Constitutive Musashi1 expression impairs mouse postnatal development and intestinal homeostasis

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ABSTRACT Evolutionarily conserved RNA-binding protein Musashi1 (Msi1) can regulate developmentally relevant genes. Here we report the generation and characterization of a mouse model that allows inducible Msi1 overexpression in a temporal and tissue-specific manner. We show that ubiquitous Msi1 induction in ~5-wk-old mice delays overall growth, alters organ-to-body proportions, and causes premature death. Msi1-overexpressing mice had shortened intestines, diminished intestinal epithelial cell (IEC) proliferation, and decreased growth of small intestine villi and colon crypts. Although Lgr5-positive intestinal stem cell numbers remained constant in Msi1-overexpressing tissue, an observed reduction in Cdc20 expression provided a potential mechanism underlying the intestinal growth defects. We further demonstrated that Msi1 overexpression affects IEC differentiation in a region-specific manner, with ileum tissue being influenced the most. Ileal of mutant mice displayed increased expression of enterocyte markers, but reduced expression of the goblet cell marker Mucin2 and fewer Paneth cells. A higher hairy and enhancer of split 1:mouse atonal homolog 1 ratio in ilea from Msi1-overexpressing mice implicated Notch signaling in inducing enterocyte differentiation. Together, this work implicates Msi1 in mouse postnatal development of multiple organs, with Notch signaling alterations contributing to intestinal defects. This new mouse model will be a useful tool to further elucidate the role of Msi1 in other tissue settings.

INTRODUCTION
Most metazoans develop from a single fertilized egg that divides repeatedly to produce an embryo with pluripotent stem cells capable of forming the diverse tissue structures of an organism. Precise spatial and temporal gene expression, in response to internal and external developmental cues, regulates the biological events that occur during embryonic and fetal development (Wilczynski et al., 2012). Proper coordination of cellular processes such as cell patterning, proliferation, differentiation, and survival is crucial for normal tissue development and functioning. As such, perturbations in the genetic control systems governing these cellular processes can have deleterious effects on a developing organism or on the health of an adult. For example, dysregulated gene expression is associated with various birth defects (Bittel et al., 2011) and cancers (Sanz-Pamplona et al., 2014). Therefore, identifying and characterizing molecular regulators of gene expression could illuminate potential therapeutic targets for human diseases.

RNA-binding proteins (RBPs) are now appreciated as essential players in the posttranscriptional control of gene expression. One such RBP is Musashi1 (Msi1), an evolutionary conserved RBP that was originally discovered in Drosophila melanogaster (Nakamura et al., 1994) and has homologues in mouse (Sakakibara et al., 1996), human (Good et al., 1998), rat (Nagata et al., 2006), and zebrafish (Shibata et al., 2012) to name a few. Mammalian Msi1 regulates various RNA metabolic processes through binding to motifs in the coding sequences (CDS), introns, and untranslated regions (UTRs) of
target mRNAs (Imai et al., 2001; Ohyama et al., 2012; Katz et al., 2014; Zearfoss et al., 2014; Li et al., 2015; Uren et al., 2015). The best-characterized role of mammalian Mis1 is in translational repression of targets (Imai et al., 2001; Battelli et al., 2006; Spears and Neufeld, 2011; Katz et al., 2014; Li et al., 2015; Chen et al., 2017). Mis1 interacts with sequence-specific motifs in the 3′-UTRs of target mRNAs and competes with eIF4G for interaction with the poly(A)-binding protein, consequently inhibiting translation initiation (Kawahara et al., 2008). It has also been shown that Mis1 can stabilize RNA (Cambuli et al., 2015; Nahas et al., 2016), promote translation (Kuwako et al., 2010; Uren et al., 2015; Cragle et al., 2019; Lin et al., 2019), and influence alternative splicing (Li et al., 2015; Uren et al., 2015; Murphy et al., 2016) of direct targets. In addition, numerous direct mRNA targets of Mis1 that are involved in key cellular processes such as cell cycle, proliferation, metabolism, survival, and migration have been identified using both in vitro and in vivo systems (de Sousa Abreu et al., 2009; Vo et al., 2012; Li et al., 2015; Uren et al., 2015). However, the regulatory effects of Mis1 on the majority of those targets have yet to be fully determined.

Mis1 expression is enriched in stem and progenitor cells of various mammalian tissues including brain (Sakakibara et al., 1996), mammary (Clarke et al., 2005), hair (Sugiyama-Nakagiri et al., 2006), stomach (Nagata et al., 2006), pancreas (Szbat et al., 2011), testis (Sutherland et al., 2014), and intestine (Kayahara et al., 2003). The expression pattern of Mis1 and its large pool of developmentally relevant target mRNAs implicate Mis1 in tissue development and in the renewal of adult tissues. For example, targeted Mis1 disruption in the developing mouse brain resulted in obstructive hydrocephalus, improper cell proliferation and differentiation (Sakakibara et al., 2002), and impaired neural cell motility (Kuwako et al., 2010). Moreover, Mis1 deficiency diminished regeneration of the intestinal epithelial tissue following irradiation-induced injury in adult mice (Yousefi et al., 2016). The importance of Mis1 in early development is further emphasized by findings that Mis1 expression is higher in some embryonic tissues, for example, in mouse brain, but decreases as the organism matures (Sakakibara et al., 1996).

Aberrant Mis1 expression has been implicated in the pathogenesis of several human cancers, including glioblastoma (Muto et al., 2012; Vo et al., 2012; Uren et al., 2015; Chen et al., 2017), colorectal (Sureban et al., 2008; Li et al., 2015), breast (Wang et al., 2010; Lagadec et al., 2014), lung, and prostate cancers (Katz et al., 2014). Most of these tumors exhibit Mis1 levels higher than that of uninvolved tissue, implicating up-regulated Mis1 expression and activity in driving oncogenesis. The potential oncogenic effects of Mis1 were supported by evidence that Mis1 overexpression can transform normal cells. Exogenous Mis1 expression in cultured primary rat intestinal cells enhanced cell proliferation, activated Wnt and Notch signaling pathways, and induced tumors in a xenograft mouse model (Rezza et al., 2010). In contrast, the knockdown of Mis1 impaired growth of xenografts derived from different cancer cell lines (Sureban et al., 2008; Wang et al., 2010; Muto et al., 2012; Vo et al., 2012), indicating that Mis1 up-regulation is essential for sustaining cancer cell proliferation and growth. Furthermore, high Mis1 expression increased the growth of mouse intestinal organoids (Cambuli et al., 2015; Li et al., 2015). In addition, elevated Mis1 promoted cell migration (Uren et al., 2015; Chiou et al., 2017; Gong et al., 2017) and augmented chemoresistance (Chen et al., 2016; Chiou et al., 2017) of various cancer cell types. Taken together, these studies show that independent manipulation of Mis1 expression can alter cell biology and thus implicate Mis1 as a potential therapeutic target.

Over 80% of colorectal cancers have inactivating mutations in the Adenomatous polyposis coli (Apc) gene, which encodes a tumor suppressor and Wnt signaling antagonist. Mis1 is highly up-regulated in mouse intestinal tissue on Apc loss (Sansom et al., 2004) and in intestinal tumors expressing mutated Apc (Potten et al., 2003). These results, together with the identification of Mis1 as a Wnt target gene (Rezza et al., 2010), led us to consider if a functional relationship exists between Mis1 and Apc. Our previous in vitro studies demonstrated that APC mRNA is a target of Mis1 and revealed a mutual-inhibitory relationship between Mis1 and APC in human colonocytes that express wild-type APC (Spears and Neufeld, 2011). We proposed that this relationship is critical for maintaining a balance between proliferation and differentiation of intestinal epithelial cells (IECs) and is disrupted in intestinal tumors expressing truncated Apc.

