Author Correction: Lipid peroxidation regulates long-range wound detection through 5-lipoxygenase in zebrafish

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Correction to: Nature Cell Biology https://doi.org/10.1038/s41556-020-0564-2, published online 31 August 2020.

In the version of this Letter originally published, the morpholino sequences in the Methods section ‘morpholino injections’ were incorrect. "One-cell-stage embryos were injected with 2.3 nl of 250–500 µM duox morpholino 1 (MO1: 5′-AAGCGTCACTAATATAATGTTGGA-3′; Gene Tools) or misprime morpholino (MP: 5′-TCCCTTTAGATTACCTTACGGCA-3′; Gene Tools)2, together with 200 µM p53 morpholino (5′-ATGCTCAACTATAATGGACATT-3′; Gene Tools)38 diluted in water” should instead read "One-cell-stage embryos were injected with 2.3 nl of 250–500 µM duox morpholino 1 (MO1: 5′-AGTGAATTAGAGAAATGCACCTTT-3′; Gene Tools) or misprime morpholino (MP: 5′-AGTCATTACAGAAATCAGCTT-3′; Gene Tools)38 diluted in water.” The error has been corrected.

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Author Correction: Non-canonical Wnt/PCP signalling regulates intestinal stem cell lineage priming towards enteroendocrine and Paneth cell fates

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Correction to: Nature Cell Biology https://doi.org/10.1038/s41556-020-00617-2, published online 4 January 2021

In the version of this Letter originally published, one of the analysed single-cell RNA sequencing samples contained cell duplicates from another sample (Control_7_FVR (with 90% FVR enrichment) contained the cells from sample Control_5_FVR (with 50% FVR enrichment)) due to an error that occurred during processing of single-cell RNA-seq libraries in the cell ranger pipeline. None of the conclusions change, but this affects the plots and maps shown in Figs 3b–e and 5a–d, Extended Data Figs. 4c–g, 5 and 8b–f, and source data for Fig. 3c. Th
...
a
Wild-type mice
Reporter mice

SI crypt isolation

Rare lineage enrichment
by flow cytometry

scRNAseq
(10X Genomics)

After QC
60,000 cells

Computational analysis

Transcriptome-based
lineage tree

b
No enrichment
(wild-type mice)

50% FVR enrichment
(FltpZV+/+)

90% FVR enrichment
(FltpZV+/+)

50% FVF enrichment
(Foxa2FVF/FVF)

c
Cell type frequency (%)

High

Low

None

d

ISC
EC pro
EC
GC pro
GC
Early GC
GC
PC pro
PC
EEC pro
EEC
TC pro
TC

e
Number of cells (×10³)

ISC
EC pro
EC
GC pro
GC
PC pro
PC
EEC pro
EEC
TC pro
TC

scRNAseq
(10X Genomics)

SI crypt isolation

After QC
60,000 cells

Rare lineage enrichment
by flow cytometry

Computational analysis

Transcriptome-based
lineage tree

Wild-type mice
Reporter mice
**Fig. 3** | Original and corrected.
Fig. 5 | Original and corrected.
Extended Data Fig. 4 | Original and corrected.
Extended Data Fig. 5 | Original and corrected.
Extended Data Fig. 8 | Original and corrected.

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