

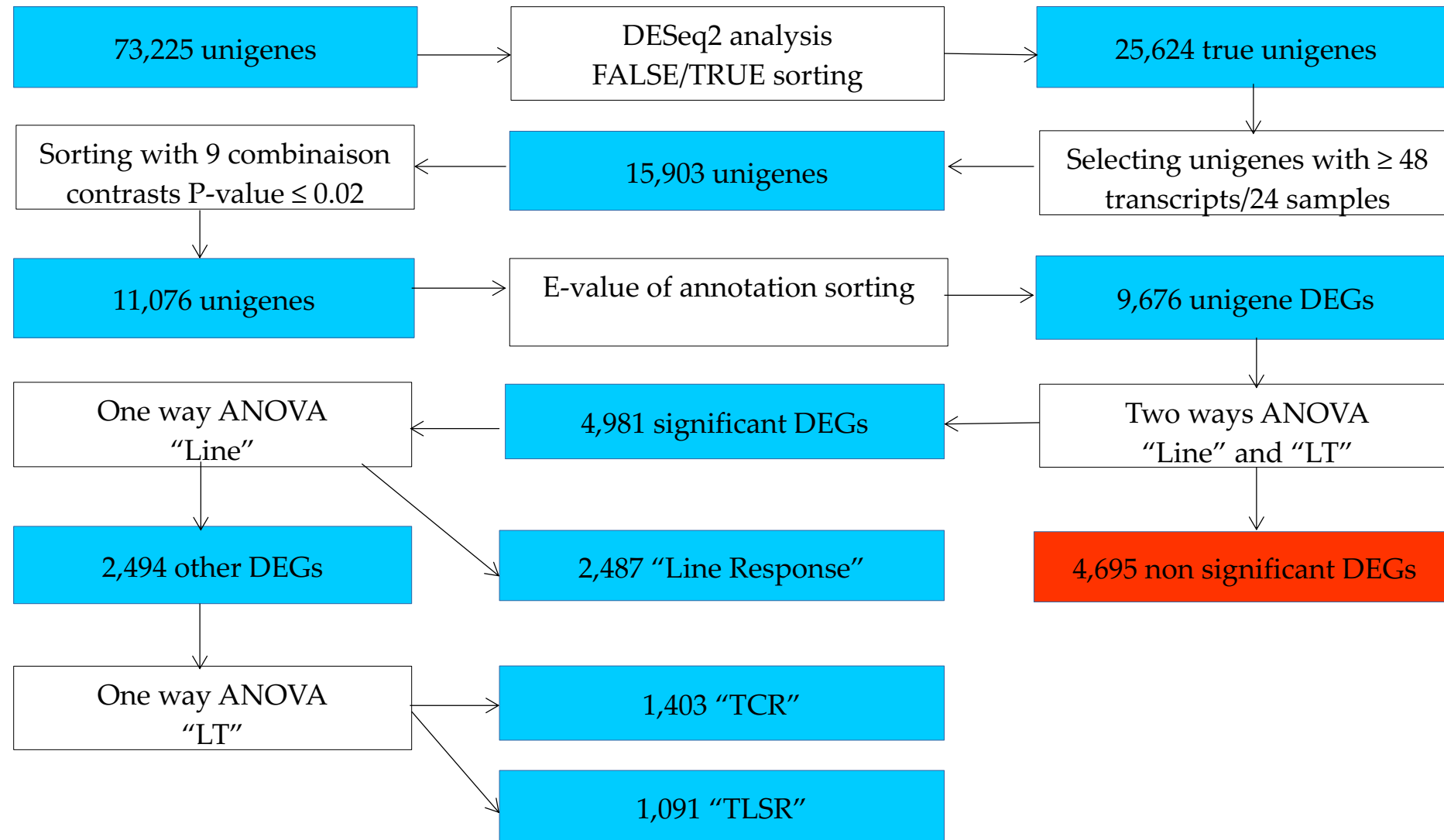


Figure S1. Statistical analysis and clustering workflow leading to three sets of differentially expressed genes (DEGs). Blue colored boxes show the gene numbers, uncolored boxes represent statistical analyses, and red box show non significant DEGs.

