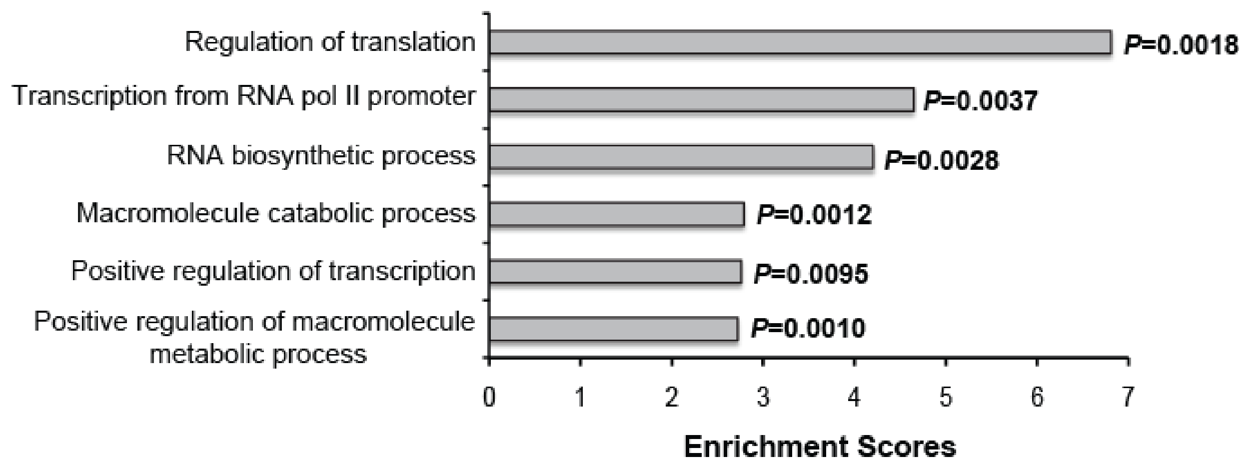



**Figure S1. Gene Ontology (GO) analysis of transcripts with altered splicing induced by EGFRvIII.**

GO analysis of transcripts that contain MADS+ identified changes in alternative splicing. P-value is generated by DAVID Functional Annotation Tool and is a modified Fisher exact p-value.

