Supplementary Table 1.

Overview on data extracted from all studies. Red indicates results only used for comparison of IDH and MGMT prediction in Section 4.5. ML = machine learning; DL = deep learning; T1pc = T1 post-contrast; SVM = support vector machines; GBM = Glioblastoma; HGG = High Grade Glioma; LGG = Low Grade Glioma; IDH = Isocitrate dehydrogenase; RB1 = Retinoblastoma protein; MGMT = O6-methylguanine-DNA-methyltransferase; PPV = positive predictive value; NPV = negative predictive value

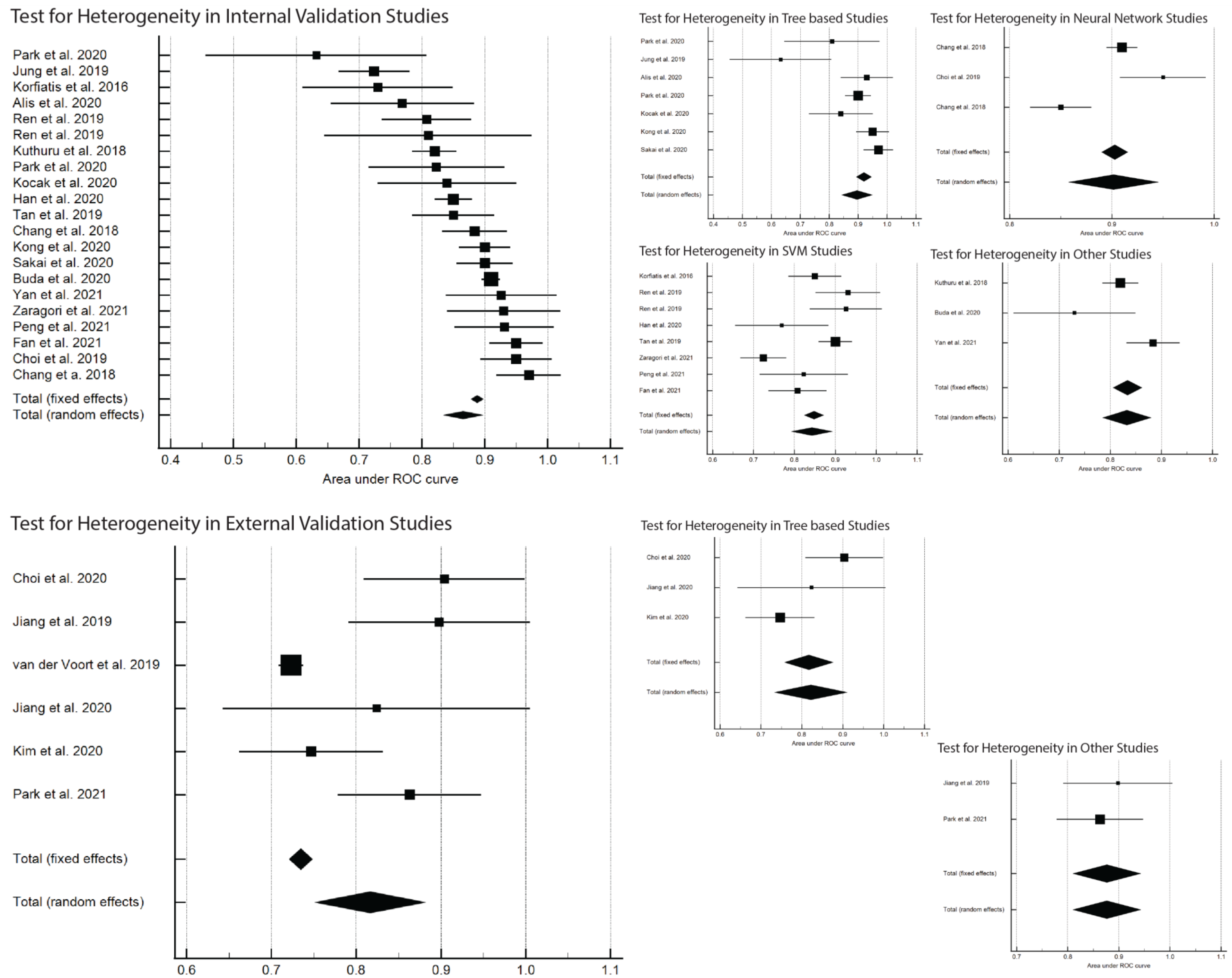
Reference	*Number of Patients (Total)*	*Tumor Type*	*Dataset*	*Overall ML or DL*	*Prediction Results Reported from which Cohort*	*Best Results Subtype*	*Best Results Algorithm*	*Type of Algorithm*	*Sequences*	*Accuracy (ACC)*	*Area under the ROC Curve (AUC)*	*Sensitivity*	*Specificity*	*Comment*
Park et al. 2020[1]	120	GBM IDH-Wildtype	Single Center	ML	Time Split Validation Cohort	RB1	random forest	Tree based	T1, T1pc, T2, FLAIR, DWI, fMRI		0.81 (95% CI: 0.64-0.97)			
Lee et al. 2019[2]	123	GBM	Single Center	ML	Time Split Validation Cohort	IDH	gradient boosting	Tree based	T1pc, T2, FLAIR, DWI, fMRI	83.40%				
Kanas et al. 2017[3]	86	GBM	Database	ML	Cross-Validation from Initial Study Population	MGMT	KNN	Other	T1, T1pc, FLAIR	73.60%		85.2%	66.3%	
Su et al. 2020[4]	122	midline glioma or brainstem Glioma	Single Center	ML	Time Split Validation Cohort	Histone H3 K27M	TPOT (decision tree)	Tree based	FLAIR	86.40%	0.85	0.8	0.917	
Chen et al. 2018[5]	47	HGG (nos)	Single Center	ML	Cross-Validation from Initial Study Population	IDH	MNMC (Multilabel Nonlinear Matrix)		T1, DWI, fMRI	87.00%	0.886	92.3%	84.9%	
Chen et al. 2018[5]	47	HGG (nos)	Single Center	ML	Cross-Validation from Initial Study Population	MGMT	MNMC (Multilabel Nonlinear Matrix)		T1, DWI, fMRI	74.60%	0.787			
Liu et al. 2018[6]	55	midline glioma or brainstem Glioma	Single Center	DL	Cross-Validation from Initial Study Population	Histone H3 K27M	SVM (Prediction based on features extracted by CNN)	SVM	T1	96.52%	0.953	96.67%		
Choi et al. 2020[7]	136	GBM	Single Center. Database	ML	External Validation Cohort	IDH	random forest	Tree based	T2	86.8%	0.904 (95 % CI: 0.81–1.0)	91.6%	75%	
Hedyehzadeh et al. 2020[8]	166	GBM	Database	DL	Holdout Testing Cohort in Initial Study Population	EGFR	deep CNN regression	Neural Network	T1, T1pc, T2, FLAIR					
Li et al. 2019[9]	193	GBM	Database. Multicenter	ML	External Validation Cohort	MGMT	random forest	Tree based	T1, T1pc, T2, FLAIR	80%	0.88	70%	86%	
Qian et al. 2019[10]	69	GBM	Multicenter	ML	Holdout Testing Cohort in Initial Study Population	MGMT	random forest	Tree based	FDOPA PET	80.00%		83%	67%	
Li et al. 2018[11]	225	GBM	Database + Multicenter	ML	External Validation Cohort	IDH	random forest	Tree based	T1, T1pc, T2, FLAIR	97%	0.96	80%	99%	
Jung et al. 2019[12]	41	midline glioma or brainstem Glioma	Multicenter	ML	Cross-Validation from Initial Study Population	Histone H3 K27M	random forest	Tree based	T1, T1pc, T2	63.30%	0.632 (95% CI: 0.456–0.808)	45.80%	88.20%	
Zhang et al. 2017[13]	120	HGG (nos)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	random forest	Tree based	T1, T1pc, T2, FLAIR, DWI	89.00%	0.9231			
Lo et al. 2020[14]	39	GBM	Database, Multicenter	ML	Cross-Validation from Initial Study Population	IDH	logistic regression	Other	T1pc	90.00%		57%	97%	
Korfiatis et al. 2016[15]	155	GBM	Single Center	ML	Cross-Validation from Initial Study Population	MGMT	SVM	SVM	T1pc, T2		0.85 (95% CI: 0.78–0.91)	80.3%	81.3%	
Hajianfar et al. 2019[16]	82	GBM	Database	ML	Cross-Validation from Initial Study Population	MGMT	decision tree	Tree based	T1pc, FLAIR		0.78			
Korfiatis et al. 2017[17]	155	GBM	Single Center	DL	Holdout Testing Cohort in Initial Study Population	MGMT	ResNet	Neural Network	T2	94.40%				
Li et al. 2019[18]	109	GBM	Database	ML	External Validation Cohort	PTEN	SVM	SVM	T1pc, T2	82.50%		78.70%	95.50%	
Calabrese et al. 2020[19]	199	GBM	Single Center, Database	ML	External Validation Cohort	ATRX	Random forest	Tree based	T1, T1pc, T2, FLAIR, (DWI only in testing cohort)		0.72	75%	75%	
Calabrese et al. 2020[19]	199	GBM	Single Center, Database	ML	External Validation Cohort	IDH	Random forest	Tree based	T1, T1pc, T2, FLAIR, (DWI only in testing cohort)		0.63			

