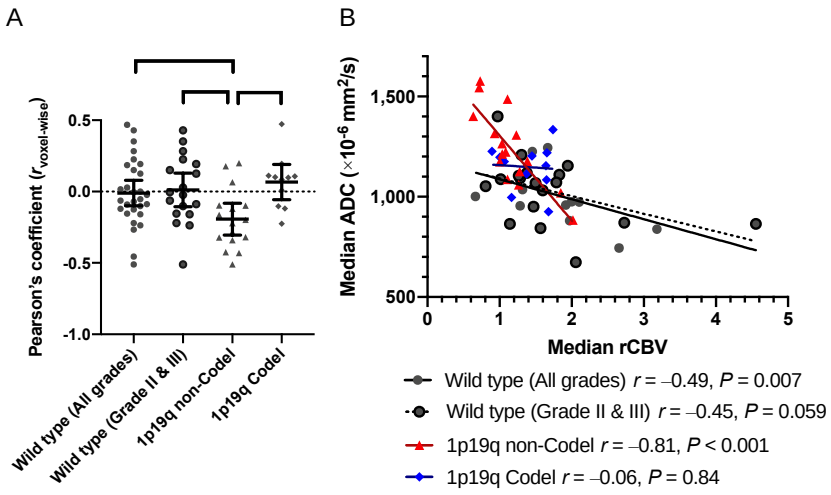
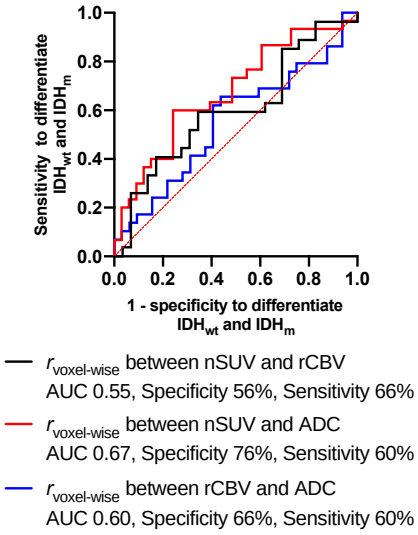
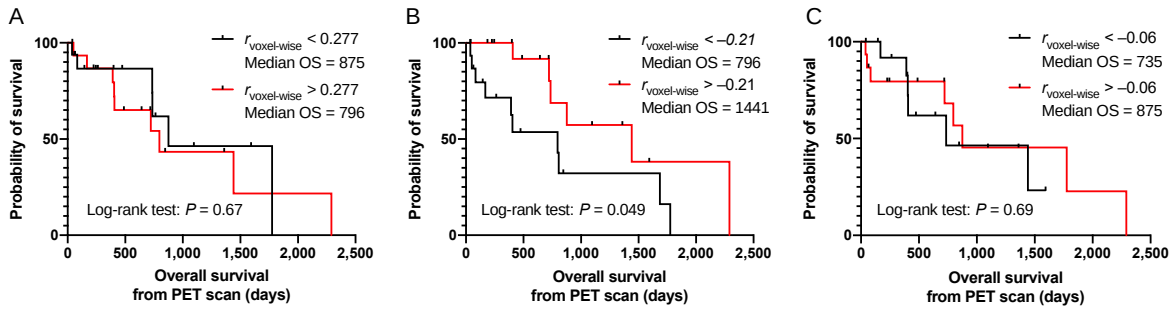


