

Table S1. Summary of the number of cancer and normal samples in each of the 13 analyzed TCGA datasets.

Cancer type		Number of RNA-seq libraries analyzed			Number of methylation libraries analyzed			Number of patients with survival data		
Abbreviation	Full name	Cancer	Healthy	Combined	Cancer	Healthy	Combined	Alive	Dead	Combined
BLCA	Bladder Urothelial Carcinoma	414	19	433	418	21	439	231	181	412
BRCA	Breast invasive carcinoma	1102	113	1215	793	97	890	946	151	1097
COAD	Colon adenocarcinoma	478	41	519	313	38	351	357	102	459
HNSC	Head and Neck squamous cell carcinoma	500	44	544	528	50	578	305	223	528
KIRC	Kidney renal clear cell carcinoma	538	72	610	324	160	484	360	177	537
KIRP	Kidney renal papillary cell carcinoma	288	32	320	275	45	320	247	44	291
LIHC	Liver hepatocellular carcinoma	371	50	421	377	50	427	245	132	377
LUAD	Lung adenocarcinoma	533	59	592	473	32	505	334	188	522
LUSC	Lung squamous cell carcinoma	502	49	551	370	42	412	285	219	504
PRAD	Prostate adenocarcinoma	498	52	550	502	50	552	490	10	500
STAD	Stomach adenocarcinoma	375	32	407	395	2	397	271	172	443
THCA	Thyroid carcinoma	502	58	560	507	56	563	491	16	507
UCEC	Uterine Corpus Endometrial Carcinoma	551	35	586	438	46	484	457	91	548