Reference	*Number of Patients (Total)*	*Tumor Type*	*Dataset*	*Overall ML or DL*	*Prediction Results Reported from which Cohort*	*Best Results Subtype*	*Best Results Algorithm*	*Type of Algorithm*	*Sequences*	*Accuracy (ACC)*	*Area under the ROC Curve (AUC)*	*Sensitivity*	*Specificity*	*Comment*
Calabrese et al. 2020[19]	199	GBM	Single Center, Database	ML	Cross-Validation from Initial Study Population	MGMT	Random forest	Tree based	T1, T1pc, T2, FLAIR, DWI		0.55			
Yamashita et al. 2019[20]	112	GBM IDH-Wildtype	Single Center	ML	Cross-Validation from Initial Study Population	TERT	SVM	SVM	T1, T1pc, DWI	74.10%	0.776	85.7%	54.8%	
Han et al. 2018[21]	262	GBM	Database	DL	Holdout Testing Cohort in Initial Study Population	MGMT	CNN	Neural Network	T1, T2, FLAIR	66.00%	0.67			
Xi et al. 2018[22]	118	GBM	Single Center, Multicenter	ML	External Validation Cohort	MGMT	SVM	SVM	T1, T1pc, T2	80.00%		87.5%	75%	
Le et al. 2020[23]	53	GBM IDH-Wildtype	Database	ML	Cross-Validation from Initial Study Population	MGMT	XGBoost	Tree based	T1, T1pc, T2, FLAIR	83.02%	0.702			
Alis et al. 2019[24]	142	HGG (nos)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	random forest	Tree based	T1pc, FLAIR, DWI	86.95%	0.93 (95% CI: 0.82–1)	60%	100%	
Akbari et al. 2018[25]	129	GBM	Single Center	ML	Holdout Testing Cohort in Initial Study Population	EGFR	SVM	SVM	T1, T1pc, T2, FLAIR, DWI DSC	87.00%	0.86	78.6%	90%	
Ahmad et al. 2019[26]	71	HGG (nos)	Single Center	DL	Holdout Testing Cohort in Initial Study Population	IDH	ResNet	Neural Network	T2	86.70%				
Crisi et al. 2020[27]	59	GBM	Single Center	DL	Cross-Validation from Initial Study Population	MGMT	multilayer perceptron (MLP)	Neural Network	T1pc, T2, FLAIR, DWI, DSC		0.84	75%	85%	
Yu et al. 2017[28]	92	LGG	Single Center	ML	Cross-Validation from Initial Study Population	IDH	AdaBoost	Tree based	FLAIR	72.00%	0.7	41%	85%	
Fukuma et al. 2019[29]	164	Grade II + III	Multicenter	ML	Cross-Validation from Initial Study Population	IDH	SVM	SVM	T1, T1pc, T2, FLAIR	73.10%				
Fukuma et al. 2019[29]	108	IDH-mutant Glioma	Multicenter	ML	Cross-Validation from Initial Study Population	pTERT	SVM	SVM	T1, T1pc, T2, FLAIR	79.80%				
Ren et al. 2019[30]	57	LGG	Single Center	ML	Cross-Validation from Initial Study Population	IDH	SVM	SVM	T1, T1pc, T2, FLAIR, DWI	94.74%	0.931 (95% CI: 0.842–1)	100%	85.71%	
Ren et al. 2019[30]	36	IDH-mutant Glioma	Single Center	ML	Cross-Validation from Initial Study Population	ATRX	SVM	SVM	T1, T1pc, T2, FLAIR, DWI	91.61%	0.926 (95% CI: 0.824–1)	94.74%	88.24%	
Yu et al. 2016[31]	110	LGG	Single Center	ML	Time Split Validation Cohort	IDH	AdaBoost	Tree based	FLAIR	90.00%	0.8	100%	50%	
Zhang et al. 2018[32]	103	LGG	Database	ML	Holdout Testing Cohort in Initial Study Population	IDH	SVM	SVM	T1, T1pc, T2, FLAIR	80.00%	0.792	85%	70%	
Zhang et al. 2018[32]	70	IDH-mutant Glioma	Database	ML	Holdout Testing Cohort in Initial Study Population	p53	SVM	SVM	T1, T1pc, T2, FLAIR	85.00%	0.869	84.6%	85.7%	
Li et al. 2017[33]	119	LGG	Single Center	DL	Time Split Validation Cohort	IDH	CNN	Neural Network	T1pc, FLAIR	92.44%	0.9521	94.38%	86.67%	
Jiang et al. 2019[34]	122	Grade II + III	Single Center, Database	ML	External Validation Cohort	MGMT	Multiple ML classifiers (SVM. random forest. AdaBoost)	Other	T1pc, T2	88.60%	0.898 (95% CI: 0.786-1.000)	82.1%	85.7%	
Kuthuru et al. 2018[35]	108	Grade II + III	Database	ML	Cross-Validation from Initial Study Population	IDH	dictionary learning approach with structured incoherence (DLSI)	Other	T1, T1pc, T2, FLAIR		0.82 (95% CI: 0.79-0.86)			
van der Voort et al. 2019[36]	413	LGG	Single Center, Database	ML	External Validation Cohort	1p/19q	SVM	SVM	T1pc, T2	69.80%	0.723 (95% CI: 0.708–0.737)	73.2%	61.7%	
Shofty et al. 2018[37]	47	IDH-mutant Glioma	Single Center	ML	Cross-Validation from Initial Study Population	1p/19q	Bagged Trees	Tree based	T1pc, T2, FLAIR	87.00%	0.87	92%	83%	
Akkus et al. 2017[38]	159	LGG	Single Center	DL	Holdout Testing Cohort in Initial Study Population	1p/19q	SGD (CNN configuration)	Neural Network	T1pc, T2	87.70%		93.30%	82.22%	