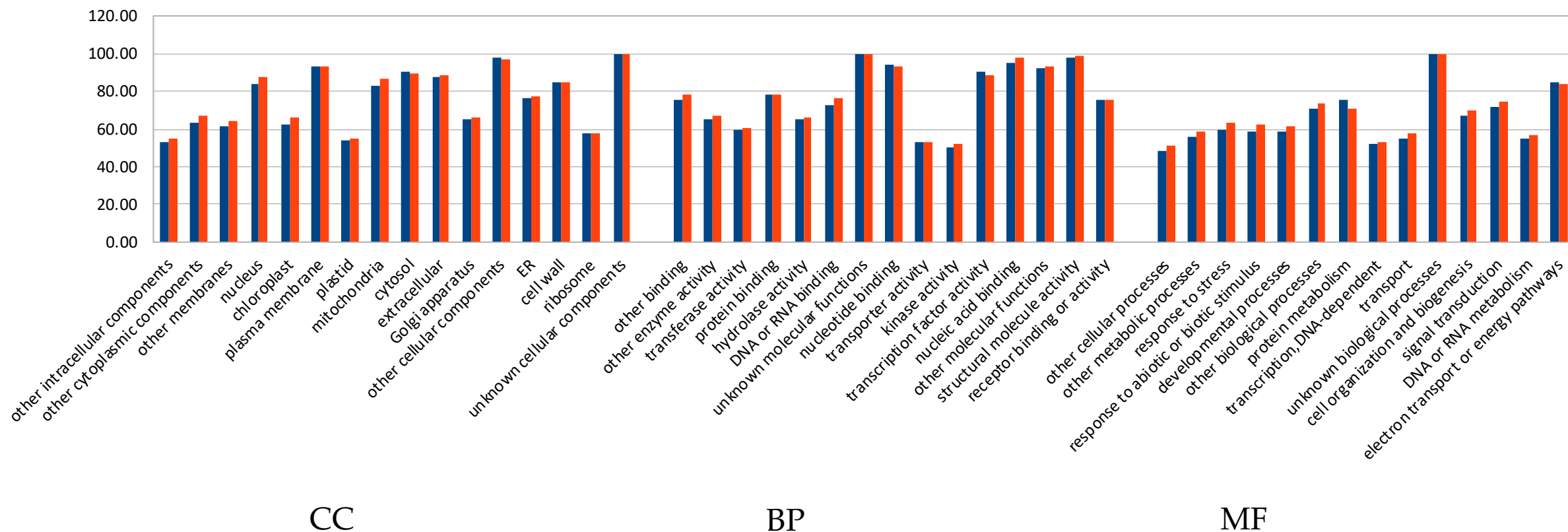
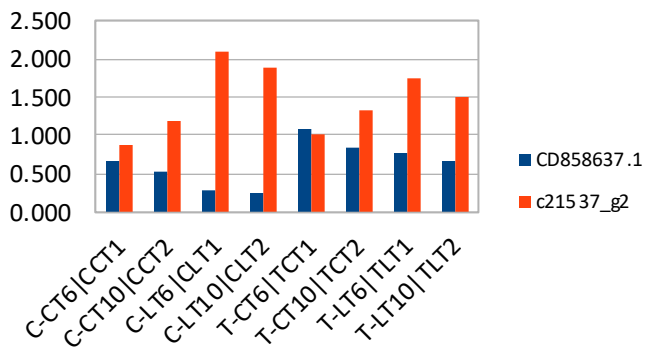
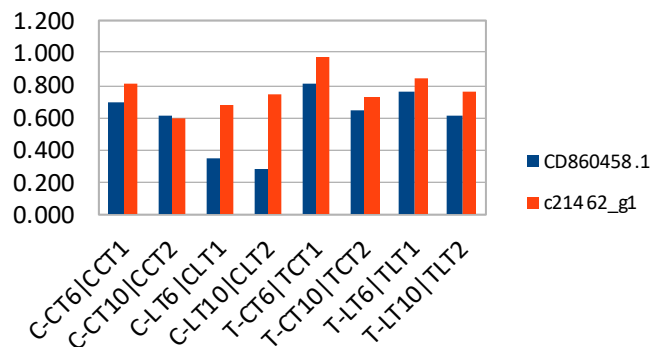
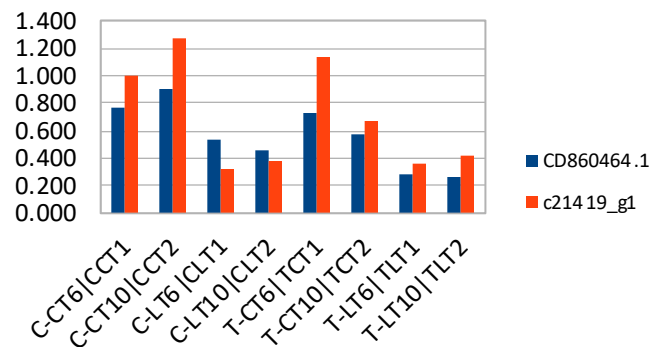
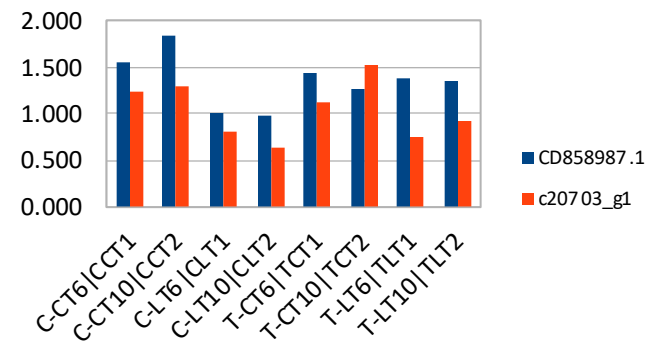
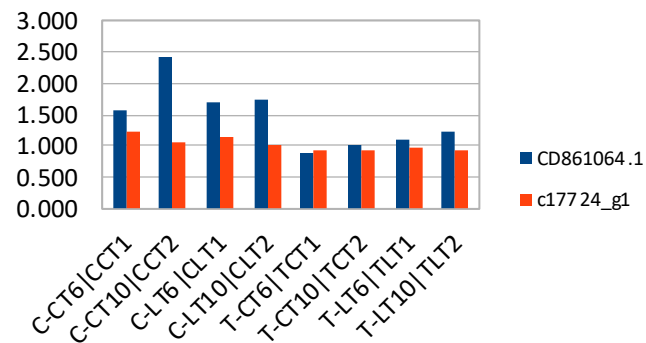
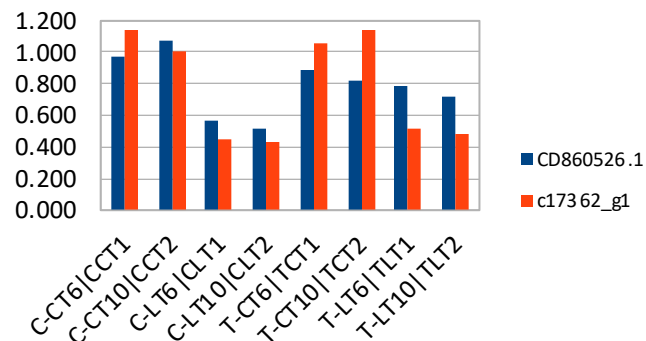
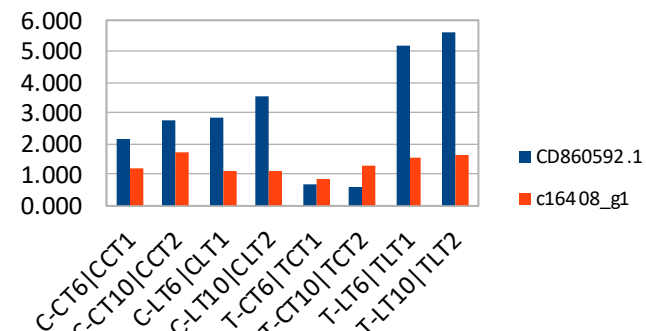
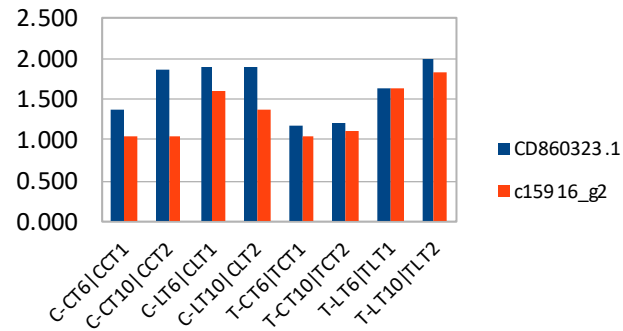
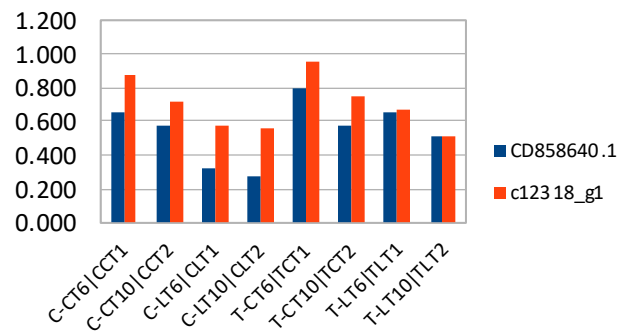
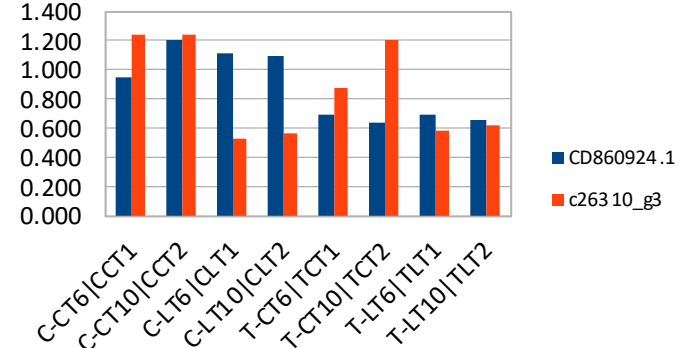
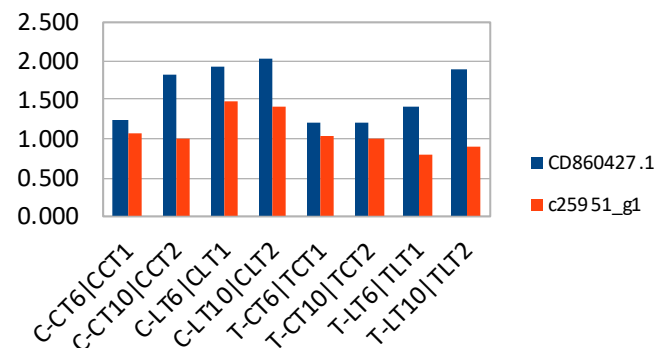
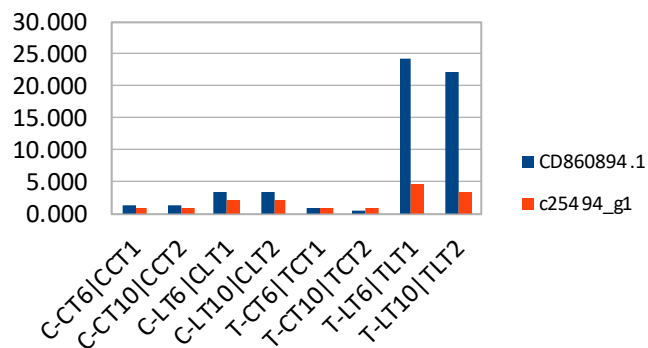
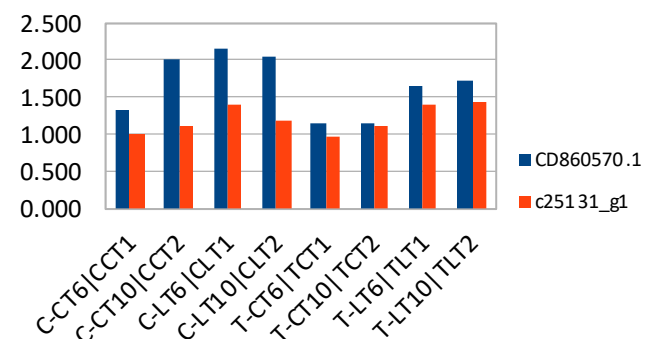
