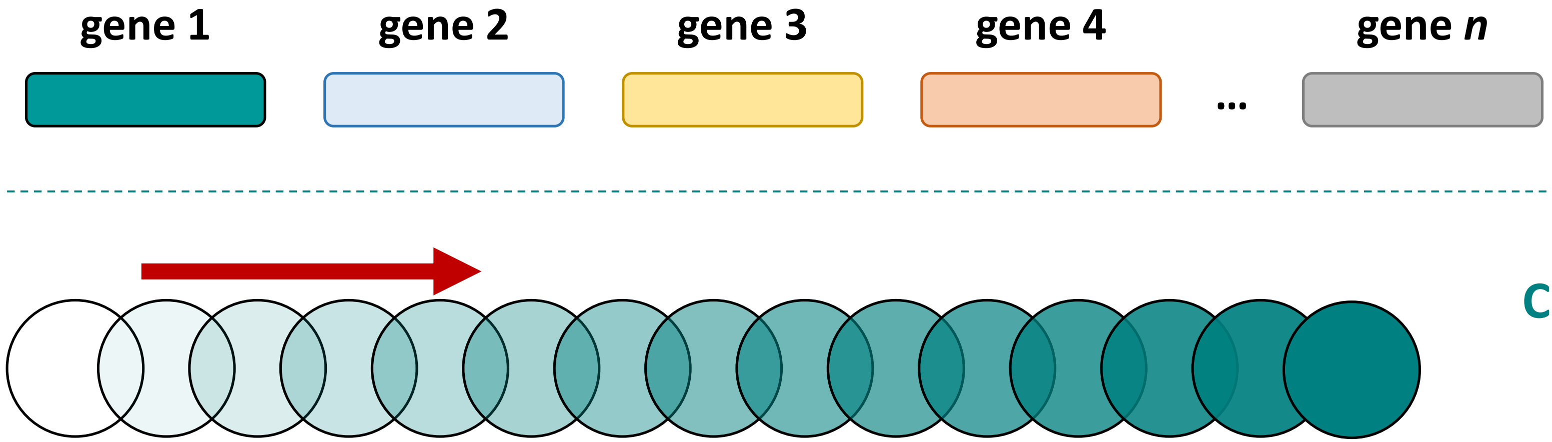
Coffee

Rapeseed

Wheat

Phenotypes of agricultural importance are “complex”

