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# Global Increase of p16<sup>INK4a</sup> in APC-deficient Mouse Liver Drives Clonal Growth of p16<sup>INK4a</sup> Negative Tumors

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## **Abstract**

Reduction of  $\beta$ -catenin (CTNNB1) destroying complex components, e.g. adenomatous polyposis coli (APC), induces  $\beta$ -catenin signaling and subsequently triggers activation of genes involved in proliferation and tumorigenesis. Though diminished expression of APC has organ specific and threshold dependent influence on the development of liver tumors in mice, the molecular basis is poorly understood. Therefore, a detailed investigation was conducted to determine the underlying mechanism in the development of liver tumors under reduced APC levels. Mouse liver at different developmental stages was analyzed in terms of  $\beta$ -catenin target genes including *Cyp2e1*, *Glul* and *Ihh* using real-time RT-PCR, reporter gene assays and immunohistological methods with consideration of liver zonation. Data from human livers with mutations in *APC* derived from FAP patients were also included. Hepatocyte senescence was investigated by determining p16<sup>INK4a</sup> expression level, presence of senescence-associated  $\beta$ -galactosidase (SA- $\beta$ -Gal) activity and assessing ploidy. A  $\beta$ -catenin activation of hepatocytes does not always result in  $\beta$ -catenin positivity but unexpectedly also in mixed and  $\beta$ -catenin negative tumors. In summary, a senescence inducing program was found in hepatocytes with increased  $\beta$ -catenin levels and a positive selection of hepatocytes lacking p16<sup>INK4a</sup>, by epigenetic silencing, drives the development of liver tumors in mice with reduced APC expression (*Apc*<sup>580S</sup> mice). The lack of p16<sup>INK4a</sup> was also detected in liver tumors of mice with triggers other than APC reduction.

## **Implications**

Epigenetic silencing of *p16*<sup>Ink4a</sup> in selected liver cells bypassing senescence is a general principle for development of liver tumors with  $\beta$ -catenin involvement in mice independent of the initial stimulus.

## **Introduction**

Genesis of hepatocellular carcinoma (HCC) is not fully understood, though several carcinogenic pathways involved in this process were identified (1) among them the Wnt/ $\beta$ -catenin pathway. Activated  $\beta$ -catenin (CTNNB1) signaling contributes to approximately 30% of HCCs (2, 3) and is characterised by nuclear and/or cytoplasmic staining of  $\beta$ -catenin (4) which contrasts to cell membranous staining of unaffected liver. Consequently, Wnt/ $\beta$ -catenin target genes, i.e. *glutamine synthetase (Glu1)* (5), are upregulated in  $\beta$ -catenin positive HCCs. Induction of  $\beta$ -catenin signaling in HCCs is caused by gain of function mutations in  *$\beta$ -catenin* (6) or mutations in genes coding for components of the  $\beta$ -catenin destruction complex, i.e. AXIN1 (7) or AXIN2 (8). Though, mutations of adenomatous polyposis coli (*APC*) gene, a further constituent of  $\beta$ -catenin destruction complex, are rarely detected in primary liver cancer (9), methylation of *APC* promoter seems significant in HCC suggesting functional importance of altered APC levels (10). In contrast, other malignancies of gastrointestinal cancer, i.e. colon and rectal cancers, are strongly predisposed to *APC* germline mutations, as found in familial adenomatous polyposis (FAP, (11)). Recently, context specific responsiveness for Wnt/ $\beta$ -catenin signaling has been suggested necessary to develop cancer following APC reduction (12). Buchert reported development of HCCs in livers of aged homozygous *Apc*<sup>580S</sup> mice expressing reduced APC levels (13). Unexpectedly, HCCs of this model display a downregulation of the Wnt-target gene (14) *Axin2*, suggesting its reduction in tumors might have promoted HCC formation at the long latencies observed in these mice.

However, the tumors lacked hypermethylation of *Axin2* promoter (12). Moreover, additional events causing tumorigenesis in this model were still unclear as mutations in oncogenes, i.e. *Hras*, were not observed. Therefore, the mechanism of how APC reduction promotes HCC development remains ambiguous and important to elucidate.

Here we investigate potential mechanisms supporting development of HCCs in livers with reduced APC levels. To this end, we utilise *Apc*<sup>580S</sup> mice (13) exhibiting elevated  $\beta$ -catenin levels and investigate deregulation of Wnt signaling during all stages of HCC development. By comparing expression pattern in isolated hepatocytes and liver tissue of transgenic mice with different levels of  $\beta$ -catenin, which were generated with the help of the tet-inducible expression system, we inferred a concerted action of a senescence inducing program in hepatocytes with increased  $\beta$ -catenin levels and a positive selection for hepatocytes with loss of cell-cycle inhibitor p16<sup>INK4a</sup> (CDKN2A) (15) as driver for the development of liver tumors in *Apc*<sup>580S</sup> mice.

## **Materials and Methods**

### **Mice**

An overview of transgenic mice is presented in Supplementary Table S1. *Apc*<sup>580S</sup> (13) mice, termed *Apc*<sup>homo</sup>, carry a homozygous floxed exon 14 *Apc* allele. *Ctnnb1*<sup>flox/flox</sup> (16) mice, termed *Ctnnb1*<sup>homo</sup>, were purchased from Jackson Laboratories. Three knock-out (KO) mice, *Apc*<sup>KO</sup>, *Ctnnb1*<sup>KO</sup> and *Apc*<sup>KO</sup>/*Ctnnb1*<sup>KO</sup> were obtained by interbreeding of floxed mice with liver specific inducible *Cre* mice (17) carrying inducible *P<sub>tet</sub>Cre-recombinase* (*LC-1*) and tetracycline controlled transactivator (*TA*<sup>LAP2</sup>) transgenes (18). Homozygous *P<sub>tet</sub>Cre-Apc*<sup>homo</sup> mice were bred with homozygous *TA*<sup>LAP2</sup>-*Apc*<sup>homo</sup> mice to obtain *P<sub>tet</sub>Cre-TA*<sup>LAP2</sup>-*Apc*<sup>homo</sup> which after induction by doxycycline withdrawal result in *Apc*<sup>KO</sup> (for breeding schema see Supplementary Fig.S1). Accordingly, interbreeding was performed with *Ctnnb1*<sup>homo</sup> and combined *Apc*<sup>homo</sup>/*Ctnnb1*<sup>homo</sup> mice leading to *Ctnnb1*<sup>KO</sup> or *Apc*<sup>KO</sup>/*Ctnnb1*<sup>KO</sup> mice (Supplementary Tab.S1). *Conductin*<sup>+lacZ</sup> mice in which the reporter enzyme  $\beta$ -galactosidase is controlled by endogenous *Conductin* (*Axin2*) promoter were interbred with *Apc*<sup>homo</sup> mice and other lines specified above to obtain *Apc*<sup>hetero</sup>/*Conductin*<sup>+lacZ</sup>, *Apc*<sup>homo</sup>/*Conductin*<sup>+lacZ</sup> and

*Apc*<sup>KO</sup>/*Conductin*<sup>+lacZ</sup> mice, respectively. Mice used in proliferation tests received a unique BrdU injection (i.p., 10mM, 0.01ml/g body weight) two hours before killing.

### **Human tissue samples**

Human specimens were provided by the Tissue Bank of the National Center for Tumour Diseases (Heidelberg, Germany, ethics proposal 206/2005, University Heidelberg). 14 formalin-fixed, paraffin-embedded liver specimens mostly taken from partial hepatectomies for liver metastases of colorectal cancer excised far from the metastases were investigated. Seven patients had clinically known FAP.

### **Histochemistry and immunohistochemistry**

Immunohistochemistry was performed as described (19, 20). Briefly, 5- $\mu$ m paraffin sections were dewaxed with xylol and hydrated through downward alcohol series. Antigen retrieval was assessed by microwaving in citrate buffer (pH 6.0). Slides were equilibrated in Tris-buffered saline (pH 7.4), quenched with H<sub>2</sub>O<sub>2</sub>, blocked with biotin/avidin, and goat serum and Blocking Reagent (VECTOR<sup>TM</sup> M.O.M. Immunodetection Kit) for mouse antibodies respectively, and incubated with primary antibodies (listed in Supplementary Tab.S2) overnight at 4°C. Corresponding biotinylated secondary antibodies were coated for 1 hour at room temperature. After washing slides were incubated with extravidin-POD conjugate and washed three times before staining with 3,3'-diaminobenzidine-tetrahydrochloride (DAB). POD oxidises DAB producing a brown precipitate. For p16<sup>INK4a</sup> immunohistochemistry human liver sections were stained automatically by a Ventana Nexes autostainer (Ventana, Tucson, USA) using CINtec<sup>®</sup> p16 (E6H4) immunohistochemistry.

