## Supplementary

**Table S1** GSEA analysis parameters

| ID | Set size | Enrichment score | NES | P value | P.adj | Q value | Rank | Leading edge | Core enrichment |
|---|---|---|---|---|---|---|---|---|---|
| BIOCARTA_IL17_PATHWAY | 15 | 0.66595252 | 1.78186992 | 0.00429241 | 0.02290126 | 0.01623349 | 4,921 | Tags =53%, list =14%, signal =46% | CXCL8/CSF3/CD58/CD3D/IL6/CD8A/CD2/CD3G |
| BIOCARTA_IL5_PATHWAY | 11 | 0.76802588 | 1.88512828 | 0.00122301 | 0.00874124 | 0.0061962 | 3,287 | Tags =55%, list =9%, signal =50% | IL5RA/HLA-DRA/HLA-DRB5/IL6/IL4/HLA-DRB1 |
| KEGG_OXIDATIVE_PHOSPHORYLATION | 119 | 0.62565731 | 2.62167224 | 1E−10 | 4.4263E−09 | 3.1376E−09 | 7,816 | Tags =64%, list =22%, signal =50% | ATP6V0A4/NDUFA4/COX7B/NDUFA2/NDUFB3/UQCRQ/NDUFB5/ATP5ME/ATP6V0E1/ATP5MF/UQCR11/COX7A2/NDUFB6/COX6A1/ATP5MG/COX17/NDUFA1/NDUFAB1/SDHD/NDUFB2/NDUFB1/COX5B/ATP5PF/ATP5PO/ATP6V0B/PPA2/UQCRH/COX7C/ATP5F1E/NDUFB4/NDUFC1/NDUFS4/NDUFC2/ATP5PB/UQCR10/ATP5MC1/ATP5PD/ATP6V1G1/COX6CP3/NDUFA6/NDUFB7/SDHC/SDHB/NDUFB9/UQCRHL/COX7A2L/NDUFS3/COX8A/NDUFA5/ATP5MC3/COX6B1/COX7B2/NDUFS5/ATP5F1C/NDUFB10/COX6C/NDUFA3/ATP4B/NDUFB8/COX11/CYC1/NDUFA8/COX4I1/UQCRFS1/ATP6V1F/PPA1/ATP6V1E2/NDUFS8/NDUFS6/ATP5MC2/COX5A/ATP5MC1P5/COX6A2/ATP6V1E1/UQCRB/NDUFA11 |
| REACTOME_CD22_MEDIATED_BCR_REGULATION | 61 | 0.91547246 | 3.38766602 | 1E−10 | 4.4263E−09 | 3.1376E−09 | 1,049 | Tags =75%, list =3%, signal =73% | IGHV4-39/IGLV3-27/IGKV3-15/IGKV1-5/IGLV2-8/IGKV3-20/IGKV1-16/IGLV7-43/IGKV1-33/IGHV3-33/IGKV3-11/IGKV1D-33/IGLV2-23/IGLV6-57/IGHV4-59/IGHV3-13/IGKV2-30/IGHV1-2/IGKV2D-40/IGHV3-11/IGLV1-44/IGKV4-1/IGHV1-46/IGLV3-19/IGKV1-17/IGHV2-5/IGKV3D-20/IGLC3/IGHV3-30/IGLV1-40/IGHV3-53/IGHV3-48/IGKV2D-28/IGLV3-21/IGHV3-7/IGKV2D-30/IGKV5-2/IGLV3-25/IGLV3-1/IGHV3-23/IGLV2-14/IGHD/IGLC2/IGKV1D-16/IGHV1-69/IGKV1-12 |
| REACTOME_FCERI_MEDIATED_NF_KB_ACTIVATION | 136 | 0.76147327 | 3.25688964 | 1E−10 | 4.4263E−09 | 3.1376E−09 | 3,671 | Tags =46%, list =10%, signal =42% | IGHV4-39/IGLV3-27/IGKV3-15/IGKV1-5/IGLV2-8/IGKV3-20/IGKV1-16/IGLV7-43/IGKV1-33/IGHV3-33/IGKV3-11/IGKV1D-33/IGLV2-23/IGLV6-57/IGHV4-59/IGHV3-13/IGKV2-30/IGHV1-2/IGKV2D-40/IGHV3-11/IGLV1-44/IGKV4-1/IGHV1-46/IGLV3-19/IGKV1-17/IGHV2-5/IGKV3D-20/IGLC3/IGHV3-30/IGLV1-40/IGHV3-53/IGHV3-48/IGKV2D-28/IGLV3-21/IGHV3-7/IGKV2D-30/IGKV5-2/IGLV3-25/FCER1A/IGLV3-1/IGHV3-23/IGLV2-14/IGLC2/IGKV1D-16/IGHV1-69/IGKV1-12/PSMA8/SKP1/IGHV2-70/IGHV4-34/IGKV1D-12/PSMA1/RPS27A/PSMA5/IGLV1-47/PSMA7/PSMD10/PSMB3/SEM1/PSMD13/PSMD14/IGKV2-28/UBE2N |
| REACTOME_FCGR3A_MEDIATED_IL10_SYNTHESIS | 95 | 0.82583691 | 3.33873873 | 1E−10 | 4.4263E−09 | 3.1376E−09 | 1,049 | Tags =51%, list =3%, signal =49% | IGHV4-39/IGLV3-27/IGKV3-15/IGKV1-5/IGLV2-8/IGKV3-20/IGKV1-16/IGLV7-43/IGKV1-33/IGHV3-33/IGKV3-11/IGKV1D-33/IGLV2-23/IGHG1/IGLV6-57/IGHV4-59/IGHV3-13/IGKV2-30/IGHV1-2/IGKV2D-40/IGHV3-11/IGHG2/IGLV1-44/IGKV4-1/IGHV1-46/IGLV3-19/IGKV1-17/IGHV2-5/IGKV3D-20/IGLC3/IGHV3-30/IGLV1-40/IGHV3-53/IGHV3-48/IGKV2D-28/IGLV3-21/IGHV3-7/IGKV2D-30/IGKV5-2/IGLV3-25/IGLV3-1/IGHV3-23/IGLV2-14/IGLC2/IGKV1D-16/IL10/IGHV1-69/IGKV1-12 |

