**Main folder name:** **Scopelliti, Bauer et al- cell met 2018.**

**Folder organization :**

* 1 “Scopelliti, Bauer-Cordero-Cell Metabolism,2018.pdf”- accepted version of the paper.
* 1 folder “**Main**” including the data relative to the main figures.
* 1 folder “**Supplementary**” including the data relative to the supplementary figures.

The two folders contain a subfolder for each figure, with a separate sub folder for each panel containing the raw and processed data.

**Details of contents:**

**“Main” Folder:**

**Fig1**:

**1A-qpcr burs whole-gut-gutless**:

1 .xlsx file containing the processed data.

1.pzfx file containing the plotted data.

1 folder “**whole flies qpcr burs**” containing: 2 .eds files with the raw data, 2 .xls files with the extracted values, 1 .xlsx file containing the processed data and 1 .pzfx data containing the plotted data.

1 folder “**gutless**” containing: 2 .eds files with the raw data,1 .xls file containing the processed data, 1 .pzfx file containing the plotted data.

**1B anti burs fed starv guts:**

1 folder “**fed**” containing: 2 .lsm files of the raw confocal images and 3 .tiff files extracted from the raw .lsm files and following processing.

1 folder “**starved**” containing: 2 .lsm files of the raw confocal image and its maximal intensity projection and 3 .tiff files extracted from the raw .lsm files and following processing.

1 .txt file describing the image processing.

**1B-D-E burs intensity quantification**

3 folder **“burs overexpression”, “dvts glut1ir fed starved refed suc burs(R) pros(G)” and “IMGS burs staining for quantification”** containing subfolders with the raw images (.lsm), selected ROI and relative processing for each genotype/conditions.

2 .pzfx files with the plotted data.

**1C -qpcr burs dicer voila fed starv+ glut1**

1 “**qpcr dvts w vs glut1ir**” subfolder containing the qPCR raw data (.eds), theextracted values (.xls) and the plotted data (.pzfx file).

1 .xls file with the normalization calculations.

1 .pzfx file with the plotted data.

**1D Glut1 IR tiffs after adjustments**

1 folder “**originals**” containing the raw confocal images (.lsm) and the converted and processed (.tiff).

2 .tiff and 2 .jpg files of the images processing.

1.txt file describing the image processing.

**1E burs overexpression refeeding burs staining**

1 subfolder “**Images**”, containing the raw confocal images (.lsm) and the converted and processed (.tiff).

1 .txt file describing the image processing.

**1F survival starvation mutants**

1 .pzfxfile with the plotted data.

**1G survival starvation voila burs**

1 .pzfxfile with the plotted data.

**Fig2**:

**2A TAG mutants**

1 .wsp file with raw data.

1 .xls file with the exported values and calculations.

1 .pzfx file with the plotted data.

**2B lipid droplets mutants**

.lsm raw confocal files and relative .tiff conversions.

**2C TAG dvoilats burs glut1 IR**

2 .xls files with the raw and calculations.

1 .pzfx file with the plotted data.

**2D lipid droplets gvoila glut1**

.lsm raw confocal files and relative .tiff conversions.

**2E-glycemia burs ir**

1 .wsp file with the raw data.

1 .pzfx data with the plotted data.

**2F-metabolomics**

1 subfolder “**de novo lipogenesis**” containing: 1 .xls file with the raw values and 2 .pzfx files with the plotted data.

1 subfolder “**Oliver/13 glucose**” containing: 5 .xls files with the raw values and normalizations, 4 .pzfx flies with the plotted data and 2 .pptx files with plotted figures.

**2G-H- o2 consumption**

1 subfolder “**3d dvts**>” containing: 3 .xls files containing the raw O2 values and calculations and 3 .pdf files containing the raw protein values.

1 subfolder “**o2 consumption in mitos 3d w vs burs**”containing: 3 .xls files (in each folder) containing the raw protein values, 1 .xls file containing the raw O2 values and calculations and 2 .pzfx files with the plotted data.

2 .pzfx files with the plotted data.

**2I-J-recovery after cold coma**

1 .pzfx files with the plotted data.

**fig3:**

**3A-B WB**

1 folder “**WB**” containing then raw blots (.tiff and .png).

2 .pzfx files with the plotted data.

**3C brain+ gut neurons rk cd8gfp**

1 .lsm file with the raw confocal image.

1 folder “**gut neurons**” containing the raw .lsm file and the converted .tiff and .jpg images.

**3D TAG rk shi**

1 “**Bradford**” folder containing 1 .wsp raw file and 1 .xlsx file with the extracted values.

1 “**FFA**” folder containing 1 .wsp raw file and 1 .xlsx file with the extracted values.

1 “**TAG**” folder containing 1 .wsp raw file and 1 .xlsx file with the extracted values.

1 “**jpg**” folder containing 4 .jpg figures.

