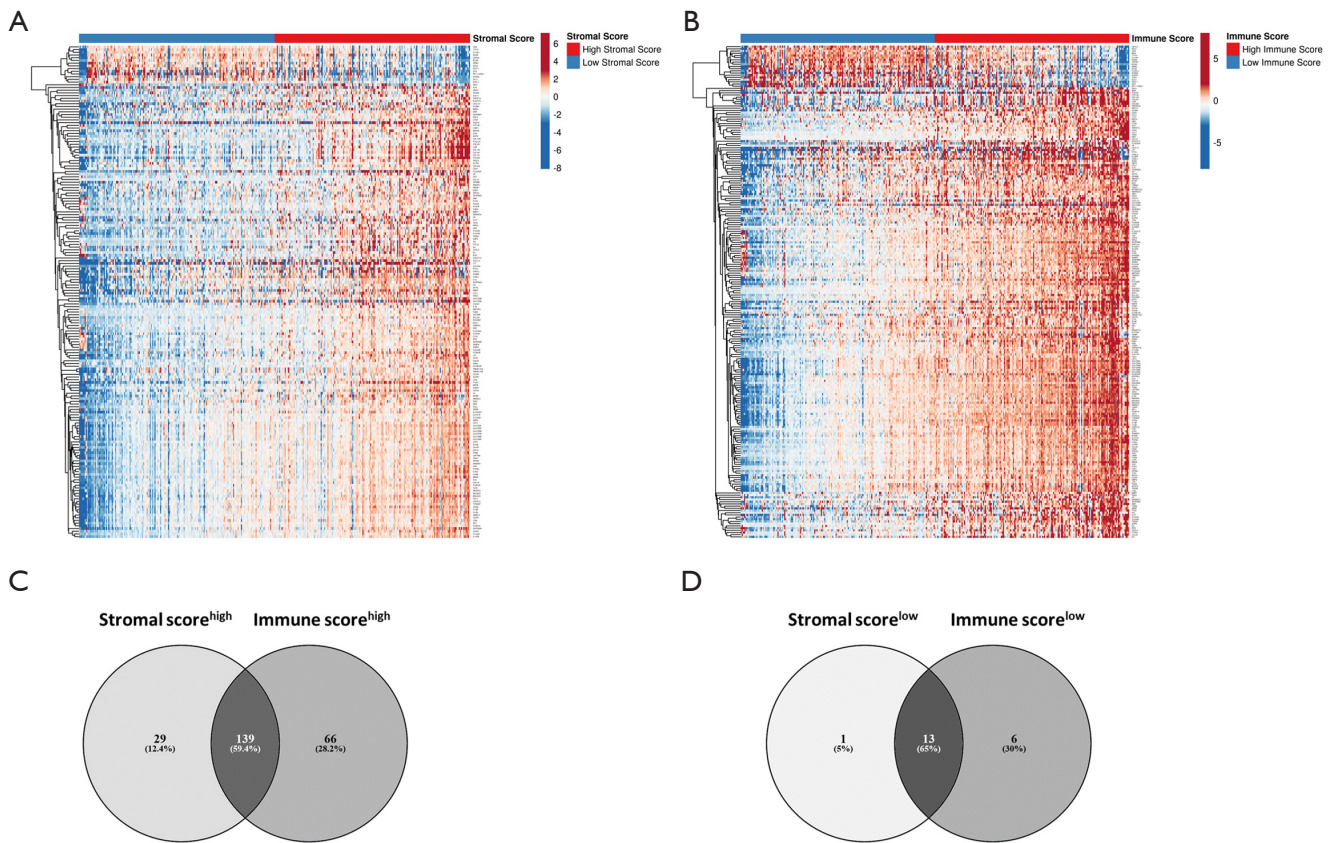
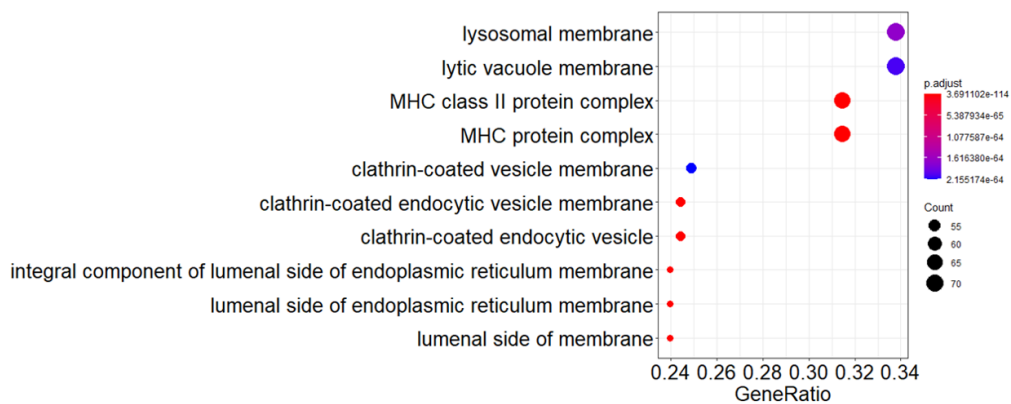


