

Table 1: Top-ranked pathways from enrichment analysis of the filtered/raw Transcriptomics data set. The 4th, 5th, and 6th column contain the number of filtered/selected features (F) which could be assigned to an entry in the corresponding pathway, the number of matched metabolites (M) in the corresponding pathway, and the number of matched genes (G). The last columns contain the estimated false discovery rates (FDRs) based on a marker/feature-based SEA (M-SEA), entry-based SEA (E-SEA), and sample-based SEA (S-SEA). The pathways are sorted according to the S-SEA FDRs.

<b>Pathway enrichment analysis of Transcriptomics data</b>								
	DB	Pathway	F	M	G	M-SEA	E-SEA	S-SEA
1	KEGG	Glucosinolate biosynthesis	12	0	9	4.936e-05	0.0009647	0.1373
2	AraCyc	hydroxyjasmonate sulfate bio-synthesis	3	0	2	0.01173	0.1399	0.1373
3	KEGG	alpha-Linolenic acid metabolism	27	0	16	2.778e-13	1.523e-07	0.1373
4	AraCyc	traumatin and (Z)-3-hexen-1-yl acetate biosynthesis	13	0	6	3.287e-06	0.08067	0.1373
5	KEGG	Fatty acid elongation	11	0	9	0.02166	0.01983	0.1373
6	KEGG	Plant hormone signal transduction	38	0	34	0.1314	0.1399	0.1373
7	KEGG	Phenylalanine, tyrosine and tryptophan biosynthesis	22	0	17	8.786e-07	0.0003148	0.1373
8	AraCyc	very long chain fatty acid biosynthesis I	6	0	4	0.4122	0.921	0.1658
9	AraCyc	superpathway of phenylalanine, tyrosine and tryptophan biosynthesis	16	0	13	9.035e-05	0.1359	0.1658
10	AraCyc	tryptophan biosynthesis	11	0	8	3.266e-05	0.06561	0.1658