

Table S1. A summary of the datasets used in this study.**TCGA cohorts**

Cancer type	Full name	Number of tumor samples	Number of <i>KALRN</i> -mutated samples	Number of <i>KALRN</i> -wildtype samples
CESC	Cervical Squamous-Cell Carcinoma And Endocervical Adeno-Carcinoma	199	11	188
COAD	Colon Adenocarcinoma	219	20	199
ESCA	Esophageal Carcinoma	185	15	170
GBM	Glioblastoma Multiforme	316	33	283
PRAD	Prostate Adenocarcinoma	499	7	492
READ	Rectum Adenocarcinoma	81	5	76
SARC	Sarcoma	259	9	250
SKCM	Skincutaneous Melanoma	472	106	366
STAD	Stomach Adenocarcinoma	379	34	345
UCEC	Uterine Corpus Endometrial Carcinoma	248	29	219
Pan-cancer	Pan-cancer	2995	407	2588

Cancer cohorts with immunotherapy

Cancer type	Dataset ID	Number of tumor samples	Number of <i>KALRN</i> -mutated samples	Number of <i>KALRN</i> -wildtype samples	References
Melanoma	Allen cohort	100	18	82	[1]
Melanoma	Hugo cohort	37	11	26	[2]
Melanoma	Riaz cohort	45	5	40	[3]
Non-small cell lung cancer	Rizvi cohort	30	3	27	[4]
lung cancer	Hellmann cohort	75	11	64	[5]

References

- [1] Van Allen EM, Miao D, Schilling B, et al: Genomic correlates of response to CTLA-4 blockade in metastatic melanoma. *Science* 350:207-11, 2015.
- [2] Hugo W, Zaretsky JM, Sun L, et al: Genomic and Transcriptomic Features of Response to Anti-PD-1 Therapy in Metastatic Melanoma. *Cell* 165:35-44, 2016.

- [3] Riaz N, Havel JJ, Makarov V, et al: Tumor and Microenvironment Evolution during Immunotherapy with Nivolumab. *Cell* 171:934-949 e16, 2017.
- [4] Rizvi NA, Hellmann MD, Snyder A, et al: Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. *Science* 348:124-8, 2015.
- [5] Hellmann MD, Nathanson T, Rizvi H, et al. Genomic Features of Response to Combination Immunotherapy in Patients with Advanced Non-Small-Cell Lung Cancer. *Cancer Cell*. 33(5):843-852 e4, 2018.