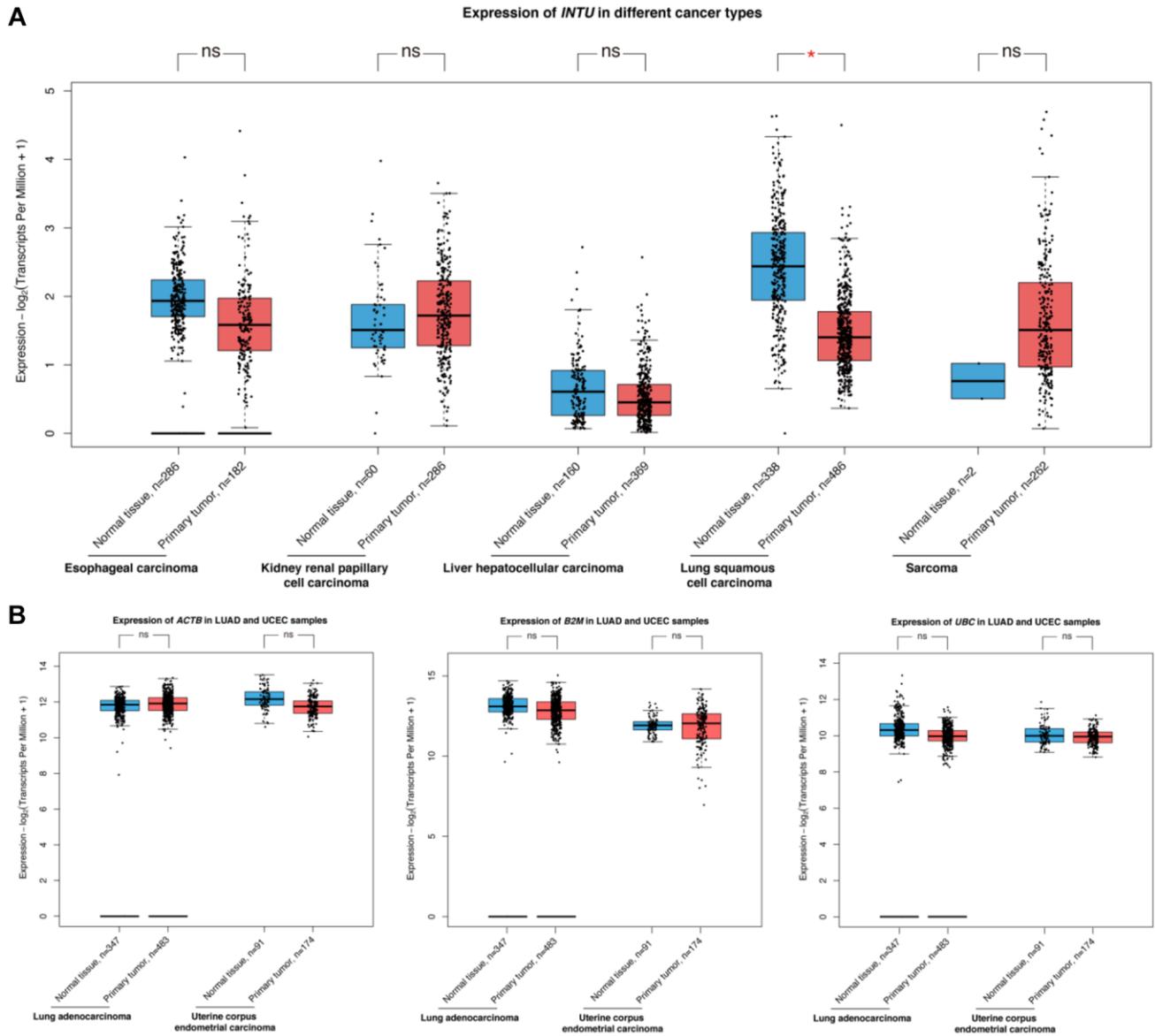
