**Table S1**

General architecture and processes of the TriAnnot pipeline V3.5 (full analysis) with a description of each module.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Panels** | **Modules or Steps** | **Software**(1) | **DataBanks**(2) | **Tasks** | **Module or Stepdependency** | **Remarks** |
| I | 01 | 16,3,4 | 1,2,4,6,7,8,9,10,11 | Repeats annotation |  | Transposable Elements (TEs) masking + masking of univec hits and *E. coli* hits |
| I | 02 | 2 | 3 | Similarity searches (BLASTX) |  | TEs proteins |
| I | 03 | 15 | 5 | TEs annotation |  |  |
| I | 04 | 21 | 73 | GTtallymer |  |  |
|  |
| II | 05 | 7,8,9,10,11 | **-** | *ab initio* gene prediction | 01 | Augustus uses a maize or wheat matrix; FGeneSH uses a monocot matrix; GeneMarkHMM uses either wheat or barley or maize or rice matrix; GeneID uses wheat matrix. |
| II | 06 | 2,20 | 12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,50,53,56,59,62,65,70 | Transcripts spliced alignments | 01 | BLASTN/exonerate: spliced alignments for nucleic biological evidences. |
| II | 07 | 2,20 | 41,42,43,44,45,46,47,51,54,57,60,63,66,67,68,69,72 | Protein spliced alignments | 01 | BLASTX/exonerate: spliced alignments for protein biological evidences. |
| II | 08 | 1with 2 & 5 | 47,70,71 | SIMsearchgene modelssimilarity only | 05 | Annotation of gene model of Categories 00, 01, 02 and 03. Need a soft-masked genome sequence. |
| II | 08 | 12 | 17,47 | EuGenegene models*ab initio* & similarities | 01,05,06,07 | EuGene is used here only as a combiner based on *ab initio* gene prediction (augustus wheat), similarity data (BLASTN/exonerate) against *Triticum aestivum* ESTs, similarity data (BLASTN/exonerate against SIMnuc) and similarity data (BLASTX/exonerate against SIMprot).  |
| II | 08 | - | - | Merge betweenSIMsearch, EuGene and augustus | 05,08 | For each locus the best category is kept with the following priority:Cat 0 > Cat 1 > Cat 2 > Cat 3 (SIMsearch) >Cat 4 (EuGene) > Cat5 (augustus) |
| II | 09 | 2,13 | 29,41,42,48,54 | **Functional annotation**(3) | 08 | known function BLASTP: UniProtKB/Swiss-Prot >80% identity & >80% coverageputative function BLASTP: UniProtKB/Swiss-Prot + UniProtKB/TrEMBL >45% identity & >50% coverage without hypothetical proteindomain containing protein PfamA and Gene Ontology (GO)expressed sequences TBLASTN: Plant ESTs databank > 45% identity & >50% coverageconserved unknown function BLASTP: UniProtKB/Swiss-Prot + UniProtKB/TrEMBL 45% identity & 50% coverage hypothetical protein onlyhypothetical protein (only *ab initio*) |
| II | 10 | 2,20 | 46,51,54,57,60,63,66,67,68,69,72 | Best hits | 08 | BLASTP/exonerate: spliced alignments for best hit protein.The pipeline verifies also amino acids gaps leading to check the absence or addition of exon within the gene model |
| II | 11 | 14 | **-** | Protein domains, gene ontology | 08 | Uses only PfamA, Prosit, SMART and Gene Ontology (GO terms) |
|  |
| III | 12 | 2 | 37,38,39,40,49,52,55,58,61,64 | BLASTN againstorganelles genomes andpseudo molecules |  | For Conserved Non Coding Sequences – CNSsGenome model pseudo molecules: *Arabidopsis thaliana* (TAIR); Rice (IRGSP); Rice (MSU); Maize (MSO); Sorghum (DOE); *Brachypodium distachyon* (JGI).  |
| III | 13 | 2 | 51,54,57,60,63,66 | BLASTX against protein databanks |  | Proteins derived from CDS annotation from Genome models such as: *Arabidopsis thaliana* (TAIR); Rice (IRGSP); Rice (MSU); Maize (MSO); Sorghum (DOE); *Brachypodium distachyon* (JGI) |
| III | 14 | 18 | **-** | tRNA annotation |  |  |
|  |
| IV | 15 | 17 | **-** | SSRs annotation |  | The parameters of TRF are tuned to find mainly microsatellites: minimum score=30; maximum period=5 |

