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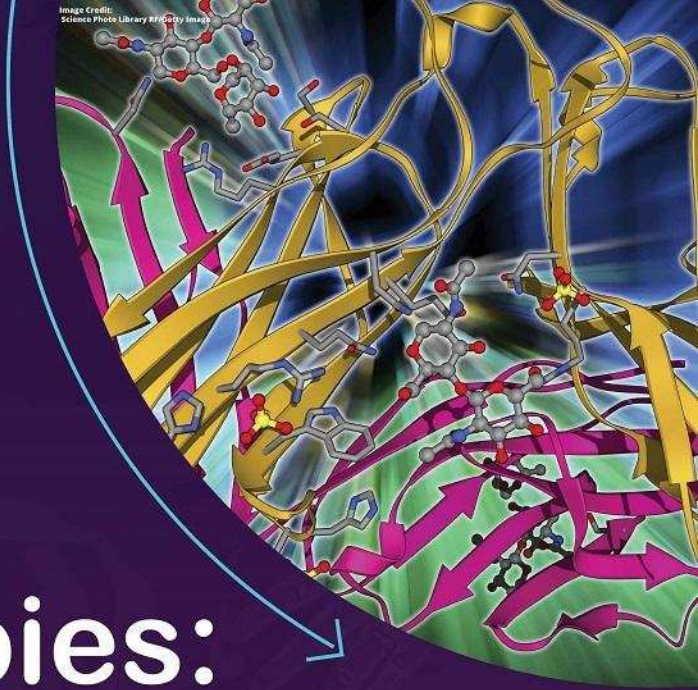


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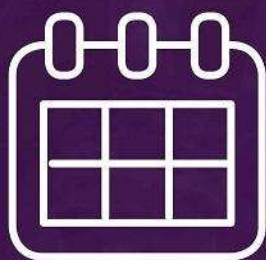
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Wnt/ β -Catenin Signaling Activates Expression of the Bone-Related Transcription Factor RUNX2 in Select Human Osteosarcoma Cell Types

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ABSTRACT

Osteosarcoma is the most common malignant bone tumor in children and adolescents. Metastasis and poor responsiveness to chemotherapy in osteosarcoma correlates with over-expression of the runt-related transcription factor RUNX2, which normally plays a key role in osteogenic lineage commitment, osteoblast differentiation, and bone formation. Furthermore, WNT/ β -catenin signaling is over-activated in osteosarcoma and promotes tumor progression. Importantly, the WNT/ β -catenin pathway normally activates RUNX2 gene expression during osteogenic lineage commitment. Therefore, we examined whether the WNT/ β -catenin pathway controls the tumor-related elevation of RUNX2 expression in osteosarcoma. We analyzed protein levels and nuclear localization of β -catenin and RUNX2 in a panel of human osteosarcoma cell lines (SAOS, MG63, U2OS, HOS, G292, and 143B). In all six cell lines, β -catenin and RUNX2 are expressed to different degrees and localized in the nucleus and/or cytoplasm. SAOS cells have the highest levels of RUNX2 protein that is localized in the nucleus, while MG63 cells have the lowest RUNX2 levels which is mostly localized in the cytoplasm. Levels of β -catenin and RUNX2 protein are enhanced in HOS, G292, and 143B cells after treatment with the GSK3 β inhibitor SB216763. Furthermore, small interfering RNA (siRNA)-mediated depletion of β -catenin inhibits RUNX2 expression in G292 cells.

Conflicts of interest: None.

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Thus, WNT/ β -catenin activation is required for RUNX2 expression in at least some osteosarcoma cell types, where RUNX2 is known to promote expression of metastasis related genes. *J. Cell. Biochem.* 118: 3662–3674, 2017. © 2017 Wiley Periodicals, Inc.

KEY WORDS: CANCER; OSTEOSARCOMA; Wnt/ β -CATENIN; RUNX2 TRANSCRIPTION FACTOR; ONCOGENE

Osteosarcoma is the most frequent primary malignant bone tumor in children and adolescents [Young and Miller, 1975]. The highest incidence of osteosarcoma is during the second decade of life, which suggests a relationship between bone growth and tumor development [Fraumeni et al., 1967; Cotterill et al., 2004], as well as dysregulation of osteoblast differentiation [Wagner et al., 2011]. Multiple studies suggest that RUNX2 is a key pathological factor in osteosarcoma [Martin et al., 2011, 2014]. Importantly, over-expression of RUNX2 in transgenic mice within the osteoblast lineage inhibits osteoblast maturation [Liu et al., 2001; Geoffroy et al., 2002]. Hence, aberrant expression of RUNX2 may contribute to compromised osteoblast growth and differentiation relationships that are evident in osteosarcoma [Stein et al., 1994].

Upregulation of the WNT/ β -catenin pathway is also associated with development of osteosarcoma [Hoang et al., 2004a; Wunder et al., 2007; Kansara et al., 2014; Martins-Neves et al., 2016a,b; Techavichit et al., 2016; Zanotti and Canalis, 2016]. Consequently, several attractive molecular strategies for therapeutic intervention are being considered that target WNT signaling in osteosarcoma [Papa et al., 2015; Bravo et al., 2017; Goldstein et al., 2016; Horne et al., 2016; Shen et al., 2016]. WNT signaling normally stimulates osteoblast maturation by activating RUNX2 expression, albeit that part of this mechanism may occur independent of the WNT responsive transcription factor LEF1 [Gaur et al., 2005; Mbalaviele et al., 2005; Kahler et al., 2006; Galindo et al., 2007; Ling et al., 2010; Schoeman et al., 2015]. These findings collectively suggest that the developmental interplay between RUNX2 and WNT is deregulated in osteosarcoma, thus motivating studies to examine the extent to which RUNX2 expression depends on WNT signaling in bone cancer cells.

Analysis of genomic DNA from osteosarcoma patients with amplification of the 6p12-p21 chromosomal interval, which spans the RUNX2 locus, increases RUNX2 gene copy number and aberrantly elevates RUNX2 expression [Lau et al., 2004; Lu et al., 2008; Sadikovic et al., 2009]. RUNX2 protein and mRNA levels are frequently elevated in clinical osteosarcoma specimens and osteosarcoma cell culture models, although there are major variations in expression [Thomas et al., 2004; Andela et al., 2005; Lu et al., 2008; Luo et al., 2008; Nathan et al., 2009; Pereira et al., 2009; Sadikovic et al., 2009; Won et al., 2009; Kurek et al., 2010; Shapovalov et al., 2010; Lucero et al., 2013]. Loss of p53 that is frequently observed in osteosarcoma increases RUNX2 gene expression by relieving repression by miR-34 [van der Deen et al., 2012, 2013]. Increased expression of RUNX2 in osteosarcoma has been associated with increased tumorigenicity, tumor progression, metastases, poor prognosis, and lower survival [Won et al., 2009; Kurek et al., 2010; Sadikovic et al., 2010; van der Deen et al., 2012, 2013]. RUNX2 levels are normally modulated during cell cycle and up-regulated with respect to cessation of cell growth in pre-osteoblastic cells [Pratap et al., 2003; Galindo et al., 2005], but this

mechanism is dysregulated in osteosarcoma [Galindo et al., 2005; Young et al., 2007a; San Martin et al., 2009; Lucero et al., 2013]. In osteosarcoma cells, RUNX2 controls expression of a number of cancer-related genes [van der Deen et al., 2012, 2013] and interacts with several subnuclear factors involved in the DNA damage response [Yang et al., 2015]. The later findings may be linked to the observation that increased expression of RUNX2 is associated with unfavorable prognosis for chemotherapy in pediatric osteosarcoma patients [Martin et al., 2014].

