## Methods

### Sequence Processing

A total of 7232 chromatogram files from two sets of replicate samples, two each for needle and cambium, were processed using an IPython {Perez:2007hy} notebook and various utilities. The chromatograms were converted using Phred {Ewing:1998uq} into FASTA sequences with a trimming cutoff probability of 0.01 (i.e., Phred score = 20), and sequences which were less than 100 bases long were excluded. These ESTs, from all replicates, were combined into a single file (where all of the sequence identifiers indicated the source and replicate of the EST). The combined file was processed, first using SeqClean {Chen:2007hs}, screening for both vectors using the Univec {Cochrane:2010hn} database and contamination from *E. coli* K-12 substr. DH10B. The cleaned and trimmed ESTs were, in each case, assembled into unigenes using iAssembler {Zheng:2011kt}. The representation of the number of sequence fragments from each tissue and replicate were calculated from the output from iAssembler {Zheng:2011kt}, which tracks which individual FASTA sequences (decorated with the source tissue/replicate combination) were assembled into each unigenes. These counts were used to assess differential unigene expression.

The assembled unigenes were aligned to a custom local copy of the UniProtKB database. This database was created from the most current release of the Swiss-Prot as of 4/1/15. Briefly, the accessions from the plant taxonomic division were extracted and were used to extract FASTA sequences from the entire UniProt database. The top 10 blastx {Altschul:1990dw} alignments for each unigene, having e-values < 1e-5, were retained for annotation using Blast2GO {Gotz:2008kq}.

### Differential Gene Expression

To determine whether assembled unigenes were differentially expressed in either needle or cambium, counts across replicates were combined for each tissue. These cambium and needle counts were used as input to the online version of IDEG6 {Romualdi:2003tk} at http://telethon.bio.unipd.it/bioinfo/IDEG6/. All test statistics were evaluated, but determination of differential expression was based on FDR-corrected p-values {Benjamini:1995ws} calculated from the general χ2 p-values from IDEG6. We chose to rely on the FDR (q < 0.05) method of correction rather than Bonferonni due the overly conservative nature of that method. We did not employ the false discovery rate correction of {\*Storey:2003cj} because the distribution of p-values from our data did not meet the asymptotic assumptions of that method.

### Gene Ontology

Blastx results were imported into Blast2GO using default parameters, keeping at most 10 hits with a high-scoring pair (HSP) length of at least 33 amino acids. Annotations were assigned using the default parameters (e-value: 1e-6, annotation cutoff: 55, GO weight: 5, HSP-hit coverage cutoff: 0, taxonomy filtering: none) and evidence code weights. The full suite of InterPro 5 {Jones:2014fn} mappings were performed for each unigene and these results were merged with existing annotations. Unigene annotations were also augmented with ANNEX and mapped to enzyme code and KEGG pathways {Kanehisa:2000jn}. The resulting annotations were exported to a text file for further analysis.

Differential GO term analysis was computed for needle and cambium using the topGO R package {Alexa:2010wb} which provides tests for GO terms while accounting for the GO graph topology. The GO hierarchy was trimmed to only include terms with two or more annotated unigenes (i.e., nodesize=2). Each set of unigenes, which were deemed to be differentially expressed in either needle or cambium, was tested using a one-tailed Fisher’s exact test and assessed for significance at two different levels, either having an uncorrected p-value less than 0.05 or a corrected {Benjamini:1995ws} p-value < 0.05. In all, six tests for differentially expressed GO terms were conducted with each tissue type evaluated against each of three GO ontologies: Biological Process, Cellular Component, and Molecular Function. Those terms which passed the raw p-value criterion where annotated with a single asterisk, and those which passed the FDR-corrected p-value were annotated with a double asterisk. Multiple test correction for GO term significance is often performed, and we include these results. However, due to the nested structure and non-independence of terms in the GO hierarchy, as well as the methodology employed in topGO, we question whether or not multiple test correction is appropriate in our case, which is why we also include those terms which pass raw p < 0.05 evaluation.

