

**Table S1:** The transcriptional levels of CIRBP and INPP5K in different types of gynecological cancer and normal tissues (ONCOMINE).

Gene symbol	Types of gynecology cancer vs. Norma	Fold change	t-test	p-value	Ref	PMID
CIRBP	Cervical squamous cell carcinoma vs. Normal	1.801	5.612	4.24E-7	Scotto Cervix 2	18506748
	Cervical squamous cell carcinoma vs. Normal	1.362	6.305	1.61E-4	Biewenga Cervix	18191186
	Cervical Squamous Cell Carcinoma Epithelia vs. Normal	1.658	4.310	1.01E-4	Zhai Cervix	17974957
CIRBP	Ovarian Serous Adenocarcinoma vs. Normal	5.365	9.222	1.63E-5	Adib Ovarian	14760385
	Ovarian Carcinoma vs. Normal	4.637	15.090	1.79E-10	Bonome Ovarian	18593951
	Ovarian Serous Surface Papillary Carcinoma vs. Normal	4.238	13.077	3.16E-9	Welsh Ovarian	11158614
	Ovarian Serous Adenocarcinoma vs. Normal	3.801	9.944	1.61E-11	Yoshihara Ovarian	19486012
	Ovarian Serous Cystadenocarcinoma vs. Normal	3.177	13.192	7.24E-7	TCGA Ovarian	
	Ovarian Endometrioid Adenocarcinoma vs. Normal	2.900	4.272	0.001	Lu Ovarian	15161682
	Ovarian Mucinous Adenocarcinoma vs. Normal	2.327	3.294	0.004	Lu Ovarian	15161682
	Ovarian Serous Adenocarcinoma vs. Normal	1.880	5.334	2.07E-5	Lu Ovarian	15161682
	Ovarian Clear Cell Adenocarcinoma vs. Normal	1.615	3.335	0.004	Lu Ovarian	15161682
	Ovarian Serous Adenocarcinoma vs. Normal	1.538	12.974	1.21E-7	Hendrix Ovarian	16452189
INPP5K	Cervical Squamous Cell Carcinoma vs. Normal	1.23	2.880	0.003	Scotto Cervix 2	18506748
	Cervical Non-Keratinizing Squamous Cell Carcinoma vs. Normal	1.207	3.067	0.005	TCGA Cervix (DNA)	
	Cervical Squamous Cell Carcinoma vs. Normal	1.103	5.522	1.86E-7	TCGA Cervix (DNA)	
INPP5K	Ovarian Serous Adenocarcinoma vs. Normal	1.950	6.543	1.43E-7	Yoshihara Ovarian	19486012
	Ovarian Serous Surface Papillary Carcinoma vs. Normal	4.267	2.093	0.041	Welsh Ovarian	11158614
	Ovarian Serous Adenocarcinoma vs. Normal	1.143	2.498	0.021	Adib Ovarian	14760385
	Ovarian Endometrioid Adenocarcinoma vs. Normal	1.052	2.916	0.003	Hendrix Ovarian	16452189
	Ovarian Serous Adenocarcinoma vs. Normal	1.029	1.989	0.030	Hendrix Ovarian	16452189

### Supplementary figure legends

**Figure.S1:** Functional enrichment of prognostic genes in CESC (Metascape). (A) Heatmap of enriched terms across the included prognostic genes colored by P-values. (B) GO terms identified in the GO analysis of the prognostic genes in the categories biological processes, cellular components, and molecular functions with 20 minimum P-values. (C) Networks of enriched terms and MCODE components identified in the gene lists.

**Figure.S2:** Functional enrichment of prognostic genes in UCEC (Metascape). (A) Heatmap of enriched terms across the included prognostic genes colored by P-values. (B) GO terms identified in the GO analysis of the prognostic genes in the categories biological processes, cellular components, and molecular functions with 20 minimum P-values. (C-D) Networks of enriched terms and MCODE components identified in the gene lists.

**Figure.S3:** Functional enrichment of prognostic genes in OV (Metascape). (A) Heatmap of enriched terms across the included prognostic genes colored by P-values. (B) GO terms identified in the GO analysis of the prognostic genes in the categories biological processes, cellular components, and molecular functions with 20 minimum P-values. (C) Networks of enriched terms and MCODE components identified in the gene lists.

**Figure.S4:** Functional enrichment of 70 overlapping and intersecting prognostic genes in gynecological cancers (Metascape). (A) Number of overlapping and intersecting prognostic genes. (B) Heatmap of enriched terms across the 70 included prognostic genes colored by P-values. (C) PPI network. (D) Networks of enriched terms and MCODE components identified in the gene lists.

**Figure.S5:** Correlation between the expression level of CIRBP/INPP5K and the clinicopathologic features (including TP53 mutation) of gynecologic cancers (UALCAN),  $P < 0.05$ .

**Figure.S6:** CIRBP expression in gynecologic cancers tissues. (A) CIRBP expression in tumor cells. (B) CIRBP Localized to the nucleoplasm. (C) CIRBP expression in

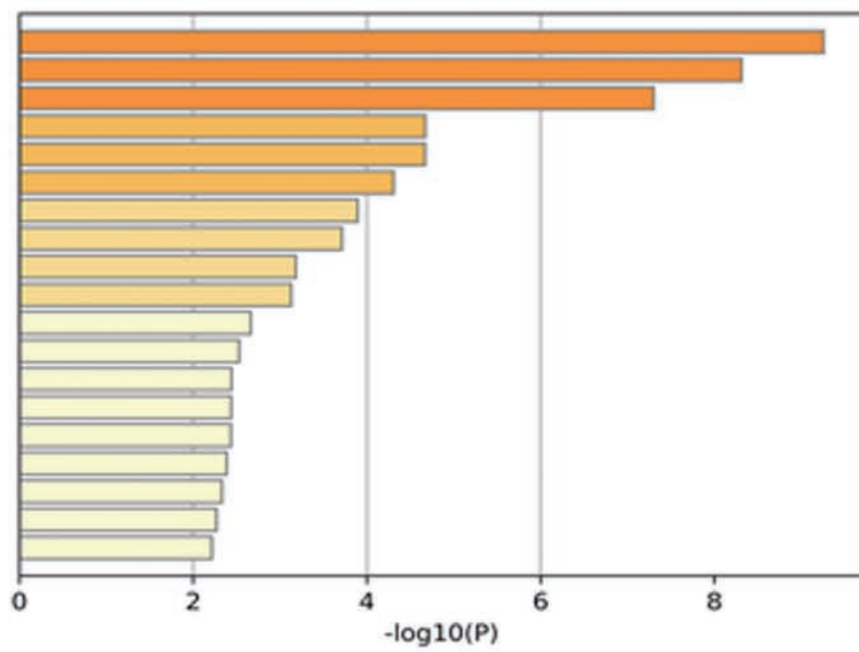
immune cells. ( The data from Cell Atlas: <https://www.proteinatlas.org> )

**Figure.S7:** Correlation between the DNA methylation level of CIRBP and the clinicopathologic features (including TP53 mutation) of gynecologic cancers (UALCAN),  $P < 0.05$ .

**Figure.S8:** Correlation between the DNA methylation level of INPP5K and the clinicopathologic features (including TP53 mutation) of gynecologic cancers (UALCAN),  $P < 0.05$ .

**Figure.S9:** Prognostic value of APA events of CIRBP and INPP5K in gynecological cancer patients (Kaplan–Meier plotter). Patients were divided into high (red) and low (blue) PDUI value groups based on the best cut-off values using the R package.

**A**



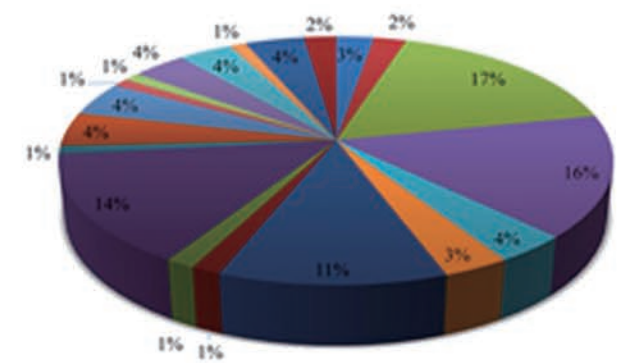
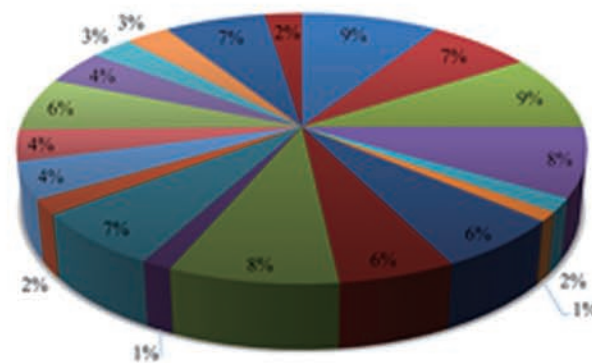
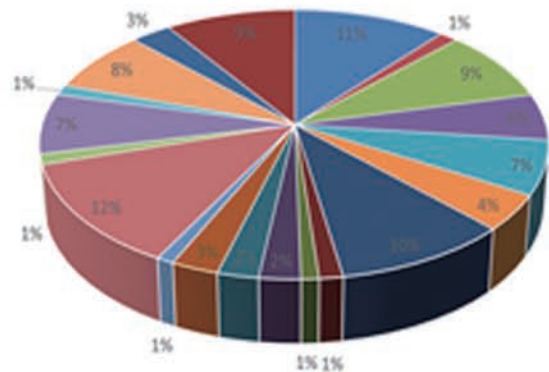
hsa04640: Hematopoietic cell lineage  
 hsa03030: DNA replication  
 hsa04060: Cytokine-cytokine receptor interaction  
 hsa04110: Cell cycle  
 hsa04657: IL-17 signaling pathway  
 hsa04066: HIF-1 signaling pathway  
 hsa04064: NF-kappa B signaling pathway  
 hsa05219: Bladder cancer  
 hsa05010: Alzheimer's disease  
 hsa05340: Primary immunodeficiency  
 hsa00564: Glycerophospholipid metabolism  
 hsa00520: Amino sugar and nucleotide sugar metabolism  
 hsa04014: Ras signaling pathway  
 hsa00250: Alanine, aspartate and glutamate metabolism  
 M00101: Cholesterol biosynthesis, squalene 2,3-epoxide => cholesterol  
 hsa04514: Cell adhesion molecules (CAMs)  
 hsa05166: HTLV-I infection  
 hsa04144: Endocytosis  
 M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP

**B**

**Cellular Components**

**Biological Processes**

**Molecular Functions**



- external side of plasma membrane
- alpha-beta T cell receptor complex
- chromosomal region
- coated vesicle membrane
- mitochondrial membrane part
- nuclear chromosome, telomeric region
- mitochondrial matrix
- nuclear lamina
- DNA replication factor C complex
- intrinsic component of mitochondrial inner membrane

- tertiary granule lumen
- replication fork
- HAUS complex
- Golgi membrane
- filopodium membrane
- early endosome
- BLOC complex
- focal adhesion
- melanosome
- centrosome

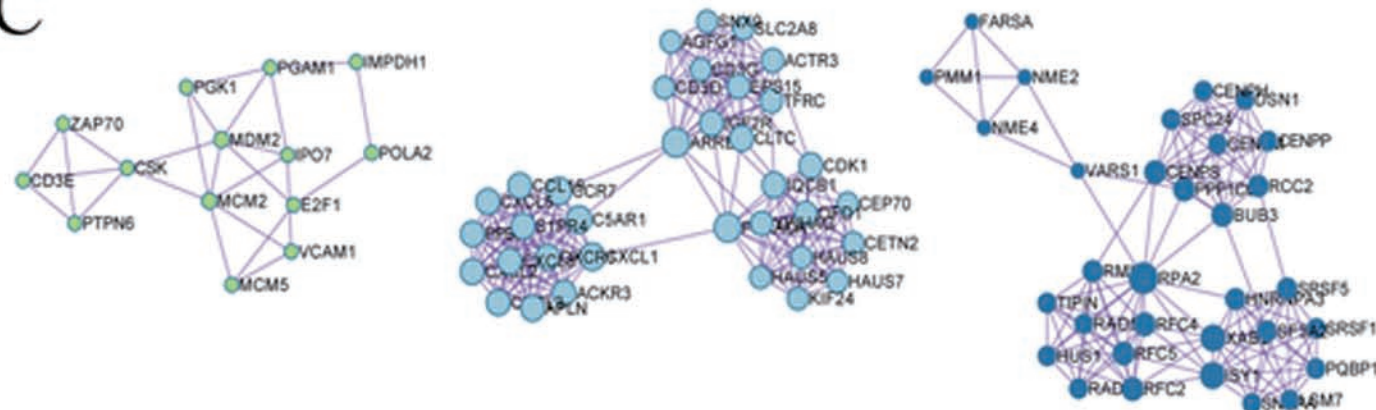
- lymphocyte activation
- leukocyte migration
- carbohydrate derivative biosynthetic process
- nucleotide metabolic process
- pyrimidine ribonucleoside metabolic process
- 4-hydroxyproline metabolic process
- generation of precursor metabolites and energy
- small molecule catabolic process
- cytokine-mediated signaling pathway
- positive T cell selection

- mitotic cell cycle phase transition
- nuclear DNA replication
- DNA conformation change
- signal transduction by p53 class mediator
- apoptotic signaling pathway
- viral life cycle
- negative regulation of leukocyte activation
- regulation of leukocyte mediated immunity
- leukocyte activation involved in immune response
- antibiotic metabolic process

- CXCR chemokine receptor binding
- cytidine deaminase activity
- oxidoreductase activity
- kinase binding
- virus receptor activity
- manganese ion binding
- cell adhesion molecule binding
- toxic substance binding
- intramolecular transferase activity, phosphotransferases
- protein domain specific binding