The canonical WNT signaling pathway and its protein mediator β -catenin are essential for development, stem cell maintenance and tissue regeneration [Beachy et al., 2004; Gordon and Nusse, 2006]. In the absence of WNT signaling, inactivation of the canonical WNT signaling pathway is achieved by targeting β -catenin into a multi-protein complex which is formed by Axin, the tumor suppressor APC (adenomatous polyposis coli protein) and the kinases CK1 α and GSK3 β . Ultimately, GSK3 β phosphorylates β -catenin and thereby targets it for proteasomal degradation [Polakis, 2007]. When WNT ligands bind to Frizzled and LRP5/LRP6 receptors in the cell surface, cytoplasmic Dvl (dishevelled) antagonizes GSK3 β -dependent phosphorylation of β -catenin. Once the phosphorylation of β -catenin is reduced, it dissociates from the Axin/APC/CK1 α /GSK3 β complex, stabilizes and accumulates in the cytoplasm [Vielhaber and Virshup, 2001; Knippschild et al., 2005]. Increased cytoplasmic β -catenin levels favor the subsequent β -catenin nuclear accumulation, allowing association with TCF/LEF transcription factors and subsequent activation of genes that contribute to cancer progression and metastasis [Polakis, 2007]. Thus, nuclear β -catenin accumulation is crucial for cancer progression, which explains the increased expression of genes involved in progression and survival of tumor cells [Bienz and Clevers, 2000; Brembeck et al., 2006].

Alterations within the WNT/ β -catenin signaling pathway have been described in human osteosarcoma cell lines and clinical osteosarcoma samples, which strongly support a possible role for WNT/ β -catenin signaling in the pathobiology and progression of human osteosarcoma. Specifically, the WNT/ β -catenin pathway is upregulated in metastatic osteosarcoma cell lines and higher grade osteosarcoma as well as hyper-activated in bone tumors and clinical samples [Haydon et al., 2002; Srivastava et al., 2006; Daino et al., 2009; Flores et al., 2012; Ma et al., 2013]. Moreover, elevated WNT/ β -catenin signaling in osteosarcoma cell lines and patient specimens is associated with chemotherapy resistance and tumor cell survival [Rajkumar and Yamuna, 2008; Zhang et al., 2011a; Ma et al., 2013; Wu et al., 2014], tumorigenesis and metastasis [Hoang et al., 2004a; Guo et al., 2008; Kansara et al., 2009; Rubin et al., 2010], tumor progression [Hoang et al., 2004b; Leow et al., 2009], and decreased overall survival [Hoang et al., 2004a; Chen et al., 2008].

In this study, we systematically examined the relationship between WNT/ β -catenin signaling and RUNX2 gene expression in a panel of six human osteosarcoma cell lines. Our results indicate

that activation of the WNT/ β -catenin pathway enhances RUNX2 expression in osteosarcoma and thus may regulate expression of RUNX2 dependent genes that support tumor progression or metastasis.

MATERIALS AND METHODS

CELL CULTURE

Human osteosarcoma cell lines were obtained from the American Type Culture Collection (ATCC, Manassas, VA). Osteosarcoma cells were maintained in culture medium supplemented with 10–15% fetal bovine serum (FBS) (HyClone Laboratories Inc, Logan, UT) plus 2 mM L-glutamine and a penicillin-streptomycin cocktail at 37°C and 5% CO₂ according to the recommendations of ATCC. The growth medium was changed every 2 days. SAOS (alias SaOS-2) cells were cultured in McCoy's medium (Sigma-Aldrich, St Louis, MO) supplemented with 15% FBS. U2OS and G292 cells were cultured in McCoy's medium with 10% FBS. MG63 and HOS cells were grown in DMEM medium (Gibco, Life Technologies, Grand Island, NY) with 10% FBS. 143B cells were maintained in DMEM medium, 1 mM sodium pyruvate, 100 μ g/ml of bromodeoxyuridine and 10% FBS. Alternatively, after 72 h cells were treated with 10 μ M of SB216367 (Sigma-Aldrich), and cultured for 24 h.

WESTERN BLOT ANALYSIS

RUNX2, β -catenin and β -actin were analyzed by Western blot analysis as described previously [Galindo et al., 2005]. Briefly, equal amounts of total cellular proteins collected in the presence of the proteasome inhibitor MG132 (Calbiochem, San Diego, CA) and Complete[®] cocktail of protease inhibitor (Roche Diagnostics, Mannheim, Germany) were resolved in 10% SDS-PAGE and transferred to polyvinylidene difluoride membranes (Perkin Elmer, Boston, MA). Blots were incubated with a 1:2,000 dilution of each primary antibody for 1 h. RUNX2-specific mouse monoclonal antibody 8G5 (MBL International, Woburn, MA), β -catenin mouse monoclonal antibody 610154 (BD Transduction Lab, Bedford, MA) and actin goat polyclonal antibody sc-1615 (Santa Cruz Biotechnology Inc., Santa Cruz, CA) were acquired commercially. Membranes were incubated with the respective horseradish peroxidase-conjugated secondary antibody (sc-2005 anti-mouse or sc-2020 anti-goat) (Santa Cruz Biotechnology Inc.) for 1 h. Immuno-reactive protein bands were visualized on a Kodak BioMax Light film (Carestream Health Inc, Rochester, NY) using a chemiluminescence detection kit (Thermo Scientific, Rockford, IL). Signal intensities were quantified by densitometry.

