

CTHRC1 Acts as a Prognostic Factor and Promotes Invasiveness of Gastrointestinal Stromal Tumors by Activating Wnt/PCP-Rho Signaling¹ Ming-Ze Ma^{*,2}, Chun Zhuang^{†,2}, Xiao-Mei Yang^{*}, Zi-Zhen Zhang[†], Hong Ma^{*}, Wen-Ming Zhang[‡], Haiyan You^{*}, Wenxin Qin^{*}, Jianren Gu^{*}, Shengli Yang^{*}, Hui Cao[†] and Zhi-Gang Zhang^{*}

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Abstract

Gastrointestinal stromal tumors (GISTs) are the major gastrointestinal mesenchymal tumors with a variable malignancy ranging from a curable disorder to highly malignant sarcomas. Metastasis and recurrence are the main causes of death in GIST patients. To further explore the mechanism of metastasis and to more accurately estimate the recurrence risk of GISTs after surgery, the clinical significance and functional role of collagen triple helix repeat containing-1 (CTHRC1) in GIST were investigated. We found that CTHRC1 expression was gradually elevated as the risk grade of NIH classification increased, and was closely correlated with disease-free survival and overall survival in 412 GIST patients. *In vitro* experiments showed that recombinant CTHRC1 protein promoted the migration and invasion capacities of primary GIST cells. A luciferase reporter assay and pull down assay demonstrated that recombinant CTHRC1 protein activated noncanonical Wnt/PCP-Rho signaling but inhibited canonical Wnt signaling. The pro-motility effect of CTHRC1 on GIST cells was reversed by using a Wnt5a neutralizing antibody and inhibitors of Rac1 or ROCK. Taken together, these data indicate that CTHRC1 may serve as a new predictor of recurrence risk and prognosis in post-operative GIST patients and may play an important role in facilitating GIST progression. Furthermore, CTHRC1 promotes GIST cell migration and invasion by activating Wnt/PCP-Rho signaling, suggesting that the CTHRC1-Wnt/PCP-Rho axis may be a new therapeutic target for interventions against GIST invasion and metastasis.

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Introduction

Gastrointestinal stromal tumors (GISTs) are mesenchymal neoplasms that usually arise in the stomach or small intestine and typically cause bleeding, anaemia and pain [1]. It is believed that GISTs originate from interstitial cells of Cajal [2] and may also derive from gastrointestinal smooth muscles or gut stem cells [3]. The pathological features of GISTs range from benign neoplasms to fatal sarcomas [1,4]. Most gastrointestinal stromal tumors stain positively for KIT [5,6], Ki67 [7] and anoctamin 1; exon mutations [6] in KIT or PDGFRA genes in approximately 80% or 10% of GISTs, respectively, have been demonstrated [1]. More than 60% of GIST patients can be cured by surgical resection [8,9]. The use of imatinib mesylate (Gleevec; Novartis) adjuvant treatment [8] is recommended in advanced GIST

Abbreviations: CTHRC1, collagen triple helix repeat containing 1; DFS, disease-free survival; ECM, extracellular matrix; GIST, gastrointestinal stromal tumors; OS, overall survival; qRT-PCR, quantitative real-time polymerase chain reaction

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patients with postoperative recurrence risk, and the survival rate can be improved; however, secondary imatinib resistance is common [10].

Micrometastases and overt metastases are the main causes of death in malignant tumors, and this is the case in GIST patients as well [11,12]. Approximately 40% GISTs patients had metastatic lesions when definitively diagnosed, and more than 10% patients exhibited overt metastases [1]. Therefore, developing new predictors that can be used to estimate the risk of metastasis and postoperative recurrence is urgent.

Extracellular matrix (ECM) proteins play important roles in regulating tumor invasion and metastasis [13-15]. Given the secretary property, ECM proteins are also ideal candidates for tumor serum biomarkers and therapeutic targets.

Collagen triple helix repeat containing-1(CTHRC1) is a 28-kD extracellular matrix glycoprotein containing an NH2-terminal signaling peptide for extracellular secretion, a short collagen triple helix repeat of 36 amino acids, and a COOH-terminal globular domain [16]. CTHRC1 was initially found in a screen for differentially expressed genes in balloon-injured versus normal rat arteries [16]. It has been reported that the CTHRC1 protein positively regulates the Wnt-PCP pathway by stabilizing formation of the Wnt ligand and Frizzled receptor complex [17] in developmental morphogenesis [17]. CTHRC1 has recently been shown to be highly expressed in human pancreatic cancer tissues [18], hepatocellular carcinoma [13], gastric cancer [19], and colorectal cancer [20], and it promotes invasion and metastasis in these cancers. Several studies revealed that CTHRC1 regulates cancer cell motility and invasiveness through activating the Wnt-PCP pathway [18]. However, the clinical significance and functional role of CTHRC1 in GIST remain unclear. In this study, we first examined the expression of CTHRC1 and its correlation with the clinicopathological parameters of GIST. Then, we further analyzed the relationship between CTHRC1 expression and the survival of GISTs patients and identified CTHRC1 as a novel prognostic factor of GIST. Finally, we demonstrated that CTHRC1 promoted migration and invasion of primary GIST cells through activated Wnt/PCP-Rho signaling.

Materials and Methods

Ethics Statement

We obtained approval from the Regional Ethical Committees, Renji Hospital, School of Medicine, Shanghai Jiao Tong University, Shanghai, China for the use of clinical GIST patients' tissues. All the patients joined this study have signed informed consent. Ethical approval number, 2012031.

Patients

The inclusion criteria for our study were as follows: 1) a distinct pathologic diagnosis of GIST (CD117 positive in immunohistochemistry staining) ; 2) primary GIST cases without history of other solid tumors; 3) accepted radical surgery treatment without tumor residual; 4) without any chemotherapy, radiotherapy or other anticancer therapies before surgery; 5) availability of complete clinicopathologic and follow-up data; 6) obtained informed consent of patients and approval of the ethics committee of Renji Hospital for the use of samples. A total of 412 GIST cases, pathologic diagnosed and treated range from September 2004 to September 2013, were retrospectively identified from the hospitalization archives of Department of General Surgery, Renji Hospital, Shanghai, China. The paraffin-embedded tissue samples of these patients were used for tissue microarray construction and immunohistochemical staining. The clinicopathologic parameters include patients' age, gender, pathogenic site, histological type, tumor size (cm), number of mitoses/50 high-power fields (HPF), tumor rupture, mutation type and imatinib adjuvant treatment regimens. The risk of GIST behavior was classified into very low, low, intermediate, and high-risk categories according to the modified National Institute of Health (NIH) consensus [21,22]. In our study, the criterion of imatinib adjuvant therapy is at least twelve months uninterrupted drugs at a dose of 400mg/day. All the patients involved in our research accepted physical examination once a month during the first year after surgery and every six months thereafter. High risk GIST patients were accepted computed tomography (CT) or magnetic resonance imaging (MRI) of abdomen and pelvis at three-months intervals during the first three years after surgery, and subsequently at six-months intervals until five years after surgery. Complete follow-up data for GIST patients in cohort were available. Patients were followed until September 2013. Overall survival (OS) was defined as the time from surgery to death or the last follow-up examination. Disease free survival (DFS) was defined from the date of surgery until the detection of tumor recurrence or last observation.

Tissue Microarray Construction

Tissue microarrays were constructed by Suzhou Xinxin Biotechnology (Xinxin Biotechnology Co, Suzhou, China). Tissue paraffin blocks of GIST samples were stained with hematoxylin-eosin to confirm the diagnoses and marked at fixed points with most typical histological characteristics under a microscope. Two 1.6 mm cores per donor block were transferred into a recipient block tissue microarrayer, and each dot array contained fewer than one hundred and sixty dots. Three-micron-thick sections were cut from the recipient block and transferred onto glass slides using an adhesive tape transfer system for ultraviolet cross linkage.

Immunohistochemistry Stain

The tissue microarray glass slides were baked at 55°C for one hour, and then de-paraffinized gradually through xylene, 50% xylene, gradient concentrations of ethanol until immersed in tap water. Tissue sections were blocked for peroxidase activity with 0.3% Hydrogen peroxide at 37°C for 30mins. Antigen retrieval was carried out via boiling in 10mmol/L citrate buffer (pH6.0) for fifteen mins. Then the tissues were incubated with CTHRC1 antibody (mouse monoclonal antibody, 1:100 dilution, Huaan Biotechnology, Hangzhou, China) overnight at 4°C. Next day, the tissues were washed with phosphate buffer solution (PBS) for three times and incubated with HRP-labelled anti-mouse secondary antibody (1:200dilution, Dako, Carpinteria , CA, USA) for one hour at room temperature. Immunostaining was carried out using diaminobenzidine substrate chromogen (Dako, Carpinteria, CA, USA) method and chromogenic reaction was controlled under microscope. After immunostaining, tissues were immersed into hematoxylin for nuclear staining. The TMA slides were then dehydrated through gradient concentrations of ethanol, cleared with xylene, and coverslipped with neutral balsam (Shenggong, Shanghai, China). The staining results were judged by two pathologists according to criterion as follows: 0: weak, no staining was observed; 1+, 25% to 50% of the tumor cells were weak or moderate staining; 2+, strong, more than 50% tumor cells were moderate or strong staining. 1 + and 2 + scores were identified as positive staining, while 0 score means negative staining. Negative controls for primary and secondary antibodies were shown in Figure W3. Total RNA Extraction

and Quantitative Real-time PCR Total RNA was extracted from 29 fresh GIST tissues using Trizol reagent (Takara, Dalian, China) followed the manufacturer instructions. The reverse-transcription reactions were carried out with random primers and M-MLV Reverse Transcriptase (Takara, Dalian, China). The 29 cases of cDNA were used for templates of quantitative real-time PCR reaction in SYBR-Green method. All the qPCR reactions were performed on a StepOne TM real-time PCR System (Applied Biosystems, Foster City, CA,USA). *Beta-actin* was used as an internal control. The 2^{- Δ Ct} method was used to quantify the relative *CTHRC1* expression levels. The forward and reverse *CTHRC1* primer sequences were: 5'-TGGTATTTCACATTCAATGGAGCTG-3' and 5'-TGGGTA--ATCTGAACAAGTGCCAAC-3', respectively.

