

Table S1 Effects of R:FR on differential metabolites in tomato plant under salt stress

Number	Metabolite name	Compound classification	P-value
1	Galacturonic acid	carbohydrates	0.018
2	Alpha-d-glucose		0.007
3	Cellobiose		0.033
4	Glucosamine		0.016
5	Trehalose-6-phosphate		0.032
6	Mannitol		0.001
7	D-fucose		0.015
8	Sorbitol		0.033
9	Palatinitol		0.028
10	Methyl alpha-d-fructofuranoside		0.038
11	Isocitric acid	Organic acids	0
12	Alpha-ketoglutarate		0
13	Fumaric acid		0.012
14	3-hydroxybutyric acid		0
15	Glucaric acid gama-lactone		0.036
16	2-oxo-propanoic acid		0.003
17	Orotic acid		0.032
18	Citraconic acid		0.003
19	Itaconic acid		0.003
20	Erucic acid		0
21	4-hydroxymandelic acid	Phenolics	0.004
22	1,2,4-benzenetriol		0
23	Biphenyl		0
24	Beta-tocopherol		0.019
25	O-phosphoserine	Amino acids	0
26	Tyramine		0.001
27	Serotonin		0
28	Adenosine-5'-monophosphate	Nucleosides	0.019
29	1-methyladenosine		0.022
30	Udp-glucuronic acid		0
31	5-methyluridine		0.03
32	Cytidine-5-monophosphate		0.046

33	4-pentenoic acid		0.007
34	Maltitol	Lipids	0.032
35	Dodecanol		0
36	Uracil		0
37	Thymine		0
38	Xanthine		0.001
39	Xylonolactone	Organoheterocyclic	0
40	Alloxanoic acid		0.005
41	Maleimide		0
42	Propane-1,3-diol		0

Table S2 The number of differentially expressed metabolites (DEMs) from tomato fruits exposed to different R/FR and salt stress

Group dass	regulation	Carbohy- drates	Organic acids	Amino acids	Phenols	Nucleo- tides	Lipids	Organic- heterocyclic	Total
L/CK	Up-regulated	3	5	10	4	2	4	8	36
	Down-regulated	2	1	0	0	2	1	0	6
Na/CK	Up-regulated	3	5	1	3	1	4	8	25
	Down-regulated	0	1	2	0	1	2	1	7
Na+L	Up-regulated	4	5	0	3	1	3	3	19
/Na	Down-regulated	2	1	0	0	3	0	0	6

Table S3 Effect of R:FR on metabolic pathway in tomato fruit under salt stress

KEGG ID	Metabolic pathway name	Rich-factor	P-value
sly00020	Citrate cycle (TCA cycle)	0.150	0.000
sly00660	C5-Branched dibasic acid metaboLism	0.088	0.001
sly00650	Butanoate metabolism	0.071	0.002
sly00051	Fructose and mannose metabolism	0.056	0.004
sly00040	Pentose and glucuronate interconversions	0.054	0.005
sly00240	Pyrimidine metabolism	0.046	0.007
sly00220	Arginine biosynthesis	0.087	0.009
sly00250	Alanine, aspartate and glutamate metabolism	0.071	0.013
sly00520	Amino sugar and nucleotide sugar metabolism	0.020	0.028
sly00052	Galactose metabolism	0.043	0.032
sly00053	Ascorbate and aldarate metabolism	0.041	0.036
sly00072	Synthesis and degradation of ketone bodies	0.167	0.037
sly00630	Glyoxylate and dicarboxylate metabolism	0.032	0.056
sly00350	Tyrosine metabolism	0.026	0.084
sly00190	Oxidative phosphorylation	0.063	0.095
sly00230	Purine metabolism	0.021	0.117
sly00430	Taurine and hypotaurine metabolism	0.045	0.129
sly00232	Caffeine metabolism	0.045	0.129
sly00290	Valine, leucine and isoleucine biosynthesis	0.043	0.134
sly00770	Pantothenate and CoA biosynthesis	0.033	0.171
sly00620	Pyruvate metabolism	0.032	0.177
sly00010	Glycolysis / Gluconeogenesis	0.032	0.177
sly00410	beta-Alanine metabolism	0.031	0.182
sly00300	Lysine biosynthesis	0.029	0.197
sly00500	Starch and sucrose metabolism	0.027	0.207
sly00908	Zeatin biosynthesis	0.026	0.217
sly00340	Histidine metabolism	0.021	0.256
sly00310	Lysine degradation	0.020	0.270
sly00260	Glycine, serine and threonine metabolism	0.020	0.270
sly00970	Aminoacyl-tRNA biosynthesis	0.019	0.279
sly00760	Nicotinate and nicotinamide metabolism	0.018	0.292

sly00360	Phenylalanine metabolism	0. 017	0. 314
sly00270	Cysteine and methionine metabolism	0. 016	0. 327
sly01040	Biosynthesis of unsaturated fatty acids	0. 014	0. 352
sly00130	Ubiquinone and other terpenoid-quinone biosynthesis	0. 014	0. 361
sly00380	Tryptophan metabolism	0. 012	0. 408
sly02010	ABC transporters	0. 011	0. 444
sly00950	Isoquinoline alkaloid biosynthesis	0. 008	0. 539