

# Transcriptional regulation of *WNT2B* based on the balance of Hedgehog, Notch, BMP and WNT signals

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**Abstract.** We cloned and characterized human *WNT2B* in 1996, and then others cloned and characterized mouse, chicken, and zebrafish *WNT2B* orthologs. *WNT2B* is expressed in several types of human cancer, such as basal cell carcinoma, gastric cancer, breast cancer, head/neck squamous cell carcinoma, cervical cancer and leukemia. *WNT2B* is one of canonical WNTs transducing signals through Frizzled (FZD) and LRP5/LRP6 receptors to  $\beta$ -catenin-TCF/LEF signaling cascade. Here, refined integrative genomic analyses on *WNT2B* orthologs were carried out to elucidate its transcriptional mechanisms. GLI-, double FOX-, HES/HEY-, bHLH-, and Sp1-binding sites within mammalian *WNT2B* promoter were well conserved. Because *GLI1*, *FOXA2*, *FOXC2*, *FOXE1*, *FOXF1* and *FOXLI* are direct target genes of Hedgehog-GLI2 signaling cascade, Hedgehog signals should induce *WNT2B* upregulation through GLI family members as well as FOX family members. Notch, BMP and Hedgehog signals inhibit *WNT2B* expression via HES/HEY-binding to N-box, whereas BMP and WNT signals inhibit bHLH transcription factor-induced *WNT2B* expression via ID1, ID2, ID3, MSX1 or MSX2. Together these facts indicate that Hedgehog signals and bHLH transcription factors are involved in *WNT2B* upregulation, which is counteracted by BMP, WNT and Notch signals. Mesenchymal BMP induces IHH expression in gastrointestinal epithelial cells, and then epithelial Hedgehog induces *WNT2B* and BMP4 expression in mesenchymal cells. NF- $\kappa$ B signals induce SHH upregulation, and *WNT2B* is upregulated in inflammatory bowel disease (IBD). BMP-IHH and inflammation-SHH signaling loops are involved in *WNT2B* upregulation during embryogenesis, adult tissue homeostasis, and carcinogenesis.

## Introduction

WNT family members are lipid-modified glycoproteins involved in embryogenesis and carcinogenesis (1-5). We cloned and characterized human *WNT2B*/*WNT13* as the 13th member of the mammalian WNT family in 1996 (6), and others then characterized mouse, chicken, and zebrafish *WNT2B* orthologs (7-9). Human *WNT2B* shows 66.9% total amino-acid identity with human *WNT2*, while mouse *Wnt2b* shows 71.1% total amino-acid identity with mouse *Wnt2*. The *WNT2B-ST7L-CAPZA1* locus at human chromosome 1p13.2 and the *WNT2-ST7-CAPZA2* locus at human chromosome 7q31.2 are paralogous regions within the human genome (10). Human *WNT2B* gene consisting of seven exons encodes multiple isoforms due to alternative splicing using alternative promoters (11). *WNT2B2* isoform rather than *WNT2B1* is evolutionarily conserved.

*WNT2B2* functions as a canonical WNT to transduce signal through Frizzled (FZD) receptor and LRP5/6 co-receptor (12). In the absence of canonical WNT signaling,  $\beta$ -catenin is phosphorylated by Casein kinase 1 $\alpha$  (CK1 $\alpha$ ) and glycogen synthase kinase 3 $\beta$  (GSK3 $\beta$ ), and then is ubiquitinated by  $\beta$ TRCP1 (FBXW1)- or  $\beta$ TRCP2 (FBXW11)-containing ubiquitin-ligase complex for its degradation in the proteasome system (13-17). Canonical WNT signals induce assembly of FZD-Dishevelled complex and LRP5/6-AXIN complex to release  $\beta$ -catenin from AXIN-APC degradation complex (18-20), which results in stabilization and nuclear translocation of  $\beta$ -catenin for the transcriptional activation of target genes, such as *MYC* and *CCND1* (21-23).

WNT signaling cascades cross-talk with Hedgehog, BMP/TGF- $\beta$ , FGF, and Notch signaling cascades to constitute the stem-cell signaling network (24-26). Dysregulation of the stem-cell signaling network due to epigenetic and genetic alterations leads to congenital abnormality and carcinogenesis (27-29).

