

Supplementary

Table S1 Baseline information of 57 patients with uterine carcinosarcoma available from the TCGA database.

Variables	Total Patients (N = 57)
Age, years	
Mean \pm SD	71.20 \pm 10.67
Median	71.00
Survival time, days	
Mean \pm SD	865.05 \pm 851.86
Median	587.00
Gender	
Female	57 (100.00%)
Race	
Caucasian	44 (77.19%)
African-american	9 (15.79%)
Asian	4 (7.02%)
Cancer stage	
Stage 1	22 (38.60%)
Stage 2	5 (8.77%)
Stage 3	20 (35.09%)
Stage 4	10 (17.54%)

SD, Standard deviation.

Table S2. Summary of multidimensional external validation results base on multiple databases

Database	JUP		RALG		ADA		NUD		NUD		HPR		IMPDH		PDE4A		Results
			PS1				T9		T2		T1		1				
	N	U	N	U	N	U	N	U	N	U	N	U	N	U			
The human protein atlas	-	N	N	N	N	N	-	N	↑	N	↓	N	-	N	N	N	NUDT2 was high-expressed, while HPRT1 was low-expressed in normal cerebral cortex in uterine (Figure S1).
GEPIA	↓	↑	↑	↓	↓	↑	↑	↓	↑	↓	↓	↑	↓	↑	↑	↓	RALGPS1, NUDT9, NUDT2, and PDE4A expressed highly in normal tissue and lowly in UCS; JUP, ADA, HPRT1, and IMPDH1 expressed lowly in normal uterine and highly in UCS (Figure S3).
UCSC xena	N	↑	N	↓	N	↑	N	↓	N	↓	N	↑	N	↑	N	↓	RALGPS1, NUDT9, NUDT2, and PDE4A expressed lowly in UCS; JUP, ADA, HPRT1, and IMPDH1 expressed highly in UCS (Figure S4).
GTEx	-	N	-	N	↓	N	↑	N	↑	N	-	N	-	N	↑	N	NUDT9, NUDT2, and PDE4A was high-expressed, while ADA was low-expressed in normal uterine tissue (Figure S5).
UALCAN	N	↑	N	-	N	↑	N	↓	N	↓	N	N	N	↑	N	-	NUDT9 and NUDT2 expressed lowly in UCS; JUP, ADA, and IMPDH1 expressed highly in UCS (Figure S6).

Linkedomics	N ↑	N ↓	N ↑	N ↓	N ↓	N ↑	N ↑	N ↓	N ↓	RALGPS1, NUDT9, NUDT2, and PDE4A expressed lowly in UCS; JUP, ADA, HPRT1, and IMPDH1 expressed highly in UCS (Figure S7).
	A	A	A	A	A	A	A	A	A	
cBioportal	N ↑	N ↓	N ↑	N ↓	N ↓	N ↑	N ↑	N ↓	N ↓	RALGPS1, NUDT9, NUDT2, and PDE4A expressed lowly in UCS; JUP, ADA, HPRT1, and IMPDH1 expressed highly in UCS (Figure S8).
	A	A	A	A	A	A	A	A	A	
Oncomine	N ↑	N ↓	N ↑	N ↓	N ↓	N ↑	N ↑	N ↓	N ↓	RALGPS1, NUDT9, NUDT2, and PDE4A expressed lowly in UCS; JUP, ADA, HPRT1, and IMPDH1 expressed highly in UCS (Figure S9).
	A	A	A	A	A	A	A	A	A	
CCLE	N ↑	N ↓	N ↑	N ↓	N ↓	N ↑	N ↑	N ↓	N ↓	RALGPS1, NUDT9, NUDT2, and PDE4A were low-expressed in tumor cell line; JUP, ADA, HPRT1, and IMPDH1 were high-expressed in tumor cell line in CCLE (Figure S10)
	A	A	A	A	A	A	A	A	A	

Note: “N” was defined as normal; “U” was defined as Uterine carcinosarcoma; “↑” was defined as a significantly high-expressed gene; “↓” was defined as a significantly low-expressed gene; “NA” was defined as “Not available”; “ND” was defined as “Not detected”; “-” was defined as a gene with no significant difference in expression.

Abbreviations: UCS, Uterine Carcinosarcoma; GTEX, Genotype-Tissue Expression; CCLE, Cancer Cell Line Encyclopedia; GEPIA, Gene Expression Profiling Interactive Analysis.

Table S3. Summary of the overall survival and stage of multidimensional external validation results base on multiple databases

Database	JUP (SF)	RALGPS1 (ASE gene)	ADA (pathway gene)	NUDT9 (pathway gene)	NUDT2 (pathway gene)	HPRT1 (pathway gene)	IMPDH1 (pathway gene)	PDE4A (pathway gene)
UALCAN	K-M: P=0.034 Stage: P=0.037	K-M: P=0.077 Stage: P=0.188	K-M: P=0.018 Stage: P=0.009	K-M: P=0.07 Stage: P=0.219	K-M: P=0.083 Stage: P=0.001	K-M: P=0.042 Stage: P=0.087	K-M: P=0.019 Stage: P=0.0075	K-M: P=0.00017 Stage: P=0.003
LinkedOmics	K-M: P=0.64	K-M: P=0.028	K-M:P=0.150	K-M: P=0.024	K-M: P=0.093	K-M: P=0.004	K-M: P=0.040	K-M: P=0.0017
PROGeneV2	K-M: P=0.68	K-M: P=0.030	K-M: P=0.16	K-M: P=0.024	K-M: P=0.06	K-M: P=0.004	K-M: P=0.050	K-M: P=0.002
GEPIA	K-M: P=0.28 stage: P=0.09	K-M: P=0.2 stage: P=0.389	K-M: P=0.03 stage: P=0.02	K-M: P=0.06 stage: P=0.554	K-M: P=0.024 stage: P=0.08	K-M: P=0.009 stage: P=0.33	K-M: P=0.024 stage: P=0.03	K-M: P=0.00015 stage: P=0.0001
KaplanMeier plotter	P=0.0057	P=0.2	P=4.6e-08	P=0.0001	P=0.0033	P=0.03	P=0.029	P=0.048

