Additional file. Information regarding the software, tools, and databases used in the methodology.

Software, tools, and databases	Web page	Version	Reference
NSCLC-Radiogenomics collection	https://wiki.cancerimagingarchive.net/display/Public/NSCLC+Radiogenomics		[1]
gcrma human dataset			[2]
Slice-O-Matic	https://www.tomovision.com/products/sliceomatic.html	v.5.0	
Cutoff Finder		v1.0	[3]
rpart	https://cran.r-project.org/web/packages/rpart/index.html	v4.1	
RStudio	https://www.rstudio.com/	v.4.1.0	
R	https://cran.r-project.org/	v3.5.1	
easyROC	http://www.biosoft.hacettepe.edu.tr/easyROC/	v. 1.3.1	[4]
Human Protein Atlas	http://www.proteinatlas.org	v18.1	[5]
Cytoscape	https://cytoscape.org/	v3.7.2	[6]
CytoNCA	https://apps.cytoscape.org/apps/cytonca	v2.1.6	[7]
GTEx portal	https://www.gtexportal.org/	V8	[8]
cellxgene Data Portal	https://cellxgene.cziscience.com	v0.16.0	
The Cancer Imaging Archive	http://cancerimagingarchive.net		[9]
BioGPS	http://biogps.org/		[10]
SankeyMATIC	http://sankeymatic.com/		
Cancer Cell Line Encyclopedia portal	https://portals.broadinstitute.org/ccle		[11]
TCGA-110CL Cell Line Panel	https://comphealth.ucsf.edu/app/tcga-110		[12]
Human Cancer Model Initiative catalog	https://ocg.cancer.gov/programs/hcmi/		
CIBERSORTx	https://cibersortx.stanford.edu/		[13]
Immune Cell Abundance Identifier	http://bioinfo.life.hust.edu.cn/ImmuCellAI#!/		[14]
CellPhoneDB	https://www.cellphonedb.org/		[15]
EnrichR	https://maayanlab.cloud/Enrichr/		[16,17]
Biojupies	https://amp.pharm.mssm.edu/biojupies/		[18]
ClustVis	https://biit.cs.ut.ee/clustvis/		[19]

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