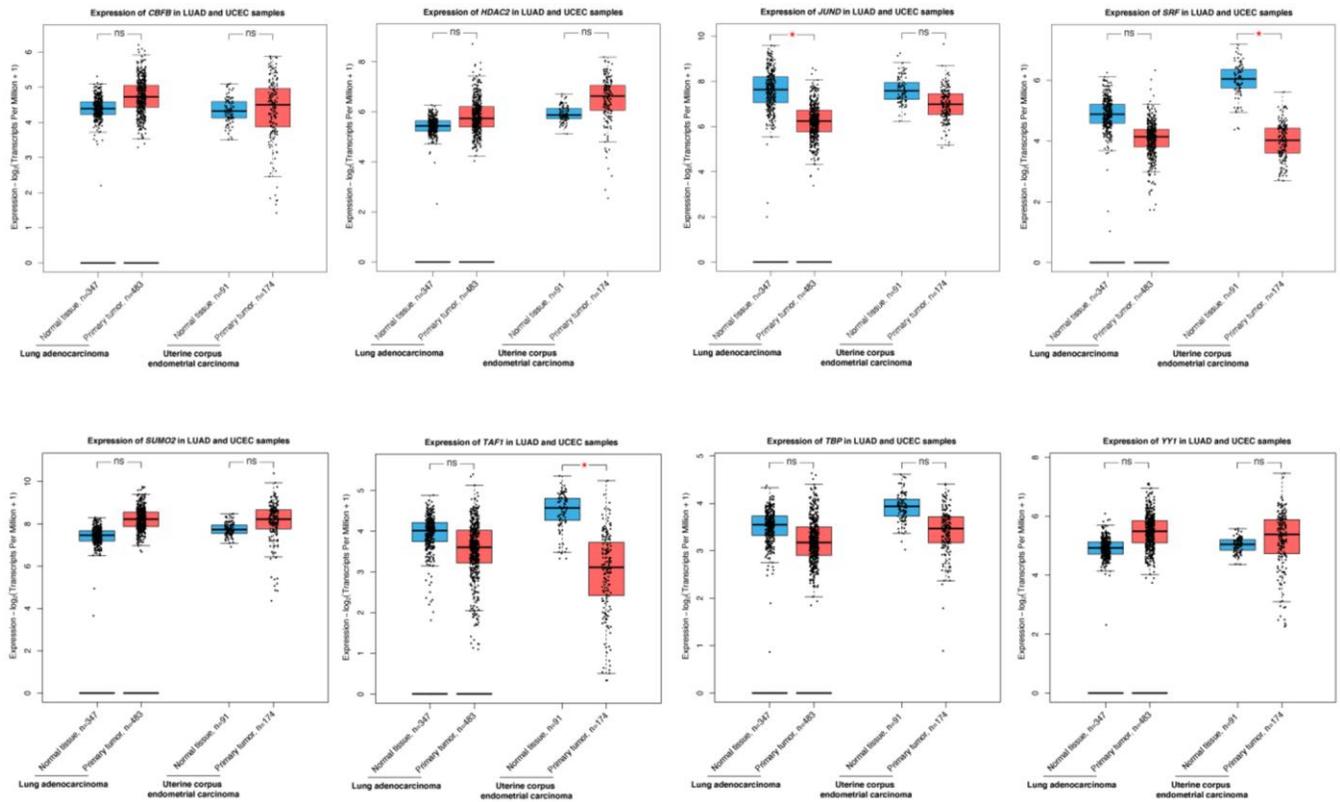


