**Main folder name:** **2019\_Johansson\_Naszai\_CELL-STEM-CELL.** "RAL GTPases Drive Intestinal Stem Cell Function and Regeneration through Internalization of WNT Signalosomes"

Note: This file and associate data files correspond to the Drosophila data in the above paper.

**Folder organization :**

* All figures in a pdf format named **FigureX** or **FigureSX** (for supplementary figures)
* 1 folder per figure named **FigureX** or **FigureSX** (for supplementary figures)
* 1 subfolder per panel named **FigureXPanelY** or **FigureSXPanelY**
* 1 README file describing organisation and content of data

**Details of content (Folders are in bold):**

**Figure 1**:

* **Figure1PanelA**: 3 folders **RalA and Delta, RalA and ArmPros, RalA and SuH-LacZ** corresponding to figure panels
* **Figure1PanelB**: **RawData** folder: 3 files .xls = raw data QPCR for rpl32, RalA upon targeted RalA knock-down in different cell-types **ProcessedData** folder: 3 files .pzfx, 3 image files .emf = graph used in publication
* **Figure1PanelB’**: **RawData** folder: 2 files .xls = QPCR data for rpl32, delta, and Rala in sorted ISCs, EBs and whole midguts. 1 file .pzfx = data used for publication.
* **Figure1PanelC**: 6 folders named the condition they represent: 5 files in each, 1 .czi = maximum intensity projection of confocal image, 4 .tif = exported images of all channels together and the three individual channels
* **Figure1PanelD**: 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **Figure1PanelE**: 2 folders named the condition they represent. 5 files in each, 1 .czi = maximum intensity projection of confocal image, 4 .tif = exported images of all channels together and the three individual channels
* **Figure1PanelF:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **Figure1PanelG:** 4 folders named the condition they represent: 4 files in each .tif = exported images of all channels together and the three individual channels
* **Figure1PanelH: RawData** folder: 4 folders containing .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript.
* **Figure1PanelI: RawData** folder: 3 folders containing .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript, 1 file .emf = graph used in publication
* **Figure1PanelJ:** 2 folders named the condition they represent: 4 files in each .tif = exported images of all channels together and the three individual channels
* **Figure1PanelK:** **RawData** folder: 2 folders containing .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript
* **Figure1PanelL: RawData** folder: 2 folders containing .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript
* **Figure1PanelM:** 1 file .czi = z-stack confocal image of wing disc
* **Figure1PanelN:** 1 file .pzfx = quantification of staining intensity

**FigureS1**:

* **FigureS1PanelA:** 1 file .czi = tile scan image, 1 file .tif = exported image
* **FigureS1PanelB:** 4 folders named the conditions they represent containing the .tif images for the figure
* **FigureS1PanelC:** 1 file .pzfx = quantification of clone size
* **FigureS1PanelD:** 4 folders named the conditions they represent containing the .tif images for the figure
* **FigureS1PanelE:** 1 file .pzfx = quantification of clone size
* **FigureS1PanelF:** 2 folders named the conditions they represent containing the .tif images for the figure
* **FigureS1PanelG:** 1 file .pzfx = quantification of cell type distribution

**Figure 2**:

* **Figure2PanelA:** 8 folders named the conditions they represent containing images of the figure panel
* **Figure2PanelB:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **Figure2PanelC:** 4 folders named the conditions they represent containing images of the figure panel
* **Figure2PanelD: RawData** folder: containing .czi and .lsm z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript
* **Figure2PanelE:** 4 files .tif = exported images of all channels together and the three individual channels
* **Figure2PanelF:** 1 file .pzfx = quantification of staining intensity
* **Figure2PanelG:** 4 folders named the conditions they represent containing images of the figure panel
* **Figure2PanelH:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **Figure2PanelI:** 4 folders named the conditions they represent containing images of the figure panel
* **Figure2PanelJ:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **Figure2PanelK:** 4 folders named the conditions they represent containing images of the figure panel
* **Figure2PanelL: RawData** folder: .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript

**FigureS2**:

* **FigureS2PanelA:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **FigureS2PanelB:** 4 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelC:** 2 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelD:** 2 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelE:** 1 file .pzfx = quantification of clone size
* **FigureS2PanelF:** 2 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelG:** 1 file .pzfx = quantification of staining intensity
* **FigureS2PanelH:** 1 file .pzfx = quantification of staining intensity
* **FigureS2PanelI:** 2 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelJ:** 1 file .pzfx = quantification of staining intensity
* **FigureS2PanelK:** 1 file .pzfx = quantification of staining intensity
* **FigureS2PanelL:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **FigureS2PanelM:** 1 file .pzfx = pH3 counts in posterior midguts with genotypes and treatments indicated
* **FigureS2PanelN:** 4 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelO: RawData** folder: containing .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript
* **FigureS2PanelP:** 4 folders named the conditions they represent containing images of the figure panel
* **FigureS2PanelQ: RawData** folder: containing .czi z-stack confocal images quantified. 1 file .pzfx = result of quantification using the custom script indicated in the manuscript