

Characterization and Regulatory Mechanism Evaluation of C8orf33 in Hepatocellular Carcinoma through Multiomics Profiling

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23 Supplementary Table 1

24 Abbreviations from the TCGA database for 33 cancers

Cancer Type	Abbreviations
ACC	Adrenocortical carcinoma
BLCA	Bladder urothelial carcinoma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and Endocervical adenocarcinoma
CHOL	Cholangiocarcinoma
COAD	Colon adenocarcinoma
DLBC	Lymphoid neoplasm diffuse large B-cell lymphoma
ESCA	Esophageal carcinoma
GBM	Glioblastoma multiforme
HNSC	Head and neck squamous cell carcinoma
KICH	Kidney chromophobe
KIRC	Kidney renal clear cell carcinoma
KIRP	Kidney renal papillary cell carcinoma
LAML	Acute myeloid leukemia
LGG	Brain lower grade glioma
LIHC	Liver hepatocellular carcinoma
LUAD	Lung adenocarcinoma
LUSC	Lung squamous cell carcinoma
MESO	Mesothelioma
OV	Ovarian serous cystadenocarcinoma
PAAD	Pancreatic adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate adenocarcinoma
READ	Rectum adenocarcinoma
SARC	Sarcoma
SKCM	Skin cutaneous melanoma
STAD	Stomach adenocarcinoma
TGCT	Testicular germ cell tumors
THCA	Thyroid carcinoma
THYM	Thymoma
UCEC	Uterine corpus endometrial carcinoma
UCS	Uterine carcinosarcoma
UVM	Uveal melanoma

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27 Supplementary Table 2

28 The relevant primer sequences

Primer name	Sequence (5'to3')
h-MIF-F	GAACCGCTCCTACAGCAAGC
h-MIF-R	GGCCGCGTTCATGTCGTAAT
mus-CD74-F	CATGGATGGCGTGAAGTGA
mus-CD74-R	GTGGCTCTTTAGGTGGAGCC
mus-CXCR4-F	AGGGGAGTGCTATTTGCTCC
mus-CXCR4-R	AAGCAGGGTTCCTTGTGGA
mus-CD44-F	ACGAGTGCAACTACAGCCTTG
mus-CD44-R	CCGTACCAGGCATCTTCGTT
h-GAPDH-F	ACAACCTTGGTATCGTGGAAGG
h-GAPDH-R	GCCATCACGCCACAGTTTC
mus-GAPDH-F	ACTCCACTCACGGCAAATTC
mus-GAPDH-R	TCTCCATGGTGGTGAAGACA