- carboxyl-O-methyltransferase activity
- protease binding
- cytokine binding
- phosphatidylserine 1-acylhydrolase activity
- DNA clamp loader activity
- protein N-terminus binding
- oxidoreductase activity, acting on NAD(P)H
- lipopeptide binding
- protein tyrosine kinase activity
- amide transmembrane transporter activity

**C**

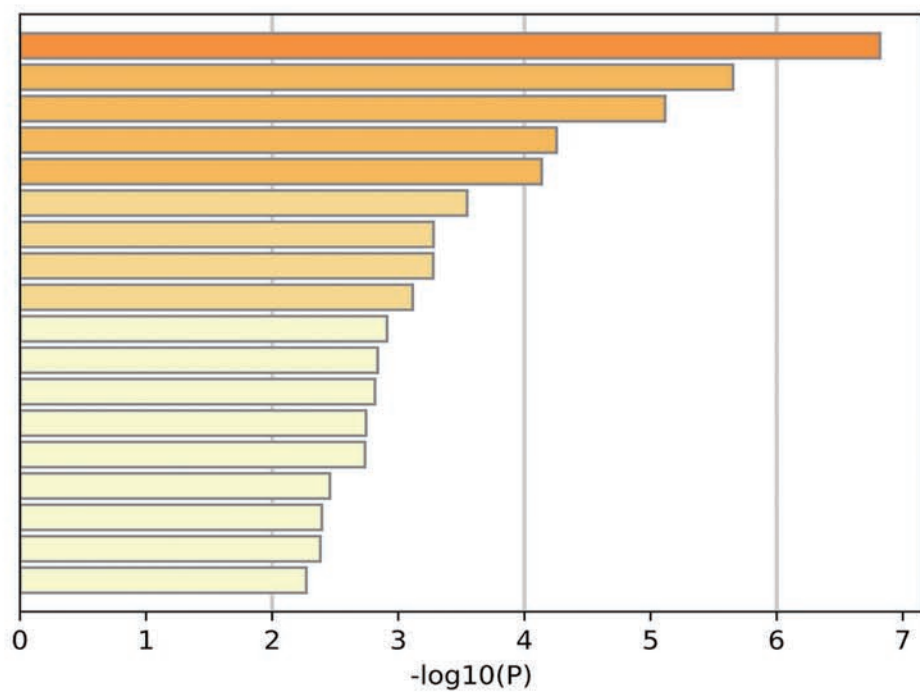


MCODE\_1 ciliary basal body-plasma membrane docking (Log10(P)=-18.1)  
 MCODE\_1 chemokine-mediated signaling pathway (Log10(P)=-16.4)  
 MCODE\_1 cellular response to chemokine (Log10(P)=-15.9)  
 MCODE\_2 Spliceosome (Log10(P)=-13.0)  
 MCODE\_2 condensed chromosome (Log10(P)=-12.7)  
 MCODE\_2 chromosomal region (Log10(P)=-12.3)  
 MCODE\_3 G1/S transition of mitotic cell cycle (Log10(P)=-8.2)  
 MCODE\_3 cell cycle G1/S phase transition (Log10(P)=-8.0)  
 MCODE\_3 positive regulation of T cell activation (Log10(P)=-7.1)

Fig.S1



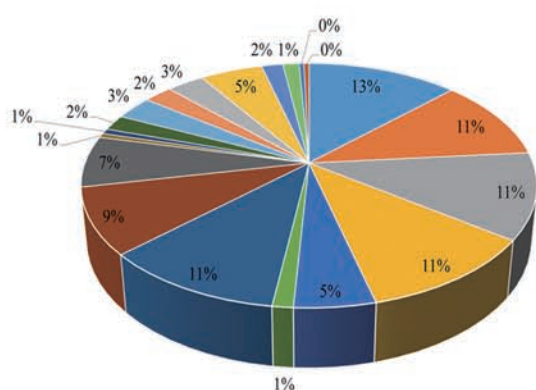
A



hsa04110: Cell cycle  
 hsa04658: Th1 and Th2 cell differentiation  
 hsa05166: HTLV-I infection  
 hsa05219: Bladder cancer  
 hsa05169: Epstein-Barr virus infection  
 hsa04141: Protein processing in endoplasmic reticulum  
 hsa04064: NF-kappa B signaling pathway  
 hsa05164: Influenza A  
 hsa04211: Longevity regulating pathway  
 hsa05418: Fluid shear stress and atherosclerosis  
 hsa04514: Cell adhesion molecules (CAMs)  
 hsa00564: Glycerophospholipid metabolism  
 hsa00250: Alanine, aspartate and glutamate metabolism  
 hsa04940: Type I diabetes mellitus  
 hsa00600: Sphingolipid metabolism  
 hsa01212: Fatty acid metabolism  
 M00089: Triacylglycerol biosynthesis  
 hsa00051: Fructose and mannose metabolism

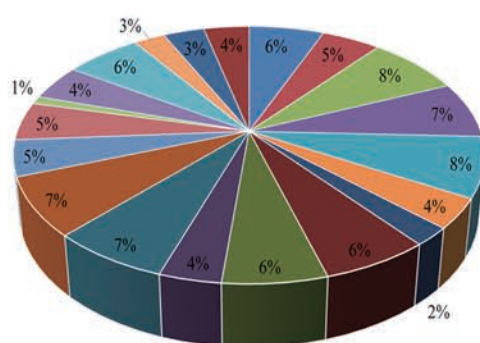
B

## Cellular Components



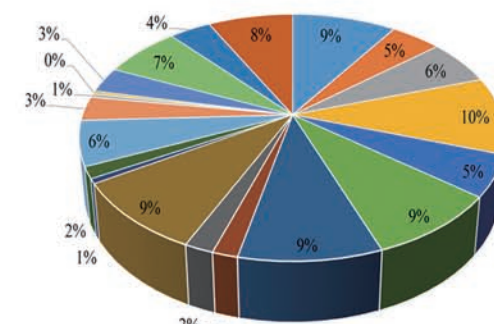
- microtubule organizing center
- cilium
- lytic vacuole
- perinuclear region of cytoplasm
- trans-Golgi network
- rough endoplasmic reticulum membrane
- mitochondrial envelope
- cell body
- cell-substrate junction
- alpha-beta T cell receptor complex
- endoplasmic reticulum chaperone complex
- lipid droplet
- integral component of endoplasmic reticulum membrane
- melanosome
- spindle pole
- membrane raft
- intercellular bridge
- myelin sheath
- dendritic filopodium
- insulin-like growth factor ternary complex

## Biological Processes



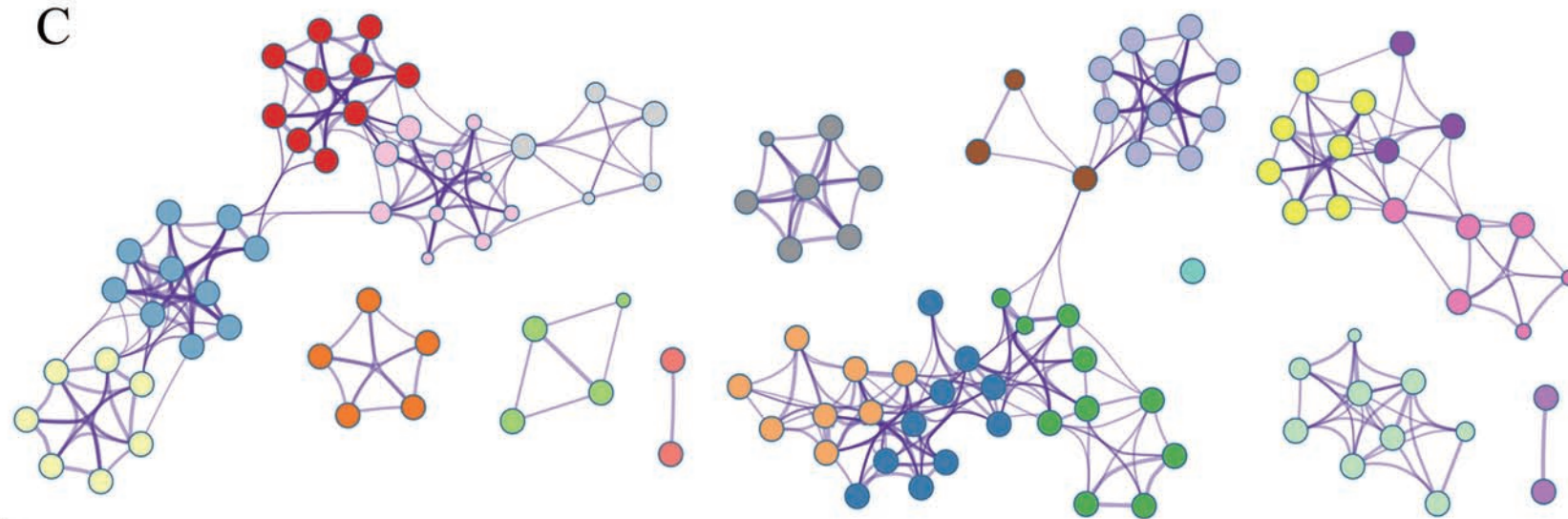
- T cell activation
- leukocyte activation involved in immune response
- positive regulation of cellular protein localization
- regulation of establishment of protein localization
- positive regulation of programmed cell death
- cilium organization
- regulation of growth
- gland development
- microtubule-based process
- positive T cell selection
- response to endoplasmic reticulum stress
- regulation of multi-organism process
- response to estradiol
- chordate embryonic development
- lymphocyte activation involved in immune response
- microtubule-based movement
- urogenital system development

## Molecular Functions



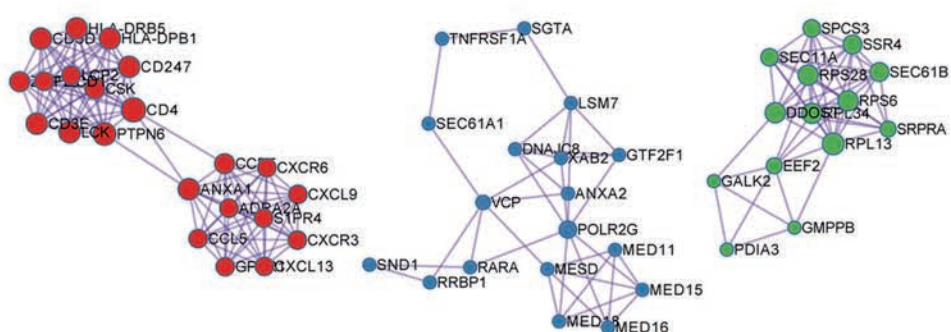
- protein kinase binding
- transcription corepressor activity
- nucleoside binding
- kinase activity
- nucleoside-triphosphatase regulator activity
- transcription factor binding
- protein domain specific binding
- p53 binding
- ATPase binding
- lipid binding
- cyclin-dependent protein serine/threonine kinase inhibitor activity
- calcium-dependent protein binding
- DNA-binding transcription activator activity, RNA polymerase II-specific
- protein C-terminus binding
- CD4 receptor binding
- very-low-density lipoprotein particle receptor activity
- transferase activity, transferring hexosyl groups
- GTPase binding
- microtubule binding
- peptidase activity

C



- T cell activation
- positive regulation of cellular protein localization
- positive regulation of programmed cell death
- microtubule organizing center
- regulation of growth
- cilium
- Cell cycle
- microtubule-based process
- response to endoplasmic reticulum stress
- response to estradiol
- lytic vacuole
- mitotic cell cycle phase transition
- regulation of protein stability
- leukocyte activation involved in immune response
- regulation of establishment of protein localization
- gland development
- positive T cell selection
- Th1 and Th2 cell differentiation
- protein kinase binding
- regulation of multi-organism process

D

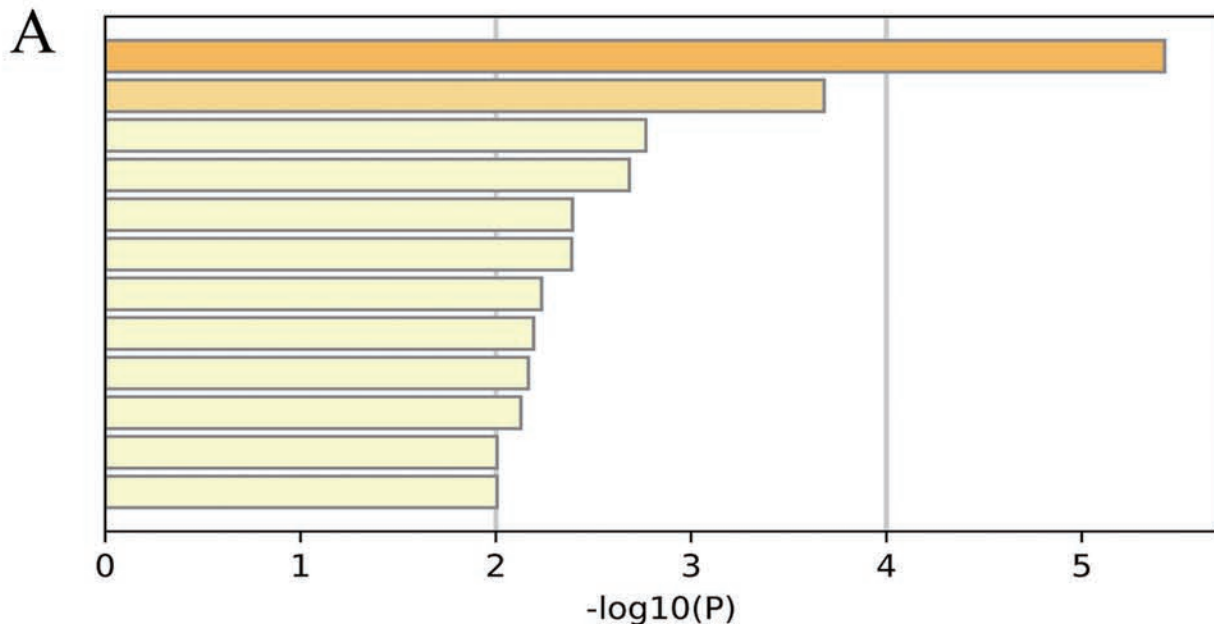


- MCODE1
- MCODE2
- MCODE3

MCODE\_1 T cell receptor signaling pathway ( $\text{Log}_{10}(P)=-17.2$ )  
 MCODE\_1 T cell receptor signaling pathway ( $\text{Log}_{10}(P)=-15.8$ )  
 MCODE\_1 positive regulation of cell-cell adhesion ( $\text{Log}_{10}(P)=-15.8$ )  
 MCODE\_2 mediator complex ( $\text{Log}_{10}(P)=-7.9$ )  
 MCODE\_2 transcription coregulator activity ( $\text{Log}_{10}(P)=-6.9$ )  
 MCODE\_2 transcription initiation from RNA polymerase II promoter ( $\text{Log}_{10}(P)=-6.6$ )  
 MCODE\_3 protein targeting to ER ( $\text{Log}_{10}(P)=-13.0$ )  
 MCODE\_3 establishment of protein localization to endoplasmic reticulum ( $\text{Log}_{10}(P)=-12.9$ )  
 MCODE\_3 protein localization to endoplasmic reticu ( $\text{Log}_{10}(P)=-12.2$ )