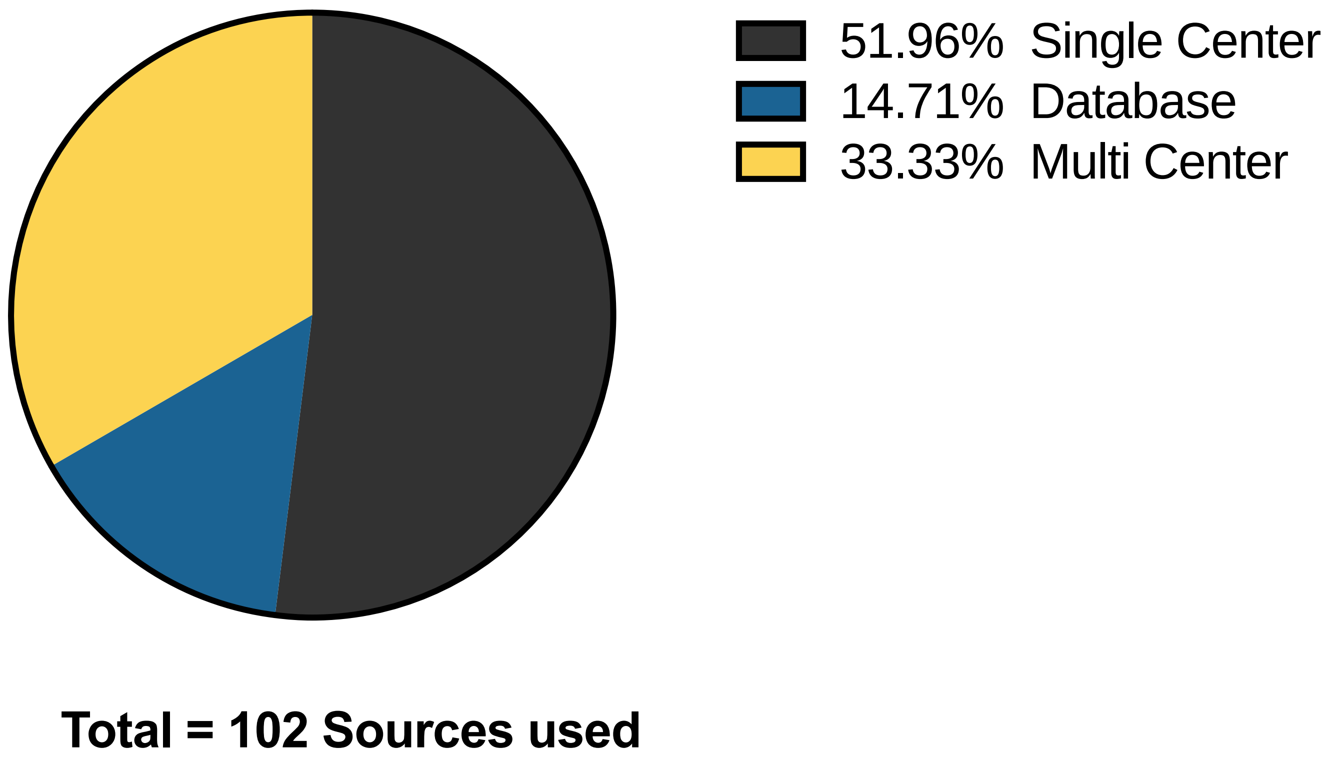
Reference	Number of Patients (Total)	Tumor Type	Dataset	Overall ML or DL	Prediction Results Reported from which Cohort	Best Results Subtype	Best Results Algorithm	Type of Algorithm	Sequences	Accuracy (ACC)	Area under the ROC Curve (AUC)	Sensitivity	Specificity	Comment
Ali et al. 2020[39]	161	LGG	Multicenter	DL	Cross-Validation from Initial Study Population	IDH	multi-stream convolutional autoencoder (CAE)	Neural Network	T1, T1pc, FLAIR	78.57%				
Eichinger et al. 2017[40]	79	Grade II + III	Single Center	ML	Cross-Validation from Initial Study Population	IDH	Neural Network	Neural Network	DTI	92.10%	0.952			
Jiang et al. 2020[41]	116	Grade II + III	Single Center, Database	ML	External Validation Cohort	TERT	Random Forest	Tree based	T1pc, T2	85.20%	0.824 (95% CI: 0.638–1.000)	70%	94.10%	
Park et al. 2020[42]	168	LGG	Single Center	ML	Cross-Validation from Initial Study Population	IDH	Random Forest	Tree based	T1pc, T2, FLAIR, DTI		0.900 (95% CI: 0.855–0.945)			
Matsui et al. 2020[43]	217	Grade II + III	Single Center	DL	Cross-Validation from Initial Study Population	IDH	ResNet	Neural Network	T1, T2, FLAIR, MRS, MET PET	68.70%				
Kocak et al. 2020[44]	107	LGG	Database	ML	Cross-Validation from Initial Study Population	1p/19q	Random forest	Tree based	T1pc, T2	84.00%	0.840 (95% CI: 0.729–0.950)	90.2%	71.7%	
Han et al. 2020[45]	59	Grade II + III	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	SVM	SVM	T1, T1pc, T2, FLAIR	79.90%	0.769 (95% CI: 0.641–0.869)	88.7%	56.3%	
Nalawade et al. 2019[46]	260	mixed (LGG. HGG)	Database	DL	Holdout Testing Cohort in Initial Study Population	IDH	Dense Net 161	Neural Network	T2	90.50%	0.95	83.1%	94.8%	
De Looze et al. 2018[47]	381	mixed (LGG. HGG)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	Random forest	Tree based	T1, T1pc, T2, FLAIR, DWI		0.88	81%	77%	
Kim et al. 2019[48]	143	mixed (LGG. HGG)	Database	ML	Holdout Testing Cohort in Initial Study Population	1p/19q	random forest (based on CNN features)	Tree based	T1, T1pc, T2, FLAIR	72.1%	0.691 (SD: 0.146)	87%	56.7%	
Bangalore Yoganada et al. 2020[49]	214	Glioma (nos)	Database	DL	Cross-Validation from Initial Study Population	IDH	U-Net	Neural Network	T1pc, T2, FLAIR	97.22%	0.99	98%	97%	
Sudre et al. 2020[50]	333	IDH-mutant Glioma	Multicenter	ML	Cross-Validation from Initial Study Population	IDH	Random Forest	Tree based	T2, FLAIR, DSC	71.00%		65%	77%	
Gao et al. 2020[51]	348	mixed (LGG. HGG)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	Ki67	random forest	Tree based	T1pc	80.00%	0.849	91%	80%	
Gao et al. 2020[51]	338	mixed (LGG. HGG)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	S100	random forest	Tree based	T1pc	95.00%	0.604	94%	97%	
Gao et al. 2020[51]	367	mixed (LGG. HGG)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	GFAP	random forest	Tree based	T1pc	81.00%	0.718	74%	81%	
Diamandis et al. 2018[52]	84	Glioma (nos)	Single Center, Database	ML	External Validation Cohort	IDH	Random Forest	Tree based	T1, T1pc, T2, FLAIR, MRS	94.20%				
Lu et al. 2018[53]	95	GBM	Database, Multicenter	ML	External Validation Cohort	IDH	SVM	SVM	T1pc, T2, FLAIR	88.90%	0.975	95.70%	100.00%	
Lu et al. 2018[53]	83	LGG	Database, Multicenter	ML	External Validation Cohort	IDH	SVM	SVM	T1pc, T2, FLAIR, DWI	91.70%		85.70%	100.00%	
Lu et al. 2018[53]	86	IDH-mutant Glioma	Database, Multicenter	ML	External Validation Cohort	1p/19q	SVM	SVM	T1pc, T2, FLAIR	80.00%	0.922	88.50%	86.20%	
Ozturk-Isik et al. 2020[54]	112	mixed (LGG. HGG)	Single Center	ML	Cross-Validation from Initial Study Population	IDH	SVM	SVM	T1, T1pc, T2, MRS, DSC	97.90%		95.51%	96.25%	
Kesler et al. 2019[55]	234	mixed (LGG. HGG)	Single Center	ML	Cross-Validation from Initial Study Population	IDH	Random Forest	Tree based	T1	89.00%	0.95	90%	89%	