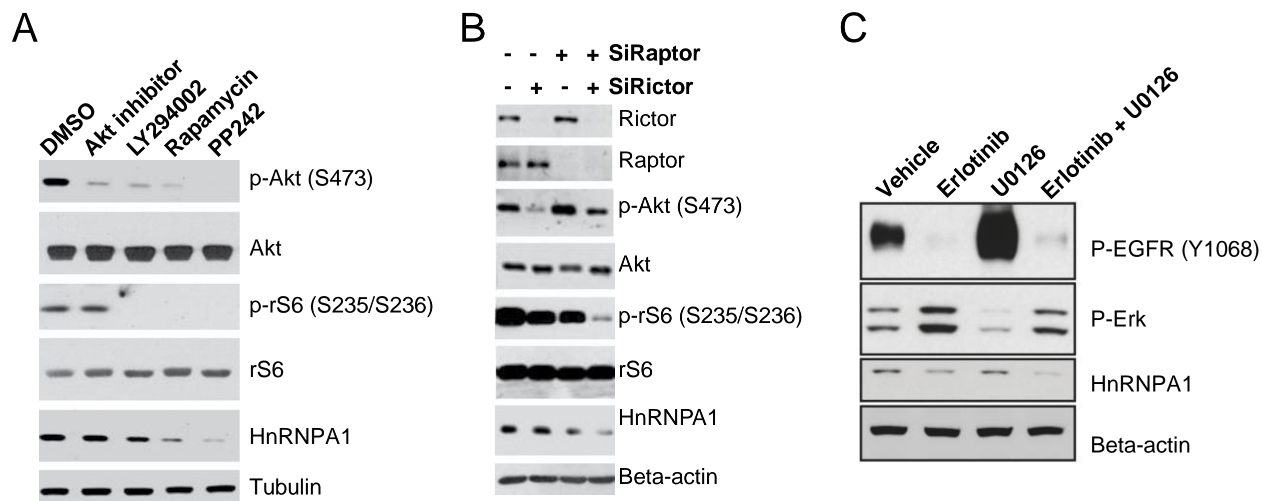


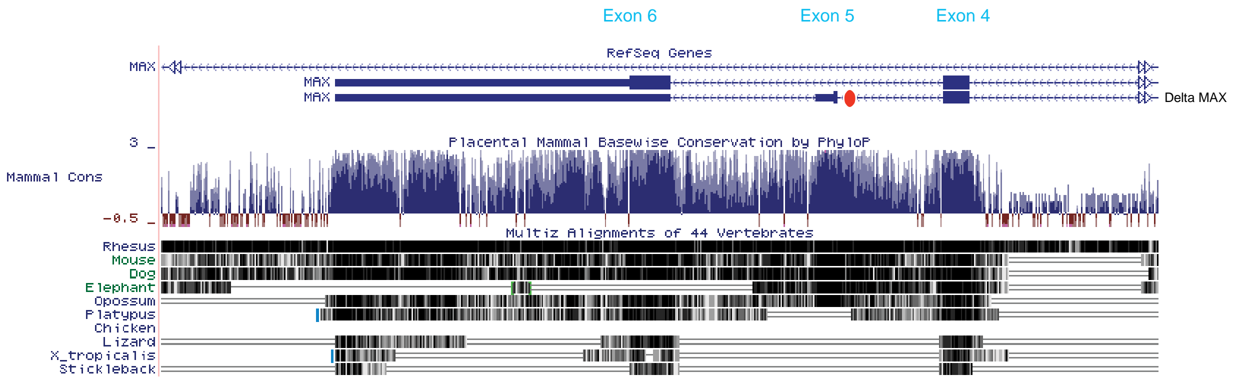

**Figure S2. Inhibition of mTOR decreases hnRNPA1 expression in U87-EGFRvIII cells.**

(A) Pharmacological inhibition of mTOR in U87-EGFRvIII cells inhibits expression of hnRNPA1.

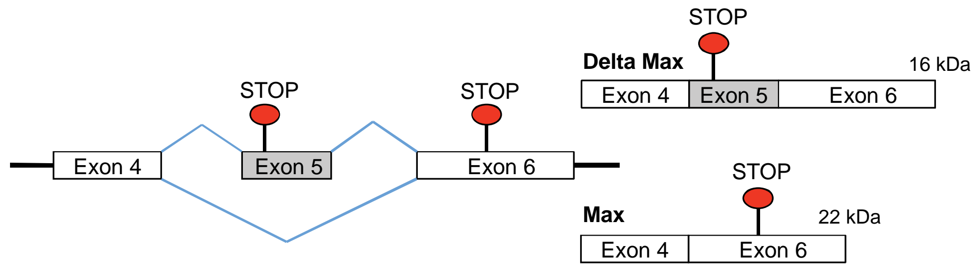
(B) Genetic inhibition of mTOR by rictor and raptor knockdown inhibits hnRNPA1 expression.

(C) Combination of eroltinib and U0126 for 24 hours inhibits hnRNPA1 expression in U87-EGFRvIII cells.

A




B




C

```
                     10        20        30        40        50        60
Max        MSDNDDIEVESDEEQPRFQSAADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASR
           ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Delta Max  MSDNDDIEVESDEEQPRFQSAADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASR
                     10        20        30        40        50        60

                     70        80        90       100       110       120
Max        AQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRALEKARSSAQLQTNYPSSDN
           ::::::::::::::::::::::::::::::::::::::
Delta Max  AQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQGESES-----------------
                     70        80        90       100

                    130       140       150       160
Max        SLYTNAKGSTISAFDGGSDSSSESEPEEPQSRKKLRMEAS

Delta Max  ----------------------------------------
```

Figure S3

**Figure S3. Data from the UCSC genome browser web site shows high conservation within the intronic region upstream of Max exon 5.**

(A) The red spot shows the location of the potential hnRNPA1 binding site within the highly conserved intronic region.

(B) Schematic illustrating Max exon 5 splicing generating the C-terminal truncated Delta Max.

(C) The amino acids highlighted in gray are unique to Delta Max carboxy-terminus and are encoded by exon 5.

