SUPPLEMENTARY MATERIALS

Clinical efficacy of ONC201 in H3K27M-mutant diffuse midline gliomas is driven by disruption of integrated metabolic and epigenetic pathways

Supplementary Data

Data S1. Protocol for NCT03416530, ONC201-014: ONC201 in Newly Diagnosed Diffuse Intrinsic Pontine Glioma and Recurrent/Refractory Pediatric H3K27M Gliomas.

Data S2. Protocol for NCT03134131, ONC201-018: Expanded Access to ONC201 for Patients with H3K27M-mutant and/or Midline High Grade Gliomas.

Supplementary Tables

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Table S3. Individual cases from historical control datasets.

Table S4. Summary of historical control datasets.

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Fig. S15. ONC201 does not cause hypermethylation leading to a glioma CpG island methylator phenotype.

Fig. S1. Selection method for planned efficacy analysis of ONC201 in patients with H3K27M-DMG.

All patients enrolled in completed arms of ONC201-014 at the recommended phase 2 dose (RP2D) and all patients enrolled in ONC201-018 with thalamic and brainstem tumors treated with ONC201 were screened. One hundred-and-eight total patients with thalamic and brainstem DMG were screened. Thirty-six total patients were excluded (5 patients from ONC201-014 and 31 patients from ONC201-018) due to unconfirmed H3K27M mutation status, inability to verify follow-up date at time of analysis, or inability to satisfy requirement for recurrent or non-recurrent disease after irradiation. Seventy-one total patients met the inclusion criteria and were included in final analysis, of which 35 enrolled following irradiation prior to recurrence while 36 enrolled with recurrent disease.



Fig. S2. Progression-free survival from diagnosis of trial patients with non-recurrent H3K27M-DMG treated with ONC201.

Kaplan-Meier curve (Y-axis, % PFS; X-axis, time in months) showing PFS from diagnosis for non-recurrent H3K27M-DMG patients treated with ONC201 by study (ONC201-014, blue, n=24; ONC201-018, light blue, n=11; and ONC201-014/018 combined, orange, n=35).

Progression-free survival (PFS) in non-recurrent H3K27M-mutant DMG



Fig. S3. Swimmers' plot of ONC201 response by recurrence status, tumor location, and ONC201 trial.

Detailed treatment information for each patient (Y-axis) segregated by (top) recurrence status, (middle) tumor location, and (bottom) ONC201 trial: yellow bar = months from starting ONC201 treatment; gray bar = radiotherapy; blue bar = treatment to end or screen; white bar = time off treatment with survival; black triangle = progression; red circle = death; black arrow = alive at end of analysis.



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Fig. S4. ONC201 efficacy is independent of TP53 mutation status and chromosomal instability.

(A) Bar graph showing percentage of responders (n=10) and non-responders (n=10) bearing (left) *TP53* mutations and/or (right) chromosomal instability (CIN).

(**B**) Box plots demonstrating association of *TP53* mutation status with (left) increased CIN (p<0.0001) and (middle) CIN loss scores (p<0.0001) but not with (right) CIN gain scores (p=0.09).

(C-D) Kaplan-Meier curves comparing (C) OS from diagnosis and (D) PFS from diagnosis for 6 patients with non-recurrent H3K27M-DMG treated with ONC201 from the ONC201-014 arm stratified by TP53 status (yellow = wildtype; blue = mutant).

(E-F) Kaplan-Meier curves comparing (E) OS from diagnosis and (F) PFS from diagnosis for 6 patients with non-recurrent H3K27M-DMG treated with ONC201 from the ONC201-014 arm stratified by CIN status (yellow = low; blue = high).



Fig. S5. Cox proportional hazard regression to assess the effect of ONC201 after adjusting for confounders.

(A) Cox proportional hazard regression analysis (X-axis, HR = hazard ratio) of OS was performed to assess for possible confounders (Y-axis, gender, age, and tumor location) between ONC201-treated or untreated (historical dataset, see **Supplementary Fig. S6**) non-recurrent H3K27M-DMG (larger HR = larger effect of confounder).

