

Table S1 ESCRT-III Gene Location on TISDIB dataset

Symbol	Chromosomal Location	Location	Subcellular Location										
			Cytoplasm	cytosol	Membrane	Lipid-anchor	Endosome membrane	Late endosome membrane	Peripheral membrane protein	Cytoplasmic side	Midbody Nucleus envelope	Cytoplasm Nucleus envelope	
CHMP2A	19q13.43	chr19:58551566-58555124 (GRCh38)							Y	Y	Y		
CHMP2B	3p 12.1	chr3:87227271-87255548 (GRCh38)	Y	Y					Y	Y			
CHMP3	2p 11.2	chr2:86503430-86620493 (GRCh38)	Y	Y	Y	Y	Y	Y	Y				
CHMP4B	20q11.22	chr20:33811304-33854366 (GRCh38)	Y	Y					Y	Y		Y	
CHMP4C	8q21.13	chr8:81732434-81759515 (GRCh38)	Y	Y					Y	Y		Y	
CHMP5	9p13.3	chr9:33264879-33282069 (GRCh38)		Y				Y	Y				
CHMP6	17q25.3	chr17:80991598-81009517 (GRCh38)				Y		Y	Y				
CHMP7	8p21.2	chr8:23243637-23262000 (GRCh38)											Y

Table S2 ESCRT-III Gene Synonyms on TISDIB dataset

Symbol	Aliases, Synonyms
CHMP2A	Cytoplasmic side Note = Localizes to the midbody of dividing cells. Localized in two distinct rings on either side of the Fleming body. BC-2; CHMP2; VPS2; VPS2A; putative breast adenocarcinoma marker (32kD); VPS2 homolog A (S. cerevisiae); chromatin modifying protein 2A; BC2; VPS2 homolog A; putative breast adenocarcinoma marker BC-2; vacuolar protein sorting-associated protein 2-1; vps2-1; hVps2-1; Chromatin-modifying protein 2a
CHMP2B	Cytoplasm, cytosol Late endosome membrane Peripheral membrane protein DKFZP564O123; CHMP2.5; VPS2B; VPS2 homolog B (S. cerevisiae); chromatin modifying protein 2B; ALS17; VPS2-2; VPS2 homolog B; vacuolar protein-sorting-associated protein 2-2; hVps2-2; Vacuolar protein sorting-associated protein 2-2; Chromatin-modifying protein 2b
CHMP3	Late endosome membrane Note = Localizes to the midbody of dividing cells. NEDF; CGI-149; VPS24; vacuolar protein sorting 24 (yeast); vacuolar protein sorting 24 homolog (S. cerevisiae); 25.1 protein; CHMP family, member 3; chromatin-modifying protein 3; neuroendocrine differentiation factor; vacuolar protein sorting 24 homolog; vacuolar protein sorting-associated protein 24; hVps24
CHMP4B	Midbody Nucleus envelope Note = Recruited to the nuclear envelope by CHMP7 during late anaphase. Localizes transiently to the midbody arms immediately before abscission dJ553F4.4; Shax1; SNF7-2; VPS32B; C20orf178; chromosome 20 open reading frame 178; chromatin modifying protein 4B; CTPP3; CTRCT31; Vps32-2; SNF7 homolog associated with Alix 1; Snf7 homologue associated with Alix 1; chromatin-modifying protein 4b; hSnf7-2; hVps32-2; vacuolar protein sorting-associated protein 32-2; vacuolar protein-sorting-associated protein 32-2
CHMP4C	Midbody ring Note=Localizes to the midbody during late cytokinesis. During its recruitment, localizes initially to the midbody arms, before being directed to the central region, the midbody ring, also called Flemming body. Phosphorylation at Ser-210 by AURKB triggers localization to midbody ring MGC22825; Shax3; VPS32C; Snf7 homologue associated with Alix 3; chromatin modifying protein 4C; SNF7-3; SNF7 homolog associated with Alix 3; chromatin-modifying protein 4c; hSnf7-3; hVps32-3; vacuolar protein sorting-associated protein 32-3; vps32-3
CHMP5	Peripheral membrane protein Note = Localizes to the midbody of dividing cells. Localized in two distinct rings on either side of the Fleming body HSPC177; CGI-34; Vps60; C9orf83; SNF7DC2; chromosome 9 open reading frame 83; chromatin modifying protein 5; PNAS-2; SNF7 domain containing 2; SNF7 domain-containing protein 2; apoptosis-related protein PNAS-2; chromatin-modifying protein 5; hVps60; vacuolar protein sorting-associated protein 60
CHMP6	Lipid-anchor Note = Localizes to endosomal membranes FLJ11749; VPS20; chromatin modifying protein 6; chromatin-modifying protein 6; hVps20; vacuolar protein sorting-associated protein 20
CHMP7	Cytoplasm Nucleus envelope Note = Diffused localization, with some punctate distribution, especially in the perinuclear area (PubMed:16856878). Localizes to the nucleus envelope during late anaphase MGC29816; CHMP family, member 7; chromatin-modifying protein 7

