

## Expanded View Figures

**Figure EV1. *Huwe1* is an intestinal tumour suppressor gene commonly mutated in human CRC.**

- A cBioPortal OncoPrints of *HUWE1* mutation rate in CRC identified during sequencing projects.
- B cBioPortal OncoPrints of *HUWE1* mutation rates in a range of human cancers.
- C UbcH7 pulldown of *HUWE1* HECT domain containing point mutations identified in colorectal cancer sequencing projects.
- D Quantification of total tumour numbers per colon in sacrificed *Vil Apc*, *Vil Apc Huwe1<sup>het</sup>* and *Vil Apc Huwe1<sup>hom</sup>* mice. Deletion of *Huwe1* led to a significant increase in the number of tumours per colon (Mann–Whitney,  $n \geq 3$ ). Mean and standard deviation are plotted.

**A**  
**TCGA, 2012**

Altered in 13 (7%) of cases



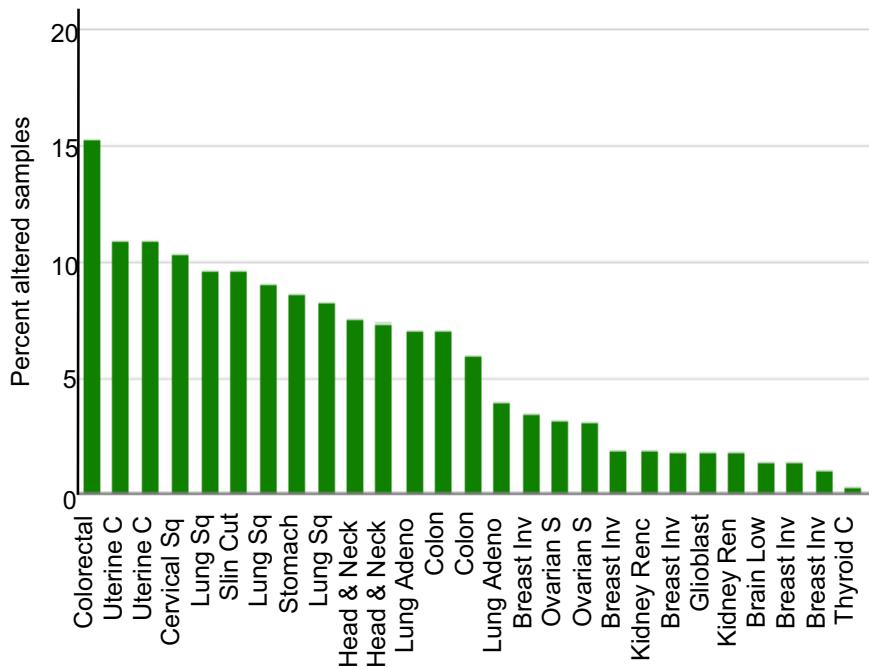