All relevant analysis code can be found in IPython notebooks at http://www.github.com/cfriedline/black\_spruce. Raw data files can be accessed from the iPlant Data Store at https://de.iplantcollaborative.org/de/?type=data&folder=/iplant/home/cfriedline/pub\_data/black\_spruce, and the unigenes can be found in NCBI dbEST under accessions XXXX—XXXX.

## Results

### Sequence data

A total of 7232 chromatogram files were obtained from sequencing for two biological replicates

(e.g., P32, P40) for two tissue types: needle and cambium. Following processing with Phred and

filtering by length, 5996 raw ESTs were combined into a single file for downstream analysis. After processing with SeqClean, 5938 ESTs remained; 2842 were trimmed and 58 were removed from the dataset, either by mapping to E. coli (34), low complexity (1), or length/shortq (23). Assembly of the fragments resulted in 1945 unigenes with an average coverage of ~ ESTs per unigenes (range=[1, 274] ESTs/unigene). Descriptive information about the raw and assembled ESTs can be found in Table 1.



Table : EST statistics for needle and cambium ESTs. The number of singletons relates to the count from each sample that is the only EST present in an assembled unigene. Length distribution refers to the ESTs that were used to assemble unigenes.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample** | **Tissue** | **Raw ESTs** | **Assembled ESTs** | **Singletons** | **Mean length/sd (min, max)** |
| P32 | Cambium | 1829 | 1526 | 189 | 435/157 (100, 850) |
| P40 | Cambium | 1628 | 1677 | 246 | 510/139 (101, 851) |
| P32 | Needle | 1926 | 1475 | 525 | 507/168 (102, 850) |
| P40 | Needle | 1849 | 1260 | 142 | 425/147 (100, 772) |

We find no significant differences between combined cambium and needle read lengths (Welch’s t = 1.16, df = 5633.37, p-value=0.25), which is important because length bias could influence annotation results with higher proportions of longer genes being associated with higher numbers of GO terms {Mi:2012ec}. Additionally the first two PCA axes of the counts for each sample accounts for a significant proportion of variance (69%) in the data, as shown in Figure 1. From the PCA, several observations can be made. PC1 accounts for the variance in EST counts/unigene largely in needle but also largely in unigenes that are found in both tissues. Accordingly, PC2 tracks the variance in cambium-specific unigene expression. There is also a strong relationship between replicates in both tissue types, lending credence to their biological replicability and ability to be combined for downstream analyses. Finally, the expression of unigenes in cambium appears to be nearly perfectly orthogonal to the expression of unigenes in the needles, highlighting the underlying biological differences between tissue types.Macintosh HD:Users:chris:Dropbox:Documents:science:postdoc:papers:black_spruce:manuscript:count_pca.pdf

Figure : PCA of unigene counts, colored by presence (count > 0) of a unigene in a tissue type

### Gene expression

The data in this study are largely organized into two main types: unigenes and ontology. Unigenes are derived from the assembly of quality-controlled and filtered ESTs. The count of individual ESTs that make up each unigene are taken directly as measures of expression of that unigene in the tissue under study, after combining replicates across tissue types. For example, unigene UN0003 was assembled from 1 EST in P32C and 1 EST in P40C, and was not found in either needle tissue sample; its expression, therefore, would be 2 in cambium and 0 in needle. For simplicity, the terms unigene and gene in this study, can be considered to be synonyms. Unigenes are also assigned to genes in UniProtKB using blastx, and these assignments are used to derive ontological terms from the GO database. As such, each unigene may be assigned to multiple GO terms, which can exist in any layer of the GO hierarchy, some of which may be nested into increasingly more general terms. This tree-like structure, therefore, creates a degree of non-independence between terms which must be accounted for in methods determining significant enrichment.

The 1945 unigenes were tested for differential expression (DE) using IDEG6. Expression levels across tissue types were largely similar, with 3203 ESTs in cambium and 2735 in needle. Overall, we found 221 significantly expressed unigenes uncorrected p-values < 0.05 and 57 with FDR-corrected (q-value) general χ2 p-values < 0.05.

