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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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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
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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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
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* 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)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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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.)

**Group allocation**

* 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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Samples were randomly allocated to the treatment or control groups. No masking was used during group allocation, data collection and/or data analysis.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
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* Avoid stating that data files are “available upon request”

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.