

| Acronym | Full name |
|--|--|
| TCGA | The Cancer Genome Atlas |
| GEO | Gene Expression Omnibus |
| LUAD | lung adenocarcinoma |
| SKCM | skin cutaneous melanoma |
| HNSC | head and neck squamous cell carcinoma |
| TME | tumor microenvironment |
| RMA | robust multi-array average |
| SD | stable disease |
| RNA-seq | RNA-sequencing |
| RECIST | Response Evaluation Criteria in Solid Tumors |
| TMB | Tumor mutation burden |
| CNA | Copy number alteration |
| NMF | Non-negative matrix factorization |
| MTL | Multitask learning |
| DGE | different gene expression analysis |
| GSEA | Gene set enrichment analysis |
| ssGSEA | Single-sample gene set enrichment analysis |
| CRLCN | Cells-receptors-ligands communication networks |
| MOCDE | Molecular Complex Detection |
| ESTIMATE Estimation of STromal and Immune cells in MAlignant Tumours using Expression data | |
| PSM | propensity score matching |
| ORA | over-representation analysis |
| GO | Gene Ontology |
| ROC | receiver operating characteristic |
| FDR | false discovery rate |
| LDF | low dimensional features |
| CNACB | CNA count burden |

Supplementary table9 Table of acronyms.