**Seshagiri et al., 2012**

Altered in 11 (15%) of cases

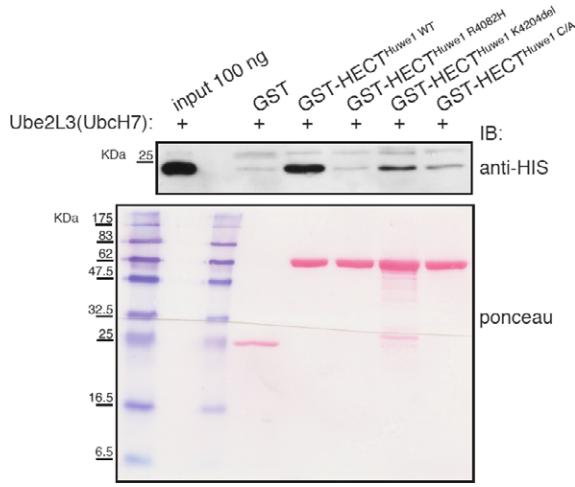


**B**

Percent sample alteration for each cancer study with mutation data: *HUWE1*



**C**



**D**

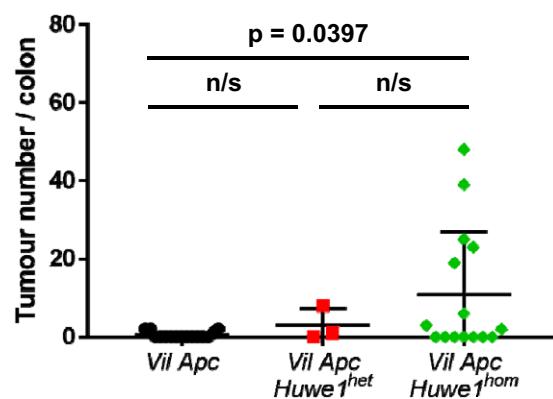
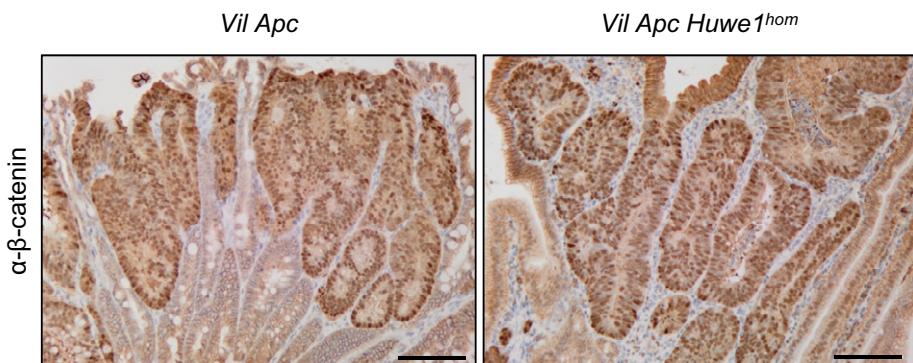
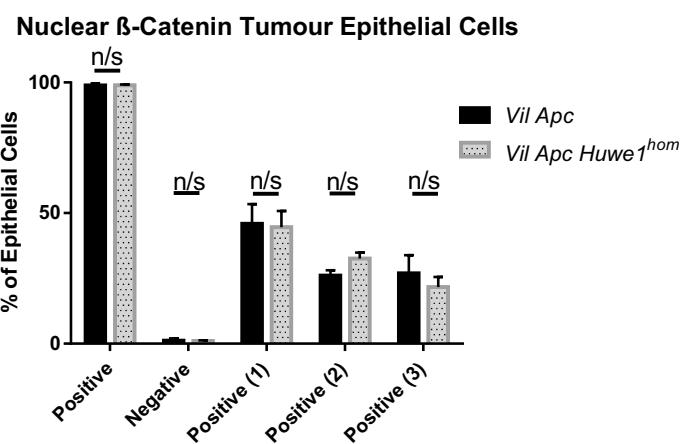
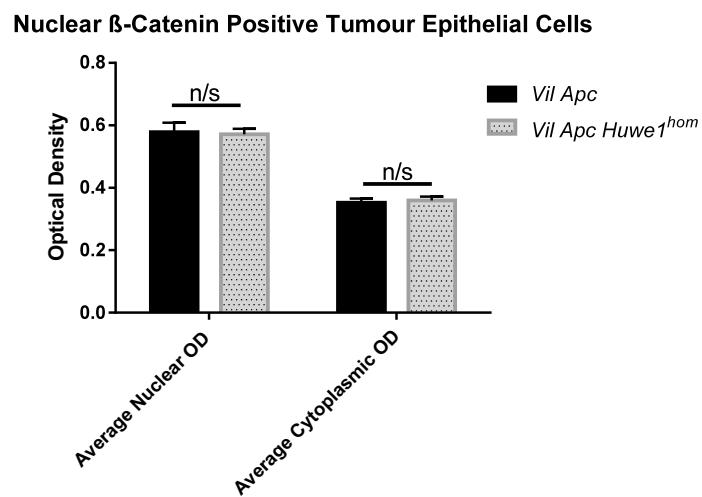


Figure EV1.

**A****B****C**

**Figure EV2.** *Huwe1*-deficient tumours display β-catenin nuclear localisation.

A β-Catenin IHC of *Vil Apc* and *Vil Apc Huwe1<sup>hom</sup>* adenomas demonstrating nuclear localisation. Scale bars = 100 μm.

B Quantification of percentage of nuclear β-catenin-positive cells in *Vil Apc* and *Vil Apc Huwe1<sup>hom</sup>* adenomas. Values 1, 2 and 3 represent low, medium and high OD, respectively (Mann–Whitney,  $n = 3$  versus 3). Data are mean and SEM.