Table S3 Categories and Cases of ESCRT mutation types on TCGA-UCEC project

Mutation categories	Mutation types	CHMP2A	CHMP2B	CHMP3	CHMP4B	CHMP4C	CHMP5	CHMP6	CHMP7
somatic mutation	Missense	36	41	30	26	40	23	30	58
	Stop Gained	4	5	4	2	3	2	1	5
	Frameshift	2	1	1	3	1			5
	Stop Lost			1			1		
	Moderate	36	41	30	26	40	23	30	58
	High	6	6	6	5	4	3	1	6
SSM, CNV	SSM Affected Cases	21	26	15	22	14	19	9	36
	CNV Gains	26	11	8	22	14	21	53	3
	CNV Losses	23	23	9	11	5	5	7	32
VEP impact mutation	modifier	22	31	16	12	9	16	3	43
	moderate	10	10	7	5	7	8	4	13
	low	4	4	3	5	2	3	5	6
	high	1	1	4	2	1	1	1	3
SIFT impact mutation	tolerated	3	3	4	3	5	6	1	9
	deleterious	7	7	5	2	2	2	3	4
	deleterious_low_confidence								1
	tolerated_low_confidence								1
Polyphen impact mutation	benign	3	4	5	4	4	7	2	9
	probably_damaging	5	7	3	1	2	1	2	3
	unknown	2							2
	possibly_damaging	2	2	2		1		2	1
Consequence type mutation	non_coding_transcript_exon_variant	8	9	11			5		39
	3_prime_UTR_variant	3	15	4	12	9	10		34
	downstream_gene_variant	17	20	10			7	2	32
	missense_variant	10	10	7	5	7	8	4	13
	upstream_gene_variant	5	1				4		13
	intron_variant	3	2	4			2	2	12
	synonymous_variant		3	1	5	2	3	4	5
	start_lost			1					
	5_prime_UTR_variant	4	7					1	2
	frameshift_variant								2
	splice_acceptor_variant						1	1	1
	splice_region_variant	1	1					1	1
	stop_gained	1	1		1	1			
Type mutation	single base substitution	22	30	16	23	17	22	9	41
	small insertion		3			1			
	small deletion		2		1	1			2
Variant caller mutation	varscan2	20	27	12	20	13	19	9	36
	muse	20	25	14	20	15	21	8	34
	mutect	21							32
	mutect2		29	15	20	19	22	8	
	somaticsniper	18	23	10	16		17	8	30

SSM, simple somatic mutation; SNV, single nucleotide variation.

Table S5 Relations between abundance of Tumor-infiltrating lymphocytes (TILs) and gene expression by spearman correlations in EC

Symbol	CHMP2A		CHMP2B		CHMP3		CHMP4B		CHMP4C		CHMP5		CHMP6		CHMP7	
TISIDB																
	rho	P	rho	P	rho	P	rho	P	rho	P	rho	P	rho	P	rho	P
Act CD8	0.389	<2.2e-16	-0.086	0.0438	-0.045	0.293	0.206	1.35e-06	-0.144	0.000769	0.064	0.133	0.243	1.06e-08	0.099	0.0212
Tcm CD8	0.09	0.0351	-0.06	0.163	0.102	0.0169	0.236	2.58e-08	-0.071	0.0977	0.128	0.0027	0.135	0.00155	0.026	0.543
Tem CD8	0.168	8.14e-05	-0.097	0.0228	-0.057	0.184	0.103	0.0157	-0.17	6.81e-05	-0.023	0.596	0.15	0.000461	-0.045	0.293
Act CD4	-0.232	4.33e-08	0.0329	3.86e-15	0.125	0.00345	-0.03	0.486	0.136	0.00147	0.289	7.83e-12	-0.153	0.000351	0.15	0.000458
Tcm CD4	0.308	2.62e-13	0.064	0.136	0.087	0.0429	0.259	9.49e-10	-0.013	0.77	0.166	1e-04	0.17	6.64e-05	0.132	0.00193
Tem CD4	-0.274	8.49e-11	0.434	<2.2e-16	0.303	5.57e-13	-0.008	0.857	0.186	1.26e-05	0.363	<2.2e-16	-0.197	3.78e-06	0.181	2.22e-05
Tfh	0.158	0.000209	0.144	0.00074	-0.066	0.124	0.14	0.00104	-0.225	1.12e-07	0.025	0.554	0.119	0.00522	-0.074	0.0849