When considering only those unigenes that are associated with one or more GO terms, this number is reduced to 113 significantly DE unigenes. Of these 113, 47 are found in cambium and 64 are found in needle tissue. Across all ontologies, the cambium DE unigenes had 4 ± 5 GO terms, ranging from 1—23 terms per unigene; the needle differentially expressed unigenes had 7 ± 7 GO terms, ranging from 1—37 terms per unigene. More details on the GO terms assigned to needle and cambium DE unigenes can be found in Supplemental Table 1 and Supplemental Table 2.

### Gene ontology

As input to topGO, we considered the 47 cambium and 64 needle DE unigenes in order to test for GO enrichment among the two sets of unigenes. These data are summarized in Table 2.

Table : Counts of GO terms by tissue for each ontology for the set of 976 unigenes associated with at least one GO term. The first number indicates the number of significant GO terms and the second indicates the number of possible unigenes testable for that ontology defined as a GO term associated with at least two unigenes.

|  |  |  |  |
| --- | --- | --- | --- |
|  | Ontology | | |
| Tissue | BP | CC | MF |
| Cambium | 23/771 | 11/549 | 41/846 |
| Needle | 58/771 | 45/549 | 51/846 |
|  |  |  |  |

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Figure : Top and significant GO terms for each tissue type for each ontology. A maximum of 20 terms are displayed in each case, consisting of: 1) all GO terms which are enriched at raw p-value < 0.05 (\*) or FDR-corrected p-value (\*\*) and 2) The most abundant GO terms.