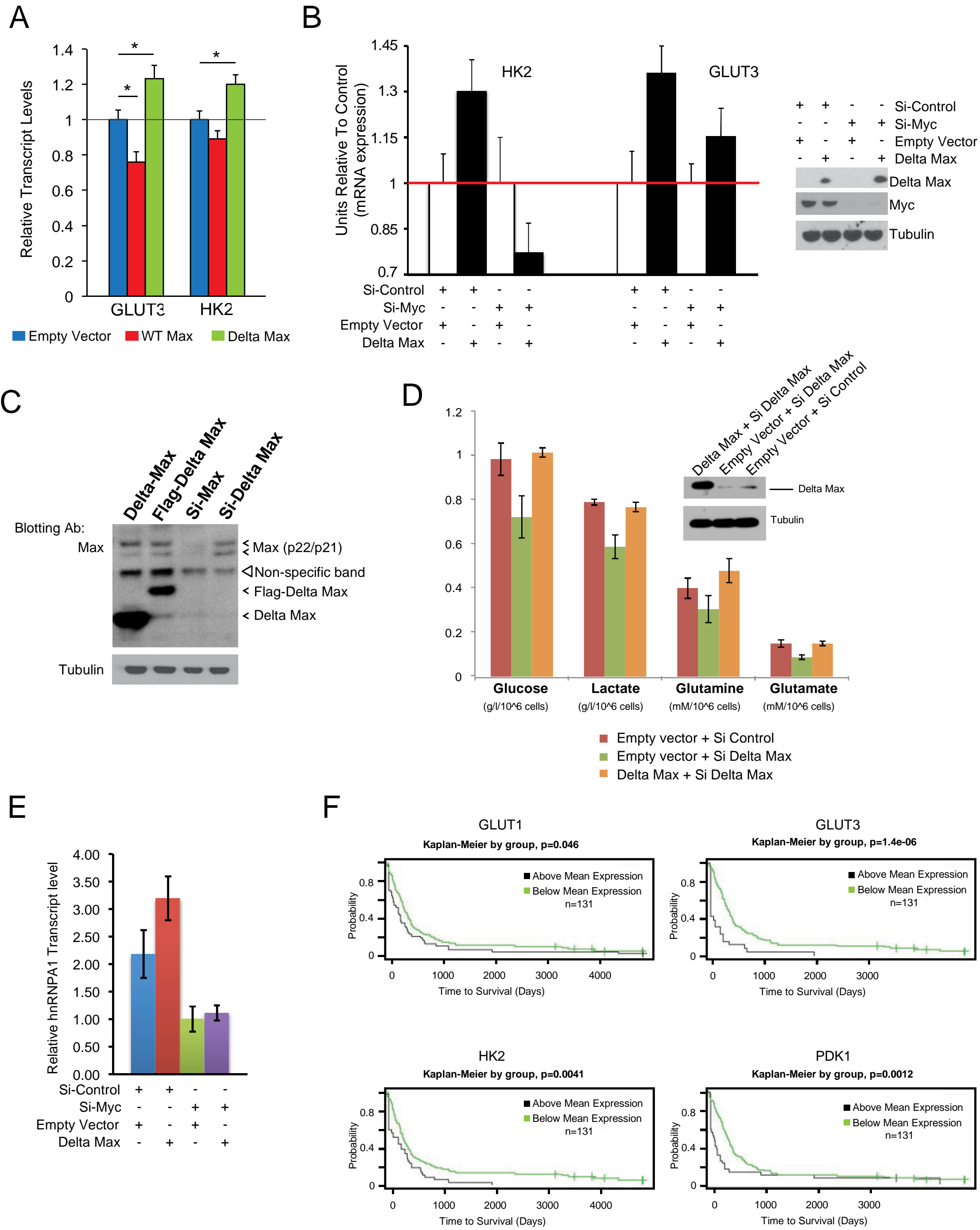



**Figure S4**

**Figure S4. Delta Max overexpression augments Myc-dependent gene expression and promotes aerobic glycolysis.**

(A) Relative transcript level of GLUT3 and HK2 in U87 cells overexpressing Delta Max or wild-type (WT) Max.

(B) HK2 and GLUT3 transcript levels in U87-EGFRvIII cells overexpressing Delta Max with or without Myc.