Table S4. Summary of multidimensional external validation

Database	JUP (SF)	RALGPS1 (ASE gene)	ADA (pathway gene)	NUDT9 (pathway gene)	NUDT2 (pathway gene)	HPRT1 (pathway gene)	IMPDH1 (pathway gene)	PDE4A (pathway gene)
The human protein atlas	Normal medium	not detected	not detected	normal medium	normal high	normal low	normal medium	not detected
PROGgeneV2	K-M: P=0.68	K-M: P=0.030	K-M: P=0.16	K-M: P=0.024	K-M: P=0.06	K-M: P=0.004	K-M: P=0.050	K-M: P=0.002
GEPIA	K-M: P=0.28 stage: P=0.09 normal low tumor high	K-M: P=0.2 stage: P=0.389 normal high tumor low	K-M: P=0.03 stage: P=0.02 normal low tumor high	K-M: P=0.06 stage: P=0.554 normal high tumor low	K-M: P=0.024 stage: P=0.08 normal high tumor low	K-M: P=0.009 stage: P=0.33 normal low tumor high	K-M: P=0.024 stage: P=0.03 normal low tumor high	K-M: P=0.00015 stage: P=0.0001 normal high tumor low
UCSC xena	early stage high	early stage high	early stage low	early stage low	early stage high	early stage high	early stage high	early stage low
GTEX	normal median	normal median	normal low	normal high	normal high	normal medium	normal medium	normal high
UALCAN	K-M: P=0.034 Stage: P=0.037	K-M: P=0.077 Stage: P=0.188	K-M: P=0.018 Stage: P=0.009	K-M: P=0.07 Stage: P=0.219	K-M: P=0.083 Stage: P=0.001	K-M: P=0.042 Stage: P=0.087	K-M: P=0.019 Stage: P=0.0075	K-M: P=0.00017 Stage: P=0.003
LinkedOmics	K-M: P=0.64	K-M: P=0.028	K-M: P=0.15	K-M: P=0.024	K-M: P=0.093	K-M: P=0.004	K-M: P=0.040	K-M: P=0.0017
cBioportal	tumor high	tumor low	tumor high	tumor low	tumor low	tumor high	tumor high	tumor low
Oncomine	tumor high	tumor low	tumor high	tumor low	tumor low	tumor high	tumor high	tumor low

CCLE	tumor high	tumor low	tumor high	tumor low	tumor low	tumor high	tumor high	tumor low
String								
KaplanMeier plotter	P=0.0057	P=0.2	P=4.6e-08	P=0.0001	P=0.0033	P=0.03	P=0.029	P=0.048