(**B**) Cox proportional hazard regression analysis (X-axis, HR = hazard ratio) of OS after excluding early deaths from historical cohort was performed to assess for possible confounders (Y-axis, gender, age, and tumor location) between ONC201-treated or untreated (historical dataset, see **Supplementary Fig. S6**) non-recurrent H3K27M-DMG (larger HR = larger effect of confounder).



В

Multivariate analysis excluding early deaths (Cox proportional hazard regression)



Fig. S6. Survival of patients with H3K27M-DMG treated with ONC201 *versus* ONC201untreated historical controls.

(A) Kaplan-Meier curve (Y-axis, % overall survival; X-axis, time in months) comparing OS from diagnosis for 35 patients with non-recurrent H3K27M-DMG treated with ONC201 from both studies (n=35, orange, median OS = 21.7 months) *versus* OS in historical controls (n=274, gray, median OS = 12 months). Historical controls derived from Pratt *et al.* (2018) *Acta Neuropathologica*.

(**B**) Kaplan-Meier curve (Y-axis, % overall survival; X-axis, time in months) comparing OS from recurrence for 36 patients with recurrent H3K27M-DMG treated with ONC201 from both studies (n=36, orange, median OS = 9.3 months) *versus* OS in historical controls (n=99, gray, median OS = 8.1 months). Historical controls derived from Castel *et al.* (2018) *Acta Neuropathol Commun*, Lobon-Iglesias *et al.* (2018) *J Neuro Oncology*, and an unpublished cohort from the Gustave Roussy Institute, France.

(C) Kaplan-Meier curve (Y-axis, % overall survival; X-axis time in months) comparing OS from diagnosis for 35 patients with non-recurrent H3K27M-DMG treated with ONC201 from both studies *versus* OS in historical controls by anatomic location (thalamus or brainstem). ONC201-treated thalamic H3K27M-DMG (n=15, orange, median OS = 20.9 months) *versus* historical thalamic H3K27M-DMG (n=68, gray, median OS = 14.5 months). ONC201-treated brainstem H3K27M-DMG (n=20, blue, median OS = 21.7 months) *versus* historical brainstem H3K27M-DMG (n=206, brown, median OS = 11.9 months). Historical controls derived from Pratt *et al.* (2018) *Acta Neuropathologica*.

(**D**) Kaplan-Meier curve (Y-axis, % overall survival; X-axis, time in months) comparing OS from diagnosis for 35 patients with non-recurrent H3K27M-DMG treated with ONC201 from both studies (n=35, orange, median OS = 21.7 months) *versus* OS in historical controls screened for early deaths (defined as OS <3 months from diagnosis, n=254, gray, median OS = 12.7 months). Historical controls derived from Pratt *et al.* (2018) *Acta Neuropathologica*.



Fig. S7. Survival of patients with H3K27M-DMG treated with ONC201 versus ONC201untreated patients (PNOC003 or HERBY Phase II trials).

(A) Kaplan-Meier curve (Y-axis, % overall survival; X-axis, time in months) comparing OS from diagnosis for patients with non-recurrent brainstem H3K27M-DMG treated with ONC201 (n=20, orange; median OS = 21.7 months) *versus* non-recurrent brainstem DMG from PNOC003 (n=28, gray, median OS = 11.6 months). Data for the PNOC003 trial derived from Kline *et al.* (2022) *Clin Cancer Res.*

(**B**) Kaplan-Meier curve (Y-axis, % overall survival; X-axis, time in months) comparing PFS from diagnosis for patients with non-recurrent brainstem H3K27M-DMG treated with ONC201 (n=20, orange; median PFS = 11.2 months) *versus* non-recurrent brainstem DMG from PNOC003 (n=25; gray, median PFS = 8.1 months). Data for the PNOC003 trial derived from Kline *et al.* (2022) *Clin Cancer Res.*

(C) Kaplan-Meier curve (Y-axis, % overall survival; X-axis, time in months) comparing OS from diagnosis for patients with non-recurrent thalamic H3K27M-DMG treated with ONC201 (n=15, orange; median OS = 26 months) *versus* non-recurrent thalamic DMG from HERBY Phase II (n=24, gray; median OS = 14.2 months). Data for the HERBY Phase II trial derived from Grill *et al.* (2018) *J Clin Oncol.*



Fig. S8. Molecular attributes of patients with H3K27M-DMG treated with ONC201.