1 .wsp file with the raw data.

1 .xls file with the calculations.

1 .pzfx file with the plotted data.

**3E survival rk shi**

1 .pzfx file with the plotted data.

2 .jpg files with the plots.

**3F survival upon starvation rkir**

1 .pzfx file with the plotted data.

**3G lipidtox FB nsyb w rk ir**

2 .lsm files with the raw confocal images.

4 .tiff from the .lsm files.

**3H-glycemia nsyb dlgrir**

1 .wsp file with the raw data.

1 .xlsx file with the extracted values.

2 .pzfx files with the plotted data.

**3I TAg nsyb rk ir**

3 .wsp files with the raw data.

3 .xlsx files with the extracted values.

1 .xlsx with the calculations.

1 .xlsx file with the relative calculations.

1 .pzfx file with the plotted data.

**3J 02 consumption**

1 subfolder “**3d dnsybts**>” containing: 1 .xls files containing the raw O2 values and calculations, 1 .xls files with the calculations, 3 .pdf files containing the raw protein values and 1 .pzfx file with the plotted data.

2 .pzfx files with the plotted data.

**3k-metabolomics**

1 subfolder “**de novo lipogenesis**” containing: 1 .xls file with the raw values and 2 .pzfx files with the plotted data.

1 subfolder “**Oliver/13 glucose**” containing: 5 .xls files with the raw values and normalizations, 4 .pzfx flies with the plotted data and 2 .pptx files with figures plotted.

**fig4:**

**4A**

1 subfolder “**NV+BR**” containing: 1 .wsp file with the raw proteins readings, 1 .xls file with the extracted proteins values, 2 .xlsx files with the calculations, 1 .pzfx file with the plotted data and 1 subfolder “**NV+BR def**” containing: 1 .xlsx files with the calculations and 4 .jpg files with the plotted figures, 1 “**protein**” folder containing 1 .wsp file with the raw data and 1 .xlsx file with the extracted values and 1 “**TAG**” folder containing 1 .wsp file with the raw data and 1 .xlsx file with the extracted values.

1 .pzfx file with the plotted data.

**4B**

1 .pzfx file with the plotted data.

**4C**

2 .pzfx files with the plotted data.

1 folder “**4C**” containing: 3 .wsp raw data, 3 .xlsx files with the extracted values and 1 .xlsx file with the calculations.

**4D**

2 .lsm files with the raw confocal images.

2 .tiff files from the raw data.

**4E**

1 .pfzx file with the plotted data.

1 jpg file of the plot.

**fig5**

**5A-qpcr akh**

1 folder “**raw data”** containing the raw .eds files and the extracted values (.xlsx).

2 .xlsx files with the calculations.

1 . pzfx file with the plotted data.

**5B-AKH staining+rk-MyrGFP**

1 folder “**lower**” with the raw .czi and processed .lsm and .tiff confocal pictures.

1 folder “**upper**” with the raw .lsm confocal picture.

**5C transtango**

1 folder “**dlgr2 trantango**” with the raw and processed confocal pictures.

1 folder “**transtango ctr**” with the raw and processed confocal pictures.

**5D calexa**

2 .lsm raw confocal pictures and 2 converted .tiff files.

**5E TAG akh A-SAP**

1 .xls file with the calculations.

1 .pzfx file with the plotted data.

1 .jpg file with the plot.

1 folder “**Bradford**” containing 1 .wsp raw file and the extracted values (.xlsx).

1 folder “**TAG**” containing 1 .wsp raw file and the extracted values (.xlsx).

**5F starvation survival AKH IR+ rk**

1 .pzfx file with the plotted data.

**5G TAG dnsybts> rkirgd plus akhIR**

1 .xls file with the calculations.

1 .pzfx file with the plotted data.

1 folder “**raw data**” containing: 2 .wsp files containing the raw data, 2 .xlsx files with the extracted values and 1 .pdf file with the raw protein data.

**5H-lipidtox snyb rkir +akh ir**

1 folder “**FB akh+rk irs lipidtox**” containing the raw .lsm file and the processed .tiffs.

1 folder “**FB rk IR lipidtox**” containing the raw .lsm file and the processed .tiff.

**5I starvation survival nsyb AKH IR burs5569**

1 .pzfx file with the plotted data.

**5J tag nsyb>akhir 5569**

2 .xls files with the calculations.

1 .pzfx file with the plotted data.

1 folder “**raw data**” containing: 4 .wsp files containing the raw data, 1 .xlsx files with the extracted values and 1 .pdf file with the raw protein data.

**5K starvation survival rescue bur5569 PLC-IP3R**

1 .pzfx file with the plotted data.

**5L TAG rescue plc-ip3r-hsl**

1 .pzfx file with the plotted data.