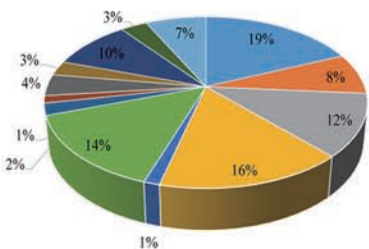
Fig.S2



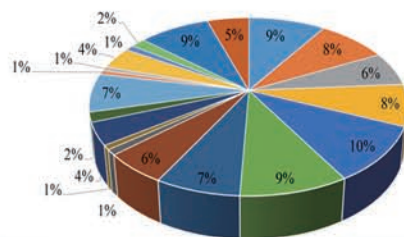


hsa03040: Spliceosome  
 hsa05200: Pathways in cancer  
 hsa05340: Primary immunodeficiency  
 hsa04141: Protein processing in endoplasmic reticulum  
 hsa00650: Butanoate metabolism  
 hsa03050: Proteasome  
 hsa04115: p53 signaling pathway  
 hsa04919: Thyroid hormone signaling pathway  
 hsa05012: Parkinson's disease  
 hsa04261: Adrenergic signaling in cardiomyocytes  
 hsa04612: Antigen processing and presentation  
 hsa03018: RNA degradation

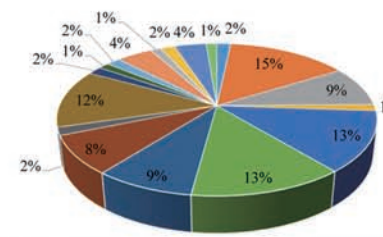
**B Cellular Components**



**Biological Processes**

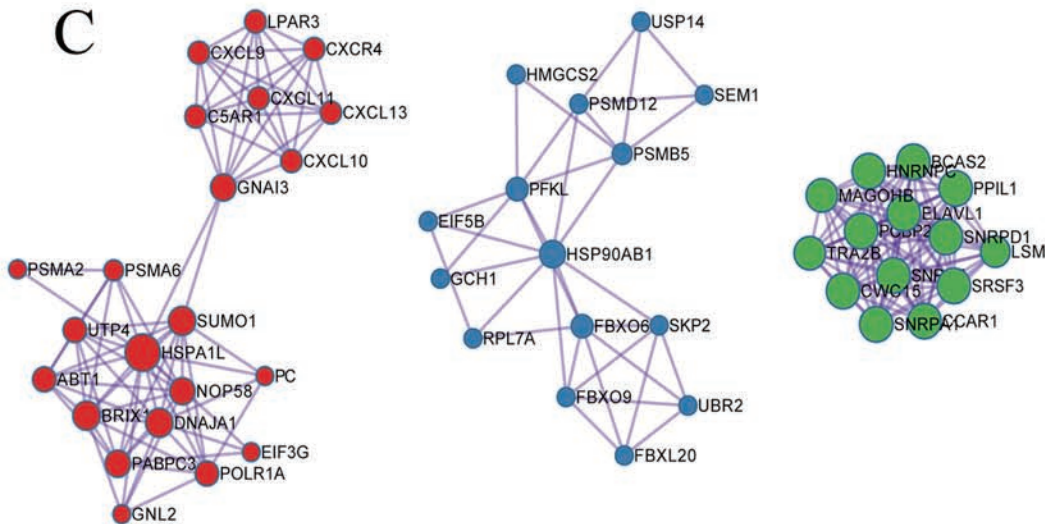


**Molecular Functions**



- transferase complex
- spliceosomal complex
- mitochondrial matrix
- mitochondrial envelope
- MHC class I peptide loading complex
- Golgi membrane
- COP9 signalosome
- methylosome
- fibrillar center
- proteasome complex
- nuclear envelope
- organelle envelope lumen
- membrane raft
- negative regulation of cell cycle
- regulation of cellular protein localization
- RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
- proteasomal protein catabolic process
- cytokine-mediated signaling pathway
- regulation of cell adhesion
- leukocyte differentiation
- negative regulation of proteolysis
- regulation of cell-cell adhesion mediated by integrin
- delamination
- cell cycle arrest
- negative regulation of carbohydrate metabolic process
- DNA repair
- positive regulation of T cell tolerance induction
- vesicle fusion with endoplasmic reticulum-Golgi intermediate compartment (ERGIC) membrane
- response to temperature stimulus
- negative regulation of ERAD pathway
- protein K48-linked ubiquitination
- regulation of cellular response to stress
- cellular amino acid metabolic process
- CXCR3 chemokine receptor binding
- transcription factor binding
- ubiquitin-like protein ligase binding
- PH domain binding
- transcription coregulator activity
- kinase binding
- ubiquitin-like protein transferase activity
- enzyme inhibitor activity
- exodeoxyribonuclease activity
- protein domain specific binding
- protein binding involved in protein folding
- transcription corepressor binding
- NF-kappaB binding
- structural constituent of ribosome
- metalloendopeptidase inhibitor activity
- hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides
- ligase activity
- polypeptide N-acetylgalactosaminyltransferase activity

**C**

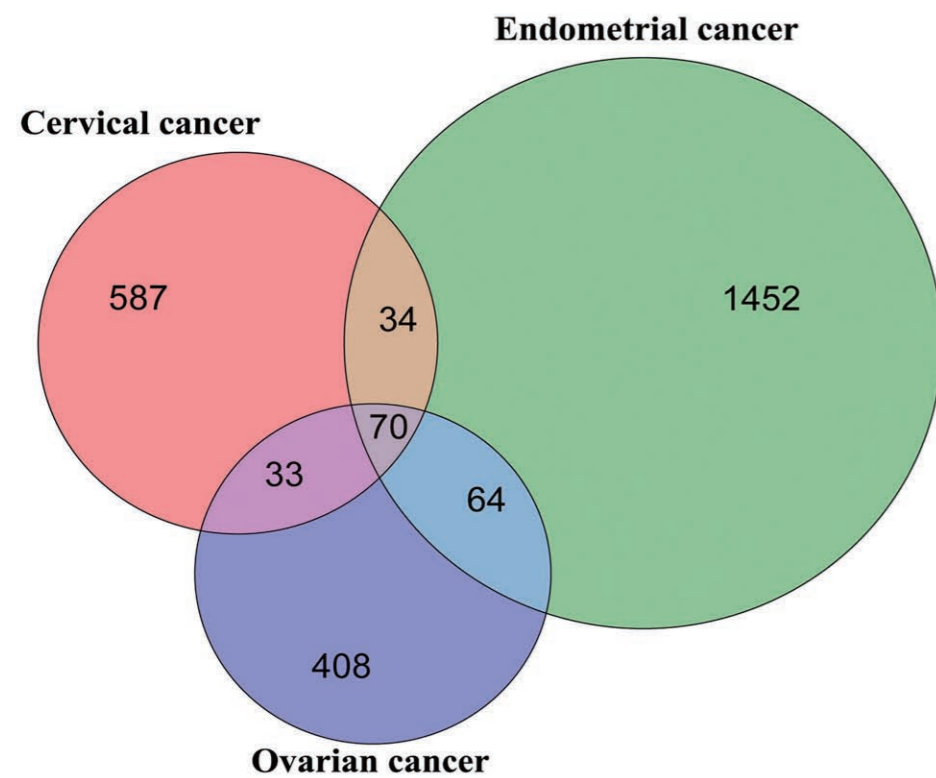


- MCODE\_1 CXCR3 chemokine receptor binding ( $\log_{10}(P)=-11.6$ )
- MCODE\_1 CXCR chemokine receptor binding ( $\log_{10}(P)=-8.8$ )
- MCODE\_1 Chemokine signaling pathway ( $\log_{10}(P)=-7.9$ )
- MCODE\_2 proteasome-mediated ubiquitin-dependent protein catabolic process ( $\log_{10}(P)=-12.2$ )
- MCODE\_2 proteasomal protein catabolic process ( $\log_{10}(P)=-11.7$ )
- MCODE\_2 SCF-dependent proteasomal ubiquitin-dependent protein catabolic process ( $\log_{10}(P)=-10.8$ )
- MCODE\_3 RNA splicing, via transesterification reactions with bulged adenosine as nucleophile ( $\log_{10}(P)=-25.9$ )
- MCODE\_3 mRNA splicing, via spliceosome ( $\log_{10}(P)=-25.9$ )
- MCODE\_3 RNA splicing, via transesterification reactions ( $\log_{10}(P)=-25.9$ )

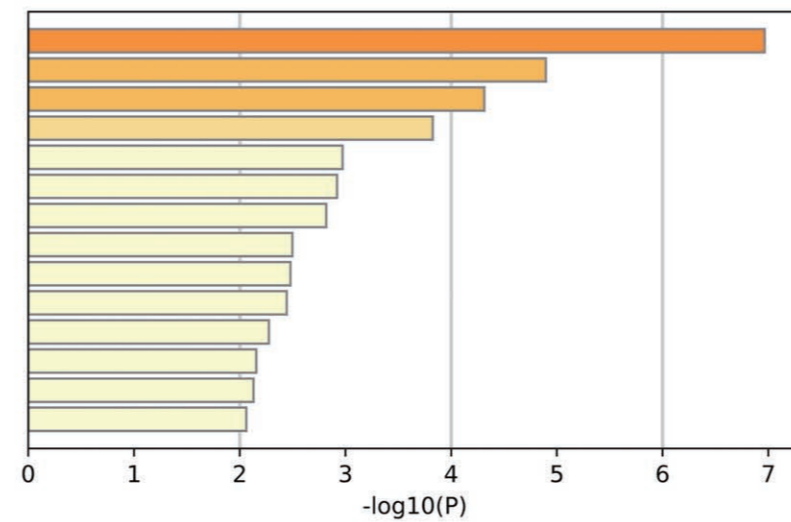
Fig.S3



A

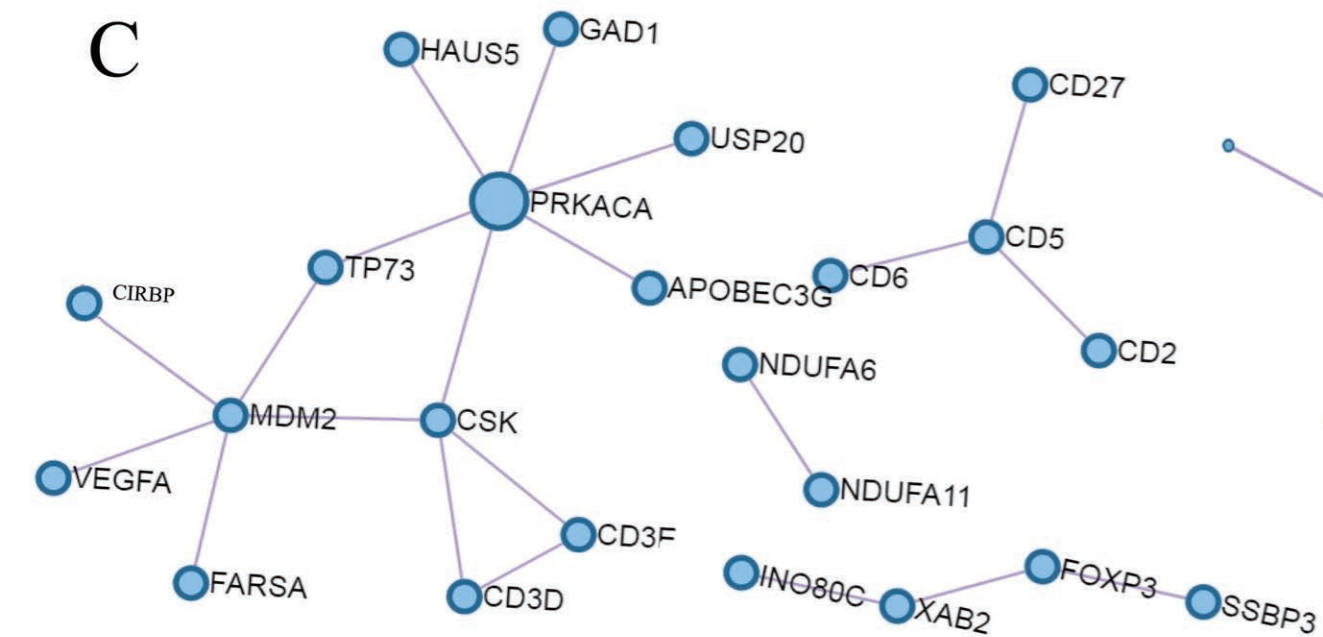


B



GO:0042110: T cell activation  
 GO:0045869: negative regulation of single stranded viral RNA replication via double stranded DNA intermediate  
 hsa04115: p53 signaling pathway  
 GO:2000117: negative regulation of cysteine-type endopeptidase activity  
 GO:0050891: multicellular organismal water homeostasis  
 GO:0006281: DNA repair  
 GO:0016575: histone deacetylation  
 GO:0048709: oligodendrocyte differentiation  
 GO:0097164: ammonium ion metabolic process  
 GO:1902749: regulation of cell cycle G2/M phase transition  
 GO:0044455: mitochondrial membrane part  
 GO:0007498: mesoderm development  
 hsa04120: Ubiquitin mediated proteolysis  
 GO:0001228: DNA-binding transcription activator activity, RNA polymerase II-specific