**Figure S1** Analysis workflow of the current study.



**Figure S2** Differential analysis of gene-expression profiles related to stromal and immune scores in patients with GBM-RT. (A,B) Heatmap for DEGs generated by comparing groups with (A) high and low stromal score groups, and (B) groups with high and low immune score. DEGs were determined using the limma package of R software, with the criteria of  $P < 0.05$  and  $|\log_2 \text{fold-change}| > 1$ . (C,D) Venn diagrams of intersecting DEGs in groups with high or low stromal/immune scores.



**Figure S3** GO-based enrichment analysis of 139 DEGs in term of CCs.

**Table S1** Top 20 GO terms of biological process

Ontology	ID	Description	GeneRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	72/207	2.22E-98	4.52E-95	3.28E-95	72
BP	GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	72/207	3.59E-98	4.52E-95	3.28E-95	72
BP	GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	71/207	4.92E-97	4.13E-94	3.00E-94	71
BP	GO:0048002	Antigen processing and presentation of peptide antigen	76/207	5.37E-82	3.38E-79	2.45E-79	76
BP	GO:0002478	Antigen processing and presentation of exogenous peptide antigen	75/207	7.73E-82	3.89E-79	2.82E-79	75
BP	GO:0019884	Antigen processing and presentation of exogenous antigen	75/207	4.28E-81	1.79E-78	1.30E-78	75
BP	GO:0019882	Antigen processing and presentation	77/207	1.42E-79	5.11E-77	3.71E-77	77
BP	GO:0034341	Response to interferon-gamma	73/207	1.43E-78	4.50E-76	3.27E-76	73
BP	GO:0071346	Cellular response to interferon-gamma	66/207	6.76E-70	1.89E-67	1.37E-67	66
BP	GO:0060333	Interferon-gamma-mediated signaling pathway	54/207	6.00E-63	1.51E-60	1.10E-60	54
BP	GO:0050852	T cell receptor signaling pathway	52/207	5.45E-50	1.25E-47	9.06E-48	52
BP	GO:0050851	Antigen receptor-mediated signaling pathway	54/207	5.70E-49	1.20E-46	8.68E-47	54
BP	GO:0002399	MHC class II protein complex assembly	23/207	3.42E-47	6.15E-45	4.46E-45	23
BP	GO:0002503	Peptide antigen assembly with MHC class II protein complex	23/207	3.42E-47	6.15E-45	4.46E-45	23
BP	GO:0002501	Peptide antigen assembly with MHC protein complex	23/207	1.01E-44	1.69E-42	1.23E-42	23
BP	GO:0002396	MHC protein complex assembly	23/207	6.55E-41	1.03E-38	7.48E-39	23
BP	GO:0042102	Positive regulation of T cell proliferation	36/207	8.13E-41	1.20E-38	8.74E-39	36
BP	GO:0050671	Positive regulation of lymphocyte proliferation	37/207	2.18E-38	3.05E-36	2.21E-36	37
BP	GO:0032946	Positive regulation of mononuclear cell proliferation	37/207	2.73E-38	3.62E-36	2.63E-36	37
BP	GO:0070663	Regulation of leukocyte proliferation	43/207	1.44E-37	1.81E-35	1.31E-35	43

