

## Extrachromosomal DNA is associated with decreased immune cell infiltration and antigen presentation, represents a potential cancer immune evasion mechanism

Tao Wu, Chenxu Wu, Xiangyu Zhao, Guangshuai Wang, Wei Ning, Ziyu Tao, Fuxiang Chen, Xue-Song Liu

**Supplementary Table 1: List of datasets and software used in this study**

data/software	resource
TCGA somatic mutation	<a href="https://gdc-hub.s3.us-east-1.amazonaws.com/download/GDC-PANCAN.mutect2_snv.tsv.gz">https://gdc-hub.s3.us-east-1.amazonaws.com/download/GDC-PANCAN.mutect2_snv.tsv.gz</a>
TCGA mRNA expression	<a href="https://toil-xena-hub.s3.us-east-1.amazonaws.com/download/tcga_RSEM_gene_tpm.gz">https://toil-xena-hub.s3.us-east-1.amazonaws.com/download/tcga_RSEM_gene_tpm.gz</a>
TCGA ecDNA information	Kim H, Nguyen N P, Turner K, et al. Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers[J]. Nature genetics, 2020, 52(9): 891-897.
ESTIMATE	R estimate package: <a href="https://bioinformatics.mdanderson.org/estimate/rpackage.html">https://bioinformatics.mdanderson.org/estimate/rpackage.html</a>
Immune cell infiltration estimation	TIMER webserver: <a href="http://timer.comp-genomics.org/">http://timer.comp-genomics.org/</a> , including the results calculated by TIMER, CIBERSORT, quanTIseq, xCell, and MCP-counter algorithms
Leukocyte fraction	Thorsson V, Gibbs D L, Brown S D, et al. The immune landscape of cancer[J]. Immunity, 2018, 48(4): 812-830. e14. ( <a href="https://gdc.cancer.gov/about-data/publications/panimmune">https://gdc.cancer.gov/about-data/publications/panimmune</a> )
Immunophenoscore (IPS)	Charoentong P, Finotello F, Angelova M, et al. Pan-cancer immunogenomic analyses reveal genotype-immunophenotype relationships and predictors of response to checkpoint blockade[J]. Cell reports, 2017, 18(1): 248-262.
Tumor inflammation signature (TIS)	Danaher P, Warren S, Lu R, et al. Pan-cancer adaptive immune resistance as defined by the Tumor Inflammation Signature (TIS): results from The Cancer Genome Atlas (TCGA)[J]. Journal for immunotherapy of cancer, 2018, 6(1): 1-17. Use GSVA to calculate TIS.
Cytolytic activity score (CYT)	Geometric mean of expression of GZMA and PRF1 genes
TCGA samples immune subtype	1.Thorsson V, Gibbs D L, Brown S D, et al. The immune landscape of cancer[J]. Immunity, 2018, 48(4): 812-830. e14. ( <a href="https://gdc.cancer.gov/about-data/publications/panimmune">https://gdc.cancer.gov/about-data/publications/panimmune</a> ) 2.Bagaev A, Kotlov N, Nomie K, et al. Conserved pan-cancer microenvironment subtypes predict response to immunotherapy[J]. Cancer Cell, 2021, 39(6): 845-865. e7.
maf2vcf	<a href="https://github.com/mskcc/vcf2maf/blob/main/maf2vcf.pl">https://github.com/mskcc/vcf2maf/blob/main/maf2vcf.pl</a>
neoantigen prediction software: NeoPredPipe	<a href="https://github.com/MathOnco/NeoPredPipe">https://github.com/MathOnco/NeoPredPipe</a>