UCEC

Clinical stage: combination of TNM results for each patient, based on patient history, physical examination, and any imaging done before initiation of treatment.

Stage 0 - cancer *in situ,*

Stage I -early-stage cancer; a small tumor without spreading to the lymph nodes or other parts of the body.

Stage II and III - larger cancers or tumors with possible spreading to lymph nodes but not to other parts of the body.

Stage IV - advanced or metastatic cancer.

Histology_type - Histologic subtype of Uterine Corpus Endometrial Carcinoma submitted for TCGA

msi_status_7-marker_call - MSI (microsatellite instability) in cancer genome:

MSI-H – MSI-high,

MSI-L – MSI-low,

MSS – MS-stable.

tumor_grade – classification of the microscopic cell appearance abnormality and deviations in their rate of growth with the goal of predicting developments at tissue level.

GX: Grade cannot be assessed (undetermined grade).

G1: Well differentiated (low grade).

G2: Moderately differentiated (intermediate grade).

G3: Poorly differentiated (high grade).

G4: Undifferentiated (high grade).

X_PANCAN_DNAMethyl_UCEC

Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays revealed four unique subtypes (based on PMID: 23636398).

Cluster 1 - heavily methylated subtype reminiscent of the CpG island methylator phenotype(CIMP) described in colon cancers and glioblastomas, associated with the MSI subtype and attributable to promoter hypermethylation of MLH1.

Cluster 3 – a serous-like cluster with minimal DNA methylation changes, composed primarily of serous tumours and some endometrioid tumours .

X_PANCAN_DNAMethyl_PANCAN

Genome-wide DNA methylation pattern within different UCEC samples submitted for TCGA.

THCA

histological_type - Histologic subtype of Thyroid Cancer submitted for TCGA.

meth_Cluster – Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays revealed four unique subtypes (based on PMID: 25417114):

CpG island methylated – hypermethylation of a large number of CpG sites in islands and shores,

Follicular – few methylation changes compared to normal thyroid.

mRNA_Cluster_number – Different THCA subtypes based on mRNA expression profiling (based on PMID: 25417114).

pathologic_M – Characterization of the distant metastasis.

MX: Metastasis cannot be measured.

M0: Cancer has not spread to other parts of the body.

M1: Cancer has spread to other parts of the body.

pathologic_T – characterization of the size and extent of the main tumor.

TX: Main tumor cannot be measured.

T0: Main tumor cannot be found.

T1, T2, T3, T4: Refers to the size and/or extent of the main tumor. The higher the number after the T, the larger the tumor or the more it has grown into nearby tissues. T's may be further divided to provide more detail, such as T3a and T3b.

pathologic_N – characterization of the regional lymph nodes**.**

NX: Cancer in nearby lymph nodes cannot be measured.

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N1, N2, N3: Refers to the number and location of lymph nodes that contain cancer. The higher the number after the N, the more lymph nodes that contain cancer.

pathologic_stage – combination of TNM results for each patient.

Stage 0 - cancer *in situ.*

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Stage IV - advanced or metastatic cancer.

PRAD

histological_type – histologic subtypes of Prostate Adenocarcinoma submitted for TCGA.

clinical_M – characterization of the distant metastasis.

MX: Metastasis cannot be measured.

M0: Cancer has not spread to other parts of the body.

M1: Cancer has spread to other parts of the body.

methylation_cluster – Unsupervised hierarchical clustering of the most variably hypermethylated

CpGs identified four epigenetically distinct groups of prostate cancers (based on PMID: 26544944).

mRNA_cluster – different PRAD subtypes based on mRNA expression profiling (based on PMID: 26544944).

mRNA_subtype – Molecular subtypes of prostate cancer based on known and novel genetic drivers of the disease; four are characterized by gene fusions ,three are defined by gene mutations (based on PMID: 26544944).

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LUSC

expression_subtypes_LUSC – Whole-transcriptome expression profiles generated by RNA sequencing and by microarrays (based on PMID: 22960745).

histological_type – histologic subtypes of tumors submitted for TCGA.

PANCAN_Cluster_Cluster_PANCAN – Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays.

PANCAN_DNAMethyl_PANCAN – Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays .

PANCAN_UNC_RNAseq_PANCAN_K16 – Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays.

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Smoking_history

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5 –Current Reformed Smoker, Duration Not Specified

LUAD

expression_subtypes_LUAD – lung adenocarcinoma subtypes based on mRNA expression (based on PMID: 25079552).

histological_type – histologic subtypes of tumors submitted for TCGA.

PANCAN_Cluster_Cluster_PANCAN – Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays.

PANCAN_DNAMethyl_PANCAN – Unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays.

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LIHC

HBV-consensus -clinical or molecular evidence of HBV infection.

HCV_consensus - serological and/or molecular markers of HCV infection.

Histological_type - histologic subtypes of tumors submitted for TCGA.

Hypermethylation.Cluster.Laird.group – unsupervised clustering of HCC using CpG sites showing cancer-specific DNA hypermethylation (based on PMID: 28622513).

