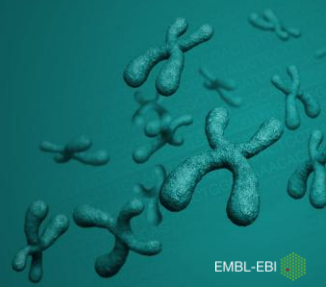
Wheat Genomes in Ensembl Plants

Paul Kersey



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Ensembl empowered

- A platform for genome annotation, analysis and browsing, developed jointly by the EBI and Wellcome Trust Sanger Institute
- Modules for handling variation data, comparative genomics, gene prediction etc.
- Multiple points of access to data: web-based application, Perl and REST-ful APIs, public mySQL databases, BioMart data mining tool, DAS client and server, FTP
- Upload your own data and compare to reference annotation
- Originally developed for vertebrate genomes, subsequently extended to non-vertebrate species ("Ensembl Genomes")

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vertebrates (ensembl.org)

bacteria.ensembl.org

fungi.ensembl.org

protists.ensembl.org

plants.ensembl.org

metazoa.ensembl.org

empowered

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Data

- Genomic sequence
- Gene / transcript / protein models
- External references
- Mapped cDNAs, proteins, microarray probes, BAC clones, repeats, markers etc. etc.
- Variation data:
  - sequence variants
  - structural variants
- Comparative data:
  - gene trees, orthologues, paralogues
  - pairwise whole genomic alignments, syntenic regions

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Wheat data in Ensembl Plants (release 21)

- Version1.0 of the chromosome survey sequence assembly generated by the International Wheat Genome Sequencing Consortium.
- Version 2.0 of the IWGSC gene models called on the survey sequence
  - Version 2.1 due in next release (March 2014)
- Whole genome alignments against Brachypodium and rice
- Alignments to wheat Unigenes and RNA-seq data

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Chromosome survey sequence: plans for the next release (release 22, due March 2014)

- Whole genome alignments
  - Against barley, *Triticum uratu* and *Aegilops taucshcii*
  - Wheat AvB, AvD, BvD
- Alignment to wheat full length ESTs
- Additional RNA-seq alignments

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Genome assemblies from Brenchley *et al*.

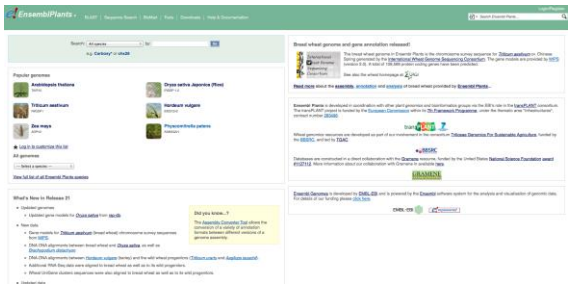
- The wheat genome assemblies generated by Brenchley et al. (PMID: 23192148) have also been aligned to the survey sequence, Brachypodium and barley
  - Homeolegous variants inferred between the 3 wheat genomes (from this work) are also displayed in the context of the gene models from Brachypodium and barley

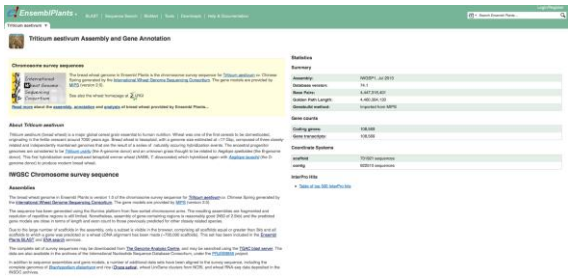
Diploid progenitor genomes

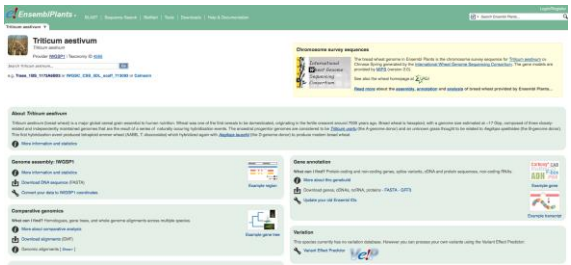
- *Aegilops tauschii* and *Triticum uratu* are also included in Ensembl Plants
- These genomes have been aligned to rice, and to relevant RNA-seq reads.
- These genomes and other more distant relatives (e.g. barley, Brachypodium, and rice) are all included in gene-centric comparative analyses

