

Figure S1 Volcano plots of ESCO2 expression across different datasets. (A) GSE26566 dataset. (B) GSE32225 dataset. (C) GSE132305 dataset. Blue indicates “down”, gray indicates “stable”, and red indicates “up”.

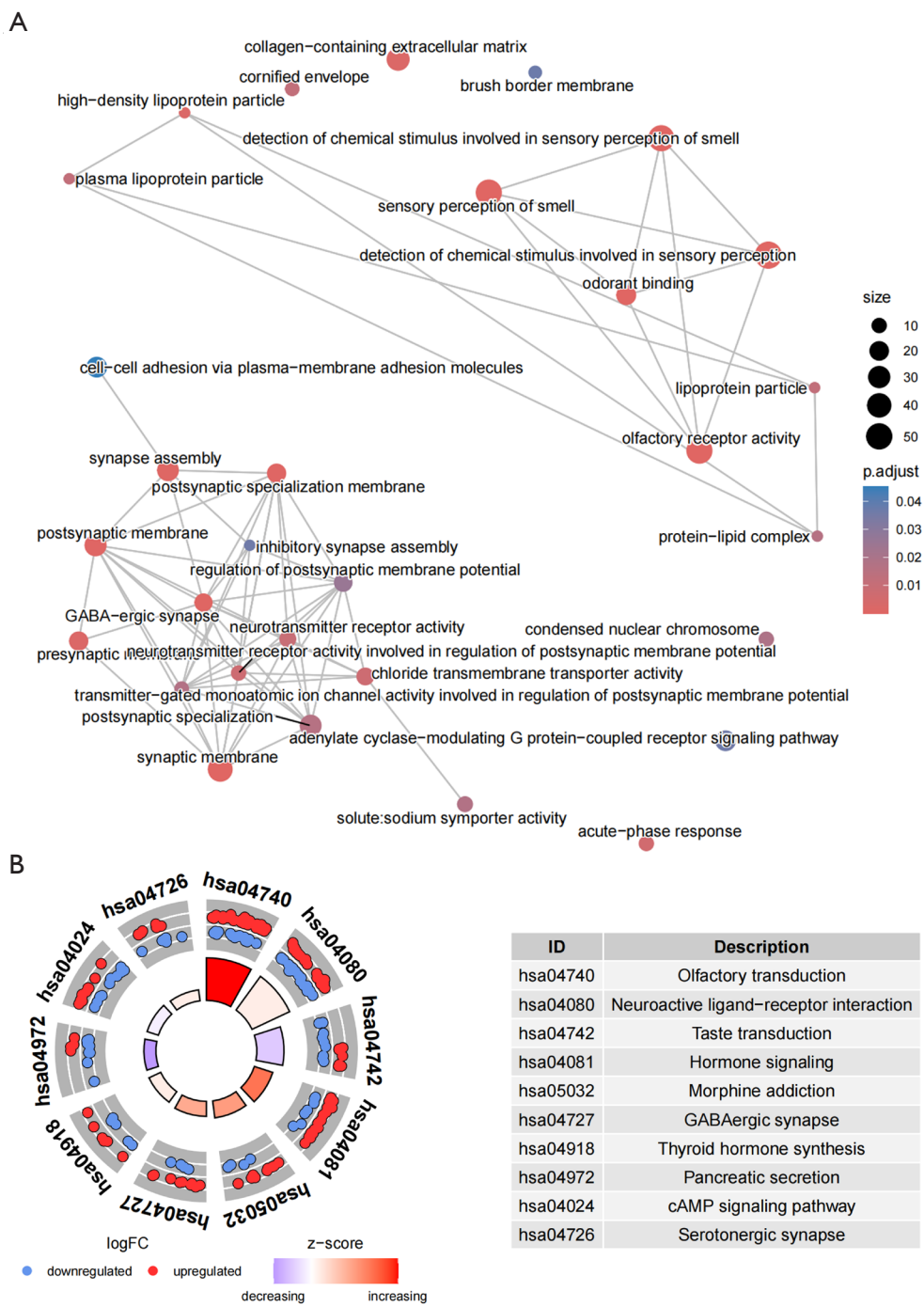


Figure S2 Enrichment analysis plots of ESCO2-related differentially expressed genes. (A) Mesh diagram of GO enrichment analysis results, each dot represents a GO Term. (B) Circle diagram of KEGG enrichment analysis, the outer ring of the circle diagram corresponds to each KEGG pathway, the dots on each KEGG module are the corresponding genes, and the inner ring of the circle diagram is the z-score of each KEGG pathway. ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

