Off-target *In Vitro* Profiling Demonstrates that Remdesivir Is a Highly Selective Antiviral Agent

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Abstract

Remdesivir (RDV, GS-5734), the first FDA-approved antiviral for the treatment of COVID-19, is a single diastereomer monophosphoramidate prodrug of an adenosine analogue. It is intracellularly metabolized into the active triphosphate form, which in turn acts as a potent and selective inhibitor of multiple viral RNA polymerases. RDV has broad-spectrum activity against members of the coronavirus family such as SARS-CoV-2, SARS-CoV, and MERS-CoV, as well as filoviruses and paramyxoviruses. To assess potential for off-target toxicity, RDV was evaluated in a set of cellular and biochemical assays. Cytotoxicity was evaluated in a set of relevant human cell lines and primary cells. In addition, RDV was evaluated for mitochondrial toxicity under aerobic and anaerobic metabolic conditions, and for the effects on mitochondrial DNA content, mitochondrial protein synthesis, cellular respiration, and induction of reactive oxygen species. Lastly, the active 5'-triphosphate metabolite of RDV, GS-443902, was evaluated for potential interaction with human DNA and RNA polymerases. Among all of the human cells tested under 5-14 days of continuous exposure, RDV's CC_{50} values ranged from 1.7 to >20 μM, resulting in selectivity indices (SI, CC_{50}/EC_{50}) from >170 to 20,000, with respect to RDV anti-SARS-CoV-2 activity (EC_{50} of 9.9 nM in human airway epithelial cells). Overall, the cellular and biochemical assays demonstrated a low potential of RDV for off-target toxicity including mitochondria-specific toxicity, consistent with the reported clinical safety profile.

Introduction

Nucleoside/tide analogs have played a key role in the treatment of viral infections caused by DNA viruses such as herpes virus and hepatitis B virus as well as RNA viruses such as human immunodeficiency virus (HIV) and hepatitis C virus (HCV) (1, 2). Studies over the past several decades have significantly expanded our knowledge on the potential off-target effects for this class of compounds including inhibition of host nucleic acid polymerases such as human mitochondrial DNA polymerase γ (POL γ) (3) and mitochondrial RNA polymerase (POLRMT) (4, 5) as well as perturbation of nucleotide metabolism, mitochondrial respiration, and dNTP/NTP pools (6). Importantly, suitable methods to evaluate the potential for these types of toxicities are currently available.

Remdesivir (RDV, GS-5734) is a single diastereomer monophosphoramidate prodrug of an adenosine analog (Fig. 1). Remdesivir has broad-spectrum activity against coronaviruses (SARS-CoV-2, SARS-CoV, and MERS-CoV) (7, 8), filoviruses (Ebola virus [EBOV] and Marburg virus) (9, 10), and paramyxoviruses (respiratory syncytial virus [RSV], Nipah virus, and Hendra virus) (11, 12). RDV the first FDA-approved antiviral for the treatment of COVID-19. . Its safety has been evaluated in two Phase I studies in healthy volunteers (13) and multiple Phase III studies in Ebola-infected (14) and SARS-CoV-2-infected patients (15-17). These studies demonstrated RDV as an effective antviral agent with a favorable benift/risk profile and RDV addresses a serious unmet medical need to the treatment of patients with COVID-19. It is intracellularly metabolized to its active triphosphate form (GS-443902, Fig. 1), which in turn acts as a potent and selective inhibitor of multiple viral RNA polymerases. Additional metabolites are formed both intracellularly and systemically in plasma including alanine metabolite (GS-704277), parent nucleoside (GS-441524), and mono-and di-phosphate metabolites. To assess the

potential off-target toxicity of RDV, the drug and its metabolites including parent nucleoside analog (GS-441524), intermediate metabolite MetX (GS-704277), and active triphosphate metabolite (GS-443902) (Fig. 1) were characterized in a broad panel of cellular and biochemical assays.

RESULTS

Evaluation of cytotoxicity

Cytotoxicity in human cell lines and primary cells. The cytotoxicity of RDV and GS-441524 was tested in four immortalized human cell lines (laryngeal, hepatoma, prostate, and lymphoblastoid transformed cell lines) and in seven primary human cell types including primary human hepatocytes (PHH), primary renal proximal tubule epithelial cells (RPTECs), quiescent and stimulated human peripheral blood mononuclear cells (PBMCs), and human hematopoietic progenitor cells including erythroid, myeloid, and megakaryoid progenitors (Table 1). These cells were chosen for their reported high sensitivity to or potential organ toxicity associated with nucleoside/tide analogs (6). ATP level was used as an indication of cell viability. After 5-14 days of continuous exposure to RDV, the CC_{50} values ranged from 1.7 to > 20 μM, resulting in selectivity indices (SI, CC_{50}/EC_{50}) from >170 to 20,000, with respect to RDV anti-SARS-CoV-2 activity (EC_{50} of 9.9 nM in human airway epithelial cells [HAE]) (18). Among the four cell lines tested, the MT-4 cell line was the most sensitive towards RDV and GS-441524, consistent with reports using other nucleoside/tide analogues (5, 19). Among the seven primary cell types tested, PHH showed the lowest CC_{50} towards RDV, suggesting that PHHs are susceptible to RDV-mediated toxicity.

The parent nucleoside GS-441524 showed no cytotoxicity up to 100 μM in any of the cell lines tested, except in MT-4 (CC_{50} = 69 ± 26 μM). Among the primary human cells, GS-441524

showed no toxicity at the highest concentration tested (100 µM), except in the three human hematopoietic progenitor cells (CC_{50} = 9.6-13.9 µM after 11-14 days of exposure).

Effect on production of reactive oxygen species. Reactive oxygen species (ROS) including peroxides, superoxides, and hydroxyl radicals are natural byproducts of normal cell metabolism and have important roles in cell signaling and homeostasis. However, excessive production of ROS can be induced by drugs and may result in cellular damage and cell death (20). In this study, we evaluated the potential effects of RDV on ROS generation in HepG2 cells, a human hepatic cell line. After a 24-hour incubation, RDV-treated cells showed no significant increase in ROS levels at concentrations up to 50 µM, and a 60% increase at 100 µM (p = 0.042 compared with DMSO control) accompanied by a parallel 60% decrease in cell viability, indicating that ROS is unlikely to be the driver of cytoxicity (Figure 2). In comparison, the control compound menadione showed > 3-fold increase in ROS levels after a 30-minute incubation.

