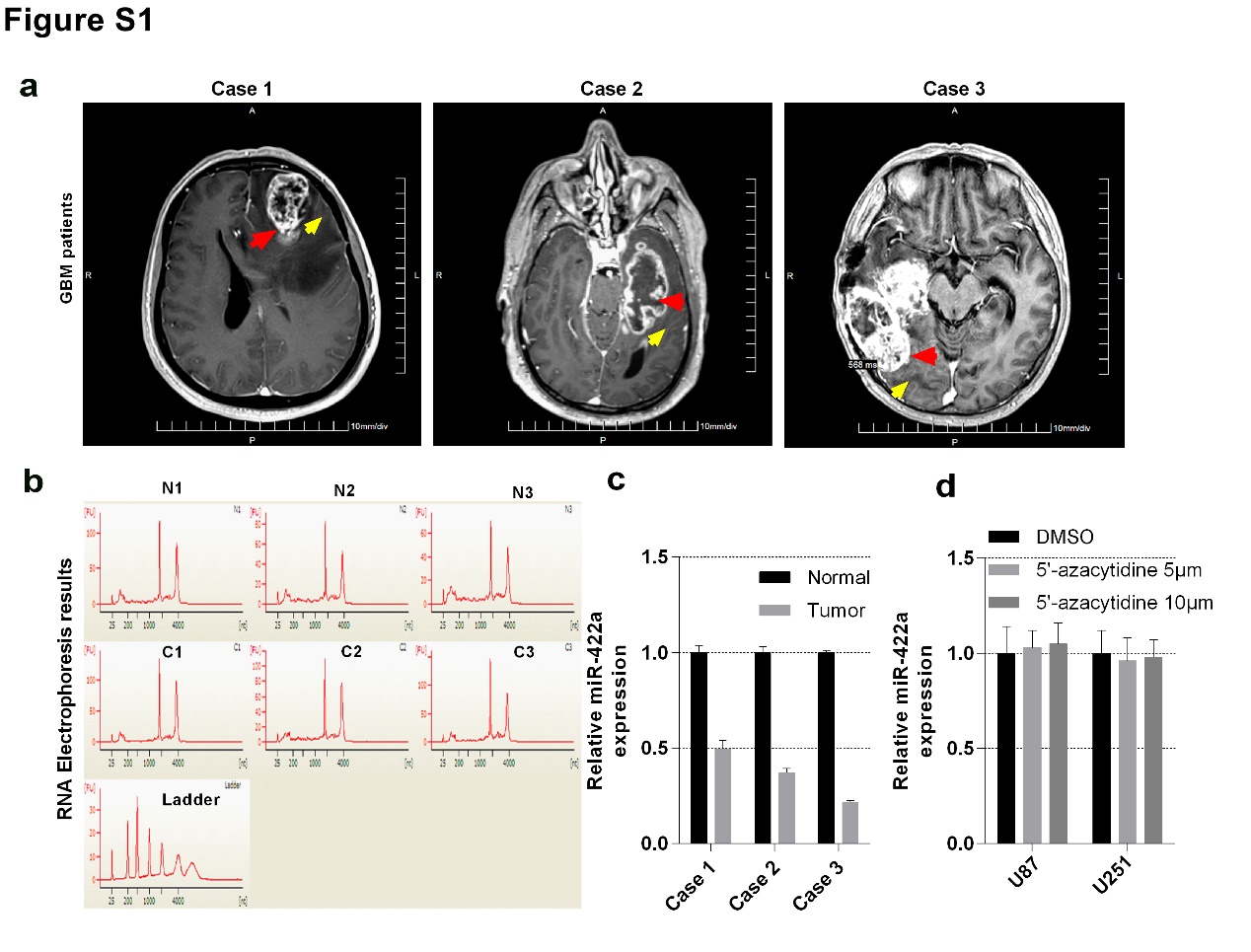
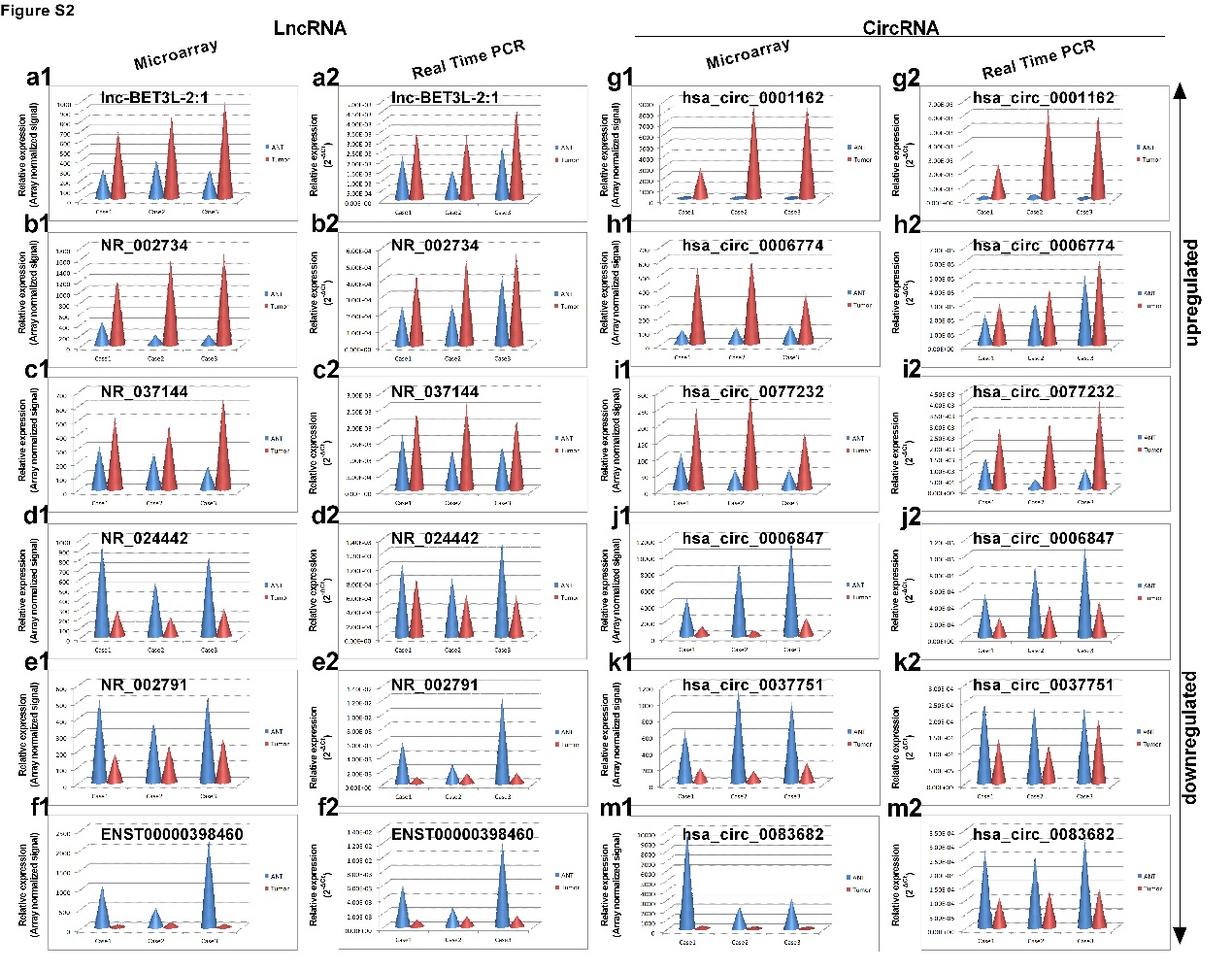
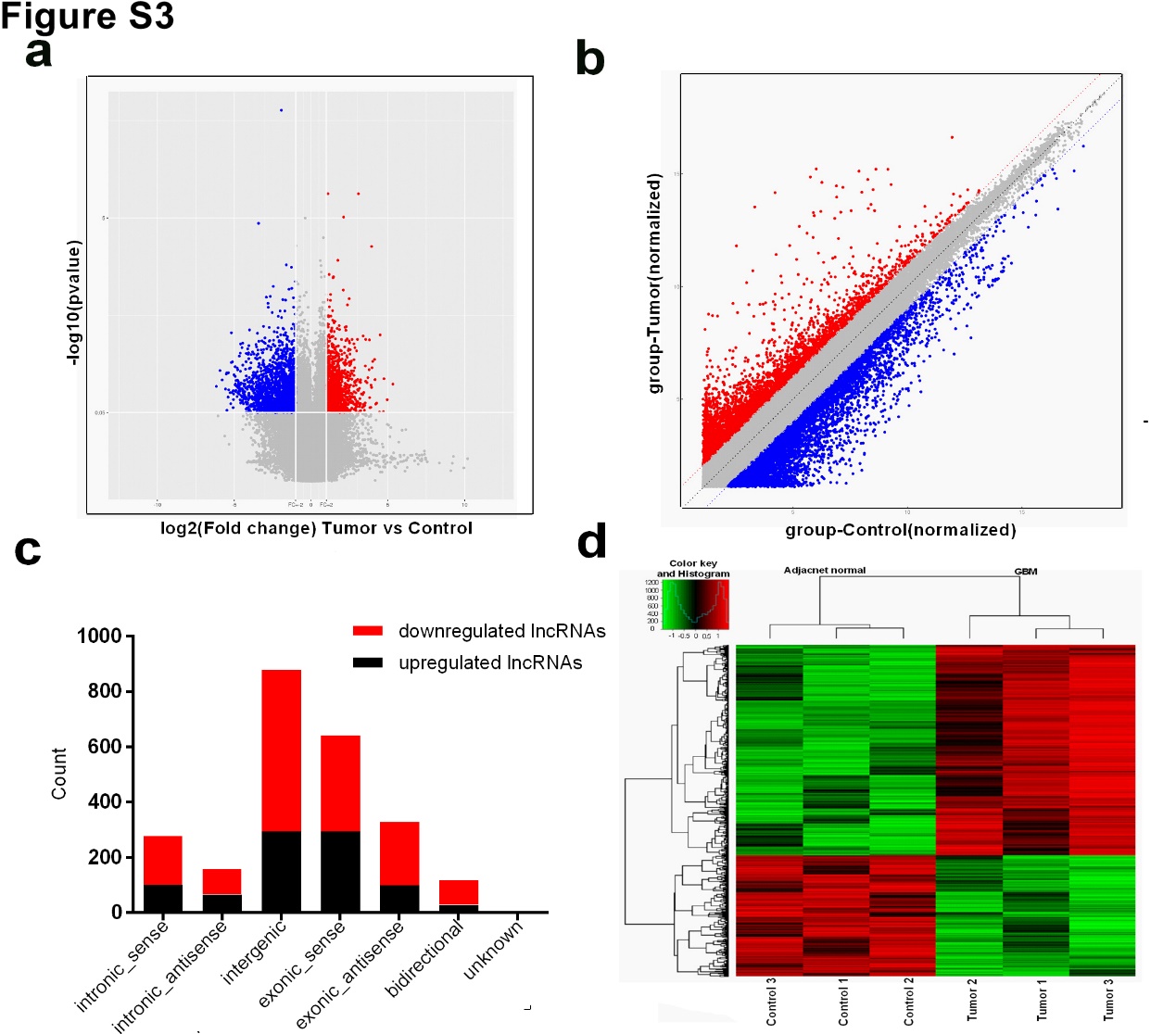
**Supplementary Figures**



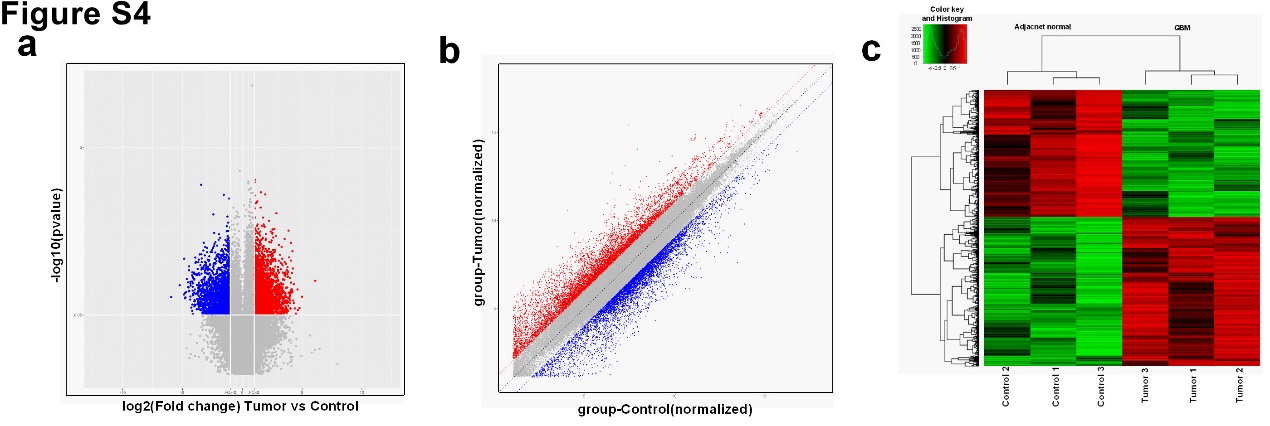
**Figure S1. Identification of three cases with low expression of miR-422a. (a)** Patients diagnosed with GBM were detected by enhanced MRI. The red arrows represent GMB tissues, while yellow arrows represent adjacent normal tissues. MRI, magnetic resonance imaging. **(b)** RNA electrophoresis results were analysed with the 3 paired GBM tissues. **(c)** miR-422a level was measured by qRT-PCR in GBM tumour and adjacent normal tissues. **(d)** U87 and U251 cells were treated with DMSO, 5′-azacytidine (5 µM), and 5′-azacytidine (10 µM). qRT-PCR was used to detect the expression of miR-422a. Data are the mean ± s.e.m. of three experiments, Student’s *t*-test.



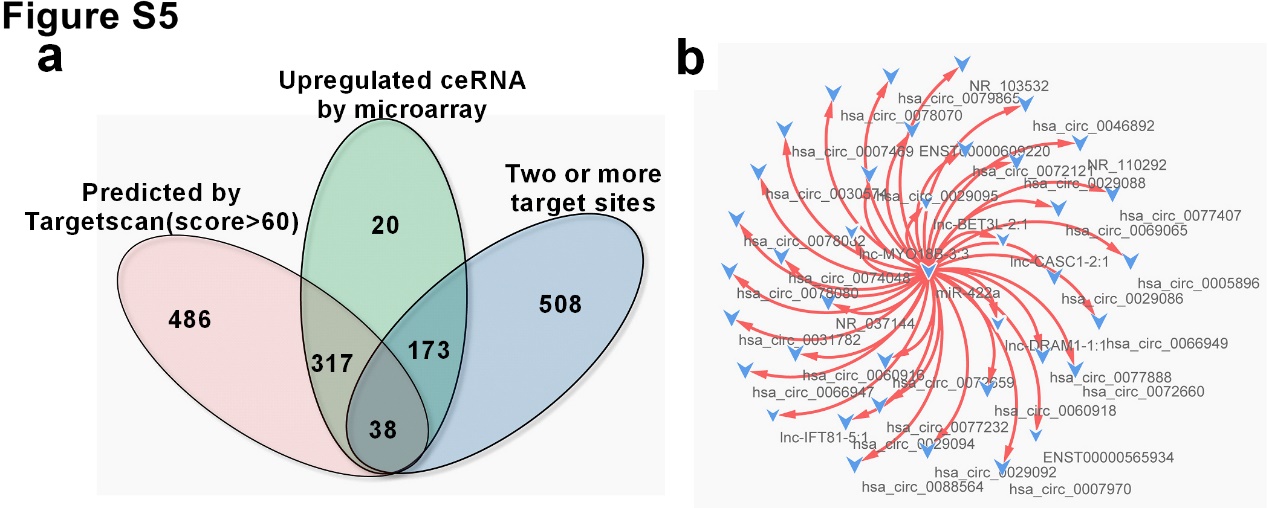
**Figure S2. Validation of microarray results by qRT-PCR analysis of six randomly selected lncRNAs and six randomly selected circRNAs in three cases.** (a1–f2) Expression of six lncRNAs (lnc-BET3L-2.1, NR\_002734, NR\_037144, NR\_024442, NR\_002791, and ENST00000398460) detected by microarray and qRT-PCR. (g1–m2) Expression of six circRNAs (hsa\_circ\_0001162, hsa\_circ\_0006774, hsa\_circ\_0077232, hsa\_circ\_0006847, hsa\_circ\_0037751, and hsa\_circ\_0083682) detected by microarray and qRT-PCR assays. Data from qRT-PCR are mean ± s.e.m. of three experiments, Student’s *t*-test.