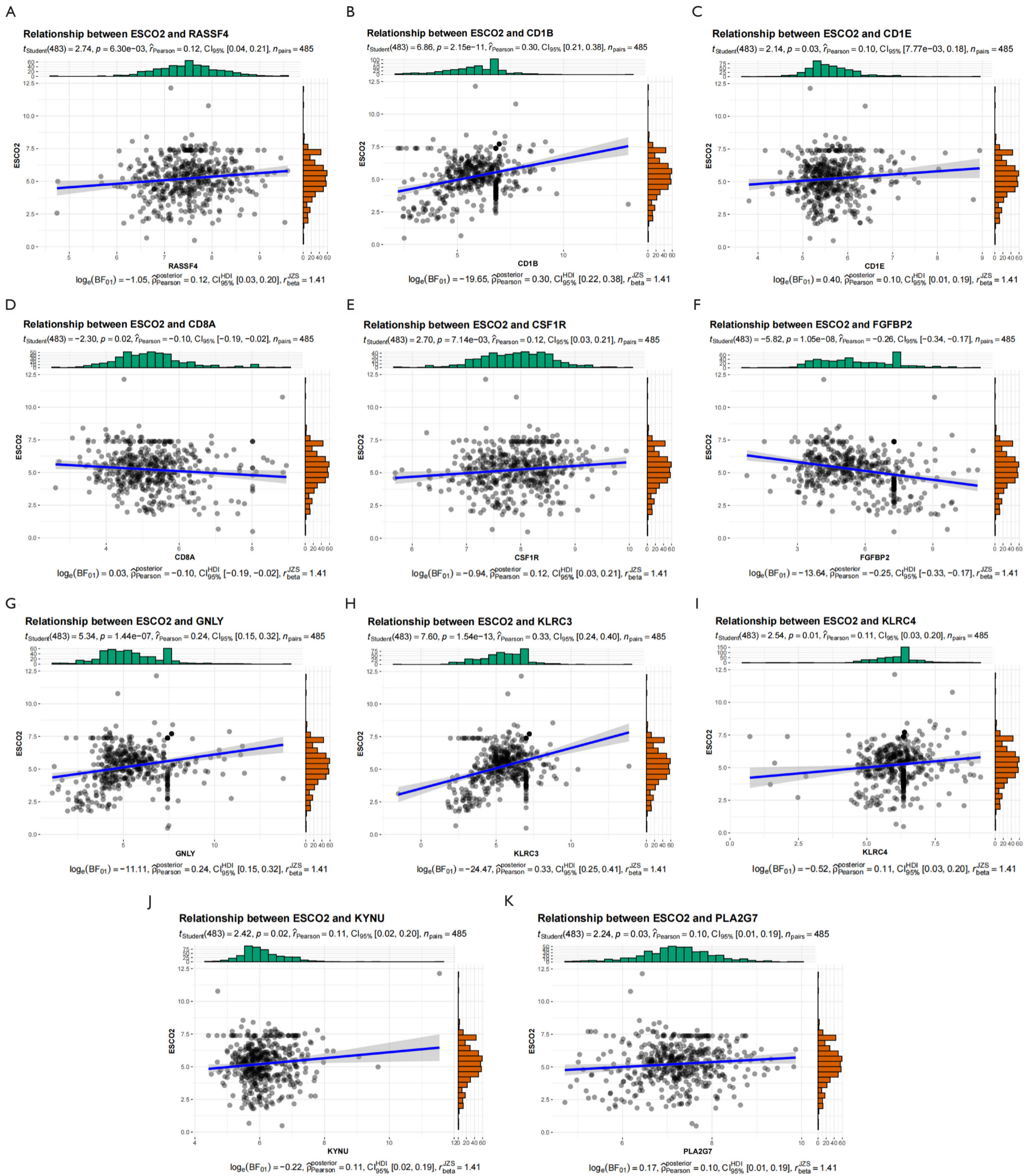


Figure S3 Correlation between ESCO2 and immune cell markers. (A) Correlation between ESCO2 and RASSF4. (B) Correlation between ESCO2 and CD1B. (C) Correlation between ESCO2 and CD1E. (D) Correlation between ESCO2 and CD8A. (E) Correlation between ESCO2 and CSF1R. (F) Correlation between ESCO2 and FGFBP2. (G) Correlation between ESCO2 and GNLY. (H) Correlation between ESCO2 and KLRC3. (I) Correlation between ESCO2 and KLRC4. (J) Correlation between ESCO2 and KYNU. (K) Correlation between ESCO2 and PLA2G7. ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; FGFBP2, fibroblast growth factor binding protein 2.

Gene	HR	lower 95%CI	upper 95%CI		pvalue
Age	1.051	0.985	1.122		0.134
Gender	1.497	0.431	5.200		0.525
Stage	1.682	0.994	2.846		0.053
T	1.577	0.723	3.440		0.252
M	4.784	0.845	27.068		0.077
N	6.376	1.267	32.079		0.025

0.5
Hazard ratios

Figure S4 Statistical data table for ESCO2 showing risk ratios (HR), 95% confidence intervals (lower 95% CI and upper 95% CI), and P values for different factors (age, gender, stage, T, M, N). ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2.