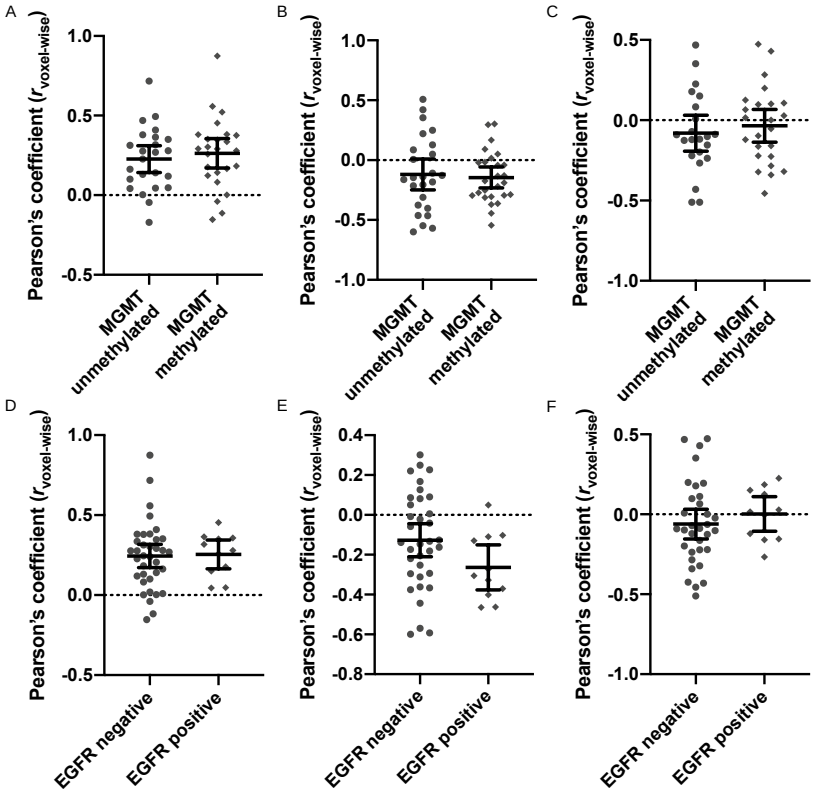
SUPPLEMENTAL FIGURE 1 Voxel-wise and patient-wise correlations between rCBV and ADC. A) The voxel-wise Pearson's correlation coefficients demonstrate that only $IDH_{m\text{-}non\text{-}codel}$ shows a significant negative correlation between rCBV and ADC. Bars denote the mean values and 95% confidential interval. * and ** mean $P < 0.05$ and < 0.01, respectively. B) IDH_{wt} with all grades and $IDH_{m\text{-}non\text{-}codel}$ exhibit significant negative correlations between median rCBV and ADC.



SUPPLEMENTAL FIGURE 2 Receiver operating characteristic curves to differentiate between IDH_{wt} and IDH_m gliomas.

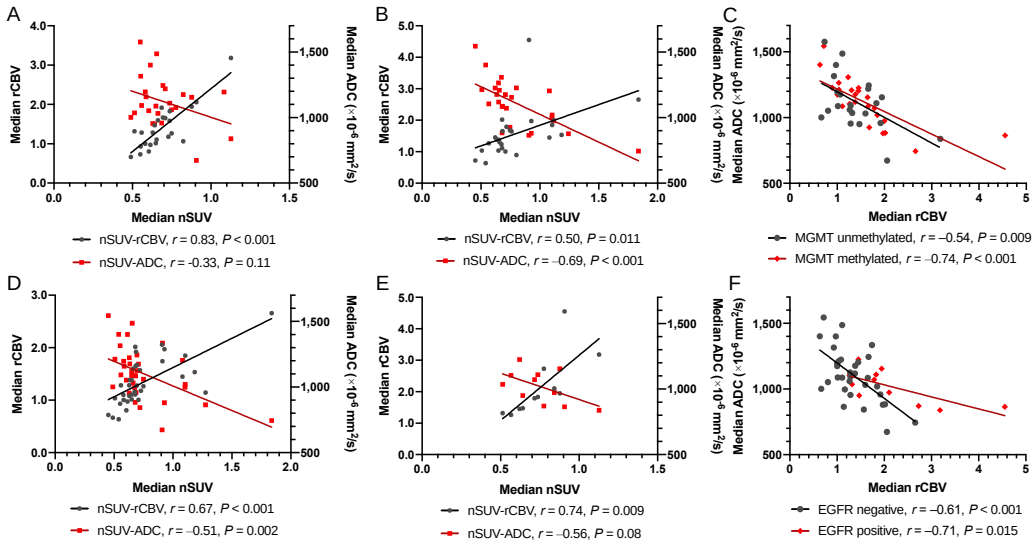


SUPPLEMENTAL FIGURE 3 Kaplan-Meier to differentiate OS of IDH_{wt} gliomas with $r_{voxel\text{-}wise}$ A) between nSUV and rCBV, B) between nSUV and ADC, and C) between rCBV and ADC. Gliomas are stratified by the median value of $r_{voxel\text{-}wise}$.