C Quantification of β-catenin staining intensity in *Vil Apc* and *Vil Apc Huwe1<sup>hom</sup>* adenomas (Mann–Whitney,  $n = 3$  versus 3). Data are mean and SEM.

**Figure EV3. Intestinal homoeostasis following *Huwe1* deletion.**

- A Scoring of number of BrdU-positive cells per half-crypt in control and *Huwe1*-deficient small intestines (Mann–Whitney,  $n = 4$  versus 4). Mean and SD are plotted.
- B Lysozyme IHC demonstrating mislocalised lysozyme expression in *Huwe1*-deficient small intestine. Scale bars = 200  $\mu\text{m}$ . Black arrows indicate mislocalized lysozyme positive staining.
- C Quantification of lysozyme-positive cell mislocalisation (per cent of crypts displaying mislocalised lysozyme-positive cells). Significant lysozyme-positive cell mislocalisation observed upon *Huwe1* deletion (Mann–Whitney,  $P = 0.0179$ ,  $n = 3$  versus 5). Mean and SD are plotted.
- D High-magnification image of lysozyme-positive villus cells in *Huwe1*-deficient intestine. Note typical goblet cell morphology (black arrows). Scale bar = 20  $\mu\text{m}$ .
- E qRT–PCR data of WNT target genes in control and *Huwe1*-deleted small intestine (Mann–Whitney,  $n = 4$  versus 6, \*\* $P = 0.0048$ ). Mean and SD are plotted.
- F qRT–PCR data of WNT target genes in *Apc* and *Apc Huwe1*-deleted small intestine (Mann–Whitney,  $n = 3$  versus 3, \* $P = 0.04$ ). Mean and SD are plotted.
- G  $\beta$ -Catenin IHC of control and *Huwe1*-deleted small intestine. Note no gross changes in  $\beta$ -catenin localisation following *Huwe1* deletion. Scale bars = 100  $\mu\text{m}$ .

