**Main folder name:** **RawData-Parvyet al. 2019-elife.** "The antimicrobial peptide Defensin cooperates with Tumour Necrosis Factor to drive tumour cell death in *Drosophila*"

**Folder organization :**

* 1 folder per figure named **FigureX** or **FigureXFigureSupY** (for figure supplement)
* 1 subfolder per panel named **FigureXpanelY** or **FigureXFigureSupYpanelZ**
* In each figure folder 2 subfolders 1 for raw data (named **RawData**), 1 for processed data (named **ProcessedData**)
* 1 README file describing organisation and content of raw data
* **Batch\_quantify\_modified.ijm**: Fiji macro to quantify colocalization between def and dcp1 or annexin V staining

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

**Figure1**:

* **Figure1panelA**: 1 file .ppt slide working model
* **Figure1panelB**: **RawData** folder: 4 files .xls = raw data QPCR for rpl32, def, drs, cecA1, dro and AttA; **ProcessedData** folder: 1 file .pzfx
* **Figure1panelC**: **RawData** folder: 1 file .xls = raw data QPCR; **ProcessedData** folder: 1 file .pzfx
* **Figure1panelD**: **RawData** folder: 2 files .xls = raw data QPCR for rpL32 and def; **ProcessedData** folder: 1 file .pzfx
* **Figure1panelE**: 1 file .ppt slide defensin mutation map

**Figure1FigureSup1**: 1 file .xls raw data flies survival, 1 file .pdf with graphs

**Figure2**:

* **Figure2panelA-B**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure2panelC-E’**: **RawData** folder: 3 files .lsm raw pictures named by genotype; **ProcessedData** folder: 3 files .tif processed pictures named by genotype
* **Figure2panelF**: **RawData** folder: 2 files .xls = raw data QPCR for rpL32 or def (note that this files also contain dlg versus dlg;imd results); **ProcessedData** folder: 1 file .pzfx
* **Figure2panelG**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure2panelI-J’**: **RawData** folder: 2 files .lsm raw pictures named by genotype; **ProcessedData** folder: 2 files .tif processed pictures named by genotype
* **Figure2panelK-L**: **RawData** folder: 2 folders containing raw pictures of tumours (.lsm) for experiments 1 or 2 (each tumour named with genotype followed by -T1/-T2/…/-TX), 2 files .xls raw data measurements made with Volocity for both experiments; **ProcessedData** folder: 1 file .pzfx
* **Figure2panelM**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx

**Figure2FigureSup1**:

* **Figure2FigureSup1panelA-B**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure2FigureSup1panelC-E’**: **RawData** folder: 3 files .lsm; **ProcessedData** folder: 3 files .tif
* **Figure2FigureSup1panelF-G**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure2FigureSup1panelH-J’**: **RawData** folder: 3 files .lsm; **ProcessedData** folder: 3 files .tif

**Figure3**:

* **Figure3panelA**: **RawData** folder: 1 file .xls = raw data QPCR for *rpl32* and *def*; **ProcessedData** folder: 1 file .pzfx
* **Figure3panelB**: **RawData** folder: 1 files .lsm; **ProcessedData** folder: 1 files .tif
* **Figure3panelC**: **RawData** folder: 1 files .lsm; **ProcessedData** folder: 1 files .tif
* **Figure3panelD**: **RawData** folder: 1 file .xls = raw data QPCR for *rpl32* and *def* (note that this file also contains results for Figure6panelF made at the same time); **ProcessedData** folder: 1 file .pzfx
* **Figure3panelE-F**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure3panelG-H’**: **RawData** folder: 2 files .lsm raw pictures named by genotype; **ProcessedData** folder: 2 files .tif processed pictures named by genotype
* **Figure3panelI**: **RawData** folder: 2 file .xls = raw data QPCR for *rpl32* or *def* (note that these files also contain results for *UAS-def* driven by *btl-gal4*); **ProcessedData** folder: 1 file .pzfx
* **Figure3panelJ-K**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure3panelL-M’**: **RawData** folder: 2 files .lsm raw pictures named by genotype; **ProcessedData** folder: 2 files .tif processed pictures named by genotype (note that dcp1 staining is in green, and red staining correspond to a UAS-rfp expression driven by btl-gal4)