Our original intention of generating an inducible Mis1 gain-of-function mouse model was to characterize the oncogenic properties of Mis1 in an in vivo setting. Given the broad range of cancers that exhibit up-regulation of Mis1, we also aimed to develop a mouse model that could be a valuable tool to the field as a whole in delineating the pathological functions of Mis1 in cancers originating from different tissues. Unexpectedly, we identified altered organ and animal size in our tamoxifen (TAM)-inducible ubiquitous Mis1-overexpressing mice and therefore embarked on a study to determine the effects of Mis1 overexpression on postnatal development. Here we report that young transgenic mice ubiquitously expressing Mis1 failed to thrive and died prematurely. These mice had stunted body and organ sizes and shorter intestines, indicating that ectopic Mis1 expression disrupted their normal postnatal development. Our data show that Mis1 up-regulation had varying effects on IEC differentiation along the proximal-to-distal axis of mouse intestines, suggesting that Mis1 has region-specific functions in the intestine. It is worth noting that while this study was underway, Cambuli et al. (2015) and Li et al. (2015) generated and characterized two distinct Mis1 gain-of-function mouse models. Notably, our findings both confirm and conflict with the intestinal phenotypes observed in these studies.

**RESULTS**

**Generation of conditional and inducible Mis1-overexpressing mice**

Up-regulated Mis1 levels have been detected in tumors originating from many tissues including colon and brain (Sureban et al., 2008; Katz et al., 2014; Chen et al., 2017). To study the consequences of Mis1 up-regulation in a living organism, we developed a double-transgenic mouse model that enabled conditional and inducible overexpression of Mis1, dependent on Cre-recombinase (Cre) activity (Figure 1). Briefly, a Mis1 transgene, controlled by a strong promoter, but with aloxP-flanked transcription termination sequence blocking expression, was inserted into the Rosa26 locus (Figure 1A; Supplemental Figure S1A). These “Rosa26Mis1/Msi1Tr” mice can be bred with mice that express active Cre to induce Mis1 overexpression. For the current study, homozygous Mis1 transgenic mice were bred with hemizygous ubiquitin (UBC)-Cre-tamoxifen-inducible estrogen receptor (ER)2 mice which express an inactive form of Cre in all cells under the control of the ubiquitin promoter (Figure 1B; Ruzankina et al., 2007). We utilized a whole-body mouse model for Mis1 overexpression because we were interested in the potential for tumorigenesis in any tissue. Following Cre activation with a single TAM injection, double-transgenic mice (Rosa26Tr/+;UBC-CreER2) overexpressed Mis1 ubiquitously. Littermate control mice (Rosa26Tr/+)) were heterozygous for the Mis1
transgene (Figure 1, C and D), but were UBC-CreER\textsuperscript{T2} null; therefore, they expressed only endogenous Msi1 even after TAM injection. Single- and double-transgenic mice were phenotypically indistinguishable before TAM administration. For simplification, TAM-injected Rosa26\textsuperscript{Msi1\textsuperscript{+/+}} and Rosa26\textsuperscript{Msi1\textsuperscript{+/+}};UBC-CreER\textsuperscript{T2} mice will be referred to as control and Msi1\textsuperscript{O/E} (Msi1-overexpressing) mice, respectively.

For our initial analysis, mice were given one intraperitoneal injection of TAM at 4–5 wk of age and then sacrificed 3 days (d) later (days postinjection, dpi). Immunofluorescence analysis showed elevated Msi1 protein levels in lung, heart, liver, kidney, small intestine, and colon tissues of Msi1\textsuperscript{O/E} mice when compared with controls (Figure 1E). Ubiquitous up-regulation of Msi1 was more pronounced in the kidney, small intestine, and colon epithelia of Msi1\textsuperscript{O/E} mice relative to other tissues.
Taken together, these results indicate efficient Msi1 induction as early as 3 d following TAM administration and show the successful generation of an inducible Msi1 knock-in transgenic mouse.

Severe growth retardation in Msi1-overexpressing mice

After confirming efficient Msi1 overexpression in various tissues of our TAM-injected double-transgenic mice, we set up a long-term experiment to determine whether Msi1 overexpression could induce tumor development in tissues that display elevated Msi1 expression during human tumorigenesis. Unexpectedly, ubiquitous Msi1 up-regulation resulted in lethality in 15% of the mice by 14 dpi at which time all mice were killed because many had lost ∼20% of their body weight and appeared morbid. The 14-day period from TAM injection to tissue harvesting was too short for analysis of potential tumor formation; therefore, we examined consequences of ubiquitous Msi1 overexpression on overall postnatal development of mice.

Although all mice had positive growth during the initial week following TAM-administration, weights of the Msi1O/E mice lagged behind their littermate controls (Figure 2A). Unexpectedly, we observed growth retardation in Msi1O/E mice starting at 2 dpi, with drastic weight loss from 10 dpi onward. When compared with controls, Msi1O/E mice had significantly lower body weights and shorter body lengths at 14 dpi (Figure 2, B and C). This stunted growth phenotype was further emphasized by significantly shorter intestines at 7 and 14 dpi (Figure 2, D and E) and significantly smaller organs at 14 dpi (Figure 2F).

Although Msi1O/E mice showed a global decrease in body size, the reduction was not uniform as seen by their differentially altered organ proportions (Figure 2, G and H, and Supplemental Figure S2). When organ weights were normalized to body weights and then expressed as a percentage of similarly normalized organ proportions in wild-type mice, the spleen and lung proportions were significantly lower in the Msi1O/E mice by 14 dpi (Figure 2H). In contrast, Msi1 overexpression resulted in increased relative brain size. There were no differences in the normalized sizes of heart, kidney, and thymus. Compared to control mice, small intestinal length to body length proportions of Msi1O/E mice were significantly reduced at both 7 and 14 dpi (Figure 2G). The colon proportions also trended to be reduced in Msi1O/E mice, but were not statistically different from littermate controls. Notably, only the liver and small intestine proportions were significantly altered in Msi1O/E mice at 7 dpi, with the liver proportion being larger (Figure 2H).

TAM toxicity and mere activation of Cre have each been linked to various phenotypes in mice (Huh et al., 2012; Bohn et al., 2018). To investigate this possibility, we analyzed body and organ sizes of TAM-injected C57BL/6 wild-type mice either with or without the UBC-CreER2 transgene (Supplemental Figure S3). No significant differences in body weight, body length, intestinal lengths, or organ weights were observed at 14 dpi, indicating that TAM administration or Cre expression alone was not sufficient to cause the stunted growth pattern we observed in Msi1O/E mice. Therefore, we conclude that the ubiquitous overexpression of Msi1 in developing mice results in severe growth retardation that is characterized by altered body and organ sizes.

Analysis of transgene expression and function in Msi1O/E intestinal epithelia

Our previous studies suggested a potential role for Msi1 in the regulation of IEC functions (Spears and Neufeld, 2011). Given that the small intestines of Msi1O/E mice were the only tissues that showed significantly altered sizes at both 7 and 14 dpi (Figure 2, D and G), we focused the rest of our study on analyzing the effects of Msi1 overexpression in the intestinal epithelium. It has been reported that TAM and its active metabolite, N-desmethyltamoxifen, are cleared out of mouse brain at 7 dpi (Jahn et al., 2018). To avoid confounding results that could be caused by residual TAM or CreER2 genome toxicity (Valny et al., 2016; Bohn et al., 2018), we did not analyze the intestinal phenotype at time points earlier than 7 dpi. Furthermore, the gut–brain axis can influence intestinal functioning and pathology (Gue et al., 1997; Tache and Perdue, 2004) and since Msi1 is expressed in the central nervous system of postnatal and adult mice (Sakakibara and Okano, 1997), the 7-day wait period was essential for accurate comparison of the intestinal phenotypes of control and Msi1O/E mice.

