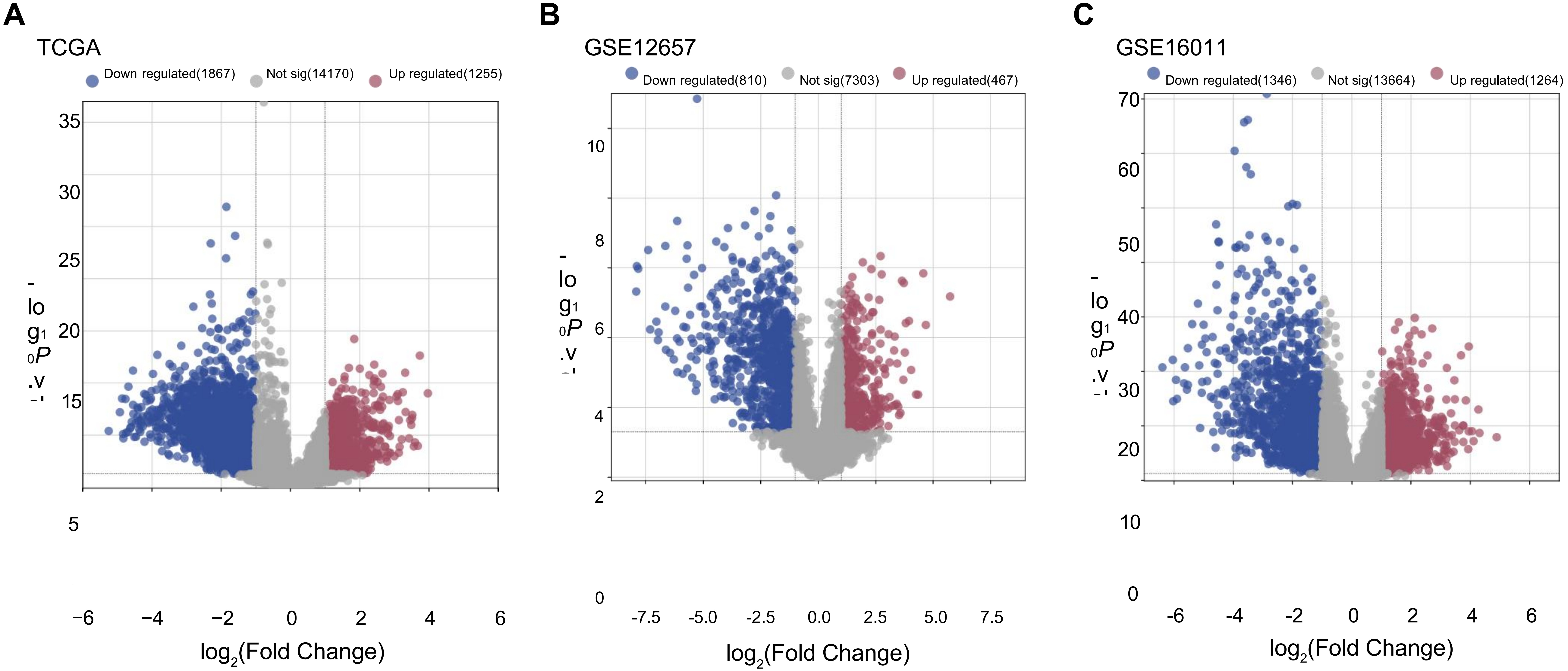
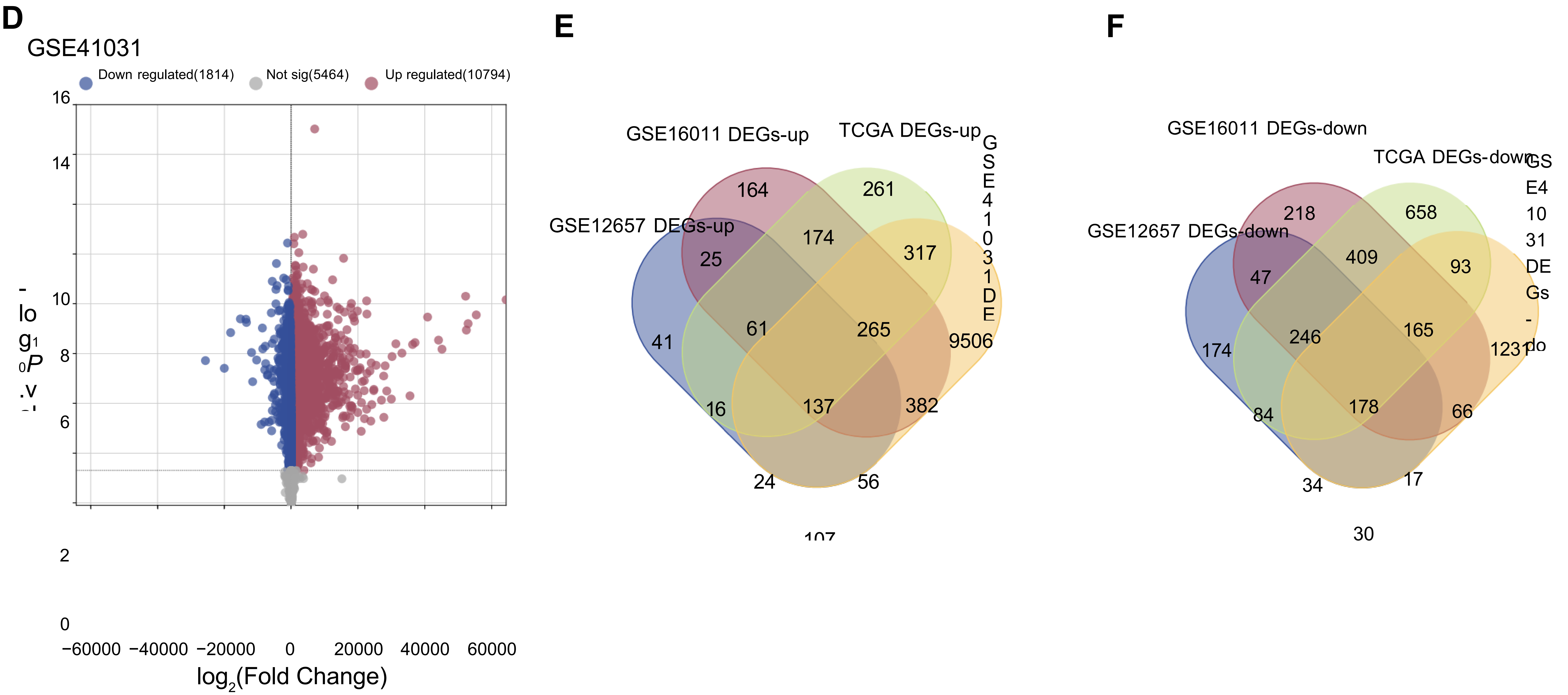

A
TCGA
Down regulated(1867)
Not sig(14170)
Up regulated(1255)
35
30
25
20
15
5
-log10P.val
−6
−4
−2
0
2
4
6
log2(Fold Change)
B
GSE12657
Down regulated(810)
Not sig(7303)
Up regulated(467)
10
8
6
4
2
0
-log10P.val
-7.5
-5.0
-2.5
0.0
2.5
5.0
7.5
log2(Fold Change)
C
GSE16011
Down regulated(1346)
Not sig(13664)
Up regulated(1264)
70
60
50
40
30
20
10
0
-log10P.val
-6
-4
-2
0
2
4
6
log2(Fold Change)



Supplementary Figure S1. Identification of differentially expressed genes (DEGs) in glioma samples. **A–D** – DEG screening of The Cancer Genome Atlas (TCGA)-glioma dataset (**A**), GSE12657 dataset (**B**), GSE16011 dataset (**C**), and GSE41031 dataset (**D**). Red represents up-regulated DEGs, and purple represents down-regulated DEGs. **E, F** – Cross-analysis was performed on the up-regulated DEGs and down-regulated DEGs of the TCGA-glioma data set, GSE12657 data set, GSE16011 data set, and GSE41031 data set, respectively