

Supplementary Information

1. Flavonoid Associated Gene in *P.minus*

Table S1. Of 48 unique transcripts related to secondary metabolite, 11 unique transcripts flavonoid associated gene was found in *P.minus*

Gene	EC Number	Similarity	E-value	Species	EST
Flavonoid					
naringenin-chalcone synthase	2.3.1.74	96	2e-80	<i>Fallopia multiflora</i>	321541_P61_D12_M13F-pUC-40cn260
leucoanthocyanidin dioxygenase	1.14.11.19	95	1e-04	<i>Phytolacca americana</i>	cn202
		95	7e-52	<i>Fagopyrum esculentum</i>	cn203
shikimate O-hydroxycinnamoyltransferase	2.3.1.133	79	8e-56	<i>Ricinus communis</i>	R008.D07.ab1
flavanone 3-dioxygenase	1.14.11.9	75	2e-26	<i>Camelia sinensis</i>	R005.C12.ab1
leucoanthocyanidin reductase	1.17.1.3	74	4e-74	<i>Ricinus communis</i>	R003.E05.ab1
caffeoyl-CoA O-methyltransferase	2.1.1.104	87	1e-38	<i>Arabidopsis thaliana</i>	R009.E03.ab1
flavonol synthase	1.14.11.23	75	2e-26	<i>Camelia sinensis</i>	R005.C12.ab1
				<i>Arabidopsis thaliana</i>	S013.F07
				<i>Carthamus tinctorius</i>	S018.D09
leucoanthocyanidin dioxygenase	1.14.11.19	90	3e-24	<i>Phytolacca americana</i>	S001.A10

Table S2. Primers for genes of interest and two housekeeping genes with the length of the amplified product.

Genes	Accession	EST	Primer sequences	Length	Size amplicon (bp)
Flavonoid Genes					
Flavonol synthase (FLS)	JG705819	R005.C12	<i>pm</i> FLS fwd : 5' AGGAGTCTGGTGAACAAGGAG 3'	22	128
			<i>pm</i> FLS rev : 5' TTGGTTGCGTATGCTGAAGG 3'	21	
Naringenin chalcone synthase (CHS)	JG745304	cn260	<i>pm</i> CHS fwd : 5' ACTTGCCCTCGTCGCCTTGA 3'	19	116
			<i>pm</i> CHS rev : 5' CTCCCTCTTCTGGATTGC 3'	18	
Leucoanthocyanidin dioxygenase (LDOX)	JG745247	cn203	<i>pm</i> LDOX fwd : 5' TGCTGAGGATGGTGATGGTGTC 3'	22	143
			<i>pm</i> LDOX rev : 5' ACGGACGTGAGTGCCTTGAC 3'	20	
Internal control					
β-actin	JG744126	292178_P55_F5_M13F	<i>pm</i> B-actin fwd : 5' AGCCGCCACTGAGCACAAT 3'	19	131
			<i>pm</i> B-actin rev : 5' GGTCCTCTTCCAGACTTCCATGA 3'	23	
Tubulin			<i>pm</i> TUB fwd: 5' TACCAGCCACCAACCGTAGTCC 3'	22	150
			<i>pm</i> TUB rev: 5' CCAACCTCCTCGTAGTCTTTCTCAA 3'	25	

2. Gene Ontology Anotation

Figure S1. Distribution of unigenes with GO terms associated with biological processes, molecular functions and cellular components. The grouped *P. minus* EST sequences were assigned GO terms according to Blast2Go software. (a) Biological process; (b) Cellular component; (c) Molecular function.

