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WTAP is a promising diagnosis and treatment biomarker that inhibits the proliferation and invasion of melanoma cells

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Wilms' tumor 1-associating protein (WTAP) is ubiquitously expressed in many tissues and plays an important role in physiological processes and tumor development. Here, we investigated the specific biological role and underlying mechanism of WTAP in melanoma. We determined the expression of WTAP and its correlation with clinicopathological features in paraffin-embedded tissues. We investigated the effects of WTAP on melanoma cells via a CCK-8 assay, a colony formation assay, an EdU assay, a Transwell assay, and subcutaneous xenograft experiments. We then applied RNA sequencing to further screen candidate targets, and NT5E was selected as the downstream gene of WTAP. Finally, a series of rescue assays, together with nucleotidase assays and ELISA, were adopted to confirm the function of NT5E in melanoma progression. We demonstrated that WTAP expression was downregulated in melanoma, which was associated with a poor prognosis, and that WTAP expression served as an independent predictor of melanoma survival. Functionally, WTAP hindered the proliferation, growth, migration, and invasion of melanoma cells. Furthermore, NT5E was identified as the downstream effector of WTAP and was subsequently found to rescue the increased proliferation, migration, and invasion of melanoma cells induced by WTAP deficiency. Moreover, knockdown of WTAP increased the expression of NT5E, MMP2, and N-cadherin, and simultaneous transfection with siNT5E reversed the increased expression of MMP2 and N-cadherin. Moreover, increased NT5E expression caused by forced WTAP inhibition in melanoma promoted the hydrolysis of AMP to produce more adenosine and further abrogated the secretion of IFN-γ by PBMCs. We found that WTAP expression is significantly downregulated and restrains the progression of melanoma via the downstream effects of NT5E on immunosuppression and molecular adhesion. This study revealed that WTAP plays a crucial inhibitory role in melanoma oncogenesis and highlighted WTAP as a potential novel diagnosis and therapeutic target for melanoma.

Key words: Wilms' tumor 1-associated protein (WTAP); melanoma; ecto-5'-nucleotidase (NT5E); immunosuppression; adhesive molecule

Melanoma is one of the most aggressive human cancers, which originates from melanocytes, namely, melanin-producing cells that are located mainly in the skin, but are also found in the mucosa, uvea, and leptomeninges. The incidence of melanoma has rapidly increased over the course of the last few decades, far exceeding that of other types of malignant tumors [1]. Melanoma is characterized by a tendency to metastasize, and patients with metastatic disease have a worse prognosis [2]. The 5-year relative survival rate of patients with localized or regional melanoma has been shown to be 98% and 64%, respectively, whereas in patients with metastatic melanoma, the 5-year survival rate is only 20% [3]. Cutaneous melanoma, which is driven by exposure to ultraviolet radiation from sunshine or tanning beds [4, 5], is responsible for the majority of melanoma cases, accounting for >75% of skin cancer-associated deaths [3]. Over the last few decades, great progress has been made in terms of elucidating the underlying mechanisms of cutaneous melanoma at the molecular, cellular, and organismal levels; however, the 5-year survival rate remains unsatisfactorily low. Therefore, a more in-depth understanding of the mechanism of melanoma development is urgently required to facilitate the

development of novel therapies that may be used to target this potentially fatal disease.

N6-methyladenosine (m6A) modification, the most prevalent internal modification of mRNAs [6, 7], has been reported to fulfil several roles in the regulation of gene expression in eukaryotes, including its participation in RNA stability, splicing, and translation efficacy [8]. This dynamic and reversible modification is catalyzed by the m6A methyltransferase complex, in which Wilms' tumor 1-associated protein (WTAP) serves as a key regulatory subunit to stabilize the core catalytic components methyltransferases methyltransferase-like 3 (METTL3) and methyltransferase-like 14 (METTL14), ensuring their proper localization to nuclear speckles and efficient m6A deposition on target RNAs [9, 10]. As a key component of m6A, WTAP has been shown to be essential in many cellular processes, including alternative splicing, X chromosome inactivation, and cell cycle regulation [11–13]. Moreover, dysregulation of WTAP has been shown to be linked to multiple cancers, where it often acts as an oncogenic driver, contributes to the aggressive features of various types of cancers, including hepatocellular carcinoma, osteosarcoma, ovarian cancer, and colorectal cancer [14–17]. Meanwhile, the tumor suppressor role of WTAP has been reported in several bioinformatics studies [18–20]. However, the biological role of WTAP in melanoma, one of the most aggressive malignancies, has yet to be fully elucidated. Feng et al. [21] downloaded the RNA sequencing transcriptomic data and clinical information of patients with melanoma from the Genotype Tissue Expression and The Cancer Genome Atlas databases, and identified that WTAP is an independent protective prognostic factor for melanoma patients. Finally, the function of WTAP in melanoma cells was verified via plasmid transfection into A375 cells. Despite these advances in our knowledge, however, how WTAP affects melanoma progression has yet to be fully elucidated.

Ecto-5'-nucleotidase (NT5E; also known as CD73) is a 70 kDa glycosylphosphatidylinositol-anchored cell surface protein that is widely distributed in the outer leaflet of the plasma membrane. As a nucleotidase, NT5E catalyzes the hydrolysis of adenosine monophosphate (AMP) into adenosine and phosphate. A high level of NT5E gene expression in tumor cells has been shown to be conducive to the accumulation of the immunosuppressive molecule adenosine in the tumor microenvironment, thereby promoting tumor growth and metastasis [22]. In addition, NT5E-generated adenosine was able to mediate the immune evasion of tumor cells via attenuating the functions of multiple types of immune cells, resulting in immune escape and further tumor growth and metastasis [23]. In addition to its effects on adenosine, NT5E has also been shown to function as an adhesive molecule that regulates cellular interactions with components of the extracellular matrix (ECM) to mediate cancer cell adhesion and migration, as well as stemness [24–26]. There is increasing evidence to show that NT5E is overexpressed in numerous types of cancer, and that this high expression is positively associated with tumor malignancy and poor outcomes [27–29]. In light of its multiple effects on tumor progression as a potential checkpoint, anti-NT5E therapy has recently attracted attention as an emerging area for therapeutic intervention in terms of cancer immunotherapy, especially in combination with conventional therapy and/or treatment with other immune checkpoint inhibitors [30–32]. An in-depth study demonstrated that an absence of NT5E improved survival in a murine model of glioblastoma treated with anti-CTLA-4 and anti-PD-1 antibodies, and these researchers further concluded that NT5E acts as a specific immunotherapeutic target that is capable of improving anti-tumor immune responses to immune checkpoint therapies in glioblastoma [32]. A previous study also reported that NT5E blockade may limit both the production and activation of immunosuppressive adenosine molecules within the tumor microenvironment, thereby overcoming the development of immune resistance [33]. Furthermore, as previously reported, NT5E expression was shown to be correlated with the plasticity of melanoma cells, thereby expediting the transition from a proliferative to an aggressive phenotype [34]. In view of these findings, the present study aimed to provide novel insights into the molecular pathogenesis of melanoma, and the results obtained suggest that targeting WTAP via the potential downstream effects of NT5E on immunosuppression and adhesion holds promise as a novel means of therapeutic intervention.

Patients and methods

Public datasets. The Gene Expression Profiling Interactive Analysis (GEPIA) database (https://gepia.cancer-pku.cn/) was utilized to compare WTAP expression levels across various cancer types and their corresponding normal tissues, as well as to evaluate the correlation between WTAP expression and prognostic outcomes in melanoma patients.

Clinical samples and ethics. Paraffin-embedded tissue samples from 55 patients with melanoma who underwent surgical excision between January 2009 and December 2018 were obtained from the Department of Pathology of Shijiazhuang People's Hospital. Complete clinicopathological data, including follow-up information for all 55 patients, were collected from the medical records room of Shijiazhuang People's Hospital. The duration of follow-up was between January 2019 and March 2024. The inclusion criteria were as follows: i) a confirmed pathological diagnosis of melanoma; and ii) no prior therapy received by the patient before surgery. The exclusion criteria were as follows: i) a previous history of malignant tumor; and ii) a previous history of immune system disease. The paraffin-embedded samples were used for subsequent immunohistochemistry analysis, as detailed below, to confirm the association between the expression of WTAP and the prognosis of patients with melanoma. All patients involved in the present study signed written informed consent statements prior to the surgery, and this

study was approved by the Ethics Committee of Shijiazhuang People's Hospital (Approval No. 2024101).

Immunohistochemistry (IHC). According to the manufacturer's protocol, IHC staining was conducted via the UltraSensitive TMSP (Mouse/Rabbit) IHC Kit (#PV-9000, ZSGB-Bio, China) with the following primary antibodies: anti-WTAP antibody (1:1000, #60188-1-Ig, Proteintech, China), anti-NT5E antibody (1:500, #12231-1-AP, Proteintech, China), anti-MMP2 antibody (1:200, #10373-2-AP, Proteintech, China), and anti-N-cadherin antibody (1:4000, #22018-1-AP, Proteintech, China). Briefly, the 4 μm paraffin-embedded slides were deparaffinized with xylene, followed by rehydration with a decreasing alcohol gradient and PBS washing three times. The sections were then immersed with endogenous peroxidase blocker for 20 min at room temperature to suppress endogenous peroxidase activity, and after three times washing by PBS, the tissue sections were transferred into Citrate Antigen Retrieval Solution (#C1032, Solarbio, China) and heated in a pressure cooker at high pressure for 2 min for antigen retrieval. Thereafter, the slides were incubated with diluted antibodies at 4 °C overnight. Next, the slides were in turn incubated with reaction strengthening fluid and enhanced enzyme-labeled goat anti-Mouse/Rabbit IgG polymer at 37 °C for 20 min, respectively. Finally, color development was carried out with DAB (#ZLI-9018, ZSGB-Bio, China) for 5 min at room temperature, and then, slides were counterstained with Harris hematoxylin (#BA4097, Baso, China), dehydrated using a series of increasing alcohol concentrations, and cover-slipped. The WTAP staining score for each patient was computed by multiplying the staining intensity grade (a grade of 0, 1, 2, or 3 indicated negative, weakly positive, moderately positive or strongly positive staining, respectively) and positive percentage score (a score of 0, 1, 2, or 3 indicated a positive percentage of 0–25%, 26–50%, 51–75% or 76–100%, respectively).

Cell lines and cell culture. Human melanoma cell lines A875 (TCH C203) and A375 (TCH C114) were provided by Suzhou Haixing Biosciences Co., Ltd. Both cell lines were authenticated by short tandem repeat profiling analysis, and mycoplasma contamination was ruled out using the MycoEasy Rapid Mycoplasma Test Kit (#CA6101024, Cellapy, China). Routinely, the cells were cultured in Gibco® Dulbecco's modified Eagle's medium (DMEM, Gibco, USA) supplemented with 10% fetal bovine serum (FBS, Gibco, USA) and 1% penicillin/streptomycin (Invitrogen, USA) in a 5% CO_2 humidified atmosphere at 37 °C.

RNA interference. Small interfering RNAs (siRNAs) directed against WTAP (termed siWTAP) and NT5E (termed siNT5E) and negative control RNAs (termed siNC) were synthesized by RiboBio (Guangzhou, China). Transient transfection was performed with Invitrogen™ Lipofectamine® 2000 Reagent (Invitrogen, USA) according to the standard protocol. Cells transfected with siWTAP or siNT5E were harvested 48 h post-transfection for RT-qPCR and immunoblotting analyses or functional assays. For rescue experiments, siWTAP was transfected first (for 24 h), followed by siNT5E transfection (for an additional 24 h). The sequences of the siRNAs used were as follows: siWTAP-1: 5'-GGAACAGACTAAAGACAAA-3'; siWTAP-2: 5'-CTAAGAGAGTCTGAAGAAA-3'; siWTAP-3: 5'-GAAGCATATGTACAAGCTT-3'; siNT5E-1: 5'-GGAGATGGGTTCCAGATGA-3'; siNT5E-2: 5'-GATCGAGTTTGATGAAAGA-3'; siNT5E-3: 5'-GATGGCTCCTCTCAATCAT-3'.