1 folder “**TAG FB rescue**”containing: 3 .wsp files containing the raw data, 4 .xlsx files with the extracted values and calculations and 1 .pzfx file with the plotted data.

**“Supplementary” Folder:**

**S1**

**S1A-Staining burs brain**

1 folder “**brain fed anti burs**” with the raw .lsm confocal images and the converted .tiff.

1 folder “**brain starv anti burs**” with the raw .lsm confocal images and the converted .tif.

1 folder “**DP anti burs**” with the raw .lsm confocal images and the converted .tiff.

**S1B- qPCR burs gut-gutless**

1 .pzfx file with the plotted data.

1 .xlsx file with thw calculations.

2 .eds files with the raw data.

**S1C- qPCR Glut1- voila glut1 IR**

1 folder “**qpcr dvts w vs glut1ir**” containing: 3 .eds files with the raw data, 3 .xlsx files with the extracted values, 1 .xlsx file with the calculations and 1 .pzfx file with the plotted data.

1 folder “**qpcr glut1 dvoilats glut1**” containing: 1 .xlsx file with the calculations, 1 .pzfx file with the plotted data and 1 .jpg file with the plot.

**S1D- staining burs - voila burs**

4 .lsm files with the raw confocal files.

2 .tiff files and 6 .jpg files from the raw data.

**S1E- TAG CTR bursIR-glut1 IR**

2 .pzfx files with the plotted data.

1 folder “**14d 29 degrees**” containing: 1 .xslx file with the calculations and 1 folder “**raw data**” containing 1 .pdf file with the raw protein data, 1 .swp file with the raw data and 1 .xlsx file with the extracted values and 1 folder “**out of std**” containing out of standard raw and extracted data.

**S2**

**S2A-food intake burs5569**

1 .pzfx file with the plotted data.

1 .wsp file with the raw data.

1 .xlsx file with the extracted values.

1 .xlsx file with the calculations .

1 folder “**W 3dd ZT0**” containing 1 .wsp raw data and 1 .xlsx file with the extracted values.

**S2B- food intake voila bursIR**

1 .pzfx file with the plotted data.

1 .wsp file with the raw data.

1 .xlsx file with the extracted values.

1 .xlsx file with the calculations.

**S2C- 2NBDG burs5569**

1 .pzfx file with the plotted data.

1 .xlsx file with the raw data.

**S2D-2NBDG voila burs IR**

1 .pzfx file with the plotted data.

1 .xlsx file with the raw data.

**S2E- excreted glucose voila burs IR**

2 .wsp files with the raw data .

1 .pzfx file with the plotted data.

1 .xlsx file with the extracted values and calculations.

**S2F-G- excreted TAG-FFA voila burs IR**

1 .wsp file with the raw data .

1 .pzfx file with the plotted data.

1 .xlsx file with the extracted values and calculations.

**S2H- glycemia burs&rk mutants**

1 .wsp file with the raw data .

1 .pzfx file with the plotted data.

2 .xlsx files with the extracted values and calculations.

1 folder “**glycemia in rk mutants**” containing:1 .wsp files with the raw data, 1 .pzfx file with the plotted data and2 .xlsx files with the extracted values and calculations.

**S2I-J- circulating TAG&FFA voila burs IR**

2 .wsp files with the raw data.

1 .pzfx file with the plotted data.

2 .xlsx files with the extracted values and calculations.

**S2K-L- locomotor activity voila burs IR& mutants**

2 .pzfx files with the plotted data.

1 folder “**fly tracking**” containing a subfolder “**videos w vs 5569**” containing all movies, 1 .pfzx file with the plotted data, 1 .xlsx file with the calculations and 2 .pptx files containing representative videos and plotting.

1 folder “**video tracking IRs**” containing 1 .pfzx file with the plotted data and 2 subfolders for the two genotypes containing the movies and the data plotting.

**S3**

**S3A-staining dlgr2-GFP VM**

1 .lsm raw confocal image.

1 .jpg extracted from the raw image.

**S3B-Surv after starvation how-dlgr2 IR**

1 .pzfx with the plotted data.

**S3C-glycemia how-dlgr2 IR**

1 .wsp file with the raw data.

1 .pzfx file with the plotted data.

1 .xlsx file with the extracted values and calculations.

**S3D-L-N-TAG how; lsp;dsrf-dlgr2 IR**

3 .wsp files with the raw data.

1 .pzfx file with the plotted data.

4 .xlsx files with the extracted values and calculations.

**S3E-O-TAG rescue how-dlgr2 IR**

1 .pzfx file with the plotted data.

1 folder “**TAG rk1 rescue**” containing 3 .wsp raw files, 3 .xlsx files with the extracted values, 1 .xlsx file with the calculations.

**S3F- Burs band intensity WBs fed starv**

1 .pzfx file with the plotted data.

