

Figure S1 Single sample Gene Set Enrichment Analysis (ssGSEA) of LGG cohort in TCGA. Enrichment scores of 28 immune cells in 505 LGG samples of TCGA cohort.

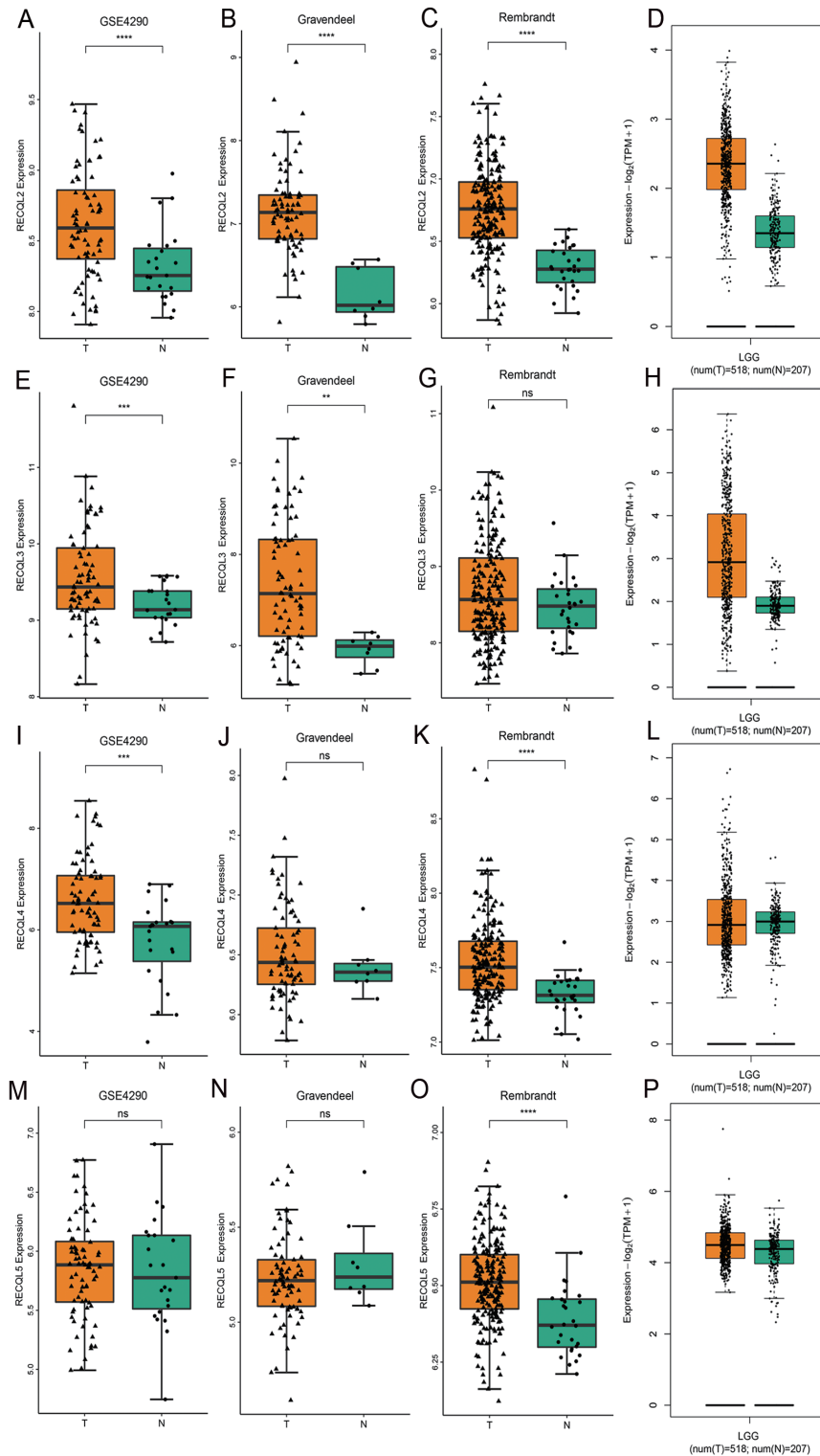


Figure S2 Expression analysis of RecQ DNA helicases. Differential expression analysis of RECQL2 in GSE4290 (A), Gravendeel (B), Rembrandt (C) and GEPIA2 datasets (D). Differential expression analysis of RECQL3 in GSE4290 (E), Gravendeel (F), Rembrandt (G) and GEPIA2 datasets (H). Differential expression analysis of RECQL4 in GSE4290 (I), Gravendeel (J), Rembrandt (K) and GEPIA2 datasets (L). Differential expression analysis of RECQL5 in GSE4290 (M), Gravendeel (N), Rembrandt (O) and GEPIA2 datasets (P). **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, no significance. LGG, low-grade glioma; T, tumor; N, non-tumor.

Table S1 Summary of clinical pathological characteristics for different cohorts

Characteristic	Training cohort (TCGA)	Validation cohort (CGGA)
Number	505	418
Age (years)		
<41	249 (49.3%)	217 (51.9%)
≥41	256 (50.7%)	201 (48.1%)
Gender		
Female	226 (44.8%)	177 (42.3%)
Male	279 (55.2%)	241 (57.7%)
WHO grade		
G2	245 (48.5%)	186 (44.5%)
G3	260 (51.5%)	232 (55.5%)
IDH mutation status		
Wildtype	94 (18.6%)	102 (24.4%)
Mutant	411 (81.4%)	316 (75.6%)
1p/19q codeletion status		
Non-codel	338 (66.9%)	289 (69.1%)
Codel	167 (33.1%)	129 (30.9%)
MGMT promoter status		
Unmethylated	89 (17.6%)	172 (41.1%)
Methylated	416 (82.4%)	246 (58.9%)

Age, age at pathological diagnosis of glioma; IDH, isocitrate dehydrogenase; MGMT, O6-methylguanine-DNA methyltransferase.

Table S2 Univariate Cox regression analysis of OS in TCGA and CGGA cohorts

Covariates	TCGA cohort (n=505)			CGGA cohort (n=418)		
	HR	95% CI	P	HR	95% CI	P