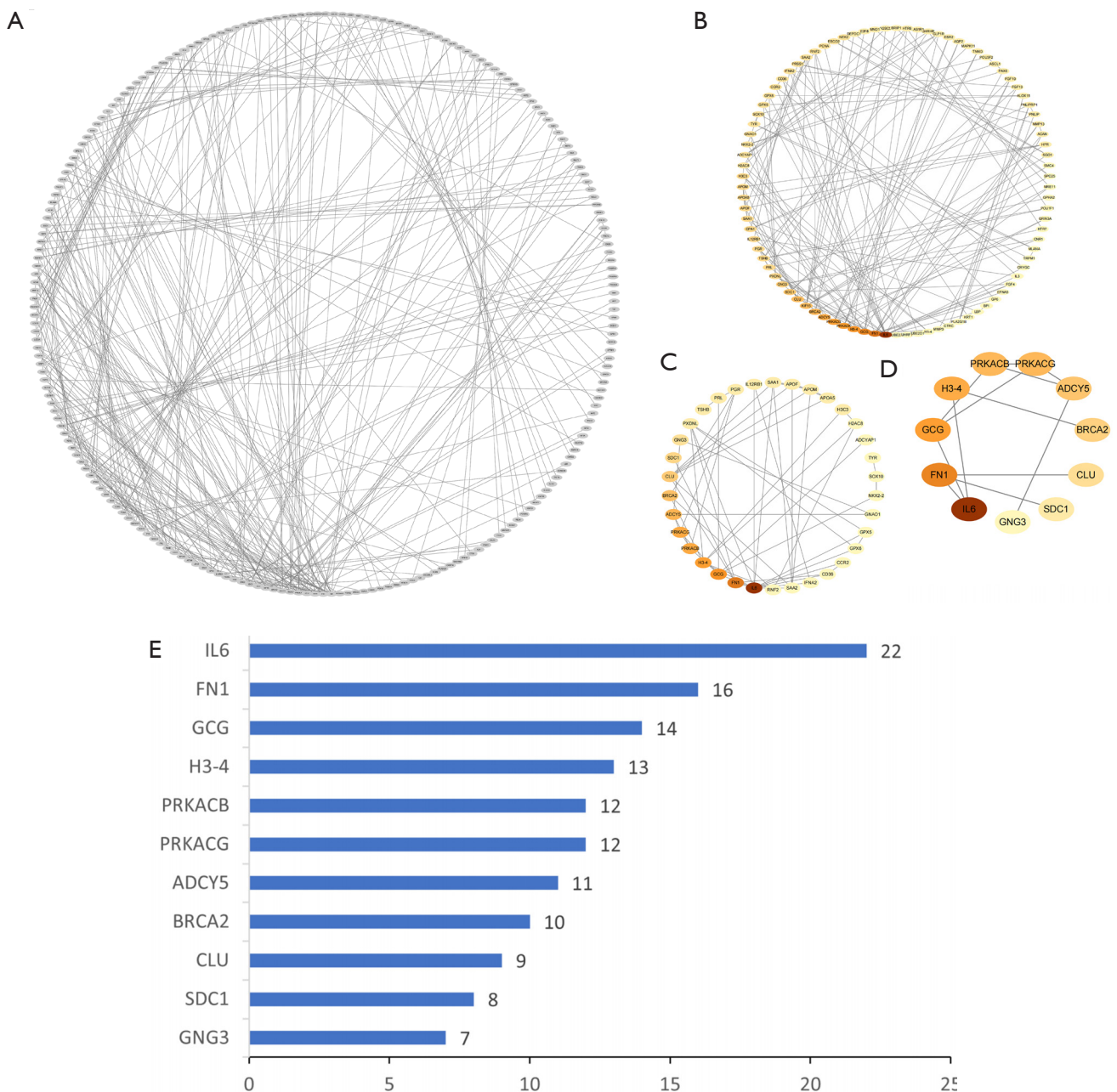


Figure S5 PPI network of differentially expressed genes. (A) PPI network construction for ESCO2-related differentially expressed genes based on the STRING database. (B) Key submodule 1 in the PPI network. (C) Key submodule 2 in the PPI network. (D) Key submodule 3 in the PPI network. (E) Degree values of the PPI network. ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; PPI, protein-protein interaction; STRING, search tool for the retrieval of interaction gene/proteins.

