**List of files**

Association files, imported from the PO subversion repository revision 1772 (<http://palea.cgrb.oregonstate.edu/viewsvn/Poc/trunk/associations/?pathrev=1772>):

po\_temporal\_gene\_arabidopsis\_tair.assoc

po\_growth\_genemodel\_zea\_MaizeGDB.assoc

Edited the association files so that they only contain rows for the classes of interest (subclasses of plant pro-ebryo stage) and removed one association from proembryo stage that wasn’t IEP (inferred by experimental procedure) or IDA (inferred by direct assay):

Zm\_concatenate\_files\_all\_columns.txt

At\_concatenate\_files\_all\_columns.txt

Extracted only column with gene names (col. 10 for Arabidopsis and col. 2 for maize) then removed any duplicate row. This left two files with just the lists of genes for all plant embryo development stages:

At\_embryo\_genes\_uniq.txt

Zm\_embryo\_genes\_uniq.txt

The two files above were used as input for the InParanoid analysis (to determine homolog clusters). The output files were the orthologs from the supercluster algorithm:

At\_Zmays\_cluster.txt

At\_Zmays\_inpara\_Zea\_mays.txt

The first column is a cluster id and will tell you if more than one cluster pair are orthologs.  All genes with the cluster ID is the same are considered orthologs of each other.

The file above contains many genes that are not present in our association files. They were removed by deleting all rows for maize genes didn’t start with GRMZ (using grep -v -e EF -e AY -e AF -e AC At\_Zmays\_inpara\_Zea\_mays.txt )

This left 23185 rows (without header):

At\_Zmays\_inpara\_Zea\_mays\_GRZM.txt

Then removed ortho scores less than 0.5. Leaves 20096 rows (without header).

At\_Zmays\_inpara\_Zea\_mays\_50.txt

Need to create a file from **At\_Zmays\_inpara\_Zea\_mays\_50.txt** that removes “.1” from all the At gene ids and removes duplicate rows, with just two columns: id and gene.

First made file with id, gene, and score. Saved as **At\_ortho\_ids\_scores.txt**.

Removed the column with scores and saved as **At\_ortho\_ids.txt**.

**3/15/13**

Files to use (under analysis/files with ortho ids):

**At\_ortho\_ids.txt** – contains unique rows, with only columns for id and gene, with only those rows that had scores >= 0.50 for At genes. (13630 rows)

**Zm\_ortho\_ids.txt** – contains unique rows, with only columns for id and gene, with only those rows that had scores >= 0.50 for Zm genes. (10557 rows)

Need to create sets of overlapping orthoids from the two files – that is, all orthoids which are present in both At and Zm, plus a set of those that are only present in At and those that are only present in Zm. Based on a small sample, there are no genes that aren’t present in both species (which there shouldn’t be, because this list only contains those genes that passed through the Inparanoid analysis), but this is across all stages. First need to separate out by stage and compare each stage. Need to go back to the lists of genes for each stage and create new files that just have orthoid plus gene, by matching to Xx\_ortho\_ids.txt.

Atbilat.txt – 13823 rows

Atexcot.txt – 13914 rows

Atglob.txt - 13763 rows

Atmature.txt – 13322 rows

Atproemb.txt – 10 rows

Zmcoleop.txt – 25065 rows

Zmproemb.txt – 27117 rows

Zmtruelf.txt – 28663 rows

3/20/2013

Add ortho ids to the above files using the Excel match function.

Atbilat\_orthos.txt – 9781 rows

Atexcot\_orthos.txt – 9831 rows

Atglob\_orthos.txt – 9741 rows

Atmature\_orthos.txt – 9519 rows

Atproemb\_orthos.txt – 8 rows

Zmcoleop\_orthos.txt – 8483 rows

Zmproemb\_orthos.txt – 8705 rows

Zmtruelf\_orthos.txt – 8765 rows

**3/23/2013**

Compare two lists of genes (http://nemates.org/MA/progs/Compare.html)

For straight gene lists (without orthos, within one species)

Do the intraspecific comparison with only ortho genes.