**S3G- Burs band intensity voila-burs IR**

1 .pzfx file with the plotted data.

**S3H-TAG voila OSBP**

1 .xlsx file with the calculations.

1 .pzfx file with the plotted data.

1 folder “**lipids vts> osbp 14d 29**” containing: 1 .xlsx files with the calculations, 1 .pzfx file with the plotted data, 1 floder “**raw data**” containing 1 .pdf file with raw protein measurements, 1 .wsp raw file and 1 .xlsx file with the extracted values.

**S3I- Survival after starv voila OSBP**

1 .pzfx file with the plotted data.

2 .jpg files with the plots.

**S3J-staining FB dlgr2-RS**

1 .lsm raw confocal image ..

**S3K-survival after starvantion lps2-dlgr2 IR**

1 .pzfx file with the plotted data.

**S3M- survival after starvation dsrf-dlgr2 IR**

1 .pzfx file with the plotted data.

**S4**

**S4A- food intake nsyb-dlgr2 IR**

1 .wsp file with the raw data.

1 .pzfx file with the plotted data.

1 .xlsx file with the extracted values and calculations.

**S4B-C excreted glucose& FFA nsyb-dlgr2 IR**

7 .wsp files with the raw data.

2 .pzfx files with the plotted data.

2 .xlsx files with the extracted values and calculations.

**S4D- 2-NBDG nsyb-dlgr2 IR**

2 .pzfx files with the plotted data.

1 .xlsx file with the raw data and calculations.

**S4E- recovery after chill coma nsyb-dlgr2 IR+akhIR**

1 .pzfx file with the plotted data.

**S4F-O2 consumption nsyb-dlgr2 IR+akh IR**

1 .pzfx file with the plotted data.

1 folder “**3d dnsybts>**” containing 4 .xlsx files with the raw data and calculations, 4 .pdf files with the protein measurements and 1 .pzfx file with the plotted data.

**S5**

**S5A- qPCR inr-thor**

1 .pzfx file with the plotted data.

1 folder “**qpcrs cuticles**” containing 3 .xlsx files with the raw data and calculations, 1 .eds file with the raw data.

**S5B- qPCRs dilp2-3-5**

1 .pzfx file with the plotted data.

1 .xlsx file with the calculations.

1 folder “**qpcrs heads**” containing 4 .eds files with the raw data, 4 .xlsx files with the extracted data, 1 .pfzx file with the plotted data.

**S5C- tGPH staining**

2 .lsm raw confocal images.

2 .tiffs derived from the raw data.

**S6**

**S6A-Staining AKH; dlgr2-myrGFP**

2 .lsm raw confocal images.

**S6B-Survival after starvation AKH-dlgr2 IR**

1 .pzfx file with the plotted data.

**S6C-TAG AKH-dlgr2IR**

1 .pzfx file with the plotted data.

3 .wsp files with the raw data.

3 .xlsx files with the extracted values.

1 .xlsx file with the calculations.

**S6D-Staining AKH; nSyb-RFP**

1 .lsm raw confocal images.

1.tiff image derived from the raw data.

**S6E-qPCR nsyb-AKH IR**

1 .pzfx file with the plotted data.

1 folder “**S6E-14d old flies akh expression**” containing: 1 .pzfx file with the plotted data, 2 .xlsx files with the extracted values and calculations and 1 subfolder “**raw data**” containing 4 .edt raw files and 4 .xlsx files with the extracted values.

**S6F-TAG CTRs dlgr2IR-AKHIR**

2 .pzfx files with the plotted data.

1 .xlsx file with the extracted values and calculations.

1 subfolder “**14d 29 degrees**” containing 1 .xlsx with the calculations and a folder “**raw data**” with 1 .swp raw data file, 1 .xlsx extracted values and 1 .pdf with the proteins levels.

**S6G-TAG CTRs FB-IRs**

1 .pzfx file with the plotted data

1 subfolder “**TAG FB rescue**” containing 4 .xlsx files with the extracted values and calculations, 3 .swp raw data file, 1 .pzfx file with the plotted values.

**S6H-TAG CTRs IRs alone**

2 .pzfx files with the plotted data.

1 subfolder “**7d 25 degrees**” containing 2 .pfzx files with the plotted data, 1 .xlsx with the calculations and a folder “**raw data**” with 1 .swp raw data file, 1 .xlsx extracted values and 1 .pdf with the proteins levels.

**S6I-TAG CTRs IRs +burs5569**

1 .pzfx file with the plotted data

1 .xlsx file with the calculations

1 subfolder “**S6I-TAG CTRs IRs +burs5569**” containing 1 .pfzx file with the plotted data

1 subfolder “**raw data**” with 1 .swp raw data file, 1 .xlsx with the extracted values and 1 .pdf with the proteins levels.

**S6J- pH3 counts**

1 .pzfx file with the plotted data.