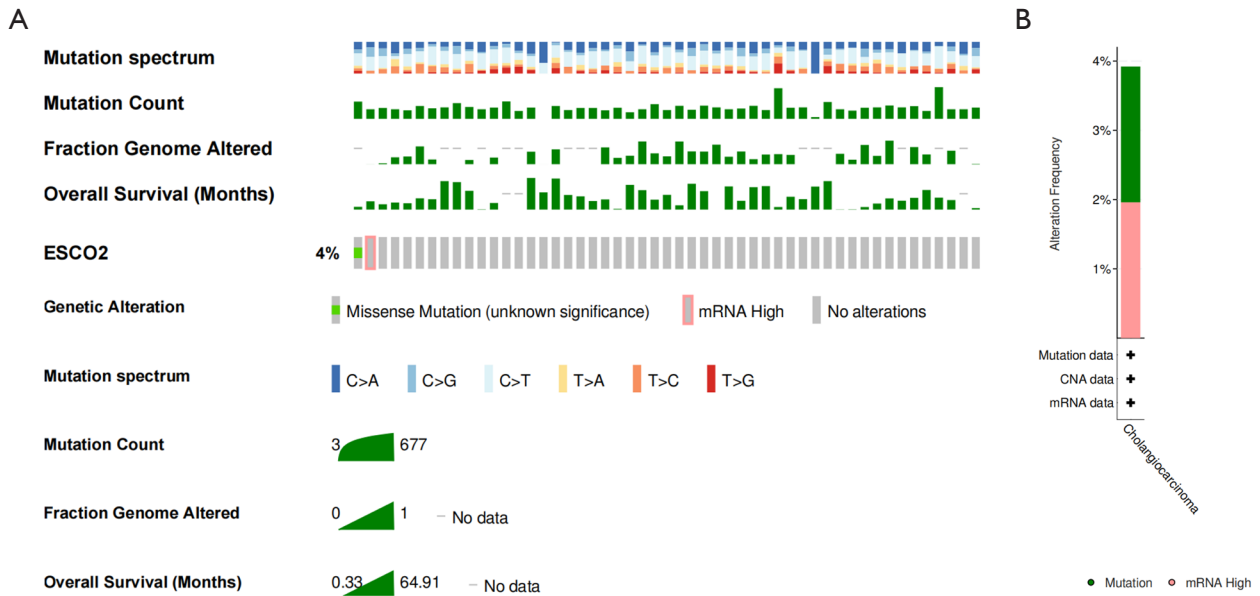


Figure S6 mRNA expression of ESCO2 in relation to its CNA mutations. (A) Set plot of mRNA expression of ESCO2 correlating with CNA mutations using Cbioportal analysis. (B) Box plot of mRNA expression of ESCO2 correlating with CNA mutations using Cbioportal analysis. ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; **CNA, copy number alteration**.