Western Blotting

Fresh GIST tissues were lysed in tissue protein extraction reagent (Invitrogen). Primary GIST cells were lysed in Western and IP lysis buffer (P0013, Beyotime, Jiangsu, China) supplemented with 1mM PMSF (Adamas beta, Shanghai, China). The lysis buffer includes, 20mM Tris (pH7.5), 150mM NaCl, 1%Triton X-100, sodium pyrophosphate, β -glycerophosphate, EDTA, Na3VO4, leupeptin.

Proteins were separated by 10% SDS-PAGE under reducing condition, followed by blocking in phosphate-buffered saline/Tween-20 containing 1%BSA (Bovine Serum Albumin). The NC (Nitrocellulose filter membrane) or PVDF (Polyvinylidenefluoride) membrane was incubated with antibodies for CTHRC1(1:1000, mouse, Huaan, Hangzhou, China) , JNK (1:1000, Rabbit source, Cell Signaling Technology), RhoA (1:1000,Rabbit,CST), Rac1(1:1000,Mouse, Millipore) ,Cdc42 (1:1000,Mouse) and species-specific secondary antibodies. Bound the IRDye 680 anti-mouse (LI-COR, 1:20000) and IRDye 800 anti-rabbit (LI-COR, 1:10000) secondary antibodies were revealed by Odyssey imaging system (LI-COR). Wnt5a neutralizing antibody (R&D), Wnt3a neutralizing antibody (R&D), NSC23766 (Rac1 inhibitor, Merck Millipore, effective dose: 50 μM), Y-27632 (ROCK inhibitor, effective dose: 100 μM).

CTHRC1 Recombinant Protein Expression, Purification and Verification

CTHRC1 ORF were cloned into the episomal expression vector V152 (Figure W1B) with pCEP-Pu-Strep II-tag (C-terminal) inframe and the sequence of the BM-40 (SPARC/osteonectin) signal



Figure 1. CTHRC1 expression in GIST tissues. (A) Relative mRNA expression of *CTHRC1* in low-risk group was significantly lower than those in the intermediate- and high-risk groups. (B) Western blotting analysis showed that CTHRC1 expression in high-risk GIST patients was significantly higher than those of low-risk or intermediate-risk groups. Tubulin was included as a loading control. (C) Representative image of immunohistochemical staining of CTHRC1 in low-risk, intermediate-risk and high-risk GIST tissues. Original magnification: a, b, c, $100 \times$; d, e, f, $200 \times$. Scale bars, 5 μ m (*, P < 0.05).

peptide downstream of the CMV promoter. CTHRC1 was recombinant expressed in EBNA-293 cells after transfecting reconstructed plasmid by using X-tremeGENE 9 DNA Transfecting Reagent (Roche, Mannheim, Germany). Forty eight hours after transfection, the EBNA-293 cells were screening with puromycin (Sigma-Aldrich, St. Louis, MO) at a dose of 2μ g/ml in DMEM supplemented with 10% FBS for seven days, then the culture media were collected and applied to the Strep Tactin sepharose column(IBA, Gottingen, Germany). After this, the column was washed with binding buffer and eluted by elution buffer containing 2.5 mM desthiobiotin. The collected fractions were further quantified by Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, Wilmington, DE) and BCA Protein Assay Kit (Pierce. Biotechnology Inc, Rockford, IL) and identified by western blotting assay.

In Vitro Migration and Invasion Assays

For the transwell migration assay, 4×10⁴ primary GIST cells were placed on the top chamber of each insert with the noncoated membrane (Millicell). Cells were trypsinized and resuspended in DMEM and 700-900µL of medium supplemented with 10% fetal bovine serum added rCTHRC1 protein followed gradient doses of 0 nM, 1 nM, 20 nM, 50 nM respectively were injected into the lower chamber. After 24 hours for GIST cells in the migration assays, any cells remaining in the top chambers or on the upper membrane of the inserts were carefully removed. After fixation and staining in a dye solution containing 0.1% crystal violet and 20% methanol, cells adhering to the lower membrane of the inserts were counted and imaged through an IX71 inverted microscope (Olympus Corp. Tokyo, Japan). We carried out invasion assay by adding 100µl matrigel (BD Bioscience, Franklin Lakes, NJ) into top chamber of transwell and placed 8×10⁴ primary GIST cells onto the matrigel. 48 hours later, the transwell for invasion was ceased and staining.

Cell Viability Assay

Cell viability was detected using a standard Cell Counting Kit-8 assay. Primary GIST cells were seeded into 96-well plates (100µl per well) at a density of 3×10^4 cells per ml. Cells in four divided groups were added rCTHRC1 protein followed gradient doses of 0 nM, 1 nM, 20 nM, 50 nM respectively. We added 10µl of reagent from Cell Counting Kit-8 (Dojindo, Kumamoto, Japan) to each well for detection at day 1, 2, 3, 4, 5. After two hours of incubation at 37°C, the optical density was measured using microplate reader at a wavelength of 450nm.

Cell Isolation and Primary Cell Culture

Fresh surgical GIST tissues were gently minced with scissors, washed twice with phosphate-buffered saline (PBS), and then filtered through the steel mesh with 200 μ m pore diameter. After washed in cold PBS, cell pellets were resuspended in RPMI-1640 medium supplemented with 20% fetal calf serum (FCS; Gibco, France) and seeded onto culture dishes. The primary GIST cells were cultured in incubator with 5%CO2 and 37 degrees centigrade. The culture medium for primary GIST cells were changed twice every three days . The successfully isolated primary GIST cells were shown in Figure 3A.

Pull Down Assay

Pull down assays were conducted as reported [23]. Primary GSIT cells cultured in 100 mm dishes were serum-starved for 24 hours and treated with rCTHRC1 at a dose of 20 nM or desthiobiotin buffer for 2 hours. The primary antibodies used included the following: mouse

primary antibody against Rac1 (Millipore, 1:1000) and rabbit primary antibody against RhoA, Cdc42 (Cell Signaling Technology, 1:1000).

Luciferase Reporter Assay

Primary GIST cells were seeded in 96-well plates and transfected with mixture of 100 ng TCF/catenin reporter plasmid (Wnt/ β catenin signaling), or 100 ng ATF2 reporter plasmid (Wnt/PCP signaling), and 10 ng Renilla following the recommended protocol for the Lipofectamine 2000 transfection system. One group of GIST cells were treated with rCTHRC1 protein at a concentration of 20 nM. After 48 hours of incubation, firefly and Renilla luciferase activities were measured using the dual-luciferase reporter assay system (Promega, Madison, WI) from the cell lysates.

Statistical Analysis

Statistical analyses were conducted using SPSS 16.0 software (Chicago, IL, USA). We performed chi-squared tests in cross tables to assess the relationships between expression levels of *CTHRC1* and clinicopathological factors. Overall survival (OS) and Disease-free survival (DFS) were calculated using Kaplan-Meier method. The survival distributions were compared through log-rank test. All statistical tests were two-sided. One-way analysis of variance (ANOVA, Post-hoc testing) was used to compare groups (Table W1). *P* value less than 0.05 was considered statistically significant.

Results

CTHRC1 Expression Is Gradually Elevated in Accordance with GIST Risk Grades

To investigate the CTHRC1 expression level in GIST tumor tissues with different risk grades, we first evaluated the mRNA

Table 1. Relationship between CTHRC1 expression and clinicopathologic features of GISTpatients(*, P < 0.05; **, P < 0.01).

Variable		CTHRC	CTHRC1(n = 412)		
		Low	High	Р	
Age ^{\$}	≤59 years	31	49	0.458	
0	>59 years	114	218		
Gender	Male	65	158	0.005	
	Female	80	109		
Tumor site	Stomach	100	128	< 0.001	
	Small bowel	28	93		
	Colon	12	9		
	Other sites	5	37		
Tumor size(cm)	≤2	30	7	< 0.001	
	>2&≤5	102	61		
	>5&≤10	9	127		
	>10	4	72		
Mitoses per 50 HPFs	≤5	138	170	< 0.001	
	>5&≤10	2	52		
	>10	5	45		
Modified NIH criteria	Very low risk	30	2	< 0.001	
	Low risk	101	51		
	Intermediate risk	4	58		
	High risk	10	156		
NIH invasion	1	30	2	< 0.001	
	2	101	51		
	3	4	58		
	4	5	101		
	5	5	55		
Tumor bleeding	No	131	220	0.030	
	Yes	14	47		

Abbreviations: HPF, high power field of the microscope; NIH, National Institutes of Health.

The P value in bold emphasize statistical significance (P<0.001). ^{\$} Median age of total 412 patients was 59 years.

expression level of *CTHRC1* in fresh GIST tissue samples by quantitative PCR (qPCR). The results showed that *CTHRC1* mRNA expression levels in GIST tumor tissues of the intermediate- and high-risk groups were higher than those of the low-risk group (Figure 1*A*). We further compared the protein expression level of CTHRC1 in GIST tissues with different risk grades. The three low-risk, two intermediate-risk and five high-risk samples were analyzed by western blotting. The results showed that the CTHRC1 protein expression level in the high-risk group was significantly higher than that of the intermediate- and low-risk groups (Figure 1*B*).