Reference	*Number of Patients (Total)*	*Tumor Type*	*Dataset*	*Overall ML or DL*	*Prediction Results Reported from which Cohort*	*Best Results Subtype*	*Best Results Algorithm*	*Type of Algorithm*	*Sequences*	*Accuracy (ACC)*	*Area under the ROC Curve (AUC)*	*Sensitivity*	*Specificity*	*Comment*
Tan et al. 2019[56]	105	Glioma (nos)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	SVM	SVM	T1, T1pc, T2, FLAIR, DWI, fMRI	87.10%	0.900 (95% CI: 0.859–0.941)	86.7%	87.5%	
Chang et al. 2018[57]	259	mixed (LGG. HGG)	Database	DL	Holdout Testing Cohort in Initial Study Population	IDH	CNN	Neural Network	T1, T1pc, T2, FLAIR	94.00%	0.91 (95% CI: 0.89–0.92)			
Chang et al. 2018[57]	259	mixed (LGG. HGG)	Database	DL	Holdout Testing Cohort in Initial Study Population	MGMT	CNN	Neural Network	T1, T1pc, T2, FLAIR	83.00%	0.81			
Kong et al. 2020[58]	96	Grade II + III	Single Center	ML	Holdout Testing Cohort in Initial Study Population	1p/19q	Random Forest	Tree based	T1pc, T2	100.00%	0.950 (95% CI: 0.886–1.000)	80%	97.1%	
Bisdas et al. 2018[59]	37	Grade II + III	Single Center	ML	Cross-Validation from Initial Study Population	IDH	SVM	SVM	T1pc, T2, FLAIR, DWI, DKI	83.80%	0.88	92%	64%	
Kim et al. 2020[60]	155	Grade II + III	Single Center	ML	External Validation Cohort	IDH	random forest	Tree based	T1, T1pc, T2, FLAIR, DWI, DSC	65.30%	0.747 (95% CI: 0.663–0.832)	53.6%	86.7%	
Pan et al. 2019[61]	151	midline glioma or brainstem Glioma	Single Center	ML	Holdout Testing Cohort in Initial Study Population	Histone H3 K27M	random forest	Tree based	T1, T1pc, T2	84.40%	0.8298			
Goya-Outi et al. 2019[62]	30	midline glioma or brainstem Glioma	Single Center	ML	Cross-Validation from Initial Study Population	Histone H3 K27M	SVM (based on Imaging + clinical features)	SVM	T1, T1pc, T2, FLAIR					F1-Score: 0.84
Yogananda et al. 2020[63]	368	mixed (LGG. HGG)	Database	DL	Cross-Validation from Initial Study Population	1p/19q	U-Net	Neural Network	T2	93.46%	0.953			
Li et al. 2018[64]	272	Grade II + III	Single Center	ML	Holdout Testing Cohort in Initial Study Population	p53	SVM	SVM	T2	70.70%	0.763	62.2%	85.1%	
Ge et al. 2020[65]	167	mixed (LGG. HGG)	Database	DL	Holdout Testing Cohort in Initial Study Population	IDH	CNN	Neural Network	T1, T1pc, T2, FLAIR	86.53%		73.75%	92.73%	
Bumes et al. 2020[66]	34	mixed (LGG. HGG)	Single Center	ML	Cross-Validation from Initial Study Population	IDH1	SVM	SVM	F-18-FET-PET + H-MRS	88.20%	0.83	95.5%	75%	
Sakai et al. 2020[67]	100	Glioma (nos)	Single Center	ML	Cross-Validation from Initial Study Population	IDH1	XGBoost	Tree based	T1pc, FLAIR, DWI	90.00%	0.97 (95% CI: 0.898-1.000)			
Li et al. 2018[68]	186	Grade II + III	Databases (TCGA training, CGGA external validation)	ML	External Validation Cohort	ATRX	SVM	SVM	T2	76.90%	0.725	57.1%	85.7%	
Lu et al. 2020[69]	181	GBM	Single Center	ML	Holdout Testing Cohort in Initial Study Population	MGMT	Decision forest	Tree based	T1, T1pc	67.27%				
Chen et al. 2020[70]	87	GBM	Database	DL	Holdout Testing Cohort in Initial Study Population	MGMT	CNN	Neural Network	T1pc	80.40%	0.8866			
Chen et al. 2020[70]	106	GBM	Database	DL	Holdout Testing Cohort in Initial Study Population	MGMT	CNN	Neural Network	FLAIR	82.70%	0.9052			
Buda et al. 2020[71]	110	Grade II + III	Multicenter + Database	DL	Cross-Validation from Initial Study Population	Molecular information put into different Clusters (CoC)	CNN	Neural Network	FLAIR		0.730 (95% CI: 0.605-0.844)			
Sun et al. 2019[72]	239	Glioma (nos)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	VEGF	SVM	SVM	T2	72.30%	0.702	67.9%	70.6%	
Li et al. 2021[73]	572	LGG	Single Center	DL	Holdout Testing Cohort in Initial Study Population	IDH	CNN	Neural Network	T1, T1pc, T2	80.00%	0.89	81%	79%	