Tgd	0.264	4.23e-10	0.001	0.981	0.103	0.0161	0.219	2.4e-07	-0.017	0.69	0.082	0.0556	0.211	7.25e-07	0.218	3.03e-07
Th1	0.073	0.0864	-0.044	0.305	-0.018	0.675	0.028	0.515	-0.153	0.000341	0.048	0.262	0.085	0.0474	-0.102	0.0172
Th17	0.215	4.26e-07	-0.153	0.00033	-0.089	0.0377	0.003	0.95	-0.069	0.105	-0.142	0.000882	0.103	0.0161	-0.142	0.000861
Th2	-0.383	<2.2e-16	0.297	1.7e-12	0.223	1.45e-07	-0.194	5.48e-06	0.147	0.000586	0.142	0.000875	-0.242	1.2e-08	0.103	0.0161
Treg	-0.035	0.414	0.035	0.41	0.081	0.0588	0.089	0.0382	-0.101	0.018	0.143	0.000804	0.061	0.157	0.064	0.134
Act B	0.154	0.000301	-0.203	1.76e-06	-0.216	3.75e-07	0.025	0.563	-0.246	6.4e-09	-0.084	0.0501	0.111	0.00957	-0.129	0.00263
Imm B	0.018	0.676	-0.077	0.0736	-0.092	0.0317	-0.026	0.537	-0.207	1.08e-06	0.034	0.432	-0.029	0.5	-0.163	0.000132
Mem B	-0.332	2.18e-15	0.132	0.00204	0.133	0.00181	-0.083	0.0516	-0.027	0.528	-0.01	0.809	-0.134	0.0017	-0.098	0.0214
NK	0.076	0.0746	0.011	0.79	0.107	0.0121	0.119	0.00551	-0.124	0.00376	0.048	0.261	0.141	0.000967	0.051	0.231
CD56bright	0.325	8.43e-15	-0.028	0.515	0.084	0.0486	0.269	2.13e-10	-0.054	0.205	0.106	0.0135	0.216	3.6e-07	0.161	0.000161
CD56dim	0.434	<2.2e-16	-0.356	4.95e-18	-0.216	3.89e-07	0.372	<2.2e-16	-0.177	3.15e-05	-0.126	0.00325	0.355	8.26e-18	-0.09	0.0361
MDSC	0.281	2.67e-11	-0.17	7.04e-05	-0.083	0.0538	0.164	0.000119	-0.225	1.11e-07	-0.02	0.646	0.24	1.46e-08	0.029	0.497
NKT	-0.005	0.902	0.021	0.63	-0.049	0.257	0.046	0.279	-0.192	6.16e-06	0.071	0.0985	-0.012	0.778	-0.07	0.104
Act DC	0.233	3.93e-08	0.048	0.262	0.056	0.192	0.286	1.13e-11	-0.086	0.0448	0.179	2.74e-05	0.177	3.38e-05	0.038	0.375
pDC	0.239	1.72e-08	0.133	0.00188	0.08	0.0632	0.165	0.000105	-0.1	0.0199	0.093	0.029	0.102	0.0174	0.081	0.06
iDC	0.06	0.162	0.315	7e-14	0.357	4.14e-18	0.061	0.152	0.106	0.0133	0.275	7.85e-11	-0.127	0.00291	0.211	6.9e-07
Macrophage	0.212	6.41e-07	-0.123	0.00403	-0.076	0.0769	0.14	0.00109	-0.243	9.26e-09	-0.05	0.241	0.219	2.59e-07	-0.063	0.14
Eosinophil	0.103	0.0165	0.001	0.974	-0.099	0.0208	-0.099	0.0213	-0.2	2.49e-06	0.047	0.272	-0.007	0.868	-0.087	0.0425
Mast	0.164	0.00012	-0.115	0.00732	-0.074	0.0828	0.027	0.527	-0.178	3.11e-05	-0.127	0.00291	0.108	0.0113	0.018	0.617
Monocyte	0.486	<2.2e-16	-0.131	0.00217	-0.011	0.805	0.316	5.37e-14	-0.136	0.00148	0.003	0.951	0.465	<2.2e-16	0.184	1.6e-05
Neutrophil	0.101	0.0187	-0.106	0.013	-0.117	0.00628	0.024	0.581	-0.12	0.00489	-0.109	0.0106	0.048	0.263	-0.14	0.00101
GEPIA2021																
	F	p	F	p	F	p	F	p	F	p	F	p	F	p	F	p
UCEC tumor	577.17	<1e-15	451.02	<1e-15	680.18	<1e-15	533.94	<1e-15	590.94	<1e-15	688.49	<1e-15	393.59	<1e-15	786.80	<1e-15
UCEC normal	83.86	<1e-15	137.56	<1e-15	163.87	<1e-15	128.64	<1e-15	222.59	<1e-15	207.66	<1e-15	46.59	<1e-15	193.17	<1e-15
Uterus	2022.39	<1e-15	1686.46	<1e-15	2523.61	<1e-15	1657.34	<1e-15	1572.16	<1e-15	2213.29	<1e-15	1499.31	<1e-15	2643.63	<1e-15

