Selective Activation of the Thyroid Hormone Receptor Beta (TRβ) Induces Tumor Suppression and Increases Efficacy of Therapeutic Agents

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Abstract

Thyroid hormone receptor beta (TRβ) is a recognized tumor suppressor in numerous solid

cancers. The molecular signaling of TRβ has been elucidated in several cancer types

through re-expression models. Remarkably, the potential impact of selective activation of

endogenous TRβ tumor progression remains largely unexplored. We used cell-based

and *in vivo* assays to evaluate the effects of the TRβ agonist sobetirome (GC-1) on a

particularly aggressive and dedifferentiated cancer, anaplastic thyroid cancer (ATC).

Here we report that GC-1 reduced tumorigenic phenotypes, decreased cancer stem-like

cell population, and increased the efficacy of current therapeutics. GC-1 induced re-

differentiation of the ATC cells and increased sodium-iodide transporter (NIS) expression

and restored iodide uptake. GC-1 alone was as effective as Sorafenib in blunting tumor

growth *in vivo*. These results indicate that selective activation of TRβ not only induces a

tumor suppression program *de novo* but enhances the effectiveness of anti-cancer

agents.

Statement of Significance: Selective activation of TRβ reduces aggressive cancer cell

phenotype, cancer stem cell population, tumor growth and increases the efficacy of

current therapeutics. TRβ is a novel diagnostic biomarker and therapeutic target.

INTRODUCTION

There is compelling evidence that the nuclear receptor thyroid hormone receptor beta (TRβ) is a suppressor of tumor progression, invasion, and metastases in multiple solid tumors including thyroid, breast, colon and other cancers(1). Cell-based and animal studies reveal that liganded TRβ induces apoptosis, reduces an aggressive phenotype, decreases cancer stem cell populations, and slows tumor growth through modulation of a complex transcriptional network (2-9) . Transcriptional regulation by TRβ is critical for its function as a tumor suppressor because it acts as both a signal transducer and facilitator of long-term epigenetic programming for maintenance of cell identity. Our recent studies revealed that TRβ in the presence of triiodothyronine (T$_3$) induced a tumor-suppressive transcriptomic program and cell redifferentiation in aggressive thyroid and breast cancer cells (2,10). We identified several key mechanisms by which activation of TRβ could reduce tumor progression, implicating thyroid hormone signaling as a therapeutic opportunity in advanced cancers. Recent studies in breast (8), colon (11), and liver (5) cancers also emphasize this untapped therapeutic potential (12,13).

Thyroid hormones, thyromimetics and their metabolites can activate TRα as well as TRβ. Yet, the use of non-selective TRβ ligands, such as T$_3$, is problematic as a therapeutic approach due to the adverse side-effects of hyperthyroidism and the potential for cardiovascular events as a result of aberrant TRα activity. To subvert these negative side effects, TRβ-selective thyromimetics have been developed (14,15). Several of these drugs have been shown to be effective for treatment of metabolic and neurodegenerative disorders in clinical trials(15). In particular, the TRβ agonist sobetirome (GC-1)

preferentially binds to and activates TRβ and induces the same transcriptomic response

as T_3 (15, 16) and has been successful in early clinical trials for treatment of dyslipidemia

(16-19). Despite their potential benefits demonstrated by numerous preclinical studies,

TRβ agonists remain untested as cancer therapeutics as single agents or in combination

with other treatments.

Here, we investigated the potential impact of a selective TRβ agonist in an

aggressive thyroid cancer model. The global incidence of thyroid cancer is increasing

faster than any other solid tumor (20,21). While prognoses for patients with differentiated

tumors receiving standard therapies are generally very good, outcomes for patients with

resistant or recurrent disease and poorly differentiated thyroid cancers (PDTC) are

extremely poor (22). Due to a lack of effective therapies, patients with advanced or

metastatic anaplastic thyroid cancer (ATC) have a higher mortality rate than all other

endocrine cancers combined (23). ATC tumors are refractory to radioiodine therapy due

to loss of the sodium-iodide symporter (NIS) expression, and traditional chemotherapy is

of limited benefit.

Activation of phosphatidylinositol 3-kinase (PI3K)–Akt–mammalian target of

rapamycin (mTOR) pathway (PI3K-Akt) and mitogen-activated protein kinase (MAPK)

signaling are recognized drivers of thyroid oncogenesis and blocking this activity is a

therapeutic focus. Yet inhibitors of the major components of these signaling cascades

rarely provide a durable response as resistance quickly develops. Current molecular

diagnostics provide a rationale for intervention with combination therapies (24). However,

combination treatments have not yielded significantly improved responses due to

development of resistance, and there are still no curative options (14). Therefore, there

remains an urgent need for innovative and less toxic therapeutics for ATC (25-27).

In our studies we establish the effects of GC-1 alone and in combination with

therapeutic agents in ATC cells with diverse genetic backgrounds (28). GC-1 alone

decreases the aggressive phenotype and increases the effectiveness of MAPK, PI3K,

and cell cycle inhibitors. GC-1 significantly increases expression of thyroid-specific genes,

inducing re-differentiation in ATC cells. Importantly, we observe an increase in NIS protein

which leads to enhanced iodide uptake implicating potential restoration of functionality.

