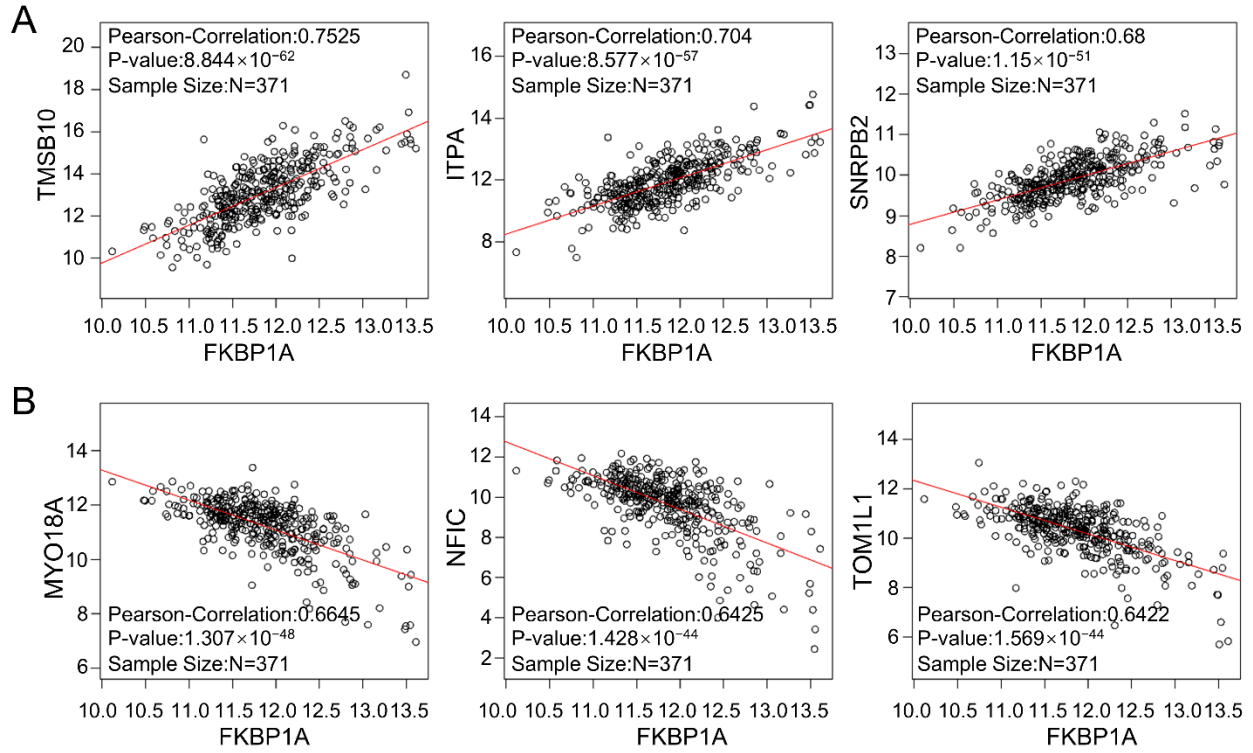
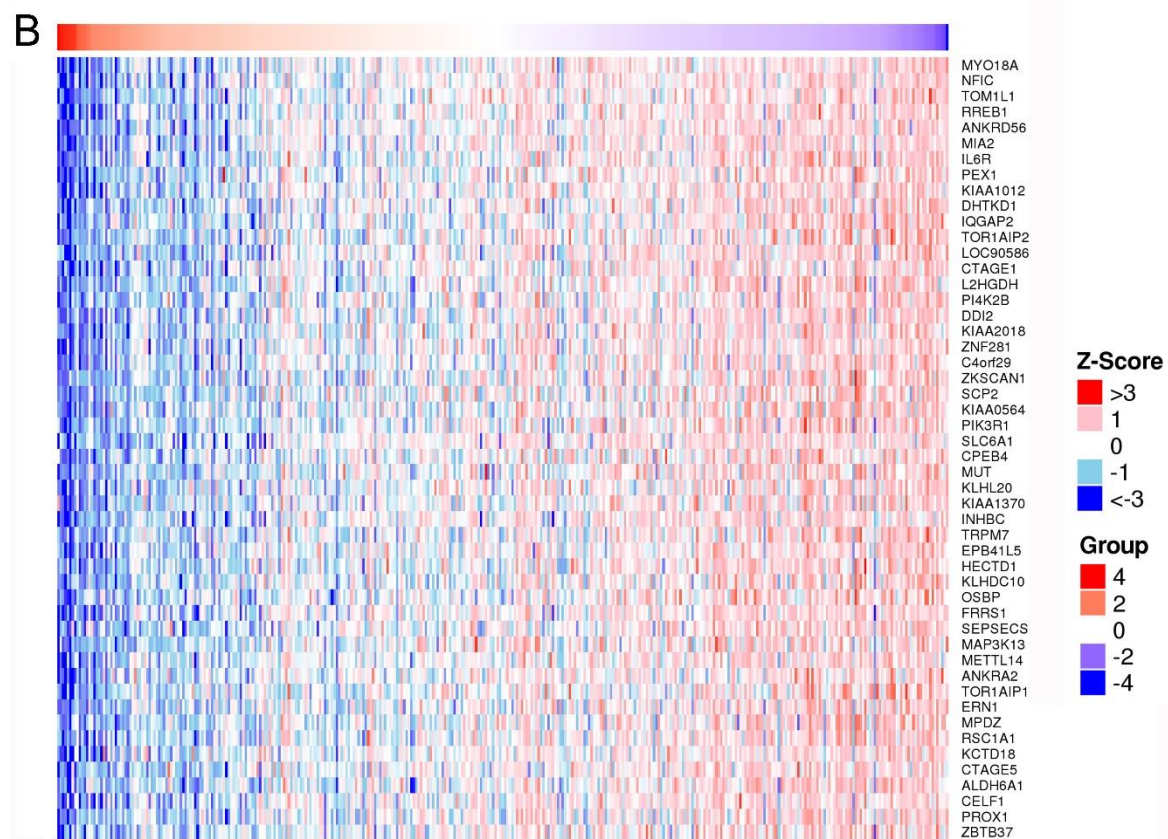
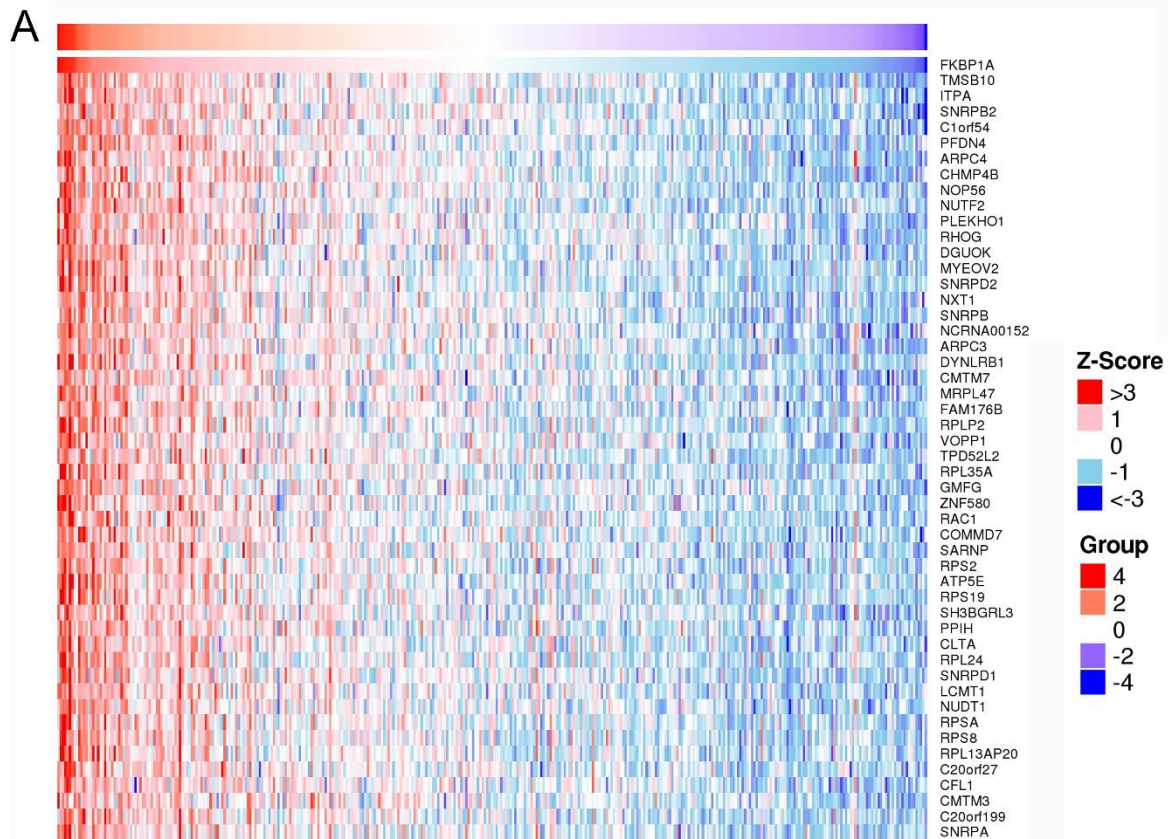


Supplementary Table S1. Expression levels of *FKBP1A* in HCCDB database

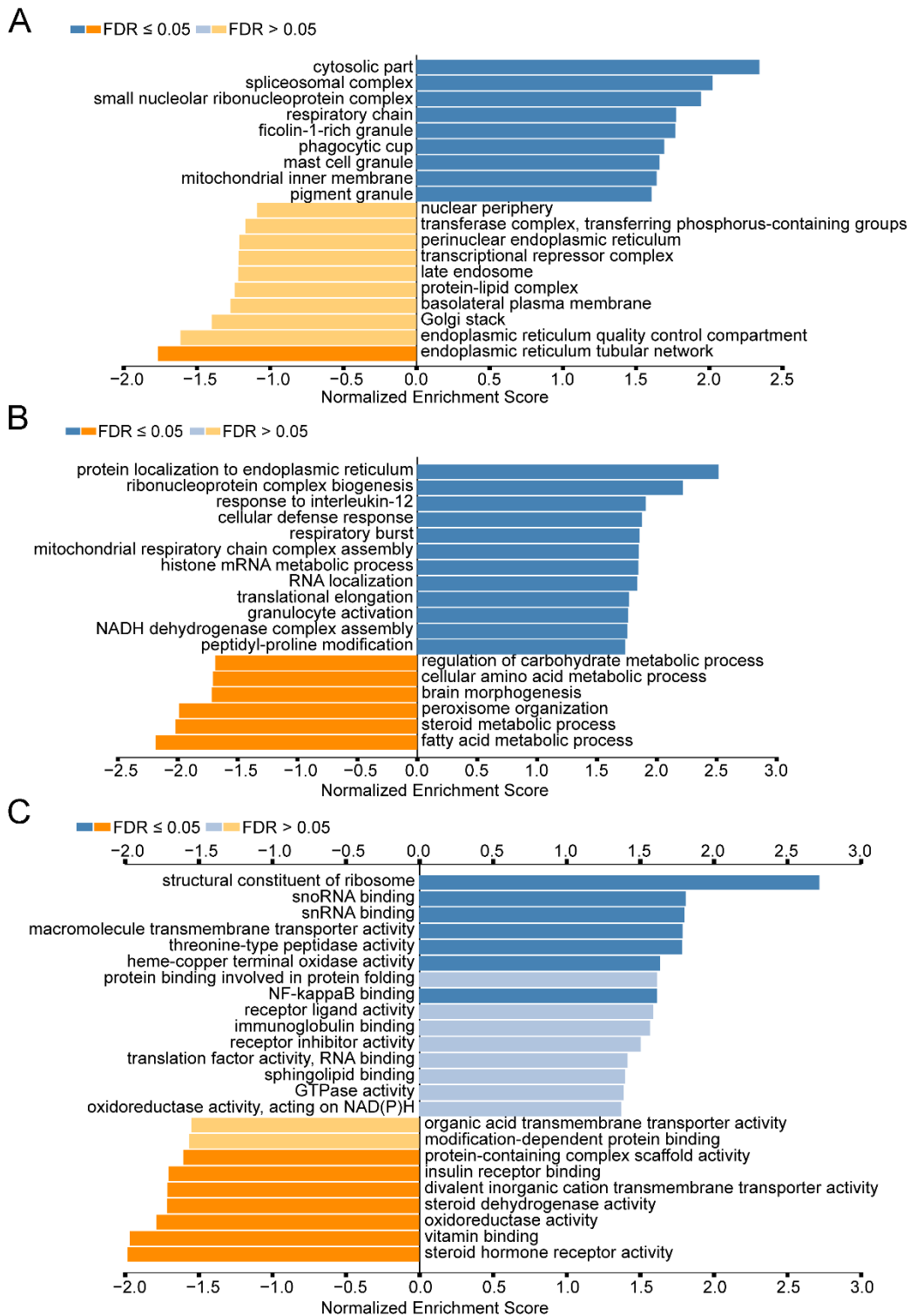
Dataset	P-value	Type	Nums	Mean	STD	IQR
HCCDB1	0.000001070	HCC	100	11.34	0.3667	0.4914
		Adjacent	97	11.10	0.3168	0.3249
HCCDB3	0.0001361	HCC	268	7.896	1.791	2.210