(C) Immunoblot demonstrating specific knockdown of Delta Max in U87-EGFRvIII cells.

(D) Overexpression of siRNA resistant Delta Max in U87 cells transfected with siRNA to Delta Max rescues glycolysis as measured by Nova BioProfile (n=3; shown is the mean$\pm$SD).

(E) RT-qPCR for hnRNPA1 with or without Myc and with or without Delta Max overexpression (n=3; shown is the mean$\pm$SD).

(F) Survival plots of 131 primary GBM patients stratified by expression of the indicated glycolytic genes. The single p-value is based on the difference of the two curves, and was calculated using the log-rank test.

## SUPPLEMENTAL TABLES

**Table S1. Alternative splicing events included in each Gene Ontology (GO) enrichment term.** Listed are the transcripts that are grouped into each of the terms listed in Figure 1D. Coordinates for the EGFRvIII regulated alternative exon are listed for each transcript. P-value for each term was generated by a modified Fisher exact test using the DAVID Bioinformatics Tool. Terms shown all displayed p-values $< 0.01$ and are ranked from most significant to least.

**Table S1.** Alternative splicing events included in each GO enrichment term.

## Biological Process

### 1) positive regulation of macromolecule metabolic process

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| DOCK7 | dedicator of cytokinesis 7 | chr1:62783206-62783298 |
| ECE1 | endothelin converting enzyme 1 | chr1:21420827-21420922 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| PSMB3 | proteasome (prosome, macropain) subunit, beta type, 3 | chr17:34170210-34170387 |
| PSMB7 | proteasome (prosome, macropain) subunit, beta type, 7 | chr9:126207417-126207532 |
| RAG1AP1 | recombination activating gene 1 activating protein 1 | chr1:153376661-153376822 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | chr12:6310280-6310353 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 2) macromolecule catabolic process

| Transcript | Description | Exon Coordinates |
|---|---|---|
| FBXO22 | FBXO22 opposite strand (non-protein coding); F-box protein 22 | chr15:73983887-73984025 |
| PCNP | PEST proteolytic signal containing nuclear protein | chr3:102781376-102781538 |
| SENP1 | SUMO1/sentrin specific peptidase 1 | chr12:46769213-46769343 |
| UPF3A | UPF3 regulator of nonsense transcripts homolog A (yeast) | chr13:114066414-114066520 |
| ASB8 | ankyrin repeat and SOCS box-containing 8 | chr12:46830137-46830190 |
| ARIH2 | ariadne homolog 2 (Drosophila) | chr3:48957573-48957618 |
| CHID1 | chitinase domain containing 1 | chr11:883427-883519 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| PSMB3 | proteasome (prosome, macropain) subunit, beta type, 3 | chr17:34170210-34170387 |
| PSMB7 | proteasome (prosome, macropain) subunit, beta type, 7 | chr9:126207417-126207532 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| RNF34 | ring finger protein 34 | chr12:120324928-120324993 |
| USP8 | ubiquitin specific peptidase 8 | chr15:48563764-48563850 |

### 3) regulation of translation

| Transcript | Description | Exon Coordinates |
|---|---|---|
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| ANKHD1 | ankyrin repeat and KH domain containing 1 | chr5:139895131-139895307 |
| EIF4G2 | eukaryotic translation initiation factor 4 gamma, 2 | chr11:10779784-10779897 |
| EIF4H | eukaryotic translation initiation factor 4H | chr7:73242513-73242572 |
| IGF2BP2 | insulin-like growth factor 2 mRNA binding protein 2 | chr3:186873023-186873151 |
| RPS5 | ribosomal protein S5 | chr19:63596155-63596364 |

### 4) cellular macromolecule catabolic process

| Transcript | Description | Exon Coordinates |
|---|---|---|
| FBXO22 | FBXO22 opposite strand (non-protein coding); F-box protein 22 | chr15:73983887-73984025 |
| PCNP | PEST proteolytic signal containing nuclear protein | chr3:102781376-102781538 |
| SENP1 | SUMO1/sentrin specific peptidase 1 | chr12:46769213-46769343 |
| UPF3A | UPF3 regulator of nonsense transcripts homolog A (yeast) | chr13:114066414-114066520 |
| ASB8 | ankyrin repeat and SOCS box-containing 8 | chr12:46830137-46830190 |
| ARIH2 | ariadne homolog 2 (Drosophila) | chr3:48957573-48957618 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| PSMB3 | proteasome (prosome, macropain) subunit, beta type, 3 | chr17:34170210-34170387 |
| PSMB7 | proteasome (prosome, macropain) subunit, beta type, 7 | chr9:126207417-126207532 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| RNF34 | ring finger protein 34 | chr12:120324928-120324993 |
| USP8 | ubiquitin specific peptidase 8 | chr15:48563764-48563850 |

