

Study	Number of samples	Data type
Lung Adenocarcinoma (TCGA, PanCancer Atlas)	566	RNA seq
Lung Squamous Cell Carcinoma (TCGA, PanCancer Atlas)	487	
Adrenocortical carcinoma (TCGA PanCancer Atlas)	92	
Cholangiocarcinoma (TCGA PanCancer Atlas)	36	
Bladder Urothelial Carcinoma (TCGA PanCancer Atlas)	411	
Colorectal Adenocarcinoma (TCGA PanCancer Atlas)	594	
Breast Invasive Carcinoma (TCGA PanCancer Atlas)	1084	
Brain Lower Grade Glioma (TCGA PanCancer Atlas)	514	
Glioblastoma multiforme (TCGA PanCancer Atlas)	592	
Cervical Squamous Cell Carcinoma (TCGA, PanCancer Atlas)	297	
Esophageal Adenocarcinoma (TCGA, PanCancer Atlas)	182	
Stomach Adenocarcinoma (TCGA, PanCancer Atlas)	440	
Uveal melanoma (TCGA, PanCancer Atlas)	80	
Head and Neck Squamous Cell Carcinoma (TCGA, PanCancer Atlas)	523	
Kidney Renal Clear Cell Carcinoma (TCGA, PanCancer Atlas)	512	
Kidney Chromophobe (TCGA, PanCancer Atlas)	65	
Kidney Renal Papillary Cell Carcinoma (TCGA, PanCancer Atlas)	283	
Liver Hepatocellular Carcinoma (TCGA, PanCancer Atlas)	372	
Diffuse Large B-Cell Lymphoma (TCGA, PanCancer Atlas)	48	
Acute Myeloid Leukemia (TCGA, PanCancer Atlas)	200	

Ovarian Serous Cystadenocarcinoma (TCGA, PanCancer Atlas)	585	
Pancreatic Adenocarcinoma (TCGA, PanCancer Atlas)	184	
Mesothelioma (TCGA, PanCancer Atlas)	87	
Prostate Adenocarcinoma (TCGA, PanCancer Atlas)	494	
Skin Cutaneous Melanoma (TCGA, PanCancer Atlas)	442	
Pheochromocytoma and Paraganglioma (TCGA, PanCancer Atlas)	178	
Sarcoma (TCGA, PanCancer Atlas)	255	
Testicular Germ Cell Tumors (TCGA, PanCancer Atlas)	149	
Thymoma (TCGA, PanCancer Atlas)	123	
Thyroid Carcinoma (TCGA, PanCancer Atlas)	500	
Uterine Corpus Endometrial Carcinoma (TCGA, PanCancer Atlas)	529	
Uterine Carcinosarcoma (TCGA, PanCancer Atlas)	57	

Supplementary table 1: studies used for data analysis.

Gene	Function
<i>PKD1L2</i>	G-protein-coupled receptor
<i>S100P</i>	Calcium sensor and contribute to cellular calcium signaling
<i>OSGIN1</i>	Regulates the differentiation and proliferation through the regulation of cell death
<i>NMRAL2P</i>	Nuclear factor
<i>TXNRD1</i>	Reduces disulfideprotein thioredoxin (Trx) to its dithiol-containing form

Supplementary table 2: Common gene functions between those overexpressed with *SMARCA4* disruptive mutation and those overexpressed with CNV loss.

Source	Term_name	Term_id	Adjusted_p_value	Genes
GO:MF	Lipid antigen binding	GO:0030882	1.352E-05	CD1A CD1E CD1C
GO:MF	Endogenous lipid antigen binding	GO:0030883	1.352E-05	CD1A CD1E CD1C
GO:MF	Exogenous lipid antigen binding	GO:0030884	1.352E-05	CD1A CD1E CD1C
GO:MF	Lipopeptide binding	GO:0071723	1.613E-04	CD1A CD1E CD1C
GO:BP	Antigen processing and presentation, endogenous lipid antigen via MHC class Ib	GO:0048006	4.356E-05	CD1A CD1E CD1C
GO:BP	Antigen processing and presentation, exogenous lipid antigen via MHC class Ib	GO:0048007	1.522E-04	CD1A CD1E CD1C
GO:BP	Antigen processing and presentation of lipid antigen via MHC class Ib	GO:0048003	1.522E-04	CD1A CD1E CD1C
GO:BP	Antigen processing and presentation via MHC class Ib	GO:0002475	0.008	CD1A CD1E CD1C
GO:BP	Regulation of leukocyte mediated cytotoxicity	GO:0001910	0.014	CD1A CD1E CX3CR1 CD1C
GO:BP	Antigen processing and presentation of endogenous antigen	GO:0019883	0.019	CD1A CD1E CD1C
GO:BP	Regulation of cell killing	GO:0031341	0.024	CD1A CD1E CX3CR1 CD1C
GO:BP	Positive regulation of T cell mediated cytotoxicity	GO:0001916	0.036	CD1A CD1E CD1C
GO:BP	T cell mediated immunity	GO:0002456	0.047	CD1A CD1E MYO1G CD1C
GO:CC	External side of plasma membrane	GO:0009897	0.032	CD1A CD1E CD207 CX3CR1 CD1C
GO:CC	Cell surface	GO:0009986	0.035	CD1A CD1E FCER1A CD207 CX3CR1 ROS1 CD1C
KEGG	Hematopoietic cell lineage	KEGG:04640	0.032	CD1A CD1E CD1C
KEGG	Amoebiasis	KEGG:05146	0.043	CD1A CD1E CD1C

Supplementary table 3: Functions of the group of genes downregulated when there is mutation and when there is CNV loss.

A	B	Neither	A Not B	B Not A	Both	Log2 Odds Ratio	p-Value	q-Value	Tendency
SMARCA4	TP53	304	23	611	57	0.302	0.458	0.687	Co-occurrence
SMARCA4	KRAS	740	64	175	16	0.080	0.882	0.882	Co-occurrence

Supplementary figure 2: Co-occurrence analysis performed in CBioportal (mutual exclusivity tab).

Appendix

CBioPortal is an open-access, for interactive exploration of multidimensional cancer genomics data sets.

CBioPortal provides access to molecular profiles and clinical attributes from large-scale cancer genomics projects.

g.Profiler is a public web server to perform statistical enrichment analysis from user-provided gene lists.

GeneCards is an integrated database of human genes that provides concise genomic related information, on all known and predicted human genes.

TIMER 2.0 is a comprehensive resource for systematical analysis of immune infiltrates across diverse cancer types. Gene (Immune association) associates immune infiltrates and gene expression.

KM Plotter provides correlation between the expression of all genes (mRNA, miRNA, protein, & DNA) and survival in samples from 21 tumor types. In the immunotherapy section, KM plotter provides information regarding outcome of patients treated with anti-PD(L)1 and anti-CTLA4 therapies.