Corrigendum

Hypoxia regulates glutamate receptor trafficking through an HIF-independent mechanism

Eun Chan Park, Piya Ghose, Zhiyong Shao, Qi Ye, Lijun Kang, XZ Shawn Xu, Jo Anne Powell-Coffman and Christopher Rongo

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Correspondence to: rongo@waksman.rutgers.edu

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Since the online publication of this paper, the authors have noticed that the photomicrographs in three figure panels (Figure 1B, Figure 1C, and Figure 4D) were accidentally interchanged. The animals display the same phenotype in all three of these panels. Thus, the conclusions drawn from these figures and from the paper remain unchanged.

The panels in Figure 1B, Figure 1C, and Figure 4D have now been replaced with the correct photomicrographs.

The authors apologize for any inconvenience caused.

Figure 1 Oxygen levels and EGL-9 regulate GLR-1 trafficking. GLR-1::GFP fluorescence in (A) wild-type animals under normoxia, (B) *egl-9(sa307)* mutants under normoxia, (C) wild-type animals under hypoxia, and (D) *egl-9(sa307)* mutants under hypoxia. GLR-1 is localized to elongated accumulations (arrows), quantified per length of ventral cord dendrites in (E, F). Red bars indicate normoxia, whereas blue bars indicate hypoxia. ANOVA followed by Dunnett's multiple comparison with wild type, normoxia (* $P < 0.01$). $N = 15$ –35 animals per condition and/or genotype. Error bars indicate s.e.m. Bar, 5 μm.

Figure 4 EGL-9 interacts with LIN-10 to regulate GLR-1 trafficking. (A) Schematic of LIN-10 protein. Coloured boxes indicate the CID, PTB, PDZ1, and PDZ2 domains. Vertical lines indicate putative CDK-5 phosphorylation sites in the amino-terminus, with the number corresponding to the proline residue in the CDK-5 consensus sequence. Horizontal lines indicate the fragments of LIN-10 protein tested for interaction with the EGL-9 catalytic domain via yeast two-hybrid. ‘+++’ Indicates a strong interaction (positive for all four reporters), whereas ‘+’ indicates a weak interaction (positive for 1–3 reporters). GLR-1::GFP fluorescence in (B) wild type, normoxia; (C) *lin-10(e1439)*, normoxia; (D) wild type, hypoxia; and (E) *lin-10(e1439)*, hypoxia. Arrows indicate accumulations of GLR-1::GFP in elongated, internal compartments. (F) Quantification of the number of GLR-1::GFP-containing elongated compartments in the indicated genotypes. * $P < 0.01$ compared with wild type, normoxia, and # $P < 0.01$ compared with wild type, hypoxia, by ANOVA followed by Dunnett’s multiple comparison. (G, H) GFP::EGL-9E fluorescence and (I, J) LIN-10::mCherry fluorescence in (G, I, K) a neuron cell body (PVC) and (H, J, L) the ventral cord. (K, L) Merged images. (M) The mean spontaneous reversal frequency and (N) the mean nose touch mechanosensory response are plotted for the indicated genotypes. Red bars indicate normoxia, whereas blue bars indicate hypoxia. ANOVA followed by Dunnett’s multiple comparison with wild type, normoxia (* $P < 0.01$) or wild type, hypoxia (# $P < 0.01$). $N = 20$ –30 animals per condition and/or genotype. Error bars indicate s.e.m. Bar, 5 μ m.