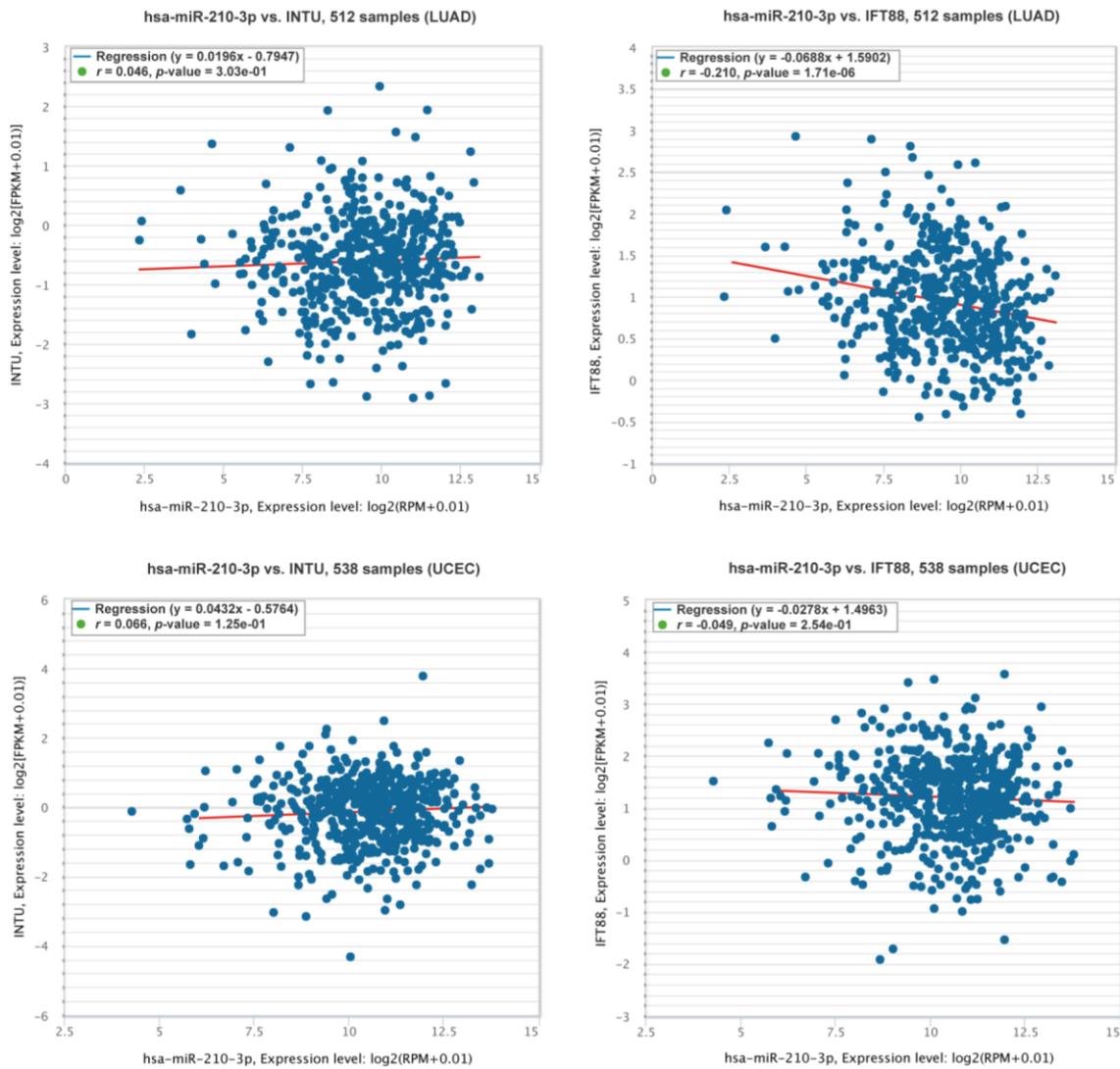
SUPPLEMENTARY FIGURES



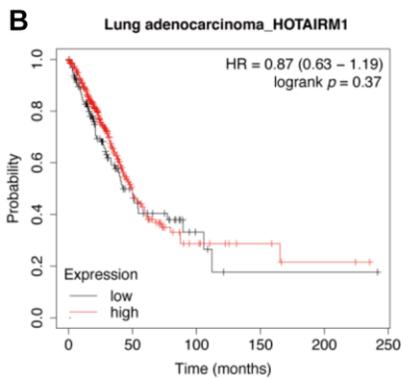
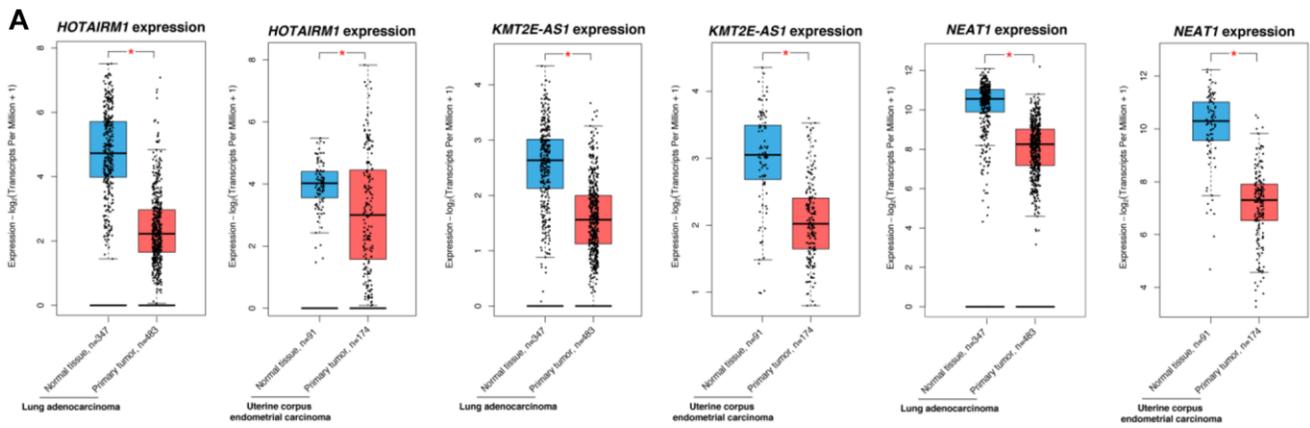
Supplementary Figure 1. Evaluation of *INTU* and housekeeping gene levels in different cancer types. (A) The expression of *INTU* was significantly downregulated in LUSC tumor samples. The *INTU* expression was not significantly altered in ESCA, KIRP, LIHC and SARC tumor samples when compared to their respective normal control samples. **(B)** The expression of housekeeping genes *ACTB*, *B2M* and *UBC* was not altered in LUAD and UCEC tumor samples when compared to their respective normal control samples.



Supplementary Figure 2. Examination of *CBFB*, *HDAC2*, *JUND*, *SRF*, *SUMO2*, *TAF1*, *TBP* and *YY1* levels in LUAD and UCEC samples. None of the transcription factors examined showed significant change of expression in both LUAD and UCEC tumor samples.

