



Corrigendum: Transcriptomic Profiling of Zebrafish Hair Cells Using RiboTag

Maggie S. Matern¹, Alisha Beirl², Yoko Ogawa¹, Yang Song³, Nikhil Paladugu¹, Katie S. Kindt² and Ronna Hertzano^{1,3,4*}

¹ Department of Otorhinolaryngology Head and Neck Surgery, University of Maryland School of Medicine, Baltimore, MD, United States, ² Section on Sensory Cell Development and Function, National Institute on Deafness and Other Communication Disorders, Bethesda, MD, United States, ³ Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD, United States, ⁴ Department of Anatomy and Neurobiology, University of Maryland School of Medicine, Baltimore, MD, United States

Keywords: inner ear, hair cells, zebrafish, RiboTag, RNA-Seq

A Corrigendum on

Transcriptomic Profiling of Zebrafish Hair Cells Using RiboTag

by Matern, M. S., Beirl, A., Ogawa, Y., Song, Y., Paladugu, N., Kindt, K. S., et al. (2018). *Front. Cell Dev. Biol.* 6:47. doi: 10.3389/fcell.2018.00047

Although the reported fold change values and statistics were accurate, there was a mistake in the CPM values shown in **Supplementary Dataset 1** in the original article. This mistake has been corrected and it has resulted in a slight change in the number of transcripts meeting the CPM cutoff for expression ($n = 17,164$), enrichment ($n = 2,379$), and depletion ($n = 2,258$). These corrected numbers of expressed, enriched and depleted transcripts are now reflected in the text, as well as in **Figure 3a**. The gene ontology and ZEOGS analyses have been redone and changes have been made to **Tables 1–3**, and **Supplementary Table 2**. The genes chosen for validation now fall within the top 100 enriched transcripts rather than the top 50; therefore, **Supplementary Table 3** has been changed to show the top 100 enriched transcripts. The scientific conclusions made from these analyses have not changed in any way.

A fourth input sample, which was included in the original analysis, was missing from **Supplementary Dataset 1** and **Supplementary Table 1** in the original article. This sample has now been added to both the files. Sentence one in the subsection “RNA sequencing and informatics” under “Materials and Methods”, now reads “RNA from 5 dpf *Tg(myo6b:RiboTag)* zebrafish IN and IP samples was submitted in biological quadruplicates for RNA-Seq at the UMSOM Institute for Genome Sciences.” The following sentence has also been added: “One IP sample had a high intergenic content suggestive of DNA contamination and was excluded from the analysis.” Finally, sentence two in paragraph one of the subsection “RNA sequencing of IP and IN samples from *Tg(myo6b:RiboTag)* zebrafish” under “Results”, now reads “We therefore performed RNA-Seq on IP and IN samples in at least three biological replicates from 5 dpf *Tg(myo6b:RiboTag)* zebrafish”.

The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way.

The original article has been updated.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fcell.2018.00084/full#supplementary-material>

OPEN ACCESS

Edited and reviewed by:

Kelvin Y. Kwan,
Rutgers University, The State
University of New Jersey,
United States

*Correspondence:

Ronna Hertzano
rhertzano@som.umaryland.edu

Specialty section:

This article was submitted to
Epigenomics and Epigenetics,
a section of the journal
*Frontiers in Cell and Developmental
Biology*

Received: 06 June 2018

Accepted: 17 July 2018

Published: 27 August 2018

Citation:

Matern MS, Beirl A, Ogawa Y, Song Y,
Paladugu N, Kindt KS and Hertzano R
(2018) Corrigendum: Transcriptomic
Profiling of Zebrafish Hair Cells Using
RiboTag. *Front. Cell Dev. Biol.* 6:84.
doi: 10.3389/fcell.2018.00084

TABLE 1 | Gene ontology analysis of hair cell enriched genes.