SEMI-QUANTITATIVE PCR AND RNA-seq ANALYSIS

Gene expression analyses were performed using semi-quantitative PCR as described previously [Varela et al., 2016] as a reproducible method that permits direct visualization of amplified cDNAs. Quantitation of mRNA expression detected by PCR was subsequently validated with next generation RNA sequencing (RNA-seq) data that were concurrently generated for SAOS, MG63 and U2OS cell lines using procedures we previously described [Dudakovic et al., 2014]. For RT-PCR analysis, total RNA was

isolated from osteosarcoma cells using TRIzol reagents (Invitrogen, Carlsbad, CA) according to the manufacturer's specifications. Total RNA was separated in a 1% agarose-formaldehyde gel. Ethidium bromide staining of the gels was used to assess RNA quality of samples. Purified RNA (3 μ g) was treated with RQ1RNase-Free DNase (Promega, Madison, WI) and subjected to reverse transcription using random hexamer primers (Promega) with M-MLV reverse transcriptase (Promega) according to the manufacturer's recommendations. Gene expression was assessed by PCR using the following specific human gene primers (0.5 pmol/ μ l): *RUNX2* (forward primer: 5'-CCGACGACAACCGCACCAT-3', reverse primer: 5'-CGTCCGGCCCACAAATCTC-3'), *β -catenin/CTNNB1* (forward primer: 5'-TGGTGCCAGGGAGAACCC-3', reverse primer: 5'-CCCACCCTCGAGCCCTCTC-3'), *DKK1* (forward primer: 5'-AACCGGCACGGTTTCGTGGG-3', reverse primer: 5'-CGCAGCGGTACGGCTGGTAG-3'), *TCF4* (forward primer: 5'-TGGCCCTGAGAGGCAGCCAT-3', reverse primer: 5'-GGTCTCATCGTCATTATTGCTAGAT-3'), *LEF1* (forward primer: 5'-CCAGC-TATTGTAAACACCTCA-3', reverse primer: 5'-TTCAGATGTAGG-CAGCTGTC-3'), *LRP5* (forward primer: 5'-CAGCCTG AC GCACCCCTTCG-3', reverse primer: 5'-CACCTCCT CGG CTCCTGCCT-3'), *LRP6* (forward primer: 5'-GCTGGAATG-GATGGTTCAAGTCG-3', reverse primer: 5'-CAGAATGGATTTCACGCAGACCC-3'), *WNT3A* (forward primer: 5'-GTTGG GCCACAG-TATTCCTC-3', reverse primer: 5'-ATCCCACCAAACCTCGATGTC-3'), *WNT10B* (forward primer: 5'-GAATGCGAATCCACAACAACAG-3', reverse primer: 5'-TTGCGG TTGTGGGT ATCAATGAA-3'), *Alkaline Phosphatase/ALPL* (forward primer: 5'-AGTGCTCTGCG-CAGGATTGGA-3', reverse primer: 5'-CACACAGGTAG GCG GTGGCG-3'), *OC/BGLAP* (forward primer: 5'-CTGGCCAGG-CAGGTGCGAAG-3', reverse primer: 5'-CAGGCCAGCAGAGCGA-CACC-3'), and *GADPH* (forward primer: 5'-CCTT CATT GACCT CAACTA-3', reverse primer: 5'-GGCCATCCACAGTCTTCT-3'). PCR amplification of cDNAs was carried out using 1 \times PCR buffer (Promega) containing 0.2 mM dNTPs (Promega), 1.5 mM MgCl (Promega), 0.06 U/ μ l of Taq polymerase (Invitrogen) by incubation for 5 min at 94°C and 20–30 amplification cycles of synthesis were applied to avoid product saturation (1 min at 94°C, 1 min at 52–62°C, and 1 min at 72°C), followed by a final extension step at 72°C for 6 min. Aliquots of the resulting products (5 μ l) were visualized in 1% agarose gels by ethidium bromide staining.

IMMUNOHISTOCHEMISTRY

Cell were washed twice with PBS and collected in a 1.5 ml tube using a scraper followed by centrifugation at 380g for 2 min. The cell pellets were fixed for 24 h, dehydrated and embedded in paraffin using standard procedures. Paraffin-embedded cells were sectioned (5 μ m), adhered to glass slides and rehydrated. Antigens were recovered by treatment with retrieval buffer (1 mM Tris, 0.5 mM EGTA, pH 9.0). Sections were blocked with PBS supplemented with 1% bovine serum albumin. Then sections were incubated with RUNX2 (M70) rabbit polyclonal antibody sc-10758 (Santa Cruz Biotechnology Inc.) or anti- β -catenin antibody, washed, and incubated with the indicated biotinylated secondary antibody. Finally, antibodies bound to specific antigens were detected using a biotin-streptavidin detection system.