CTHRC1 Protein Expression Level Is Closely Correlated with Risk Grade of NIH Classification, and Prognosis of GIST

The clinicopathological significance of CTHRC1 was further examined using a tissue microarray which contained 412 GIST tissue samples. The immunohistochemistry staining results showed that 145 (35.2%) cases showed CTHRC1 low expression, 267 (64.8%) cases showed CTHRC1 high expression (Figure 1*C*). The correlations between CTHRC1 expression and the clinicopathological parameters are shown in Table 1. We found that the expression level of CTHRC1 was higher in the patients with high NIH grade, large tumor size (>10 cm) or increased mitotic figures

than those with low NIH grade, small tumor size (<10 cm), fewer mitotic figures with statistical significance (P < 0.05). Interestingly, we found that there was a significant difference between male (70.85%) and female (57.67%) GIST patients in frequency of high CTHRC1 levels. The statistical analysis suggested that CTHRC1 expression was not correlated with age, histological type, or tumor rupture. We further investigated the correlation between CTHRC1 expression and overall survival (OS) or disease-free survival (DFS) of GIST patients. The OS in the CTHRC1 negative (low) group (five-year OS rates, 100%, 145/145) was remarkably superior than that in the CTHRC1 positive (high) expression group (five-year OS rates, 90.6%, 242/267) (Figure 2A). The DFS in the CTHRC1 negative (low) group (five-year DFS rates, 95.2%, 138/145) was significantly higher than that in the CTHRC1 positive (high) expression group (five-year DFS rates, 76.8%, 205/267) (Figure 2B). In summary, CTHRC1 expression in GIST tumor tissues was closely correlated with OS and DFS of GIST patients.

Correlation between CTHRC1 Expression and the Efficacy of Imatinib Adjuvant Treatment

According to the NIH classification guideline, intermediate- or high-risk GIST patients require adjuvant treatment with imatinib. In



Figure 2. (A) Kaplan-Meier analysis of overall survival related to the expression of CTHRC1 in 412 GIST patients. (B) Kaplan-Meier analysis of disease-free survival related to the expression of CTHRC1 in 412 GIST patients. (C) Among CTHRC1-negative intermediate- and high-risk GIST patients, there was no significant difference in DFS between the groups with or without imatinib adjuvant treatment. (D) Among CTHRC1-positive intermediate- and high-risk GIST patients, no significant difference between the imatinib treatment group and the surgery alone group were observed.



Figure 3. (A) Immunofluorescent staining showed the morphology of primary GIST cells isolated from the GIST tissues of three patients. The green fluorescence represents phalloidin for F-actin staining, whereas the blue fluorescence represents DAPI for nuclear staining. (B) Cell viability of primary GIST cells treated with rCTHRC1 protein at doses of 0 nM, 1 nM, 20 nM, 50 nM were measured using CCK-8 assay for six days. (C) Representative images (left) of GIST cells that migrated to the bottom of transwell filter (8 μ m, pore diameter) and statistical analysis (right) of the cell migration stimulated with rCTHRC1 protein or vehicle. (D) Representative images (left) of GIST cells that invaded through Matrigel to the bottom of transwell filter (8 μ m, pore diameter) and statistical analysis (right) of the cell invasiveness stimulated with rCTHRC1 protein or vehicle. The results shown are mean±SD of migration, and invading cells were photographed at 200 × magnification per field. (*, *P* < 0.05; **, *P* < 0.01).

this study, we analyzed the correlation between the efficacy of imatinib adjuvant treatment and CTHRC1 expression. Among 14 CTHRC1- negative intermediate- and high-risk GIST patients, there was no correlation between imatinib treatment and patient prognosis (Figure 2*C*). The difference in DFS between the imatinib treatment group and the surgery treatment only group was not statistically significant (P = 0.255). Notably, among 214 CTHRC1- positive

intermediate- and high-risk GIST patients, the DFS rate in the imatinib treatment group were higher than that in the surgery only group within 3 years of follow-up. However, the differences in 5-year DFS rates in the two groups were not statistically significant (P = 0.313) (Figure 2D). Therefore, the expression of CTHRC1 can not predict the efficacy of imatinib adjuvant treatment in our current study.



Figure 4. (A) Dual-luciferase reporter assay showed that rCthrc protein inhibited Wnt/ β -catenin signaling of primary GIST cells in a dosedependent manner. The results shown are mean ±SD of relative firefly/Renilla ratio. (B) Noncanonical Wnt/PCP signaling of GIST cells was activated by rCTHRC1 protein in a dose-dependent manner. (C) The inhibitory effect of rCTHRC1 on Wnt/ β -catenin signaling was partially blocked by Wnt5a monoclonal neutralizing antibody. (D) The promoting effect of rCTHRC1 protein on Wnt/PCP signaling was almost blocked by Wnt5a monoclonal neutralizing antibody. (E) The promoting effect of Wnt3a on Wnt/ β -catenin signaling was almost blocked by Wnt3a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catenin signaling was almost blocked by Wnt3a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catenin signaling was almost blocked by Wnt3a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catenin signaling was almost blocked by Wnt5a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catenin signaling was almost blocked by Wnt3a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catening was almost blocked by Wnt5a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catening was almost blocked by Wnt5a monoclonal neutralizing antibody. (F) The promoting effect of Wnt5a on Wnt/ β -catening was almost blocked by Wnt5a

Recombinant CTHRC1 Protein Promotes GIST Cell Migration and Invasion in a Dose-dependent Manner

To explore the biological functions of CTHRC1 as a secreted protein, CTHRC1 was recombinantly expressed in EBNA-293 cells, and further purified and verified by western blotting (Figure W2). Then, the purified recombinant CTHRC1 (rCTHRC1) protein was applied to primary GIST cells in a migration and Matrigel invasion assay. Compared to the vehicle group, GIST cell migration and invasion were significantly enhanced by rCTHRC1 protein at doses of 1 nM, 20 nM, and 50 nM (Figure 3, *C* and *D*). Moreover, the promotion of cell motility by the rCTHRC1 protein was dose-dependent. However, primary cell viability was not remarkably affected by rCTHRC1 protein based on the cell viability assay (Figure 3*B*). These results demonstrate that CTHRC1 is a potent pro-invasion factor that facilitates GIST cell invasion in a dose-dependent manner.

CTHRC1 Activates Wnt/PCP-Rho Signaling in Primary GIST Cells

To understand the underlying mechanism by which CTHRC1 promotes GIST cell migration and invasion, we examined the activation of the canonical Wnt pathway and the non-canonical Wnt pathway. GIST cells were transfected with a Wnt// β -catenin reporter plasmid (TCF/catenin plasmid) and negative control counterpart plasmid or non-canonical Wnt/PCP pathway reporter plasmid (ATF2 plasmid). Recombinant CTHRC1 or vehicle control was added 24 hours after transfection, and luciferase activity was determined. The results showed that Wnt/ β -catenin signaling was inhibited while the noncanonical Wnt/PCP signaling was activated by rCTHRC1 protein in primary GIST cells (Figure 4, *A* and *B*). The effects of rCTHRC1 protein on Wnt signaling was blocked by a Wnt5a neutralizing antibody (Figure 4, *C* and *D*). We also verified the block effect of Wnt3a and Wnt5a neutralizing antibodies (Figure 4, *E* and *F*). We further confirmed the



Figure 5. (A) Analysis of the active and total RhoA,Rac1 and Cdc42 in primary GIST cells treated with rCTHRC1 protein by pull-down assay.(B) Quantitative analysis of grey value for active Rac1/-total Rac1 ratio using ImageJ software. (C) Quantitative analysis of grey value for active RhoA/-total RhoA ratio using ImageJ software. (D) Quantitative analysis of grey value for active Cdc42/ total Cdc42 ratio using ImageJ software. (E) Rac1 G-LISA assay was used to assess the levels of GTP-bound Rac1 in GIST cells treated with rCTHRC1 protein. (F) RhoA G-LISA assay was used to assess the levels of GTP-bound RhoA in GIST cells treated with rCTHRC1 protein. (*, P < 0.05; **, P < 0.01).

inhibitory effect of CTHRC1 on Wnt/ β -catenin signaling using western blotting assy. The level of phosphorylated β -catenin, which indicates the degradation of β -catenin, was increased in primary GIST cells treated with rCTHRC1 (Figure 6, *B* and *F*). In addition, the level of GSK3 β , which phosphorylates β -catenin on Ser-33/Ser-37/Thr-41 was increased in rCTHRC1 treated primary GIST cells (Figure 6, *B* and *D*). Therefore, we confirmed that CTHRC1 inhibits the canonical Wnt/ β -catenin pathway in primary GIST cells.

The downstream molecules of the Wnt/PCP pathway mainly include the small GTPase family, such as Rac1, RhoA and Cdc42, which play important roles in cancer cell migration and invasion. Using a Rho GTPases pull-down assay, we found that the rCTHRC1 protein enhanced the activity of RhoA and Rac1 but not Cdc42 (Figure 5, *A-D*).

To further confirm the above results, the GLISA assay, another approach to measure the activities of Rho GTPases, was performed. It also demonstrated that the activities of RhoA and Rac1 were significantly enhanced by rCTHRC1 treatment in primary GIST cells, which is consistent with the results of the Rho GTPases pull-down assay (Figure 5, *E* and *F*).

Furthermore, the phosphorylation of c-Jun N terminal kinase (JNK), another downstream molecule of the Wnt/PCP pathway, and Wnt5a were also elevated by rCTHRC1 treatment (Figure 6, *A*, *C* and *E*). These results suggested that CTHRC1 may promote GIST cell invasion through the Wnt/PCP-Rho-JNK pathway.

