Electronic Supplementary Material (ESI) for Biomaterials Science.

Supplementary Information

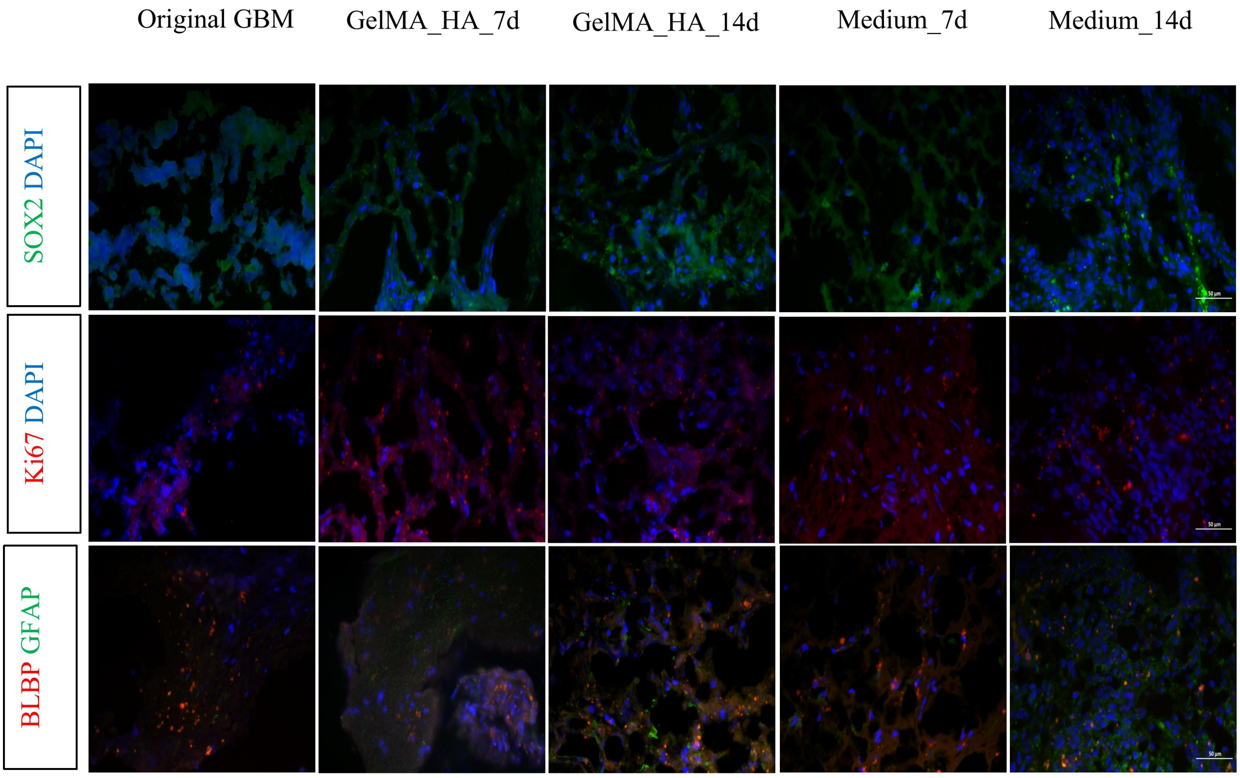

Figure S1.Immunofluorescence staining of SOX2, KI67, BLBP, GFAP in Original GBM and GBOs. Scale bar 50 μm.