Human *WNT2B* is expressed in fetal brain, lung, kidney, adult heart, brain, placenta, lung, prostate, testis, ovary, small intestine, colon, and also in several types of human cancer, such as basal cell carcinoma, gastric cancer, breast cancer, head/neck squamous cell carcinoma, cervical cancer, and leukemia (6,11,30-34). *WNT2B* is upregulated in liver and biliary epithelial cells of patients with primary biliary cirrhosis (35), and in colonic mucosa of patients with inflammatory bowel disease (36). *WNT2B* is upregulated in some types of human cancer and in some tissues with chronic inflammation;

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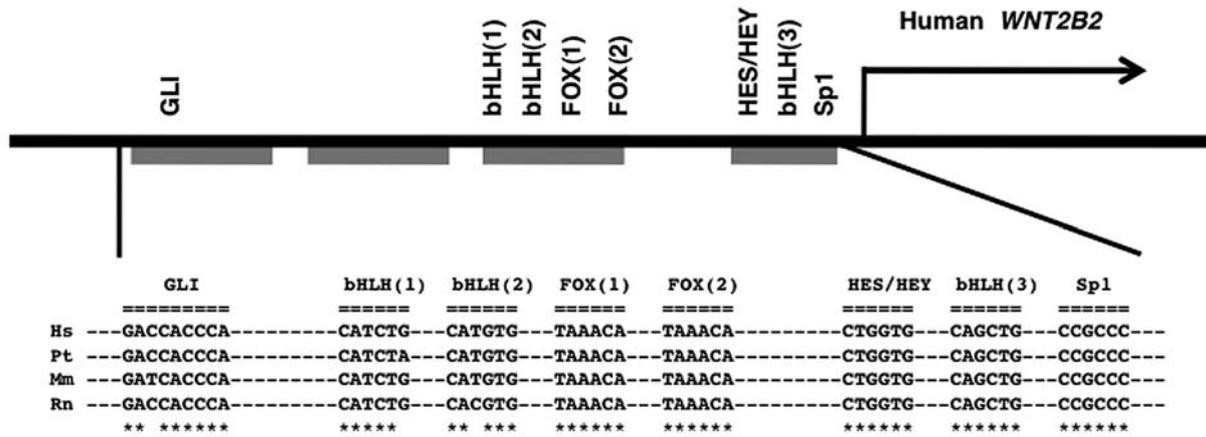


Figure 1. Conserved transcription factor-binding sites within *WNT2B* promoter. Human genome around the *WNT2B2* promoter is shown by the bold bar. Evolutionarily conserved regions are shown by the gray bars. Nucleotide sequences of promoter region of human (Hs), chimpanzee (Pt), mouse (Mm), and rat (Rn) *WNT2B* orthologs are aligned in the bottom. GLI-, double FOX-, HES/HEY-, bHLH-, and Sp1-binding sites within mammalian *WNT2B* promoter are well conserved.

however, the mechanisms of *WNT2B* transcription remain unclear. Here, refined integrative genomic analyses are carried out to elucidate the transcriptional mechanisms of *WNT2B* with an emphasis on the stem-cell signaling network.

## Materials and methods

**Comparative genomic analyses.** Human genome sequences corresponding to human *WNT2B2* isoform (NM\_024494.2) were searched for by using BLAST programs, as previously described (37-40). Conserved transcription factor-binding sites within the *WNT2B2* promoter were then searched for based on manual inspection, as previously described (41-44).

**Regulatory network analyses.** Literature on *WNT2B*, Hedgehog, BMP, and Notch signaling molecules in PubMed and Medline databases was critically evaluated to extract knowledge on the regulation of GLI, FOX, bHLH, ID and MSX family transcription factors. The mechanisms of *WNT2B* transcription were then investigated based on our data of conserved transcription factor-binding sites within the *WNT2B* promoter and in-house knowledgebase of transcription factors regulated by the stem-cell signaling network.

## Results

**Comparative genomics on *WNT2B* promoter.** Because the region around the *WNT2B2* promoter is GC-rich (45), transcription start sites (TSSs) of human *WNT2B2* mRNA have been predicted to show 'broad peak' pattern, as is usual for other GC-rich promoters. Indeed, NM\_024494.2 *WNT2B2* RefSeq was extended to the 496-bp 5'-position compared with NM\_024494.1 *WNT2B2* RefSeq. Comparative integromics analyses of the *WNT2B* promoter were carried out again in this study by using up-to-date in-house knowledgebase on the transcription-factor network.

BLAST programs using the NM\_024494.2 *WNT2B2* RefSeq as a query sequence revealed that the TSS of human *WNT2B2* mRNA was located within AL354760.11 and AC140714.1 genome sequences. BLAST programs next revealed that the distal promoter region (-2447 ~ -2043

position from TSS) and the proximal promoter region (-701 ~ -213 position from TSS) were well conserved between human *WNT2B* genome sequence and mouse *Wnt2b* genome sequence AC166156.4 (Fig. 1).

