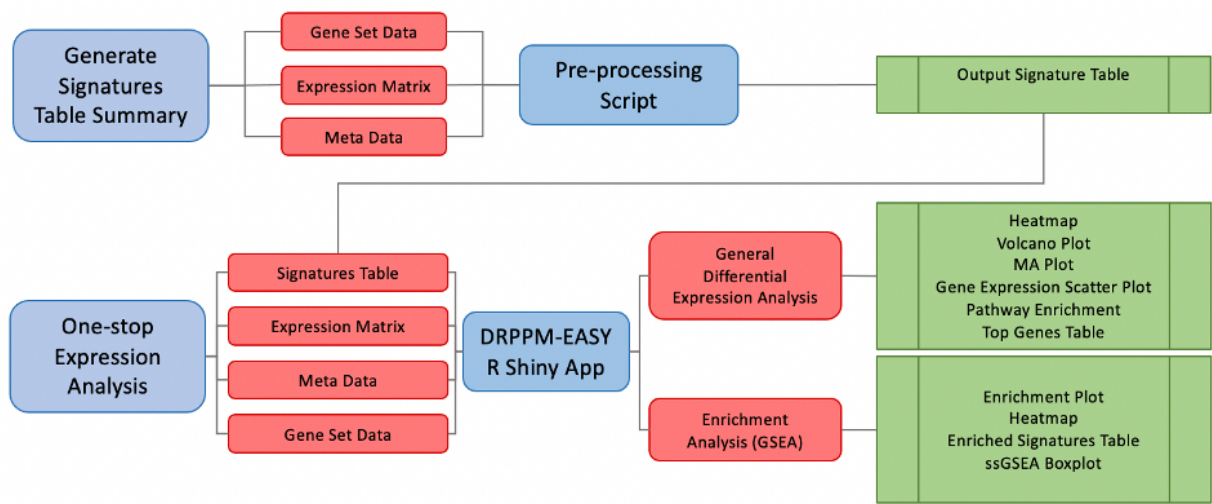
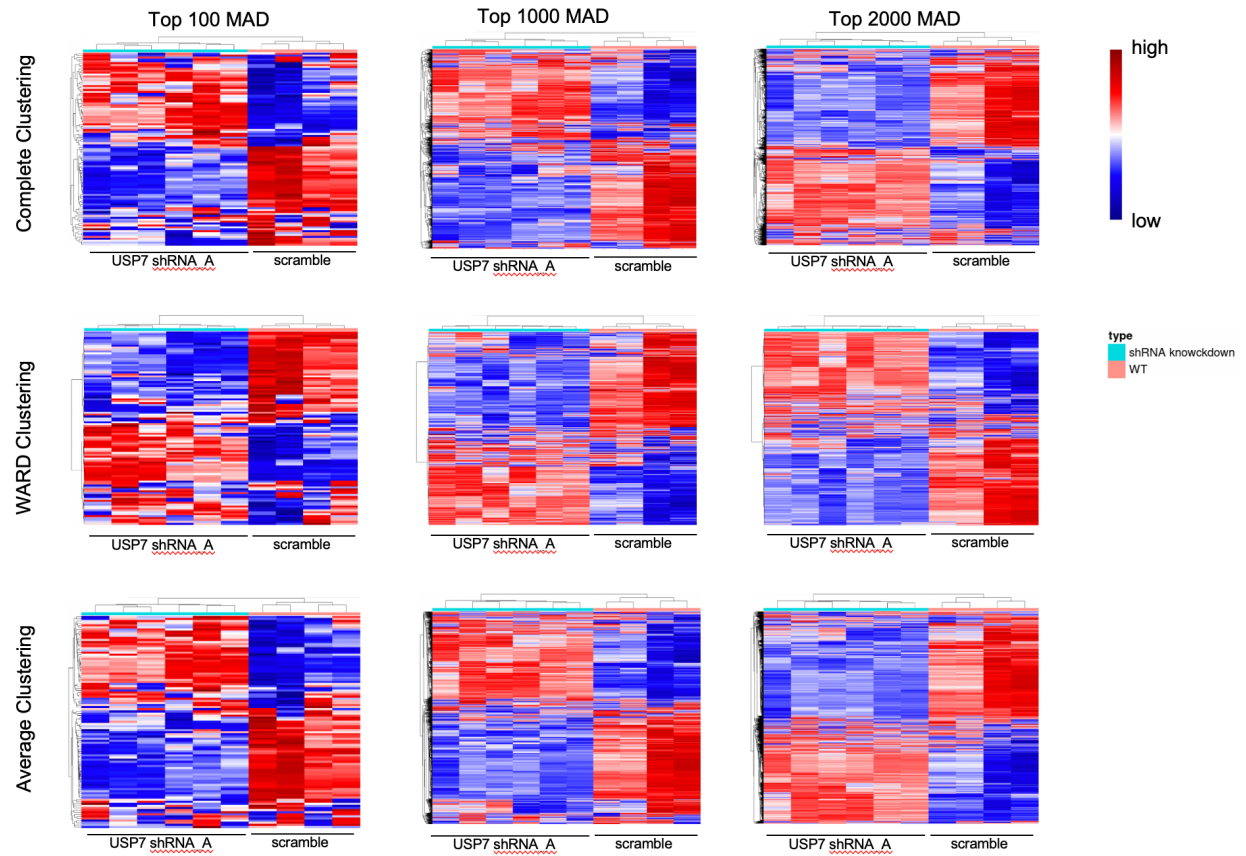