Table S6 Survival analysis of ESCRT genes in EC patients

Dataset	Symbol	CHMP2A	CHMP2B	CHMP3	CHMP4B	CHMP4C	CHMP5	CHMP6	CHMP7
TCGA	p	0.2	0.1		0.037	0.86	0.69	0.13	0.19
TISIDB	Log-rank p	0.0203	0.274	0.183	0.118	0.101	0.426	0.28	0.984
GEPIA									
OS	Log-rank p	0.14	0.91	0.85	0.45	0.22	0.68	0.97	0.14
	HR (high)	0.6	0.91	1.1	1.3	0.64	0.86	0.99	0.59
DFS	Log-rank p	0.016	0.12	0.97	0.89	0.16	0.17	0.19	0.027
	HR (high)	0.44	0.6	0.99	1	0.63	0.63	0.64	0.47

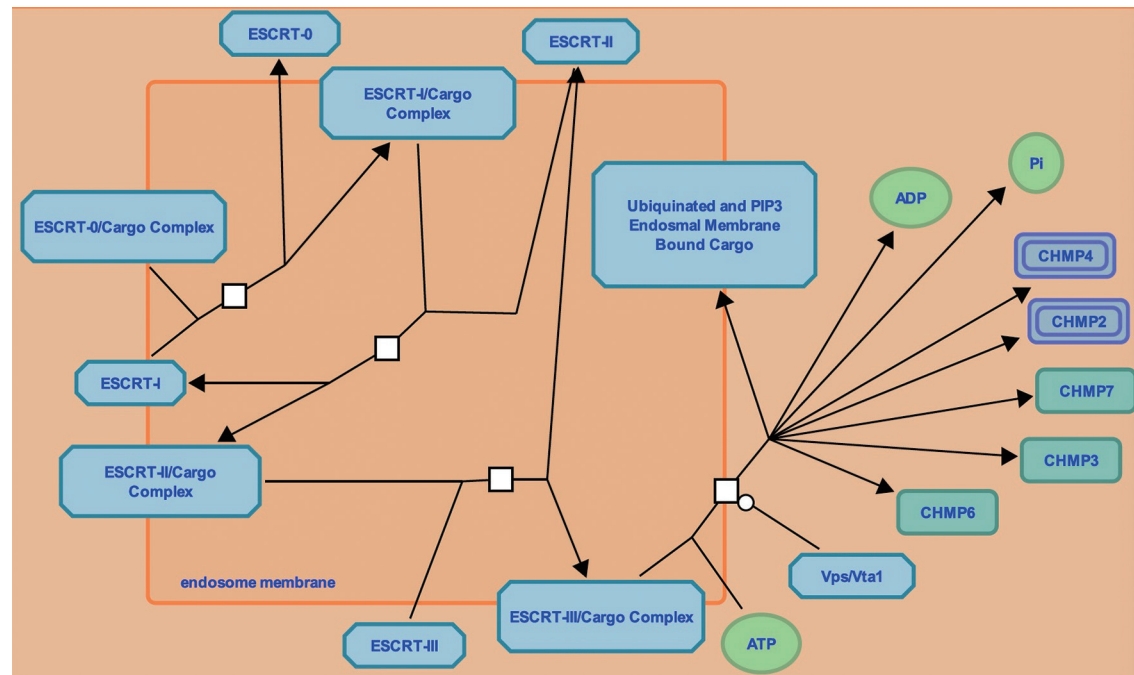


Figure S1 Endosomal sorting required for transport complex III (ESCRT-III) pathway. Cited from: TISIDB (<http://cis.hku.hk/TISIDB/index.php>). ESCRT, endosomal sorting complex required for transport, CHMP, charged multivesicular body protein.

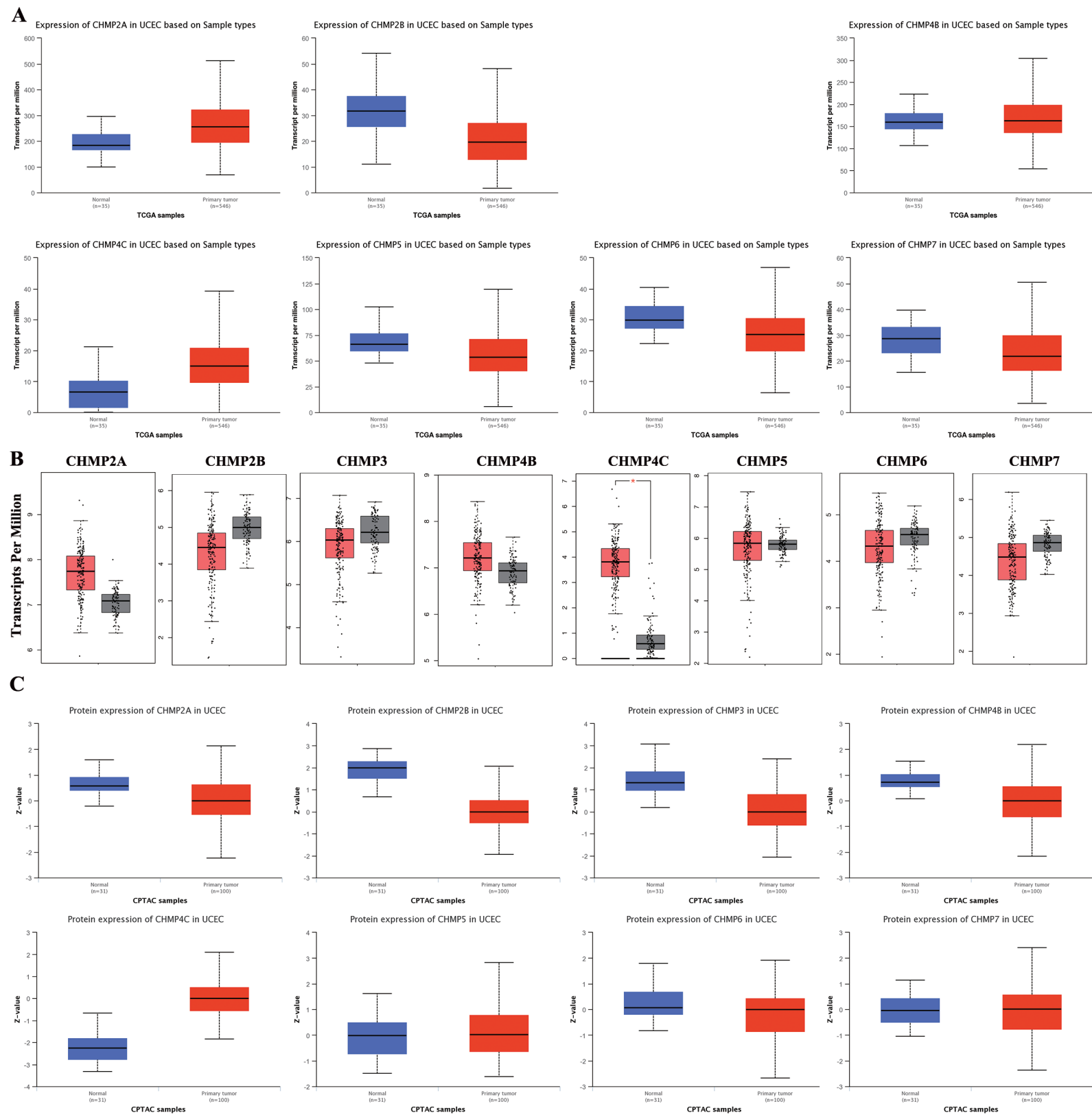


Figure S2 A comparison of the expression levels of the endosomal sorting complex required for transport (ESCRT) pathway genes between EC and normal endometrial tissue samples. The gene expression profile across tumor samples and paired normal tissues are displayed by bar plot. The height of bar represents the median expression of EC tumor type or normal tissue. The X axis represents the association between ESCRT pathway gene expression in EC and normal endometrial tissue, while the Y axis represents the TPM (A), in UALCAN analysis on TCGA-UCEC database, and (B), in GEPIA analysis on TCGA-UCEC and GTEx- Uterus database. (C) Z-values represent the standard deviations from the median of Z-values across EC and normal group samples. *, $P < 0.05$ compared with normal endometrial tissues with boxplots. TPM: Transcripts Per Million; ESCRT: endosomal sorting complex required for transport; CHMP: charged multivesicular body protein; TCGA: dataset of the Cancer Genome Atlas database; UCEC: uterine corpus endometrial carcinoma.