Table 1. Primer sequences and reaction conditions.

Gene	Primer sequence	Annealing temperature	Product size, bp
WTAP	F: 5'-TTCCCAAGAAGGTTCGATTG-3' R: 5'-TGCAGACTCCTGCTGTTGTT-3'	57 °C	192
CHGB	F: 5'-TCTATCCCTCCGACAGCCAA-3' R: 5'-CGTCGTTTGTCCACCTCAGA-3'	59 °C	412
IKBKGP1	F: 5'-GCACCTCTCCAGCCTCCATC-3' R: 5'-CGCTTTTGTGTACCTTTGTGTATCTC-3'	57 °C	113
NT5E	F: 5'-CTCCTCTCAATCATGCCGCT-3' R: 5'-TGGATTCCATTGTTGCGTTCA-3'	59 °C	174
SLC7A11	F: 5'-TGGAACGAGGAGGTGGAGAA-3' R: 5'-TGGTGGACACAACAGGCTTT-3'	57 °C	264
FUT1	F: 5'-CCCCTGCATCCCCGATCT-3' R: 5'-GGTCTGGACACAGGATCGAC-3'	57 °C	195
CTH	F: 5'-CTCACTGTCCACCACGTTCA-3' R: 5'-CTGTTTGTACAGTACTTAGCCCC-3'	55 °C	138
GAPDH	F: 5'-AATCCCATCACCATCTTCCA-3' R: 5'-TGGACTCCACGACGTACTCA-3'	57 °C	82

Abbreviations: WTAP-Wilms' tumor 1-associating protein; NT5E-ecto-5'-nucleotidase; CHGB-Chromogranin B; IKBKGP1-Inhibitor of Kappa Light Polypeptide Gene Enhancer in B-cells, Kinase Gamma Pseudogene 1; SLC7A11-Solute Carrier Family 7 Member 11; FUT1-Fucosyltransferase 1; CTH-Cystathionine Gamma-Lyase; GAPDH-Glyceraldehyde-3-Phosphate Dehydrogenase

Plasmid transfection. The WTAP-overexpressing plasmid (RC209632, termed oeWTAP) and empty vector (#PS100001, termed oeVector) were constructed by OriGene Technologies, Inc. Plasmid transfection in A875 and A375 cells was performed using jetPRIME® Versatile DNA/siRNA transfection reagent (Polyplus-transfection SA), and 48 h later, the transfection efficiency was evaluated. Cells that had been successfully transfected were harvested for subsequent functional experiments. No selection markers were used in the present study.

RNA isolation and quantitative real-time PCR (RT-qPCR). Total RNA was isolated from A875 and A375 cells using TRIzol Reagent (Invitrogen, USA), followed by RNA concentration and quality assessment using a NanoDrop One spectrophotometer (Applied Biosystems, USA). Total RNA (2 μg) was reverse transcribed into cDNA using GoScript™ Reverse Transcription Mix (Promega, USA) according to the manufacturer's instructions. For mRNA expression analysis, the cDNA was amplified using GoTaq® qPCR Master Mix (Promega, USA) with an Applied Biosystems™ StepOne Plus Real-Time PCR system (Applied Biosystems, USA). Relative expression levels were normalized against those of GAPDH and calculated using the $2^{-\Delta\Delta cq}$ method [35]. All the RT-qPCR reactions were performed in triplicate technical replicates for each biological replicate to ensure data reliability and reproducibility, and the details of all primers used (including their sequences) are shown in Table 1.

Protein isolation and western blot. A875 and A375 cells were seeded in 6-well plates and routinely maintained in complete DMEM medium in a 5% CO_2 humidified atmosphere at 37 °C. After achieving full cell adhesion and desired confluency, cells were transfected with either siRNA or plasmids, with detailed methodologies provided in "RNA interference" and "Plasmid transfection" above. Forty-eight hours later, total cellular proteins were extracted via precooled RIPA buffer (Sevenbio, China) containing protease inhibitors (Sevenbio, China), and a BCA protein assay kit (Sevenbio, China) was used to evaluate the protein concentration. An Omni-Easy™ Protein Sample Loading Buffer (LT101S, EpiZyme, China) was adopted to mix with 1:4 (v/v) protein sample, followed by incubation at 100 °C for 5 min. Then, 30 μg total cellular proteins were subjected to electrophoresis on an SDS-PAGE (10%, Biotides, China) and transferred to a PVDF membrane (Millipore, USA) followed by membrane incubation in rapid blocking buffer (#G2052-500 ml, Servicebio, China) for 10 mins at room temperature to prevent non-specific binding. After incubation with primary anti-WTAP (1:10000, #60188-1-Ig, Proteintech, China), anti-NT5E (1:1000, #12231-1-AP, Proteintech, China), anti-MMP2 (1:800, #10373-2-AP, Proteintech, China), anti-N-cadherin (1:3000, #22018-1-AP, Proteintech, China) and anti-β-actin (1:2500, #20536-1-AP, Proteintech, China) antibodies at 4 °C overnight, the membranes were then incubated with HRP-conjugated goat anti-mouse antibody (#SA00001-1, Proteintech, China) or HRP-conjugated goat anti-rabbit antibody (#SA00001-2, Proteintech, China) at 37 °C for 1 h. Finally, the signals were detected via a ChemiDoc TM MP Imaging system (Bio-Rad Laboratories, Inc.) after the PVDF membrane had been immersed in SuperKine TM ECL reagent (#BMU102-CN2, Abbkine, China) for 2 min. All the western blot experiments were performed with triplicate independent biological replicates to ensure data reliability and reproducibility.

Cell proliferation assay. Cell proliferation ability was assessed with a Cell Counting Kit-8 (CCK-8, Kumamoto, Japan) based on the reduction of WST-8 (a water-soluble tetrazolium salt) to a water-soluble orange formazan via intracellular dehydrogenases in metabolically active cells. The absorbance at 450 nm is directly proportional to the number of viable cells. Pretreated cells were seeded into a 96-well plate at 2×10^3 cells/well with five replicates and cultured for 1, 2, 3, 4, or 5 days at 37 °C. At the same time, cell-free blank wells were prepared to rule out the potential impact of background absorbance. Absorbance at 450 nm was detected by using the microplate reader (Tecan Group, Ltd.) daily to evaluate cell proliferation. To guarantee the robustness and repeatability of the experimental results, all CCK-8 assays were conducted using three independent biological replicates.

Colony formation assay. A total of 1.5×10^3 transfected A875 or A375 cells were inoculated into 6-well plates and incubated routinely in DMEM at 37 °C for 1-2 weeks until visible colonies formed (colonies typically consist of >50 cells). Colonies were fixed with 4% paraformaldehyde (#P0099, Beyotime, China) at room temperature for 30 min and subsequently stained with 0.1% crystal violet (#C0121, Beyotime, China) at room temperature for 15 min. Visible cell clusters were captured under a light microscope (Olympus Corporation), and the numbers of cell colonies were quantified using ImageJ software (version 1.8.0; National Institutes of Health). Each colony formation experiment was carried out in triplicate with biologically independent samples for enhanced data reliability and reproducibility.

5-Ethynyl-2'-deoxyuridine (EdU) assay. A VF 555 Click-iT EdU Universal Cell Proliferation Detection Kit (#HY-K1086, MedChemExpress, USA) was used to assess the cell proliferation ability with triplicate independent biological replicates. According to the manufacturer's protocol, transfected A875 or A375 cells were plated on glass coverslips in 12-well plates at a density of 3×10^5 cells/well. After 24 h of routine inoculation, the cells were incubated with 50 μM EdU buffer at 37 °C for 2 h, fixed with 4% formaldehyde, and permeabilized with 0.5% Triton X-100. Then, 500 μl Click-iT working buffer was added to each well, and the nuclei were stained with 4',6-diamidino-2-phenylindole (DAPI) (#SI103-11, Sevenbio, China). Finally, images were captured using a confocal microscope (LSM 900, Zeiss, Germany).

Wound healing assay. Pretreated A875 or A375 melanoma cells in the exponential growth phase were seeded in a six-well plate. After 24 h incubation at 37 °C, when the

cell confluence had reached 90%, a 200 μl pipette tip was used to create two vertical bottom lines on the cells. The cells were rinsed three times and then cultured in fresh serum-free medium. Images of the cell monolayer were taken using an inverted microscope (Leica, Germany) at 0 h and 48 h. The scratch wound healing rate was assessed by measuring the migration distance using the following method: Cell migration rate (%) = [(wound width at 0 h – wound width at 48 h) / wound width at 0 h] × 100%. For enhanced data reliability and reproducibility, each wound healing experiment was carried out in triple independent biological samples.

Transwell migration and invasion assays. Transwell assays were implemented in 24-well Transwell™ plates (Corning Incorporated, USA) with an 8 μm pore size insert. For migration assay, single-cell suspensions with 4×10^4 post-transfection cells were prepared with 100 μl of DMEM free of FBS. These cells were seeded into the upper chamber, and the bottom chamber was filled with 600 μl of DMEM supplemented with 20% FBS. For invasion assay, the Transwell membranes were pre-coated with 20 μl 1:7 diluted Matrigel (BD Biosciences, Franklin Lakes, NJ, USA) and allowed to solidify at 37 °C overnight. The subsequent steps followed the same protocol as the migration assay. After 48 h incubation at 37 °C, a wet cotton swab was used to wipe away the non-migrating cells on the upper surface of the membrane, whereas the invasive cells at the bottom were fixed with 4% paraformaldehyde and stained with 0.1% crystal violet. Images of the migrated cells were captured using an inverted microscope (Leica, Germany) in five random fields in each filter, and the numbers of cells were counted using ImageJ software (version 1.8.0). All migration and invasion assays were conducted using three independent biological replicates.

RNA-seq analysis. Total RNA was extracted from A875 cells following transfection with siWTAP-2 or siNC via TRIzol Reagent. Total RNA was quantified using a NanoDrop ND 2000 spectrophotometer, and RNA integrity was examined using an Agilent Bioanalyzer 2100 (Agilent Technologies, USA). Library construction and RNA-seq analysis were subsequently performed at Applied Protein Technology (Beijing, China) with an Illumina NovaSeq 6000 System (Illumina, USA), followed by computational analysis, which was also provided by this company.

Immunofluorescence assay. Pretreated cells were seeded on glass coverslips in 12-well plates at a density of 1×10^5 cells/well. After 24 h incubation at 37 °C, 4% paraformaldehyde and 0.3% Triton X-100 were added to each well for 15 and 5 min, respectively, to fix and permeabilize the cells, followed by blocking non-specific binding with 10% BSA. Anti-NT5E antibody (1:100, #12231-1-AP, Proteintech, China) was added to each well and incubated with the contents of the wells at 4 °C overnight, followed by incubation with goat anti-rabbit IgG (1:200, #SA00013-2, Proteintech, China) at room temperature for 1 h. After the cells had been stained with DAPI, images of the cells were captured using a confocal microscope (LSM 900, Zeiss, Germany).

Ectonucleotidase assay. To determine the enzymatic activity of NT5E hydrolysis, an ectonucleotidase assay was performed as previously described [36]. In brief, A875 or A375 cells pretreated with siWTAP were reseeded into 24-well plates at a density of 1.0×10^5 cells/well. After 24 h incubation at 37 °C, 200 μl reaction medium containing 2 mM $MgCl_2$, 120 mM NaCl, 5 mM KCl, 10 mM glucose, 20 mM HEPES, and 2 mM AMP (#HY-A0181, MedChemExpress, USA) as the substrate was added to each reaction, and incubated at 37 °C for 45 min. Subsequently, 200 μl incubation medium was rapidly withdrawn and heat-inactivated at 95 °C for 90 s to halt the enzymatic activity, and the mixture was subsequently centrifuged at 16,000 × g at 4 °C for 30 min. The level of soluble free inorganic phosphate in each sample was detected with a Malachite Green Phosphate Detection Kit (#S0196S, Beyotime, China) according to the manufacturer's instructions. In addition, (α,β-methylene) diphosphate (APCP) (#HY-112502, MedChemExpress, USA) was applied to investigate its effects on NT5E function, and 20 μM APCP was added to each sample 15 min prior to the addition of the substrate AMP. At the same time, the same volume of solvent was added as a control.