Atbilat.txt vs. Atexcot.txt

13798 genes in list 1. 13898 genes in list 2.

List comparison type: AND

13476 genes meet the comparison criteria.

Atbilat.txt vs. Atglob.txt

13798 genes in list 1. 13739 genes in list 2.

List comparison type: AND

12800 genes meet the comparison criteria.

Atbilat.txt vs. Atmature.txt

13798 genes in list 1. 13319 genes in list 2.

List comparison type: AND

13147 genes meet the comparison criteria.

Atexcot.txt vs. Atglob.txt

13898 genes in list 1. 13739 genes in list 2.

List comparison type: AND

12786 genes meet the comparison criteria.

Atexcot.txt vs. Atmature.txt

13898 genes in list 1. 13319 genes in list 2.

List comparison type: AND

13147 genes meet the comparison criteria.

Atglob.txt vs. Atmature.txt

13739 genes in list 1. 13319 genes in list 2.

List comparison type: AND

12575 genes meet the comparison criteria.

------------------------------------

Zmcoleop.txt vs. Zmproemb.txt

25065 genes in list 1. 27117 genes in list 2.

List comparison type: AND

24569 genes meet the comparison criteria.

Zmcoleop.txt vs. Zmtruelf.txt

25065 genes in list 1. 28663 genes in list 2.

List comparison type: AND

24801 genes meet the comparison criteria.

Zmproemb.txt vs. Zmtruelf.txt

27117 genes in list 1. 28663 genes in list 2.

List comparison type: AND

26045 genes meet the comparison criteria.

------------------------------------

genes = orthoids in these files (may be more than one gene per ortho group)

Atbilat\_orthos.txt vs Zmcoleop\_orthos.txt

7855 genes in list 1. 6878 genes in list 2. List comparison type: AND 6606 genes meet the comparison criteria.

Atbilat\_orthos.txt vs Zmproemb\_orthos.txt

7855 genes in list 1. 7011 genes in list 2. List comparison type: AND 6807 genes meet the comparison criteria.

Atbilat\_orthos.txt vs Zmtruelf\_orthos.txt

7855 genes in list 1. 7063 genes in list 2. List comparison type: AND 6853 genes meet the comparison criteria.

------------------------------------

Atexcot\_orthos.txt vs Zmcoleop\_orthos.txt

7906 genes in list 1. 6878 genes in list 2. List comparison type: AND 6641 genes meet the comparison criteria.

Atexcot\_orthos.txt vs Zmproemb\_orthos.txt

7906 genes in list 1. 7011 genes in list 2. List comparison type: AND 6843 genes meet the comparison criteria.

Atexcot\_orthos.txt vs Zmtruelf\_orthos.txt

7906 genes in list 1. 7063 genes in list 2. List comparison type: AND 6890 genes meet the comparison criteria.

------------------------------------

Atglob\_orthos.txt vs Zmcoleop\_orthos.txt

7805 genes in list 1. 6878 genes in list 2. List comparison type: AND 6579 genes meet the comparison criteria.

Atglob\_orthos.txt vs Zmproemb\_orthos.txt

7805 genes in list 1. 7011 genes in list 2. List comparison type: AND 6741 genes meet the comparison criteria.

Atglob\_orthos.txt vs Zmtruelf\_orthos.txt

7805 genes in list 1. 7063 genes in list 2. List comparison type: AND 6774 genes meet the comparison criteria.

------------------------------------

Atmature\_orthos.txt vs Zmcoleop\_orthos.txt

7691 genes in list 1. 6878 genes in list 2. List comparison type: AND 6474 genes meet the comparison criteria.

Atmature\_orthos.txt vs Zmproemb\_orthos.txt

7691 genes in list 1. 7011 genes in list 2. List comparison type: AND 6692 genes meet the comparison criteria.

Atmature\_orthos.txt vs Zmtruelf\_orthos.txt

7691 genes in list 1. 7063 genes in list 2. List comparison type: AND 6729 genes meet the comparison criteria.