It is well established that there is heterogeneity in tissue morphology, cell populations, and gene expression along the proximal-to-distal axis of mouse intestinal tissue. Therefore, we examined effects of Msi1 overexpression on the jejunum, ileum, and colon as separate entities.

First we analyzed Msi1 RNA and protein expression in the intestinal epithelial tissue. Elevated Msi1 mRNA levels were confirmed in IECs isolated from jejunum, ileum and colon segments of Msi1O/E mice compared with their injected control littermates (Figure 3A). Furthermore, immunofluorescent staining showed increased Msi1 protein levels in intestinal tissue sections of Msi1O/E mice (Figure 3B). Bright fluorescent signal in the villi stroma of both control and Msi1O/E mice was due to nonspecific tissue autofluorescence (white arrows, Figure 3C) and absent from the intestinal epithelium.

We observed that recombination of the Msi1 knock-in transgene approached but did not reach 100% efficiency. We provide, as an example, an image of small intestinal tissue of Msi1O/E, which displayed some areas of low Msi1 protein expression (within the dashed-white line, Figure 3D) comparable to endogenous Msi1 levels in control tissue. This mosaicism was not surprising, given recombination efficiencies reported for other Cre-LoxP systems (Ruzankina et al., 2007).

To determine whether the transgenic Msi1 protein in Msi1O/E mice was functioning properly, we analyzed Jagged1 (Jag1) expression. Jag1 mRNA is a validated Msi1 target; Msi1 binds to Jag1 mRNA and inhibits its translation, resulting in diminished Jag1 protein levels (Katz et al., 2014). We performed immunofluorescence staining for Jag1 and observed a significant decrease in Jag1 protein expression and fluorescence intensity in colon epithelia at 7 dpi (Figure 4, A and B). These results are consistent with Jag1 response to Msi1-overexpression in mouse neural stem cells (Katz et al., 2014) and indicate that the Msi1 transgene is functioning as expected.

Msi1 overexpression results in subtle effects on intestinal crypt and villi architecture

To assess whether the shorter intestines in Msi1-overexpressing mice were related to changes in the overall structure of the intestinal epithelium, we analyzed crypt and villi morphology. Histological analyses of hematoxylin and eosin-stained tissue showed no overt differences between control and Msi1-overexpressing mice (Figure 5A), indicating that normal gross crypt-villi architecture was maintained in the intestinal epithelial tissue of Msi1O/E mice.

Intestinal development during the first 6 weeks of postnatal life in wild-type C57BL/6 mice is characterized by a gradual increase in small intestine length, crypt depth, and villus height (Dehmer et al., 2018). To avoid confounding results that could be caused by residual TAM or CreER2 genome toxicity (Valny et al., 2016; Bohn et al., 2018), we did not analyze the intestinal phenotype at time points earlier than 7 dpi. Furthermore, the gut–brain axis can influence intestinal functioning and pathology (Gue et al., 1997; Tache and Perdue, 2004) and since Msi1 is expressed in the central nervous system of postnatal and adult mice (Sakakibara and Okano, 1997), the 7-day wait period was essential for accurate comparison of the intestinal phenotypes of control and Msi1O/E mice.

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height and crypt depth and width of control mice had positive growth, while crypt density decreased (Figure 5, B–E). Although the overall patterns of Msi1\textsuperscript{O/E} villi and crypt change over the 7-day period tended to be similar to those of control tissue, the mean sizes of these changes were smaller and we observed some notable differences. For instance, the jejunum villi height and distal colon crypt depth of Msi1\textsuperscript{O/E} mice had significant negative growth rates when compared with controls. Second, the proximal and distal colon crypts of Msi1\textsuperscript{O/E} mice either changed in the opposite direction to that of control mice or barely changed between 7 and 14 dpi. In summary, although there were no exaggerated alterations in crypt-villi morphology of Msi1\textsuperscript{O/E} mice, the overall decrease in intestinal growth observed was consistent with the shorter intestinal lengths.
Decreased proliferation in intestinal epithelia with Msi1 overexpression

To test the hypothesis that altered IEC proliferation could contribute to the shorter intestines and reduced intestinal growth rates of Msi1<sup>OE</sup> mice, we stained and scored intestinal tissue for the proliferative cell marker Ki-67. Representative images of Ki-67 immunofluorescence at 7 dpi are shown in Figure 6A. The percentage of Ki-67-positive IECs in crypts of the jejunum, ileum, and colon did not differ between control and Msi1-overexpressing mice at 7 dpi (Figure 6B). In contrast, by 14 dpi, there were significantly fewer proliferative IECs in all three intestinal segments of Msi1<sup>OE</sup> mice compared with controls (Figure 6, C and D). This decrease in the population of Ki-67-positive cells is consistent with the stunted intestinal lengths and intestinal growth rates of Msi1<sup>OE</sup> mice.

Our Msi1<sup>OE</sup> mice displayed cell proliferation and crypt-villi growth phenotypes contrary to previous reports in other Msi1 mouse models (Cambuli et al., 2015; Li et al., 2015). To test for mutations that might have occurred in the Rosa26<sup>Msi1</sup> transgene which were potentially acting on the Msi1 wild-type alleles in a dominant negative manner, we verified the sequence of the Rosa26<sup>Msi1</sup> transgene. The Msi1 transgene locus was amplified from genomic DNA by PCR (Supplemental Figure S1, B–D) and sequenced. We utilized genomic DNA that was extracted from tail biopsies of Rosa26<sup>Msi1/Msi1</sup> pups. Our sequencing results showed no mutations in the transgene, and the sequence of the isolated locus was 100% identical to the published CDS of mouse Msi1 isoform 1 (Supplemental Figure S1E).

Therefore, we conclude that ubiquitous overexpression of Msi1 results in decreased intestinal cell proliferation, shorter intestinal lengths, and stunted crypt-villi growth rates.

Msi1 overexpression has region-specific effects on intestinal cell differentiation

A possible mechanism for decreased IEC proliferation in mice overexpressing Msi1 is increased differentiation of transit-amplifying progenitor cells. To test this possibility, we first utilized Alcian blue to label goblet cells. Intestinal tissue from both control and Msi1-overexpressing mice displayed a general distribution of goblet cells similar to previous reports, with numbers increasing from jejunum to colon (Figures 7A and Supplemental Figure S4, A and B). Quantification revealed a significantly higher proportion of goblet cells in villi from Msi1<sup>OE</sup> mice ileum at 7 dpi and both jejunum villi and ileum crypts at 14 dpi. We were unable to quantify Alcian blue-positive cells in the colon segments due to the high percentage of goblet cells in that tissue (Supplemental Figure S4B).

As a secondary method to evaluate goblet cells, we measured expression of Muc2 (Muc2), a secretory mucin that is produced by goblet cells. In contrast to Alcian blue staining results, Muc2 RNA levels were significantly reduced in IECs from Msi1<sup>OE</sup> ileum compared with controls at 14 dpi (Figure 7B). Significant differences in Muc2 expression in the other intestinal segments were not observed.

Next, we examined Paneth and enteroendocrine cell differentiation by immunostaining for lysozyme and chromogranin A (Chga), respectively. Msi1<sup>OE</sup> tissue had slightly fewer lysozyme-stained Paneth cells per crypt in all segments, with significant decreases in 7 dpi ileum (Figure 7C). In contrast, enteroendocrine cells from 7 dpi jejunum segments showed an increase, albeit insignificant, in Msi1<sup>OE</sup> mice (p = 0.0698, Supplemental Figure S4C).