Finally, GC-1 alone reduced tumor growth of ATC cells in xenografts as effectively as

Sorafenib. The combination of GC-1 and Sorafenib maximally suppressed tumor growth.

These observations indicate that activation of TRβ with isomer-selective agonists may be

an effective and practical adjuvant therapeutic strategy.

RESULTS

GC-1 blocks the tumorigenic phenotype of ATC cells transduced with TRβ.

We previously demonstrated that T_3 (10 nM) treatment of transduced SW1736

cells, in which TRβ is re-expressed (SW-TRβ), induced a tumor suppression

transcriptomic program and reduced cell growth when compared to cells transduced with

empty vector (SW-EV) (2). We therefore tested the ability of GC-1 (10 nM) to reduce ATC

phenotypes. We found that GC-1 similarly decreased cell growth in four days (**Fig. 1A**).

There was a 50% reduction in the overall growth rate of SW-EV cells and 75% reduction

in SW-TRβ cells (**Fig. 1B**), indicating potent activation of endogenous TRβ. There was

also a modest decrease in the cell migration rate of upon treatment with GC-1 (**Fig. 1C**).

As cancer stem cells
are thought to be responsible
for tumor initiation and
recurrence, targeting these
cells is key to successful
treatment. Therefore, we
tested whether thyroid
cancer stem cells are
responsive to GC-1.
Thyrosphere formation is
robust in SW-EV cells, and
GC-1 induced a significant
reduction in growth (**Fig. 1D**).
Re-expression of TRβ (SW-
TRβ) reduces thyrosphere
growth and addition of GC-1
reduces thyrosphere
formation by approximately
80% (**Fig. 1D**). These results
indicate that GC-1 can
activate TRβ to reduce the
thyroid cancer stem cell
population.

Figure 1. GC-1 blocks tumorigenic phenotypes in ATC cells transduced with TRβ. A. Growth curves demonstrate that SW-TRβ growth is significantly decreased after treatment with GC-1 for 4 days (n=3). Significance (* $p < 0.05$) was determined by a two-way ANOVA and Tukey's multiple comparisons test. **B**. Area under the curve (AUC) analysis of growth curve data. Significance (* $p < 0.05$) was determined by t-test. **C.** Treatment with GC-1 slows migration of SW-TRβ and SW-EV cells measured by scratch assay. Significance (* $p < 0.05$) was determined by t-test. D. GC-1 repressed thyrosphere formation in SW-TRβ and SW-EV cells (n=4). Significance (* $p < 0.05$) was determined by t-test. E. Immunoblot demonstrates that 5 days of GC-1 treatment induces apoptosis in SW-TRβ cells assessed by cleavage of PARP and caspase 3 (n=3).

Apoptotic signaling is central to ligand-activated TRβ modulation of the ATC

aggressive phenotype (2). Thus, we assessed the effects of GC-1 on PARP and caspase

3 cleavage by immunoblot as markers of late-stage apoptosis (**Fig. 1E**). GC-1 significantly

increased cleavage of PARP and caspase 3 in SW-TRβ consonant with increased

apoptotic signaling. Combined, these results indicate that GC-1 can activate TRβ to

reduce the aggressive phenotype in transduced ATC cells with TRβ re-expressed and

recapitulate effects seen with T_3 at comparable concentrations.

GC-1 slows growth of parental ATC cells.

Once we confirmed that GC-1 induces the same phenotypic changes in our

transduced ATC cell line model, it was critical to assess whether selective activation of

endogenous TRβ would induce similar effects in unmodified ATC cell lines (28). SW1736,

8505C, OCUT2, and KTC-2 cells all harbor *BRAF^V600E* and *TERT* driver mutations, but

otherwise have diverse mutational backgrounds (summarized in **Fig. 2A**). Endogenous

TRβ expression is low in all four ATC cell lines when compared with normal thyroid cells

(29). Treatment of each cell line with 10 nM GC-1 for four days yielded a modest but

significant decrease in cell growth (**Fig. 2B-E**). Treatment with 10 nM T_3 did not alter

growth of any of the cell lines. This result suggests that even low levels of endogenous

TRβ can be selectively activated with GC-1, and GC-1 is more effective at promoting

tumor suppressor activity than T_3.

Figure 2: GC-1 slows growth of parental ATC cells. A. Summary of mutated genes in four ATC cell lines implemented in this study (17). B-E. Relative cell growth of unmodified ATC cell lines was measured by cell counting assay after 4 days of treatment with 10 nM GC-1 or 10 nM T_3. Significance (* $p<0.05$) was determined by a two-way ANOVA followed by Dunnett's multiple comparisons test; 3 independent experiments were performed per treatment group.