GO biological process complete	# in Reference	# in input	# expected	Fold enrichment	FDR	Genes
miRNA mediated inhibition of translation	9	5	0.21	24.32	0.00252	<i>trim71 tnrc6b tnrc6a tnrc6c1 ago2</i>
Skeletal muscle contraction	23	5	0.53	9.52	0.0373	<i>CU929259 tnni1c tnn1b CU929259 tnni1d</i>
detection of mechanical stimulus	25	5	0.57	8.76	0.0496	<i>tmc2a loxhd1a loxhd1b denn2a lhfp15a</i>
sensory perception of mechanical stimulus	48	7	1.1	6.37	0.0283	<i>tmc2a pcdh15b atp2b1a lhfp15a mecp2 BX572619 dcdc2b</i>
neuromast development	62	8	1.42	5.64	0.0237	<i>atoh1a pcsk5a slc12a5b atp2b1a pho BX572619 erbb2 dcdc2b</i>
Steroid hormone mediated signaling pathway	77	9	1.76	5.11	0.0198	<i>vdra abhd2a pparα thrab rorb rorc nr6a1b thrb nr0b2a</i>
mRNA metabolic process	299	19	6.84	2.78	0.0182	<i>celf4 ptbp3 qkib rbbp6 rbmx2 crnk1 snmp70 tnrc6a nova2 rbm25a exosc7 qkia kiaa0907 exosc3 coil snrpa aqr dicer1 ago2</i>
Transcription, DNA-templated	841	43	19.24	2.23	0.00093	<i>hdac4 hoxb1a pou6f2 vdra nfia rest stat2 hoxb3a foxh1 brf2 pparα hoxc6b bhlhe41 hoxa1a thrab rorb ncoa1 gtf2a11 nfat5a eed rorc bhlhe41 nrarα mef2a nr6a1b clocka med19a pou2f1b tcf3a jarid2b thrb onecut2 BX005395 twistn onecut1 mecp2 ccnd1 hoxa1a znf367 nr0b2a pou2f2a asx2 nfic</i>
Regulation of transcription, DNA-templated	1703	71	38.97	1.82	0.00092	<i>hdac4 hoxb1a nkap pou6f2 pde8b vdra nfia rest mkl2a stat2 hoxb3a foxh1 brf2 pparα hoxc6b has2 tcf3a bhlhe41 hoxa1a thrab gfi1aa trps1 rorb atoh1a foxj3 ncoa1 crebrf zfx4 fosl1a nfat5a eed rfx7 rorc tomm20a ches1 mef2b nrarα CU633479 mef2a nr6a1b clocka hmbx1b med19a pou2f1b tcf3a jarid2b thrb BX511021 cica onecut2 pbxip1b zfx3 BX005395 onecut1 mecp2 rbpja foxb1b ccnd1 hnf1a hoxa1a tcl1xr1b mycbp znf367 nr0b2a pou2f2a crtc1a ago2 asx2 nfic dot11 rbpjb</i>

TABLE 2 | Gene ontology analysis of hair cell depleted genes.

GO biological process complete	# in Reference	# in Input	# expected	Fold enrichment	FDR	Genes
Antibiotic catabolic process	4	3	0.07	41.55	0.024	<i>esd cat amdhd2</i>
ATP synthesis coupled electron transport	43	7	0.78	9.02	0.00537	<i>AC024175.9 (associated with mt-nd4l mt-cyb mt-nd2 mt-co1 mt-nd4 mt-nd5)</i>
Detection of light stimulus	38	6	0.69	8.75	0.0176	<i>opn1mw1 gnat2 rho lamc1 opn1sw1 (also associated with opn1sw2)</i>
Pyruvate metabolic process	43	6	0.78	7.73	0.0275	<i>hkdc1 aldoca eno2 pdha1b aldooa pkmb</i>
ATP biosynthetic process	64	8	1.16	6.93	0.00767	<i>hkdc1 aldoca eno2 AC024175.9 (associated with mt-atp6) aldooa BX901937 pkmb</i>
Visual perception	97	12	1.75	6.85	0.00022	<i>opn1mw1 kera gnat2 rho lamc1 cryaa crx aoc2 irbp vsx2 opn1sw1 (also associated with opn1sw2)</i>
Proton transmembrane transport	57	7	1.03	6.8	0.0194	<i>atpv0e2 AC024175.9 (associated with mt-co1 mt-atp6) BX901937 atp6v0b atp6v1b2</i>
Regulation of cell growth	97	9	1.75	5.14	0.0179	<i>igfbp7 osgn1 ncaldb chma1 casp9 epb41i3b lamtor2 dpysl2b arl3l1</i>
Coenzyme biosynthetic process	116	9	2.1	4.3	0.0436	<i>aldoca eno2 sprα mat2al pdha1b aldooa ndufa9b pkmb</i>
Nucleobase-containing compound catabolic process	153	11	2.77	3.98	0.0239	<i>hkdc1 aldoca eno2 upf3a smg5 pcid2 polr2gl aldooa dis3 dnase1i3l pkmb</i>
Cellular protein localization	497	23	8.99	2.56	0.0115	<i>vps11 copb1 ap2m1b ap4e1 smg5 tomm40l vps29 pcid2 glrb chma1 atg9a copa wipi2 epb41i3b BX901937 grpel2 nmd3 hsc70 sx1b nappb pttg1ipb sec24d lamtor2</i>
Protein transport	530	24	9.59	2.51	0.0113	<i>arcn1b vps11 rab4a copb1 ap2m1b ap4e1 smg5 tomm40l vps29 pcid2 rab10 tsg101a atg9a copa tvp23b BX901937 (associated with Zgc:165520 vps37c) grpel2 nmd3 snx1b nappb jagr1a pttg1ipb sec24d</i>

(Continued)

