THE CANCER GENOME ATLAS
National Cancer Institute
National Human Genome Research Institute

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The Somatic Genomic Landscape of Glioblastoma

Cell, Volume 155 Issue 2. 462-477, [10.1016/j.cell.2013.09.034]

Abstract

We describe the landscape of somatic genomic alterations based on multidimensional and comprehensive characterization of more than 500 glioblastoma tumors (GBMs). We identify several novel mutated genes as well as complex rearrangements of signature receptors, including EGFR and PDGFRA. TERT promoter mutations are shown to correlate with elevated mRNA expression, supporting a role in telomerase reactivation. Correlative analyses confirm that the survival advantage of the proneural subtype is conferred by the G-CIMP phenotype, and MGMT DNA methylation may be a predictive biomarker for treatment response only in classical subtype GBM. Integrative analysis of genomic and proteomic profiles challenges the notion of therapeutic inhibition of a pathway as an alternative to inhibition of the target itself. These data will facilitate the discovery of therapeutic and diagnostic target candidates, the validation of research and clinical observations and the generation of unanticipated hypotheses that can advance our molecular understanding of this lethal cancer.

Associated Data Files

These data represent a data freeze from Oct 10, 2012. Please note that more recent data are available via the TCGA Data Portal.

The data are supported by different organizations. All data marked by [DCC] are DCC-validated archives. All data marked by [Supplementary] were created by the manuscript authors and you should contact the corresponding author for support.

Sample Lists - below are links to cumulative list of samples for the publication

Full GBM Sample List

After the data freeze for this paper, several blood normal samples were found to be mistakenly labelled as tissue normals. The table below lists the aliquots from this publication that were affected. The GBM sequence data list has been revised, and the original with incorrect barcodes can be found here. Note that the BAM file names for these samples contains the original, incorrect, barcode.

Incorrect Barcode	Correct Barcode
TCGA-19-5958-11A-01D-1696-08	TCGA-19-5958-10A-01D-1696-08
TCGA-19-5951-11A-01D-1696-08	TCGA-19-5951-10A-01D-1696-08
TCGA-19-5955-11A-01D-1696-08	TCGA-19-5955-10A-01D-1696-08
TCGA-19-5960-11A-01D-1696-08	TCGA-19-5960-10A-01D-1696-08
TCGA-19-5959-11A-01D-1696-08	TCGA-19-5959-10A-01D-1696-08
TCGA-19-5954-11A-01D-1696-08	TCGA-19-5954-10A-01D-1696-08
TCGA-19-5952-11A-01D-1696-08	TCGA-19-5952-10A-01D-1696-08
TCGA-19-5950-11A-01D-1696-08	TCGA-19-5950-10A-01D-1696-08
TCGA-19-5947-11A-01D-1696-08	TCGA-19-5947-10A-01D-1696-08

- GBM data freeze list (tab-delimited text format) (53M)
- GBM sequence data list (tab-delimited text format)(184K)

Copy Number Tables

- TCGA_GBM_PCT_CNA_Annotation.txt
- TCGA_GBM_PCT_CNA_Physical_triplet.txt
- TCGA_GBM_PCT_CNA_Summary.txt

Mutations

- TCGA_GBM_PCT_hg19_combined_snp_indel.maf.pct
- TCGA_GBM_PCT_hg19_combined_snp_indel_description.txt

Open access MAF file
- broad.mit.edu_GBM.IlluminaGA_DNASeq.Level_2.100.1.0.tar.gz
- broad.mit.edu_GBM.IlluminaGA_DNASeq.Level_2.100.1.0.tar.gz.md5

Gene Expression

Level 3 Data Archives
- GBM.Gene_Expression.Level_3.tar (79M)
- GBM.Gene_Expression.Level_3.tar.md5

Level 2 Data Archives
- GBM.Gene_Expression.Level_2.tar (133M)
- GBM.Gene_Expression.Level_2.tar.md5

Level 1 Data Archives
- GBM.Gene_Expression.Level_1.tar (1.4G)

In This Section

- About the Data
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- GBM.Gene_Expression.Level_1.tar.md5