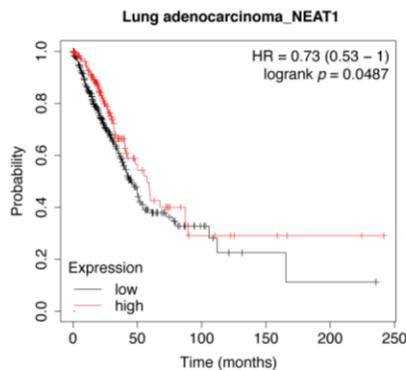


Supplementary Figure 3. Evaluation of the correlation between *hsa-miR-210-3p* expression and *INTU* and *IFT88* levels in LUAD and UCEC tumor samples. No significant correlation was detected between the expression of *hsa-miR-210-3p* and mRNA levels of *INTU* and *IFT88* in LUAD and UCEC tumor samples, except for in LUAD tumor samples, expression of *hsa-miR-210-3p* negatively correlated with *IFT88* mRNA level.



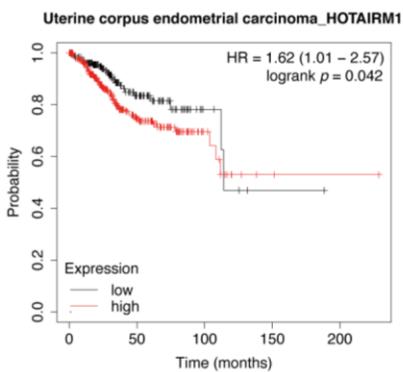
Expression range of the *HOTAIRM1* probe: 1 - 1965

Cutoff value to differentiate low and high expression groups: 32



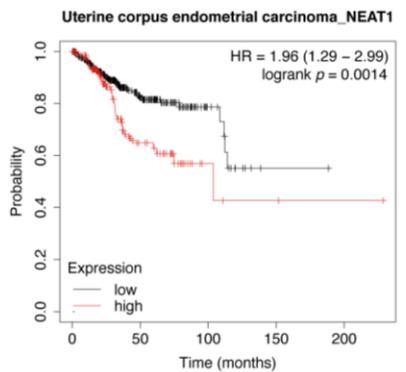
Expression range of the *NEAT1* probe: 539 - 842740