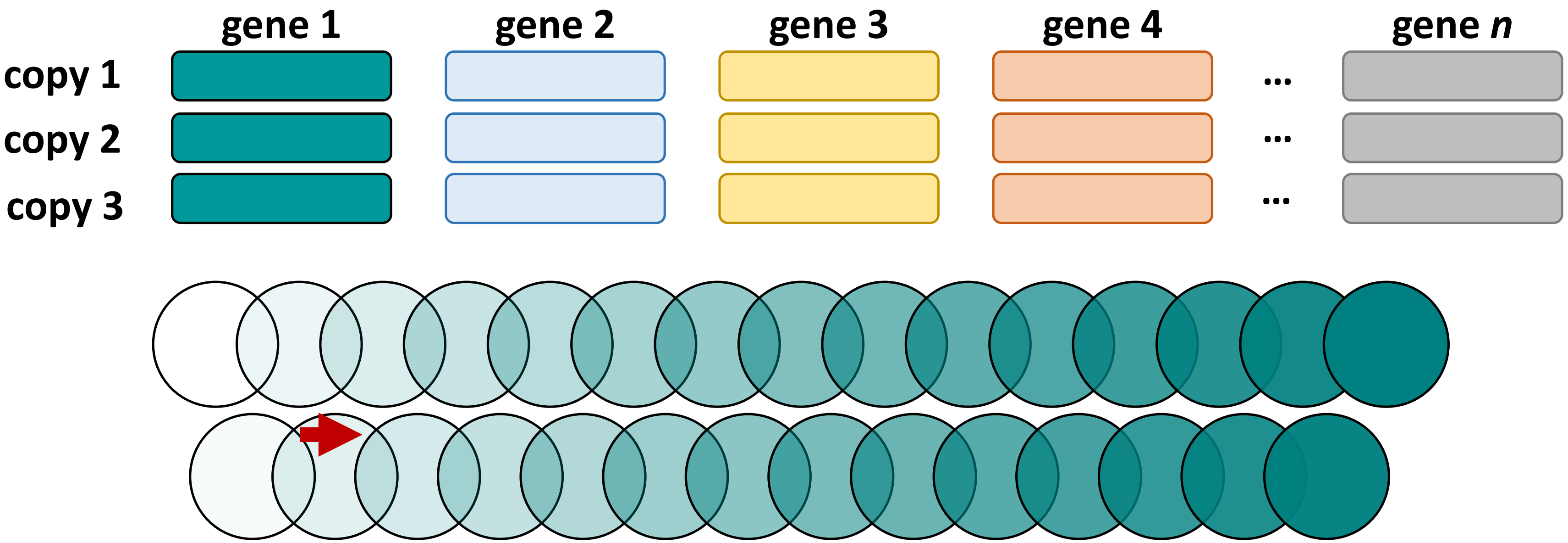
Diploids



Continuous phenotypic variation

Polyploids

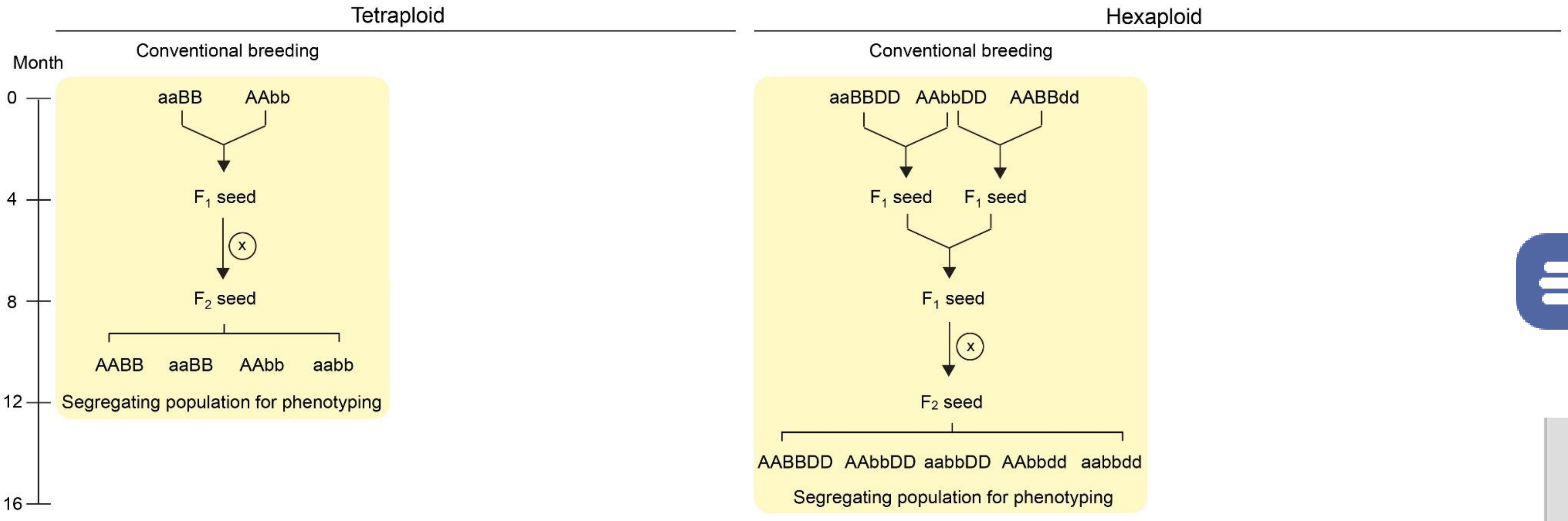
Multiple genes

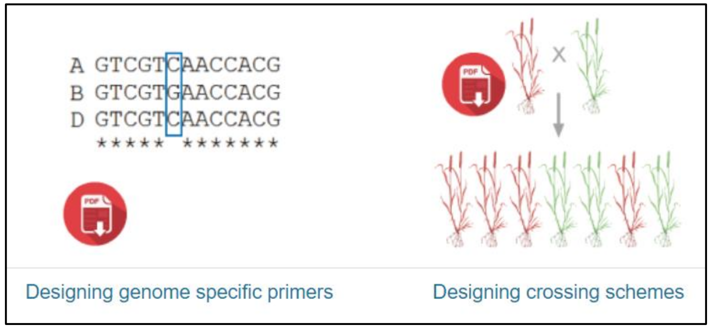


Multiple copies

Functional Redundancy

Combining mutations for full gene knock-outs



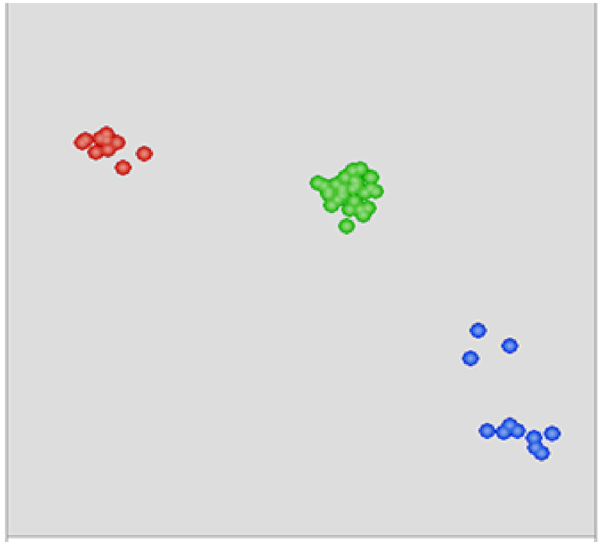


```
A GTCGTCAACCACG
B GTCGTGAACCACG
D GTCGTCAACCACG
  ***** *******
```

Designing genome specific primers

Designing crossing schemes

polymarker



Ramirez-Gonzalez, Uauy, Caccamo 2015 *Bioinformatics*

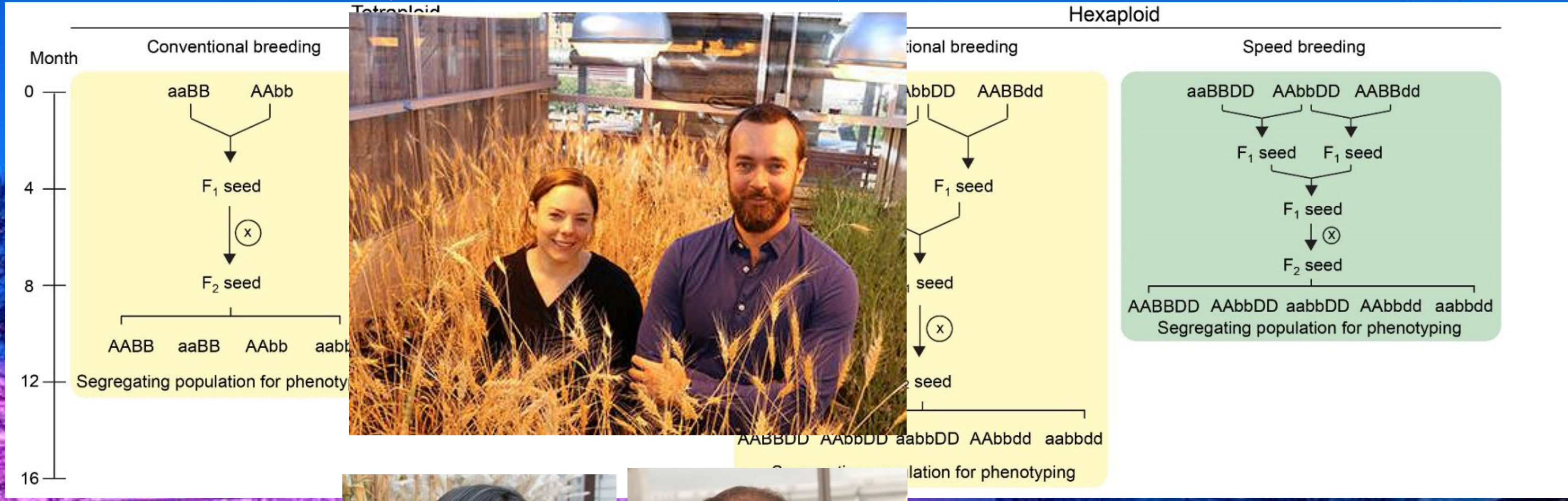
Speed Breeding

Cadenza 38 days after sowing

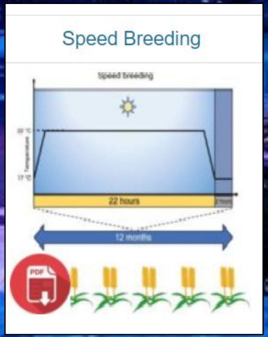
Normal growth

Accelerated growth

Amy Watson & Lee Hickey (Univ Queensland)