CTHRC1-induced Primary GIST Cell Migration and Invasion Is Wnt5a and Wnt/PCP Signaling-dependent

We further investigated whether Wnt3a (a ligand of canonical Wnt/ β -catenin pathway) and Wnt5a (a ligand of noncanonical Wnt/PCP pathway) are involved in CTHRC1-induced GIST cell migration and invasion by using neutralizing antibodies of Wnt3a and Wnt5a. The data illustrated that the migration- and invasion-promoting activities of rCTHRC1 at a dose of 20 nM were not



Figure 6. (A) The expression of Wnt5a and the phosphorylation of JNK were examined after treatment with rCTHRC1 by western blotting. (B) The phosphorylation of GSK3 β and β -catenin were examined after treatment with rCTHRC1 by western blotting. (C) Quantitative analysis of grey value for Wnt5a using ImageJ software. The relative expression of Wnt5a induced by rCTHRC1 at 0', 5', 10', 30' was compared with the grey value of Wnt5a induced by rCTHRC1 at 60'. (D) Quantitative analysis of grey value for phospho-GSK3 β /total GSK3 β ratio using ImageJ software. (E) Quantitative analysis of grey value for phospho-JNK/total JNK ratio using ImageJ software. (F) Quantitative analysis of grey value for phospho- β -catenin/total β -catenin ratio using ImageJ software. (*, P < 0.05; **, P < 0.01).



Figure 7. (A) The promotive effect of rCTHRC1 protein was blocked by Wnt5a neutralizing antibody but not blocked by Wnt3a neutralizing antibody shown from cell migration assay in vitro. (B) Quantification analysis of migrated cells were performed for six randomly selected fields (original magnification: $200 \times$). (C) The promotive effect of rCTHRC1 protein was partially blocked by Rac1 inhibitor (NSC23766) as well as ROCK inhibitor (Y-27632) shown from cell migration assay. (D) Quantification analysis of migrated cells were performed for six randomly selected fields (original magnification: $200 \times$). (*, P < 0.05; **, P < 0.01).

affected by the Wnt3a neutralizing antibody (Figure 7, *A* and *B*, Figure 8, *A* and *B*). However, the promoting effects of rCTHRC1 on GIST cell migration and invasion were almost completely blocked by the Wnt5a neutralizing antibody (Figure 7, *A* and *B*, Figure 8, *A* and *B*). We further investigated whether the promoting effects of CTHRC1 on GIST cells motility are Wnt/PCP signaling-dependent by using inhibitors of ROCK and Rac1, which are key downstream molecules of the Wnt/PCP pathway. The results showed that both ROCK and Rac1 inhibitors treatment inhibits the promoting effects of rCTHRC1 on GIST cell migration and invasion (Figure 7, *C* and *D*, Figure 8, *C* and *D*).

Taken together, these data indicated that the CTHRC1-induced GIST cell migration and invasion is Wnt5a and noncanonical Wnt/PCP signaling dependent (Figure 9).

Discussion

GISTs have a variable malignancy degree ranging from a curable disorder to highly malignant sarcomas [1,8]. The majority of GISTs stain positive for KIT oncoproteins in immunohistochemical assays [3,24]. KIT is a stem cell growth factor receptor that plays proproliferative and anti-apoptotic roles in GIST progression [5,6]. GIST patients treated with the KIT targeted inhibitor, – imatinib, showed prolonged median recurrence-free survival of 12 to 24 months [1,21]. Recurrence and metastasis in GIST patients are the major causes of treatment failure or even death [7,25,26]. Thus, new predictive biomarkers for recurrence and an understanding of the mechanisms of GIST metastasis are urgently needed.

By analyzing the GIST microarray dataset (GSE21315) from the GEO database (Figure W1*A*), we found that *CTHRC1* expression in GIST with liver metastasis was remarkably higher than in primary GIST tissues(fold change>3, P < 0.05). This result strongly suggested that CTHRC1 may play important roles in regulating GIST metastasis. The NIH classification published in 2002 was widely accepted as standard for predicting the prognosis of GIST patients [27,28]. According to the NIH classification, the risk assessments are based on tumor size and the number of mitotic figures. We have analyzed the correlation between CTHRC1 expression and GIST clinicopathological parameters and found that the CTHRC1



Figure 8. (A) The pro-invasion effect of rCTHRC1 protein was blocked by Wnt5a neutralizing antibody but not blocked by Wnt3a neutralizing antibody shown from cell invasion assay in vitro. (B) Quantification analysis of migrated cells were performed for six randomly selected fields (original magnification: $200 \times$). (C) The pro-invasion effect of rCTHRC1 protein was partially blocked by Rac1 inhibitor (NSC23766) as well as ROCK inhibitor (Y-27632) shown from cell invasion assay. (D) Quantification analysis of migrated cells were performed for six randomly selected fields (original magnification: $200 \times$). (* , P < 0.05; **, P < 0.01).

expression levels were closely related to NIH classification, tumor size and the number of mitotic figures. These analyses suggest that CTHRC1-positive GISTs exhibit a greater likelihood of malignant behavior and more aggressive features. Moreover, there was a significant difference between male and female GIST patients in frequency of high CTHRC1 levels (Table 1). It has been reported that *CTHRC1* is associated with attenuated inflammatory arthritis severity in males, but not in females [29,30]. The naive mice assay showed that the expression and inducibility of *CTHRC1* were highly dependent on sex [29,30]. Among naive wild-type BALB/c mice, *CTHRC1* expression was remarkably higher in males than in females. Moreover, *CTHRC1* was one of the major sex-affected differentially expressed genes [29,30]. Therefore, sex disparities may cause the difference between male and female GIST patients in high CTHRC1 expression rates.

The Kaplan-Meier curves analysis revealed that CTHRC1 expression was closely correlated with OS and DFS of GIST patients. GIST patients with CTHRC1-positive tumors had shorter OS and DFS than CTHRC1-negative patients. Therefore, we identified that

CTHRC1 is an available predictor of poor prognosis including OS and DFS in GIST patients. In addition, the great clinical value of CTHRC1 in predicting the recurrence risk of postoperative GIST patients may contribute to improving the clinical therapeutic effects.

Tumor microenvironments including components of extracellular matrix protein play crucial roles in promoting tumor invasion and metastasis [31]. CTHRC1, a secreted ECM protein, has been reported to be up-regulated in many solid tumors. In hepatocellular carcinoma, CTHRC1 is up-regulated and promotes tumor invasion and predicts poor prognosis [13]. CTHRC1 plays a promoting role in pancreatic cancer progression and metastasis by enhancing the migration ability of cancer cells [18]. These accumulating data indicate that CTHRC1 is an important regulator of tumor invasion and metastasis in the tumor microenvironment. In the present study, we have found that CTHRC1 expression in GIST tissue is gradually elevated in accordance with risk grading. Based on an *in vitro* functional assay, CTHRC1 was considered to be an invasion-promoting protein and ultimately contributed to gastrointestinal stromal tumor metastasis and recurrence.



Figure 9. CTHRC1 induced cell signaling alteration and its related cell movement.

Although the functional roles of CTHRC1 in tumor cell invasion and metastasis have been well established, the underlying mechanisms of how CTHRC1 promotes cancer cell invasion remains unclear. It has been reported that CTHRC1 acts as a Wnt cofactor that selectively activates the PCP pathway in the inner ear developmental process [17]. In the present study, we showed that CTHRC1 promotes GIST cell invasion by activating Wnt/PCP signaling, which is supported by the following evidence. First, the luciferase reporter assay and western blotting showed that recombinant CTHRC1 protein activated the PCP pathway of Wnt signaling of primary GIST cells in a dose-dependent manner. Second, the pro-invasion activity of the rCTHRC1 protein was blocked by the neutralizing antibody of Wnt5a (a ligand for Wnt/PCP pathway [32,33]) and the inhibitors of Rac1 and ROCK (the downstream molecules of Wnt/PCP signaling [34,35]).

CTHRC1 promoted tumor cells migration by activating Rac1 and resulted in metastasis of pancreatic cancer [18]. The overexpression of *CTHRC1* promotes tumor invasion by activating RhoA in hepatocellular carcinoma [13]. Accordingly, we demonstrated the promoting effect of CTHRC1 on both RhoA and Rac1 in GIST cells.

Moreover, we further verified that the pro-invasion activity of CTHRC1 in GIST cells was dependent on the Wnt5a/PCP-Rho axis by blocking the Wnt5a/PCP-Rho pathway with neutralizing antibodies and specific inhibitors. The noncanonical Wnt/PCP pathway transmits signaling from the cell-surface Frizzled receptorcoupled Wnt5a protein, via the Dvl-RhoA/Rac1-JNK-ATF2/c-Jun cascade [36-38], to the nucleus. Noncanonical Wnt/PCP signaling plays important roles in promoting cell migration [39] and formation of cell protrusions [40,41]. The small Rho GTPases Rac1, RhoA and Cdc42, are key executors of Wnt/PCP related cell migration [42,43]. RhoA controls the assembly of actin to generate contractile forces [44,45], while Rac1 and Cdc42 promote actin polymerization contributing to the formation of protrusive forces [46,47]. Therefore, the efficient cell movement requires synergistic actions of the three Rho GTPases [48-50]. In this study, we have shown that CTHRC1, a secreted protein, transduces outside-in signals through the Wnt/PCP pathway and coordinates the action of the three Rho GTPases to promote GIST cell migration and invasion.