RNA immunoprecipitation (RIP). To investigate WTAP-NT5E regulatory interactions, RIP assays were performed in A875 and A375 cells transfected with either siWTAP or control siNC for 48 h using the Magna RIP™ Kit (Millipore, USA) following standardized protocols. Cells were lysed in RIP lysis buffer for 15 min at 4 °C, followed by centrifugation at 12,000 × g for 10 min. The resulting supernatant was collected and incubated with protein A/G magnetic beads conjugated with anti-WTAP antibody (1:1000, #ab195380, USA) or anti-IgG antibody (1:5000, #10284-1-AP, Proteintech, China) in RIP immunoprecipitation buffer (containing 0.5 M EDTA and RNase inhibitor) overnight at 4 °C. Bead complexes were washed six times with ice-cold RIP wash buffer, followed by proteinase K digestion (55 °C, 30 min) to release RNA. Recovered RNA was purified using TRIzol Reagent and analyzed by RT-qPCR to quantify NT5E transcript enrichment in WTAP pulldowns relative to IgG controls.

Actinomycin D assay. Following transfection with either siWTAP or negative control siNC, A875 and A375 cells were exposed to 2 μg/ml actinomycin D (Act D) for 0, 4, 8, 12, and 24 h to inhibit *de novo* RNA transcription. Total RNA was isolated at the indicated time points and analyzed by RT-qPCR. The expression levels of NT5E were normalized to GAPDH as an internal control, and the relative half-life of NT5E was subsequently determined to assess its stability under WTAP knockdown conditions.

Enzyme-linked immunosorbent assay (ELISA). Peripheral blood mononuclear cells (PBMCs) isolated from healthy donors via a human PBMC separation kit (#P5290, Solarbio, China) were incubated in Gibco® RPMI-1640 medium (Gibco, USA) supplemented with 10% FBS and 1% penicillin/streptomycin in a humidified atmosphere at 37 °C containing

5% CO_2. One day later, the PBMCs (2×10^5 cells/well) were replated in 24-well plates and incubated in 150 µl RPMI-1640 medium supplemented with FBS and penicillin/streptomycin and 50 µl supernatant from cultures of melanoma cells or melanoma cells silenced with siNC, siWTAP, or siNT5E. Phytohemagglutinin (PHA) (10 µg/ml, #HY-N7038, MedChemExpress, USA) was added to stimulate the PBMCs to produce interferon-γ (IFN-γ). In certain experiments, 2 mM AMP or 20 µM APCP was added to each well. AZD4635 (50 nM, #HTL1071, MedChemExpress, USA), an A_{2A} adenosine receptor antagonist, was added to each reaction to clarify the immunosuppressive role of adenosine as mediated by WTAP. Finally, the level of IFN-γ in the PBMC culture supernatant was quantified 24 h after treatment using an IFN-γ detection ELISA kit (#KE00146, Proteintech, China) according to the manufacturer's protocol.

Subcutaneous xenograft experiments. Twelve 4-week-old male nude mice were provided by HuaFuKang Bioscience in Beijing. All mice were maintained under standard conditions in a sterile, temperature-controlled environment (temperature 20–26 °C and humidity approximately 50%) to ensure the animals' comfort. After the mice had been allowed to adapt to local rearing conditions for 1 week, 2×10^6 A375 cells were resuspended in 100 µl PBS and inoculated subcutaneously into the left flank of the mice. After 1 week, following the formation of palpable punctate tumor masses that were visible to the naked eye, the mice were randomly divided into two groups, and cholesterol-modified siWTAP-2 or siNC (RiboBio, China) was injected intratumorally at a concentration of 10 nmol/mouse once every week. The mice's health and behavior were monitored every day, and the tumor volume and body weight of each mouse were recorded twice weekly, and the tumor volume was calculated using the formula volume = length × width^2 × 0.5. The maximum diameters of the tumors in each mouse did not exceed 2 cm. Seven days post the fourth inoculation (day 35 post tumor cell injection), all 12 mice survived the experiment and were subsequently euthanized, and the tumors were completely removed for histological analysis. The detailed procedure for the humane euthanasia of mice was as follows: first, anesthesia was induced by placing the mouse under a face mask with 3–4% isoflurane in oxygen at a flow rate of 0.5–1 l/min for 2–5 min until the corneal reflex was completely absent. Secondly, the isoflurane concentration was set at 1.5–2% to ensure the maintenance of an anesthetic state, and firm pressure was applied at the base of the skull while gently pulling the tail to separate the cervical vertebrae from the skull. Thirdly, death was confirmed by checking for the absence of reflexes again. The *in vivo* experiments were approved by the Animal Care Committee of Shijiazhuang People's Hospital (Approval No. 2024002).

Statistical analysis. SPSS software version 21.0 (IBM Corp.) and GraphPad Prism software 8.0 (Dotmatics) were used to analyze the data and to generate the graphs, respectively. For measurement data, Student's t-test was used to compare two groups, while for datasets involving multiple group comparisons, one-way ANOVA (for parametric data) was adopted, followed by LSD post hoc tests. The chi-square test was used to analyze clinical data. Patient prognosis was analyzed using the Kaplan-Meier method, and $p\leq0.05$ and $p\leq0.01$ were considered to indicate a statistically significant difference and highly statistically significant difference, respectively.

Table 2. Clinicopathological features of melanoma patients.

Characteristics	Level	Low	High	χ^2	p-value
n		26	29		
Age (years)	<60	11	16	0.908	0.341
	≥60	15	13		
Sex	Male	16	13	1.536	0.215
	Female	10	16		
Stage	I	2	6	9.193	0.027
	II	6	14		
	III	10	7		
	IV	8	2		
T classification	T2	8	19	6.827	0.033
	T3	11	7		
	T4	7	3		
N classification	N0	11	19	5.053	0.168
	N1	5	6		
	N2	7	2		
	N3	3	2		
M classification	M0	11	16	0.908	0.341
	M1	15	13		

Note: a chi-square test was used to compare groups with low and high WTAP expression; *p < 0.05

Results

WTAP acts as a cancer suppressor in melanoma. To explore WTAP expression in human melanoma tissues and its effect on melanoma malignancy, the GEPIA dataset (https://gepia.cancer-pku.cn/) was adopted to examine the expression patterns of WTAP across various cancer types, and the analysis revealed that WTAP is significantly downregulated in Skin Cutaneous Melanoma (SKCM) compared to normal tissues (Figure 1A). Additionally, patients with low WTAP expression demonstrated a worse prognosis (Figure 1B).

To further validate our findings, we collected 55 human melanoma tissue samples and examined the expression of WTAP via IHC (Figure 1C). To further identify the correlation between the WTAP expression level and aggressive progression of melanoma, the 55 patients with melanoma were divided into two groups according to the median staining score: A group with low WTAP expression (n=26) and another group with high WTAP expression (n=29). As shown in Table 2, WTAP expression was found to be negatively associated with the clinical stage and T classification of patients with melanoma, demonstrating that

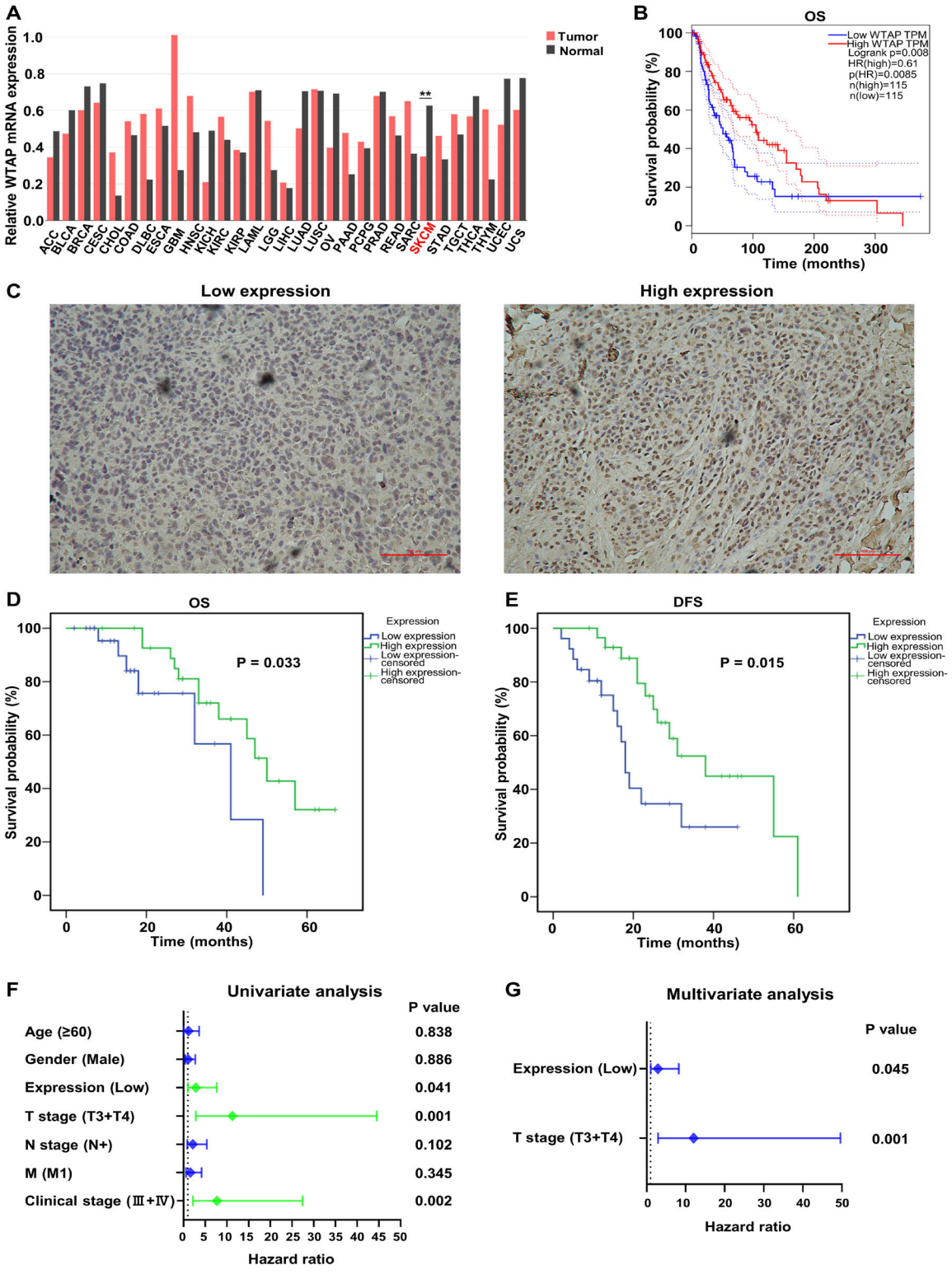

Figure 1. WTAP expression was downregulated in melanoma. A) The expression levels of WTAP mRNA across various cancers were analyzed by the GEPIA datasets. B) Kaplan-Meier survival curves for OS in melanoma patients were generated using data from the GEPIA datasets. C) The protein expression of WTAP in melanoma tissues was analyzed by IHC (n = 55) (magnification, ×200). D, E) Kaplan-Meier survival curves of OS and DFS in melanoma patients were constructed based on WTAP immunohistochemical staining. The log-rank test was used to compare differences between the two groups. F, G) Forest plots were constructed based on the outcomes of univariate and multivariate analyses of several factors associated with the OS and RFS of melanoma patients. *p<0.05, **p<0.01

low WTAP expression is an aggressive characteristic of melanoma. Moreover, the clinical data analysis suggested that patients with lower WTAP expression had worse overall survival (OS) and disease-free survival (DFS) rates (Figures 1D, 1E). Furthermore, univariate analysis disclosed that WTAP expression, pathological T stage, and clinical stage were significantly related to OS (Figure 1F), whereas multivariate analysis suggested that WTAP expression and pathological T stage were independent risk factors for OS (Figure 1G). Taken together, these findings confirmed that low WTAP expression is associated with a poor prognosis in patients with melanoma, demonstrating that WTAP may fulfil a suppressive role in melanoma progression.