------------------------------------

Atproemb\_orthos.txt vs Zmcoleop\_orthos.txt

5 genes in list 1.  
6878 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria.

Atproemb\_orthos.txt vs Zmproemb\_orthos.txt

5 genes in list 1.  
7011 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria.

Atproemb\_orthos.txt vs Zmtruelf\_orthos.txt

5 genes in list 1.  
7063 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria.

------------------------------------

Atbilat\_orthos.txt vs. Atexcot\_orthos.txt

7855 genes in list 1. 7906 genes in list 2. List comparison type: AND 7776 genes meet the comparison criteria.

Atbilat\_orthos.txt vs. Atglob\_orthos.txt

7855 genes in list 1. 7805 genes in list 2. List comparison type: AND 7565 genes meet the comparison criteria.

Atbilat\_orthos.txt vs. Atmature\_orthos.txt

7855 genes in list 1. 7691 genes in list 2. List comparison type: AND 7651 genes meet the comparison criteria.

Atbilat\_orthos.txt vs. Atproemb\_orthos.txt

7855 genes in list 1.  
5 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria

------------------------------------

Atexcot\_orthos.txt vs. Atglob\_orthos.txt

7906 genes in list 1. 7805 genes in list 2. List comparison type: AND 7570 genes meet the comparison criteria.

Atexcot\_orthos.txt vs. Atmature\_orthos.txt

7906 genes in list 1. 7691 genes in list 2. List comparison type: AND 7661 genes meet the comparison criteria.

Atexcot\_orthos.txt vs. Atproemb\_orthos.txt

7906 genes in list 1.  
5 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria.

------------------------------------

Atglob\_orthos.txt vs. Atmature\_orthos.txt

7805 genes in list 1. 7691 genes in list 2. List comparison type: AND 7475 genes meet the comparison criteria.

Atglob\_orthos.txt vs. Atproemb\_orthos.txt

7805 genes in list 1.  
5 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria.

------------------------------------

Atmature\_orthos.txt vs. Atproemb\_orthos.txt

7691 genes in list 1.  
5 genes in list 2.  
List comparison type: AND  
5 genes meet the comparison criteria.

**Zm ortho intraspecific comparisons:**

Zmcoleop\_orthos.txt vs. Zmproemb\_orthos.txt

6878 genes in list 1.

7011 genes in list 2.

List comparison type: AND

5962 genes meet the comparison criteria.

Zmcoleop\_orthos.txt vs. Zmtruelf\_orthos.txt

6878 genes in list 1.

7063 genes in list 2.

List comparison type: AND

6007 genes meet the comparison criteria.

Zmproemb\_orthos.txt vs. Zmtruelf\_orthos.txt

7011 genes in list 1.

7063 genes in list 2.

List comparison type: AND

6884 genes meet the comparison criteria.

See results summary in **Overlap\_summary.xlsx**

----------------------------------------------------------

Compare GO enrichment for the lists of genes that overlap versus those that don’t for a few sets.

**11/23/2013**

Extract lists of genes that do not overlap between the stages using <http://nemates.org/MA/progs/Compare.html>.

See results in the folder “no overlap genes” under “stage specific sets”

**First for At only:**

Need to redo this using TAIR10 as reference.

**Settings:**

Analysis tool: SEA

Supported species: Arabidopsis thaliana

Query list: genes from files like “Atbilat\_not\_Atexcot.txt”

Reference from selected background: Arabidopsis genome locus (TAIR 9)

Advanced options: GO slim

**Atglob.txt vs. Atmature.txt**

List comparison type: 1NOT2

1164 genes meet the comparison criteria.

Agrigo job#: 590428029 (with Plant GO slim)

Agrigo job#: 926535914 (with complete GO)

Doesn’t seem to change the categories, just the order of their significance. Will use plant slim

With GO slim, 11/29/13:

Agrigo job#: 631894729

1140 genes in query list. 87 significant GO terms. Figure saved as At\_glob\_not\_mature.png

List comparison type: 2NOT1

744 genes meet the comparison criteria.