C



D

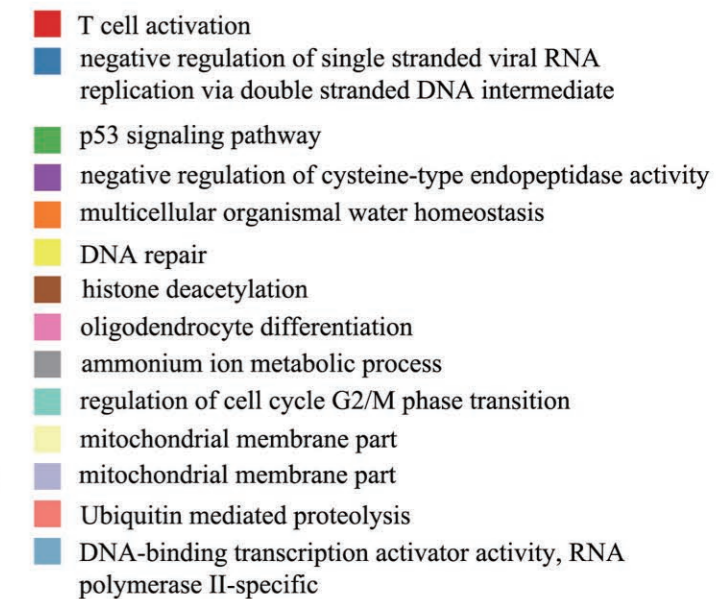
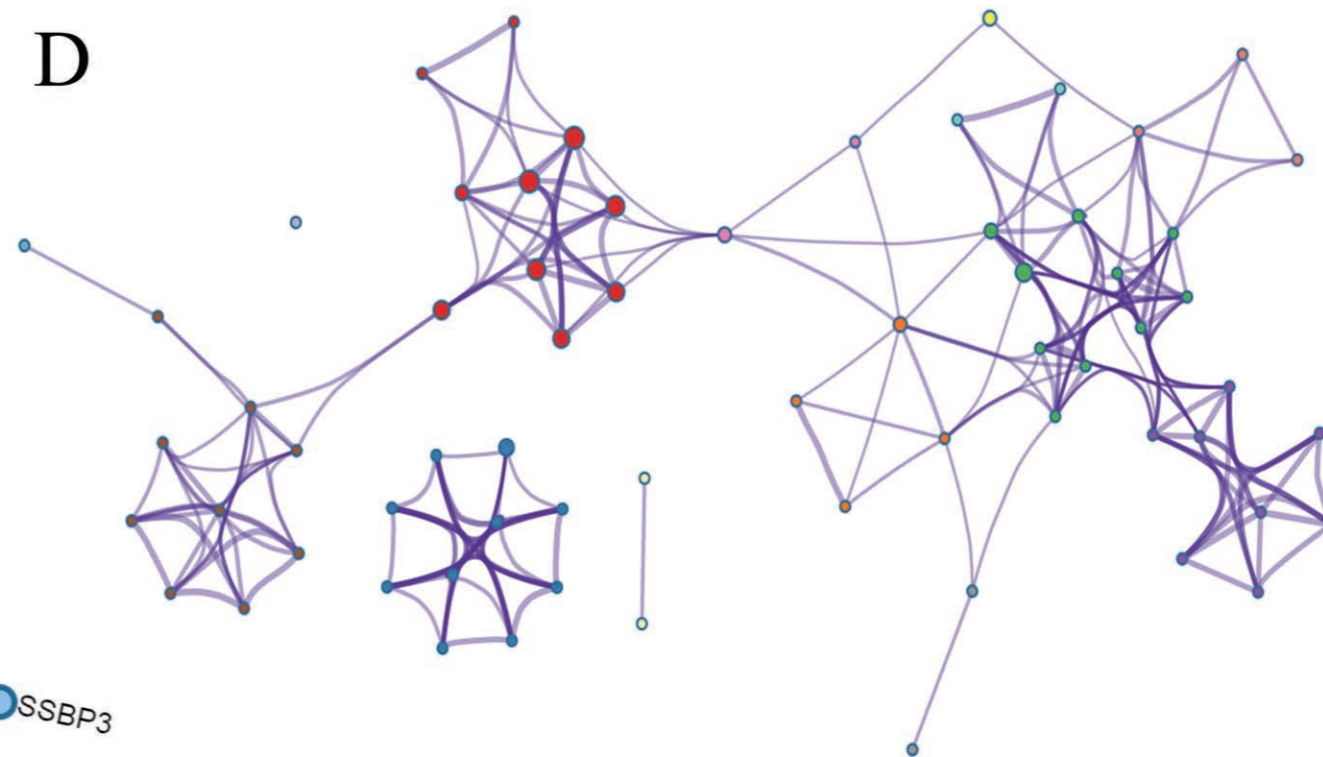


