NRG Oncology/RTOG-98-02 Data Dictionary
NCTN/NCORP Data Archive
Dictionary for *NCT00003375-D1-Dataset.csv*
PMID: 32706640

Randomized and eligible patients from NRG Oncology/RTOG-98-02.

See also the companion datasets/data dictionaries

- NCT00003375-D2-Dataset.csv   NCT00003375-D2-Data-Dictionary.pdf
- NCT00003375-D3-Dataset.csv   NCT00003375-D3-Data-Dictionary.pdf

Data can be used to approximate published study findings, but exact reproduction of previous manuscripts may not be possible in some cases (e.g., when data must be modified for de-identification purposes or have undergone further data cleaning).

Variables in this dataset that contain limited high-dimensional "omic" data are provided in addition to the clinical data in an "as-is" state without all the same quality-control procedures that are performed on the clinical data by the NCTN/NCORP Data Archive. It may not be possible to fully reproduce the results of the genomic analyses included in the publication. For example, the "omic" data provided may be a subset of the data used in the publication or may not reflect certain aspects of the data processing.

Note: The following errors will be corrected in the primary publication.
1. Figure 1 reports 116 with patient samples submitted for biomarker analysis. The actual count is 118 patients.
2. Table 2 reports p value of 0.47 for neurologic function. The corrected p value is 0.14.
3. Supplementary Figure 3 – Overall Survival (3A) dead/total should be 26/43 for IDH1 non-mutant and 33/69 for IDH1 mutant (p=0.046; HR=0.60 (0.36 – 1.00)). Progression-free Survival (3B) Failure/total should be 33/43 for IDH1 non-mutant and 41/69 for IDH1 mutant (p=0.004; HR=0.51 (0.32 - 0.81)).

#	Variables	Description	Format/Coding for categorical data
1	study_no	Study number	Character
2	patid	De-identified ID	Character
3	arm	Assigned treatment	1=RT alone 2=RT + PCV *Note: covariate in cox model (reference=1)*
4	age	Age (years)	Continuous *Note: covariate in cox model (continuous)*
5	sex	Sex	1=male 2=female *Note: covariate in cox model (reference=2)*
6	race	Race	1=White 2=Hispanic or Latino 3=Black or African American 4=Asian 6=American Indian or Alaskan Native
7	KPS	Karnofsky performance status (KPS) at baseline	60 70 80 90 100

#	Variables	Description	Format/Coding for categorical data
8	KPS_cox	KPS group used in cox model for multivariate analyses	0=status 60,70, or 80 1=status 90,100 *Note: covariate in cox model (reference=1) if analysis_inclusion=1 (Blank if analysis_inclusion=2).*
9	surgery	Prior surgery	1=Biopsy 2=Partial Resection 3=total resection
10	surgery_cox	Surgery group used in cox model for multivariate analyses	0=Biopsy 1=Resection *Note: covariate in cox model (reference=1) if analysis_inclusion=1 (Blank if analysis_inclusion=2).*
11	nf	Neurologic function (baseline)	0=no symptoms 1=minor symptoms 2=moderate symptoms; fully active 3=moderate symptoms; less than fully active
12	nf_cox	Neurologic function group used in cox model for multivariate analyses	0=no symptoms 1=minor/moderate symptoms *Note: covariate in cox model (reference=0) if analysis_inclusion=1 (Blank if analysis_inclusion=2).*
13	histology	Histology from central review	1=Astrocytoma 2=Oligodendroglioma 3=Oligoastrocytoma, astro dominant 4=Oligoastocytoma, astro=oligo 5=Oligoastrocytoma, olig dominant
14	histology_cox	Histology group used in cox model for multivariate analyses	1=astrocytoma 2=mixed oligoastrocytoma 3=oligodendroglioma *Note: covariate in cox model (reference=3) if analysis_inclusion=1 (Blank if analysis_inclusion=2).*
15	submitted_samples	Patient samples submitted for biomarker analysis	0=No 1=Yes
16	submitted_idh_ihc	Submitted for IDH1R132H IHC of patients who submitted samples	0=No 1=Yes *Note: blank for patients with no samples submitted (n=133)*
17	submitted_sequencing	Submitted to the targeted sequencing panel which consisted of IDH1, IDH2, ATRX, CIC, and FUBP1	0=No 1=Yes *Note: blank for patients with no samples submitted (n=133)*
18	submitted_1p19q	Submitted for 1p/19q analysis of patients who submitted samples	0=No 1=Yes *Note: blank for patients with no samples submitted (n=133)*
19	submitted_mgmt	Submitted for MGMT analysis of patients who submitted samples	0=No 1=Yes *Note: blank for patients with no samples submitted (n=133)*
20	analysis_inclusion	Indicator for inclusion of analysis in IDH 1/2, 1p/19q, and WHO subgroup	1=In analysis 2=Not in analysis *Note: variable used for table 1 and supplementary figure 1*
21	1p_19q__quality	Analysis platform used to call 1p/19q (450k and/or Oncoscan)	0=Submitted, but too poor data quality to call 1p/19q 1-450K 1-450K/Onco 1-Onco *Note: blank indicates not done*