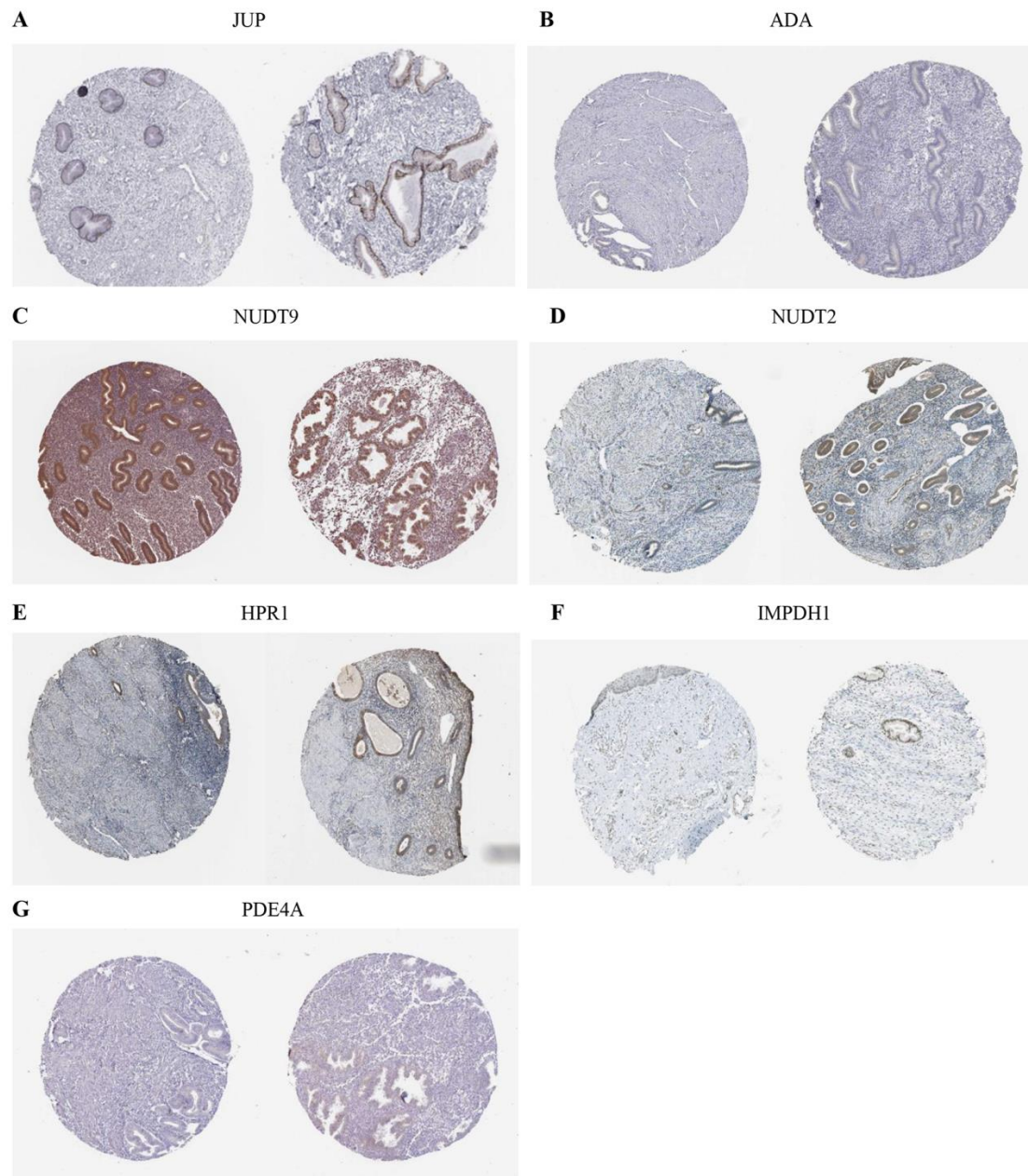


Figure S1 The Human Protein Atlas database validation. (A) JUP was medium expressed in normal uterine tissues and high expressed in UCS; (B) ADA was medium expressed in normal uterine tissues and high expressed in UCS; (C) NUDT9 was medium expressed in normal uterine tissues and high expressed in UCS; (D) NUDT2 was high expressed both in normal uterine tissues and UCS; (E) The expression of HPR1 was relatively low in normal tissues compared to that in tumor tissues; (F) IMPDH1 was medium expressed in normal uterine tissues and low expressed in UCS; (G) PDE4A was not detected in normal uterine tissues and medium expressed in UCS.

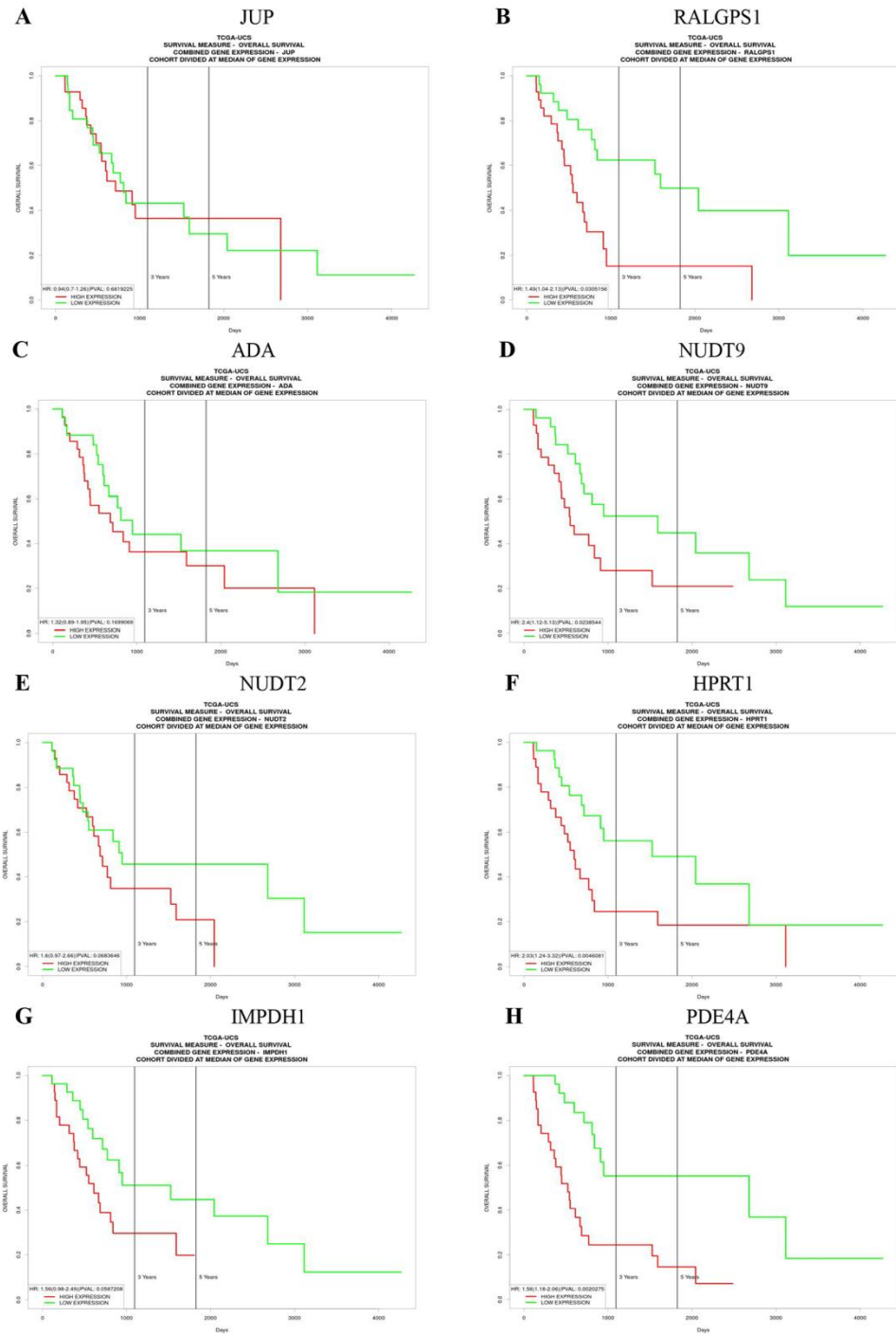


Figure S2 PROGgeneV2 database validation. RALGPS1 (B), NUDT9 (D), HPRT1 (F), and PDE4A (H) were significantly correlated with patients' prognosis.