Hypermethylation.Cluster.Laird.group.1

Hypomethylation.Cluster.Laird.group – unsupervised clustering of HCC using CpG sites showing cancer-specific DNA hypomethylation (based on PMID: 28622513).

Hypomethylation.Cluster.Laird.group.1

mRNA.clusters.5.group.NMF.Hoadley.group – liver hepatocellular carcinoma subtypes based on mRNA expression.

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KIRP

DNA_methylation_subtype – molecular subtyping by means of a DNA methylation platform revealed three subtypes of papillary renal-cell carcinoma (PRCC), one of which showed widespread DNA hypermethylation patterns characteristic of CIMP-associated tumors (the other subtypes are identified as cluster 1 and cluster 2) (based on PMID: 26536169).

histological_subtype – histologic subtypes of tumors submitted for TCGA.

mRNA_subtype– Kidney Renal Papillary Cell Carcinoma subtypes based on mRNA expression (based on PMID: 26536169).

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KIRC

mRNA_cluster – Unsupervised clustering methods identified four stable subsets in mRNA expression data sets (based on PMID: 23792563).

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tumor_grade – classification of the microscopic cell appearance abnormality and deviations in their rate of growth with the goal of predicting developments at tissue level.

GX: Grade cannot be assessed (undetermined grade)

G1: Well differentiated (low grade)

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G4: Undifferentiated (high grade)

KICH

histological_type_eosinophilic.1_classic.0 – histologic subtypes of chromophobe renal cell carcinoma samples submitted for TCGA. 1 – eosinophilic, 0 – classic.

pathologic_N – characterization of the regional lymph nodes**.**

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HNSC

clinical_N – characterization of the regional lymph nodes**.**

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clinical_stage – combination of TNM results for each patient.

Stage 0 - cancer *in situ.*

Stage I -early-stage cancer; a small tumor without spreading to the lymph nodes or other parts of the body.

Stage II and III - larger cancers or tumors with possible spreading to lymph nodes but not to other parts of the body.

Stage IV - advanced or metastatic cancer.

histlogical_type – histologic subtypes of Head and Neck Squamous Cell Carcinoma samples submitted for TCGA.

Hpv.status.ish – HPV testing based on HPV16 in situ hybridization (ISH).

Hpv.status.p16 – HPV testing based on p16 immunohistochemistry.

histological_type – histologic subtypes of Head and Neck Squamous Cell Carcinoma samples submitted for TCGA.

Methylation_subype – unsupervised clustering of DNA methylation data generated from Illumina InfiniumDNAmethylation arrays revealed four unique subtypes (based on PMID: 25631445).

RNA_subtype – Head and Neck subtypes based on mRNA expression (based on PMID: 25631445).

pathologic_N – characterization of the regional lymph nodes**.**

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ESCA

columnar_metaplasia_present – replacement of the normal stratified squamous epithelium lining of the esophagus by simple columnar epithelium with goblet cells.

columnar_mucosa_dysplasia – a pre-malignant lesion the esophagus associated with Barrett's esophagus; considered the precursor of esophageal adenocarcinoma.

histological_type – histologic subtypes of Esophageal Carcinoma samples submitted for TCGA.

histologic_grade - classification of the microscopic cell appearance abnormality and deviations in their rate of growth with the goal of predicting developments at tissue level.

GX: Grade cannot be assessed (undetermined grade)

G1: Well differentiated (low grade)

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H.PYLORI-Infection – status of patient's *Helicobacter pylori* infection.

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BRCA

ER.status – the presence of estrogen receptors on the surface of the cancer cell

HER2.Final.Status – the presence of a growth-promoting protein (HER2) on the surface of the cancer cell

histological_type – histologic subtypes of Breast Cancer samples submitted for TCGA.

Integrated.Clusters.with.PAM50 – Breast Cancer subtypes based on mRNA expression integrated with PAM50 tumor profiling test.

Methylation.Clusters – genome-wide DNA methylation pattern within different Breast Cancer samples submitted for TCGA (based on PMID: 23000897).

Cluster 3 – a hyper-methylated phenotype significantly enriched for Luminal B mRNA-subtype and under-represented for PIK3CA and MAP3K1/MAP2K4 mutations.

Cluster 5 – the lowest levels of DNA methylation, overlapped with the Basal-like mRNA-subtype, and a high frequency of TP53 mutations.

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Stage IV - advanced or metastatic cancer.

PR.status - the presence of progesterone receptors on the surface of the cancer cell.

BLCA

histological_subtype – histologic subtypes of Bladder Cancer samples submitted for TCGA.

neoplasm_histologic_grade – measure of anaplasia in a sampled tumors.

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X_PANCAN_Cluster_Cluster_PANCAN – genome-wide DNA methylation pattern within different BLCA samples submitted for TCGA.

X_PANCAN_DNAMethyl_BLCA – genome-wide DNA methylation pattern within different BLCA samples submitted for TCGA.

X_PANCAN_DNAMethyl_PANCAN – genome-wide DNA methylation pattern within different BLCA samples submitted for TCGA.

X_PANCAN_UNC_RNAseq_PANCAN_K16 – genome-wide DNA methylation pattern within different BLCA samples submitted for TCGA.