### **Senescence associated $\beta$ -galactosidase (SA- $\beta$ -Gal)**

Frozen liver samples were cut and mounted on Superfrost plus slides (Menzel, Braunschweig, Germany). Slides were dried 1 hour at room temperature and fixed with 0.5% glutaraldehyde in PBS 5 min at room temperature. After washing in PBS slides were incubated in 40 mM Na<sub>2</sub>HPO<sub>4</sub>, 40 mM citrate pH 6.0, stained overnight at 37°C with 1 mg/ml 5-bromo-4-chloro-

3-indolyl-beta-D-galactoside (X-Gal) in 40 mM citric acid, sodium phosphate, pH 6.0, 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 150 mM NaCl and 2 mM MgCl<sub>2</sub> and counterstained with hematoxylin.

### **Reporter enzyme**

Sections were fixed in 2% paraformaldehyde and 0.2% glutaraldehyde in PBS pH 7.4 for 30 min at room temperature, washed three times for 15 min with 2 mM MgCl<sub>2</sub>, 0.01% Nonidet P-40 in PBS and stained with 1 mg/ml X-Gal, 5 mM K<sub>3</sub>Fe(CN)<sub>6</sub>, 5 mM K<sub>4</sub>Fe(CN)<sub>6</sub> for 36–40 h at 37 °C in the dark. Slides were counterstained with nuclear fast red.

### **Isolation of hepatocytes, cell culture and transfection**

Primary hepatocytes were isolated and cultivated as described (20) by collagenase perfusion (21). Pericentral and periportal hepatocytes were isolated by a modified digitonin/collagenase perfusion technique (22, 23) and transfected with TOP-Gau reporter plasmids (24) using Effectene (Qiagen). *Apc* silencing *in vitro* was achieved by transfection with *Apc* siRNA (APCMSS202103, APCMSS202104, APCMSS202105, Invitrogen, 4nM) using Interferin (PeqLab).

### **Gaussia luciferase assay**

Gaussia luciferase activity was measured in 10 µl supernatant of transfected hepatocytes with 50 µl assay reagent on Orion-II microplate luminometer (Titertek-Berthold).

### **RNA isolation and quantitative real-time reverse transcription PCR (qRT-PCR)**

Total RNA was isolated using PeqGOLD RNA Pure isolation system (Peqlab). RNA quality was assessed by gel electrophoresis and purity was estimated using the A260/A280 ratio. Concentration was adjusted to 0.5 mg/ml. qRT-PCR was performed as described (20) using primers listed in Supplementary Table S3. RNA load was normalised with the housekeeping gene *cyclophilin* (*Ppia*). Standard curves of serial dilutions from total RNA were used for transforming ct-values to concentration values depicted as arbitrary units.

### **Methylation-specific PCR**



DNA from tumor and surrounding liver tissue was isolated using NucleoSpin tissue kit (Macherey&Nagel). DNA methylation was tested with the bisulfite conversion method using the EZ DNA-Methylation-Gold kit (Zymo Research) and *p16<sup>Ink4a</sup>* promoter-specific primers (25) Supplementary Table S3).

### **Clinical Chemistry**

Alanine aminotransferase (ALAT) and glutamate dehydrogenase (GLDH) were measured on an automated clinical chemistry analyzer (Modular PPE, Roche).

### **Flow cytometry**

Hepatocytes were counted and 200,000 cells were resuspended in 100  $\mu$ l wash buffer (PBS, 5% FCS). After washing, 500  $\mu$ l prechilled ethanol (-20°C) was added slowly with continuous mixing avoiding agglutination. Hepatocytes were kept on ice, washed twice with 1 ml PBS/5% FCS and incubated for 1 hour with RNase A (1mg/ml PBS) at 37°C. Suspensions were brought up to 200  $\mu$ l with PBS/5% FCS and 20  $\mu$ l propidium iodide (1 mg/ml) was added. This hepatocyte suspension was measured on a flow cytometer (FACScan, BD Biosciences) for determining the ploidy grade.

### **Statistical analysis**

All data are expressed as mean  $\pm$  S.E.M. Statistical analysis was performed by Student's t-test or Mann-Whitney test using SigmaPlot 11 (SSP Science). The accepted level of significance was set at  $p < 0.05$ .

## **Results**

### **Activation of $\beta$ -catenin initiates AXIN2 expression in selected/individual HCCs of aged *Apc<sup>homo</sup>* mice**

Using liver sections  $\beta$ -catenin signaling was investigated by immunohistochemistry in hepatocytes of young (8 weeks) and aged (10 months) *Apc<sup>homo</sup>* and compared to *Apc<sup>KO</sup>* mice representing a positive control for  $\beta$ -catenin activation (Figs.1A-D). This staining displayed

only few hepatocytes with activated  $\beta$ -catenin (nuclear expression) both in liver tissue from young *Apc<sup>homo</sup>* mice and tissue adjacent to tumors in aged mice. Liver tumors and their prestages in aged *Apc<sup>homo</sup>* mice exhibit, unexpectedly, a highly heterogeneous  $\beta$ -catenin staining in the same animal. Both  $\beta$ -catenin negative (Fig.1C,C') and  $\beta$ -catenin positive (Fig.1D,D') tumors were detected. Moreover, if tumors contained activated  $\beta$ -catenin they always displayed membrane-bound  $\beta$ -catenin providing a mixed phenotype, while an exclusively nuclear or cytoplasmic staining was never detectable.

Quantification of the universal and direct Wnt/ $\beta$ -catenin target gene, *Axin2* mRNA level in liver tissue extracts (Fig.1E), expectedly revealed a significant elevation in *Apc<sup>homo</sup>* and *Apc<sup>KO</sup>* and a decrease by trend in *Ctnnb1<sup>KO</sup>* mice (only 2 animals were investigated due to sudden early death of *Ctnnb1<sup>KO</sup>* mice) and a significant decrease in *Apc<sup>KO</sup>/Ctnnb1<sup>KO</sup>* mice compared to controls (both heterozygous and wild-type mice). In contrast, *Axin2* mRNA levels in tumor extract (containing several tumors) were not significantly altered (Fig.1E). However, re-evaluation of macroscopically visible tumors and subsequent resection of individual tumors of each liver revealed different individual *Axin2* mRNA levels (Fig.1F). Thereby, in the same animal either up- or downregulation of the  $\beta$ -catenin responsive target *Axin2* occur in individual HCCs. To functionally validate activation of  $\beta$ -catenin signaling *in vitro* we transfected a TCF-reporter, which allows monitoring activity of  $\beta$ -catenin triggers, in isolated primary hepatocytes (Fig.1G). Hepatocytes from *Apc<sup>homo</sup>* mice show a 5fold induction of *Gaussia* luciferase activity compared to controls, and in turn represent about one-fifth of luciferase activity obtained in *Apc<sup>KO</sup>* mice (Fig.1G), thus supporting *Axin2* mRNA data.

*In vivo* we also confirmed the elevated activation of  $\beta$ -catenin signaling in *Apc<sup>homo</sup>* mice utilizing the Wnt reporter mouse *Conductin<sup>+lacZ</sup>* in which the reporter gene  $\beta$ -galactosidase is expressed in response to the endogenous *Conductin* (*Axin2*) promoter. In *Apc<sup>hetero</sup>/Conductin<sup>+lacZ</sup>* mice  $\beta$ -galactosidase was detected only in pericentral hepatocytes as

a weak spot-like staining within the nucleus of the first row of cells around central veins and rarely in the second row, while midzonal or periportal hepatocytes were never positively marked (Fig.1H). In *Apc<sup>homo</sup>* mice (Fig.1J) the expression zone expanded and staining intensity increased. Here, several individual midzonal hepatocytes show  $\beta$ -galactosidase activity.

### **$\beta$ -catenin target genes are heterogenously expressed in tumors and lesions**

We examined expression of common  $\beta$ -catenin target genes, *Glul* and *Cyp2e1* (*Cytochrome P450 2E1*) (Fig.2A), representing classical pericentrally (pc) expressed proteins within livers of *Apc<sup>homo</sup>* mice at different ages. Additionally, we inspected the pattern of typical periportally (pp) expressed proteins, carbamoyl phosphate synthetase I (CPS) and E-cadherin, which are expected to be conversely localized to pc-specific proteins (Fig.2A). Liver tissue of *Apc<sup>homo</sup>* mice showed age-dependent up-regulation of  $\beta$ -catenin target genes, *Cyp2e1* and *Glul*, supporting data from Buchert and colleagues (12), who investigated five-months-old mice. The cellular proportion of the pericentral expression type in the zonal expression pattern starts to increase at age 3 weeks and is nearly completed at age 8 weeks. Later on, in mice, over five months old (Fig.2A), first cancerous lesions appear. Although there was a slight increase of hepatocytes exhibiting nuclear/cytoplasmic  $\beta$ -catenin in aged *Apc<sup>homo</sup>* mice, GLUL expression never spread over the whole lobulus.

The shifted zonal expression pattern of pericentral and periportal proteins in liver parenchyma of *Apc<sup>homo</sup>* mice as a result of a continuous moderate activation of  $\beta$ -catenin signaling raised the question whether zonal shifting in liver parenchyma also occurs in patients with *APC*-repressing mutations. Thus we examined the zonal expression pattern of GLUL in paraffin sections of livers of FAP patients (Fig.2B). In six out of seven FAP liver samples enlargement of the GLUL positive zone was detected. In two of these six samples GLUL positive focal

nodular hyperplasia was demonstrated (Fig.2B, top right), whereas GLUL positive nodules were not present in controls.