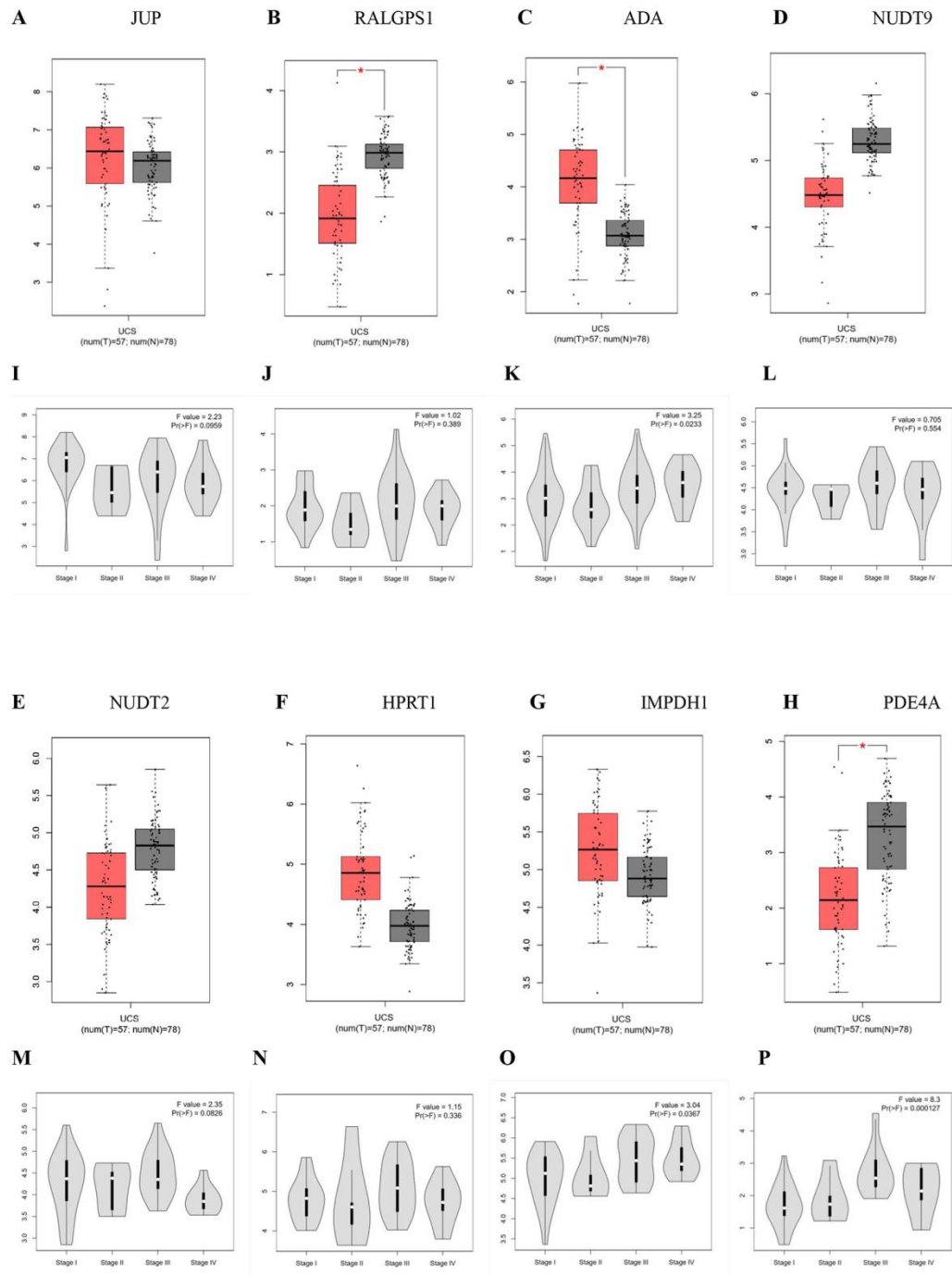


Figure S3 GEPIA database validation. RALGPS1 (B), NUDT9 (D), NUDT2 (E), and PDE4A (H) were significantly down regulated in tumor tissues. ADA (K), IMPDH1 (O), and PDE4A (P) were significantly correlated with clinical stage.

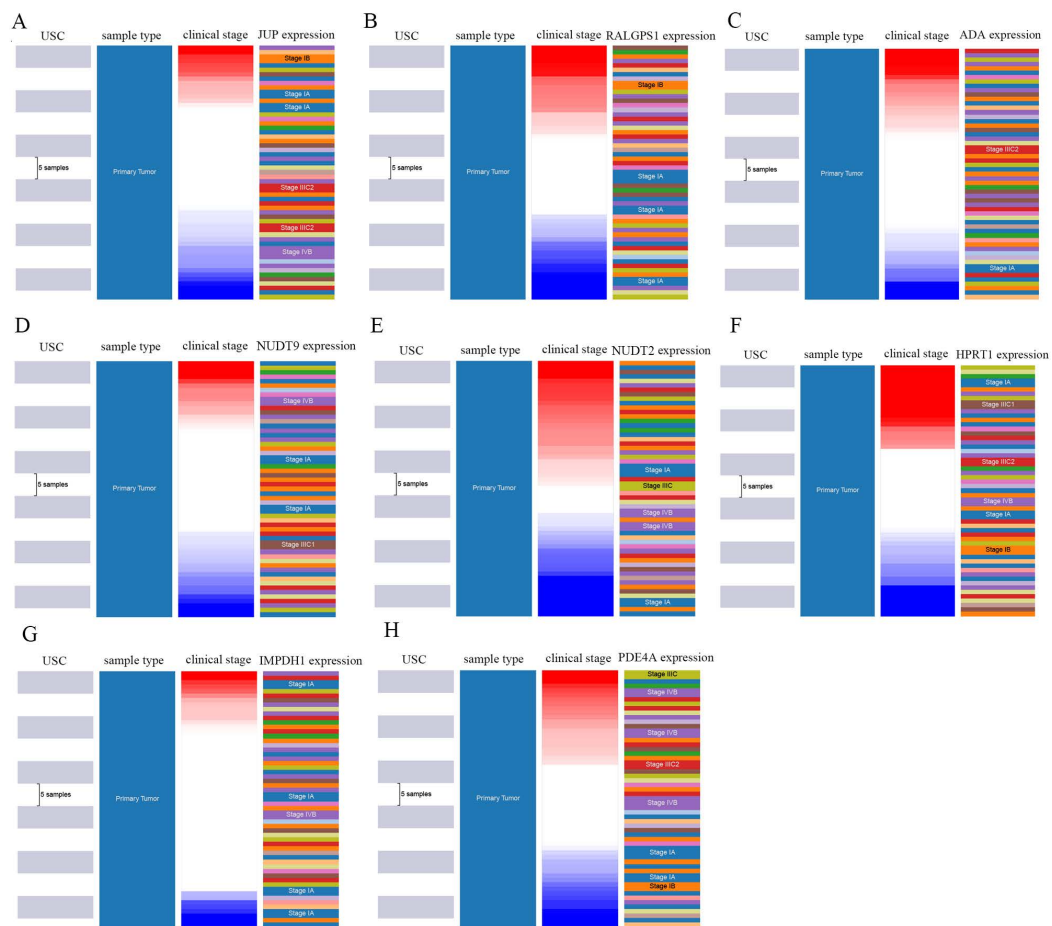


Figure S4 UCSC xena database validation. The expression levels of JUP (A), RALGPS1 (B), NUDT2 (E), HPRT1 (F), and IMPDH1 (G) were relatively high expressed in early stage UCS patients compared to advanced UCS patients. ADA (C), NUDT9 (D), and PDE4A (H) were relatively low expressed in early stage UCS patients compared to advanced UCS patients.