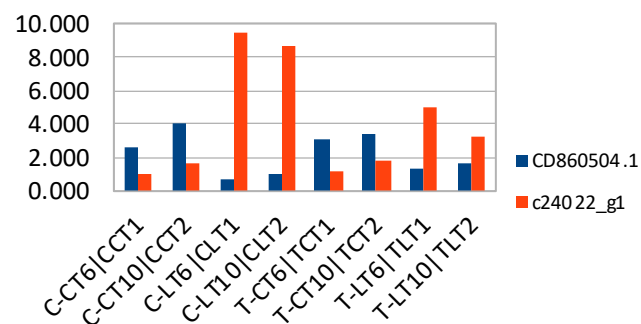
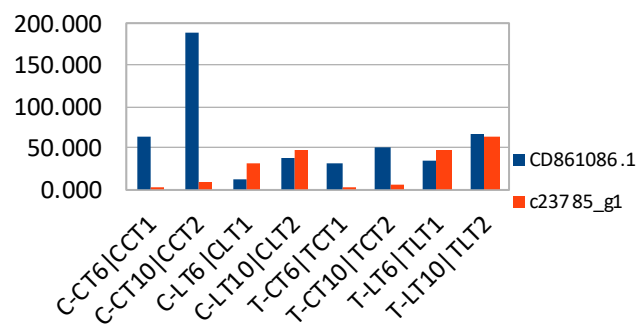
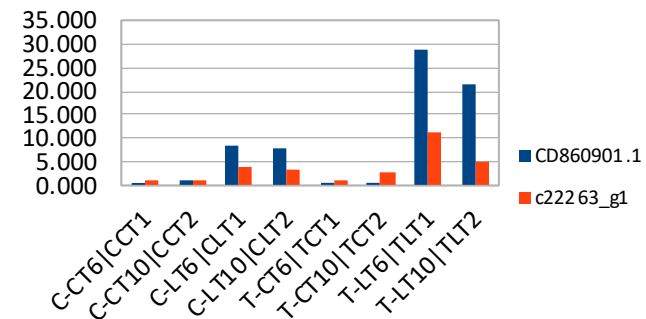
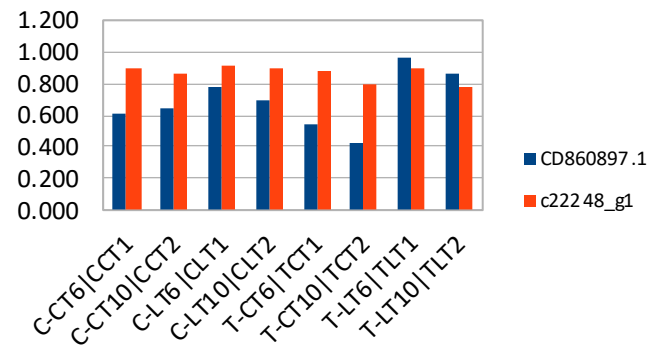
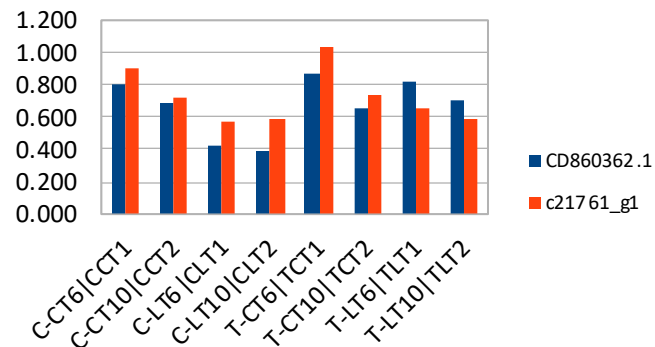
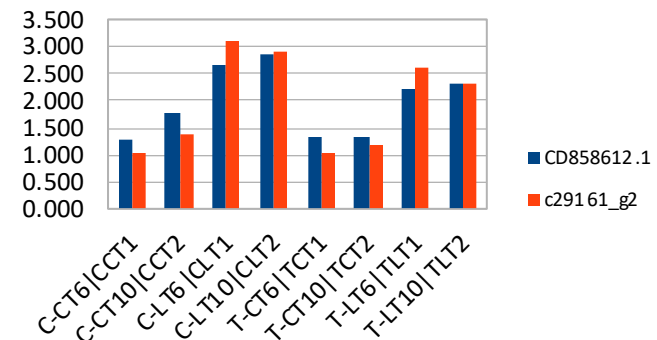
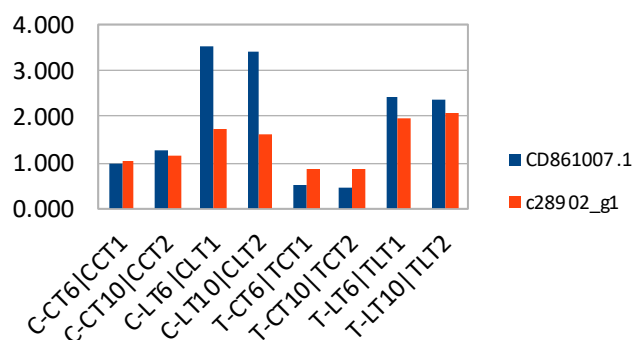
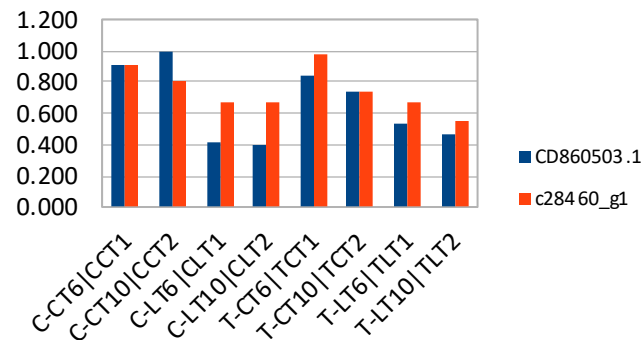
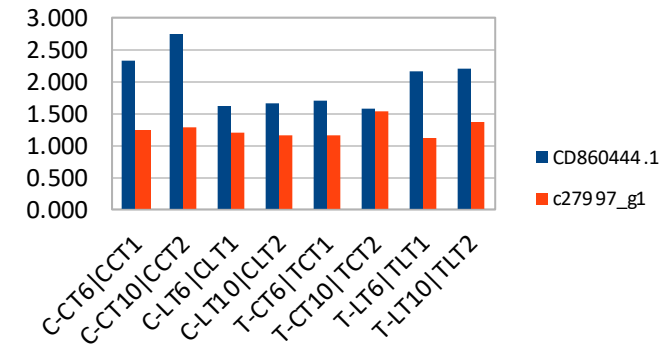
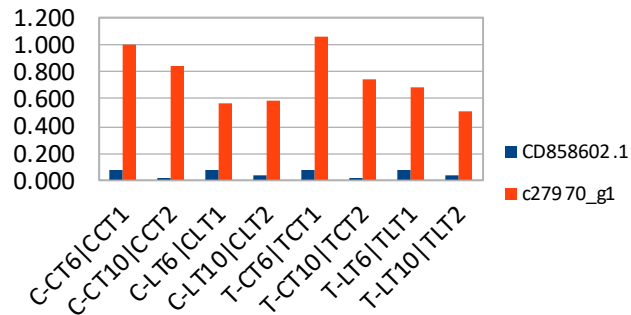
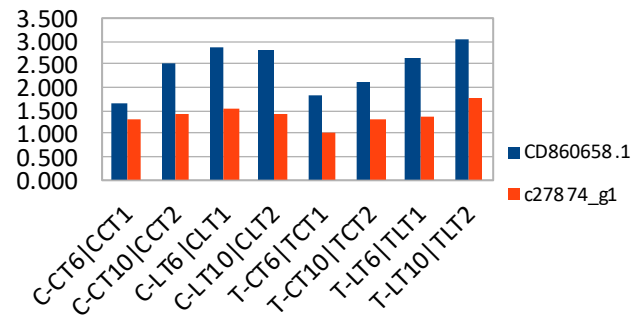
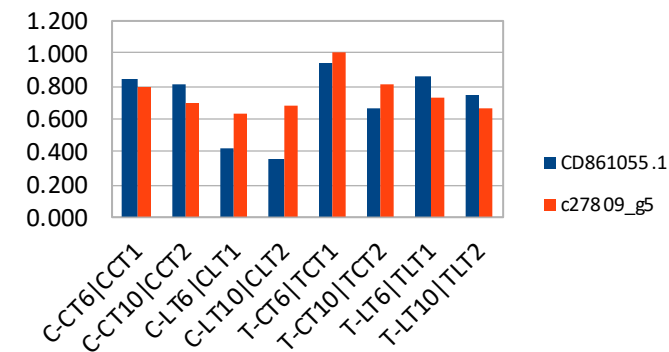
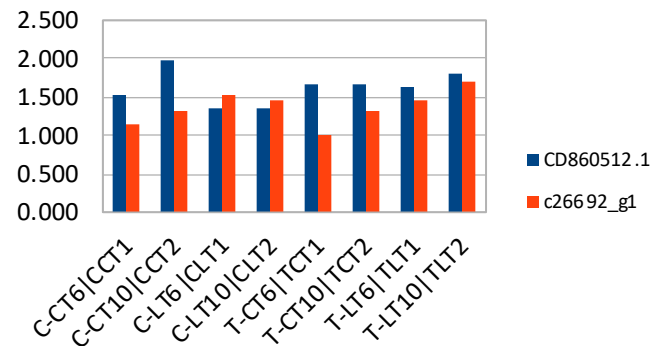
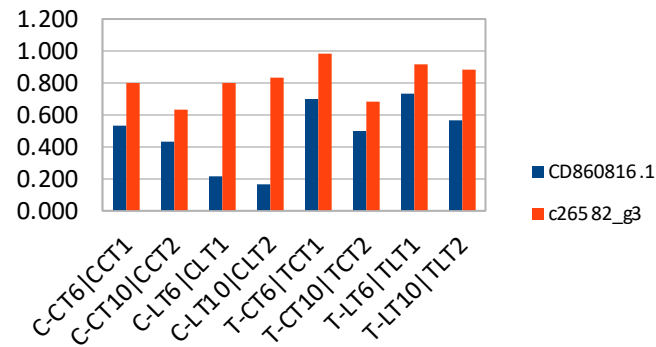