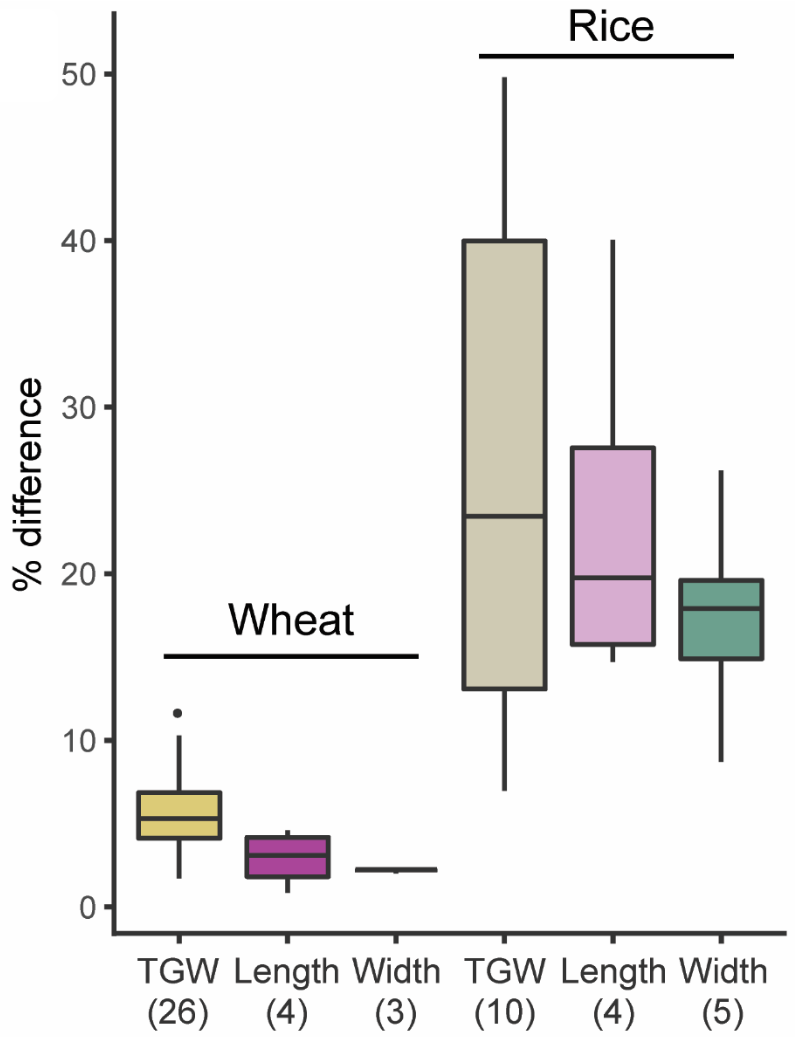


Sreya Ghosh & Brande Wulff (JIC)



Watson et al 2018 *Nature Plants*
Ghosh et al 2018 *Nature Protocols*

QTL effects in wheat are subtle compared to diploid

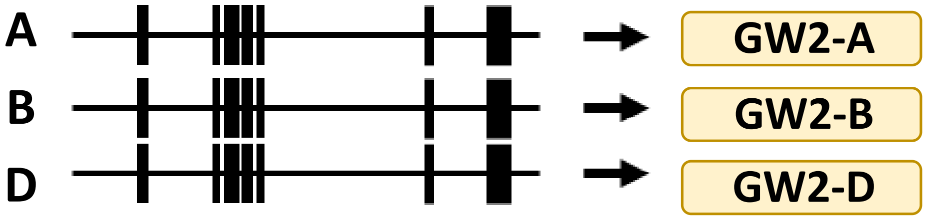


Brinton and Uauy 2018 *JIPB*

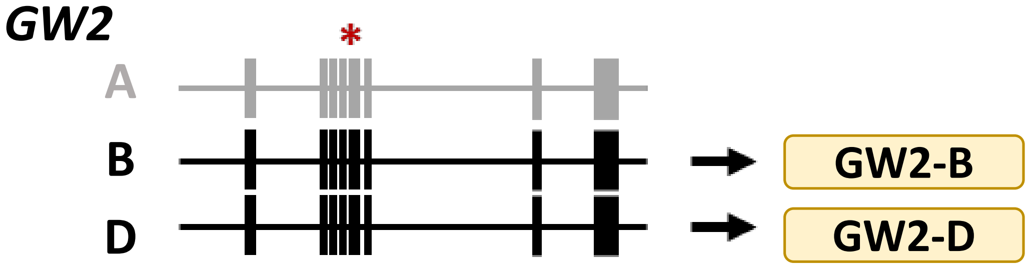
Combining mutations to overcome redundancy

Wildtype

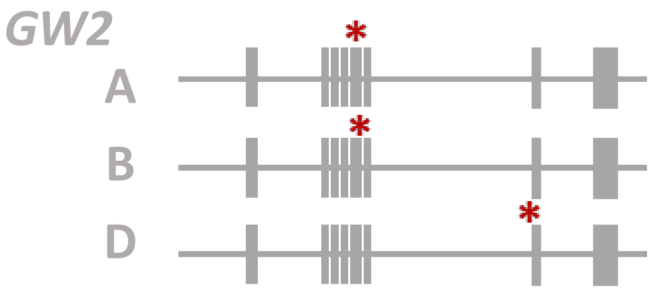
Grain Width 2 (GW2)



Single mutant



Triple mutant



James Simmonds (JIC)

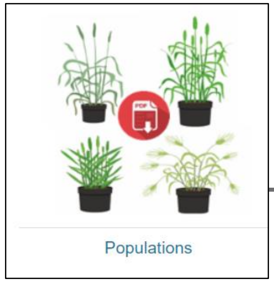
Simmonds et al 2016 *TAG*
Wang et al 2018 *TAG*

20 grains

Increase grain weight

Natural diversity populations

Collection	Short description	Number of accessions	Genotyping	Data/seed availability	More information/ Reference
Wheat diversity panels					
Watkins historic collection of landrace wheats	World collection of wheat landraces grown as farmer saved seed before the 1930s. Genetically stable collection developed by two generations of single seed descent	829 accessions (core set of 119 represent majority of assayed genotypic variation). $F_{4:5}$ mapping populations against Paragon, mainly for the core set.	35K Axiom breeders array (***Allen et al., 2017***); subset exome sequenced (***Gardiner et al., 2018***)	**Genotype**: https://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/axiom_download.php **Seed**: https://www.seedstor.ac.uk/ (store codes WATDE0001-WATDE1063)	http://wisplandracepillar.jic.ac.uk/results_resources.htm ; ***Wingen et al., 2014***; ***Wingen et al., 2017***
NIAB, UK	8-way (parents Alchemy, Brompton, Claire, Hereward, Rialto, Robigus, Xi19, Soissions); 16-way (Banco, Bersee, Brigadier, Copain, Cordiale, Flamingo, Gladiator, Holdfast, Kloka, Maris Fundin, Robigus, Slejpner, Soissons, Spark, Steadfast, Stetson)	NIAB 8-way MAGIC:>1,000 RILs; NIAB 16-way MAGIC: ~600 RILs	35K Axiom breeders array. Genome sequence (Claire, Robigus, others underway). Exome capture sequence of 16-way parents. Skim-seq of all RILs underway.	**Claire and Robigus genomes**: https://opendata.earlham.ac.uk/opendata/data/Triticum_aestivum/EI/v1.1/ **Genotyping and Seed**: https://www.niab.com/research/research-projects/resources	***Mackay et al., 2014***; ***Gardner et al., 2016***