TABLE 2 | Continued

GO biological process complete	# in Reference	# in Input	# expected	Fold enrichment	FDR	Genes
System development	2,933	79	52.94	1.49	0.0437	<i>tfap2b cdh7 tyrp1b inpp5b wif1 vps11 rab4a ecrg4b igfbp7 copb1 slc2a2 slc35b2 col17a1b ponzr1 epb41b ncaldb fosab rab10 slc4a1a PPP1CC pou4f2 slc33a1 dacha ruvbl2 chrna1 snapc2 gdpd3a celsr2 copa rapsn ephb4a smyd1b casp9 lingo2a inpp5kb mcm3 olfm2a aldoaa grhl2a rtn4r BX470189 fez1 lamc1 dhps cryaa itm2bb id4 klhl40a camk1db crx lrfn4b rel lhx1a jagn1a inab scinla lamb2 padi2 anos1a slitrk6 zic6 CRIP2 plppr1 pttg1ipb sec24d polr3b ugdh SLITRK1 atp6v0b dpysl2b mab21l2 pou3f1 arl3l1 hpse lrrn1 PDCL3 dnase1l3l spry4 six3a</i>

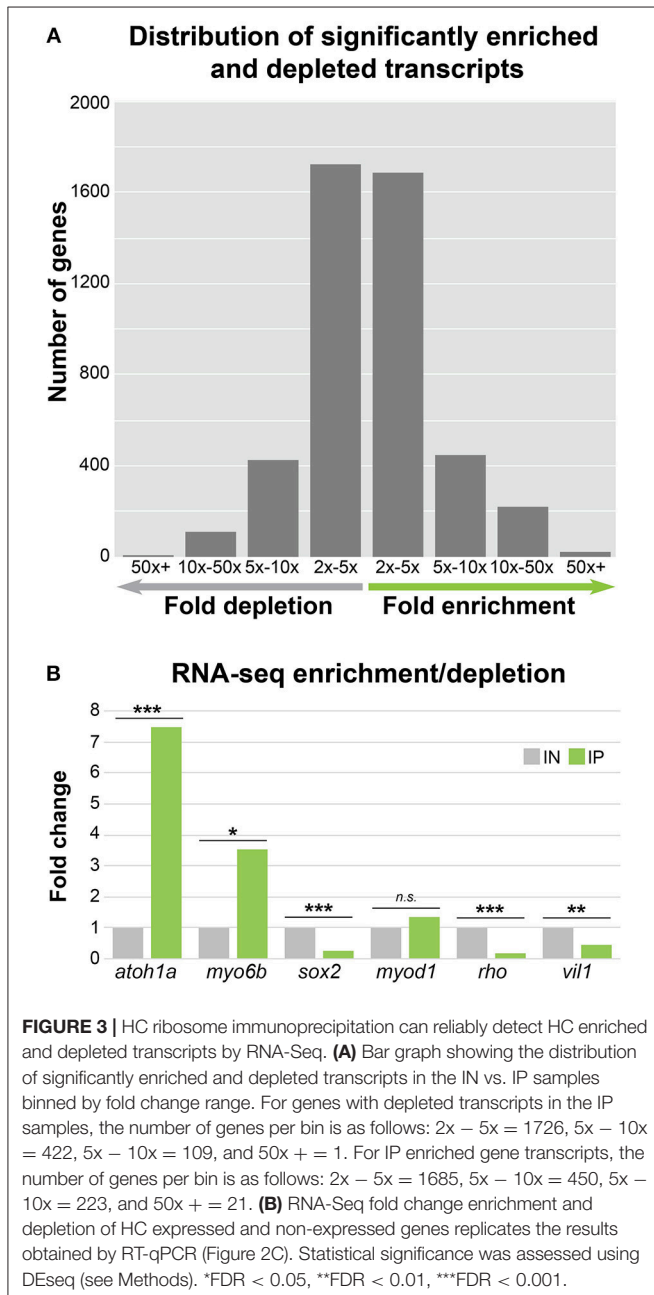


TABLE 3 | ZEOGS analysis of HC enriched transcripts.

Anatomical term	Corrected p-value	Genes
Neuromast	0.00052	<i>cabp2b morn3 pcsk5a rorb s100t atp2b1a gfii1a ofota wasa pho bdnf pvalb8 tmc2a tmc2b s100s myclb atoh1a</i>
Levator operculi	0.06849	<i>tnnc1b smyhc2</i>
Hair cell anterior macula	0.07032	<i>atp2b1a tmc2a ofota</i>
Hyohyoideus	0.07515	<i>myha tnnc1b smyhc2</i>
Olfactory epithelium	0.0832	<i>tnks1bp1 cnga3a s100t dlg2 bdnf s100s s100a1 elavl3</i>
Olfactory bulb	0.0915	<i>klf7a mef2aa fabp10b plxn2b s100t dlg2 bdnf pvalb8 s100s cadm1b igdccc3</i>
Hair cell posterior macula	0.09839	<i>atp2b1a tmc2a</i>

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Copyright © 2018 Matern, Beirl, Ogawa, Song, Paladugu, Kindt and Hertzano. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.