Consensus transcription factor-binding sites within the conserved promoter regions were searched for with manual inspection based on in-house knowledgebase. Double bHLH-binding sites [bHLH(1) and bHLH(2)] and double FOX-binding sites [FOX(1) and FOX(2)] within the distal promoter region of human *WNT2B* gene were conserved in mouse *Wnt2b* promoter (Fig. 1). HES-binding site, bHLH-binding site [bHLH(3)], and Sp1-binding site within the proximal promoter region of human *WNT2B* gene were also conserved in mouse *Wnt2b* promoter (Fig. 1).

Conservation of transcription factor-binding sites in other mammalian species was then searched for. Rat *Wnt2b* gene was located within AC106372.5 genome sequence, as previously described (45). Chimpanzee *WNT2B* gene was located within NW\_001229591.1 genome sequence. The bHLH(1)-binding site was not conserved in chimpanzee *WNT2B* promoter, whereas the bHLH(2)-binding site was not conserved in rat *Wnt2b* promoter. Together these facts indicate that FOX(1)-, FOX(2)-, HES-, bHLH(3)-, and Sp1-binding sites were conserved in human *WNT2B*, chimpanzee *WNT2B*, mouse *Wnt2b*, and rat *WNT2B* promoters (Fig. 1).

**Hedgehog signaling cascades and *WNT2B*.** Hedgehog signals are transduced through Patched family receptors to activate Smoothened signal transducer, which results in stabilization and nuclear accumulation of GLI family members for transcriptional activation of Hedgehog target genes (29,46-48). Hedgehog signaling cascade is aberrantly activated in basal cell carcinoma (49-51), gastric cancer (52,53), breast cancer (54), and other tumors. *WNT2B* is expressed in basal cell carcinoma (32), gastric cancer (6), breast cancer (31), and other tumors, as mentioned above. Because Hedgehog signaling activation and *WNT2B* expression co-existed in several types of human cancer, we investigated the causal link between Hedgehog signaling activation and *WNT2B* expression.

Consensus GLI-binding site was located at the position -4636 ~ -4628 from the human *WNT2B* TSS (Fig. 1). The

