Table S2: Data collection and processing procedures for public <u>DNA methylation</u> datasets in BTECH.

Track Description	Data Resource	Title	Methods	PubMed ID	Analysis Procedures
Track Description	Data Resource	1140	Withous		Anarysis i roccuures
Brain methylation profile	http://transcript ome.affymetrix.c om/download/D ataMethPaper/	Microarray-based DNA methylation profiling: technology and applications.	Microarry hybridization	16428248	Download and uplift to the current genome coordinates
Hypomethylated regions in adult normal brain	Publication	Large-scale structure of genomic methylation patterns	Enzyme digestion followed by sequecing	16365381	Kindly provided by Dr. T.H. Bestor's group
Hypermethylated regions in adult normal brain	Publication	Large-scale structure of genomic methylation patterns	Enzyme digestion followed by sequecing	16365381	Kindly provided by Dr. T.H. Bestor's group
Human epigenome project	http://www.epig enome.org/	DNA methylation profiling of human chromosomes 6, 20 and 22.	Bisulfite DNA sequencing	17072317	Download from the HEP site
GBM_The Cancer Genome Atlas_Methylation	http://www.canc ergenome.nih.go v/	The Cancer Genome Atlas	HG-U133A	Available from TCGA	Download from site
Astrocytomas_Hypomet hylated_Regions	http://www.ncbi. nlm.nih.gov/geo /query/acc.cgi?a cc=GSE19391	CpG island hypermethylation in human astrocytomas	Microarry hybridization	20233874	Download from the GEO site
Astrocytomas_CpG Island	http://www.ncbi. nlm.nih.gov/geo /query/acc.cgi?a cc=GSE19391	CpG island hypermethylation in human astrocytomas	Microarry hybridization	20233874	Download from the GEO site

Methylation Associated SNP Clusters (MASCs)	Publication	SNP-based Prediction of the Human Germ Cell Methylation Landscape	Computation analysis	19442638	Extract from publication
MAS Intensity	Publication	SNP-based Prediction of the Human Germ Cell Methylation Landscape	Computation analysis	19442638	Extract from publication