**Figure4**:

* **Figure4panelA-B’’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 2 files .tif whole and cropped tumour
* **Figure4panelC-C’**: **RawData** folder: 1 files .lsm; **ProcessedData** folder: 1 files .tif
* **Figure4panelD-E’’**: **RawData** folder: 1 files .lsm; **ProcessedData** folder: 2 files .tif whole and cropped tumour
* **Figure4panelE-E’’**: **RawData** folder: 1 files .lsm; **ProcessedData** folder: 1 files .tif
* **Figure4panelF**: **RawData** folder: 1 file .xls = measurements made with BatchQuantify and 1 folder containing the raw pictures 10 files .lsm; **ProcessedData** folder: 1 file .pzfx
* **Figure4panelG-G’**: **RawData** folder: 1 files .lsm; **ProcessedData** folder: 1 files .tif
* **Figure4panelH-H’’**: **RawData** folder: 2 files, 1 .czi raw picture, 1 .tif raw picture tif format; **ProcessedData** folder: 1 file .tif cropped picture

**Figure4FigureSup1**:

* **Figure4FigureSup1panelA**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure4FigureSup1panelB**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure4FigureSup1panelC**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure4FigureSup1panelD**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif

**Figure5**:

* **Figure5panelA**: **RawData** folder: 2 files .xls = raw data QPCR for *rpl32* and *def*; **ProcessedData** folder: 1 file .pzfx
* **Figure5panelB-C**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure5panelD-E’**: 2 files .lsm raw pictures named by genotype; **ProcessedData** folder: 2 files .tif processed pictures named by genotype
* **Figure5panelF**: **RawData** folder: 1 file .xls = raw data QPCR for *rpl32* and *def*; **ProcessedData** folder: 1 file .pzfx
* **Figure5panelG-RAWDATA**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure5panelI-J’**: 2 files .lsm raw pictures named by genotype; **ProcessedData** folder: 2 files .tif processed pictures named by genotype

**Figure6**:

* **Figure6panelA**: **RawData** folder: 1 file .xls = raw data QPCR for *rpl32* and *def*; **ProcessedData** folder: 1 file .pzfx
* **Figure6panelB-C**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure6panelD-E’**: **RawData** folder: 2 files .lsm raw pictures named by genotype; **ProcessedData** folder: 2 files .tif processed pictures named by genotype
* **Figure6panelF**: **RawData** folder: 1 file .xls = raw data QPCR for *rpl32* and *def*; **ProcessedData** folder: 1 file .pzfx
* **Figure6panelG-RAWDATA**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure6panelI-K’**: **RawData** folder: 3 files .lsm raw pictures named by genotype; **ProcessedData** folder: 3 files .tif processed pictures named by genotype
* **Figure6panelL-M**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure6panelN-O**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx

**Figure7**:

* **Figure7panelA-B’’**: **RawData** folder: 1 file .xls ; **ProcessedData** folder: 2 files .tif whole and cropped tumour
* **Figure7panelC**: **RawData** folder: 1 file .xls = measurements made with BatchQuantify and 1 folder **RawPictures** containing 18 files .lsm; **ProcessedData** folder: 1 file .pzfx
* **Figure7panelD**: **RawData** folder: 2 files .xls = raw data QPCR for *rpl32* and *def*; **ProcessedData** folder: 1 file .pzfx
* **Figure7panelE**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7panelF**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7panelG**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7panelH**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7panelI**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7panelJ**: **RawData** folder: 1 folder **RawPictures** containing the raw pictures organized by dates of experiments and by genotypes, 1 file .xls = measurements made with Fiji; **ProcessedData** folder: 1 file .pzfx
* **Figure7panelK**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours organized by injection product (PBSvsDef) and labelled by genotype (followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx
* **Figure1panelA**: 1 file .ppt slide model

**Figure7FigureSup1**:

* **Figure7FigureSup1panelA**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup1panelB**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup1panelC-C’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif

**Figure7FigureSup2**:

* **Figure7FigureSup2panelA-A’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup2panelB-B’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup2panelC-C’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup2panelD-D’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup2panelE-E’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup2panelF-F’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif

**Figure7FigureSup3**:

* **Figure7FigureSup3panelA-A’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup3panelB-B’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 1 file .tif
* **Figure7FigureSup3panelC-D’’**: **RawData** folder: 1 file .lsm; **ProcessedData** folder: 2 files .tif 1 for whole tumour and 1 for enlargement
* **Figure7FigureSup3panelE-F**: **RawData** folder: 1 folder **RawPictures** containing pictures of tumours (each named with genotype followed by -T1/-T2/…/-TX), 1 file .xls raw data measurements made with Volocity; **ProcessedData** folder: 1 file .pzfx **Figure7FigureSup3panelG-H’**: **RawData** folder: 2 files .lsm; **ProcessedData** folder: 2 files .tif