Evaluation of mitochondrial toxicity

Cytotoxicity under aerobic metabolic conditions. Some nucleoside analogues have the potential to affect mitochondrial functions via diverse mechanisms. One approach to assess mitochondrial function is a comparison of effects on cell viability in the presence of glucose-favoring glycolysis (ie, anaerobic metabolism) and galactose-favoring oxidative phosphorylation (ie, aerobic metabolism). The latter condition may sensitize cells to compounds affecting mitochondrial functions (21). However, the predictability of this assay has not been validated for nucleoside/tide analogues (6). Using intracellular ATP quantification as a readout for cell viability, the effects of glucose and galactose on the cytotoxicity of RDV and GS-441524 were assessed in the HepG2 hepatoma cell line, which was previously identified as a suitable model for testing compounds under aerobic conditions (Table 2) (21). In addition, a similar study was

done using the PC-3 prostate-derived cell line, a model of rapidly proliferating cells. The CC_{50} values of RDV in HepG2 cells were 3.7 and 11.1 μM in the presence of glucose and galactose, respectively (Table 2), indicating that aerobic conditions did not enhance the cytotoxicity of RDV. In contrast, aerobic conditions in PC-3 cells enhanced RDV cytotoxicity by 6-fold (CC_{50} = 1.4 in galactose culture vs 8.9 μM in glucose culture). The divergent results from HepG2 and PC-3 cells suggest that the observed effects are cell line-dependent.

The parent nucleoside GS-441524 did not show any cytotoxicity in either PC-3 or HepG2 cells at the highest concentrations tested (100 μM), irrespective of the metabolic conditions (Table 2). Puromycin, used as general cytotoxic control, exhibited similar cytotoxicity in both cell types in the presence of glucose or galactose. The lack of a known nucleoside mitotoxin prevented us from using one as a positive control in this study.

Effect on mitochondrial DNA. The potential effect of RDV and GS-441524 on mitochondrial DNA (mtDNA) was assessed in vitro by quantitative real-time polymerase chain reaction (qPCR) analysis following continual treatment of HepG2 cells for 10 days. Dideoxycytidine (ddC), a known inhibitor of mtDNA replication, was used as a positive control. HepG2 cells treated with RDV showed a lack of dose response indicating the lack of a specific effect on mtDNA synthesis. The effect of the parent nucleoside GS-441524 on mtDNA content was overall minimal (Table S1).

Effect on mitochondrial protein synthesis. The effect of RDV and GS-441524 on mitochondrial protein synthesis was assessed following a 5-day incubation with PC-3 cells. This particular cell model was chosen for its prior successful use in the studies of mitochondrial toxins (6). The selective effect of a compound on mitochondrial protein synthesis was determined by quantification of the level of cytochrome oxidase subunit 1 (COX-1; encoded by mtDNA) and

127 succinate dehydrogenase A (SDH-A; encoded by nuclear DNA) (5, 19). RDV affected the levels
128 of COX-1 and SDH-A to a similar extent, with CC_{50} values of 8.9 and 8.6 μM, respectively
129 (Table 3, Figure 3). These effects manifested in the same range of concentrations as the
130 cytotoxicity measured by cellular ATP levels, indicating a lack of any selective effect of RDV on
131 mitochondrial protein synthesis. GS-441524 showed no effect on protein synthesis up to the
132 highest concentration tested (100 μM) (Table 3, Figure 3). Chloramphenicol was used as a
133 positive control, and its specific effect on mitochondrial protein synthesis was consistent with
134 published data (5, 19).
135 *Effect on mitochondrial respiration*. RDV and GS-441524 were further evaluated for their
136 effects on mitochondrial spare respiratory capacity in the human cell-lines PC-3 and HepG2 and
137 the primary cells PHH and RPTEC by measuring the rate of oxygen consumption (OCR) using a
138 Seahorse Extracellular Flux Analyzer (5, 22-24). Overall, there was a lack of a specific effect on
139 cellular respiration among the four cellular systems tested. The cellular respiration of RDV-treated
140 cells decreased in parallel with decreases in ATP level and total DNA level in HepG2, PHH, and
141 RPTEC, indicating a lack of specific inhibition of cellular respiration (Table 4, Figure 4). The
142 most profound effect of RDV on spare mitochondrial respiratory capacity was seen in PC-3 cells,
143 where RDV inhibited mitochondrial spare respiratory capacity with a
144 CC_{50} value (CC_{50} = 2.5 μM) lower than those for the inhibition of ATP level and total DNA
145 (CC_{50} = 24.0 and 12.5 μM, respectively). Among all four cell systems, GS-441524 showed no
146 effect on mitochondrial respiration at the highest concentration tested (100 μM) (Table 4, Figure
147 S1). In contrast, the positive control chloramphenicol showed specific inhibition of
148 mitochondrial respiration and minimal impact on ATP level and total DNA (Figure S2).

GS-704277, a major intermediate RDV metabolite was evaluated for its effect on mitochondrial spare respiratory capacity, ATP levels, and total DNA in PHH after both an acute 4-hour treatment and a chronic 3-day incubation, the default condition in the experiments described in the previous paragraph. After the 4-hour incubation, RDV-treated PHH showed parallel decreases in mitochondrial spare respiratory capacity (21%-27%) and cellular ATP levels (17%-31%), indicating lack of mitochondria-specific toxicity (Figure S3). After a 3-day treatment with RDV, PHH showed parallel decreases in mitochondrial spare respiratory capacity, ATP levels, and total DNA, with CC_{50} values of 7.6, 7.8, and 13.4 μM, respectively, indicating general toxicity instead of specific mitochondrial toxicity (Table 4, Figure 4). Neither of the two major systemic metabolites of RDV, GS-704277 nor GS-441524, exhibited any effects on mitochondrial spare respiratory capacity, ATP levels, or total DNA at the highest concentration tested (100 μM) after either a 4-hour or a 3-day treatment (Table 4, Figure S1, S3-S4).

Profiling of the active triphosphate metabolites

Formation of active 5'-triphosphate metabolite GS-443902 in cells

Formation of GS-443902 from RDV and GS-441524 was measured in HEp-2, PC-3, and PHH cells after 24-hour continuous incubation of the compounds. As shown in Figure 5 and Table S2, RDV formed 43 ± 6, 153 ± 16, and 45 ± 23 pmole/10^6 cells of GS-443902 in HEp-2, PC-3, and PHH cells, respectively. In contrast, GS-441524 formed 7.8-23-fold less active metabolites in these cells, at 5.5 ± 1.1, 6.6 ± 4.9 and 1.9 ± 1.6 pmole/10^6 cells, respectively.