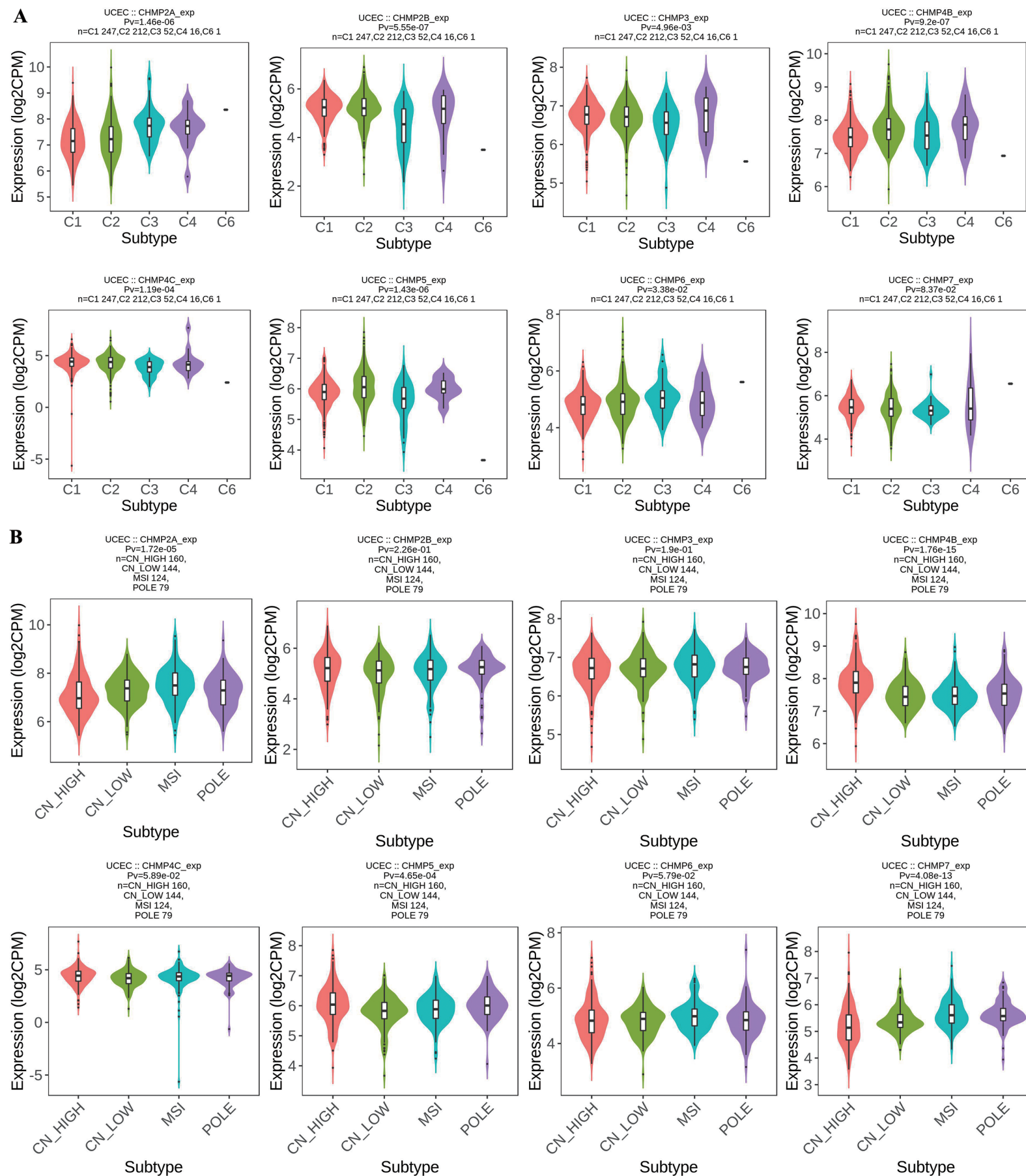


Figure S3 Association between the ESCRT pathway gene expression and the EC immune and molecular subtype. The Y axis represents the log2CPM of expression, which has been determined by the Kruskal-Wallis test $-\log_{10}(p\text{-value})$. (A) Immune subtype: C1 (wound healing) (n=247); C2 (IFN-gamma dominant) (n=212); C3 (inflammatory) (n=52); C4 (lymphocyte depleted) (n=16); C5 (immunologically quiet) (n=0); C6 (TGF- β dominant) (n=1). (B) Molecular subtype: Molecular subtype: POLE (DNA polymerase epsilon) (n=79), low copy number (CN-LOW) (n=144), high copy number (CN-HIGH) (n=160), and microsatellite instability (MSI) (n=124).

