

The role of LRP1B in the LUAD

Supplementary Table 1. Differentially regulated genes in RNA-seq

shLRP1B-1	shLRP1B-2	shLRP1B-3	shNC-1	shNC-2	shNC-3	shLRP1B
2.881786	0	0	6.334299	8.204781	2.958071	0.960595
203.6462	352.7641	159.5777	3287.501	4332.124	2468.017	238.6627
320.8389	128.8184	450.1994	11.7637	20.51195	19.72047	299.9522
1415.918	830.383	1057.863	219.8907	188.71	242.5618	1101.388
4.802977	12.88184	6.340837	110.3978	130.2509	114.3787	8.00855
350.6173	219.9821	98.28297	9.953899	24.61434	11.83228	222.9608
268.9667	228.9003	412.1544	41.62539	33.84472	54.2313	303.3405
70.12347	90.17285	46.49947	374.6285	592.7954	347.0803	68.93193

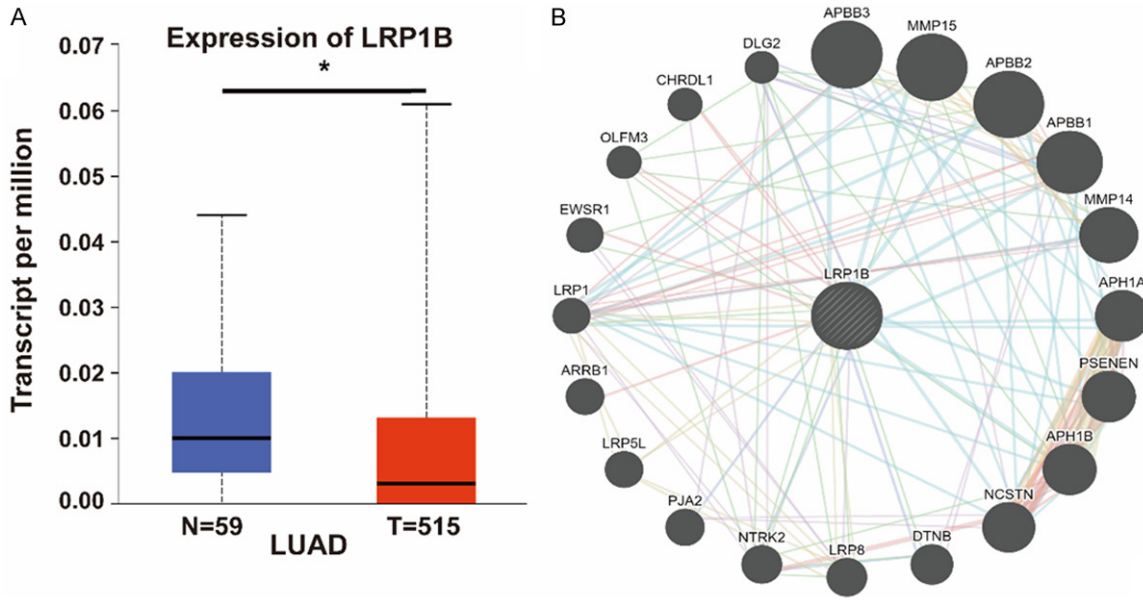
Supplementary Table 2. The relative levels of JAK-STAT3 signaling pathway-related molecules in A549 cells with knockdown of LRP1B versus control cells (n = 3)

shNC-3	shLRP1B	shNC	log2FoldCh	p value	padj	gene_name
2.958071	0.960595	5.832384	-2.577934	0.138215	1	LRP1B
7.88819	78.39484	7.415519	3.421497	7.99E-07	0.000287	IL6
52.25926	208.9918	45.49232	2.199126	1.80E-07	8.28E-05	IFNL1
195.2327	777.8646	142.0965	2.453392	7.72E-10	9.81E-07	IL11
5.916142	17.66553	5.04884	1.821249	0.066796	0.555054	IL7R
623.167	1462.691	519.2951	1.493837	1.93E-05	0.003668	SOCS3
169.5961	259.7961	135.1594	0.9427	0.007996	0.192901	STAT5A
713.8812	719.9657	603.1456	0.255364	0.406481	0.837585	ACSF3