(A) Correlation between gene expression levels (RNA) and best tumor response in non-recurrent H3K27M-mutant DMG. Best tumor response was defined as percentage radiographic reduction in tumor area relative to diagnosis. Spearman's ρ statistic (**P*<0.05) was used to estimate a rank-based measure of association between gene expression and radiographic response.

(**B**) Significant TCA cycle-related genes (red) with positive correlation from **Fig. 3C** are depicted. Genes with Spearman's coefficient >5 and <5 (Y-axis) are plotted against gene rank (X-axis).

PDHB = Pyruvate Dehydrogenase B; SDHB = Succinate Dehydrogenase B; FH = Fumarate Hydratase; and ACLY = ATP Citrate Lyase.

(C-D) Significant (C) mitochondrial OXPHOS- and (D) steroid biosynthesis-related genes (black) with positive correlation from Fig. 3C are depicted. Genes with Spearman's coefficient >5 and <5 (Y-axis) are plotted against gene rank (X-axis).

NDUFB6 = NADH:Ubiquinone Oxidoreductase Subunit B6; COX16 = Cytochrome C Oxidase Assembly Factor 16; ATP1A1 = ATPase Na+/K+ Transporting Subunit Alpha 1; NDUFAB1 = NADH:Ubiquinone Oxidoreductase Subunit AB1; COX11 = Cytochrome C Oxidase Assembly Factor 11; ATP6V0A1 = ATPase H+ Transporting V0 Subunit A1; PPA1 = Inorganic Pyrophosphatase 1; and NDUFA6 = NADH:Ubiquinone Oxidoreductase Subunit A6.

SQLE = Squalene Epoxidase; DHCR7 = 7-Dehydrocholesterol Reductase; LIPA = Lipase A, Lysosomal Acid Type; MSMO1 = Methylsterol Monooxygenase 1; SC5D = Sterol-C5-Desaturase; and HSD17B7 = Hydroxysteroid 17-Beta Dehydrogenase 7.

(E) Significant T cell receptor signaling pathway-related genes (black) with negative correlation from Fig. 3C are depicted. Genes with Spearman's coefficient >5 and <5 (Y-axis) are plotted against gene rank (X-axis).

CD247; CD28; ZAP70 = Zeta Chain of T Cell Receptor Associated Protein Kinase 70; MAP2K7 = Mitogen-Activated Protein Kinase Kinase 7; ITK = IL2 Inducible T Cell Kinase; NFATC1 = Nuclear Factor Of Activated T Cells 1; and IKBKB = Inhibitor Of Nuclear Factor Kappa B Kinase Subunit Beta.











Fig. S9: Survival of H3K27M-DMG mice models treated with ONC201.

(A) Cartoon depicting procedure for generating immune-competent *in utero* electroporation mouse models of H3K27M-DMG. "PPK" mice harbor dominant-negative TP53, PDGFRA D842V, and H3F3A (H3.3) K27M mutations.

(**B**) Kaplan-Meier curves comparing OS from days post-birth in ONC201-treated (orange, n=6) *versus* vehicle (black, n=7) PPK mice models. Mice were treated with 125 mg/kg ONC201 once a week.

(C) Kaplan-Meier curves comparing OS from days post-implantation in ONC201-treated (orange, n=10) *versus* vehicle (black, n=9) patient-derived xenograft mice models. Mice were treated with 100 mg/kg ONC201 once a week.



С



Fig. S10. Integrative analysis of *in vitro* and human tumor metabolic gene expression in response to ONC201.

(A) Mouse pharmacokinetic study to assess brain penetration and tissue concentrations of ONC201. Schema (left) showing mice (n=3) injected intraperitoneally (IP) with 15 mg/kg of ONC201. After 30 minutes, plasma and tissues from midline locations harboring H3K27M-DMGs (spinal cord = blue, brainstem = teal, thalamus = green) were harvested. Bar graph (right) showing ONC201 concentrations (Y-axis, μ M) assessed by LC/MS quantification from plasma and three midline brain locations (n=3 per location).