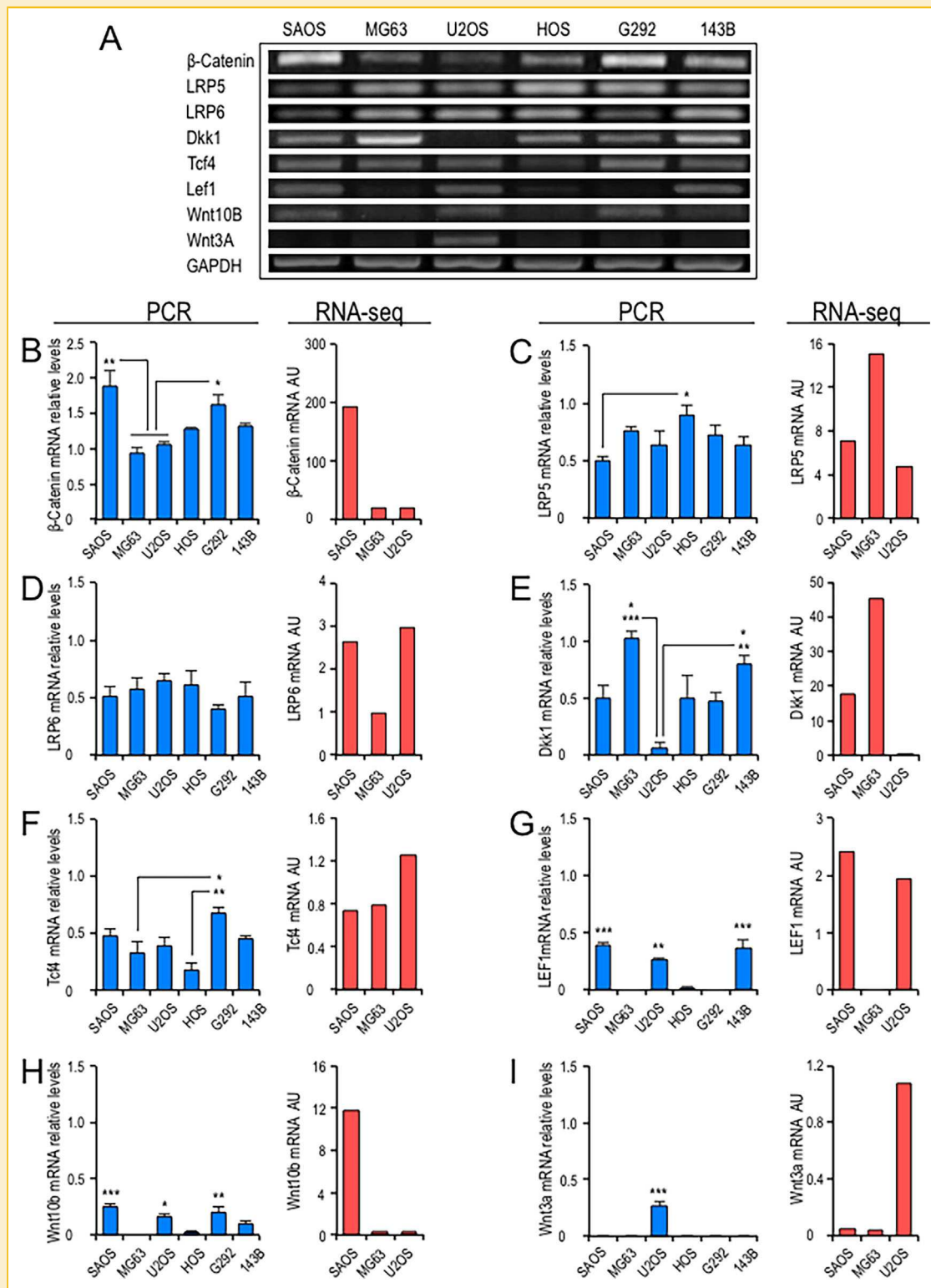


Fig. 1. Expression of Wnt/ β -catenin signaling pathway components in human osteosarcoma cell lines. The mRNA levels of β -Catenin/*CTNNB1*, *LRP5*, *LRP6*, *DKK1*, *TCF4*, *LEF1*, *WNT10B*, and *WNT3A* were assessed by RT-PCR and RNA-seq in SAOS, MG63, U2OS, HOS, G292, and 143B osteosarcoma cells (A–I). The graphs below depict quantitation of the RT-PCR data (left graphs) and RNAseq data (right graphs) as indicated upon normalization to *GAPDH* (B–I). All data are presented as mean \pm SEM. Statistical significance was determined by Tukey post-hoc tests (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$). *DKK1*: MG63 and 143B cells versus the others four osteosarcoma cell lines (* $P < 0.05$); *LEF1*: SAOS and 143B cells versus MG63, HOS and G292 cells (*** $P < 0.001$), U2OS cells versus MG63, HOS, and G292 cells (** $P < 0.01$); *WNT10B*: SAOS cells versus MG63 and HOS cells (*** $P < 0.001$), G292 cells versus MG63 and HOS cells (** $P < 0.01$), U2OS cells versus MG63 and HOS cells (* $P < 0.05$).

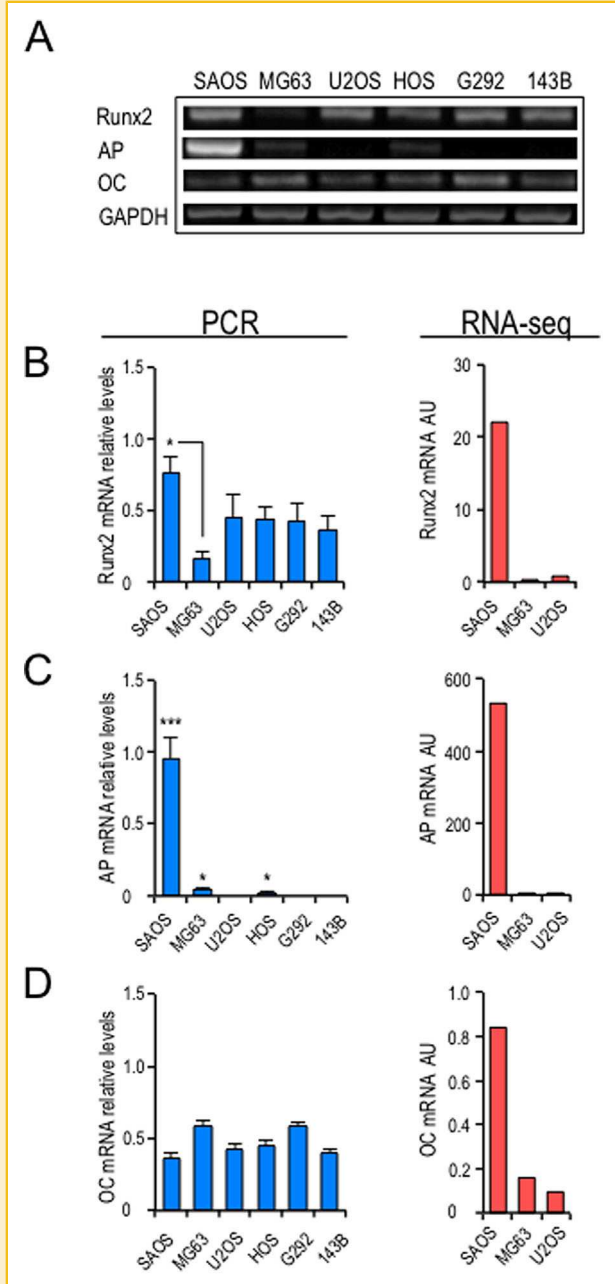


Fig. 2. Expression of *RUNX2* and bone differentiation markers in human osteosarcoma cell lines. Expression of mRNAs for *RUNX2* and the bone differentiation markers alkaline phosphatase (AP, *ALPL*) and osteocalcin (OC, *BGLAP*) were examined by RT-PCR in the human osteosarcoma cell lines SAOS, MG63, U2OS, HOS, G292, and 143B (A). The graphs show quantification of the RT-PCR data (left graphs) and RNAseq data (right graphs) relative to *GAPDH* mRNA (B–D) and are presented as mean \pm SEM. Statistical significance was determined by Tukey post-hoc tests (* $P < 0.05$; *** $P < 0.001$). AP: SAOS cells versus the others five osteosarcoma cell lines (*** $P < 0.001$), MG63 and HOS cells versus U2OS, G292, and 143B cells (* $P < 0.05$).

RNA INTERFERENCE

RNA interference experiments were carried out using commercially available siRNAs (Dharmacon, Lafayette, CO). Specific siRNA (h) for

RUNX2 (ON-TARGET plus, SMARTpool) and β -catenin (ON-TARGET plus, SMARTpool) were designed to inhibit *RUNX2* and β -catenin gene expression. Control non-silencing (ns) RNA (ON-TARGET plus, Non-targeting Pool) was used as negative control in our experiments, because this pool of nsRNA has no discernible off-target effects on cell growth parameters examined in our study. Cells were plated in 60 mm plates at a density of 3×10^5 cells/plate and cultured for 24 h in DMEM with 10% FBS in absence of antibiotics at 40–60% of confluence. Subsequently, cells were washed in PBS, and transfected in 2 ml of Opti-MEM medium (Gibco, life Technologies) plus 2.5 to 5 μ l of a 20 μ M stock solution of each siRNA pool (final concentration of 25–50 nM) and 12 μ l of Oligofectamine 2000 (Invitrogen). Concentrated complete DMEM ($3 \times$; 1 ml) was added 4 h after transfection to obtain approximately 3 ml of culture medium with standard final concentrations of penicillin-streptomycin cocktail, 2 mM L-glutamine, and 10% FBS. After siRNA transfection, cells were incubated for 48 h and *RUNX2* and β -catenin knock down efficiency was confirmed by Western blot analysis as described above.