(1) Software number (see table below)

(2) Databanks number (see Supplementary Table 2)

(3) The functional annotation follows a modification of the IWGSC annotation guide line.

List of software used within the TriAnnot pipeline V3.5

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Number** | **Softwares** | **Version** | **URL** | **References** |
| 1 | SIMsearch | AUG 2011 | Developed by T. Itoh’s bioinformatics Group at NIAS, Japan | - |
| 2 | BLAST | 2.2.21 | ftp://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST  | ([Altschul et al., 1997](#_ENREF_1)) |
| 3 | wu-BLAST | 2.2.6 | http://www.advbiocomp.com/blast.html  | Advanced Biocomputing LLC |
| 4 | cross-match | 0.990329 | http://www.incogen.com/public\_documents/vibe/details/crossmatch.html  | Green P. *et al*. |
| 5 | est2genome | EMBOSS\_6.1.0 | ftp://ftp.sanger.ac.uk/pub/pmr/  | ([Mott, 1997](#_ENREF_13)) |
| 6 | Gmap | 2010-03-09 | http://research-pub.gene.com/gmap/  | ([Wu and Watanabe, 2005](#_ENREF_29)) |
| 7 | GeneID | 1.3 | http://www1.imim.es/software/geneid/index.html  | ([Guigo et al., 1992](#_ENREF_7)) |
| 8 | GeneMarkHMMgmhmm2 | 2.2a | http://opal.biology.gatech.edu/GeneMark/  | ([Lukashin and Borodovsky, 1998](#_ENREF_12))([Lomsadze et al., 2005](#_ENREF_10)) |
| 9 | GeneMarkHMMgmhmm3 | 3.9d | http://opal.biology.gatech.edu/GeneMark/ | ([Lukashin and Borodovsky, 1998](#_ENREF_12))([Lomsadze et al., 2005](#_ENREF_10)) |
| 10 | FGeneSH | 3.1.1 | http://linux1.softberry.com/berry.phtml  | SoftBerry |
| 11 | augustus | 2.4 | http://augustus.gobics.de/  | ([Stanke and Waack, 2003](#_ENREF_23)) |
| 12 | EuGene | 4.0 | http://eugene.toulouse.inra.fr/  | ([Schiex et al., 2001](#_ENREF_19)) |
| 13 | HMMER | 3.0 | http://hmmer.janelia.org/software | ([Durbin R, 1998](#_ENREF_4)) |
| 14 | InterProsScan | 4.6 | http://www.ebi.ac.uk/interpro/  | ([Zdobnov and Apweiler, 2001](#_ENREF_30)) |
| 15 | TEannot | 1.4 | http://urgi.versailles.inra.fr/index.php/urgi/Tools/REPET  | ([Quesneville et al., 2005](#_ENREF_17)) |
| 16 | RepeatMasker | 3.2.6 | http://www.repeatmasker.org/  | ([Smit, 1993](#_ENREF_22)) |
| 17 | TRF | 4 | http://tandem.bu.edu/  | ([Benson, 1999](#_ENREF_2)) |
| 18 | tRNAscan-SE | 1.23 | http://lowelab.ucsc.edu/tRNAscan-SE/  | ([Lowe and Eddy, 1997](#_ENREF_11)) |
| 19 | GBrowse | 1.70 | http://gmod.org/wiki/Main\_Page  | Generic Model Organism Database (GMOD) |
| 20 | exonerate | 2.2.0 | http://www.ebi.ac.uk/~guy/exonerate/  | ([Slater and Birney, 2005](#_ENREF_21)) |
| 21 | GTtallymer | 1.3.4 | http://seqanswers.com/wiki/Tallymer  | ([Kurtz et al., 2008](#_ENREF_9)) |