Interaction with host RNA and DNA polymerases. The active triphosphate metabolite GS-443902 was tested in multiple biochemical assays to assess its interaction with key human DNA and RNA polymerases. The enzymatic activities of human DNA polymerases α and β, as well as that of RNA polymerase II, were unaffected by GS-443902 up to 200 μM, the highest concentration

tested (Table 5). In addition, GS-443902 was tested for its incorporation into nucleic acids by host mitochondrial DNA and RNA polymerases using a single nucleotide incorporation assay. GS-443902 was a poor substrate of mtDNA polymerase γ with no detectable incorporation when tested under the supratherapeutic concentration of 50 μM [vs C_{max} of 6 μM at 150 mg dose in clinic (13). It was also a poor substrate for POLRMT, with a rate of incorporation equal to 5.8% relative to ATP when tested under supratherapeutic concentration of 500 μM (Table 6). This result contrasts with the significantly higher incorporation rates of 92% and 112%, for the triphosphate forms of BMS-986094 and balapiravir, respectively, two anti-HCV nucleosides associated with clinical toxicity (5). Together, these data further support the hypothesis about low potential of RDV to induce mitochondrial toxicity.

Molecular target screen

In addition to the aforementioned known off-targets of nucleoside/tide anlaogues, the RDV-containing diastereomeric mixture GS-466547 and the parent nucleoside GS-441524 were screened against a panel of 87 targets consisting of receptors, ion channels, transporters, and enzymes involved in a wide range of biological processes (Table S3). At 10 μM, none of the compounds showed detectable interaction with any of the 87 targets tested.

DISCUSSION

RDV is a single diastereomer monophosphoramidate prodrug of an adenosine analog with broad-spectrum antiviral activity. Using a prodrug as a way to deliver an active molecule may potentially result in intracellular accumulation of the less cell-permeable metabolites depending on the activity of the enzymes participating in the metabolism of a particular drug and its conversion into the active form. Therefore, detailed examination of the functional consequences of the exposure to high doses is critical for the evaluation of the drug safety.

This study presents a detailed characterization of RDV in a panel of in vitro cytotoxicity and off-target screening assays, undertaken to identify potential safety and toxicitiy liabilities. In this report, the general cytoxicity of RDV measured as CC_{50} following a 5- to 14-days of continuous exposure to the drug ranged from 1.7 μM to >20 μM in selected human cell lines and primary human cells. It is worth noting that the RDV exposure in these cell culture studies was significantly higher than the systemic exposure of RDV for the repeated dosing of 150 mg in humans (plasma C_{max} = 2720 ng/mL = 4.5 μM, $t_{1/2}$ = 1.11 hr) (13). The parent nucleoside and major systemic metabolite GS-441524 showed less cytotoxicity than RDV. The differences in toxicity between these two compounds are likely due to the significantly lower active triphosphate in GS-441524-treated cells than in RDV-treated cells, as observed in this study as well as other studies (18). However, RDV and GS-441524 showed similar levels of toxicity in three hematopoietic progenitor cells. Cell-dependent cytotoxicity has been widely observed for nucleoside/tide analogs, which can be affected by the duration of compound exposure (5-day versus 14-day), compound permeability, intracellular activation, and differential cellular characteristics including replication rate and bioenergetic status (5).

Among the primary cells tested, PHH showed the highest sensitivity to RDV, possibly due to high cellular permeability and efficient intracellular metabolism leading to high levels of the triphosphate metabolite. This observation could shed light on the liver enzyme elevations observed in healthy volunteers treated with repeated doses of RDV (13). In contrast, the two main RDV metabolites in plasma, GS-704277 and GS-441524, are unlikely to contribute to clinical liver toxicity, due to their low permeability and ineffective intracellular metabolism or limited systemic exposure. In two Phase I studies, RDV was evaluated in healthy subjects with single-dose IV administration (across the dose range of 3-225 mg; N=78 RDV and 18 placebo)

or multiple doses of 150 mg once daily for 7 or 14 days (N=16 RDV and 8 placebo) (13). Overall, RDV was well tolerated in both studies, and all adverse events were Grade 1 or 2 in severity. In the repeat-dose study, reversible, treatment-emergent Grade 1 or 2 alanine aminotransferase (ALT) (50% RDV, 13% placebo) and aspartate aminotransferase (AST) (44% RDV, 0% placebo) elevations were observed . Because transaminase elevations have been observed in patients with COVID-19 (25), the potential of RDV to exacerbate transaminase elevations in patients with COVID-19 may be difficult to discern. This has been supported by multiple RDV clinical trials. First, an open-label study (N=397 RDV) without a placebo control arm showed little difference between 5-day and 10-day RDV treatment durations for adverse events of elevations in ALT (6% and 8%, respectively) or AST (5% and 7%, respectively) (15). Second, in a study of RDV in 584 hospitalized patients with moderate COVID-19, patients were randomized at a 1:1:1 ratio to receive 10-day RDV, 5-day RDV, or standard of care treatment; there was little difference between the three arms for adverse events of elevations in ALT (32%, 34%, and 39%, respectively) or AST (32%, 32%, and 33%, respectively); Grade 3 or 4 adverse events were reported less frequently for patients who received RDV (ALT: 3%, 2%, and 8%, respectively; AST: 1%, 3%, and 6%, respectively) (17). Finally, in the recently completed double-blind study of RDV versus placebo in 1062 hospitalized patients with COVID-19, adverse events of increased amino transferase levels, including ALT, AST, or both were reported in 6% of subjects treated with RDV for up to 10 days compared with 11% of subjects in the placebo group, indicating lack of specific drug-induced liver enzyme elevation (16). All of these reports consistently support minimal contribution of RDV to transaminase elevations in patients with COVID-19.

To understand whether the cytotoxicity is associated with mitochondrial toxicity, we measured the effects of RDV on mitochondrial DNA content, protein level, and cellular respiration. In HepG2 cells, RDV showed a lack of a specific dose-dependent effect on mtDNA synthesis. Similarly, RDV did not show specific inhibition of a mitochondria DNA-coded protein (CC_{50} of 8.9 μM) over a nuclear DNA-coded protein (CC_{50} of 8.6 μM) in PC-3 cells. Additional biochemical assays showed that the active triphosphate metabolite GS-443902 was a poor substrate for mitochondria DNA and RNA polymerases even when tested at supra-physiological concentrations of 50 and 500 μM, respectively. A recent paper reported the effects of RDV on cellular toxicity through a transcriptomic analysis, and reported effects of RDV on mitochondrial function (31). However, it is not clear whether the results were due to specific mitochondrial toxicity or general cellular toxicity. In addition, the relation between specific gene expression and mitochondrial toxicity has not been fully validated.