STATISTICAL ANALYSIS

The data were represented as mean \pm SEM with a minimum of three independent samples and analyzed using one-way ANOVA with Tukey post-hoc tests, or by Student's *t*-test. *P*-value of less than 0.05 was considered statistically significant.

RESULTS

WNT/ β -CATENIN EXPRESSION IN OSTEOSARCOMA CELL LINES

To determine the status of Wnt/ β -catenin expression in osteosarcoma, we first analyzed expression of several Wnt/ β -catenin related genes in six human osteosarcoma cell lines (SAOS, MG63, U2OS, HOS, G292, and 143B) (Fig. 1). Expression of mRNA levels for β -catenin/*CTNNB1*, *LRP5*, *LRP6*, *DKK1*, *TCF4*, *LEF1*, *WNT10B*, and *WNT3A* was determined by RT-PCR. The mRNA levels for these genes were further validated in three of the lines (SAOS, MG63, U2OS) using RNA-seq data that were generated in parallel. All six osteosarcoma lines express the WNT co-receptors *LRP5* and *LRP6* at comparable mRNAs levels when normalized to *GAPDH* as detected by either PCR or RNA-seq (Fig. 1). However, these cell lines exhibit differences in the expression of other WNT signaling components. For example, SAOS, U2OS, G292, and 143B cells express alternatively high levels of positive WNT signaling components, including β -catenin/*CTNNB1* and the WNT-responsive transcription factors *TCF4* and/or *LEF1*, as well as the ligand *WNT10B* and/or *WNT3A*. In contrast, MG63 and HOS cells express minimal levels of *TCF4*, *LEF1*, *WNT10B*, and *WNT3A*. Yet, MG63 cells express the highest levels of the WNT inhibitor *DKK1*. Interestingly, 143B cells which are a metastatic derivative of HOS cells, express higher levels of *TCF4*, *LEF1*, and *WNT10B* than the parental cells, suggesting that increased expression of these WNT signaling components accompanies metastatic osteosarcoma progression of HOS cells. Taken together, the observed modulations in the mRNA levels of distinct WNT signaling components may reflect intrinsic differences in the potential for WNT signaling, unless other members of these gene

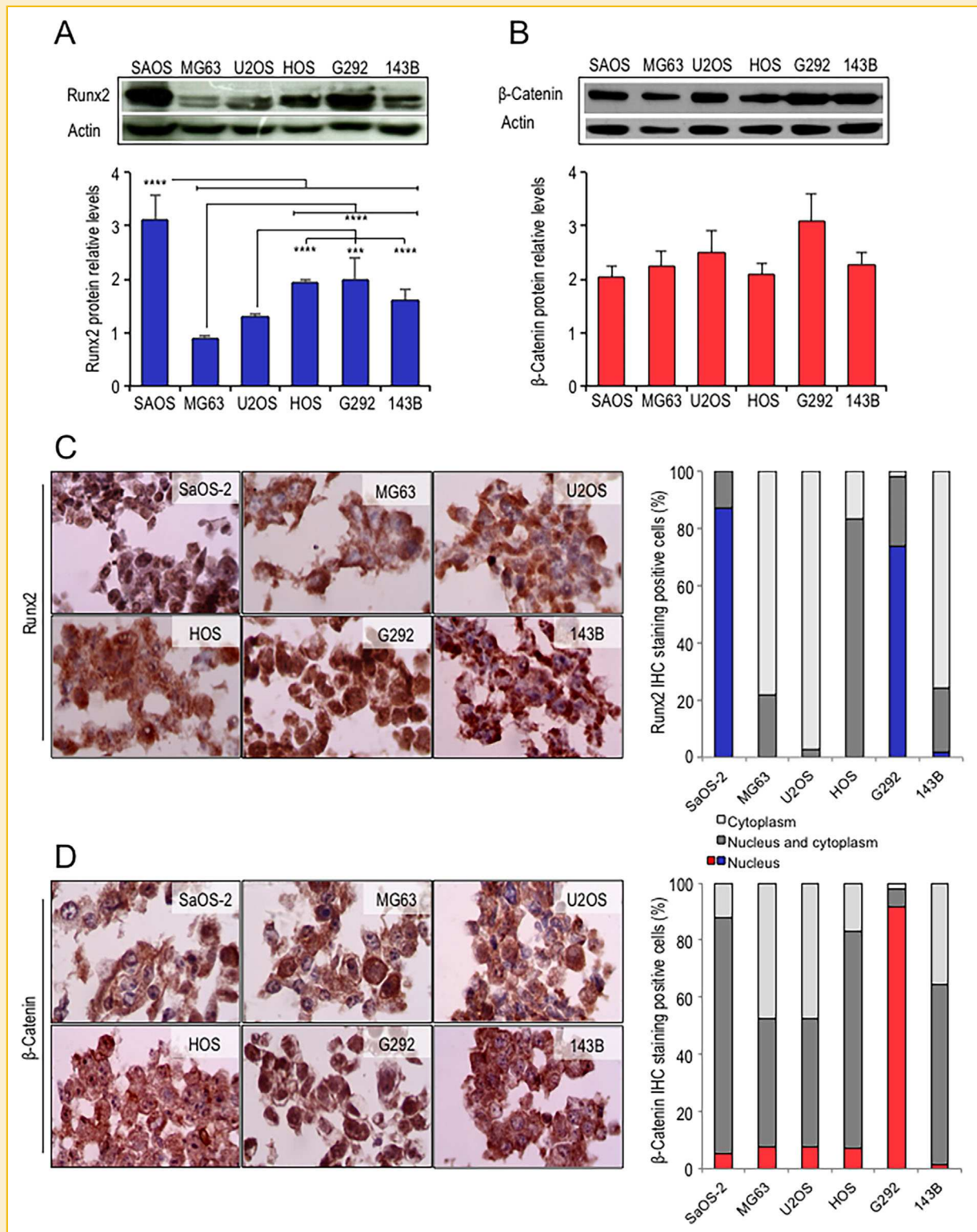


Fig. 3. Human osteosarcoma cell lines exhibit different nuclear expression pattern of β -catenin and RUNX2. Western blot analysis was performed to evaluate protein levels of RUNX2 (A) and β -catenin protein (B) in our panel of osteosarcoma cell lines as indicated. The bar graphs in each case show quantification for both proteins relative to β actin and are presented as mean \pm SEM. Statistical significance was determined by Tukey post-hoc tests (** $P < 0.001$; **** $P < 0.0001$). Each osteosarcoma cell line was grown up to 70% of confluence and fixed in paraformaldehyde for immunohistochemical detection of RUNX2 (C) and β -catenin (D). Magnification 400 \times . The graphs show the percentage of cell with RUNX2- or β -catenin-immunohistochemical staining in nucleus, nucleus and cytoplasm or cytoplasm.