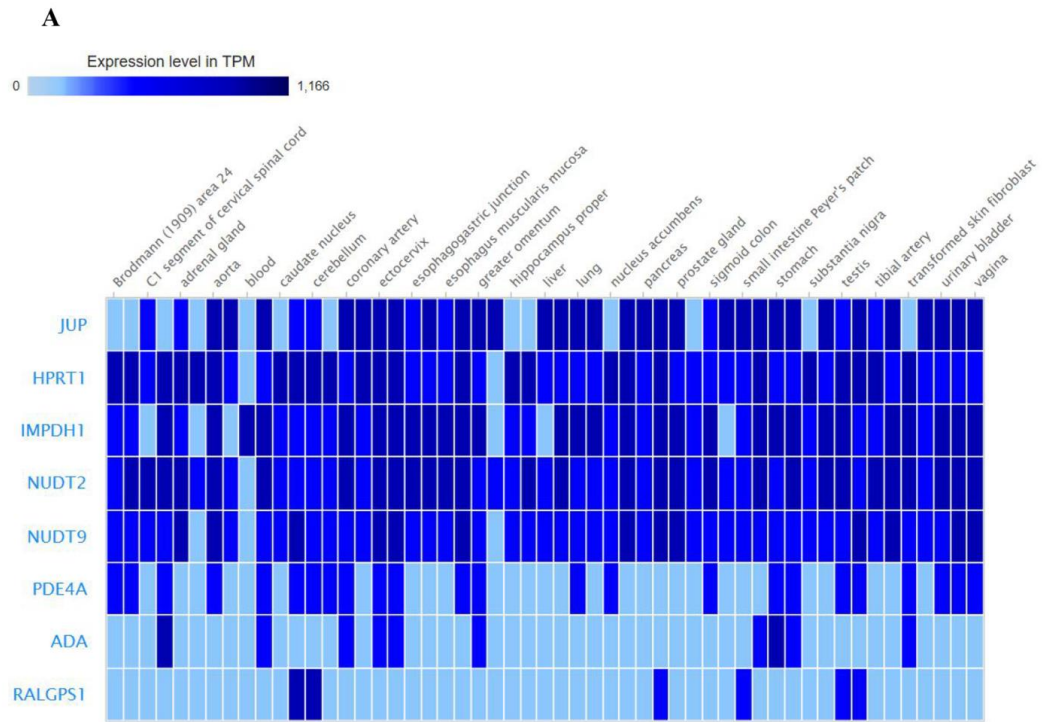


Figure S5 GTEx database validation. Heatmaps shown the expression levels of the genes in different normal tissues.