**Table S2** Top 20 GO terms of molecular function (MF)

Ontology	ID	Description	GeneRatio	pvalue	p.adjust	qvalue	Count
MF	GO:0042605	Peptide antigen binding	50/208	1.03E-68	3.02E-66	2.42E-66	50
MF	GO:0032395	MHC class II receptor activity	36/208	2.20E-56	3.24E-54	2.59E-54	36
MF	GO:0003823	Antigen binding	50/208	5.31E-56	5.22E-54	4.17E-54	50
MF	GO:0042277	Peptide binding	56/208	2.26E-46	1.67E-44	1.33E-44	56
MF	GO:0023026	MHC class II protein complex binding	30/208	3.09E-46	1.82E-44	1.46E-44	30
MF	GO:0033218	Amide binding	57/208	3.34E-44	1.64E-42	1.31E-42	57
MF	GO:0023023	MHC protein complex binding	30/208	2.36E-41	9.96E-40	7.96E-40	30
MF	GO:0140375	Immune receptor activity	44/208	6.29E-40	2.32E-38	1.85E-38	44
MF	GO:0030247	Polysaccharide binding	15/208	6.36E-21	2.08E-19	1.67E-19	15
MF	GO:0030246	Carbohydrate binding	19/208	4.48E-10	1.32E-08	1.06E-08	19
MF	GO:0061134	Peptidase regulator activity	17/208	1.21E-09	3.23E-08	2.58E-08	17
MF	GO:0004866	Endopeptidase inhibitor activity	15/208	3.66E-09	9.00E-08	7.19E-08	15
MF	GO:0030414	Peptidase inhibitor activity	15/208	5.86E-09	1.33E-07	1.06E-07	15
MF	GO:0061135	Endopeptidase regulator activity	15/208	6.67E-09	1.41E-07	1.12E-07	15
MF	GO:0070628	Proteasome binding	7/208	1.71E-08	3.37E-07	2.69E-07	7
MF	GO:0004867	Serine-type endopeptidase inhibitor activity	10/208	1.07E-07	1.97E-06	1.57E-06	10
MF	GO:0008009	Chemokine activity	8/208	3.22E-07	5.58E-06	4.46E-06	8
MF	GO:0019864	IgG binding	4/208	2.43E-06	3.98E-05	3.18E-05	4
MF	GO:0035325	Toll-like receptor binding	4/208	5.63E-06	8.74E-05	6.98E-05	4
MF	GO:0042379	Chemokine receptor binding	8/208	5.95E-06	8.77E-05	7.01E-05	8

**Table S3** Top 20 GO terms of cellular components

Ontology	ID	Description	GeneRatio	pvalue	p.adjust	qvalue	Count
CC	GO:0042613	MHC class II protein complex	67/213	2.38E-116	3.69E-114	2.03E-114	67
CC	GO:0042611	MHC protein complex	67/213	2.96E-99	2.30E-97	1.26E-97	67
CC	GO:0030669	Clathrin-coated endocytic vesicle membrane	52/213	3.26E-79	1.68E-77	9.26E-78	52
CC	GO:0045334	Clathrin-coated endocytic vesicle	52/213	1.76E-73	6.81E-72	3.74E-72	52
CC	GO:0071556	Integral component of luminal side of endoplasmic reticulum membrane	51/213	2.35E-70	6.07E-69	3.34E-69	51
CC	GO:0098553	Luminal side of endoplasmic reticulum membrane	51/213	2.35E-70	6.07E-69	3.34E-69	51
CC	GO:0098576	Luminal side of membrane	51/213	4.53E-69	1.00E-67	5.52E-68	51
CC	GO:0005765	Lysosomal membrane	72/213	8.71E-66	1.69E-64	9.29E-65	72
CC	GO:0098852	Lytic vacuole membrane	72/213	1.19E-65	2.06E-64	1.13E-64	72
CC	GO:0030665	Clathrin-coated vesicle membrane	53/213	1.39E-65	2.16E-64	1.19E-64	53
CC	GO:0030134	COPII-coated ER to Golgi transport vesicle	54/213	1.59E-65	2.24E-64	1.23E-64	54
CC	GO:0012507	ER to Golgi transport vesicle membrane	51/213	2.82E-65	3.64E-64	2.00E-64	51
CC	GO:0032588	Trans-Golgi network membrane	51/213	1.36E-64	1.62E-63	8.91E-64	51
CC	GO:0030666	Endocytic vesicle membrane	58/213	1.99E-60	2.20E-59	1.21E-59	58
CC	GO:0030660	Golgi-associated vesicle membrane	51/213	2.09E-57	2.16E-56	1.19E-56	51
CC	GO:0030136	Clathrin-coated vesicle	53/213	5.25E-56	5.09E-55	2.80E-55	53
CC	GO:0005798	Golgi-associated vesicle	54/213	3.85E-55	3.51E-54	1.93E-54	54
CC	GO:0030662	Coated vesicle membrane	53/213	1.54E-53	1.32E-52	7.27E-53	53
CC	GO:0030139	Endocytic vesicle	61/213	1.81E-53	1.47E-52	8.11E-53	61
CC	GO:0030176	Integral component of endoplasmic reticulum membrane	51/213	6.62E-51	5.13E-50	2.82E-50	51