SNP

Level 3 Data Archives
- GBM.SNP.Level_3.tar (20M)
- GBM.SNP.Level_3.tar.md5

miRNA Expression

Level 3 Data Archives
- unc.edu_GBM.H-miRNA_8x15K.Level_3.1.8.0.tar.gz (2.9M)

Level 2 Data Archives
- unc.edu_GBM.H-miRNA_8x15K.Level_2.1.8.0.tar.gz (8.1M)

Level 1 Data Archives
- unc.edu_GBM.H-miRNA_8x15K.Level_1.1.8.0.tar.gz (776M)

Methylation

Methylation Summary Information
- TCGA_GBM_dnameth_calls_20120112_ver3.txt
- TCGA_GBM_dnameth_scores_20120112_ver3.txt
- DNA.methylation.k6.txt
- TCGA_GBM_dnameth_call_categories.txt

Level 3 Data Archives
- GBM.HumanMethylation27.Level_3.tar (177M)
- GBM.HumanMethylation27.Level_3.tar.md5
- GBM.HumanMethylation450.Level_3.tar (1.2G)
- GBM.HumanMethylation450.Level_3.tar.md5

Level 2 Data Archives
- GBM.HumanMethylation27.Level_2.tar (121M)
- GBM.HumanMethylation27.Level_2.tar.md5
- GBM.HumanMethylation450.Level_2.tar (1.2G)
- GBM.HumanMethylation450.Level_2.tar.md5
- GBM.HumanMethylation_OMA002_CPI.Level_2.tar (1.4M)
- GBM.HumanMethylation_OMA002_CPI.Level_2.tar.md5
- GBM.HumanMethylation_OMA003_CPI.Level_2.tar (1.3M)
- GBM.HumanMethylation_OMA003_CPI.Level_2.tar.md5

Level 1 Data Archives
- GBM.HumanMethylation27.Level_1.tar (219M)
- GBM.HumanMethylation27.Level_1.tar.md5
- GBM.HumanMethylation450.Level_1.tar (1.1G)
- GBM.HumanMethylation450.Level_1.tar.md5
- GBM.HumanMethylation_OMA002_CPI.Level_1.tar (5M)
- GBM.HumanMethylation_OMA002_CPI.Level_1.tar.md5
- GBM.HumanMethylation_OMA003_CPI.Level_1.tar (6.6M)
- GBM.HumanMethylation_OMA003_CPI.Level_1.tar.md5

Reverse Phase Protein Array (RPPA)

Level 3 Data Archives
- mdanderson.org_GBM.MDA_RPPA_Core.Level_3.1.0.0.tar.gz
- mdanderson.org_GBM.MDA_RPPA_Core.Level_3.1.0.0.tar.gz.md5

Level 2 Data Archives
- mdanderson.org_GBM.MDA_RPPA_Core.Level_2.1.0.0.tar.gz
- mdanderson.org_GBM.MDA_RPPA_Core.Level_2.1.0.0.tar.gz.md5

Level 1 Data Archives
- mdanderson.org_GBM.MDA_RPPA_Core.Level_1.1.0.0.tar.gz (987M)
- mdanderson.org_GBM.MDA_RPPA_Core.Level_1.1.0.0.tar.gz.md5

Clinical

- GBM.Clinical.tar (56M)
- GBM.Clinical.tar.md5

Supplementary Data

- ceRNAs and target genes.docx
- Expression_signatures.xlsx
- Exome_Sequencing.xlsx
- Genomic_Rearrangements.xlsx
- miRNA-mRNA-network.xls
- Molecular_features_of_long-term-survivors.xlsx
- Molecular_subtype_classification.xlsx
- Pathways_enriched_in_GBM_gene_ceRNAs.xlsx
- RPPA signaling module scores per sample.xlsx

Additional Information

- Receptor_Tyrosine_Kinase_Gene_Expression_Data.zip - Receptor Tyrosine Kinase Gene Expression Data (using RT-PCR and Nanostring)
- TCGA Wiki
  - Descriptions of TCGA data are provided in the TCGA Data Primer
- Genomic Data Commons Portal

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