		Adjacent	243	7.311	1.644	1.835
		Cirrhotic	40	10.23	1.665	1.871
		Healthy	6	6.262	0.2864	0.4250
HCCDB4	4.570e-31	HCC	240	8.183	0.6289	0.9086
		Adjacent	193	7.536	0.4386	0.5385
HCCDB6	1.390e-24	HCC	225	6.447	0.6841	0.9070
		Adjacent	220	5.824	0.5076	0.6724
HCCDB7	0.03196	HCC	80	14.12	0.5324	0.7195
		Adjacent	82	13.93	0.5670	0.8197
HCCDB11	0.06864	HCC	88	8.013	0.5790	0.5815
		Adjacent	48	8.260	0.8235	0.7188
HCCDB12	0.00001900	HCC	81	7.966	0.4326	0.6260
		Adjacent	80	7.692	0.3512	0.4174
HCCDB13	0.2174	HCC	228	5.860	0.9144	1.029
		Adjacent	168	5.726	0.7040	0.9128
HCCDB15	9.180e-18	HCC	351	11.84	0.5789	0.7500
		Adjacent	49	11.33	0.2762	0.4200
HCCDB16	9.020e-9	HCC	60	9.202	0.3315	0.3739
		Adjacent	60	8.857	0.2765	0.3266
HCCDB17	3.500e-10	HCC	115	9.109	0.4034	0.6050
		Adjacent	52	8.661	0.3780	0.4300