Cutoff value to differentiate low and high expression groups: 17650



Expression range of the *HOTAIRM1* probe: 0 - 4033

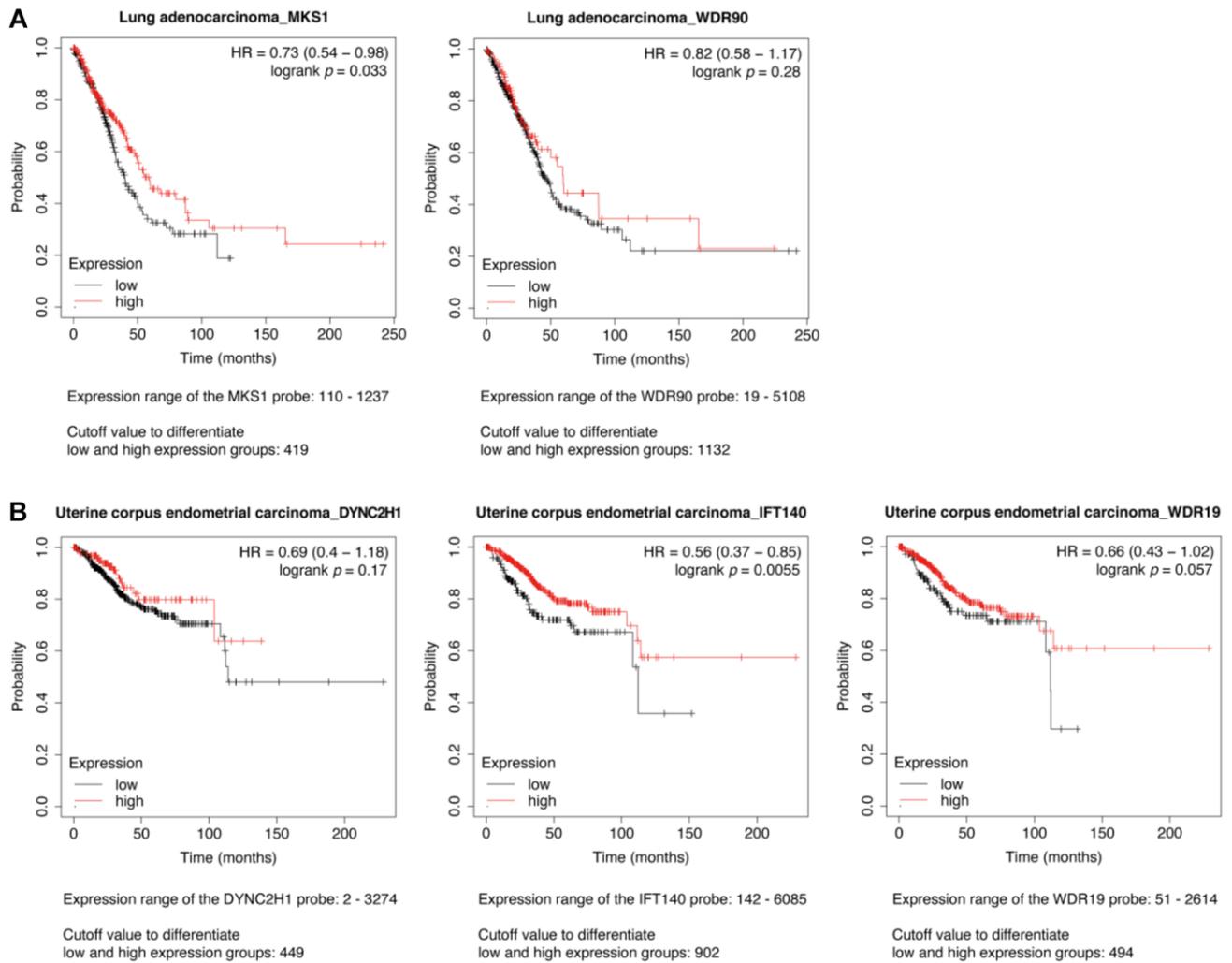
Cutoff value to differentiate low and high expression groups: 29