Taken together, we conclude that RDV has low potential for the off-target toxicities described for other nucleoside analogs including mitochondrial toxicity. Furthermore, neither RDV nor its systemic metabolites induced ROS formation *in vitro* or interacted with any of the 87 targets in the molecular screen. Consistent with the clinical observations of drug-related elevations of liver transaminases following multiple doses of RDV, primary hepatocytes showed high *in vitro* susceptibility to RDV. In clinical settings of COVID-19 treatment in hospitalized patients, the risk associated with possible RDV-related liver enzyme elevations is substantially lower compared to its established benefits in hospitalized COVID-19 patients.

MATERIALS AND METHODS

Reagents. Remdesivir (RDV, GS-5734), its parent nucleoside GS-441524, metabolite intermediate GS-704277 (Met X), and 5'-triphosphorylated metabolite GS-443902 were

263 synthesized by Gilead Sciences, Inc (Foster City, CA). Nucleotide triphosphates (TP) used as
264 positive controls including decitabine-TP (5-aza-2'-deoxyCTP), 2'CMe-GTP (active metabolite
265 of BMS-986094), 4'-CN-CTP (active metabolite of Balapiravir/RG1626) were synthesized by
266 Gilead Sciences, Inc. 3'-deoxy ATP, 3'-deoxy GTP, 3'-deoxy CTP, 3'-deoxy UTP were
267 purchased from TriLink BioTechnologies (San Diego, CA). Control compounds for CC_{50} assays
268 such as dideoxycytidine (ddC), puromycin, chloramphenicol, menadione, aphidicolin, and α-
269 amanitin were purchased from Sigma-Aldrich (St. Louis, MO). All radioactively labeled
270 nucleoside triphosphates (NTPs) were purchased from PerkinElmer (Shelton, CT).
271 **Cell lines and primary cells.** The following cell lines were obtained from the indicated sources:
272 HEp-2 (laryngeal carcinoma; ATCC), HepG2 (hepatoblastoma; ATCC), PC-3 (prostate
273 metastatic carcinoma; ATCC), and MT-4 [human T-cell leukemia virus 1 (HTLV-1)-transformed
274 human T lymphoblastoid cells; NIH AIDS Research and Reference Reagent Program].
275 Cryopreserved primary human RPTEC were obtained from LifeLine Cell Technology
276 (Frederick, MD) and isolated from the tissue of human kidney. Freshly isolated PHH were from
277 Bioreclamation IVT (Westbury, NY) or Life Technologies (Carlsbad, CA). Human PBMC were
278 isolated from human buffy coats which were obtained from healthy volunteers (Stanford Blood
279 Bank, Palo Alto, CA).
280 **Cell culture**. The HepG2 galactose-adapted cell line was established by culturing HepG2 cells in
281 glucose-free DMEM (Gibco, Carlsbad, CA) supplemented with 10% FBS, 100 units/mL
282 penicillin, 100 units/mL streptomycin, 2 mM glutamine, 1 mM sodium pyruvate, and 10 mM
283 galactose for 3 weeks prior using in the assays. The PC-3 galactose-adapted cell line was
284 established by culturing PC-3 cells in glucose-free Kaighn's F12 media supplemented with 10%
285 FBS, 100 units/mL penicillin, 100 units/mL streptomycin, and 7 mM galactose for 3 weeks prior

using in the assays. The cells were passaged twice per week to maintain sub-confluent densities. The cell culture procedures of RPTEC and PHH were following vendor's recomendation. PBMCs were isolated from human buffy coats using standard Ficoll separation and stimulated as described elsewhere (19) and were tested at both quiescent and stimulated stages. The stimulated PBMCs were obtained from quiescent PBMCs stimulated with 10 units per mL of recombinant human interleukin 2 (hIL-2) and 1 µg per mL phytohemagglutinin P (PHA-P) for 48 hrs prior to drug treatment. Normal human primary bone marrow (BM) light-density cells were from three different lots obtained from AllCells (Emeryville, CA) or Lonza (Walkersville, MD). All primary human cells were cultured according to the manufacturer's protocols. All cells were cultured at 37 °C in a 5% CO_2 incubator with 90% humidity unless noted otherwise.

General cytotoxicity and cell viability.

Cytotoxicity in human cell-lines, PHH, RPTEC, and PBMC. Cells were treated with compounds for 4 hours to 14 days depending on assay type. Culture of freshly isolated PHH cells required fresh medium every 24-48 hours so compounds and medium were refreshed on Day 0, 2, and 4 or Day 0, 1, 3 during the 5-day culture. After the incubation period, cell viability was measured by the addition of CellTiter Glo viability reagents (Promega, Madison, WI). The luminescence signal was quantified on an EnVision or Victor™ luminescence plate reader (Perkin-Elmer, Waltham, MA) after the cells were incubated with the reagents for 10 min at room temperature. The compound concentration that caused a 50% decrease in the luminescence signal (CC_{50}), a measure of toxicity, was calculated by nonlinear regression using a sigmoidal dose-response (variable slope) equation as described in Data Analysis Section.

Cytotoxicity in human hematopoietic progenitor cells. The effects of the compounds on the proliferation of human erythroid, myeloid, and megakaryoid progenitors were tested in

MethoCult84434, a methylcellulose-based colony assay conducted by StemCell Technology (Vancouver, Canada) (26). After 11-14-day culture, the hematopoietic progenitor colonies (CFU-E, BFU-E, CFU-GM, and CFU-GEMM [E, erythroid; BFU, burstforming unit; GM, granulocyte/macrophage; GEMM, multilineage progenitors]) were enumerated and the CC_{50} values were calculated as described in Data Analysis section.