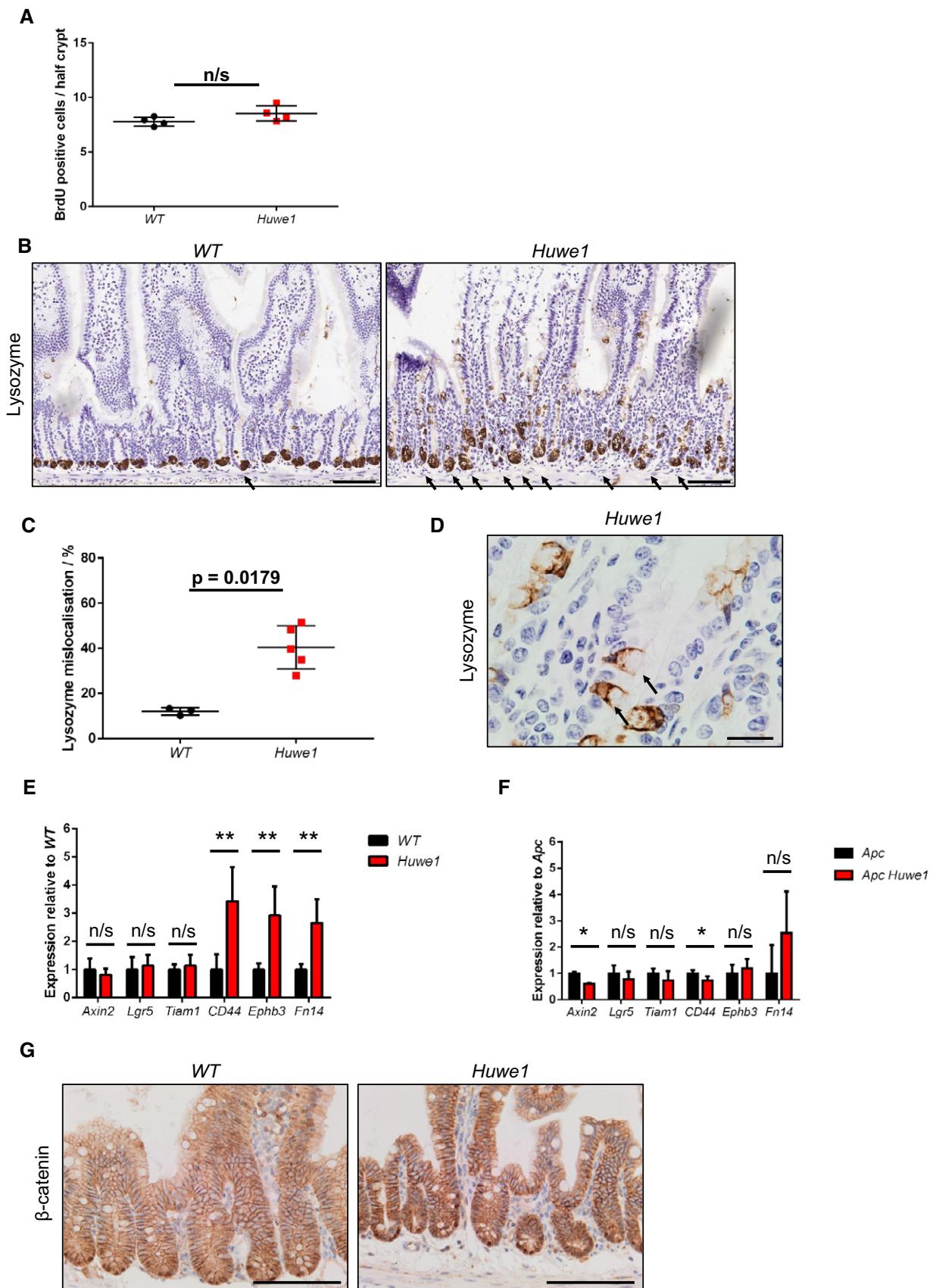
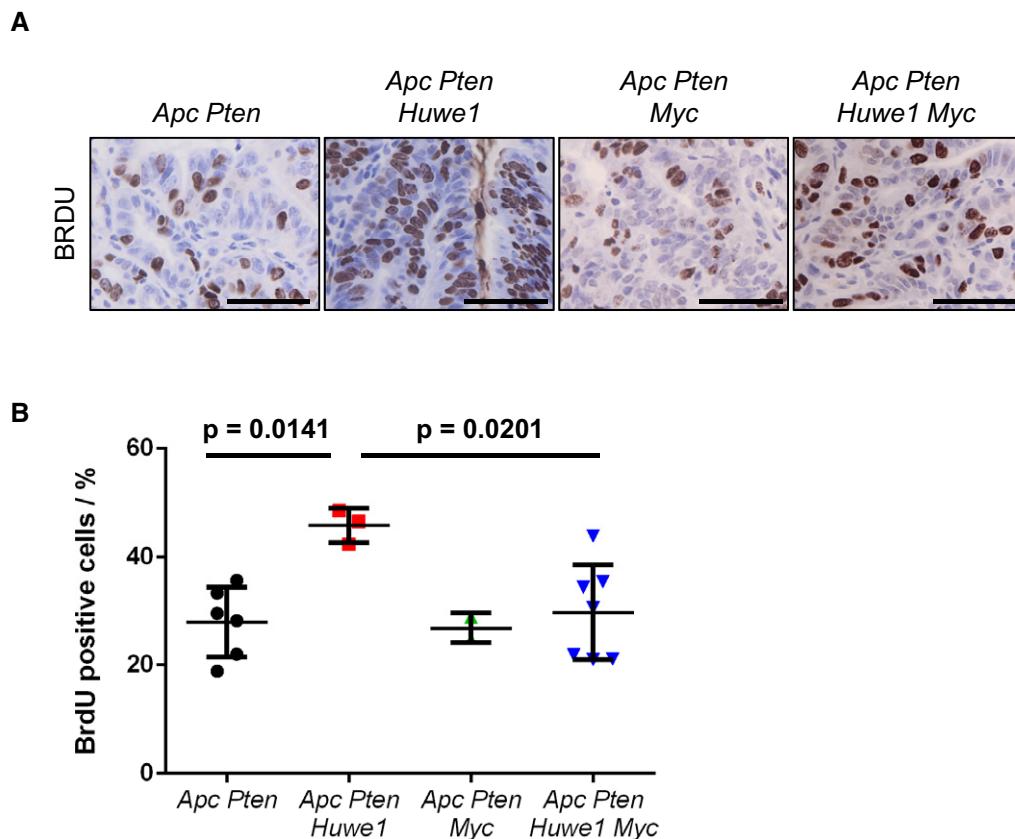