## References

{papers2\_bibliography}

## Supplemental Information

Supplemental Table : GO terms associated with DE cambium genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **UNIQID** | **P32C** | **P40C** |  | **GO Terms** |
| UN0010 | 5 | 0 |  | GO:0005773,GO:0005794,GO:0005886,GO:0005543,GO:0008060,GO:0006605,GO:0009555,GO:0016043,GO:0044763 |
| UN0040 | 4 | 0 |  | GO:0006950 |
| UN0045 | 3 | 0 |  | GO:0046872 |
| UN0050 | 8 | 0 |  | GO:0046872 |
| UN0126 | 0 | 3 |  | GO:0005618,GO:0005739,GO:0005777,GO:0005829,GO:0009507,GO:0009516,GO:0004028,GO:0005524,GO:0008802,GO:0009414,GO:0009651,GO:0009737,GO:0046686,GO:0055114,GO:0071454,GO:0006544,GO:0006563,GO:0006566 |
| UN0132 | 0 | 4 |  | GO:0005774,GO:0031966,GO:0045271,GO:0003824,GO:0005975,GO:0006511,GO:0009853,GO:0051788,GO:0080129 |
| UN0173 | 1 | 2 |  | GO:0008289,GO:0006869 |
| UN0176 | 0 | 5 |  | GO:0005578,GO:0005618,GO:0009506,GO:0009740,GO:0009744,GO:0009749,GO:0009750,GO:0009751,GO:0010162,GO:0010286,GO:0080167 |
| UN0178 | 9 | 0 |  | GO:0046872 |
| UN0192 | 30 | 0 |  | GO:0046872 |
| UN0201 | 0 | 5 |  | GO:0046872 |
| UN0204 | 1 | 2 |  | GO:0046872 |
| UN0209 | 2 | 3 |  | GO:0005509 |
| UN0213 | 2 | 1 |  | GO:0046872 |
| UN0214 | 5 | 27 |  | GO:0006950,GO:0009415 |
| UN0215 | 0 | 20 |  | GO:0015035,GO:0006662,GO:0045454,GO:0006118 |
| UN0222 | 2 | 0 |  | GO:0046872 |
| UN0228 | 4 | 10 |  | GO:0008289,GO:0006869 |
| UN0234 | 5 | 0 |  | GO:0046872 |
| UN0251 | 1 | 2 |  | GO:0046872 |
| UN0260 | 3 | 0 |  | GO:0004568,GO:0005975,GO:0006032,GO:0016998 |
| UN0274 | 4 | 0 |  | GO:0004190,GO:0006508 |
| UN0283 | 19 | 19 |  | GO:0006950,GO:0009415 |
| UN0289 | 0 | 2 |  | GO:0046872 |
| UN0298 | 1 | 3 |  | GO:0046872 |
| UN0299 | 1 | 5 |  | GO:0005829,GO:0005886,GO:0009507,GO:0003824,GO:0046872,GO:0009628,GO:0019438,GO:0032787,GO:0042742,GO:0044711,GO:0050832,GO:1901362 |
| UN0332 | 2 | 3 |  | GO:0046872 |
| UN0354 | 48 | 3 |  | GO:0046872 |
| UN0355 | 7 | 3 |  | GO:0046872 |
| UN0357 | 18 | 19 |  | GO:0046872 |
| UN0359 | 7 | 5 |  | GO:0046872 |
| UN0363 | 0 | 4 |  | GO:0046872 |
| UN0365 | 2 | 0 |  | GO:0005840,GO:0003735,GO:0006412,GO:0042254 |
| UN0369 | 3 | 0 |  | GO:0004857,GO:0030599,GO:0005982,GO:0005985 |
| UN0370 | 11 | 0 |  | GO:0006950,GO:0009415 |
| UN0381 | 1 | 2 |  | GO:0003849,GO:0000162,GO:0006571,GO:0009094 |
| UN0416 | 5 | 0 |  | GO:0020037 |
| UN0439 | 1 | 2 |  | GO:0005840,GO:0003735,GO:0006412,GO:0042254 |
| UN0442 | 5 | 0 |  | GO:0080048 |
| UN0633 | 2 | 0 |  | GO:0006950,GO:0009415 |
| UN0635 | 0 | 2 |  | GO:0046872 |
| UN0647 | 3 | 0 |  | GO:0046872 |
| UN0662 | 0 | 6 |  | GO:0005886,GO:0005215,GO:0006810 |
| UN0664 | 0 | 2 |  | GO:0046872 |
| UN0685 | 0 | 3 |  | GO:0005840,GO:0003735,GO:0006412,GO:0042254 |
| UN0775 | 0 | 2 |  | GO:0005739,GO:0005819,GO:0009524,GO:0009536,GO:0009574,GO:0055028,GO:0008017,GO:0000280,GO:0000911,GO:0007020,GO:0009624,GO:0009791,GO:0016458,GO:0016570,GO:0031116,GO:0040029,GO:0044249,GO:0044711,GO:0048731,GO:0052096,GO:0090304,GO:1901576,GO:0045298 |
| UN0838 | 0 | 3 |  | GO:0005634,GO:0005783,GO:0005829,GO:0005515,GO:0008142,GO:0046872,GO:0006888,GO:0008202,GO:0009567,GO:0009610,GO:0009644,GO:0009697,GO:0009863,GO:0031348,GO:0042542,GO:0045087,GO:0046482 |