Detection of intracellular reactive oxygen species (ROS) level. HepG2 cells were seeded at densities of 12×10^3 cells per well in 96-well plates with a final volume of 160 µL per well. The cells were incubated overnight at 37 ºC in a 5% CO_2 and 90% humidity incubator with EMEM medium supplemented with 10% FBS (HyClone, Logan, UT), 100 units/mL penicillin and 100 µg/mL streptomycin (P/S) (Gibco, Carlsbad, CA). On the next day (Day 1), cells in 42 out of the 96-well plate were treated with RDV for 24 hours. RDV was added to the cell culture plate directly using an HP D300 Dispenser (Hewlett-Packard, Palo Alto, CA) with a starting concentration of 100 µM, with two-fold dilutions to generate a total of 6 concentration points with six replicates for each concentration and 6 wells without RDV as negative controls. On the day of the ROS assay (Day 2), 18 wells out of the remaing untreated 54 wells on the orignial 96-well plate were incubated with either 0 µM, 100 µM, or 200 µM menadione (Sigma-Aldrich, St. Louis, MO) for 30 minutes, with 6 replicates for each treatment. A mixture of CellROX Deep Red reagent and NucBlue Hoechst 33342 was added to the cells treated with menadione, RDV, and DMSO. The final DMSO concentration was 0.5% in all wells. The cell culture plate was incubated in a 37 ºC incubator for 30 minutes. The cell culture plate was then washed 3-4 times with 200 µL/well of 1× PBS buffer without Ca^{2+} and Mg^{2+} (Corning, Corning, New York), followed by a final addition of 100 µL 1× PBS in each well. The assay plate was scanned using a Cellomics™ ARRAYSCAN VTI (Thermo Fisher Scientific, Waltham, MA) High Content

Screening Instrument with two channels. One channel measured the intensity of CellROX Deep Red using excitation/emission at 640/665 nm, while the other channel measured the signal intensity from NucBlue/Hoechst 3334 using excitation/emission at 360/460 nm. The ATP level was measured using CellTiter Glo viability reagents (Promega, Madison, WI) in cells treated with RDV for 24 hours in a parallel experiment.

Data analysis.

Data analysis of Calculation of CC_{50} and IC_{50} values. The CC_{50} values were defined as the concentration causing 50% decrease in cell viability, DNA level, protein level, or spare respiratory capacity in comparison to the DMSO control. The IC_{50} values were defined as the concentration causing 50% decrease in product formation in the biochemical assays. Data were analyzed using GraphPad Prism 8.0 (La Jolla, CA). The CC_{50} and IC_{50} values were calculated by non-linear regression analysis using sigmoidal dose-response (variable slope) equation (four parameters logistic equation):

$Y = 100/(1+10^{((LogCC_{50}-X)*Hillslope)})$

$Y = 100/(1+10^{((LogIC_{50}-X)*Hillslope)})$

where X is the log of the concentration of the test compound, Y is the response. The CC_{50} or IC_{50} values were calculated as an average of three or more independent experiments.

*Data analysis of measuring mitochondrial DNA***.** The relative amount of mitochondrial DNA (mtDNA) in treated samples was determined using a relative quantification method based upon the $2^{-\Delta\Delta C}{}_T$ formula (27). The amount of mtDNA in compound treated samples relative to the DMSO treated controls (% mtDNA) was calculated based upon the following formula:

$\%\ \text{mtDNA} = 100 \times 2^{-\Delta\Delta C}{}_T$

$\Delta\Delta C_T = \Delta C_{T,\ \text{treated}} - \Delta C_{T,\ \text{control}}$

$\Delta C_{T,\ treated} = (C_T,\ cyt\ b - C_T,\ \beta\text{-actin})_{treated}$

$\Delta C_{T,\ control} = (C_T,\ cyt\ b - C_T,\ \beta\text{-actin})_{control}$

C_T, cyt b and C_T, β-actin represent the cycle threshold values for the amplification of cytochrome b and β-actin, respectively, as determined by the computational analysis of amplification curves using the ABI Prism software. The final results are presented as the mean % mtDNA ± SD from 2 independent experiments, each performed in triplicate. The $2^{-\Delta\Delta C_T}$ method was validated for cytochrome b and β-actin genes by determining the ΔC_T values for amplification reactions containing various amounts of total cellular DNA. Minimal differences were observed in the ΔC_T values in samples containing 5 to 40 ng of total cellular DNA; indicating that neither the amplification nor detection efficiencies of cytochrome b and β-actin were affected by the amount of DNA template within the dilution range relevant for the quantitative analysis performed (Table S5).

Measuring mitochondrial DNA. mtDNA was generated by real-time PCR from total DNA isolated from HepG2 cells using the QIAamp DNA Mini Kit (Qiagen, Valencia, CA) according to the manufacturer's protocol. Real-time PCR reactions were performed using TaqMan universal mastermix (Applied Biosystems, Foster City, CA) in an ABI Prism 7900HT Fast Real-Time PCR System (Applied Biosystems). Quantification of mtDNA was achieved by amplification of a fragment of the mitochondrial specific cytochrome b gene using the primers and probe. The oligonucleotide sequence of the primer and probe was used as cytochrome b forward CCTTCCACCCTTACTACACAATCAA, cytochrome b reverse GGTCTGGTGAGAATAGTGTTAATGTCA, and cytochrome b FAM-ACGCCCTCGGCTTAC-BHQ1. Chromosomal DNA was quantified by the amplification of a fragment of the β-actin gene using a β-actin Assay-on-Demand kit (Applied Biosystems).

Amplification reactions for the quantification of mitochondrial and chromosomal DNA were performed independently using approximately. HepG2 cell culture and compounds' treatment was based on a previously published method (19, 28).

Mitochondrial protein synthesis assay. PC-3 cells were treated with the compounds for 5 days and analyzed with the MitoTox MitoBiogenesis in-cell enzyme-linked immunosorbent assay (ELISA) kit (MitoSciences/Abcam, Eugene, Oregon) as described previously (5, 19). The assay uses quantitative immunocytochemistry to measure the protein levels of nuclear DNA-encoded succinate dehydrogenase (SDH-A; Complex II) and mitochondrial DNA-encoded cytochrome c oxidase (COX-1; Complex IV) in cultured cells.