GC-1 increases the efficacy of selected therapeutic agents

Based on our previous work on activation of TRβ in ATC cells, we hypothesized that GC-1 could enhance the efficacy of therapeutics that target selective pathways. Cell viability was calculated following treatment for three days with increasing concentrations of the PI3K inhibitor Buparlisib (pan-PI3K inhibitor) or Alpelisib (PI3Kα mutant inhibitor) for OCUT2 cells which harbor a gain-of-function *PIK3CA* mutation (**Fig. 3A**), the cell cycle inhibitor Palbociclib (**Fig. 3B**), or the multi-tyrosine kinase inhibitor Sorafenib (**Fig. 3C**), with or without 10 nM GC-1. Each therapeutic agent decreased cell viability in three days

Figure 3. GC-1 increases efficacy of inhibitors. Cell viability of unmodified ATC cell lines was measured by SRB assay after 3 days of treatment with increasing concentrations buparlisib or alpelisib (A), sorafenib (B), or palbociclib (C) simultaneously in combination with 10 nM GC-1. Significance (* $p<0.05$) was determined by a two-way ANOVA followed by Sidak's multiple comparisons test; 3 independent experiments were performed per each treatment group.

in a dose-dependent manner. The addition of GC-1 significantly increased the efficacy of

these agents at lower concentrations. For example, 1 μM Buparlisib was required to

reduce cell viability below 50% in the absence of GC-1, but when combined with 10 nM

GC-1 this could be achieved with 0.1-0.5 μM Buparlisib (**Fig. 3A**). Similar trends were

observed with all four therapeutics and across the panel of cell lines used.

GC-1 enhances the effects of therapeutic agents on cell migration

In addition to reducing cell viability, many therapeutics target pathways that are

involved in cell migration. To further evaluate the ability of GC-1 to enhance the efficacy

of select therapeutics, cells were treated with the indicated inhibitors at concentrations

determined to be effective based on cell viability assays (**Fig. 3**), and migration was

observed by assessing wound closure. Each inhibitor was able to successfully slow

migration, and this effect was increased when each of the inhibitors were combined with

GC-1, except for Buparlisib in KTC-2 cells (**Fig. 4B-E**). Notably, GC-1 alone was able to

prevent wound closure of all cell lines with similar success as each inhibitor alone (**Fig.**

4A-E). These findings are similar to what we previously observed in experiments using

endogenous thyroid hormone, T$_3$, indicating GC-1 is a suitable alternative for TRβ

activation for slowing migration.

Figure 4. GC-1 enhances the effects of inhibitors on cell migration. Cell migration was measured by scratch assay. Representative images demonstrate reduced scratch closure after two days when ATC cells are treated with GC-1 (A). Area under the curve (AUC) analysis shows SW1736 (B), 8505C (C), OCUT2 (D), and KTC-2 (E) cells all exhibit lower rates of scratch closer after treatment with GC-1 alone and further reduced scratch closure rates after combined treatment with GC-1 and inhibitors. Significance (* p<0.05) was determined by t-test.

GC-1 blocks tumorsphere outgrowth and increases efficacy of therapeutic agents.

Current treatment options for ATC primarily target hyperproliferative cells, but

aggressive cancers like ATC are enriched for long-lived cancer stem cells that are thought

to be a major mechanism for therapy resistance and tumor recurrence. We previously

demonstrated that ligand-activated TRβ regulates genes related to stemness in ATC cells

and that GC-1 could block thyrosphere outgrowth in our modified ATC cells (**Fig. 1D**). We

therefore tested the hypothesis that GC-1 could prevent thyrosphere outgrowth after an

initial treatment with an inhibitor that targets proliferation.

Figure 5. GC-1 blocks thyrosphere outgrowth and increases the efficacy of therapeutic agents. Thyrosphere growth was determined for ATC cells after 3 days of treatment with 0.5 μM buparlisib or alpelisib (A), 10 μM sorafenib (B), or 1 nM palbociclib (C) under adherent culture conditions, followed by plating in conditions for spheroid growth in the presence of 10 nM GC-1 for 7 days. GC-1 alone and each therapeutic agent significantly blocked sphere formation in all cell types. GC-1 in addition to each therapeutic agent further inhibited or completely blocked sphere formation. Significance (* p<0.05) was determined by two-way ANOVA followed by Sidak's multiple comparisons test; 3 independent experiments were performed per each treatment group; n=3 per analyses.

ATC cells were treated with the indicated inhibitor or vehicle for three days,

followed by re-plating in non-adherent conditions. We again observed that GC-1 alone

could reduce thyrosphere formation in unmodified ATC cell lines (**Fig. 5A-C**). None of the

inhibitors could completely prevent thyrosphere outgrowth when used alone; however,

Sorafenib was the most effective overall (**Fig. 5C**). The addition of GC-1 upon removal of

each inhibitor blocked nearly all thyrosphere outgrowth. This effect was consistent across

all four cell lines and all three inhibitors used. This suggests that GC-1 may be particularly

effective at blocking cancer stem cell expansion.

GC-1 promotes re-differentiation of ATC cell lines.

