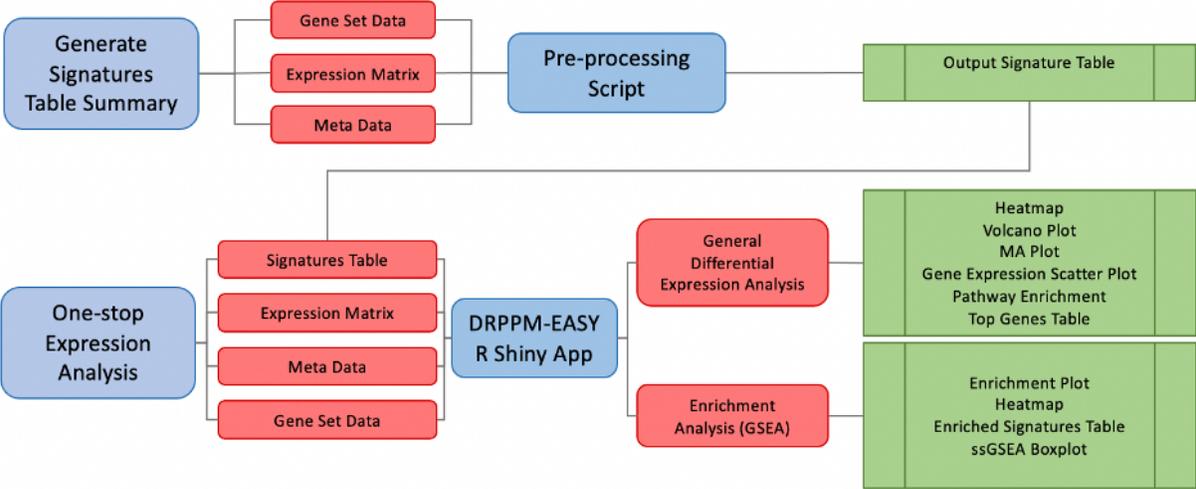
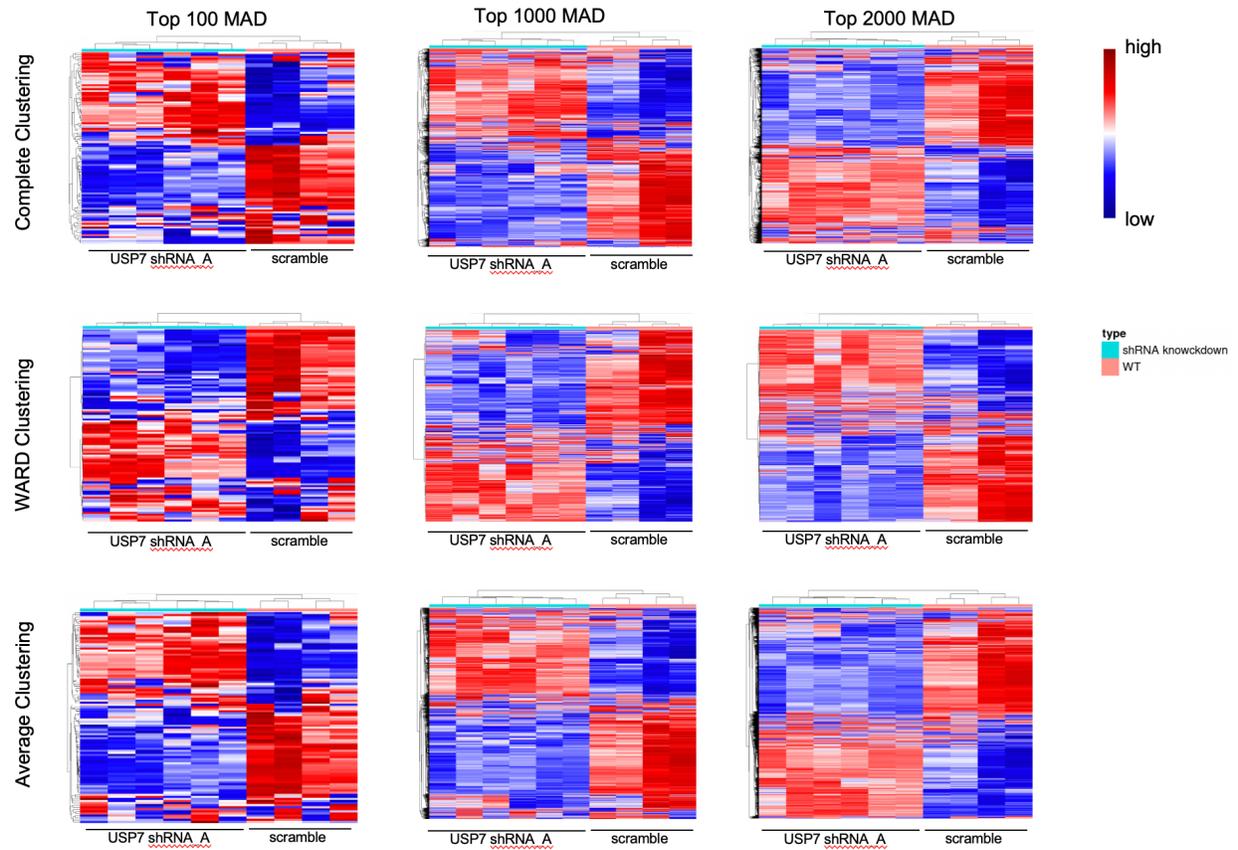