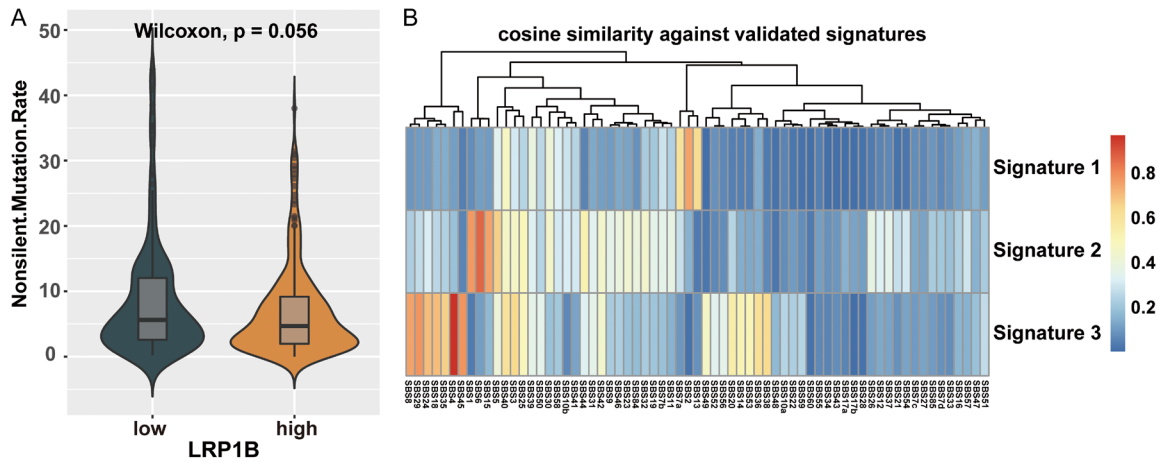
Supplementary Table 3. Gene and primer sequence

Target	Primer Name	Sequence (5'-3')
LRP1B	LRP1B-human-F	TGCCATTGAAGTGGTTGTGG
	LRP1B-human-R	AGCCATCTAGTTTGCCACT
IL6	IL6-human-F	ACTCACCTCTTCAGAACGAATTG
	IL6-human-R	CCATCTTTGGAAGGTTTCAGGTTG
JAK1	JAK1-human-F	GTTTGCCCTGTATGACGAGAAC
	JAK1-human-R	ACCTCATCCGGTAGTGGAGC
JAK2	JAK2-human-F	TCGGSATCGAACTGGACTA
	JAK2-human-R	ATCGGATTGCTGAATGCAA
STAT3	STAT3-human-F	ACCAGCAGTATAGCCGCTTC
	STAT3-human-R	GCCACAATCCGGGCAATCT
GAPDH	GAPDH-human-F	CGCTGAGTACGTCGTGGAGTC
	GAPDH-human-R	GCTGATGATCTTGAGGCTGTTGTC