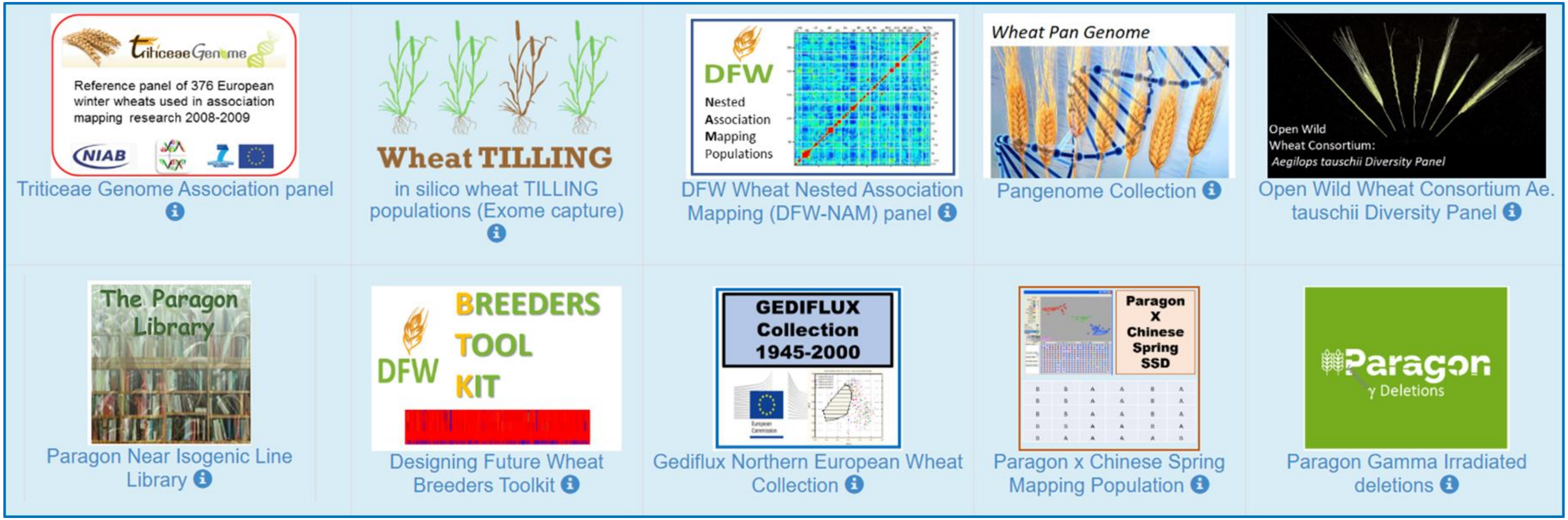


Adamski et al 2020 *eLife*
(Table 2)


Keith Gardner


James Cockram (NIAB)

Publicly available germplasm collections (eg SeedStor)



Triticeae Genome Association panel ℹ

in silico wheat TILLING populations (Exome capture) ℹ

DFW Wheat Nested Association Mapping (DFW-NAM) panel ℹ

Pangenome Collection ℹ

Open Wild Wheat Consortium Ae. tauschii Diversity Panel ℹ

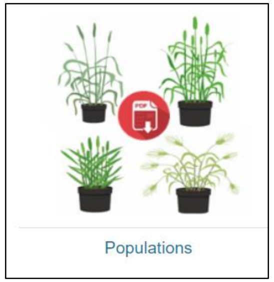
Paragon Near Isogenic Line Library ℹ

Designing Future Wheat Breeders Toolkit ℹ

Gediflux Northern European Wheat Collection ℹ

Paragon x Chinese Spring Mapping Population ℹ

Paragon Gamma Irradiated deletions ℹ

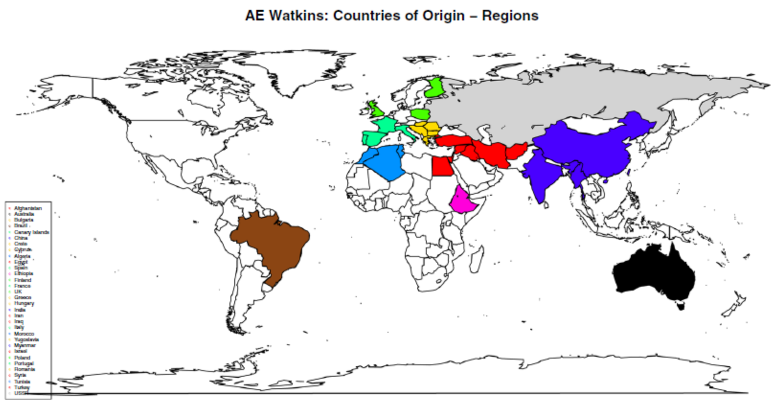

Populations

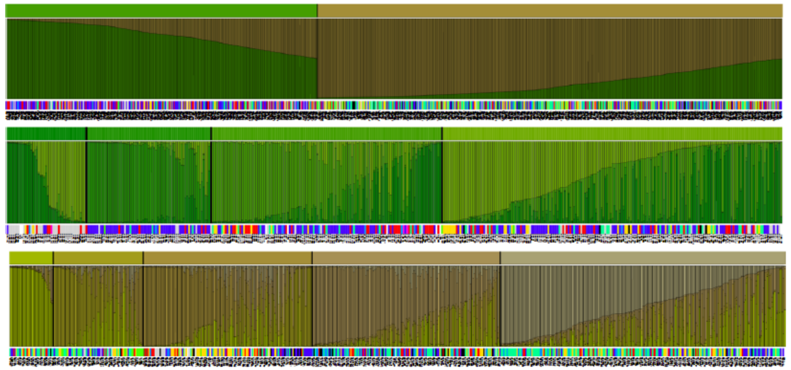
Adamski et al 2020 *eLife*
(Table 2)

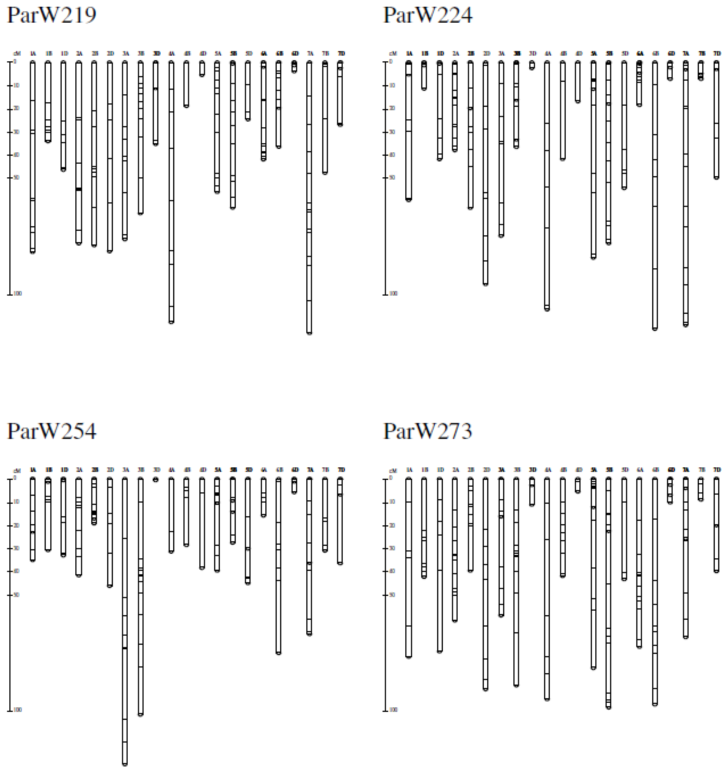
https://www.seedstor.ac.uk/search-browsecollections.php