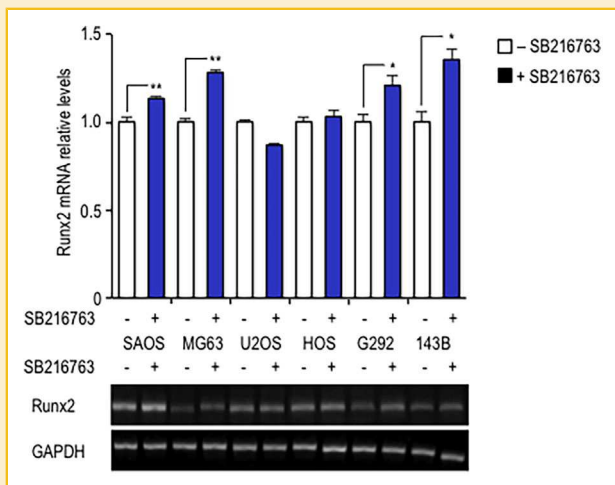


Fig. 4. *RUNX2* mRNA levels are differentially induced after treatment with GSK3 β inhibitor in human osteosarcoma cell lines. SAOS, MG63, U2OS, HOS, G292, and 143B osteosarcoma cell lines were grown up to 70% of confluence and then treated with SB216763 for 24 h. *RUNX2* mRNA levels were assessed by RT-PCR. The graphs depict data of *RUNX2* mRNA values normalized to *GAPDH* and relative to untreated cells. All data are presented as mean \pm SEM. (* $P < 0.05$ and ** $P < 0.01$).

families or post-transcriptional mechanisms compensate for the observed changes in gene expression in osteosarcoma cells.

EXPRESSION AND CELLULAR LOCALIZATION OF β -CATENIN AND *RUNX2* IN OSTEOSARCOMA CELL LINES

Expression analysis indicates that mRNA is expressed for *RUNX2* across all six osteosarcoma cell lines (Fig. 2). SAOS cells exhibit the highest *RUNX2* mRNA levels compared to the others five osteosarcoma cell lines. *RUNX2* mRNA levels are also detected in U2OS, HOS, G292, and 143B cells, but it is barely detected in MG63. These PCR results were confirmed using RNA-seq data for *RUNX2* mRNA in SAOS, MG63, and U2OS cells, although RNA-seq is less effective in detecting *RUNX2* mRNA in U2OS cells (Fig. 2). Expression profiles of the bone markers alkaline phosphatase (“AP”; *ALPL*) and osteocalcin (“OC”; *BGLAP*) show that both are only co-expressed to a significant degree in SAOS cells, and to a lesser extent in U2OS cells. Specifically, SAOS cells, which have the highest relative mRNA levels for *RUNX2* also robustly express *AP/ALPL* and *OC/BGLAP* (Fig. 2). The PCR and RNA-seq data together in most cases show good concordance in expression levels detected in SAOS, MG63 and U2OS cells for the mRNAs of *RUNX2*, bone phenotypic markers and different WNT signaling components.

Western blot analysis of *RUNX2* protein levels in all the osteosarcoma cell lines shows that SAOS cells exhibit the highest expression of *RUNX2*, consistent with the high mRNA levels observed in this cell type (Fig. 3A). For comparison, total cellular β -catenin protein expression relative to β -actin is very similar in all six cell lines (Fig. 3B). *RUNX2* protein is detected in HOS, G292, and 143B cells, but to a lesser extent in U2OS cells and MG63 cells (Fig. 3B). These findings are consistent with data we previously

reported [Lucero et al., 2013]. The reduced levels of *RUNX2* protein in MG63 are attributable to low mRNA levels (see Fig. 2), while the discordance between *RUNX2* mRNA and protein levels in U2OS cells may be due to expression of the p53 responsive miRNA miR-34 that suppresses *RUNX2* protein accumulation [Zhang et al., 2011b; van der Deen et al., 2013].

Because both β -catenin and *RUNX2* can exhibit changes in subcellular localization, we analyzed whether these proteins localize to the nucleus (Fig. 3C and D). Nuclear accumulation of both *RUNX2* and β -catenin protein is evident to different degrees in nuclei from all six cell lines. Nuclear localization of *RUNX2* is most evident in SAOS and G292 cells but is clearly more cytoplasmic in MG63 and U2OS cells (Fig. 3C), which expresses low levels of *RUNX2* protein (Fig. 3A). Nuclear accumulation of β -catenin is most pronounced in G292 cells (Fig. 3D), consistent with these cells having an mRNA expression profile for WNT signaling components high levels of β -catenin/*CTNNB1*, *TCF4*, *WNT10B*, and low levels of *DKK1* that is conducive for WNT signaling and β -catenin stabilization (see Fig. 1).

STABILIZATION OF β -CATENIN DIFFERENTIALLY INCREASES *RUNX2* PROTEIN LEVELS IN OSTEOSARCOMA CELLS

To determine if WNT/ β -catenin pathway modulates *RUNX2* expression in osteosarcoma, we treated cells with the GSK3 β inhibitor SB216763. *RUNX2* mRNA levels increase modestly in SAOS, MG63, G292, and 143B cells treated with SB216763 compared to control cells (Fig. 4). More importantly, treatment with the GSK3 β inhibitor results in up-regulation of both β -catenin and *RUNX2* protein levels in HOS, G292, and 143B cells (Fig. 5). Because G292 cells exhibit robust nuclear accumulation of β -catenin, we examined the effect of siRNA-mediated knockdown of β -catenin on *RUNX2* expression in this cell type. Control experiments show that β -catenin and *RUNX2* proteins are each down-regulated by their respective siRNAs in G292 cells (Fig. 6A and B). As expected, treatment of G292 cells with siRNA against β -catenin (25 or 50 nM), but not with control non-silencing RNA, reduces *RUNX2* protein expression by 2–3 fold depending on the dose. For comparison, treatment of cells with *RUNX2* siRNA (50 nM) reduces *RUNX2* levels by approximately 2 fold, independent of the presence of the β -catenin siRNA (Fig. 6C). Therefore, siRNA depletion of β -catenin is at least as effective in down-regulating *RUNX2* as direct depletion of *RUNX2* by siRNA for *RUNX2*.