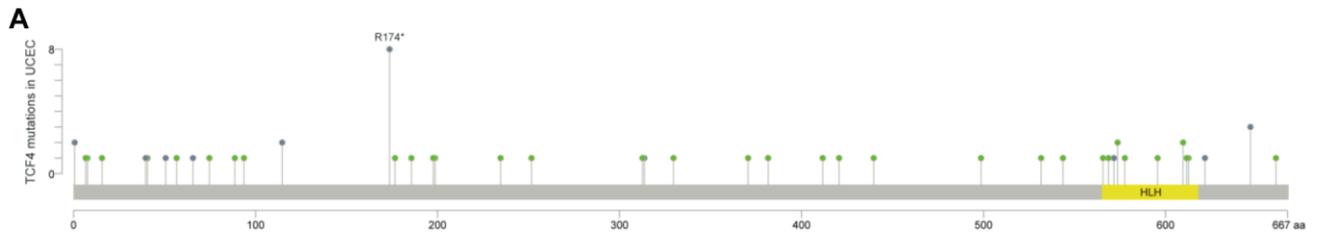
Expression range of the *NEAT1* probe: 170 - 467509

Cutoff value to differentiate low and high expression groups: 8208

Supplementary Figure 4. Evaluation of the expression and prognostic significance of lncRNAs in LUAD and UCEC tumor samples. (A) The expression of *HOTAIRM1*, *KMT2E-AS1* and *NEAT1* was significantly downregulated in LUAD and UCEC tumor samples. (B) The LUAD patients with decreased *NEAT1* level showed reduced survival probabilities. Higher levels of *HOTAIRM1* and *NEAT1* were found associated with poor survival probabilities in UCEC patients. No correlation between *HOTAIRM1* level and OS probabilities was detected in LUAD patients.



Supplementary Figure 5. Evaluation of the prognostic significance of enriched Hh-related genes in LUAD and UCEC patients. (A) Decreased level of *MKS1* correlated with poor OS probabilities in LUAD patients, whilst the *WDR90* level didn't show a significant correlation with OS probabilities in LUAD patients. (B) The UCEC patients with lowered *IFT140* level showed decreased OS probabilities. Neither *DYNC2H1* nor *WDR19* level significantly correlated with OS probabilities in UCEC patients.