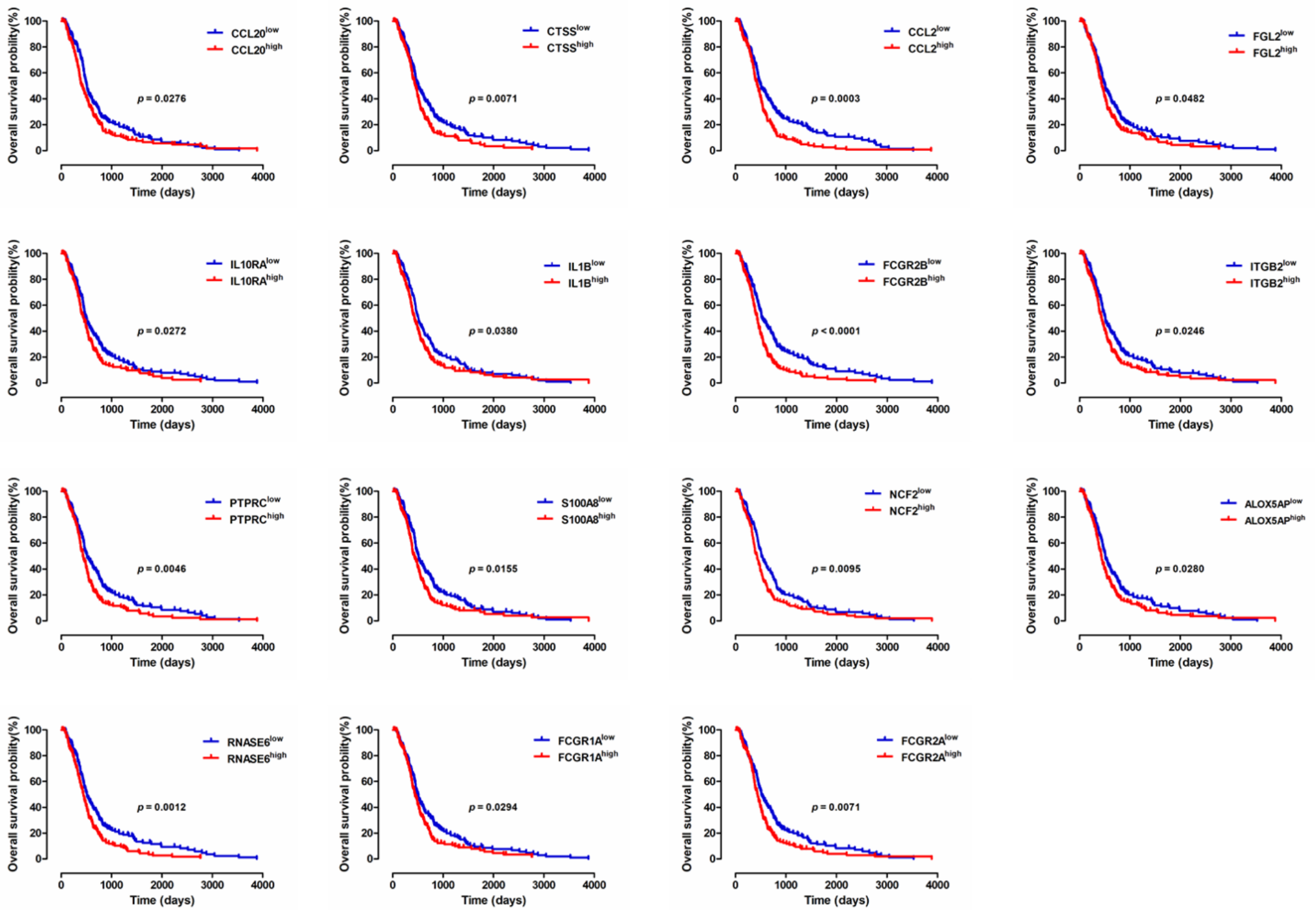
**Table S4** Enrichment of KEGG pathways