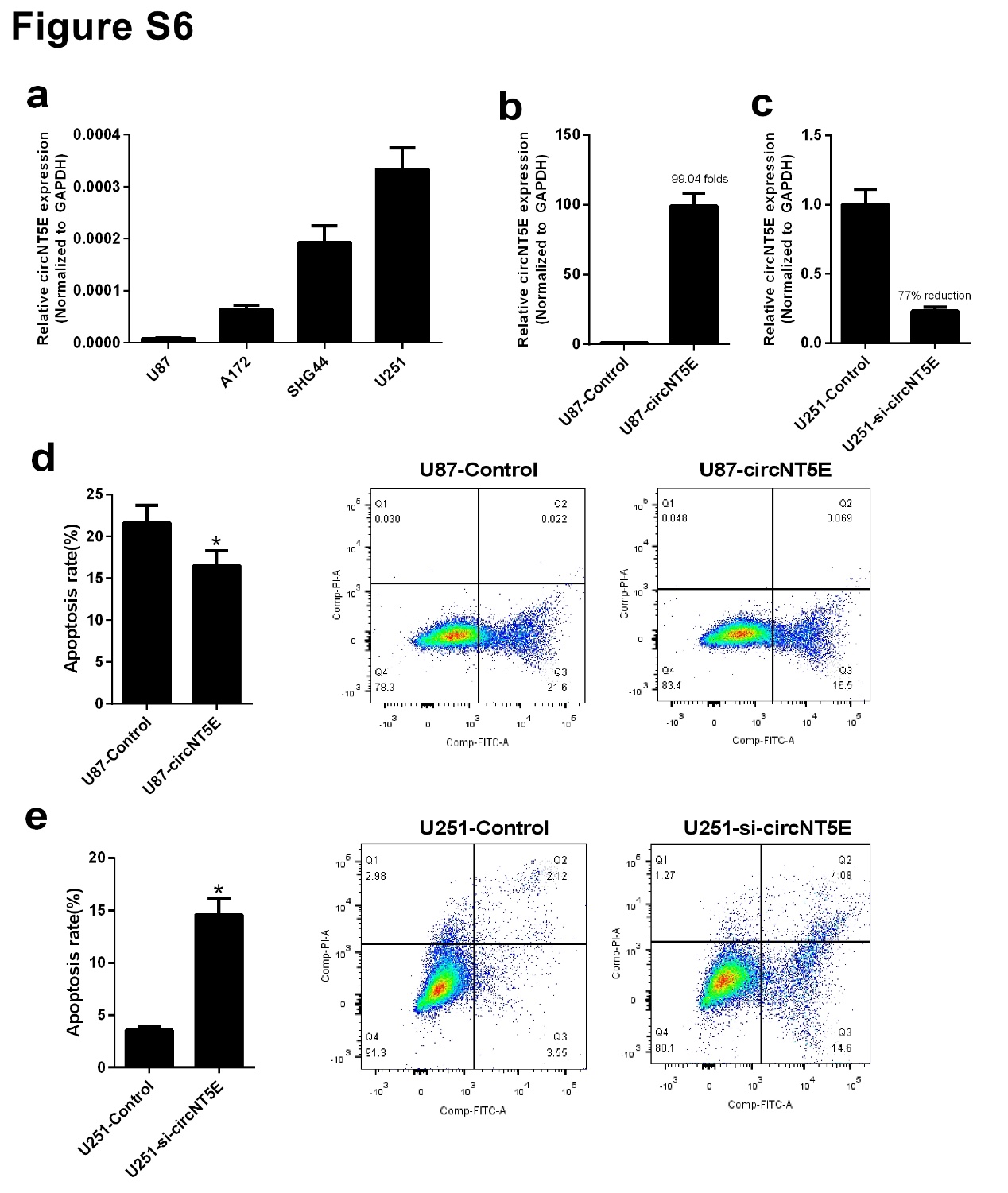
**Figure S3. Identification of differentially expressed lncRNAs in GBM tumour and adjacent normal tissues. (a)** Volcano plot indicates lncRNA expression data. The vertical lines represent to 2-fold up- and downregulation, and horizontal lines represent *P* value of 0.05. The red and blue points represent differentially expressed lncRNAs showing significant differences, and the grey points represent the lncRNAs that did not show significant differences. **(b)** Scatter plot also shows the differentially expressed lncRNAs in GBM tumour and adjacent normal tissues. **(c)** Types and counts of differentially regulated lncRNAs detected by microarray (fold change > 2.0, *P* < 0.05). The lncRNAs are classified into 6 types according to the relationship and genomic loci with their associated coding genes. One lncRNA may be associated with several mRNAs for disparate relationships. **(d)** Heat map of differentially expressed lncRNAs.



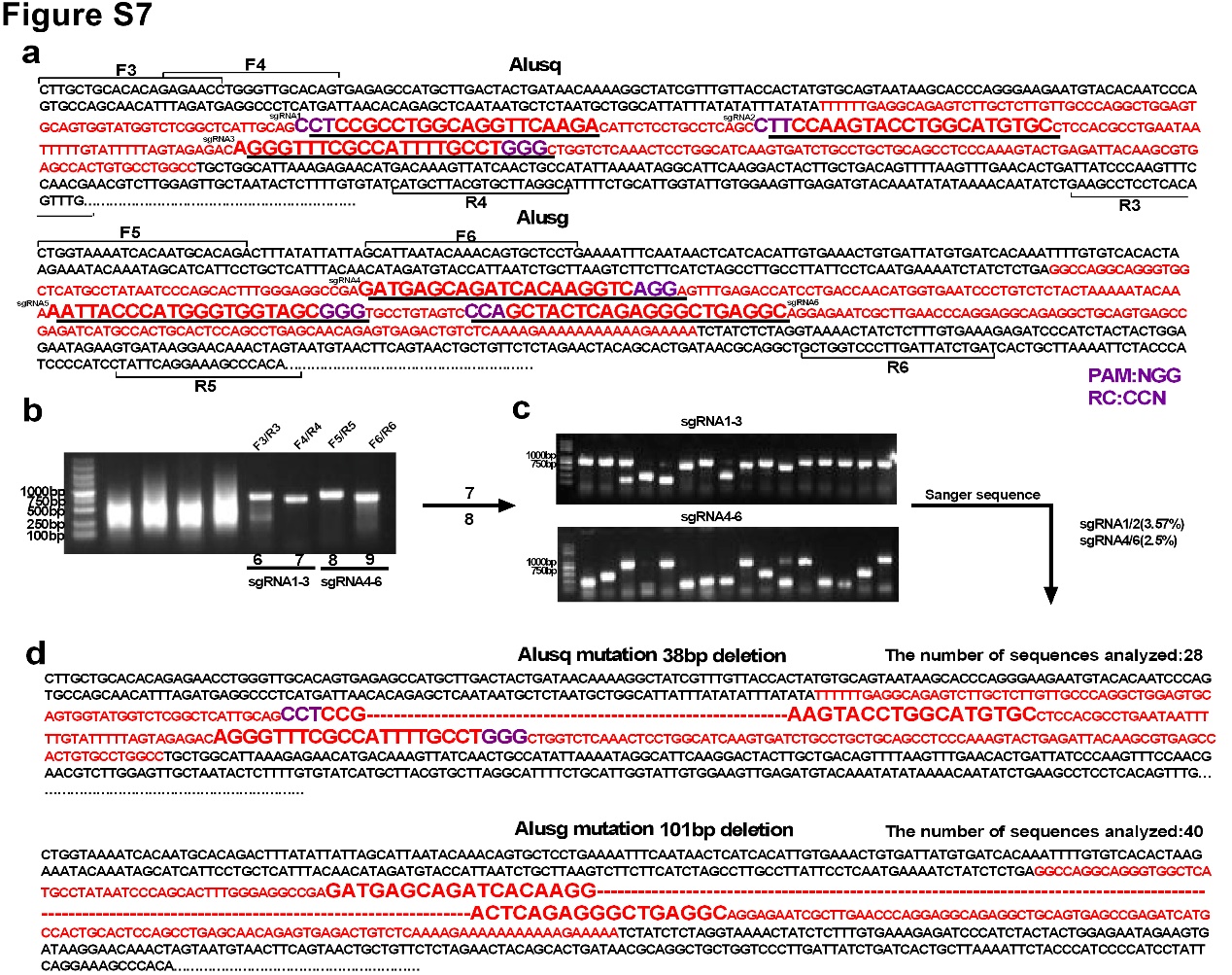
**Figure S4. Identification of differentially expressed circRNAs in GBM tumour and adjacent normal tissues. (a)** Volcano plot showing circRNAs expression data. The vertical lines represent to 2-fold up- and downregulation, and the horizontal lines represent *P* value of 0.05. The red and blue points represent differentially expressed circRNAs showing significant differences, and the grey points represent circRNAs that did not show significant differences. **(b)** Scatter plot also shows differentially expressed circRNAs in GBM tumour and adjacent normal tissues. **(c)** Heat map of differentially expressed circRNAs.



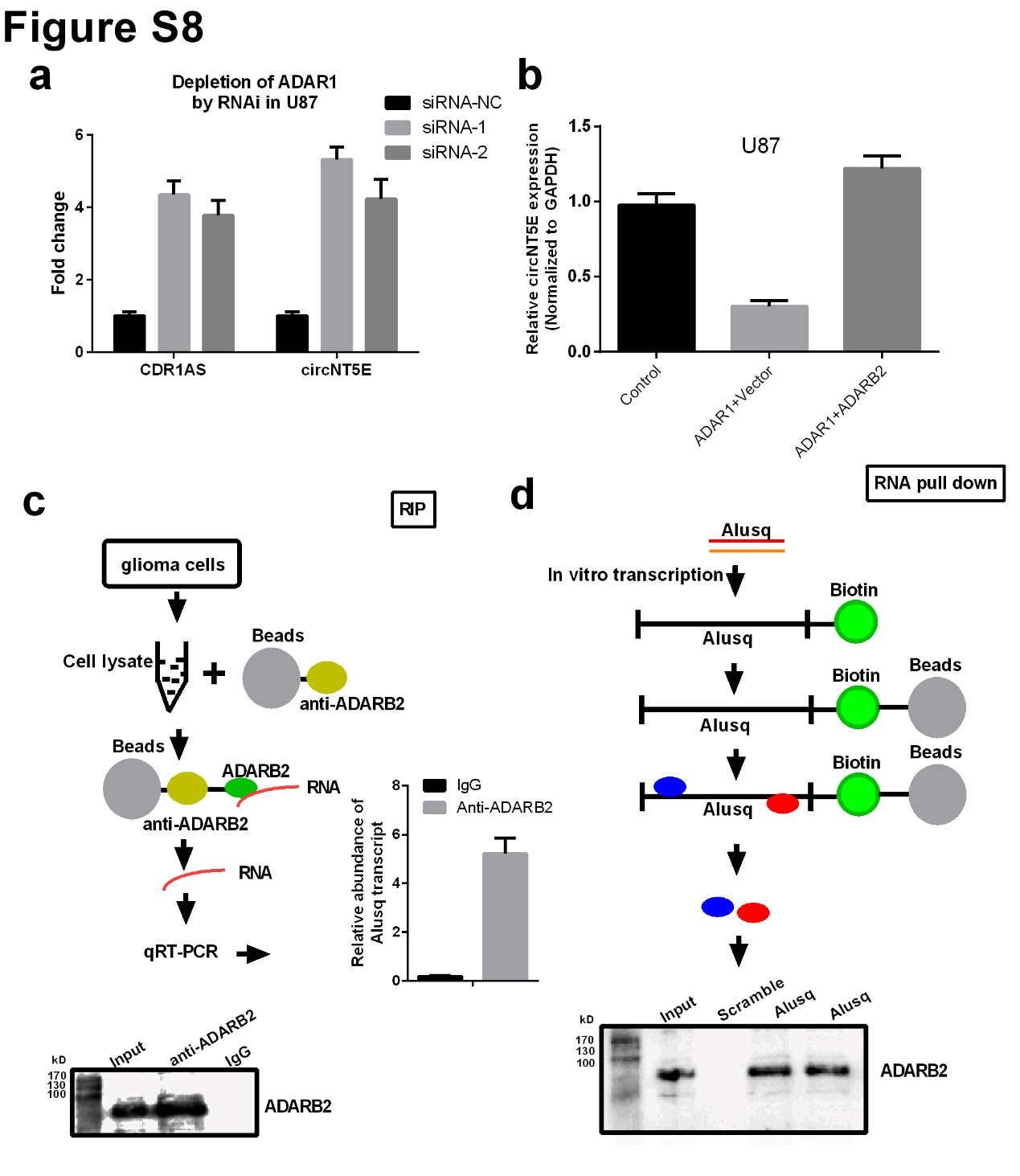
**Figure S5. Screen of possible interaction between lncRNA/circRNAs and miR-422a in glioblastoma. (a)** Venn diagram showing the possible logical interaction relationships among lncRNA/circRNAs and miR-422a in glioblastoma. **(b)** Global view of 38 circRNA/lncRNAs that may interact with miR-422a in glioblastoma by using microarray and bioinformatics screening approaches.



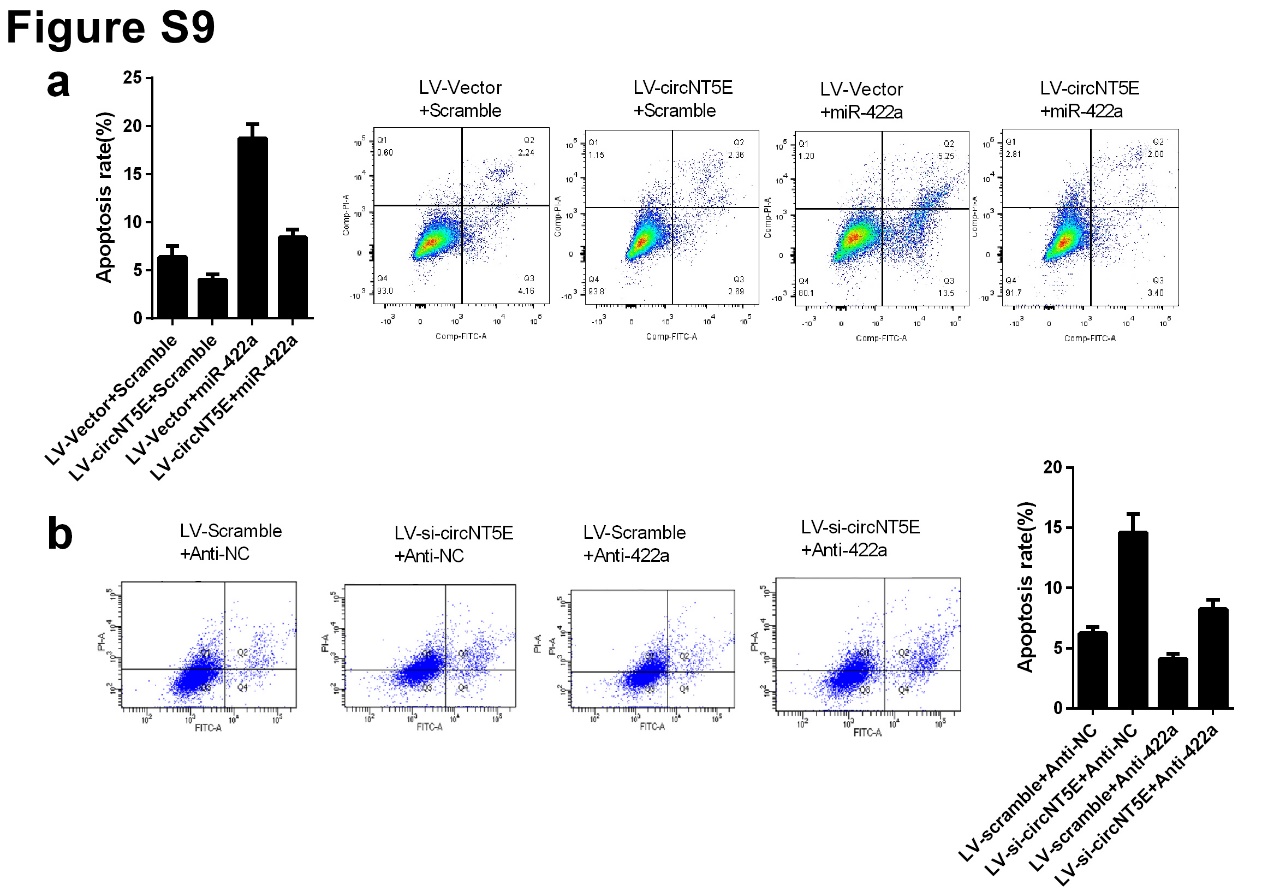
**Figure S6. CircNT5E affects the cell apoptosis of glioblastoma. (a)** qRT-PCR was performed to detect the expression level of circNT5E in four GBM cell lines (U87, A172, SHG44, and U251). GAPDH mRNA was used as an internal control. **(b–c)** qRT-PCR was performed to detect the expression level of circNT5E in stable LV-circNT5E-transfected U87 cells and LV-si-circNT5E-transfected U251 cells. **(d–e)** Results of cell apoptosis 7-AAD/Annexin V staining assay quantified by flow cytometry from treated U87 and U251 cells. Data are mean ± s.e.m. \**P* < 0.05 (Student’s *t*-test).