Agrigo job#: 361454077

719 genes in the query list. 71 significant GO terms. Figure saved as At\_mature\_not\_glob.png

**SEAcompare:**

**Atbilat.txt vs. Atexcot.txt**

List comparison type: 1NOT2

322 genes meet the comparison criteria.

List comparison type: 2NOT1

422 genes meet the comparison criteria.

**Atbilat.txt vs. Atglob.txt**

List comparison type: 1NOT2

998 genes meet the comparison criteria.

List comparison type: 2NOT1

939 genes meet the comparison criteria.

**Atbilat.txt vs. Atmature.txt**

List comparison type: 1NOT2

651 genes meet the comparison criteria.

Agrigo job#: 688600946

has GO terms like seed development, embryonic development, others that are not in mature stage (see comparison on Agrigo)

List comparison type: 2NOT1  
172 genes meet the comparison criteria.

Agrigo job#: 237066171

**Atexcot.txt vs. Atglob.txt**

List comparison type: 1NOT2

1112 genes meet the comparison criteria.

List comparison type: 2NOT1

953 genes meet the comparison criteria.

**Atexcot.txt vs. Atmature.txt**

List comparison type: 1NOT2

751 genes meet the comparison criteria.

List comparison type: 2NOT1  
172 genes meet the comparison criteria.

**Between species**

**Comparison between species for specific stages**

Need to redo this. Should have compared coleoptilar to cotyledonary, because they now are siblings.

Compared bilateral to coleoptilar stage, because cp is a subclass of bl stage, so they should be most similar (but they aren’t actually).

**Atbilat\_orthos.txt vs. Zmcoleop\_orthos.txt**

List comparison type: 1NOT2

1249 genes meet the comparison criteria.

Output: Atbilat\_not\_ Zmcoleop.txt

List comparison type: 2NOT1  
272 genes meet the comparison criteria.

Output: Zmcoleop\_not\_Atbilat.txt

**Convert ortho ids back into gene names for At:**

Match Atbilat\_not\_ Zmcoleop.txt to to At\_ortho\_ids.txt using =IF(ISERROR(MATCH(A1,$E$1:$E$1249,0)),"",B1)

Saved as match\_At\_orthos\_to\_bilatnotcoleop.xls

Sorted column B to produce just list of At genes (1562 genes – not sure if all of them were in the original list because this back converts to everything in the orhtolog family. Should match to Atbilat\_orthos.txt to insure it only has the genes in the original list.

Match Atbilat\_not\_ Zmcoleop.txt to Atbilat\_orthos.txt using =IF(ISERROR(MATCH(A1,$E$1:$E$1249,0)),"",B1)

Sort only At gene names that match orthos.

Save working file as match\_Atbilt\_not\_Zmcoleop.xlsx in (in no overlap genes)

Saved list of At genes only match\_At\_orthos\_to\_bilatnotcoleop.txt

**Convert ortho ids back into gene names for Zm:**

Match to Zmcoleop\_not\_Atbilat.txt to Zmcoleop\_orthos.txt using =IF(ISERROR(MATCH(A1,$E$1:$E$1249,0)),"",B1)

Save working file as match\_Zm\_orthos\_to\_coleopnotbilat.xlsx (in no overlap genes)

Save list of Zm genes as match\_Zm\_orthos\_to\_coleopnotbilat.txt

**Convert OrthoIDs that are in Zmcoleop but not in Atbilat back to At gene IDs**

Match Zmcoleop\_not\_Atbilat.txt to At\_ortho\_ids.txt (under stage specific sets) using =IF(ISERROR(MATCH(A1,$E$1:$E$1249,0)),"",B1)

Save working file as match\_Atorthos\_to\_coleopnotbilat.xlsx (in files with orthoids)