Precancerous lesions and tumors of aged *Apc<sup>homo</sup>* mice, however, feature surprising heterogeneity regarding the expression of the  $\beta$ -catenin target genes, *Glul* and *Cyp2e1* (Fig.3). As expected from nuclear/cytoplasmic  $\beta$ -catenin staining pattern and *Axin2* mRNA quantification tumors with pericentral, periportal or the mixed expression program were detected within an individual animal (Fig.3).

### **p16<sup>INK4a</sup> expression is regulated by $\beta$ -catenin and loss of p16<sup>INK4a</sup> is characteristic for all tumors and precancerous lesions**

The mechanism driving carcinogenesis in *Apc<sup>homo</sup>* mice seems obscure, because  $\beta$ -catenin dependent hepatocyte proliferation is supposed not to be cell-autonomous (26) and tumors with homogenously nuclear  $\beta$ -catenin staining were not found in our experiments. Moreover, hyperproliferation neither of hepatocytes carrying nuclear or cytoplasmic  $\beta$ -catenin nor of pre-programmed GLUL positive hepatocytes occurs in *Apc<sup>homo</sup>* mice (Supplementary Fig.S2). A pronounced proliferation in non-tumorous liver parenchyma was detected in livers of *Apc<sup>KO</sup>* mice only (Supplementary Fig.S2,C) compared to coeval *Apc<sup>homo</sup>* and control mice (Supplementary Fig.S2A,B). However, the hyperproliferation in *Apc<sup>KO</sup>* mice is accompanied with ruin of hepatocytes by necrosis (Fig.7A,B; black arrows). However, preliminary microarray experiments comparing the mRNA expression pattern of pericentral hepatocytes from *Apc<sup>homo</sup>* mice to periportal hepatocytes from *Apc<sup>hetero</sup>* mice, indicate alterations of tumor suppressor levels in pericentral hepatocytes. Furthermore, tumor suppressor *p16<sup>INK4a</sup>* was recently identified as a  $\beta$ -catenin target gene (27). Both results suggest *p16<sup>INK4a</sup>* as a possible key regulator for tumorigenesis in *Apc<sup>homo</sup>* mice. Consequently, we analyzed *p16<sup>INK4a</sup>* immunohistochemically and detected a very high cytoplasmic amount of *p16<sup>INK4a</sup>* in nearly all hepatocytes in aged *Apc<sup>homo</sup>* mice independently of their acinar location (Supplementary

Fig.S3,S4). Livers of FAP patients were also examined concerning expression of p16<sup>INK4a</sup>. Hereby both stainings manually performed with monoclonal antibody D7D7 used for detection of p16<sup>INK4a</sup> negative lesions in mice (not shown) and automatically performed with monoclonal antibody E6H4 (CINtec® p16,) (Supplementary Fig.S3) detected a pronounced incidence of p16<sup>INK4a</sup> in all livers samples of FAP patients compared to normal liver. Thereby a preference of p16<sup>INK4a</sup> expression in pericentral areas was observed in both FAP livers and controls (frames in Supplementary Fig.S3J,K and the corresponding magnifications J' and K').

Simultaneously, loss of p16<sup>INK4a</sup> protein in all mouse liver tumors and precancerous lesions (Fig.4A) was detected. Serial sections of liver tissue from mice at age 10 months or older showing macroscopically visible tumors corroborate the p16<sup>INK4a</sup> negativity of tumors and prestages independently on whether a periportal or pericentral expression program was followed (Fig.4A). Cells within the p16<sup>INK4a</sup> negative tumors proliferate which is shown by BrdU incorporation (Supplementary Fig.S2E,E'). In contrast tumor surrounding hepatocytes which are characterized by high p16<sup>INK4a</sup> expression do not proliferate (Supplementary Fig.S2E').

To confirm p16<sup>INK4a</sup> protein deficiency as a general hallmark of HCCs in mice with abnormal  $\beta$ -catenin signaling, we stained liver sections harbouring tumors, which initial causative event had been identified as activating mutations in exon 3 of the CTNNB1 proto-oncogene, leading to constitutively active Wnt/ $\beta$ -catenin signaling, ((28), Fig.4C) and tumors, which developed after transfection of *Apc*<sup>flax/flax</sup> mice using a virally encoded *Cre-recombinase* ((29), Fig.4B). All tumors including those with different genesis were p16<sup>INK4a</sup> protein negative. In contrast, liver tumors of aged *Apc*<sup>homo</sup> mice displayed no reduction of other tumor suppressors i.e. p19<sup>ARF</sup>, p15<sup>INK4b</sup> or p21<sup>CIP1</sup> (data not shown). Higher *p16*<sup>INK4a</sup> mRNA expression level was found in pericentral hepatocytes of *Apc*<sup>homo</sup> mice (moderate activation of  $\beta$ -catenin signaling)

and hepatocytes of *Apc*<sup>KO</sup> mice (highest  $\beta$ -catenin signaling) compared to hepatocytes of *Apc*<sup>hetero</sup> mice (low  $\beta$ -catenin signaling) (Fig.5B).

### **Cause of p16<sup>INK4a</sup> deficiency in tumors of *Apc*<sup>homo</sup> mice**

The downregulation of p16<sup>INK4a</sup> protein in tumors of *Apc*<sup>homo</sup> mice matches data on kidney (30), showing that only bypassing senescence caused by p21<sup>CIP1</sup> triggers renal tumors in *Apc*<sup>homo</sup> mice. In liver *p16*<sup>Ink4a</sup> silencing seems to meet this function.

To validate if p16<sup>INK4a</sup> reduction is epigenetically regulated *p16*<sup>Ink4a</sup> promoter methylation was examined. Only 1 out of 7 tumors displayed a methylation-specific PCR product (Fig.5A). Next, we investigated the transcriptional level by quantifying *p16*<sup>Ink4a</sup> mRNA by qRT-PCR. No reduction of *p16*<sup>Ink4a</sup> mRNA was detected in tumors compared to surrounding normal liver tissue of *Apc*<sup>homo</sup> mice (Fig.5B, right). In contrast, paradoxically, an increase of *p16*<sup>Ink4a</sup> mRNA level was detected in all tumors lacking *p16*<sup>Ink4a</sup> promoter methylation (Fig.5B and Supplementary Fig.S5). The p16<sup>INK4a</sup> reduction seems post-transcriptionally regulated, probably by increased degradation of p16<sup>INK4a</sup> protein which would explain increased *p16*<sup>Ink4a</sup> mRNA levels as compensatory mechanism. Recently, p16<sup>INK4a</sup> degradation was suggested to occur ubiquitin-independently by PSME3 proteasome (31). Hence, we quantified *Psme3* in tumor and liver extracts and found an up-regulation exclusively in tumor tissue (Fig.5C). Tumor T2-2 in which the *p16*<sup>Ink4a</sup> promoter is methylated shows no up-regulation of *Psme3* but demonstrates alternatives for p16<sup>INK4a</sup> reduction in certain cases. Accordingly, this tumor was excluded for statistical analysis of *Psme3* mRNA.

### **Consequences of altered p16<sup>INK4a</sup> expression**

Overexpression of tumor suppressors, e.g. p16<sup>INK4a</sup>, leads to induction of senescence associated  $\beta$ -galactosidase (SA- $\beta$ -Gal; GLB1) (32, 33), activation of the facultative stem cell compartment, oval cells, in phases with proliferation demand (33) and polyploidisation of hepatocytes (33). In all stages of life more SA- $\beta$ -Gal was detected in cryosections of *Apc*<sup>homo</sup> compared to *Apc*<sup>hetero</sup> mice (Fig.6B). However, stronger upregulation of SA- $\beta$ -Gal was found

in livers of *Apc<sup>KO</sup>* mice (Fig.6C) and the strongest reactivity was observed in tissue surrounding tumors and precancerous lesions (Fig.6D). Isolated primary hepatocytes of aged mice revealed in FACS analysis an increase of >16N-ploidy in *Apc<sup>homo</sup>* and *Apc<sup>KO</sup>* mice (Fig.6E), whereas hepatocytes with 4N-ploidy decreased significantly in *Apc<sup>KO</sup>* mice and by trend in *Apc<sup>homo</sup>* mice. Immunohistological stainings with anti-pan-cytokeratin antibody specific for oval cells (34), show their activation in *Apc<sup>homo</sup>* mice starting at age 5 months. In livers of mice older than 10 months both around macroscopically identifiable tumors and areas of cancer-prestages a border of oval cells was visible (Fig.6J,K, arrows). Hence the question arose what trigger, preferably produced by tumors, could activate oval cell compartment in *Apc<sup>homo</sup>* mice.