(**B**) Dose response curves (Y-axis, cell viability normalized to vehicle treatment) for four low passage H3.3K27M-DMG, patient-derived cell lines (DIPG007, QCTB-R095, DIPGXIII*P, and SF7761; n=3 for each cell line) at indicated concentrations of ONC201 (X-axis, μ M) for 72 hours. Values (right) for half maximal inhibitory concentration (IC₅₀) and ONC201 efficacy (maximal effect, E_{max}) are indicated.

(C) Seahorse time course data of glycolysis stress test showing extracellular acidification rate (ECAR, mPH/min/10,000 cells, Y-axis) plotted against time (minutes, X-axis) in H3.3K27M-DMG cells DIPG007, QCTB-R095, and DIPGXIII*P. Each cell line (n=6-8) was untreated (black) or treated with vehicle (blue), 5 μ M ONC201 (red), or 10 μ M ONC201 (orange).

(**D**) Seahorse time course data of oxidative phosphorylation stress test showing oxygen consumption rate (OCAR, pMols/min/10,000 cells, Y-axis) plotted against time (minutes, X-axis) in H3.3K27M-DMG cells DIPG007, QCTB-R095, and DIPGXIII*P. Each cell line (n=6-8) was untreated (black) or treated with vehicle (blue), 5 μ M ONC201 (red), or 10 μ M ONC201 (orange).

(E) Pathway impact analysis plot of upregulated genes and metabolites from Fig. 4A and Fig. 4B (X-axis, pathway impact, ONC201 *versus* vehicle; Y-axis, corresponding -Log10 *P*).

(**F**) Immunoblots for Hexokinase 2 (HK2) in H3.3K27M DIPG-XIII*P, DIPG007, and SF7761 treated with or without indicated concentrations of ONC201 for 48 hours. Vinculin was probed as loading control.

(G) Schema (left) of [¹³C₆]-glucose tracing into the TCA cycle indicating predicted mass isotopes (M+3 or M+2) for each metabolite. Bar graph (right) showing fraction enrichment (Y-axis) for M+3 pyruvate (Pyr), M+3 lactate (Lac), M+2 α -ketoglutarate (α -KG), M+2 fumarate (Fum), M+2 malate (Mal), and M+2 aspartate (Asp) are indicated in cells treated with vehicle (blue) or 5 μ M ONC201 (red). n=3 replicates per condition.



VINCULIN Inos-P met 6 •Nitrogen met G Glucose (m+6) Cys & Met met 100-4 Arg syn HK2 • Vehicle -Log10 P Pyr fractional enrichment (m+3) Lac 000 • ONC201 75-(m+3) Aspartate ^{●●} (m+2) PDH • 50-2 GIn & Glu met Cit (m+2) 25 Mal (m+2) PPP α-KG ∞ (m+2) 0 0000 [¹³C_e]-Glucose tracing 0-PYNNYS Lac NX3 FUT NAL ASP NX2 0.0 1.0 1.5 0.5 2.0 Fum (m+2) OGDH Glutamate (m+2) Pathway Impact Suc •• (m+2)

Fig. S11. ONC201-mediated L2HG production increases H3K27me3 in H3K27M-DMG cells.

(A) Representative traces from enantiomer-specific mass spectroscopy for L-2HG from DIPG-XIII*P cells treated with vehicle (blue) or ONC201 (red, 5 μ M, 48 hours); note earlier retention time between 27-29 minutes.

(**B**) Representative trace from enantiomer-specific mass spectroscopy for D-2HG in IDH1 R132H-mutant TB096 patient-derived cell line; note later retention time between 32-35 minutes.

(C) H3.3K27M (DIPG007 and DIPGXIII*P) and H3.1K27M (DIPGIV) cells were treated with indicated concentrations of ONC201 for 48 hours. Cells were probed for H3K27me3 and total H3 (as loading control). Arrowhead indicates increased H3K27me3 across all cell lines.

(**D**). H3.3K27M and H3WT expressing isogenic mouse neuronal stem cells (mNSC) were treated with ONC201 (5 or 10 μ M) for 48 hours. Cells were probed for H3K27me3 and total H3 (as loading control). Arrowhead indicates increased H3K27me3.

(E-F). Image-J based quantification of H3K27me3/total H3 ratios (Y-axis) from H3.3K27M mNSC (E) and H3WT mNSC (F) in **Supplementary Fig. S11D**.

