

Figure S1. Expression profiles of GSDME in tumor and normal tissues from TCGA using GEPIA online tool. GEPIA, Gene Expression Profiling Interactive Analysis; TCGA, The Cancer Genome Atlas; GSDME, gasdermin E; N, normal; T, tumor.

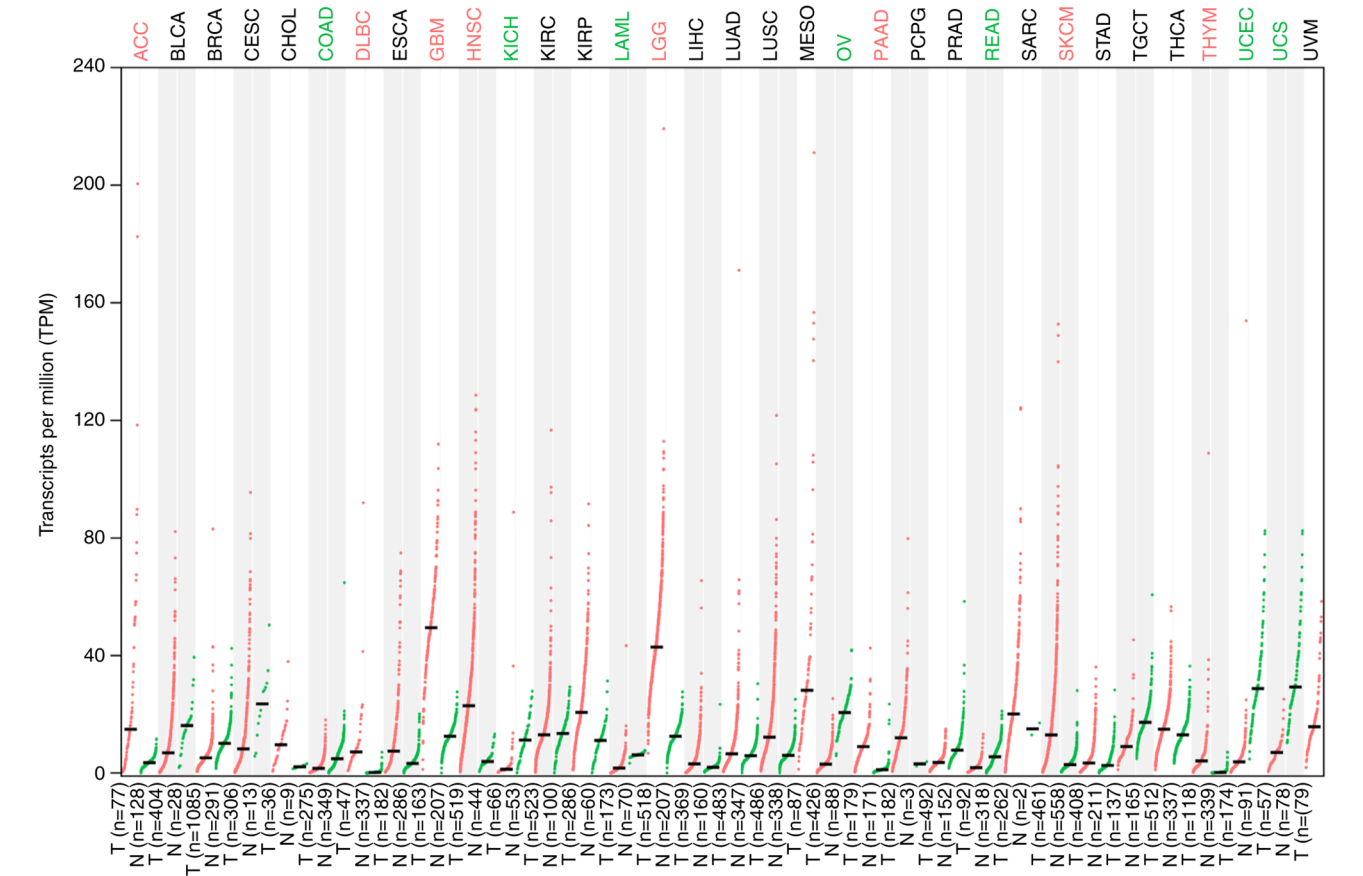


Table SI. Sequences of primers and transfection sequences used.