Watkins NAM population

http://wisplandracepillar.jic.ac.uk/





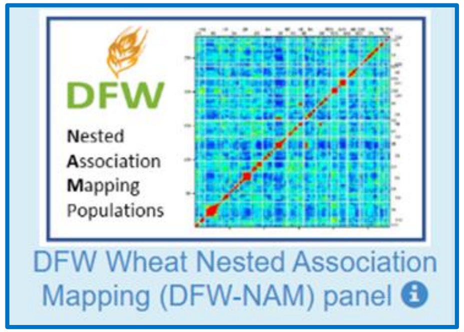


DESIGNING FUTURE WHEAT

>100 F_6 ”off-the shelf” mapping populations (many phenotyped)

Simon Griffiths (JIC)

Luzie Wingen (JIC)

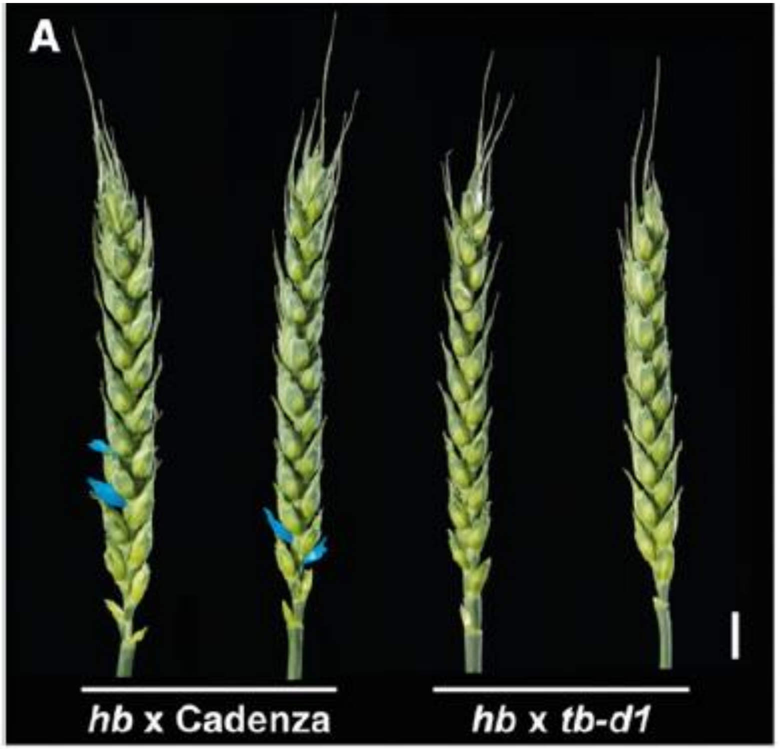


DFW

Nested Association Mapping Populations

DFW Wheat Nested Association Mapping (DFW-NAM) panel

Wingen et al 2014 *TAG*
Wingen et al 2017 *Genetics*



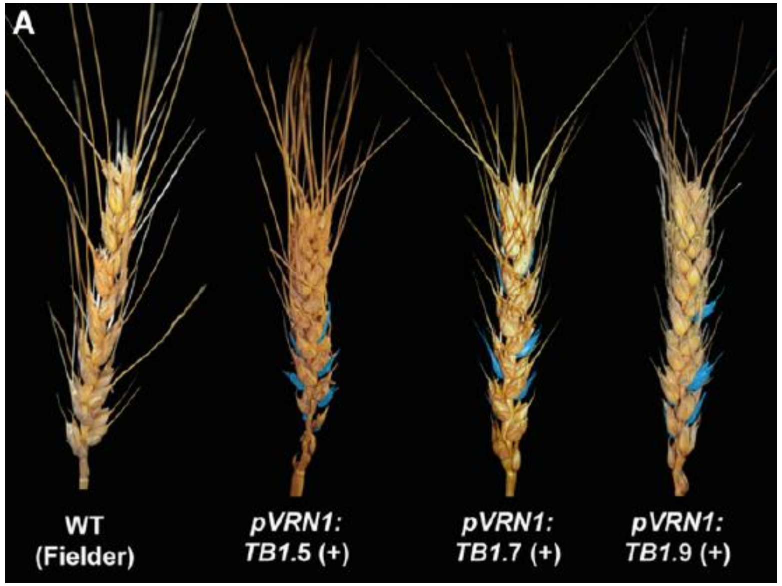
Original allele (*hb*) from CSIRO 4-way MAGIC

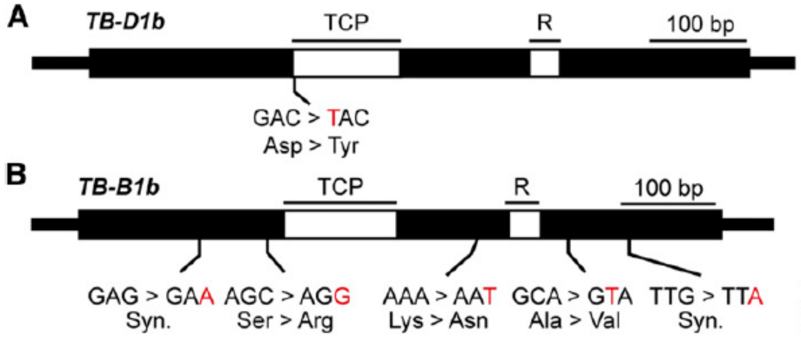
Candidate gene validated with TILLING mutant (*tb-d1*)

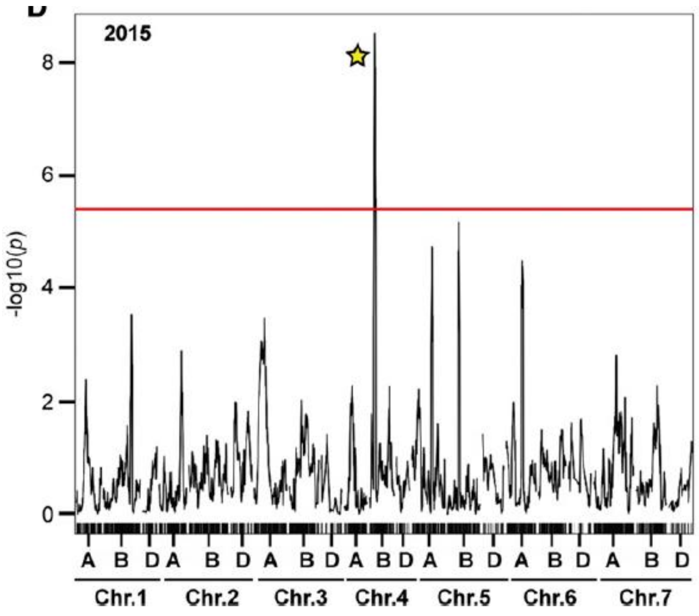
Functional validation with transgenic lines (Fielder)