Fig.S4



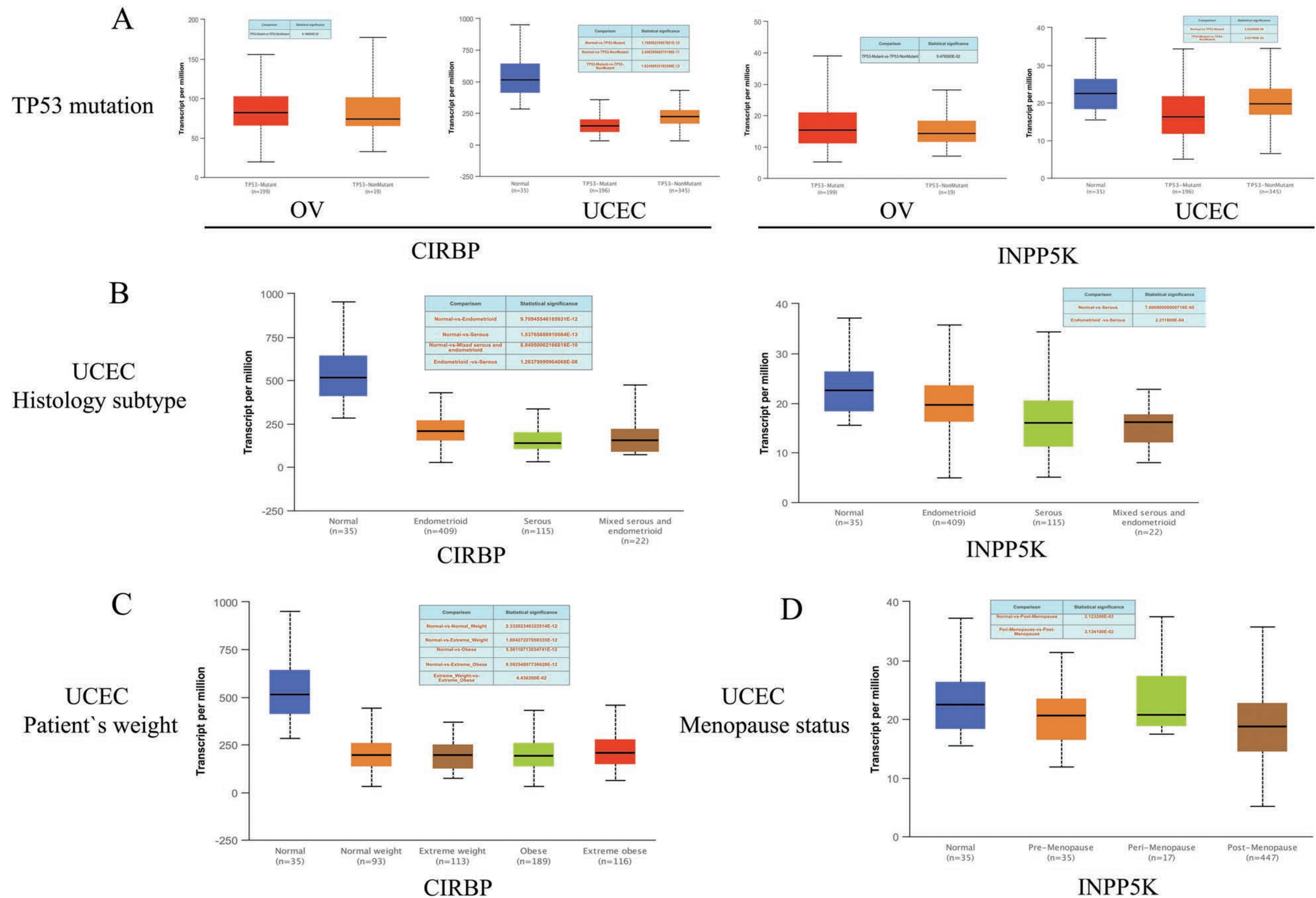


Fig.S5



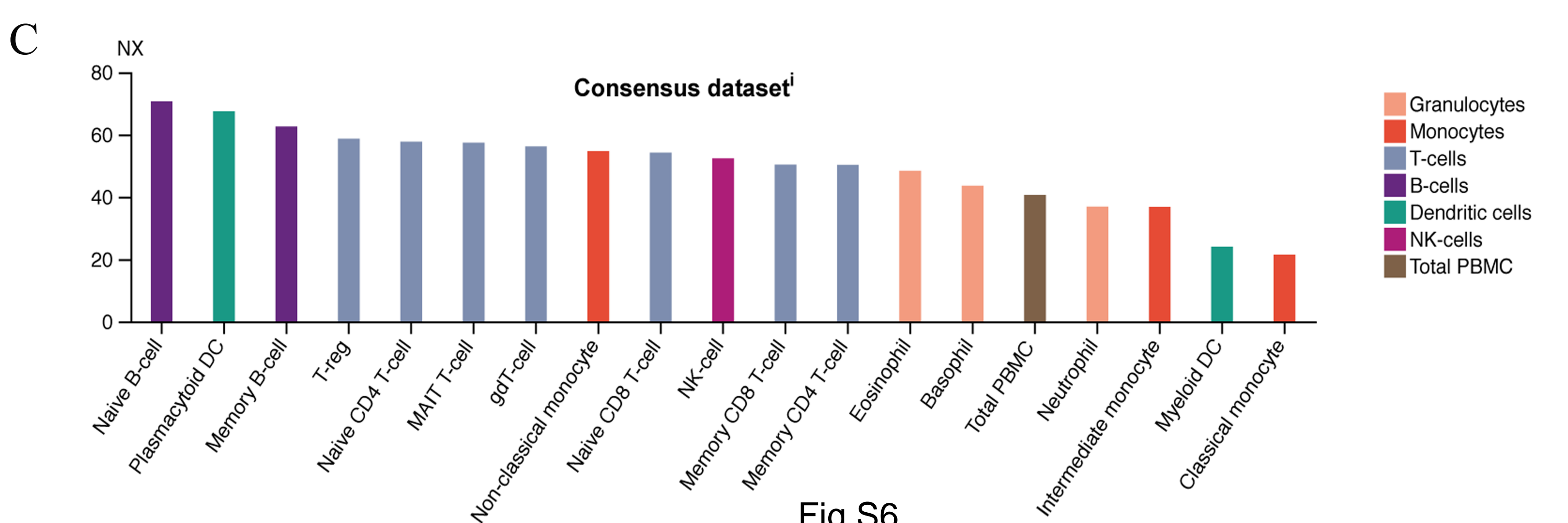
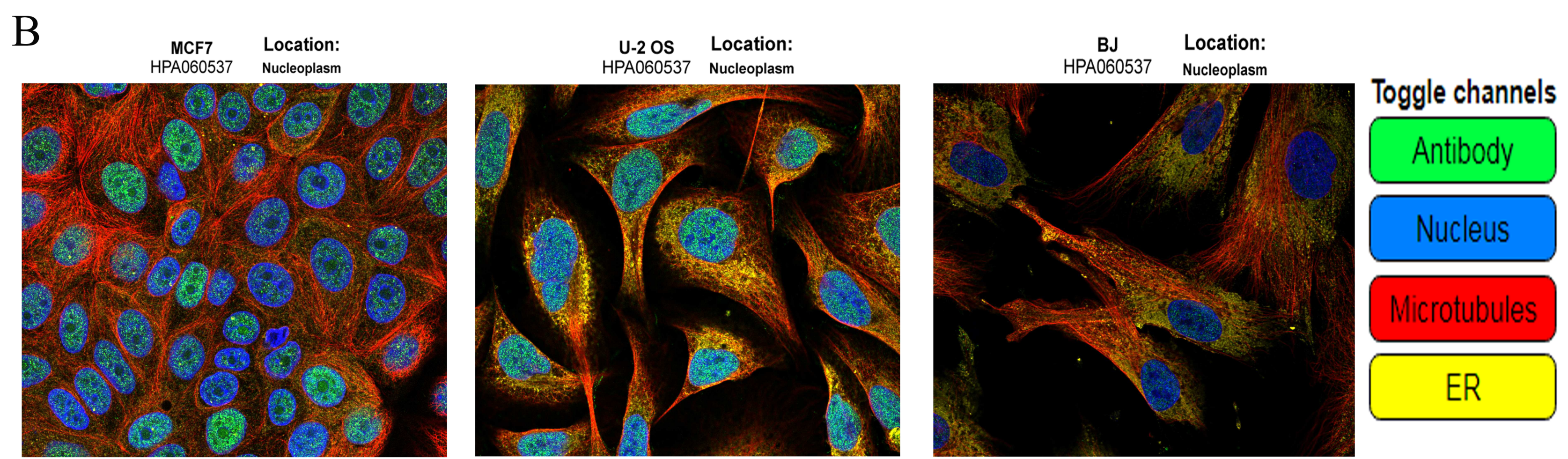
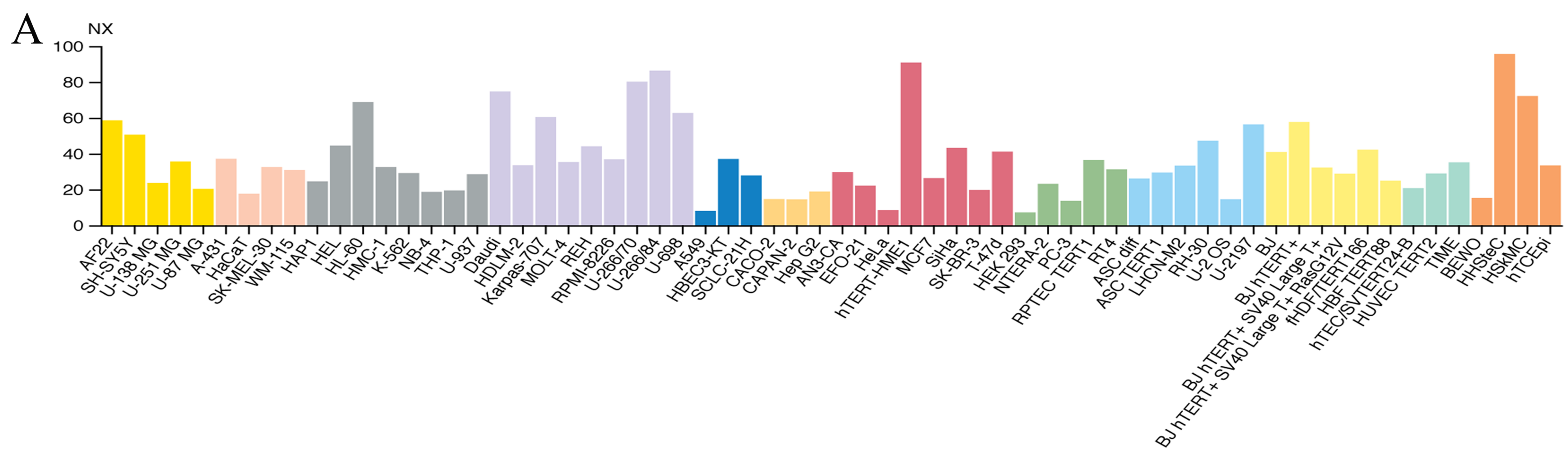
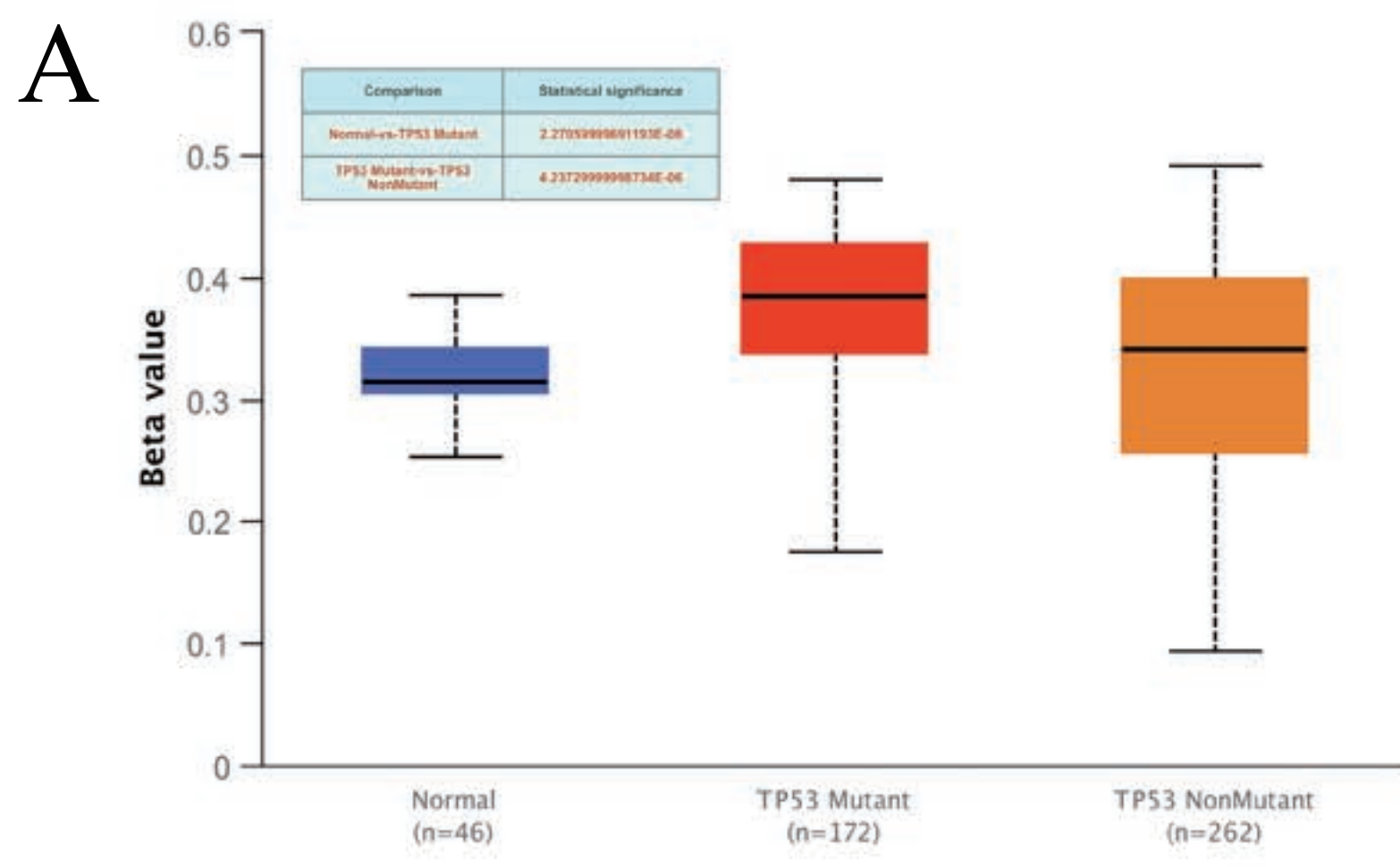
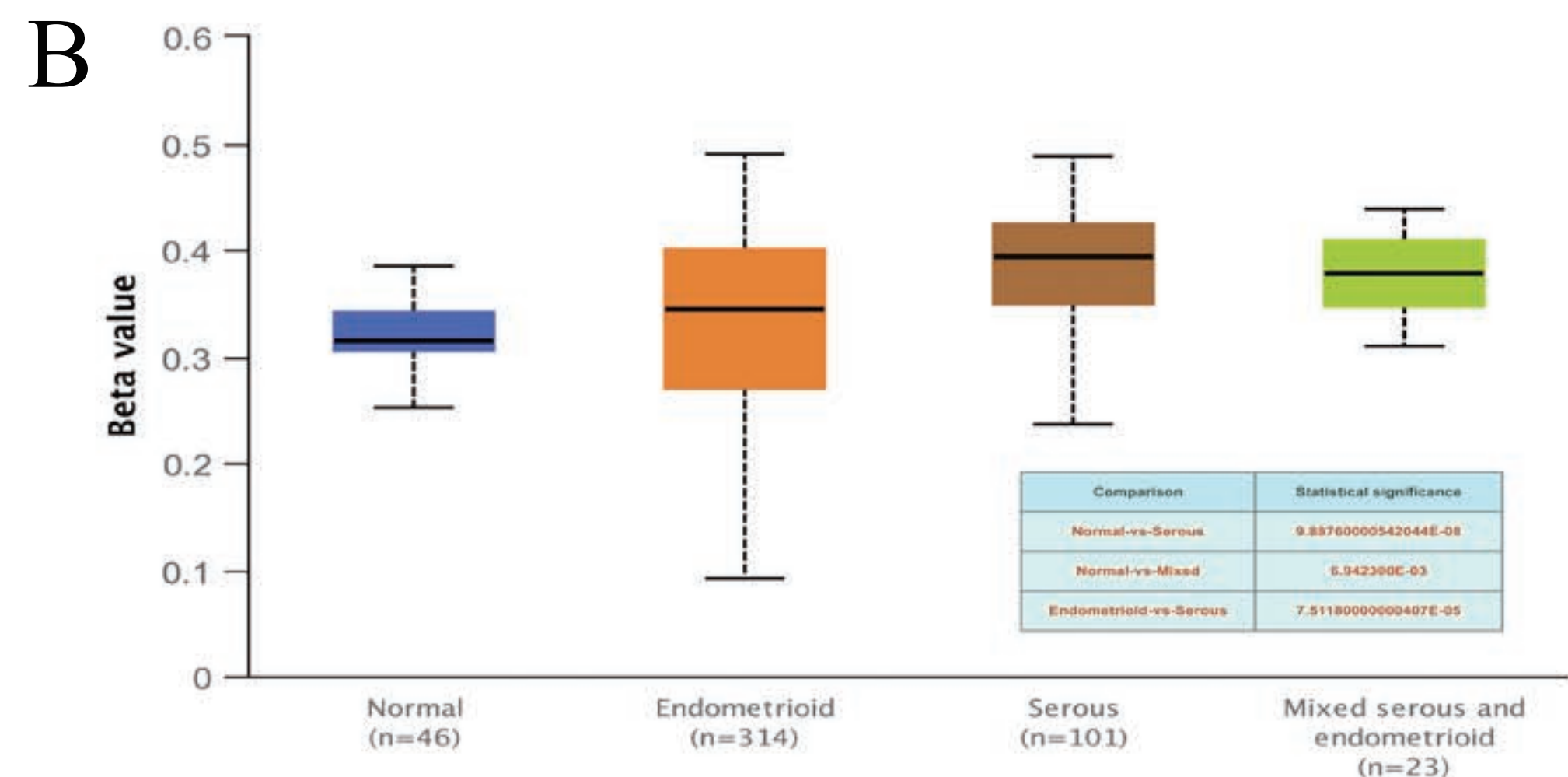