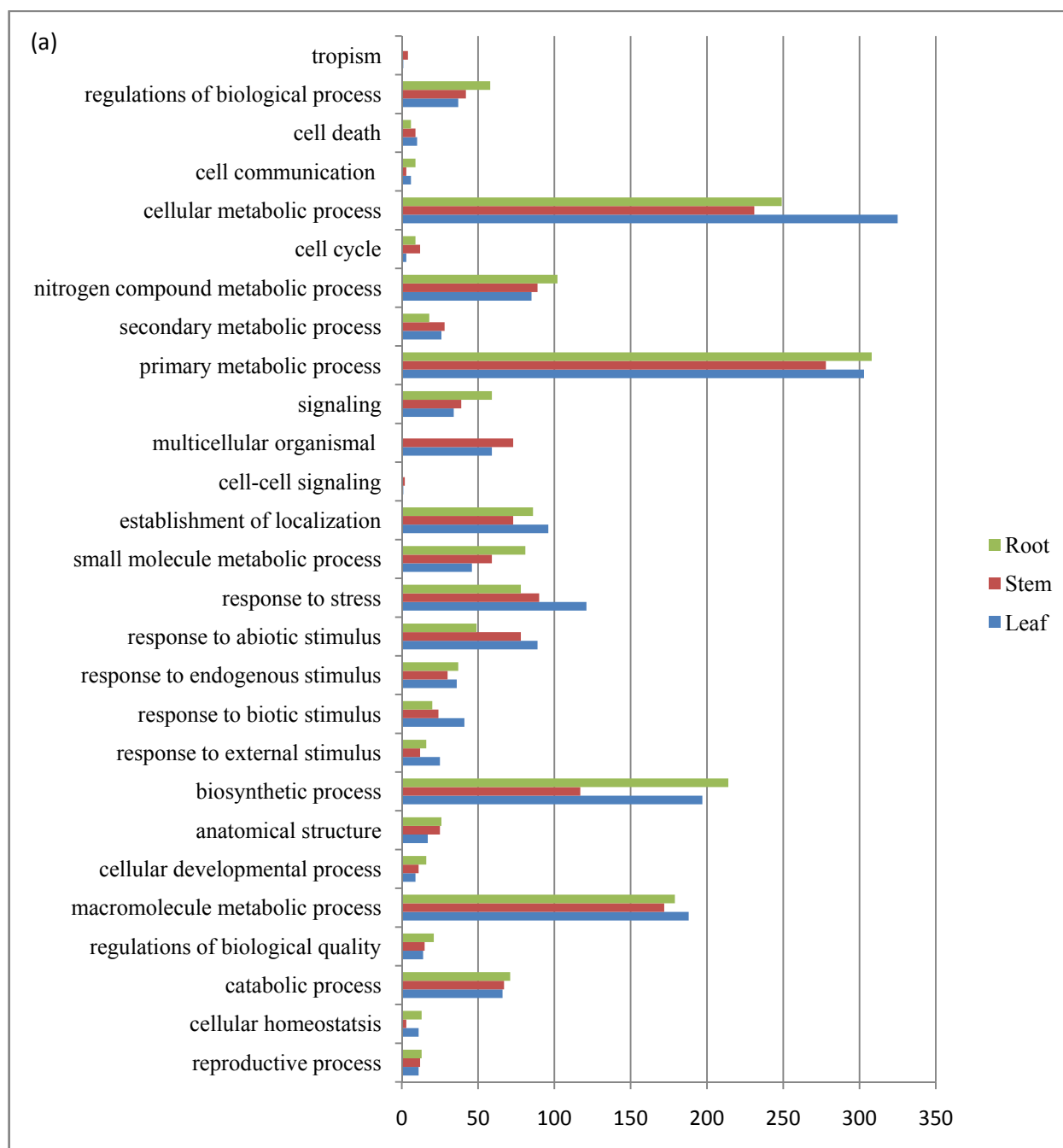


Figure S1. Cont.