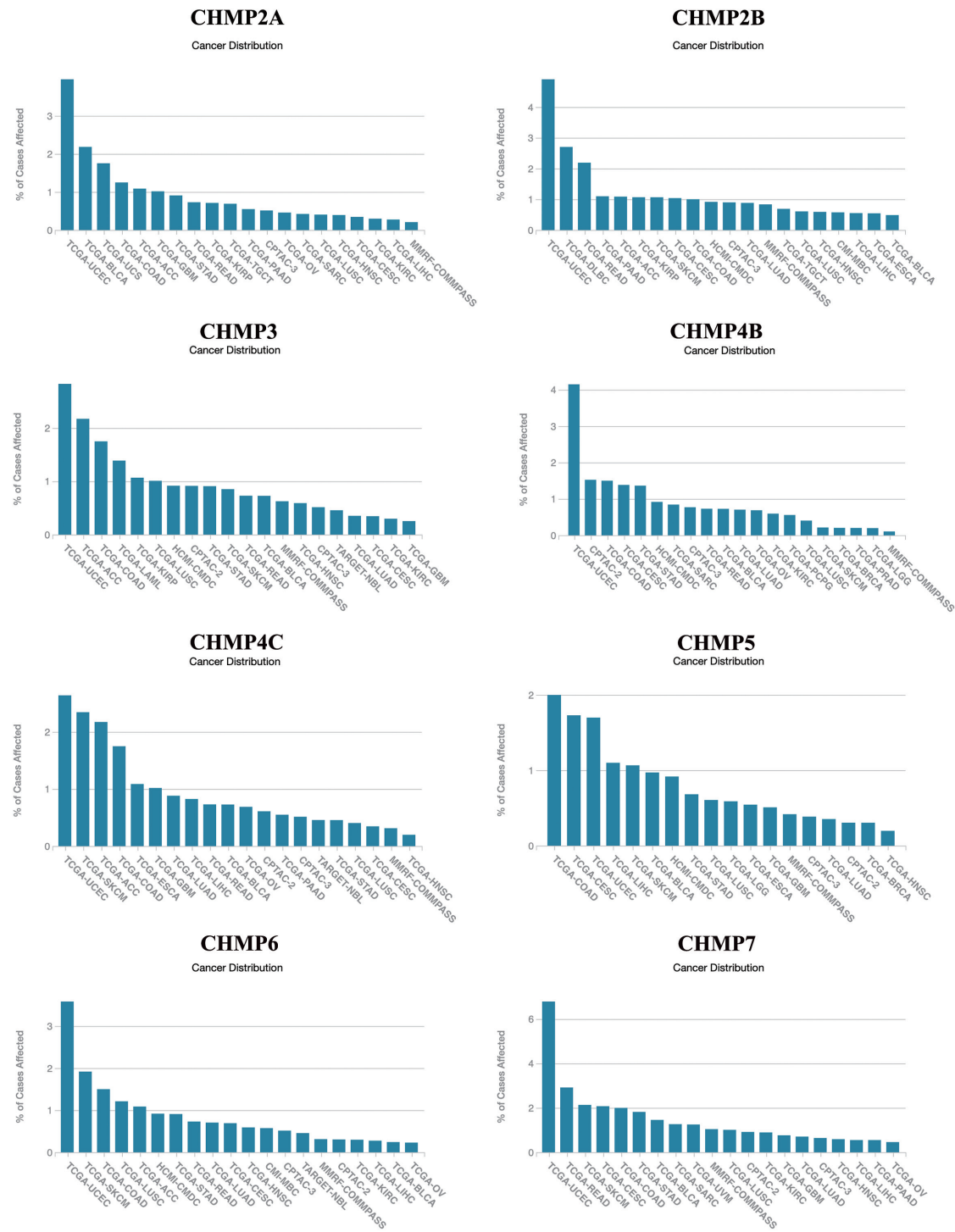


Figure S4 Correlations among the ESCRT pathway gene expression with Transcripts Per Million (TPM) by Pearson correlation analysis.