Save list of At genes that as **match\_Atorthos\_to\_coleopnotbilat.txt**

**Compare GO profile of match\_Atorthos\_to\_coleopnotbilat.txt (genes in coleop in maize but not in bilat in At) to Atblat.txt**

First match\_Atorthos\_to\_coleopnotbilat.txt vs. Atbilat.txt. There shouldn’t be any overlap. No overlap (good!)

match\_Atorthos\_to\_coleopnotbilat.txt in Agrigo, Agrigo job#: 690980667

289 genes in query list, 19 significant GO terms

Atbilat.txt in Agrigo, Agrigo job#: 817011459

13536 genes in the query list, 124 significant GO terms

**Compare all embryo stage genes for At versus Zm**

From Justin E. , re. the file **At\_Zmays\_inpara\_Zea\_mays.txt**

“I believe the file will contain ones from the list you sent me.  However, it could be that if InParanoid decided that another At gene was in the cluster, that will be in the file as well.  In other words, if say At1G10040 was in your list, and At1G10050 was not, but InParanoid figured they were in a cluster together, they both would be in that file.”

Need to check this to see if it has only the genes from **At\_embryo\_genes\_uniq.txt**

and **Zm\_embryo\_genes\_uniq.txt**  or if it has extra genes from the ortho families.

Confirmed that **At\_otho\_ids.txt** has only a subset of genes from **At\_embryo\_genes\_uniq.txt** (the genes that belong to Inparanoid ortho families).

Saves list of orthos only as **At\_embryo\_orthos.txt.**

However, **Zm\_orthod\_ids.txt** has genes that are not in **Zm\_embryo\_genes\_uniq.txt**. Created a new file with only the Zm orthos that match genes in Zm\_embryo\_genes\_uniq.txt using:

=IF(ISERROR(MATCH(B1,$E$1:$E$297802,0)),"",B1)

Saved as **Zm\_ortho\_ids\_match\_Zm\_embryo\_genes\_uniq.xlxs**.

Saved list of orthos only as **Zm\_embryo\_orthos.txt.**

**At\_embryo\_orthos.txt vs. Zm\_embryo\_orthos.txt**

List comparison type: 1NOT2

988 genes meet the comparison criteria.

(save list as Atembryo\_not\_Zmembryo.txt in no overlap genes)

List comparison type: 2NOT1  
0 genes meet the comparison criteria.

>>No genes match the second test because the list of orthologs was generated from the input list of At genes, and so only includes Zm genes that have an ortholog in the At set. yay.

**June 2015:** **New Between species**

**Comparison between species for specific stages**

Redo comparing coleoptilar stage to cotyledonary stage, because they now are siblings.

**Atexcot\_orthos.txt vs. Zmcoleop\_orthos.txt**

List comparison type: 1NOT2

7906 genes in list 1. 6878 genes in list 2.

List comparison type: 1NOT2

1265 genes meet the comparison criteria.

Output: Atexcot\_not\_ Zmcoleop.txt

7906 genes in list 1.  
6878 genes in list 2.  
List comparison type: 2NOT1  
237 genes meet the comparison criteria.

Output: Zmcoleop\_not\_Atexcot.txt

**Convert ortho ids back into gene names for At:**

Match Atexcot\_not\_ Zmcoleop.txt to to At\_ortho\_ids.txt using =IF(ISERROR(MATCH(A1,$E$1:$E$1249,0)),"",B1)

Sorted column B to produce just list of At genes.

Saved as match\_At\_orthos\_to\_excotnotcoleop\_extras.txt

Not all of them are in the original list because this back converts to everything in the ortholog family. Should match to Atexcot\_orthos.txt to insure it only has the genes in the original list.

Match Atexcot\_not\_ Zmcoleop.txt to Atbilat\_orthos.txt using =IF(ISERROR(MATCH(A1,$D$1:$D$1265,0)),"",B1)

Match only At gene names from match\_At\_orthos\_to\_excotnotcoleop.txt that match genes in Atbilat\_orthos.txt.