Fig.S6

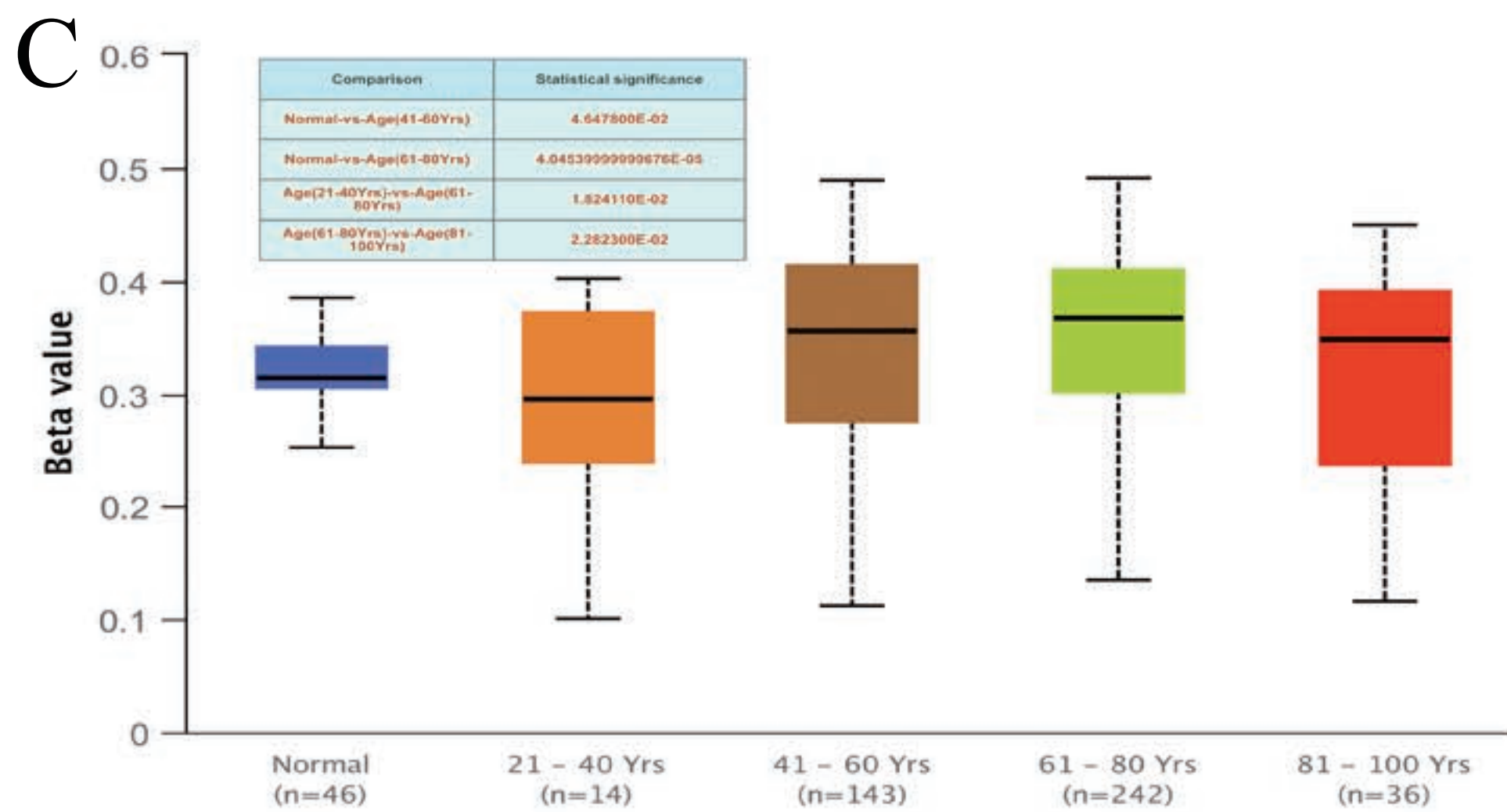




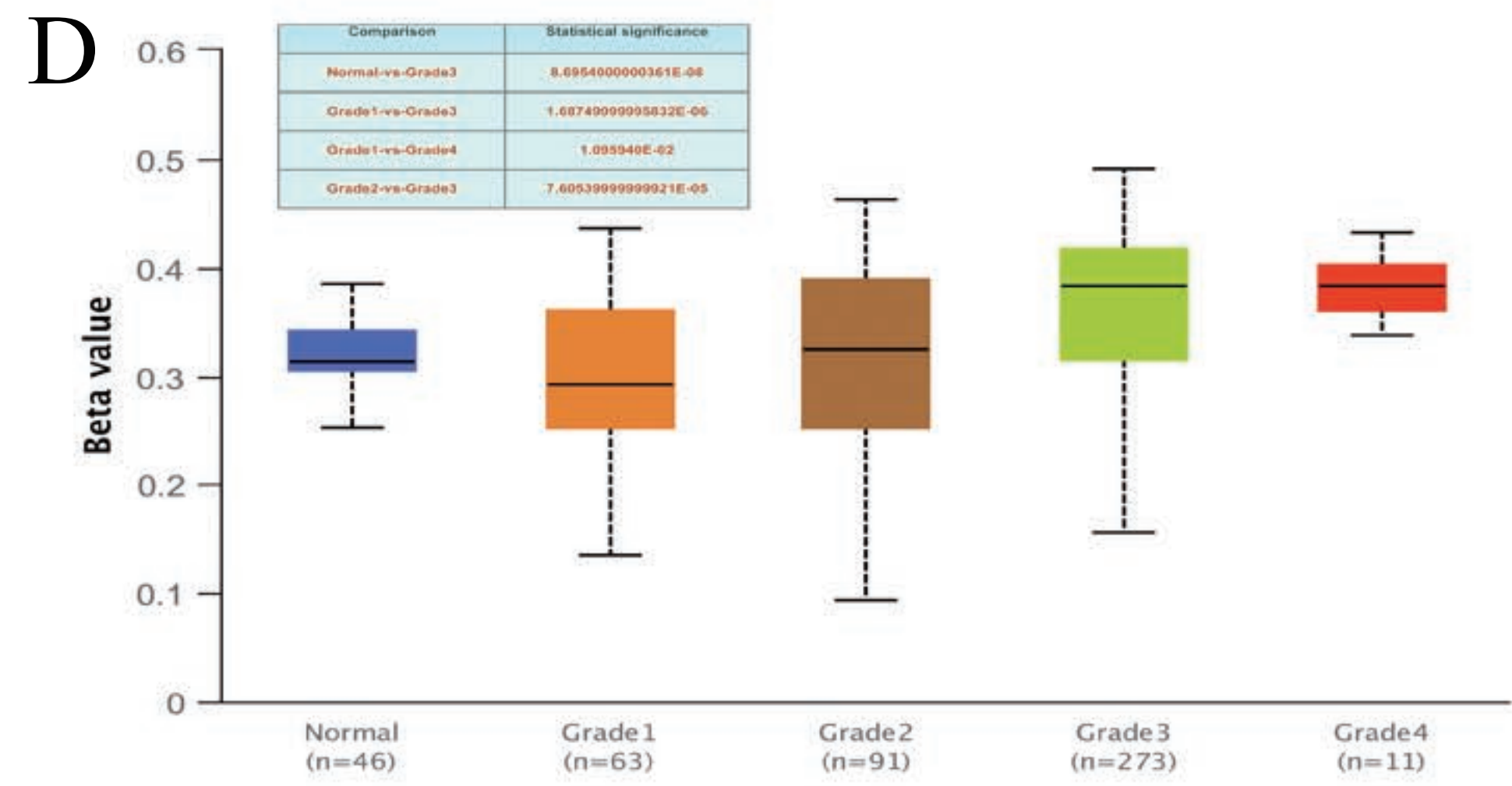
UCEC TP53 mutation



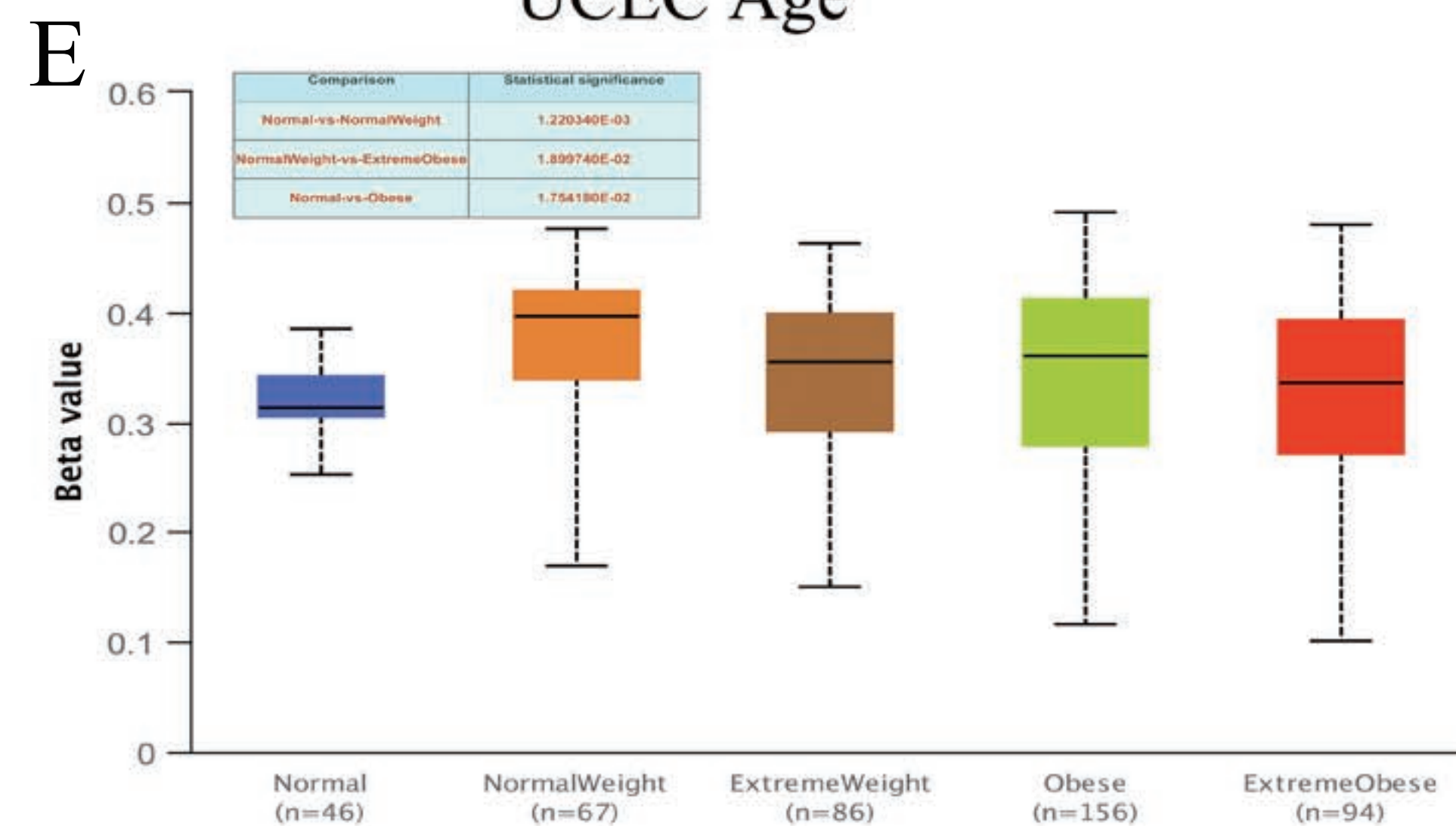
UCEC Histology subtype



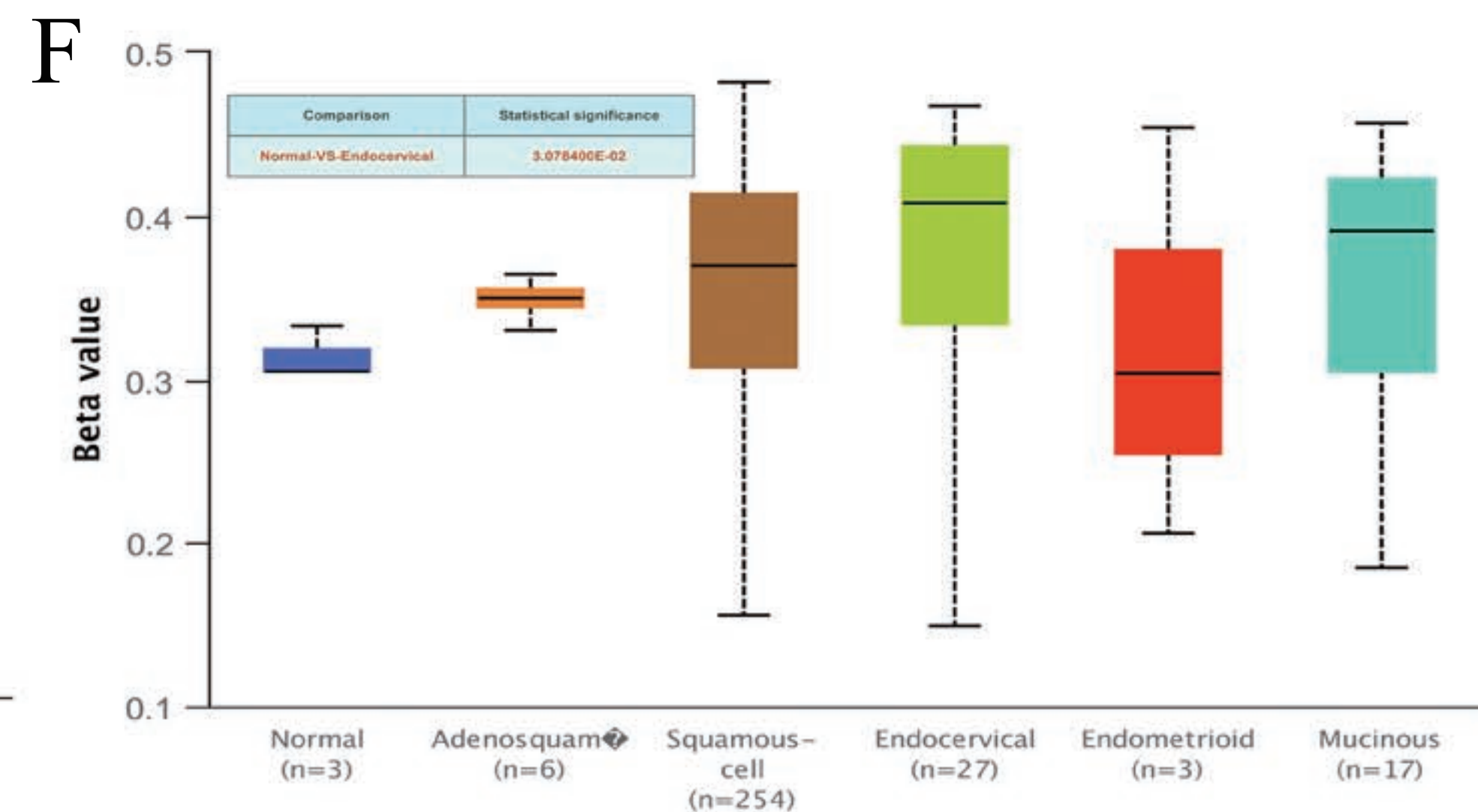
UCEC Age



UCEC Tumor grade



UCEC Weight