WTAP suppresses melanoma cell proliferation, migration, and invasion. To elucidate the biological functions of WTAP in melanoma cells, three specific siRNAs directed against WTAP were used to knock down the expression of WTAP in A875 and A375 melanoma cells, and potential alterations in cell function were subsequently examined via a series of functional experiments. The knockdown efficiency of siRNAs targeting WTAP was first evaluated by RT-qPCR and western blotting analyses. As shown in Figure 2A and Supplementary Figure S1A, the results from both RT-qPCR and western blotting experiments revealed that siRNA-1 and siRNA-2 had greater knockdown efficiency compared with siRNA-3. Therefore, siRNA-1 and siRNA-2 were selected to downregulate endogenous WTAP expression in subsequent *in vitro* assays, and siRNA-2 was utilized to silence WTAP expression in RNA-seq and *in vivo* assays. The results of the CCK-8, EdU, and colony formation assays demonstrated that a deficiency of WTAP led to substantial enhancement of the proliferative and clonogenic capabilities of A875 and A375 cells (Figures 2B, 2C; Supplementary Figure S2A). Furthermore, the results of the wound healing and Transwell assays revealed that WTAP downregulation clearly increased the migration and invasion of both cell types (Figures 2D, 2E). Moreover, to further examine the role of WTAP in melanoma cells, WTAP was overexpressed via a suitably designed plasmid, and the efficiency of transfection was confirmed via RT-qPCR and western blotting analyses (Figure 3A; Supplementary Figure S1B). WTAP was found to negatively influence cell proliferation, as transfected A875 and A375 cells overexpressing WTAP exhibited decreased proliferative and clonogenic capabilities compared with those in the control group (Figures 3B, 3C; Supplementary Figure S2B). In addition, the forced overexpression of WTAP led to a marked depletion of the migration and invasion rates of both cell types, as shown in Figures 3D and 3E. Taken together, these data highlighted that WTAP, which acts as a tumor suppressor protein, has a pivotal role in suppressing the proliferation, migratory, and invasive capabilities of melanoma cells.

NT5E is the functional downstream target of WTAP in melanoma cells. To further explore the potential functional mechanism via which WTAP exerts a tumor suppressive effect in melanoma, transcriptome sequencing was employed to explore the transcriptional alterations in both siWTAP-2 A875 cells and parallel control siNC A875 cells. $|Log2FC|>1$ and $p<0.05$ were adopted as thresholds to identify altered genes following the deletion of WTAP in A875 cells, and 6 upregulated and 8 downregulated genes were identified as potential downstream genes, as shown in volcano plots and heatmaps (Figures 4A, 4B). To further narrow the scope of downstream targets, numerous previously published studies were consulted, and the genes Chromogranin B (CHGB), Inhibitor of nuclear factor kappa B kinase subunit gamma pseudogene 1 (IKBKGP1), NT5E, Solute carrier family 7 member 11 (SLC7A11), Fucosyltransferase 1 (FUT1), and Cystathionine gamma-lyase (CTH) were identified as potential targets involved in WTAP-mediated melanoma progression. RT-qPCR assays were subsequently performed to assess the impact of WTAP on each candidate gene. As shown in Figure 4C, NT5E was consistently found to be clearly upregulated upon transfecting both A875 and A375 cells with siWTAPs. Subsequently, immunofluorescence analysis was used to specifically identify the protein expression and subcellular localization of NT5E in siWTAP-transfected melanoma cells (Figure 4D). NT5E expression (shown by the green coloration) was clearly increased in both A875 and A375 cells following transfection with siWTAPs, as indicated by increased and brighter fluorescence levels located in the cell membrane and cytoplasm. Collectively, our findings identified NT5E as the key downstream effector of WTAP-mediated tumor suppression in melanoma.

Further analysis of the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway revealed that 5 differentially expressed genes were enriched in 10 pathways (Figure 4E). The primary downstream gene NT5E was enriched in 3 pathways, namely, pyrimidine metabolism, nicotinate and nicotinamide metabolism, and metabolic pathways. As demonstrated by previous studies, NT5E was able to hydrolyze AMP to produce extracellular adenosine, and this NT5E-adenosine pathway, has been reported both to extensively participate in cancer progression, metastasis, and drug resistance, and to directly or indirectly affect pyrimidine metabolism, nicotinate and nicotinamide metabolism, and metabolic pathways [37–39]. Based on the present evidence, we proposed that the NT5E-adenosine axis contributes to WTAP-dependent tumor regulation in melanoma. Therefore, to further confirm the activity of NT5E in melanoma cells, an AMPase hydrolysis assay was employed to evaluate NT5E function in melanoma cells following knockdown with siNC or siWTAPs. A875 or A375 cells were incubated with AMP, and the production of inorganic phosphate was assessed using the malachite green method. As shown in Figure 4F, in both A875 and A375 cells, WTAP knockdown led to a significant increase in inorganic phosphate production, which further confirmed that the elevated expression and function of NT5E in A875 and A375 cells were driven by transfection with the siWTAPs.

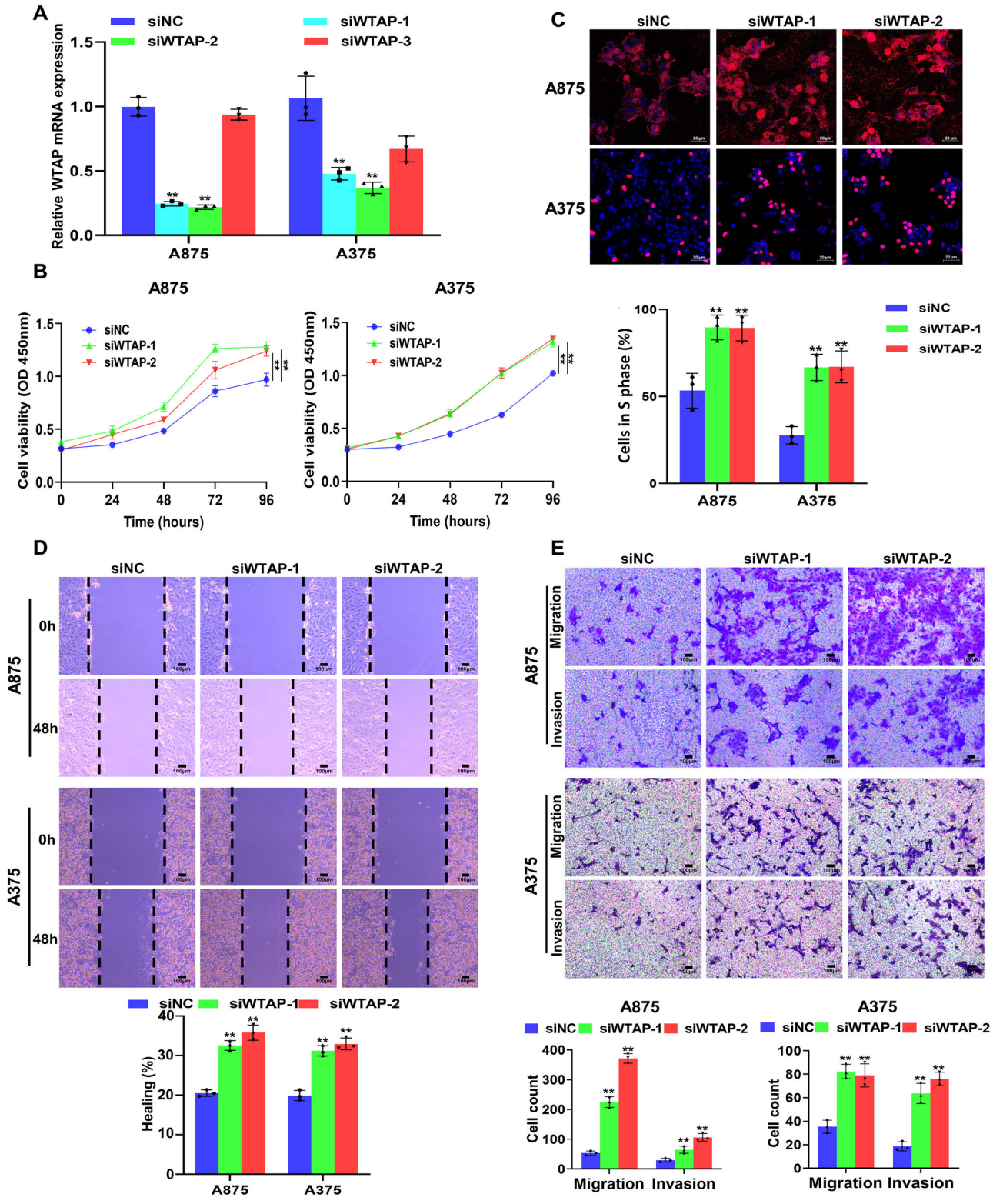

Figure 2. Deletion of WTAP enhanced the growth and invasion of melanoma cells. A) Negative control or siRNA (siWTAP-1, siWTAP-2, and siWTAP-3) was transfected into A875 and A375 cells, and the knockdown efficiency was determined by RT-qPCR. B, C) Melanoma cell proliferation was detected via CCK-8 and EdU assays (magnification, ×200). D, E) Wound healing and Transwell assays were applied to compare melanoma cell migration and invasion (magnification, ×100). **p<0.01