Figure S2. Functional classification of assembled unigenes carried out using Gene Ontology. The distribution of the cellular component (CC), molecular function (MF) and biological processes (BP), obtained from the whole transcriptome assembly (blue bars) is compared with that of the *A. thaliana* whole genome (red bars).







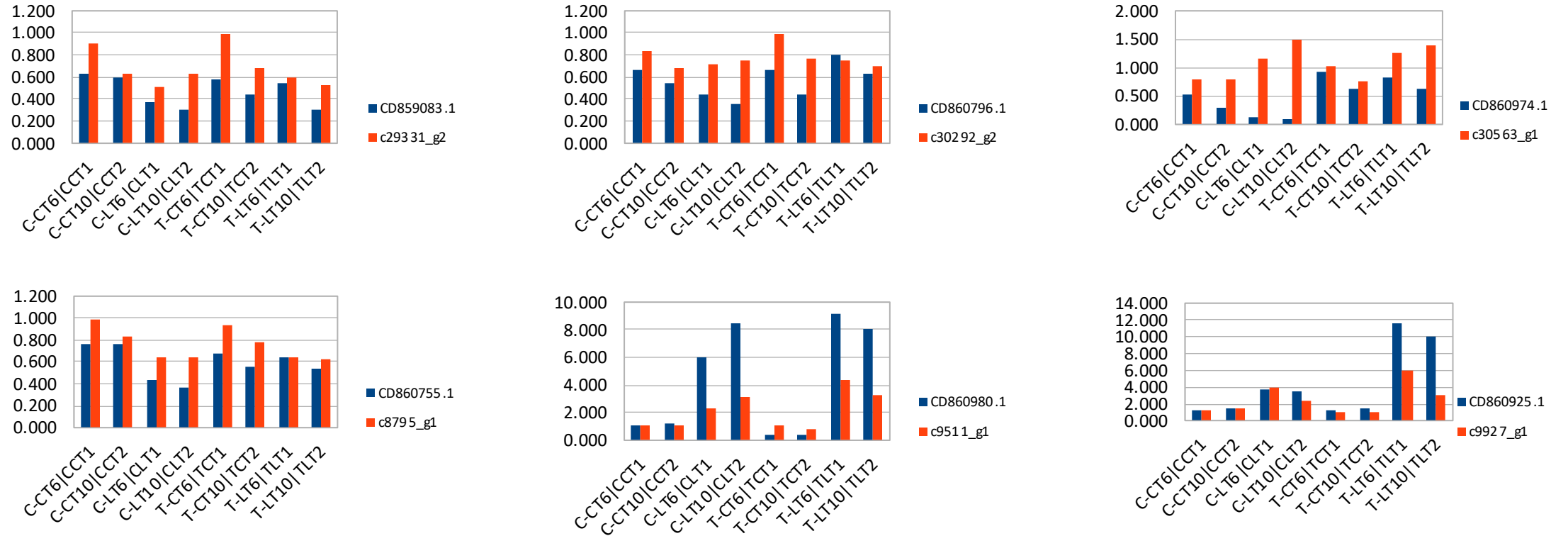
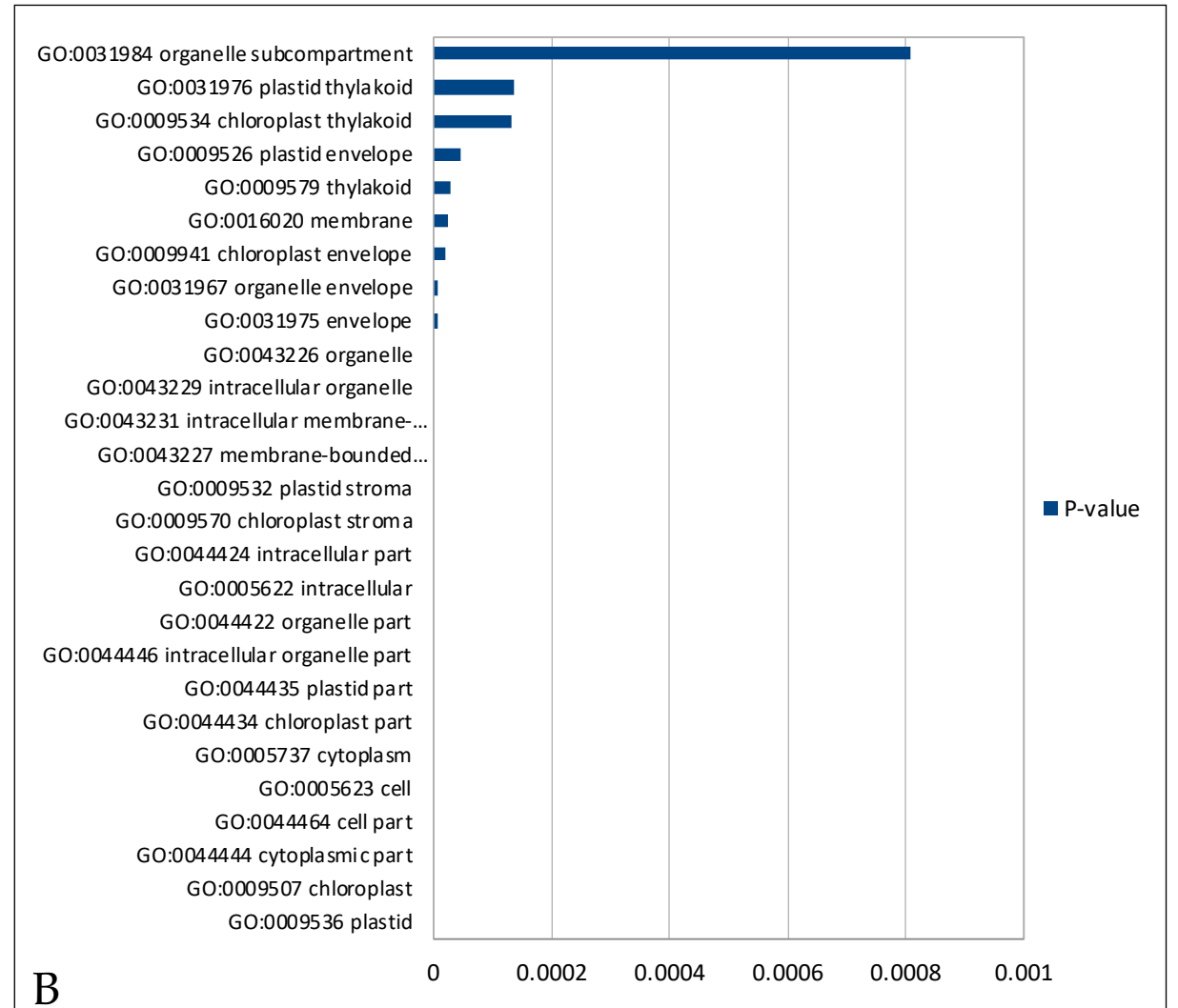
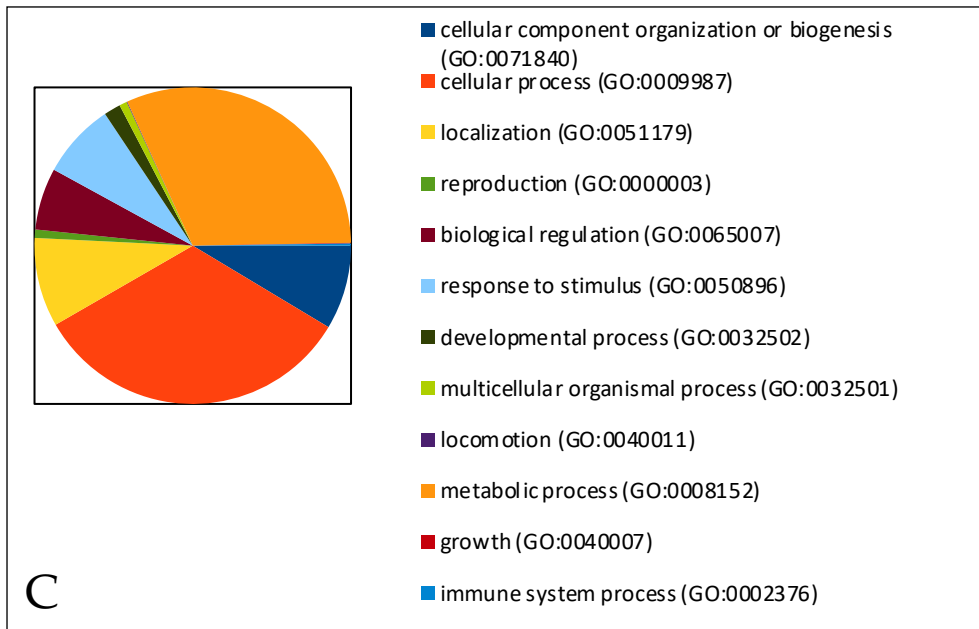
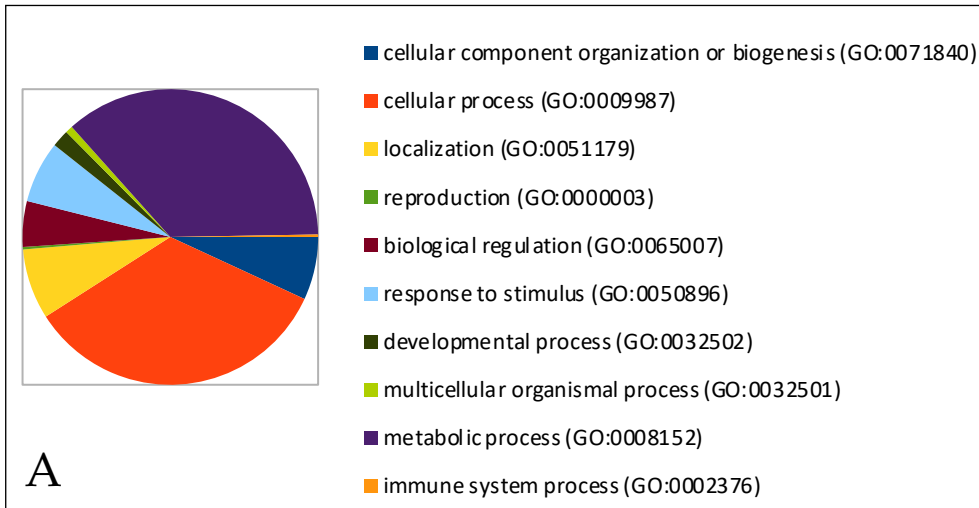
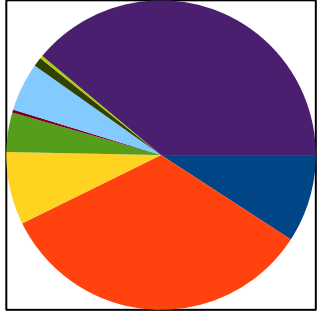
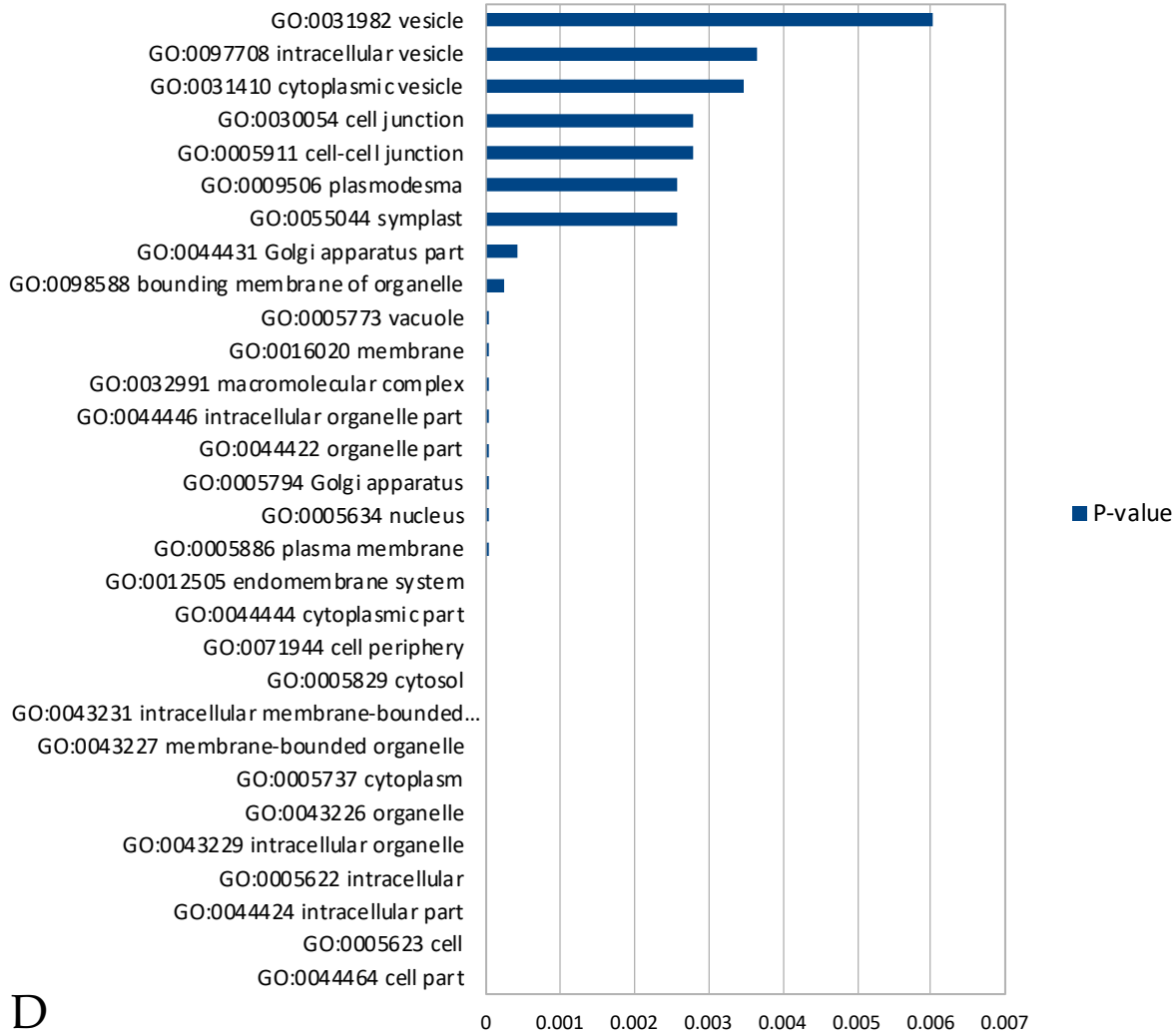