Mitochondrial respiration in cell lines and primary cells. Mitochondrial respiration was monitored by measuring the rate of oxygen consumption (OCR) of the cells after 4-hour or 3-day treatments with the compounds, using a Seahorse extracellular flux analyzer (XFe-96) based on published protocols (5, 22-24) and modified from a previously published method (5). The OCR signals were normalized by cell numbers using DNA content which method was based on a previously published method (5). The optimized cell seeding of PC-3, HepG2, RPTEC, and PHH were seeded at densities of 5×10^3, 5×10^3, 7.5×10^3, and 25×10^3 cells per well, respectively, in XF 96-well plates (Seahorse Bioscience, North Billerica, MA) with a final volume of 160 µL per well. The cells were incubated with compounds for 3 days except PHH which received compound treatment for 4 hours or 3 days. Compounds were added to the assay plate directly using an HP D300 Dispenser (Hewlett-Packard, Palo Alto, CA) with 2-fold dilutions to give a total of 9 concentration points with six replicates. On the day of the assay, the cell culture medium was replaced with XF assay medium (pH 7.4) containing 10 mM glucose and 1 mM freshly prepared pyruvate. The mitochondrial respiration was monitored by measuring the rate of

oxygen consumption (OCR) on a Seahorse Extracellular Flux (XFe-96) Analyzer based on published protocols (5, 22-24). All concentrations were final after mixing unless noted otherwise. Multiple parameters were measured after the sequential injection of the ATP synthase inhibitor oligomycin (2 µM for all cell models), the uncoupler FCCP (0.25 µM for PC-3, 0.5 µM for HepG2 and PHH, 1.5 µM for RPTEC), and a mixture of the mitochondrial Complex I inhibitor rotenone and the Complex III inhibitor antimycin A (0.5 µM of each for all cell models) (Mito Stress Test Kit, Seahorse Biosciences) (22-24). The spare respiratory capacity was obtained by subtracting the rate of basal respiration from the rate of maximal respiration and normalized to the cell number obtained from DNA level measurements. The data reported for each treatment are the average of the results from six replicates. The methods of detection of measuring ATP level in parallel experiments was based on a previously published method (5).

Biochemical assays.

DNA and RNA templates and primers. The DNA polymerase alpha and gamma inhibition assays utilized a 78-mer DNA template and a 19-mer DNA primer: D78 5'-ACACATGATACTACGAATTTTATGCTTCCAATGCCTTACAGTTCTCTAGCGGTGGCG CCCGAACA GGGACCTGAAAGC-3' and D19 5'-GTCCCTGTTCGGGCGCCAC-3' were purchased from Integrated DNA Technologies (Coralville, IA). Activated fish sperm DNA was purchased from USB/Affymetrix (Santa Clara, CA) and used as a template for the DNA polymerase beta inhibition assay. The DNA template used in the RNA POLII inhibition assay was a 1,188 bp restriction fragment containing the cytomegalovirus (CMV) immediate early promoter (Promega, Madison, WI). For single nucleotide incorporation, a DNA 19-mer primer and a DNA 36-mer template were used for POL γ–catalyzed reactions whereas a RNA 12-mer primer and a DNA 18-mer template were used for POLRMT-catalyzed reactions (Table S6). All

primers were 5'-labeled with ^{32}P-γ-ATP (3000 Ci/mmol) and T4-kinase (New England Biolabs, Ipswich, MA). In brief, a mixture containing 100 μM of primer, 0.4 unit/μL T4-kinase, 1× T4-kinase reaction buffer, and 4 μCi/μL (0.4 μM) ^{32}P-γ-ATP was incubated at 37 °C for 60-120 min, followed by heat-inactivation at 65 °C for 5-10 minute. 5'-32P-R12/D18 were annealed at a 1:1.1 molar ratio at a concentration of 10 μM in a solution of 10 mM Tris-HCl (pH 8.0) and 0.1 mM EDTA using a thermocycler where samples were heated for 1 minute at 90 °C and cooled to 10 °C at a rate of 5 °C per minute. 5'-^{32}P-D18/D36 were annealed at a 1:1.1 molar ratio at 10 μM in a solution containing 10 mM Tris-HCl (pH 8.0) and 0.1 mM EDTA. Samples were heated at 90 °C for 10 minutes, cooled at 50 °C for 30 minutes and placed on ice for 10 minutes.

Enzymatic inhibition assays. Human DNA polymerase alpha, isolated from HeLa cell extracts, was from CHIMERx (Madison, WI). Recombinant human DNA polymerase beta, expressed in *E. coli*, was a gift from Zucai Suo at The Ohio State University. Recombinant human DNA polymerase gamma (including both the large subunit and the small subunit) was cloned, expressed, and purified from insect cells by Gilead Sciences (Foster City, CA) (19). RNA PolII was purchased as part of the HeLaScribe nuclear extract in vitro transcription system kit from Promega (Madison, WI). The recombinant human POLRMT and the transcription factors mitochondrial transcription factor A (mtTFA) and B2 (mtTFB2) were purchased from Enzymax (Lexington, KY). The inhibition of DNA polymerases alpha, beta, and gamma, POLRMT, and PolII has been described previously in detail (4, 19, 29).

Single nucleotide incorporation assay by human mitochondrial DNA Pol γ. All concentrations were given as the final concentration. 1.2 nM DNA Pol γ large subunit and 3.4 nM Pol γ accessory subunit were preincubated on ice for 5 minutes and added to reaction mixture containing 50 mM Tris-HCl (pH 8.0), 2 mM DTT, 0.2 mg/mL BSA, 200 nM D19/D36 p/t and 10

mM $MgCl_2$. Reactions were heated for 37 °C and initiated by addition of 50 µM natural dNTP or analogs, plus 50 µM dGTP (for T or C template) or dCTP (for A or G template). At 0, 0.5, 2, 5, 10, 30, and 60 min, 10 µL of the reaction mixture was removed and quenched with10 µL of gel loading buffer containing 100 mM EDTA, 80% formamide, and 1% bromophenol blue, and heated for 65 °C for 5 minutes. The samples were run on a 20% polyacrylamide gel (8 M urea) and the gel was exposed to a phosphorimager screen. The substrate and the incorporation products, D19 and D20-28, were quantified using a Typhoon Trio Imager and Image Quant TL software.

Single nucleotide incorporation assay by human mitochondrial POLRMT. The assay was modified based on a published report (30). All concentrations are final concentration. A mixture of MTCN buffer (50 mM MES, 25 mM Tris-HCl, 25 mM CAPS, and 50 mM NaCl, pH 7.5), 200 nM 5'-^{32}P-R12/D18, 10 mM $MgCl_2$, 1 mM DTT, and 376 nM POLRMT (Enzymax, Lexington, KY) was pre-inclubated at 30 °C for 1 min. The reaction was started by addition of 500 µM natural NTP or NTP analogs. At 0.17, 0.5, 2, 5, 10, and 30 minutes, 3 µL of the reaction mixture was removed and quenched with10 µL of gel loading buffer containing 100 mM EDTA, 80% formamide, and 1% bromophenol blue, and heated for 65 °C for 5 minutes. The samples were run on a 20% polyacrylamide gel (8 M urea) and the gel was processed and analyzed in the same way as described above.