SUPPLEMENTAL FIGURE 4 Voxel-wise Pearson's coefficient between FDOPA uptake, rCBV, and ADC in different MGMT methylation or EGFR amplification status. A) The $r_{voxel\text{-}wise}$ between FDOPA uptake and rCBV has a positive correlation in MGMT unmethylated (0.23, 95% CI [0.14, 0.31]) and methylated gliomas (0.26, 95% CI [0.17, 0.36]). B) The $r_{voxel\text{-}wise}$ between FDOPA uptake and ADC has a negative correlation in MGMT unmethylated (−0.12, 95% CI [−0.25, 0.01]) and methylated gliomas (−0.15, 95% CI [−0.23, −0.06]). C) The $r_{voxel\text{-}wise}$ between

rCBV and ADC has no significant correlation in MGMT unmethylated (−0.08, 95% CI [−0.19, 0.03]) nor methylated gliomas (−0.03, 95% CI [−0.13, −0.07]). D) The $r_{\text{voxel-wise}}$ between FDOPA uptake and rCBV has a positive correlation in EGFR negative (0.24, 95% CI [0.17, 0.32]) and positive gliomas (0.25, 95% CI [0.16, 0.34]). E) The $r_{\text{voxel-wise}}$ between FDOPA uptake and ADC has a negative correlation in EGFR negative (−0.13, 95% CI [−0.21, −0.04]) and positive gliomas (−0.26, 95% CI [−0.38, −0.15]). F) The $r_{\text{voxel-wise}}$ between rCBV and ADC has no significant correlation in EGFR negative (−0.06, 95% CI [−0.15, 0.03]) nor positive gliomas (0.002, 95% CI [−0.11, 0.11]). Bars denote the mean values and 95% confidential interval. No pair-wise comparisons between the different molecular status show significant differences.



SUPPLEMENTAL FIGURE 5 Patient-wise Pearson's correlation coefficients between median nSUV, median rCBV, and ADC in different MGMT methylation or EGFR amplification status. A) In MGMT unmethylated gliomas, there is a significant positive correlation between the FDOPA uptake and rCBV, and a weak negative (not significant) correlation between the FDOPA uptake and ADC. B) In MGMT methylated gliomas, there is a significant positive correlation between the FDOPA uptake and rCBV, and a significant negative correlation between the FDOPA uptake and ADC. The patient-wise correlation of nSUV and rCBV is significantly stronger in MGMT unmethylated gliomas than in methylated gliomas. C) Both MGMT unmethylated and methylated gliomas demonstrate significant negative correlations between median rCBV and ADC. D) In EGFR positive gliomas, there is a significant positive correlation between FDOPA uptake and rCBV, and a negative correlation between FDOPA uptake and ADC. E) In EGFR positive gliomas, there is a significant positive correlation between FDOPA uptake and rCBV and a negative correlation (not significant) between FDOPA uptake and ADC. F) Both EGFR negative and positive gliomas demonstrate significant negative correlations between median rCBV and ADC. There are no significant differences in the correlation strength between FDOPA uptake, rCBV, and ADC with different EGFR statuses.