Figure S3. Individually comparisons of thirty-three qPCR and RNAseq data. Blue and red bars represent the qPCR and the RNA-seq data, respectively. For more details, see figure 1 and figure 2.

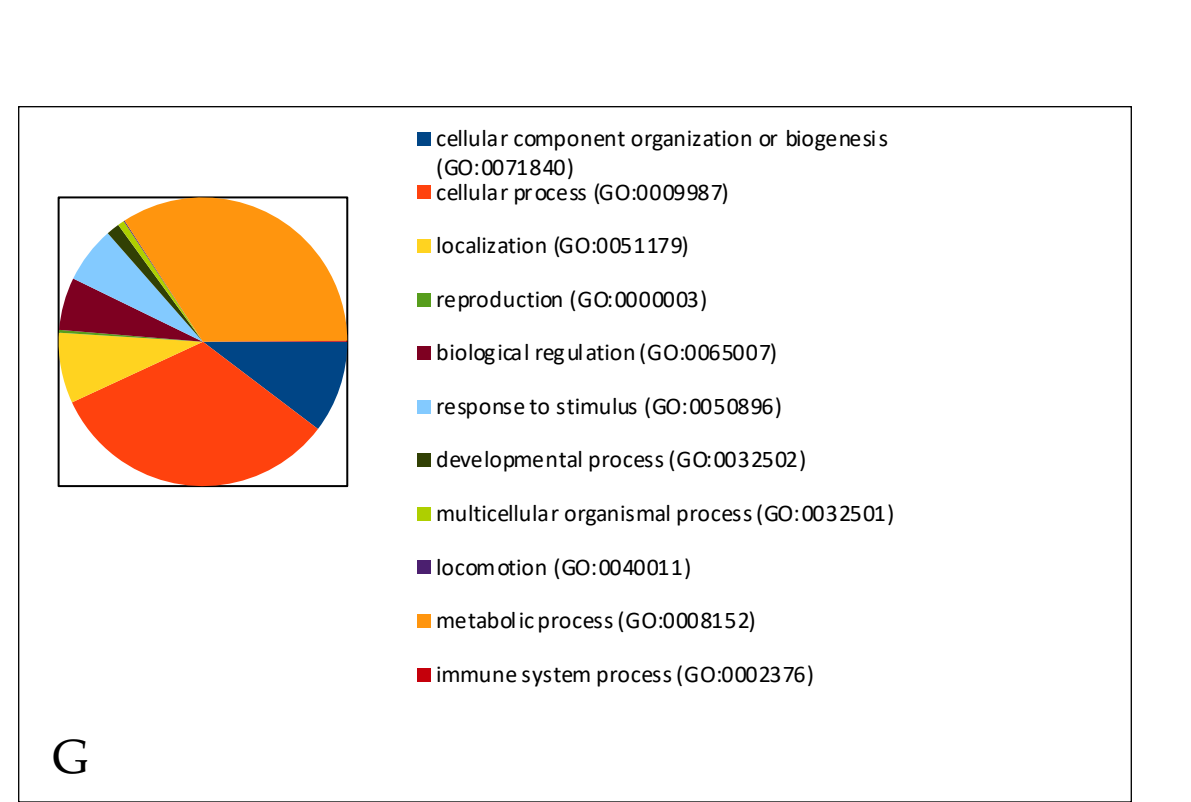
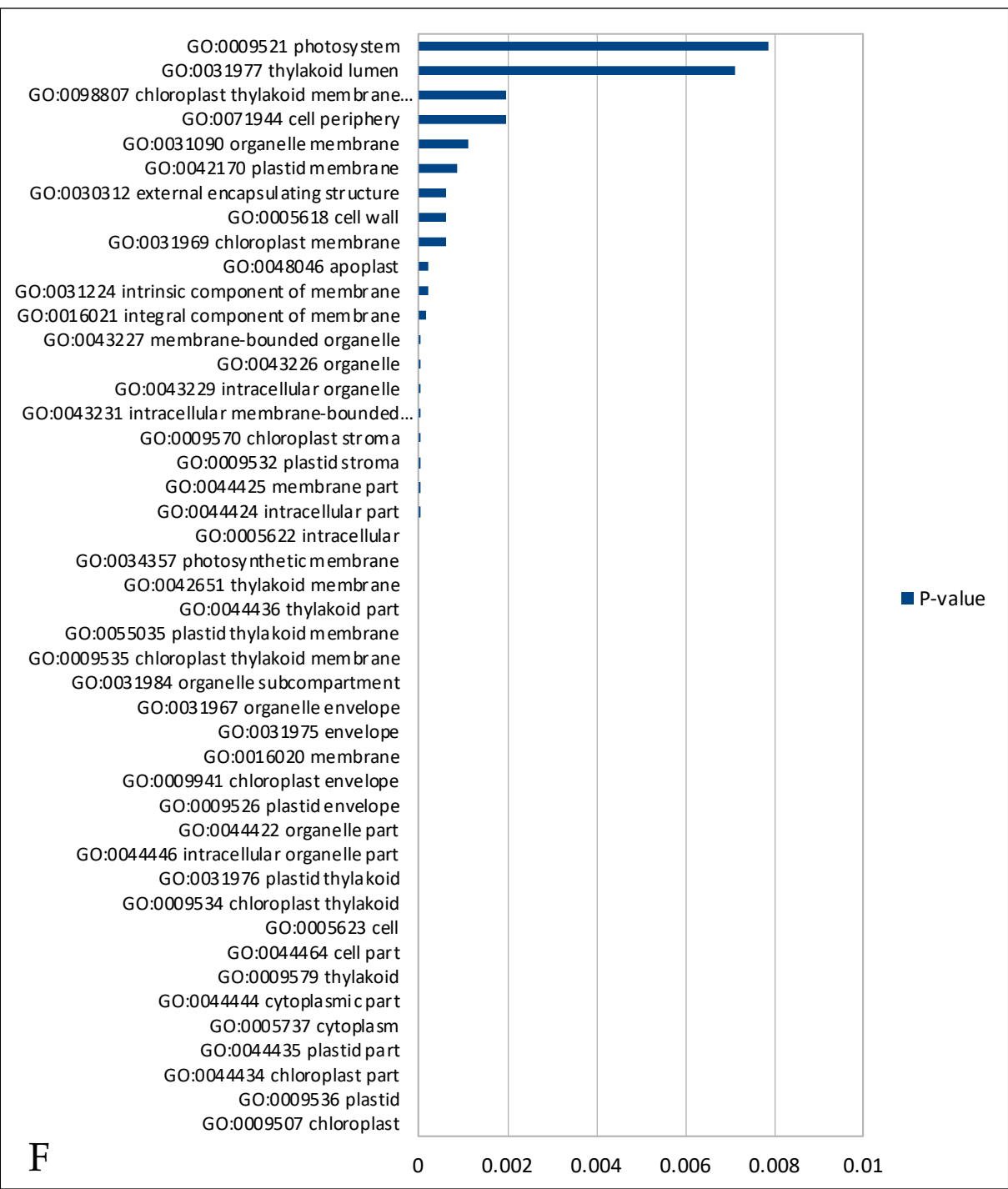