Age	1.06	1.045–1.075	<0.001	1.015	1.001–1.028	0.031
Gender	1.076	0.752–1.538	0.69	1.085	0.83–1.417	0.552
Grade	3.377	2.273–5.015	<0.001	2.911	2.173–3.899	<0.001
IDH	0.155	0.107–0.225	<0.001	0.422	0.318–0.561	<0.001
1p/19q	0.388	0.242–0.621	<0.001	0.269	0.188–0.386	<0.001
MGMT	0.388	0.264–0.569	<0.001	0.817	0.627–1.064	0.134
RECQL1	1.685	1.394–2.037	<0.001	1.612	1.395–1.863	<0.001

OS, overall survival; HR, hazard ratio; CI, confidence interval; P, P value; IDH, IDH mutation status; 1p/19q, 1p/19q codeletion status; MGMT, MGMT promoter status.

Table S3 Gene Ontology (GO) annotation of High RECQL1 expression group by GSEA

Subtype	Name	NES	NOM P value	FDR q value
BP	GOBP_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	2.3368735	0	0.004080848
	GOBP_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	2.31915	0	0.004081
	GOBP_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	2.317956	0	0.002721
	GOBP_NEGATIVE_REGULATION_OF_CATABOLIC_PROCESS	2.307437	0	0.004081
	GOBP_HOMEOSTASIS_OF_NUMBER_OF_CELLS	2.306452	0	0.002721
CC	GOCC_CELL_DIVISION_SITE	2.302822	0	0.002551
	GOCC_CLEAVAGE_FURROW	2.286551	0	0.001134
	GOCC_NUCLEAR_ENVELOPE	2.281711	0	9.72E-04
	GOCC_NUCLEAR_MEMBRANE	2.257516	0	6.64E-04
	GOCC_CELL_SUBSTRATE_JUNCTION	2.253693	0	5.71E-04
MF	GOMF_KINASE_REGULATOR_ACTIVITY	2.306612	0	0.003265
	GOMF_TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	2.291345	0	0.001275
	GOMF_HORMONE_RECEPTOR_BINDING	2.291316	0	0.0012
	GOMF_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	2.280161	0	9.79E-04
	GOMF_ATPASE_ACTIVITY	2.27769	0	9.07E-04

GSEA, Gene Set Enrichment Analysis; BP, biological process; CC, cellular component; MF, molecular function; NES, normalized enrichment score; NOM P value, nominal P value; FDR q value, false discovery rate.

