

Erratum to: *MGMT* methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status

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In the original paper, one of the author names was misspelled and should read David R. Macdonald.

On behalf of the investigators of the European Organisation for Research and Treatment of Cancer and the National Cancer Institute of Canada Clinical Trials Group.

The online version of the original article can be found under doi:10.1007/s00401-012-1016-2.

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One of the methylation probe names in the abstract was misspelled and should read cg12434587 (not cg1243587). The authors wish to add the following statement that was missing in the Acknowledgments:

The results published here are in part based upon data generated by The Cancer TCGA Genome Atlas pilot project established by the NCI and NHGRI. Information about TCGA and the investigators and institutions who constitute the TCGA research network can be found at <http://cancergenome.nih.gov/>. The dbGaP accession number to the specific version of the TCGA data set is phs000178.v5.p5.

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