SUPPLEMENTAL TABLE 1 Detailed patient demographics and molecular information

ID	Sex	Age	WHO grade	IDH mutation status	1p/19q codeletion status	MGMT methylation status	EGFR amplification status	Surgical procedure	Date between PET scan and censored date (days)	Final status
1	Male	64	IV	Wild-type	–	Methylated	Positive	GTR	1776	Deceased
2	Female	76	IV	Wild-type	–	Methylated	Negative	STR	167	Deceased
3	Female	66	IV	Wild-type	–	Methylated	Negative	STR	719	Alive
4	Female	47	IV	Wild-type	–	Methylated	Negative	STR	1685	Deceased
5	Male	54	IV	Wild-type	–	Methylated	–	STR	37	LFU
6	Male	74	IV	Wild-type	–	Methylated	–	Biopsy	50	Deceased
7	Male	36	IV	Wild-type	–	Unmethylated	Positive	STR	404	Deceased
8	Female	55	IV	Wild-type	–	Unmethylated	Positive	STR	847	LFU
9	Male	74	IV	Wild-type	–	Unmethylated	Negative	GTR	41	LFU
10	Female	26	IV	Wild-type	–	Unmethylated	Negative	Biopsy	734	Deceased
11	Male	77	IV	Wild-type	–	Unmethylated	Negative	STR	735	Deceased
12	Male	56	IV	Wild-type	–	Unmethylated	Negative	STR	245	LFU
13	Female	63	IV	Wild-type	–	Unmethylated	Negative	STR	406	Deceased
14	Male	76	IV	Wild-type	–	–	Positive	Biopsy	82	Deceased
15	Female	68	III	Wild-type	–	Methylated	Positive	GTR	1594	Alive
16	Female	60	III	Wild-type	–	Methylated	Positive	STR	796	Deceased
17	Male	59	III	Wild-type	–	Methylated	Negative	STR	1096	LFU
18	Female	61	III	Wild-type	–	Methylated	–	STR	1361	LFU
19	Male	48	III	Wild-type	–	Unmethylated	Positive	STR	474	Alive
20	Female	59	III	Wild-type	–	Unmethylated	Positive	STR	722	Deceased
21	Male	58	III	Wild-type	–	Unmethylated	Positive	STR	875	Deceased
22	Male	53	III	Wild-type	–	Unmethylated	Negative	STR	399	LFU
23	Male	62	III	Wild-type	–	Unmethylated	Negative	STR	226	LFU
24	Male	64	III	Wild-type	–	Unmethylated	Negative	STR	145	Alive
25	Female	60	III	Wild-type	–	Unmethylated	Negative	Biopsy	391	Deceased
26	Male	60	III	Wild-type	–	Unmethylated	–	STR	806	Deceased
27	Female	63	III	Wild-type	–	–	Positive	Biopsy	488	LFU
28	Male	68	III	Wild-type	–	–	Negative	STR	38	Deceased
29	Male	63	III	Wild-type	–	–	Negative	STR	65	LFU
30	Male	63	II	Wild-type	–	Methylated	Positive	STR	642	LFU
31	Male	61	II	Wild-type	–	Unmethylated	Negative	STR	1441	Deceased
32	Male	64	II	Wild-type	–	Unmethylated	Negative	STR	187	Alive
33	Male	69	II	Wild-type	–	Unmethylated	Negative	STR	263	Alive
34	Female	54	II	Wild-type	–	–	Negative	Biopsy	57	LFU
35	Male	50	II	Wild-type	–	–	–	STR	763	LFU
36	Female	63	II	Wild-type	–	–	–	Biopsy	2291	Deceased
37	Male	38	III	Mutant	non-Codeleted	Methylated	Negative	Biopsy	1149	LFU
38	Female	47	III	Mutant	non-Codeleted	Methylated	Negative	STR	656	Alive
39	Male	35	III	Mutant	non-Codeleted	Methylated	Negative	STR	502	Alive
40	Male	55	III	Mutant	non-Codeleted	Methylated	Negative	Biopsy	357	LFU
41	Female	41	III	Mutant	non-Codeleted	Methylated	–	STR	118	LFU
42	Female	25	III	Mutant	non-Codeleted	Unmethylated	Negative	Biopsy	1530	LFU
43	Male	36	II	Mutant	non-Codeleted	Methylated	Negative	GTR	1921	LFU
44	Male	34	II	Mutant	non-Codeleted	Methylated	Negative	STR	1336	LFU
45	Male	79	II	Mutant	non-Codeleted	Methylated	Negative	STR	159	Alive
46	Male	57	II	Mutant	non-Codeleted	Methylated	Negative	STR	747	Alive
47	Female	27	II	Mutant	non-Codeleted	Methylated	–	GTR	1423	LFU
48	Female	36	II	Mutant	non-Codeleted	Unmethylated	Negative	STR	1110	Alive
49	Male	39	II	Mutant	non-Codeleted	Unmethylated	Negative	Biopsy	347	LFU
50	Female	25	II	Mutant	non-Codeleted	Unmethylated	–	STR	1790	Alive
51	Male	22	II	Mutant	non-Codeleted	–	Negative	STR	1099	LFU
52	Male	39	II	Mutant	non-Codeleted	–	Negative	STR	712	Alive
53	Male	67	III	Mutant	Codeleted	Methylated	Negative	STR	1110	LFU
54	Male	53	III	Mutant	Codeleted	Unmethylated	Negative	STR	321	LFU
55	Female	35	III	Mutant	Codeleted	Unmethylated	–	GTR	4291	LFU
56	Male	33	III	Mutant	Codeleted	–	–	STR	3958	LFU
57	Female	48	II	Mutant	Codeleted	Methylated	Negative	GTR	1713	Alive
58	Male	43	II	Mutant	Codeleted	Methylated	Negative	STR	29	Deceased
59	Female	47	II	Mutant	Codeleted	Methylated	–	GTR	2779	Alive
60	Female	48	II	Mutant	Codeleted	Methylated	–	Biopsy	222	LFU
61	Male	36	II	Mutant	Codeleted	Methylated	–	STR	3263	Alive
62	Female	28	II	Mutant	Codeleted	Unmethylated	–	GTR	1232	LFU
63	Male	61	II	Mutant	Codeleted	Unmethylated	–	GTR	166	Alive
64	Female	25	II	Mutant	Codeleted	Unmethylated	–	GTR	166	Alive
65	Male	37	II	Mutant	Codeleted	–	Negative	STR	362	Alive

66	Male	56	II	Mutant	Codeleted	–	Negative	GTR	740	Alive
67	Male	39	II	Mutant	Codeleted	–	–	STR	3590	LFU
68	Male	52	II	Mutant	Codeleted	–	–	STR	1637	LFU

STR = subtotal resection; GTR = gross total resection; LFU = lost to follow-up

SUPPLEMENTAL TABLE 2 A linear mixed effect model between FDOPA uptake and rCBV or ADC with different molecular status

Tumor type		Wild-type (n = 36)		*P* value	Mutant 1p/19q non-codel (n = 16)		*P* value	Mutant 1p/19q codel (n = 16)		*P* value
Voxel-wise mixed effect model between nSUV and rCBV	β_0	0.99	[1.23, 1.25]		-0.21	[-0.38, -0.05]		1.08	[0.90, 1.26]	
	β_1	1.24	[1.23, 1.25]	< 0.001	2.52	[2.51, 2.53]	< 0.001	0.76	[0.74, 0.77]	< 0.001
	b_{0m}	0.69	[0.54, 0.88]		0.34	[0.24, 0.48]		0.33	[0.22, 0.48]	
	ε_{im}	1.48	[1.47, 1.47]		1.04	[1.04, 1.04]		1.24	[1.24, 1.24]	
Voxel-wise mixed effect model between nSUV and ADC	β_0	1169	[1128, 1211]		1669	[1606, 1730]		1023	[969, 1076]	
	β_1	-157	[-159, -155]	< 0.001	-649	[-651, -646]	< 0.001	187	[184, 190]	< 0.001
	b_{0m}	121	[95, 153]		127	[90, 178]		101	[69, 146]	
	ε_{im}	250	[249, 250]		258	[258, 258]		249	[248, 249]	