Supplementary Figure S1.



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

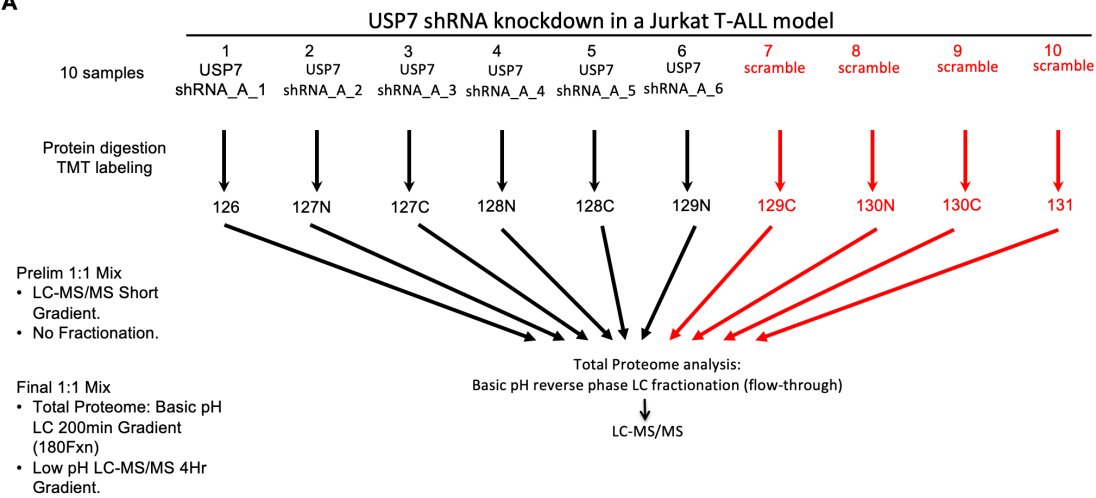
Supplementary Figure S2.



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

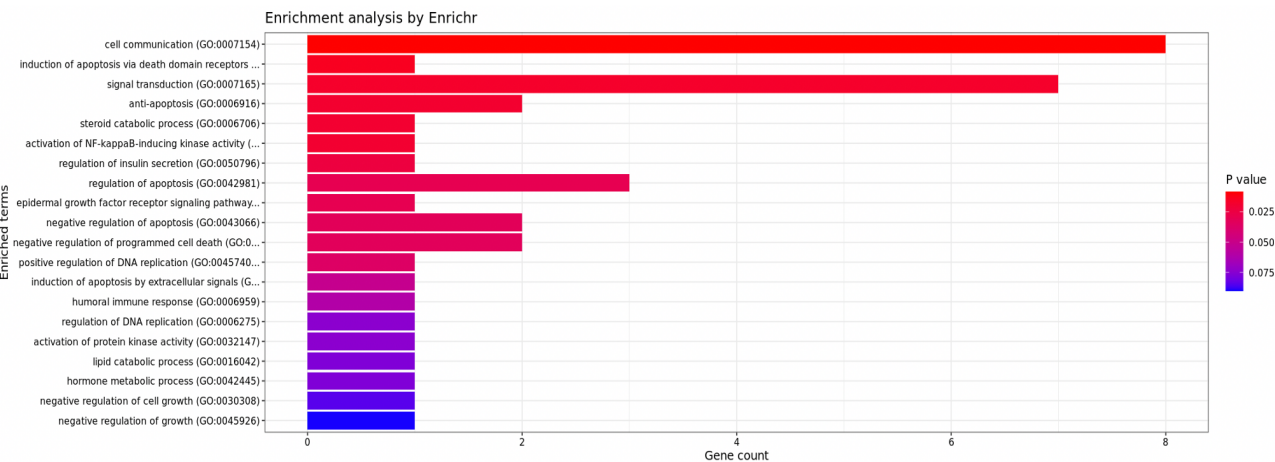
Supplementary Figure S3. A) Experimental design of the total proteome profiling of the USP7 knockdown experiment. B, C) Upregulated pathway ranked based on Jaccard index, Odds Ratio, and Cohen's Kappa in the KEGG database (B) and the HALLMARK database (C).