Recently, Indian hedgehog (IHH) was confirmed as an activator of hepatic stem cells produced by dying hepatocytes (35). We found *Ihh* up-regulated both in cultured hepatocytes after *Apc* siRNA treatment (Fig.6F) and in *Apc<sup>KO</sup>* mice (Fig.6F) thus confirming *Ihh* increase in livers of *AhCre-Apc<sup>KO</sup>* mice (36). These data combined with a trend of *Ihh* reduction in hepatocytes of *Ctnnb1<sup>KO</sup>* mice confirm *Ihh* as direct target of  $\beta$ -catenin (37). The up-regulation of *Ihh* mRNA level in tumors (Fig.6F) supports a role as death signal of hepatocytes, and cell damage should be expected.

### **Evidence of hepatocyte damage**

Necrotic cell death occurs in *Apc<sup>KO</sup>* mice of every age but also in old *Apc<sup>homo</sup>* mice with tumors and prestages (Fig.7A,B). Additionally apoptotic death, featured by numerous Councilman bodies (Fig.7C), seems to play a role in hepatocyte loss of *Apc<sup>homo</sup>* mice, at least in aged mice, even though caspase-3 detection failed in all liver slides (not shown). As elevated liver enzymes in serum clearly indicate necrotic loss of hepatocytes, we measured characteristic liver parameters in serum of *Apc<sup>homo</sup>*, *Apc<sup>hetero</sup>* and *Apc<sup>KO</sup>* mice. Although a slight, non-significant raise of ALAT and GLDH activities was detected age-dependently in *Apc<sup>homo</sup>* up to the age of 12 months (Fig.7D,F), a significant difference of these enzyme

activities as shown for old mice (Fig.7B,D) between *Apc<sup>homo</sup>* and *Apc<sup>hetero</sup>* mice (controls) could be measured at all these ages (not shown). In contrast, serum levels of tumor harbouring mice and *Apc<sup>KO</sup>* mice were increased up to 10fold compared to age related *Apc<sup>homo</sup>* mice (Fig.7A-D).

Additionally DNA damage was observed by anti- $\gamma$ -H2AX staining in all tumors and their prestages (Fig.7K). Moreover, large quantities of  $\gamma$ -H2AX positive nuclei were detected in *Apc<sup>KO</sup>* mice (Fig.7J).

## **Discussion**

Reduced APC expression leads to permanent activation of  $\beta$ -catenin and consequently, to upregulation of Wnt/ $\beta$ -catenin target genes and a pericentral expression program (12, 28, 38). Conversely, *Hras* mutations cause a periportal expression program (28). Unexpectedly, livers of *Apc<sup>homo</sup>* mice, providing a model of half-maximal  $\beta$ -catenin activation, develop phenotypically different tumors. Some of them are distinguished by the expression of the Wnt-target gene *Glul* and others by detection of E-cadherin, which is actually downregulated by sufficient  $\beta$ -catenin activation and belongs to the periportal expression program. Other Wnt-target genes, i.e. *Axin2*, are reduced or unchanged in such tumors ((12), present study). Likewise, the periportally expressed protein CPS is heterogeneously expressed.

The tumor suppressor *p16<sup>INK4a</sup>*, recently identified as a  $\beta$ -catenin target gene (27), was completely lost at protein level in all tumors and precancerous lesions investigated here and results in bypassing senescence as recently also found in human HCC and hepatoblastoma (39, 40).

Our data suggest the epigenetic silencing of *p16<sup>INK4a</sup>* in selected liver cells is a common factor for development of liver tumors. Firstly, APC reduction leads to overexpression of *p16<sup>INK4a</sup>* in the unaffected healthy liver of *Apc<sup>homo</sup>* mice and in hepatocytes of *Apc<sup>KO</sup>* mice with highly



activated  $\beta$ -catenin signaling. Subsequently, elevated p16<sup>INK4a</sup> induces senescence and protects from tumorigenesis as recently shown by others for pre-malignant hepatocytes in mice (41). Necessarily, increased ALAT and GLDH levels in *Apc*<sup>homo</sup> mice indicate loss of pericentrally programmed hepatocytes, which culminates in permanent proliferative stress of residual hepatocytes, being still senescent by p16<sup>INK4a</sup> overexpression. Thereby no fully replicative senescence seems to occur, because growth and physiological function of liver of *Apc*<sup>homo</sup> mice are not limited up to a critical age of about 10 months when tumors develop. Because the replicative capacity of hepatocytes is impaired by p16<sup>INK4a</sup> overexpression, a physiologically required hepatocyte replacement generates a selective pressure, both forcing the initiation of *p16*<sup>Ink4a</sup> silencing in selected populations of hepatocytes and promoting subsequent proliferation of clusters of p16<sup>INK4a</sup> negative hepatocytes. We hypothesize this sequence of events because no single p16<sup>INK4a</sup> negative hepatocyte was detected in younger animals before precancerous lesions occur and hyperproliferation does also not occur by moderate/half-maximal activated hepatocytes.

It seems irrelevant which metabolic program (pericentral/periportal phenotype) is followed by *p16*<sup>Ink4a</sup> silenced cells. The most relevant process responsible for silencing of *p16*<sup>Ink4a</sup> function is the specific p16<sup>INK4a</sup> removal, most likely by PSME3 mediated proteasomal digestion.

The p16<sup>INK4a</sup> overexpression induced by diminished APC levels supports faster ageing and death of hepatocytes, which therefore contain a diminished proliferative capacity. A similar explanation can be supposed to pericentral hepatocytes, which have a continuous  $\beta$ -catenin signaling (42), and might also be relevant in liver parenchyma of FAP patients as shown here by GLUL expression. P16<sup>INK4a</sup> up-regulation as a consequence of *APC*-repressing mutations also occurs in hepatocytes of FAP patients and likely protects from liver cancer in early stages of life in the majority of cases. The higher incidence of hepatoblastoma in children with FAP (43) and the frequent occurrence of p16<sup>INK4a</sup> loss in hepatoblastoma (40) underscores the significance of the tumor suppressor p16<sup>INK4a</sup> in  $\beta$ -catenin activated liver parenchyma.

The escalation of ALAT and GLDH concentrations in *Apc<sup>KO</sup>* mice indicates a massive decay of hepatocytes probably causing sudden death of *Apc<sup>KO</sup>* mice 10 to 14 days after conditional knockout. The strong  $\gamma$ -H2AX staining in *Apc<sup>KO</sup>* mice verifying the replicative stress in *Apc<sup>KO</sup>* hepatocytes supports this suggestion.

The IHH signal delivered by dying hepatocytes is obviously not sufficient to activate an adequate number of oval cells to replace lost cells. This also applies to tumors whose elevated *Ihh* levels might follow, additionally to activation by  $\beta$ -catenin, damage induced signals, similarly as reported on radiated hepatocytes (44). Even if sufficient oval cells were activated, their subsequent differentiation into hepatocytes would ultimately end in their decline.

Summarizing, our data suggest the epigenetic silencing of *p16<sup>Ink4a</sup>* in selected liver cells bypassing senescence is a common principle for the development of tumors in mouse liver with  $\beta$ -catenin involvement independent of the initial stimulus.

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## Figure legends

### Figure 1

Activation of canonical  $\beta$ -catenin signaling in liver of  $Apc^{homo}$  mice

**A-D)** Immunohistochemistry of mouse liver sections with anti- $\beta$ -catenin antibody.

Though some hepatocytes with nuclear  $\beta$ -catenin are detected in liver parenchyma of young  $Apc^{homo}$  mice (**A,A'**), the staining pattern is mainly comparable to normal liver (not shown) with  $\beta$ -catenin detection at hepatocyte membrane. A pronounced nuclear staining of  $\beta$ -catenin is induced in  $Apc^{KO}$  mice (**B,B'**). Aged  $Apc^{homo}$  mice have clusters of hepatocytes with nuclear  $\beta$ -catenin staining (**C and right edge in C'**) and have both tumor prestages and tumors without nuclear  $\beta$ -catenin (**C'**) and with nuclear  $\beta$ -catenin (**D,D'**). **C'** and **D'** represent larger magnifications of framed areas in **C** and **D**. Scale bar, A,B,C,D, 1200  $\mu$ m; A',B',C',D', 40  $\mu$ m.

**E-F)** Quantification of *Axin2* mRNA (**E**) in livers of different transgenic mice and tumor tissue of aged  $Apc^{homo}$  mice by qRT-PCR; \*,  $p < 0.05$ ,  $n > 4$ , t-test, and (**F**) in single individual tumors of aged  $Apc^{homo}$  mice. T represents individual tumors, i.e. T2-1 indicates tumor 2 in mouse 1.

**G-J)** Differential activation of  $\beta$ -catenin. (**G**) Activity of the *Top-Gau* luciferase reporter (containing two sets of three copies of TCF binding site and a soluble *Gaussia princeps* luciferase) displays differential  $\beta$ -catenin activation *in vitro* in cultured primary hepatocytes (hep) of  $Apc^{homo}$ ,  $Apc^{KO}$  and  $Ctnnb1^{KO}$  mice related to control mice 48 hours post transfection,  $p < 0.05$ ,  $n = 4$  (For each group hepatocytes of four different animals were used), Mann-Whitney test.

Demonstration of Wnt/ $\beta$ -catenin signaling in liver sections of  $Apc^{hetero}/Conductin^{+/lacZ}$  mice (**H**) and  $Apc^{homo}/Conductin^{+/lacZ}$  mice (**J**) by enzyme-immunohistochemistry of  $\beta$ -

galactosidase using X-Gal as substrate displays a distinct turquoise reaction product. Scale bar, 50  $\mu$ m.

## Figure 2

Immunohistochemistry of marker proteins zonally expressed in mouse and human liver

(A) Spreading of pericentral (GLUL, CYP2E1) and periportal (CPS, E-cadherin) specific proteins over the liver lobe in *Apc<sup>homo</sup>* mice at different ages

Using rabbit anti-CPS I, mouse anti-GLUL, mouse anti-E-cadherin and rabbit anti-CYP2E1 antibodies the distribution of indicated pericentral and periportal proteins is immunohistochemically demonstrated (brown, DAB). Liver sections of 8 week old *Apc<sup>hetero</sup>* mice, used as controls, show the localisation of the proteins in normal mouse liver, because no differences were detected between C57BL/6 and *Apc<sup>hetero</sup>* mouse liver at different ages (not shown). Central veins were indicated by cv, portal tracts by pv. Bar represents 100  $\mu$ m.

(B) Distribution of the pericentral marker enzyme GLUL in human liver sections

Immunohistochemistry with anti-GLUL antibody (brown, DAB) was performed on representative normal human liver sections and liver sections of FAP patients.

## Figure 3

Expression of typical pericentral and periportal proteins in tumors and precancerous lesions in aged *Apc<sup>homo</sup>* mice (>10 months)

Serial liver sections of different tumor harbouring mice were immunohistochemically stained using antibodies against GLUL and CYP2E1, which represent pericentrally expressed proteins in normal liver and CPS and E-cadherin, which exhibit periportal expressed proteins in normal mouse liver. From left to right the following HCC phenotypes are shown: GLUL positive, GLUL negative, mixed phenotype and tumor prestages. Scale bar, 100  $\mu$ m.

## Figure 4

p16<sup>INK4a</sup> expression in HCCs of mouse liver

(A) Serial liver sections of tumor-containing *Apc*<sup>homo</sup> (13) mouse, (B) *Apc*<sup>flox/flox</sup> mouse *in vivo* transfected with adenoviral *Cre* (29) and (C) mice with chemically induced HCCs (28) were incubated either with anti-GLUL and anti-p16<sup>INK4a</sup> or anti-E-cadherin and anti-p16<sup>INK4a</sup> antibodies. Positively labelled signals are brown (DAB). Chemically induced tumors had been generated by a N-nitrosodiethylamine/ phenobarbital initiation protocol, with a single i.p. dosage of the nitrosamine (90µg/g body weight) at 6 weeks of age followed by phenobarbital-containing diet (0.05%) for 6 months. Scale bar, 100 µm.

### Figure 5

Cause of p16<sup>INK4a</sup> reduction in mouse liver tumors

A) Methylation-specific PCR proved epigenetic silencing of *p16*<sup>Ink4a</sup> promoter.

DNA of seven different tumors was examined by PCR using primers specific for methylated (m) and unmethylated (um) *p16*<sup>Ink4a</sup>-promoter. As controls a methylated DNA (positive-m; Zymed research) and DNA of tumor T1-1 surrounding liver tissue of an *Apc*<sup>homo</sup> mouse (homo-m, homo-um) were used. Abbreviations: see legend of Fig.1B.

B) Quantification of *p16*<sup>Ink4a</sup> expression in isolated hepatocytes and liver tissue extracts by qRT-PCR.

Mean relative mRNA content of pericentral hepatocytes of *Apc*<sup>homo</sup> (pc-*Apc*<sup>homo</sup>, n=6), hepatocytes of *Apc*<sup>KO</sup> (hep-*Apc*<sup>KO</sup>, n=3) and *Apc*<sup>homo</sup> (hep-*Apc*<sup>homo</sup>, n=3) mice, and *Apc*<sup>homo</sup> liver tissue (tissue-*Apc*<sup>homo</sup>, n=6) and tumor tissue of *Apc*<sup>homo</sup> mice (n=7) was compared to the mean value provided by hepatocytes of 5 control animals which were used as reference. The highest, but equal, *p16*<sup>Ink4a</sup> expression was measured in tumor and surrounding liver tissue of *Apc*<sup>homo</sup> mice, \*, p<0.05, Mann-Whitney test. Tissue of tumor 2-2 possesses decreased p16<sup>INK4a</sup> mRNA compared to control (see Supplementary Fig.S5).

C) QRT-PCR of *Psmc3* mRNA in liver extracts of indicated mice and tumors of *Apc<sup>homo</sup>* mice and in separately isolated individual tumors (see also legend Fig.1), \*,  $p < 0.05$ , Mann-Whitney test.

## Figure 6

Signals of senescence in *Apc<sup>homo</sup>* mice

(A-D) Enzyme-histochemistry of SA- $\beta$ -Gal in liver cryosections of control (*Apc<sup>hetero</sup>*) (A), *Apc<sup>homo</sup>* (B), *Apc<sup>KO</sup>* (C) and tumor-containing aged *Apc<sup>homo</sup>* mice (D). The turquoise color is the reaction product of SA- $\beta$ -Gal activity with substrate X-Gal at pH 6.0. Dotted line in D marks the border between tumor, visible on the upper right edge, and non-tumor. Scale bar, 50  $\mu$ m.

Altered hepatocyte ploidy and DNA content respectively was determined by flow cytometry analysis using propidium iodide staining (E). *Apc<sup>hetero</sup>* mice possess more hepatocytes with 4N DNA content than *Apc<sup>KO</sup>* mice. Hepatocytes with higher ploidy,  $>16N$ , were over-represented in *Apc<sup>homo</sup>* and *Apc<sup>KO</sup>* mice compared to controls (*Apc<sup>hetero</sup>*), \*,  $p < 0.05$ , t-test. (F) *Ihh* mRNA was measured by qRT-PCR in isolated hepatocytes and in extracts of whole liver. Data represent fold change in positive direction for induction and in negative direction for repression of *Ihh* mRNA. The ratio of *Ihh* mRNA in *Apc<sup>hetero</sup>* mouse liver normalised to *cyclophilin* mRNA represents the benchmark, \*,  $p < 0.05$ , Mann-Whitney test.

Abbreviations: hep, total hepatocytes; pc, pericentral hepatocytes; tissue, liver tissue; hep-wt-*Apc*-si, C57BL/6-hepatocytes transfected with *Apc* siRNA.

(G-K) Depiction of oval cells by cytokeratin immunoreactivity.

Liver sections of *Apc<sup>hetero</sup>* (G) and *Apc<sup>homo</sup>* (H-K) mice, each 10 months old, were immunohistochemically stained with an anti-cytokeratin antibody combined to a biotinylated secondary antibody (brown; DAB) Arrows indicate the remarkable border of oval cells surrounding tumor prestages. Scale bar, 50  $\mu$ m.

## Figure 7

Evidence of hepatocyte damage in *Apc<sup>homo</sup>* and *Apc<sup>KO</sup>* mice

**(A-C)** Hematoxylin/Eosin staining of liver sections of *Apc<sup>KO</sup>* (**A**) and old *Apc<sup>homo</sup>* mice (**B,D**) demonstrating the ruin of hepatocytes by necrosis (black arrows in **A** and **B**) and by apoptosis (black arrows in **C**).

**(D-G)** Serum enzyme activity of GLDH (**D**) and ALAT (**F**) in *Apc<sup>homo</sup>* and *Apc<sup>KO</sup>* mice at different ages and compared to activities in control mice (*Apc<sup>hetero</sup>*) as indicated (**E,G**), Mann-Whitney test, \*,  $p < 0.02$ .

**(E-G)** Immunohistochemistry with rabbit anti- $\gamma$ -H2AX detects DNA damage in (**H**) control (*Apc<sup>hetero</sup>*), (**J**) *Apc<sup>KO</sup>* and (**K**) *Apc<sup>homo</sup>* mice (brown nuclei, DAB). The dashed line in (**G**) marks the border to the tumor (\*). Scale bar, 50  $\mu$ m.

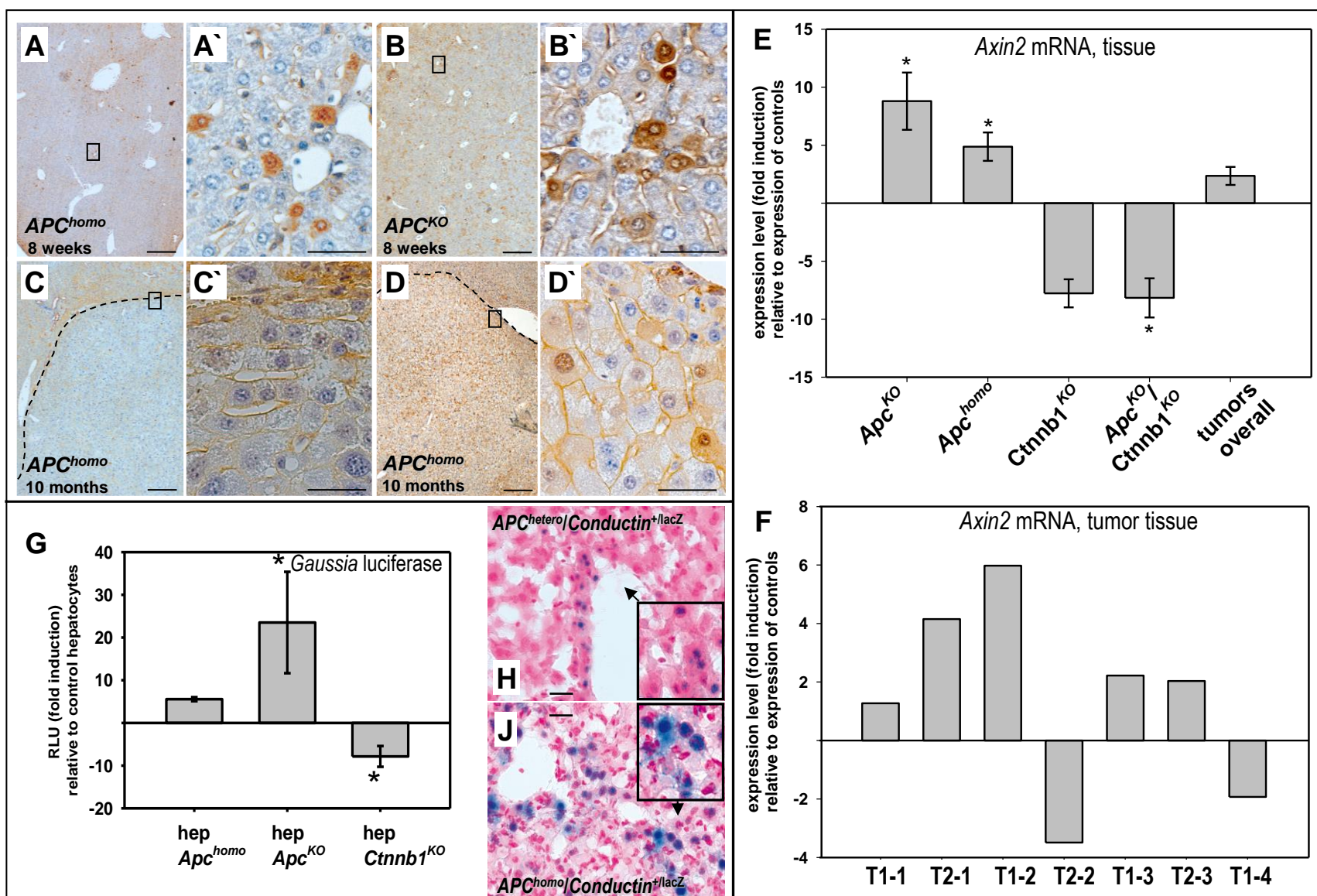


Figure 1



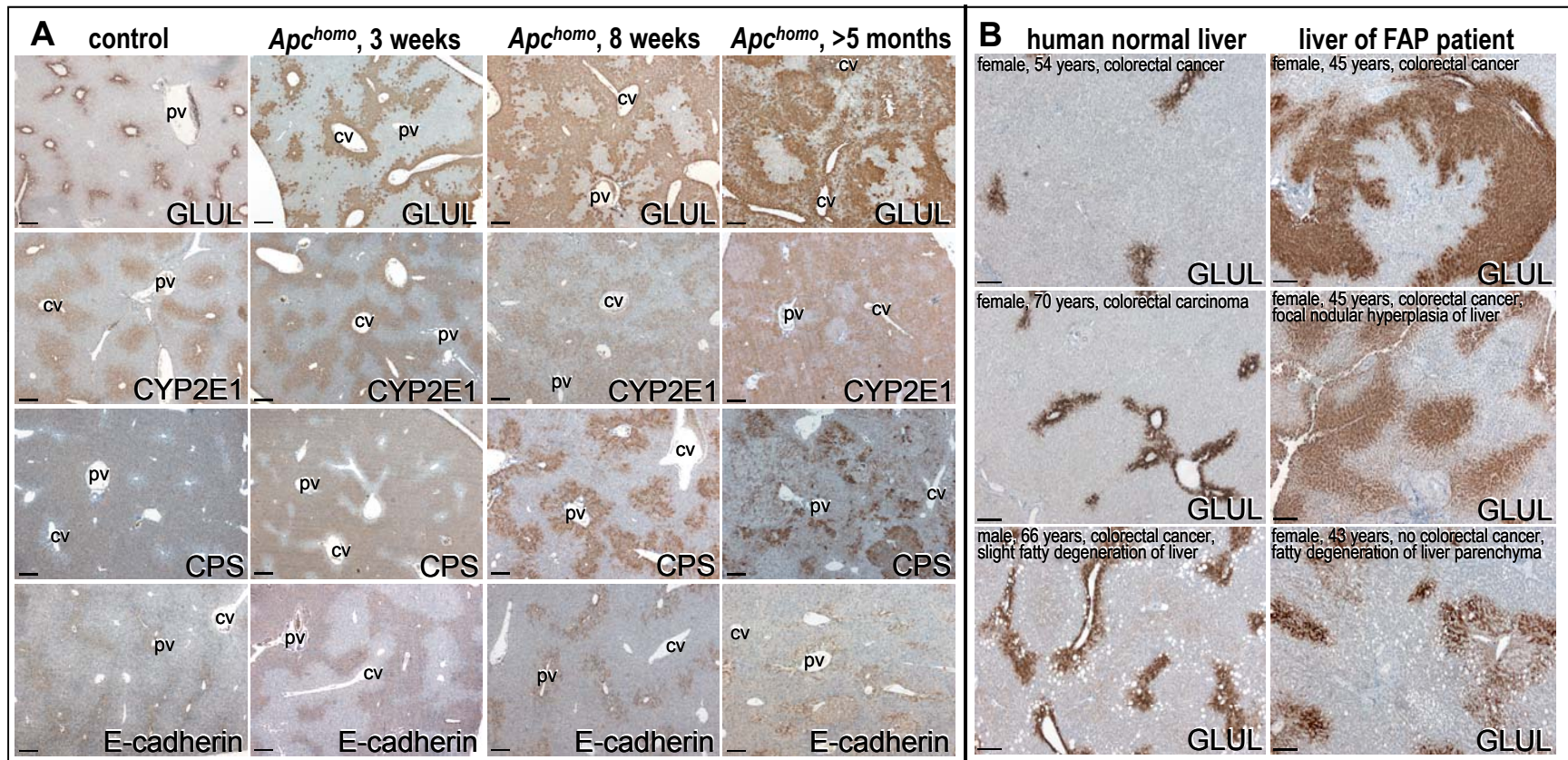


Figure 2

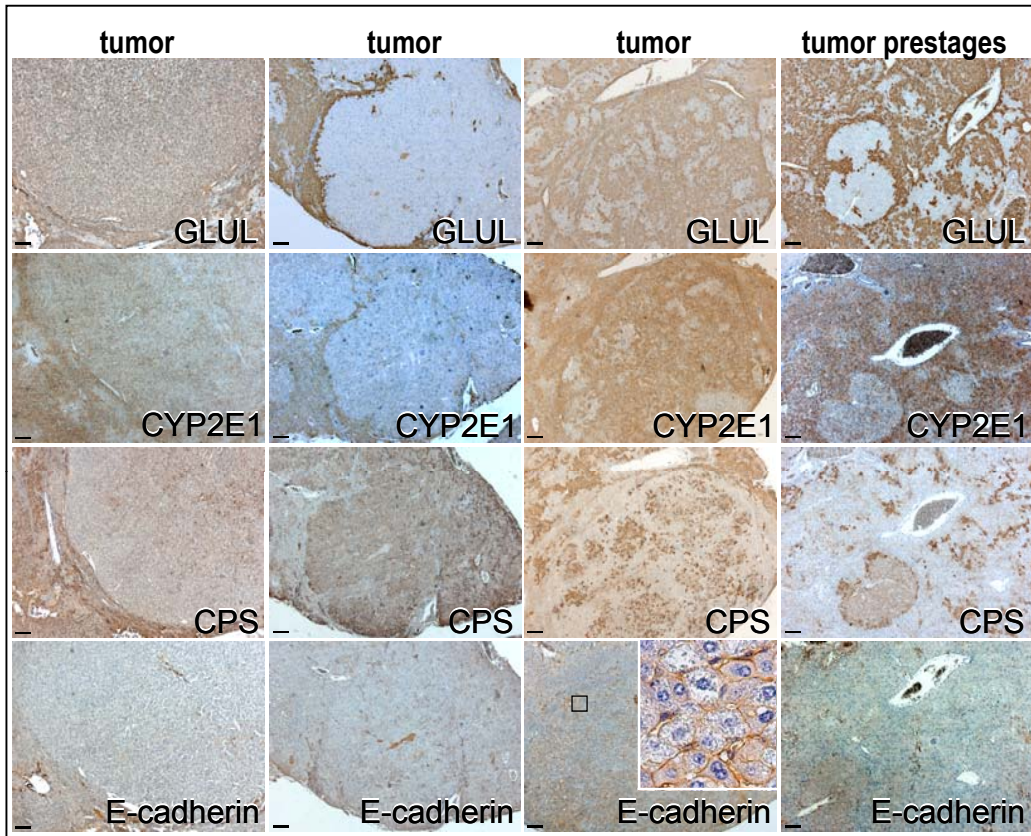


Figure 3

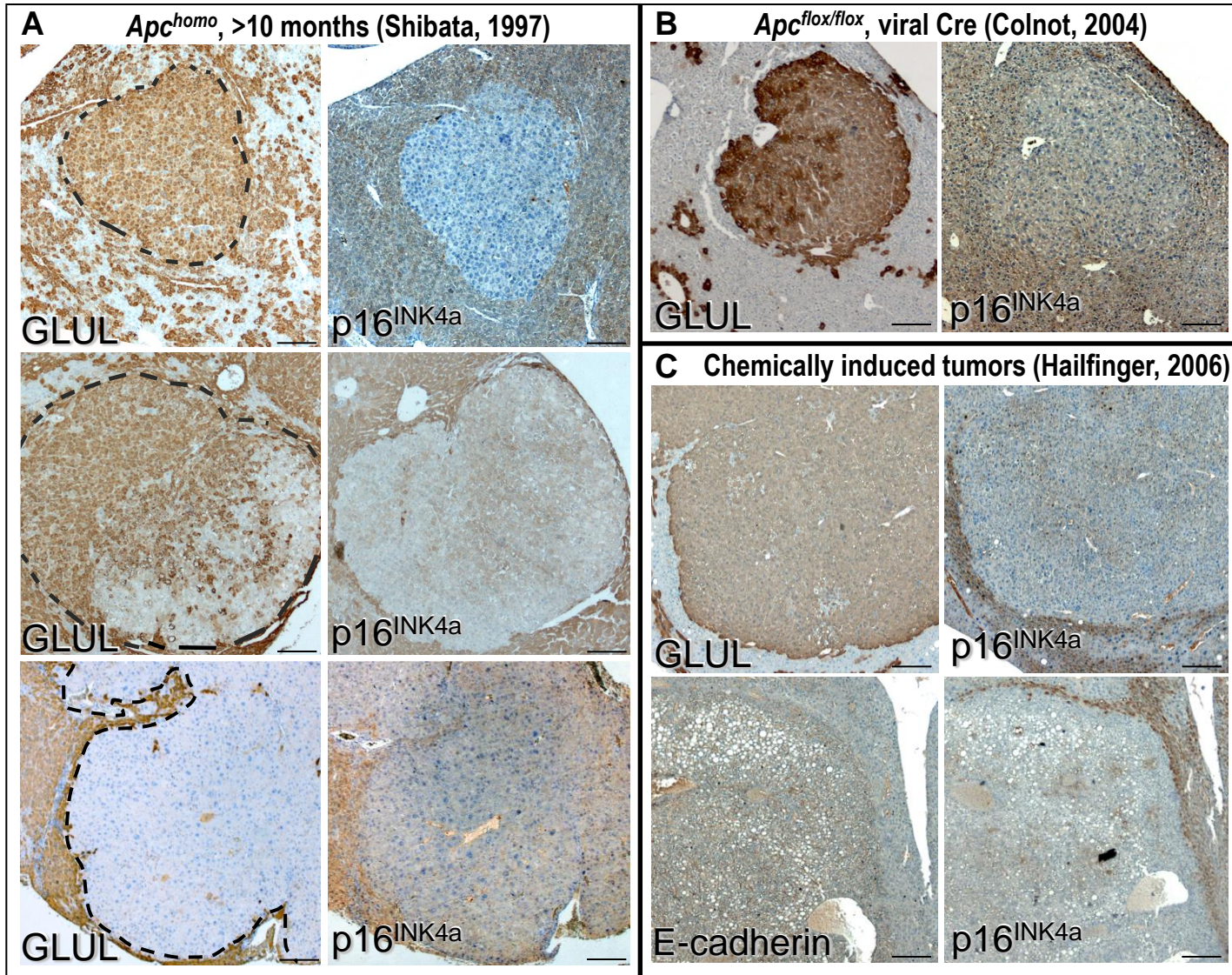


Figure 4

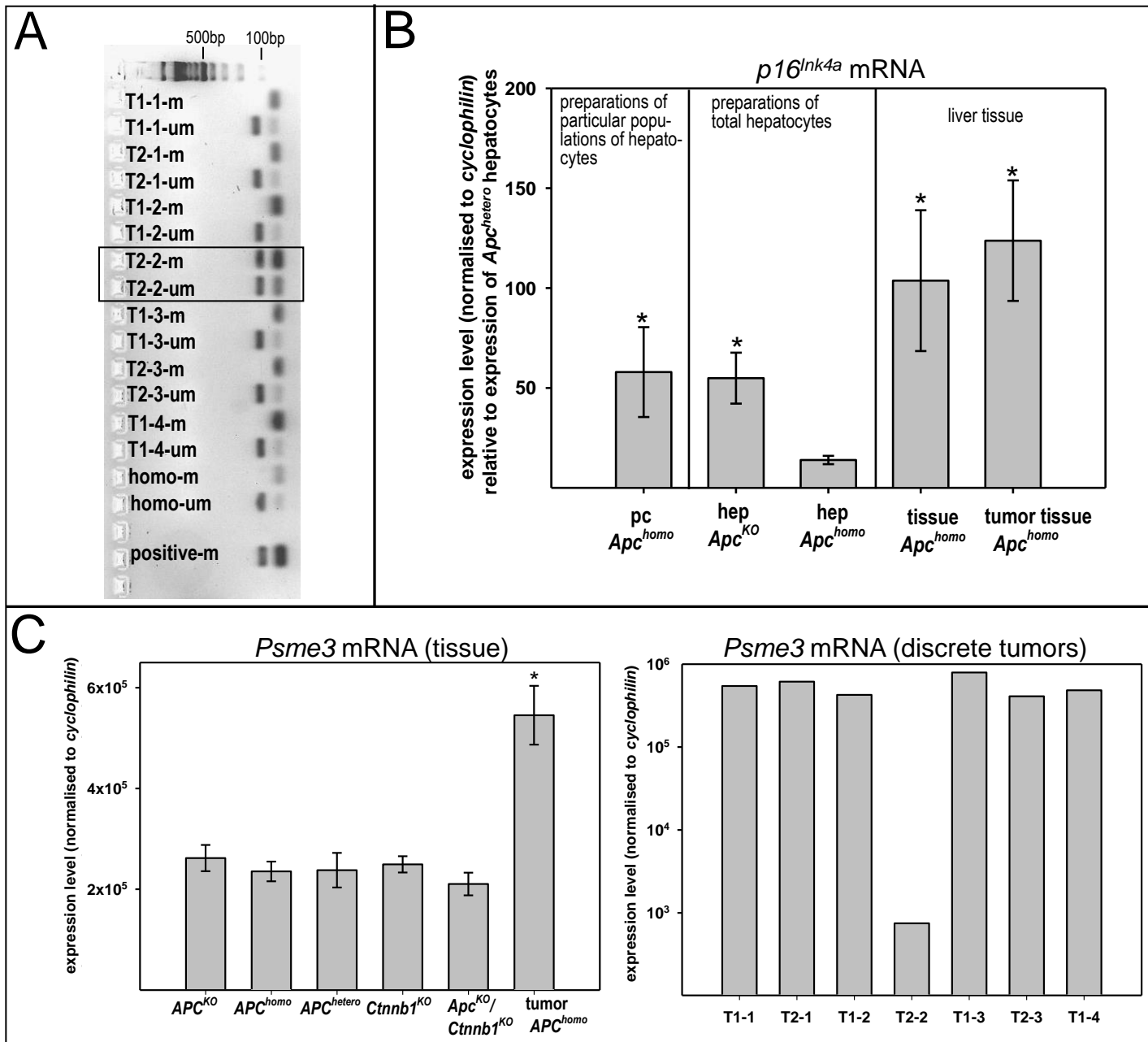


Figure 5

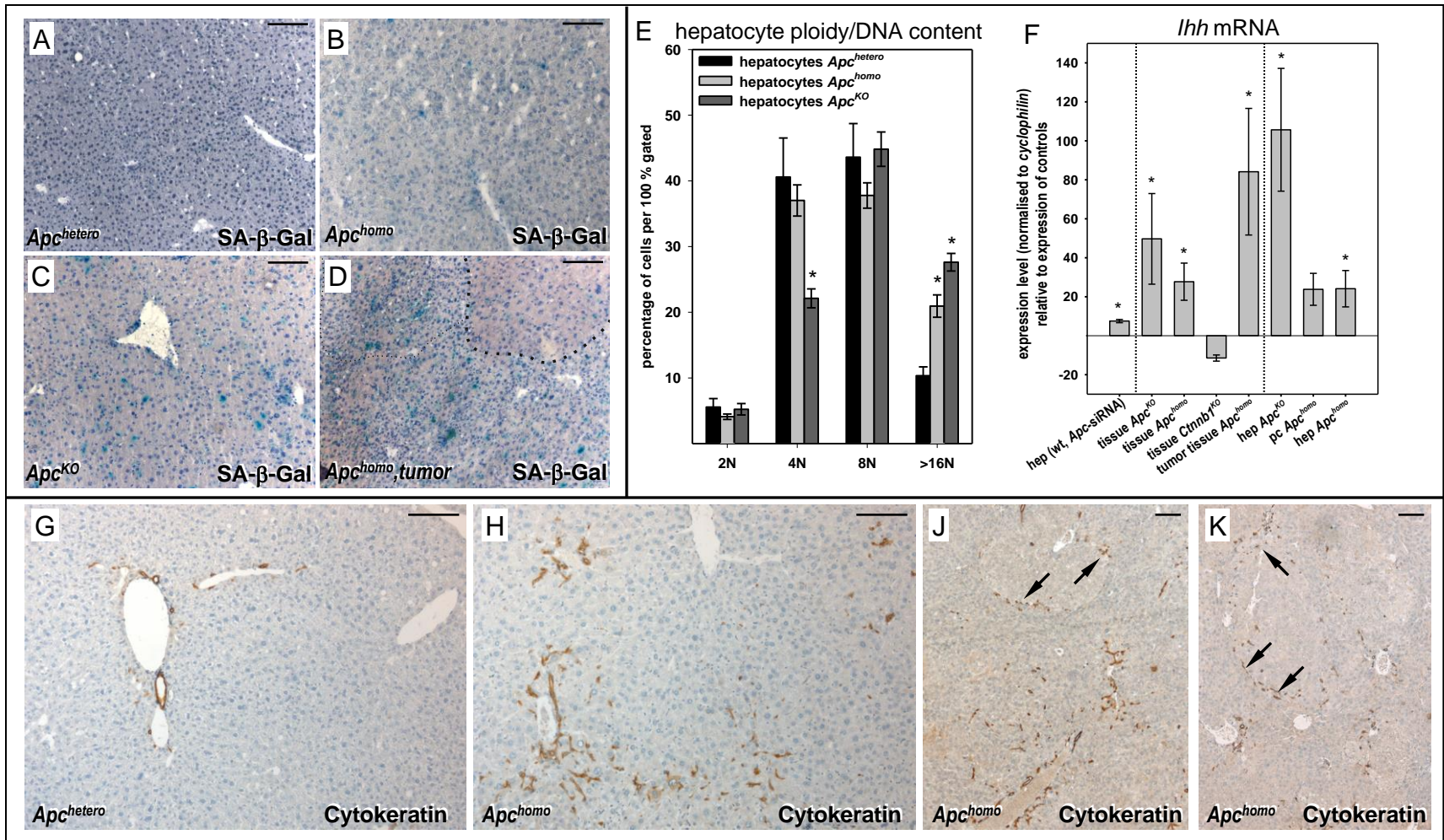


Figure 6

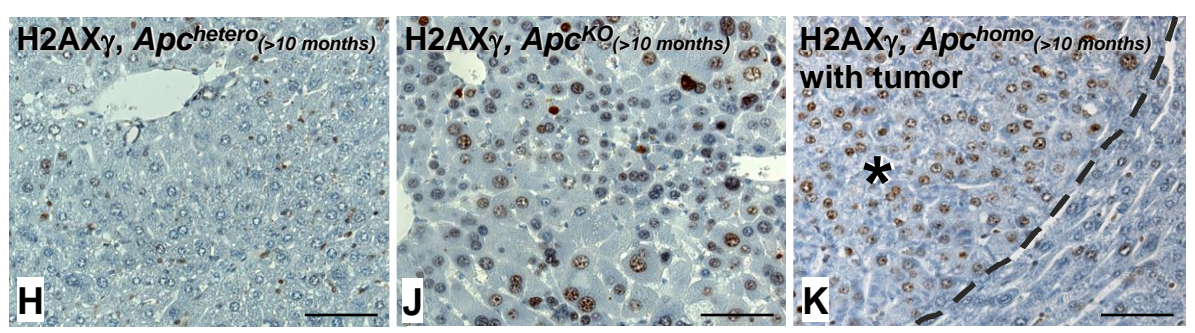
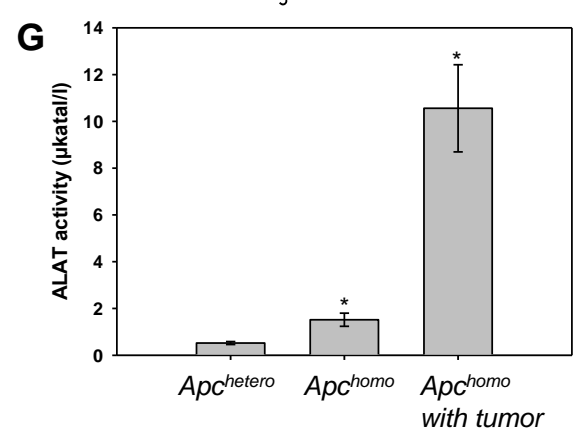
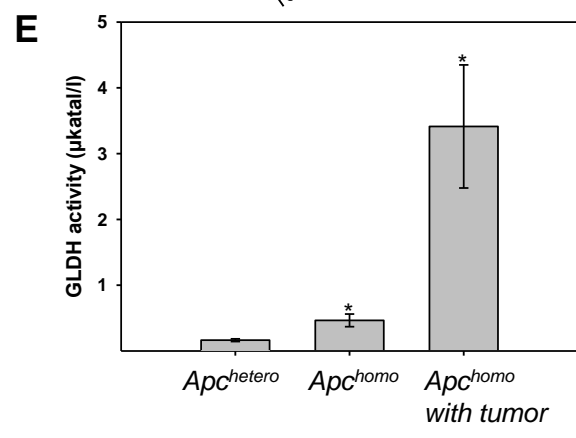
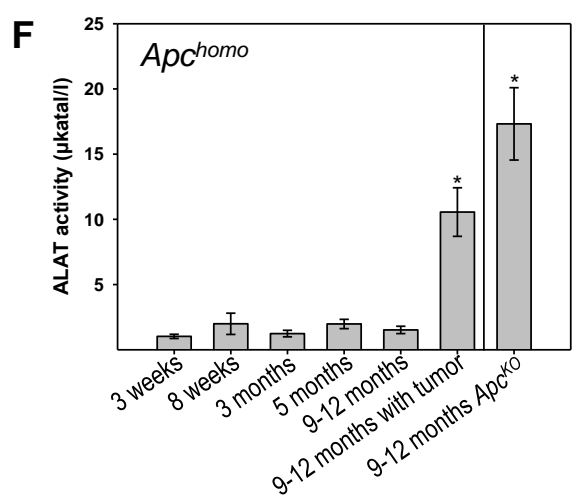
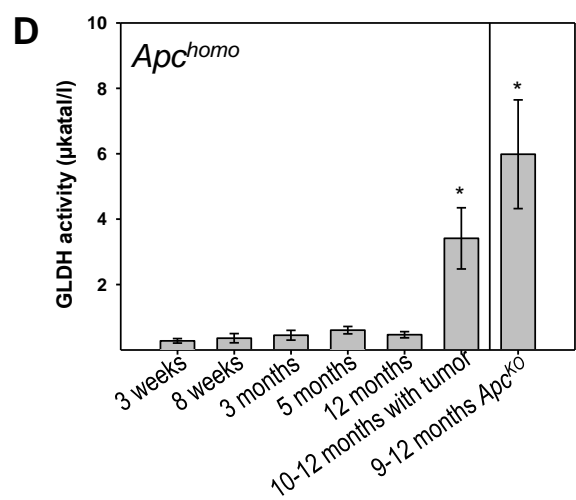
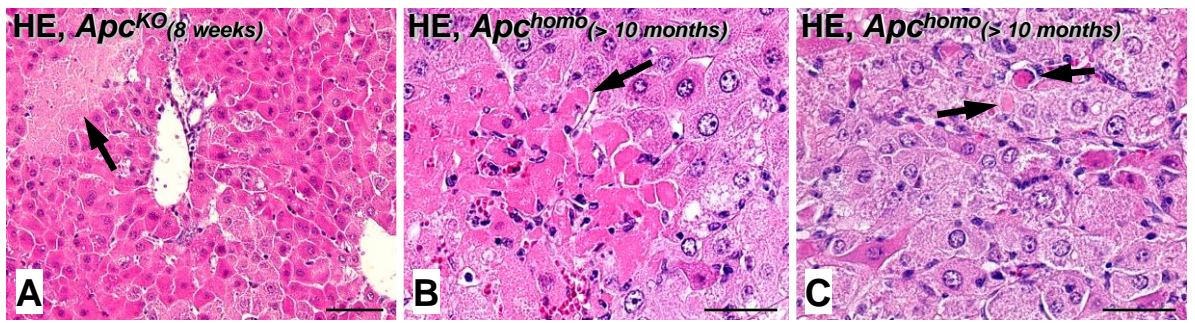


Figure 7