Identify natural variation

NIAB 8-way MAGIC QTL identifies B genome (*TB-B1*)







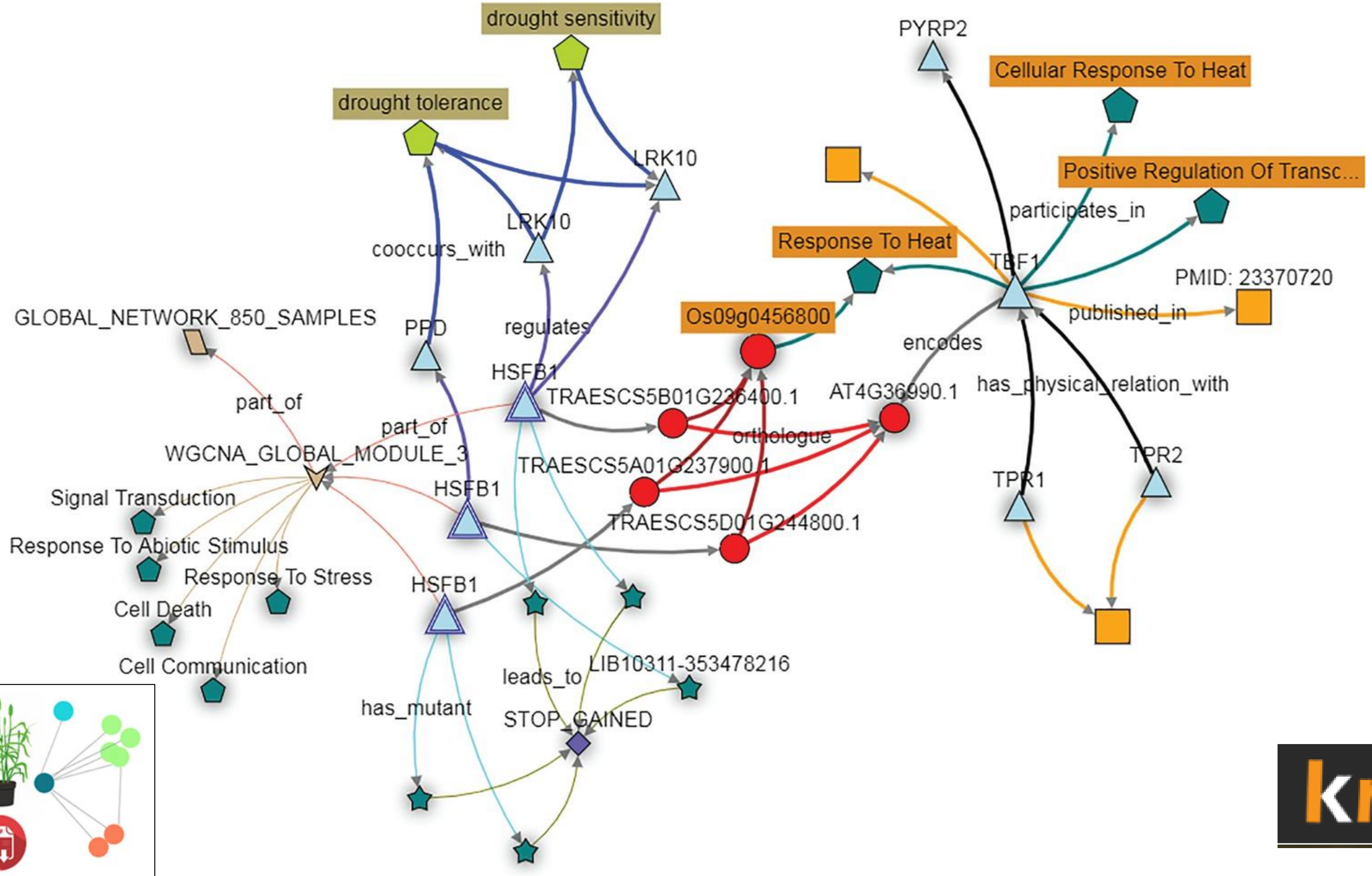
Laura Dixon (Leeds)

Scott Boden (Adelaide)

Dixon et al 2018 *Plant Cell*

Knowledge Networks

https://knetminer.rothamsted.ac.uk/Triticum_aestivum/



Keywan Hassani-Pak
(Rothamsted)

knetminer

Hassani-Pak et al 2020 *bioRxiv*

From one cultivar to over 10 sequenced cultivars

Curtis Pozniak
University of Saskatchewan

10+ GENOME PROJECT

10+ GENOME PROJECT

Variety	Habit	Origin
Lancer	spring	Australia
Mace	spring	Australia
CDC Landmark	spring	Canada
CDC Stanley	spring	Canada
Paragon	spring	UK
Cadenza	spring	UK
Weebil	spring	CIMMYT
Robigus	winter	UK
Claire	winter	UK
Arina	winter	Switzerland
Julius	winter	Germany
Norin-61	winter	Japan
Jagger	winter	US
SY Mattis	winter	Syngenta
Kronos	spring	US
Svevo	spring	Italy
Zavitan	-	Israel

Bread wheat (6x)

Durum wheat (4x)

Wild emmer (4x)

Variety	Habit	Origin
Lancer	spring	Australia
Mace	spring	Australia
CDC Landmark	spring	Canada
CDC Stanley	spring	Canada
Paragon	spring	UK
Cadenza	spring	UK
Weebil	spring	CIMMYT
Robigus	winter	UK
Claire	winter	UK
Arina	winter	Switzerland
Julius	winter	Germany
Norin-61	winter	Japan
Jagger	winter	US
SY Mattis	winter	Syngenta
Kronos	spring	US
Svevo	spring	Italy
Zavitan	-	Israel

Sean Walkowiak
(Canadian Grain Commission)

Variety	Habit	Origin
Lancer	spring	Australia
Mace	spring	Australia
CDC Landmark	spring	Canada
CDC Stanley	spring	Canada
Paragon	spring	UK
Cadenza	spring	UK
Weebil	spring	CIMMYT
Robigus	winter	UK
Claire	winter	UK
Arina	winter	Switzerland
Julius	winter	Germany
Norin-61	winter	Japan
Jagger	winter	US
SY Mattis	winter	Syngenta
Kronos	spring	US
Svevo	spring	Italy
Zavitan	-	Israel

New Results

W2RAP: a pipeline for high quality, robust assemblies of large complex genomes from short read data