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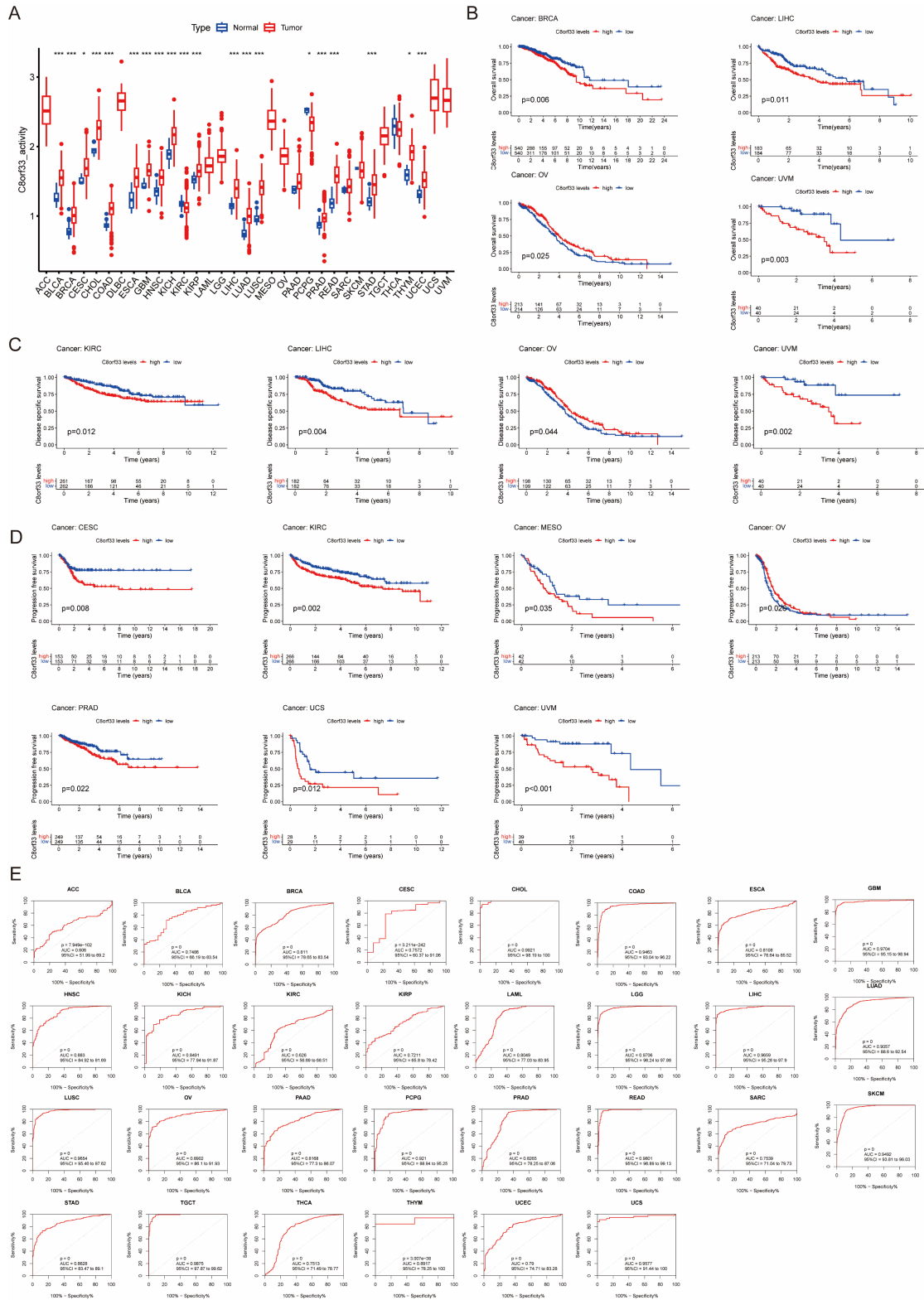
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Supplementary Figure 1. Pan-Cancer Analysis of C8orf33 Expression and Prognostic Value.