(G) Immunoblots for H3K27me3 and total H3 (as loading control) in H3.3K27M DIPG007 and SF7761 cell lines treated with indicated concentrations of L-2HG or vehicle.

(H) Immunoblots for H3K27ac and total H3 (as loading control) in H3.3K27M DIPG007, SF7761, and mNSC cell lines treated with indicated concentrations of ONC201 or vehicle.

(I) Immunoblots for HIF-1 α in 293T and H3.3K27M DIPG007 and DIPGXIII*P cell lines. Cells were treated with 200 μ M of HIF-1 α stabilizer deferoxamine as positive control or with indicated concentrations of ONC201. β -actin was probed as loading control.



Fig. S12. ONC201-induced increase in H3K27me3 is mediated by lactate dehydrogenase.

(A) Immunoblot for LDHA in DIPG007 cells transduced with two independent shRNAs against LDHA. Vinculin was used as loading control.

(**B**) Immunoblots for H3K27me3 and total H3 (as loading control) in DIPG007 cells with or without LDHA knockdown or treated with LDH pharmacologic inhibitors GSK-2837808A or oxamate in the presence and absence of ONC201 (5 μ M, 48 hours). Arrowhead indicates no change in H3K27me3.

(C) (Left) Immunoblot for L-2HGDH in DIPG007 cells with or without L-2HGDH overexpression. Vinculin was used as loading control. (Right) Cells with L-2HGDH overexpression were treated with ONC201 (5 μ M, 48 hours) or vehicle and probed for H3K27me3 and total H3 (as loading control). Arrowhead indicates no change in H3K27me3.

(**D**) (Left) Immunoblot for D-2HGDH in DIPG007 cells with or without D-2HGDH overexpression. Vinculin was used as loading control. (Right) Cells with D-2HGDH overexpression were treated with ONC201 (5μ M, 48 hours) or vehicle and probed for H3K27me3 and total H3 (as loading control). Arrowhead indicates increase in H3K27me3.

(E) Immunoblots for OGDH in DIPG007 cells transduced with two independent shRNAs against OGDH. HSP90 was used as loading control. Cells were probed for H3K27me3, H3K36me3, H3K9me3, H3K4me3, H3K27M and total H3 (as loading control). Arrowhead indicates increases in H3K27me3 and H3K36me3.

(F) ClpP was knocked down (KD) in DIPG007 cells. Cells with or without ClpP knockdown were treated with indicated concentrations of ONC201 for 48 hours and then probed for ClpX, NDUFA12, cleaved PARP, and OGDH. α -tubulin was used as loading control.

(G) Normalized cell counts (Y-axis) were plotted against increasing concentrations of ONC201 (X-axis) in DIPG007 cells with ClpP KD (green) or expressing empty vector control (blue).

(H) Immunoblots for H3K27me3 and total H3 (as loading control) in DIPG007 cells with ClpP KD treated with 5 or 10 μ M ONC201 for 48 hours. Arrowhead indicates no change in H3K27me3.



Fig. S13. ONC201 alters genomic chromatin accessibility and H3K27ac distribution in H3K27M-DMG cells.

(A) Venn diagram depicting overlap of genes with decreased chromatin accessibility (ATAC-seq) and downregulated gene expression by RNA-seq in DIPG007 cells treated with ONC201 (5 μ M, 48 hours) *versus* vehicle.

(**B**) Venn diagram depicting overlap of genes with decreased H3K27ac enrichment at promoters and enhancers and downregulated gene expression by RNA-seq in DIPG007 cells treated with ONC201 (5 μ M, 48 hours) *versus* vehicle.

(C) Venn diagram depicting overlap of genes with decreased chromatin accessibility (ATAC-seq), decreased H3K27ac enrichment at promoters and enhancers, and downregulated gene expression by RNA-seq in DIPG007 cells treated with ONC201 (5 μ M, 48 hours) *versus* vehicle.

(**D**) GSEA pathway analysis of 348 downregulated genes from Venn diagram in **Supplementary Fig. S13C** relating to cell cycle regulation and differentiation-related pathways (purple).

(E) Transcription factor motif analysis of downregulated H3K27ac and ATAC-seq genes showing enrichment of early lineage neuro-developmental transcription factors including *SOX10*, *SOX21*, and *SOX3*.