Taken together, we have demonstrated that CTHRC1 expression level is closely correlated with risk grade of NIH classification and prognosis of GIST, indicating that CTHRC1 served as a new predictor of recurrence risk and prognosis in post-operative GIST patients. Furthermore, we have shown that CTHRC1 promotes GIST cell migration and invasion by activating the Wnt/PCP-Rho signaling, suggesting that the CTHRC1- Wnt/PCP-Rho axis may be a new therapeutic target for interventions against GIST invasion and metastasis.

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These authors declare no conflict of interest.

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Supplementary materials



Reconstruction of CTHRC1 recombinant protein

Figure W1. (A) Analysis of *CTHRC1* differential expression in metastatic GIST and primary GIST based on data from GEO Database (GSE21315). (B) Schematic diagram of V152 vector which was used to reconstruct *CTHRC1*-StrepII recombinant plasmid.



Figure W2. Verification of affinity purified CTHRC1 protein by Coomassie Brilliant Blue staining and Western blotting.

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Negative control for primary antibody

Negative control for secondary antibody

Figure W3. Negative controls for primary and secondary antibodies in GIST TMA immunohistochemistry staining assay (original magnification:100 ×).

Table W1. ANOVA analysis (post-hoc testing) for statistics of figures.

Multiple Comparisons						
(I) 1 = low risk,	(J) 1 = low risk,	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
2 = intermediate risk, 3 = high risk	2 = intermediate risk, 3 = high risk				Lower Bound	Upper Bound
Figure 1A						
1	2	-1.53243*	.57014	.031	-2.9405	1244
	3	-1.47190 *	.58777	.046	-2.9235	0203
2	1	1.53243*	.57014	.031	.1244	2.9405
	3	.06053	.62280	.995	-1.4776	1.5986
3	1	1.47190*	.58777	.046	.0203	2.9235
	2	06053	.62280	.995	-1.5986	1.4776
VAR00001						
Tukey HSD						
Multiple Comparisons						
(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inter	val
					L D l	I I D J

					Lower Bound	Upper Bound
Figure 3B						
Day0						
0	1	0040000	.0094810	.973	034361	.026361
	20	0160000	.0094810	.389	046361	.014361
	50	0013333	.0094810	.999	031695	.029028
1	0	.0040000	.0094810	.973	026361	.034361
	20	0120000	.0094810	.607	042361	.018361
	50	.0026667	.0094810	.992	027695	.033028
20	0	.0160000	.0094810	.389	014361	.046361
	1	.0120000	.0094810	.607	018361	.042361
	50	.0146667	.0094810	.456	015695	.045028
50	0	.0013333	.0094810	.999	029028	.031695
	1	0026667	.0094810	.992	033028	.027695
	20	0146667	.0094810	.456	045028	.015695
VAR00001						
Tukey HSD						

Table W1. (continued)	able W1. (continued)								
Multiple Comparisons									
(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inte	rval			
					Lower Bound	Upper Bound			
Figure 3B									
Day1									
0	1	.0023333	.0055578	.973	015465	.020131			
	20	0216667*	.0055578	.019	039465	003869			
	50	0230000*	.0055578	.014	040798	005202			
1	0	0023333	.0055578	.973	020131	.015465			
	20	0240000 *	.0055578	.011	041798	006202			
	50	0253333 *	.0055578	.008	043131	007535			
20	0	.0216667*	.0055578	.019	.003869	.039465			
	1	.0240000*	.0055578	.011	.006202	.041798			
	50	0013333	.0055578	.995	019131	.016465			
50	0	.0230000 *	.0055578	.014	.005202	.040798			
	1	.0253333 *	.0055578	.008	.007535	.043131			
	20	.0013333	.0055578	.995	016465	.019131			
VAP00001									

VAR00001 Tukey HSD

Multiple Comparisons

(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 3B Day2						
0	1	0596667 *	.0133083	.009	102285	017049
	20	0253333	.0133083	.299	067951	.017285
	50	0746667*	.0133083	.002	117285	032049
1	0	.0596667 *	.0133083	.009	.017049	.102285
	20	.0343333	.0133083	.120	008285	.076951
	50	0150000	.0133083	.684	057618	.027618
20	0	.0253333	.0133083	.299	017285	.067951
	1	0343333	.0133083	.120	076951	.008285
	50	0493333 *	.0133083	.025	091951	006715
50	0	.0746667*	.0133083	.002	.032049	.117285
	1	.0150000	.0133083	.684	027618	.057618
	20	.0493333 *	.0133083	.025	.006715	.091951
VAR00001						

Tukey HSD

(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 3B						
Day3						
0	1	0046667	.0051962	.806	021307	.011973
	20	0223333*	.0051962	.011	038973	005693
	50	02833333 *	.0051962	.003	044973	011693
1	0	.0046667	.0051962	.806	011973	.021307
	20	0176667*	.0051962	.038	034307	001027
	50	0236667*	.0051962	.008	040307	007027
20	0	.0223333 *	.0051962	.011	.005693	.038973
	1	.0176667*	.0051962	.038	.001027	.034307
	50	0060000	.0051962	.669	022640	.010640
50	0	.0283333*	.0051962	.003	.011693	.044973
	1	.0236667*	.0051962	.008	.007027	.040307
	20	.0060000	.0051962	.669	010640	.022640
VAR00001 Tukey HSD						

Table W1. (continued)	able W1. (continued)								
Multiple Comparisons	Multiple Comparisons								
(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inte	rval			
					Lower Bound	Upper Bound			
Figure 3B Day4									
0	1	0030000	.0072111	.974	026092	.020092			
	20	.0173333	.0072111	.154	005759	.040426			
	50	0753333*	.0072111	.000	098426	052241			
1	0	.0030000	.0072111	.974	020092	.026092			
	20	.0203333	.0072111	.086	002759	.043426			
	50	0723333*	.0072111	.000	095426	049241			
20	0	0173333	.0072111	.154	040426	.005759			
	1	0203333	.0072111	.086	043426	.002759			
	50	0926667*	.0072111	.000	115759	069574			
50	0	.0753333*	.0072111	.000	.052241	.098426			
	1	.0723333*	.0072111	.000	.049241	.095426			
	20	.0926667*	.0072111	.000	.069574	.115759			
VAR00001									

Tukey HSD

Multiple Comparisons

(I) concentration (J) concentration Mean Difference (I-J) Std. Error Sig. 95% Confidence Interval Lower Bound Upper Bound Figure 3B Day5 0 1 .0146667 .0078916 .316 -.010605 .039938 -.040728 20 -.0660000 * .0078916 .000 -.091272 50 -.0893333* .0078916 .000 -.114605 -.064062 .010605 0 -.0146667 .0078916 .316 -.039938 1 20 -.0806667* .0078916 .000 -.105938 -.055395 50 -.1040000* .0078916 .000 -.129272 -.078728 .091272 20 0 .0660000* .000 .040728 .0078916 1 .0806667* .0078916 .000 .055395 .105938 -.02333333 .0078916 .071 -.048605 .001938 50 50 0 .0893333* .0078916 .000 .064062 .114605 .1040000* .0078916 .000 .078728 .129272 1 -.001938 .048605 20 .0233333 .0078916 .071 VAR00001

Tukey HSD

(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 3B						
Day6						
0	1	0046667	.0106797	.970	038867	.029533
	20	0750000 *	.0106797	.001	109200	040800
	50	1590000 *	.0106797	.000	193200	124800
1	0	.0046667	.0106797	.970	029533	.038867
	20	0703333*	.0106797	.001	104533	036133
	50	1543333*	.0106797	.000	188533	120133
20	0	.0750000*	.0106797	.001	.040800	.109200
	1	.0703333*	.0106797	.001	.036133	.104533
	50	0840000 *	.0106797	.000	118200	049800
50	0	.1590000*	.0106797	.000	.124800	.193200
	1	.1543333*	.0106797	.000	.120133	.188533
	20	.0840000*	.0106797	.000	.049800	.118200
VAR00001						
Tukey HSD						

Multiple Comparisons							
(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inte	rval	
					Lower Bound	Upper Bound	
Figure 3C							
0	1	-6.50000*	1.69558	.005	-11.2458	-1.7542	
	20	- 55.50000 *	1.69558	.000	-60.2458	-50.7542	
	50	-69.16667*	1.69558	.000	-73.9125	-64.4208	
1	0	6.50000 *	1.69558	.005	1.7542	11.2458	
	20	-49.00000*	1.69558	.000	- 53.7458	-44.2542	
	50	-62.66667 *	1.69558	.000	-67.4125	- 57.9208	
20	0	55.50000 *	1.69558	.000	50.7542	60.2458	
	1	49.00000 *	1.69558	.000	44.2542	53.7458	
	50	- 13.66667 *	1.69558	.000	-18.4125	-8.9208	
50	0	69.16667*	1.69558	.000	64.4208	73.9125	
	1	62.66667*	1.69558	.000	57.9208	67.4125	
	20	13.66667*	1.69558	.000	8.9208	18.4125	

VAR00001

Tukey HSD

Multiple Comparisons

(I) concentration	(J) concentration	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 3D						
0	1	-23.66667*	3.28549	.000	- 32.8625	-14.4708
	20	-55.50000*	3.28549	.000	-64.6959	-46.3041
	50	-72.16667*	3.28549	.000	-81.3625	-62.9708
1	0	23.66667*	3.28549	.000	14.4708	32.8625
	20	-31.83333*	3.28549	.000	-41.0292	-22.6375
	50	-48.50000*	3.28549	.000	- 57.6959	- 39.3041
20	0	55.50000*	3.28549	.000	46.3041	64.6959
	1	31.83333 *	3.28549	.000	22.6375	41.0292
	50	- 16.66667 *	3.28549	.000	-25.8625	-7.4708
50	0	72.16667 *	3.28549	.000	62.9708	81.3625
	1	48.50000 *	3.28549	.000	39.3041	57.6959
	20	16.66667*	3.28549	.000	7.4708	25.8625
VAR00001						