To quantify differentiation into the absorptive enterocyte lineage, we measured RNA levels of two enterocyte markers, sucrase-isomaltase (Sis) and lactase (Lac), in IECs isolated from different intestinal sections (Murayama et al., 2009). Sis but not Lac expression was significantly decreased in jejenum IECs from Msi1<sup>OE</sup> at 7 dpi (Figure 7D). In contrast, both Sis and Lac RNA levels were significantly higher (4.5-fold and 8-fold increase, respectively) in 14 dpi ileum of mice overexpressing Msi1 (Figure 7, D and E). No changes were observed in the other segments.

Collectively, these results suggest that Msi1 overexpression affects IEC differentiation, but not in the same way for each intestinal region. Ileum tissue at 14 dpi seemed the most dramatically altered by Msi1 overexpression, showing significant decreases in goblet cell marker RNA and increases in enterocyte marker RNAs. Canonical Notch signaling is a major regulator of IEC differentiation and is predicted to inhibit secretory cell differentiation and thus support an absorptive enterocyte cell fate (Fre et al., 2005). In contrast, high expression of Notch antagonist mouse atonal homolog 1 (Math1) promotes commitment of progenitor cells to the secretory cell lineage (VanDussen and Samuelson, 2010). We hypothesized that the status of Notch signaling would vary among the three intestinal tissue segments, with more Notch signaling in 14 dpi ileum. To test this, we assessed expression of downstream Notch effector, hairy and enhancer of split 1 (Hes1) and its antagonistic target Math1.

Though we expected Hes1 and Math1 expression to be inversely altered, we instead found that both antagonists were significantly up-regulated (67 and 76% increase, respectively) in 14 dpi Msi1<sup>OE</sup> colon compared with controls (Figure 7, F and G). In contrast, 14 dpi ileum had significantly lower Math1 expression (70% reduction) and also lower Hes1 expression (32% reduction, p = 0.0547). No changes in Hes1 and Math1 expression were seen in any intestinal segments at 7 dpi or in jejunum at 14 dpi. Because Hes1 and Math1 act as antagonists to control IEC differentiation, we analyzed the ratio of Hes1-to-Math1 RNA as a readout of Notch activity. Consistent with the reduced Muc2 and elevated enterocyte marker RNA levels in 14 dpi ileum of Msi1<sup>OE</sup> mice, we also found a significantly higher Hes1-to-Math1 ratio (Figure 7H). The only other significant change was a lower Hes1-to-Math1 ratio seen in 7 dpi colons of Msi1<sup>OE</sup> mice compared with their wild-type littermates. This decreased Notch readout was consistent with observed trends of decreased enterocyte and increased goblet cell marker RNAs.

Taken together, our findings suggest that Msi1 regulates IEC differentiation in a temporal and region-specific manner, potentially through modulation of Notch activity in some regions.

Ubiquitous Msi1 overexpression does not alter Numb protein expression in intestinal epithelia

To further investigate a potential mechanism underlying altered expression of Hes1 and Math1 in 14 dpi ileal and colon epithelia, we analyzed the expression of Numb, an antagonist of Notch signaling. It has been reported that Msi1 protein can bind to Numb mRNA and inhibit its translation, resulting in reduced Numb protein amounts and in potentiation of Notch signaling (Imai et al., 2001). We performed immunostaining for Numb (Figure 8A) and quantified Numb fluorescence intensity in 14 dpi intestinal epithelial tissue (Figure 8B). Numb expression pattern revealed a decreasing gradient from the jejunum to the colon. In addition, we observed higher Numb protein expression in jejunum and ileum villi than in crypts. However, our analysis showed no significant differences in relative Numb protein fluorescence intensity between control and Msi1<sup>OE</sup> intestinal epithelial tissue. Thus, these data suggest that altered Hes1 and Math1 expression in 14 dpi Msi1<sup>OE</sup> epithelia is not due to modified Numb protein levels.
Msi1 impairs development, gut homeostasis

FIGURE 3: Up-regulation of Msi1 expression in the Msi1 knock-in mouse model. (A) Evaluation of Msi1 overexpression in isolated IECs by RT-qPCR. Data were analyzed using an unpaired two-tailed t test on ΔΔCt values. Expression was normalized to Gapdh. Graphical data represent mean ± SEM for each genotype (7 dpi, control jejunum, n = 4, ileum, n = 4; colon, n = 5; Msi1OE, n = 5; 14 dpi, control, n = 5, Msi1OE, n = 4 mice). Each mouse is shown as an individual blue point representing the mean relative Jag1 intensity in the crypt epithelia (control) or red diamond (Msi1OE) in colon tissue at 7 dpi. Scale bars represent 50 µm.

Decreased Cdc20 expression in Msi1-overexpressing ileum IECs

Another possibility for the reduced IEC proliferation observed in mice with overexpressed Msi1 is fewer intestinal stem cells (ISCs). Loss of ISCs has been correlated with diminished cell proliferative abilities and villi shortening (Zhou et al., 2013). Lgr5-positive cells represent actively dividing ISCs in intestinal crypts. For ISC analysis, we focused on 14 dpi ileum because it was the most severely affected tissue with regard to differentiation. We found that the number of ISCs expressing Lgr5 RNA as detected by in situ hybridization did not differ between control and Msi1OE tissue in 14 dpi ileum (Figure 9, A and B). Therefore, the decrease in IEC proliferation that we observed was likely not the result of alterations in the population of Lgr5-positive ISCs.

To gain insight into the mechanism underlying the decreased proliferation observed when Msi1 is overexpressed for 14 d, we looked at expression levels for “Cancer Pathway” genes using a PCR array. Of the 84 genes in the panel, 12 transcripts showed expression changes greater than 25% in small intestine samples from three 7 dpi Msi1OE mice (Supplementary Table S2). Of these transcripts, the only gene classified as a cell cycle regulator was Cdc20. Cdc20 is required for cell cycle exit and its down-regulation has been shown to induce mitotic arrest (Eichhorn et al., 2013). RNA extracted from 14 dpi ileum was tested for Cdc20 expression levels using independent primers for RT-qPCR. Notably, Cdc20 expression was significantly decreased (~70%) in Msi1OE IECs (Figure 9C), consistent with less proliferation also seen in this tissue.

Collectively, our data suggest that whole-body induction of Msi1 disrupts the proliferative capacity of IECs, resulting in a considerable reduction of transit-amplifying progenitors, region-specific changes in differentiation, and an overall decrease in intestinal growth and, consequently, in shortening of small intestines and colons.

DISCUSSION

In this study, we generated and characterized a novel Cre-inducible mouse model that facilitates conditional transgenic overexpression of Msi1. Our main aim for generating this transgenic mouse was to investigate the oncogenic properties of Msi1 in vivo. The second goal was to provide the Msi1 research field with a valuable resource that can be used to further the overall understanding of the pathological roles played by Msi1 in tumors originating from different tissues. We utilized a TAM-dependent UBC-CreERΔ2 strain to drive whole-body expression of our Msi1 knock-in transgene in order to identify tissues that were altered by Msi1 overexpression and could be characterized further.

Here we report that Msi1 expression was up-regulated in various tissues, including kidney, lung, liver, and intestinal epithelium, at 3 d after activation of Cre. However, the ubiquitous overexpression of Msi1 in juvenile mice (4–5 wk old) resulted in a failure to thrive and premature death. Two weeks after Msi1 induction, the Msi1OE mice had smaller body and organ weights, as well as shorter intestinal lengths when compared with littermate controls. Mouse pups are not fully developed when they are born and it has been shown that neonatal organs, including the intestines, grow rapidly during the early postnatal period (~6 wk) (Cheng and Bjerknes, 1985; Dehmer et al., 2011). Therefore, our findings suggest that whole-body
overexpression of Msi1 severely impairs the postnatal development process in mice. However, this stunted growth phenotype of Msi1 O/E mice was not seen in every tissue, but rather showed selective alterations in organ proportions. It is possible that this selectivity was due to unequal organ sensitivities to up-regulated Msi1 or differences in normal baseline Msi1 levels in different organs.