ID	Description	GeneRatio	pvalue	p.adjust	qvalue	Count
hsa05150	Staphylococcus aureus infection	20/88	7.12E-21	1.00E-18	6.30E-19	20
hsa05152	Tuberculosis	22/88	1.19E-17	8.37E-16	5.25E-16	22
hsa05140	Leishmaniasis	16/88	8.32E-17	3.54E-15	2.22E-15	16
hsa04145	Phagosome	20/88	1.00E-16	3.54E-15	2.22E-15	20
hsa04610	Complement and coagulation cascades	15/88	1.11E-14	3.12E-13	1.96E-13	15
hsa05323	Rheumatoid arthritis	15/88	4.49E-14	1.05E-12	6.61E-13	15
hsa05332	Graft-versus-host disease	10/88	1.63E-11	3.28E-10	2.06E-10	10
hsa05310	Asthma	9/88	2.48E-11	4.37E-10	2.74E-10	9
hsa04640	Hematopoietic cell lineage	13/88	3.79E-11	5.95E-10	3.73E-10	13
hsa05321	Inflammatory bowel disease (IBD)	11/88	7.94E-11	1.12E-09	7.02E-10	11
hsa05322	Systemic lupus erythematosus	14/88	1.79E-10	2.30E-09	1.44E-09	14
hsa05133	Pertussis	11/88	4.61E-10	5.42E-09	3.40E-09	11
hsa04612	Antigen processing and presentation	11/88	6.15E-10	6.27E-09	3.93E-09	11
hsa04940	Type I diabetes mellitus	9/88	6.23E-10	6.27E-09	3.93E-09	9
hsa04672	Intestinal immune network for IgA production	9/88	2.15E-09	2.02E-08	1.27E-08	9
hsa05145	Toxoplasmosis	12/88	2.51E-09	2.22E-08	1.39E-08	12
hsa05164	Influenza A	14/88	3.49E-09	2.89E-08	1.82E-08	14
hsa05330	Allograft rejection	8/88	5.62E-09	4.40E-08	2.76E-08	8
hsa04061	Viral protein interaction with cytokine and cytokine receptor	11/88	9.22E-09	6.84E-08	4.29E-08	11
hsa05416	Viral myocarditis	9/88	1.40E-08	9.90E-08	6.21E-08	9
hsa05320	Autoimmune thyroid disease	8/88	8.91E-08	5.98E-07	3.75E-07	8
hsa05134	Legionellosis	8/88	1.60E-07	1.03E-06	6.44E-07	8
hsa04659	Th17 cell differentiation	10/88	2.18E-07	1.34E-06	8.39E-07	10
hsa04668	TNF signaling pathway	10/88	3.36E-07	1.98E-06	1.24E-06	10
hsa04514	Cell adhesion molecules (CAMs)	11/88	5.43E-07	3.06E-06	1.92E-06	11
hsa04657	IL-17 signaling pathway	9/88	7.46E-07	4.05E-06	2.54E-06	9
hsa05169	Epstein-Barr virus infection	12/88	1.68E-06	8.78E-06	5.50E-06	12
hsa04658	Th1 and Th2 cell differentiation	8/88	6.61E-06	3.33E-05	2.09E-05	8
hsa04933	AGE-RAGE signaling pathway in diabetic complications	8/88	1.23E-05	5.99E-05	3.75E-05	8
hsa05142	Chagas disease (American trypanosomiasis)	8/88	1.43E-05	6.48E-05	4.06E-05	8
hsa05146	Amoebiasis	8/88	1.43E-05	6.48E-05	4.06E-05	8
hsa05144	Malaria	6/88	1.57E-05	6.84E-05	4.29E-05	6
hsa04064	NF-kappa B signaling pathway	8/88	1.64E-05	6.84E-05	4.29E-05	8
hsa04060	Cytokine-cytokine receptor interaction	13/88	1.65E-05	6.84E-05	4.29E-05	13
hsa05166	Human T-cell leukemia virus 1 infection	11/88	2.43E-05	9.81E-05	6.15E-05	11
hsa04620	Toll-like receptor signaling pathway	7/88	0.000134	0.000524	0.000329	7
hsa05168	Herpes simplex virus 1 infection	15/88	0.000252	0.00096	0.000602	15
hsa05132	Salmonella infection	9/88	0.000398	0.001479	0.000927	9
hsa04380	Osteoclast differentiation	7/88	0.000482	0.001741	0.001092	7
hsa05020	Prion diseases	4/88	0.000543	0.001915	0.001201	4
hsa04621	NOD-like receptor signaling pathway	8/88	0.000787	0.002706	0.001697	8
hsa04062	Chemokine signaling pathway	8/88	0.001043	0.003501	0.002195	8
hsa04666	Fc gamma R-mediated phagocytosis	5/88	0.003433	0.011258	0.00706	5
hsa04210	Apoptosis	6/88	0.00367	0.011759	0.007374	6
hsa01523	Antifolate resistance	3/88	0.004575	0.014336	0.00899	3
hsa04623	Cytosolic DNA-sensing pathway	4/88	0.004898	0.015014	0.009415	4
hsa04625	C-type lectin receptor signaling pathway	5/88	0.005532	0.016595	0.010407	5
hsa05221	Acute myeloid leukemia	4/88	0.006098	0.017912	0.011233	4
hsa05143	African trypanosomiasis	3/88	0.007544	0.021709	0.013614	3
hsa04217	Necroptosis	6/88	0.007804	0.022008	0.013801	6
hsa04611	Platelet activation	5/88	0.011428	0.031596	0.019814	5
hsa05135	Yersinia infection	5/88	0.01381	0.037446	0.023482	5
hsa05167	Kaposi sarcoma-associated herpesvirus infection	6/88	0.017255	0.045636	0.028618	6
hsa05162	Measles	5/88	0.017477	0.045636	0.028618	5
hsa05130	Pathogenic Escherichia coli infection	6/88	0.018505	0.046593	0.029218	6
hsa05202	Transcriptional misregulation in cancer	6/88	0.018505	0.046593	0.029218	6