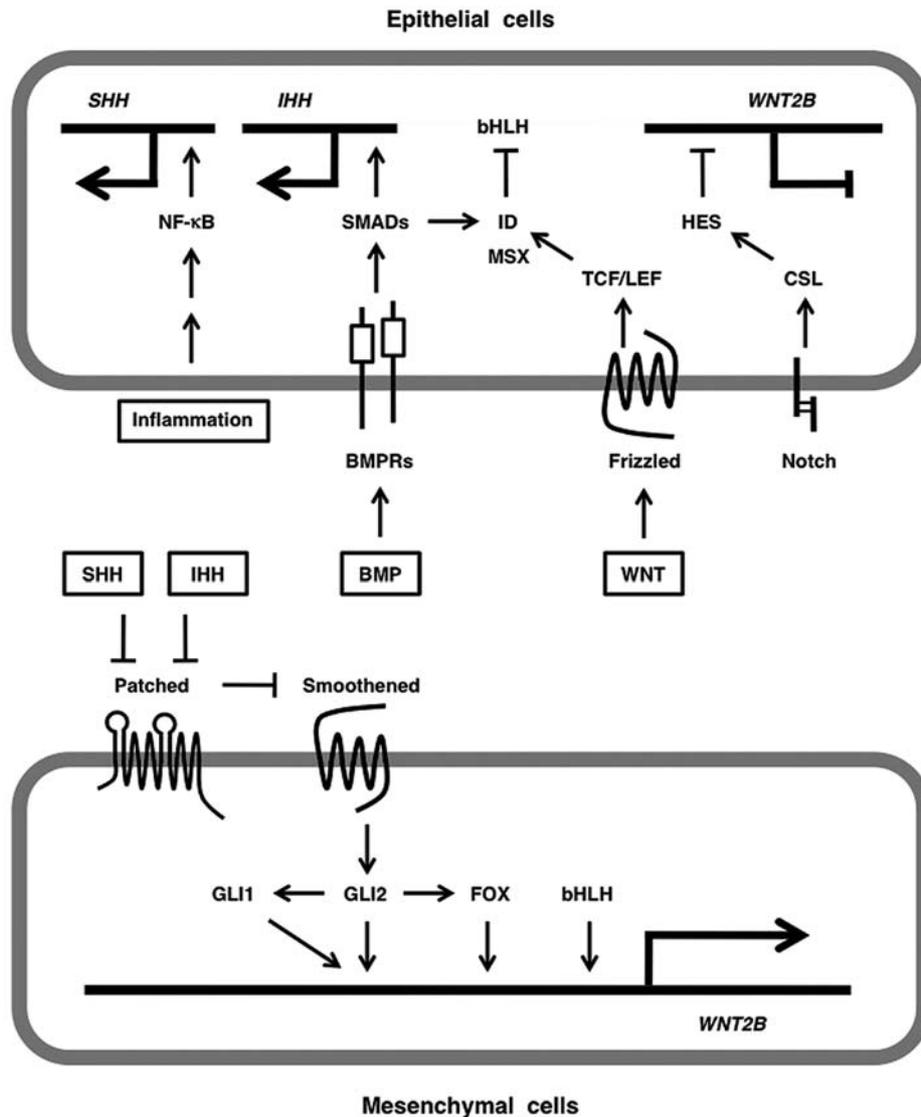


Figure 2. BMP-IHH-WNT2B and Inflammation-SHH-WNT2B signaling loops. Mesenchymal BMP induces *IHH* expression via SMADs in gastrointestinal epithelial cells, and inflammation induces *SHH* expression via NF-κB in epithelial cells. *WNT2B* expression is repressed in gastrointestinal epithelial cells by BMP and WNT signals via ID and MSX family members, and also by Notch signals via HES/HEY family members. *IHH* and *SHH* activate Hedgehog signaling cascades in mesenchymal cells to upregulate *WNT2B* expression via GLI and FOX family members, in cooperation with bHLH transcription factors.

GLI-binding site at about 5 kb upstream of human *WNT2B* TSS was completely conserved in chimpanzee *WNT2B* and rat *WNT2b* promoters, and was almost conserved in mouse *WNT2b* promoter except one base substitution (Fig. 1). *GLI1*, *FOXA2*, *FOXC2*, *FOX E1*, *FOXF1* and *FOXL1* are direct target genes of Hedgehog-GLI signaling cascade (29), and double FOX-binding sites within human *WNT2B* promoter were completely conserved in chimpanzee *WNT2B*, rat *WNT2b*, and mouse *Wnt2b* promoters, as mentioned above. Hedgehog signals should induce *WNT2B* upregulation through GLI and FOX family members (Fig. 2).

**BMP signaling cascades and WNT2B.** BMP signals are transduced through BMP receptors to SMAD1, SMAD5 or SMAD8 effectors to regulate transcription of target genes in cooperation with SMAD4 (55). *ID1*, *ID2*, *ID3*, *MSX1*, *MSX2*, *HES1*, *HEY1*, and *IHH* are representative target genes of BMP signaling cascades (56-58). *ID1*, *ID2* and *ID3* are HLH transcription factors functioning as inhibitors of tissue-specific

bHLH transcription factors. *MSX1* and *MSX2* are homeobox transcription factors functioning as inhibitors of tissue-specific bHLH transcription factors. *HES1* and *HEY1* are N-box-binding transcriptional repressors to downregulate tissue-specific bHLH transcription factors. BMP signals downregulate *WNT2B* expression due to the repression of bHLH-induced transcription via *ID1*, *ID2*, *ID3*, *MSX1*, *MSX2*, *HES1* or *HEY1*.

In adult mouse intestine, *Wnt2b* is expressed in mesenchymal cells (59), whereas *Indian Hedgehog (Ihh)* is expressed in differentiated epithelial enterocytes (60). We previously underscored the role of BMP-IHH signaling loop in the gastrointestinal homeostasis and carcinogenesis (61). Because epithelial *IHH* is able to induce mesenchymal *WNT2B* expression as mentioned above, we propose the BMP-IHH-*WNT2B* signaling loop in this study.

Based on these facts, it was concluded that BMP signals directly downregulate *WNT2B* expression in intestinal epithelial cells through the impediment of the bHLH-driven transcription,

and also that BMP signals indirectly upregulate *WNT2B* expression in intestinal mesenchymal cells through Hedgehog-mediated transcription (Fig. 2).