While investigating the molecular basis underlying intestinal shortening in Msi1-overexpressing mice, we also found a significant decrease in epithelial cell proliferation in the small intestine and colon at 14 dpi. Further analysis revealed no difference in the number of Lgr5-positive stem cells. However, we found reduced Cdc20 expression in ileum IECs at 14 dpi. Knockout of Cdc20 in both young and adult mice has been reported to induce metaphase arrest in proliferating IECs as well as to decrease Ki-67-positive cells (Manchado et al., 2010). Thus, our results suggest that the impaired IEC proliferation that we observed in Msi1-overexpressing mice could be due to down-regulation of Cdc20. Future work will investigate whether Msi1 can directly bind to Cdc20 RNA and the consequence of this interaction, or if Msi1 influences expression of Cdc20 indirectly.

FIGURE 5: Effects of Msi1 up-regulation on intestinal crypt and villi architecture. (A) Representative hematoxylin and eosin-stained images for small intestine and colon epithelia at 7 and 14 dpi. Scale bar, 50 µm. Growth analysis as percentage change at 14 dpi relative to size at 7 dpi for (B) villi height, (C) crypt depth, (D) crypt width, and (E) crypt density. Each data point in the scatter plots indicates the mean percentage change for a single mouse (7 dpi, control = 5, Msi1 O/E jejunum = 6, ileum = 5, colon = 5; 14 dpi, control = 5, Msi1 O/E jejunum = 6, ileum = 5, colon = 5). Technical replicates per mouse: n ≥ 29 villi for height measurements; n ≥ 21 crypts for crypt depth and width measurements; n ≥ 15 images for crypt density analysis. Mean ± SEM. Nested two-tailed t test analysis. *p < 0.05, **p < 0.01.
The intestine increases in length and diameter during the early postnatal period, resulting in a larger digestive and absorptive epithelial surface area. These changes are driven by increased IEC proliferation, villi height and width, as well as crypt depth, density, and diameter (Cheng and Bjerknes, 1985; Dehmer et al., 2011). Our crypt morphology analysis revealed an overall but marginal decrease in growth between 7 and 14 dpi. Jejunum villi height and distal colon crypt depth were substantially reduced by 14 dpi. Taken together, the shorter intestines, decreased crypt-villus growth, and altered cell proliferation suggest that the intestines of Msi1-overexpressing mice have reduced luminal surface area, which may compromise their nutrient acquisition and overall health.

Here we show that Msi1 up-regulation had region-specific effects on IEC differentiation; the ileum of Msi1\(^{O/E}\) mice was more responsive to Msi1 up-regulation than the jejunum and colon. We detected enhanced enterocyte marker expression as well as increased Hes1-to-Math1 expression ratios in the ileum segments 2 wk after Msi1 induction. These results indicate that ubiquitous Msi1 overexpression promoted secretory cell differentiation, potentially through modulating the activities of Math1 and Hes1. Consistent with a role for Notch in regulating IEC differentiation, we saw decreased Paneth cell numbers in the ileum a week after Msi1 induction. This finding agrees with in vitro studies that have shown inhibition of Paneth cell differentiation in response to Msi1 overexpression (Murayama et al., 2009). Inexplicably, there were no differences in Paneth cell numbers in 14 dpi ileum tissue. Moreover, Muc2 was down-regulated in the ileum at 14 dpi, but there were no changes in Muc2 in the other intestinal segments. Contrary to expectations, there were more goblet cells (Alcian blue) in the jejunum and ileum of Msi1\(^{O/E}\) mice. It is possible that the goblet cells from Msi1-overexpressing mice were making less Muc2 as a way to compensate for the increased goblet cell numbers or as a result of the high Hes1-to-Math1 expression ratio. Additional RNA expression analysis of other goblet cell markers will be required to test this compensation model.

Msi1 protein can bind to Numb mRNA and inhibit its translation (Imai et al., 2001). Consequently, Msi1 overexpression has been shown to activate the Notch signaling pathway (Imai et al., 2001; Rezza et al., 2010). In IEC differentiation, high Notch
signaling repressed the intestinal secretory cell lineage, resulting in more enterocytes (Fre et al., 2005). Although our results from the 14 dpi ileum section were mostly consistent with Notch activation, Numb was not differentially expressed between Msi1O/E and control mice. In addition, we did not observe differences in Numb expression in 14 dpi jejunum and colon sections. Thus, these findings show

**FIGURE 7:** Altered intestinal cell differentiation with Msi1 up-regulation. (A) Representative images for goblet cells stained using Alcian blue and Nuclear Fast Red (left), and quantification of Alcian blue-positive cells in small intestine epithelia (right) (7 dpi, control jejunum, n = 5; ileum, n = 6, Msi1O/E jejunum, n = 5, ileum, n = 5; 14 dpi, control jejunum, n = 5, ileum, n = 5, Msi1O/E jejunum, n = 6, ileum, n = 5). N ≥ 30 villi per mouse. (B) Representative merged immunofluorescent images for lysozyme (Paneth cell marker) staining and quantification of positive cells in small intestinal epithelia (7 dpi, control jejunum, n = 4, ileum, n = 4, Msi1O/E jejunum, n = 5, ileum, n = 4; 14 dpi, control jejunum, n = 4, ileum, n = 4, Msi1O/E jejunum, n = 4, ileum, n = 4). N ≥ 25 crypts per mouse. Analyses of (B) Muc2, (D) Sis, (E) Lac, (F) Hes1, and (G) Math1 RNAs in IECs harvested from 7- and 14 dpi mice (7 dpi, control jejunum, n = 4, ileum, n = 4, colon, n = 5; Msi1O/E, n = 5; 14 dpi, control, n = 5, Msi1O/E, n = 4 mice). There were three technical replicates assayed for each mouse. Expression was normalized to Gapdh. (H) The ratios of Hes1-to-Math1 RNA levels were calculated from data presented in F and G with p value determined using ΔCt values. Graphical data represent mean ± SEM for each genotype. Each mouse is shown as an individual blue circle (control) or a red diamond (Msi1O/E). Data in A and C were analyzed using a nested two-tailed t test and in B and D–H analyzed using an unpaired two-tailed t test. *p < 0.05, **p < 0.01. Scale bars, 50 µm.
that Msi1 up-regulation did not modulate Numb expression in our Msi1\textsuperscript{O/E} mice, in contrast to the established Msi1/Numb/Notch relationship. However, this inconsistency between Msi1 and Numb expression patterns has been reported in other mouse models. No significant changes in Numb translation were observed in neural stem cells that were derived from tetracycline-Msi1 mice and treated with doxycycline to induce Msi1 overexpression (Katz et al., 2014). In contrast, Msi1 deficiency in Msi1-knockout mice resulted in the down-regulation of Numb protein expression and delayed gastric regeneration, indicating that Msi1 is required for translational activation of Numb (Takahashi et al., 2013). Taken together, our results show that the high Hes1-to-Math1 expression ratio in 14 dpi ileum IECs was not due to altered Numb expression. Although the high Hes1-to-Math1 ratio suggested Notch activation, more work is needed to determine whether the changes in ileum IEC differentiation were due to modulations of Notch signaling or on transcription factors that function downstream of Hes1 and Math1. In addition, future studies are required to unravel the complicated region-specific effects of Msi1 up-regulation on IEC differentiation.