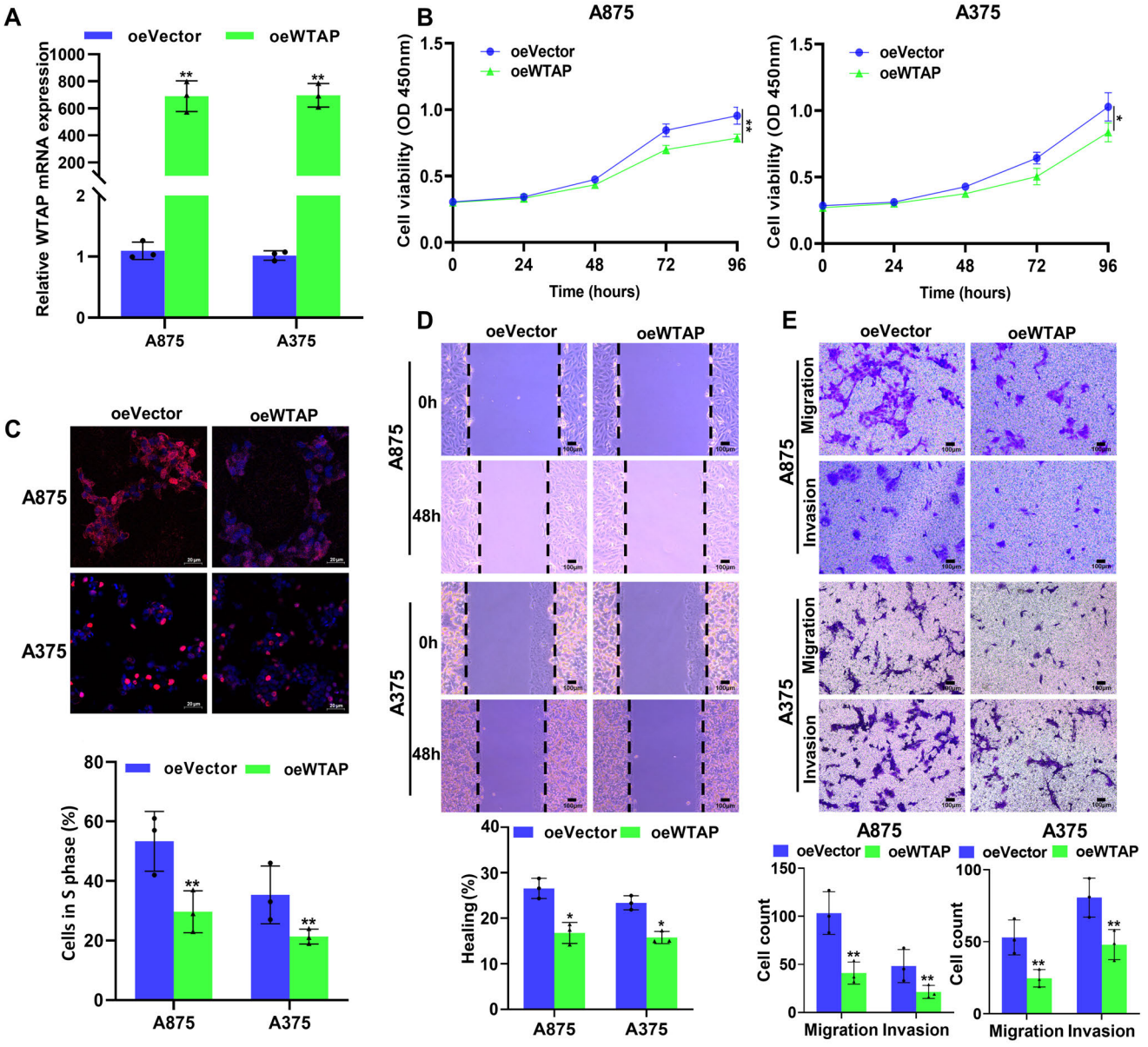

Figure 3. WTAP overexpression weakened the growth and invasion of melanoma cells. A) The plasmid for WTAP overexpression and the control vector were transfected into A875 and A375 cells, and the efficiency of infection was determined by RT-qPCR. B, C) The proliferation of melanoma cells was detected by CCK-8 and EdU assays (magnification, ×200). D, E) The migration and invasion of melanoma cells were evaluated via a wound healing and Transwell assays (magnification, ×100). *p<0.05, **p<0.01

Inhibition of NT5E abrogated the effects of WTAP depletion in A875 and A375 cells. To further determine whether the biological effect of WTAP on melanoma cells was mediated by NT5E, a series of rescue experiments were performed. CCK-8 and colony formation assays revealed that the deletion of NT5E led to a substantial reversal of the increases in the cell proliferative (Figure 5A) and colony formation (Figure 5B) capabilities of both A875 and A375 cells caused by the silencing of WTAP. Moreover, the depletion of NT5E also led to a marked suppression of the increased migration and invasion rates of A875 and A375 cells that resulted from the attenuation of WTAP (Figures 5C, 5D). Collectively, these data suggested that silencing WTAP effectively promoted the malignant progression of melanoma cells through enhancing the activity of downstream NT5E.

WTAP suppressed melanoma progression via NT5E-mediated immunosuppression and molecular adhesion. A growing body of evidence indicated that WTAP is widely involved in RNA modifications associated with pre-mRNA splicing, miRNAs, lncRNAs, circRNA processing,

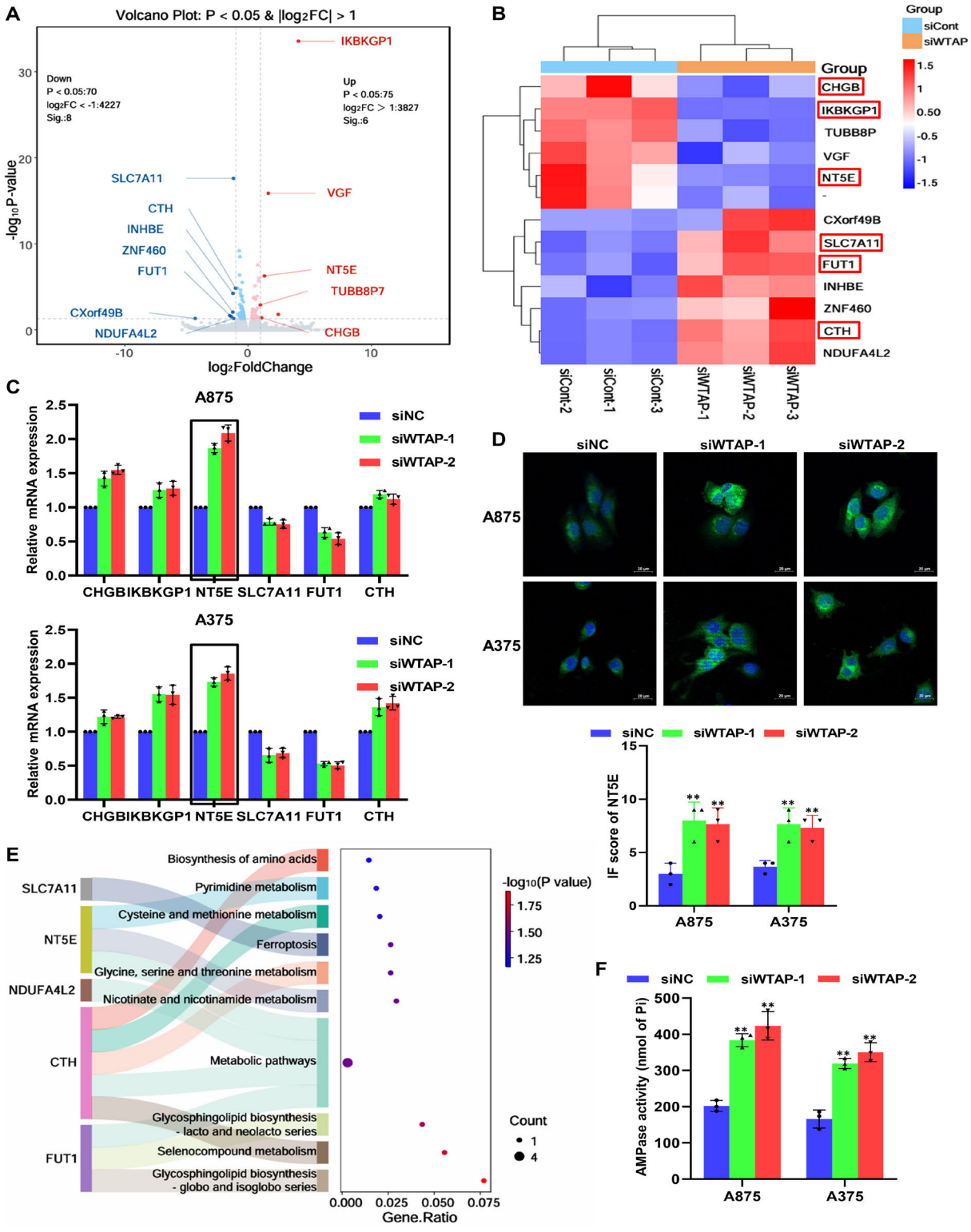

Figure 4. NT5E was proven to be a downstream target of WTAP in melanoma progression. A, B) Volcano plots and heatmaps were generated from the differentially expressed genes identified via RNA-seq. C) Relative mRNA expression levels of representative genes in A875 and A375 cells treated with siWTAP-2. D) Immunofluorescence staining of NT5E in A875 and A375 cells transfected with siWTAP (magnification, ×200). E) Enrichment analysis for representative KEGG pathways in WTAP target genes. F) AMPase activity of A875 and A375 cell culture supernatants in the siWTAP and siNC groups. **p<0.01

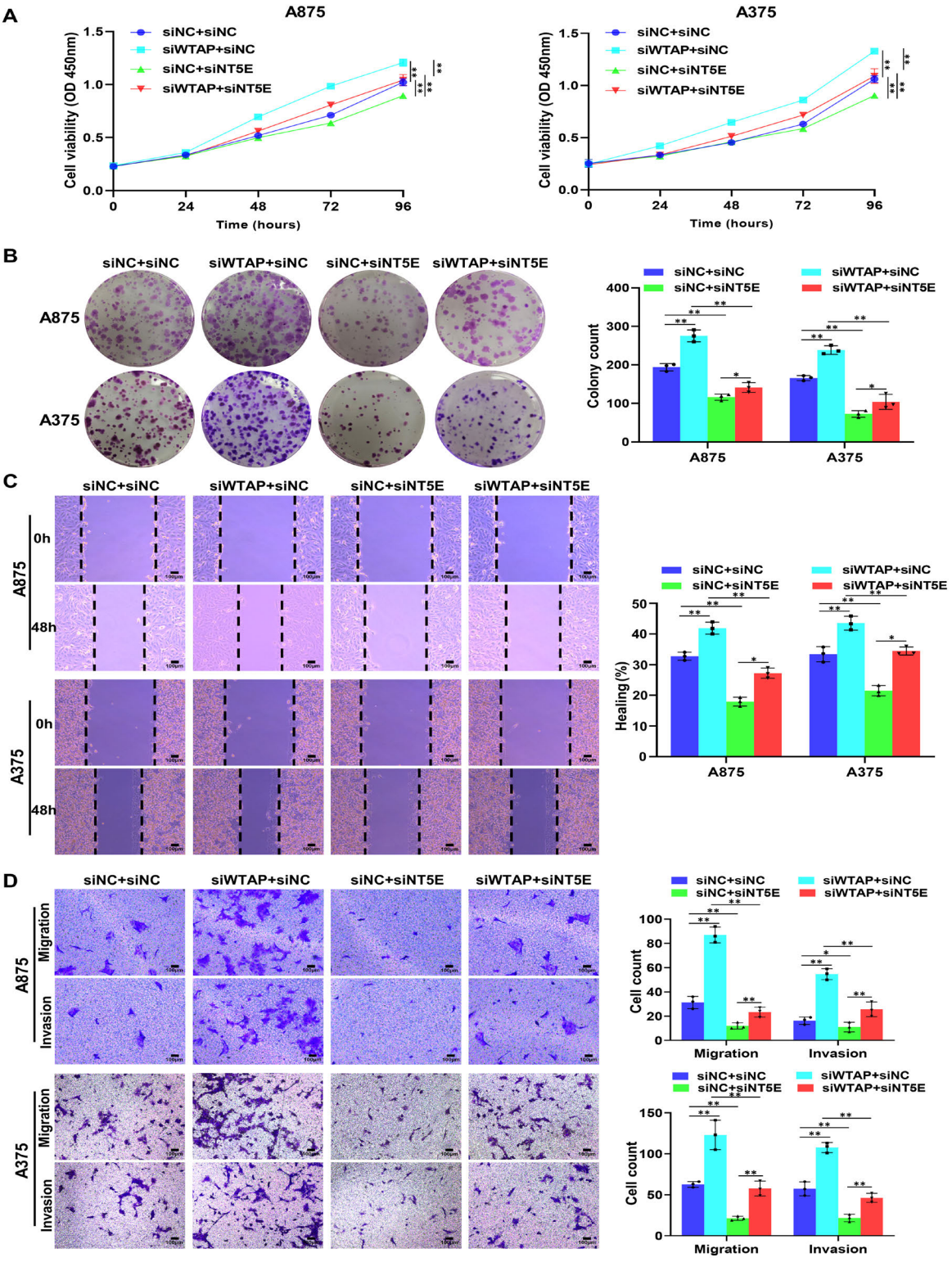

Figure 5. siNT5E reversed the effects of siWTAP on increasing the proliferation and metastasis of melanoma cells. A, B) Compared with the siNC+siNC group, the siNC+siNT5E group presented suppressed proliferation and colony formation in melanoma cells, and compared with the siWTAP+siNC group, the siWTAP+siNT5E group presented impaired proliferation and colony formation in melanoma cells. C, D) The migration and invasion of melanoma cells were lower in the siNC+siNT5E group than in the siNC+siNC group, and the migration and invasion of melanoma cells were lower in the siWTAP+siNT5E group than in the siWTAP+siNT5E group (magnification, ×100). *p<0.05, **p<0.01

translation efficiency, and mRNA stability [40, 41]. Our present study also provides direct evidence that WTAP depletion elevates NT5E transcript levels (Figures 4A–4C). In addition, to further confirm whether WTAP could regulate NT5E mRNA, a RIP assay was implemented with A875 or A375 cell lysates and either WTAP antibody or control rabbit IgG. As shown in Figure 6A, NT5E mRNA was detected in the WTAP immunocomplexes, but not in the control IgG immunocomplexes, and depletion of WTAP led to an increase in NT5E mRNA abundance in melanoma cell supernatants. Actinomycin D chase experiments demonstrated that WTAP knockdown significantly reduced the decay rate of NT5E mRNA in melanoma cells, indicating WTAP-mediated destabilization of NT5E transcripts (Figure 6B).

