Supplementary Table II. Nucleotides, phosphorylated intermediates and acetyl-CoA levels of fully expanded leaves from 8-week-old plants of the SCoAL transgenic lines. All metabolite analyses were performed from the same tissue samples. Data presented are mean \pm SE of determinations on six individual plants per genotype. Values set in bold type were determined by the *t*-test to be significantly different (*P* < 0.05) from the wild type.

Metabolite	nmol min ⁻¹ gFW ¹											
	WT			AL18			RL40			RL25		
Glc6P	76.2	±	3.6	99.6	±	4.6	67.7	±	10.4	94.9	±	5.8
Glc1P	20.6	±	2.1	16.4	±	1.7	13.4	±	2.5	22.5	±	2.6
Fru6P	17.9	±	2.0	23.6	±	2.1	17.8	±	2.9	17.2	±	2.8
3-PGA	506	±	105	534	±	50	465	±	34	591	±	29
Pi	3.1	±	0.7	4.1	±	0.5	2.5	±	0.4	4.2	±	0.6
∑ hexose -P	115.8	±	7.3	144.1	±	3.1	98.7	±	14	132.7	±	8.8
UDP-Gluc	26	±	1.6	26	±	0.5	26	±	1.0	27	±	1.1
UDP	44	±	4.5	50	±	4.5	43	±	3.3	33	±	2.3
UTP	11	±	0.6	10	±	0.6	11	±	0.5	13	±	0.3
∑ Uridinylates	83	±	6.3	75	±	11.2	80	±	4.5	72	±	2.8
UTP / UDP	0.3	±	0.03	0.2	±	0.03	0.3	±	0.02	0.4	±	0.03
ADP	6	±	0.5	4	±	0.4	6	±	0.4	5	±	0.6
ATP	18	±	1.6	17	±	0.9	16	±	0.8	19	±	0.9
∑ Adenylates	24	±	1.8	21	±	0.9	21	±	1.1	24	±	1.3
ATP / ADP	3.1	±	0.4	4.0	±	0.4	2.9	±	0.2	4.0	±	0.3
CDP	55	±	4.3	53	±	2.6	54	±	1.9	49	±	4.1
CTP	2.6	±	0.4	2.5	±	0.3	2.5	±	0.4	2.6	±	0.3
GDP	5.8	±	0.9	3.2	±	0.3	4.6	±	1.2	4.5	±	1.2
GTP	3.2	±	0.3	3.5	±	0.5	2.6	±	0.5	3.6	±	0.2
Acetyl -CoA	7.7	±	1.0	6.9	±	0.5	7.3	±	1.0	8.4	±	0.7
CoASH	2.0	±	0.3	1.8	±	0.3	1.8	±	0.6	2.0	±	0.5
Total CoA	9.7	±	1.3	8.7	±	1.1	9.1	±	0.8	10.4	±	0.4