Supplementary Figure S1.



Supplementary Figure S1. Schematic of the GSEA pre-processing.

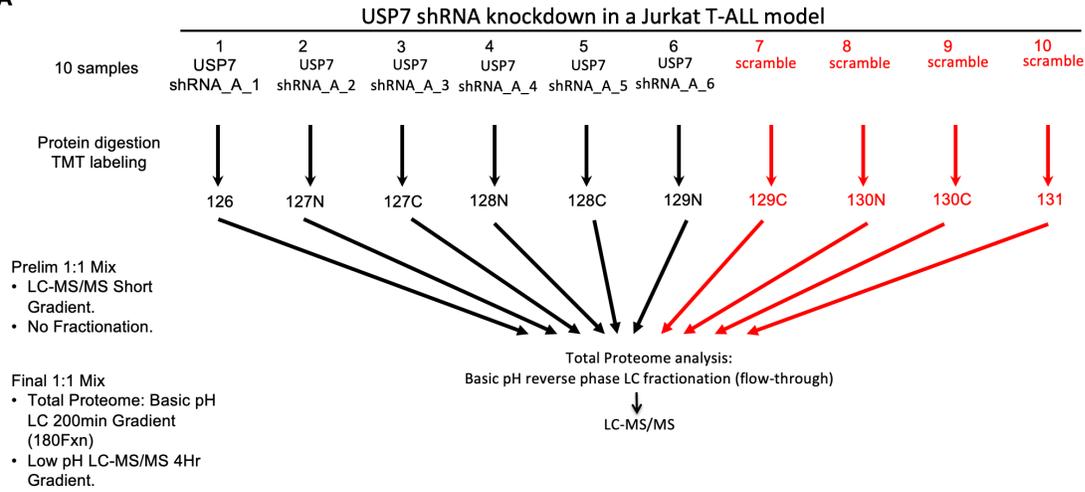
## Supplementary Figure S2.



**Supplementary Figure S2.** Unsupervised hierarchical clustering of Jurkat samples after USP7 KD. Each row represents distinct clustering algorithms: Complete, WARD, and Average. Each column represents different number of variable genes selected by Mean Absolute Deviation (MAD).

### Supplementary Figure S3.

A



B

GeneSets	Top Enriched Pathways
KEGG_SPLICEOSOME	1
KEGG_RNA_POLYMERASE	2
KEGG_PYRIMIDINE_METABOLISM	3
KEGG_LYSOSOME	4
KEGG_HUNTINGTONS_DISEASE	5
KEGG_TGF_BETA_SIGNALING_PATHWAY	6
KEGG_PURINE_METABOLISM	7
KEGG_CELL_CYCLE	8
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	9
KEGG_P53_SIGNALING_PATHWAY	10