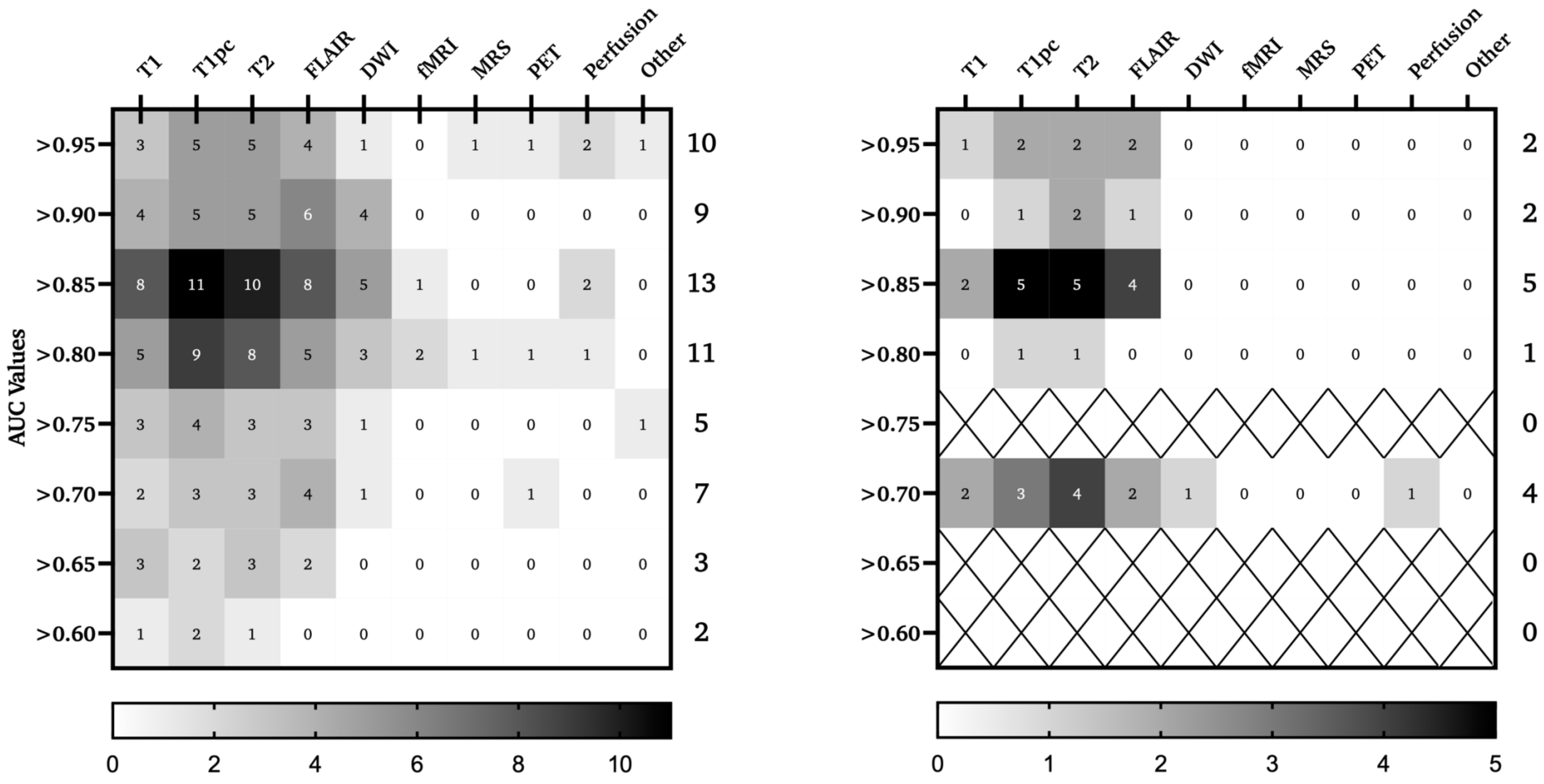
Reference	*Number of Patients (Total)*	*Tumor Type*	*Dataset*	*Overall ML or DL*	*Prediction Results Reported from which Cohort*	*Best Results Subtype*	*Best Results Algorithm*	*Type of Algorithm*	*Sequences*	*Accuracy (ACC)*	*Area under the ROC Curve (AUC)*	*Sensitivity*	*Specificity*	*Comment*
Li et al. 2021[73]	334	IDH-mutant Glioma	Single Center	DL	Holdout Testing Cohort in Initial Study Population	1p/19q	CNN	Neural Network	T1, T1pc, T2	83.00%	0.85	85%	79%	
Li et al. 2021[73]	444	mixed (LGG. HGG)	Single Center	DL	Holdout Testing Cohort in Initial Study Population	IDH	CNN	Neural Network	T1, T1pc, T2	74.00%	0.66	47%	80%	
Kandemirli et al. 2021[74]	109	midline glioma or brainstem Glioma	Multicenter	ML	Holdout Testing Cohort in Initial Study Population	Histone H3 K27M	XGBoost	Tree based	T1, T1pc, T2, FLAIR, DWI	72.70%	0.737			
Yan et al. 2021[75]	357	mixed (LGG. HGG)	Single Center	DL	Holdout Testing Cohort in Initial Study Population	IDH	Bayesian-regularization neural networks (BRNN)	Neural Network	T1, T1pc, T2, FLAIR, DWI	82.40%	0.884 (95% CI: 0.830–0.934)	75%	89.8%	
Zaragori et al. 2021[76]	72	Glioma (nos)	Single Center	ML	Cross-Validation from Initial Study Population	1p/19q	SVM	SVM	18F-FDOPA PET		0.724 (95% CI: 0.669-0.782)			
Yogananda et al. 2021[77]	274	Glioma (nos)	Database	DL	Cross-Validation from Initial Study Population	MGMT	3D-dense-UNet	Neural Network	T2	94.73%	0.93	96.31%	91.66%	
Wagner et al. 2021[78]	115	Pediatric LGG	Single Center, Mult Center	ML	External Validation Cohort	BRAF	random forest	Tree based	T1pc, T2, FLAIR		0.85			
Peng et al. 2021[79]	105	mixed (LGG. HGG)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	SVM	SVM	T1pc, T2, fMRI	77.00%	0.823 (95% CI: 0.715-0.931)	76.5%	77.6%	
Park et al. 2021[80]	111	LGG	Multicenter + Database	ML	External Validation Cohort	TERT or EGFR as molecular features of glioblastomas	(SVM + XGBoost + AdaBoost + linear discriminant analysis) + RFE	Other	T1, T1pc, T2, FLAIR		0.863 (95% CI: 0.778–0.947)			
Fan et al. 2021[81]	157	LGG	Database	ML	Cross-Validation from Initial Study Population	1p/19q	SVM	SVM	T1, T1pc, T2	75.80%	0.8079 (95% CI: 0.733–0.8755)	58.46%	88.04%	
Decuyper et al. 2021[82]	738	mixed (LGG. HGG)	Database, Single Center	DL	External Validation Cohort	IDH	3D U Net	Neural Network	T1pc, either T2 or FLAIR	75.58%	0.8623	84.38%	70.37%	
Cao et al. 2021[83]	102	mixed (LGG. HGG)	Single Center	ML	Holdout Testing Cohort in Initial Study Population	IDH	random forest	Tree based	T1, T1pc, T2, FLAIR, DWI	74.30%	0.849	72.4%	76.1%	
Choi et al. 2019[84]	463	Glioma (nos)	Single Center	DL	Holdout Testing Cohort in Initial Study Population	IDH	Recurrent Neural Network	Neural Network	T1, T1pc, T2, FLAIR, DSC	91.70%	0.95 (95% CI. 0.898–0.982)	92.1%	91.5%	
Chang et al. 2018[85]	469	mixed (LGG, HGG)	Multicenter + Database	DL	Holdout Testing Cohort in Initial Study Population	IDH	CNN	Neural Network	T1, T1pc, T2	82.10%	0.85 (95% CI: 0.82-0.88)	79.1%	87.00%	



Supplementary Figure 1. Forest plots on all studies eligible for metanalysis. *27 Studies reported AUC values with 95% CI from the previously mentioned 95 studies and were eligible for this meta-analysis. The studies were split up into internal validation (n=21/77) and external validation (n=6/18) studies and were tested separately with a random effects model. Within the internal validation studies, an overall AUC of 0.865 (95% CI 0.834 to 0.897) was attained. Testing for heterogeneity resulted in an inconsistency of 82.70% (95% CI 74.61 to 88.22) with significance of p < 0.0001. Due to high heterogeneity in internal validation studies, we conducted a subgroup analysis divided by types of prediction models used (See 3.4 and Figure 5). While the inconsistency in seven Tree based studies (69.34% with 95% CI 32.56% to 86.06% and p = 0.0033), eight SVM based (80.12% with 95% CI 61.48% to 89.74% and p < 0.0001) and three other studies (71.74% with 95% CI 4.25% to 91.66% and p = 0.0291) was smaller while still being relatively high, the inconsistency was even higher within three Neural Network-based studies with 88.66% (95% CI 68.74% to 95.89% with p = 0.0001).*
Within external validation studies the overall random effect AUC was 0.816 with 95% CI from 0.751 to 0.882. We only were able to conduct subgroup analysis on three Tree based studies (Inconsistency of 65.89% 95% CI from 0% to 90.19%) with p = 0.0001) and two other studies (Inconsistency of 0% with p = 0.6149).