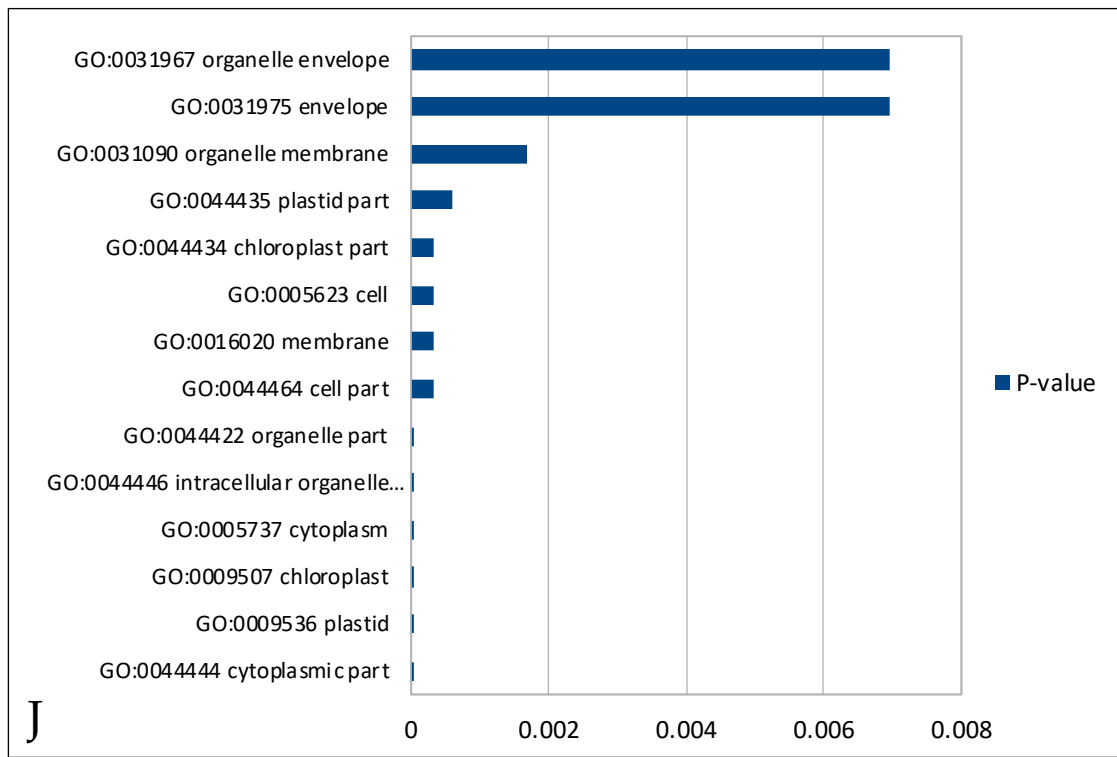
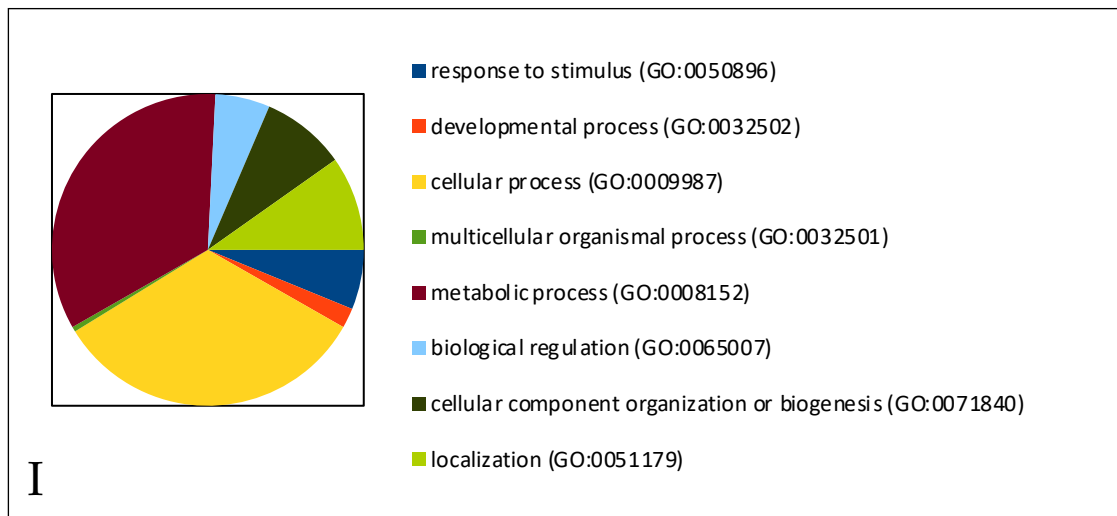
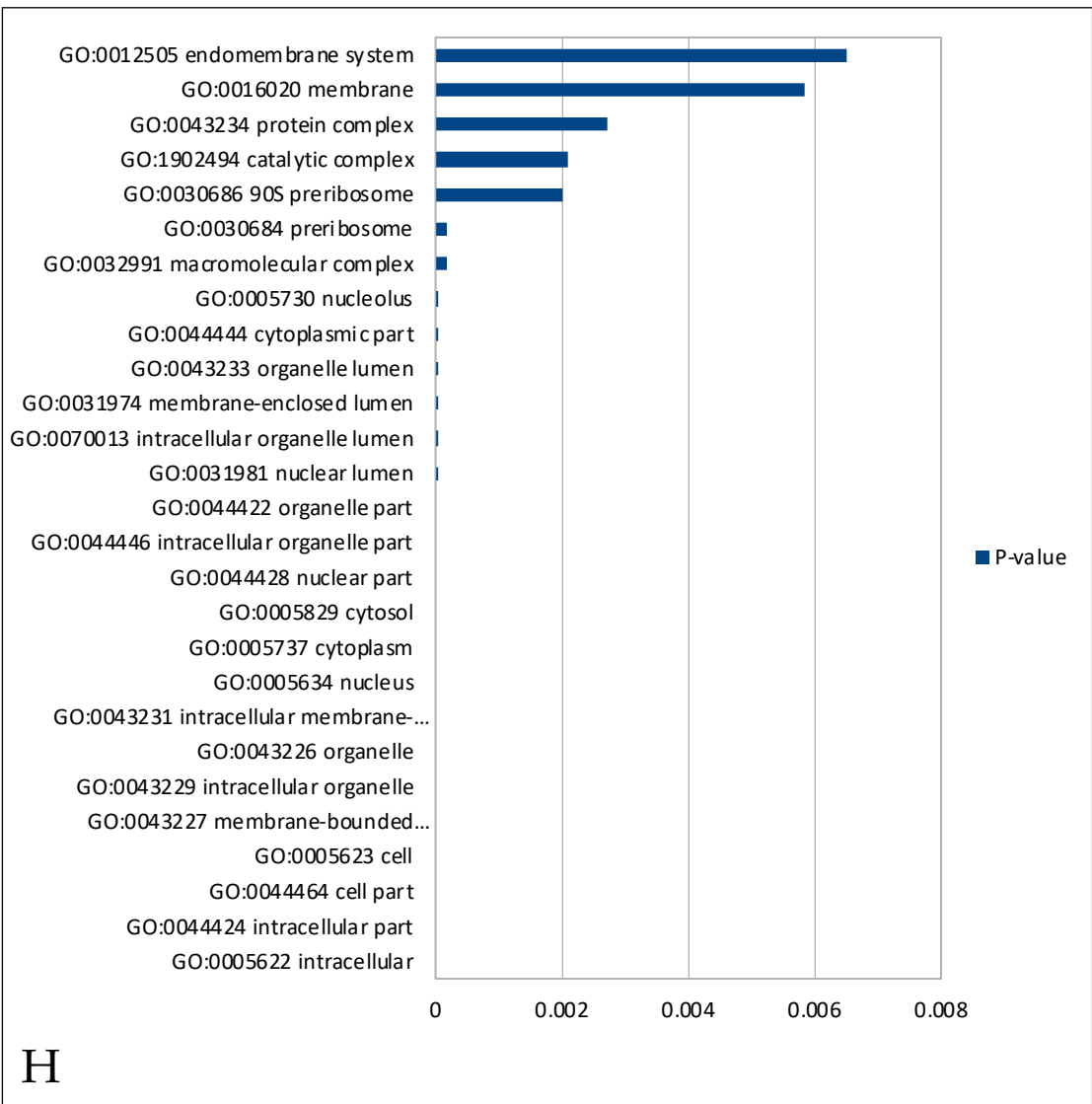
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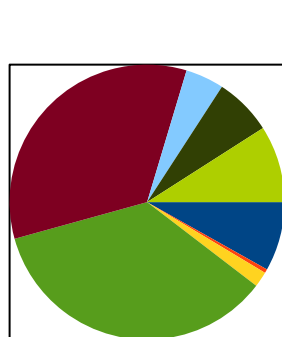
E