### 5) transcription, DNA-dependent

| Transcript | Description | Exon Coordinates |
|---|---|---|
| AFF4 | AF4/FMR2 family, member 4 | chr5:132301240-132301331 |
| ADRM1 | adhesion regulating molecule 1 | chr20:60316819-60316921 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | chr17:43489393-43489482 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| STAT1 | signal transducer and activator of transcription 1, 91kDa | chr2:191583338-191583420 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 6) RNA biosynthetic process

| Transcript | Description | Exon Coordinates |
|---|---|---|
| AFF4 | AF4/FMR2 family, member 4 | chr5:132301240-132301331 |
| ADRM1 | adhesion regulating molecule 1 | chr20:60316819-60316921 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | chr17:43489393-43489482 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| STAT1 | signal transducer and activator of transcription 1, 91kDa | chr2:191583338-191583420 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 7) positive regulation of transcription, DNA-dependent

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | chr12:6310280-6310353 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 8) positive regulation of RNA metabolic process

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | chr12:6310280-6310353 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 9) positive regulation of gene expression

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| RAG1AP1 | recombination activating gene 1 activating protein 1 | chr1:153376661-153376822 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | chr12:6310280-6310353 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 10) transcription from RNA polymerase II promoter

| Transcript | Description | Exon Coordinates |
|---|---|---|
| AFF4 | AF4/FMR2 family, member 4 | chr5:132301240-132301331 |
| ADRM1 | adhesion regulating molecule 1 | chr20:60316819-60316921 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | chr17:43489393-43489482 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| STAT1 | signal transducer and activator of transcription 1, 91kDa | chr2:191583338-191583420 |

### 11) positive regulation of transcription from RNA polymerase II promoter

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | chr12:6310280-6310353 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 12) positive regulation of transcription

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | chr12:6310280-6310353 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

## Molecular Function

### 1) transcription regulator activity

| Transcript | Description | Exon Coordinates |
|---|---|---|
| AFF4 | AF4/FMR2 family, member 4 | chr5:132301240-132301331 |
| CNOT2 | CCR4-NOT transcription complex, subunit 2 | chr12:68974284-68974341 |
| SETD8 | SET domain containing (lysine methyltransferase) 8 | chr12:122439933-122440054 |
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| CUTA | cutA divalent cation tolerance homolog (E. coli) | chr6:33492675-33492724 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MTA1 | metastasis associated 1 | chr14:104986741-104986791 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | chr17:43489393-43489482 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| STAT1 | signal transducer and activator of transcription 1, 91kDa | chr2:191583338-191583420 |
| SSBP4 | single stranded DNA binding protein 4 | chr19:18403163-18403228 |
| SF1 | splicing factor 1 | chr11:64297478-64297553 |
| SFRS2 | splicing factor, arginine/serine-rich 2 | chr17:72243449-72243552 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |
| ZNF207 | zinc finger protein 207 | chr17:27721132-27721214 |

### 2) RNA polymerase II transcription factor activity

| Transcript | Description | Exon Coordinates |
|---|---|---|
| CNOT2 | CCR4-NOT transcription complex, subunit 2 | chr12:68974284-68974341 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | chr16:68159899-68159952 |
| SF1 | splicing factor 1 | chr11:64297478-64297553 |
| USF2 | upstream transcription factor 2, c-fos interacting | chr19:40452546-40452746 |

### 3) transcription cofactor activity

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SETD8 | SET domain containing (lysine methyltransferase) 8 | chr5:135516263-135516346 |
| CUTA | cutA divalent cation tolerance homolog (E. coli) | chr6:33492675-33492724 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | chr17:43489393-43489482 |
| RNF14 | ring finger protein 14 | chr5:141338052-141338579 |
| SF1 | splicing factor 1 | chr11:64297478-64297553 |
| SFRS2 | splicing factor, arginine/serine-rich 2 | chr17:72243449-72243552 |

