CORRECTION

Correction: Phosphorylated Ribosomal Protein S6 Is Required for Akt-Driven Hyperplasia and Malignant Transformation, but Not for Hypertrophy, Aneuploidy and Hyperfunction of Pancreatic β-Cells

The PLOS ONE Staff

The first author's name appears incorrectly in the article citation. The correct citation is: Wittenberg Dreazen A, Azar S, Klochendler A, Stolovich-Rain M, Avraham S, Birnbaum L, et al. (2016) Phosphorylated Ribosomal Protein S6 Is Required for Akt-Driven Hyperplasia and Malignant Transformation, but Not for Hypertrophy, Aneuploidy and Hyperfunction of Pancreatic β -Cells. PLoS ONE 11(2): e0149995. doi:<u>10.1371/journal.pone.0149995</u>.

<u>Table 1</u> appears incorrectly in the published article. The last six rows are duplicates of the six above them. Please see the correct <u>Table 1</u> and its caption below. The publisher apologizes for the error.



 $\label{eq:characteristic} \begin{array}{l} \mbox{Citation: The $PLOS$ ONE Staff (2016) Correction:} \\ \mbox{Phosphorylated Ribosomal Protein S6 Is Required for} \\ \mbox{Akt-Driven Hyperplasia and Malignant} \\ \mbox{Transformation, but Not for Hypertrophy, Aneuploidy} \\ \mbox{and Hyperfunction of Pancreatic β-Cells. PLoS ONE} \\ \mbox{11(5): e0155281. doi:10.1371/journal.pone.0155281} \end{array}$

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Table 1. List of proteins that selectively interact with unphosphorylatable form of rpS6. Whole cell extract from HEK293 cells infected with pS6^[5S]-GFP, pS6^[5A]-GFP, pS6^[5A]-GFP or pEGFP-N1, was subjected to GFP pull-down, and the bound proteins were size fractionated by SDS-polyacrlamide gel electrophoresis. Mass spectrometric analysis of proteins in each lane was performed as described in "material and Methods" and proteins, selectively bound to pS6^[5A]-GFP in two independent experiments, are presented (numbers separated by slash [/] represent results obtained in each of the two individual analyses).

Gene name	Protein	Function	Location	Area ^a	Coverage ^b	No. of unique peptides ^c
PSIP1	PC4 and SFRS1-interacting protein 1 (LEDGF)	Repair of DNA double- strand breaks	Nucleus	1.141E6/ 1.705E7	5.28/17.55	3/8
TOP2B	Topoisomerase (DNA) II beta	DNA replication, transcription and repair	Nucleus	7.922E6/ 2.783E7	19.62/8.98	18/7
SRSF4	Serine/arginine-rich splicing factor 4	Splicing	Nucleus	2.327E6/ 3.816E7	7.89/11.54	3/2
ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	Transporter (?)	Peroxysomal and mitochondrial membranes	1.584E6/ 9.683E6	6.83/3.95	3/2
NDUA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 9	Accessory subunit of Complex I	Mitochondria	5.180E5/ 8.213E6	8.49/9.28	3/3
SYQ	Glutaminyl-tRNA synthetase	Translation	Cytoplasm	1.596E6/ 5.299E6	6.32/5.42	4/3

^a Area—displays the average area of the three unique peptides with the largest peak area, based on extracted ion currents (XICs).

^b Coverage—displays the percentage of the protein sequence covered by identified peptides.

^c No. of unique peptides—Displays the number of peptide sequences unique to a protein group.

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Reference

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