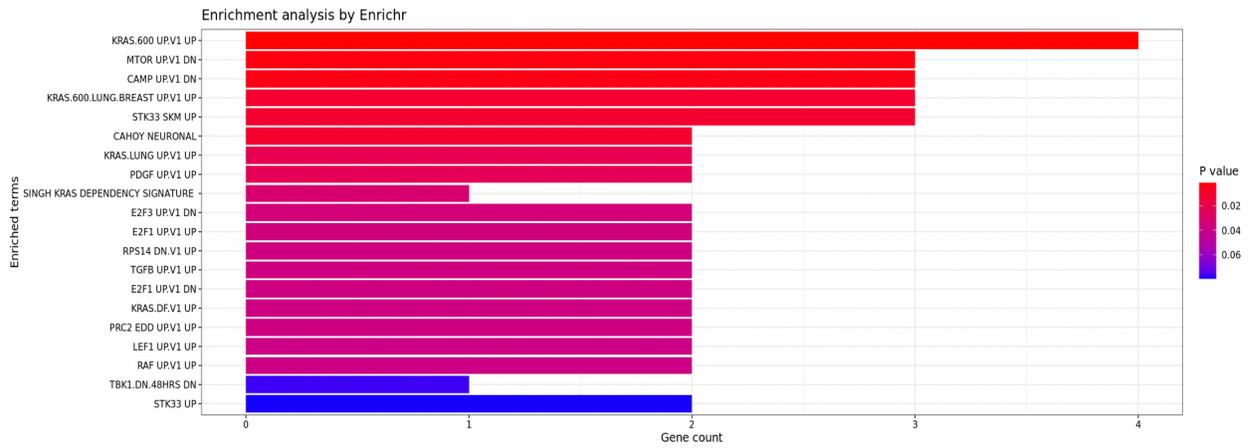
C

GeneSets	Top Enriched Pathways
HALLMARK_UV_RESPONSE_UP	1
HALLMARK_INTERFERON_GAMMA_RESPONSE	2
HALLMARK_G2M_CHECKPOINT	2
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	4
HALLMARK_MYC_TARGETS_V2	5
HALLMARK_ALLOGRAFT_REJECTION	6
HALLMARK_E2F_TARGETS	7
HALLMARK_MYC_TARGETS_V1	8
HALLMARK_ESTROGEN_RESPONSE_EARLY	9
HALLMARK_INTERFERON_ALPHA_RESPONSE	10

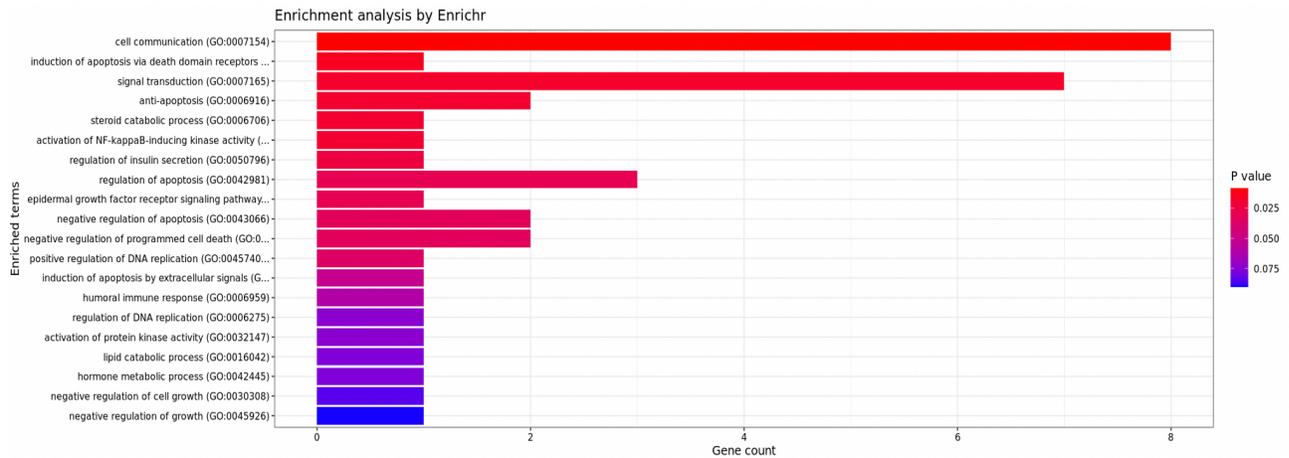
**Supplementary Figure S3.** A) Experimental design of the total proteome profiling of the USP7 knockdown experiment. B, C) Upregulated pathway ranked based on Jaccard index, Odds Ratio, and Cohen's Kappa in the KEGG database (B) and the HALLMARK database (C).

## Supplementary Figure S4.

A



B



**Supplementary Figure S4.** Pathway enrichment analysis of genes differentially upregulated in KRAS mutated samples in NSCLC. A) Pathway analysis using the MsigDB Oncogenic Signature database. B) Pathway analysis using the GO Biological Process Gene Signatures.

# Supplementary Figure S5.

**A**

(CCLE Integrative Expression Analysis) Intro and Methods **Data Input** Expression Scatter Plot Reciprocal GSEA Reciprocal vsGSEA Statistical Analysis

Step1: User Data Input Step2: CCLE Data Selection Step3: Designate Comparison Groups

**User Matrix Input**

Matrix Name:

User Matrix:

Expression Matrix File Upload

Browse...

Check if Header in Meta File

Meta Matrix File Upload

Browse...

