

CORRECTION

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Correction to: RNA_{seq} and quantitative proteomic analysis of *Dictyostelium* knock-out cells lacking the core autophagy proteins ATG9 and/or ATG16

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Following publication of the original article [1], it was reported that there was an error in Table 3. The corrected Table 3 is included in this Correction article and the original article has been updated.

The original article can be found online at <https://doi.org/10.1186/s12864-021-07756-2>.

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Table 3 GO term enrichment analysis of DEPs in ATG9⁻, ATG16⁻ and ATG9⁻/16⁻

Strain	Enriched categories for up-regulated proteins					
	Biological process	E	Molecular function	E	Cellular component	E
ATG9 ⁻	No GO term enrichment		No GO term enrichment		No GO term enrichment	
ATG16 ⁻	No GO term enrichment		No GO term enrichment		Phagocytic vesicle	3
ATG9 ⁻ /16 ⁻	macroautophagy	6			autophagosome	9
	lipid catabolic process	3	acyl-CoA oxidase activity	15	peroxisome	6
	fatty acid oxidation	9	carboxylic acid binding	9		
	arginine biosynthetic process	22	acetyl-CoA:L-glutamate N-acetyltransferase activity	34		
	actin cytoskeleton organization	6	actin filament binding	5	actin cytoskeleton	5
	regulation of phagocytosis	7			phagocytic cup	6
	chemotaxis	4	G protein-coupled receptor binding	14	heterotrimeric G-protein complex	12
	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	8	G-protein beta/gamma-subunit complex binding	15		
	regulation of GTPase activity	3	phosphoric ester hydrolase activity	3		
negative regulation of organelle organization	5			mitochondrial inner membrane	3	
Enriched categories for down-regulated proteins						
ATG9 ⁻	membrane lipid biosynthetic process	22	fatty acid synthase activity	>100	integral component of ER membrane	21
	fatty acid elongation	93	very-long-chain 3-ketoacyl-CoA synthase activity	>100		
ATG16 ⁻	fatty acid elongation	28			No GO term enrichment	
	phospholipid catabolic process	19	phospholipase activity	11		
	pyrimidine nucleoside monophosphate biosynthetic process	26	acid phosphatase activity	19		
	purine ribonucleoside monophosphate biosynthetic process	19				
	peptidyl-proline modification	10				
ATG9 ⁻ /16 ⁻	oxidation-reduction process	2	glutathione transferase activity	14	cell surface	7
			serine-type exopeptidase activity	13	extracellular space	5
			cis-trans isomerase activity	8	phagocytic vesicle	4
			calcium ion binding	4	vacuole	3

E enrichment (rounded integer), ER endoplasmic reticulum

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