A large body of evidence has shown that soluble NT5E, a major enzyme involved in the production of extracellular adenosine via the hydrolysis of AMP, is able to suppress the function of T cells and to fulfil an oncogenic role [42]. The expression of soluble NT5E has been confirmed to be higher in patients with melanoma, demonstrating its potential as a predictive biomarker for immunotherapy [43]. In this series of experiments, AMPase activity and IFN-γ production in the supernatant of the melanoma cell cultures were examined to further evaluate the NT5E activity. As shown in Figure 6C, compared with that of the siNC group, AMPase activity in the siWTAP group was clearly increased, whereas the addition of NT5E inhibitor APCP to the supernatant impaired this NT5E-mediated AMPase activity. As shown in Figure 6D, A875 and A375 cell culture supernatants were collected and subsequently incubated with PBMCs, and PHA was added to the reaction mixtures to stimulate the production of IFN-γ by PBMCs. PBMCs without PHA activation did not produce any discernible level of IFN-γ; however, compared with that in activated cells without AMP, the production of IFN-γ in PBMCs was substantially impaired when the substrate AMP was added to the culture supernatant. Moreover, the addition of the NT5E inhibitor APCP partly reversed the reduced secretion of IFN-γ compared with that in activated cells treated with AMP alone. As shown in Figure 6E, the secretion of IFN-γ by PBMCs in the presence of AMP with or without the NT5E inhibitor APCP was found to be depleted in the culture supernatant from siWTAP-treated A875 or A375 cells. However, knocking down NT5E (siNT5E) rescued the decreased IFN-γ production induced by both the siWTAP-treated A875 and A375 cell supernatants, as shown in Figure 6F. Overall, it was demonstrated that the increased expression of NT5E promoted by siWTAP in both A875 and A375 cell cultures contributed to the hydrolysis of AMP to produce more adenosine, which thereby subsequently abrogated the secretion of IFN-γ by PBMCs. Both the endogenous deletion of NT5E by siNT5E treatment and exogenous inhibition of NT5E by APCP were shown to suppress both its ability to produce adenosine and its immunosuppressive effect on PBMCs. To further validate the role of the NT5E-adenosine pathway in WTAP-driven melanoma progression, an A_{2A} adenosine receptor antagonist, AZD4635, was added to further ELISA assays. As shown in Figure 6G, the addition of AZD4635 to the reaction enhanced secretion of IFN-γ compared to the control experiments, suggesting that adenosine fulfils a critical role in NT5E-mediated IFN-γ production, which further confirmed that the NT5E-adenosine pathway contributed to WTAP-mediated tumor suppression.

NT5E has an oncogenic role in tumor progression that is mediated via both enzymatic and nonenzymatic activity [44]. In melanoma cells, the enzymatic function of NT5E is associated with the cancer invasion process, whereas its nonenzymatic action is to increase cell migration and ECM adhesion through the activation of focal adhesion kinase [44]. To further understand the functional mechanism of NT5E in WTAP-mediated melanoma regression, the expression levels of the Epithelial-Mesenchymal Transition (EMT)-associated markers Matrix Metalloproteinase 2 (MMP2) and N-cadherin in A875 and A375 cells were determined via western blotting. As shown in Figures 7A and 7B, in WTAP-silenced melanoma cells, the expression level of NT5E, as well as that of MMP2 and N-cadherin, was simultaneously increased. Moreover, NT5E deletion in melanoma cells resulted in the downregulation of N-cadherin and MMP2 expression, whereas the expression of WTAP was not significantly altered (Figures 7C, 7D). Furthermore, in the co-transfection assay, NT5E deficiency led to a reversal of the increase in MMP2 and N-cadherin expression induced by siWTAP in both A875 and A375 cells (Figures 7E, 7F).

WTAP suppressed melanoma tumorigenesis *in vivo*. To elucidate the role of WTAP in melanoma tumorigenesis *in vivo*, a xenograft melanoma tumorigenesis assay was performed by subcutaneously injecting A375 cells into nude mice (Figure 8A). The results obtained revealed that WTAP depletion promoted tumorigenesis, resulting in markedly larger tumor volumes and weights compared with the control mice (Figures 8B–8D). IHC analysis subsequently revealed that the xenograft tumors affected by siWTAP exhibited increased levels of NT5E, MMP2, and N-cadherin expression (Figure 8E). Taken together, these results suggested that WTAP exerts tumor-inhibiting effects on melanoma.

Discussion

Melanoma is the most malignant skin tumor with high invasive and metastatic potential, which is associated with poor outcomes [2]. Currently, cutaneous melanoma remains the leading cause of cutaneous cancer-associated deaths globally [3]. The multidisciplinary treatment of cutaneous melanoma is complicated, and therapeutic methods ranging from traditional surgery and chemotherapy to immunotherapy have gradually been developed in recent years [45]. m6A methylation is the predominant dynamic mRNA modification that occurs in all mammals [46], and aberrant m6A modifications have been ubiquitously identified in numerous

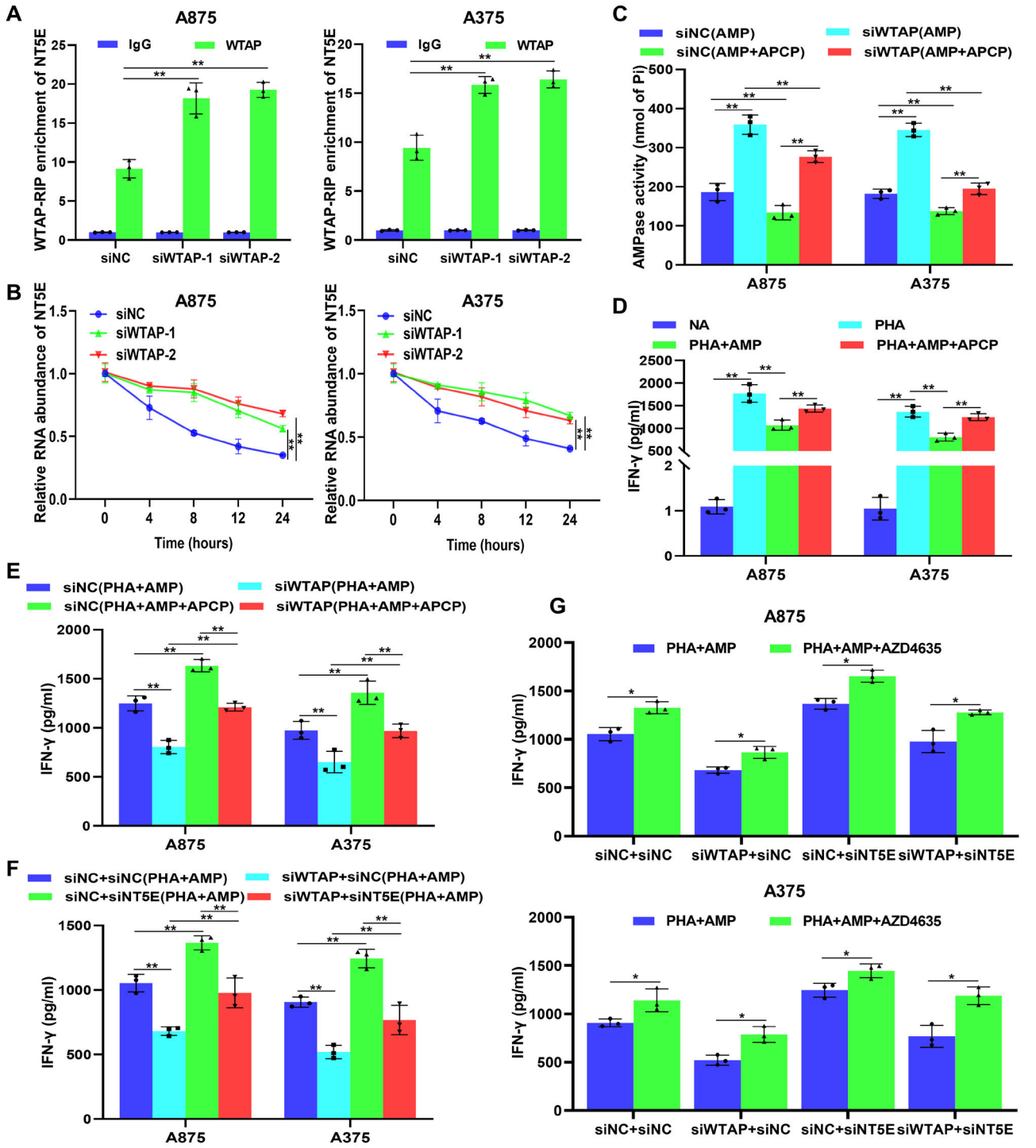

Figure 6. NT5E-mediated immunosuppression is involved in WTAP-dependent suppression of melanoma progression. A) A875 and A375 cell lysates were supplemented with anti-WTAP and anti-IgG antibodies to determine whether WTAP interacts with NT5E mRNA. B) The actinomycin D assay was adopted to examine NT5E stability changes in WTAP-knockdown melanoma cells. C) AMPase activity was determined in the supernatants of siWTAP- and siNC-transfected melanoma cell cultures. AMP was used as a substrate, APCP was used as an inhibitor, and the amount of released inorganic phosphate was measured via the Malachite Green assay. D) ELISA was used to measure IFN-γ levels in the supernatants of PBMC cultures with or without the PHA activator and melanoma cell cultures with or without the NT5E substrate AMP and the selective NT5E inhibitor APCP. E) IFN-γ levels in the supernatant of PHA-activated PBMCs cultured with supernatant from siWTAP or siNC melanoma cells in the presence of AMP with or without APCP were measured via ELISA. F) ELISA was performed to detect IFN-γ levels in the supernatant of PHA-activated PBMC cultures treated with culture supernatant of melanoma cells transfected with both siWTAP and siNT5E by the addition of AMP and APCP in every reaction. G) The secretion of IFN-γ was detected via ELISA in each reaction with or without AZD4635. *p<0.05, **p<0.01

