

Table 1 DAVID function annotation clusters of mapped sequences

<b>Annotation Cluster 1</b>		<b>Enrichment Score: 1.5568309284413362</b>	
Category	Term	Count of genes	PValue
SP_PIR_KEYWORDS	Photosystem I	4	0.007
GOTERM_CC_FAT	GO:0009522~photosystem I	4	0.010
GOTERM_CC_FAT	GO:0009521~photosystem	4	0.083
GOTERM_CC_FAT	GO:0034357~photosynthetic membrane	4	0.092
<b>Annotation Cluster 2</b>		<b>Enrichment Score: 1.3464086767695658</b>	
Category	Term	Count of genes	PValue
SP_PIR_KEYWORDS	transit peptide	6	2.22E-04
UP_SEQ_FEATURE	transit peptide: Chloroplast	6	2.22E-04
SP_PIR_KEYWORDS	photosynthesis	5	3.35E-02
GOTERM_BP_FAT	GO:0015979~photosynthesis	5	3.73E-02
SP_PIR_KEYWORDS	thylakoid	5	0.130
GOTERM_CC_FAT	GO:0009579~thylakoid	5	0.137
SP_PIR_KEYWORDS	plastid	6	0.379
SP_PIR_KEYWORDS	chloroplast	6	0.379
GOTERM_CC_FAT	GO:0009507~chloroplast	6	0.466
GOTERM_CC_FAT	GO:0009536~plastid	6	0.466
<b>Annotation Cluster 3</b>		<b>Enrichment Score: 1.3190315921745306</b>	
Category	Term	Count of genes	PValue
GOTERM_MF_FAT	GO:0046872~metal ion binding	4	0.038
GOTERM_MF_FAT	GO:0043169~cation binding	4	0.051
GOTERM_MF_FAT	GO:0043167~ion binding	4	0.056
<b>Annotation Cluster 4</b>		<b>Enrichment Score: 0.21221159852893356</b>	
Category	Term	Count of genes	PValue
SP_PIR_KEYWORDS	transmembrane	3	0.591
UP_SEQ_FEATURE	transmembrane region	3	0.591
GOTERM_CC_FAT	GO:0016021~integral to membrane	3	0.636
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	3	0.636