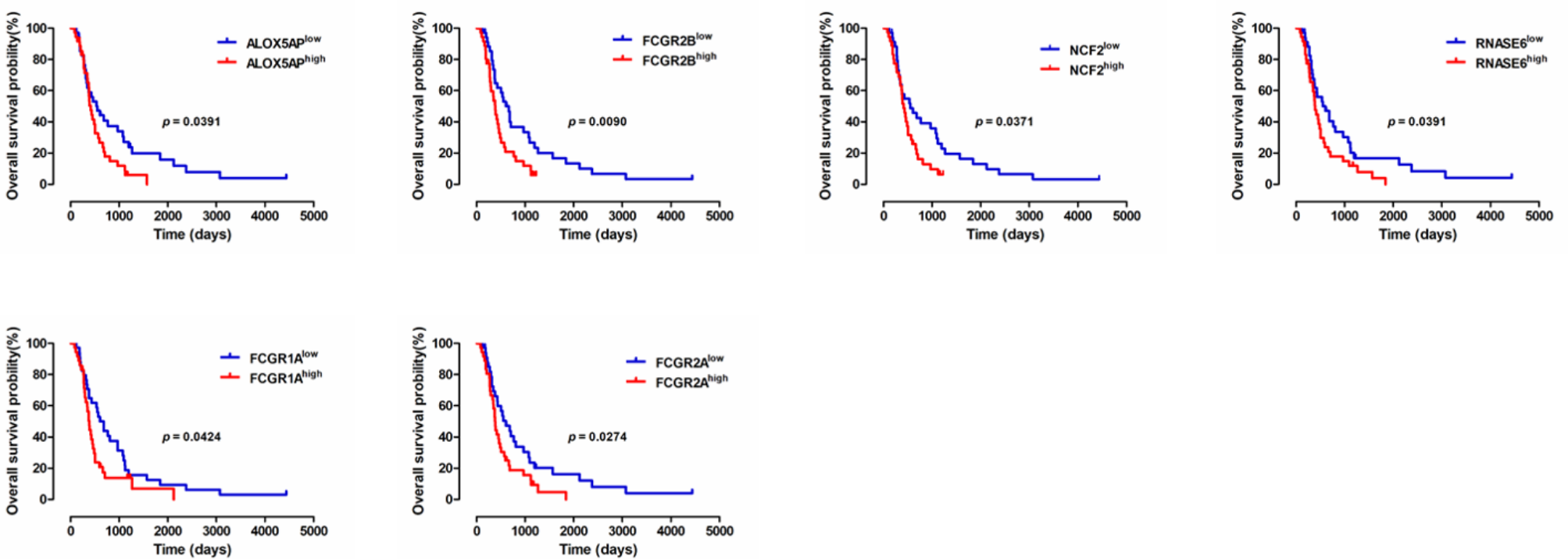
**Table S5** Correlation of the selected DEGs with the OS of patients with GBM-RT identified by Cox regression analysis in TCGA database