**Table S2**

List of databanks used within the TriAnnot pipeline V3.5

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Number** | **Databanks(1)** | **Release** | **http and/or ftp URLs for downloading** | **References** |
|  | **Repeat Databanks** |  |  |  |
| 1 | TREP\_total | 10 | http://wheat.pw.usda.gov/ITMI/Repeats/index.shtml  | ([Wicker et al., 2002](#_ENREF_28)) |
| 2 | TREP\_nr |
| 3 | TREP\_prot |
| 4 | TREP\_plus | FCREP-all-1.2 | TREPplus = TREPtotal + F. Choulet annotated TEs***Databank not publicly available*** | ([Choulet et al., 2010](#_ENREF_3)) |
| 5 | TREP\_cons | JAN2010 | \* 58 are consensus made from TE copies already in TREP release 10 (for which there is no consensus) and from TE copies found by Choulet *et al.* The number of copies used to make the consensus is in the sequence headers (“msa” stands for “multiple sequence alignment”)\* 188 are TE copies (already in TREP release 10) belonging to known families for which there are less than 3 copies, thus no consensus are made for these families\* 63 are TE copies (already in TREP release 10) that are “unnamed”, thus no consensus are made for these families\* 140 are TE copies (Choulet *et al.*) that are “unnamed”, thus no consensus are made for these families\* 91 are consensus already in TREP release 10***Databank not publicly available*** | ([Flutre et al., 2011](#_ENREF_6)) |
| 6 | TIGR\_Fam\_Repeats | V2-V3.3 | *Gramineae, Fabaceae, Solanaceae, Brassicaceae*ftp://ftp.tigr.org/pub/data/TIGR\_Plant\_Repeats/  | TIGR, US |
| 7 | TIGR\_GSS\_Repeats | JUL2004 | *Arabidopsis, Brassica, Glycine, Lotus, Lycopersicon, Medicago, Oryza, Sorghum, Triticum, Zea*ftp://ftp.tigr.org/pub/data/TIGR\_Plant\_Repeats/TIGR\_GSS\_Derived\_Repeats/  |
| 8 | MIPS\_repeat | 8.3 | ***Databank not publicly available*** | K. Mayer (MIPS) |
| 9 | ALL\_Repbase | 16.03 | http://www.girinst.org/server/RepBase/index.php  | ([Jurka et al., 2005](#_ENREF_8)) |
| 10 | univec | 6.0 | http://www.ncbi.nlm.nih.gov/VecScreen/UniVec.html ftp://ftp.ncbi.nih.gov/pub/UniVec/README.uv  | NCBI-GenBankKitts *et al.* unpublished |
| 11 | Ecoli | 107 | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Molecule: genomic dnaembl-Class: stdembl-Description: complete&genomeembl-Organism: Escherichia&coli | EBI-EMBL, UK |
|  | **Nucleic Databanks** |  |  |  |
| 12 | PlnCpltCDS (3) | 107 | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Division: plnembl-Molecule: mrnaembl-Class: stdembl-Description: complete&cds | EBI-EMBL, UK |
| 13 | PlnMrnaSTD (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Division: plnembl-Molecule: mrnaembl-Class: std | EBI-EMBL, UK |
| 14 | PoaMrnaSTD (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Division: plnembl-Molecule: mrnaembl-Class: stdembl-Taxon: Poaceae | EBI-EMBL, UK |