HCCDB18	3.000e-39	HCC	212	6.092	0.5949	0.7875
		Adjacent	177	5.292	0.4774	0.4800



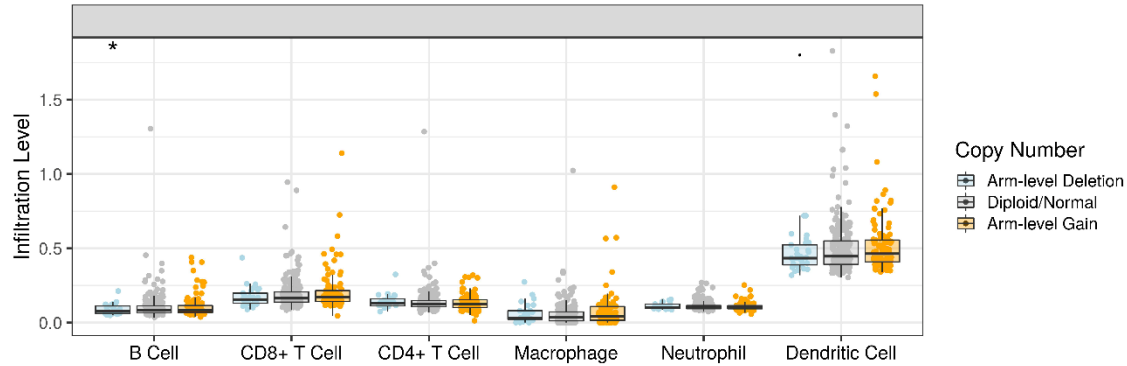
Supplementary Figure S1. The top3 co-expression genes with *FKBP1A* were analyzed in LIHC from the LinkedOmics database. (A-B) The scatter plot shows the Pearson correlation of *FKBP1A* expression with the top3 positively correlated genes (A) and negatively correlated genes (B) in LIHC.