**Canonical WNT signaling cascades and *WNT2B*.** Canonical WNT signals are transduced through FZD and LRP5/6 receptors to activate transcription of target genes via the  $\beta$ -catenin-TCF/LEF complex, as mentioned above. MYC is a key target of canonical WNT signaling activation in colorectal cancer (22). MYC is one of bHLH-LZ transcription factors binding to the CACGTG motif to regulate cellular proliferation and differentiation (62). Manual inspection in this study revealed that consensus TCF/LEF- or MYC-binding site within *WNT2B* promoter was not conserved in mammals (data not shown). WNT and BMP signals synergistically induce upregulation of *ID2*, *MSX1*, and *MSX2* mRNAs (63). Because *ID2*, *MSX1* and *MSX2* are involved in the inhibition of bHLH-mediated transcription as mentioned above, it was predicted that canonical WNT signals downregulate *WNT2B* expression via *ID* and *MSX* family members (Fig. 2).

**Notch signaling cascades and *WNT2B*.** Notch ligands induce Notch signaling activation through the NICD-CSL complex, and *HES1*, *HES5*, *HEY1*, *HEY2* and *HEYL* are representative target genes of Notch signaling cascades (64-67). Manual inspection in this study revealed that the consensus CSL-binding site within *WNT2B* promoter was not conserved among mammals (data not shown). On the other hand, HES/HEY-binding N-box within proximal promoter region of *WNT2B* was conserved in mammals (Fig. 1). Together these facts indicate that Notch signals downregulate *WNT2B* expression via HES/HEY family members (Fig. 2).

**Chronic inflammation and *WNT2B*.** Chronic inflammation in tumor microenvironment is advantageous for tumor progression, because mediators or effectors of chronic inflammation support the proliferation and survival of tumor cells (68,69). NF- $\kappa$ B and STAT3 are representative transcription factors involved in inflammation-associated carcinogenesis. Because *WNT2B* is upregulated in chronic inflammation-associated diseases such as primary biliary cirrhosis (35) and inflammatory bowel disease (35,36), we next investigated the causal link between chronic inflammation and *WNT2B* expression. Consensus STAT3-binding site was not identified conserved in the *WNT2B* promoter region in this study (data not shown), while *in silico* prediction of NF- $\kappa$ B-binding site is not practical at present. Recently, *Sonic Hedgehog* (*Shh*) was identified as an NF- $\kappa$ B target gene (70). Because epithelial Hedgehog induces *WNT2B* upregulation in mesenchymal cells as mentioned above, we propose the inflammation-SHH-WNT2B signaling loop (Fig. 2).

## Discussion

Refined integrative genomic analyses on *WNT2B* orthologs were carried out to elucidate the transcriptional mechanisms of *WNT2B* in this study. GLI- and double FOX-binding sites within the distal promoter region as well as HES/HEY-, bHLH- and Sp1-binding sites within the proximal promoter region were well conserved in mammalian *WNT2B* orthologs (Fig. 1).

GLI-binding site in human *WNT2B* promoter was completely conserved in chimpanzee *WNT2B* and rat *Wnt2b* promoters, and was almost conserved in mouse *Wnt2b* promoter except one base substitution (Fig. 1). Double FOX-binding sites within human *WNT2B* promoter were completely conserved in chimpanzee *WNT2B*, rat *Wnt2b*, and mouse *Wnt2b* promoters (Fig. 1). Hedgehog signals initially stabilize the GLI2 activator to upregulate primary Hedgehog target genes, such as *GLI1*, *FOXA2*, *FOXC2*, *FOXE1*, *FOXF1* and *FOXLI*. Hedgehog-GLI2-induced GLI1 upregulation augments the Hedgehog signaling quantitatively as well as qualitatively (29). Based on the conserved GLI- and double FOX-binding sites within distal *WNT2B* promoter region, it was concluded that Hedgehog signals should induce *WNT2B* upregulation through GLI and FOX family members (Fig. 2).

HES/HEY- and bHLH-binding sites in human *WNT2B* promoter were completely conserved in chimpanzee *WNT2B*, rat *Wnt2b*, and mouse *Wnt2b* promoters (Fig. 1). Notch and BMP signals upregulate HES/HEY family members to repress *WNT2B* transcription, whereas BMP and WNT signals upregulate *ID* and *MSX* family members to impede bHLH-induced *WNT2B* upregulation. Notch, BMP, and WNT signals synergistically repress *WNT2B* transcription due to the impediment of the bHLH-induced *WNT2B* transcription (Fig. 2).

We emphasized the BMP-IHH signaling loop to maintain the homeostasis of stem-cell signaling network (61), and Kasperczyk *et al* reported the NF- $\kappa$ B-SHH signaling loop during chronic inflammation (70). These facts were combined with the results of this study to propose that the BMP-IHH and inflammation-SHH signaling loops are involved in *WNT2B* upregulation during embryogenesis, adult tissue homeostasis, and carcinogenesis.

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