| 15 | PlnFL (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Division: plnembl-Molecule: mrnaembl-Class: stdembl-Description: full&insert or FLI\_CDNA | EBI-EMBL, UK |
| 16 | TaFL (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Division: plnembl-Molecule: mrnaembl-Class: stdembl-Description: FLI\_CDNAembl-Taxon: Triticum|Aegilopshttp://trifldb.psc.riken.jp/download.pl for 6146 FLcDNAhttp://trifldb.psc.riken.jp/download/ver.2.0/TaRFL5740.fas.gz for 5740 FLcDNAhttp://trifldb.psc.riken.jp/download/ver.3.0/TaRFL4905.fas.gz for 4905 FLcDNA | EBI-EMBL, UKRiken, Japan |
| 17 | TaEST (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession embl-Division: plnembl-Organism: Triticum&aestivumembl-Class: est | EBI-EMBL, UK |
| 18 | HvFL (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSessionembl-Division: plnembl-Molecule: mrnaembl-Class: stdembl-Description: FLI\_CDNAembl-Taxon: Hordeum |
| 19 | HvEST (3) | http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession embl-Division: plnembl-Organism: Hordeum&vulgareembl-Class: est |
| 20 | AT\_unigene (3) | 70 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Arabidopsis\_thaliana/  | ([Wheeler et al., 2003](#_ENREF_27)) |
| 21 | HV\_unigene (3) | 56 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Hordeum\_vulgare/  |
| 22 | OS\_unigene (3) | 80 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Oryza\_sativa/  |
| 23 | TA\_unigene (3) | 56 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Triticum\_aestivum/  |
| 24 | ZM\_unigene (3) | 77 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Zea\_mays/  |
| 25 | SB\_unigene (3) | 29 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Sorghum\_bicolor/  |
| 26 | SO\_unigene (3) | 14 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Saccharum\_officinarum/  |
| 27 | HS\_unigene (3) | 224 | http://www.ncbi.nlm.nih.gov/unigene ftp://ftp.ncbi.nih.gov/repository/UniGene/Homo\_sapiens/  |
| 28 | embl\_pl | 107 | ftp://ftp.ebi.ac.uk/pub/databases/embl/release/   | EBI-EMBL class std, UK |
| 29 | embl\_est\_pln | EBI-EMBL class est, UK |
| 30 | embl\_pat\_pln | EBI-EMBL class pat, UK |
| 31 | embl\_sts\_pln | EBI-EMBL class sts, UK |
| 32 | embl\_gss\_pln | EBI-EMBL class gss, UK |
| 33 | embl\_htg\_pln | EBI-EMBL class htgs, UK |
| 34 | embl\_htc\_pln | EBI-EMBL class htc, UK |
| 35 | embl\_tsa\_pln | EBI-EMBL class tsa, UK |
| 36 | embl\_wgs\_pln | EBI-EMBL class wgs, UK |
| 37 | WH\_embl\_mito | AP008982 | http://www.ncbi.nlm.nih.gov/nuccore/78675232?  | ([Ogihara et al., 2005](#_ENREF_15)) |
| 38 | WH\_embl\_chloro | AB042240 | http://www.ncbi.nlm.nih.gov/nuccore/13928184?  | ([Ogihara et al., 2002](#_ENREF_14)) |