It is noteworthy that most phenotypes of our Msi1\textsuperscript{O/E} mice differ considerably from those of other Msi1-overexpressing mouse models (Cambuli et al., 2015; Li et al., 2015). Whereas our study used a ubiquitous and TAM-inducible model and focused on the early postnatal development stage, Li et al. (2015) utilized a doxycycline-inducible collagen promoter to drive Msi1 expression in adult mice (Li et al., 2015). In the Cambuli et al. (2015) study, Msi1 overexpression was intestine epithelial cell-specific, driven by a noninducible villin promoter from embryonic day 11 (Cambuli et al., 2015). In contrast to our findings, both the inducible collagen promoter-driven adult mouse model and the villin-promoter driven model reported increased IEC proliferation in the small intestine, which correlated with enhanced stem cell marker expression and numbers. However, similar to our 7 dpi findings, Cambuli et al. (2015) showed no differences in colon IEC proliferation. In terms of IEC differentiation, Li et al. (2015) reported a decrease in the overall number of differentiated cells, whereas Cambuli et al. (2015) observed no differences. Although Msi1 overexpression was lethal in our mice around 2 wk after induction, Msi1 driven by a collagen promoter resulted in lethality within 3 d (Li et al., 2015). Discrepancies between these three mouse models could be due to the age at which Msi1 transgene expression was initiated and the tissue- and cell-type specificity of the expression. Another consideration is that our Msi1\textsuperscript{O/E} mice overexpress Msi1 in all cells and tissues. This might be the reason that our study is the first to report differences in mouse body and organ weights. Ongoing studies are investigating the roles of Msi1 in early postnatal development using an intestine-specific inducible mouse strain. Preliminary results suggest that overexpressing Msi1 in the intestines of ~5-wk-old mice does not cause premature death.

In summary, we have successfully developed a conditional and Cre-inducible Msi1 knock-in line by targeting the Rosa26 locus. Msi1 overexpression appears to have a global inhibitory effect on mouse postnatal development, with prominent phenotypes observed in intestines, liver, spleen, lung, and brain. Our detailed analysis of intestinal tissue revealed roles for Msi1 in the maintenance of intestinal homeostasis which might be important for future therapies that manipulate Msi1 activity. Msi1 up-regulation for 14 d promoted enterocyte and inhibited goblet cell differentiation marker expression in the ileum, consistent with a measured elevated readout of Notch signaling. At earlier stages, the ileum showed depressed Paneth cell numbers, also consistent with elevated Notch signaling. In addition to this analysis of intestinal phenotypes, the Cre-inducible Msi1 model will be a useful tool for future investigations of the regulatory functions of Msi1 in other tissues and cell types at different developmental stages.

FIGURE 8: Ubiquitous Msi1 overexpression does not alter Numb immunostaining in 14 dpi intestinal epithelial tissue. (A) Representative immunofluorescence images for Numb (gray, red) and DAPI (blue) in small intestine and colon tissue at 14 dpi. Scale bars represent 50 µm. (B) Quantification of Numb fluorescence intensity. Each data point represents the mean relative Numb fluorescence intensity in the villus or crypt epithelia for a single mouse (four mice per genotype). For each mouse, 13 images were analyzed, and intensity was measured on the brightest one or two 361-µm² epithelial sections per image. Mean ± SEM. Nested two-tailed t test analysis.
black, strain C57BL/6, offspring (G1) indicated successful germline transmission. To genotype G1 mice, PCR was performed on genomic DNA from tail snips and PCR amplicons were analyzed using a Caliper LabChip GX device. Homozygous and heterozygous Msi1 knock-in mice will be referred to as Rosa26<sup>Mul/Msi1</sup> and Rosa26<sup>Mul/1</sup>, respectively.

### Mice breeding and genotyping

Hemizygous B6.Cg-Tg(UBC-Cre-ERT2)1Ejb/J (Ruzankina et al., 2007) male breeders were purchased from The Jackson Laboratory (#008085). Rosa<sup>Mul/Msi1</sup> females were crossed with the UBC-CreERT2 male to produce pups that were single transgenic Rosa<sup>Mul/1</sup> or double-transgenic Rosa<sup>Mul/1</sup>/UBC-CreERT2. Additional control mice were obtained from breeding a C57BL6/wild-type female with a UBC-CreERT2 male. Tail-snips from 3-wk-old pups were digested in 0.2 mg/ml Proteinase K (ThermoFisher, #EO0491) at 55°C overnight and heat-inactivated at 95°C for 10 min to extract genomic DNA. Primers used to genotype for Msi1 were: Msi1 WT Forward (WT<sub>F</sub>) 5′-CTCTTCCTCCGTGATCTGCAACTC-3′; Msi1 WT Reverse (WT<sub>R</sub>) 5′-CATGTCTTAATACCTCTGAGTGG-3′; Msi1 knock-in Forward (KI<sub>F</sub>) 5′-GGCAGGCTTGATGATG-3′; Msi1 knock-in Reverse (KI<sub>R</sub>) 5′-CCCAAGGCCACAAAGAC-3′. PCR conditions, using OneTaq DNA polymerase (New England Biolabs [NEB], #M0482S), were 95°C for 5 min, 35 cycles (95°C for 30 s, 60°C for 30 s, and 72°C for 1 min) and 72°C for 10 min. Msi1 WTprimers amplified a 299-base pair sequence of the endogenous Rosa26 locus (see Figure 1A). The binding sites for WT primers were also in the Rosa26 knock-in allele, but there was no amplification due to the large transgenic vector inserted between the primer binding sites. The Msi1 knock-in primers amplified a 492-base pair fragment. Primers used to identify Cre were: Cre<sub>F</sub> 5′-GACGCCAGGGTGAAGGAAG-3′ and Cre<sub>R</sub> 5′-CCAGAAGTCATCTTGAGCGC-3′. PCR conditions were 94°C for 3 min, 35 cycles (94°C for 30 s, 59°C for 1 min, 68°C for 30 s, and 68°C for 5 min and the Cre fragment size was 225 base pairs. To confirm the DNA quality of Rosa26<sup>Mul/1</sup> mouse samples analyzed for Cre, an internal control fragment (492 base pairs) was amplified using the Msi1 knock-in primers.

### Sequencing the Rosa26<sup>Mul1</sup> transgene

The transgenic Msi1 CDS was isolated from genomic DNA by PCR using primers PF<sub>1</sub> and PR<sub>1</sub> (Supplemental Figure S1B). Primers PF<sub>1</sub> and PR<sub>2</sub> amplified a 1174-base pair product which included 61 base pairs upstream and 24 base pairs downstream of the transgenic Msi1 CDS (1089 base pairs). The genomic DNA was extracted from tail snips of 3-wk-old pups as mentioned above, and PCR was performed on samples from three independent Rosa26<sup>Mul1/Msi1</sup> transgenic mice and one negative control Rosa26<sup>Mul</sup> (Msi1 wild-type) mouse. Primer sequences were: PF<sub>1</sub> 5′-CTCGTCGACCTATAACCTTGATAG-3′ and PR<sub>1</sub> 5′-CTGTAATTTAATCTTACCCAGCGC-3′. PCR conditions, using Q5 High-Fidelity DNA Polymerase (NEB, #M0492S), were 98°C for 2 min 30 s, 35 cycles (98°C for 30 s, 59°C for 1 min, 68°C for 30 s) and 68°C for 5 min and the Cre fragment size was 225 base pairs. The PCR product was then purified using a QIAquick PCR Purification Kit (Qiagen). To confirm the DNA quality of Rosa26<sup>Mul/1</sup> mouse samples analyzed for Cre, an internal control fragment (492 base pairs) was amplified using the Msi1 knock-in primers.
Information reference sequence for mouse Msi1 CDS isoform 1 (NM_008629.2; assessed on 07/30/2020). Sequence alignment was performed using the MultAlin software (Corpet, 1988).