Supplemental Table : GO terms associated with DE needle genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **UNIQID** | **P32N** | **P40N** |  | **GO Terms** |
| UN0063 | 2 | 1 |  | GO:0010181,GO:0016491,GO:0055114 |
| UN0078 | 3 | 3 |  | GO:0016020,GO:0008152 |
| UN0083 | 1 | 1 |  | GO:0016021,GO:0016758 |
| UN0155 | 1 | 2 |  | GO:0016020,GO:0005215,GO:0006810 |
| UN0160 | 0 | 2 |  | GO:0046872 |
| UN0162 | 0 | 6 |  | GO:0004014,GO:0006557,GO:0006597,GO:0008295,GO:0006525,GO:0006560 |
| UN0163 | 4 | 2 |  | GO:0005737,GO:0045431,GO:0046872,GO:0050589,GO:0007033,GO:0009611,GO:0009718,GO:0009733,GO:0009744,GO:0009753,GO:0010023,GO:0010224,GO:0016045,GO:0080167 |
| UN0165 | 0 | 2 |  | GO:0009522,GO:0009523,GO:0009535,GO:0016021,GO:0016168,GO:0046872,GO:0009765,GO:0018298 |
| UN0166 | 2 | 3 |  | GO:0009573,GO:0009579,GO:0009941,GO:0016020,GO:0048046,GO:0004497,GO:0016984,GO:0009637,GO:0009853,GO:0010114,GO:0010218,GO:0019253,GO:0055114,GO:0046487 |
| UN0170 | 3 | 0 |  | GO:0004672,GO:0005524,GO:0006468 |
| UN0177 | 10 | 4 |  | GO:0009570,GO:0003700,GO:0005524,GO:0005667,GO:0045449 |
| UN0183 | 2 | 2 |  | GO:0016020,GO:0005215,GO:0006810 |
| UN0194 | 3 | 0 |  | GO:0009570,GO:0003700,GO:0005524,GO:0005667,GO:0045449 |
| UN0195 | 1 | 16 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0196 | 5 | 0 |  | GO:0005829,GO:0009535,GO:0009570,GO:0009941,GO:0010319,GO:0048046,GO:0005515,GO:0005524,GO:0008974,GO:0000165,GO:0006098,GO:0006364,GO:0006612,GO:0009409,GO:0009595,GO:0009637,GO:0009697,GO:0009735,GO:0009773,GO:0009862,GO:0009867,GO:0009902,GO:0010103,GO:0010114,GO:0010200,GO:0010207,GO:0010218,GO:0010310,GO:0010363,GO:0019253,GO:0019344,GO:0031348,GO:0035304,GO:0042742,GO:0043900,GO:0050832,GO:0015976 |
| UN0197 | 5 | 0 |  | GO:0000287,GO:0010333,GO:0008152 |
| UN0208 | 2 | 1 |  | GO:0009522,GO:0016021,GO:0015979 |
| UN0210 | 0 | 6 |  | GO:0016020,GO:0009765 |
| UN0211 | 1 | 5 |  | GO:0008289,GO:0006869 |
| UN0227 | 0 | 4 |  | GO:0004497,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0232 | 4 | 2 |  | GO:0004497,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0240 | 9 | 0 |  | GO:0004332,GO:0006096,GO:0006000,GO:0006013,GO:0006020,GO:0006094,GO:0006098,GO:0015976 |
| UN0243 | 23 | 59 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0247 | 2 | 1 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0252 | 4 | 2 |  | GO:0009055,GO:0006118 |
| UN0253 | 2 | 2 |  | GO:0016620,GO:0055114 |
| UN0269 | 2 | 0 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0270 | 3 | 1 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0276 | 4 | 0 |  | GO:0005739,GO:0005794,GO:0009517,GO:0009522,GO:0009533,GO:0009783,GO:0010287,GO:0016021,GO:0016168,GO:0046872,GO:0006364,GO:0009637,GO:0009644,GO:0009744,GO:0009765,GO:0010114,GO:0010155,GO:0010196,GO:0010218,GO:0018298,GO:0019344 |
| UN0281 | 1 | 1 |  | GO:0005739,GO:0005794,GO:0009517,GO:0009522,GO:0009533,GO:0009783,GO:0010287,GO:0016021,GO:0016168,GO:0046872,GO:0006364,GO:0009637,GO:0009644,GO:0009744,GO:0009765,GO:0010114,GO:0010155,GO:0010196,GO:0010218,GO:0018298,GO:0019344 |
| UN0285 | 17 | 5 |  | GO:0009522,GO:0016021,GO:0015979 |
| UN0302 | 5 | 0 |  | GO:0010181,GO:0016491,GO:0055114 |
