**Supplementary Materials**

**Supplementary Table S1. Software versions and database URLs used in this study**

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| --- | --- | --- |
| **Software/Database** | **Version** | **URL** |
| R | 4.5.2 | [**https://www.r-project.org/**](https://www.r-project.org/) |
| Bioconductor | 3.22 | [**https://www.bioconductor.org/**](https://www.bioconductor.org/) |
| sva | 3.56.0 | [**https://bioconductor.org/packages/sva**](https://bioconductor.org/packages/sva) |
| mice | 3.19.0 | [**https://cran.r-project.org/package=mice**](https://cran.r-project.org/package=mice) |
| glmnet | 4.1-10 | [**https://cran.r-project.org/package=glmnet**](https://cran.r-project.org/package=glmnet) |
| pROC | 1.18.5 | [**https://cran.r-project.org/package=pROC**](https://cran.r-project.org/package=pROC) |
| survival | 3.8-3 | [**https://cran.r-project.org/package=survival**](https://cran.r-project.org/package=survival) |
| survminer | 0.5.1 | [**https://cran.r-project.org/package=survminer**](https://cran.r-project.org/package=survminer) |
| rms | 8.1-0 | [**https://cran.r-project.org/package=rms**](https://cran.r-project.org/package=rms) |
| ggplot2 | 4.0.1 | [**https://cran.r-project.org/package=ggplot2**](https://cran.r-project.org/package=ggplot2) |
| Seurat | 5.4.0 | [**https://cran.r-project.org/package=Seurat**](https://cran.r-project.org/package=Seurat) |
| TCGA (UCSC Xena) | v36.0 | [**https://xena.ucsc.edu**](https://xena.ucsc.edu/) |
| GEO | – | [**https://www.ncbi.nlm.nih.gov/geo/**](https://www.ncbi.nlm.nih.gov/geo/) |
| GTEx Portal | – | [**https://gtexportal.org**](https://gtexportal.org/) |
| HCCDB | – | [**http://lifeome.net/database/hccdb/**](http://lifeome.net/database/hccdb/) |
| BEST | – | [**https://rookieutopia.com/BEST/**](https://rookieutopia.com/BEST/) |
| TNMplot | – | [**https://tnmplot.com**](https://tnmplot.com/) |
| KM Plotter | – | [**https://kmplot.com**](https://kmplot.com/) |
| IHGA | – | [**https://ihga.cancer-pku.cn/**](https://ihga.cancer-pku.cn/) |
| DepMap | – | [**https://depmap.org/portal/**](https://depmap.org/portal/) |
| GENI | – | [**https://geni.heilbrunn-lab.org/**](https://geni.heilbrunn-lab.org/) |
| CellTracer | – | [**http://www.regenmedlab.org/celltracer/**](http://www.regenmedlab.org/celltracer/) |
| GDSC | – | [**https://www.cancerrxgene.org/**](https://www.cancerrxgene.org/) |
| CTRP | – | [**https://portals.broadinstitute.org/ctrp/**](https://portals.broadinstitute.org/ctrp/) |
| PRISM | – | [**https://depmap.org/portal/prism/**](https://depmap.org/portal/prism/) |
| TCGAplot | 4.0.0 | [**https://github.com/tjhwangxiong/TCGAplot**](https://github.com/tjhwangxiong/TCGAplot) |
| Hiplot Pro | – | [**https://hiplot.com.cn**](https://hiplot.com.cn/) |

一張含有 文字, 螢幕擷取畫面, 字型, 數字 的圖片

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**Supplementary Figure S1. Pathway enrichment analysis of differentially expressed genes.**  
To identify biological processes associated with the altered gene signature, we performed an enrichment analysis using the Enrichr web platform. The list of differentially expressed genes was inputted into Enrichr, and the BioPlanet 2019 database was selected to query for significantly enriched pathways. The bar chart ranks the top 10 enriched pathways based on the negative logarithm of their *p*-values, with longer bars indicating higher statistical significance. "One-carbon metabolism" and "Cysteine and methionine metabolism" were identified as the most significant metabolic alterations.