**User Expression Data**

Show  entries

	JK.S1.ERCC.S22	JK.S1.ERCC.S23	JK.S2.ERCC.S24	JK.S3.ERCC.S25	JK.A2.1.ERCC.S26	JK.A2.2.ERCC.S27	JK.A2.3.ERCC.S28	JK.A2.4.ERCC.S29	JK
CALML5	5076.7808	3047.11731	2854.50039	5032.49028	873.807708	14482.88276	16782.90874	15048.19104	
HBA1	21234.1036	117614.6915	49569.92969	211539.8302	77002.21983	198991.7212	5317.039757	10208.41737	
JAM3	12390.0834	111455.6286	76504.7477	75734.02977	35512.29008	32546.61794	33980.49137	31124.16232	
NRN1	67769.54448	53038.42882	50910.14739	41332.80797	20425.23618	17006.69156	21525.32069	16218.66237	
TNRC4	50063.21673	49132.24054	28227.31234	29388.43162	13552.68376	14156.82619	11451.78205	13537.26236	
DNT7	86051.73961	68034.44933	71179.70883	81405.26224	29734.78234	31425.58827	27618.04269	31759.89134	
SELBNP1	40235.60956	67463.30087	50112.60882	50117.38715	36117.83755	31126.38742	7331.125117	11021.28424	

**B**

(CCLE Integrative Expression Analysis) Intro and Methods **Data Input** Expression Scatter Plot Reciprocal GSEA Reciprocal vsGSEA Statistical Analysis

Step1: User Data Input Step2: CCLE Data Selection Step3: Designate Comparison Groups

**Subset Expression Data:**

Sample Choices:

Select Sample Subset:

Condition Selection:

Log Transform Expression Data:

Label for Project Data:

**Meta Data**

Show  entries

SampleName	Type
ACH-00001.NKNCVARS	Female
ACH-00001.0NC00001	Female
ACH-00004.T0Y11D	Female
ACH-00001.OV56	Female
ACH-00010.CADV4	Female
ACH-00018.OV408	Female
ACH-00025.OV424	Female
ACH-00032.JH52	Female
ACH-00037.JH57	Female
ACH-00038.OV219	Female

**Expression Data**

Show  entries

SampleName	AD
ACH-00001.NKNCVARS	66.63
TNRC4	0
TNRC4	0
SPN1	164.34
SCY3	3.29
CTH112	17.66
FGA	0.03
GH1	0.68
FGS2	60.00
SC2	28.87
MPN	19.10

**Name Map Guide**

Show  entries

SampleName	CCLE Name
ACH-00001.NKNCVARS	NKNCVARS_OVARY
ACH-00001.0NC00001	0NC00001_OVARY
ACH-00004.T0Y11D	T0Y11D_OVARY
ACH-00001.OV56	OV56_OVARY
ACH-00010.CADV4	CADV4_OVARY
ACH-00018.OV408	OV408_OVARY
ACH-00025.OV424	OV424_OVARY
ACH-00032.JH52	JH52_OVARY
ACH-00037.JH57	JH57_OVARY
ACH-00038.OV219	OV219_OVARY

**C**

Download Meta Data Download Expression Data Download Name Map

Step1: User Data Input Step2: CCLE Data Selection Step3: Designate Comparison Groups

Show  entries

**Comparison Groups From User Data:**

Comparison Group 1:

Comparison Group 2:

**Comparison Groups From CCLE Data:**

Comparison Group 1:

Comparison Group 2:

Label Group 1 and Group 2:

Group 1 Label:

Group 2 Label:

Download Compiled Meta Table:

File Name for Download:

SampleName	Type
JK.A2.1.ERCC.S26	USP7KO_or_HJWE1mut
JK.A2.2.ERCC.S27	USP7KO_or_HJWE1mut
JK.A2.3.ERCC.S28	USP7KO_or_HJWE1mut
JK.A2.4.ERCC.S29	USP7KO_or_HJWE1mut
JK.S2.ERCC.S24	USP7wt
JK.S3.ERCC.S25	USP7wt
JK.S1.ERCC.S22	USP7wt
JK.S1.ERCC.S23	USP7wt
JK.S2.ERCC.S24	USP7wt
JK.S3.ERCC.S25	USP7wt
ACH-00001.NKNCVARS	USP7wt
ACH-00001.0NC00001	USP7wt
ACH-00004.T0Y11D	USP7wt
ACH-00001.OV56	USP7wt
ACH-00010.CADV4	USP7wt
ACH-00018.OV408	USP7wt

**Supplementary Figure S5.** Screen shot showing the user option to upload user data in the DRPPM-Large Project Integration function. (CCLE example). **A)** Step 1. The user can upload a matrix and its associated sample meta-information file. **B)** Step 2. The user will select the CCLE sample cohort to analyze and select the phenotype for the group comparison. **C)** Step3. Harmonizes the sample grouping between the two datasets.