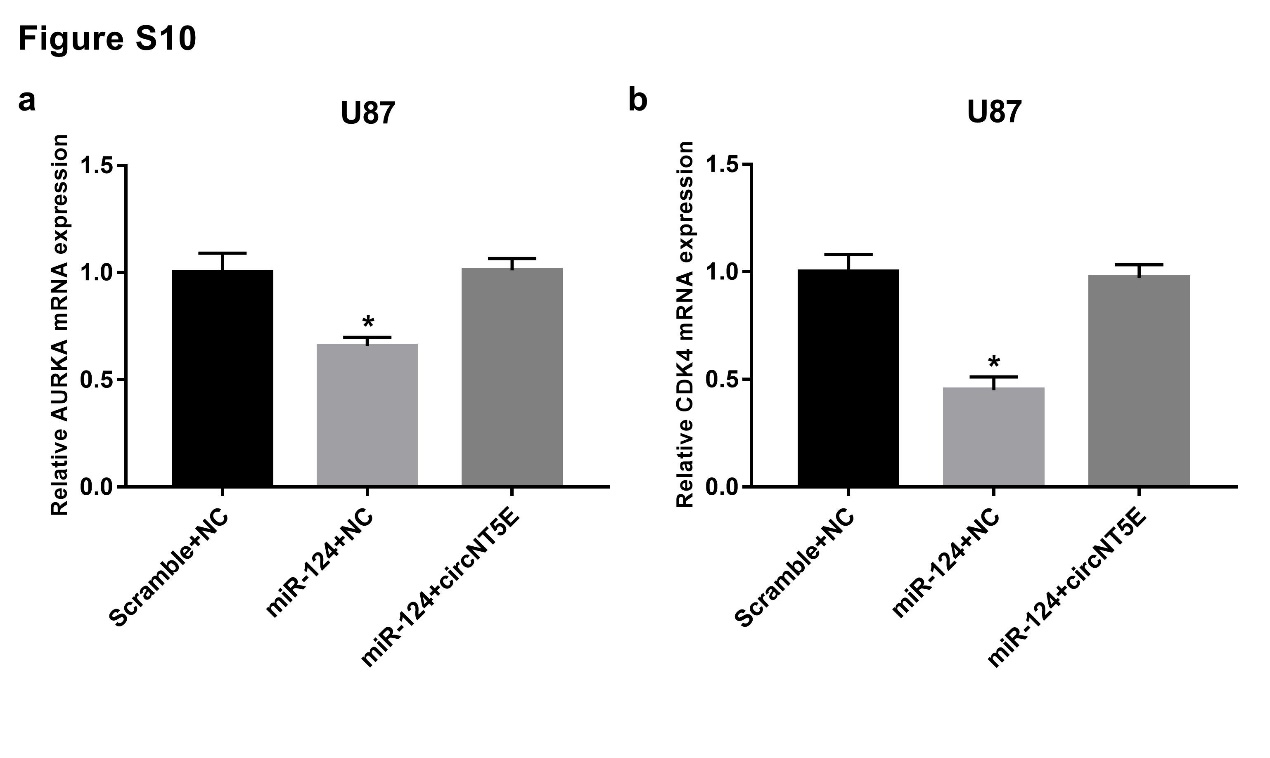
**Figure S7. CRISPR/Cas9 system targeting Alusq and Alusg.** (a) Sequence of the wild-type Alusq and Alusg (red coloured words); CCN and NGG are the PAM sequence, which was recognized by Cas9 (purple words); F3/R3, F4/R4, F5/R5, and F6/R6 are the four paired primer design sites for amplifying the wild-type or mutant Alu sequence; sgRNA1–6 are sites targeted by CRISPR/Cas9, sgRNA = small guide RNA. (b) PCR results of U87 genome by specific primers, lines 6 and 7 indicate U87 cells transfected with sgRNA1-3, while lines 8–9 show U87 cells transfected with sgRNA4–6. (c&d) The fragments in lines 7 and 8 were sub-cloned and subjected to Sanger sequencing.



**Figure S8. ADARB2 directly interacts with the Alusq region of NT5E pre-mRNA.** (a) circNT5E expression upon knockdown of ADAR1 in U87 cells, circRNA-CDRAS1 was a positive control, which is regulated by ADAR1. (b) qRT-PCR assay results indicated that ADARB2 restored circNT5E expression, which was inhibited by ADAR1. (c) qRT-PCR analysis of Alusq region of NT5E pre-mRNA in the immunoprecipitates of ADARB2 compared to the IgG control. Schematic diagram of RIP assay (left panel); qRT-PCR result is shown (right panel); western blot indicated that ADARB2 was pulled down by anti-ADARB2, input as a positive control, and IgG was a negative control. (d) RNA pull-down experiment showed the interaction between ADARB2 and Alusq region of NT5E pre-mRNA. Biotin-labelled Alusq fragment was incubated with U87 cell lysates, and enriched ADARB2 was detected by western blotting. The scramble sequence was used as a control. Data are mean± s.e.m., n = 3 biological replicates.



**Figure S9. CircNT5E regulates cell apoptosis by miR-422a in glioblastoma. (a–b)** U87 cells were transfected with LV-vector+scramble, LV-circNT5E+scramble, LV-vector+miR-422a, and LV-circNT5E+miR-422a; U251 cells were transfected with LV-scramble+anti-NC, LV-si-circNT5E+anti-NC, LV-scramble+anti-422a, and LV-si-circNT5E+anti-422a. Results of cell apoptosis 7-AAD/Annexin V staining assay quantified by flow cytometry from treated U87 and U251 cells. Data are mean ± s.e.m.n = 3 biological replicates.



**Figure S10. CircNT5E functions as an efficient miRNA sponge in glioblastoma.** (h) U87 cells were transfected with scramble+NC, miR-124+NC or miR-124+circNT5E. Expression levels of AURKA and CDK4 mRNA were measured by qRT-PCR. Data in a–b are the mean ± s.e.m. of three experiments, \*P<0.05, Student’s t-test.

**Supplementary Tables**

Supplementary Table 1 clinical patients information (N/A means no data)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ID | Sex | Year | WHO（Grade） | MGMT | GFAP | Olig-2 | EMA | Ki-67 | Vimentin | NeuN | NF | CK | S-100 | P53 | MMP-9 | PTEN | Syn | CDs | VEGF | IDH1 |
| 2870492 | Male | 17 | I | + | ++ | N/A | N/A | <1% | N/A | N/A | N/A | N/A | + | <1% | + | + | N/A | N/A | N/A | N/A |
| 1556250 | Female | 46 | I | 5%-10% | N/A | 2+ | N/A | >4% | - | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1198476 | Female | 23 | I | 20-30% | + | - | + | 2%-5% | + | N/A | N/A | - | N/A | - | N/A | N/A | N/A | N/A | N/A | N/A |
| 1713980 | Male | 47 | I | - | ++ | +++ | - | 2%-3% | ++ | + | + | N/A | ++ | N/A | N/A | N/A | N/A | CD3-CD20-CD68+CD34+ | N/A | N/A |
| 1390857 | Male | 56 | II | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1060699 | Female | 45 | II | 2% | +++ | N/A | - | <1% | N/A | N/A | N/A | N/A | ++ | - | +/- | N/A | N/A | N/A | N/A | N/A |
| 0091885 | Female | 44 | II | 5%-10% | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1552583 | Female | 60 | II | 2%-5% | + | + | N/A | 2%-5% | N/A | N/A | N/A | N/A | N/A | 50%-60% | + | N/A | N/A | N/A | N/A | N/A |
| 1377690 | Female | 38 | III | 2% | + | + | N/A | 3%-5% | + | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1835308 | Female | 63 | III | <1% | + | + | N/A | 8% | N/A | N/A | N/A | N/A | N/A | + | N/A | N/A | N/A | N/A | N/A | N/A |
| 1205271 | Female | 45 | III | - | +++ | N/A | N/A | 5% | N/A | N/A | N/A | N/A | ++ | - | N/A | - | N/A | CD34- | N/A | N/A |
| 1059368 | Female | 55 | III | 2% | + | N/A | - | 7%-8% | + | N/A | N/A | N/A | + | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1734521 | Male | 45 | III | + | + | + | N/A | <1% | N/A | N/A | N/A | - | N/A | - | N/A | N/A | N/A | N/A | N/A | N/A |
| 1190246 | Female | 34 | III | 20% | +++ | N/A | ++ | 2% | +++ | N/A | N/A | N/A | +++ | + | N/A | ++ | N/A | CD68+ | N/A | N/A |
| 219332 | Male | 47 | III | - | ++ | N/A | + | 2% | N/A | N/A | N/A | N/A | ++ | - | N/A | +/- | N/A | CD34- | N/A | N/A |
| 1198351 | Male | 37 | III | 8% | + | N/A | N/A | <2% | N/A | N/A | N/A | N/A | + | + | N/A | - | N/A | CD34+ | N/A | N/A |
| 1457517 | Male | 50 | III | >90% | - | + | - | 50%-60% | N/A | N/A | N/A | N/A | N/A | 30%-40% | N/A | N/A | N/A | N/A | N/A | N/A |
| 0510987 | Male | 51 | III | <5% | + | N/A | N/A | 10% | N/A | N/A | N/A | N/A | + | N/A | N/A | +/- | N/A | CD34+ | N/A | N/A |
| 1903007 | Male | 66 | III | - | + | + | - | 40% | + | - | N/A | - | N/A | +/- | N/A | N/A | N/A | N/A | N/A | N/A |
| 1351734 | Male | 32 | III | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1309303 | Male | 12 | III | 2%-5% | - | + | N/A | 70%-80% | + | N/A | - | - | + | 10%-15% | N/A | N/A | + | N/A | N/A | N/A |
| 0089326 | Male | 44 | IV | + | +++ | N/A | N/A | 5%-10% | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 2907331 | Male | 69 | IV | 5% | + | N/A | - | N/A | ++ | N/A | N/A | N/A | N/A | + | N/A | - | N/A | N/A | N/A | N/A |
| 2754818 | Male | 64 | IV | + | - | N/A | - | >25% | N/A | N/A | - | N/A | + | +++ | N/A | N/A | N/A | N/A | N/A | N/A |
| 1383534 | Male | 39 | IV | 10% | + | + | + | 15% | + | + | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1036693 | Male | 60 | IV | 5% | + | N/A | + | 40% | + | N/A | N/A | + | + | N/A | N/A | N/A | N/A | CD34- | N/A | N/A |
| 1152417 | Female | 35 | IV | 3% | + | + | - | 20% | N/A | N/A | - | N/A | N/A | - | N/A | N/A | N/A | CD56+ | N/A | - |
| 1752197 | Male | 55 | IV | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1474282 | Male | 47 | IV | - | + | + | N/A | 70%-80% | + | + | - | - | N/A | N/A | N/A | N/A | N/A | CD199+ | N/A | N/A |
| 1683343 | Male | 57 | IV | + | + | + | - | 20% | + | N/A | N/A | - | N/A | N/A | N/A | N/A | N/A | CD34+ | N/A | N/A |
| 0266417 | Male | 43 | IV | +/- | + | + | - | 60% | + | N/A | N/A | - | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 1450350 | Male | 13 | IV | N/A | + | + | N/A | 20% | + | N/A | N/A | N/A | + | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| 2218546 | Female | 62 | IV | - | + | + | - | 20%-30% | N/A | N/A | N/A | N/A | N/A | 20%-30% | N/A | N/A | N/A | N/A | N/A | N/A |
| 1044951 | Male | 44 | IV | - | + | N/A | - | 15% | +++ | N/A | N/A | - | +++ | + | N/A | + | N/A | N/A | N/A | N/A |
| 1287563 | Male | 74 | IV | + | + | + | + | 30%-40% | N/A | N/A | N/A | N/A | + | 1% | + | N/A | N/A | N/A | + | N/A |
| 2744946 | Female | 42 | IV | 5% | + | N/A | - | >40% | + | N/A | N/A | N/A | - | N/A | N/A | - | N/A | CD68- | N/A | N/A |
| 2739745 | Female | 60 | IV | 15% | +++ | N/A | - | 20% | ++ | N/A | N/A | N/A | + | +++ | N/A | - | + | CD99+ | N/A | N/A |
| 1722707 | Male | 50 | IV | 70%-80% | + | + | - | 15%-20% | + | - | N/A | N/A | + | - | N/A | N/A | N/A | CD56+CD99- | N/A | N/A |
| 0547181 | Male | 40 | IV | - | + | + | N/A | 15% | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |

**Supplementary Table 2 Primers and RNA sequences used in this study**

|  |  |
| --- | --- |
| **List of oligonucleotide**  **sequences** | **5'--> 3'** |
| **primers for Real-time PCR and RT-PCR** |  |
| NR\_103532-F | CACCGAGACCAACAGAGTCA |
| NR\_103532-R | TGATGCCATAGTCCCTCCTT |
| ENST00000565934-F | GCATGTTGCTGTTCCTGATG |
| ENST00000565934-R | TGTCTCGCTTTGACGCAATA |
| ENST00000609220-F | TGAAAAGACCAAAGTCAATTAAAA |
| ENST00000609220-R | TCACTCATGTTTCCTGTTTTGG |
| NR\_110292-F | CAATGCTTTTGCCCAGGTAT |
| NR\_110292-R | TCCGGTCCTGAATATCTTTGTT |
| lnc-CASC1-2:1-F | TCAAAACAACTCCATCGGAAG |
| lnc-CASC1-2:1-R | TCAGCTCCCAAAAGTGTTCC |
| lnc-DRAM1-1:1-F | GCACCAACTCACTGTCCAAG |
| lnc-DRAM1-1:1-R | GGAGGTTTGCTCCTGGTTTT |
| lnc-IFT81-5:1-F | TCAGGGATAGCCACATTTTCT |
| lnc-IFT81-5:1-R | TGCACATGCTGAAGACTGC |
| NR\_037144-F | CTTTACCTCCCTGCCATGAA |
| NR\_037144-R | GCAGCCATCATACAACCTCA |
| hACTB-FO-1 | CGTGGACATCCGCAAAGA |
| hACTB-RE-1 | GAAGGTGGACAGCGAGGC |
| GAPDH\_diver\_F | GTATTGGGCGCCTGGTCACC |
| GAPDH\_diver\_R | CGGCTGGCGACGCAAAAGAA |
| hsa-miR-377-3p\_F: | ATCACACAAAGGCAACTTTT |
| hsa-miR-590-3p\_F: | TAATTTTATGTATAAGCTAGT |
| hsa-miR-132-5p\_F: | ACCGTGGCTTTCGATTGTTACT |
| hsa-miR-153-3p: | TTGCATAGTCACAAAAGTGATC |
| has-miR140\_F: | CAGTGGTTTTACCCTATGGTAG |
| has-miR-340-5p\_F: | TTATAAAGCAATGAGACTGATT |
| has-miR-422a\_F: | ACTGGACTTAGGGTCAGAAGGC |
| hsa-miR-146a-5p\_F: | TGAGAACTGAATTCCATGGGTT |
| has-miR-495\_F: | GAAGTTGCCCATGTTATTTTCG |
| has-miR-129\_F: | AAGCCCTTACCCCAAAAAGCAT |
| has-miR-218\_F: | TTGTGCTTGATCTAACCATGT |
| has-miR-708\_F: | AAGGAGCTTACAATCTAGCT |
| has-miR-205\_F: | TCCTTCATTCCACCGGAGTCTG |
| has-miR-134\_F: | TGTGACTGGTTGACCAGAGGGG |
| has-miR-124\_F: | CGTGTTCACAGCGGACCTTG |
| has-miR-148a-3p\_F: | TCAGTGCACTACAGAACTTTGT |
| has-miR-338\_F: | AACAATATCCTGGTGCTGAGTG |
| has-miR-329\_F: | GAGGTTTTCTGGGTTTCTGTTTC |
| has-miR-335\_F: | TCAAGAGCAATAACGAAAAATGT |
| has-miR-185\_F: | TGGAGAGAAAGGCAGTTCCTGA |
| U6-S | CTCGCTTCGGCAGCACA |
| U6-A | AACGCTTCACGAATTTGCGT |
| CDRAS1-F | ACGTCTCCAGTGTGCTGA |
| CDRAS1-R | CTTGACACAGGTGCCATC |
| PI3KCA-F | ACTCTCAGCAGGCAAAGACC |
| PI3KCA-R | ATTCAGTTCAATTGCAGAAGGAG |
| NR\_037144-F | AGGTGACCACCGGAAAGAAG |
| NR\_037144-R | CTTCTTCATGGCAGGGAGGT |
| NR\_002734-F | CGATGCTCCCACATCCTTAC |
| NR\_002734-R | GTTTTTGTTTGAGGGGTCCA |
| lnc-BET3L-2:1-F | TGATTGAAGCATTTCTTAGCTCTC |
| lnc-BET3L-2:1-R | TCTTGGTTTGTCAGCAGCATC |
| ENST00000398460-F | TCCGAGGGGAAATGTTTAGAGC |
| ENST00000398460-R | GCCCAACCTATCCAGCTTTGA |
| NR\_002791-F | GCCAGGAAGCAACAGAGAG |
| NR\_002791-R | TGCTGATCGAACTGATAATTTG |
| NR\_024442-F | AGTATCCAAACAGGAGTGGCT |
| NR\_024442-R | AGGGATTTCACGCTGGCTG |
| ADARB2-F | CCTAAACACCAAGGCGAGAT |
| ADARB2-R | AAAACTAACGGGGCACACTG |
| FOXO4-F | TCCCATCATTTCCTGTGTCA |
| FOXO4-R | CACACTTCCCCACTCCAATC |
| CCK-F | CAACCACACACCTCACCAGAA |
| CCK-R | ACCAGGAGTCACAGATGAAGA |
| SOX4-F | GCTCAAAGACAGCGACAAGA |
| SOX4-R | CTGGGCCGGTACTTGTAGTC |
| EGFR-F | CCTAATCTGTGTGTGCCCTGT |
| EGFR-R | ATTGGATGGGGTGGATATTG |
| linear NT5E-F | GAGGACACTCCAACACATTT |
| liner NT5E-R | TTAGAAGAATGGGATTTCCA |
| hsa\_circ\_0083682-F | GATCGATGTTAAACGTCACAGCA |
| hsa\_circ\_0083682-R | ACGTGTAGCTCATCTTGGAGG |
| hsa\_circ\_0006847-F | CACCCAGGCTGGAGAGACA |
| hsa\_circ\_0006847-R | TCACAGCCAGGAGGGATCTT |
| hsa\_circ\_0037751-F | GCAGCCCAACTCCACCAA |
| hsa\_circ\_0037751-R | TCCCGGAAGGCGAAGTG |
| hsa\_circ\_0001162-F | GAGCCAGTTTGCCGGATA |
| hsa\_circ\_0001162-R | ATCTGCGCCTCCACTCCT |
| hsa\_circ\_0006774-F | TGCTGTGTACCTGCCCAAT |
| hsa\_circ\_0006774-R | TCTCCTCGGCCATCTCAG |
| hsa\_circ\_0005896-F | CTTTCCCGCTCTAACTTTTCAGAT |
| hsa\_circ\_0005896-R | TTAGTCCAAACTGAAATACCCCTGTA |
| hsa\_circ\_0007469-F | ACAATTTGATTGATTTCTGTCCCTTA |
| hsa\_circ\_0007469-R | GGCCCCACCGTTAGTATTTCA |
| hsa\_circ\_0007970-F | TTTTGGTTCCAAGCAGAAGG |
| hsa\_circ\_0007970-R | GTCAGCACCAGGGCTTTCTA |
| hsa\_circ\_0029086-F | TGCCACTTTGAGTGAAAAGG |
| hsa\_circ\_0029086-R | TCACTGATTGGTCGGCTACA |
| hsa\_circ\_0029088-F | TCAGGGAAAATGCTACAACACT |
| hsa\_circ\_0029088-R | ACTTCTCTCGCCAACCAAAA |
| hsa\_circ\_0029092-F | CCTTGGAGTCTACCAGTTTGC |
| hsa\_circ\_0029092-R | TAAGTCCGCCGATTTTCATC |
| hsa\_circ\_0029094-F | TTTGCCATACTGCTCCCTTA |
| hsa\_circ\_0029094-R | TGTTGAATTTTTAAAAGCTGAAGGT |
| hsa\_circ\_0029095-F | ACGAGCACAAAAGATTTGGTCAT |
| hsa\_circ\_0029095-R | AAAAAATCCACTGTATGTAAGAAGTAGCA |
| hsa\_circ\_0030574-F | GGGCAATTCTCAGGAAAAATC |
| hsa\_circ\_0030574-R | CACAGCCACAGAGACCACAC |
| hsa\_circ\_0031782-F | GGCTCTTTTCCAAGAAGTGG |
| hsa\_circ\_0031782-R | AGACTGAAGAGCTTCTGTGAGG |
| hsa\_circ\_0060916-F | GGTAGTCCAGCATCCAGCTC |
| hsa\_circ\_0060916-R | GGCTGCAGCATATTCACAAA |
| hsa\_circ\_0060918-F | TTGTGTGCCTGCTGGTAGTC |
| hsa\_circ\_0060918-R | AAGTCAATCCCAGCAACCTG |
| hsa\_circ\_0066947-F | TCTTCTTTCTTGTGGCATCTCCTT |
| hsa\_circ\_0066947-R | CCAATCCTCAAACATAGGTGTAACC |
| hsa\_circ\_0066949-F | GGCAGTAGGTTTAAGCAAGGTTACA |
| hsa\_circ\_0066949-R | CCCATAAACAGAAAAATCGATACCA |
| hsa\_circ\_0069065-F | CGGAATGCAGCCACCAA |
| hsa\_circ\_0069065-R | CGGCTCACATTCCTTGAAGTC |
| hsa\_circ\_0072121-F | GTAACCCGGAGCCCTGTGA |
| hsa\_circ\_0072121-R | TTCTTTCCCATCATGCTGGAT |
| hsa\_circ\_0072659-F | CAGTGTGAAAGCAAATGTGACAGTA |
| hsa\_circ\_0072659-R | TCACGGTAAAGTTTGGCAACCT |
| hsa\_circ\_0072660-F | AATGCAGCAGTGTGAAAGCA |
| hsa\_circ\_0072660-R | GTCATTCAGCCACCAAGGTT |
| hsa\_circ\_0074048-F | AATAAACCTCAAAACCTGCCC |
| hsa\_circ\_0074048-R | GCAACTTTATTAGCAGCTCGGC |
| hsa\_circ\_0077232-F | AGATAAGCTCTTTGGTCGGA |
| hsa\_circ\_0077232-R | CGAATGTCCCAGTGCAATAA |
| hsa\_circ\_0077407-F | GAACTGCTGAAAAAGTCCATCA |
| hsa\_circ\_0077407-R | ACTGGACTGTAACAAGGTTTCCA |
| hsa\_circ\_0077888-F | TGGAGATGGCCGAGATGAG |
| hsa\_circ\_0077888-R | GGGCTGTAGCCACTACTTGTAATTACT |
| hsa\_circ\_0078070-F | GGTTACCTGCCTGTCCAGACA |
| hsa\_circ\_0078070-R | GACAACTTTATCCCAGCTGAAGAGA |
| hsa\_circ\_0078080-F | ACAACCCAAAAGGGATGGAT |
| hsa\_circ\_0078080-R | TTCACCTGTTCAGCCTCAAG |
| hsa\_circ\_0078082-F | CTCAACATATCAAAAGTGCCAAAAA |
| hsa\_circ\_0078082-R | TCTTCAGTCCAACGGCATACTG |
| hsa\_circ\_0079865-F | TTCGCCCTTGTTGGATCTTA |
| hsa\_circ\_0079865-R | TGGCATTGGTGAGAAGAGTG |
| hsa\_circ\_0088564-F | CTCTTTCTGAGGAGCTGTTACTGA |
| hsa\_circ\_0088564-R | ATGTCTTTGTTTGCCCACCT |
|  |  |
| **Oligos for cloning of gRNAs** |  |
| sgRNA-1-S | 5’- CACCGTCTTGAACCTGCCAGGCGG -3’ |
| sgRNA-1-AS | 5’- AAACCCGCCTGGCAGGTTCAAGAC -3’ |
| sgRNA-2-S | 5’- CACCGCACATGCCAGGTACTTGGA -3’ |
| sgRNA-2-AS | 5’- AAACTCCAAGTACCTGGCATGTGC -3’ |
| sgRNA-3-S | 5’- CACCGAGGGTTTCGCCATTTTGCCT -3’ |
| sgRNA-3-AS | 5’- AAACAGGCAAAATGGCGAAACCCTC -3’ |
| sgRNA-4-S | **5’-** CACCGATGAGCAGATCACAAGGTC **-**3’ |
| sgRNA-4-AS | 5’- AAACGACCTTGTGATCTGCTCATC -3’ |
| sgRNA-5-S | 5’- CACCGAATTACCCATGGGTGGTAGC -3’ |
| sgRNA-5-AS | 5’- AAACGCTACCACCCATGGGTAATTc -3’ |
| sgRNA-6-S | 5’- CACCGCCTCAGCCCTCTGAGTAGC -3’ |
| sgRNA-6-AS | 5’- AAACGCTACTCAGAGGGCTGAGGC -3’ |
|  |  |
| **Primers to amplify genomic deletions** |  |
| F3 | CTTGCTGCACACAGAGAACC |
| R3 | CAAACTGTGAGGAGGCTTCA |
| F4 | GAGAACCTGGGTTGCACAGT |
| R4 | GCCTAAGCACGTAAGCATGA |
| F5 | CTGGTAAAATCACAATGCACAGA |
| R5 | TGTGGGCTTTCCTGAATAGG |
| F6 | GCATTAATACAAACAGTGCTCCTG |
| R6 | CAGATAATCAAGGGACCAGCA |
|  |  |
| **FISH probes** |  |
| circNT5E | CTTCAAACACTAAATTTGTCCGACCAAACAGCTTATCTTC |
| miR-422a | GCCTTCTGACCCTAAGTCCAGT |
|  |  |
| **siRNAs** |  |
| ADAR1-1#-F | CGCAGAGUUCCUCACCUGUTT |
| ADAR1-1#-R | CGGUGGGCUCUGCG |
| ADAR1-2#-F | GGAUGCAAAUCAAGAGAAATT |
| ADAR1-2#-R | UUUCUCUUGUUUGCUCC |
| Scramble/siRNA control-F: | UUCUCCGAACGUGUCACGUTT |
| Scramble/siRNA control-R: | ACGUGACACGUUCGGAGAATT |
| si-circNT5E | CTCTTTGGTCGGACAAATTTA |
|  |  |
| **List of Antibodies** | **Source and indentifier** |
| anti-NT5E/CD73 | ProteintechTM, Cat No.:12231-1-AP |
| anti-SOX4 | Abcam, ab80261, Cat No.:GR279180-1 |
| anti-ADARB2 | Abnova, Cat No.:PAB22715 (Lot:A95452);Santa Cruz, Cat No.: sc-73410 |
| anti-Smad2 | ProteintechTM, Cat No.:12570-1-AP |
| anti-pSmad2(S467) | Abcam, ab53100, Cat No.:GR540308-12 |
| anti-Akt(S473) | ProteintechTM, Cat No.:10176-2-AP |
| anti-pAkt | Cell Signaling Technology, Cat No.:9271T |

**Supplementary Table 3: GBM-related tumor suppressor miRNAs extracted from the literature.**

|  |  |
| --- | --- |
| Name | Reference(Pubmed ID) |
| miR-377 | 24951112 |
| miR-590-3p | 26556542 |
| miR-132 | 25983322/27522003/27698888/25720694/26898440/26604788 |
| miR-153 | 27215075/23397238/27295037/21213215 |
| miR-140 | 27498787 |
| miR-340-5p | 25831237/25817794 |
| miR-146a/146b-5p | 25326894/26916895/26320176/26239619/23796692/20874002/19265686 |
| miR-495 | 25759932/23594394/27220777 |
| miR-129 | 26510428 |
| miR-218 | 26889813/26572167/24368849/24357514/23950210/20933503/25789001/25943352/26012781/26133092/26137139/26407971/23243056 |
| miR-708 | 23754151 |
| miR-205 | 26230475/23683741/22159356 |
| miR-134 | 25564273/23467648 |
| miR-124 | 21196113/18577219/23624896/24861879/26554866/24497408/23936026/25112530/23817964/26530859/24954504/23761023 |
| miR-148ab-3p/152 | 27446363/25971746/25218589/25224277 |
| miR-338 | 27739438/26936749 |
| miR-329 | 23866847 |
| miR-335 | 22644918/22172575 |
| miR-185 | 21962230/26458593 |

**Supplementary Word-1. The sequences of Alu elements of circNT5E analysis.**

>hg19\_hub\_1\_salzman\_circRNAs range=chr6:86170955-86215509 5'pad=10000 3'pad=10000 strand=+ repeatMasking=none