## Cellular Compartment

### 1) eukaryotic translation initiation factor 4F complex

| Transcript | Description | Exon Coordinates |
|---|---|---|
| ANKHD1 | ankyrin repeat and KH domain containing 1 | chr5:139895131-139895307 |
| EIF4G2 | eukaryotic translation initiation factor 4 gamma, 2 | chr11:10779784-10779897 |
| EIF4H | eukaryotic translation initiation factor 4H | chr7:73242513-73242572 |

### 2) macromolecule catabolic process

| Transcript | Description | Exon Coordinates |
|---|---|---|
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MTA1 | metastasis associated 1 | chr14:104986741-104986791 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| RNF34 | ring finger protein 34 | chr12:120324928-120324993 |
| SRRM1 | serine/arginine repetitive matrix 1 | chr1:24846157-24846286 |
| SFRS2 | splicing factor, arginine/serine-rich 2 | chr17:72243449-72243552 |

### 3) membrane-enclosed lumen

| Transcript | Description | Exon Coordinates |
|---|---|---|
| FKBP10 | FK506 binding protein 10, 65 kDa | chr17:37226836-37226981 |
| SMAD5 | SMAD family member 5 | chr5:135516263-135516346 |
| AK2 | adenylate kinase 2 | chr1:33250262-33250310 |
| APP | amyloid beta (A4) precursor protein | chr21:26291546-26291602 |
| FN1 | fibronectin 1 | chr2:215953779-215954048 |
| FXR1 | fragile X mental retardation, autosomal homolog 1 | chr3:182171557-182171637 |
| GTF2H1 | general transcription factor IIH, polypeptide 1, 62kDa | chr11:18313877-18314069 |
| GTF2H2 | general transcription factor IIH, polypeptide 2, 44kDa | chr5:69205247-69205280 |
| LEF1 | lymphoid enhancer-binding factor 1 | chr4:109222191-109222274 |
| MED21 | mediator complex subunit 21 | chr12:27070620-27070734 |
| MTA1 | metastasis associated 1 | chr14:104986741-104986791 |
| MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) | chr7:104465809-104465882 |
| PTBP1 | polypyrimidine tract binding protein 1 | chr19:750413-750443 |
| PTBP1 | polypyrimidine tract binding protein 1 | chr19:756513-756569 |
| RNF34 | ring finger protein 34 | chr12:120324928-120324993 |
| SRRM1 | serine/arginine repetitive matrix 1 | chr1:24846157-24846286 |
| STAT1 | signal transducer and activator of transcription 1, 91kDa | chr2:191583338-191583420 |
| SF1 | splicing factor 1 | chr11:64297478-64297553 |
| SFRS2 | splicing factor, arginine/serine-rich 2 | chr17:72243449-72243552 |
| ZNF207 | zinc finger protein 207 | chr17:27721132-27721214 |

**Table S2. Analysis of TCGA dataset identifies a correlation between EGFRvIII and hnRNPA1 in GBM**. Analysis was restricted to the classical, mesenchymal and neural subtypes of GBM, and data analyzed for hnRNPA1 expression in tumors definitively defined by the TCGA as EGFRvIII+ vs. those for which EGFRvIII expression could not be clearly identified. HnRNAPA1 expression was higher in the EGFRvIII+ tumors (p=0.00881). Correlations were computed with Pearson correlation coefficient.

**(Table S2 is a separate Excel File)**

**Table S3. Analysis of TCGA dataset identifies a correlation between hnRNPA1 and glycolytic genes**. Expression of glycolytic genes correlated with hnRNPA1 expression in GBM from TCGA dataset. Correlations were computed with Pearson correlation coefficient.