#	Variables	Description	Format/Coding for categorical data
22	del_both	1p/19q deletion	0=non-co-deleted 1=co-deleted *Note: blank indicates not done*
23	idh1_2	IDH 1/2 status by sequencing and IHC	0=wild type 1=mutant (IDH1 R132H/C/S/G or IDH2 R172K) *Note: blank indicates not done*
24	IDH1_Mutation_Sequencing	IDH1 mutation sequencing	NA=Not available, although the case was submitted for sequencing NS=Not submitted for sequencing N385fs R132C R132G R132H R132H/A410T WT=Wild-type *Note: blank indicates not done*
25	IDH2_Mutation_Sequencing	IDH2 mutation sequencing	NA=Not available, although the case was submitted for sequencing NS=Not submitted for sequencing R172K R261C WT=Wild-type *Note: blank indicates not done*
26	idh_ihc	IDH1R132H IHC	0=negative 1=positive *Note: blank indicates not done*
27	idhdel	WHO-defined molecular subgroup	0=IDH 1/2 Wild Type 1=IDH 1/2 Mutant w 1p/19q non-codeleted 2=IDH 1/2 Mutant w 1p/19q codeleted 9=missing IDH 1/2 or 1p/19q *Note: covariate in cox model (reference=0) if analysis_inclusion=1 (Blank if analysis_inclusion=2)*
28	mgmt	MGMT status	1=Methylated 2=Unmethylated *Note: blank indicates not done*
29	cic_inclusive	CIC inclusive mutation	0=non-mutant 1=mutant *Note: blank indicates not done*
30	cic_deleterious	CIC deleterious mutation	0=non-mutant 1=mutant *Note: blank indicates not done*
31	atrx_inclusive	ATRX inclusive mutation	0=non-mutant 1=mutant *Note: blank indicates not done*
32	atrx_deleterious	ATRX deleterious mutation	0=non-mutant 1=mutant *Note: blank indicates not done*
33	fubp1_inclusive	FUBP1 inclusive mutation	0=non-mutant 1=mutant *Note: blank indicates not done*
34	fubp1_deleterious	FUBP1 deleterious mutation	0=non-mutant 1=mutant *Note: blank indicates not done*

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#	Variables	Description	Format/Coding for categorical data
35	TERT_Mutation	TERT Mutation	C228T -124 bp C250T -146 bp NA=Not available WT=Wild-type *Note: blank indicates not done*
36	tert	All TERT mutations are deleterious	0=non-mutant 1=mutant *Note: blank indicates not done*
37	TP53_Mutation	TP53 Mutation	G245S/C NA=Not available R175H R248Q/L R273C/S R273H/L WT=Wild-type Y163C Y220C *Note: blank indicates not done*
38	tp53	All TP53 mutations are deleterious	0=non-mutant 1=mutant *Note: blank indicates not done*
39	OncoSNP_BRAF	BRAF Mutation	NA=Not available Non-Mutated *Note: blank indicates not done*
40	OncoSNP_EGFR	EGFR Mutation	Mutated NA=Not available Non-Mutated *Note: blank indicates not done*
41	OncoSNP_KRAS	KRAS Mutation	NA=Not available Non-Mutated *Note: blank indicates not done*
42	OncoSNP_NRAS	NRAS Mutation	Mutated NA=Not available Non-Mutated *Note: blank indicates not done*
43	OncoSNP_PIK3CA	PIK3CA Mutation	Mutated NA=Not available Non-Mutated *Note: blank indicates not done*
44	OncoSNP_PTEN	PTEN Mutation	NA=Not available Non-Mutated *Note: blank indicates not done*
45	survival	Survival status	0=Alive 1=Dead
46	survival_years	Time since randomization to death/last follow-up (years)	Continuous
47	PFS	progression-free survival status	0=Alive without progression 1=Progressed or death due to any cause
48	PFS_years	Time since randomization to progression or date of death, or last follow-up if alive without progression (years)	Continuous

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