Supplementary Figure 2. Overall data sources used in 85 studies. Due to 17 studies using multiple sources of data, the overall number raises to 102.



	T1	T1pc	T2	FLAIR	DWI	fMRI	MRS	PET	Perfusion	Other	
>0.95	3	5	5	4	1	0	1	1	2	1	10
>0.90	4	5	5	6	4	0	0	0	0	0	9
>0.85	8	11	10	8	5	1	0	0	2	0	13
>0.80	5	9	8	5	3	2	1	1	1	0	11
>0.75	3	4	3	3	1	0	0	0	0	1	5
>0.70	2	3	3	4	1	0	0	1	0	0	7
>0.65	3	2	3	2	0	0	0	0	0	0	3
>0.60	1	2	1	0	0	0	0	0	0	0	2

	T1	T1pc	T2	FLAIR	DWI	fMRI	MRS	PET	Perfusion	Other	
>0.95	1	2	2	2	0	0	0	0	0	0	2
>0.90	0	1	2	1	0	0	0	0	0	0	2
>0.85	2	5	5	4	0	0	0	0	0	0	5
>0.80	0	1	1	0	0	0	0	0	0	0	1
>0.75											0
>0.70	2	3	4	2	1	0	0	0	1	0	4
>0.65											0
>0.60											0

Supplementary Figure 3. Different sequences and radiological imaging techniques used. Included studies for reported AUC values for their pipelines. Only 74 studies reported AUC values. We divided internally validated data (n=60/74) on the left from externally validated data (n=14/74) on the right. Numbers on the right of the heatmap indicate overall included number of studies represented in the respective AUC spectrum.

Score / Domain	*D1 - D*	*D1 - V*	*D2 - D*	*D2 - V*	*D3 - D*	*D3 - V*	*D4 - D*	*D4 - V*	*Overall ROB*
LOW	88.23%	82.35%	62.35%	82.35%	80%	88.24%	0	0	0
HIGH	7.06%	0	4.71%	5.89%	3.53%	0	100%	100%	100%
UNCLEAR	4.71%	17.65%	32.94%	11.76%	16.47%	11.76%	0	0	0

Supplementary Figure 4. PROBAST scores from each domain. ROB = risk of bias.

1. Park, J.E., et al., *Prediction of Core Signaling Pathway by Using Diffusion- and Perfusion-based MRI Radiomics and Next-generation Sequencing in Isocitrate Dehydrogenase Wild-type Glioblastoma.* Radiology, 2020. **294**(2): p. 388-397.
2. Lee, M.H., et al., *Prediction of IDH1 Mutation Status in Glioblastoma Using Machine Learning Technique Based on Quantitative Radiomic Data.* World Neurosurg, 2019. **125**: p. e688-e696.
3. Kanas, V.G., et al., *Learning MRI-based classification models for MGMT methylation status prediction in glioblastoma.* Comput Methods Programs Biomed, 2017. **140**: p. 249-257.
4. Su, X., et al., *Automated machine learning based on radiomics features predicts H3 K27M mutation in midline gliomas of the brain.* Neuro Oncol, 2020. **22**(3): p. 393-401.
5. Chen, L., et al., *Multi-Label Nonlinear Matrix Completion With Transductive Multi-Task Feature Selection for Joint MGMT and IDH1 Status Prediction of Patient With High-Grade Gliomas.* IEEE Trans Med Imaging, 2018. **37**(8): p. 1775-1787.
6. Liu, J., et al., *A Cascaded Deep Convolutional Neural Network for Joint Segmentation and Genotype Prediction of Brainstem Gliomas.* IEEE Trans Biomed Eng, 2018. **65**(9): p. 1943-1952.
7. Choi, Y., et al., *IDH1 mutation prediction using MR-based radiomics in glioblastoma: comparison between manual and fully automated deep learning-based approach of tumor segmentation.* Eur J Radiol, 2020. **128**: p. 109031.
8. Hedyehzadeh, M., et al., *A Comparison of the Efficiency of Using a Deep CNN Approach with Other Common Regression Methods for the Prediction of EGFR Expression in Glioblastoma Patients.* J Digit Imaging, 2020. **33**(2): p. 391-398.
9. Li, Z.-C., et al., *Multiregional Radiomics Phenotypes at MR Imaging Predict MGMT Promoter Methylation in Glioblastoma*, in *World Congress on Medical Physics and Biomedical Engineering 2018*. 2019. p. 143-146.
10. Qian, J., et al., *Prediction of MGMT Status for Glioblastoma Patients Using Radiomics Feature Extraction From (18)F-DOPA-PET Imaging.* Int J Radiat Oncol Biol Phys, 2020. **108**(5): p. 1339-1346.
11. Li, Z.C., et al., *Multiregional radiomics profiling from multiparametric MRI: Identifying an imaging predictor of IDH1 mutation status in glioblastoma.* Cancer Med, 2018. **7**(12): p. 5999-6009.
12. Jung, J.S., et al., *Differentiation between spinal cord diffuse midline glioma with histone H3 K27M mutation and wild type: comparative magnetic resonance imaging.* Neuroradiology, 2019. **61**(3): p. 313-322.
13. Zhang, B., et al., *Multimodal MRI features predict isocitrate dehydrogenase genotype in high-grade gliomas.* Neuro Oncol, 2017. **19**(1): p. 109-117.
14. Lo, C.M., et al., *Computer-aided diagnosis of isocitrate dehydrogenase genotypes in glioblastomas from radiomic patterns.* Medicine (Baltimore), 2020. **99**(8): p. e19123.
15. Korfiatis, P., et al., *MRI texture features as biomarkers to predict MGMT methylation status in glioblastomas.* Med Phys, 2016. **43**(6): p. 2835-2844.
16. Hajianfar, G., et al., *Noninvasive O6 Methylguanine-DNA Methyltransferase Status Prediction in Glioblastoma Multiforme Cancer Using Magnetic Resonance Imaging Radiomics Features: Univariate and Multivariate Radiogenomics Analysis.* World Neurosurg, 2019. **132**: p. e140-e161.
17. Korfiatis, P., et al., *Residual Deep Convolutional Neural Network Predicts MGMT Methylation Status.* J Digit Imaging, 2017. **30**(5): p. 622-628.
18. Li, Y., et al., *Radiogenomic analysis of PTEN mutation in glioblastoma using preoperative multi-parametric magnetic resonance imaging.* Neuroradiology, 2019. **61**(11): p. 1229-1237.
19. Calabrese, E., J.E. Villanueva-Meyer, and S. Cha, *A fully automated artificial intelligence method for non-invasive, imaging-based identification of genetic alterations in glioblastomas.* Sci Rep, 2020. **10**(1): p. 11852.
20. Yamashita, K., et al., *Predicting TERT promoter mutation using MR images in patients with wild-type IDH1 glioblastoma.* Diagn Interv Imaging, 2019. **100**(7-8): p. 411-419.
21. Han, L.K., M. R., *MRI to MGMT: predicting methylation status in glioblastoma patients using convolutional recurrent neural networks.* Biocomputing, 2018.
22. Xi, Y.B., et al., *Radiomics signature: A potential biomarker for the prediction of MGMT promoter methylation in glioblastoma.* J Magn Reson Imaging, 2018. **47**(5): p. 1380-1387.
23. Le, N.Q.K., et al., *XGBoost Improves Classification of MGMT Promoter Methylation Status in IDH1 Wildtype Glioblastoma.* J Pers Med, 2020. **10**(3).
24. Alis, D., et al., *Machine learning-based quantitative texture analysis of conventional MRI combined with ADC maps for assessment of IDH1 mutation in high-grade gliomas.* Jpn J Radiol, 2020. **38**(2): p. 135-143.
25. Akbari, H., et al., *In vivo evaluation of EGFRvIII mutation in primary glioblastoma patients via complex multiparametric MRI signature.* Neuro Oncol, 2018. **20**(8): p. 1068-1079.
26. Ahmad, A.S., S.; Shah, A.; Gore, S.; Santosh, V.; Saini, J.; Ingalhalikar, M.; Ieee,, *Predictive and discriminative localization of IDH genotype in high grade gliomas using deep convolutional neural nets.* 2019.
27. Crisi, G. and S. Filice, *Predicting MGMT Promoter Methylation of Glioblastoma from Dynamic Susceptibility Contrast Perfusion: A Radiomic Approach.* J Neuroimaging, 2020. **30**(4): p. 458-462.
28. Yu, J., et al., *Anatomical location differences between mutated and wild-type isocitrate dehydrogenase 1 in low-grade gliomas.* Int J Neurosci, 2017. **127**(10): p. 873-880.
29. Fukuma, R., et al., *Prediction of IDH and TERT promoter mutations in low-grade glioma from magnetic resonance images using a convolutional neural network.* Sci Rep, 2019. **9**(1): p. 20311.