Tukey HSD

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inter	95% Confidence Interval	
					Lower Bound	Upper Bound	
Figure 4A (Mutant TC	CF)						
0	1	01200	.02143	.941	0806	.0566	
	20	02933	.02143	.550	0980	.0393	
	50	04333	.02143	.257	1120	.0253	
1	0	.01200	.02143	.941	0566	.0806	
	20	01733	.02143	.849	0860	.0513	
	50	03133	.02143	.500	1000	.0373	
20	0	.02933	.02143	.550	0393	.0980	
	1	.01733	.02143	.849	0513	.0860	
	50	01400	.02143	.911	0826	.0546	
50	0	.04333	.02143	.257	0253	.1120	
	1	.03133	.02143	.500	0373	.1000	
	20	.01400	.02143	.911	0546	.0826	
VAR00001 Tukey HSD							

Multiple Comparisons							
(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inte	rval	
					Lower Bound	Upper Bound	
Figure 4A (TCF)							
0	1	.19167 *	.02076	.000	.1252	.2582	
	20	.30900 *	.02076	.000	.2425	.3755	
	50	.46600 *	.02076	.000	.3995	.5325	
1	0	19167 *	.02076	.000	2582	1252	
	20	.11733 *	.02076	.002	.0508	.1838	
	50	.27433 *	.02076	.000	.2078	.3408	
20	0	30900 *	.02076	.000	3755	2425	
	1	11733 *	.02076	.002	1838	0508	
	50	.15700 *	.02076	.000	.0905	.2235	
50	0	46600 *	.02076	.000	5325	3995	
	1	27433 *	.02076	.000	3408	2078	
	20	15700 *	.02076	.000	2235	0905	
VAR00001							

Tukey HSD

Multiple Comparisons

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inte	95% Confidence Interval	
					Lower Bound	Upper Bound	
Figure 4B							
0	1	- 1.92467 *	.41532	.007	-3.2547	5947	
	20	-2.50733 *	.41532	.001	-3.8373	-1.1773	
	50	-6.96000*	.41532	.000	- 8.2900	-5.6300	
1	0	1.92467 *	.41532	.007	.5947	3.2547	
	20	58267	.41532	.531	-1.9127	.7473	
	50	-5.03533*	.41532	.000	-6.3653	-3.7053	
20	0	2.50733*	.41532	.001	1.1773	3.8373	
	1	.58267	.41532	.531	7473	1.9127	
	50	-4.45267 *	.41532	.000	-5.7827	-3.1227	
50	0	6.96000 *	.41532	.000	5.6300	8.2900	
	1	5.03533*	.41532	.000	3.7053	6.3653	
	20	4.45267 *	.41532	.000	3.1227	5.7827	
VAR00001							

Tukey HSD

(I) 1 = 0nm,	(J) 1 = 0nm,	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
2 = 20nm, 3 = 0nm+Wnt5a mAb, 4 = 20nm+Wnt5a mAb	2 = 20nm, 3 = 0nm+Wnt5a mAb, 4 = 20nm+Wnt5a mAb				Lower Bound	Upper Bound
Figure 4C						
1	2	.33467 *	.03334	.000	.2279	.4414
	3	.04400	.03334	.577	0628	.1508
	4	.16100 *	.03334	.006	.0542	.2678
2	1	33467 *	.03334	.000	4414	2279
-	3	29067 *	.03334	.000	3974	1839
	4	17367 *	.03334	.004	2804	0669
3	1	04400	.03334	.577	1508	.0628
	2	.29067 *	.03334	.000	.1839	.3974
	4	.11700 *	.03334	.033	.0102	.2238
4	1	16100 *	.03334	.006	2678	0542
	2	.17367*	.03334	.004	.0669	.2804
	3	11700 *	.03334	.033	2238	0102
VAR00001 Tukey HSD						

Multiple Comparisons								
(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Inte	95% Confidence Interval		
					Lower Bound	Upper Bound		
Figure 4D								
1	2	- 2.75433 *	.27391	.000	-3.6315	-1.8772		
	3	1.07233*	.27391	.019	.1952	1.9495		
	4	32100	.27391	.659	-1.1981	.5561		
2	1	2.75433*	.27391	.000	1.8772	3.6315		
	3	3.82667 *	.27391	.000	2.9495	4.7038		
	4	2.43333*	.27391	.000	1.5562	3.3105		
3	1	-1.07233*	.27391	.019	- 1.9495	1952		
	2	- 3.82667 *	.27391	.000	-4.7038	-2.9495		
	4	-1.39333*	.27391	.004	-2.2705	5162		
4	1	.32100	.27391	.659	5561	1.1981		
	2	-2.43333*	.27391	.000	- 3.3105	- 1.5562		
	3	1.39333*	.27391	.004	.5162	2.2705		
MADOOOOI								

VAR00001

Tukey HSD

Multiple Comparisons

(I) 1 = NC,	(J) 1 = NC,	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
2 = +Wnt3a, 3 = +Wnt3a mAb, 4 = Wnt3a+Wnt3a mAb	2 = +Wnt3a, 3 = +Wnt3a mAb, 4 = Wnt3a+Wnt3a mAb				Lower Bound	Upper Bound
Figure 4E						
1	2	47433 *	.04523	.000	6192	3295
	3	.17733 *	.04523	.019	.0325	.3222
	4	.16567 *	.04523	.026	.0208	.3105
2	1	.47433*	.04523	.000	.3295	.6192
2	3	.65167*	.04523	.000	.5068	.7965
	4	.64000 *	.04523	.000	.4951	.7849
3	1	17733 *	.04523	.019	3222	0325
	2	65167 *	.04523	.000	7965	5068
	4	01167	.04523	.994	1565	.1332
4	1	16567 *	.04523	.026	3105	0208
	2	64000 *	.04523	.000	7849	4951
	3	.01167	.04523	.994	1332	.1565
VAR00001						

Tukey HSD

(I) 1 = NC,	(J) 1 = NC,	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
2 = + Wnt5a, 3 = + Wnt5a mAb, 4 = Wnt5a+Wnt5a mAb	2 = + Wnt5a, 3 = + Wnt5a mAb, 4 = Wnt5a+Wnt5a mAb				Lower Bound	Upper Bound
Figure 4F						
1	2	-3.02767*	.20239	.000	-3.6758	-2.3795
	3	1.02867 *	.20239	.004	.3805	1.6768
	4	17100	.20239	.832	8191	.4771
2	1	3.02767 *	.20239	.000	2.3795	3.6758
-	3	4.05633*	.20239	.000	3.4082	4.7045
	4	2.85667 *	.20239	.000	2.2085	3.5048
3	1	-1.02867 *	.20239	.004	- 1.6768	3805
	2	-4.05633*	.20239	.000	-4.7045	- 3.4082
	4	- 1.19967 *	.20239	.002	-1.8478	5515
4	1	.17100	.20239	.832	4771	.8191
	2	-2.85667*	.20239	.000	-3.5048	-2.2085
	3	1.19967 *	.20239	.002	.5515	1.8478
VAR00001 Tukey HSD						

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 5B						
0	5	58300 *	.05290	.000	7571	4089
	10	12600	.05290	.197	3001	.0481
	30	40433 *	.05290	.000	5784	2302
	60	13600	.05290	.150	3101	.0381
5	0	.58300*	.05290	.000	.4089	.7571
	10	.45700 *	.05290	.000	.2829	.6311
	30	.17867*	.05290	.044	.0046	.3528
	60	.44700 *	.05290	.000	.2729	.6211
10	0	.12600	.05290	.197	0481	.3001
	5	45700 *	.05290	.000	6311	2829
	30	27833 *	.05290	.003	4524	1042
	60	01000	.05290	1.000	1841	.1641
30	0	.40433*	.05290	.000	.2302	.5784
	5	17867 *	.05290	.044	3528	0046
	10	.27833*	.05290	.003	.1042	.4524
	60	.26833 *	.05290	.003	.0942	.4424
60	0	.13600	.05290	.150	0381	.3101
	5	44700 *	.05290	.000	6211	2729
	10	.01000	.05290	1.000	1641	.1841
	30	26833 *	.05290	.003	4424	0942

Multiple Comparisons

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 5C						
0	5	20667 *	.01588	.000	2589	1544
	10	39767 *	.01588	.000	4499	3454
	30	52167 *	.01588	.000	5739	4694
	60	53733 *	.01588	.000	5896	4851
5	0	.20667 *	.01588	.000	.1544	.2589
	10	19100 *	.01588	.000	2433	1387
	30	31500 *	.01588	.000	3673	2627
	60	33067 *	.01588	.000	3829	2784
10	0	.39767 *	.01588	.000	.3454	.4499
	5	.19100*	.01588	.000	.1387	.2433
	30	12400*	.01588	.000	1763	0717
	60	13967 *	.01588	.000	1919	0874
30	0	.52167*	.01588	.000	.4694	.5739
	5	.31500*	.01588	.000	.2627	.3673
	10	.12400 *	.01588	.000	.0717	.1763
	60	01567	.01588	.855	0679	.0366
60	0	.53733 *	.01588	.000	.4851	.5896
	5	.33067 *	.01588	.000	.2784	.3829
	10	.13967 *	.01588	.000	.0874	.1919
	30	.01567	.01588	.855	0366	.0679
VAR00001						