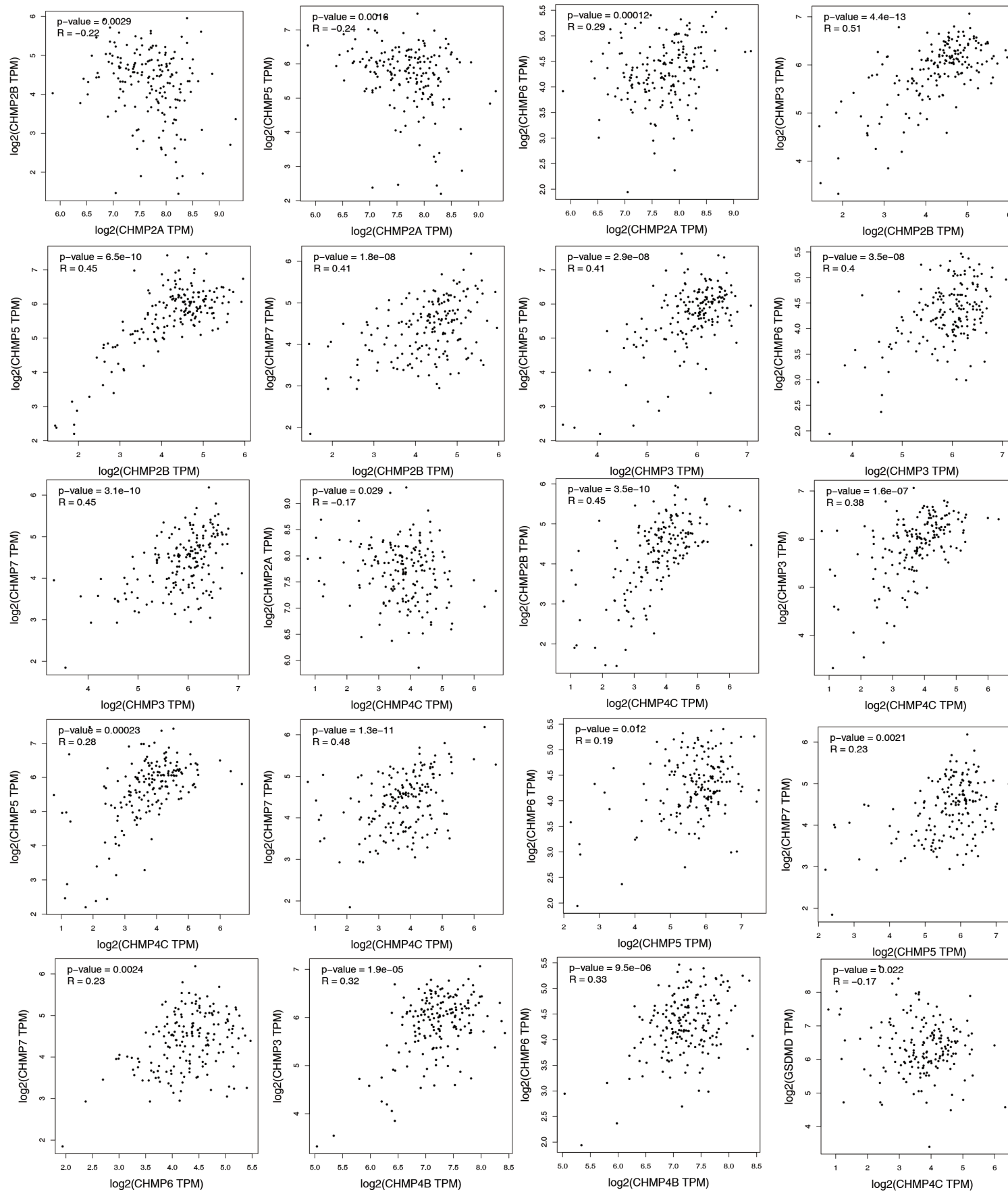


Figure S5 The ESCRT pathway gene mutations across different cancer types compared with those in EC. This was based on the TCGA database. Different genes are represented in the waterfall plot column. ACC, Adrenocortical carcinoma, BRCA, Breast invasive carcinoma, BLCA, Bladder urothelial carcinoma, CESC, Cervical squamous cell carcinoma, COAD, Colon adenocarcinoma, CPTAC-2, CPTAC-Breast, Colon, Ovary, CPTAC-3, CPTAC-Brain, Head and Neck, Kidney, Lung, Pancreas, Uterus, CMI-MBC, Count Me In (CMI): The Metastatic Breast Cancer (MBC) Project, DLBC, Lymphoid Neoplasm Diffuse Large B-cell Lymphoma, ESCA, Esophageal carcinoma, GBM, Glioblastoma multiforme, HNCMI-CMDC, NCI Cancer Model Development for the Human Cancer Model Initiative, HNSC, Head and Neck squamous cell carcinoma, KIRC, Kidney renal clear cell carcinoma, KIRP, Kidney renal papillary cell carcinoma, LAML, Acute Myeloid Leukemia, LUAD, Lung adenocarcinoma, LUSC, Lung squamous cell carcinoma, LIHC, Liver Hepatocellular Carcinoma, LGG, Brain Lower Grade Glioma, MMRF-COMMPASS, Multiple Myeloma CoMMpass Study, OV, Ovarian serous cystadenocarcinoma, PAAD, Pancreatic adenocarcinoma, PRAD, Prostate adenocarcinoma, READ, Rectum adenocarcinoma, SARC, Sarcoma, STAD, Stomach adenocarcinoma, SKCM, Skin cutaneous melanoma, TARGET-NBL, Neuroblastoma, TGCT, Testicular Germ Cell Tumors, UCS, Uterine carcinosarcoma, UCEC, Uterine corpus endometrial carcinoma.

