Supplement 1 – Search terms, quality assessment and data extraction tables

Table S1. Search terms

Glioma	(glioma OR gliomas OR glioblastoma OR glioblastomas OR astrocytoma OR astrocytomas OR astrocytic OR oligodendrogli* OR oligoastrocyt*).tiab
AND	
Classification	(histology OR histologic OR molecular OR genetic OR mutation OR mutant OR mutated OR co-delet* OR pathophysiologic* OR methyl* OR MGMT OR amplifi* OR EGFR).tiab
AND	
Localization *(For research question 1 only)*	(location* OR localization* OR lobe* OR radiographic* OR radiologic*) .tiab
AND	
Extent of resection *(For research question 2 only)*	("extent of resection" OR "extent of surgery" OR "gross total resection" OR "complete resection" OR "complete surgical resection" OR "subtotal resection" OR "subtotal surgical resection" OR "incomplete resection" OR "incomplete surgical resection" OR "partial resection" OR "partial surgical resection" OR "type of surgery" OR debulking).tiab

Table S2. Quality assessment signaling questions and score

Signaling question	**Maximum number of points**
Was the study population clearly specified and defined?	2
Was the participation rate of eligible persons at least 50%?	1
Was the study performed in a population of at least 50 participants?	1
Were participants selected consecutively (uniform application of inclusion and exclusion criteria and participants from the same or similar populations)?	2
Was mutational status clearly defined, valid, reliable, and implemented consistently across all study participants?	2
Was anatomical localization (question 1) or EoR / type of surgery (question 2) clearly defined, valid, reliable, and implemented consistently across all study participants?	3
Were the outcome assessors blinded to the mutational status of the examined tumors?	1
Does the study sample match the review domain in its full breadth (minimization of selection bias)?	4
Maximum number of points	16

Table S3. Definition of data extraction items

Study	first author and year of publication
Selection of participants	duration and years of sample collection, inclusion and exclusion criteria
Patient characteristics	number of participants, gender distribution, age (either mean or median, and range), type of glioma (histology, grade and distribution hereof)
Molecular markers	molecular markers investigated
Anatomical localization (research question 1)	anatomical localizations reported
Extent of resection (research question 2)	threshold(s) applied for EoR or types of surgery compared
Statistics	statistical tests performed
Outcomes	conclusions regarding relation of molecular markers to - localization (research question 1) and/or - EoR or type of surgery (research question 2) and reported frequencies of occurrence regarding these relations

Supplement 2 – Quality assessment scoring system

Points / Quality item	0	1	2	3	4
Description of study population: 1. Age 2. Tumor type (histological or molecular) 3. Tumor grade	Two or more characteristics are missing	One of three characteristics is missing	All three characteristics are described	x	x
Participation rate of eligible persons	< 50% or unknown	≥ 50%	x	x	x
Sample size	< 50 participants	≥ 50 participants	x	x	x
Consecutive selection of participants: 1. Time period 2. In- and/or exclusion criteria 3. Number of persons in- or excluded per criterion	Items other than no. 3 are missing	Only item 3 is missing	All three items are described	x	x
Determination of mutation status	Unknown	Fluorescence in situ hybridiza-tion or immuno-histochemistry	Polymerase chain reaction / next generation sequencing	x	x
Determination of anatomical location / extent of resection	Unknown	CT, 'radiological' or 'imaging' (unspecified whether this indicates MRI)	MRI (anatomical location: without defining anatomical locations EoR: application of other sequences than described in the adjacent column or without specifying applied sequences)	MRI (anatomical location: with definitions of allocated anatomical locations EoR: application of T2 or FLAIR sequences in low-grade and T1 sequences with contrast in high-grade glioma)	x
Blinding	Not applied or unknown	Applied	x	x	x
Minimization of selection bias	A maximum of 4 points can be allocated for this quality item. The following features are grounds for deduction of points. - Selection based on tumor grade (-1 point) - Selection based on tumor histology, mutation status, anatomical location or treatment (-2 points per selection criterion) - No mention of selection (in- or exclusion) criteria (-4 points)				