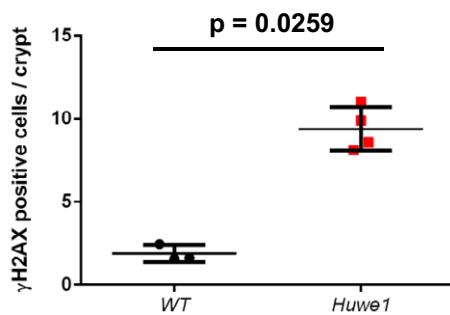
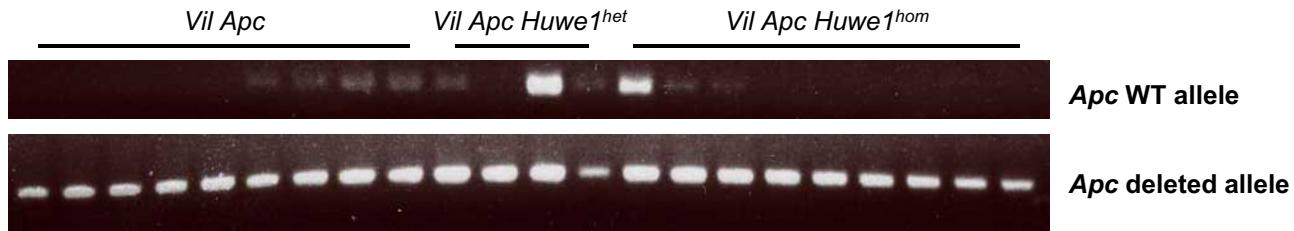
Figure EV3.



**Figure EV4.** HUWE1 suppresses tumourigenesis via regulation of MYC.

A BrdU IHC of *Vil Apc Pten*, *Vil Apc Pten Huwe1*, *Vil Apc Pten Myc* and *Vil Apc Pten Huwe1 Myc* tumours. Scale bars = 50  $\mu$ m.

B Quantification of BrdU IHC in *Vil Apc Pten*, *Vil Apc Pten Huwe1*, *Vil Apc Pten Myc* and *Vil Apc Pten Huwe1 Myc* tumours (Mann–Whitney,  $n \geq 3$ ). Data plotted are mean and SD.

**A****B****Figure EV5.** *Huwe1*-deficient tumours display *Apc* LOH.

A Quantification of  $\gamma$ -H2AX IHC demonstrating increased number of nuclei staining positive following *Huwe1* deletion (Mann–Whitney,  $n = 3$  versus 4). Data plotted are mean and SD.