- cellular component organization or biogenesis (GO:0071840)
- cellular process (GO:0009987)
- localization (GO:0051179)
- biological regulation (GO:0065007)
- reproduction (GO:0000003)
- response to stimulus (GO:0050896)
- developmental process (GO:0032502)
- locomotion (GO:0040011)
- metabolic process (GO:0008152)



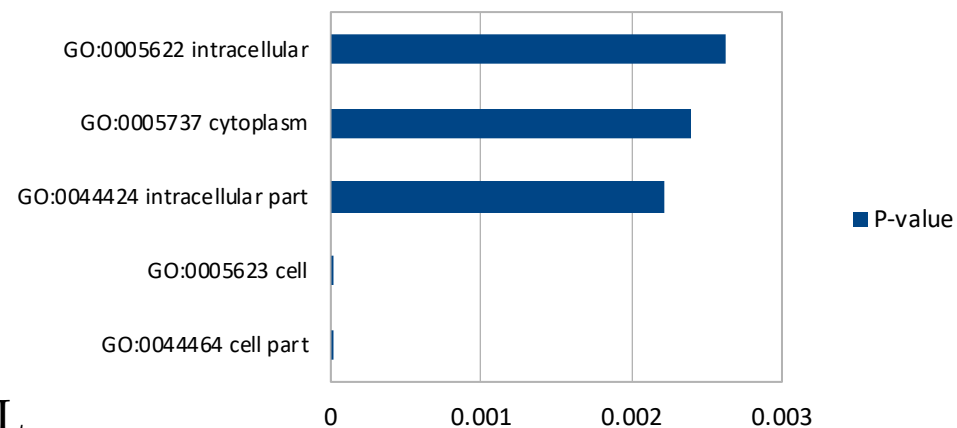


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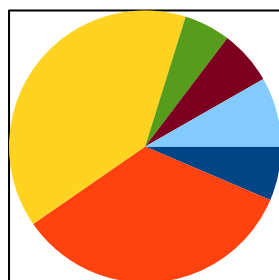


- response to stimulus (GO:0050896)
- immune system process (GO:0002376)
- developmental process (GO:0032502)
- cellular process (GO:0009987)
- metabolic process (GO:0008152)
- biological regulation (GO:0065007)
- cellular component organization or biogenesis (GO:0071840)
- localization (GO:0051179)

L

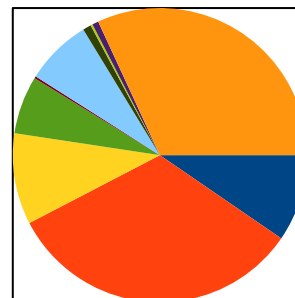


M



- response to stimulus (GO:0050896)
- cellular process (GO:0009987)
- metabolic process (GO:0008152)
- biological regulation (GO:0065007)
- cellular component organization or biogenesis (GO:0071840)
- localization (GO:0051179)

N



- cellular component organization or biogenesis (GO:0071840)
- cellular process (GO:0009987)
- localization (GO:0051179)
- biological regulation (GO:0065007)
- reproduction (GO:0000003)
- response to stimulus (GO:0050896)
- developmental process (GO:0032502)
- rhythmic process (GO:0048511)
- multicellular organismal process (GO:0032501)
- metabolic process (GO:0008152)

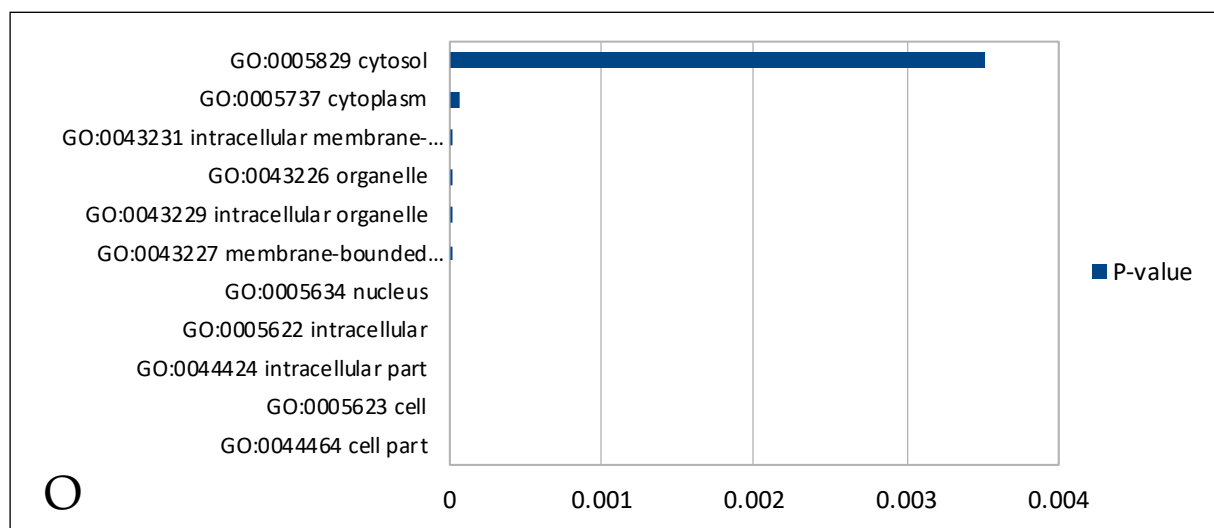


Figure S4. Enrichment of GO terms related to “Biological Processes (BP)” (pie chart) and “Cellular Component (CC)” (horizontal histogram, classes are sorted by *p*-value, most significant at the bottom). **(A)** BP and **(B)** CC of the LR Ch up-expressed subset; **(C)** BP and **(D)** CC of the LR Te up-expressed subset; **(E)** BP and **(F)** CC of the TCR down-expressed subset; **(G)** BP and **(H)** CC of the TCR up-expressed subset; **(I)** BP and **(J)** CC of the TLSR **a** subset; **(K)** BP and **(L)** CC of the TLSR **b** subset; **(M)** BP the TLSR **c** subset; and **(N)** BP and **(O)** CC of the TLSR **d** subset.

Table S1. Statistical overview of sequencing and transcriptome assembly data.

Items	Trinity	TransRate
Number of libraries	24	24
Total number of clean reads	793,583,651	743,950,152
Number of reads in Champagne	432,811,373	405,452,636
Number of reads in Terese	360,772,278	338,497,516
# contigs present only in Champagne	5,845	5,689
# contigs present only in Terese	6,257	5,186
# contigs (≥ 0 bp)	150,342	122,194
# contigs (≥ 1000 bp)	67,384	49,454
Total length (≥ 0 bp)	176,909,219	133,129,560
Total length (≥ 1000 bp)	137,299,244	99,332,177
# contigs	100,020	76,267
Minimum length of contigs (bp)	201	201
Average length of contigs (bp)	1,177	1,089
Largest contig (bp)	12,528	11,608
Total length	161,140,190	118,787,279
GC (%)	38.13	38.04
N50	1,961	1,904
N75	1,294	1,242
L50	27,830	21,098
L75	52,994	40,289
# N's per 100 kbp	0	0
Number of unigenes	81,321	73,225

Table S2. KEGG pathways repartition in each subset of DEGs, divided into two sub-categories of KEGG classification. The Ch up and Te up correspond to “Line Response” followed by two columns of “Temperature Common Response” and the last four columns referring to the “Temperature Line Specific Response”.

	Ch up	Te up	TCR down	TCR up	TLSR a	TLSR b	TLSR c	TLSR d
1. Metabolism								
1.0 Global and overview maps								
Metabolic pathways	114	106	82	55	38	28	10	27
Biosynthesis of secondary metabolites	75	66	57	31	30	17	7	13
Carbon metabolism	11	18	16	7	5	3	3	1
2-Oxocarboxylic acid metabolism	2	3	4	5	2	2		1
Fatty acid metabolism	3	1	4	2	3	3		
Biosynthesis of amino acids	16	14	10	9	4	4	1	2
1.1 Carbohydrate metabolism								
Glycolysis / Gluconeogenesis	6	10	5	3	1	1		1
Citrate cycle (TCA cycle)	2	2	2	5		2		
Pentose phosphate pathway		7	3				2	1
Pentose and glucuronate interconversions	2	4					1	1
Fructose and mannose metabolism	1	8	1		1			2
Galactose metabolism	3	5		2				
Ascorbate and aldarate metabolism	5	3	4		1		1	1
Starch and sucrose metabolism	8	10	5	8	6	3	1	2
Amino sugar and nucleotide sugar metabolism	8	9	5	2	4		1	
Pyruvate metabolism	7	9	3	2	2	1	1	1
Glyoxylate and dicarboxylate metabolism	3	4	10	1	4	2		
Propanoate metabolism			2	1	2		2	
Butanoate metabolism	1		1	1	1	1		
C5-Branched dibasic acid metabolism		1		2				
Inositol phosphate metabolism	2	5	1	2	1	4		
1.2 Energy metabolism								