Administration of TAM
Four- to 5-wk-old mice, both sexes, were given intraperitoneal injections with a single dose of 75 mg/kg body weight TAM solution (MP Biomedicals, #156738). TAM was prepared under sterile conditions by dissolving in 10:1 sunflower oil/ethanol mixture; 10% of the mixture was evaporated before administration into mice. Both control (Rosa<sup>Msi1<sup>-/-</sup></sup> mice and the Cre-containing (Rosa<sup>Msi1<sup>-/-</sup>,UBC-CreERT2) mice were injected with TAM. Mice were killed by CO₂ asphyxiation followed by cervical dislocation at 3, 7, or 14 d post-TAM injections. Age-matched littermates were used for all experiments.

Body weight, organ weights, and length measurements
Mice were weighed daily at approximately the same time. Final body weights were measured immediately after mouse sacrifice. To obtain total body lengths, mice were laid facedown on a flat surface and body length was measured from the base of the skull to the anus. Organs were promptly excised and weighed, or their lengths were measured. Organ-to-body weight proportions for liver, kidneys, thymus, spleen, lungs, and brain were calculated by dividing the weight of the organ by the body weight of the mouse. Intestinal length-to-body length proportions were also determined for the small intestine and colon. For comparison, organ proportions for each mouse were normalized to the average organ proportion of Rosa<sup>Msi1<sup>-/-</sup></sup> control mice.

Tissue sample preparation and immunofluorescence
The small intestine was divided into three sections: duodenum, ileum, and jejunum. The duodenum was the most proximal 5 cm and was not further analyzed. Jejunum and ileum sections were the proximal two-thirds and distal third of the remaining small intestinal tissue, respectively. The jejunum, ileum, and colon tissues were flushed with 10% saline-buffered formalin, cut lengthwise, individually rolled into “Swiss rolls,” and fixed in 10% saline-buffered formalin for 24 h. Mouse heart, lung, and kidney that were harvested at 3 d post-TAM injections were fixed in 10% saline-buffered formalin for 24 h, whereas liver samples were fixed for 48 h. The tissue was then stored in 70% ethanol before paraffin embedding.

In brief, for immunofluorescence staining, 4-µm tissue sections were deparaffinized 3x in xylene substitute for a total of 30 min, rehydrated in a graded ethanol series (100, 95, 80, 70, and 50%) for each concentration, and permeabilized in methanol (0.1% Tween20) for 15 min on a shaker. Slides were washed 2x in absolute methanol for 5 min each, followed by a phosphate-buffered saline (PBS) wash. Antigen retrieval was achieved by incubating slides in 0.01 M citrate buffer (0.05% Tween20, pH 6.2) in a 90–95°C water bath for 40 min. Slides were incubated for 2 h in a PBS-blocking buffer containing 2% normal goat serum, 0.1% Triton X-100, 0.05% Tween20, 5% cold-fish skin gelatin, and 10% bovine serum albumin (wt/vol). Sections were then incubated with primary antibodies overnight at 4°C. Primary antibodies used were Msi1 (1:1000 Millipore, #MABE268 clone 7B11.1), Jag1 (1:50 Cell Signaling Tech (D4Y1R), #70109), Ki-67 (1:400 Cell Signaling Tech, #D3B5), Isyozyme (1:500 DakoCytomation, #EC 3.2.17), ß-catenin (1:500 BD Transduction, #610154), and Numb (1:500 Cell Signaling Tech (C29G11), #2756). Slides were rinsed 3x in PBS for 15 min total, incubated with Alexa Fluor secondary antibodies (1:1000 Invitrogen) for 1 h at room temperature, and rinsed 3x in PBS before counterstaining with DAPI (Invitrogen, #P36962).

Immunoperoxidase staining
After deparaffinization, rehydration, permeabilization, and methanol washes; slides were incubated in 3% H₂O₂ methanol (100%) for 20 min. Antigen retrieval, blocking, and primary antibody (SP-1 Chga, Immunomark, #20085), incubation steps were similar to those for immunofluorescence staining. Goat anti-rabbit HRP–conjugated secondary antibody (1:1000 Bio-Rad, #172-1019) and 3,3′-diaminobenzidine tetrahydrochloride substrate (Invitrogen, #00-2020) were used. Tissue sections were counterstained with Gill’s Hematoxylin (American MasterTech, HXGHE1LT) for 5 min followed by a 2-min water rinse. Bluing was achieved by dipping slides in 0.2% ammonia water for 30 s. Slides were then rinsed in water for 2 min, dehydrated in ethanol (50, 70, 80, 95, 100%) for a minute each, and washed 2x in xylene-substitute for 10 min total before application of mounting solution (Biocare Medical, EM897L).

Hematoxylin and eosin staining
Deparaffinized slides were rehydrated in ethanol (5 min in 100%, 2 min in 90%, and 2 min in 70%) 2x for each concentration. Then slides were washed 2x in water for 2 min, stained with Gill’s Hematoxylin for 8 min, washed in water for 2 min, and then blued as above. This was followed by two rinses in water for a minute each, incubation in 95% ethanol for a minute, and staining with Eosin Y (Fisher Scientific, 314-630) for a minute. After dehydrration in ethanol (95, 100%) for 2 min with two changes for each concentration, slides were briefly washed in xylene substitute and then mounting solution (Biocare Medical, EM897L) was applied.

Alcian blue staining
For goblet cell staining, deparaffinized slides were rehydrated in ethanol (100, 95, 80, 70, 50%) for 5 min each and then washed 2x in water for 5 min. Slides were stained in 1% (wt/vol) Alcian blue solution (Sigma Aldrich, dissolved in 3% acetic acid, pH 2.5) for 30 min followed by two washes in water for 5 min each. Counterstaining was achieved by incubating slides with Nuclear Fast Read (Newcomer Supply, 1255A) for 5 min. Slides were then washed 2x in water for a total of 4 min. This was followed by dehydration in ethanol (50, 70, 80, 95, 100%) for a min each, three xylene washes for 5 min each, and application of mounting solution.

RNA in situ hybridization
RNA in situ hybridization was performed using the RNAscope 2.5 HD Detection Kit (ACD) according to manufacturer’s protocol. Briefly, after deparaffinization and hydrogen peroxide treatment (ACD, #322335), antigen retrieval on 4-µm tissue sections was achieved by boiling slides in 1x Target Retrieval Reagent (ACD, #322000) in a 99–102°C water bath for 15 min. Slides were dipped in 100% ethanol and air-dried at room temperature. Then, protease (ACD, #322331) was performed at 40°C for 30 min. This was followed by hybridization using target probes for Lgr5 (ACD, #312171) at 40°C for 2 h. Mm-Polk2a (ACD, #312471) and dapB (ACD, #310043) probes were used for the positive and negative control sections, respectively. The signal was amplified and detected using the Red Detection Reagent (ACD, #322360). Counterstaining was achieved by incubating slides in 50% Gill’s Hematoxylin for 2 min at room temperature and then blued in 0.02% ammonia water for 10 s. After dehydration at 60°C for 15 min, slides were dipped in xylene before application of mounting solution (Biocare Medical, EM897L).