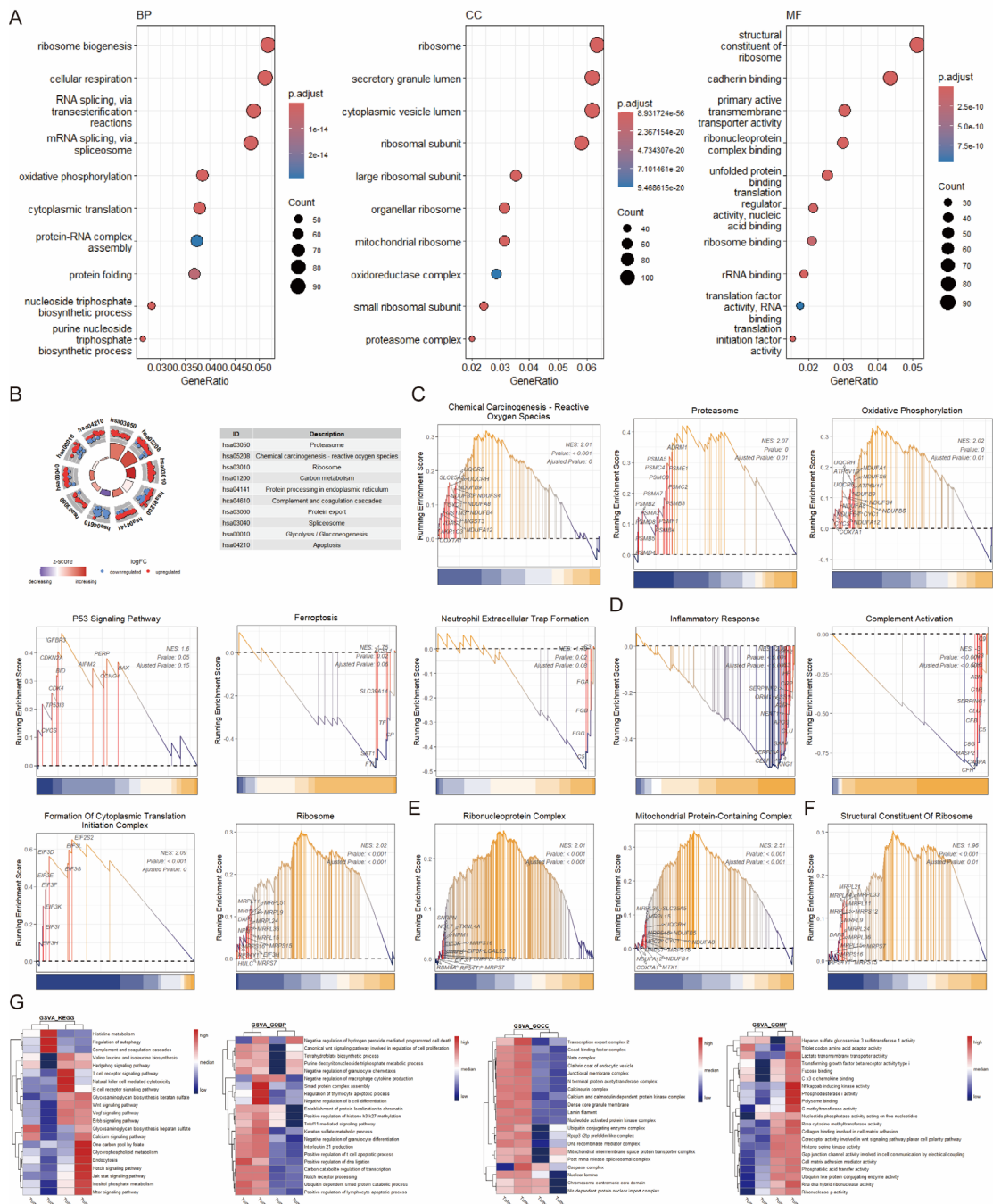
(A) Box plots comparing C8orf33 activity in tumor versus non-tumor tissues across a pan-cancer cohort.

(B-D) Kaplan-Meier survival analysis for Overall Survival (OS), Disease-Specific Survival (DSS), and Progression-Free Interval (PFI) in patient cohorts stratified by C8orf33 expression levels.

(E) ROC curves evaluating the diagnostic potential of C8orf33 to distinguish tumor from normal tissues.



Supplementary Figure 3. Functional annotation and pathway analysis of the Tumor-Epi3 subpopulation. (A, B) Results from Gene Ontology (GO) (A) and KEGG (B) pathway enrichment analyses performed on the differentially expressed genes identified in the Tumor-Epi3 subpopulation. (C-F) Representative Gene Set Enrichment Analysis (GSEA) plots illustrating the enrichment of selected KEGG pathways and GO terms. (G) Gene Set Variation Analysis (GSVA) heatmap showing pathway activities across parenchymal subpopulations.



Supplementary Figure 4. Cell Communication between Tumor Parenchymal Cells and Lymphocytes.

(A) UMAP visualization of 132,998 lymphocytes, clustered into 11 subtypes.

(B, C) Density plot (B) and stacked plot (C) showing the distribution and proportion of lymphocyte subtypes across samples.