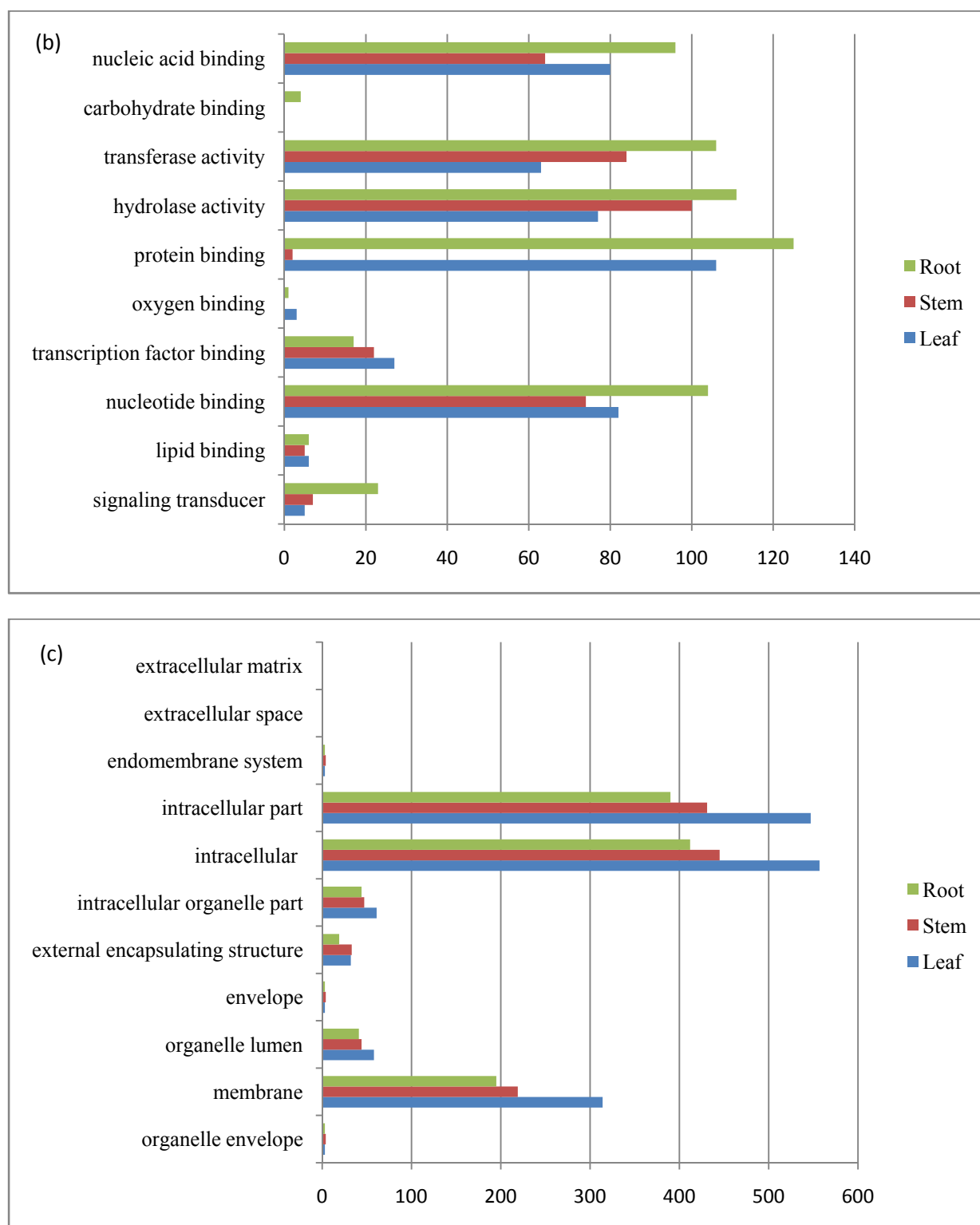
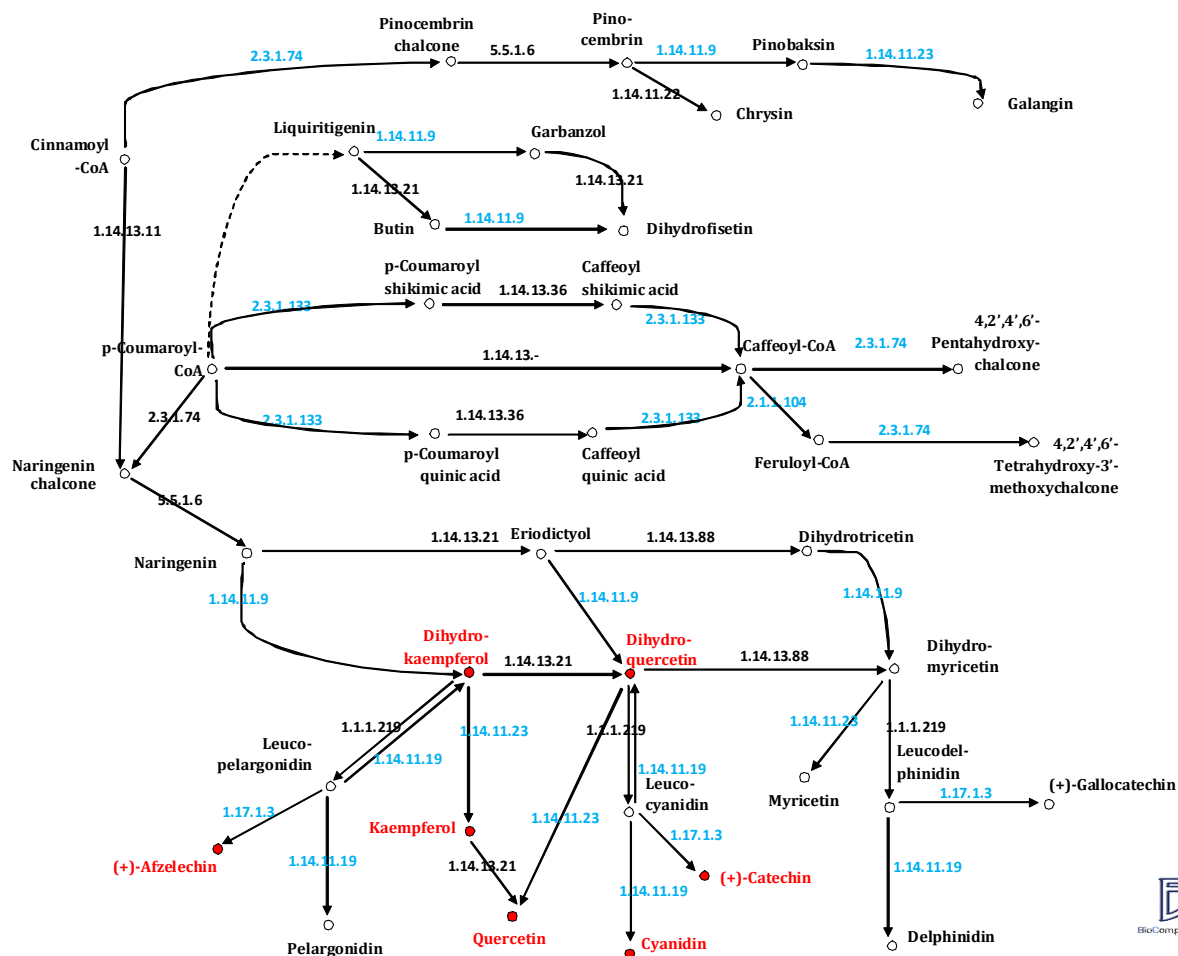


Figure S2. Flavonoid Biosynthesis Pathway in *P.minus*. This pathway was constructed with integrated of EST data (Blue) and metabolomic data (Red).



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