Microscope image acquisition and analysis
Immunofluorescence images were acquired using a Zeiss (Axiovert 41) microscope and Hamamatsu (C10600) digital camera. A Nikon Microscope image acquisition and analysis
Immunofluorescence images were acquired using a Zeiss (Axiovert 41) microscope and Hamamatsu (C10600) digital camera. A Nikon
(Eclipse 80i) microscope equipped with a ProgRes C3 (Jenoptik) digital camera was used to capture immunohistochemistry, H&E, and Alcian blue images. RNA in situ hybridization images were acquired using a Leica (MZFLIII) dissecting microscope and a Leica DFC 320 camera. Slides were assigned coded IDs and images were taken by an investigator who was blinded to sample genotype. An additional blinding step was performed, before image analysis, by renaming each acquired image with a random four-letter code (generated using Excel). Images and slides were decoded after completion of measurements and/or counting analysis. Image brightness and levels were adjusted in Photoshop (Adobe) using identical settings for matched experiments.

Jag1 and Numb immunofluorescence signal intensities were measured using ImageJ software. For Jag1, signal intensities were measured on the brightest four 150-µm² regions per image, and for consistency purposes, these four regions were within the bottom two-thirds of crypts. For Numb, measurements were taken on the brightest one or two 361-µm² regions per image, in the villus and/or crypt epithelium. Intensity data were analyzed using the corrected total cellular fluorescence method (CTCF). CTCF = Integrated fluorescence of background – (Area of selected tissue region × mean fluorescence of background readings). The background readings were measured from negative control (no primary antibody, secondary only) slides.

**Isolation of mouse IECs and RNA preparation**

Jejunum, ileum, and colon epithelial cells were isolated as previously described with minor modifications (Zeineldin and Neufeld, 2012; Zeineldin et al., 2012). Intestinal tissue pieces were incubated in 0.04% sodium hypochlorite solution for 5 min on ice and then incubated in Solution B (2.7 mM KCl, 150 mM NaCl, 1.2 mM KH₂PO₄, 68 mM Na₂HPO₄, 1.5 mM EDTA, 0.5 mM DTT) for 10 min on ice. The isolated cells were centrifuged at 1000 rpm for 10 min at 4°C. Cell pellets were resuspended in Trizol (Life Technologies, #15596-026), 4 ml for jejunum, 2 ml for ileum, and 1 ml for colon, for total RNA extraction using the manufacturer’s protocol; with the isopropanol incubation step at 20°C overnight to optimize RNA precipitation. DNase I (NEB, #M0303S) digestion was performed to remove genomic DNA contaminants from the resuspended RNA, followed by further purification on RNeasy columns (Qiagen, #74104).

**Differential target expression analysis using RT² Profiler PCR Array**

Jejunum intestinal epithelium cells were isolated from mice 7 d after TAM administration. Total RNA was extracted using Trizol (Life Technologies, #15596-026) and purified on RNeasy columns (Qiagen, #74104). Then complementary DNA (cDNA) synthesis was performed using 1 µg purified total RNA and the RT² First Strand Kit (Qiagen, #330401) following the manufacturer’s protocol. This kit included a gDNA elimination step. Prepared cDNA was mixed with the RT² SYBR green (Qiagen, #330502) and dispensed in a 96-well RT² Profiler PCR Array for the Mouse Cancer PathwayFinder (Qiagen, #330231 PAMM-0332A) according to manufacturer’s recommendations. A single array was used for each individual mouse (three mice per genotype) and assayed in a DNA Engine Opticon 2 System (MJ Research). Target expression was analyzed using the ΔΔCt method and normalized to the average cycle threshold (CT) values of the five housekeeping genes provided in the array. For the initial analysis, targets with an expression change greater or less than 25% of the control samples were considered to be differentially expressed in Msi1-overexpressing samples.

**cDNA generation and gene expression analysis**

Purified total RNA (1µg) was used to generate cDNA. A 17-µl reaction mixture containing RNA, Random Primer 6 (NEB, #512305), dNTPs (NEB, #N04475), and nuclease-free water was incubated at 65°C for 5 min and quickly put on ice. M-MLV Reverse Transcriptase (1 µl, NEB, #M0253S) and 2 µl of enzyme buffer were added to the reaction mixture. For negative controls, nuclease-free water was used instead of reverse transcriptase. The final concentration was 6 µM for Random Primer 6, and 0.75 mM for dNTPs. PCR conditions for cDNA generation were 25°C for 5 min, 42°C for 1 h, and inactivation at 65°C for 20 min. The cDNA product was diluted 1:5 with nuclease-free water and stored at −20°C in aliquots to avoid repeated freeze–thaw cycles. For RT-qPCR, 1.6 µl of 1:10 further diluted cDNA was mixed with 300 nM of each target primer, and 1× SYBR Green (DyNAamo HS, ThermoFisher, #F-140 or PowerUp, Thermofisher, #A25742) in a 20-µl reaction mix and assayed in a DNA Engine Opticon 2 System (MJ Research) according to manufacturer’s recommendations. Four to five independent RNA samples were used for each genotype and three technical replicates were assayed for each mouse. Targets analyzed were Cdc20, Hes1, Lac, Math1, Msi1, Muc2, and Sis. Ct values for the housekeeping gene Gapdh were used as an internal control and for normalizing target Ct values. Primer sequences for targets are shown in Table 1.

The PCR efficiency of each primer pair was determined by performing a standard curve using 1:5 or 1:10 serial-diluted cDNA. To enhance precision, only raw Ct values of the triplicate reactions that varied by <0.6 were used to calculate the mean Ct value for each biological sample. The ΔΔCt method was used to analyze expression

**TABLE 1: RT-qPCR primer sequences and efficiencies.**

| Gene | Forward primer (5′-3′) | Reverse primer (5′-3′) | Efficiency |
|------|-----------------------|-----------------------|------------|
| Cdc20 | TTCGTGTTTGGAGACGGATTG | ACCTTGGAACTAGATTGCCA | 101.31%b |
| Gapdh | TGGGCTTCTCTTTCCTAC | GAGTTGCTGTAGAAGTCGCA | 96.61%a, 91.54%b |
| Hes1 | CCACCCAGGTCTCACAGCA | AATGCCGGAAGTCTTTTC | 90.6%b |
| Lac | CACTCTCTACAGGAGAAGG | AGGAATTCACAGGAGCCCTT | 90.29%b |
| Math1 | ATCCGGTTTACCAACAGCG | CCTTCCGACAGGGGTAGC | 100.08%b |
| Msi1 | ATATGGTTGATTGGATGCT | CGGGAACAACTGGGTAGTGA | 92.03%b |
| Muc2 | GATGCACTCAGTGGTGGG | TCAGGTGTGTGATCTTCGCA | 99.58%a |
| Sis | TGACTACGACATAACGGGG | TCATATGTTGTAGCTAGTCTC | 92.31%a |

a Primer efficiencies and expression levels assayed using DyNAamo HS SYBR Green.

b Assays that were performed using PowerUp SYBR Green.
levels for targets with primer efficiencies that differed by less than $\pm 5\%$ from the GAPDH primer efficiency. For those targets, an unpaired two-tailed $t$-test was performed on grouped nonaveraged $\Delta Ct$ values to determine statistical significance in expression levels between control and mutant samples. In contrast, Cdc20 and Math1 efficiencies differed from Gapdh by $>5\%$; therefore, expression levels were calculated according to the method described by Pfaffl (2001), and data were analyzed using an unpaired two-tailed $t$-test on grouped nonaveraged fold change values.

**Statistical analysis**

All data analysis was performed using GraphPad Prism 8 software. Data for body and organ weights, lengths or proportions, and RT-qPCR data were analyzed using an unpaired two-tailed $t$-test. Nested $t$ tests were used to analyze data for experiments where multiple technical measurements were taken from each mouse. These experiments included analysis of cell proliferation, morphological measurements, and cell differentiation staining. Sample sizes for mice, carys, and vili analyzed are given in the figure legends.

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