Bernardo Clavijo, Gonzalo Garcia Accinelli, Jonathan Wright, Darren Heavens, Katie Barr, Luis Yanes, Federica Di Palma

doi: https://doi.org/10.1101/110999

Clavijo et al 2017 *bioRxiv*

Bernardo Clavijo
(Earlham Institute)

Earlham Institute
Decoding Living Systems

Currently available

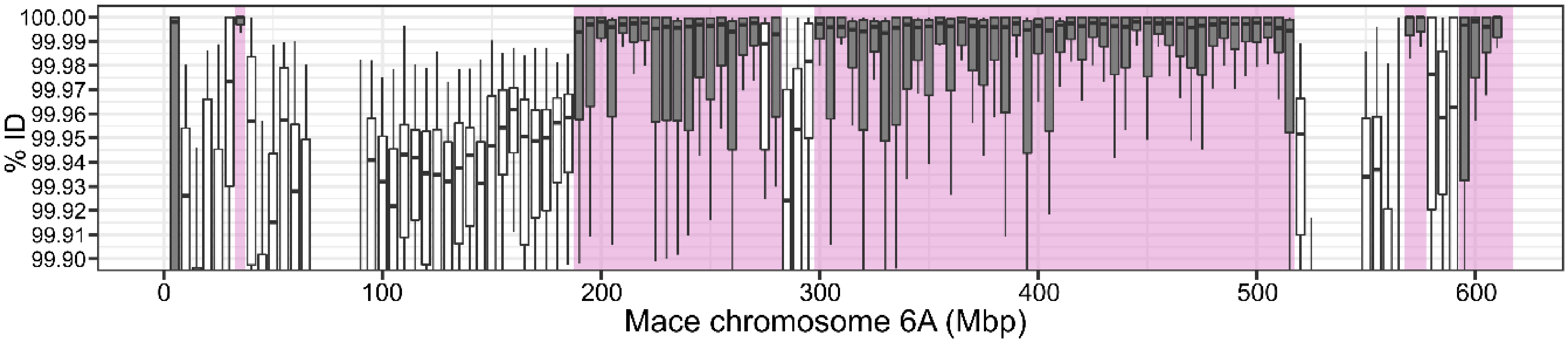
Variety	Habit	Origin		Website
CDC Landmark	spring	Canada	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Arina	winter	Switzerland	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Julius	winter	Germany	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Jagger	winter	US	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Zavitan	-	Israel	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Lancer	spring	Australia	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Mace	spring	Australia	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Norin-61	winter	Japan	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
CDC Stanley	spring	Canada	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
SY Mattis	winter	Syngenta	10G	http://webblast.ipk-gatersleben.de/wheat_ten_genomes/
Svevo	spring	Italy	Interomics	https://www.interomics.eu/durum-wheat-genome
Paragon	spring	UK	Earlham	https://wheatis.tgac.ac.uk/grassroots-portal/blast
Cadenza	spring	UK	Earlham	https://wheatis.tgac.ac.uk/grassroots-portal/blast
Robigus	winter	UK	Earlham	https://wheatis.tgac.ac.uk/grassroots-portal/blast
Claire	winter	UK	Earlham	https://wheatis.tgac.ac.uk/grassroots-portal/blast
Kronos	spring	US	Earlham	https://wheatis.tgac.ac.uk/grassroots-portal/blast

Fei Lu (CAS)
25 *Triticum/Aegilops* ssp.
Zhou et al 2020 *bioRxiv*

Coming to EnsemblPlants Soon!

ACTGCGT
Genome assemblies

Using the wheat pangenome to define haplotypes

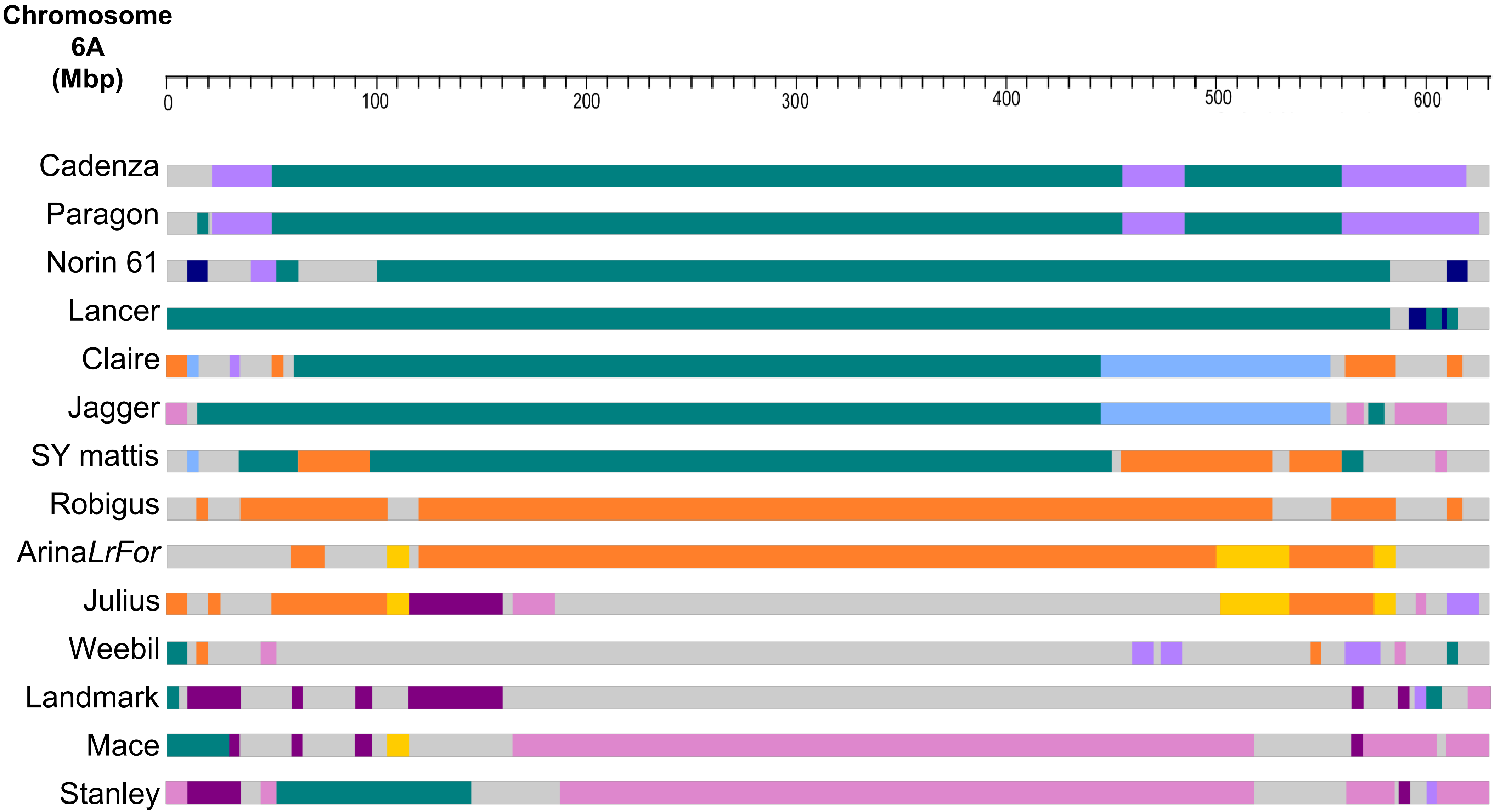


Jemima Brinton
(JIC)