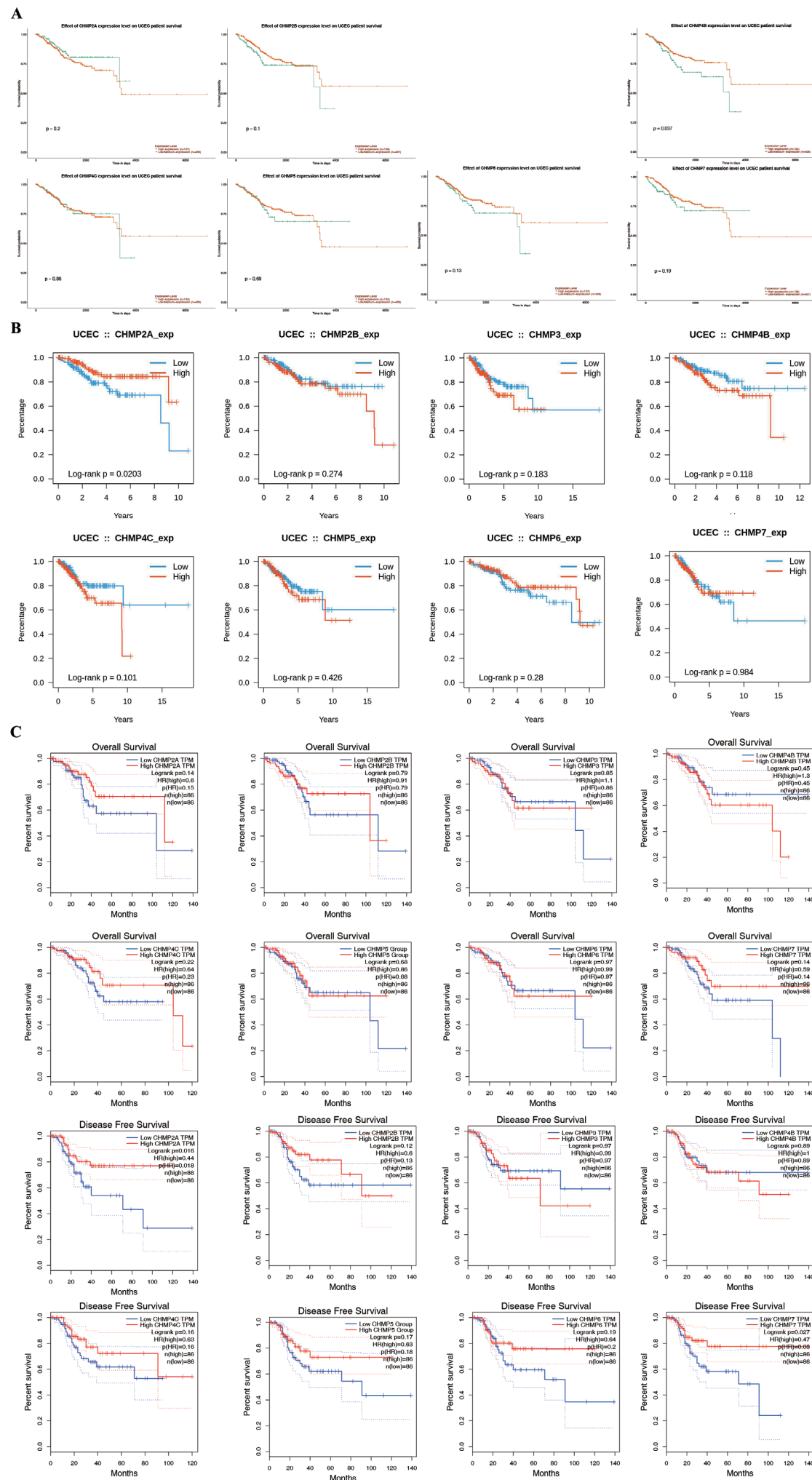


Figure S6 The survival analysis of the ESCRT genes. (A) Kaplan-Meier survival analysis for OS in UALCAN; (B) OS in TISDIB; (C) Univariate cox-regression analysis for OS and DFS in GEPIA Row: Percentage of survival, Column Axis Units: (A) Days; (B) Years; (C) Months. HR, Hazard Ratio.

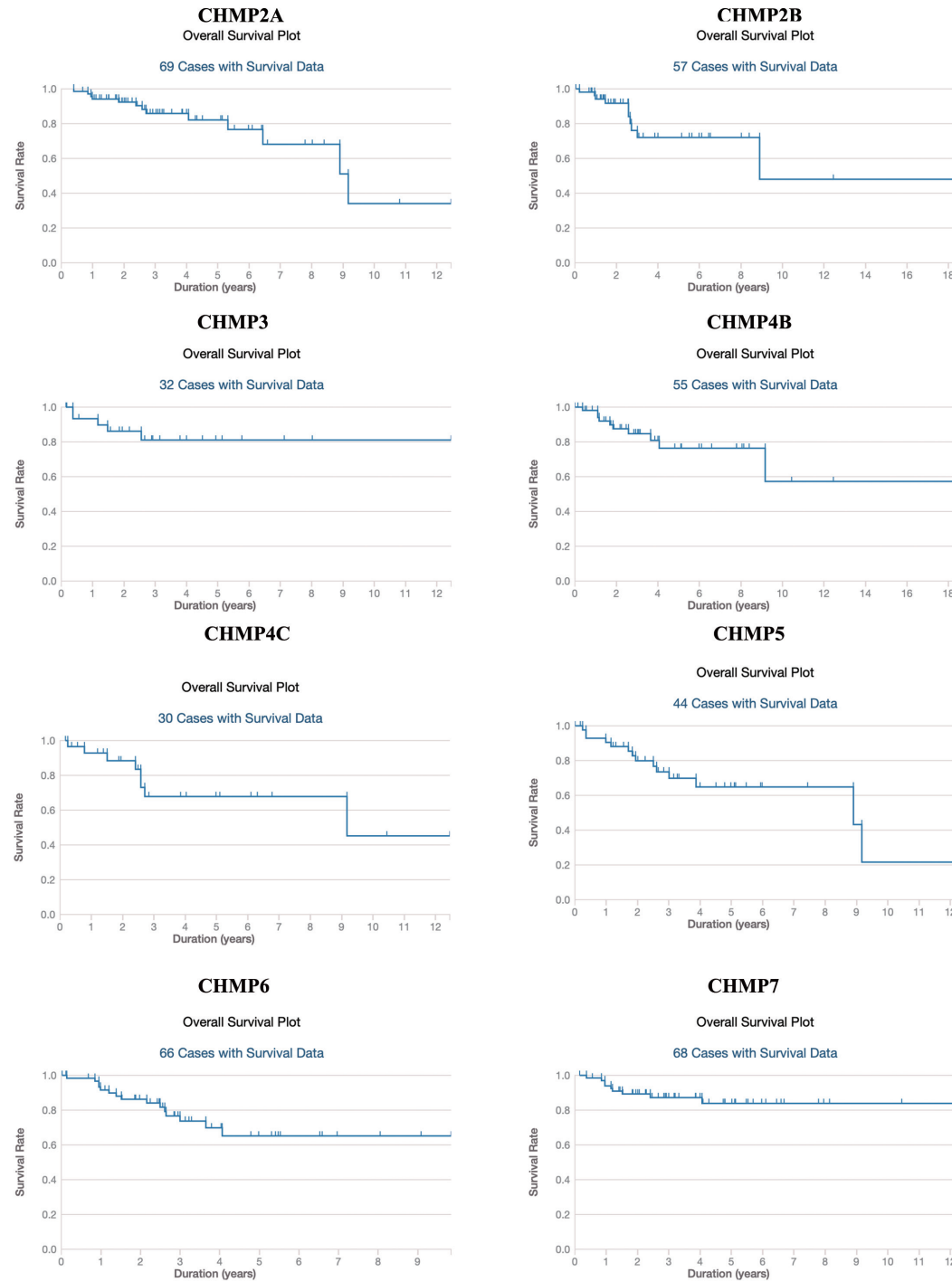


Figure S7 Survival analysis on ESCRT-III mutation genes: CHMP2A, CHMP2B, CHMP3, CHMP4B, CHMP5, CHMP6, CHMP7.