GSEA, gene set enrichment analysis; P.adj, adjusted P value.

**Table S2** Cox's regression analysis of factors associated with OS in GBM

| Characteristics | Total (N) | Univariate analysis | | Multivariate analysis | |
|---|---|---|---|---|---|
| | | HR (95% CI) | P value | HR (95% CI) | P value |
| IDH status | 161 | | <0.001 | | |
| WT | 149 | Reference | – | Reference | – |
| Mut | 12 | 0.301 (0.138–0.654) | 0.002 | 0.389 (0.171–0.886) | 0.025 |
| Age | 168 | | 0.072 | | |
| ≤60 years | 87 | Reference | – | Reference | – |
| >60 years | 81 | 1.365 (0.973–1.915) | 0.072 | 1.224 (0.848–1.767) | 0.281 |
| SMIM20 | 168 | | 0.004 | | |
| Low | 84 | Reference | – | Reference | – |
| High | 84 | 1.670 (1.174–2.375) | 0.004 | 1.606 (1.109–2.327) | 0.012 |
| Gender | 168 | | 0.886 | | |
| Female | 59 | Reference | – | – | – |
| Male | 109 | 1.026 (0.719–1.466) | 0.887 | – | – |
| Karnofsky performance score | 128 | | 0.440 | – | – |
| ≤80 | 36 | Reference | – | – | – |
| >80 | 92 | 0.838 (0.538–1.305) | 0.434 | – | – |

OS, overall survival; GBM, glioblastoma multiforme; HR, hazard ratio; CI, confidence interval; IDH, immature dendritic cell; WT, wild type; Mut, mutant.