In transduced cells, TRβ activation with T_3 reduces the aggressive phenotype

partially through re-differentiation. Therefore, we investigated the potential for GC-1 to

promote re-differentiation in parental SW1736 cells. Gene expression analysis using RT-

qPCR revealed that 24 hours of GC-1 exposure increased levels of thyroid-specific gene

transcripts (**Fig. 6A**). This transcriptomic program is summarized by the thyroid

differentiation score (TDS), which significantly increased in GC-1-treated cells (**Fig. 6B**).

Additionally, GC-1 alone decreased the overall number of $CD24^-/CD44^+$ cells present in

the monolayer population as evident by RT-qPCR (**Sup. Fig. 1A**). We also observed a

decrease in the ATC markers *ALCAM* (CD166) and *ALDH1A1* (**Sup. Fig. 1B**).

218   Intriguingly, *SLC5A5* expression was increased with 24 hours of GC-1 (**Fig. 6A**).

219 Therefore, we further investigated NIS protein levels after 48 hours of GC-1 treatment.

220 Both nascent and mature (glycosylated) NIS protein significantly increased following GC-

221 1 treatment (**Fig. 6C-D**). Iodide uptake into cells also increased (**Fig. 6E**), indicating that

222 the increased NIS protein was functional. These findings reveal a novel function of GC-1

Figure 6. GC-1 induces expression of redifferentiation markers in SW1736 cells. A. RT-qPCR for thyroid differentiation markers was performed on SW1736 cells treated with or without 10 nM GC-1 for 24 hours. mRNA levels in cells treated with GC-1 are relative to the untreated cells. Significance (* p<0.05) was determined by Student's unpaired t test; 3 independent experiments were performed per treatment group. B. Thyroid differentiation score (TDS) was calculated using the expression level of the genes in panel A, excluding *THRB*, as previously described (10, 17). Significance (* p<0.0001) was determined by Student's unpaired t test. C. SW1736 cells were treated with or without 10 nM GC-1 in triplicate for 48 hours prior to protein extraction and analysis via immunoblot. Normal-like thyroid Nthy-ORI cells were used as a positive control. D. Relative NIS/GAPDH protein levels from (C) were quantified via ImageJ, and significance (* p<0.01) was determined by Student's unpaired t test. E. Iodide uptake was measured after 48 hours of GC-1 treatment. Significance was determined by Student's unpaired t test. (* p<0.001).

to induce re-differentiation in an ATC cell line model and offers a promising target to

increase NIS levels and iodide uptake.

GC-1 blunts tumor growth as effectively as Sorafenib *in vivo.*

To validate our cell-based findings *in vivo*, the effect of GC-1 alone or in

combination with Sorafenib was tested in a xenograft study. GC-1 blunted tumor growth

with no significant change in tumor volume over the treatment period similar to Sorafenib

and the combination of both treatments (Fig. 7A). At day 16 of treatment, GC-1 induced

a significant 60% reduction in tumor mass as did Sorafenib (Fig. 7B, C). The potential for

drug synergy was masked due to the equivalent efficacy with Sorafenib at these doses

(7A-C). Of note, All mouse groups exhibited similar weight gains over the course of

treatment (Fig. 7D). Immunofluorescence image analysis (HALO) on excised tumors

revealed diminished Ki67 in all treatment groups (Fig. 7E-F). The combination of GC-1

and Sorafenib resulted in a significant reduction in Ki67 expression (Fig. 7F). Region of

Interest (ROI) analysis revealed distribution of Ki67 expression preferential in cells along

the periphery of the tumor samples.

Figure 7. GC-1 inhibits tumor growth as effectively as Sorafenib in an ATC xenograft model. Nude mice were injected subcutaneously with 1×10^6 8505C cells. Tumors were established after 1 week. Mice were assigned to 4 treatment groups by weight and injected i.p. daily for 16 days with vehicle control, 10 mg/kg sorafenib, 0.3 mg/kg GC-1, or a combination of sorafenib and CP. (A) Percent change in tumor volumes from day 1 of treatment; *** $p<0.001$ (B) Representative excised tumors from each treatment. No evidence of metastases was noted in any group. Reduced vascularization was observed with GC-1 treatment. (C) Tumors were excised on Day 16 and weighed. Sorafenib (blue), GC-1 (red) induced a 60% reduction in final tumor mass with no difference between the two treatments. The combined treatments did not further reduce the tumor mass over the time period. Significance indicated ** $p<0.01$. (D) Mice were weighed three times a week following drug injections to monitor toxicity. No significant change in animal weight was noted for any group. (E) Representative images of tumors stained for Ki-67 are illustrated. Regions of interest containing only tumor tissue were outlined on each tiled image. Nuclear detection was set to the DAPI channel and the nuclear detection settings were optimized to accurately segment nuclei in the images. (F) Images were analyzed using HALO image analysis (Indica Labs, Albuquerque NM; version 3.3.45) utilizing the HighPlex FL module (version 4.1.3). Quantification of Ki-67 fluorescent intensity per cell is summarized. Sorafenib and GC-1 decreased Ki-67 but only significantly in combination; ** $p<0.01$.