Tukey HSD

(I) time	(J) time	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interv	95% Confidence Interval	
					Lower Bound	Upper Bound	
Figure 5D							
0	5	.03000	.03961	.937	1004	.1604	
	10	01000	.03961	.999	1404	.1204	
	30	.00667	.03961	1.000	1237	.1370	
	60	02333	.03961	.974	1537	.1070	
5	0	03000	.03961	.937	1604	.1004	
	10	04000	.03961	.845	1704	.0904	
	30	02333	.03961	.974	1537	.1070	
	60	05333	.03961	.671	1837	.0770	

Table W1. (con	tinued)					
10	0	.01000	.03961	.999	1204	.1404
	5	.04000	.03961	.845	0904	.1704
	30	.01667	.03961	.992	1137	.1470
	60	01333	.03961	.997	1437	.1170
30	0	00667	.03961	1.000	1370	.1237
	5	.02333	.03961	.974	1070	.1537
	10	01667	.03961	.992	1470	.1137
	60	03000	.03961	.937	1604	.1004
60	0	.02333	.03961	.974	1070	.1537
	5	.05333	.03961	.671	0770	.1837
	10	.01333	.03961	.997	1170	.1437
	30	.03000	.03961	.937	1004	.1604
VAR00001						

Tukey HSD

Multiple Comparisons

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 5E						
0	1	11033 *	.02696	.015	1967	0240
	20	32633*	.02696	.000	4127	2400
	50	47333 *	.02696	.000	5597	3870
1	0	.11033 *	.02696	.015	.0240	.1967
	20	21600*	.02696	.000	3023	1297
	50	36300*	.02696	.000	4493	2767
20	0	.32633 *	.02696	.000	.2400	.4127
	1	.21600 *	.02696	.000	.1297	.3023
	50	14700*	.02696	.003	2333	0607
50	0	.47333 *	.02696	.000	.3870	.5597
	1	.36300 *	.02696	.000	.2767	.4493
	20	.14700 *	.02696	.003	.0607	.2333
VAR00001						

Tukey HSD

Multiple Comparisons

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 5F						
0	1	15167*	.01790	.000	2090	0943
	20	39267 *	.01790	.000	4500	3353
	50	51900 *	.01790	.000	5763	4617
1	0	.15167 *	.01790	.000	.0943	.2090
	20	24100*	.01790	.000	2983	1837
	50	36733*	.01790	.000	4247	3100
20	0	.39267 *	.01790	.000	.3353	.4500
	1	.24100 *	.01790	.000	.1837	.2983
	50	12633*	.01790	.000	1837	0690
50	0	.51900 *	.01790	.000	.4617	.5763
	1	.36733 *	.01790	.000	.3100	.4247
	20	.12633 *	.01790	.000	.0690	.1837
VAR00001 Tukey HSD						

(I) VAR00002	(J) VAR00002	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Figure 6C						
0	5	08967 *	.02012	.008	1559	0234
	10	37167*	.02012	.000	4379	3054
	30	56933*	.02012	.000	6356	5031
	60	74133*	.02012	.000	8076	6751
5	0	.08967 *	.02012	.008	.0234	.1559
	10	28200*	.02012	.000	3482	2158
	30	47967 *	.02012	.000	5459	4134
	60	65167 *	.02012	.000	7179	5854

278.e10 CTHRC1 Promotes Invasion of Gastrointestinal Stromal Tumors and

Table W1. (continued)						
10	0	.37167*	.02012	.000	.3054	.4379
	5	.28200 *	.02012	.000	.2158	.3482
	30	19767 *	.02012	.000	2639	1314
	60	36967 *	.02012	.000	4359	3034
30	0	.56933*	.02012	.000	.5031	.6356
	5	.47967 *	.02012	.000	.4134	.5459
	10	.19767 *	.02012	.000	.1314	.2639
	60	17200 *	.02012	.000	2382	1058
60	0	.74133 *	.02012	.000	.6751	.8076
	5	.65167 *	.02012	.000	.5854	.7179
	10	.36967 *	.02012	.000	.3034	.4359
	30	.17200*	.02012	.000	.1058	.2382
VAR00001						
Tukey HSD						

Multiple Comparisons

(I) time	(J) time	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interv	/al
					Lower Bound	Upper Bound
Figure 6D						
0	5	23467*	.02028	.000	3014	1679
	10	82533*	.02028	.000	8921	7586
	30	68733*	.02028	.000	7541	6206
	60	46233 *	.02028	.000	5291	3956
5	0	.23467 *	.02028	.000	.1679	.3014
	10	59067 *	.02028	.000	6574	5239
	30	45267 *	.02028	.000	5194	3859
	60	22767 *	.02028	.000	2944	1609
10	0	.82533 *	.02028	.000	.7586	.8921
10	5	.59067 *	.02028	.000	.5239	.6574
	30	.13800*	.02028	.000	.0712	.2048
	60	.36300*	.02028	.000	.2962	.4298
30	0	.68733*	.02028	.000	.6206	.7541
	5	.45267 *	.02028	.000	.3859	.5194
	10	13800*	.02028	.000	2048	0712
	60	.22500*	.02028	.000	.1582	.2918
60	0	.46233*	.02028	.000	.3956	.5291
	5	.22767 *	.02028	.000	.1609	.2944
	10	36300*	.02028	.000	4298	2962
	30	22500 *	.02028	.000	2918	1582
VAR00001						

Tukey HSD

(I) time	(J) time	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interv	val
					Lower Bound	Upper Bound
Figure 6E						
0	5	.02467	.02220	.797	0484	.0977
	10	33967 *	.02220	.000	4127	2666
	30	26100 *	.02220	.000	3341	1879
	60	37767 *	.02220	.000	4507	3046
5	0	02467	.02220	.797	0977	.0484
	10	36433 *	.02220	.000	4374	2913
	30	28567 *	.02220	.000	3587	2126
	60	40233 *	.02220	.000	4754	3293
10	0	.33967 *	.02220	.000	.2666	.4127
	5	.36433 *	.02220	.000	.2913	.4374
	30	.07867 *	.02220	.034	.0056	.1517
	60	03800	.02220	.469	1111	.0351
30	0	.26100*	.02220	.000	.1879	.3341
	5	.28567 *	.02220	.000	.2126	.3587
	10	07867 *	.02220	.034	1517	0056
	60	11667 *	.02220	.003	1897	0436
60	0	.37767 *	.02220	.000	.3046	.4507
	5	.40233 *	.02220	.000	.3293	.4754
	10	.03800	.02220	.469	0351	.1111
	30	.11667 *	.02220	.003	.0436	.1897
data						
Tukey HSD						

Multiple Compa	Multiple Comparisons								
(I) time	(J) time	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval				
					Lower Bound	Upper Bound			
Figure 6F									
0	5	43533 *	.01941	.000	4992	3715			
	10	83733 *	.01941	.000	9012	7735			
	30	77067 *	.01941	.000	8345	7068			
	60	78267 *	.01941	.000	8465	7188			
5	0	.43533*	.01941	.000	.3715	.4992			
	10	40200 *	.01941	.000	4659	3381			
	30	33533 *	.01941	.000	3992	2715			
	60	34733 *	.01941	.000	4112	2835			
10	0	.83733*	.01941	.000	.7735	.9012			
	5	.40200*	.01941	.000	.3381	.4659			
	30	.06667 *	.01941	.040	.0028	.1305			
	60	.05467	.01941	.104	0092	.1185			
30	0	.77067 *	.01941	.000	.7068	.8345			
	5	.33533*	.01941	.000	.2715	.3992			
	10	06667 *	.01941	.040	1305	0028			
	60	01200	.01941	.969	0759	.0519			
60	0	.78267 *	.01941	.000	.7188	.8465			
	5	.34733 *	.01941	.000	.2835	.4112			
	10	05467	.01941	.104	1185	.0092			
	30	.01200	.01941	.969	0519	.0759			
data									

Tukey HSD

(I) 1 = 0nm,	(J) 1 = 0nm,	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence In	terval
2 = 20nm, 3 = 0nm+Wnt3a mAb, 4 = 20nm+Wnt3a mAb, 5 = 0nm+Wnt5a mAb, 6 = 20nm+Wnt5a mAb	2 = 20nm, 3 = 0nm+Wnt3a mAb, 4 = 20nm+Wnt3a mAb, 5 = 0nm+Wnt5a mAb, 6 = 20nm+Wnt5a mAb				Lower Bound	Upper Bound
Figure 7B						
1	2	- 53.00000 *	4.10916	.000	-65.4984	-40.5016
	3	33333	4.10916	1.000	-12.8317	12.1651
	4	-49.50000*	4.10916	.000	-61.9984	-37.0016
	5	-4.50000	4.10916	.879	- 16.9984	7.9984
	6	- 13.33333 *	4.10916	.031	-25.8317	8349
2	1	53.00000*	4.10916	.000	40.5016	65.4984
	3	52.66667*	4.10916	.000	40.1683	65.1651
	4	3.50000	4.10916	.955	-8.9984	15.9984
	5	48.50000*	4.10916	.000	36.0016	60.9984
	6	39.66667*	4.10916	.000	27.1683	52.1651
3	1	.33333	4.10916	1.000	-12.1651	12.8317
	2	- 52.66667*	4.10916	.000	-65.1651	-40.1683
	4	-49.16667*	4.10916	.000	-61.6651	- 36.6683
	5	-4.16667	4.10916	.910	- 16.6651	8.3317
	6	-13.00000*	4.10916	.038	-25,4984	5016
4	1	49.50000*	4.10916	.000	37.0016	61,9984
	2	-3.50000	4.10916	.955	-15,9984	8,9984
	3	49.16667*	4,10916	.000	36.6683	61.6651
	5	45.00000 *	4.10916	.000	32,5016	57.4984
	6	36.16667*	4.10916	.000	23.6683	48.6651
5	1	4 50000	4 10916	879	-7 9984	16 9984
-	2	-48 50000 *	4 10916	000	-60 9984	- 36 0016
	3	4 16667	4 10916	910	-8 3317	16 6651
	4	-45 00000 *	4 10916	000	-57 4984	- 32 5016
	6	-8 83333	4 10916	290	-21 3317	3 6651
6	1	13 33333*	4 10916	031	8349	25 8317
0	2	- 39,66667*	4 10916	.000	-52 1651	-27.1683
	3	13 00000 *	4 10916	.000	5016	25 4984
	6	36.16667*	4.10916	.000	/8 6651	23.6683
		8 83333	4 10916	290	-36651	-25.0005
VAR00001)	0.03333	4.10/10	.270	- 5.0051	21.331/
Tukey HSD						