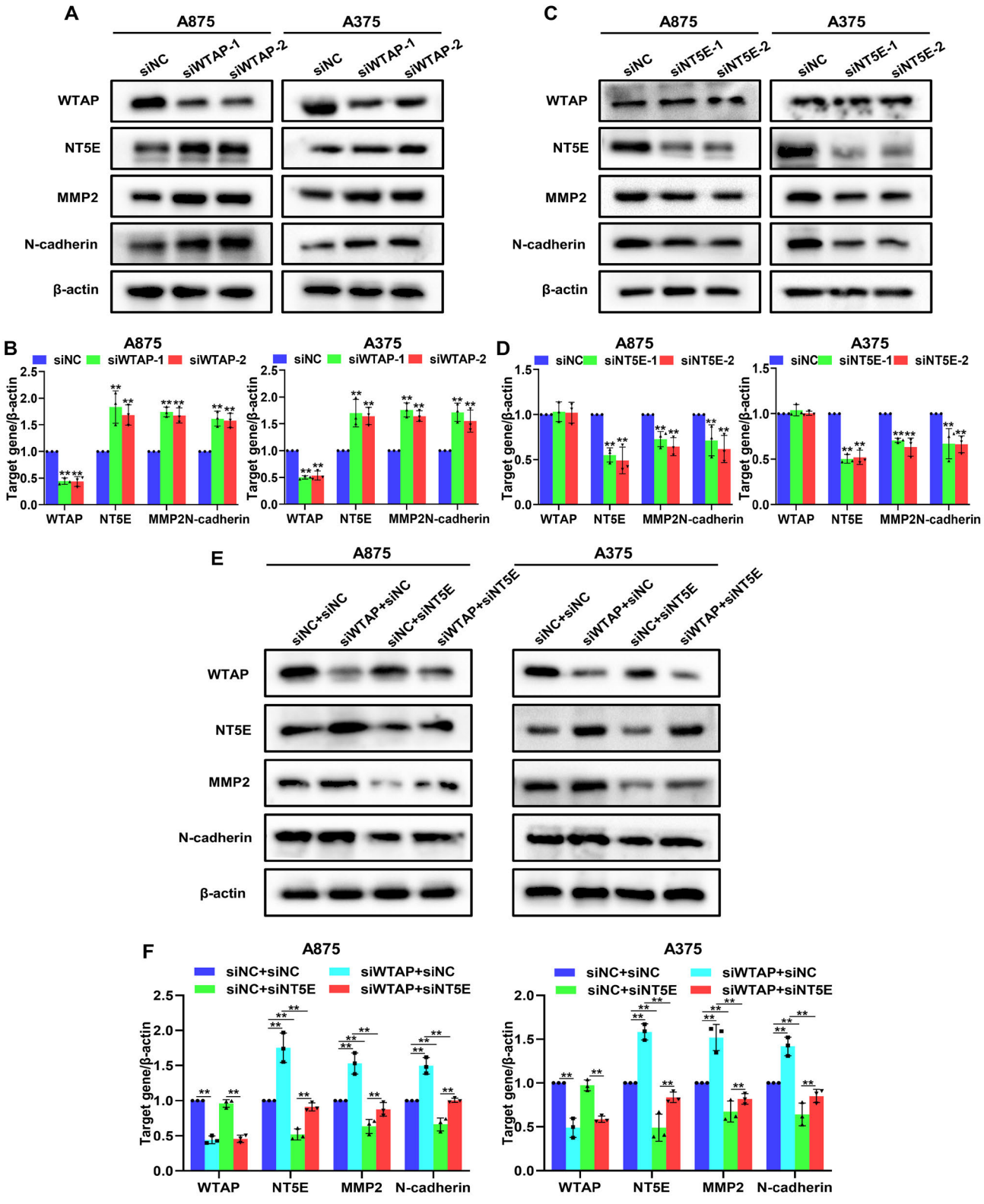

Figure 7. WTAP expression was assessed in melanoma cells transfected with siWTAP, siNT5E, or both. A–D) The protein expression of WTAP, NT5E, MMP2, and N-cadherin in the siWTAP and siNT5E groups compared with that in the siNC group was assessed via western blotting. E, F) The protein expression of WTAP, NT5E, MMP2, and N-cadherin in A875 and A375 cells was observed after transfection with siWTAP, siNT5E, and both siWTAP and siNT5E. **p<0.01

types of cancers, including melanoma [47–49]. METTL3 drives aberrant uridine cytidine kinase 2 upregulation via m6A-dependent RNA stabilization, thereby activating the Wnt/β-catenin signaling axis to promote melanoma metastasis [47]. METTL14, while sharing functional synergy with METTL3 in m6A deposition, exhibits unique roles in modulating melanoma cell invasiveness through regulation of metastasis-associated transcripts [48]. Conversely, the m6A reader protein YTH N6-methyladenosine RNA binding protein 3 (YTHDF3) suppresses melanoma metastasis by binding m6A-modified lysyl oxidase-like 3 mRNA and destabilizing it, highlighting the context-dependent duality of m6A-mediated regulation in melanoma [49]. With respect to WTAP function in melanoma, Feng et al. [21] demonstrated an association between WTAP expression and prognosis in patients with melanoma through analyzing databases, and

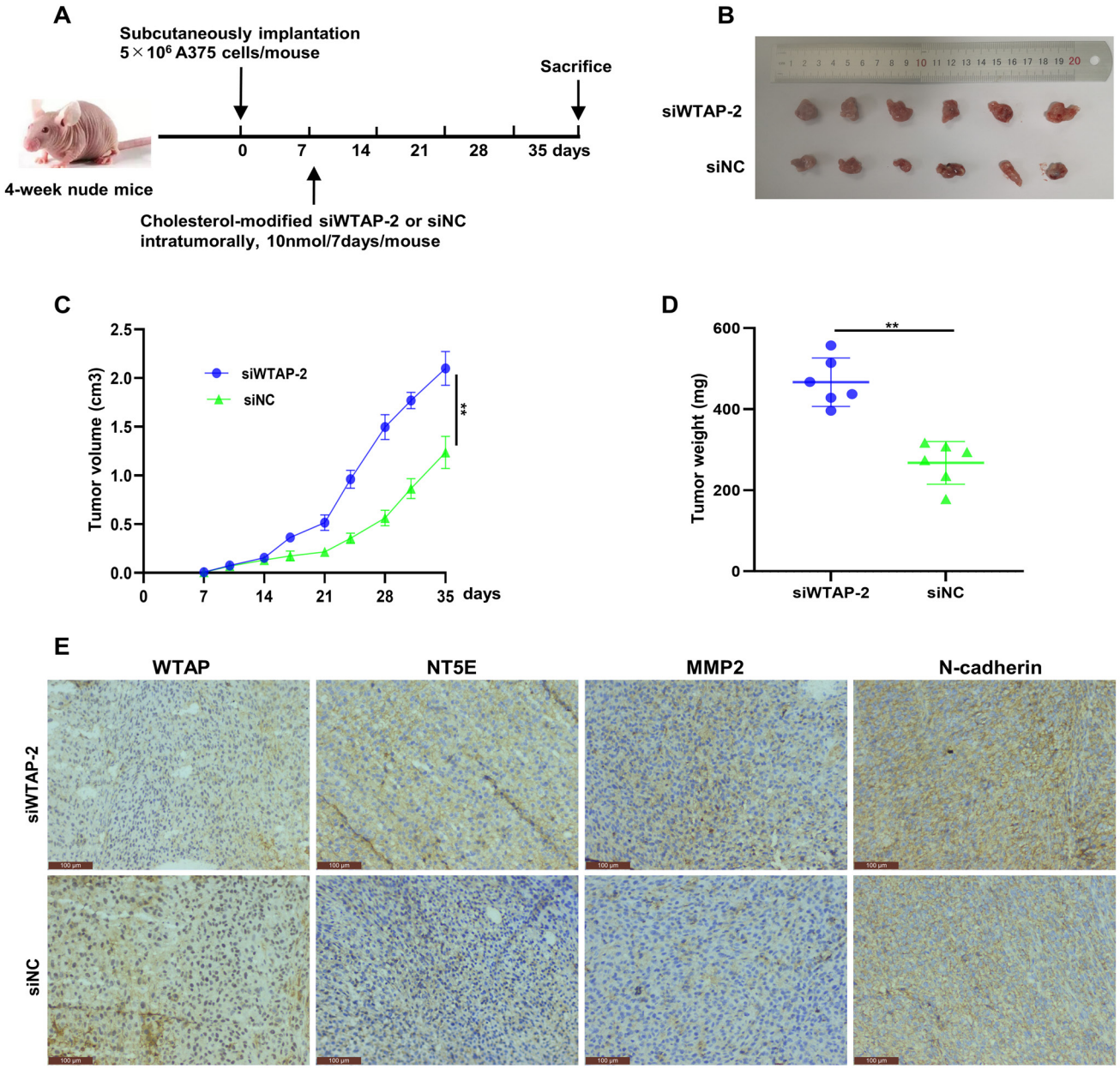

Figure 8. WTAP inhibited melanoma cell growth *in vivo*. A) Schematic diagram of the groups in the xenotransplantation model. B) Images of xenografts in the indicated groups. C, D) Volume (C) and weight (D) of subcutaneous xenograft tumors. E) Representative IHC images of WTAP, NT5E, MMP2, and N-cadherin in xenograft tumors from the siWTAP-2 and siNC groups (magnification, ×200). **p<0.01

further performed functional assays in which A375 cells were used to overexpress WTAP. However, the underlying mechanism via which WTAP suppresses melanoma progression has yet to be fully elucidated.

In the present study, both the expression and mechanism of action of WTAP in the development of melanoma were carefully investigated. WTAP was found to be downregulated in melanoma tissues, and WTAP expression was significantly negatively correlated with clinical stage and T stage, according to the IHC analysis of melanoma tissues. In addition, WTAP expression, pathological T stage, and clinical stage were strongly related to OS, and WTAP expression and pathological T stage were found to be independent risk factors for OS. Subsequently, the role of WTAP in the proliferation and invasion of melanoma cells was explored. A series of functional assays revealed that an attenuation of WTAP expression led to substantial increases in cell proliferation and invasion, whereas WTAP overexpression led to a decrease in the proliferation and invasion of melanoma cells. Furthermore, data obtained from *in vivo* animal experiments confirmed the tumor suppressor function of WTAP in melanoma cells, as melanoma xenografts generated with siWTAP cells formed larger tumors in nude mice compared with the tumors generated with control cells. Subsequently, NT5E was identified as a potential downstream target via RNA-seq analysis, and an ectonucleotidase assay and ELISA were then performed with the aim of verifying NT5E expression and function in cells with silenced WTAP expression. The rescue and western blot assays that were performed demonstrated that silencing NT5E abrogated the upregulated effects and EMT-associated gene expression caused by WTAP depletion in melanoma cells. Mechanistically speaking, RIP and actinomycin D experiments demonstrated that WTAP binds to the mRNA of the downstream gene NT5E and destabilizes it, thereby suppressing melanoma progression. Collectively, these data suggested that WTAP suppresses melanoma progression via NT5E-regulated EMT and adenosine pathway.

By contrast, abundant evidence has shown that WTAP contributes to aggressive features in other malignant tumors, where it serves as a considerable risk factor [14–17]. For example, WTAP is highly expressed in hepatocellular carcinoma and is associated with poor survival. Functionally, WTAP increases the proliferation and growth of hepatocellular carcinoma cells, and the overexpression of WTAP was found to promote the progression of hepatocellular carcinoma through reducing the expression of the downstream suppressor gene ETS proto-oncogene 1 [14]. In addition, WTAP is highly upregulated in osteosarcoma tissue, and as an oncogene, WTAP was shown to facilitate the proliferation and metastasis of osteosarcoma cells by regulating the stability of the downstream suppressor gene homeobox containing 1 [15]. WTAP is a conserved nuclear protein that functions as a partner of Wilms' tumor 1 (WT1) [50], which was previously identified as an inactivated tumor suppressor gene in a subset of pediatric renal cancers [51]. Additionally, WT1 has been described as a tumor suppressor in various kinds of cancer [52, 53]. With regard to WTAP as a tumor suppressor gene, as shown in Figure 1A, the GEPIA dataset revealed that WTAP is significantly downregulated in several cancer types, including SKCM, thyroid carcinoma, breast invasive carcinoma, kidney chromophobe, and lung adenocarcinoma. Through a systematic literature review, we identified only 3 robust bioinformatics studies supporting the tumor-suppressive role of WTAP [18–20]. However, no experimental studies have explicitly validated its tumor-suppressive function, and the precise molecular mechanisms underlying this activity remain unclear due to the absence of detailed mechanistic investigations. In our present study, a RIP assay was implemented with A875 or A375 cell lysates and WTAP antibody, and NT5E mRNA was detected in the WTAP immunocomplexes, and depletion of WTAP led to an increase in NT5E mRNA abundance in melanoma cell supernatants. Further actinomycin D chase experiments demonstrated that WTAP knockdown significantly reduced the decay rate of NT5E mRNA in melanoma cells, all of which suggested that WTAP was able to bind to NT5E mRNA and exerts tumor-suppressive effects in melanoma by modulating NT5E mRNA stability. Each tumor, therefore, evolves in its own unique way, and in the case of melanoma, WTAP may exhibit behavior as a tumor suppressor gene, fulfilling a suppressive role in melanoma progression.