B

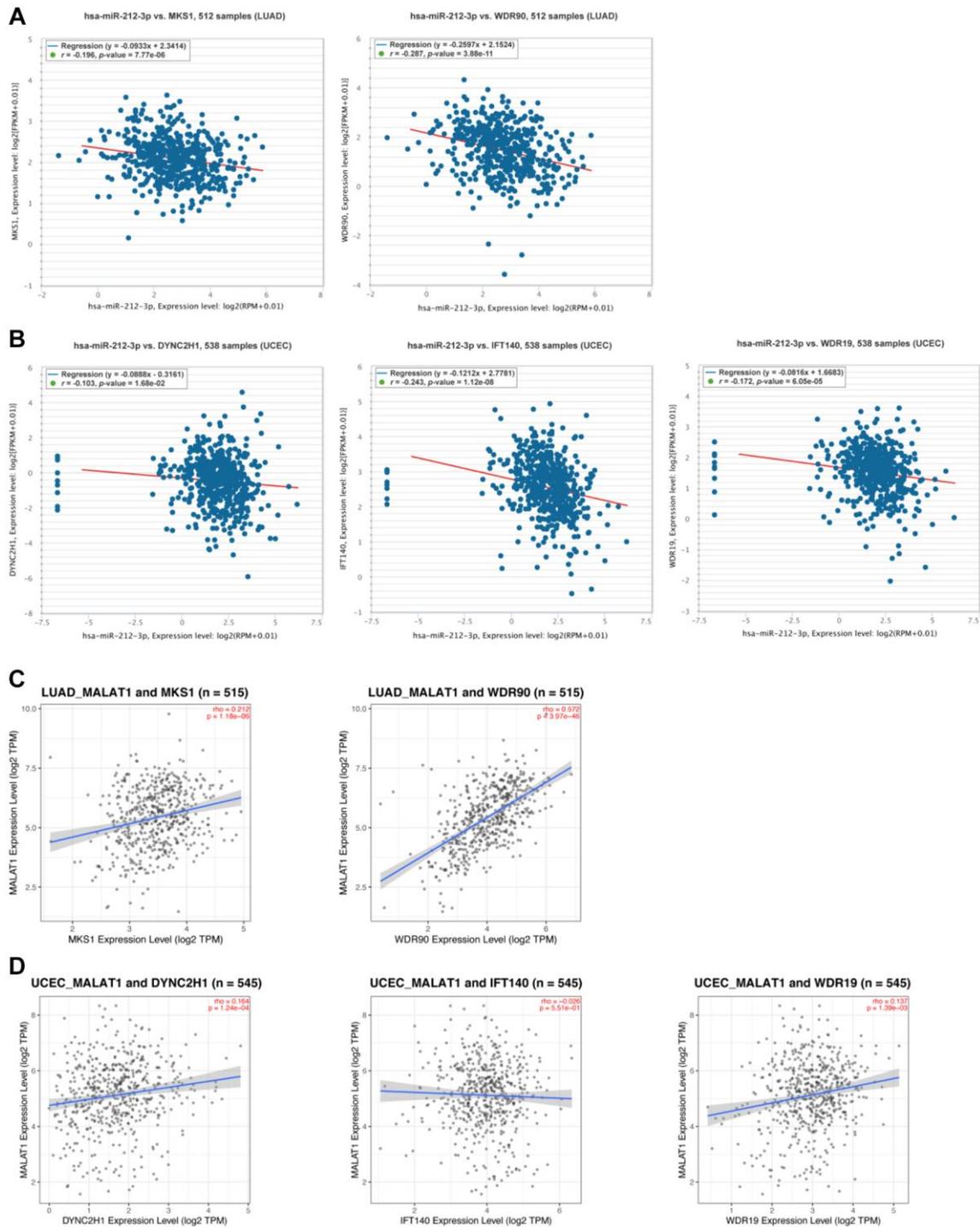
Cancer type	Sample ID	TCF4 mutation			Functional Impacts	
		Amino acid change	HGVSc	Mutation type	SIFT	MutationAssessor
Uterine Corpus Endometrial Carcinoma	TCGA-AP-A056-01	R174*	ENST00000356073.4:c.520C>T	Nonsense	N/A	N/A
Uterine Corpus Endometrial Carcinoma	TCGA-AX-A05Z-01					
Uterine Corpus Endometrial Carcinoma	TCGA-B5-A0JY-01					
Uterine Corpus Endometrial Carcinoma	TCGA-B5-A11E-01					
Uterine Corpus Endometrial Carcinoma	TCGA-B5-A1MR-01					
Uterine Corpus Endometrial Carcinoma	TCGA-BS-A0UF-01					
Uterine Corpus Endometrial Carcinoma	TCGA-EO-A3AV-01					
Uterine Corpus Endometrial Carcinoma	TCGA-QF-A5YS-01					

C

TCF4 protein

	174
Human	TKKVRKVP
Chimpanzee	TKKVRKVP
Cattle	TKKVRKVP
Pig	TKKVRKVP
Rat	TKKVRKVP
Mouse	TKKVRKVP
Frog	AKKVRKVP
	.*****

Supplementary Figure 6. Illustration of the mutations in TCF4 protein from LUAD and UCEC tumor samples. (A) A relative higher mutation frequency was identified at TCF4^{R174} residue from UCEC tumor samples. **(B)** The detailed mutation site of TCF4^{R174} mutant protein from UCEC tumor samples. **(C)** The TCF4^{R174} residue was highly conserved among different species.



Supplementary Figure 7. The *MALAT1-hsa-miR-212-3p* signaling axis regulates enriched Hh-related genes in LUAD and UCEC samples. (A) The expression of *hsa-miR-212-3p* was found negatively associated with the mRNA levels of *MKS1* and *WDR90* in LUAD samples. **(B)** Negative correlation was determined between *hsa-miR-212-3p* expression and mRNA levels of *DYNC2H1*, *IFT140* and *WDR19* in UCEC samples. **(C)** The expression of *MALAT1* positively correlated with the levels of *MKS1* and *WDR90* in LUAD samples. **(D)** The expression of *MALAT1* positively correlated with the levels of *DYNC2H1* and *WDR19* in UCEC samples. No significant correlation was determined between *MALAT1* and *IFT140*.