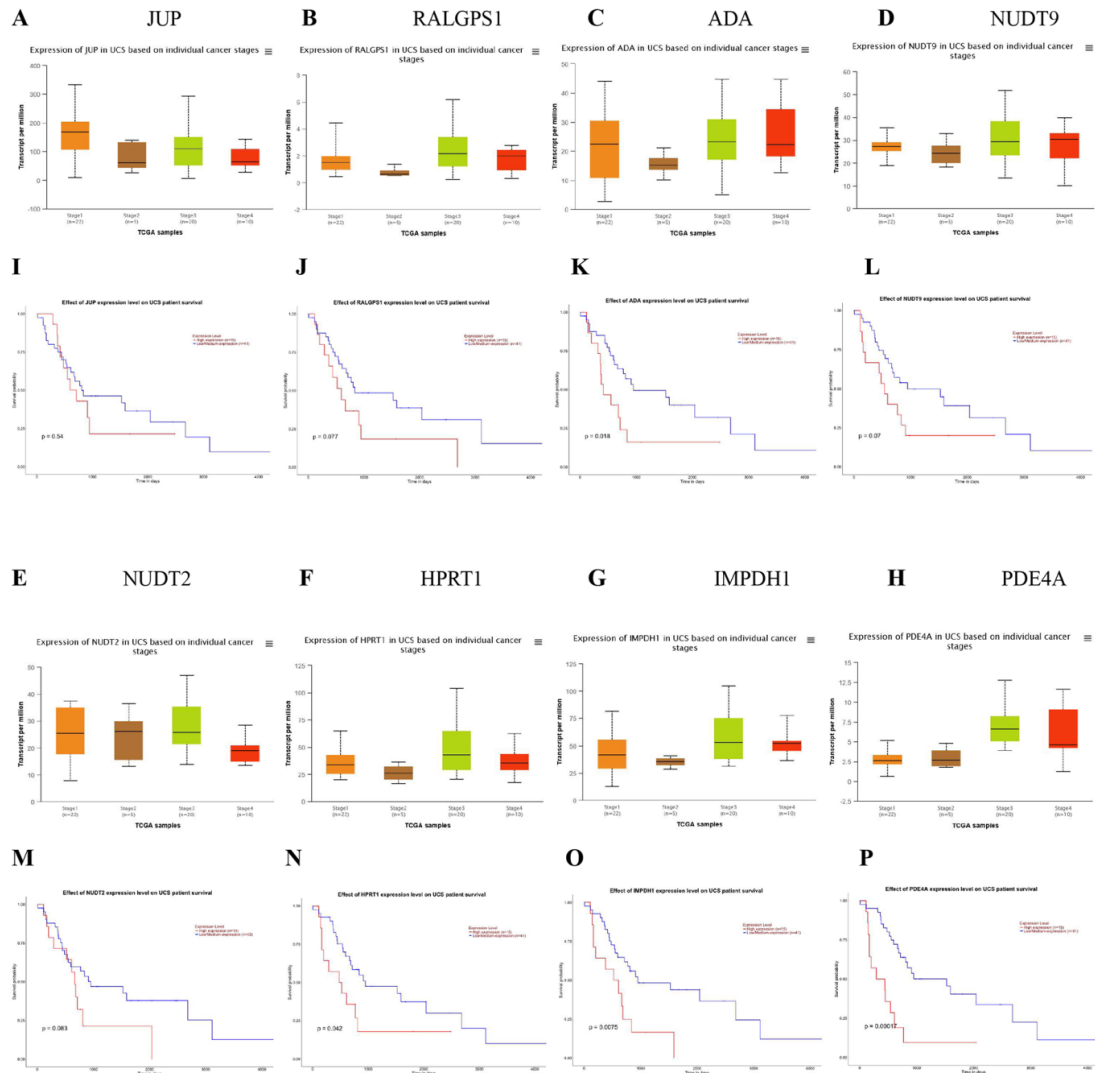


Figure S6 UALCAN database validation. JUP (A), ADA (C), NUDT2 (E), IMPDH1 (G), and PDE4A (H) were all differentially expressed between tumor and normal tissues with significance. Besides, ADA (K), HPRT1 (N), IMPDH1 (O), and PDE4A (P) were significantly correlated with patients' prognosis.

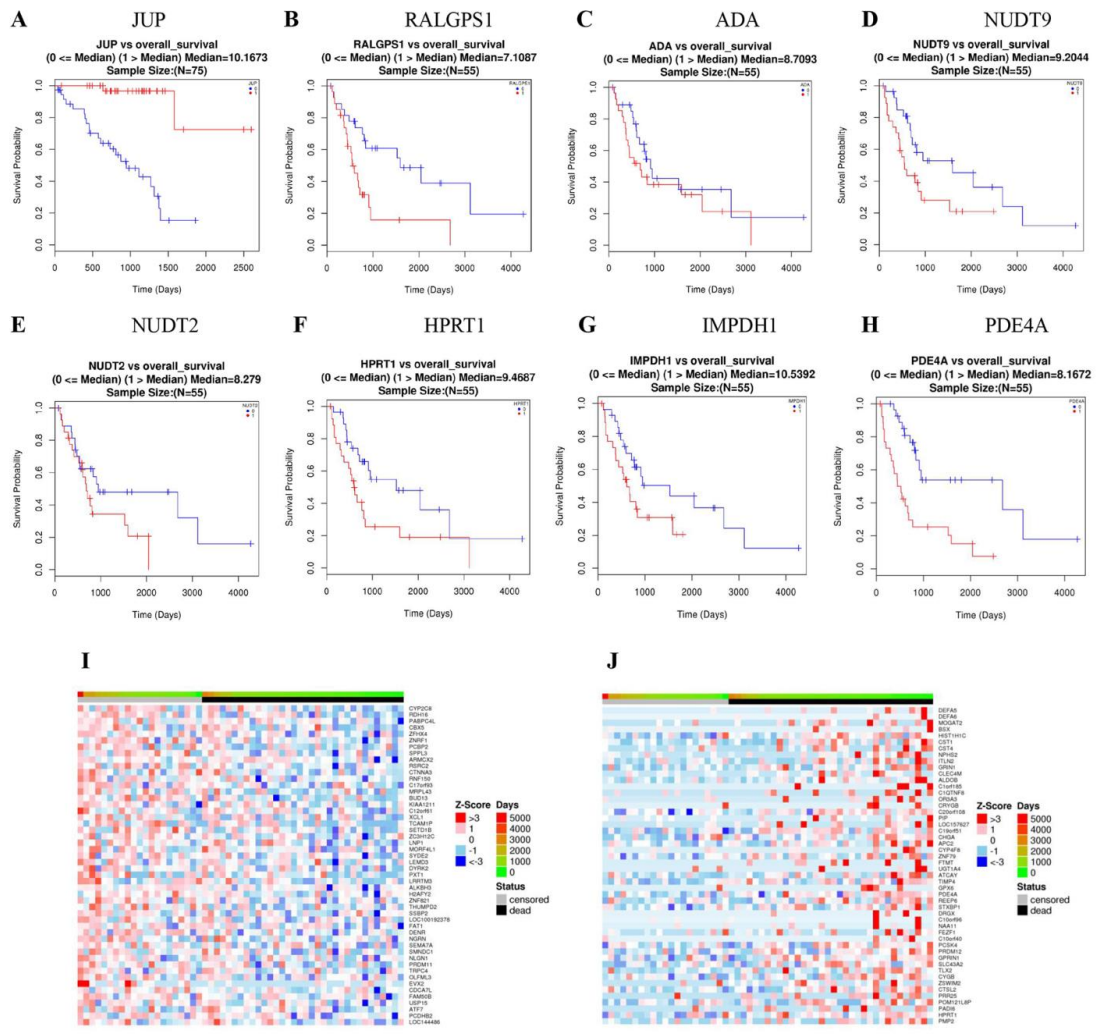


Figure S7 LinkedOmics database validation. K-M curves shown high expression of RALGPS1 (B), NUDT9 (D), HPRT1 (F), IMPDH1 (G), and PDE4A (H) were positively related to negative prognosis in patients with UCS. (I, J) Heatmaps shown the genes which have noteworthy correlation coefficient with RALGPS1.