CEC Histology subtype

Fig. S7



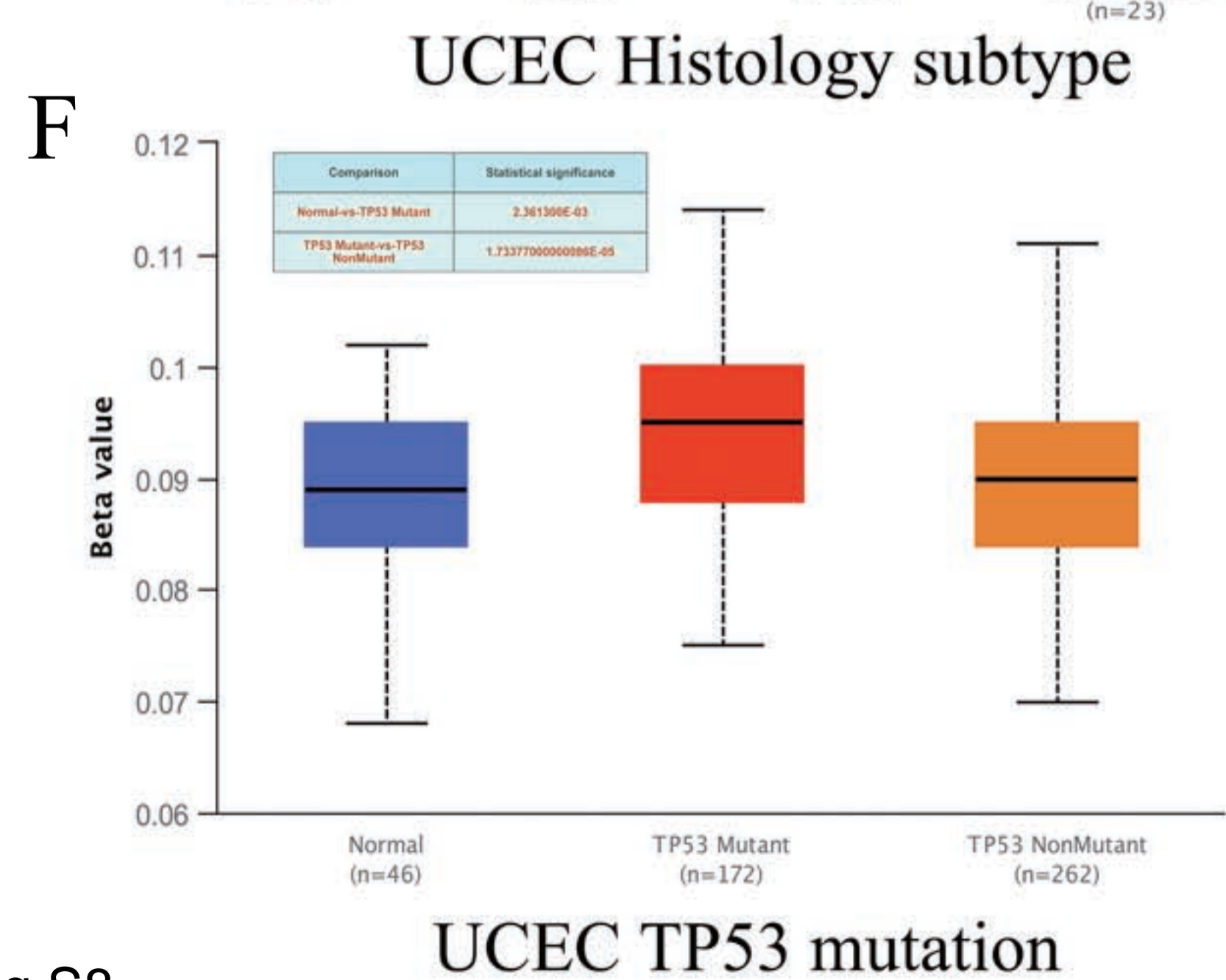
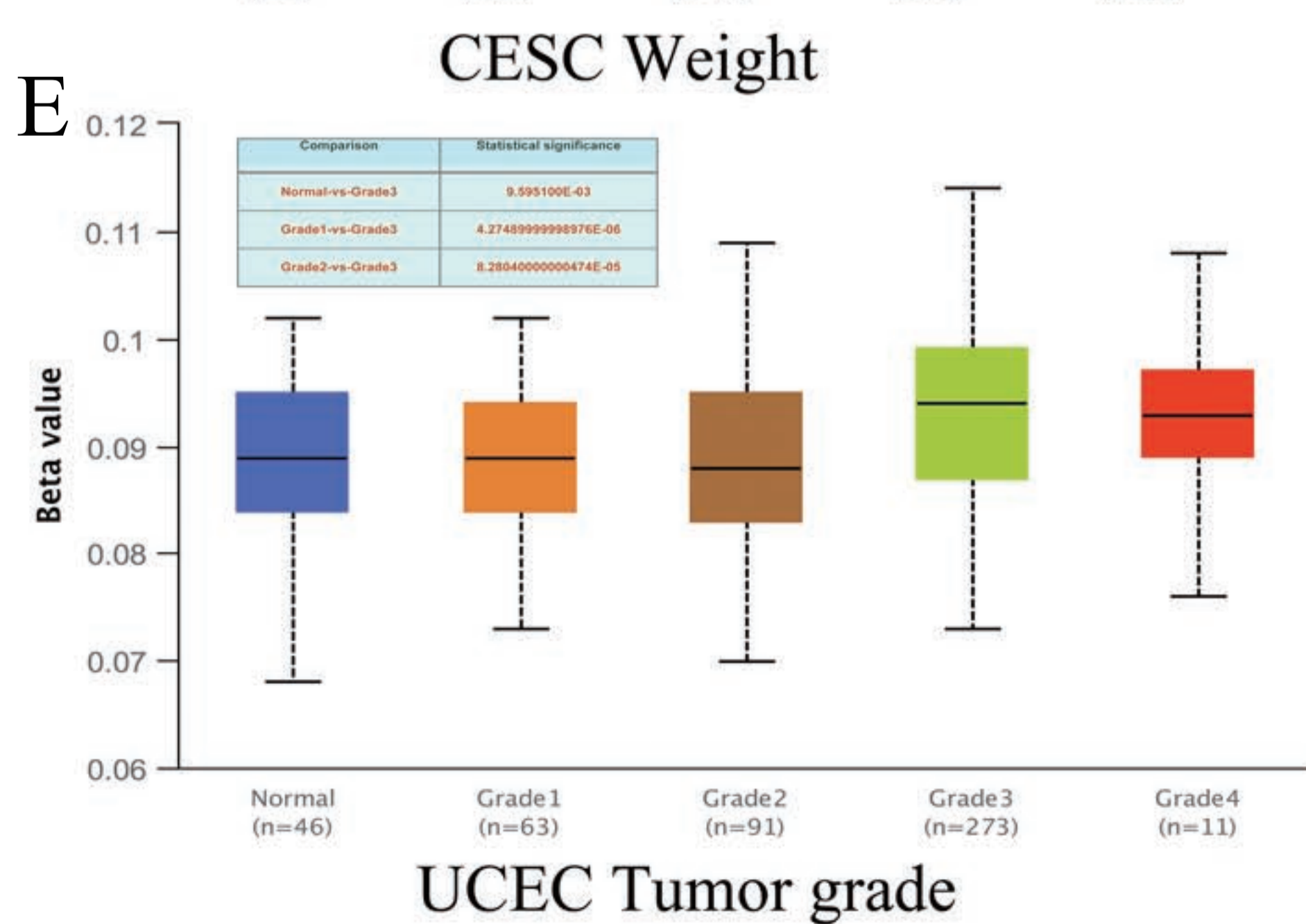
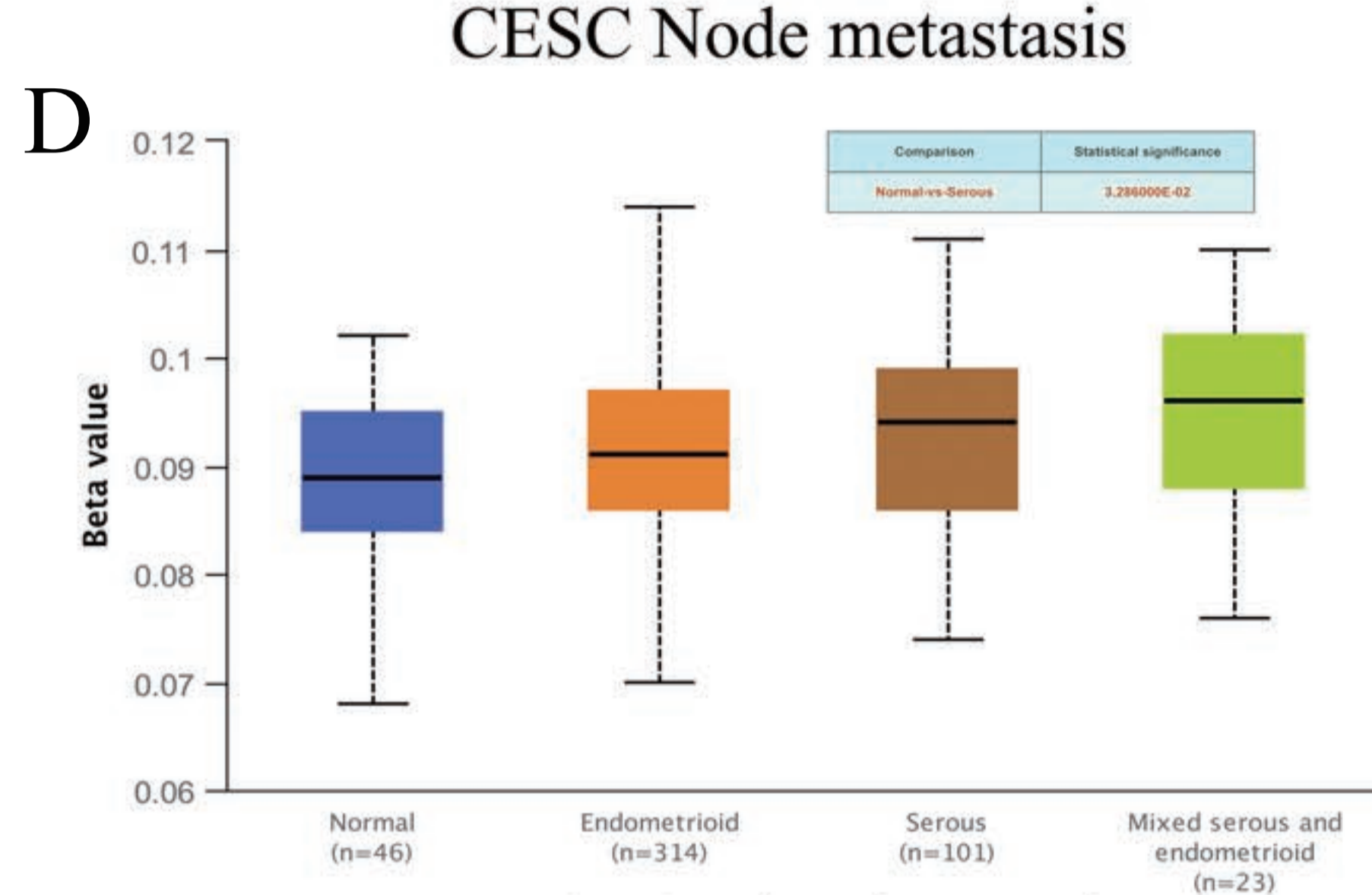
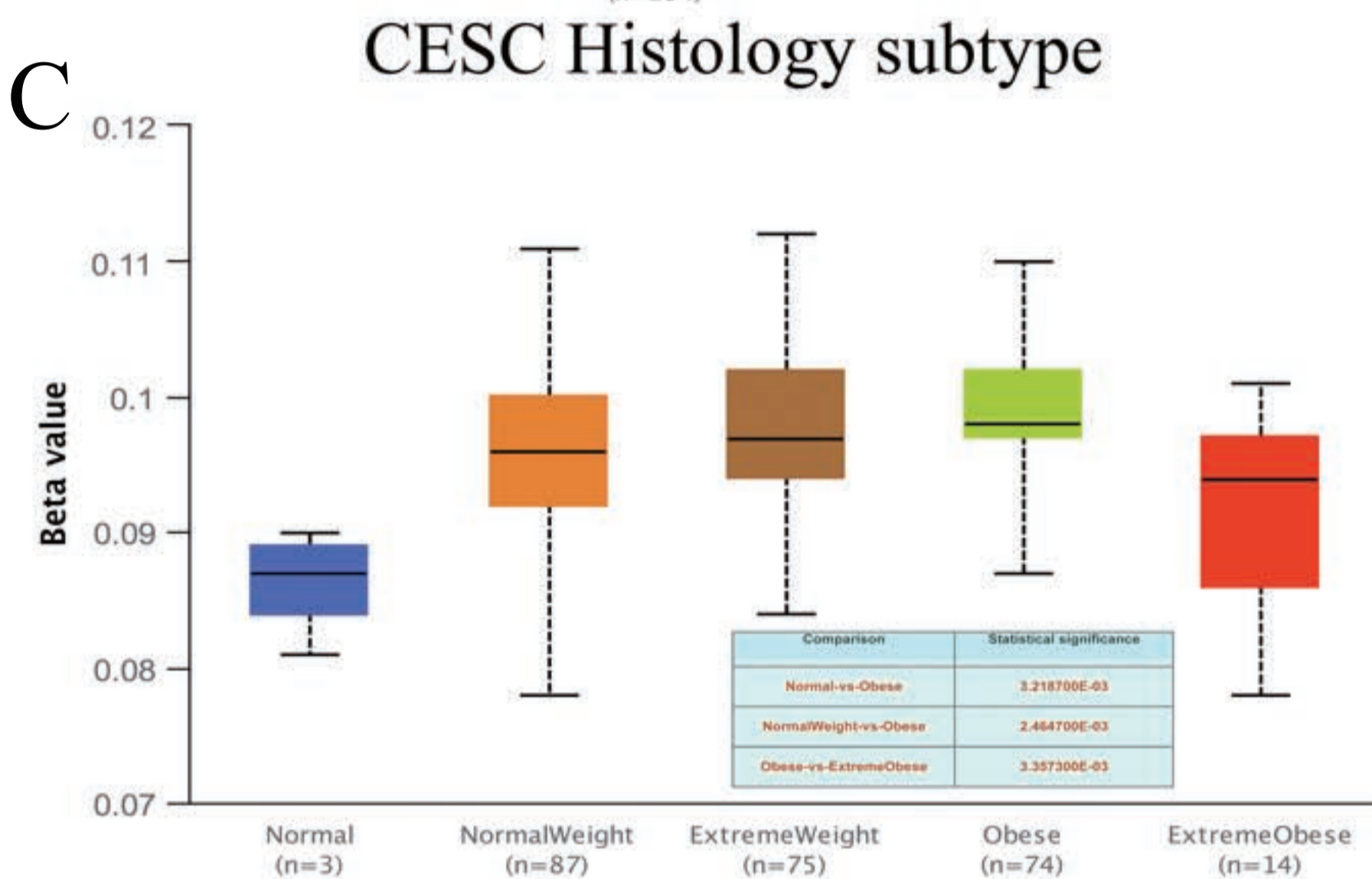
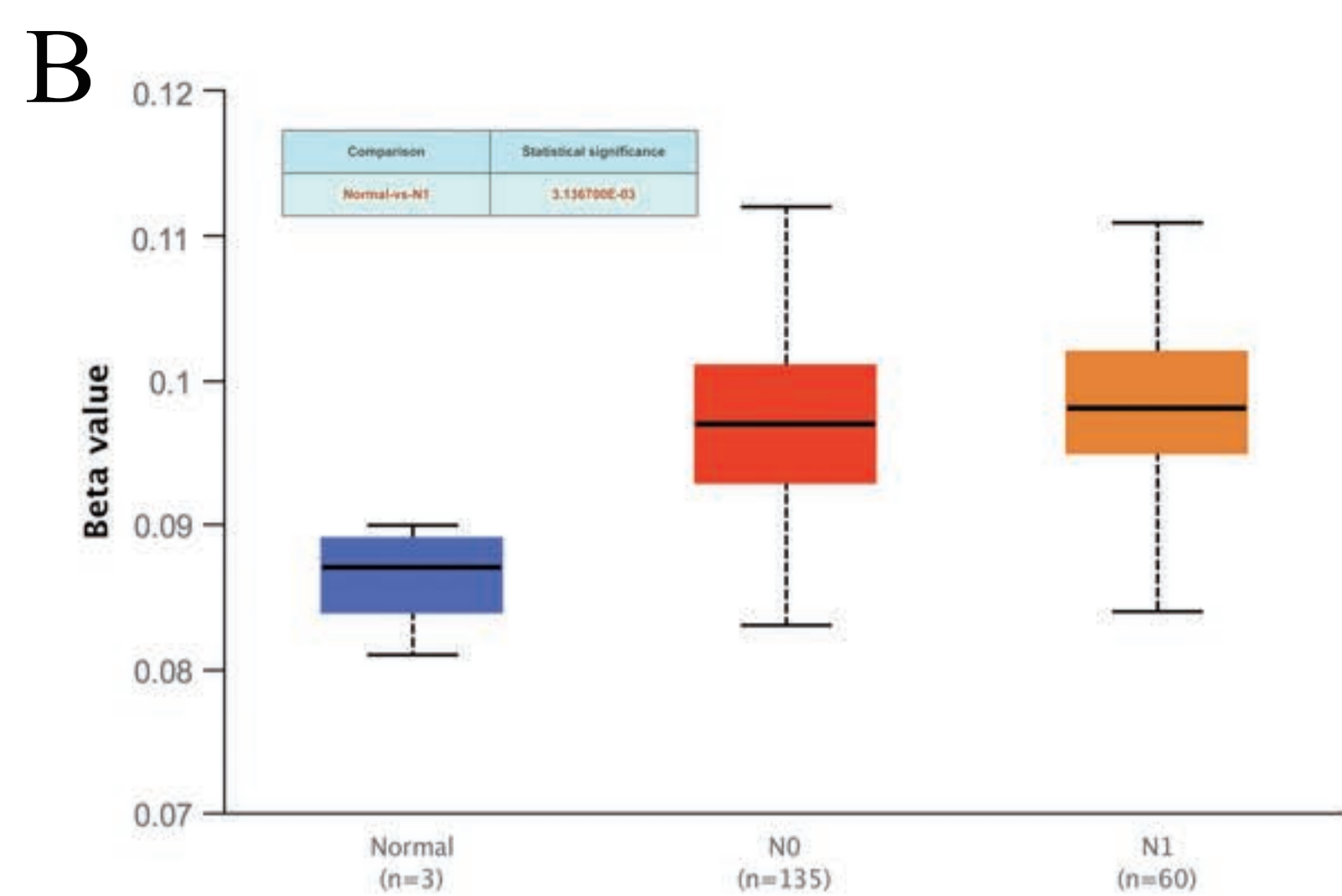
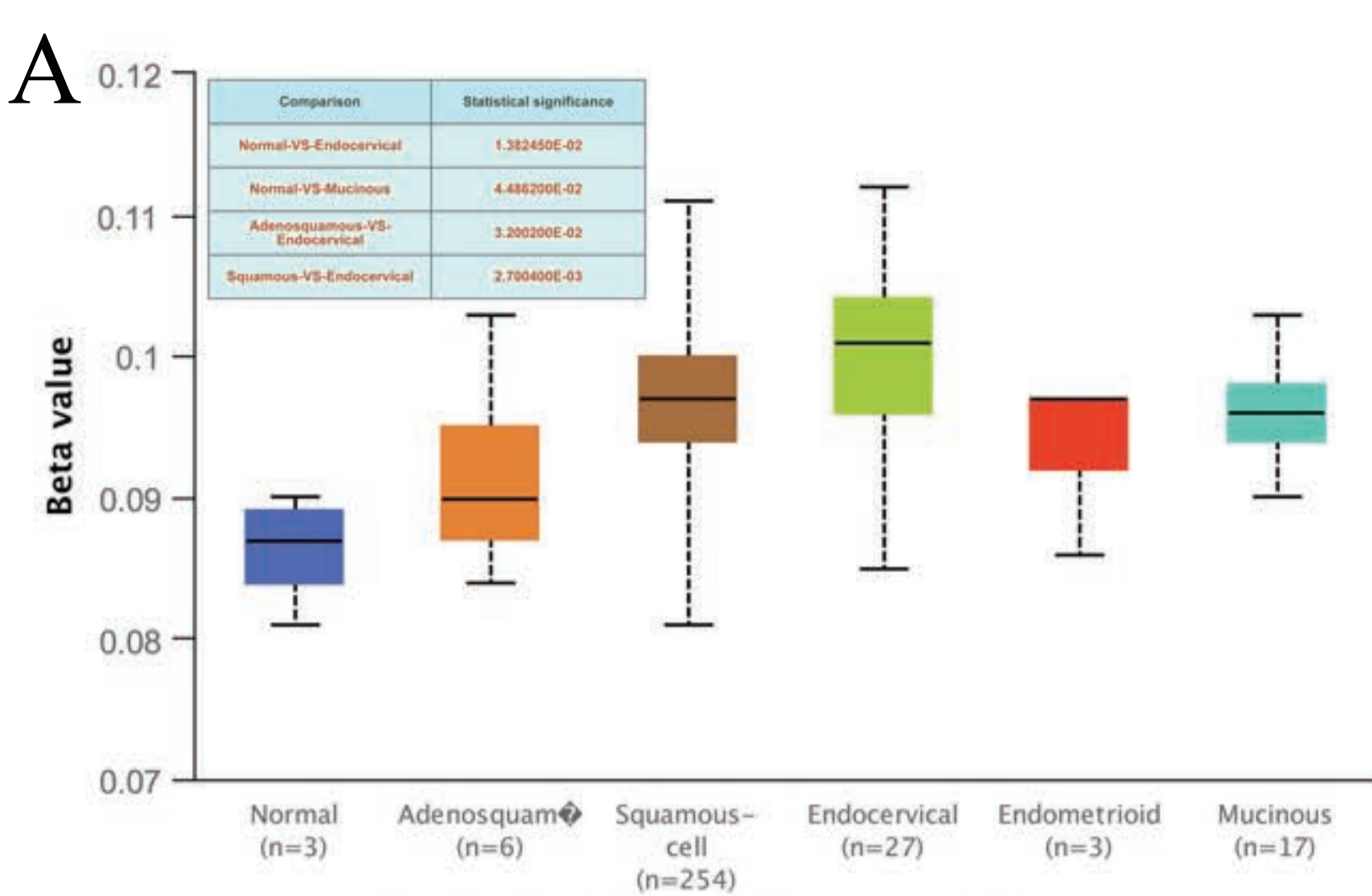