Saved list of At genes only match\_At\_orthos\_to\_excotnotcoleop.txt

**Convert ortho ids back into gene names for Zm:**

Match to Zmcoleop\_not\_Atexcot.txt to Zmcoleop\_orthos.txt using =IF(ISERROR(MATCH(A1,$D$1:$D$237,0)),"",B1)

Save list of Zm genes as match\_Zm\_orthos\_to\_coleopnotexcot.txt

**Convert OrthoIDs that are in Zmcoleop but not in Atexcot back to At gene IDs**

Match Zmcoleop\_not\_Atexcot.txt to At\_ortho\_ids.txt (under stage specific sets) using =IF(ISERROR(MATCH(A1,$D$1:$D$237,0)),"",B1)

Save working file as match\_Atorthos\_to\_coleopnotexcot.xlsx (in files with orthoids)

Save list of At genes that as match\_Atorthos\_to\_coleopnotexcot.txt

**Compare GO profile of match\_Atorthos\_to\_coleopnotexcot.txt (genes in coleop in maize but not in excot in At) to Atexcot.txt**

Now AgriGo only has TAIR10, so need to use that.

Settings:

1. Select analysis tool: SEA

2. Select species:

supported species

Arabidopsis TAIR10

Query list: paste in list of genes from **match\_At\_orthos\_to\_excotnotcoleop.txt** or **match\_Atorthos\_to\_coleopnotexcot.txt**

3. Select reference: suggested backgrounds, TAIR10

4. Advance options:

PlantGO slim

Others as default

Results: http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=202830895

## Analysis Brief Summary

**Job ID:** 202830895 [Useful within 7 days]

**Job Name:** excotnotcoleop

**Species:**

**GO type:** Plant GO slim

**Background/Reference:** Customized

**Annotated number in query list:** 1538 [ [[http://bioinfo.cau.edu.cn/agriGO/images/page_copy.png](http://bioinfo.cau.edu.cn/agriGO/tmp/202830895.annotated_ID.txt)Download](http://bioinfo.cau.edu.cn/agriGO/tmp/202830895.annotated_ID.txt) ]

**Annotated number in background/reference:** 28397

**Significant GO terms:** 65 [ [[http://bioinfo.cau.edu.cn/agriGO/images/arrow_down.png](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=202830895%23detailtable)Details](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=202830895" \l "detailtable) ]

## Analysis Brief Summary

**Job ID:** 250031567 [Useful within 7 days]

**Job Name:** coleopnotexcot

**Species:**

**GO type:** Plant GO slim

**Background/Reference:** Customized

**Annotated number in query list:** 267 [ [[http://bioinfo.cau.edu.cn/agriGO/images/page_copy.png](http://bioinfo.cau.edu.cn/agriGO/tmp/250031567.annotated_ID.txt)Download](http://bioinfo.cau.edu.cn/agriGO/tmp/250031567.annotated_ID.txt) ]

**Annotated number in background/reference:** 28397

**Significant GO terms:** 14

**SEACompare of the two jobs above**

Results saved in analyses folder as **cotyledon\_coleoptile\_comparison.xlsx**

## Analysis Brief Summary

**Job ID:** 900997977 [Useful within 7 days]

**Job Name:** Atexcot

**Species:**

**GO type:** Plant GO slim

**Background/Reference:** Customized

**Annotated number in query list:** 13817 [ [[http://bioinfo.cau.edu.cn/agriGO/images/page_copy.png](http://bioinfo.cau.edu.cn/agriGO/tmp/900997977.annotated_ID.txt)Download](http://bioinfo.cau.edu.cn/agriGO/tmp/900997977.annotated_ID.txt) ]

**Annotated number in background/reference:** 28397

**Significant GO terms:** 134 [ [[http://bioinfo.cau.edu.cn/agriGO/images/arrow_down.png](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=900997977%23detailtable)Details](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=900997977" \l "detailtable) ]

Results saved in analyses folder as **SEA\_excotonly.xlsx**

Use SEACOMPARE to compare jobs 250031567 (coleopnotexcot) and 900997977 (Atexcot).