DISCUSSION

Gene regulatory pathways governed by WNT/ β -catenin and *RUNX2* are both synergistically involved in osteoblast growth and differentiation, and are each compromised in osteosarcoma. Therefore, we examined the relationship between expression of WNT signaling components and *RUNX2* in osteosarcoma cells. One key findings of this paper is that the mRNA levels of distinct WNT signaling components (e.g., *DKK1*, *TCF4*, *LEF1*, *WNT10B*, and *WNT3A*) are highly variable among six osteosarcoma cell lines, while others (e.g., *LRP5* and *LRP6*) are relatively constant. Interestingly, β -catenin protein levels are very similar in all six

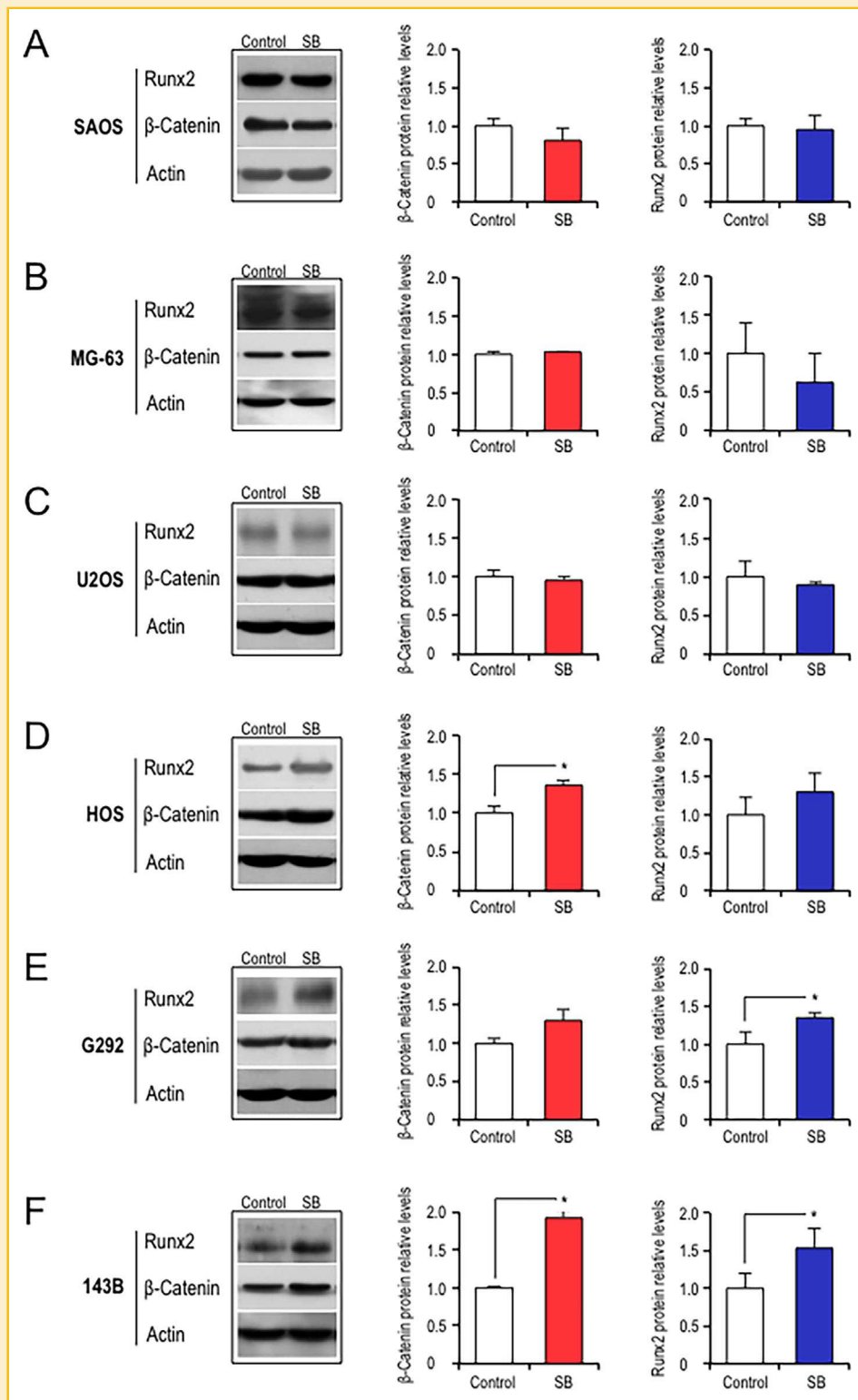


Fig. 5. RUNX2 protein levels are differentially up-regulated after treatment with GSK3 β inhibitor in human osteosarcoma cell lines. SAOS, MG63, U2OS, HOS, G292, and 143B osteosarcoma cell lines were grown up to 70% of confluence and then treated with the GSK3 β inhibitor SB216763 (SB) for 24 h. RUNX2 and β -catenin protein levels were assessed by Western blot analysis (A–F). Graphs depict data of RUNX2 and β -catenin protein values normalized to β -actin. All data are presented as mean \pm SEM. (* $P < 0.05$).

