

Additional file 16.

Mapman functional group	Up-regulated				Down-regulated			
	Yukon		Col-0		Yukon		Col-0	
	Number of genes ¹	<i>p</i> -value ²	Number of genes ¹	<i>p</i> -value ²	Number of genes ¹	<i>p</i> -value ²	Number of genes ¹	<i>p</i> -value ²
Photosynthesis	12	<i>3.46E-041</i>	1	6.53E-001	502	<i>1.49E-129</i>	13	<i>1.78E-004</i>
Major CHO metabolism	24	9.90E-002	9	<i>1.55E-004</i>	23	5.10E-001	2	5.35E-001
Minor CHO metabolism	21	7.61E-001	3	3.82E-001	14	1.35E-001	1	1.00E+000
Glycolysis	51	<i>4.45E-012</i>	2	3.51E-001	19	9.46E-001	1	7.34E-001
Fermentation	11	<i>1.46E-002</i>	3	<i>9.67E-003</i>	5	1.00E+000	ND	NA
Gluconeogenese/ glyoxylate cycle	6	7.87E-002	ND	NA	2	1.00E+000	ND	NA
Oxidative pentose phosphate cycle	11	1.39E-001	ND	NA	13	7.61E-002	ND	NA
TCA / organic acids transformation	22	2.74E-001	2	3.77E-001	45	<i>7.03E-007</i>	8	<i>1.78E-004</i>
Mitochondrial electron transport	16	<i>4.08E-002</i>	1	1.00E+000	12	<i>1.82E-005</i>	1	1.00E+000
Cell wall	60	5.13E-001	6	7.53E-001	160	<i>1.38E-026</i>	3	6.49E-001
Lipid metabolism	70	8.40E-001	6	6.06E-001	133	<i>2.92E-007</i>	6	6.34E-001
Nitrogen metabolism	10	5.85E-001	2	1.57E-001	24	<i>5.30E-005</i>	2	1.79E-001
Amino acid metabolism	60	7.84E-001	4	6.76E-001	115	<i>4.34E-007</i>	3	1.00E+000
Sulfur assimilation	ND	NA	ND	NA	12	<i>1.56E-004</i>	ND	NA
Metal handling	32	<i>5.06E-004</i>	ND	NA	14	4.37E-001	ND	NA
Secondary metabolism	62	1.02E-001	10	1.26E-001	80	<i>1.82E-002</i>	4	1.00E+000
Hormone metabolism	62	1.00E+000	3	6.35E-001	152	<i>4.45E-015</i>	19	<i>1.19E-004</i>
Cofactor and vitamine metabolism	13	8.32E-001	ND	NA	9	3.04E-001	1	6.09E-001
Tetrapyrrole synthesis	2	<i>1.97E-002</i>	ND	NA	35	<i>5.31E-008</i>	2	2.61E-001
Stress	212	<i>6.16E-012</i>	10	9.64E-001	191	<i>2.08E-002</i>	5	1.79E-001
Redox regulation	43	7.23E-001	1	8.18E-001	60	1.00E+000	5	2.61E-001
Polyamine metabolism	13	<i>7.68E-007</i>	ND	NA	ND	NA	ND	NA
Nucleotide metabolism	27	6.90E-001	2	7.73E-001	20	1.73E-001	1	1.00E+000
Biodegradation of Xenobiotics	18	<i>1.58E-007</i>	ND	NA	2	4.04E-001	ND	NA
C1 metabolism	6	1.00E+000	ND	NA	8	9.70E-001	1	5.38E-001
Misc	247	<i>5.57E-005</i>	37	<i>2.26E-005</i>	392	<i>2.06E-025</i>	26	5.62E-002
RNA	350	4.81E-001	18	1.27E-001	303	<i>1.65E-008</i>	26	6.96E-001
DNA	34	<i>4.63E-005</i>	3	<i>2.88E-002</i>	42	<i>9.46E-007</i>	1	<i>1.27E-003</i>
Protein	552	7.55E-001	25	1.08E-001	375	<i>1.32E-049</i>	30	2.98E-001
Signalling	162	6.04E-001	11	9.64E-001	177	5.93E-001	16	5.05E-001
Cell	92	3.14E-001	5	6.04E-001	130	9.77E-001	4	3.86E-001
Micro RNA, natural antisense, etc	ND	NA	2	1.00E+000	ND	NA	3	6.34E-001
Development	109	<i>2.42E-002</i>	6	1.00E+000	83	7.04E-002	2	1.81E-001
Transport	164	<i>1.97E-002</i>	21	<i>2.34E-002</i>	179	3.70E-001	8	6.68E-001
Not assigned	2016	<i>5.01E-007</i>	100	3.06E-001	2379	<i>3.45E-021</i>	117	9.75E-001

¹Number of genes was found in each significant gene lists identified from the respective RNA hybridized to species-specific arrays.

²*p*-value from Fisher's exact test with false discovery rate controlled by Benjamini and Hochberg (1995) method. *P*-values highlighted in bold and italic were significant ($p < 0.05$) for the proportion of genes in a functional group that was over- or under-represented, respectively, in the respective gene list compared to all corresponding genes represented on the array.

ND, not detected; NA, not available.