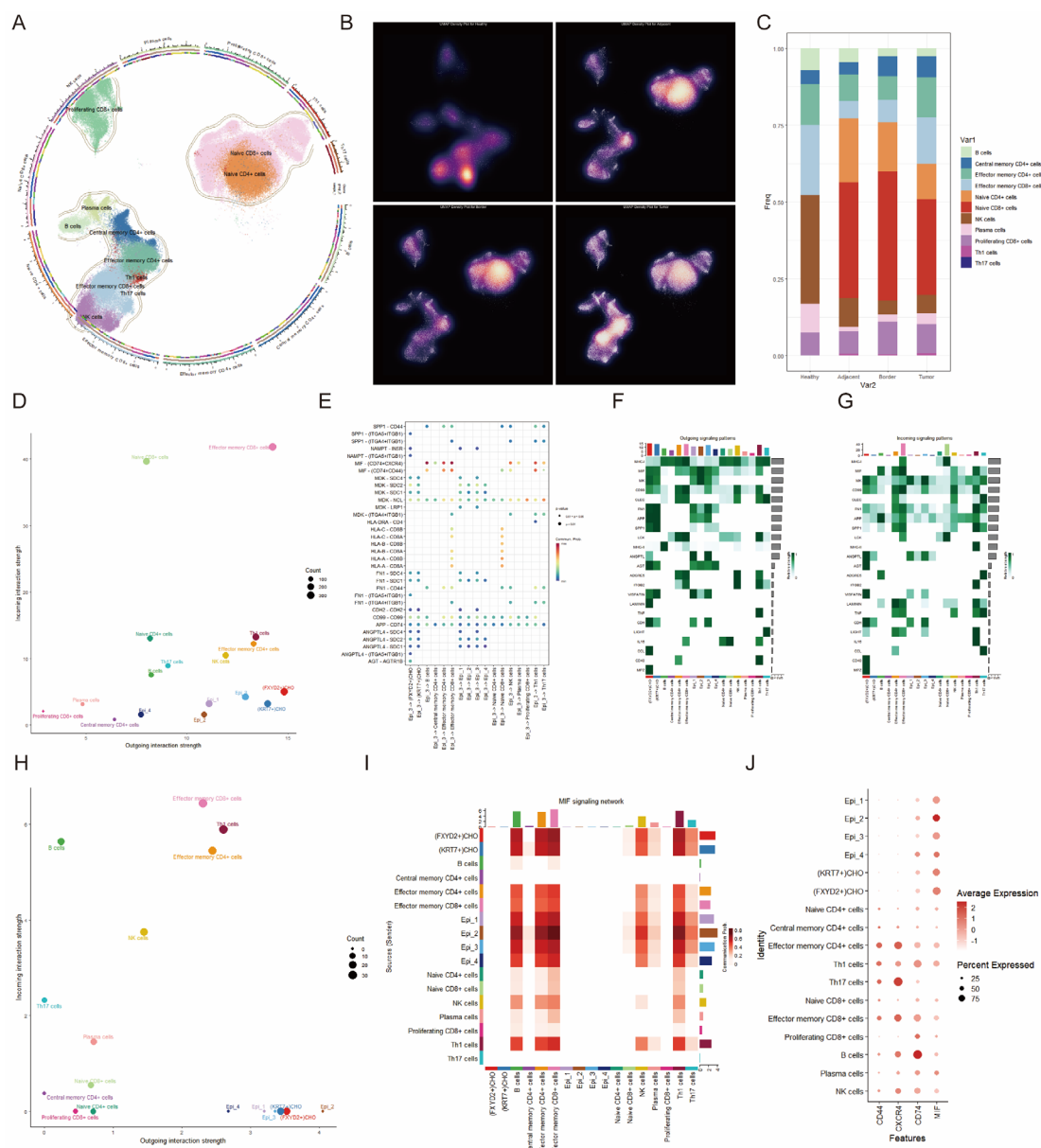
(D) Scatter plot illustrating the overall interaction strength between parenchymal cells and lymphocytes.

(E) Bubble plot of ligand-receptor interactions between the Tumor-Epi3 subpopulation and lymphocyte subsets.

(F, G) Heatmaps showing outgoing (F) and incoming (G) signaling pathway contributions.

(H-J) Analysis of the MIF signaling pathway, showing interaction strength (H, I) and expression of ligands and receptors (J).

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