Ricardo Ramirez-Gonzalez
(JIC)

Brinton et al 2020 *unpublished*

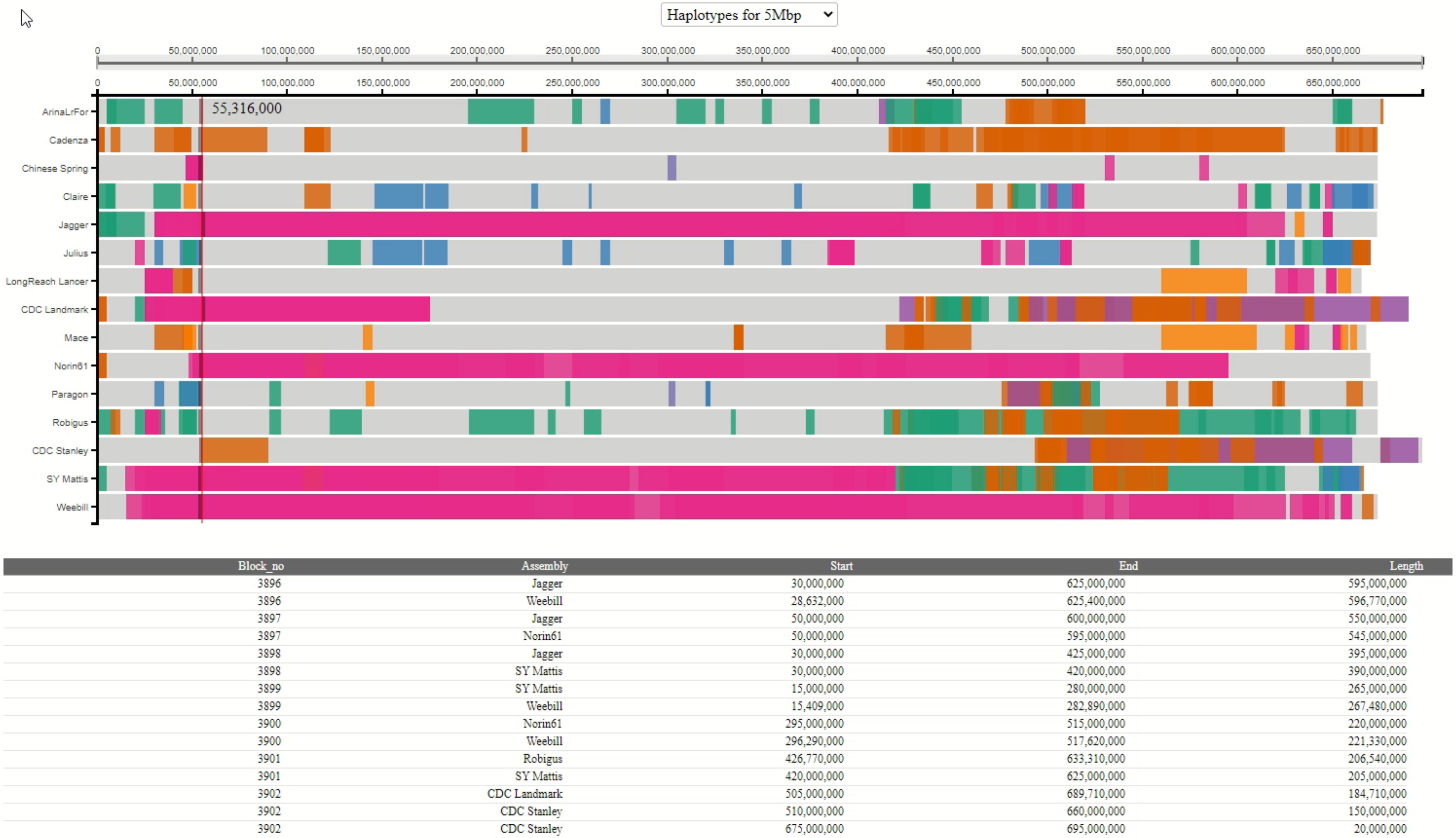
Defining haplotypes across all cultivars (chr 6A)



Brinton et al 2020 *unpublished*

Visualisation interface (chr 4B example)

http://www.crop-haplotypes.com/



Block_no	Assembly	Start	End	Length
3896	Jagger	30,000,000	625,000,000	595,000,000
3896	Weebill	28,632,000	625,400,000	596,770,000
3897	Jagger	50,000,000	600,000,000	550,000,000
3897	Norin61	50,000,000	595,000,000	545,000,000
3898	Jagger	30,000,000	425,000,000	395,000,000
3898	SY Mattis	30,000,000	420,000,000	390,000,000
3899	SY Mattis	15,000,000	280,000,000	265,000,000
3899	Weebill	15,409,000	282,890,000	267,480,000
3900	Norin61	295,000,000	515,000,000	220,000,000
3900	Weebill	296,290,000	517,620,000	221,330,000
3901	Robigus	426,770,000	633,310,000	206,540,000
3901	SY Mattis	420,000,000	625,000,000	205,000,000
3902	CDC Landmark	505,000,000	689,710,000	184,710,000
3902	CDC Stanley	510,000,000	660,000,000	150,000,000
3902	CDC Stanley	675,000,000	695,000,000	20,000,000

Brinton et al 2020 *unpublished*

VIRTUAL CONFERENCE

PLANT GENOMES IN A CHANGING ENVIRONMENT

12-14 October, 2020

Abstracts due 01 September

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Wenbo Ma – UC Riverside, USA / The Sainsbury Lab, UK
Sarah McKim – University of Dundee, UK
Jane Parker – Max Planck Institute, Germany
Corné Pieterse – Utrecht University, The Netherlands
Michael Purugganan – New York University, USA

Concluding thoughts

- Open-access resources to enable biological understanding
- Polyploidy 'hides' useful phenotypic variation
- Be collaborative and open
- For more info:
    - www.wheat-training.com
    - Adamski et al 2020 *eLife*

VIRTUAL CONFERENCE

PLANT GENOMES
IN A CHANGING
ENVIRONMENT

12-14 October, 2020

Abstracts due 01 September

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Wheat (and human) diversity

10+ GENOME PROJECT

DESIGNING FUTURE WHEAT

IWYP International Wheat Yield Partnership
Research to Deliver Wheat for the Future

erc
European Research Council
Established by the European Commission

@CristobalUauy

UKRI Biotechnology and Biological Sciences Research Council

cristobal.uauy@jic.ac.uk