| Gene                | Primer sequences (5'-3')                                                             |
|---------------------|--------------------------------------------------------------------------------------|
| GSMDE               | F: CCCAGGATGGACCATTAAGTGT<br>R: GGTTCAGGACCATGAGTAGTT                                |
| Caspase-3           | F: GGAAGCGAATCAATGGACTCTGG<br>R: GCATCGACATCTGTACCAGACC                              |
| Caspase-9           | F: GTTTGAGGACCTTCGACCAGCT<br>R: CAACGTACCAGGAGCCACTCTT                               |
| Bcl-2               | F: ATCGCCCTGTGGATGACTGAGT<br>R: GCCAGGAGAAAATCAAACAGAGGC                             |
| Bcl-xl              | F: GCCACTTACCTGAATGACCACC<br>R: AACCAGCGGTTGAAGCGTTCCT                               |
| Bax                 | F: TCAGGATGCGTCCACCAAGAAG<br>R: TGTGTCCACGGCGGCAATCATC                               |
| NEAT1               | F: TGGCTAGCTCAGGGCTTCAG<br>R: TCTCCTTGCCAAGCTTCCTTC                                  |
| PVT1                | F: GGGGAATAACGCTGGTGGAA<br>R: CCCATGGACATCCAAGCTGT                                   |
| OIP5-AS1            | F: TGCGAAGATGGCGGAGTAAG<br>R: TAGTTCCTCTCCTCTGGCCG                                   |
| MALAT1              | F: ATGCGAGTTGTTCTCCGTCT<br>R: TATCTGCGGTTTCCTCAAGC                                   |
| SNHG1               | F: ACGTTGGAACCGAAGAGAGC<br>R: GCAGCTGAATTCCCCAGGAT                                   |
| GAPDH               | F: TGCACCACCAACTGCTTAGC<br>R: GGCATGGACTGTGGTCATGAG                                  |
| Hsa-miR-370         | F: CAGGTCACGTCTCTGCAGTT<br>R: GCGAGCACAGAATTAATACGAC                                 |
| Hsa-miR-375         | F: GCGACGAGCCCCTCGCACAAA<br>R: GCGAGCACAGAATTAATACGAC                                |
| Hsa-miR-376         | F: GTAGATTCTCCTTCTATGAG<br>R: GCGAGCACAGAATTAATACGAC                                 |
| Hsa-miR-379         | F: TATGTAACATGGTCCACTAA<br>R: GCGAGCACAGAATTAATACGAC                                 |
| Hsa-miR-448         | F: TTGCATATGTAGGATGTCCC<br>R: GCGAGCACAGAATTAATACGAC                                 |
| Hsa-miR-452         | F: AACTGTTTGCAGAGGAACT<br>R: GCGAGCACAGAATTAATACGAC                                  |
| U6                  | F: CTCGCTTCGGCAGCACA<br>R: AACGCTTCACGAATTTGCGT                                      |
| pre-miR-370 cloning | F: TAGAAGCTTAGGTGTGCAAGGCGGGCTACT<br>R: TATCTCGAGAACCCTCCATCCCACCTCTGA               |
| pre-miR-375 cloning | F: TAGAAGCTTGCCGCAGATGCGTTCAGGTGA<br>R: TATCTCGAGCTCTCCCACCCGTACGGTTGA               |
| pre-miR-376 cloning | F: TAGAAGCTTAAGCTCGTCTGCCTCATGTGA<br>R: TATCTCGAGTCTGTGTCTGTCCGTCCTGTA               |
| pre-miR-379 cloning | F: TAGAAGCTTCTCAGAAAGCTTTCTGGAAGT<br>R: TATCTCGAGACATCAACCATGAGCCACAGA               |
| pre-miR-448 cloning | F: TAGAAGCTTCATTTACACAGAGAAGCATCA<br>R: TAGCTCGAGTCTAGTGATGCAGCTCTAGCA               |
| pre-miR-452 cloning | F: TAGAAGCTTGGTGGTAGGGATGATTGGAGA<br>R: TAGCTCGAGAGGTCAGAGTTGTAACCTCGA               |
| GSDME 3'UTR         | F: GCTCTAGATGTCATATGTGAAGTACGT<br>R: GGAATTCCATATGAGTTCAAAGTTTCTTTAATAGAAT           |
| GSDME 3'UTR Mut1    | F: GAACTGTAAAGGTCCGCAATGCGTTAAAGTTGACC<br>R: GGTCAACTTTTAAACGCATTGCGGACCTTTAACAGTTCT |

Table SI. Continued.

| Gene                 | Primer sequences (5'-3')                                                       |
|----------------------|--------------------------------------------------------------------------------|
| GSDME 3'UTR Mut2     | F: TGGGACCCTAGCTCTATGTCTTTTATGTGACCTT<br>R: AAGGTCACATAAAAGACATAGAGCTAGGGTCCCA |
| siNEAT1-1            | S: UUAAGAUUGAGAUUUACCCAG<br>AS: GGGUAAAUCUCAUCUUAATT                           |
| siNEAT1-2            | S: GGAAAGUUUCUAAGCAACUUCUCACUU<br>AS: GUGAGAAGUUGCUUAGAAACUUUCC                |
| siGSDME              | S: GCGGUCCUAUUUGAUGAUGAA<br>AS: UUCAUCAUCAAAUAGGACCGC                          |
| miR-375 mimics       | S: UUUGUUCGUUCGGCUCGCGUGA<br>AS: ACGCGAGCCGAACGAACAAAUU                        |
| miR-379 mimics       | S: UAUGUAACAUGGUCCACUAACU<br>AS: UUAGUGGACCAUGUUACAUAAU                        |
| miR-448 mimics       | S: UUGCAUAUGUAGGAUGUCCCAU<br>AS: GGGACAUCCUACAUAUGCAAUU                        |
| Control miRNA mimics | S: GGUCCUAUUUGAUGAUGAATT<br>AS: UUCAUCAUCAAAUAGGACCGC                          |
| Control siRNA        | S: GGUCCUAUUUGAUGAUGAATT<br>AS: UUCAUCAUCAAAUAGGACCGC                          |

The underlined sequences correspond to the restriction enzyme sequence. F, forward; R, reverse; S, sense; AS, anti-sense; Mut, mutant; UTR, untranslated region; MALAT1, metastasis-associated lung adenocarcinoma transcript 1; NEAT1, nuclear paraspeckle assembly transcript 1; OIP5-AS1, OIP5 antisense RNA 1; PVT1, Pvt1 oncogene; SNHG1, small nucleolar RNA Host Gene 1; GSDME, gasdermin E; miRNA/miR, microRNA; si, small interfering.