Developing and analysing novel tools to study endogenous WNT signalling in mice

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Publication date
2021

Citation for published version (APA):
Chapter 4

A novel Axin2 knock-in mouse model for visualization and lineage tracing of WNT/CTNNB1 responsive cells

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Adapted from
Genesis (2020) 58:e23387
DOI: 10.1002/dvg.23387
Abstract

WNT signal transduction controls tissue morphogenesis, maintenance and regeneration in all multicellular animals. In mammals, the WNT/CTNNB1 (Wnt/β-catenin) pathway controls cell proliferation and cell fate decisions before and after birth. It plays a critical role at multiple stages of embryonic development, but also governs stem cell maintenance and homeostasis in adult tissues. However, it remains challenging to monitor endogenous WNT/CTNNB1 signalling dynamics in vivo. Here, we report the generation and characterization of a new knock-in mouse strain that doubles as a fluorescent reporter and lineage tracing driver for WNT/CTNNB1 responsive cells. We introduced a multicistronic targeting cassette at the 3’ end of the universal WNT/CTNNB1 target gene Axin2. The resulting knock-in allele expresses a bright fluorescent reporter (3xNLS-SGFP2) and a doxycycline-inducible driver for lineage tracing (rtTA3). We show that the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 strain labels WNT/CTNNB1 responsive cells at multiple anatomical sites during different stages of embryonic and postnatal development. It faithfully reports the subtle and dynamic changes in physiological WNT/CTNNB1 signalling activity that occur in vivo. We expect this mouse strain to be a useful resource for biologists who want to track and trace the location and developmental fate of WNT/CTNNB1 responsive stem cells in different contexts.

Introduction

WNT/CTNNB1 (Wnt/β-catenin) signalling controls multiple stages of development in the mammalian embryo, ranging from primary axis formation (Liu et al., 1999) to mammary gland morphogenesis (Chu et al., 2004). Postnatally, WNT/CTNNB1 responsive stem cells regulate tissue homeostasis, regeneration and wound healing (Nusse & Clevers, 2017). Over the years, different genetically engineered mouse strains have been generated to capture these dynamic processes in vivo (Figure 1a).

Multiple reporter lines allow visualization of cells with active WNT/CTNNB1 signalling, either directly (e.g., GFP) or indirectly (e.g., lacZ). Some strains report active WNT/CTNNB1 signalling using an artificial reporter construct with concatemerized TCF/LEF sites, analogous to the first in vivo WNT/CTNNB1 reporter mouse, TOP-GAL (Cho, Smallwood, & Nathans, 2017; DasGupta & Fuchs, 1999; Ferrer-Vaquer et al., 2010; Maretto et al., 2003). Although these transgenic strains continue to be highly useful, they likely do not fully recapitulate the endogenous pattern of WNT/CTNNB1 signalling activity due to integration of this reporter cassette into a random or exogenous locus (Cho et al., 2017; Yu, Liu,
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Costantini, & Hsu, 2007). Moreover, different expression patterns can be detected when multiple lines are compared in the same tissue (Al Alam et al., 2011). Although truly universal WNT/CTNNB1 target genes are rare, the negative feedback regulator Axin2 has been shown to reliably report cells with active WNT/CTNNB1 signalling (Lustig et al., 2001). Accordingly, it can be used to track the developmental fate of WNT/CTNNB1 responsive stem cells in postnatal tissues (Van Amerongen, Bowman, & Nusse, 2012).

All existing models suffer from some drawbacks. Specifically, none of the available strains combine the expression of a sensitive fluorescent reporter gene and a lineage tracing driver from an unperturbed, physiological locus. Therefore, we generated a novel mouse strain, $\text{Axin2}^{P2A-\text{rtTA3-T2A-3xNLS-SGFP2}}$, in which the knock-in cassette allows both direct visualization and doxycycline-dependent lineage tracing of WNT/CTNNB1 responsive cells. Our model faithfully recapitulates the endogenous Axin2 expression pattern, while leaving normal Axin2 expression intact.
Figure 1: Design and generation of the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 knock-in allele. (a) Overview of WNT/CTNNB1 reporter and lineage tracing strains that are available from public repositories. Information was retrieved from the International Mouse Strain Resource (IMSR) at http://www.findmice.org. Strains are subdivided by four criteria: whether it is a random transgenic insertion (Tg) or a targeted insertion (Rosa26 or Axin2 locus); whether the targeted Axin2 allele still produces a functional AXIN2 protein; whether the strain carries a reporter that can directly visualize WNT/CTNNB1 responsive cells; whether the strain can be used for lineage tracing experiments. n.a., not applicable, FP, fluorescent protein, asterisk "*" requires Cre-mediated removal of a stop-cassette before the reporter becomes functional. (b) Schematic representation of the mouse Axin2 locus (chr11:108920349 - 108950781, mm10).
coordinates). Most existing Axin2 knock-in strains target the 5’ end of the gene by introducing the knock-in cassette at the start codon (ATG) in exon 2. This disrupts the endogenous Axin2 coding sequence. (c) Cartoon depicting the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 targeting construct. A multicistrionic targeting cassette was cloned immediately upstream of the Axin2 stop codon (TGA) in exon 11. The PGK-Neo-polyA cassette, flanked by FRT sites (indicated by triangles), was used for selection of embryonic stem cells and was removed prior to establishing the colony. (d) Targeted locus after removal of the PGK-Neo-polyA selection cassette. The approximate location of the primers used for the genotyping PCR depicted in (g) is indicated with equilibrium arrows. (e) The 3’ knock-in allele is designed to give rise to a single transcript in which the Axin2 5’ UTR, coding sequence and 30 UTR are left intact. (f) Following translation, the self-cleaving P2A and T2A sequences ensure that the polypeptide is cleaved into a fully functional AXIN2 protein, a doxycycline activatable rtTA3 driver for lineage tracing, and a bright green fluorescent protein that localizes to the nucleus (3xNLS-SGFP2). (g) Genotyping PCR of wildtype, heterozygous and homozygous animals. Wildtype allele = 257 bp, knock-in allele = 461 bp

Results and Discussion

We designed our new Axin2 knock-in allele to meet specific criteria. First, we targeted the 3’ end of the gene to maintain endogenous Axin2 expression and to preserve both 5’ and 3’ regulatory control (Figure 1b–d, Figure S1). Second, we wanted a single allele to function as both a reporter and a lineage tracing driver (Figure 1e,f). Third, we designed the reporter to serve as a direct readout of Axin2 activity and to be suitable for live cell imaging. For this reason, we incorporated a fluorescent protein rather than a lacZ reporter gene. Based on prior experience, we expected Axin2 expression to be relatively low. Therefore, we concentrated the reporter signal in the nucleus by fusing the SGFP2 gene to a strong nuclear localization signal (3xNLS). Finally, for lineage tracing purposes we chose a doxycycline rather than a tamoxifen inducible system, because tamoxifen can affect the outgrowth of hormone responsive tissues such as the mammary gland (Shehata, van Amerongen, Zeeman, Giraddi, & Stingl, 2014), as well as impair embryonic development, pregnancy and delivery (Ved, Curran, Ashcroft, & Sparrow, 2019). To promote equimolar expression of AXIN2, rtTA3, and 3xNLS-GFP2, self-cleaving 2A peptides were favoured over IRES sequences (Goedhart et al., 2011).
Figure 2: Functional validation of the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 allele. (a and b) Cartoons depicting the response of the knock-in allele to downstream WNT/CTNNB1 signalling, either by activation by WNT proteins in vivo (a) or by treatment with CHIR99021, a specific GSK3 inhibitor (b). Cells with active WNT/CTNNB1 signalling will induce Axin2,
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resulting in the expression of 3xNLS-sGFP expression (depicted as green nuclei). (c–f) Dot plots showing the dose-dependent induction of Axin2 mRNA expression in wildtype (c) and heterozygous (d) mouse embryonic fibroblasts (MEFs), as measured by qRT-PCR in n = 3 independent MEF isolates. Rpl13a was used as a reference gene, values in the DMSO treated control were set to 1. (e and f) Same as for (c and d), but showing rtTA3 (e) and SGFP2 (f) mRNA expression in heterozygous MEFs. (g) Confocal microscopy images of fixed mouse embryonic fibroblasts (MEFs), showing the dose-dependent induction and direct detection of SGFP2. Scalebar is 100 μm. (h) Quantification of the experiment described and depicted in (g). Fixed MEFs were counterstained with DAPI to allow nuclear segmentation, after which the relative SGFP2 expression levels were calculated by correcting for the fluorescence intensity of the DAPI signal. This experiment was performed for n = 3 independent MEF isolates. One experiment is shown here. The results for two additional MEF isolates are shown in Figure S2. (i) The rtTA3 transcriptional activator is induced together with SGFP2, but only becomes active in the presence of doxycycline (DOX). This results in activation of tetO-driven transgenes (tetO-Tg). (j) Western blot showing the WNT/CTNNB1-dependent induction of SGFP2 and the WNT/CTNNB1- and DOX-dependent induction of a FLAG-tagged protein expressed from a tetO-responsive allele in whole cell lysates from MEFs after treatment with different combinations of CHIR99021 (5 μM) and DOX (1 μg/ml). These MEFs were isolated from embryos carrying both the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 knock-in allele and a tetO-responsive FLAG-Wnt5a transgene.