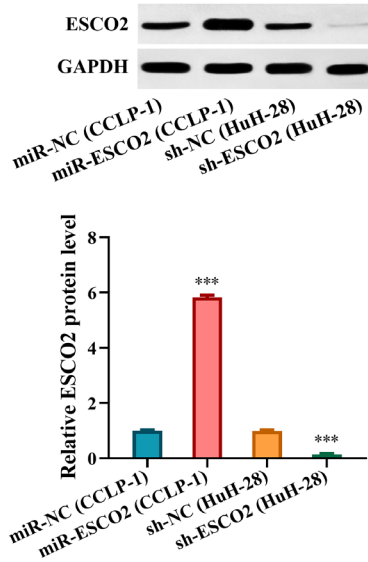


Figure S7 WB detection of ESCO2 protein expression levels following ESCO2 overexpression/silencing. ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; WB, Western blot.

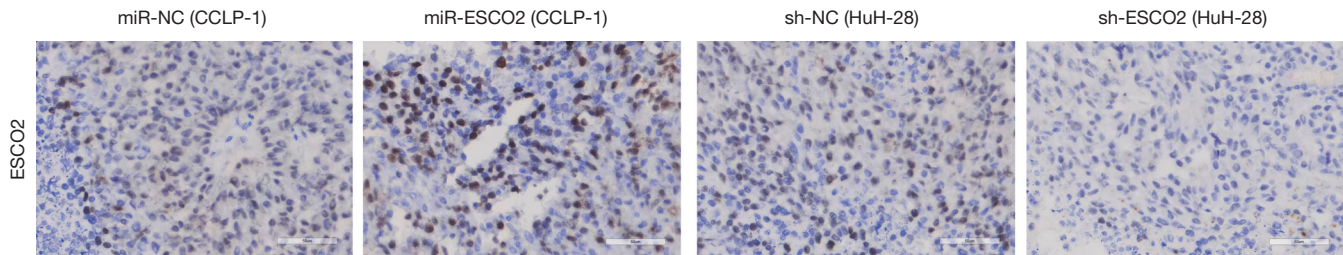


Figure S8 Immunohistochemical staining for ESCO2 in tumor sections. Scale: 50 μ m.

Table S1 Information about the data set and the number of samples it contains, as well as its sources

DataSet	Tumor	Normal	Platform	Origin
GSE26566	104	6	GPL6104	GEO
GSE32225	149	6	GPL8432	GEO
GSE132305	182	38	GPL13667	GEO
TCGA	35	9	TCGA	TCGA

GEO, Gene Expression Omnibus; TCGA, The Cancer Genome Atlas.

Table S2 Primer sequence

Genetics	Sequences
ESCO2	Forward primer: 5'-CACTGGGACGCACCCAAAA-3'
	Reverse primer: 5'-CACTTGCCTTGTGCGAAAAG-3'
GAPDH	Forward primer: 5'-GACAGTCAGCCGCATCTTCT-3'
	Reverse primer: 5'-GCGCCCAATACGACCAAATC-3'

Table S3 KEGG enrichment results based on ESCO2 differential gene (top 10 sorted by P value)