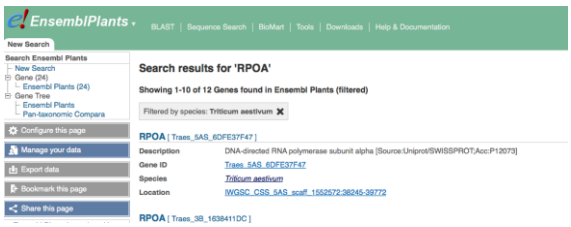
Sequence

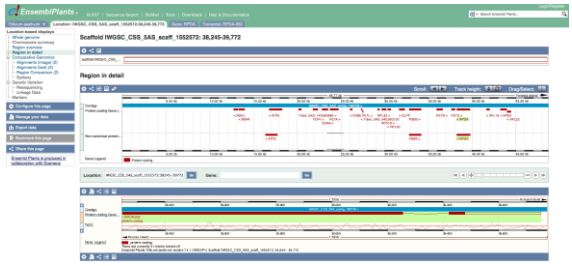
- The chromosome survey sequence (and its annotations) are available to search via BLAST and other search alignment algorithms.
- EST-based search (with onward genomic mapping) also available

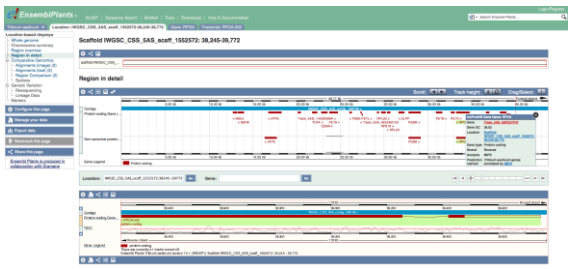







EnsemblPlants
BLAST | Sequence Search | BioMart | Tools | Downloads | Help & Documentation
New Search
Search Ensembl Plants
New Search
Gene (24)
Ensembl Plants (24)
Gene Tree
Ensembl Plants
Pan-taxonomic Compara
Configure this page
Manage your data
Export data
Bookmark this page
Share this page
Search results for 'RPOA'
Showing 1-10 of 12 Genes found in Ensembl Plants (filtered)
Filtered by species: Triticum aestivum
RPOA [Traes_5AS_6DFE37F47]
Description
DNA-directed RNA polymerase subunit alpha [Source:Uniprot/SWISSPROT;Acc:P12073]
Gene ID
Traes_5AS_6DFE37F47
Species
Triticum aestivum
Location
IWGSC_CSS_5AS_scaff_1552572:38245-39772
RPOA [Traes_3B_1638411DC]


Scaffold IWGSC_CSS_5AS_scaff_1552572: 38,245-39,772
Region in detail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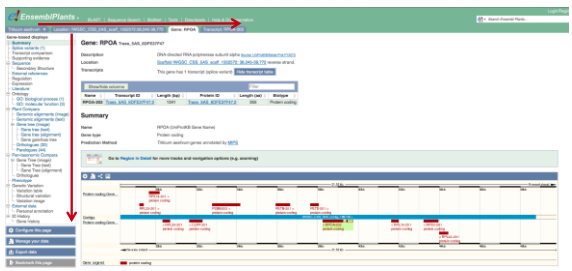
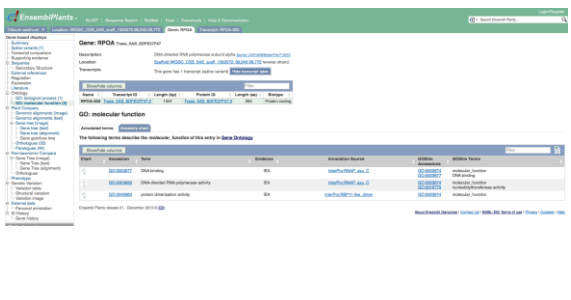
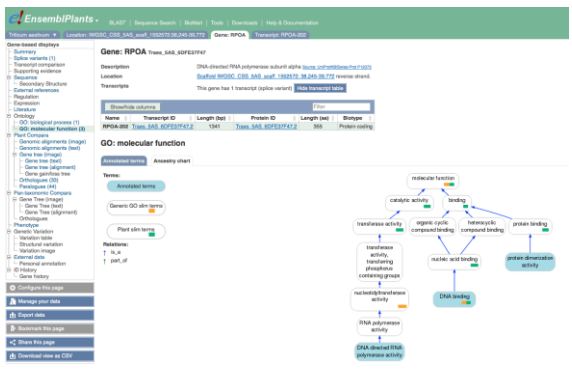
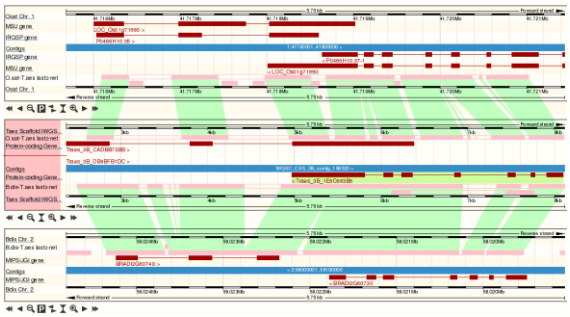
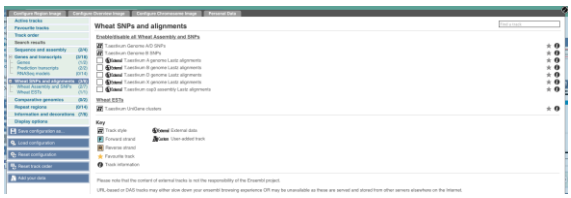
Region in detail