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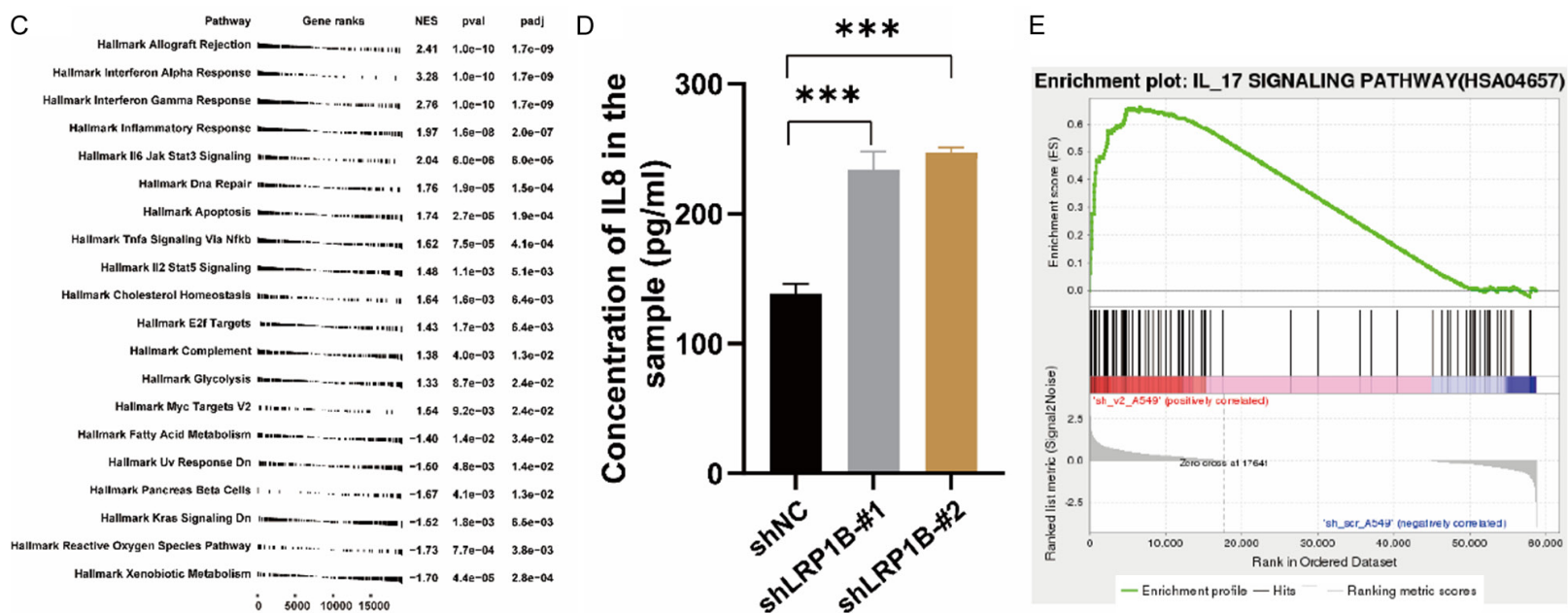


Supplementary Figure 1. In LUAD cohort, expression of LRP1B in normal tissues and tumor tissues and LRP1B's protein-protein interaction network. A. The expression status of the LRP1B gene in normal or tumor was analyzed through GEPIA2 (*P < 0.05). B. The interaction of LRP1B related proteins in LUAD in GeneMANIA portal.



Supplementary Figure 2. Comparison of nonsilent mutation rate and extraction of mutation signatures. A. Comparison of nonsilent mutation rate between LRP1B low-expression group with LRP1B high-expression group in TCGA. B. Cosine similarity analysis of extracted mutational signatures against the 67 identified signatures in COSMIC (Version 3) with heatmap illustration.

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Supplementary Figure 3. Low expression of LRP1B significantly elevates the activity of the IL6-JAK-STAT3, IL17 signaling pathway et al inflammation signaling. A, B. GO enrichment analysis of differentially expressed genes, the left side represents up-regulated expression, and the right side is to be down-regulated expression. BP, CC, and MF represent biological pathways, cellular components, and molecular functions obtained by GO analysis, respectively. C. Data Display about KEGG pathway enrichment analyses of differentially expressed genes in Control and Knock down LRP1B of A549. D. A549 cells with knockdown of LRP1B and control cells were seeded for 12 hours before medium replacement. Culture supernatants were collected 48 hours after medium replacement and the IL-8 levels were detected by ELISA ($***P < 0.001$). E. GSEA of IL17 signaling pathway to assess specific enrichment of A549 cells with knockdown of LRP1B versus control cells.