

**Table S1** Clinical features. Clinical information overview of the OV cohort integrated with AS profiles from TCGA data portal

Level	Overall
N	318
Age (median [IQR])	58.50 [51.00, 68.00]
Days to last follow-up (median [IQR])	948 [445, 1579]
Status (%)	
Alive	141 (44.3)
Dead	177 (55.7)
Race (%)	
Asian	10 (3.1)
White	278 (87.4)
Black or African American	21 (6.6)
American Indian or Alaska native	1 (0.3)
Not reported	8 (2.5)
FIGO stage (%)	
Stage IIA	3 (0.9)
Stage IIB	3 (0.9)
Stage IIC	11 (3.5)
Stage IIIA	6 (1.9)
Stage IIIB	11 (3.5)
Stage IIIC	237 (74.5)
Stage IV	45 (14.2)
Unknown	2 (0.6)

OV, ovarian serous cystadenocarcinoma; AS, alternative splicing; TCGA, The Cancer Genome Atlas.

**Table S2** Detailed information of 58 independent prognostic factors

Gene	HR	Lower	Upper	P value	Type	Exon
<i>NPEPPS</i>	2.2395	1.4745	3.4013	0.000156	AA	14.1
<i>UFSP2</i>	1.8259	1.1817	2.8214	0.006692	AA	10.1
<i>EEF1D</i>	0.3720	0.2402	0.5760	9.31e-06	AA	8.1.1
<i>SRRT</i>	4.1182	2.7083	6.2621	3.61e-11	AA	19.1
<i>POLDIP3</i>	0.5075	0.3272	0.7869	0.00244	AA	3.1
<i>IMMT</i>	0.5752	0.3566	0.9277	0.023361	AA	6.1
<i>SLC25A3</i>	2.0004	1.3094	3.0561	0.001342	AA	1.4
<i>ISOC2</i>	0.6000	0.3989	0.9024	0.014156	AA	4.1
<i>COPS7A</i>	2.3717	1.5161	3.7101	0.000155	AD	1.4
<i>KLK11</i>	0.6520	0.4327	0.9825	0.040931	AD	5.2
<i>KBTBD4</i>	0.6407	0.4172	0.9838	0.041880	AD	1.2
<i>ZGPAT</i>	1.5319	1.0029	2.3400	0.048476	AD	2.2
<i>NME6</i>	1.5584	1.0275	2.3636	0.036823	AD	1.3
<i>VEGFA</i>	1.6714	1.0867	2.5708	0.019363	AD	7.2:7.3
<i>FAM134C</i>	1.5020	0.9255	2.4375	0.099609	AP	2.1
<i>PIGV</i>	2.8141	1.8381	4.3082	1.92e-06	AP	1
<i>UBR4</i>	0.4092	0.2647	0.6325	5.77e-05	AP	86.1
<i>C12orf23</i>	1.5888	1.0120	2.4943	0.044231	AP	4.1
<i>FGD4</i>	0.5192	0.3402	0.7924	0.002374	AP	4
<i>ZNF266</i>	2.9253	1.8460	4.6359	4.89e-06	AP	6.1
<i>GJA9</i>	0.4178	0.2734	0.6383	5.45e-05	AP	2.1
<i>RPS6KA3</i>	1.8166	1.2044	2.7400	0.004416	AP	3
<i>CUL1</i>	2.6272	1.6977	4.0656	1.45e-05	AP	3
<i>BARX2</i>	0.5372	0.3524	0.8191	0.003885	AP	3.1
<i>ACTR3</i>	3.1419	1.7864	5.5258	7.07e-05	AT	13
<i>ZNF131</i>	2.9838	1.9536	4.5572	4.21e-07	AT	9.3
<i>NR4A3</i>	0.6250	0.4117	0.9488	0.027318	AT	9
<i>LAG3</i>	1.9284	1.2420	2.9941	0.003438	AT	5.2
<i>ATP6V0E1</i>	0.5184	0.3410	0.7881	0.002110	AT	4
<i>KIAA2013</i>	3.0489	1.9391	4.7938	1.38e-06	AT	3
<i>LEF1</i>	2.1721	1.3956	3.3806	0.000589	AT	13
<i>NF544</i>	0.3561	0.2324	0.5456	2.10e-06	AT	10.2
<i>C1orf85</i>	2.1322	1.3355	3.4040	0.001513	AT	7
<i>DDX19B</i>	0.6454	0.4238	0.9828	0.041284	AT	8
<i>NEMF</i>	0.2646	0.1496	0.4691	4.92e-06	ES	4.1

Table S2 (continued)

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Gene	HR	Lower	Upper	P value	Type	Exon
<i>TNRC6A</i>	0.5018	0.3324	0.7575	0.001032	ES	13
<i>TATDN1</i>	1.9961	1.3154	3.0289	0.001160	ES	2.1
<i>LETMD1</i>	0.4463	0.2925	0.6810	0.000182	ES	1.3:2:3.2:4
<i>ABHD12</i>	2.4057	1.6016	3.6134	2.35e-05	ES	3
<i>BTBD3</i>	2.0454	1.3419	3.1177	0.000877	ES	3
<i>NOL8</i>	0.4797	0.3072	0.7492	0.001241	ES	4
<i>CAMLG</i>	1.8165	1.2070	2.7338	0.004206	ES	3.1
<i>PLEKHA5</i>	0.2409	0.1308	0.4436	4.90e-06	ES	9
<i>SRRM1</i>	0.5322	0.3406	0.8315	0.005603	ES	4:05
<i>TSEN2</i>	2.2470	1.4654	3.4455	0.000206	ES	6
<i>ELN</i>	0.4528	0.3002	0.6830	0.000158	ES	5
<i>RHOT1</i>	7.2572	4.4697	11.7831	1.10e-15	ES	19.3
<i>SLC38A9</i>	0.2915	0.1664	0.5107	1.64e-05	ES	7
<i>ZNF846</i>	0.5154	0.3430	0.7746	0.001426	ES	5
<i>FKBP5</i>	2.1638	1.1441	4.0922	0.017589	ES	4:5:6:7
<i>MAPK8</i>	0.5746	0.3819	0.8645	0.007848	ME	7 8
<i>NDUFAF6</i>	2.3221	1.4873	3.6255	0.000210	ME	12 13
<i>THNSL2</i>	0.4692	0.3039	0.7243	0.000636	ME	9 10
<i>RAB43</i>	1.7873	1.1692	2.7322	0.007317	RI	4.2
<i>SLC39A1</i>	2.0447	1.3683	3.0553	0.000483	RI	4.2
<i>NPIP4</i>	0.5022	0.3329	0.7576	0.001026	RI	9.14
<i>KIF9</i>	1.8236	1.1563	2.8758	0.009738	RI	2.2
<i>MAGED2</i>	0.4341	0.2797	0.6737	0.000198	RI	5.2:5.3:5.4

HR, hazard ratio; AA, alternate acceptor site; AD, alternate donor site; AP, alternate promoter; AT, alternate terminator; ES, exon skip; ME, mutually exclusive exons; RI, retained intron; Exon, expression region.