

Supplementary Materials

Table S1. qRT-PCR Oligonucleotide sequences.

Primer	Oligonucleotide Sequence (5'-3')
Thau_F	CATCTCTTTGGTTGATGGTT
Thau-R	GAATAGTTGGTGGGAGAACA
Amp-F	CATGGAGGATACGAGTTCAT
Amp-R	CAAGCTTTATTGGGACAAC
StilB-F	ACAAAAGTATACCCACCAG
StilB-R	AGATGTTGCGTCTGAAAGTT
Myb-F	ACAACGAAATCAAGAACCAC
Myb-R	ACTGTTGAAAGCATTGGAT
Chiti_F	TTTGGTTCCTTTTCTTTG
Chiti_R	CACAGCTACAGTTTGGAGCA
Chloro_F	ATGCATCTCCTATGCCTTG
Chloro_R	CACAGCTACAGTTTGGAGCA

Table S2. Summary of the De novo assembly statistics.

Metric	Value
Total number of contigs	306,164
N° of contigs >=200 bp	306,164
N° of contigs >=500 bp	63,969
N° of contigs >=1000 bp	17,772
N° of contigs >=2000 bp	2994
N° of contigs >=4000 bp	86
N° of contigs >= 6000 bp	3
Total length of contigs	133,362,131
Largest contig	6451
GC %	43.28
N50	440

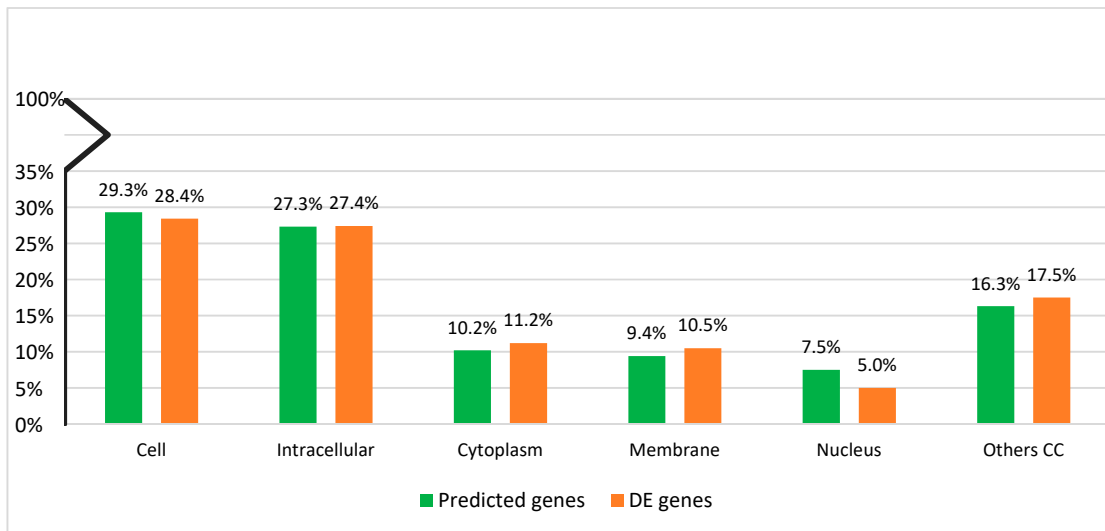


Figure S1. Gene Ontology analysis of RNA-Seq data. Distribution of the most representative biological process subcategories. The results for predicted genes are shown in green and for DEG in orange.

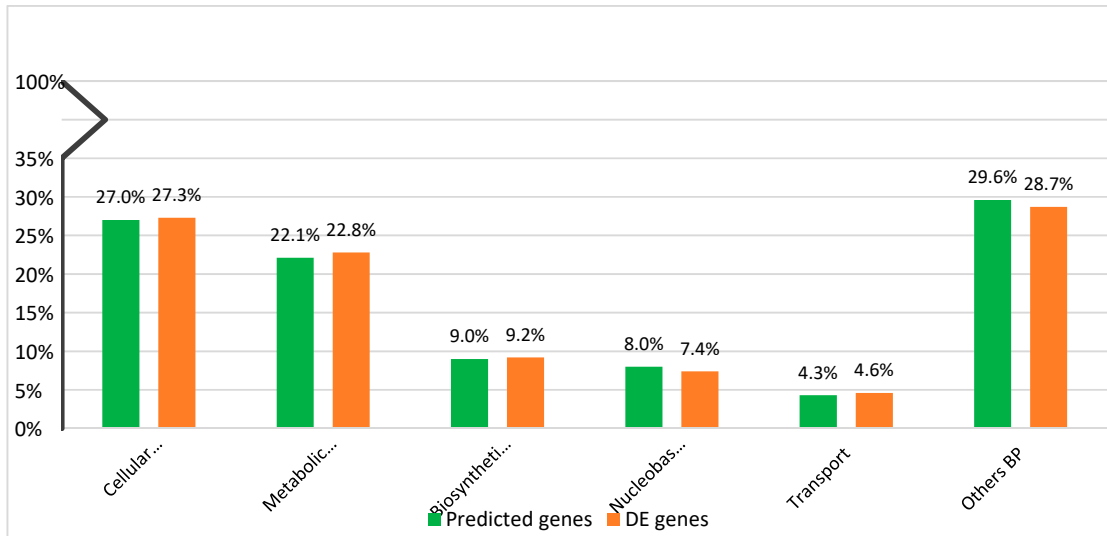


Figure S2. Gene Ontology analysis of RNA-Seq data. Distribution of the most representative cellular component subcategories. The results for predicted genes are shown in green and for DEG in orange.

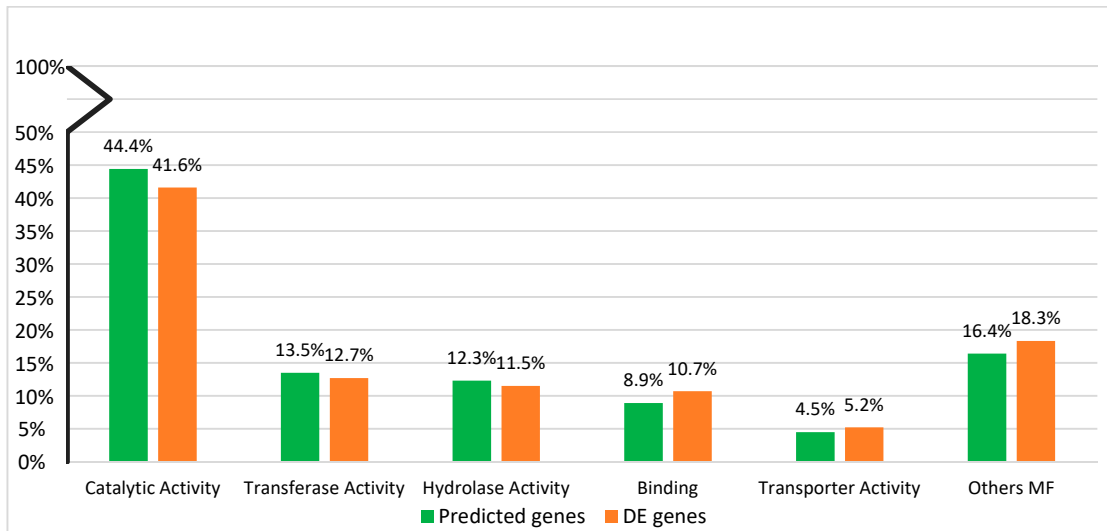


Figure S3. Gene Ontology analysis of RNA-Seq data. Distribution of the most representative biological process subcategories. The results for predicted genes are shown in green and for DEG in orange.