Ontology	ID	Description	Gene ratio	Bg ratio	Rich factor	P value	P adjust	q value	Count
BP	GO:0050907	Detection of chemical stimulus involved in sensory perception	55/690	479/18,986	0.114823	3.9E-14	1.67E-10	1.62E-10	55
BP	GO:0050911	Detection of chemical stimulus involved in sensory perception of smell	49/690	431/18,986	0.113689	1.47E-12	3.16E-09	3.05E-09	49
MF	GO:0004984	Olfactory receptor activity	49/700	429/18,737	0.114219	3.35E-12	2.56E-09	2.34E-09	49
BP	GO:0007608	Sensory perception of smell	49/690	459/18,986	0.106754	1.48E-11	2.11E-08	2.04E-08	49
MF	GO:0005549	Odorant binding	21/700	122/18,737	0.172131	4.59E-09	1.76E-06	1.6E-06	21
CC	GO:0097060	Synaptic membrane	42/710	453/19,960	0.092715	1.61E-08	6.79E-06	6.36E-06	42
BP	GO:0007416	Synapse assembly	28/690	269/18,986	0.104089	6.11E-07	0.000657	0.000635	28
CC	GO:0098982	GABAergic synapse	16/710	107/19,960	0.149533	1.18E-06	0.000249	0.000233	16
CC	GO:0099634	Postsynaptic specialization membrane	19/710	157/19,960	0.121019	3.27E-06	0.000459	0.00043	19
CC	GO:0045211	Postsynaptic membrane	29/710	321/19,960	0.090343	4.52E-06	0.000476	0.000446	29
BP	GO:0006953	Acute-phase response	10/690	48/18,986	0.208333	7.05E-06	0.00606	0.005859	10
CC	GO:0062023	Collagen-containing extracellular matrix	33/710	430/19,960	0.076744	3.14E-05	0.002261	0.00212	33
CC	GO:0034364	High-density lipoprotein particle	7/710	27/19,960	0.259259	3.33E-05	0.002261	0.00212	7
BP	GO:0060078	Regulation of postsynaptic membrane potential	17/690	151/18,986	0.112583	3.6E-05	0.025763	0.024909	17
MF	GO:0099529	Neurotransmitter receptor activity involved in regulation of postsynaptic membrane potential	10/700	56/18,737	0.178571	3.73E-05	0.007899	0.007197	10
CC	GO:0042734	Presynaptic membrane	19/710	186/19,960	0.102151	3.76E-05	0.002261	0.00212	19
MF	GO:0015108	Chloride transmembrane transporter activity	15/700	120/18,737	0.125	4.12E-05	0.007899	0.007197	15
BP	GO:1904862	Inhibitory synapse assembly	7/690	29/18,986	0.241379	6.3E-05	0.036251	0.03505	7
MF	GO:0030594	Neurotransmitter receptor activity	13/700	97/18,737	0.134021	6.4E-05	0.009812	0.008939	13
BP	GO:0007188	Adenylate cyclase-modulating G protein-coupled receptor signaling pathway	24/690	274/18,986	0.087591	6.75E-05	0.036251	0.03505	24
BP	GO:0098742	Cell-cell adhesion via plasma-membrane adhesion molecules	24/690	280/18,986	0.085714	9.47E-05	0.045211	0.043713	24
MF	GO:1904315	Transmitter-gated monoatomic ion channel activity involved in regulation of postsynaptic membrane potential	9/700	53/18,737	0.169811	0.000137	0.017454	0.015903	9
MF	GO:0015370	Solute:sodium symporter activity	11/700	79/18,737	0.139241	0.000164	0.017648	0.016079	11
MF	GO:0046943	Carboxylic acid transmembrane transporter activity	18/700	185/18,737	0.097297	0.000204	0.017648	0.016079	18
MF	GO:0005342	Organic acid transmembrane transporter activity	18/700	186/18,737	0.096774	0.000219	0.017648	0.016079	18

ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; MF, molecular function; CC, cellular component.

Table S4 KEGG enrichment results based on ESCO2 differential gene (top 10 sorted by P value)

ID	Description	Gene ratio	Bg ratio	P value	P adjust	q value	Count
hsa04740	Olfactory transduction	53/370	453/8541	1.82E-11	5.52E-09	5.05E-09	53
hsa04080	Neuroactive ligand-receptor interaction	46/370	370/8541	5.81E-11	8.81E-09	8.05E-09	46
hsa04742	Taste transduction	17/370	86/8541	1.19E-07	1.2E-05	1.09E-05	17
hsa04081	Hormone signaling	25/370	219/8541	8.21E-06	0.000622	0.000568	25
hsa05032	Morphine addiction	14/370	91/8541	3.27E-05	0.001982	0.001811	14
hsa04727	GABAergic synapse	13/370	89/8541	0.000108	0.005463	0.004992	13
hsa04918	Thyroid hormone synthesis	11/370	75/8541	0.000351	0.015186	0.013875	11
hsa04972	Pancreatic secretion	13/370	106/8541	0.00063	0.023844	0.021785	13
hsa04024	cAMP signaling pathway	21/370	226/8541	0.000777	0.026162	0.023903	21
hsa04726	Serotonergic synapse	13/370	115/8541	0.001361	0.041224	0.037665	13

ESCO2, establishment of sister chromatid cohesion N-acetyltransferase 2; KEGG, Kyoto Encyclopedia of Genes and Genomes.