***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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Generally accepted sample sizes were used. Sample size was determined according to standard practices and to our previous experience. Sample size and associated statistics are indicated in each figure legend.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Experimental findings were reliably reproduced. The number of experiments and the number of independent biological and/or technical replicates are indicated in each figure legend. No data were excluded from the analyses. RNA sequencing data have been deposited in the National Center for Biotechnology Information Gene Expression Omnibus (GEO) and a private link was shared with reviewers.

**Statistical reporting**

* Statistical analysis methods should be described and justified
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
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Statistical analyses for all relevant numeric data sets are summarized in the figure legends. We described the statistical tests used, N values, definitions of centers, methods of multiple test correction, etc. for each experiment in figure legends. We reported p-values for each experiment in figure legends.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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Please indicate the figures or tables for which source data files have been provided:

**Figure 3**: Source data is provided, including:

- Figure 3—source data 1. Differentially Expressed Genes in Duodenum Intestine-Chip vs. Duodenal Organoids.

- Figure 3—source data 2. Differentially Expressed Genes in Adult Duodenum vs. Duodenal Organoids.

- Figure 3—source data 3. Differentially Expressed Genes Common in Duodenum Intestine-Chip and Adult Duodenum versus Duodenal Organoids.

- Figure 3—source data 4. Enriched GO Terms from a List of Differentially Expressed Genes Common in Duodenum Intestine-Chip and Adult Intestine versus Duodenal Organoids.

Additional file related to this figure:

- Supplementary Table 1. RNAseq Datasets Downloaded from Public Databases.

**Supplementary Figure 2**: Source data is provided, including:

- Supplementary Figure 2—source data 1. Differentially Expressed Genes in Duodenal Organoids vs. Adult Duodenum.

- Supplementary Figure 2—source data 2. Differentially Expressed Genes in Duodenum Intestine-Chip vs. Adult Duodenum.