Supplement 3 – Quality assessment

Table S4. Assessment of methodological quality and risk of bias of studies included for Research Question 1

	Description of study population	Participation rate ≥ 50%	No. of participants ≥ 50	Consecutive inclusion of participants	Reliable determination of mutational status	Reliable determination of localization	Blinding	Minimization of selection bias	Quality score
Arita 2018[1]	+	-	+	-	+	+	-	+	10 (IDH, 1p/19q, TERT, MGMT)
Izquierdo 2019[2]	+	-	+	=	+	+	-	-	8 (TERT)
Kanazawa 2019[3]	+	-	-	=	+	+	+	+	11 (IDH, 1p/19q, MGMT)
Kim 2018[4]	+	-	+	=	+	+	+	+	13 (IDH, TERT, MGMT)
Li 2018[5]	+	-	+	=	+	+	+	-	9 (IDH, MGMT)
Park 2018[6]	+	-	+	+	+	+	+	+	13 (IDH)
	+	-	+	+	=	+	+	+	12 (1p/19q)
Villanueva-Meyer 2018[7]	=	-	+	=	=	+	+	+	10 (IDH)
Wang 2018[8]	+	-	+	=	=	+	+	=	9 (1p/19q)
Williams 2018[9]	+	-	+	+	+	-	-	+	10 (MGMT)
	+	-	+	+	+	-	-	=	8 (TERT)
Akyerli 2018[10]	+	-	+	-	+	-	-	+	8 (TERT)
Darlix 2017[11]	+	+	+	+	+	+	+	+	14 (IDH, 1p/19q)
Delfanti 2017[12]	+	+	-	+	=	+	+	+	12 (IDH, 1p/19q)
Lasocki 2017[13]	=	+	+	+	=	+	-	=	9 (IDH)
Pai 2017[14]	+	+	+	+	=	-	-	=	9 (1p/19q)
Patel 2018[15]	+	-	+	+	=	-	-	+	9 (IDH)
Wijnenga 2018[16]	+	+	+	+	+	-	-	=	10 (IDH, 1p/19q)
Yang 2016[17]	+	-	+	=	+	+	-	=	10 (IDH)
Yuan 2016[18]	=	-	+	=	=	+	-	=	8 (MGMT, P53, EGFR)

Zhang 2016[19]	+	-	+	=	+	-	-	+	9 (IDH)
	+	-	+	=	=	-	-	+	8 (EGFR)
Eckel-Passow 2015[20]	+	-	+	=	+	=	-	+	11 (IDH, TERT)
	+	-	+	=	=	-	-	+	9 (1p/19q)
Sun 2015[21]	+	-	+	=	=	+	+	+	11 (IDH, TERT)
Kizilbash 2014[22]	=	+	+	+	+	+	-	-	9 (IDH)
Nishiyama 2014[23]	+	-	+	=	+	+	-	+	11 (IDH, 1p/19q)
Qi 2014[24]	+	-	+	=	+	+	+	=	10 (IDH)
Reclacowicz 2013[25]	+	+	-	+	=	-	-	+	9 (1p/19q)
Carrillo 2012[26]	+	-	+	-	+	+	+	-	8 (MGMT)
Singh 2012[27]	+	-	-	+	+	-	-	=	8 (MGMT)
Hirose 2011[28]	+	-	+	=	+	-	-	+	9 (1p/19q)
Kim 2011[29]	+	-	+	=	=	+	+	=	9 (1p/19q)
Drabycz 2010[30]	+	+	+	+	+	+	+	+	14 (MGMT)
Metellus 2010[31]	+	-	-	=	+	+	+	=	10 (IDH)
Sherman 2010[32]	=	+	+	+	=	+	+	=	10 (1p/19q)
Scheie 2008[33]	+	+	+	+	+	+	-	=	11 (1p/19q)
Mut 2007[34]	+	-	+	=	=	+	+	+	11 (P53)

Table S5. Assessment of methodological quality and risk of bias of studies included for Research Question 2