| 39 | refSeq\_chloro | APR2011 | ftp://ftp.ncbi.nlm.nih.gov/refseq/release/README ftp://ftp.ncbi.nlm.nih.gov/refseq/release/plastid/  | NCBI-GenBank |
| 40 | refSeq\_mito | ftp://ftp.ncbi.nlm.nih.gov/refseq/release/README ftp://ftp.ncbi.nlm.nih.gov/refseq/release/mitochondrion/  |
|  | **Protein Databanks** |  |  |  |
| 41 | uniprot\_sprot | 2011\_04 | http://us.expasy.org/sprot/ ftp://ftp.uniprot.org/pub/databases/uniprot/README   | ExPASy Proteomics Server |
| 42 | uniprot\_trembl |
| 43 | uniprot\_uniref100 | http://us.expasy.org/sprot/ ftp://ftp.uniprot.org/pub/databases/uniprot/uniref/uniref100/  |
| 44 | uniprot\_uniref90 | http://us.expasy.org/sprot/ ftp://ftp.uniprot.org/pub/databases/uniprot/uniref/uniref90/  |
| 45 | uniprot\_uniref50 | http://us.expasy.org/sprot/ ftp://ftp.uniprot.org/pub/databases/uniprot/uniref/uniref50/  |
| 46 | nr | APR2011 | ftp://ftp.ncbi.nlm.nih.gov/blast/db/FASTA/ ftp://ftp.ncbi.nlm.nih.gov/blast/db/README  | NCBI |
| 47 | refSeqPlnProt | ftp://ftp.ncbi.nlm.nih.gov/refseq/release/plant/ ftp://ftp.ncbi.nlm.nih.gov/refseq/release/README  |
|  | **Protein Domains** |  |  |  |
| 48 | PfamA | 25 | http://pfam.sanger.ac.uk/ | ([Sammut et al., 2008](#_ENREF_18))([Finn et al., 2010](#_ENREF_5)) |
|  | **Model Genomes& Proteomes** |  |  |  |
|  | *Arabidopsis thaliana* |  |  | **TAIR**http://www.arabidopsis.org/([The Arabidopsis Genome Initiative, 2000](#_ENREF_25)) |
| 49 | genoAtTAIR | 9 | ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR9\_genome\_release/TAIR9\_chr\_all.fas  | - |
| 50 | cdsAtTAIR (3) | 10 | ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR9\_genome\_release/ TAIR10\_sequences/TAIR10\_cds\_20101214  | - |
| 51 | protAtTAIR | ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR9\_genome\_release/ TAIR10\_sequences/TAIR10\_pep\_20101214 | - |
|  | *Oryza sativa***MSU** |  | http://rice.plantbiology.msu.edu/annotation\_pseudo\_current.shtml  | **MSU**http://rice.plantbiology.msu.edu/  |
| 52 | genoOsMSU | 6.1 | ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic\_Projects/o\_sativa/annotation\_dbs/pseudomolecules/version\_6.1/all.dir/all.con  | - |
| 53 | cdsOsMSU (3) | ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic\_Projects/o\_sativa/annotation\_dbs/pseudomolecules/version\_6.1/all.dir/all.cds | - |
| 54 | protOsMSU | ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic\_Projects/o\_sativa/annotation\_dbs/pseudomolecules/version\_6.1/all.dir/all.pep | - |
|  | *Oryza sativa***IRGSP** |  |  | **IRGSP**http://rapdb.dna.affrc.go.jp/([Tanaka et al., 2008](#_ENREF_24)) |
| 55 | genoOsIRGSP | 5 | http://rapdb.dna.affrc.go.jp/download/latest/  🡺 file IRGSPb5.fa.masked.gz | - |