Fig.S8



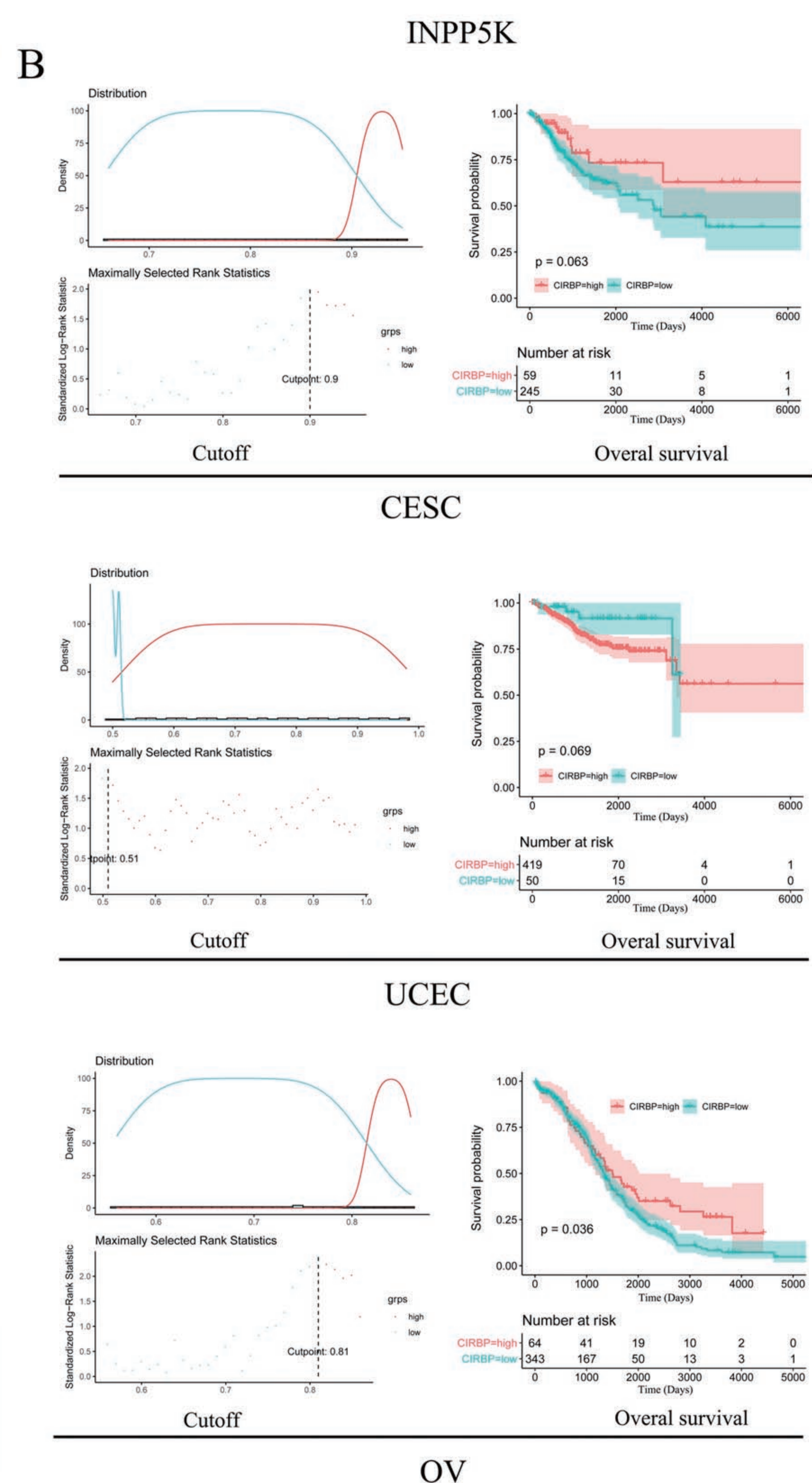
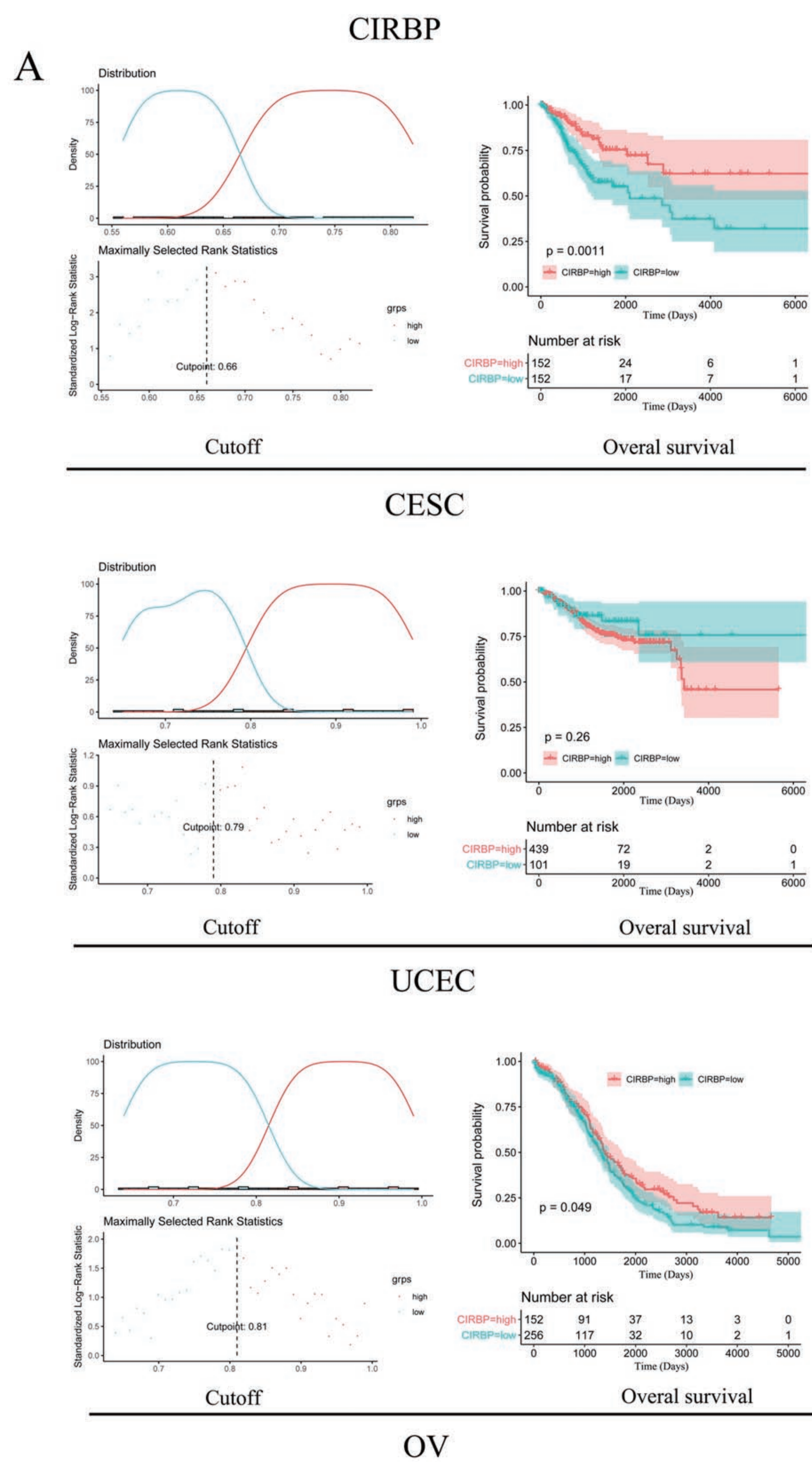


Fig.S9