	Description of study population	Participation rate ≥ 50%	No. of participants ≥ 50	Consecutive inclusion of participants	Reliable determination of mutational status	Reliable determination of extent of resection	Blinding	Minimization of selection bias	Quality score
Gessler 2019[35]	+	+	+	+	+	+	+	=	13 (MGMT)
Aoki 2018[36]	+	-	+	-	+	-	-	+	8 (IDH, 1p/19q)
Delfanti 2017[12]	+	-	+	+	=	-	-	+	9 (IDH, 1p/19q)
Eseonu 2017[37]	=	+	-	=	-	+	+	=	8 (1p/19q)
Patel 2018[15]	+	-	+	+	=	+	+	+	13 (IDH)
Wijnenga 2018[16]	+	+	+	+	+	+	-	=	13 (IDH, 1p/19q)
Yan 2017[38]	+	-	-	-	+	+	-	=	8 (MGMT)
Jungk 2016[39]	+	+	-	+	=	+	-	=	10 (IDH)
Tang 2016[40]	+	-	-	=	+	+	-	=	9 (IDH)
Cordier 2015[41]	+	+	+	=	+	+	-	=	12 (IDH, 1p/19q)
	+	+	+	=	=	+	-	=	11 (P53)
Eckel-Passow 2015[20]	+	-	+	=	=	-	-	+	9 (IDH, 1p/19q, TERT)
Aihara 2014[42]	+	+	-	+	+	-	-	=	9 (MGMT)
Kizilbash 2014[22]	=	+	+	+	+	+	-	-	9 (IDH)
Qi 2014[24]	+	-	+	=	+	+	+	=	10 (IDH)
Zhang 2014[43]	+	+	-	+	+	-	-	=	9 (IDH, TERT)
	+	+	-	+	=	-	-	=	8 (1p/19q)
Singh 2012[27]	+	-	-	+	+	-	-	=	8 (MGMT)
Hirose 2011[28]	+	-	+	=	+	+	-	+	11 (1p/19q)
Mut 2007[34]	+	-	+	=	=	-	-	+	8 (P53)

Supplement 4 – Data on other mutations

Mutation status and anatomical location

TERT promoter mutation

Multiple studies describe correlations between TERT promoter mutation status and anatomical location. TERT-mutant tumors were more frequently found in the frontal[1,2,4] and parietal lobe[2]. Studies report conflicting correlations between TERT mutation and localization in the temporal[1,2] and insular lobe[2,10]. TERT-wildtype gliomas would more often be located in the brainstem[2], midline[4] and cerebellum[9] compared to TERT-mutant tumors. However, results of several studies demonstrate absence of an association between TERT mutation status and anatomical location[20,21] or midline localization[21].

MGMT promoter methylation

Several studies report associations between MGMT promoter methylation status and anatomical location. A high frequency of MGMT-wildtype tumors in the right medial frontal lobe is described.[18] However, comparative results regarding frontal[1,5] and temporal[3,5] localization of gliomas stratified by MGMT promoter methylation status are ambivalent. Unmethylated tumors have been found more frequently in the basal ganglia[1] and showed surface[3] and multifocal[26] localization more often compared to methylated tumors. In contrast, findings of multiple studies do not suggest a correlation between MGMT methylation and tumor localization.[4,9,26,27,30]

EGFR gene amplification

Studies that performed EGFR analyses report that gliomas displaying EGFR-overexpression were relatively often localized around the left anterior horn of the lateral ventricle[18] and predominantly in the hemispheres without affecting the midline[19].

P53 mutation

One study describes finding high frequencies of P53-mutant tumors in the anterior temporal lobe, left insula and left lentiform nucleus.[18] Another concluded that different degree of P53 expression did not predict preference for lesion location.[34]

Mutation status and EoR

TERT promoter mutation

Findings of studies that performed TERT promoter mutation analyses demonstrate no correlation between mutation status and EoR.[20,43]

MGMT promoter methylation

None of the findings of the included studies suggested a correlation between MGMT promoter methylation status and EoR.[27,35,38,42]

P53 mutation

Studies report absence of an association between P53 mutation status and EoR.[34,41]

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