(F) Heatmaps showing chromatin accessibility (ATAC-seq) at promoters and enhancers (+/- 2Kb from peak center) in DIPG007 cells treated with vehicle or ONC201 (5 μ M ONC201 for 48 hours; n=2 replicates per condition).

(G) Heatmaps showing genomic H3K27ac at promoters and enhancers (+/- 2Kb from peak center) in DIPG007 cells treated with vehicle or ONC201 (5μ M ONC201 for 48 hours, n=2 replicates per condition).

(H) Venn diagram depicting overlap of genes with increased chromatin accessibility (ATAC-seq) and upregulated gene expression by RNA-seq in DIPG007 cells treated with ONC201 (5 μ M, 48 hours) *versus* vehicle.

(I) GSEA pathway analysis of 1096 upregulated genes from Venn diagram in **Supplementary** Fig. S13H.

(J) Venn diagram depicting overlap of genes with increased H3K27ac enrichment at promoters and enhancers and upregulated gene expression by RNA-seq in DIPG007 cells treated with ONC201 (5 μ M, 48 hours) *versus* vehicle.

(K) GSEA pathway analysis of 818 upregulated genes from Venn diagram in **Supplementary** Fig. S13J.

(L) Venn diagram depicting overlap of genes with increased chromatin accessibility (ATAC-seq), increased H3K27ac enrichment at promoters and enhancers, and upregulated gene expression by RNA-seq in DIPG007 cells treated with ONC201 (5 μ M, 48 hours) *versus* vehicle.

(M) GSEA pathway analysis of 223 upregulated genes from Venn diagram in **Supplementary** Fig. S13L.









positive regulation of protein metabolic processestablishment of protein localization regulation of intracellular signal transduction phosphorylationneurogenesis-

Η Upregulated RNA-seq 3301 4248 ATAC-seq 1096



10 -Log10 P

20

30

0





Κ



Μ



H3K27ac



Fig. S14. ONC201 increases global H3K27me3 in patient samples.

(A) Representative H3K27me3 IHC images from H3K27M-DMG patients who were treated (n=6) or untreated (n=4) with ONC201 from the Children's National Hospital (CNH) cohort.

(**B**) Volcano plot of H3K27me3 sites (X-axis, Log₂ fold change between ONC201-treated / untreated H3K27M-DMGs) plotted against -Log10 false discovery rate (FDR). We detected 360 autosomal sites that gained H3K27me3 and 85 autosomal sites that showed decreased H3K27me3 enrichment.

(C) Autosomal sites that gained H3K27me3 from **Supplementary Fig. S14B** were compared with H3K27me3-enriched regions in IDH1 mutant gliomas (n=6) and were found to have no overlap. Data for IDH1 mutant gliomas derived from Wu *et al.* (2020).

FIGURE S14 A

В

CNH cohort

H3K27M non-ONC201



С



Fig. S15. ONC201 does not cause hypermethylation leading to a glioma CpG island methylator phenotype.

(A) Hierarchical clustering of H3K27M-DMGs and lower-grade IDH-mutant gliomas with a G-CIMP phenotype based on methylation values. The heatmap displays 1,000 CpG probes with the highest variance across all samples. *Methylation class*: IDH low-grade (blue) and H3K27M-DMG (red). *Therapy*: ONC201 (yellow) and other (gray). *CpG island status*: yes (green) and no (white).

(**B**) Principal components derived from highly variable (S.D. >0.2) CpG sites showing ONC201treated H3K27M-DMGs (white), untreated H3K27M-DMG controls (red), and lower-grade IDH-mutant gliomas with a G-CIMP phenotype (blue).

(C) Average DNA methylation values for highly variable CpG probes (S.D. >0.2) located within CpG islands for ONC201-treated H3K27M-DMGs (yellow), untreated H3K27M-DMG controls (gray), and lower-grade IDH-mutant gliomas (blue). Only sites that are hypermethylated in lower-grade IDH-mutant gliomas relative to ONC201-treated or untreated H3K27M-DMG controls are shown.







5,667 CpG probes Most variable s.d. > 0.2 b(A IDH, LG) > b(DMG, K27M) CpG islands