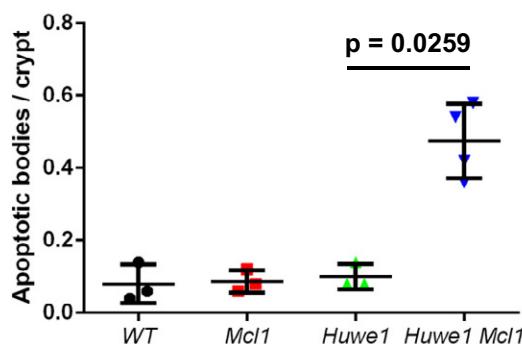
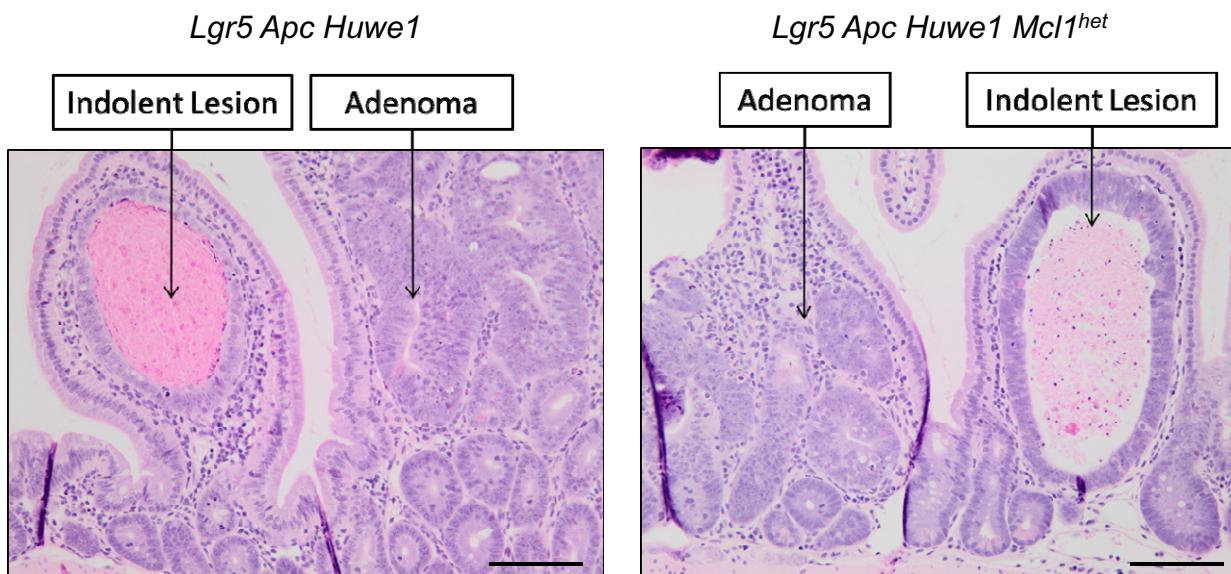
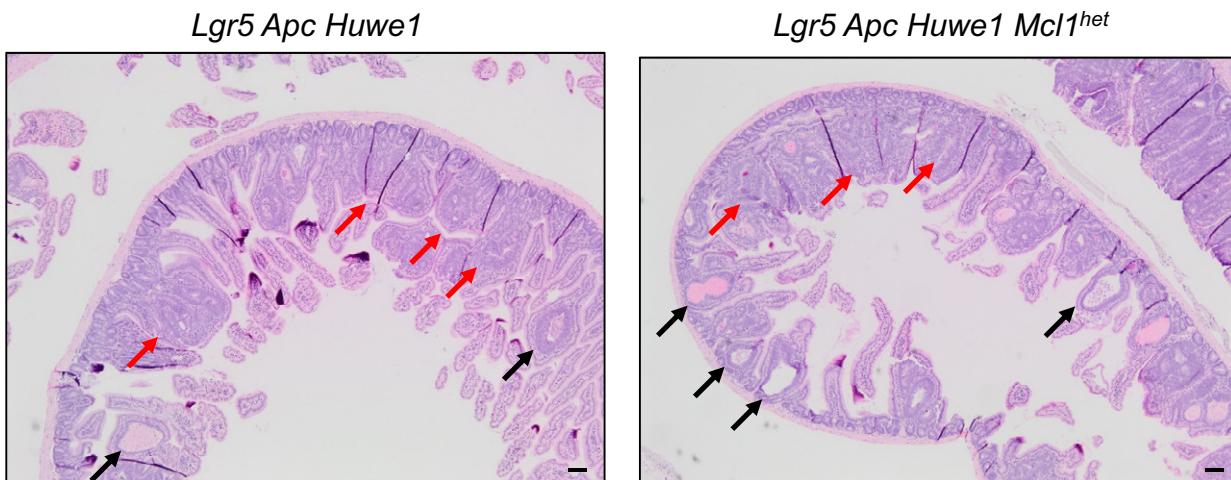
B *Apc* LOH PCR analysis of tumours isolated from *Vil Apc*, *Vil Apc Huwe1<sup>het</sup>* and *Vil Apc Huwe1<sup>hom</sup>* mice. The majority of tumours display *Apc* LOH.

**Figure EV6.** *MCL1* protects *Huwe1*-deficient tumours from apoptosis.

A Quantification of scoring of apoptotic bodies in control, *Mcl1*<sup>fl/fl</sup>, *Huwe1*<sup>fl/fl</sup> and *Huwe1*<sup>fl/fl</sup> *Mcl1*<sup>fl/fl</sup> deleted intestines (Mann–Whitney,  $P = 0.0259$ ,  $n = 3$  vs 4). Data are mean and SD.

B Classification of adenoma and indolent lesions observed in *Lgr5 Apc Huwe1* (left panel) and *Lgr5 Apc Huwe1 Mcl1<sup>het</sup>* (right panel) mice. Scale bars = 100  $\mu$ m.

C Image of intestines from *Lgr5 Apc Huwe1* (left panel) and *Lgr5 Apc Huwe1 Mcl1<sup>het</sup>* (right panel) mice. Adenomas indicated by red arrows and indolent lesions by black arrows. Note the decreased ratio of adenomas/indolent lesions observed in *Mcl1<sup>het</sup>* intestines. Scale bars = 100  $\mu$ m.

**A****B****C****Figure EV6.**