| | **HNRNPA1** | **SLC2A3 (Glut3)** | **HK2** | **SLC2A1 (Glut1)** | **PDHK1 (PDK1)** |
|---|---|---|---|---|---|
| **HNRNPA1** | **1** | **0.179484606** | **0.238654** | **0.080826701** | **0.027049** |
| **SLC2A3 (Glut3)** | **0.179485** | **1** | **0.570375** | **0.589632526** | **0.580685** |
| **HK2** | **0.238654** | **0.57037536** | **1** | **0.510702251** | **0.483486** |
| **SLC2A1 (Glut1)** | **0.080827** | **0.589632526** | **0.510702** | **1** | **0.727501** |
| **PDHK1 (PDK1)** | **0.027049** | **0.580685165** | **0.483486** | **0.727500884** | **1** |
| | | | | | |

## SUPPLEMENTAL EXPERIMENTAL PROCEDURES

### UV-crosslinking and immunoprecipitation (CLIP)

U87-EGFRvIII cells in 15 cm plates were washed twice with cold PBS, added 12.5 mls PBS then UV irradiated in a UV stratalinker 1800 UV cross-linker (Stratagene) on ice with lid off. UV crosslinking was with either 100 or 500 J/m$^2$. Cells were collected by scraping, pelleted 5 min 500xg, resuspended in 1 ml PBS, transferred to eppy tubes and pelleted at 4000rpm 4 min at 4$^o$C. PBS was removed and cell pellets frozen and stored at -80$^o$C. Cells were lysed by adding 300 ul RIPA buffer (Boston BioProducts) containing 2x half protease inhibitor cocktail (Thermo Scientific), vortexed, and placed on ice for 20 min. Lysates were clarified by centrifuging 13 min 14000rpm at 4$^o$C. Supernatant lysates were pre-cleared with 100 ul Pro A Dynabeads (Invitrogen) for 45 min on rotator 4$^o$C. Immunoprecipitation (IP) was for 2 hrs at 4$^o$C with either anti-HA Control antibody (6E2) (Cell Signaling) or with anti-hnRNPA1 9H10 clone (Sigma) with 250 ug/ml yeast tRNA. IP beads were washed 4X with RIPA buffer, resuspended in water, Dnase treated with DNase I (Ambion) for 1 hr and subsequently proteinase K (Roche) treated 1 hr, followed by phenol/Chloroform extraction, and RNA ethanol precipitated overnight at -20$^o$C. RNA was pelleted, washed with 70% ethanol, air dried and resuspended in 14 ul water, and used for cDNA synthesis with Superscript VILO (Invitrogen). Primers used for RT-PCR were: Max Intron (Forward), 5'-GCTCAGTAGCAGGCTTGGTC-3', Max Intron (Reverse), 5'-AGAGGTCAGGCCAGAAAAGA-3'. Reverse primers were $^{32}$P end-labeled and 22 cycle PCR reactions were resolved by denaturing PAGE. Radioactive signal was detected using a Typhoon phosphorimager (GE).

**Primers used for Real-Time (RT) quantitative PCR**

Primers used for Real-Time PCR were: Vinculin-F 5’-ctttgctgctacaggggaag-3’; Vinculin-R 5’-ggatatgggacgggaagttt-3’; GLUT1-F 5’-gtggagactaagccctgtcg-3’; GLUT1-R 5’-aggggcaaatcctaatggag-3’; GLUT3-F 5’-tcctggacatcctcttctgc-3’; GLUT3-R 5’-agtctgaggttgggggaact-3’; HK2-F 5’-agagaggaccccactggact-3’; HK2-R 5’-ccaaggtgaagcaaccgtat-3’; PDK1-F 5’-ggttgggaaccactctttca-3’; PDK-R 5’-gctttggttacgtggcattt-3’; hnRNPA1-F 5’-ttgtgaactcagccaagcac-3’; hnRNPA1-R 5’-cagcgtcacgatcagactgt-3’.

**Lactate production, glucose/glutamine consumption, glutamate assay**

For NOVA measures of lactate production, glucose consumption, glutamine consumption, and glutamate secretion U87-EGFRvIII cells were grown in 10 cm plates with DMEM and 5% FBS. Media changed to 5 ml for 24 hr before measuring glucose, lactate, glutamine, and glutamate in the media by NOVA BioProfile automatic analyzer (Nova Biomedical). Glucose uptake, lactate production, glutamine uptake, and glutamate production were calculated by comparing to control plates without cells. Cells were collected after measurement and cell count were used to normalize results. Experiments were performed in triplicate.