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) Info and Methods **Data Input** Expression Scatter Plot Reciprocal GSEA Reciprocal ssGSEA 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... [Upload Sample](#)

☒ Check if Header in Meta File

Meta Matrix File Upload

Browse... [Upload Sample](#)

User Expression Data

Show entries

JK.S1.3.ERCC.S22	JK.S1.3.ERCC.S23	JK.S2.2.ERCC.S24	JK.S3.3.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	5047.11731	28524.9838	50322.49028	8713.807758	14482.88278	16782.90874	15048.19104
HBA1	21234.1036	117614.6915	49559.92989	211539.8332	77002.21583	198891.7212	5317.038757	10298.41757
JAM3	123880.0834	111453.6285	76504.71477	75734.02977	35512.25008	32546.81754	33885.89157	31124.18232
NRN1	57756.54448	52038.42882	50910.14739	41332.90797	20425.23618	17036.89156	21525.32589	18218.60237
TNRC4	50063.21573	49132.24584	28237.31234	29388.43162	13552.58375	14156.82618	11451.78205	13537.26336
DNFT	8691.73951	98034.14583	71179.70883	81605.28224	29734.78734	31629.58827	27818.04289	31759.89134
SELBNP1	40335.60956	87433.90387	50172.68892	50117.38715	36117.80755	31126.38742	7331.125117	11011.28424

B

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

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

Subset Expression Data:

Sample_Changes:

Select Sample Subset:

Condition Selection:

☐ Log2 Transform Expression Data:

Label for Project Data:

CCLE

Meta Data

Show entries

SampleName	Type
ACH-000001.NKNCVARS	Female
ACH-000013.ONC0001	Female
ACH-000048.TON110D	Female
ACH-000091.ON06	Female
ACH-000103.CADN4	Female
ACH-000116.ON063	Female
ACH-000125.COV43	Female
ACH-000132.JH052	Female
ACH-000137.JH047	Female
ACH-000153.COV43	Female

Expression Data

Show entries

SampleName	ACH-000001.NKNCVARS	ACH-000013.ONC0001	ACH
TNRC4	50.85	44.81	
TM6D3	0	0.6	
SPN1	164.34	165.68	
SCYL3	3.29	2.75	
CTHPT2	17.86	15.9	
FGFR	0.03	0.02	
CHN	0.88	3.19	
FGFR2	62.02	41.87	
SCC2	28.87	17.41	
MPN1	10.10	10.35	

Name Map Guide

Show entries

SampleName	CCLE Name
ACH-000001.NKNCVARS	NKNCVARS_OVARY
ACH-000013.ONC0001	ONC0001_OVARY
ACH-000048.TON110D	TON110D_OVARY
ACH-000091.ON06	ON06_OVARY
ACH-000103.CADN4	CADN4_OVARY
ACH-000116.ON063	ON063_OVARY
ACH-000125.COV43	COV43_OVARY
ACH-000132.JH052	JH052_OVARY
ACH-000137.JH047	JH047_OVARY
ACH-000153.COV43	COV43_OVARY

C

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:

[Download](#)

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

Show entries

SampleName	Type
JK.A2.1.ERCC.S26	USP7KO_HLWEmut
JK.A2.2.ERCC.S27	USP7KO_HLWEmut
JK.A2.3.ERCC.S28	USP7KO_HLWEmut
JK.A2.4.ERCC.S29	USP7KO_HLWEmut
JK.A2.5.ERCC.S30	USP7KO_HLWEmut
JK.A2.6.ERCC.S31	USP7KO_HLWEmut
ACH-000062.DC314	USP7KO_HLWEmut
ACH-001145.DC316	USP7KO_HLWEmut
JK.S1.2.ERCC.S22	USP7wt
JK.S1.3.ERCC.S23	USP7wt
JK.S2.2.ERCC.S24	USP7wt
JK.S2.3.ERCC.S25	USP7wt
ACH-000001.NKNCVARS	USP7wt
ACH-000013.ONC0001	USP7wt
ACH-000048.TON110D	USP7wt
ACH-000091.ON06	USP7wt
ACH-000103.CADN4	USP7wt
ACH-000132.JH052	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.