DISCUSSION

There is compelling evidence that loss of expression of TRβ, a member of the thyroid hormone receptor (TR) family, through genomic modifications and epigenetic silencing is characteristic of thyroid tumors (3,30-35). Numerous pre-clinical studies demonstrate the potent anti-tumorigenic effect of robust expression of the *THRB* gene. Re-expression of silenced TRβ using demethylating agents delays thyroid tumor progression *in vivo* (36), mice expressing a c-terminal frameshift of TRβ (*Thrb^{PV}*) spontaneously develop follicular thyroid cancer (37), and *Thrb^{PV/PV} Kras^{G12D}* mice develop thyroid tumors with features of de-differentiated thyroid cancer (38). Our studies in anaplastic thyroid cancer cells revealed that activation of TRβ induces a tumor suppression transcriptomic program, re-differentiation, and reduces the aggressive phenotype (2,10).

Activation of TRβ in pre-clinical and clinical studies have yielded exciting results

with great promise for novel interventions. Patients who were rendered hypothyroxinemic

and treated with T_3 had longer survival with end-stage solid tumors (39) and T_3 treatment

enhanced chemosensitivity (40). Following tyrosine kinase inhibitor therapy, patients

demonstrated improved survival with treatment of hypothyroidism (41). Agonists have

been developed to target tissue-specific expression of the most abundant TR isomers

(42). Mimetics of T_3 that selectively act as TRβ agonists have been clinically successful

for treatment of metabolic disorders, hyperlipidemia, hypercholesterolemia, and non-

alcoholic steatohepatitis without the harmful cardiovascular effects mediated by TRα

(16,17). Our findings demonstrate that GC-1 alone decreases the ATC aggressive

phenotype in transduced cells in which TRβ is re-expressed and parental cell lines with

diverse genetic backgrounds. These results emphasize the generalizability of GC-1 to

activate a TRβ tumor suppression program.

In ATC tumors, several genetic alterations and disrupted signaling pathways are

usually found. Therefore, the aim is to inhibit or disrupt multiple pathways with

combination therapies that block cell survival and proliferation (27,43). In this study, we

tested representative drugs that target the MAPK, PI3K, and cell cycle pathways to

assess whether GC-1 could increase their effectiveness. Since we have demonstrated

that activation of TRβ in ATC represses the PI3K pathway through genomic mechanisms

(2,29), GC-1 with either Buparlisib or Alpelisib would be suppressing PI3K activity in

concert. In contrast, TRβ does not directly impact MAPK through transcriptomic

modulation so GC-1 in combination with Sorafenib demonstrated concordant effects. In

all studies, GC-1 reduced the effective concentrations required to observe a reduction in

cell viability. One of our most intriguing observations is the impact of GC-1 alone and in

combination with inhibitors on cancer stem cell growth in thyrosphere formation. In all

ATC cell types, GC-1 alone significantly reduced thyrosphere formation. Remarkably,

GC-1 in combination with any of the drug treatments nearly eliminated thyrosphere

formation.

GC-1 induced re-differentiation in the SW1736 cell line in 24 hours, demonstrating

potent transcriptional reprogramming. While we have previously demonstrated the

potential for TRβ to promote a more differentiated phenotype in ATC cells, this is the first

time we have observed the profound impact of GC-1 in a parental cell line with low TRβ

expression. Importantly, we observed a concomitant increase in NIS that led to a higher

intake of iodide. Since PDTC and ATC tumors often exhibit a marked decrease in NIS

expression and resistance to RAI therapy, the results presented here raise a provocative

implication for the use of GC-1 in combination with RAI. Critically, we found that GC-1

could blunt tumor growth as effectively as Sorafenib in a xenograft study confirming the

observations in cell-based studies. The combination of GC-1 and Sorafenib did not further

reduce the tumor volume or mass over the study period. Future studies establishing the

pharmacodynamics of GC-1 in combination with different doses of therapeutic agents will

elucidate the most effective combinatorial paradigm.

Our findings demonstrate that selective activation of TRβ with GC-1 can reduce

the aggressive phenotype, reduce the cancer stemness in ATC cells, increase the

sensitivity of these cells to therapeutic agents, and promote re-differentiation and iodide

uptake. Moreover, GC-1 treatment is as effective as the therapeutic Sorafenib in inhibiting

tumor growth. These studies provide the foundation for further investigation of the broad

impact of GC-1 on mitigating tumor progression, toxicity, and development of resistance

to treatment.

MATERIALS AND METHODS

Culture of thyroid cell lines. Anaplastic thyroid cancer cell lines (SW1736, 8505C,

OCUT-2, and KTC-2) and the normal-like thyroid cell line Nthy-ORI were cultured in RPMI

1640 growth media with L-glutamine (300 mg/L), sodium pyruvate and nonessential

amino acids (1%) (Corning), supplemented with 10% fetal bovine serum (Peak Serum)

and penicillin-streptomycin (200 IU/L) (Corning) at 37°C, 5% CO_2, and 100% humidity.