Save results are Seacompare\_coleopnotexcot\_excot\_all.xlsx.

File that includes just the GO terms from coleopnotexcot: **Seacompare\_coleopnotexcot\_excot.xlsx**.

**REDO analysis within At, to use TAIR 10 data set:**

**Settings:**

Analysis tool: SEA

Supported species: Arabidopsis thaliana TAIR 10

Reference from selected background: Arabidopsis genome locus (TAIR 10)

Advanced options: PO slim

**Atglob\_not\_ATmature.txt**

## Analysis Brief Summary

**Job ID:** 363277779 [Useful within 7 days]

**Job Name:** AtglobNOTmature

**Species:**

**GO type:** Plant GO slim

**Background/Reference:** Customized

**Annotated number in query list:** 1156 [ [[http://bioinfo.cau.edu.cn/agriGO/images/page_copy.png](http://bioinfo.cau.edu.cn/agriGO/tmp/363277779.annotated_ID.txt)Download](http://bioinfo.cau.edu.cn/agriGO/tmp/363277779.annotated_ID.txt) ]

**Annotated number in background/reference:** 28397

**Significant GO terms:** 46 [ [[http://bioinfo.cau.edu.cn/agriGO/images/arrow_down.png](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=363277779%23detailtable)Details](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=363277779" \l "detailtable) ]

**Atmature\_not.\_Atglob.txt**

|  |
| --- |
| Analysis Brief Summary **Job ID:** 688842085 [Useful within 7 days]  **Job Name:** AtmatureNOTglob  **Species:**  **GO type:** Plant GO slim  **Background/Reference:** Customized  **Annotated number in query list:** 722 [ [[http://bioinfo.cau.edu.cn/agriGO/images/page_copy.png](http://bioinfo.cau.edu.cn/agriGO/tmp/688842085.annotated_ID.txt)Download](http://bioinfo.cau.edu.cn/agriGO/tmp/688842085.annotated_ID.txt) ]  **Annotated number in background/reference:** 28397  **Significant GO terms:** 30 [ [[http://bioinfo.cau.edu.cn/agriGO/images/arrow_down.png](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=688842085%23detailtable)Details](http://bioinfo.cau.edu.cn/agriGO/SEAresult.php?session=688842085" \l "detailtable) ] |
| |  | | --- | |  | |

**SEACOMPARE AT glob versus mature**

Save comparison results as: **seacompare\_glob\_mature.xlsx**

June 23, 2015

Extract lists of genes that are unique to each stage. Use <http://nemates.org/MA/progs/Compare.html>.

By species, compare lists of genes annotate to each stage to the complete list of genes for every stage but the one of interest.

**Generate lists for comparison:**

rwalls-iplant$ sort -u Atbilat.txt Atexcot.txt Atmature.txt > At\_minus\_glob.txt

or

IPC-HELMKE:stage\_specific\_sets rwalls-iplant$ sort -u Zmproemb.txt Zmcoleop.txt > Zm\_minus\_truelf.txt

Be sure that all files have unix returns (not Mac Classic) or the uniq and sort commands will not work as expected!

**Comparison lists, stored under files with orthoIDs/stage specific sets:**

At\_minus\_glob.txt

At\_minus\_bilat.txt

At\_minus\_excot.txt

At\_minus\_mature.txt

Zm\_minus\_proemb.txt

Zm\_minus\_coleop.txt

Zm\_minus\_truelf.txt

**Compare lists of genes in e.g., At\_minus\_glob.txt to At\_glob.txt to generate lists of unique genes in At glob. Save unique gene lists in stage specific sets folder:**

At\_glob\_u.txt 781 genes of 13739

At\_bilat\_u.txt 134 genes 0f 13798

At\_excot\_u.txt 246 genes of 13898

At\_mature\_u.txt 48 genes of 13319

Zm\_proemb\_u.txt 855 genes of 27117

Zm\_coleop\_u.txt 47 genes of 25065

Zm\_truelf\_u.txt 2169 genes of 28663