Terms	HR[exp(coef)]	coef	95% CI lower	95% CI upper	Z	P value
DLL3	0.881408	-0.12623	-0.19726	-0.05521	-3.48372	4.94E-04
BCAN	0.917235	-0.08639	-0.16807	-0.00471	-2.07305	0.038167
PLA2G2A	1.051875	0.050574	6.10E-04	0.100539	1.983877	0.04727
LTF	1.056815	0.055259	0.017223	0.093295	2.847469	0.004407
SLPI	1.060782	0.059006	0.005916	0.112097	2.178359	0.029379
CXCL10	1.064471	0.062478	0.002551	0.122406	2.04338	0.041015
COL6A3	1.065954	0.063871	0.011623	0.116118	2.395979	0.016576
FCGBP	1.068699	0.066442	0.005769	0.127116	2.146339	0.031846
PI3	1.073327	0.070763	0.005245	0.136282	2.116854	0.034272
LYZ	1.073906	0.071302	0.007092	0.135512	2.176429	0.029523
VSIG4	1.075443	0.072733	0.002282	0.143183	2.02346	0.043026
IL8	1.075938	0.073192	0.007456	0.138929	2.182266	0.02909
TREM1	1.07641	0.073631	0.002621	0.144642	2.032294	0.042124
CHI3L2	1.077258	0.074419	0.019478	0.129359	2.65483	0.007935
CXCL14	1.080297	0.077236	0.030698	0.123773	3.252858	0.001143
GPNMB	1.082401	0.079181	0.012482	0.145881	2.326751	0.019979
NNMT	1.08533	0.081884	0.030996	0.132773	3.153747	0.001612
POSTN	1.087824	0.084179	0.044279	0.124079	4.134989	3.55E-05
ALOX5AP	1.08895	0.085214	0.013445	0.156983	2.327134	0.019958
SERPINA1	1.090036	0.086211	0.013712	0.15871	2.330656	0.019772
CCL20	1.090169	0.086333	0.007298	0.165368	2.140943	0.032279
CHI3L1	1.091505	0.087558	0.040746	0.134369	3.665969	2.46E-04
F13A1	1.091961	0.087975	0.028615	0.147335	2.904795	0.003675
TNFSF10	1.092109	0.08811	0.002294	0.173927	2.012352	0.044183
RGS1	1.093359	0.089254	0.015567	0.162941	2.374022	0.017595
HLA-DMA	1.094432	0.090236	0.001664	0.178807	1.996796	0.045847
C1QA	1.095929	0.091603	0.01	0.173206	2.200141	0.027797
CP	1.099548	0.094899	0.026501	0.163298	2.719338	0.006541
SAMSN1	1.100264	0.09555	0.003059	0.188041	2.024793	0.042889
CD163	1.100454	0.095723	0.03367	0.157775	3.02344	0.002499
AIM1	1.106014	0.100762	0.02152	0.180005	2.492221	0.012695
RNASE1	1.107058	0.101706	0.018785	0.184627	2.403972	0.016218
SOD2	1.107097	0.101741	0.009082	0.194401	2.152062	0.031392
FCER1G	1.108624	0.10312	0.018343	0.187897	2.384032	0.017124
PTX3	1.109612	0.10401	0.04603	0.16199	3.515971	4.38E-04
BIRC3	1.110015	0.104373	0.012755	0.195991	2.232831	0.02556
CCL2	1.110579	0.104882	0.046226	0.163537	3.504605	4.57E-04
UBD	1.112426	0.106543	0.031787	0.1813	2.793343	0.005217
BCL2A1	1.113078	0.10713	0.02548	0.188779	2.571606	0.010123
CLEC2B	1.115707	0.109488	0.02679	0.192186	2.594891	0.009462
S100A4	1.116046	0.109792	0.036712	0.182873	2.944552	0.003234
LY96	1.116715	0.110391	0.026205	0.194577	2.570053	0.010168
C3AR1	1.118796	0.112254	0.008528	0.215979	2.121106	0.033913
FCGR1A	1.119057	0.112487	0.008706	0.216267	2.124384	0.033638
DPYD	1.121302	0.114491	0.036672	0.19231	2.883576	0.003932
S100A8	1.121341	0.114526	0.043056	0.185995	3.14072	0.001685
CTSS	1.121415	0.114592	0.017865	0.211318	2.321973	0.020234
CCR1	1.122064	0.11517	8.94E-04	0.229446	1.975298	0.048234
CD14	1.125668	0.118376	0.036756	0.199997	2.842593	0.004475
LAPTM5	1.128666	0.121036	0.022499	0.219574	2.407486	0.016063