Wildtype, heterozygous and homozygous Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 mice were born at the expected mendelian ratios from heterozygous intercrosses on a C57BL/6 background (Figure 1g, Table S1). We have not detected any phenotype (including differences in weight, fertility and lifespan up to 12 months) associated with homozygosity of the knock-in allele (data not shown). Of note, we also did not observe any shortening of the skull (data not shown), a craniosynostosis phenotype that has been reported in homozygous Axin2lacZ mice (Yu et al., 2005). This suggests that our 3’ knock-in allele retains full functionality, in contrast to 5’ Axin2 knock-in alleles, which by design disrupt endogenous Axin2 expression (de Roo et al., 2017; Lustig et al., 2001; Van Amerongen, Bowman, et al., 2012) and which may be haploinsufficient depending on the genetic background (Table S2).

For functional validation of the allele, we isolated primary mouse embryonic fibroblasts (MEFs) from E13.5 embryos that were heterozygous for the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 allele. Only cells with activated WNT/CTNNB1 signalling are predicted to induce Axin2 and to express rtTA3, as well as a bright green fluorescent protein in the nucleus (Figure 2a,b). Quantitative RT-PCR analysis confirmed that Axin2, rtTA3 and SGFP2 were all induced upon WNT/CTNNB1 pathway activation (Figure 2c–f). As expected, nuclear SGFP2 expression was induced upon dose-dependent activation of WNT/CTNNB1 signalling, as demonstrated by exposing the cells to increasing concentrations of CHIR99021 (a small molecule GSK3 inhibitor that
activates WNT/CTNNB1 signalling downstream of the WNT receptor complex) (Figure 2g,h, Figure S2).

Next, we tested if rtTA3 was capable of activating a tetO-responsive promoter in a doxycycline and CTNNB1-dependent manner (Figure 2i,j). In MEFs heterozygous for both the Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 allele and a tetO-responsive FLAG-tagged transgene, FLAG-tagged protein expression was only induced in the presence of both CHIR99021 and doxycycline, but not by either treatment alone (Figure 2j).

To determine if the knock-in allele properly reports WNT/CTNNB1 signalling during embryonic development, we isolated embryos from stages at which defined Axin2 expression domains were previously determined using RNA in situ hybridization (Jho et al., 2002). A dim SGFP2 signal could be detected in freshly isolated heterozygous or homozygous, but not wildtype embryos under a dissecting microscope (Figure S3). Homozygous embryos consistently showed a brighter GFP signal than heterozygous embryos, suggesting bi-allelic expression of Axin2.

At E8.5, SGFP2 was expressed in the head folds and the posterior neural tube (Figure 3a–c). At E10.5, we detected SGFP2 expression in the developing limb bud, in the branchial arches, and along the dorsal neural tube, including the roof plate of the developing brain (Figure 3d–f). These are the same sites where endogenous Axin2 was previously shown to be expressed via RNA in situ hybridization (Jho et al., 2002). At E12.5, prominent SGFP2 expression was visible in the mammary placodes (Figure 3g–i), recapitulating expression of the Axin2lacZ reporter at this site (Van Amerongen, Bowman, et al., 2012). Using wholemount confocal microscopy, individual SGFP2-positive nuclei could readily be distinguished in these embryos at the indicated sites (Figure 3c,e,f,i, Movies S1 and S2). Together, these experiments confirm that Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 reports endogenous WNT/CTNNB1 signalling in the developing embryo.

To test functionality of the lineage tracing module in vivo, we generated compound Axin2P2A-rtTA3-T2A-3xNLS-SGFP2; tetO-Cre; Rosa26mTmG mice and labelled WNT/CTNNB1-responsive cells in E7.5 embryos by a single intraperitoneal injection of doxycycline into timed pregnant females. At E10.5, triple-heterozygous embryos showed prominent recombination of the Rosa26mTmG reporter in the posterior half of the embryo (Figure 3j–l), consistent with posterior expression of Axin2 at the time of induction at E7.5 (Jho et al., 2002). Thus, Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 allows direct visualization and efficient lineage tracing of WNT/CTNNB1 responsive cells in the developing embryo.

Postnatally, SGFP2 expression was readily visualized in the small intestinal crypt. The strongest signal was found at the crypt bottom in so-called crypt-base-columnar cells (CBCs), which are known to be WNT/CTNNB1 responsive (Barker et al., 2007). These cells are readily identified by their distinct shape and presence among SGFP2-negative Paneth cells (Figure 4a,b). In adult mice, a gradient of
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SGFP2 signal extended into the upper portion of the crypt (Figure 4a). Axin2 expressing cells in the intestine could also be detected by immunohistochemical staining of formalin fixed paraffin embedded (FFPE) tissue sections with an anti-GFP antibody (Figure S4).

In adult triple-heterozygous Axin2P2A-rtTA3-T2A-3xNLS-SGFP2; tetO-Cre; Rosa26mTmG mice, Cre/lox mediated recombination of the Rosa26mTmG reporter allele in fast dividing, long-lived WNT/CTNNB1 responsive intestinal stem cells was efficiently induced by a single intraperitoneal injection of doxycycline in both pubertal and adult mice. Recombined cells first became visible 24–48 hr after doxycycline injection (Figure S5), after which the progeny of fast dividing, long-lived WNT/CTNNB1-responsive stem cells could be traced and seen to populate the crypt and villus compartments within 3–6 days (Figure S6). Prolonged tracing of the WNT/CTNNB1 responsive cell lineage resulted in sustained labelling of the entire crypt villus compartment as expected (Figure 4c,d), confirming that Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 labels intestinal stem cells (Van Amerongen, Bowman, et al., 2012).

We and others have previously reported the presence of Axin2-positive, WNT/CTNNB1 responsive cells in multiple endodermal and ectodermal tissues (Lim et al., 2013; Lim, Tan, Yu, Lim, & Nusse, 2016; Van Amerongen, Bowman, et al., 2012; Wang, Zhao, Fish, Logan, & Nusse, 2015). Contrary to what is observed in the intestine, tracing of cells in other tissues was less efficient in the experimental set up used. Nevertheless, scarce labelling of cells in the liver (Figure 4e,f, Movie S3) and prominent labelling of cells in the hair follicle (Figure 4g–i, Figure S7) could be detected, either by imaging wholemount tissues or FFPE sections.