SW1736-EV and SW-TRβ cells were modified by lentiviral transduction as recently

described (10). SW1736, KTC-2, and Nthy-ORI were authenticated by the Vermont

Integrative Genomics Resource at the University of Vermont using short tandem repeat

profiles (SW1736, May 2019; KTC-2, October 2019; Nthy-ORI, August 2020). 8505C and

OCUT2 were authenticated by the University of Colorado using short tandem repeat

profiles (8505C, June 2013; OCUT-2, June 2018).

Pharmacological agents. T_3 and GC-1 (Sigma-Aldrich) were suspended in 1 M NaOH

(T_3) and 100% ethanol (GC-1) for stock concentrations of 1 mM before further dilution in

culture medium. Buparlisib, Sorafenib, Palbociclib, and Alpelisib (MedChemExpress)

were suspended in 100% DMSO for stock concentrations of 50-150 mM before further

dilution in culture medium.

Cell Growth and Viability Assays. Cell growth was measured by cell counting at

discrete time points. Cells were seeded in 12- well plates, then treated with GC-1,

Buparlisib, Alpelisib, Palbociclib, or Sorafenib to establish time and concentration effects

of therapeutics on cell growth. Cell viability was determined by a Sulforhodamine B assay

(Abcam) following the manufacturer's protocol. In brief, ATC cells were plated in 96-well

clear flat-bottom plates at a density of 5,000 cells per well. Cells were fixed, stained, and

imaged using a plate reader according to manufacturer's instructions.

Migration Assay. Cell migration was determined by wound healing assay as previously

described (10, 18). Media was supplemented with GC-1 (10 nM) with and without 0.5 μM

Buparlisib, 0.5 μM Alpelisib, 1 nM Palbociclib, or 5 μM Sorafenib. Images were obtained

at 0, 16, 24, 48, and 72 hours or until 100% wound closure, depending on the cell line.

Percent closure was calculated relative to the area of the initial scratch.

Tumorsphere Assay. Tumorspheres formed from ATC cells were used to assess self-

renewal and sphere-forming efficiency as previously described (10). Where indicated,

adherent cells were treated with 0.5 μM Buparlisib, 0.5 μM Alpelisib, 1 nM Palbociclib, 5

μM Sorafenib, or vehicle for 72 hours prior to tumorsphere-forming assay. Tumorspheres

were then cultured in with or without GC-1 (10 nM) to evaluate the effects of liganded TRβ

on thyrosphere growth alone or after treatment with a therapeutic agent.

Western blot Analysis. Proteins were isolated from whole cells in lysis buffer and

visualized by Western blot as previously described (9, 10, 18). Specific proteins were

detected with the indicated antibodies (Table 1); immunoreactive proteins were detected

by enhanced chemiluminescence (Thermo Fisher Scientific) on a ChemiDoc XRS+ (Bio-

Rad Laboratories).

RNA Extraction and Quantitative Real-Time PCR (qRT-PCR). Total RNA was

extracted using RNeasy Plus Kit (Qiagen) according to manufacturer's protocol. cDNA

was generated using 5X LunaScript RT SuperMix, and mRNA expression was quantified

by qRT-PCR using 2X Luna Universal qPCR Master Mix (New England Biolabs) on a

QuantStudio 3 real-time PCR system (Applied Biosystems). Fold change in gene

expression compared to housekeeping controls was calculated using the ddCT method.

Primer sequences are indicated in Table 2.

Iodide Uptake Assay. Cells were seeded at a density of 40,000 cells per well in a 96 well

plate with or without 10 nM GC-1 for 48 hours. Media was discarded, and cells were

washed four times with warm PBS before incubation with 1 μM potassium iodide (KI,

Sigma-Aldrich) in PBS for 1 hour at 37°C. Wells were washed an additional four times

with warm PBS and 100 μL of ddH$_2$O were added to each well. 100 μl of 24 mM

ammonium cerium (IV) sulfate hydrate with 5.7% concentrated H$_2$SO$_4$ (Sigma-Aldrich)

and 100 μl of 24 mM sodium arsenite (III) with 205 mM sodium chloride (NaCl) and 50

mM sodium hydroxide (NaOH, Sigma-Aldrich) were added to each well. Plates were

incubated in the dark at room temperature for 30 minutes, and absorbance at 415 nm

was measured with a Synergy 2 Multi-Detection Microplate Reader (Agilent

Technologies).

***In Vivo* Evaluation of Sobetirome (GC-1) and Sorafenib.** The xenograft experiment

was approved by the Animal Care and Use Committee of the University of Vermont

(Protocol X0-018). Four-week-old athymic female nude mice (outbred homozygous nude

Foxn1^{nu}/Foxn1^{nu}) were purchased from Jackson Laboratory (Bar Harbor, ME, USA) and

were allowed to acclimatize for one week. Mice were given food and water *ad libitum*.