Molecular target screen of the RDV-containing diastereomeric mixture GS-466547 and parent nuc GS-441524

RDV-containing diastereometric mixture GS-466547 and parent nuc GS-441524 were tested at 10 µM in a SafetyScreen87 Panel (Eurofins Panlabs Taiwan, Ltd) (Table S3). Effects of

compounds were evaluated along with a known receptor ligand or substrate. Positive results were defined as > 50% inhibition of ligand binding.

Determination of GS-441524 and its Phosphorylated Metabolites in PC-3 and PHH.

HEp-2, PC-3, or PHH cells were seeded 0.44×10^6 or 0.88×10^6 cells/well in 12-well plate respectively. On the next day, HEp-2, PC-3, or PHH were treated with either 1 µM RDV or GS-441524, in duplicate, or 0.01% DMSO in eight replicates. After 24 hours treatment, cells were washed twice with ice-cold 0.9% NaCl then treated with 500 µL of dry ice-cold extraction buffer (0.1% potassium hydroxide and 67 mM ethylenediamine tetraacetic acid in 70% methanol, containing 0.5 µM chloro-adenosine triphosphate as internal standard). The above solution was vortexed for 5 minutes, then centrifuged at 20,000 x g for 10 minutes. Supernatant was transferred to clean 1.5 mL Eppendorf vials and loaded onto a centrifuging evaporator. Once dry, samples were reconstituted with 80 µL of 1 mM ammonium phosphate buffer (pH 7.0), and transferred to HPLC vials where a 10 µL injection was used for analysis by LC/MS/MS. Standard calibration curves for HEp-2, PC-3, or PHH were constructed based on pmol of compound per sample with known cell numbers in each sample. The standard curve was prepared by spiking an appropriate amount of GS-441524, GS-441524-MP, GS-441524-DP, and GS-443902 solution, prepared in water, into blank HEp-2, PC-3, or PHH matrix, with serial dilution to complete the calibration standard curve. Detailed HPLC and mass spectrometry parameters are provided in the Materials and Methods under Supplemental Materials.

Determination of cell volume

Measurements of the cell volume for various cell types were conducted using confocal microscope Leica SP8 (Leica Microsystems GmbH, Wetzlar, Germany) and image analysis software Imaris (Bitplane, Zürich, Switzerland). The intracellular space was labeled with a

fluorescent dye Calcein AM (1-10 µg/mL, ThermoFisher Scientific, Waltham, MA, USA), which loads into live cells with active esterases. The nuclei were labeled with DNA-binding dye Hoechst 33342 (16-32 µM, ThermoFisher Scientific, Waltham, MA, USA) to facilitate separation and correct counting of adjacent cells. The labeling was conducted by incubating the cells in a culture medium containing the dyes at 37 °C and 5% CO_2 for at least 15 min. The series of images (Z-stacks) were collected using 63x objective with numerical aperture of 1.4 at different focal planes to enable computational reconstruction of three-dimensional objects with complex shape and estimation of their volume. Calcein was excited with the white laser at 488 nm and the fluorescence signal was detected in the range of 498-600 nm using Leica HyD hybrid detector. The imaging was performed at 37 °C to avoid temperature-related changes in shape of the cells. The estimation of the cell volume was verified using the fluorescent beads of known diameter by comparison of the values obtained after calculations based on either the diameter or 3-D reconstruction. This revealed that only minor correction was needed to account for elongation of the point spread function in vertical direction for the objective with high (1.4) numerical aperture unlike for the objective with low (0.4) numerical aperture. In addition, the results of confocal imaging were confirmed using the cell counter (Cellometer K2, Nexcelom Bioscience, Lawrence, MA, USA) with imaging capabilities allowing for determining the diameter of the cells in suspension after trypsinization.

Statistical Analysis

The difference between compound-treated groups and DMSO-treated group were analyzed using ordinary one-way ANOVA (Sidak's multiple comparisons test) (GraphPad Prism 8.1) and a *p*-values less than 0.05 was defined as stastically significant.

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Figures and legends

Figure 1: Structures of RDV and major metabolites.

Figure 2: Effect of RDV on cellular ROS, ATP, and cell count after 24-hours of treatment in HepG2 cells. (A) Treatment of 3.1-50 µM of RDV showed no effect on ROS, while 100 µM of RDV caused a 60% increase in ROS ($p = 0.042$). The positive control menadione showed > 3-fold increase in ROS levels after a 30-min incubation. (B) A concentration-dependent cytotoxicity was observed during the 24-hour incubation of RDV, especially for concentrations ≥ 12.5 µM.

Figure 3: Effects of RDV and its parent nucleoside GS-441524 on mitochondrial protein synthesis after 5-days of treatment in PC-3 cells. The effects on COX-1 levels (● blue, solid lines), SDH-A (♦ green, solid lines), and ATP levels (■ red, solid lines) are shown as % of DMSO control. RDV showed non-selective inhibition of COX-1, SDH-A, and ATP levels while GS-441524 showed no effect up to 100 µM. The positive control chloramphenicol, a known mitochondrial toxin, specifically inhibited COX-1 synthesis.

Figure 4: Effect of RDV on mitochondrial respiration (spare respiratory capacity) (● blue, solid lines), ATP levels (■ red, solid lines), and total DNA (♦ green, solid lines) after a 3-day treatment in PC-3, HepG2, PHH, and RPTEC. The spare respiratory capacity was normalized by cell numbers. Overall, RDV showed simultaneous inhibition of mitochondrial respiration, ATP levels, and total DNA, except in PC-3 cells where a mitochondria-specific inhibition was observed.

Figure 5. Metabolism of RDV and GS-441524 in HEp-2, PC-3, and PHH cells. The active 5'-triphosphate levels were measured after 24-hr continuous incubation of each compound. RDV-

537 treated cells (open bars) formed 7.8-, 23-, and 23-fold higher triphosphate levels than GS-

538 441524-treated (filled bars) in HEp-2, PC-3, and PHH cells, respectively.