Finally, we established primary 3D small intestinal organoid cultures from Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 animals. One heterozygous and one homozygous organoid line were maintained for extended cultures of more than 6 months, during which the reporter remained stably expressed and did not get silenced (Figure 5, Figure S8). Similar to what we observed in embryos, the levels of SGFP2 were higher in homozygous than in heterozygous organoids (Figure S8a–d). Strongest expression of the reporter allele was observed in CBCs at the bottom of the crypt-like compartment. Expression gradually decreased along the crypt axis in the transit amplifying compartment, similar to what is observed in vivo (Figures 4a and 5a–d).
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E8.5 embryo

E10.5 embryo

E10.5 embryo (traced from E7.5)

E12.5 embryo
Figure 3: *Axin2* reports embryonic WNT/CTNNB1 signalling. (a and b) Wholemount E8.5 embryo after fixation, imaged under a dissecting microscope using brightfield (a) or fluorescent (b) settings. Arrowheads indicate the headfolds and posterior neural tube. Scalebar is 100 μm. (c) Maximum intensity projection of a wholemount confocal microscopy Z-stack of the same embryo as in (a and b). Arrowheads point to regions with individual SGFP2-positive nuclei in the headfolds and posterior neural tube. Scalebar is 100 μm. (d) Wholemount E10.5 homozygous embryo imaged under a fluorescence dissecting microscope. Arrowheads indicate expression in the developing limb bud and branchial arches, along the dorsal neural tube, and in the roof plate of the developing brain. Scalebar is 500 μm. The same embryo is depicted in Figure S2. (e and f) Wholemount confocal microscopy images of the roof plate (e) and forelimb bud (f) of an E10.5 heterozygous embryo. Individual SGFP2-positive nuclei can be distinguished and are indicated with arrowheads. Scalebar is 50 μm for (e) and 100 μm for (f). (g) Wholemount E12.5 homozygous embryo imaged under a fluorescence dissecting microscope. Scalebar is 1 mm. (h) Close up of the area highlighted in (g). Arrowheads indicate expression of the fluorescent reporter in the mammary buds. Scalebar is 500 μm. (i) Maximum intensity projection of a wholemount confocal microscopy Z-stack of the E12.5 mammary bud, showing the difference in GFP intensity between a heterozygous (HET, top) and homozygous (HOM, bottom) embryo. Nuclear SGFP2 signal can be detected in both the epithelial bud and the surrounding mesenchyme. A 3D rotation of the entire Z-stack is provided in Movies S1 (HET) and S2 (HOM). (j) Timeline for the experiment depicted in (l). Lineage tracing in WNT/CTNNB1-responsive cells was induced in utero at E7.5 by administering a single intraperitoneal injection of doxycycline (DOX) to pregnant females. Embryos were isolated and imaged at E10.5. (k) Lineage tracing principle using the Rosa26\(^{m\text{tmg}}\) reporter. Prior to Cre-mediated recombination, all cells express a membrane-localized red fluorescent protein (mT). Cre recombination results in a permanent switch to expression of a membrane-localized green fluorescent protein (mG). (l) Composite image showing Cre/lox dependent recombination in the posterior half of an *Axin2*; *tetO-Cre*; Rosa26\(^{m\text{tmg}}\) triple heterozygous embryo. Red signal reflects non-recombined cells (mT), green signal reflects recombined cells (mG). Note that expression of membrane-bound GFP in the Rosa26\(^{m\text{tmg}}\) reporter is driven by a strong CAGGS promoter, such that with the imaging and filter settings chosen the weaker endogenous 3xNLS-SGFP2 signal of the *Axin2* knock-in allele itself is not detected. The embryonic timed matings and tracing experiments were performed in two independent litters for all timepoints. Scalebar is 500 μm.
**Figure 4: Visualization and lineage tracing of WNT/CTNNB1 responsive cells in postnatal tissues.** (a) Wholemount confocal microscopy images, showing a side view of the intestinal crypts of adult heterozygous Axin2<sup>P2A-rtTA3-T2A-3xNLS-SGFP2</sup> mice. Arrowhead indicates an SGFP2-positive stem cell, flanked by two SGFP2-negative Paneth cells. Scalebar is 20 μm. (b) Wholemount confocal microscopy images, showing a bottom view of the intestinal crypts of wild type (WT, top) and homozygous (HOM) Axin2<sup>P2A-rtTA3-T2A-3xNLS-SGFP2</sup> mice. In mice carrying the Axin2 knock-in allele, direct SGFP2 expression (left) can be detected in stem cells at the bottom of the crypt, but not in the neighbouring Paneth cells. Scalebar is 50 μm. Cell outlines in (a) and (b) are visualized because the animals also express a membrane-bound tdTomato protein. (c) Timeline for the experiment depicted in (d). Lineage tracing in WNT/CTNNB1-responsive cells was induced in adult mice at P84 via a single intraperitoneal injection of doxycycline (DOX). The WNT/CTNNB1-responsive lineage was traced for 54 days. (d) Wholemount confocal microscopy images, showing a side view of the intestinal epithelium from an Axin2<sup>P2A-rtTA3-T2A-3xNLS-SGFP2; tetO-Cre; Rosa26<sup>mTmG</sup></sup> triple-heterozygous animal. Left panel shows the fluorescence signal coming from the Rosa26<sup>mTmG</sup> lineage tracing reporter allele, with the membrane restricted red colour (mT) reflecting non-recombined cells and the membrane restricted green colour (mG) reflecting recombed cells. Right panel shows the transmission. Note that expression of membrane-bound GFP in the Rosa26<sup>mTmG</sup> reporter is driven by a strong CAGGS promoter, such that with the imaging settings chosen the weaker endogenous 3xNLS-SGFP2 signal of the Axin2 knock-in allele itself is not detected. Asterisk indicates a non-recombined crypt neighbouring two traced crypts. Scalebar is 20 μm. (e) Timeline for the experiment depicted in (f). Lineage tracing in WNT/CTNNB1-responsive cells was induced in pubertal mice at P30 via a single intraperitoneal injection of doxycycline (DOX). The WNT/CTNNB1-responsive lineage was traced for 3 days. (f) Confocal microscopy images of FFPE liver sections, showing the immunofluorescent detection of the recombed mTmG allele (left) in sporadic cells adjacent to the central vein. Nuclei are counterstained with DAPI (middle). Scale bar is 20 μm. (g) Timeline for the experiment depicted in (h and i). Lineage tracing in WNT/CTNNB1-responsive cells was induced in pubertal mice at P33 via a single intraperitoneal injection of doxycycline (DOX). The WNT/CTNNB1-responsive lineage was traced for 8 days. (h) Confocal microscopy images of FFPE skin section, showing the immunofluorescent detection of the recombed mTmG allele in mutiple hair follicles. Scale bar is 100 μm. (i) Close up of the boxed area in (h), showing patches of recombed cells expressing membrane-localized mG (arrowhead) in the hair follicle (green, left). Nuclei are counterstained with DAPI (gray, right). Scale bar is 50 μm. In these qualitative lineage tracing experiments, no difference was observed between male and female mice.
Intestinal organoids provide a relevant physiological context to study the bidirectional response of the reporter, since WNT/CTNNB1 signalling can be both hyperactivated and inhibited in this setting. Direct modulation of the activity of the WNT/CTNNB1 pathway with small molecule inhibitors influenced both the intensity and the number of SGFP2-positive cells present per organoid (Figure 5e–j). Exposure to CHIR99021 resulted in a prominent increase in Axin2-positive cells along the crypt axis within 24 hr (Figure 5f,i). In contrast, incubation with the PORCN inhibitor IWP-2, which blocks the secretion of endogenous WNT proteins, completely abolished SGFP2 expression within 48 hr (Figure 5g,j). This confirms that the \(Axin2^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) reporter is sensitive to direct changes in WNT/CTNNB1 signalling and dynamically reports endogenous WNT/CTNNB1 signalling in individual cells.

In conclusion, our \(Axin2^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) model offers multiple advantages over existing mouse models (Figure 1a) and as such we expect it to be useful for investigations into the role of WNT/CTNNB1 signalling in embryonic development and adult tissue stem cells. We show that the fluorescent 3xNLS-SGFP2 reporter is expressed at multiple embryonic and postnatal stages of development (Figures 3 and 4) and dynamically reports changes in WNT/CTNNB1 signalling (Figures 2 and 5). Signal intensity of the reporter can be increased by using homozygous rather than heterozygous mice.

We also demonstrate that the new, doxycycline-inducible lineage tracing driver is suitable for embryonic and postnatal traces (Figures 3 and 4). At the same time, our model does not fully recapitulate the results that we previously obtained with the 5’ \(Axin2^{lacZ}\) or 5’ \(Axin2^{CreERT2}\) knock-in models (Lim et al., 2013; Van Amerongen, Bowman, et al., 2012). Specifically, both lacZ reporter gene expression and \(CreERT2\) driven recombination were detected in a larger set of adult cell types than sGFP2 reporter expression and rtTA3-driven Cre/lox recombination in our new 3’ knock-in model.

