

Table 1. Patient data and biosamples analyzed in this study

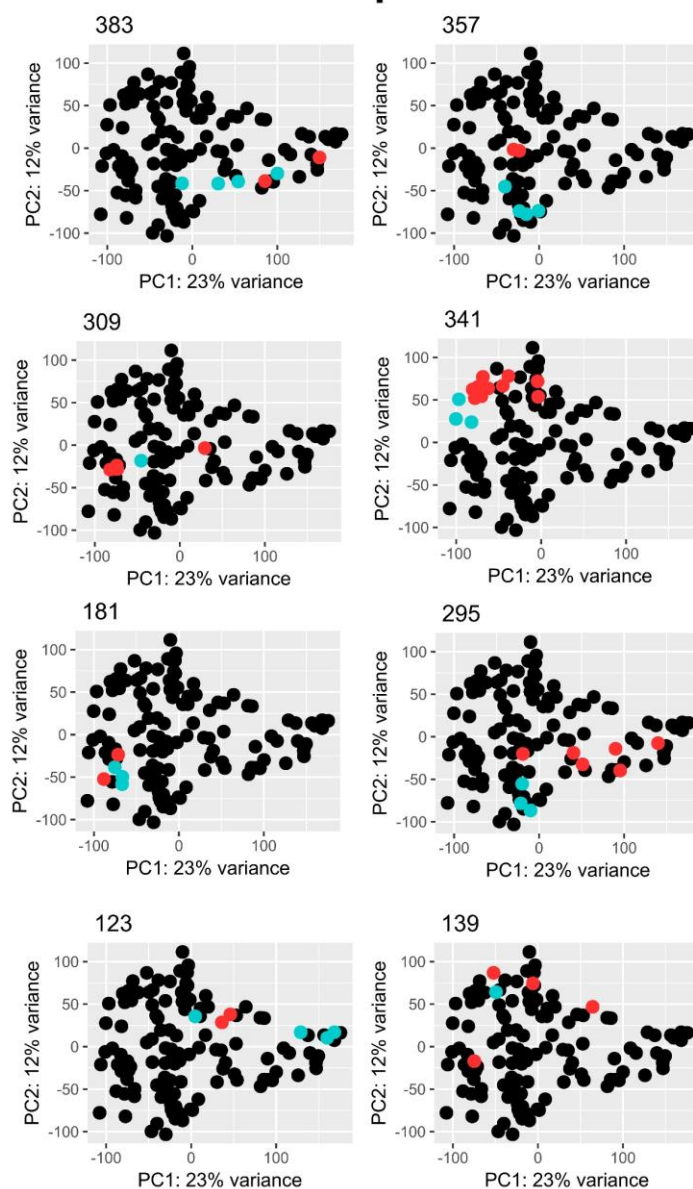
Patient ID	Sex	Age, ndGB ^a	Age, recGB ^b	TTP ^c	ndGB ^d TL, TS, N	recGB ^e TL, TS, N	GSC-ndGB ^f N	GSC-recGB ^g N
123	M	28	30; 31	32; 4	right insular 2.5 × 3; N = 2	right fronto-temporal local recurrence 2.3 × 3; N = 4 right frontal local recurrence 5 × 5; N = 5	0	0
139	M	59	60	14	left temporomesial 2 × 3; N = 4	left temporomesial local recurrence 2 × 2cm; N = 1	0	0
151	M	68	70; 71	23; 5	bifrontal 4 × 2.7 (left side) 2.5 × 2 (right side) N = 2	left frontal local recurrence 1 × 1.5; N = 2 left frontal local recurrence 6 × 4.5; N = 7	0	0
163	M	30	40	123	0	left frontal local recurrence 2.8x2.5; N = 2	0	0
181	M	57	58	4	left temporal 4 × 3; N = 2	left temporal local recurrence 7 × 4.5; N = 3	0	0
191	M	56	57	4	right frontal 6 × 5; N = 2	0	0	0
211	M	57	57	9	0	right frontal local recurrence 4 × 3; N = 1	0	0
226	M	70	71	4	0	right temporopolar local recurrence 3 × 2; N = 4	0	3
245	M	62	62	4	left temporoparietal 2.4 × 2.1; N = 1	left parietal local recurrence 4.4 × 2; N = 3	0	0
259	M	56	58	26	left temporopolar 4.5 × 6; N = 1	left temporopolar local recurrence	0	0