| 56 | cdsOsIRGSP (3) | http://rapdb.dna.affrc.go.jp/download/latest/rap\_representative.tgz 🡺 file representative\_orf\_nuc.fa http://rapdb.dna.affrc.go.jp/download/latest/rap\_predicted.tar.gz  🡺 file predicted\_orf\_nuc.fa | - |
| 57 | protOsIRGSP | http://rapdb.dna.affrc.go.jp/download/latest/rap\_representative.tgz  🡺 file representative\_orf.fa http://rapdb.dna.affrc.go.jp/download/latest/rap\_predicted.tar.gz  🡺 file predicted\_orf.fa | - |
|  | *Zea mays* |  |  | **MaizeSequence.org**http://maizesequence.org/index.html ([Schnable et al., 2009](#_ENREF_20)) |
| 58 | genoZmMSO | 5b | http://ftp.maizesequence.org/current/assembly/ ZmB73\_RefGen\_v2.masked.tar.gz  | - |
| 59 | cdsZmMSO (3) | http://ftp.maizesequence.org/current/filtered-set/ ZmB73\_5b\_FGS\_cds.fasta.gz | - |
| 60 | protZmMSO | http://ftp.maizesequence.org/current/filtered-set/ ZmB73\_5b\_FGS\_translations.fasta.gz  | - |
|  | *Sorghum bicolor* |  | ftp://ftp.jgi-psf.org/pub/JGI\_data/phytozome/v6.0/Sbicolor/README  | **Phytozome**http://www.phytozome.net/sorghum.php ([Paterson et al., 2009](#_ENREF_16)) |
| 61 | genoSbDOE | 6 | ftp://ftp.jgi-psf.org/pub/JGI\_data/phytozome/ v6.0/Sbicolor/assembly/sbi1\_n\_repeatMasker.fasta.gz | - |
| 62 | cdsSbDOE (3) | ftp://ftp.jgi-psf.org/pub/JGI\_data/phytozome/ pub/JGI\_data/phytozome/v6.0/Sbicolor/annotation/Sbicolor\_79\_cds.fa.gz | - |
| 63 | protSbDOE | ftp://ftp.jgi-psf.org/pub/JGI\_data/phytozome/ pub/JGI\_data/phytozome/v6.0/Sbicolor/annotation/Sbicolor\_79\_peptide.fa.gz | - |
|  | *Brachypodium distachyon* |  |  | **Orego State U.**http://www.brachypodium.org/([The International Brachypodium Initiative, 2010](#_ENREF_26)) |
| 64 | genoBdJGI | 8x | http://ftp.brachypodium.org/ files/8X\_ASSEMBLY/Brachypodium\_distachyon\_Bd21.main\_genome.scaffolds.fasta.tar.gz  | - |
| 65 | cdsBdJGI (3) | 1.2 | http://ftp.brachypodium.org/ files/Annotation/brachypodium\_1.2\_CDS.fa | - |
| 66 | protBdJGI | 1.2 | http://ftp.brachypodium.org/ files/Annotation/brachypodium\_1.2\_Protein.fa | - |
|  | *Triticum* |  |  |  |
| 67 | ProtTRI | 107 | Using a homemade perl program for SRS request (4) | EBI-EMBL uniprot |
|  | *Hordeum* |  |  |  |
| 68 | ProtHOR | 107 | Using a homemade perl program for SRS request (4) | EBI-EMBL uniprot |
|  | *Saccharum* |  |  |  |
| 69 | ProtSAC | 107 | Using a homemade perl program for SRS request (4) | EBI-EMBL uniprot |
|  | **Special Databanks** |  |  |  |
| 70 | SIMnuc | JUN2011 | Expertise\_CDS (CAT00) + TaFL(CAT01) + PoaFL(CAT02) + CDSplus (CAT03) (3) | Local databank |
| 71 | SIMprot | RefSeqPlnProt + protBdJGI + protOsIRGSP + ProtTRI + ProtHOR |
| 72 | protPlant | Using a homemade perl program for SRS request (4) with Taxon = *Magnoliophyta* |
| 73 | CS3B2X\_OCC1 | 2011 | Wheat cv. Chinese Spring Chromosome 3B 2X 454 sequences | Local databank([Choulet et al., 2010](#_ENREF_3)) |