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541 **Tables**

542 **Table 1: *In vitro* cytotoxicity of RDV and GS-441524 in human cell lines and primary**

543 **human cells after 5-14 day treatment**

Cells		CC_{50} (µM)[a,b]		
		RDV (SI)[c]	GS-441524	Positive Control[d]
Cell lines	HEp-2	6.0 ± 1.5 (600)	> 100	0.53 ± 0.10
	HepG2	3.7 ± 0.2 (370)	> 100	0.73 ± 0.01
	PC-3	8.9 ± 1.6 (890)	> 100	0.52 ± 0.11
	MT-4	1.7 ± 0.4 (170)	69 ± 26	0.12 ± 0.03
Primary cells	PHH	2.5 ± 0.6 (250)	> 100	1.60 ± 0.01
	RPTEC	12.9 ± 6.2 (12,900)	> 100	0.85 ± 0.01
	Quiescent PBMC	> 20 (>20,000)	> 100	5.05 ± 0.01
	Stimulated PBMC	14.8 ± 5.8 (14,800)	> 100	1.10 ± 0.01
	Erythroid progenitors	8.5 ± 1.9 (850)	13.9 ± 1.3	3.2 ± 1.6
	Myeloid progenitors	5.1 ± 2.3 (510)	11.7 ± 9.6[e]	2.2 ± 0.6
	Megakaryoid progenitors	4.9 ± 2.5 (490)	9.6 ± 2.4	2.3 ± 1.7

[a] All CC_{50} values represent the average ± SD of three or more independent experiments. Cells from three different donors were tested in the primary cell assays. The compounds were refreshed every other day during the 5-day PHH study.

[b] Treament duration: all studies are 5 days except studies for the three human hematopoietic progenitor cells where a 11- to 14-day treatment was used.

[c] Selectivity Index (SI) = CC_{50}/EC_{50}, where the an EC_{50} value of 10 nM against SARS-CoV-2 was used (18).

[d] Positive control: puromycin was used in all assays except the three human hematopoietic progenitor cells where 5-fluorouracil was used as a positive control. CC_{50} values of control compounds are consistent with historical values.

[e] The myeloid CC_{50} values for GS-441524 tested against cells from three different donors were 6.37, 22.70, and 5.93 µM, respectively.

556 **Table 2: *In vitro* cytotoxicity of RDV and GS-441524 under anaerobic and aerobic**

557 **metabolic conditions after 5-day treatment in HepG2 and PC-3 cells**

	5-day CC_{50} (µM)[a]			
	HepG2 Cells		PC-3 Cells	
Compound	**Anaerobic (Glucose)**	**Aerobic (Galactose)**	**Anaerobic (Glucose)**	**Aerobic (Galactose)**
RDV	3.7 ± 0.2	11.1 ± 1.2	8.9 ± 1.6	1.4 ± 0.1
GS-441524	> 100	> 100	> 100	> 100
Puromycin	0.73 ± 0.01	0.96 ± 0.13	0.52 ± 0.11	0.48 ± 0.01

558 [a] All CC_{50} values represent average ± SD of three or more independent experiments.

559

560 **Table 3: *In vitro* effect of RDV and GS-441524 on mitochondrial proteosynthesis after 5-**

561 **day treatment in PC-3**

	Mitochondrial and Cellular Protein Synthesis 5-day CC_{50} (µM)[a]		
Compounds	**COX-1**	**SDH-A**	**Cellular ATP**
RDV	8.9 ± 1.1	8.6 ± 1.3	11.3 ± 3.3
GS-441524	> 100	> 100	> 100
Chloramphenicol (positive control)	2.6 ± 0.6	> 25	14.1 ± 3.6

562 [a] CC_{50} values represent average ± SD of three or more independent experiments.

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565 **Table 4: *In vitro* effect of RDV and its metabolites GS-704277 and GS-441524 on**

566 **mitochondrial respiration after 3-day treatment in PC-3, HepG2, PHH, and RPTECs**

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		3-day CC_{50} (µM)[a]		
Compounds	**Cell Model**	**Spare Respiration**	**Total DNA Content**	**Cellular ATP**
RDV	PC-3	2.5 ± 0.1	12.5 ± 0.7	24.0 ± 1.4
	HepG2	10.6 ± 0.1	6.3 ± 0.9	7.9 ± 0.1
	PHH	7.6 ± 1.9	13.4 ± 1.7	7.8 ± 2.2
	RPTECs	7.3 ± 2.7	14.3 ± 3.3	16.9 ± 4.1
GS-441524	PC-3	> 100	> 100	> 100
	HepG2	> 100	> 100	> 100
	PHH	> 100	> 100	> 100
	RPTECs	> 100	> 100	> 100
GS-704277	PHH	> 100	> 100	> 100
Control chloramphenical	PC-3	4.8 ± 1.3	> 50	> 50
Control phenformin	PHH	1.9 ± 0.5	22.1 ± 1.9	9.7 ± 4.5

568 [a] CC_{50} values represent average ± SD from three or more independent experiments.
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572 **Table 5: Inhibition of host DNA and RNA polymerases by the active triphosphate**

573 **metabolite GS-443902**

	IC_{50} (μM)[a]				
Compound	**DNA Pol α**	**DNA Pol β**	**DNA Pol γ**	**RNA Pol II**	**POLRMT Pol**
GS-443902	> 200	> 200	> 200	> 200	> 200
Positive Control	Aphidicolin 4.7 ± 3.3	3′dTTP 1.9 ± 0.8	3′dTTP 1.2 ± 0.6	α-amanitin 0.0035 ± 0.0015	3′deoxy GTP 4.2 ± 1.4

574 [a] IC_{50} values represent average ± SD from three independent experiments.

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578 **Table 6: Relative rate of incorporation of the active triphosphate metabolite GS-443902 by**

579 **human mitochondrial DNA and RNA polymerases**

		Rate of Incorporation (% of natural dNTP or NTP)[a]	
Clinical Compounds	**Nucleotide Triphosphate**	**DNA Polymerase γ**	**mtRNA Polymerase**
RDV	GS-443902	0%	5.8% ± 1.4%
Decitabine	5-aza-2'-dCTP	79% ± 8%	ND
BMS-986094	2'CMe-GTP	ND	92% ± 33%
Balapiravir/RG1626	4'CN-CTP	ND	112% ± 10%

580 [a] The rate of single nucleotide incorporation was measured in the presence of 50 μM nucleotide
581 analog for DNA Pol γ and 500 μM for POLRMT and expressed as % of the natural dNTP or
582 NTP incorporation at the same concentration. Data are presented as average ± SD from three or
583 more independent experiments.

584

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