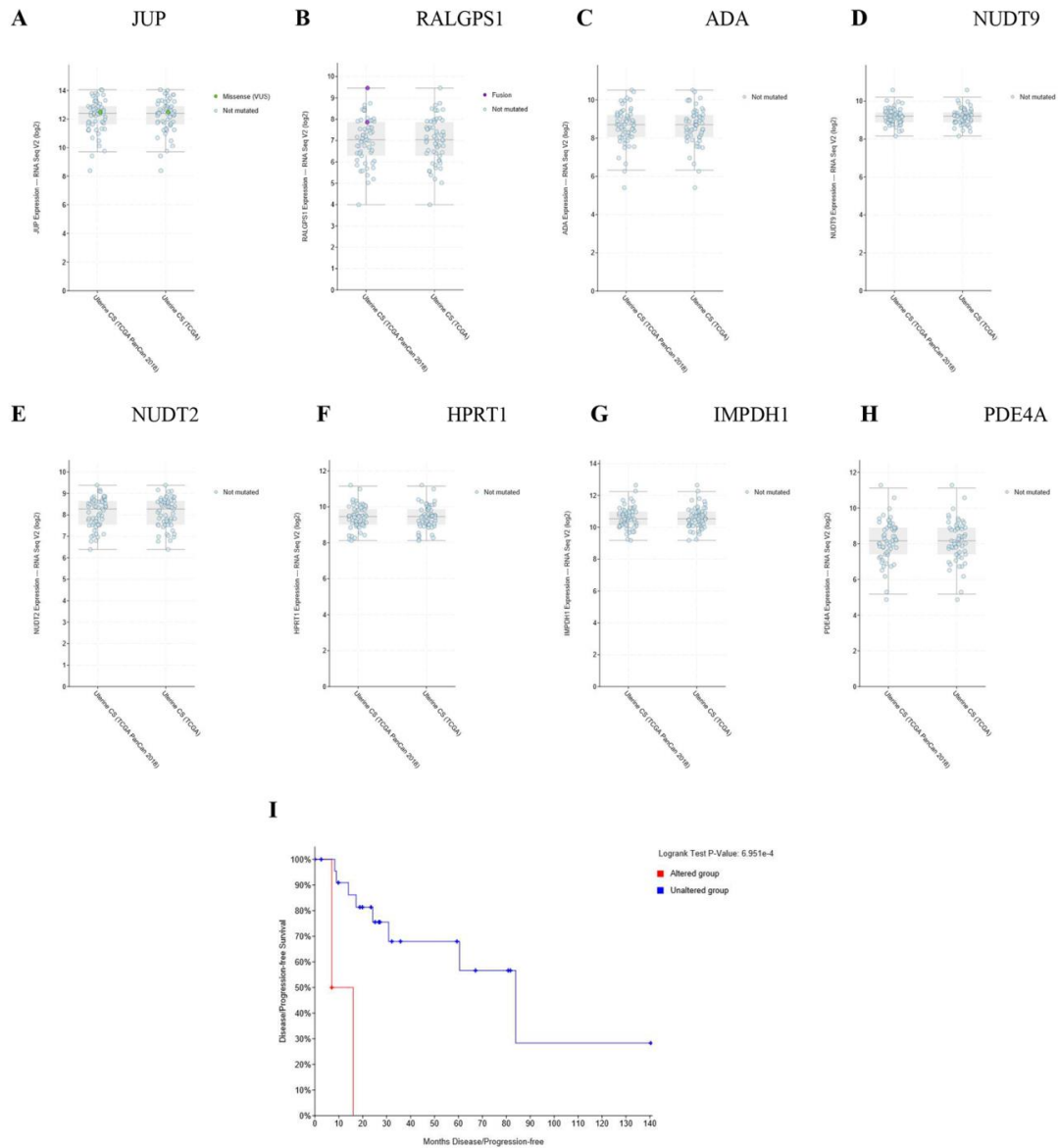


Figure S8 CBioportal database validation. Expression levels of JUP (A), RALGPS1 (B), ADA (C), NUDT9 (D), NUDT2 (E), HPRT1 (F), IMPDH1 (G), and PDE4A (H) in patients with UCS. (I) Integrated genes ($P = 0.0007$) were significantly related to prognosis.