Table S1 Differentially expressed genes between samples

Original_GBM-vs-GelMA_HA_7d			Original_GBM-vs-Medium_7d		Medium_7d-vs-GelMA_HA_7d	
Symbol	Log2 FoldChange	FDR	Log2 FoldChange	FDR	Log2 FoldChange	FDR
GFAP	-2.597172255	0	-3.662965013	0	1.065792758	5.53E-222
NES	-1.312864012	4.68E-66	-1.669851398	1.28E-80	0.356987386	0.000967645
MKI67	-0.201207091	0.143575012	-0.87731748	3.43E-11	0.676110389	5.88E-08
S100B	-1.427823654	0	-3.045761574	0	1.61793792	3.95E-185
FABP7	0.757738149	7.19E-85	-2.136482236	1.04E-254	2.894220385	0
HOPX	-1.286195919	1.16E-281	-3.902679639	0	2.616483719	0
SOX2	-0.698439703	5.28E-16	-2.840600178	1.25E-104	2.142160476	3.77E-52
OLIG2	-1.200387113	5.95E-09	-1.899633041	4.28E-14	0.699245928	0.023522179
PROM1	-11.3553511	7.65E-55	-0.21964181	1.76E-05	-11.13570929	2.42E-30
CRBN	-1.214077605	6.96E-141	-1.043848462	5.39E-96	-0.170229143	0.073143841
EGFR	-1.284649871	1.88E-188	-2.663694937	0	1.379045066	6.05E-45
CDK12	-0.14172811	0.072245125	-0.636492801	0.009132575	0.494764692	0.391545584
PTEN	-0.797487893	1.13E-95	0.123104145	1.19E-05	-0.920592037	1.11E-144
TNKS	-0.533823652	1.36E-22	-0.759449608	5.37E-35	0.225625957	0.000969898
NF1	0.178267196	0.000871638	-0.018185472	1.27E-05	0.196452668	0.244832593
MTOR	0.284825388	0.327010508	-0.255982783	0.000451192	0.540808171	0.01106217

The genes/transcripts with the parameter of false discovery rate (FDR) below 0.05 and absolute fold change≥1 were considered differentially expressed genes. Sample on the left of “vs” is control group

Table S2 Differentially expressed genes between samples

Original_GBM-vs-GelMA_HA_14d			Original_GBM-vs-Medium_14d		Medium_14d-vs-GelMA_HA_14d	
Symbol	Log2 FoldChange	FDR	Log2 FoldChange	FDR	Log2 FoldChange	FDR
GFAP	-1.1000408	0	-1.643073456	0	0.543032657	1.02E-89
NES	0.022852671	0.77959435	0.136400967	0.039413974	-0.113548296	0.06027403
MKI67	1.343954401	7.98E-55	1.066726114	1.23E-31	0.277228287	4.94E-05
S100B	-1.044582833	2.82E-195	-1.331445465	4.57E-299	0.286862632	6.63E-13
FABP7	3.147428164	0	1.459768736	0	1.687659428	0
HOPX	0.012156062	0.587664236	-1	1.57E-175	1.012156062	1.51E-202
SOX2	0.798661052	5.28E-32	-0.011846243	0.935374399	0.810507295	4.29E-39
OLIG2	1.21405312	4.23E-17	0.092589608	0.648814612	1.121463512	1.15E-17
PROM1	-11.3553511	4.41E-55	-1.693572999	2.06E-17	-9.661778098	1.12E-20
CRBN	-0.250673677	1.78E-08	-0.084559959	0.006470378	-0.166113718	0.003872649
EGFR	0.243195659	0.670842273	-2.10203981	1.71E-293	2.345235468	0
CDK12	-1.208399149	3.36E-11	-0.636492801	0.001203492	-0.571906348	0.000905418
PTEN	-1.421247294	5.68E-272	-0.65132639	8.92E-63	-0.769920904	1.40E-75
TNKS	0.309380244	5.66E-18	0.373927997	9.54E-12	-0.064547754	0.084124776
NF1	-1.281830026	2.68E-22	-1.973144508	4.26E-46	0.691314482	1.15E-06
MTOR	-1.089472446	5.04E-32	-0.426867342	1.23E-05	-0.662605104	1.67E-14

The genes/transcripts with the parameter of false discovery rate (FDR) below 0.05 and absolute fold change≥1 were considered differentially expressed genes. Sample on the left of “vs” is control group