

1 **Supplementary Tables**

2 **Table S1.** Regression of the first ten principal components **derived from Methylation** on age at diagnosis, race and gender.

PC ¹	Age			Race			Gender		
	Estimate ²	p-value ³	Prop. var ⁴	Estimate	p-value	Prop. var	Estimate	p-value	Prop. var
PC1	1.2980	-0.9303	0.0001	0.1728	0.4808	0.0025	0.5522	0.2621	0.0062
PC2	-17.477	0.2378	0.0069	0.2919	0.2331	0.0069	0.4406	0.3709	0.0039
PC3	10.843	0.4644	0.0026	-0.1728	0.4808	0.0025	0.4669	0.3429	0.0044
PC4	81.307	< 0.0001	0.1479	-0.0869	0.7234	0.0006	0.0096	0.9845	0.0001
PC5	10.164	0.4928	0.0023	0.0137	0.9554	0.0001	0.8281	0.0918	0.0139
PC6	-22.482	0.1285	0.0113	0.5794	0.0174	0.0276	-0.7314	0.1369	0.0109
PC7	-25.149	0.0888	0.0142	0.5405	0.0266	0.0239	-0.2582	0.6003	0.0014
PC8	25.342	0.0864	0.0144	0.6912	0.0044	0.0392	-0.4463	0.3649	0.0040
PC9	-9.0396	0.5419	0.0018	-0.0180	0.9414	0.0001	0.4173	0.3969	0.0035
PC10	-38.245	0.0094	0.0328	-0.1458	0.5522	0.0017	0.5321	0.2801	0.0057

3 ¹Principal components derived from methylation; ²Coefficient estimate associated with each PC; ³p-value for significance of
4 association; ⁴Proportion of variance of age at diagnosis, race and gender explained by each methylation-derived principal component.

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6 **Table S2.** Regression of the first ten principal components **derived from CNV** on age at diagnosis, race and gender.

PC ¹	Age			Race			Gender		
	Estimate ²	p-value ³	Prop. var ⁴	Estimate	p-value	Prop. var	Estimate	p-value	Prop. var
PC1	-0.0007	< 0.0001	0.0528	0.2174	0.3676	0.0019	-0.2642	0.5891	0.0007
PC2	-0.0004	0.0177	0.0134	0.2447	0.3106	0.0025	0.3453	0.4800	0.0012
PC3	0.0007	< 0.0001	0.0458	-0.2403	0.3193	0.0024	0.1464	0.7648	0.0002
PC4	-0.0001	0.6884	0.0004	-0.1344	0.5776	0.0007	1.1161	0.0221	0.0124
PC5	0.0005	0.0047	0.0189	-0.4950	0.0398	0.0101	-0.1575	0.7475	0.0003
PC6	0.0001	0.7829	0.0002	-0.2369	0.3262	0.0023	0.1383	0.7374	0.0002
PC7	-0.0004	0.0141	0.0143	0.5030	0.0367	0.0104	-0.1363	0.7806	0.0002
PC8	-0.0002	0.2216	0.0036	0.3979	0.0988	0.0065	-0.0020	0.9967	< 0.0001
PC9	0.0002	0.1691	0.0045	-0.3202	0.1843	0.0042	-0.4902	0.3159	0.0024
PC10	0.0002	0.1428	0.0051	0.1766	0.4643	0.0013	-0.5352	0.2735	0.0029

7 ¹Principal components derived from CNV; ²Coefficient estimate associated with each PC; ³p-value for significance of association;

8 ⁴Proportion of variance of age at diagnosis, race and gender explained by each CNV-derived principal component.

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11 **Table S3.** Regression of the first ten principal components **derived from SNP** on age at diagnosis, race and gender.