Oxidative phosphorylation	6	3	4	1	6	1	1	
Photosynthesis	2	1	7					
Photosynthesis - antenna proteins	1	2	1	2			1	
Carbon fixation in photosynthetic organisms	4	4	4		1		1	1
Nitrogen metabolism	4	1	1		1			1
Sulfur metabolism	3	2	2		1			
1.3 Lipid metabolism								
Fatty acid biosynthesis	2		1	1	1	2		
Fatty acid elongation	3	1	4		3		1	
Fatty acid degradation	4	3		2	2	3		
Synthesis and degradation of ketone bodies			1		1			
Cutin, suberine and wax biosynthesis	1	2			2	1	1	
Steroid biosynthesis	2	2	1		1			
Glycerolipid metabolism	8	6	3	4		2	1	2
Glycerophospholipid metabolism	8	7	4	5	2	4	1	5
Ether lipid metabolism		2		2	1	1		1
Sphingolipid metabolism	2	1	1	4		1		1
Arachidonic acid metabolism	2			1		1		
Linoleic acid metabolism	1			1				1
alpha-Linolenic acid metabolism	4	3	3	1		1		1
Biosynthesis of unsaturated fatty acids	1	2	3	1	1	1		
1.4 Nucleotide metabolism								
Purine metabolism	8	11	3	9	3	5		3
Pyrimidine metabolism	5	4		5	1	4		6
1.5 Amino acid metabolism								
Alanine, aspartate and glutamate metabolism	6	1	2	2	1	1		2
Glycine, serine and threonine metabolism	5	4	6	2	2			1
Cysteine and methionine metabolism	13	3	2	1	2	1		1
Valine, leucine and isoleucine degradation	1	5	3	1	1		2	1
Valine, leucine and isoleucine biosynthesis		2		2				
Lysine biosynthesis	2	1						1

Lysine degradation	1	5		1	1		
Arginine biosynthesis	4	1	4		1		1
Arginine and proline metabolism	3	3	2	2	1	2	
Histidine metabolism	1	1		2			1
Tyrosine metabolism	5	3		1	3	1	1
Phenylalanine metabolism	4	2	3	1	2	1	2
Tryptophan metabolism	3	5	3	1	2	1	
Phenylalanine, tyrosine and tryptophan biosynthesis	5	1	2	1	2	1	1
1.6 Metabolism of other amino acids							
beta-Alanine metabolism	4	2		1	1	2	1
Taurine and hypotaurine metabolism	1	1				1	
Phosphonate and phosphinate metabolism	1			2			1
Selenocompound metabolism	3						1
Cyanoamino acid metabolism	3	5	4	3	3	3	1
Glutathione metabolism	9	2	2	4	1	2	1
1.7 Glycan biosynthesis and metabolism							
N – Glycan biosynthesis	2	3			1		2
Other types of O – glycan biosynthesis							1
Glycosaminoglycan degradation		1	1				
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	1	2		1			1
Glycosphingolipid biosynthesis - globo and isoglobo series	1	1	1				
Glycosphingolipid biosynthesis - ganglio series			1				
Other glycan degradation	2		1	2			1
1.8 Metabolism of cofactors and vitamins							
Thiamine metabolism	1		1	1		1	
Riboflavin metabolism	2	1					
Vitamin B6 metabolism	1		1	1			
Nicotinate and nicotinamide metabolism	2	1		1	1		2
Pantothenate and CoA biosynthesis	1			2			1

Biotin metabolism	1							
Lipoic acid metabolism	1							
Folate biosynthesis		1	2				1	1
One carbon pool by folate	1	1	5		1			
Porphyrin and chlorophyll metabolism	3	1	3	1	4	1		
Ubiquinone and other terpenoid-quinone biosynthesis		1	4			2		1
1.9 Metabolism of terpenoids and polyketides								
Terpenoid backbone biosynthesis	4	2	4	1	2		1	2
Monoterpenoid biosynthesis	1	1						
Sesquiterpenoid and triterpenoid biosynthesis	1	2						
Diterpenoid biosynthesis		2	1					
Carotenoid biosynthesis	2		4		1			1
Brassinosteroid biosynthesis		1		1				
Zeatin biosynthesis	1	1	1		1			
1.10 Biosynthesis of other secondary metabolites								
Phenylpropanoid biosynthesis	9	12	9	5	4	4		2
Stilbenoid, diarylheptanoid and gingerol biosynthesis			1					
Flavonoid biosynthesis	5		2		1			
Flavone and flavonol biosynthesis	2				1			
Anthocyanin biosynthesis					1			
Indole alkaloid biosynthesis	2							
Isoquinoline alkaloid biosynthesis	3	1			2			
Tropane, piperidine and pyridine alkaloid biosynthesis	3	1		1	3			1
Betalain biosynthesis	1							
Glucosinolate biosynthesis			1	1	1			
Monobactam biosynthesis								1
Sub-toatal	467	425	334	222	179	122	45	108
2. Genetic Information Processing								
2.1 Transcription								

RNA polymerase	1	2		4		3		
Basal transcription factors	1	4	1	1				1
Spliceosome	5	11	3	18	2	2		5
2.2 Translation								
Ribosome	6	25		2		1		4
Aminoacyl-tRNA biosynthesis	3	2		2				2
RNA transport	5	11	1	13		4		6
mRNA surveillance pathway		8		14		3		7
Ribosome biogenesis in eukaryotes	2	2		21		1		5
2.3 Folding, sorting and degradation								
Protein export	2	3		2	1		1	1
Protein processing in endoplasmic reticulum	5	8	4	9	4	3	1	3
SNARE interactions in vesicular transport	1	5		2				1
Ubiquitin mediated proteolysis	4	13	3	4	1		2	2
Sulfur relay system		1				2		2
Proteasome	2	1		6		3		
RNA degradation	2	6	2	10				1
2.4 Replication and repair								
DNA replication	3	1		1	1	2		1
Base excision repair	2	6	1	1		1		
Nucleotide excision repair	4	4		2	1	2		
Mismatch repair	4	1			1	2		
Homologous recombination	1	5				2		1
Non – homologous end – joining		1		1				1
3. Environmental Information Processing								
3.1 Membrane transport								
ABC transporters	1	3		2		1		1
3.2 Signal transduction								
MAPK signaling pathway - plant	3	8		4			1	3
Phosphatidylinositol signaling system	2	6	1	3		4	1	
Plant hormone signal transduction	4	17	3	7	1	1	2	6

4. Cellular Processes

4.1 Transport and catabolism

Endocytosis	5	14	3	12	3	4		6
Phagosome	3	4	4	5	2		2	
Peroxisome	4	5	3	6	1	3	1	1
Autophagy - other	2	3		1				2

5. Organismal Systems

5.1 Environmental adaptation

Circadian rhythm - plant	2	2	2	6	3	2		3
Plant-pathogen interaction	7	8		6	1	2	1	

6. Human Diseases

6.1 Endocrine and metabolic diseases

AGE-RAGE signaling pathway in diabetic complications		1	1	1				
Sub-total	86	191	32	166	22	48	12	65
Total	553	616	366	388	201	170	57	173
Total number of genes in each subset	906	1581	520	883	253	228	131	479

Table S3. Kinases repartition in each subset of DEGs, using iTAK software. The Ch up and Te up correspond to “Line Response” followed by two columns of “Temperature Common Response” and the last four columns referring to the “Temperature Line Specific Response”.

Kinases	Ch up	Te up	TCR down	TCR up	TLSR a	TLSR b	TLSR c	TLSR d
ATN1 Like Family				1				
Calcium Dependent Protein Kinase	1	3		2		1		1
Casein Kinase I Family			1	5				3
CDC2 Like Kinase Family	2	3		2		1		
CRPK1 Like Kinase (Types 1 and 2)	3				1			
CTR1/EDR1 Kinase		3						1
Domain of Unknown Function 26 (DUF26) Kinase	4	2	1		1			
ELM1/PAK1/TOS3 Like Kinase		2						
GmPK6/AtMRK1 Family		4	2	1		1		1
IRE/NPH/PI dependent/S6 Kinase		1		3			1	2
LAMMER Kinase Family			1					
Legume Lectin Domain Kinase		2	1	1		1		
Leucine Rich Repeat Kinase I	1	1						1
Leucine Rich Repeat Kinase II & X		2					1	1
Leucine Rich Repeat Kinase III		2	3		2			
Leucine Rich Repeat Kinase IX	1	3						
Leucine Rich Repeat Kinase VI				1				
Leucine Rich Repeat Kinase X		1						
Leucine Rich Repeat Kinase XI & XII	1	7	2	1	1			3
Leucine Rich Repeat Receptor Kinase		1		1				
Leucine Rich Repeat Receptor VIII		1						
Leucine-rich transmembrane protein kinase			1					
LRK10 Like Kinase (Type 1)	2					1		
MAP2K	1	2	1	2				
MAPK Family	1	2	1	2				
Other Protein Kinase		1						
Plant External Response Like Kinase		4						1
Possible MAP2K		4						
Putative LRR receptor-like protein kinase		1		1				1
Putative receptor like protein kinase	2							
Receptor Like Cytoplasmic Kinase I		1						
Receptor Like Cytoplasmic Kinase II								1
Receptor Like Cytoplasmic Kinase IV		1						1
Receptor Like Cytoplasmic Kinase IX		1						
Receptor Like Cytoplasmic Kinase V		2		2				
Receptor Like Cytoplasmic Kinase VI				1				1
Receptor Like Cytoplasmic Kinase VII	2		1	3	1	1		3
Receptor Like Cytoplasmic Kinase VIII		1						
Receptor-like protein kinase	1	1		1	1	1		
RKF3 Like Kinase		1						
S Domain Kinase (Type 1)		1		1		2		
S Domain Kinase (Type 2)	4					1		
SNF1 Related Protein Kinase (SnRK)		5	1	3		1		1
STE20-PAK Like Protein Kinase				1				
Tousled like kinase								1
Unknown Function Kinase		4		1				
Wall Associated Kinase-like Kinase				2				
Total	26	70	16	38	7	11	2	23