Table S4 Correlation between RECQL1 expression and gene markers of immune cells

Cell type	Gene markers	LGG				Cell type	Gene markers	LGG			
		None		Purity				None		Purity	
		Cor	P value	Cor	P value			Cor	P value	Cor	P value
B cell	CD19	0.162	***	0.177	***	Monocyte	CD14	0.173	***	0.185	***
	CD20	0.146	***	0.186	***		CD115 (CSF1R)	0.118	**	0.196	***
	CD27	0.293	***	0.289	***	TAM	CD68	0.32	***	0.271	***
	CD79A	0.064	ns	0.064	ns		CCL2	0.17	***	0.145	***
T cell (general)	CD2	0.293	***	0.336	***		IL10	0.253	***	0.221	***
	CD3D	0.209	***	0.264	***	M1 Macrophage	CD64 (FCGR1A)	0.16	***	0.216	***
	CD3E	0.231	***	0.277	***		CD80	0.351	***	0.35	***
CD8+ T cell	CD8A	0.059	ns	0.15	**		IL6	0.187	***	0.197	***
	CD8B	0.005	ns	0.078	ns		INOS (NOS2)	-0.057	ns	-0.043	ns
	CD45	0.413	***	0.509	***	M2 Macrophage	CD163	0.323	***	0.321	***
Th1	T-bet (TBX21)	0.294	***	0.294	***		CD206	-0.064	ns	-0.052	ns
	STAT1	0.572	***	0.584	***		MS4A4A	0.292	***	0.301	***
	STAT4	-0.096	*	-0.034	ns		VSIG4	0.219	***	0.258	***
Th2	GATA3	0.274	***	0.304	***	Neutrophils	CD11b (ITGAM)	0.167	***	0.256	***
	STAT6	0.058	ns	0.21	***		CD15	0.312	***	0.36	***
	IL13	0.104	*	-0.119	**		CD66b (CEACAM8)	0.016	ns	-0.011	ns
Tfh	BCL6	0.222	***	0.174	***	Natural killer cell	CD56	0.158	***	0.111	*
	IL21	0.118	**	0.121	**		CD335	0.218	***	0.218	***
Th17	STAT3	0.679	***	0.675	***		KIR2DL1	0.142	**	0.152	***
	IL17A	0.095	*	0.08	ns		KIR2DL3	0.137	**	0.15	***
Treg	FOXP3	0.197	***	0.217	***		KIR3DL1	0.097	*	0.096	*
	CD25	0.299	***	0.295	***		KIR3DL2	0.087	*	0.104	*
	CCR8	0.195	***	0.212	***	Dendritic cell	CD11c (ITGAX)	0.131	**	0.2	***
	STAT5B	0.467	***	0.435	***		CD123	-0.093	*	-0.092	*
T cell exhaustion	PD-1 (PDCD1)	0.226	***	0.233	***		BDCA-1 (CD1C)	0.197	***	0.205	***
	CTLA4	0.162	***	0.204	***		BDCA-3 (CD141)	0.235	***	0.235	***
	LAG3	0.173	***	0.157	***		BDCA-4 (NRP1)	0.553	***	0.536	***
	TIM-3 (HAVCR2)	0.246	***	0.328	***						

LGG, low grade glioma; TAM, tumor-associated macrophage; Th, T helper cell; Tfh, follicular helper T cell; Treg, regulatory T cell; Cor, R value of Spearman's correlation; None, none, correlation without adjustment; Purity, correlation adjusted by purity. ns, P>0.05; *, P<0.05; **, P<0.01; ***, P<0.001.