Mice were anesthetized using 3% isoflurane delivered at 1.5 L/min, and tumors were

established by subcutaneously injecting 1×10^6 8505C cells with a 26G needle in 100 μL

of high concentration Matrigel (Corning Inc.) diluted 1:2 with base RPMI-1640 into each

flank of 24 mice. One week later, mice were sorted into four treatment groups to achieve

approximately equal body weights within each group. Mice were then administered 0.3

mg/kg GC-1, 10 mg/kg Sorafenib, both GC-1 and Sorafenib, or vehicle control every day

via intraperitoneal injection using 27G needles. Pharmacological agents were dissolved

in 100% DMSO and diluted daily in 30% DMSO, 40% PEG300, and 30% PBS and

incubated at 55°C for 10 minutes prior to vortexing to encourage complete solubilization.

Tumor dimensions were measured with digital calipers, and the volumes were calculated

by the following formula: $(\Pi \times a \times b^2) / 6$, where a represents the largest diameter and b

is the perpendicular diameter. The body weight of each animal was taken at least twice a

week to measure toxicity. After treatment for 16 days, mice were euthanized with carbon

dioxide, and the tumors were harvested, fixed with formalin (Thermo Fisher Scientific),

and stored at 4°C prior to slide sectioning and immunohistochemistry.

Immunofluorescent Analysis of Tumor Tissues. Formalin fixed paraffin embedded

human thyroid xenograft tumor blocks were sectioned at 5 μm thickness onto glass

microscope slides, dried overnight, and then baked at 60°C for one hour. Sections were

deparaffinized in three changes of xylene for 15 minutes each, then dehydrated in a series

of graded ethanols (100% x2, 95% x2, 70%, 50%, water) for 5 minutes each. Antigen

retrieval utilizing 1X DAKO target Retrieval Solution (DAKO product #S1699, lot#

11270951; Agilent Technologies, Santa Clara, CA) in 50% glycerol was performed in a

Decloaking Chamber (SP1 - 100°C for 15 min, SP2 - 90°C for 1 min). Following antigen

retrieval, slides were cooled to room temperature in the antigen retrieval solution for 20

minutes. Slides were then rinsed 2x 5 minutes in distilled water followed by 0.2% Tween-

20 for an additional 5 minutes. Tissue sections were blocked for non-specific antibody

reactivity by incubation with 10% normal goat serum diluted in phosphate buffered saline

(PBS)/ 3% bovine serum albumin (BSA)/ 0.3% Triton X-100 for 60 minutes at room

temperature. Immediately following blocking, slides were incubated with rabbit polyclonal

anti-KI-67 (Abcam, Cambridge, UK; #ab15580) at a concentration 1.4 µg/ml in PBS/3.0%

BSA/0.3% Triton X-100 overnight at 4°C. Slides were then rinsed 7x 5 minutes in

PBS/3.0% BSA and incubated with goat anti-rabbit Alexa 488 conjugated secondary

antibody (ThermoFisher, Waltham MA; #A11008) in PBS/3.0% BSA for 60 minutes at

room temperature. Staining was followed by 5x 5 minute rinses with PBS/3.0% BSA.

Samples were counterstained with 4', 6-diamidino-2-phenylindole (DAPI) (ThermoFisher,

#D1306) at a concentration of 10 µg/ml in PBS / 3.0%BSA for 15 minutes then rinsed 3x

5 minutes in distilled water. Following rinses slides were mounted with a #1.5 coverslip

and DAKO IF mounting media (Agilent; #S3023) for imaging.

Confocal Imaging of human thyroid xenograft tissue. Xenograft samples stained with

anti-KI-67 and DAPI were imaged on a Nikon A1R HD point scanning confocal

microscope with a 20x Plan Apo λ DIC objective lens (NA 0.75, WD 1000 µm) with 488

nm and 405 nm laser excitation respectively. Image acquisition was completed in

galvanometic scanning mode (Nikon Instruments Inc., Melville NY). Images of the entire

xenograft section were acquired at 12-bit resolution using the tile scan function. Images

were saved in ND2 file format in NIS Elements (version 5.2.1, Nikon, Tokyo, Japan).

Indica Labs HALO Image Analysis. Images were analyzed using HALO image analysis

(Indica Labs, Albuquerque NM; version 3.3.45) utilizing the HighPlex FL module (version

4.1.3).   Regions of interest containing only tumor tissue were outlined on each tiled

image.   Nuclear detection was set to the DAPI channel and the nuclear detection settings

were optimized to accurately segment nuclei in the images. Membrane and cytoplasmic

threshold settings were optimized for Ki-67 staining in the Alexa 488 (green) channel.

Cytoplasmic detection settings were set to 4095 (in a 12 bit image) so that no cytoplasmic

background staining would be included in the analysis. Nuclear positive signal setting

threshold was set per image, to most accurately reflect the antibody staining level

observed in the image. Percent Ki-67 positive cells were summarized.

Ethics statement and animal modeling. All animal procedures were approved by

Institutional Animal Care and Use Committee (IACUC) at the University of Vermont. All

animals were maintained in pathogen-free conditions and cared for in accordance with

IACUC policies and certification. All surgeries were performed with isoflurane anesthesia.

Temperature-controlled post-surgical monitoring was implemented to minimize suffering.