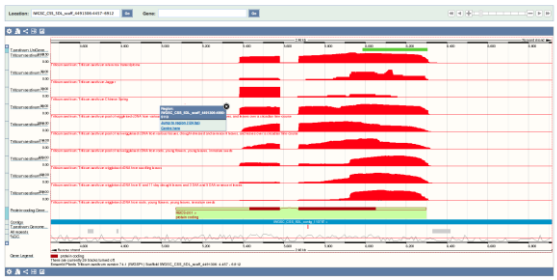

Gene: RPOA
Summary


Gene: RPOA
GO: molecular function


Gene: RPOA
GO: molecular function
molecular function
catalytic activity
binding
transferase activity
organic cyclic compound binding
heterocyclic compound binding
protein binding
nucleic acid binding
DNA binding
RNA polymerase activity
DNA-directed RNA polymerase activity



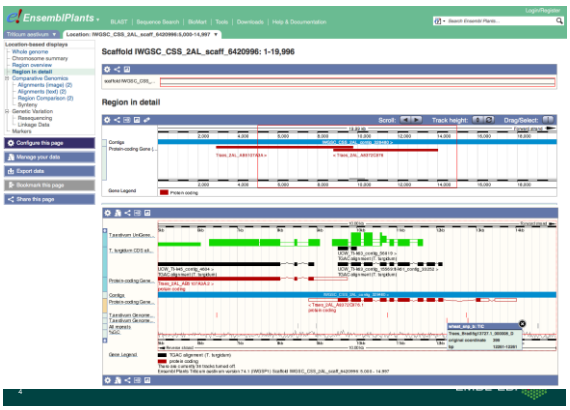




Inter-homeologeous variants

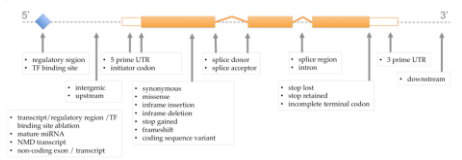
- Data from Brenchley et al. mapped onto chromosome survey sequence
- Data from chromosome survey sequence itself due in next release

	Inter-homeologue variants (total)	Inter-homeologue variants (mapped)	% variants mapped
A/D	102,593	101,570	99
B	22,959	29,638	99
Total	132,552	131,208	99



Variant Effect Predictor (VEP)

- Predicts functional consequences of known and unknown variants
- For substitutions, insertions, deletions and structural variants
- Web interface (for up to 750 variants), standalone Perl script, Perl API and REST API
- http://www.ensembl.org/info/docs/variation/vep/index.html



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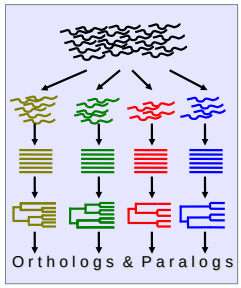
Gene tree pipeline