Systemic management of melanoma has been revolutionized by the development of targeted therapies and immunotherapies. Immune checkpoint inhibitor therapy has sparked new hope for therapies against melanoma, especially advanced melanoma. In the present study, WTAP was shown to play a tumor suppressor role in melanoma *in vitro* and *in vivo*. Through transcriptome sequencing, the downstream target gene NT5E was identified as a potential factor. As a well-studied gene, NT5E has been shown to be overexpressed in numerous types of cancer, and its high expression both contributes to tumor malignancy and is associated with poor outcomes [27–29]. In recent years, a growing body of data have shown that NT5E is considered an ideal therapeutic target for cancer therapy, especially in situations where conventional therapy and/or treatment are combined with other immune checkpoint inhibitors, since its hydrolysis produces the immunosuppressive compound adenosine, which further increases tumor growth and metastasis [22, 23]. Therefore, NT5E depletion, in general, is expected to expedite the immune response to limit tumor-mediated immune evasion, especially in advanced melanoma. In the present study, either blocking NT5E by adding APCP to the melanoma culture supernatant or inhibiting NT5E expression via siRNAs led to a marked reduction in adenosine production, thereby improving adenosine-mediated IFN-γ secretion. The addition of an A_{2A} adenosine receptor antagonist, AZD4635, to the reaction enhanced secretion of IFN-γ compared to the control exper-

iments, suggesting that adenosine fulfils a critical role in NT5E-mediated IFN-γ production, which further confirmed that the NT5E-adenosine pathway contributed to WTAP-mediated tumor suppression. These results provided further evidence in support of NT5E, downstream from WTAP, having an immunosuppressive role in melanoma progression, and these findings were consistent with the previously demonstrated immunosuppressive function of NT5E. Additionally, NT5E effects molecular adhesion to promote malignant tumor progression. The results from the western blot analysis experiments revealed that the expression levels of MMP2 and N-cadherin were upregulated in the siWTAP groups, and that reduced NT5E expression led to a reversal of the elevated levels of MMP2 and N-cadherin expression that resulted from WTAP silencing in both A875 and A375 cells. Collectively, these findings have provided sufficient evidence to enable us to conclude that novel interventions to increase WTAP expression may have the effect of attenuating the NT5E-mediated immunosuppressive role, which would thereby exert an influence on molecular adhesion to suppress melanoma progression.

In conclusion, the present study has clearly demonstrated that WTAP is downregulated in melanoma, which impedes the progression of melanoma via the downstream effects mediated by NT5E on immunosuppression and molecular adhesion. The present study has also determined that WTAP exerts a crucial inhibitory role in melanoma oncogenesis, thereby highlighting WTAP as a potentially novel diagnosis and therapeutic target in melanoma.

Supplementary information is available in the online version of the paper.

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WTAP is a promising diagnosis and treatment biomarker that inhibits the proliferation and invasion of melanoma cells

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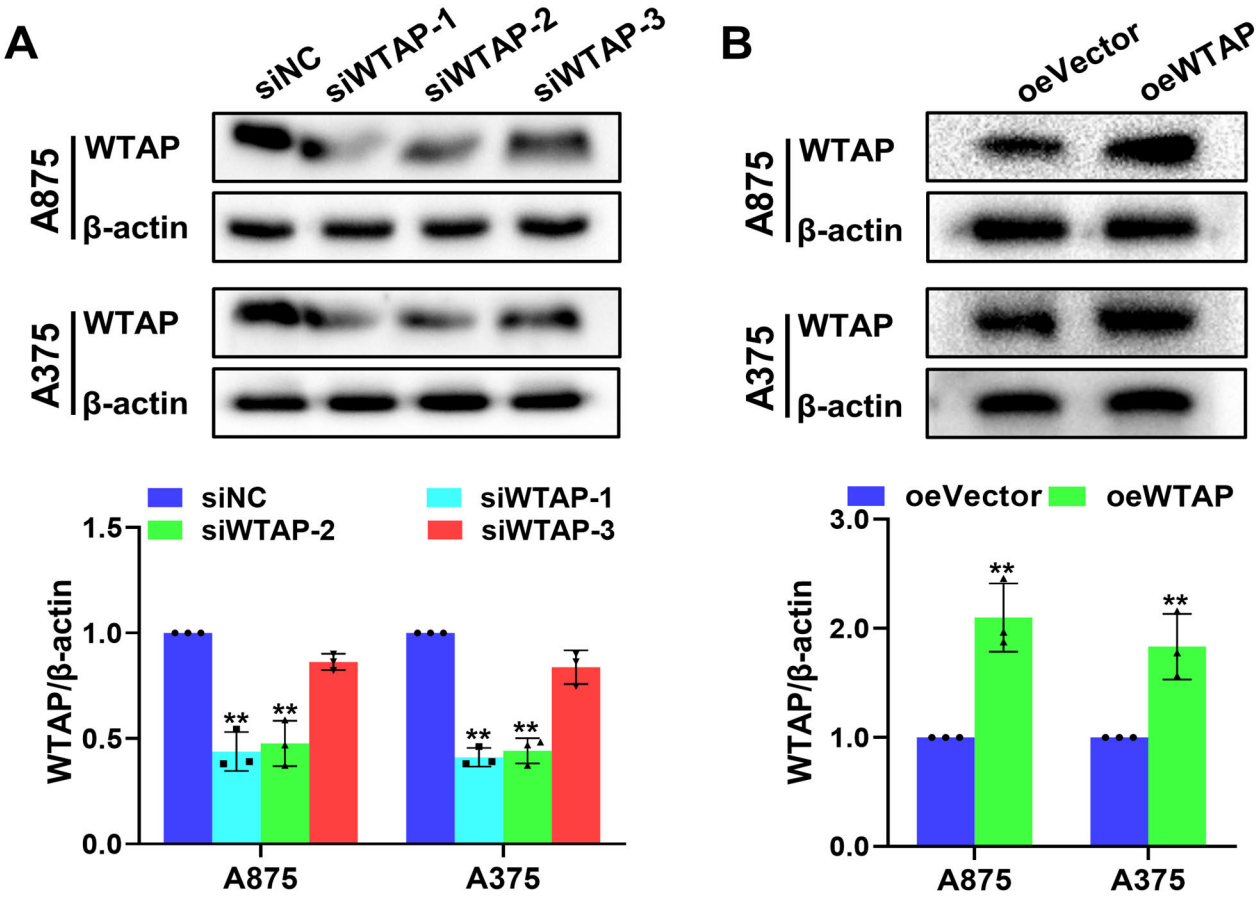
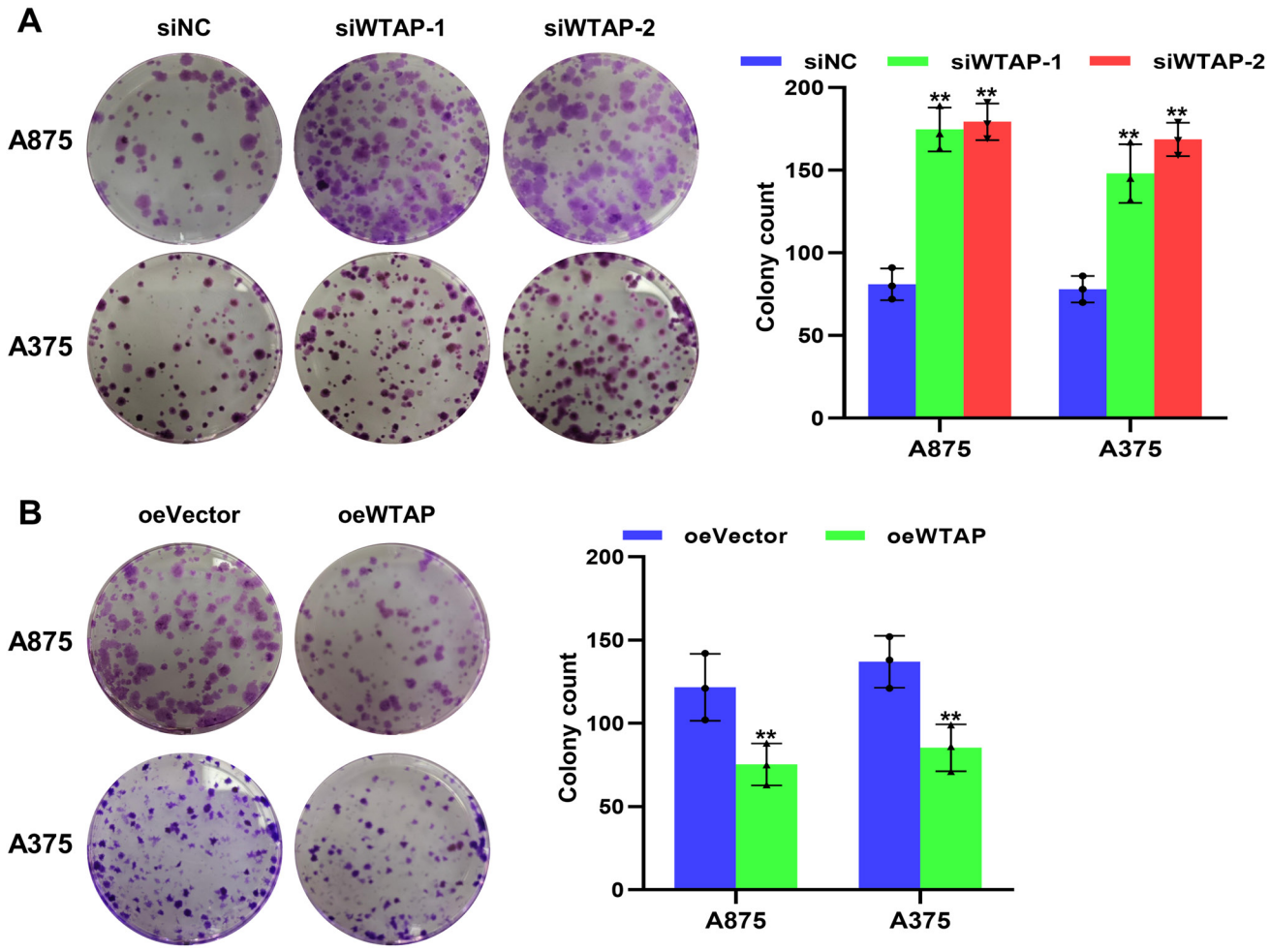
Supplementary Information



Supplementary Figure S1. Transfection efficiency of siRNA and overexpression plasmid in melanoma cells was detected by western blotting. A) Negative control or three specific siRNAs directed against WTAP was transfected into A875 and A375 cells, and the knockdown efficiency was determined by western blotting. B) The plasmid for WTAP overexpression and control vector were transfected into A875 and A375 cells, and the efficiency of infection was determined by western blotting. **p<0.01



Supplementary Figure S2. Colony formation assay in melanoma cells with WTAP silencing or overexpression. A, B) Results of the colony formation assay of melanoma cells in the siWTAP and control groups (A) or in the WTAP overexpression and control groups were exhibited (B). **p<0.01