Multiple Comparisons						
(I) $1 = 0$ nm, 2 = 20nm	(J) $1 = 0$ nm, 2 = 20nm	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Int	erval
3 = 0nm+NSC23766,	3 = 0nm+NSC23766,				Lower Bound	Upper Bound
4 = 20nm+NSC23766,	4 = 20nm+NSC23766,					
5 = 0nm+Y-27632,	5 = 0nm+Y-27632,					
6 = 20nm+Y-27632	6 = 20nm+Y-27632					
Figure 7D						
1	2	- 51.00000 *	2.31541	.000	-58.0425	-43.9575
	3	-4.16667	2.31541	.481	-11.2092	2.8759
	4	- 15.50000 *	2.31541	.000	-22.5425	-8.4575
	5	-/.1666/*	2.31541	.044	- 14.2092	1241
2	1	51 00000 *	2.31541	.001	43 9575	- 5.9375
2	3	46.83333*	2.31541	.000	39.7908	53.8759
	4	35.50000 *	2.31541	.000	28.4575	42.5425
	5	43.83333*	2.31541	.000	36.7908	50.8759
	6	40.00000 *	2.31541	.000	32.9575	47.0425
3	1	4.16667	2.31541	.481	-2.8759	11.2092
	2	-46.83333*	2.31541	.000	- 53.8759	- 39.7908
	4	- 11.33333 *	2.31541	.000	- 18.3759	-4.2908
	5	-3.00000	2.31541	.785	- 10.0425	4.0425
4	6	-6.83333	2.31541	.061	- 13.8/59	.2092
4	1	15.50000 *	2.31541	.000	8.45/5	22.5425
	2	- 55.50000	2.31341	.000	-42.3423	$\begin{array}{cccc} -52.7908 \\ 9 & -4.2908 \\ 5 & 4.0425 \\ 9 & .2092 \\ 5 & 22.5425 \\ 5 & -28.4575 \\ 8 & 18.3759 \\ 8 & 15.3759 \\ 8 & 15.3759 \\ 5 & 11.5425 \\ 1 & 14.2092 \\ 9 & -36.7908 \\ 10.0425 \\ 9 & -1.2908 \\ 9 & 3.2092 \\ 5 & 18.0425 \\ 5 & -32.9575 \\ 12 & 13.8759 \\ 25 & 2.5425 \\ 10.8759 \\ \end{array}$
	5	8 33333*	2.31541	.000	1 2908	15 3759
	6	4.50000	2.31541	.397	-2.5425	11.5425
5	1	7.16667 *	2.31541	.044	.1241	14.2092
	2	-43.83333*	2.31541	.000	- 50.8759	- 36.7908
	3	3.00000	2.31541	.785	-4.0425	10.0425
	4	-8.33333*	2.31541	.013	-15.3759	-1.2908
	6	-3.83333	2.31541	.570	-10.8759	3.2092
6	1	11.00000*	2.31541	.001	3.9575	18.0425
	2	-40.00000 *	2.31541	.000	-47.0425	- 32.9575
	3	6.83333	2.31541	.061	2092	13.8759
	4	-4.50000	2.31541	.39/	-11.5425	2.5425
VAR00001 Tukey HSD	,	5.65555	2.51911	.970	5.2672	10.0755
Multiple Comparisons						
(I) 1 = 0nm.	(I) $1 = 0$ nm.	Mean Difference (I-I)	Std Error	Sig	95% Confidence In	terval
2 = 20 nm.	2 = 20 nm.			0.8.		
3 = 0nm+Wnt3a mAb,	3 = 0nm+Wnt3a mAb,				Lower Bound	Upper Bound
4 = 20nm+Wnt3a mAb,	4 = 20nm+Wnt3a mAb,					
5 = 0nm+Wnt5a mAb,	5 = 0nm+Wnt5a mAb,					
6 = 20nm+Wnt5a mAb	6 = 20nm+Wnt5a mAb					
Figure 8B						
1	2	-71.83333*	3.48250	.000	-82.4257	-61.2410
	3	1.00000	3.48250	1.000	-9.5923	11.5923
	4	-65.33333 *	3.48250	.000	-75.9257	-54.7410
	5	-1.00000	3.48250	1.000	-11.5923	9.5923
	6	-9.33333	3.48250	.109	- 19.9257	1.2590
2	1	71.83333 *	3.48250	.000	61.2410	82.425/
	3	/2.83333*	3.48250	.000	62.2410	83.425/
	4	6.50000 70.83333 *	3.48250	.441	-4.0925	1/.0925
	5	/0.85555 62 50000 *	3.48250	.000	51 9077	81.42 <i>)</i> / 73.0923
3	1	- 1.00000	3 48250	1 000	-11 5923	9 5923
<i>ت</i>	2	-72.83333*	3.48250	.000	-83.4257	-62.2410
	- 4	-66.33333 *	3.48250	.000	-76.9257	-55.7410
	5	-2.00000	3.48250	.992	- 12.5923	8.5923
	6	- 10.33333	3.48250	.059	-20.9257	.2590
4	1	65.33333 *	3.48250	.000	54.7410	75.9257
	2	-6.50000	3.48250	.441	- 17.0923	4.0923
	3	66.33333 *	3.48250	.000	55.7410	76.9257
	5	64.33333 *	3.48250	.000	53.7410	74.9257
	6	56.00000 *	5.48250	.000	45.40//	66.5923

45.4077

Table W1. (continued)

Maldala C

4

1	1.00000	3.48250	1.000	-9.5923	11.5923
2	-70.833333*	3.48250	.000	-81.4257	-60.2410
3	2.00000	3.48250	.992	-8.5923	12.5923
4	-64.333333*	3.48250	.000	-74.9257	- 53.7410
6	-8.33333	3.48250	.191	-18.9257	2.2590
1	9.33333	3.48250	.109	-1.2590	19.9257
2	-62.50000*	3.48250	.000	-73.0923	-51.9077
3	10.33333	3.48250	.059	2590	20.9257
4	- 56.00000 *	3.48250	.000	-66.5923	-45.4077
5	8.33333	3.48250	.191	-2.2590	18.9257
	1 2 3 4 6 1 2 3 4 5	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

Tukey HSD

Multiple Comparisons

(I) 1 = 0nm,	(J) 1 = 0nm,	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Int	erval
2 = 20nm, 3 = 0nm+NSC23766, 4 = 20nm+NSC23766, 5 = 0nm+Y-27632, 6 = 20nm+Y-27632	2 = 20nm, 3 = 0nm+NSC23766, 4 = 20nm+NSC23766, 5 = 0nm+Y-27632, 6 = 20nm+Y-27632				Lower Bound	Upper Bound
Figure 8D						
1	2	-78.00000*	3.68053	.000	-89.1947	-66.8053
	3	-4.16667	3.68053	.864	-15.3613	7.0280
	4	- 5.50000	3.68053	.670	-16.6947	5.6947
	5	3.16667	3.68053	.953	-8.0280	14.3613
	6	-11.00000	3.68053	.056	-22.1947	.1947
2	1	78.00000*	3.68053	.000	66.8053	89.1947
	3	73.83333*	3.68053	.000	62.6387	85.0280
	4	72.50000*	3.68053	.000	61.3053	83.6947
	5	81.16667*	3.68053	.000	69.9720	92.3613
	6	67.00000*	3.68053	.000	55.8053	78.1947
3	1	4.16667	3.68053	.864	-7.0280	15.3613
	2	-73.83333*	3.68053	.000	-85.0280	-62.6387
	4	-1.33333	3.68053	.999	-12.5280	9.8613
	5	7.33333	3.68053	.370	-3.8613	18.5280
	6	-6.83333	3.68053	.447	-18.0280	4.3613
4	1	5.50000	3.68053	.670	-5.6947	16.6947
	2	-72.50000*	3.68053	.000	-83.6947	-61.3053
	3	1.33333	3.68053	.999	-9.8613	12.5280
	5	8.66667	3.68053	.205	-2.5280	19.8613
	6	- 5.50000	3.68053	.670	-16.6947	5.6947
5	1	-3.16667	3.68053	.953	-14.3613	8.0280
	2	-81.16667*	3.68053	.000	-92.3613	-69.9720
	3	-7.33333	3.68053	.370	-18.5280	3.8613
	4	-8.66667	3.68053	.205	-19.8613	2.5280
	6	-14.16667*	3.68053	.007	-25.3613	-2.9720
6	1	11.00000	3.68053	.056	1947	22.1947
	2	-67.00000 *	3.68053	.000	-78.1947	- 55.8053
	3	6.83333	3.68053	.447	-4.3613	18.0280
	4	5.50000	3.68053	.670	-5.6947	16.6947
	5	14.16667*	3.68053	.007	2.9720	25.3613
VAR00001 Tukey HSD						

* The mean difference is significant at the 0.05 level.