30. Ren, Y., et al., *Noninvasive Prediction of IDH1 Mutation and ATRX Expression Loss in Low-Grade Gliomas Using Multiparametric MR Radiomic Features.* J Magn Reson Imaging, 2019. **49**(3): p. 808-817.
31. Yu, J., et al., *Noninvasive IDH1 mutation estimation based on a quantitative radiomics approach for grade II glioma.* Eur Radiol, 2017. **27**(8): p. 3509-3522.
32. Zhang, X., et al., *Radiomics Strategy for Molecular Subtype Stratification of Lower-Grade Glioma: Detecting IDH and TP53 Mutations Based on Multimodal MRI.* J Magn Reson Imaging, 2018. **48**(4): p. 916-926.
33. Li, Z., et al., *Deep Learning based Radiomics (DLR) and its usage in noninvasive IDH1 prediction for low grade glioma.* Sci Rep, 2017. **7**(1): p. 5467.
34. Jiang, C., et al., *Fusion Radiomics Features from Conventional MRI Predict MGMT Promoter Methylation Status in Lower Grade Gliomas.* Eur J Radiol, 2019. **121**: p. 108714.
35. Kuthuru, S., et al., *A Visually Interpretable, Dictionary-Based Approach to Imaging-Genomic Modeling, With Low-Grade Glioma as a Case Study.* Cancer Inform, 2018. **17**: p. 1176935118802796.
36. van der Voort, S.R., et al., *Predicting the 1p/19q Codeletion Status of Presumed Low-Grade Glioma with an Externally Validated Machine Learning Algorithm.* Clin Cancer Res, 2019. **25**(24): p. 7455-7462.
37. Shofty, B., et al., *MRI radiomics analysis of molecular alterations in low-grade gliomas.* Int J Comput Assist Radiol Surg, 2018. **13**(4): p. 563-571.
38. Akkus, Z., et al., *Predicting Deletion of Chromosomal Arms 1p/19q in Low-Grade Gliomas from MR Images Using Machine Intelligence.* J Digit Imaging, 2017. **30**(4): p. 469-476.
39. Ali, M.B., et al., *Domain Mapping and Deep Learning from Multiple MRI Clinical Datasets for Prediction of Molecular Subtypes in Low Grade Gliomas.* Brain Sci, 2020. **10**(7).
40. Eichinger, P., et al., *Diffusion tensor image features predict IDH genotype in newly diagnosed WHO grade II/III gliomas.* Sci Rep, 2017. **7**(1): p. 13396.
41. Jiang, C., et al., *Conventional magnetic resonance imaging-based radiomic signature predicts telomerase reverse transcriptase promoter mutation status in grade II and III gliomas.* Neuroradiology, 2020. **62**(7): p. 803-813.
42. Park, C.J., et al., *Diffusion tensor imaging radiomics in lower-grade glioma: improving subtyping of isocitrate dehydrogenase mutation status.* Neuroradiology, 2020. **62**(3): p. 319-326.
43. Matsui, Y., et al., *Prediction of lower-grade glioma molecular subtypes using deep learning.* J Neurooncol, 2020. **146**(2): p. 321-327.
44. Kocak, B., et al., *Radiogenomics of lower-grade gliomas: machine learning-based MRI texture analysis for predicting 1p/19q codeletion status.* Eur Radiol, 2020. **30**(2): p. 877-886.
45. Han, Y., et al., *Amide Proton Transfer Imaging in Predicting Isocitrate Dehydrogenase 1 Mutation Status of Grade II/III Gliomas Based on Support Vector Machine.* Front Neurosci, 2020. **14**: p. 144.
46. Nalawade, S., et al., *Classification of brain tumor isocitrate dehydrogenase status using MRI and deep learning.* J Med Imaging (Bellingham), 2019. **6**(4): p. 046003.
47. De Looze, C., et al., *Machine learning: a useful radiological adjunct in determination of a newly diagnosed glioma's grade and IDH status.* J Neurooncol, 2018. **139**(2): p. 491-499.
48. Kim, D., et al., *Prediction of 1p/19q Codeletion in Diffuse Glioma Patients Using Pre-operative Multiparametric Magnetic Resonance Imaging.* Front Comput Neurosci, 2019. **13**: p. 52.
49. Bangalore Yogananda, C.G., et al., *A novel fully automated MRI-based deep-learning method for classification of IDH mutation status in brain gliomas.* Neuro Oncol, 2020. **22**(3): p. 402-411.
50. Sudre, C.H., et al., *Machine learning assisted DSC-MRI radiomics as a tool for glioma classification by grade and mutation status.* BMC Med Inform Decis Mak, 2020. **20**(1): p. 149.
51. Gao, M., et al., *Machine Learning-Based Radiomics Predicting Tumor Grades and Expression of Multiple Pathologic Biomarkers in Gliomas.* Front Oncol, 2020. **10**: p. 1676.
52. Diamandis, E., et al., *MR-spectroscopic imaging of glial tumors in the spotlight of the 2016 WHO classification.* J Neurooncol, 2018. **139**(2): p. 431-440.
53. Lu, C.F., et al., *Machine Learning-Based Radiomics for Molecular Subtyping of Gliomas.* Clin Cancer Res, 2018. **24**(18): p. 4429-4436.
54. Ozturk-Isik, E., et al., *Identification of IDH and TERTp mutation status using (1) H-MRS in 112 hemispheric diffuse gliomas.* J Magn Reson Imaging, 2020. **51**(6): p. 1799-1809.
55. Kesler, S.R., et al., *Pre-surgical connectome features predict IDH status in diffuse gliomas.* Oncotarget, 2019. **10**(60): p. 6484-6493.
56. Tan, Y., et al., *A radiomics nomogram may improve the prediction of IDH genotype for astrocytoma before surgery.* Eur Radiol, 2019. **29**(7): p. 3325-3337.
57. Chang, P., et al., *Deep-Learning Convolutional Neural Networks Accurately Classify Genetic Mutations in Gliomas.* AJNR Am J Neuroradiol, 2018. **39**(7): p. 1201-1207.
58. Kong, Z., et al., *Thin-Slice Magnetic Resonance Imaging-Based Radiomics Signature Predicts Chromosomal 1p/19q Co-deletion Status in Grade II and III Gliomas.* Front Neurol, 2020. **11**: p. 551771.