PC ¹	Age			Race			Gender		
	Estimate ²	p-value ³	Prop. var ⁴	Estimate	p-value	Prop. var	Estimate	p-value	Prop. var
PC1	-0.0003	0.4076	0.0033	3.3334	<0.0001	0.9129	0.2322	0.6376	0.0011
PC2	0.0003	0.3118	0.0050	-0.4629	0.0578	0.0176	-0.1743	0.7236	0.0001
PC3	0.0002	0.6533	0.0010	0.4331	0.0785	0.0151	0.7273	0.1421	0.0105
PC4	-0.0007	0.0330	0.0222	-0.1229	0.6159	0.0012	-0.5370	0.2752	0.0059
PC5	0.0001	0.8394	0.0002	0.0001	0.9999	0.0001	0.3934	0.4245	0.0031
PC6	-0.0003	0.3870	0.0037	0.0147	0.9522	0.0001	-0.2112	0.6683	0.0009
PC7	0.0001	0.8230	0.0002	0.2698	0.2705	0.0059	0.8434	0.0859	0.0145
PC8	-0.0003	0.4512	0.0028	-0.1576	0.5203	0.0021	0.3648	0.4589	0.0027
PC9	0.0006	0.0722	0.0158	0.1999	0.4146	0.0033	-0.1339	0.7859	0.0004
PC10	0.0003	0.4352	0.0030	0.1527	0.5332	0.0019	-0.3525	0.4743	0.0025

12 ¹Principal components derived from SNP; ²Coefficient estimate associated with each PC; ³*p*-value for significance of association;

13 ⁴Proportion of variance of age at diagnosis, race and gender explained by each SNP-derived principal component.

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16 **Table S4.** Regression of the first ten principal components **derived from gene expression** on age at diagnosis, race and gender.

PC ¹	Age			Race			Gender		
	Estimate ²	p-value ³	Prop. Var ⁴	Estimate	p-value	Prop. var	Estimate	p-value	Prop. var
PC1	-11.646	0.4319	0.0031	-0.1489	0.5439	0.0018	-0.6582	0.1808	0.0088
PC2	7.4834	0.6137	0.0013	0.1073	0.6617	0.0009	-0.4501	0.3608	0.0041
PC3	-3.8613	0.7946	0.0003	-0.5408	0.0265	0.0241	1.5081	0.0019	0.0462
PC4	30.817	0.0367	0.0213	-0.3723	0.1278	0.0114	-0.3094	0.5301	0.0019
PC5	9.1784	0.5359	0.0018	-0.2891	0.2379	0.0069	0.6782	0.1680	0.0093
PC6	18.392	0.2139	0.0076	-0.4619	0.0585	0.0175	0.2511	0.6104	0.0013
PC7	-29.571	0.0452	0.0196	0.4525	0.0639	0.0168	0.8961	0.0680	0.0163
PC8	20.642	0.1629	0.0096	-0.0853	0.7278	0.0006	-0.0749	0.8791	0.0001
PC9	-65.807	< 0.0001	0.0972	-0.3510	0.1514	0.0101	-1.3815	0.0047	0.0388
PC10	17.264	0.2435	0.0067	-0.1708	0.4857	0.0024	0.3609	0.4637	0.0026

17 ¹Principal components derived from gene expression; ²Coefficient estimate associated with each PC; ³*p*-value for significance of
18 association; ⁴Proportion of variance of age at diagnosis, race and gender explained by each gene expression-derived principal
19 component.

Table S5. Hazard ratio, confidence interval (95%) and p-value for clinical, demographic and chemotherapy treatments in GBM patients.

Covariate¹	Hazard ratio (95% CI)²	Pr(> z)³
Age at diagnosis	1.027 (1.019,1.034)	< 0.0001
Gender (Males)	0.986 (0.794,1.224)	0.8980
Race (European-American)	1.019 (0.634,1.640)	0.9362
Method of diagnosis (Tumor resection)	0.822 (0.574,1.178)	0.2859
Tumor purity	0.405 (0.163,1.008)	0.0539
Radiation	0.864 (0.649,1.149)	0.3145
Chemotherapy treatments (compound names)		
Temozolomide	0.651 (0.515,0.822)	0.0003
Bevacizumab	0.758 (0.516,1.113)	0.1571
Carboplatin	0.938 (0.583,1.508)	0.7920
Carmustine	0.778 (0.557,1.069)	0.1218
Erlotinib	1.200 (0.713,2.022)	0.4923
Etoposide	0.903 (0.539,1.514)	0.7001
Irinotecan	0.694 (0.445,1.084)	0.1088
Lomustine	0.587 (0.389,0.885)	0.0109
Procarbazine	1.046 (0.594,1.843)	0.8756
Tamoxifen	1.362 (0.763,2.432)	0.2966
Other Chemo	0.836 (0.612,1.141)	0.2591

¹ Clinical covariates included in the model; ²Hazard ratio and corresponding 95% confidence interval; ³p-value for significance of the covariate.