ITGB2	1.130141	0.122342	0.025103	0.219581	2.465937	0.013666
FLJ22662	1.130952	0.12306	0.026339	0.219781	2.493702	0.012642
PYCARD	1.131215	0.123292	0.016127	0.230457	2.254916	0.024139
IL10RA	1.131224	0.1233	0.023577	0.223023	2.423355	0.015378
IL1B	1.131917	0.123913	0.027372	0.220454	2.515673	0.011881
SERPINE1	1.132382	0.124323	0.046999	0.201648	3.15127	0.001626
TGFBI	1.132835	0.124723	0.044614	0.204832	3.051493	0.002277
CXorf9	1.133711	0.125496	0.016541	0.234452	2.257518	0.023976
PTPRC	1.135169	0.126782	0.028047	0.225517	2.516718	0.011845
C1orf38	1.135762	0.127304	0.013093	0.241514	2.184654	0.028914
RNASE6	1.13619	0.127681	0.027556	0.227806	2.49937	0.012441
CFI	1.13753	0.128859	0.049446	0.208272	3.180315	0.001471
S100A9	1.139868	0.130912	0.054232	0.207592	3.346154	8.19E-04
SERPINF1	1.140222	0.131223	0.045693	0.216753	3.007054	0.002638
SQRDL	1.141299	0.132167	0.032157	0.232177	2.590175	0.009593
CLEC7A	1.143047	0.133698	0.017518	0.249878	2.255491	0.024103
TLR2	1.145966	0.136248	0.031434	0.241062	2.547769	0.010841
SLA	1.147324	0.137432	0.037735	0.237129	2.70181	0.006896
PSCDBP	1.147956	0.137983	0.033347	0.242618	2.584608	0.009749
FGL2	1.149974	0.139739	0.021932	0.257547	2.324849	0.02008
GPR65	1.151432	0.141006	0.032105	0.249908	2.537767	0.011156
CSTA	1.153006	0.142373	0.066494	0.218251	3.677507	2.36E-04
IFI30	1.153156	0.142503	0.046641	0.238365	2.913577	0.003573
C1S	1.15346	0.142766	0.067038	0.218494	3.695023	2.20E-04
CECR1	1.155062	0.144154	0.051433	0.236875	3.04717	0.00231
C5AR1	1.158813	0.147396	0.046884	0.247909	2.874177	0.004051
NCF2	1.159058	0.147608	0.043079	0.252136	2.767728	0.005645
FCGR2B	1.159292	0.147809	0.074332	0.221286	3.942732	8.06E-05
FCGR2A	1.159377	0.147883	0.048799	0.246967	2.925244	0.003442
SERPING1	1.159456	0.147951	0.072158	0.223745	3.82592	1.30E-04
TMEM176B	1.159545	0.148028	0.067693	0.228362	3.611518	3.04E-04
TNFAIP3	1.161278	0.149521	0.029151	0.269891	2.434619	0.014907
CSF2RB	1.161308	0.149547	0.024369	0.274724	2.341523	0.019205
STAB1	1.161958	0.150106	0.046476	0.253737	2.838965	0.004526
RNASE2	1.162077	0.150209	0.057075	0.243344	3.16107	0.001572
CYBB	1.171486	0.158273	0.038136	0.278411	2.582118	0.00982
SERPINB1	1.180691	0.1661	0.069733	0.262467	3.378224	7.30E-04
PLAUR	1.220504	0.199264	0.084103	0.314426	3.391329	6.96E-04

OS, overall survival in terms of days.



**Figure S4** Correlation of the selected DEGs with the OS of patients in TCGA database. Survival analysis was conducted by generating Kaplan-Meier curves. DEGs were grouped based on high (red line, n=174) or low (blue line, n=174) expression levels relative to the median gene-expression level.  $P < 0.05$ , as determined by the log-rank test. OS, overall survival in terms of days.



**Figure S5** Validation of the selected DEGs in the CGGA cohort. Survival analysis was conducted by generating Kaplan-Meier curves. DEGs were grouped based on high (red line, n=36) or low (blue line, n=35) expression levels relative to the median gene expression level.  $P < 0.05$ , as determined by the log-rank test.