Patient ID	Sex	Age, ndGB ^a	Age, recGB ^b	TTP ^c	ndGB ^d TL, TS, N	recGB ^e TL, TS, N	GSC-ndGB ^f N	GSC-recGB ^g N
						4 × 1.3; N = 1		
279	M	45	45	9	left temporomesial 4.5 × 2.8; N = 3	left temporomesial local recurrence 4.2 × 3.7; N = 1	0	2
295	M	75	75	6	right temporal 6.2 × 4.5; N = 6	right temporal local recurrence two sites each 1 × 1; N = 3	1	1
309	F	73	74	14	right temporofrontal 6.1 × 4.1; N = 4	right frontoopercular local recurrence 2 × 1.5; N = 1	1	0
326	F	63	63	8	right frontal (gyrus praecentralis) 1.6 × 1.9; N = 2	right frontal (gyrus praecentralis) local recurrence 2 × 2; N = 1	0	0
341	F	54	56	31	left temporopolar 5.5 × 4; N = 11	left temporopolar local recurrence 5.2 × 4; N = 3	0	0
357	F	72	72	5	right parietal 3.1 × 2.5; N = 2	right parietal local recurrence 2.8 × 2.6; N = 4	0	0
367	F	60	60	5	right frontal 4.1 × 3.9 cm; N = 1	0	0	0
383	F	74	75	9	right frontotemporal (insula) 6 × 4; N = 2	right temporal local recurrence two herds 2 × 1 & 1 × 1; N = 4	0	0
402	F	49	49	3	right temporopolar 2.4 × 2.6; N = 2	right temporal local recurrence 1.8 × 1.8; N = 1	0	0
501	F	70	unk	unk	right temporo-insular 5.3 × 5.3; N = 8	0	2	0
459	F	18	unk	unk	left frontal (basal ganglia) 6 × 4.5; N = 2	0	2	0
565	F	42	unk	unk	left frontal 6.8 × 6.2; N = 5	0	1	0
568	F	62	unk	unk	left frontal	0	2	0

Patient ID	Sex	Age, ndGB ^a	Age, recGB ^b	TTP ^c	ndGB ^d TL, TS, N	recGB ^e TL, TS, N	GSC-ndGB ^f N	GSC-recGB ^g N
					6.8 × 4.4; N = 3			
657	F	57	unk	unk	occipital right 6.2 × 3.4; N = 1	0	2	0
677	F	74	unk	unk	left frontal 1.1 × 1.3; N = 3	0	4	0
700	M	48	49	8	0	right temporoparietal local recurrence 4 × 3; N = 5	0	4
704	M	67	67	6	0	right parietal. local recurrence 3.2 × 2.8; N = 1	0	0
649	F	66	unk	unk	right parietal 4.2 × 3.8; N = 2	0	2	0

^aPatient age at the time of initial GB diagnosis, years old; ^bPatient age at the time of recGB diagnosis, years old; ^cTime to progression, months. For the cases sequentially two times diagnosed with recGB, two TTP values are shown. “unk”, unknown. ^dTL, tumor location/ TS, tumor size (max diameter on axial plain)/ N, number of samples available from ndGBs; ^eTL, tumor location/ TS, tumor size (max diameter on axial plain, cm)/N, number of samples available from recGBs; ^fN, number of GSC cultures established from ndGBs; ^gN, number of GSC cultures established from recGBs.