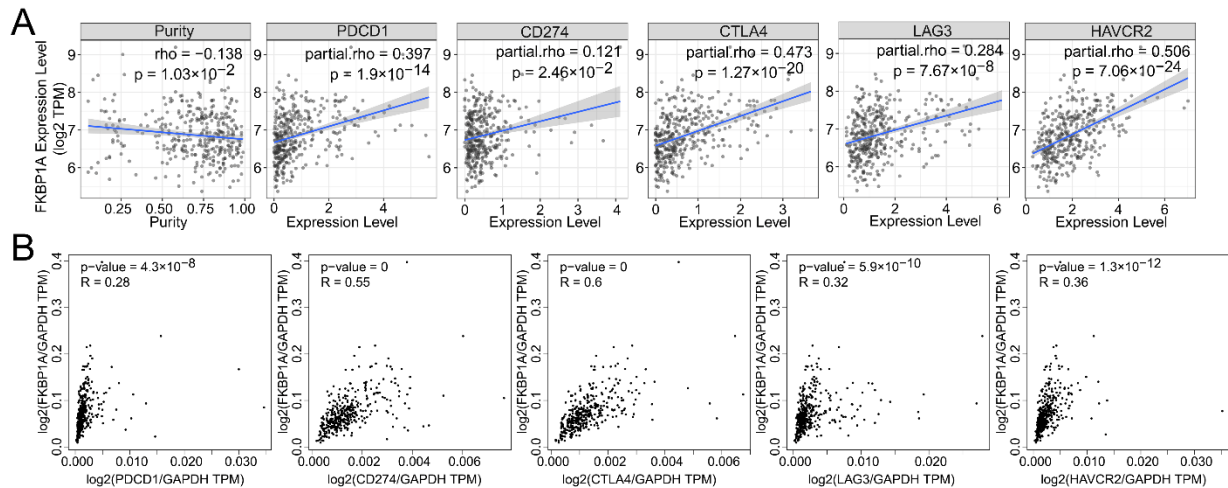
Supplementary Figure S2. Top 50 genes related to *FKBP1A* in LIHC are shown in heatmaps from the LinkedOmics database. (A-B) Heat maps showing top 50 genes positively (A) and negatively (B) correlated with *FKBP1A*. Red indicates positively correlated genes and blue indicates negatively correlated genes.



Supplementary Figure S3. The significantly enriched GO annotations of genes co-expressed with *FKBP1A* were analyzed using gene set enrichment analysis by LinkedOmics database. (A) Cellular components. (B) Biological processes. (C) Molecular functions. FDR, false discovery rate. The x-axis represents the normalized enrichment score, and the y-axis represents the term of GO. GO, Gene Ontology; FDR, false discovery rate.



Supplementary Figure S4. The infiltration level of various immune cells under somatic copy number alterations of *FKBP1A* in LIHC. $*p < 0.05$.



Supplementary Figure S5. Correlation of *FKBP1A* expression with *PD-1*, *PD-L1*, *CTLA-4*, *LAG3* and *HAVCR2* expression in LIHC. (A) Spearman correlation of *FKBP1A* with expression of *PD-1*, *PD-L1*, *CTLA-4*, *LAG3* and *HAVCR2* in LIHC adjusted by tumor purity using TIMER2.0. (B) The expression correlation of *FKBP1A* with expression of *PD-1*, *PD-L1*, *CTLA-4*, *LAG3* and *HAVCR2* in LIHC determined by GEPIA database.