Data were estimate with 95% confidence interval; Parameters fit for a linear mixed-effect model for voxel-wise analysis of nSUV and rCBV/ADC (see Eq. 1); nSUV = normalized standardized uptake value; rCBV = relative cerebral blood volume; ADC = apparent diffusion coefficient

SUPPLEMENTAL TABLE 3 Parameters of FDOPA PET and MRI in different MGMT or EGFR status

Tumor type	MGMT unmethylated (n = 27)		MGMT methylated (n = 27)		*P* value	EGFR negative (n = 36)		EGFR positive (n = 16)		*P* value
Maximum nSUV	1.46 ± 0.67	[1.20, 1.72]	1.62 ± 0.91	[1.26, 1.98]	0.89	1.55 ± 0.83	[1.28, 1.82]	1.61 ± 0.68	[1.15, 2.06]	0.50
Median nSUV	0.70 ± 0.16	[0.64, 0.76]	0.82 ± 0.30	[0.70, 0.94]	0.15	0.75 ± 0.27	[0.66, 0.84]	0.76 ± 0.18	[0.64, 0.88]	0.49
Median rCBV	1.40 ± 0.55	[1.17, 1.63]	1.57 ± 0.77	[1.25, 1.89]	0.41	1.34 ± 0.44	[1.19, 1.49]	2.15 ± 0.99	[1.48, 2.82]	0.001*
Median ADC ($\times 10^{-6}$ mm^2/s)	1122 ± 194	[1042, 1202]	1105 ± 182	[1031, 1179]	0.75	1104 ± 198	[1036, 1172]	1018 ± 128	[931, 1104]	0.17

Data were mean ± standard deviation with 95% confidence interval; * means statistically significant; MGMT = O6-methylguanine-DNA methyltransferase; EGFR = epidermal growth factor receptor; nSUV = normalized standardized uptake value; rCBV = relative cerebral blood volume; ADC = apparent diffusion coefficient

SUPPLEMENTAL TABLE 4 A linear mixed effect model between SUV uptake and rCBV or ADC with different MGMT or EGFR status

		MGMT unmethylated (n = 27)		*P* value	MGMT methylated (n = 27)		*P* value	EGFR negative (n = 36)		*P* value	EGFR positive (n = 16)		*P* value
Voxel-wise mixed effect model between nSUV and rCBV	β_0	0.56	[0.41, 0.70]		0.66	[0.39, 0.94]		0.70	[0.57, 0.83]		1.15	[0.70, 1.61]	
	β_1	1.54	[1.53, 1.55]	< 0.001	1.49	[1.48, 1.49]	< 0.001	1.22	[1.21, 1.23]	< 0.001	1.62	[1.61, 1.65]	< 0.001
	b_{0m}	0.36	[0.27, 0.48]		0.69	[0.52, 0.92]		0.40	[0.32, 0.50]		0.77	[0.51, 1.17]	
	ε_{im}	1.29	[1.28, 1.29]		1.12	[1.12, 1.12]		1.32	[1.32, 1.32]		1.57	[1.56, 1.57]	
Voxel-wise mixed effect model between nSUV and ADC	β_0	1295	[1231, 1358]		1245	[1191, 1300]		1210	[1153, 1266]		1223	[1171, 1276]	
	β_1	-226	[-228, -224]	< 0.001	-148	[-151, -146]	< 0.001	-123	[-124, -120]	< 0.001	-226	[-229, -223]	< 0.001
	b_{0m}	161	[123, 210]		139	[106, 183]		169	[133, 213]		88	[58, 133]	
	ε_{im}	266	[266, 267]		238	[238, 238]		245	[244, 245]		246	[245, 246]	

Data were estimate with 95% confidence interval; Parameter fit for linear mixed-effects model for voxel-wise analysis of nSUV and rCBV/ADC (see Eq. 1); MGMT = O6-methylguanine-DNA methyltransferase; EGFR = epidermal growth factor receptor; nSUV = normalized standardized uptake value; rCBV = relative cerebral blood volume; ADC = apparent diffusion coefficient