

Transcriptomic files processing

Preprocess - *trimmomatic*, *sortmerna*, *rcorrector*

Assembly - *rnaSPAdes*, *trinity*, *evidentialgene*

Evaluation - *busco*, *ex90n50*, *backmapping*

Annotation - *egglog*, *genera*, *mercator*

SRA

"Pinus radiata"

Samples: 141

Tissues: 5

Stresses: 4

Table S1; S2

Processed files

Final assembly

Expression

Splicing

Expression - *salmon*, *sva*, *deseq2*

Network - *wgcna*

F. enrich - *fgsea*

Splicing - *sva*, *kiss-suite* (*splice*, *2refgenome*, *de*)

Genomic features - *matt*

F. enrich - *fgsea*

Transcriptomes regulation global description

Figure 2

Transcriptomics module

Application: Stress/Tissue* var.

Integration - *mofa2*, *mytai*

Figure 4; S1

Experimental Validation*; **Figure 4**

Proteomic files processing

Identification, quantification - *proteomdiscoverer*

Pre processing - *processomics*

Imputation - *processomics*

Annotation - *genera*

PubMed/PRIDE

"Pinus radiata"

Samples: 155

Subcellular: 3

Tissues: 3 (New)

Stresses: 3

Table S3

Processed files

Proteins

Proteins - *sva*, *limma*

Network - *wgcna*

F. enrich - *fgsea*

Tissue evo patterns - *mytai*

Proteomes regulation global description

Figure 3

Proteomics module

Application: Stresses var.

Integration - *mofa2*, *mytai*

Figure 5; S1

Resource: Database

Search

Blastp

Orthologs

Public DB datasets available for future applications



***Pinus radiata* Gene Expression ATLAS**