Take canonical protein for each gene belonging to one Ensembl Genomes clade

Cluster: WU-BLASTP + Smith-Waterman all-versus-all, hcluster_sg

Align: multiple aligners consensified by M-Coffee

Build trees: PhyML-WAG + PhyML-HKY + NJ-p + NJ-dN + NJ-dS + species tree → TreeBeST-merge

Infer orthologues and paralogues

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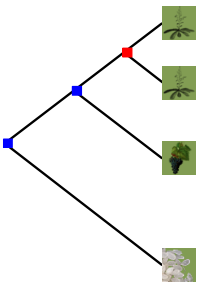
Orthologues and paralogues



Paralogues:

Any gene pairwise relationship where the ancestor node is a duplication event

Orthologues:

Any gene pairwise relationship where the ancestor node is a speciation event

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Orthology / paralogy types

- ortholog_one2one
- ortholog_one2many
- ortholog_many2many
- apparent_ortholog_one2one
- possible_ortholog (weakly supported duplication node)

- within_species_paralog
- other_paralog (too distant to be in the same tree)

- contiguous_gene_split (artefact)
- putative_gene_split (artefact)
- 94,280 wheat genes in inferred orthology relationships with 270216 genes from other creals

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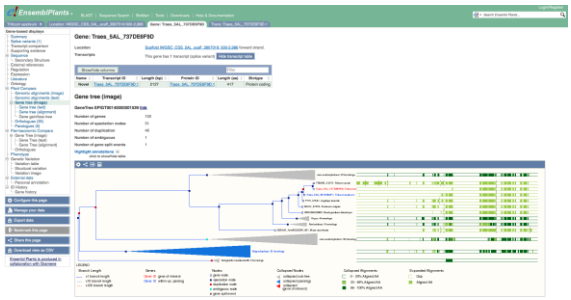

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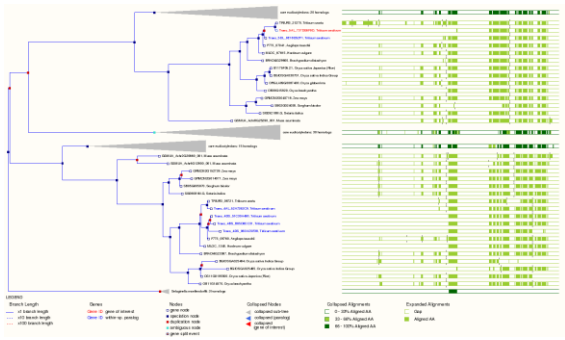

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Visualise your own data

Upload data
- Data saved by Ensembl
- 5 MB limit (and therefore not possible for large file formats)

Attach remote file
- URL-based (HTTP or FTP)
- No size limit

- Uploaded / attached tracks can be saved (to account)
- Uploaded / attached tracks can be shared with other users
- Only trivial security, do not use for sensitive data!

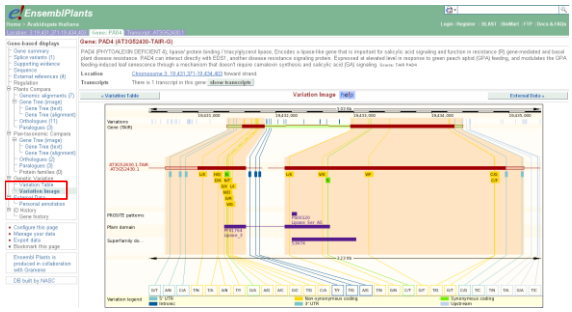
- http://www.ensembl.org/info/website/upload/index.html

Possible formats

- BAM sequence alignments (no upload)
- BED genes / features
- BedGraph continuous-valued data
- BigBed genes / features (no upload)
- BigWig continuous-valued data (no upload)
- TrackHub collection of tracks
- Gbrowse genes / features
- GFF/GTF genes / features
- PSL sequence alignments
- VCF variants (no upload)
- WIG continuous-valued data

Next release

- Improved representation of the polyploid genome
  - Preconfigured A v B v D compartive views
  - Separation of 3 wheat genomes in the gene tree analysis
- Representation of inter-homologue data as a full variation database
  - Data structure can also accommodate inter-varietal SNPs, links to phenotypes, haplotype structure etc.



Funding

- Ensembl Genomes Funded by
  - EMBL
  - EU (INFRAVEC, Microme, transPLANT, AllBio)
  - BBSRC (PhytoPath, wheat/barley/midge sequencing, UK-US collaboration, RNAcentral)
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People

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