This once again underscores that care should be taken when interpreting results from genetic reporters and, in general, when comparing expression patterns across different mouse strains. The discrepancy between the different \(Axin2\) models can be explained by one or more of the following reasons. First, our new knock-in model preserves both 5’ and 3’ transcriptional and translational regulatory control. It thus fully recapitulates endogenous \(Axin2\) expression. The direct detection of a fluorescent reporter reveals how low these expression levels really are, especially after birth. This is in agreement with the low-level and low-amplitude oscillations of \(Axin2\) expression detected by others (Sonnen et al., 2018) and something that may be obscured by the enzymatic amplification that occurs during X-gal staining in \(Axin2^{LacZ}\) mice. It may also explain reduced labelling efficiency in postnatal lineage tracing experiments. Second, the tetO-Cre line used for our studies is not leaky, but may display a high threshold to activation. In combination with the low \(Axin2\) (and
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thus low rtTA3) expression this may result in insufficient Cre activity to recombine the Rosa26mTmG allele. Whether rtTA3 or tetO-Cre, or a combination of both, is the rate limiting factor remains to be tested. Labelling efficiency might be increased in homozygous Axin2PzA-rtTA3-TzA-3xNLS-SGFP2 animals or in combination with a different tetO-Cre strain.

Summarizing, our bright fluorescent nuclear SGFP2 reporter offers straightforward detection of Axin2 expression and is expected to be compatible with live cell imaging, nuclear segmentation and thus automated cell tracking in embryonic tissues and organoids. The Axin2PzA-rtTA3-TzA-3xNLS-SGFP2 reporter is sensitive to direct changes in endogenous WNT/CTNNB1 signalling and allows monitoring of WNT/CTNNB1 sensitive cells. As such, our model can be a useful tool for the scientific community to simultaneously visualize and trace cells with active WNT/CTNNB1 signalling both in vivo and in vitro.
Figure 5: Visualization and manipulation of endogenous WNT signalling in small intestinal organoids. (a and b) Confocal microscopy (transmission) image of a fixed $Axin^{2A-}\text{rtTA3-T2A-3xNLS-SGFP2 HOM}$, $\text{Rosa26mTmG HET}$ (red) small intestinal organoid stained with anti-

lysozyme SGFP2

membrane SGFP2

nuclei SGFP2

membrane membrane membrane

DMSO CHIR99021 IWP2 DMSO CHIR99021 IWP2 DMSO CHIR99021 IWP2

SGFP2 nuclei SGFP2 nuclei SGFP2 nuclei

membrane membrane membrane

max min max min max min
Lysozyme (cyan). SGFP2 expression (depicted in red) is restricted to the crypt bottom, but does not co-localize with lysozyme staining in the large granular Paneth cells. The asterisk indicates dead material excreted into the organoid lumen that gives autofluorescence in the SGFP2 channel. SGFP2 is depicted in a red look up table for better visual representation of the subtle differences in combination with nuclear and membrane staining. Note that this organoid line is also heterozygous for the Rosa26<sup>mdTmG</sup> allele, which is used as a membrane marker in panels (c–j). (b) Close-up of the highlighted crypt section from (a). Scalebars are 30 μm (a) and 15 μm (b). For (a and b) a total of 17 organoids were imaged in a single experiment. A representative image is shown. (c) Confocal microscopy image of two crypts from a fixed Axin<sup>2P2A-rtTA3-T2A-3xNLS-SGFP2</sup> HOM; Rosa26<sup>mdTmG</sup> HET small intestinal organoid. Membrane-tdTomato is depicted in gray and 3xNLS-SGFP2 expression in red. 3xNLS-SGFP2 is expressed in a gradient along the crypt-axis, the highest expression is located at the crypt bottom and gradually declines when cells move upward. Scalebar is 30 μm. (d) Heat map showing the relative Axin2 expression superimposed on the confocal image in (c). The heat map depicts the 3xNLS-sGPF2 signal relative to a DRAQ5 nuclear staining (not shown) and is imposed on the area of the nuclei. This overlay corrects for signal intensity differences due to imaging depth and reveals differences in gene expression. Scalebar is 30 μm. For panels (c and d), a total of 14 organoids were imaged in two independent experiments. A representative image is shown. (e and f) Confocal microscopy images of crypts from fixed Axin<sup>2P2A-rtTA3-T2A-3xNLS-SGFP2</sup> HOM; Rosa26<sup>mdTmG</sup> HET (3xNLS-SGFP2, red) small intestinal organoids stained with nuclear dye DRAQ5 (gray). The organoids were treated with either DMSO for 24 hr (e), CHIR99021 for 24 hr (f), or IWP2 for 48 hr (g) before fixation. Scalebar is 30 μm. (h–j) Heat map showing relative Axin2 reporter levels superimposed on the confocal images of (e and f). The dotted lines indicate the cutoff for which the nuclei were excluded from further analysis. Note that this relative scale is not directly comparable to the one depicted in (d). Scalebar is 30 μm. For panels (e–j) a total of 51 organoids were imaged in two independent experiments (n = 14 for DMSO, n = 29 for CHIR99021, n = 8 for IWP2). Representative images of all conditions are shown.

**Methods**

### 3.1 Generation of Axin2<sup>P2A-rtTA3-T2A-3xNLS-SGFP2</sup> mice

The following considerations were made in designing the Axin2<sup>P2A-rtTA3-T2A-3xNLS-SGFP2</sup> targeting construct: P2A and T2A self-cleaving peptides were selected to ensure optimal separation of Axin2, rtTA3, and 3xNLS-SGFP2 (Daniels, Rossano, Macleod, & Ganetzky, 2014). The rtTA3 (Tet3G) transactivator was selected to ensure sensitive and tight (i.e., low background) doxycycline-dependent control for lineage tracing purposes (Das et al., 2004; Zhou, Vink, Klaver, Berkhout, & Das, 2006). The SGFP2
fluorescent protein was selected for its bright and monomeric properties (Kremers, Goedhart, Van Den Heuvel, Gerritsen, & Gadella, 2007). In anticipation of low expression levels, a triple nuclear localization signal (3xNLS) was employed to concentrate the fluorescent reporter signal for improved detection (Chertkova et al., 2017).

The Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 mouse line was generated by Ozgene Pty Ltd (Bentley WA, Australia). The final targeting construct, containing 5.5 kb and 2.8 kb homology arms, was linearized and electroporated into Bruce 4 [B6.Cg-Thy1] ES cells (Köntgen, Süss, Stewart, Steinmetz, & Bluethmann, 1993). Homologous recombinant ES cell clones (7/95) were identified by Southern hybridization and 2 independent clones were injected into goGermline blastocysts (Koentgen et al., 2016). Male chimeric mice were obtained and crossed to FLP females (OzFlp; a Rosa26 transgenic FLP deleter strain) to establish heterozygous germline offspring on a pure C57BL/6 background. The final colony was established from one of these ES cell derived chimeras. Cloning, sequencing and targeting details are provided as supplementary files available via https://osf.io/6cyab/.

3.2 Mice
All mice used for this study were maintained under standard housing conditions. Animals were housed in open or IVC cages on a 12 hr light/dark cycle and received food and water ad libitum. All experiments were performed in accordance with institutional and national guidelines and regulations and approved by the Animal Welfare Committee of the University of Amsterdam.

Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 mice were backcrossed to C57BL/6JRccHsd (Envigo) or FVB/NHan®Hsd (Envigo). These mice are currently being deposited with a public repository (official strain nomenclature: B6(Cg)-Axin2<tm1Rva>/Rva MGI:6360059). Most experiments were performed on a mixed C57BL/6 and FVB background, unless noted otherwise.

Other strains used: Rosa26 mTmG [mixed background, official strain name B6.129(Cg)-Gt(Rosa)26Sortm4(Actb-ttdTomato,-EGFP)Luo/J, Jackson labs stock number 007676, (Muzumdar, Tasic, Miyamichi, Li, & Luo, 2007)]; tetO-Cre(Bjd) [mixed background, official strain name Tg(tetO-cre)LC1Bjd, Infrafrontier EMMA ID 00753, (Schönig, Schwenk, Rajewsky, & Bujard, 2002)]; tetO-FLAG-Wnt5a [FVB background, official strain name FVB/N-Tg(tetO-Wnt5a)17Rva/J, Jackson labs stock number 022938, (Van Amerongen, Fuerer, Mizutani, & Nusse, 2012)]; Axin2CreERT2 [mixed background, official strain name B6.129(Cg)-Axin2tm1(cre/ERT2)Rnu/J, Jackson labs stock number 018867, (Van Amerongen, Bowman, et al., 2012)].

For timed matings, female mice were screened for the presence of a vaginal plug. When a plug was found, this timepoint was recorded as E0.5. For embryo
isolation, pregnant dams were euthanized at the indicated timepoints and embryos were isolated for further processing. Yolk sacs were used for genotyping all embryos.

For embryonic lineage tracing, pregnant mice were injected intraperitoneally with 375 μg doxycycline (75 μl of a filter sterilized, 5 mg/ml solution of Doxycycline Hyclate [Merck] dissolved in PBS). For postnatal lineage tracing, mice were injected intraperitoneally with a filter sterilized solution of 2 mg doxycycline (Merck), dissolved in PBS (100 or 200 μl of a filter sterilized, 20 mg/ml or 10 mg/ml stock solution). We verified that no leakiness (i.e., recombination of the Rosa26mTmG reporter in the absence of doxycycline) was detected in uninjected triple heterozygous animals. As negative controls for imaging experiments, we used littermates lacking the tetO-Cre allele, and thus also not showing recombination of the Rosa26mTmG reporter.

### 3.3 PCR genotyping

Ear clips or yolk sacs were lysed either overnight (ear clips) or for 2 hr (yolk sacs) at 55°C in 200 μl of Direct PCR tail lysis buffer (Viagen) supplemented with 200 μg/ml Proteinase K (20 mg/ml stock solution). Proteinase K was inactivated by incubating the samples at 85°C for 15–45 min. Samples were cooled to room temperature and spun down (2 min at 14,000 rpm), after which 1 μl of the supernatant was used as input for a standard 20 μl PCR reaction with 0.4 μl of Phire II polymerase (ThermoFisher, #F-124S). PCR conditions were as follows: initial denaturation at 98°C for 30 s, followed by 30 or 35 cycles of denaturation at 98°C for 5 s, annealing at the relevant temperature for 5 s, extension at 72°C for 10 s, followed by a final extension step of 72°C for 1 min. Samples were cooled to 16°C and analysed on a 2% agarose gel in standard TAE buffer. Primer sequences, annealing temperatures, number of cycles and expected band sizes are detailed in Table S3.

### 3.4 Isolation and culture of mouse embryonic fibroblasts

Mouse embryo fibroblasts (MEFs) were isolated at E13.5 as described previously (Van Amerongen et al., 2005). MEFs were cultured in DMEM supplemented with Glutamax (ThermoFisher Scientific), 10% FBS (ThermoFisher Scientific), 1% penicillin/streptomycin (ThermoFisher Scientific) and 50 μM β-mercaptoethanol (Merck) at 37°C and 5% CO2. To induce WNT/CTNNB1 signalling in these cells, CHIR99021 (BioVision) was dissolved in DMSO (Sigma Aldrich) at 6 mM and added at the concentrations described.

### 3.5 Isolation and culture of mouse intestinal organoids

Mouse intestinal organoids were established as previously described (Sato et al., 2009). Crypts were isolated from the entire length of the small intestine of one Axin2P2A-rtTA3-T2A-3xNLS-SGFP2(HOM); Rosa26mTmG(HET) animal (used for Figure 5), one Axin2P2A-rtTA3-T2A-3xNLS-SGFP2(HOM) animal and one Axin2P2A-rtTA3-T2A-3xNLS-SGFP2(HET) animal.
animal (used for the comparison of heterozygous and homozygous organoids in Figure S8) and used to establish individual organoid lines. Organoids were cultured in 10 μl Matrigel droplets (Corning) in culture medium containing advanced DMEM/F12 (ThermoFisher Scientific) supplemented with 100 U/ml Penicillin/Streptomycin (ThermoFisher Scientific), 2 mM Glutamax (ThermoFisher Scientific), 10 mM HEPES (ThermoFisher scientific), 1×B27 supplement (ThermoFisher Scientific) and 1.25 mM N-acetylCysteine (Sigma Aldrich), freshly added EGF (50 ng/ml, PeproTech), recombinant murine Noggin (100 ng/ml, PeproTech) and recombinant murine R-spondin 1 (500 ng/ml, Sinobiological Inc.) at 37˚C and 5% CO₂. For passaging, cell culture medium was removed and Matrigel was broken into small pieces by scraping, followed by vigorous pipetting with ice-cold advanced DMEM/F12. Crypts were centrifuged at 200g for 5 min at 4˚C. The supernatant was carefully removed, the pellet was resuspended in Matrigel and plated on pre-warmed plates. Medium was refreshed every other day and organoids were split once a week in a 1:3 ratio. To modulate the levels of WNT/CTNNB1 signalling at day 5 after plating, 10 μM CHIR99021 (BioVision), or 2 μM IWP-2 (Calbiochem) were added for 24 or 48 hr before fixation.

3.6 RNA isolation, cDNA synthesis, and qRT-PCR analysis
Total RNA was isolated from confluent MEF cultures using TRIzol (ThermoFisher Scientific) according to the manufacturer’s guidelines. Residual genomic DNA was removed by RQ1 RNase-free DNase treatment (Promega) according to the manufacturer’s instructions. The RNA concentration was determined using a Nanodrop spectrophotometer. cDNA was synthesized from 2 μg RNA using SuperScript IV Reverse Transcriptase (Invitrogen) and Random Hexamers (ThermoFisher Scientific), according to the manufacturer’s instructions. RiboLock RNase-inhibitor (ThermoFisher Scientific) was added during the reverse transcriptase reaction. The resulting cDNA was diluted 10-fold for subsequent qRT-PCR analysis.

qRT-PCR was performed using a QuantStudio 3 (Applied Biosystems). PCR reactions (total volume 20 μl) were set up containing 13 μl RNase-free H₂O, 4 μl 15× HOT FIREPol EvaGreen qRT-PCR Mix Plus ROX (Solis Biodyne), 0.5 μl of each specific forward and reverse primer (10 μM stock) and 2 μl of diluted cDNA template. The reactions were set up in technical triplicates in 96-well qPCR plates. One negative control (no-RT) reaction was included for each sample/primer combination. Thermal cycling was performed, starting with a hold stage at 50˚C for 2 min, an initial step at 95˚C for 15 min, followed by 40 cycles of denaturation at 95˚C for 15 s and annealing at 60˚C for 1 min. Each run was completed with a melting curve analysis. Primer sequences are detailed in Table S3.
3.7 Protein isolation and western blot analysis

Cells were harvested by lysis in RIPA buffer (150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, 0.1% SDS, 50 mM Tris–HCl, pH 8.0) supplemented with protease inhibitors (Roche). Protein concentration was determined using a Pierce BCA protein kit (BioRad), following the manufacturer’s instructions. Samples were prepared in equal amounts of protein in loading buffer [125 mM Tris–HCl (pH 6.8), 50% glycerol, 4% SDS, 0.2% Orange-G, 10% betamercaptoethanol (Merck)] and boiled at 95°C. Denatured samples were run on a 10% SDS-PAGE gel and transferred to a 0.2 μM nitrocellulose membrane (Biorad) at 30 V for 16 hr; or at 260 mA for 3 hr, both at 4°C. The blot was blocked for 1 hr at room temperature in Odyssey Blocking Buffer (LI-COR) diluted 1:1 in TBS, followed by overnight incubation with primary antibody at 4°C. Primary antibodies were used to recognize GFP (1:1,000, Thermo Fisher, A-6455), HSP90α/β (1:1,000, Santa Cruz Biotechnology, sc-13119), Flag M1 (1:2,000, Sigma, F3040), and active CTNNB1 (1:1,000, Cell Signalling Technology, 8814). After incubation with the primary antibody, blots were washed extensively with TBS-Tween (0.1%) before incubating with the secondary antibodies for 1 hr at room temperature. Secondary antibodies were IRDye 680LT anti-mouse (1:20,000, LI-COR) and IRDye 800CW anti-rabbit (1:20,000, LI-COR). For Flag M1 antibody, 1 mM calcium was added to all solutions from the addition of the first antibody on. Blots were imaged with an Odyssey Fc Dual-Model Imaging System (LI-COR). Image visualization/representation for Western blots was performed using LI-COR Image Studio Lite software. Panels were cropped in Photoshop. Original Western blots are available via https://osf.io/6cyab/.

3.8 Immunofluorescence and immunohistochemistry

GFP expression was assessed using standard immunostaining methods. 4% PFA-fixed (Merck) and paraffin-embedded tissues were cut into 15 μm sections (IHC) or 5 μm sections (IF) and floated on water. Tissues sections were picked up onto a superfrost plus slide (Thermo Scientific), deparaffinized, and then rehydrated. Antigen retrieval was performed in Sodium Citrate buffer (10 mM Sodium Citrate, 0.05% Tween 20, pH 6.0) by incubating the slides for 2.5 hr at 85°C, followed by cooling on ice. The slides were then washed with PBS for 5 min.

For immunohistochemistry, the slides were rinsed with demi water. Endogenous peroxidase activity was blocked by incubation in 0.3% hydrogen peroxide in methanol for 30 min, and then the tissues sections were rinsed with PBS. Next, tissues were circled with an ImmEdge pen (Vectorlabs) and incubated for 20 min with diluted normal blocking serum from Vectastain Elite ABC kit (PK-6101 Vector labs). Diluted GFP antibody (rabbit, GFP polyclonal antibody, A-6455 Invitrogen), was prepared by using 1:5,000 GFP antibody in blocking serum. Without rinsing the slides, this antibody was incubated for 30 min at room temperature. As a negative control, samples were only stained with the secondary
antibody. The slides were washed with PBS for 5 min for three times. Then the secondary antibody was added for 30 min, followed by three washes with PBS. At this point, Vectastain ABC reagent was prepared according to manufacturer's instructions, and allowed to stand for 30 min before use. The ABC reagent was added to the slides for 30 min, followed by three washes with PBS. Slides were rinsed in demi water and DAB peroxidase (ImmPACT HRP SK-4105) was added for 2–3 min, followed by a demi water wash. Sections were counterstained with 50% hematoxylin, dehydrated in a graded series of ethanol dilutions followed by Histoclear II (National Diagnostics), and mounted with a coverslip using Omnimount (National Diagnostics).

For immunofluorescence, the slides were rinsed with PBS and tissues were circled with an ImmEdge pen (Vectorlabs) and incubated for 45 min with 2.5% BSA in PBS. Without rinsing the slides, the GFP antibody (chicken, GFP polyclonal antibody Abcam ab13970), diluted 1:400, was incubated over night at room temperature. As a negative control, samples were only stained with the secondary antibody. The slides were washed with PBS for 5 min for three times. Then the secondary antibody, Alexa Fluor 488 (Invitrogen A11039), diluted 1:1,000, and DAPI (Invitrogen D1306, used at 1 ug/ml, stock solution 5 mg/ml in dimethylformamide) was added for 1 hr, followed by 3 washes with PBS. Next the slides were mounted with a coverslip using Mowiol (6 g glycerol, 2.4 g polyvinylalcohol 4–88 [Sigma, 81381], 6 ml MQ and 12 ml 0.2 M Tris HCL pH 8.5).

3.9 Microscopy
For imaging MEFs in the presence of DAPI, cells were fixed for 15 min in fresh 4% PFA (methanol free ampules, Thermo Scientific) diluted in PBS, and mounted in Mowiol with 1 μg/ml DAPI (Invitrogen). Fixation was carried out at 37˚C to prevent quenching of the endogenous fluorescence signal. Fixed cells were imaged using a Nikon A1 microscope. Fluorophores were excited as follows: DAPI at 405 nm, SGFP2 at 488 nm. Emission was detected as follows: DAPI 425-480 nm, SGFP2 500-555. Images were acquired using a 40× oil objective.

For wholemount confocal microscopy of embryos and tissues, samples were fixed in 4% formaldehyde for histology, buffered pH 6.9 (Merck) or 4% PFA made from 16% PFA (methanol free ampules, Thermo Scientific) diluted in PBS for 1 hr at room temperature. Tissues were dehydrated through a graded ethanol series and cleared in methylsalicylate (Sigma) as described previously (Van Amerongen, Bowman, et al., 2012) or through a graded glycerol series, as indicated in the figure legends. Imaging of whole-mount embryos, intestine, liver and skin was performed on a Leica SP8 confocal microscope. Fluorophores were excited as follows: DAPI at 405 nm, SGFP2 at 488 nm, tdTomato at 561 nm. Emission was detected as follows: DAPI 425–480 nm, SGFP2 500–555 nm, tdTomato 567–730 nm. All images were acquired using a 10× dry, 20× dry, or 40× oil objective.
Images of intestinal organoids were captured using confocal microscopy on a Leica SP8 with the LasX software. For imaging, the samples were cultured and imaged on glass chamber slides (Ibidi). Intestinal organoids were fixed in 4% formaldehyde for histology, buffered pH 6.9 (Merck) for 15 min at room temperature, the reaction was quenched with 0.15 M Glycine and the samples were permeabilized with 0.5% TritonX-100 for 10 min. The organoids were either incubated with 1 μM DRAQ5 for 10 min at room temperature, or blocked with 5% BSA blocking solution for 2 hr. To visualize Paneth cells the samples were stained with 1:500 primary antibody anti-lysozyme (Agilent) overnight at 4˚C, and 1:1,000 secondary antibody Alexa Fluor 647 (Invitrogen) for 1 hr at room temperature. Fluorophores were excited as follows: sGPF2 at 488 nm, tdTomato at 561 nm, Alexa Fluor 647/anti-lysozyme and DRAQ5 at 633 nm. Emission was detected as follows: SGFP2 HyD 494–540 nm, tdTomato HyD 568–625 nm, Alexa Fluor 647/anti-lysozyme PMT 642–696 nm, DRAQ5 PMT 665–740 nm. All images were acquired using a 40× oil or 63× water objective.

For imaging immunohistochemistry slides, pictures were taken using an Axio scope A1 microscope with a Nikon Ri2 camera and NIS F freeware. For imaging immunofluorescence slides, Pictures were taken using a Nikon A1 confocal microscope and NIS elements AR software.

Wholemount images of embryos were taken on a Leica stereomicroscope MZFLIII equipped with a Nikon Digital sight DS-Fi2 and NIS elements F freeware software.

3.10 Microscopy image analysis

Fluorescence microscopy images were processed in Fiji (Schindelin et al., 2012) using the Image 5D plugin and custom-built approaches. For the quantification of SGFP2 expression in MEFs (Figure 2c,d and Figure S2), ROIs surrounding single nuclei were selected manually in the DAPI channel using the magic wand tool. The SGFP2 nuclear signal was normalized over DAPI intensity. For each condition, three images were analyzed. This was repeated for three independent MEF lines. Data for one of the lines is shown in Figure 2, data for the other two lines are shown in Figure S2. For Figure 5, heatmaps were drawn as follows: ROIs surrounding single nuclei were selected manually in the DRAQ5 channel using the Freehand selection tool. The SGFP2 nuclear signal was normalized over DRAQ5 intensity. To determine the relative Axin2 expression a ratio of SGFP2 over DRAQ5 was calculated in Excel and imported in Fiji. An overlay was made that draws a heat map in selected ROIs based on this ratio with the ROI Color Coder plugin (Ferreira et al., 2017).

Color scheme choices: SGFP2 signal is shown in green, except for Figure 5 and Figure S6, where a red LUT was chosen to be able to overlay the SGFP2 and the nuclear signal. All lineage tracing experiments are depicted in green and red to maintain the original mTmG reporter set up (i.e., a switch from tdTomato to eGFP).
3.11 Software, statistics, and online databases
The following software was used: Fiji (https://imagej.net/Fiji/Downloads) for image analysis (Schindelin et al., 2012), R (R Development Core Team, 2017) and R studio (https://rstudio.com/products/rstudio/download/) to generate the dotplots and violin plots in Figure 2 using the ggplot2 package (Wickham, 2009), ThermoFisher Cloud software and Microsoft Excel for qRT-PCR analysis using the ddCt method, LI-COR Image Studio Lite for Western blot analysis, Graphpad PRISM for generating graphs. Final figures were compiled in Adobe Illustrator. For Figure 1a, information was retrieved from http://www.findmice.org on the seventh of January 2020.

Acknowledgements

We thank our animal caretakers for taking daily care of the mice, the van Leeuwenhoek Centre for Advanced Microscopy (LCAM, Section Molecular Cytology, Swammerdam Institute for Life Sciences, University of Amsterdam) for the use of their facilities and LCAM staff for sharing their expertise and providing technical support, Jeroen van Zon (AMOLF) for sharing the anti-Lysozyme antibody, all colleagues for stimulating discussions and Tanne van der Wal, Larissa Mourao and Dorus Gadella for feedback on the manuscript. This work was supported by a MacGillavry fellowship from the University of Amsterdam (to RvA), a career development award from KWF Kankerbestrijding (2013-6057, to RvA), a research grant from KWF Kankerbestrijding/ Alpe d’HuZes (2015-8014, to RvA) and an NWO-ALW VIDI grant (864.13.002, to RvA).
Supplementary Figures

**Figure S1: Details on the targeting strategy.** (a) Schematic representation of the mouse Axin2 locus (chr11:108920349-108950781, mm10 coordinates). (b) Most existing Axin2 knock-in strains, including our previously generated Axin2^CreERT2 driver and the frequently used Axin2^lacZ reporter, target the 5′ end of the gene by introducing the knock-in cassette at the start codon in exon 2. This disrupts the endogenous Axin2 coding sequence. (c) Cartoon depicting details of the targeting construct and its homologous recombination
into the 3′ UTR of the Axin2 locus. The targeting construct contained 5.6 kb (5′) and 2.8 kb (3′) homology arms. The Axin2 stop codon (TGA) was mutated and immediately followed by the P2A-rTA3-T2A-3xNLS-SGFP2 multicistronic knock-in cassette. The PGK-Neo-polyA cassette, flanked by FRT sites, was cloned immediately downstream of the knock-in cassette in the reverse orientation and used for selection of embryonic stem cells carrying the recombined allele. After crossing founder mice with an FLP deleter strain, the remaining FRT site immediately downstream of the knock-in cassette, otherwise leaving the Axin2 locus intact.

dose-dependent induction of 3xNLS-SGFP2 expression in a second MEF isolate

dose-dependent induction of 3xNLS-SGFP2 expression in a third MEF isolate
Figure S2: Dose-dependent induction of nuclear sGFP2 in MEFs. This figure shows the quantification of nuclear sGFP2 expression for two additional MEF isolates, supplementing the data shown in (g and h). Fixed MEFs were counterstained with DAPI to allow nuclear segmentation, after which the relative SGFP2 expression levels were calculated by correcting for the fluorescence intensity of the DAPI signal.

Figure S3: Wholemount detection of SGFP2 expression in Axin2P2A-rtTA3-T2A-3xNLS-SGFP2 embryos. Brightfield (top row) and fluorescent (bottom row) images of freshly isolated E10.5 wildtype (left), heterozygous (middle) and homozygous (right) embryos. A subtle difference in SGFP2 expression at the developing limb bud, the branchial arches, and along the dorsal neural tube, including the developing brain can be seen between heterozygous and homozygous embryos. Although we verified all genotypes by PCR, this difference in GFP intensity allowed us to distinguish wildtype, heterozygous and homozygous embryos by eye. All embryos depicted were imaged with the same exposure times (30 ms for brightfield images, 8 s for a GFP long pass filter) under a dissecting microscope. Scalebar is 500 μm. Note that size differences between embryos were not linked to the genotype, and thus most likely represent natural variation between individual embryos of the same litter.
Figure S4: Immunohistochemical detection of SGFP2 in FFPE samples. Brightfield image showing the detection of nuclear SGFP2 in a formalin fixed, paraffin embedded (FFPE) tissue section from a homozygous Axin<sub>2</sub>ΔTA3-T2A-3xNLS-SGFP2 adult (P49) animal. SGFP2 was visualized using an anti-GFP antibody and immunohistochemical detection. Nuclei are counterstained with hematoxylin. Scalebar is 10 μm. Of note, we were not capable of robustly detecting SGFP2-positive cells postnatally in other organs tested (mammary gland, liver, hair follicle and interfollicular epidermis), which most likely reflects differences in the absolute levels of WNT/CTNNB1 signalling across tissues.
Figure S5: Short-term lineage trace of WNT/CTNNB1-responsive cells in intestinal tissue. Lineage tracing in WNT/CTNNB1-responsive cells was induced in pubertal mice at P35 via a single intraperitoneal injection of doxycycline (DOX) for 24 hr (a) or 48 hr (b and c). Experimental timelines are indicated on top. Wholemount confocal microscopy images showing a side view (a, b) and bottom view (c) of the intestinal epithelium from triple-heterozygous Axin2P2A-rtTA3-T2A-3xNLS-SGFP2; tetO-Cre; Rosa26mTmG animals. The fluorescence signal is coming from the Rosa26mTmG lineage tracing reporter allele, with the red colour (mT) reflecting non-recombined cells and the green colour (mG) reflecting recombined cells 3 days after induction. Recombined cells can be detected in the intestinal crypt as early as 24 hr after labelling in the intestinal (a). After 48 hr a substantial portion of cells in the crypt (b and c) can be detected with the concentration of DOX used. Scalebar is 100 μm.

Figure S6 Lineage tracing of WNT/CTNNB1 responsive cells in intestinal tissue. Lineage tracing in WNT/CTNNB1-responsive cells was induced in pubertal mice at P30 via a single intraperitoneal injection of doxycycline (DOX). A timeline for the experiment is depicted on top. Wholemount confocal microscopy images showing a side (top) and bottom view of the intestinal epithelium from triple-heterozygous Axin2P2A-rtTA3-T2A-3xNLS-SGFP2; tetO-Cre; Rosa26mTmG animals. The WNT/CTNNB1-responsive lineage was traced for 3 and 6 days. The left panel shows a control sibling without TetO-Cre allele, in which only the 3xNLS-SGFP2
signal from the Axin2 locus is visible. The middle panel shows the fluorescence signal coming from the Rosa26<sup>mTmG</sup> lineage tracing reporter allele, with the red colour (mT) reflecting non-recombined cells and the green colour (mG) reflecting recombined cells 3 days after induction. The crypts show recombined cells, with the progeny of these stem cells starting to populate the villus compartment. The right panel shows recombined cells 6 days after induction of lineage tracing. Villi from recombined crypts are completely green. Scalebar is 100 μm.
Figure S7: Lineage tracing of WNT/CTNNB1 responsive cell in postnatal tissues. Lineage tracing in WNT/CTNNB1-responsive cells was induced in pubertal mice at P33 via a single intraperitoneal injection of doxycycline (DOX). A timeline for the experiment depicted is shown on top. Wholemount confocal microscopy images showing different tissues from triple-heterozygous $\text{Axin2}^{P2A-\text{rtTA3-T2A-3xNLS-SGFP2}_2}; \text{tetO-Cre}; \text{Rosa26}^m\text{mTmG}$ animals. The WNT/CTNNB1-responsive lineage was traced for 8 days. The bottom panel shows a control sibling without TetO-Cre allele where only the 3xNLS-SGFP2 signal from the $\text{Axin2}^{P2A-\text{rtTA3-T2A-3xNLS-SGFP2}_2}$ is detectable. (a) Wholemount confocal microscopy images showing a bottom (left) and side (right) view of the intestinal epithelium. The top panels show the fluorescence signal coming from the $\text{Rosa26}^m\text{mTmG}$ lineage tracing reporter allele, with the red colour (mT) reflecting non-recombined cells and the green colour (mG) reflecting recombined cells. Both the crypt and villi compartments show a majority of recombined cells. (b) Wholemount confocal microscopy images of fixed and cleared liver, showing the recombinant mTmG allele in sporadic cells adjacent to the central vein (top). (c) Wholemount confocal microscopy images of fixed and cleared skin, showing the recombinant mTmG allele in multiple hair follicles (top). Scale bar is 100 μm. Of note, we were not capable of tracing cells in the mammary epithelium and interfollicular epidermis, which is likely due to differences in the absolute levels of WNT/CTNNB1 signaling across tissues, doxycycline induced versus tamoxifen induced lineage tracing, the tetO-Cre line used, or a combination of the two.
**Figure S8: SGFP2 signal intensity in heterozygous versus homozygous small intestinal organoids.** (a–d) Confocal microscopy images of crypts from fixed Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HOM}\) and Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HET}\) small intestinal organoids stained with nuclear dye DRAQ5. SGFP2 is depicted in red and DRAQ5 in grey. (a and b) were imaged with settings optimized for Axin2\(^{3xNLS-SGFP2}\) \(\text{HET}\) organoids and (c and d) with settings optimal for Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HOM}\) organoids. Scalebar is 30 μm. For panels (a–d) \(n = 6\) Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HET}\) organoids and \(n = 7\) Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HOM}\) were imaged in a single experiment. (e–g) Confocal microscopy images of crypts from fixed Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HET}\) small intestinal organoids stained with nuclear dye DRAQ5. Organoids were imaged with settings optimized for Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) \(\text{HET}\) organoids. Samples were treated with DMSO for 24 hr (e), CHIR99021 for 24 hr (f), or IWP2 for 48 hr (g) prior to fixation. Scalebar is 30 μm. For panel (e–g), a total of 18 organoids were imaged in a single experiment (\(n = 9\) for DMSO, \(n = 5\) for CHIR99021, \(n = 4\) for IWP2). Representative images of all conditions are shown.


**Movie S3 Traced Axin2-positive cells in the liver.** Wholemount confocal microscopy Z-stack through a piece of formalin fixed, cleared liver tissue from a triple-heterozygous Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2};\ tetO-Cre;\ Rosa26\(^{mTmG}\) mouse that was traced for 8 days after receiving a single intraperitoneal injection of doxycycline mid puberty. The fluorescence signal comes from the Rosa26\(^{mTmG}\) lineage tracing reporter allele, with the red colour (mT) reflecting non-recombined cells and the membrane-localized green colour (mG) reflecting cells that have recombined the reporter. Movie at [https://onlinelibrary.wiley.com/action/downloadSupplement?doi=10.1002%dvg.23387&file=dvg23387-sup-0011-MovieS3.mov](https://onlinelibrary.wiley.com/action/downloadSupplement?doi=10.1002%dvg.23387&file=dvg23387-sup-0011-MovieS3.mov)

**Supplementary Table 1. Mendelian inheritance of the 3’ Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) allele.** Homozygous Axin2\(^{P2A-rtTA3-T2A-3xNLS-SGFP2}\) mice are born at the expected mendelian ratios from
heterozygous intercrosses on a C57BL/6 background. (Chi-square test, P=0.61 for both sexes combined).

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Supplementary Table 2. Non-mendelian inheritance in *Axin2* knock-in mice

By design, all 5’ *Axin2* knock-in alleles generated to date (*Axin2*\textsubscript{lacZ}, *Axin2*\textsubscript{mTq2}, *Axin2*\textsubscript{CreERT2}) are predicted to disrupt endogenous *Axin2* expression (Supplementary Figure 1). However, mice heterozygous for *Axin2* were previously reported to be phenotypically normal (van Amerongen et al., 2012; Lustig et al., 2001; Zeng and Nusse, 2010).

Although we have bred *Axin2*\textsubscript{CreERT2} mice (targeting performed in ES cells from a 129/Sv background) without any trouble at multiple different animal facilities in back-crosses to both C57BL/6J and FVB/N, we noticed that even heterozygous animals were present upon weaning at sub-mendelian ratios after rederiviation onto a C57BL/6JRj background (A, Chi-square test, P=0.00077 for both sexes combined). This coincided with the presence of a skull phenotype in some heterozygous animals, resembling that described for homozygous *Axin2*\textsubscript{lacZ} mice by (Yu et al., 2005). Sub-mendelian inheritance of the knock-in allele remained apparent during the first three generations of heterozygous backcrossing of the mice from A onto FVB/N (B, Chi-square test, P=3.5x10\textsuperscript{-6} for both sexes combined), after which wildtype and heterozygous mice were again present upon weaning at the expected ratios (C, Chi-square test, P=0.85 for both sexes combined).

These data were collected between September 2014 and April 2018 as part of our regular colony maintenance and genotyping efforts. Note that this information has been used to update the strain description on the Jackson laboratory website in August 2017. We would also like to point out that Jackson labs now reports that homozygous *Axin2*\textsubscript{CreERT2} mice are born “at a significantly reduced frequency (~5% in heterozygous crosses)”, as stated on their website (https://www.jax.org/strain/018867, accessed 5 June 2020). These observations suggest that the 5’ *Axin2*\textsubscript{CreERT2} knock-in allele is haploinsufficient on a C57BL/6JRj background. At present we have no explanation for this observation, nor do we have an explanation for why neither of these effects (haploinsufficiency and reduced numbers of homozygous animals) have been observed in *Axin2*\textsubscript{lacZ} mice, which carry a knock-in cassette at the exact same location.
### Supplementary Table 3. Primer sequences

**PCR genotyping:**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Primer</th>
<th>Description</th>
<th>Sequence (5’ to 3’)</th>
<th>details</th>
<th>Product</th>
</tr>
</thead>
<tbody>
<tr>
<td>Axin2&lt;sup&gt;P2A-rtTA3-T2A-3xNLS-SGFP2&lt;/sup&gt;</td>
<td>RVA 1786, RVA 1787, RVA 1789</td>
<td>Ozgene 01F (WT PCR)</td>
<td>CGAGCTTTTCCTGTCTTCTCTTAAAGGAATATTTCGTGGCTGTTGCCGAGCAACACGTCTATATCAG</td>
<td>T&lt;sub&gt;ann&lt;/sub&gt; = 52°C, 30 cycli</td>
<td>Wild type allele = 257 bp, Knock-in allele = 461 bp</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ozgene 02R (common)</td>
<td>GAATATTTCGTGGCTGTTGCCACACCCTTCTCCAATGTACTG</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ozgene 04F (mut PCR)</td>
<td>CAACAGCCACAACGTCTATATCAG</td>
<td></td>
<td></td>
</tr>
<tr>
<td>tetO-Wnt5a</td>
<td>RVA 6, RVA 7</td>
<td>Fw, Rv</td>
<td>ACAAAAGACGATGACGACAAGCGCACCTTCTCCAATGTACTG</td>
<td>T&lt;sub&gt;ann&lt;/sub&gt; = 55°C, 30 cycli</td>
<td>Transgenic product = 200 bp</td>
</tr>
<tr>
<td>tetO-Cre(Bjd)</td>
<td>RVA 2422, RVA 2423</td>
<td>Fw, Rv</td>
<td>TTACAGATGACATATCGAGGTAACCCAGTAGATCCAGAGG</td>
<td>T&lt;sub&gt;ann&lt;/sub&gt; = 58°C, 30 cycli</td>
<td>Transgenic product = 490 bp</td>
</tr>
<tr>
<td>Rosa&lt;sup&gt;26mTmG&lt;/sup&gt;</td>
<td>RVA 284, RVA 285, RVA 286</td>
<td>WT Fw, WT Rv, Mut Rv</td>
<td>CTCTGGCTGCTCTCTGGCGTTCTGAG</td>
<td>T&lt;sub&gt;ann&lt;/sub&gt; = 58°C, 35 cycli</td>
<td>Wild type allele = 330 bp, Knock-in allele = 250 bp</td>
</tr>
</tbody>
</table>

**qRT-PCR:**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer</th>
<th>Description</th>
<th>Sequence (5’ to 3’)</th>
</tr>
</thead>
</table>
| Axin2      | RVA 12, RVA 13 | Axin2 Fw, Axin2 Rv | AGCTGTGTGTCACCTACT
|            |         |             | CAGGCAATTTCGTCACCTCAG |
| Rpl13a     | RVA 413, RVA 414 | Rpl13a Fw, Rpl13a Rv | CCCCTCACCATGACAGAA
|            |         |             | GCCCGAGTGAACAAACTT |
| SGFP2      | RVA 1784, RVA 1785 | GFP Fw, GFP Rv | CCAGGACCGACCTATCTTCT
|            |         |             | TGCCGTCCTTGCTTGTGTCG |
| rtTA3      | RVA 276, RVA 277 | rtTA Fw, rtTA Rv | AGCGAGTCATGGCAAGA
|            |         |             | GGGGAAGCCTTGTGACA |
A novel Axin2 knock-in mouse model

References


