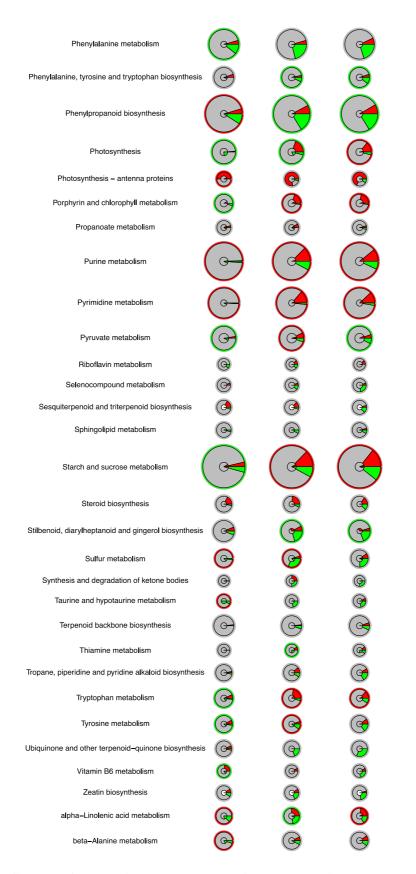
		$\frown$	
Pie size	<b>B</b>		
Number of genes / proteins 6	1 1 1 23 / 13	Ī Ī   81 / 26 123 / 36	188 / 46
	T1:T0	T8:T0	T8:T1
2-Oxocarboxylic acid metabolism	$\bigcirc$	G	$\bigcirc$
ABC transporters	$\bigcirc$	C	<b>(</b>
Alanine, aspartate and glutamate metabolisi	n 🕝	Q	Q
Amino sugar and nucleotide sugar metabolis	m 🕝		
Aminoacyl-tRNA biosynthesis	$\bigcirc$	$\bigcirc$	$\bigcirc$
Anthocyanin biosynthesis	$\odot$	©	$\odot$
Arachidonic acid metabolism	G	G	٢
Arginine and proline metabolism	<b>O</b>	$\bigcirc$	
Ascorbate and aldarate metabolism	œ	œ	G
Biosynthesis of amino acids	$\bigcirc$		
Biosynthesis of unsaturated fatty acids	Q	(C)	(C)
Biotin metabolism	G	œ	œ
Brassinosteroid biosynthesis	()	0	<b>(</b>
Butanoate metabolism	$\bigcirc$	G	¢
C5-Branched dibasic acid metabolism	O	C	$\odot$
Caffeine metabolism	0	O	0
Carbon fixation in photosynthetic organisms		œ	œ
Carbon metabolism	G		
Carotenoid biosynthesis	G	Q	œ
Citrate cycle (TCA cycle)	$\bigcirc$	$\bigcirc$	Ø
Cutin, suberine and wax biosynthesis	$\overline{\mathfrak{S}}$	<u>e</u>	©
Cyanoamino acid metabolism	œ	G	
Cysteine and methionine metabolism			
Degradation of aromatic compounds	0	Ø	œ
Diterpenoid biosynthesis	$\bigcirc$	C	G
Ether lipid metabolism	$\bigcirc$	œ	$\bigcirc$
Fatty acid biosynthesis	G	œ	G
Fatty acid degradation	œ	G	G
Fatty acid elongation	œ		œ
Fatty acid metabolism	œ		œ

	-		-
Flavone and flavonol biosynthesis	Ø	0	O
Flavonoid biosynthesis	٢	•	<b>()</b>
Folate biosynthesis	$\odot$	$(\mathbf{e})$	$(\mathbf{e})$
Fructose and mannose metabolism	$\bigcirc$		
Galactose metabolism	$\bigcirc$	œ	œ
Glucosinolate biosynthesis	G	G	C
Glutathione metabolism		G	G
Glycerolipid metabolism	œ	œ	G
Glycerophospholipid metabolism	$\bigcirc$		G
Glycine, serine and threonine metabolism	$\bigcirc$	œ	œ
Glycolysis / Gluconeogenesis	G		
Glycosaminoglycan degradation	$\bigcirc$	©	Ø
Glycosphingolipid biosynthesis – ganglio series	$\bigcirc$	G	$\bigcirc$
Glycosphingolipid biosynthesis – globo series	œ	©	Ø
Glycosylphosphatidylinositol(GPI)-anchor biosynthe	sis 🕞	O	O
Glyoxylate and dicarboxylate metabolism	œ	œ	G
Histidine metabolism	œ	O	O
Indole alkaloid biosynthesis	C	•	$\overline{\mathbf{O}}$
Inositol phosphate metabolism	$\bigcirc$	œ	G
Isoquinoline alkaloid biosynthesis	œ	œ	G
Limonene and pinene degradation	$\bigcirc$	<b>(</b>	9
Linoleic acid metabolism	Q	Q	Q
Lipoic acid metabolism	$\bigcirc$	٢	٢
Lysine biosynthesis	O	œ	œ
Lysine degradation	G	O	O
Monoterpenoid biosynthesis	G	G	G
N-Glycan biosynthesis	$\odot$		$\odot$
Nicotinate and nicotinamide metabolism	O	œ	G
Nitrogen metabolism	œ	G	@ © Ø Ø
One carbon pool by folate	O	0	
Other glycan degradation	O	Ō	© ©
Other types of O–glycan biosynthesis	O	O	O
Oxidative phosphorylation	$\bigcirc$	G	$\bigcirc$
Pantothenate and CoA biosynthesis	O	<b>O</b>	©
Pentose and glucuronate interconversions			Ø
Pentose phosphate pathway		œ	G



**Additional file 21. Correlation between RNA and protein at a pathway level.** Three pairwise comparisons based on the T0, T1, T8 time points were included. (a) The radius represents the volume (total number of genes) of the target pathway. (b)

Inner circle represents the ratio of up- and down-regulated proteins in the target pathway; gray: proteins not significantly differentially expressed; red: up-regulated proteins; green: down-regulated proteins; white: no protein detected. (c) The intermediate ring stands for ratio of up- or down-regulated genes; gray: genes not significantly differentially expressed; red: up-regulated genes; green: down-regulated genes. (d) The outer thin ring stands for the relationship between the ratios of up- and down-regulated genes and proteins in the target patwhay; red: positive correlation, green: negative correlation.