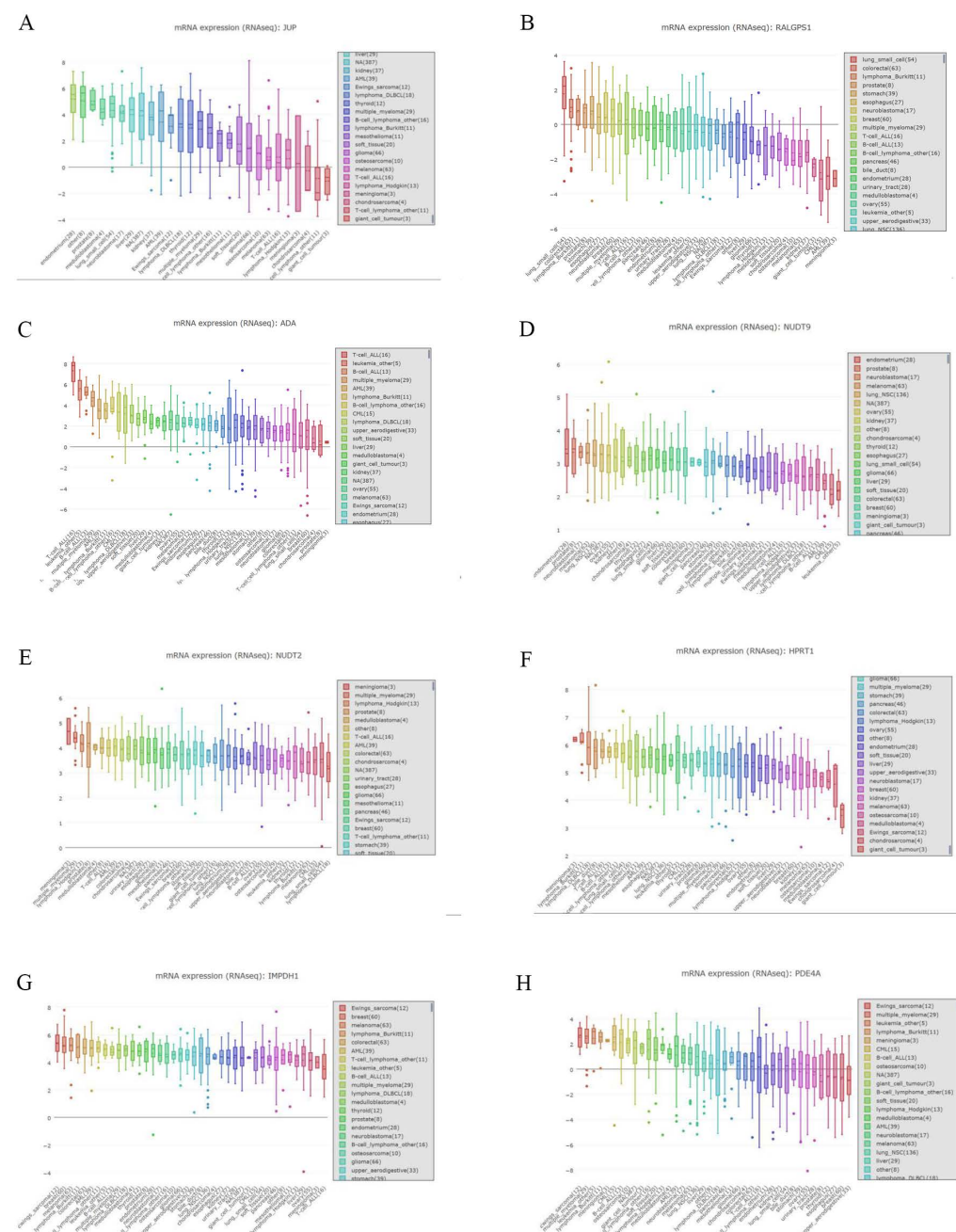


Figure S10 CCLE database validation. RALGPS1 (B), NUDT9 (D), NUDT2 (E), and PDE4A (H) were down regulated, while JUP (A), ADA (C), HPRT1 (F), and IMPDH1 (G) were significantly up regulated in different kinds of uterine cancers.

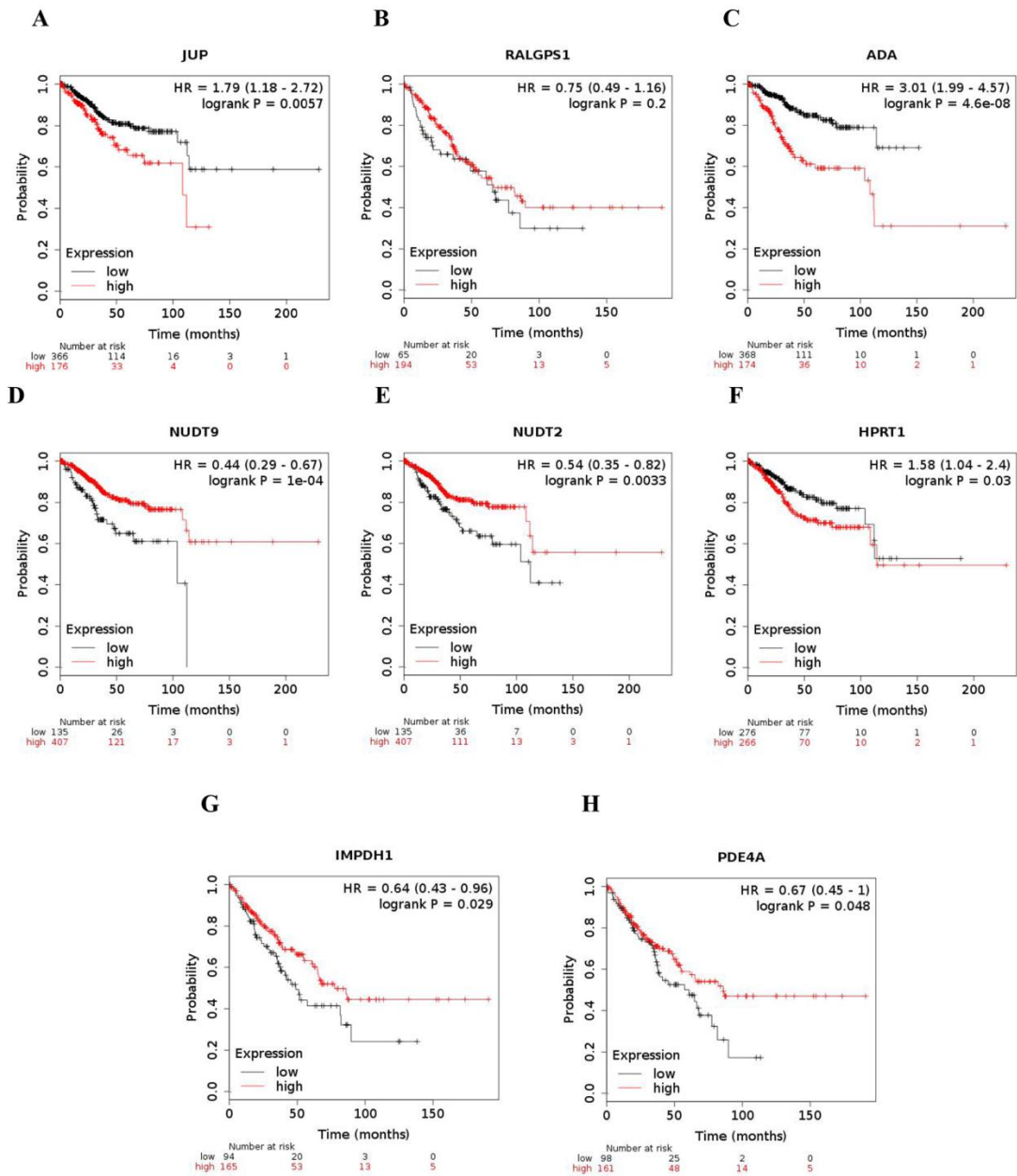


Figure S12 K-M Plotter database validation. JUP (A), ADA (C), NUDT9 (D), NUDT2 (E), HPRT1 (F), IMPDH1 (G), and PDE4A (H) were significantly correlated with patients' prognosis.