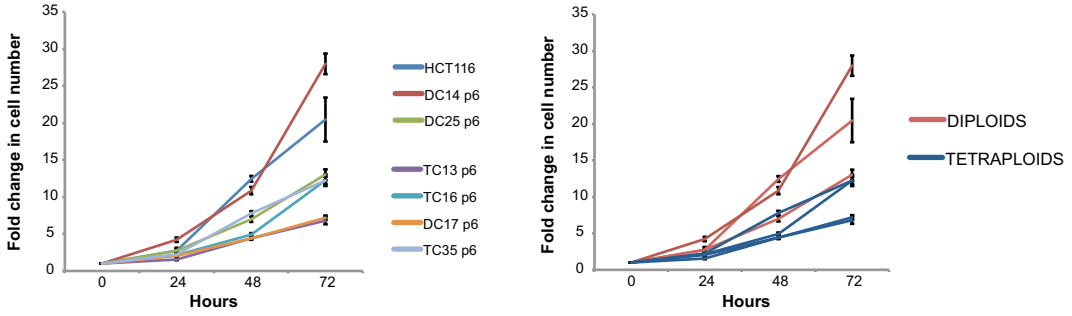
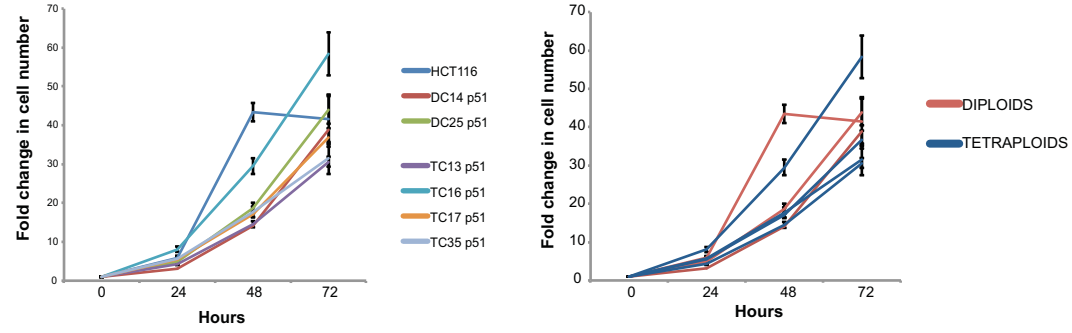
Supplementary Figure 2: Dewhurst & McGranahan et al.,

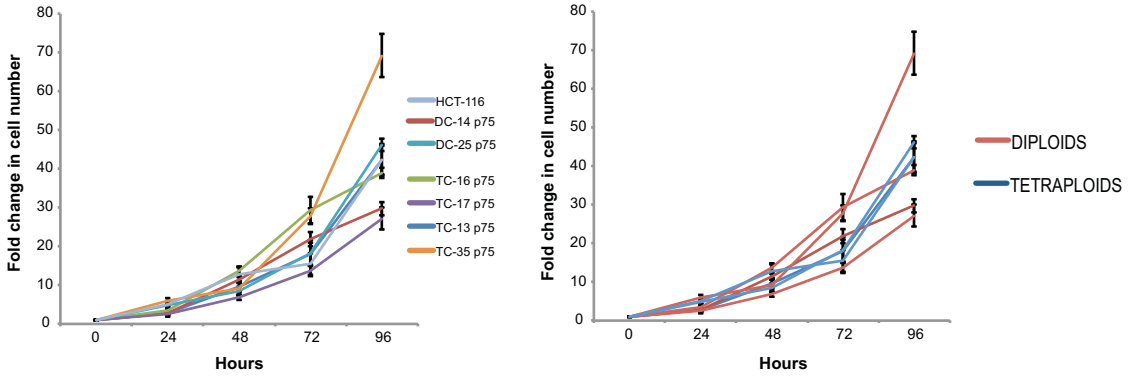
A) passage 6



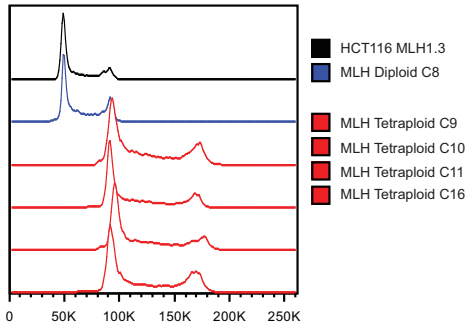
B) passage 51



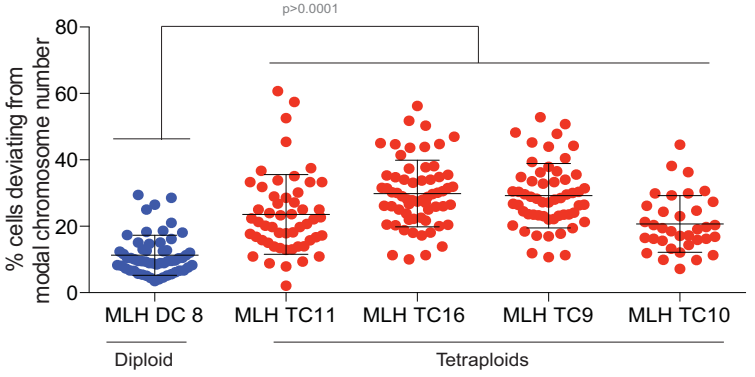
C) passage 75



D)



E)



Supplementary Figure 2

A) Proliferation at passage 6, **B)** at passage 51 and **C)** at passage 75. Proliferation was measured by seeding equal numbers of cells in multiple 96 well plates (5 well replicates for each cell line), then fixing a plate at indicated time points in 70% EtOH, before staining with DAPI and using an automated Acumen cell counter (TTP Labtech) to calculate cell number. Fold change in cell number is plotted and standard deviation between wells is indicated by error bars. Graphs on the left hand side show individual clones in different colours, whilst right-hand-side graphs show diploid clones in red and tetraploid clones in blue in order to compare growth rates between the two groups more easily.

D) DNA content analysed by flow cytometry of one diploid and four tetraploid clones derived from HCT-116_MLH1 at passage 6.

E) Clonal FISH for HCT-116_MLH1 clones. Percentage of cells per colony that deviates from the modal chromosome number in that colony (cell-to-cell variation). One diploid clone from the HCT-116_MLH1 cell line (MLH DC8) and four tetraploid clones (MLH TC11, MLH TC16, MLH TC9, MLH TC 10) are shown at passage 5. (P<0.0001, Student's T-test). The average deviation for chromosome 2 and chromosome 8 is shown.