Mice carrying anaplastic thyroid tumors were euthanized at designated time points for

tumor collection. We used signs of ulceration or a maximum individual tumor size of 2000

mm^3 as a protocol-enforced endpoint.

Statistics. All statistical analyses were performed using GraphPad Prism 9.3.1 and

assumed that variance was similar between experimental groups. Sample sizes were a

minimum of three independent experiments. Paired comparisons were conducted by

unpaired Student's t-test assuming two-tailed distribution. Group comparisons were made

by one-way ANOVA followed by Sidak's or Tukey's multiple comparison test as

appropriate. Two-way ANOVA followed by a Tukey's multiple comparison test was

conducted for multigroup analysis. Data are represented as mean ± standard deviation

or standard error of the mean where indicated. Differences were considered statistically

significant at $p \leq 0.05$ (*$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$). Area under the curve (AUC) at

the 95th confidence interval was used to evaluate statistical differences in growth and

migration assays.

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ERW: Formal analysis, Investigation. **CDD**: Formal analysis, Investigation. **JAT:**

Investigation, Writing – Review & editing. **ELB:** Conceptualization, – Review & editing.

FEC: Conceptualization, Resources, Writing-Review & editing, Supervision, Project

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SUPPLEMENT

Supplemental Figure 1. RT-qPCR for markers of stemness and proliferation was performed on

SW1736 cells treated with or without 10 nM GC-1 for 24 hours. mRNA levels in cells treated

with GC-1 are relative to the untreated cells. Significance (* p<0.05) was determined by

Student's unpaired t test; 3 independent experiments were performed per treatment group.

Antibody Table

Target	Use	Antibody	Manufacturer
PARP	WB	9542	Cell Signaling Technology
Caspase-3	WB	14220	Cell Signaling Technology
Cleaved Caspase-3	WB	9664	Cell Signaling Technology
NIS	WB	MABC1191	Sigma Aldrich
GAPDH	WB	600-401-A33	Rockland Immunochemicals
Goat anti-mouse HRP	WB	7076	Cell Signaling Technology
Mouse anti-rabbit HRP	WB	211-035-109	Jackson Immunoresearch Laboratories

Isotype	Dilution	Antibody Id	MW (kDa)
rabbit	1/1,000	AB_2160739	89,116
rabbit IgG	1/500	AB_2798429	35,19,17
rabbit IgG	1/500	AB_2070042	17,19
mouse	1/500	N/A	75
rabbit	1/5,000	AB_2107593	37
goat	1/10,000	AB_330924	
mouse	1/10,000	AB_2339150	

Primer Table

Target	Forward (5'-3')	Reverse (5'-3')
ALCAM	TCAAGGTGTTCAAGCAACCA	CTGAAATGCAGTCACCCAAC
ALDH1A1	GCACGCCAGACTTACCTGTC	CCTCCTCAGTTGCAGGATTAAAG
CD24	TGAAGAACATGTGAGAGGTTTGAC	GAAAACTGAATCTCCATTCCACAA
CD44	CCAGAAGGAACAGTGGTTTGGC	ACTGTCCTCTGGGCTTGGTGTT
DIO1	CACTGCCTGAGAGGCTCTACATA	TGTAGTTCCAAGGGCCAGAT
DIO2	CCTGGTTGCAGCACATTCAC	TTGACTAGCACTGCCTCAGC
DUOX1	CCTGGCTCTAGCATGGACAC	TCCCACGAAATGGGGTTCTG
DUOX2	GCTGCCTTCCCTTAGTGAGT	TCGCTGGCACTCCATCTTTG
FOXE1	CACGGTGGACTTCTACGGG	GGACACGAACCGATCTATCCC
GAPDH	ATGTTCGTCATGGGTGTGAA	TGTGGTCATGAGTCCTTCCA
MYC	GGCTCCTGGCAAAAGGTCA	CTGCGTAGTTGTGCTGATGT
NKX2-1	CTCGCTCATTTGTTGGCGAC	GGAGTCGTGTGCTTTGGACT
PAX8	AGTCACCCAGTCGGATTC	CTGCTCTGTGAGTCAATGCTTA
SLC5A5	GCAGTACATTGTAGCCACGAT	TGCAGATAATTCCGGTGGACA
SLC26A4	TGAAGGAAATGCCAAAGTTACG	AGTATTCCCGCAGTTTGCTGA
TG	AGGGAGAGTTTATGCCTGTCC	CAATACCCAGATACCTCAGGGAA
THRA	AGGTCACCAGATGGAAAGCG	AGTGATAACCAGTTGCCTTGTC
THRB	CACATCATCATGGTCCAGATGG	GGCGCAGCACGTTGAAAAT
TPO	GCCAACAAGCGGAGTGATTG	GGGCAGCATGTAAGGGAGAC
TSHR	TTCCCTGACCTGACCAAAGTT	ACGTCATGTAAGGGTTGTCTGT

Amplicon Size (bp)
96
129
208
151
75
125
72
132
154
143
119
163
139
122
97
148
136
92
175
76