Gene expression



Pathway activation level

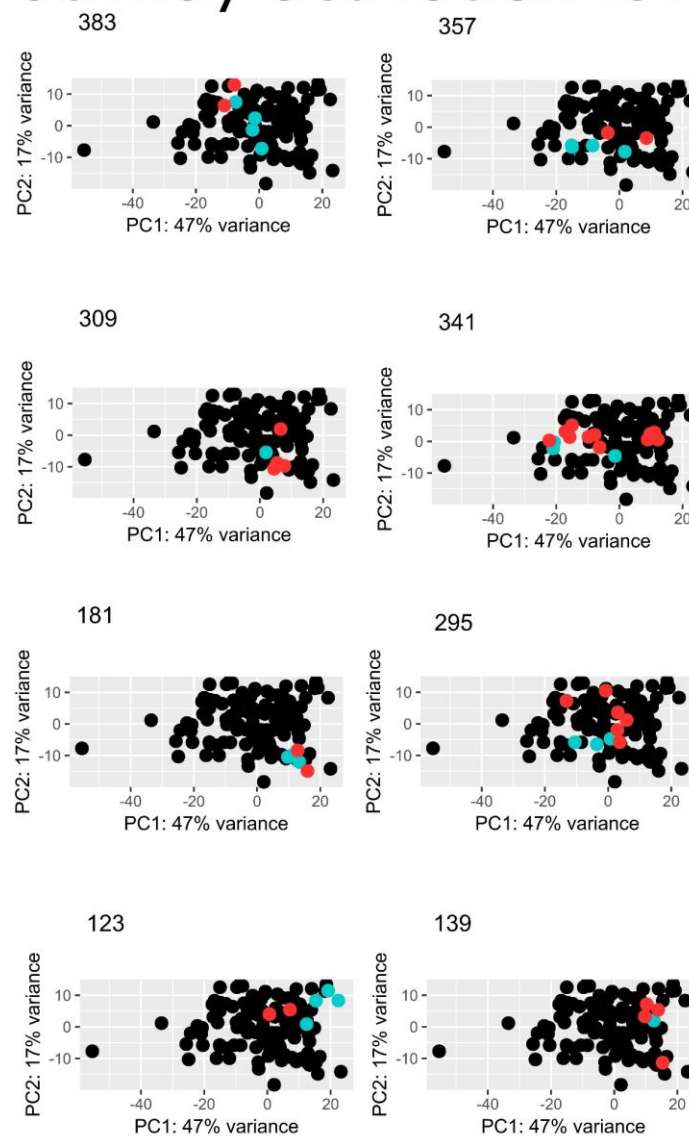
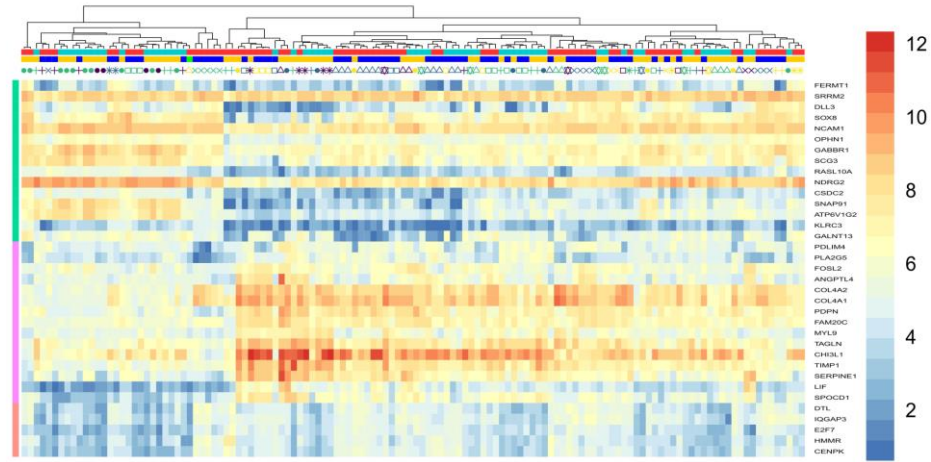


Figure S1. Principal component analysis of GBM tissue multisampling using normalized gene expression data (left panel) or pathway activation levels (right panel). Panels show colored data for patient-matched tumors at ndGB (red) and recGB (magenta) stages. Values aligned with axis show proportion of variance in percent for principal components 1 and 2, respectively;.

A



Patient ID

Gene groups

Sample type



MES
PN
PROLIF

Primary
Recurrent
Tumour size
≤ median
> median
Not available

B

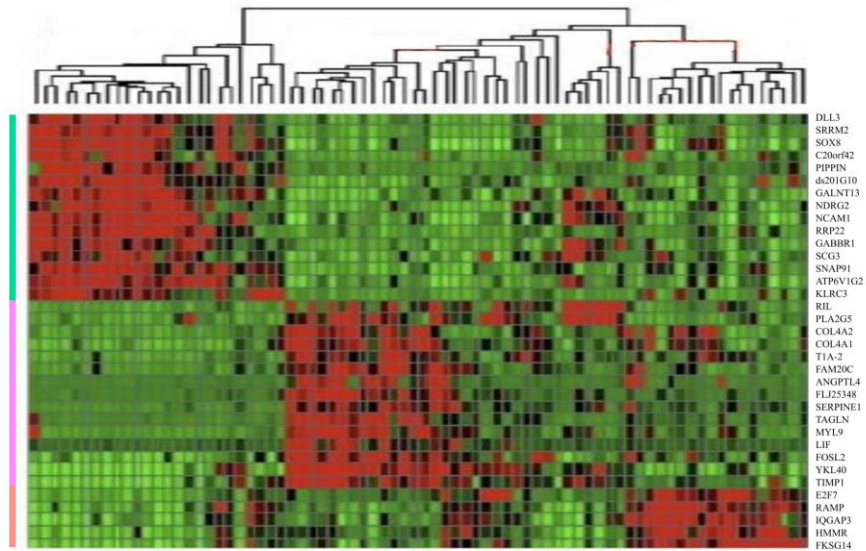


Figure S2. (A) Hierarchical clustering dendrogram of GB tissue samples. Color marker indicates tissue type (ndGB or recGB, for horizontal codes) or phenotype associated genes (PN—proneural, MES—mesenchymal, PROLIF—proliferative) according to Phillips et al. [39]. (B) Hierarchical clustering dendrogram of GB tissue samples adopted from Phillips et al. [39];.