| UN0304 | 2 | 4 |  | GO:0004014,GO:0006597,GO:0008295,GO:0006525,GO:0006560 |
| UN0309 | 2 | 2 |  | GO:0047216,GO:0006012 |
| UN0310 | 3 | 2 |  | GO:0005829,GO:0009535,GO:0009570,GO:0009941,GO:0010319,GO:0048046,GO:0005515,GO:0005524,GO:0008974,GO:0000165,GO:0006098,GO:0006364,GO:0006612,GO:0009409,GO:0009595,GO:0009637,GO:0009697,GO:0009735,GO:0009773,GO:0009862,GO:0009867,GO:0009902,GO:0010103,GO:0010114,GO:0010200,GO:0010207,GO:0010218,GO:0010310,GO:0010363,GO:0019253,GO:0019344,GO:0031348,GO:0035304,GO:0042742,GO:0043900,GO:0050832,GO:0015976 |
| UN0317 | 2 | 6 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0323 | 13 | 12 |  | GO:0006952,GO:0009607 |
| UN0326 | 2 | 33 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0331 | 1 | 4 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0333 | 8 | 0 |  | GO:0016020,GO:0005215,GO:0006810 |
| UN0338 | 15 | 21 |  | GO:0006869,GO:0009414,GO:0009651,GO:0009737 |
| UN0339 | 1 | 8 |  | GO:0004497,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0340 | 14 | 1 |  | GO:0009570,GO:0003700,GO:0005524,GO:0005667,GO:0045449 |
| UN0342 | 5 | 0 |  | GO:0016706,GO:0055114 |
| UN0343 | 1 | 3 |  | GO:0016020,GO:0009765 |
| UN0344 | 2 | 3 |  | GO:0006952,GO:0009607 |
| UN0345 | 8 | 16 |  | GO:0016020,GO:0009765 |
| UN0351 | 3 | 4 |  | GO:0004497,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0353 | 0 | 5 |  | GO:0004497,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0360 | 9 | 45 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0361 | 12 | 128 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0405 | 0 | 2 |  | GO:0004332,GO:0006096,GO:0006000,GO:0006013,GO:0006020,GO:0006094,GO:0006098,GO:0015976 |
| UN0407 | 7 | 0 |  | GO:0003746,GO:0003924,GO:0005525,GO:0005840,GO:0006448 |
| UN0408 | 2 | 3 |  | GO:0005576,GO:0009505,GO:0004104,GO:0004560,GO:0016298,GO:0019863,GO:0006952,GO:0009987,GO:0005975,GO:0016042,GO:0019814 |
| UN0409 | 0 | 4 |  | GO:0009523,GO:0015979 |
| UN0410 | 1 | 3 |  | GO:0005739,GO:0009507,GO:0009522,GO:0006098,GO:0006364,GO:0009657,GO:0009768,GO:0010207,GO:0019344,GO:0030003,GO:0035304,GO:0070838 |
| UN0415 | 3 | 0 |  | GO:0005737,GO:0016879,GO:0006529 |
| UN0425 | 2 | 0 |  | GO:0016491,GO:0055114 |
| UN0431 | 1 | 2 |  | GO:0004089,GO:0008270,GO:0015976,GO:0006730,GO:0006807 |
| UN0434 | 3 | 0 |  | GO:0009535,GO:0009538,GO:0010287,GO:0016021,GO:0006364,GO:0009657,GO:0009735,GO:0009773,GO:0010207,GO:0019344,GO:0035304 |
| UN0435 | 5 | 0 |  | GO:0000015,GO:0005634,GO:0005740,GO:0005886,GO:0009506,GO:0009570,GO:0048046,GO:0003677,GO:0004634,GO:0005507,GO:0006094,GO:0006096,GO:0006098,GO:0009409,GO:0009416,GO:0009651,GO:0009735,GO:0009737,GO:0009853,GO:0010090,GO:0046686,GO:0000162,GO:0006571,GO:0009094 |
| UN0578 | 2 | 0 |  | GO:0009533,GO:0009543,GO:0009941,GO:0030095,GO:0006098,GO:0006364,GO:0009637,GO:0009735,GO:0009902,GO:0010027,GO:0010114,GO:0010207,GO:0010218,GO:0010304,GO:0015995,GO:0016117,GO:0035304,GO:0042744,GO:0042793,GO:0045893,GO:0046686 |
| UN0612 | 0 | 2 |  | GO:0004497,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |
| UN0661 | 2 | 2 |  | GO:0004497,GO:0005515,GO:0016984,GO:0009853,GO:0019253,GO:0055114,GO:0009573,GO:0046487 |