The folder contains two subfolders, "data\_microMA" which contains data from microfluidic mutation accumulation (MA) experiments (one representative experiment for each strain), and "data\_MV" which contains data from mutation visualization (MV) experiments, used to generate Figure 2 of the paper.

**Description of "data\_microMA":**

The folder contains 4 files giving the evolution of growth rate during one representative MA experiment for 4 different strains, *mutH*, *mutT*, WT, MF1 (dataset\_microMA\_...) . Each column contains the values of one variable (time, generation or growth rate) for each time step for the mother cell of a single microchannel. The first two lines (i.e. first two values for each column) give respectively the index of the field of view and the index of the microchannel (~15channels for each field of view).

The folder also contains 4 files giving data on mortality of the mother cell for these experiments and one file with the mortality data for one representative experiment with the pMQ strain (induced with arabinose). For WT and *mutH* strains, the first 2 columns gives the index of the field of view and the index of the microchannel. The two last columns for WT and *mutH* and the two columns for *mutT*, MF1 and pMQ indicates the final state of the mother cell and the last frame. Several cases can occur : the mother cell can die during the experiment (final state=0, last frame=frame of the last division), it can stay alive and be imaged until the end of the experiment (final state=2, last frame=last frame of the movie), or imaging can stop before the end of the experiment for instance if the cells escape the channel (final state=4, last frame=last frame where the mother cell is imaged).

The folder contains also a file called " last\_frames\_for\_microMA\_analysis\_MF1"which contains 4 columns which indicate : the index of the field of view, the index of the microchannel, the final frame for analysis and the final state ("alive" or "dead"). Here the final frame for analysis is the last frame where the cell is imaged if final state=alive but if the cell dies, it gives the frame where growth rate analysis should stop (~10 generations before death).

**Description of "data\_MV":**

"interarrival\_times\_figure2" gives the inter-arrival times between successive foci (in minutes) for a *mutH* experiment

"size\_and\_focusfirstdetection\_figure2E" gives the size and number of new foci for all mother cells at all times, for a *mutH* experiment (number new foci at time ti = number of foci that arose between ti-1 and ti)

" size\_growthrate\_focusfirstdetection\_figure2G" gives the size, growth rate and number of new foci for all mother cells at all times, for *mutH* (2 experiments are pooled; number new foci at time ti = number of foci that arose between ti-1 and ti)