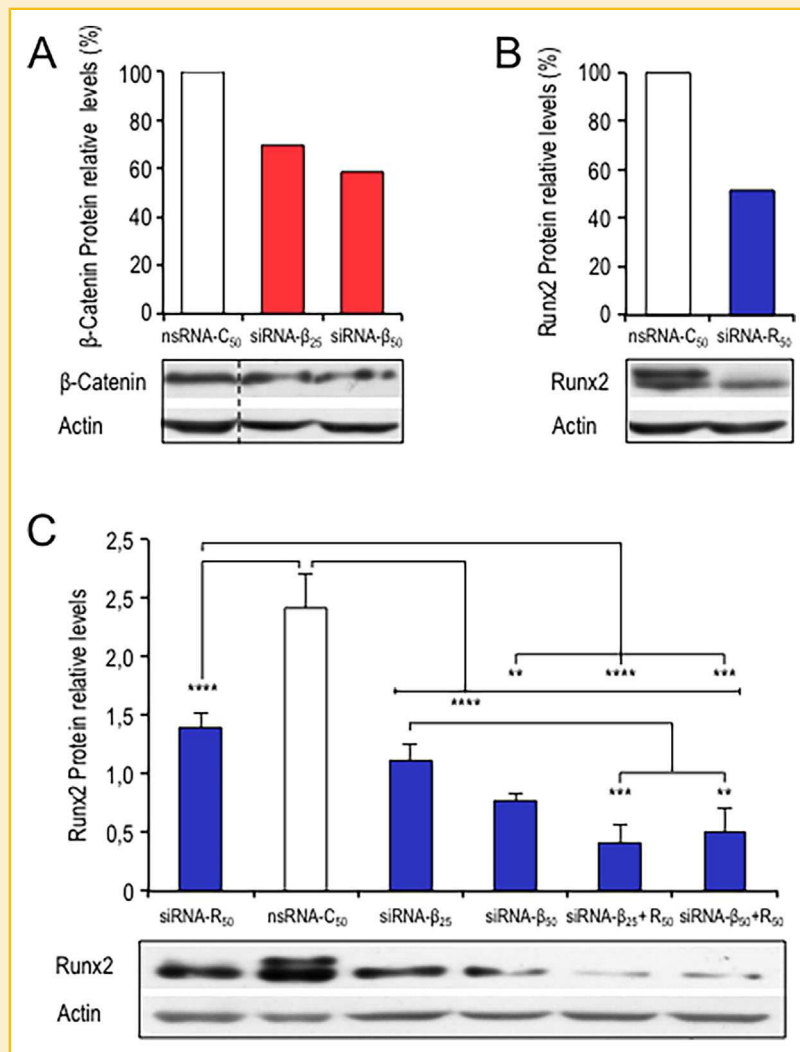


Fig. 6. β -Catenin deficiency reduces RUNX2 expression in human osteosarcoma cell line. G292 cells were treated with β -catenin siRNA (25–50 nM) (A) or RUNX2 siRNA (50 nM) (B) to assess efficiency of either siRNAs compared to control non-silencing (ns) RNA. Graphs depict data of RUNX2 and β -catenin protein values as a percentage of cells treated with control nsRNA. G292 osteosarcoma cells were transfected with β -catenin siRNA and/or RUNX2 siRNA (C) to determine if β -catenin deficiency reduces RUNX2 expression, as compared to RUNX2 siRNA or control nsRNAs. RUNX2 protein levels were assessed by Western blot analysis at day 2 after transfection. Graphs depict data of RUNX2 protein levels normalized to β -actin. All data are presented as mean \pm SEM. (** $P < 0.01$ and *** $P < 0.001$, **** $P < 0.0001$).

osteosarcoma cell lines. However, β -catenin nuclear accumulation was observed at different degrees in osteosarcoma cells. As expected, *RUNX2* mRNA and protein levels are robustly expressed in most osteosarcoma cell types, except MG63 cells that have low expression of *RUNX2* with residual protein levels showing mostly cytoplasmic localization. These expression differences suggest that cross-talk between WNT signaling and *RUNX2* activity is cell type dependent among osteosarcomas.

The strong expression of *RUNX2* in actively proliferating osteosarcoma cells is remarkable because *RUNX2* protein expression is normally increased at the cessation of proliferation and initiation of differentiation of pre-osteoblastic cells, to reinforce a quiescent state [Pratap et al., 2003; Galindo et al., 2005, 2007; Young et al., 2007b]. Regulatory mechanisms controlling *RUNX2* expression in osteosarcoma cells must balance *RUNX2* protein levels to promote

its putative oncogenic functions, while avoiding suppression of bone tumor cell growth [van der Deen et al., 2012; Lucero et al., 2013]. The growth suppressive potential of *RUNX2* is normally controlled by modulation of its protein and mRNA levels during the cell cycle [Galindo et al., 2005, 2007]. Cell cycle dependent changes of *RUNX2* protein and mRNA levels occur with respect to the G1 phase when osteoblasts monitor extra-cellular cues for competency to initiate cell cycle progression beyond the G1/S phase transition [Galindo et al., 2005, 2007]. Down-regulation of *RUNX2* in late G1 phase may be mediated by CDK-related and ubiquitin/proteasome dependent protein degradation [Galindo et al., 2005; Shen et al., 2006; Rajgopal et al., 2007]. Cell cycle control of *RUNX2* protein levels is retained in 143B, G292, HOS, and U2OS osteosarcoma cells [Lucero et al., 2013]. In this study we show that the low levels of *RUNX2* observed in MG63 and U2OS cells are mostly cytoplasmic, while the

constitutively high levels of RUNX2 proteins in SAOS cells are mostly localized in the nucleus. The remaining cell types show a mixed nuclear and cytoplasmic distribution of RUNX2. Hence, the possibility arises that cell cycle dependent changes in nuclear RUNX2 protein levels may be linked to nuclear/cytoplasmic shuttling in osteosarcoma cells.

Because RUNX2 expression is transcriptionally stimulated by WNT/ β -catenin signaling [Gaur et al., 2005], increased activation of this pathway could potentially enhance RUNX2 expression in osteosarcoma. In addition, RUNX2 controls components of multiple signaling pathways in osteosarcoma cells, including Wnt ligands [van der Deen et al., 2012], suggesting the potential for cross-talk through self-reinforcing positive feedback loops. However, RUNX2 stimulation of the mouse osteocalcin promoter is suppressed by protein/protein interactions with LEF1 and β -catenin in several osteoblastic cell types and osteosarcoma cells [Kahler and Westendorf, 2003]. Thus, both negative and positive feedback mechanisms may mediate cross-talk between RUNX2 and the WNT/ β -catenin pathway to control bone cell differentiation or progression of osteosarcoma.

Previous reports have demonstrated that RUNX2 is expressed in distinct cancer types [Ito et al., 2015]. For example, RUNX2 has been involved in tumor progression and bone metastasis in breast and prostate cancer [Pratap et al., 2005, 2006, 2008; Leong et al., 2010; Ferrari et al., 2013; McDonald et al., 2014], as well as tumorigenesis in lymphomas [Blyth et al., 2005]. In normal mammary epithelial cells RUNX2 is expressed at low levels, but it is expressed at high levels in metastatic mammary cancer cells [Selvamurugan and Partridge, 2000; Inman and Shore, 2003; Barnes et al., 2004]. RUNX2 also promotes bone metastatic properties of breast and prostate cancer cells [Brubaker et al., 2003; Javed et al., 2005; Pratap et al., 2005, 2006, 2008; Leong et al., 2010]. Enhanced expression of RUNX2 is also associated with stimulating the oncogenic potential of cells during lymphoma development [Blyth et al., 2006]. Moreover, RUNX2 is strongly expressed in human malignant melanoma, thyroid papillary carcinoma, gliomas, and pituitary tumors, which suggests that this cancer gene promotes tumorigenesis in a broad spectrum of tumors [Riminucci et al., 2003; Endo et al., 2008; Vladimirova et al., 2008; Zhang et al., 2009]. Interestingly, several studies have shown that the Wnt/ β -catenin pathway is also aberrantly expressed in breast and prostate cancer [Geyer et al., 2011; Kypta and Waxman, 2012], melanoma [Omholt et al., 2001], lymphoma [Gelebart et al., 2008], gliomas [Zhang et al., 2012], and pituitary tumors [Elston and Clifton-Bligh, 2010], as well as in thyroid papillary carcinoma [Gilbert-Sirieix et al., 2011]. These studies collectively suggest that cross-talk between Wnt/ β -Catenin signaling and RUNX2 may be operative in both osseous and non-osseous tumors.

In osteosarcoma specimens from human patients, expression of RUNX2 varies depending on tumor stage and grade, and its levels are prognostic for chemotherapy responsiveness, metastasis, and long term survival [Won et al., 2009; Kurek et al., 2010; Sadikovic et al., 2010; van der Deen et al., 2013]. One key finding of this is that WNT/ β -catenin signaling positively modulates RUNX2 protein levels in a subset of osteosarcoma cell types. WNT/ β -catenin signaling is most pronounced in G292 cells which exhibit the greatest nuclear

accumulation of β -catenin. We propose that the WNT/ β -catenin pathway may promote parameters of tumor progression in osteosarcoma at least in part by functional cross-talk including stimulation of RUNX2 gene expression.

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