59. Bisdas, S., et al., *Texture analysis- and support vector machine-assisted diffusional kurtosis imaging may allow in vivo gliomas grading and IDH-mutation status prediction: a preliminary study.* Sci Rep, 2018. **8**(1): p. 6108.
60. Kim, M., et al., *Diffusion- and perfusion-weighted MRI radiomics model may predict isocitrate dehydrogenase (IDH) mutation and tumor aggressiveness in diffuse lower grade glioma.* Eur Radiol, 2020. **30**(4): p. 2142-2151.
61. Pan, C.C., et al., *A machine learning-based prediction model of H3K27M mutations in brainstem gliomas using conventional MRI and clinical features.* Radiother Oncol, 2019. **130**: p. 172-179.
62. Goya-Outi, J.C., R.; Orlhac, F.; Philippe, C.; Boddaert, N.; Puget, E.; Buvat, I.; Frouin, V.; Grill, J.; Frouin, F.; Ieee,, *Can Structural MRI Radiomics Predict DIPG Histone H3 Mutation and Patient Overall Survival at Diagnosis Time?* 2019.
63. Yogananda, C.G.B., et al., *A novel fully automated MRI-based deep-learning method for classification of 1p/19q co-deletion status in brain gliomas.* Neurooncol Adv, 2020. **2**(1): p. vdaa066.
64. Li, Y., et al., *MRI features predict p53 status in lower-grade gliomas via a machine-learning approach.* Neuroimage Clin, 2018. **17**: p. 306-311.
65. Ge, C., et al., *Deep semi-supervised learning for brain tumor classification.* BMC Med Imaging, 2020. **20**(1): p. 87.
66. Bumes, E., et al., *Non-Invasive Prediction of IDH Mutation in Patients with Glioma WHO II/III/IV Based on F-18-FET PET-Guided In Vivo (1)H-Magnetic Resonance Spectroscopy and Machine Learning.* Cancers (Basel), 2020. **12**(11).
67. Sakai, Y., et al., *MRI Radiomic Features to Predict IDH1 Mutation Status in Gliomas: A Machine Learning Approach using Gradient Tree Boosting.* Int J Mol Sci, 2020. **21**(21).
68. Li, Y., et al., *Genotype prediction of ATRX mutation in lower-grade gliomas using an MRI radiomics signature.* Eur Radiol, 2018. **28**(7): p. 2960-2968.
69. Lu, Y., et al., *Machine learning-based radiomic, clinical and semantic feature analysis for predicting overall survival and MGMT promoter methylation status in patients with glioblastoma.* Magn Reson Imaging, 2020. **74**: p. 161-170.
70. Chen, X., et al., *Automatic Prediction of MGMT Status in Glioblastoma via Deep Learning-Based MR Image Analysis.* Biomed Res Int, 2020. **2020**: p. 9258649.
71. Buda, M., et al., *Deep Radiogenomics of Lower-Grade Gliomas: Convolutional Neural Networks Predict Tumor Genomic Subtypes Using MR Images.* Radiol Artif Intell, 2020. **2**(1): p. e180050.
72. Sun, Z., et al., *Radiogenomic analysis of vascular endothelial growth factor in patients with diffuse gliomas.* Cancer Imaging, 2019. **19**(1): p. 68.
73. Li, Y., et al., *Molecular subtyping of diffuse gliomas using magnetic resonance imaging: comparison and correlation between radiomics and deep learning.* Eur Radiol, 2022. **32**(2): p. 747-758.
74. Kandemirli, S.G., et al., *Machine Learning-Based Multiparametric Magnetic Resonance Imaging Radiomics for Prediction of H3K27M Mutation in Midline Gliomas.* World Neurosurg, 2021. **151**: p. e78-e85.
75. Yan, J., et al., *Quantitative MRI-based radiomics for noninvasively predicting molecular subtypes and survival in glioma patients.* NPJ Precis Oncol, 2021. **5**(1): p. 72.
76. Zaragori, T., et al., *(18)F-FDOPA PET for the Noninvasive Prediction of Glioma Molecular Parameters: A Radiomics Study.* J Nucl Med, 2022. **63**(1): p. 147-157.
77. Yogananda, C.G.B., et al., *MRI-Based Deep-Learning Method for Determining Glioma MGMT Promoter Methylation Status.* AJNR Am J Neuroradiol, 2021. **42**(5): p. 845-852.
78. Wagner, M.W., et al., *Radiomics of Pediatric Low-Grade Gliomas: Toward a Pretherapeutic Differentiation of BRAF-Mutated and BRAF-Fused Tumors.* AJNR Am J Neuroradiol, 2021. **42**(4): p. 759-765.
79. Peng, H., et al., *Predicting Isocitrate Dehydrogenase (IDH) Mutation Status in Gliomas Using Multiparameter MRI Radiomics Features.* J Magn Reson Imaging, 2021. **53**(5): p. 1399-1407.
80. Park, C.J., et al., *MRI Features May Predict Molecular Features of Glioblastoma in Isocitrate Dehydrogenase Wild-Type Lower-Grade Gliomas.* AJNR Am J Neuroradiol, 2021. **42**(3): p. 448-456.
81. Fan, Z., et al., *Preoperative Radiomics Analysis of 1p/19q Status in WHO Grade II Gliomas.* Front Oncol, 2021. **11**: p. 616740.
82. Decuyper, M., et al., *Automated MRI based pipeline for segmentation and prediction of grade, IDH mutation and 1p19q co-deletion in glioma.* Comput Med Imaging Graph, 2021. **88**: p. 101831.
83. Cao, M., et al., *Qualitative and Quantitative MRI Analysis in IDH1 Genotype Prediction of Lower-Grade Gliomas: A Machine Learning Approach.* Biomed Res Int, 2021. **2021**: p. 1235314.
84. Choi, K.S., S.H. Choi, and B. Jeong, *Prediction of IDH genotype in gliomas with dynamic susceptibility contrast perfusion MR imaging using an explainable recurrent neural network.* Neuro Oncol, 2019. **21**(9): p. 1197-1209.
85. Chang, K., et al., *Residual Convolutional Neural Network for the Determination of IDH Status in Low- and High-Grade Gliomas from MR Imaging.* Clin Cancer Res, 2018. **24**(5): p. 1073-1081.