(1) Databank names used within the TriAnnot pipeline

(3) These databank are post processed: polyA tails are deleted; sequences are strong-masked with RepeatMasker against the univec databank (N on 5’ and 3’ ends are deleted), and soft-masked with RepeatMasker against TREPplus. CAT00 is related to mRNA/CDS which have been already manually expertised.

(4) (([uniprot-Organism:$species\*]) & ((([uniprot-ProteinExistence:1: evidence at protein level] | [uniprot-ProteinExistence:2: evidence at transcript level]) | [uniprot-ProteinExistence:3: inferred from homology]) | [uniprot-ProteinExistence:4: predicted])). $species being the genus of interest (for example: *Arabidopsis, Triticum, Hordeum, Oryza, Zea, Sorghum, Saccharum, Brachypodium*).

**Table S3**

Parameters for TriAnnot V3.5 default analysis (step.xml).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Panel** | **Modules or steps** | **Softwares**(1) | **DataBanks**(2) | **Topic** | **Sequence status and threshold of main parameters** |
| I | 01 | 16 | 4 | TEs annotation and masking | Initial sequenceRepeatMasker cutoff 225‘qq’ parameter (rush job) about 10% less sensitive, 4 to 10 times faster than default repeat optionsmasked with lower-case and Ns |
| I | 02 | 2 | 3 | BLASTX | Initial sequenceEvalue = 10-5 |
|  |
| II | 05 | 11 | - | *ab initio* gene prediction | Masked TEs (N-masked) sequenceWheat matrix |
| II | 06 | 2, 20 | 16,17,18,53, 56,59,62,65,70 | Spliced transcript alignments. BLASTN followed by exonerate. | Masked TEs (soft-masked) sequenceFor TaEST databank: BLASTN: Evalue = 10-5 Identity = 95% Coverage = 95% exonerate coverage threshold = 95%For all other databanks: BLASTN: Evalue = 10-5 Identity = 80% Coverage = 70% exonerate coverage threshold = 80% |
| II | 07 | 2 & 20 | 41,47,54,57,60,63,66,67,68,71 | Spliced transcript alignments. BLASTX followed by exonerate | Masked TEs (soft-masked) sequenceBLASTX: Evalue = 10-5Identity = 70%Coverage = 60%exonerate coverage threshold = 70% |
| II | 08 | 1,12 | 10,13,48,72 | SIMsearchgene modelssimilarity only  | Masked TEs (soft-masked) sequencePriority = CAT,CV\_NA,ORF\_LEN,ID\_AA,ID\_NA,RANGE,EXON3’/5’ extension on |
| II | 08 | 12 | 17,70,71 | EuGenegene models*ab initio* & similarities | Masked TEs (specific IG file for EuGene)Combines: augustus\_wheat and BLASTN/exonerate of TaEST, SIMnuc and BLASTX/exonerate of SIMprot |
| II | 09 | 2,13 | 29,41,42,48,54 | Functional annotation | On proteins derived from the best gene models obtained at step08 |
| II | 10 | 2 | 46,51,54,57,60,63,66,67,68,69,72 | Best hits | On proteins derived from the best gene models obtained at step08BLASTp: Evalue = 10-5Positive = 50%Coverage = 60%Exonerate coverage threshold = 50% |
| II | 11 | 14 | - | Protein domains and gene ontology annotations | On proteins derived from the best gene models obtained at step08InterProScan default parameters (Pfam,Prosite,SMART & GO) |
|  |
| III | 12 | 2 | 39,40,49,52,55,58,61,64 | CNSsBLASTN againstorganelles genomes andpseudo molecules | Masked TEs and Genes (N-masked) sequence BLASTN: Evalue = 10-5 |
| III | 13 | 2 | 51,54,57,60,63,66 | BLASTX against protein databanks | Masked TEs and Genes (N-masked) sequence BLASTN: Evalue = 10-5 |
| III | 16 | 18 | - | Annotation of tRNA | Initial sequencetRNAscan default parameters |
|  |  |  |  |  |  |
| IV | 19 | 17 | - | Microsatellite (SSR) annotations | Initial sequencematch = 2; mismatch = 7; delta = 7; pm = 80; pi = 10; minscore = 30;maxPeriod = 5 |

(1) Software number (**see Supplementary table S1**)

(2) Databanks number (**see Supplementary table S2**)

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