CCTGGCAGCCCCATCCATGTGACCTTGAATTCTGTCCAAGTCTCATCACTTTCTATGTGTGTTGTAATGGAAAAAAGGTTACAAAACACAGTCTTTCTGGCCTGGAGTACCAAAATAGTAAAGACTTCTGTTTTGAAAGCCTCTGACAAATGAACACAACAGCCACAGTGATAACTTTAGCAGGAAATTGAACCACAAAAAGCAAGCGAGCCACAAAGCCCTGAAGGCTAAAAATGCCTCACAGGCCAAGAGGCAGTTAGGTTGCACCTGAGACAGAGGCTGCTTTCTTAACTGGGAAATGGGTGTCTCCAGATATATAAAGCTGTGAGGAGATCACCATGGCCCAGCTCTGACGAGCCACTGGTACAGCATTGTTGGTTAGTTTGCCTCAACCTGCAGCAGAGTTTTTATTCCAAGAGTTAACAGTTAGTTAGGCTTTTTCCAAAGGTTGAGATGACACCCCAACTCCCACACCCATTTCCGTCCTGCCCCAGCTTGAAACCAGGCAAAGTGAGTTAAGACATTGGGAGATGGGAGGGGACAGGAGGGGTAGAGGCCTGGCACCCCTCTCTCTTCTGTTTCAAGAGACACTTTGTGGAGTTGTCTAGAGAGACTGGGGGTAACTGCTCCTTCTGCCCCCAATCTCCCCTTAGCTCCCCACTCCTCCCTATCCTGCCAGGCCAACCACCAGCAGAGAAGGGCGCTTAGCTCCAGTGACGCTGTGAGTGAGGTACTTGTGAGGATGCATATGGTTCCTGTTGGAAATGCACGGAGGAGCAGTGAAACACCAGAAGCCCCATCCTCTCTCCTGCCCGTGCCCTCATGCCCAGCCAGCTGAATATTCCTGTGGCTTCCACTCCTGCACTGTCCCCTCAGTGTCACCTCCCCACCACATTCCCACAGCCCCACTTGCTGTGTCACCTCTCCCCTGAGGGAGAGGTGTCTTCCTGCCAGTCTCTTCACCACCAGGCTCACACAACTCCCATCCATTCACTGCAGGCTGCCAGACTGAGCTTTCCAAGCACCCCCGGACTGCCTCCAGCCCTACTTTCTCTTCAAGGCTTCCCACTTCCCTCAAAATGAAAGCCCTGACTCCTTGGACACCATACAGACCCTCCCTGATCTCCCAGCGATGCTCTTAGCAGCATCATTTTTTTTTCTGCCAGATTTTCAGGTGCCCTCAGTTCCAGGAGCACCAAATCACCTGGATGCCATGAGCTGCTTATGACACAGTTCAAGGTGTGACATCTTTGAGGTCTCTCCATAACACCTCTACTGCAGACGTCTGTCTCTGGTGTATCAGCTGTACCTTGCACACATGTCTCTAACCATCTGTCCACTGTGTCTGTCTGTTCACACATCAGATTGACCCTATGTTCTCTGTGACACCAGGTGAGCTCTGGCACCAGTGCCCAGCAGATGATTACTGAATGATTAATAAAACTACTCACTCCACCTGCTGCTTTTAAATGGGCTCCATTTTGGTATGATTTGGTGCGTGAACCATTAAAACTTTTCAGAAGTCAGGATTTGAAACAAACTTGGTAAAAAGTAGTTAAGCAATGTCTTCGTTGTAAAGTGAGAAACCAAGTTGCTTGGAAACAGGTGAAAAGCTTAGCCAGCAGCTTCACAATTCACAGCCTGGCACTCCAGTAGCCCTCTCTGGACAATTGCCCAGGTTTTCTTGTTTTCATTTCTGTGTTTTAATTTACAAGTTACCTTTATATTTCTACTAATACCTTACTGGCACTTGTTTGTGAATGAAACAATTTTTTTGAGAGTTTGTTAATTGTTCTGTGTGAGTGTGGAAAGTTTCTTTCATATAAGATCATCAATTCTTTTTTTAAAAATAGTGTTTTAGGTTTTCTCCTACATAAAGAAAGTGGTGGGGGTGAGGAGCTGGGGGTGGACCAGATGCTCACATTGTATTTCTATGATTTTGCTGTTGGAGATACTGAAGATCATTTTGCTGGGCTTTGCTCTCTTAAATTACAGAAAAGTGCATTTGGTGAAGTTTAGTGTTTTTAGTAAACATATACAAGATGTCATAGGGATAGAATTAGTGAAGGAATAGGGTTCGTGAATGAATGAGCTCAATCTTAGTAATGAAATGTTTGGAAAGCAACAGAACAAGAGAGAAAGAGCATCAGAACATGATTTAGGTACCCCATACATTTATACAAATAAAAAAAAGATCTGATTTAGGGTCATAGAAATCACATACCTAAACTGATGGTTAAACAATAAGTGGCAAGTAACAGTTTAGCTACAAAAAATGTACAGGAACACATAAGGAAAGTTACATGGGAACTTTCAGAGAGGACCAAAAAAGGTGGAATAAGATTATCTGCTCTGTTATGATCCCCTGTATTTCTCTGCTCTATGTTCTTCTCTTGGGCAGTCTTTTCCTGAGATGTTTTCATGTTATTAATCAAAAATAATAGAAACGAATAAACTAGATCAATGCATTTACAAGATTTTTTGAGTGCCTGCAGTATGCCTCGGTGTGGTGGGAACTTGGTGTACTGAGGTGAGTAGCATGATCCTGAAGAGCTTAGGAATCACTGAGTTCTCGTAAGTGCAATAGAAGAAAAACTGGTAGAAGGAAGTCAAATGAAAATACAAGTTTCTAAAGAAAATAAGTATTTACAAAGGAATTTGTCTGCATTAATTTCTGTGGAAAAGTTAGCTATGTATAGAAGAAAGAAACTTGTTAGTAATTCTTTCATTCATTCATTTATTCATTCAACAGTGAATCCCTGCCATGGTAGTACTAACTACTTGCACTGTGGTAGTGCAAGGGATACATTTGCTGTGCAAGTAGTTAGGAATTTTTTTTTTTTTTTTTTTTTTTTTTAGTGCTTTGTGTATGCTAGGCTTTATGCAAATATACAGCCAAGCACAGAGGTTAAGAACTTTGGAATCAAACCGAAGTGGTTCTAGTCCCAGCTCCCCCTTACAAATTGTGTGATCTTCAACAGTTCATTTAACTTCTCTAGATCTCAGATTTTCTCATCAGTAAAATGAGTGCAGTAAGAGTACCACCCTCACAGCATGAAATCAGATTTTCTGTACTCTTTACTAACTCACTTTCCATGACGCTGGCATGTGGCAAGTGCTGACTCAATACTGGCTCATTTCCTTAACTGCTTTTATTTTATTCATTCACTGCCATTCCAGAGGAAACTGCGGTTCTGAGATGTGCCCTGGGTCACTGCTGAGGAGCGGACGGAGCCTGGGAGGGAGCTACCCCTGCCTTGTTTCCTCACACTTTATGGGGTGGGTGTCAGGAATGAGGCTGGAGGGGAAGGCAAAACCAGATCCCTAAGAGCCCCCTGGACCCTGCTTAGGGTGTTTACTTCTATCATAAAGGCTGTGCTTCTGTAGAGACCTAAGGCAGAGAGTGCCAAGGTCAGGTTTGCATTTGAGAAAAGTTTTTCTGGCAGCAATATAAAGAATAGTTTAGCAAAAGAAATGAGAATAGCTGGAAACCCAGTTAGGAGGCTGTGGTAGTCCAGGAGCACACTAAGGCAGCAACAATAGGTGGATGGAAACTGGAGCATTTAGGTAAGGGAGAGGGATGCCAGAGGACGTGATGGTGAGGGAGAGGGAAGAGGGTGGGACTCCACCGCACCAGGGCTTCTGGCTTTATTGACTGGGTATATGGTGGCATCCTGGGCCAAGACAGTGAGTCACAGGGAAGAGGCTTTGAGCCTGGTAAGCTTGGGACACTTTTGAGACATTGGGAGGAAATGACACATGGCAGTTGACATACAGATCTAGACGTCAGGAGAAAAGTCAGGGCTGGAGATTTTCGGTTTACAGTTGAAGGTATGAGTAGGAATGAGATCATTTACTCAGTCCATCCCACCACATTGAGCACCATGAATAAGGGGCTCCTCTCCCCATGGGGCAAGAGAGGTGAAAAGACAGTCAAAGTCACTACTTTCAGGAGGATTAGGCTCAAGTTAGGATGGGGAGGTGGAGAAGGCATCAAACAAATAAATGAAAACTATAACTTCAGTTATTGCCAAGTGCTAGGAATATAATGTTGCTGTTAAACTGCAAGGTGGCTAACAAGTTGGATAGTCTTTCTTGAAGAACTGTAGAAACATTCATTAAAAACAAAATAATTTTATAGTTAAGCAAGAAAGTGATTGTACTATAACAAGGGAGACTTATTTCACCATAGGAAAAAAATCATAACATTCTAAGAATAGAAGGAAAAAATAACAATTACCCAAGCCTGCAACAACCTGTAAGACCAGATCAGCTTTTAAGAGGAAAGTTAATTAGATAACAGGAAGAGGTAAAAATGAGATCATCAGAGATGGGGGAAAAGGCAAATTTAGAAATTCTGAATTTAATAGGGGAGACAAGTATGTAGGAATATAAACACATTGTGCTTTCTCTGCACAAACACATTCACATGAGGATGTATACACAACCCTTGCAGGCACAGGTACTCAGTGAATGCCTGCGTGCCAAGGAGGGGGACAGCACTGAGCAGGAGAGGTGGCAGGGCCTGGTGGCCCAGGAGCACTCATATAGTCAGGAGACTGATATAAAAGAAAGATCCTGCTAACATGCCATTACAGAGTATGGAATGAGCAAGGAAGGAAGAGGGTGAGGCTGTAAGAGAGTGCACAGGCCCTCATTTAAATGGACGGGTCACCAGCCAGTACTTCATGCCTGTTCCTAGATGACCCACAAAGTGAAACGAAACTGGATGTGGTATTTAGCAAGTCTGAGATTTGCTGGTTTAAGTACTAAGTTAGCAAACCAGCCTTGGCAGCCAGAGCAGGTAGGGTAGGGGGCCCAAGGAGATGGGTGTATCCAGGAGGCCAATGGAGGAAGGAGAGGAAGGTTTTCTGGGAAGCCAGCTGACATGTCATGCTTTGTCAGTGGGGCCTCTGCATGGATTCCCTCCACTCCCCCCCAGCCCCCAACTCACTACGGGGAGCTGCAAAATGACAGACAATGGGTGGTTTTGTACCCAGCAGCCACTCCTCAACCAGTGAGGAATGGGAGAGAGATAAGAAGGTGGGAAACAAGGATTGCTTGTCACCATCCCTGCTCCTCCTGAAGCCCTGCGCTGGGAGCAGGTACAGAACCCGCTGAAGGTCACCTAATCATTTCACCATGGAGTTCTTCCCCAGATGTGAAACTGCTGGGACTGGAGCAAAGGGTGCCCAGAGCTGACTGGAGGAGGAAGCCAGAGCCACACTGGAACATATGGAGATGCTAGCTCCTGCCTGCTATTGAGGAACTTCATTTTCCCAGAAGAATTAGAGGACCACAGGAGTGCTTGGGAAGAAGCAATTGTGGCAACCTAGGTGAATGATGACCTAGGAGGTGAAATGAGGAAGGAGGCCTTTGGTCTCTGCCAACCATACATTTCAGGTTGCCTTTTGCTAAAGTCCTGCTGATGTTAATCATTCTCTCCAGCAGATCGCGGCTTGAATCATGGGGTCTGAAATGTGGGTTTATGAGAGAAAAACAACATGGAAAAATTGGGCAGAGGCTGGTAAATGTGAACATTCAAACCTGCCCCCAATCTGAGATGGTGGGACAGTGGACCCCTGGCCAGCTCTCCAGGTGTTGCGTATGCACATTGGCAAACCACCTTTATTAGGTGGTGTGACACCTGGGTAGCAATTCTCAAGCAATGTGATGATCTGAATGTCCCTGGGCCTGACCCAGGTGAGGAGGACACAAAATCATGCAATATGTCTCATAGAGCTTAGTCAGTTTTGAGAAATACTGGACTAATGTTATGTTTTTAAAGCACCTAATTCTTTTTCTCTTTTCTGTTTTATCTAGGCACTGGGAAATCATGAATTTGATAATGGTGTGGAAGGACTGATCGAGCCACTCCTCAAAGAGGCCAAATTTCCAATTCTGAGTGCAAACATTAAAGCAAAGGGGCCACTAGCATCTCAAATATCAGGACTTTATTTGCCATATAAAGTTCTTCCTGTTGGTGATGAAGTTGTGGGAATCGTTGGATACACTTCCAAAGAAACCCCTTTTCTCTCAAATCCAGGTATTTTCTACTTTTATAGCACTCAATGCTTGAAAATAGATGCCCTAAATCACAGCTTGGCATTATATTTATGGACTGTAGATAAAAGTAGGAACAACTGGGTAAATAGTGCACTAGAATAACACTGATAAAAGCAATCTGGTAAATTCTATGCTGTTGTTCCAAGGTACTTCTTAAAGAGATGTCCTCTTCTGCTCAGTGAACTTCTTTGTTGACAAAAACAGTATCTTTGTCTAATTCAGTGCTTTCAAAATGGGAAGAGGAGACAATGTATAGCCAGTGCTAAACAGTACAGTTTCATTTACTAGAGAATGAGAGCCTCAAAACTCACTGCCCTTCTCCTGTGGAGCCATGAGCACAGAGCCAGAGTTTTACCTCAATTTACCTTATTGCTCCTTTTCTAGGATGATTATTACATGTCCAGCTAACTCACCTTTCTCGCTTTTCATTATTCATCTCGTTTTAATGACATTCTTGTATCTGACTTTCTGGGAAATATATATAGTGGTCTTATGATATATATGGATATATATAAGTGTATGTATATACATTTATAGACATATATACACATATGTATATATAATATATATAATCTTAAGACACACACATACATATATGACACATATACATACATACATATAAGACACACACACATATATAATCTTAAGACCCTTCAAGAAACTATTTTGAGGCACTTTTATAAGAAAACTTTTTGGAATATTTTGGCAATGAGAACAAAAATGACATTTTCTTTAAATTATCCAAATTAAATGTGTTTCCATATTTGAAGAAAAAAAGGGAAAATAGGAGCCAGGGTTATCTAGAAACATGAGTTTTCATTAAGAACTAACTGATAAAGGACATATAATTGACAATTCAAAAATATATATTTACTGTTGTTGTTGTTATAAAATAAATAAGTCCAGGCCATTGGAAACAACAACAGAAAAGTCAGCTGTGTTTGCTGAGAGCAGCAAGCGGGTCCTGCAGCTGGCATAGAGGCAGAGCTGGAGGCAGGGTGGAGCGGCTGGGGCTGGAGTGGTCAGTGAGAAGAGTGAGAGAACTTGCTAAAGAACCCCCCAACCCCACCCTGGGGTCAGGTTTACTTGCTGAAGAACCTCCTTGGTCCCCTTGAGAGCTGTGTAAAACATCCCTGGGGCACAGGACATTCCAGAAGTGAGGTCAGAGTCACAAGCTAGGATGCAGGCTCCATGAGGACAGAAACCTCTGCTGTCTCACTATTGCCCAATGACTGTGCACAGTGCCTGGCATATGATAAGTCCTCAGGAAGCATTGCTGGGATGAATACATGAGAGCAGGAAGGTATAGGGGCCACAGTCACAGAACAGCAGATAGTTCCATTTCCTGGAGCATGGGTTCTGACTAGGAAAAGCTAGAAAGTTGGATCAGGGCTAGATTGTAGGGCTGAGAAGTTCAGGTGTGATTTGGAGGAAAGCATTGTCTCTTCTTTAAAAGGCACCCATAAGGAGGTAGGAGGTGCAGGTCTTGGTGGAAAGGCACAGCAGCTCCAGAAATCAAACTGCCCCAGCTGGGACTCTGACCAGCCCTTTACCAGGCTGTAACAGAGAGGGGATCAAAAGTGACACTGCTGTTTCCAGCAGCTGCTGGAAGAGAGGGCTGCATTTTGCAGGGCCCAGTGTGGGGGGAAAGGGATGGGGTGGAATAGAATGTTTCCAGGAGCACTGCTTCTTCCAAGACTACAGGCCCAGCGGCCTGGTGTGGGTTCTTCCTACAGTTCTTTGACCCTAATCAAGCCCAGTTCTCCCAGTCCTAGTGGCCTGGGCACCCACAGGGTTATAACCTGTATTTCTAGCACATTTAATCTAATTTATTTTAGCTAGATCATTAAATACCTGAAATACAACTCTCCTCATGACATCTTGAAATATAAGCCATGCTTTGTATATATGGGATGCCTGGTCCTGTGAGGTTTCTGATATAATAGAGGAATACATTCCTTTGTCCTCAGAGGCATTTCTCTGAATTTTTTTTCCTTCTTGGCAGCCATACCTTAAGCAAAAGATGGTAGCATACTCTCGACATTTAGTCATTCCCCTGGGTACCTGTCTGTGTGCCAGGCACTGTTTTAGGCACCAGGGATACTGACCAAAAAAAAAAAAGTTGCCCACTGGAGCTTACATATTCAGTGGGGGAATCAATAAATGAGTAAATGGTTTGGTATGTCAGAAGGTGCTAAGGCTGTGGAGAAGAATTAAGCAGGAGGGGAATGGCAAGTGCAGCAGGGGGGAAGGTATACCTTGTTGTTTCAAAGAGATGCTCAAGGAAAGGCTCACATAGAAGGCAACATAGCACTGAGGGTCAACGGGGAGCCCTGGGCTTCTTGGGGCAACCAACAGGAAGCAGATTGTCCTTGATGTTCTCATAATAGACAACAGTGGCAAAACTACAACTCTTGATTTTTCAACATTGCCTATGAGTTACAGACAGCCTTGCCTGTCCAACACATCTGTGAGCTGCTAATTATTAGGTTGTCATTCTGGGGCCTCCCTGGCTATGATGTCAGCCATGAATTATCTTCCATGGTAATTTGCACTTGTGGAGTTGGCTAATGTTAAGGATTCAGGAGTTCCCCTGCTGAAGCACACAGACATTCCTAAACCTCACAGTGGAACAAGGGATGCATTTCTAATAATCTTGTTACTCTTTGGATTAGTACTTTTCAAACTGGAGTTTGCAGACTCCTGCATTTTGAAAGCTTTTAATGAAATGTCATTCTCCCACCCTCCTTCCCTTGTTTAGTGTTAGTTCTTAGAAATCAGTGTAAGAACGTCTGGATCTACTGGAGGACTCCCTAGTCACAGAGTACCAGACATGACTTCAGGGCAGCATGTCTGTATTTGCAGTCATCTTCATGCCAGTGATAGCCATAAAACCTCAAAGCTTCCTCAAATGTGGCTAACAGAGCCAGTTGGAGGAACCAGTTGCCTTGCTGCACACAGAGAACCTGGGTTGCACAGTGAGAGCCATGCTTGACTACTGATAACAAAAGGCTATCGTTTGTTACCACTATGTGCAGTAATAAGCACCCAGGGAAGAATGTACACAATCCCAGTGCCAGCAACATTTAGATGAGGCCCTCATGATTAACACAGAGCTCAATAATGCTCTAATGCTGGCATTATTTATATATTTATATATTTTTTGAGGCAGAGTCTTGCTCTTGTTGCCCAGGCTGGAGTGCAGTGGTATGGTCTCGGCTCATTGCAGCCTCCGCCTGGCAGGTTCAAGACATTCTCCTGCCTCAGCCTTCCAAGTACCTGGCATGTGCCTCCACGCCTGAATAATTTTTGTATTTTTAGTAGAGACAGGGTTTCGCCATTTTGCCTGGGCTGGTCTCAAACTCCTGGCATCAAGTGATCTGCCTGCTGCAGCCTCCCAAAGTACTGAGATTACAAGCGTGAGCCACTGTGCCTGGCCTGCTGGCATTAAAGAGAACATGACAAAGTTATCAACTGCCATATTAAAATAGGCATTCAAGGACTACTTGCTGACAGTTTTAAGTTTGAACACTGATTATCCCAAGTTTCCAACGAACGTCTTGGAGTTGCTAATACTCTTTTGTGTATCATGCTTACGTGCTTAGGCATTTTCTGCATTGGTATTGTGGAAGTTGAGATGTACAAATATATAAAACAATATCTGAAGCCTCCTCACAGTTTGCAACCAAGTTCAAGCAAAACAATATCCACAACCTTAAACTAATACAACATAAAGTGAATGTAATGAGGATATTGATTTGAATTTTTATTTACTTCTTAGGGGTTTTGTATTTAATGAATAAATATGTTTTGGTTTTACTGACTCTTGAGCTTTAGTAAATTAAGGTGTTTAACCTTTGCATGTTAATATGTATATTAAGTAATATAATAAAAATTGTTAATAAATATCCATTTTATTTATTTTGTTCCTTAGGGACAAATTTAGTGTTTGAAGATGAAATCACTGCATTACAACCTGAAGTAGATAAGTTAAAAACTCTAAATGTGAACAAAATTATTGCACTGGGACATTCGGGTTTTGAAATGGATAAACTCATCGCTCAGAAAGTGAGGGGTGTGGACGTCGTGGTGGGAGGACACTCCAACACATTTCTTTACACAGGTAATTGTTTCAAAAGGATTGCATGGGCCAGGATGTCCAGATAAGCACTGTGTCTCTTTTGCCTTTGTAACTGTTATTACTCTTTTTACTGCTATTTAATATGTAATGTATATTATATGATCTATAATATATATGTAATATACATTAAATGGGAACATGTGCAAATCTTACAAACATTACTAAGAATTTATTGATTTCATGATTATAAGTCAATTCCATATATTTATGTATATAATAAATATATAAGACATAAAATATGTATAAAACATATATATACCATACATATGAAAAACAAAAAGACTATTGAGCCCCAACCAAGTCATTTATGATAGATTCTTATCAAAAAGCAACATGTCATATAAAAACTTTAAGCATAAACAAAATAATGTAAATAAGGACCTTTATAACTCAAGGTGGATTTGATTTGTAGGTTGCACAGGTAGCAGAGGCTGGACCTCGAGTGTGAGTCCTAACTCTGCTGCAGACTAGGAATATAAGTATCCTGGAAGCCACATGACCCTGGGTCCTCAGGAGAGCATGCACTCTTCCTACCCACTACCTGACTACCCCCACCACTCTCTTTTTTTCTCTCTCAAATTGGTGTTAAGTAGTTTTCATCAGAATAACTCTTTTATGATTTTTCCACTTTAAACCTATAATGTCCCAAAACTTTTGAATCTGGTTCCACCTTTCCCACTTCCCCCACCTTGCACTGCATAGATCTTTGAAGTATTCCCAAGGAAAGGAAGAAGAGGCTGGTAAACAGTTCTTCTATCAGCATTCGCAAAGAAGGCTTTGGCGTGGGAACAGCCCTCCCCTTGAAGAGGCTCCTGCTTCTACCATCCTTATGTGGGCTGTCAAAGACCATGCTATTTTGATAAAAGCGAAACTCAAAATACCCCAAACAATAAGTAGGAAATACCCAAAAACATTAAAAGGGATTATCACTAAGAAAGTAATTTTTATTTTCTTTCTAGTACTTTGGAGTATTTTCAAATAATGAATGCATGTTACTTTTGCAATCGGAAAGCAAAATATAAATTATAAAAAGGAAAGAAACACAATATTGGGTCAAAAGTCCCCATTCCTAATTCACTTGAATGACTTTGAGCAGGTCACTTAGCACCTCTGAATCTGCTAGCTTAGCTTCAAAATAGGGGATGATCATGCTCAAAGTTCCACGTTACTGTGAAAATTATATGAGATGTAAAAATATGTGAAAGCAGTTTATAAACTATAAATAGCTATATTCTGGTATGCAGCGTCATGGAGGTTGCCTGCTTATAAAAATATGTCAGTCAAAATCATAACTCACAAACTAAAGTTGGCCTTCACTTAAGAAAATACCAGTATGAATGTGTGCTAATTAAATTCCTTCACAGATATTTTACTTCTTGGTAAACACAGGCTAAGGAATAATTTCAAACTGAGTTAAACTGACAGGTTGTGAAATCAATTTATGGGTTATGACCAGTAGTAGGGCTTTTTTTTTTGACAGATAAGACTAAAATAGATTAGGCACTTACATTACTCATAAGAATGATAAATATTGTTCCATGGGAAAAGATGTATATAAGATGTCAAGAACAGCCCCAGGCACATAGCAGACAATCCATAAATGTGATGAGGATGACGACTAGCACTGGACATTGTTAGCATGGATAACATTGCAATCAAAGAGTTTCAACAACTCCATGAGGGTTAAATGAACTAAGAGAGCCAAGACGAGGAAATAATTGGAGCAGGTCACTGGGAAGCACTGGGTAGGGGTGAAGACTCAACAAAGTCCTTCTGACTCTACCACTAATGGTGGGGTCCTTTCAATGCCTGATTACCCTCATCTGTGGAATGAAGGTGATAACAACAGTACCTATTATAAGGGGTCACTGTGATTTAATATGTGTAATGAATGTATAGGTAAATGGCCTTAGCACAGGGCCTAGTATGTTAGCTGTTCTTATTTTAGTTATGTGCTGGCTCACTGGATAAGACCTGTGAAAACCCAAACCTTAGCTTTTCACTGAGGCAGTGTCAGCACCCTTGGACACACAGTGGGAGCTAGATATGTCTCCTCCCCCTTCTTCCTTTAGAATAATGGTTTCAAAAAGTTTAAACTATGACCCGTAGTAAGAAGAACATTTTAGACAGGGAGCCAAAACACACAAACATATATGTGTGTGTGCGTTCACATACGAACATGCAAAAGCACTTGTATGTGCAAACACATACAAGTGAAAGAAAACTTTCACAAAGCACATGGAATGCACCCCAACTTTTCTGTTTTACTGTTTTATTCACTTAATGCCAGCTACCACTCATTGAATTGATTTTCTTGTACTGTAGTTAATCCATGTTTCTAAAAACTCAGCTTTAAATGGGACGTGACCAAAATAATGCATGAACACTCAAAGGAGTTTCATCCCTTCATTCAGATGTGAACATTCCTGTGTTCCCCTTGACTTGTCTTTACACCATCTTAATCAATGCTGTCTTACAGCAACAATTAGTCATTCATAGCCTGTGGTTTGTGTCCATCAGTGAGTGTGCCCTGATAGACCTGAAAAGATTGGGAGACCATGCCCAGCTTCCCATTATTTCTGTAGCCTGTCCTTTGTTCCCATAACAGTACAGTCATGCCTTAGTATCTGTGGGGGATTGGTTCTAGAACTCCCTGTGGATACCAAAATCCATGGATGCTCAAGTCCCTTATATAAATGGTGTAGCATTTGCATATGACCTGTGCACATCCTCGCATATATTTTAAGTCATCTCTAGATTACTTATAATACTTGATACAATGTAAATGATATGTAAATAGTTGTTATACTGTATTGTTTAGGGAGCAAAGACAAGAAAAAATATATGTTCAGTACAGATAAAACCATCCTTTTTTAGAAAATAACTTTTTGTTCATGGCTGGCTGAATCCAACAATGCAAAACCCACAGTTAGAGACAGCCAACTGTATGTGCCTTTGCTAAGTAGATAAATTTAGTTAATGATGAAGGACTGGATGAAAGAAAGATTTGAGGATAAAAATTAGAGTTTGCTTATCTGTAAATCCTGAAGTAAATAATTACAGTCTCTGAGAAAACTGAGATAACTAATACTTAGTCATTTACTTCACATTTCATGATTGCTTACCAAGATTAAACTTGTTCTGATGAAAATCTTCACTTTTCATACTCATCGTTTTGATGAGTGAACTTAACAATTAAAGGTGGCTGGGCACAGCAGCTCATGCCTATAATCCCAGAATTTTGGGAGGCTGAGGCAGAAGAATTGCTTGAGCCCAGGAGTTCGAGACCGGCCTGGGCAAGATAGGGAGACCCCCATATCTACAAAAAAAATTTTTAAAAATTAGCCAAGTGTAGGGGCATATGCCTGTAGTCCCACCTACTCAGGAGGCTGAGGTGGGAGAATTGCTTGAATCGGGGAGGTTGAGGATGCAGTGAGCTATGATCACTCCACTGAACTCCAGTCTGAGTGACAGAGTGAAAACCCTGTCTCAACAACAGCAACAACAGCAAAAACATTAAAGGTAATTCCAGGACACAATAGGGATGAGGCATATTGCCTGTTTAAATAAACTTTCCTGGCCTTAAGAAAACAACTCTGCTGAATAATTTTATGGAATTAGAATGACATTAAAATAATGAATCTGATAAATATGATTAGTTAATAAAAATACAGTTAAAATAATACATCCCTTGGAATTTTAAATCTTACTGAGAACCATTTCTGCACGCACAGTATCCAATATACAAACACACATGGAAGAAAACCTTTCCAAAGCTCGTGGATTGCACCCTCATATTTTCTGTTCTGTTATTTGAGTTTTTAAATGCTGGTTACCACCCATTATATTAATTTTATTGTATTGTAGCTTGCTCATATTTTTTTAAAACTCAGCTTCAAATAAGGCATGACTAAAACAGTGCATGAATGGATCCCTTCCAAATGTTGAAAGTTATTCCAGTTTCTTTCCTTTCCAAGTACCATGCATATGCAGCTAACCCTAGCATTGGCTGACCAGTCTAACATCAGAGTGAAGAGAAGGGAACTTCCCTCTACAAGGCTTACAAAATGATAAAGTTACAAAGATAAGAGCTAAAATGCAAACGCTTTCTCTAAAGAAGTTAAATCCTAGAGTCACGAACTGGTCCATGTTGCTTCCTTTAGAGAAAAAAGTAGTAAAATCAGTGCAGGTTGAAACCTGCAGCAGGTACAACAGGGGACTCTATTCTCTGTGCTGTCCTTGAAGGGACTCCAAAGATGCTGTTTCTCTGTTTGCCTCCCAGTATTTTAAGTGAGTTTTGGATTCTGCAAATCAATCTGGCTAGCTATGGCCTTGGGTGAATATAAGCACCAGTTTCTATAGCCGCAAGTTAAAGGGATTTGAATTGTTAATTCTGTCATCCCTCCCATTCTAACATCCTGTTACCTAGAAAATCATCCATACATAGAGCCTGAAAGCTTACTTTTCAGGATTTGGGGAAATAAAAAAAAATTTGGTAGAATACCTCATACTTTCATTAGGCTACTGATATGAACTTAATTATTCCTCTAACTCCTTTGAGGCTCAGACCTTCTGTCCCCTGTCTTATCACTCTCATCTAATCACCTCCAAGCAATGTCCCACGTCACTGAGAATTTAGTATCCAATTTCCTATCTTCTGCTCCACTCCAGCTCCTGCCTTCACCTGGCAGAGTGTCCATGTGGGTAGTTGATCCAATACCCCAAGTTCAGAGTCCCTTGATCTCCTCAATCCAGTGACTGACACCTCCACTCCATTTCAGCAACTTCACTTCTGGGGCCACAGGCTGAGACTTGATTATCTCCAGAATTTCTCCATGTCCAAAACTGAAATGGGATAGTTCCCTTGACCCCTTCGTGGGACTCATGAAGGGGTTGTCTTGTTTACTCATCCTGCAGCTCTCAACTCCTCATGGGAGGGAGAGCACATAGGTGAGTGGGTGCAGAGGGTGGGACAAGTGCTTCTGGGTGCTGGCAGGAGTAGAACTCTGTGCGGCCCCGCAGCAGCATCTAGGTGAGTATCTGTGACCCCTGGAGCCGCAGAGGGCATGTGTTACAGTGTGCTCTTTTAGCTTTGCTGTCCATGGACAGCTTAAGTGTTTTAACAGCTCAGTGTGACAGCCCTCTGTATCCTGAACTCTTGTTCAGCAACCAGGAAGGATCAGCTTGCACGAACAAATTGAAGATGGTGAATGTGGAGAACTTTATTGCTGATGAAAATGGCTCTCAGTGGGATGGGGAGCTGGAAAGGGGATGGAGTGGGAAGGTGTCTCCCCCTGGAGTTAGGCCATCCCCAGCTGAACTCTTCTCCGAGGTCCTACCGTCAAGCCATCCCTCTGAAGTCAAGCTGCTTTTCACCAGTGTCAAGCTTCTTCTCTTCTCTCCTTCTCTGCCATTCCACTGCCAGTGGATCCTGGGGTTTTTATGGGGACAGGATGGGGGGCAGGGCGGGCCAGGGTGATTTTGGAAAAGGCAACATTCAGGCAGCAAAATGGGGATATAAAGTTCTCACTTTGGGCCACGGGTCCAGGCTTGAGGGTGGAGCCATTGCCAGGGACCCCACCCTTTTCTACCTAGTATTTCCCTGCCTCCACTCTCCAACTCTCTTATCACAGGCCTCCTATCCATAAATCTTTCTCACTCCCTTATTTTTTTTAGAGCTCACCTTCAGACTTATGAAAGCTCAAGTCTTTTGAATTCCTCTTTCCCTCCCAGTCCAGCAGGCTTCACTTCTCTCCTTGCTAGCCTGGAAGTGTCCATTACACCCTTGACTGTGTCGCGGCTGACACATGGAAGGCAGGTGTCTGGTATTGTTAAATGAACGTTAACAAGTGCAACTTCTTTAAAAAGTAAGATTTCTTTATTTGATTGATCAGTTTTTTTTTTAATTAAGTATCTAATTTCCATTGCTTCTGGATTTAGGCACACATATTGAATATAAAATTCAAAACTTTTCATGTATCTAAAGAAATAATTTTAATGACCACAGAATTTTGCTCTTAAAACAAATGGAGCTTGCAATATAATTATAACTAAGACAGACTACAAGCACCTGCTGTGTTTTCTTCATGCTGCCATCAGGCTGGTGCATAGTCTGATGGGATGGATGCATCCCTGCTGTAATAGGAATAAGTAAAGAGGGTGGGAGACTGTTGTTGGTGTTTACAATCATTATTCATCTCTCCATTAATTTTCATCCTTGCAGTTGAGATAATCTTGCCTTTTAGAACGAGAAAACAATCTTATTACTTACAACATTCACAAGACAGGGAAACACTCCTCAACAAAGAACCATTTCCTTTGGGCATTTGATAAGAACTGCTGACATCTGTGTTTATTAAGTGATGTGGGAGAATCAGCCAAGGGGCAGAGGTGTGGGTGGTAGCTTCAAAGGTAATTTCCTGACTGAGTGTGGTTGGGCATGTTGGCAATCCCAGTGTTTGCAATTCCAGTGCTTTGGGAGGCTGAGGCAGGAGCATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGCTATGATTACGCCACTGCACTCCAGCCAGTGTGACAGAGAGAGACCTTGTCTCAAAAAAAAAAAAAAAAAGGATTTTGCTTTCCTGGTCTGTTTGAATGTGGTAAGCACAAGAACTTATTTGTACTGGTGGTCACCCACTTGGGTCCTTTCAGTAAACTTCTGGCCATGGCCCAGCCTGAGCACCTGCTTCCTTTACAGAGCAAAGCCAGAGCCTTCTGGTTTGTAATTTTTGCAGCCACATAACACTGATCCATTTTAGCTGTCTCATGAAACTGCTTTCCAAGATGAAGTGAGACTATCCGAAACCAAAATCTAAAAAGAATGACTACAGAACGAATGGCAGTCCAAGGTCATTTGGCAGGGTAGAATTATAAGGAAAGGTGATGGCCAGCTACTGTGAAGTCTTAAGCCCACTCATAGGTACGAATCTCTTACCAGGACTGAAGTTTGTGTTTCCTTAACTTTGCTGCTTGATGGTCTTCTGCAAAGGATCTCATTTCTCCAGCTTTCACTGGGAAGTGGCATGGGGTTTTCGAAAGTGCTTTAAACTCTAAGAACTGGTTTCCTCTCAGGCTTAGCCACCACTAGCTGTCTGACTTTGGACAAGTTACTCAACCACTCTGAGCATCAGCTTTCTTTTTTTAAAATGGTGACAGTGATATGGCTACCTTAGAGAGTTGTGGAGATTAAGTGAGATAATATATGAACAAAATATATAAATATGTCTATATTAGACATATATGATCTGTTAAATATATTTATATATATATATAGAAAGAATATTAGAGAACTGACATATTTATCTTAGACCTACTATGTTCTAGGGCCCAGTTCTGCTCATGTATTATCTCTCTATATATATAGTATTGAGAGAGAGAAAGAGAGAGAGAGCTAGAGAAATAGAAACCAGTAGGATATATCCTATCTGAAGAACTCTAATACAGGTATTTCACTGAACAAAATGGCTTCTCCTTAAAATGTATTCCAACACCAATTTCCCCTCCTTGCTTCTCATACATATTAATTCACAGAAATTATATTGGTCATAAGGCGGTAGGACTATGAATAATTTTTTTCTTCTGCATTTGCCAAATATTCTGTAATGCTAGTTTTATTTTTATAACAAATTTTTAAAGTCCCTGTAAACCCTATAAAATTAACTACTAATCCTAAACTTGAACTGTAATACATATTTTTGTTAAATAAAAAAAAAGATATCCTAAATTTGAGAATCTAAGCTAAATTCACAAAATGACTAAATGTATCTTCTTACTCTTAAACGATAAGAAACCAGGAATGCAGTGGTTTAACCCAAACAGCCTAGGTATTCTTCACTCATTTCTCTTGTCCTCAGTATATGTTTCCCCCAGGCCAAGAAACATTTATGGCTAGGAATTCATGACTGCTCATCTGTAAGACACTCTCCAAGTACTCTGTCATGATTTGGAACCAGAGCTTTGGCCTTCCATTCCAGATGACCTCCAGGTTCTAAGCTTTATCTGAAGTACTCCACACTACATTGCACACCAGCATGATGGGAAGGAATGACTCAAGGGAACTGGGCATTCAGACCACTCACCAACTACACACAGCCTTTCACACAGCAGTAGACAACCTTTGTAGGAAGACCTCTGGCCAAATATTTATATATCAGGAGTATATCAATGTATGGTCACAGTTACCTCCTTTTTAATCTCAAGAAATAAAGTCATTACTTCTGAAAAGAACACCAGTAATGGAACTACACGGGCATGCCAAGATGAAAATTAGTCTCTCTCTCTCTCTCCACCCCATTCTTTTGGCCACTGCATTTTAAACAGGCCATAGTGATAGAACCAGAAGGTAGCTGTGTTTCGATTATTTTTGTTTTCTTATTTTTAAACATTGCTTTATAGAAGCCTGTTCTATAATGTAAGAAGTGAATAGGAATCCTAGTATCTGGAATGATGCTGAGCCATGGAGATGGCCAGATTCCATGTGAAGAGAAGAGGCTGGCAGAAAGCTAAGTATTTGCTCGCTTTCCCTACCCTGTATTCATGGAGCAGCCATTACAAAAGATGACGCACCAGACCATGGGCCTGGTCTTGCTAGGTGGTGGAGATCCAAAATGCTGGGCACTCACTGGAGCTCCGTGAAGATCTGTTGAATGAGTGACTAAATGTGTGGTGAACTGTCCCTACCTACAGGGTTCCCTGCTTTGCCCAGCCTATCAGGCTTGGGTACAAGCAGATAGCCTGGATTGGATTTCATGAGGGCTTTGTGCCCACTCTGTATACTACCGGAAGATGCATAATCTCTTTAGACTTCCTGGGTCATCACTGAAAGGCCAGAGGCAAGAATTTGAGCAGTAAATTGAAGCATGTGCAGAGTGACATAGTCTGGGCATAGATAACAGTACCTGACCCCTCAAATTCCCTAAAGTTGACATGACAGCTTGTGCATCATGGTTTGGTACAGAGATGACTGAAGAGACAGTGGTTGCTCCTCTGGTTGCTGGACACCTTTTGAATGGGCTGTGATGACTGGAGAGCGTGCTCTGTCCTGGTCACCTGAAGGTGCTCCTAGACTAGCAGAAGCAGAGACAGCAGCCAGGCCTGACTGGAGAGCTGGAGGGACTGGGTGCAGGGGACTTCTAGGCCAGCAGTTTCTGTGCTGTGCTCGGAGGGGCTCTGGTGGCAGGAACCTAGTCCTGGGTTCCAGCTCTACCAGGGTGCAGCCTGAGGAACTCAGCTTTCCTATTTATTGGCTTGCCTTGCCACAAAGGATTTCTTGTGTGTTAAAGATACTAATAGCTTAAACAAACAAACAAACAAACAAACAAACTATTGATTTAAACCACTAATCAAATCTTTGGTTTTACAAATTTAGAAAATAAAATTAGGCCCCAGGGACTAAATGTCTCTCCTATGGTCCAGAAACCAGACTGAAACTGACCTAGTAGCAAAACCCATTCTCCTGTATCCCAACTCCCAGTTCAGGTTCCTCTTCATTAGCTCCCACCCAGCTGCATAGTTGAGGACACTGAATTGAGGGGACCTGGGGTAAAGGGCTGGCACTCAGGCATCGCTGGCTTCTACATGATTCCACCACATGGAAAGCATCATAATCATGTATGATCCCTAGAAAAGTGTTTGCTAAACTCCTTAAGTTGTCATTCAACAAACATTTATCTAGCACCTACCACATGCTAGGCAAATTCTAGAGACACAGCTGCCCCTGCCCTCATGGAACTAAATGTCTTGAAAGAGATACTGGCCCTGATCAGATTTTTTAAAAATACATAATTATGCAAATAAATCATATTATATATAATTACAAAGCATGGTATGAAAGGAAAAGTACAAGATGCTGTGAAAGCGTATAAAAGGAGGACTTGGCCAAGTCTAGAGGATCATCAGTGAGTGTTCCCTGATGGACTAACATTAGGGCCAAGATCAGAAAGATGTCCAGGAGTTAACATGGTCAATAATCACTGTTAATCTTTATTAAGCATTTCCCTTGAGTCGAGTCAGGCTTCACTTGCTGCATTAACTTCTTTAATCTCCACAATAACTCTGTAAGGTAGGTGCTTTTGCTTTTTTTCCACTTTACAGATGAATAAACAAGAAGTAAAAAGATGTAACTAATTCACATGTAGCCCTCTGGCTTCAGAAGCTCTTTACTCCATAAGGTTCCTGGGCACGTGGGTGTGGTCTAGGAATGGGAAGAGGCTAAGAATGCTGAAGGGCAGACTGAATGTTCCAGATGAAGCTGGCGTGATAAGAAAGGGCCACATCATGTGGGTCTTATAGGTTATGATATTCATGTTAAAACTGTTAATGTTTTTGAAATATCTAAAACCAGGAAGTGCATGATCATATTTATGTTTTAGAAAGATCACTCAGGCTGCTGTGTGGAGACTGGAGTAGAAAGAAGCATAGAAGAGACCTACAGAGACTAGGAAGCTGTCACAGTAACCTAGGCACAAGATAGTAGTGGTCAAGACTAGCTTGCTTGAGGAAGTGTAGAGAAGTAGACAGATAAAAGGAGCATCCAAGGAGTGTACACTTCTAAGTAATTTAAAAGAAAGAGTCAAATCCCTTAGAAGCAATCATTTGAAATAACCTAATTACCAATCCTTTTTATCCAGTCCTCTTATGTTGTCCCAATTCAGGAATTCTTAAACCAGTTCTTGTGTTAAAATCATAGCATGGACTGCCTTACAACATTCTATACTTCAGTCCATTGAAAACCACATCAGGCCAGGTGCGTGGCTCATGCCTATAAGCCCAGCACTTTTGGAGGCCAAGGCGAGAGGACTGCTTGAGCCCAGGAATTGGAGACCACTGAACTCTAGCCTGGGCAACAGAATGAGACCCTGTTGAAAGAGAGAAAAGGAAGAAAGAAAGAAAAAAGAGGAAGGAAGGAGGGAAAAAAGGAAAAAAGGGAGGGAGGGAAGGTGGAAGAAAGAAAAAAAAAGAAAGAGAAAGAAAAGGCTGCTTCCTGGCACTTCTATTACCATGTGACACGAGAAGGGCAATTGTCCAGACCCACACTTAGGTTCACCACAGTCCTTGGTTCCCAGGACAGAGTCCTTTGAGGTTCCTTCAAGCACCCACACCATGCTGGAAAATGCAGGCTTTATAAACTCCAGATGTCAGTCCACAACTCCACAGCCCCATTGGGTTTGGTTCCTGGATGAATTCTCGGCTAGATGACTGGAATAGAGTTCTGGTGAACATCTTCCTTCCTGCCAAGATGACAAGTCAGGTTTCTAAAGACAGATGTGTAGCTCTTTGTGGAAAAAATATTCTGGGCACGAACATCTTCGGCTGAACGGCATGGAATGGTGTGGAAAATGTGAAGCCCTGGACTGGTTTCTGTGTCAGTGGTTTCCTGGGACTGCCGAGTTGAAGGGGAGCAGAAAGGGCTCAGCTGTGGAGGAGGCAGAGATTAGCCAAACTAGACCAGCTATCGCCCCAGCTGCATGGATAGCATCTTCCTTCTTGTTCCTGATTAAGCTCATTTAATATGCCAATGACAAAAGGATCATGAAGGTCTTTCCAAATGAATGAATGTTTTCTGGAGCTGAGATTGCTGGCTCCTATTTGCATAGTAGTGCATACTGAGGCATCTGACCGGATTACTGGATTCCTAACTTTTACATTCTTTTTAAGCTCAGATATTTCTACGGAAGGCAGAAAGATAAAGGCCAAAAAAAGATCAGGCTTGCCTAGCTCTTGGGTTTCCAGGAAACTGACAGACTCCTGATATCTGCAACTAGTGCTTTCTCTCCCTGGGCGGGGCGTTCTCCGCCACCTTGTGGACATTTGGGGAACTGCACCGCCCCAGCATCTATGATCAGAGGAACTGACAGAGGCTGCCATAACTACCTGGTCCCCTGAAATAAAAACCAGGCACCAGGTTTGCCCAAAGGAGGACCAACACATAGCAGAATGAGGCTGAGTAGGATGTTAACCTTCCATGCTGGTCTTCCATTATCACGTTATCTGCCACTGTCACAGACAACATCTGCATCCGCTACAGATGGAGATGGAACAAAGGCTTTCACTGGATCTCAAGTTGGATGCTTCTGTAAAAGTAAAGTTCCAAGACCTTTTTCTTTTTTTTCCCCAGTGACAGCAAGAAAATTGGATGTTACTATTGGCAACAACTATTTCCTGCTTGTGAAGCGTTGGTATTTGCAGTGCTTCTGCCCTGTGGTTATTGAGCTGAAAGGGGGGCTGCTCTTGACATAGGAGCATGGCAGGATTGGATTCTTCATAACATGCTACCCAGCTTGTCTTATGTGAAAAGAGAAGCCCAGAAAGAGCTTGGGACACAAAGATGCAAATCCTGGGTTTGCATTTGATTTGTTAAGTGTCCTTTCACAACCAGCTTGCAGACTTTAGGGGAAAAAAAATACATGGTAGGCTTGTGGGTAGTGGAGAAAACATAAGCTCCAGTACCTCACAGCCTGGGTTTTCAGTCTGCCTCCTCCCAACCCTCATCACATACCAGCTGTGTGACCGTGGGTACTCTGTCTATGACAATCAATTTTCTTGTCTGCAGAGTACAGATAATAGAGGACCTGCCCCATGGGAAGCTTGGAGGACTAAATGAGATTAAGCCCAGGGCCTGGCTCATGGCCGATTCTCGTAACAGGTCCATGTGTGTAATCAACATGTGCTGAAGTTCTCTGGACCCTCTGTAAATATCTAATAGGAACGACTAGCCATGGGTGTGATGAGGGAGATGCTAGAAACAGTAATGGGGTCAAATGAATCTGTCCCATAGTCTCTAATTTGAAACAGCTGAACTGTGCCATTGTCTCCTTGGAGGTAAGATATAAGCCACAGAGTGCCTGAAGCAGGTCTACAGTTAAGGAACTTAAATGTGCTAAGTGATTAAAGGCTGGGCTGCCTACTCCCTGTATGGCGACACTCTCCACCCTCCTGCATACTCTCCACTACTCCAGGCAGTGGTGGGCCTCCTAGCCTCTGGGTGATGAGCAGCTCCCACATCTCCCCTTTGAGACAGAGGCCTGCAGAACCTGACCAGTGTGAGGGCTGGCTGGGGTCAGGAGTGTGCCTGCTGGTTGGCCCTCAAGGTGAATGTGGCTCTTCTAAAAGACACCTGAAGGGATGCAGAATTTAGCAGCAAACGCCAAGAACAGCTCTTTGTCATCTCTGCATCTTCTACTAAAGATTTTAAGCTCCGAAGTATATGTCTGGGGTTTCTAGAGATTGCTATTCCCTTATAAGGGAAAAAATACACCCTTATTGTATATTTATTGAGCACCTACAATGTGCCAGGCACCCCAGCTAGGGAGTTTAGATATTTAATCCTCTCAGCTGCCCTGTAAAATAGGGATTGTTTAAAATGGATTTCGCCCACCTTATAGGCAAGGAAACTGAACTACAGTATGGTAAAGTGGCTTGGCTAATCCACCTGGCTAGTGAGAATGGAGCCACAGTGAACCTGGAGGATACTCTTCACGGCGTTCCATCTTTGTGTGCCCCACAGCACAAGCACAATGCCCGGGTCTTAGGAAGAGCTTGGTAAATGACTGCTGAGTTGAGAATGGTAGGATTCATGTACCAAAAGGGCATTTGGAAATGGGCAAATGCCCAGATAGGGCTCTGAAAGACTAGCTATGTAGAGCAACAGATGGCAAATCATCAATTTAAAACTCTGTCATCCAGCCAGTAGCCCGCTGGCCTACAGCCAGCCATGTATGTACAAGGGCTGACTTGATCAGCTGTGGCTCTTTTATTTCAGGCAATCCACCTTCCAAAGAGGTGCCTGCTGGGAAGTACCCATTCATAGTCACTTCTGATGATGGGCGGAAGGTTCCTGTAGTCCAGGCCTATGCTTTTGGCAAATACCTAGGCTATCTGAAGATCGAGTTTGATGAAAGAGGAAACGTCATCTCTTCCCATGGAAATCCCATTCTTCTAAACAGCAGCATTCCTGAAGGTAAGTGAAGTTCAGGGGAATGTTCCACCAATCTAAAATTTAGATGGCTGGATATTTTGCTCCTTCCCATTTTTTTCCTTTAATGTTTCAGGAAAAGACTATAATACTGTTGAAGAATTTAGTTTCTTCCTTGAGTTTGCCCTCTTCATGGATAGATTTAAAACACACCCAAATGCCAAAAGCCCCACTTGCTTCTTCAAGTCTTCTCAGCATCAGATTCCATACATCACTGCTTCCTCTGCCTTTTAAAATCTTGATCCTGACATGCCAAAGCCACTCTCAGCTTGTGTTTACAGGAGAGATAACTGAACTAAAGGGGTTCTAATTGGGCAGAGCGGGGCTCAAGTCCTGGCCCCCCAACTAGAGGCAGTGTGCCTTAGGCAAGTTGCCCAATCTCATGGGCCTCAGTTTCTTTATCAAATGAGGGAGTACCTTATTTATATGTCTGAGTCTATTGCGGGATCTGGCCAGCAGCCCGCAATGCAATGGGGCTCTCTCTTTGTTCCTAGGCAGATTGGCAGGTTGAGAAATAATAGACACACACAAGATAGTGAAAGCTGGGTCCAGGGGGGTCACTGCCTTCTGGTCCTGCGGTGCCAACAATGCACTGGATATACCAGCATTTATTATTAAGTTTAGTGAGGGCAGGGGTACGTTAGTGAGGGATTTAGGGTCATTTGATTATGAGGTGAGATGGTCACATGGGGATGAAGTAATTCTTTAACATAACATTTGTATGTAGAAGTACAGTACATTTGTATGTAGAAGTACAGTATGAGATAAGAATTTACAATATAGTGTGTGCGTCAGTAATTTCTAACAGAGCCTTAGAACAGAAACACAGTCTTTCCATAACCTATGATTAGCAAGATATTAATCAGCAGTAACAATTGCAACAAAAACTGGTTACAAATAATCCATGGAAACAGGACATGAAGCTAGATAACCAGTTAGACCAGAAATTCTCAGAGGGGAGTACGCCTTAACCCTAAAGAGGCCTAGAAGAGCGGCGGCAAGATGAGCGTGTTTATAGCCCTATCTTATCCATATGGACAGGCCCCCCCCATGCGTCCGTTTATAGGCTCCCCACAAGGGTCACATTCCATTCCCAGAGCTATGAACATCTGCTTTTCTGGGATAGGAATCTTGGTGATGGGAAACCTCCCTGACTGCACGTCCATTTGTAGGCTCTCTGCAGGGGGAAGCACATCACGTGCTGTTGGCTCATTGTGGCAGTCCAACCTGGCATTGTCTTTACACAATCCTGCATGCAATTTTGTATTTACAATAATCAGGAGCATTTCATCTTTTATTCCGTAGCAATAGTTTCAGGGCGTCTCCCTACATGAGTCTCAGAGTAAAAATACATTTTTATATCATTGATTTTCATATGTGTACAGAACACACTCCTGTGCTTGTCTCTCACTTTCCCTTTTCTGTTGACTATGATCATGTCAGGAAGATGAGGTGCACAGCACCCAGGTGAGCCTGTAGTCACAACACAGCCCTCTCAGTAGCCAGATGGGAAAGGGGCCCAGGACCACACTGACAGCGATAGCCCAGCTGTACCTCAGCAGGCCTTTTATAACTGCCCCTGGGCCTTTCAGAGCTCCTACCGCCACCACTAATGCTGTCCCAGGTGGGCCAATGGGTAGCTCATACAGATGTGATGAGCTGGTAGATGTTCAGAATATTCTTAAATTAAGATGCATTCCAGGTCTTATTACCAGGAAACAAAATAGAAGTTCCTAAGGAAATTTCATGGTCAAAACCAAAATGCACACAAATATGGTAAACAAATATGTTCTCACAGCAAGTAAGATAGATGATGTTTCATTCCTTTTCCAGAATTTAGCCCAGTGTGAGATTTAATTGTAGGGTACCTTCTTTTCTTTCTTCTAGATCCAAGCATAAAAGCAGACATTAACAAATGGAGGATAAAATTGGATAATTATTCTACCCAGGAATTAGGGAAAACAATTGTCTATCTGGATGGCTCCTCTCAATCATGCCGCTTTAGAGAATGCAACATGGGCAACCTGATTTGTGATGCAATGGTAAGTCATCAGCAGGAGTGGACATATGCTAGGGAGGAAGGAAAGGAAGAGGGAAGAGGAAGGAAGGATGCGAGAAGGGATAGATCGATAGCTACAGAATGAGGGATTTCAAAACATTTTTAGCCAGGGTGGTGGCATGTGCCTATAGTCCCAGCTACTCGGGAGGCTTAGGTGGGAAGATGGCTTGAGCCCAGGAGGCTGCAGTGAGCTATAATTGCACCAGTGCACTCCAGCCTGGGCAAAAGAGCGAGACTCTGTCTCTAAAATTAAATAAATATGAAAAATAAATAAAACATTAGTGCCTAAACAAAAGCCTGATGTAGCTTCATACTCAGTACCTTCTTAAGGTGCTGGAAGGAGATCAGGTAACCACCAACATACTGCTTTACAAGAACTAAAACCTTTATTTTAAGGTGTTCTTAGATGTCTGAATTTTGGATGTTGCTTTCCTTTTGTAAGATGATGCAAATGCACAAACTCTGCTACCCTGGAGATATCAACATAATAGATAAAAGCATATCTGTTTGGCCAGACTGTTTTTCACTCATCTGTTCACTTGACTCCAGAGAACCCTGGCCTTGTGTGACAGGAACCTCTTTCACAGGCACAGAAAGACAACACACAGTTTTAATGGTAATAACAAGTCCTATGGCTGAGCAAGACCAGGTATGAAGAACAAGCCCGTCTACTTGTCACCAGGCGGAATGGCCATGGTAGCTCTCTGGGGGCCTTACTGAGCCAAGGTCTCCTATGTCGGACTACTACTTCCATGGGCTCACAGCCTGCACCCAGGGAAGTCATTTCTGTCAGTGCTTGGCATGCATTGCCCAGTGCCCAGGATACAACTGCACTCGATAAATGTTTGCCGTGTAAATGACAACAATCATGCTCATGCCAAGACCAGACTCATGATGTCTCCTCAGCATCATGCAGTCAATGCCAGAGAAGTAGTTAAGGAGAAGCTGGTATATAAATGTTAAGAGAAGTCTGGAGGGAAACAACCCAGGCTGTTGGCAGTGCTTATCCACTCTGTTAAAGAGGCTAGGACAAAGGAGAGCTTTTGCTTTTTATTTATTTATTTATTTAATTAATTAATTTATTTATTTATTGAGACTGAGTCTTGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTCACTGCAACCTCCGTCCCTTGGGTTCAAGCGATTCTCCTGCTTCAGCCTCCCAAGTAGCTGGGATTAGAGGTGTCCACTACCACACCCAGCTAATTTTTGTATCTTTAGTAGAGACGGGGTTTCACCATGTTGGCTAGACTGGTCTCGAACTCCTGACCTTAGGTGATCCACCTGCCACAGCCTCCCAAAGTGCTGGGATTTACAGGTGTGAGCCACTATGCCTGGCCTTTTTTTTTTTTTTTTTTCGGCTTTTTGTCTCCTAAATGAGAATATATTCATTTTATTTCTTATAACTAAACATATATTTTGTAAAATAAAAGTAAGAATGGATGTGATTCTCCCCAGCTTCAAAAGGCTGTCTCTGTCTTTCCAAAATTGCCAACTTGGGAATCAGCTGCAGACATAGACGTGGAGGCCAGGTTCTCTTTGGCATGAGGTCTGGTGTTGAGCAGGCTCTAGGGCCAAGCCCTCAGAATCAGGCAGAGGGCATGGCCTGCCCTGGAGAAGCCTGTGCAGGAGTGACTCTGCAGGCCACCTTGCATGGGAGGCCCAGTCCCGACACCAGGGCTACAACCGAGAGACCATTTTGCTAAGGCCACCTGGCCTGACAGTATGGGAGTTTTAGGAGGGGGAAATAAGAGTTTGACATGGACTGGTAACAGTATATTTTTACTTCTGGGAGCATAAAATTAGTTCTAATTATAGTTGAGAGATCCCTGGGAACACAGCAGCAGGTGAAAAGCAGCTTTATTTCCTCACTAGAGCTAACCAGATTCCTGGAGCTGATCCTAAGGAAGAAGAGCCAGAGTAACTAGTGTAAATCTGTGCTACTGTTGCAGATTAACAACAACCTGAGACACACGGATGAAATGTTCTGGAACCACGTATCCATGTGCATTTTAAATGGAGGTGGTATCCGGTCGCCCATTGATGAACGCAACAATGGTATGCTCCCAGGCCCAGCTCCTCAGTGTGTCATGTTCTCTCTCTGATCTCCTTTTCTGTTATGGTTCTTGCCCTGAACACACCCATGTGCAGCCTCAGTTCATCTCTGCTGCCAGCCATGTACCAGAATGTCAGTCCTTTAAATTAGGGTTAGCCATTATTAAAGTCTAAAACCTAGCCTGAAGGACACACACAAGCTTGTGTGTTCTTATATGTATTCACACACAGAAGCTGCAGGTAAGGTTAGTGGAACTCAAACTTGGTCTGAATTTCTGACTTACAAAGCTATACTAGTTGTTTCTGATTTATGCAAAATAACAACAGTCACCACCTTGGCATCTGAAAAGAGACAAAATCACCAATCTTCTGTCCTGAAAAAGACATACCACTGGATTAAAATGTTACCTTAGTATATTTACAGATATCCAAGATTATATCATATGGCAAAACAAATCAACTACACAAATACTCAAGACACTCTTGTAGCCCTCCCTGATTTACTGTGAAAACCAATCAGTATCAGTATAAGGCCCCAAACGCATCCCATTGTCAGACAACAGGGACAGGTTGCAGGGGCACATTGTTTGTCTGGAGGAACGGAACAATGCAAAACAAACTACTGGAGATCCAGCCCCAAGCTAGCAGATCTAAGACTGAGCATGGTGAACTTCTGAGGCACAGCCATTTGTGAGCTCCCGCCATCTTGCCCAGTGGTGGAGTGCAGGGCCAGAGGCCTCCTAAACTCATTCCCTTCCTCAGTGTCAGGAACCACTTAGACATAGCTAATGATGCTCTATAAGCTTCCCATGTCCCCCTCATTTCTTCCCCCAGCGCTGAGGGAAACTGGTCATGGTGTAAGCATTTTCTCAAGCTATTTTCCTTCTTGCCTCATCTGTGACTACCCTCAGGCACAATTACCTGGGAGAACCTGGCTGCTGTATTGCCCTTTGGAGGCACATTTGACCTAGTCCAGTTAAAAGGTTCCACCCTGAAGAAGGCCTTTGAGCATAGCGTGCACCGCTACGGCCAGTCCACTGGAGAGTTCCTGCAGGTGGGCGGTAAGTCACCCATCCTGTAGGGCTGGCCCATCCAAAGTGACATGGCATTTCCTGCTGGTTGGCTCAGCTTCCCCTTCACCAAAATTCCTGTGGTCAAACTGGTTTGGATTTTTCCCGACCCAACACCAATACCTTACCCTTTAATGGCTGTGGACTCTCAGAGCCACTAAGATTAGGTTGGGGTCAAAGCCCCAAAGCCCCAAAGCCCTGGCAATAAGCAGTATTTGCCAAGTCTGATTTGGACATCAGATGGGCCCTCTAAGCAGGTCACCTGCTTTGAGGTCTAGTTTCTAATAAAATCTTATTTAAGCATTCAATTATTTTTTTTTTAAATCCTCTCCTCTGTTCTACTCATCGTTGCCTGGAACCATGCCAAGATTTAAAGGAATGCTGTCCAATCTGTATTAACCAGGATGATTCCTGGAAGGAGCAGCCTACTGCACAGACATACCTGAACACCTGGTTCTAGTCCCACTGTGACCTGGGGCAAGTTCTCAACCCCTCTGGGCACAGGGAGAAAACCTTTCCTGTTTATCTCATGGACTGCAGTGAAAGTTGAATGGAAATAAATGCTTCCTA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**Note:**

**1.circNT5E sequence region (Exon3-Exon9) with gray background.**

**2.10 kb intron upstream of NT5E Exon3 have one Alu sequence with red backgroup.**

**3.10 kb intron upstream of NT5E Exon9 have two Alu sequence with green and yellow backgroup.**

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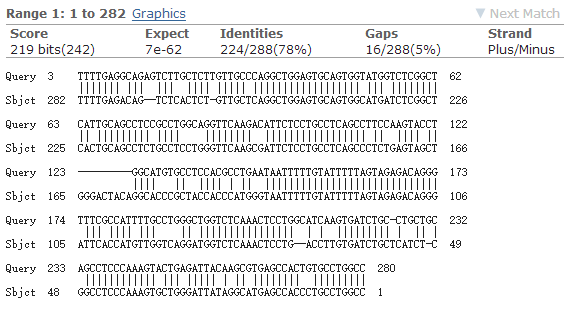
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AATTAATTAAAGAAAAATAAA

Alusq Matches Alusg:



Alusq Matches AluJb:

