

Supplementary Table 1. SBT-EOC cases used for molecular analyses

Fresh Frozen Tissue							FFPE Tissue		
Case ID	Tumour component	Oncomap	HRM (<i>KRAS</i> , <i>BRAF</i> , <i>ERBB2</i> , <i>TP53</i>)	PCR-Seq (<i>NRAS</i>)	CNV	GE	HRM (<i>TP53</i> Only)	CNV	IHC
Paired Cases									
15043	SBT & INV	✓	✓	✓	✓	✓			✓
65662	SBT & INV	✓	✓	✓	✓	✓			
65661	SBT & INV	✓	✓	✓	✓	✓			✓
9128	SBT & INV	✓	✓	✓	✓	✓			
2044	SBT & INV	✓	✓	✓	✓	✓			
3960	SBT & INV	✓	✓	✓	✓	✓			
5899	SBT & INV	✓	✓	✓	✓	✓			
65663	SBT & INV		✓	✓	✓				
65666	Inv		✓	✓	✓				
	SBT						✓		
65664	Inv		✓	✓	✓			✓	✓
	SBT						✓	✓	✓
15060	Inv		✓	✓	✓			✓	✓
	SBT						✓	✓	✓
65665	Inv		✓	✓	✓			✓	✓
	SBT						✓	✓	✓
65668	Inv		✓	✓	✓			✓	✓
	SBT						✓	✓	✓
65667	Inv		✓	✓				✓	✓
	SBT						✓	✓	✓
15018	Inv		✓	✓	✓				✓
	SBT								✓
15071	Inv		✓	✓	✓				✓
	SBT								✓
65670	Inv		✓	✓	✓				✓
	SBT								✓
8982	Inv		✓	✓					✓
	SBT								✓
Unpaired Cases									
15046	Inv		✓	✓	✓				
15014	Inv		✓	✓	✓				
65671	Inv		✓	✓	✓				
65672	SBT		✓	✓	✓				
65673	Inv		✓	✓	✓				
65674	Inv		✓	✓	✓				
65675	Inv		✓	✓	✓				
65676	Inv		✓	✓	✓				
65677	Inv		✓	✓	✓				
65678	Inv		✓	✓	✓				
65679	Inv		✓	✓	✓				

Case ID	Tumour component	Fresh Frozen Tissue					FFPE Tissue		
		Oncomap	HRM (<i>KRAS, BRAF, ERBB2, TP53</i>)	PCR-Seq (<i>NRAS</i>)	CNV	GE	HRM (<i>TP53 Only</i>)	CNV	IHC
65680	Inv		✓	✓	✓				
5349	Inv		✓	✓	✓				
7957	Inv		✓	✓	✓				
8395	Inv		✓	✓	✓				
8390	Inv		✓	✓					
2110	Inv		✓	✓					
6328	Inv		✓	✓					
9125	Inv		✓	✓					
9221	Inv		✓	✓					
10701	Inv		✓	✓					
1072	Inv		✓	✓					
11266	Inv		✓	✓					
11368	Inv		✓	✓	✓				
12237	Inv		✓	✓					
2064	Inv		✓	✓					
3539	Inv		✓	✓					
2189	Inv		✓	✓	✓				
5711	Inv		✓	✓					
6251	Inv		✓	✓					
6582	Inv		✓	✓					
7200	SBT		✓	✓	✓				
8633	Inv		✓	✓	✓				
9579	Inv		✓	✓					
10740	Inv		✓	✓					
11766	Inv		✓	✓					
3958	Inv		✓	✓					
4723	Inv		✓	✓					
6244	Inv		✓	✓	✓				
7716	Inv		✓	✓					

SBT-EOC, serous carcinoma with adjacent borderline regions; SBT, serous borderline component of SBT-EOC; Inv, invasive component of SBT-EOC; FFPE, formalin fixed paraffin embedded; HRM, high resolution melt analysis; CNV, copy number variation; GE, gene expression analysis; IHC, immunohistochemistry

Supplementary Table 2. Mutations Screened on the Sequenom/OncoMap3 Platform

Gene	OM3 Core number of assays (34 unique genes)	OM3 Extended number of assays (117 unique genes)	Gene	OM3 Core number of assays (34 unique genes)	OM3 Extended number of assays (117 unique genes)
ABL1	14	7	MADH4	-	7
ABL2	-	1	MAP2K4	-	13
ADAMTSL3	-	4	MEN1	-	6
AKT1	1	-	MET	7	5
AKT2	2	-	MLH1	1	-
AKT3	1	-	MLL3	-	5
ALK	-	10	MPL	-	3
AML1/RUNX1	-	8	MSH2	-	2
APC	16	2	MSH6	-	3
AR	-	2	MYC	6	16
ATM	-	3	MYH1	-	3
ATP8B1	-	4	NF1	-	5
AURKA	-	3	NF2	-	10
AURKB	-	1	NOTCH1	-	11
AURKC	-	3	NPM1	-	7
AXL	-	1	NRAS	30	8
BMX	-	1	NTRK1	-	1
BRAF	46	8	NTRK1	-	1
BRCA1	-	3	NTRK2	-	1
BRCA2	-	6	NTRK3	-	6
BUB1	-	2	PAK7	-	1
C14orf155	-	3	PALB2	-	3
CDH1	-	5	PDGFRA	22	15
CDK4	2	1	PDGFRB	-	3
CDKN2A	15	6	PDPK1	-	1
CEBPA	-	18	PDPK1	-	1
CREBBP	-	2	PIK3CA	18	31
CSF1R (FMS)	7	-	PIK3R1	-	13
CTNNB1	40	22	PKHD1	-	5
CUBN	-	3	PTCH	-	6
DBN1	-	2	PTEN	15	13
DDR1	-	2	PTPN11	-	14
DDR2	-	1	RAF1	-	2
EGFR	59	40	RB1	12	2
EPHA1	-	2	RET	16	4
EPHA3	-	18	RET	-	13
EPHA4	-	4	ROBO1	-	2
EPHA5	-	6	ROBO2	-	4
EPHA8	-	1	ROS1	-	4
EPHB1	-	10	SIX4	-	4
EPHB6	-	6	SMAD2	-	3
ERBB2	9	14	SMAD4	-	4
FBXW7	-	8	SMARCB1	-	9
FES	-	4	SMO	-	3
FGFR1	2	-	SPTAN1	-	4
FGFR2	7	9	SRC	1	-
FGFR3	17	11	STK11	12	7
FGFR4	-	3	SUFU	-	3
FLNB	-	5	TBX22	-	3
FLT3	12	14	TCF1	-	3
FLT4	-	1	TEC	-	1
FMS	-	3	TFDP1	-	2
FYN	-	3	TIAM1	-	3
GATA1	-	16	TIF1	-	3
GNAS	-	4	TP53	7	15
GUCY1A2	-	3	TRIM33	-	4
HRAS	19	3	TSC1	-	2
IGF1R	-	5	TSHR	-	5
JAK2	2	3	VHL	7	9
JAK3	3	1	WT1	-	2
KIT	30	17	Total Assays:	352	371
KRAS	48	10			
LRP1B	-	12			
LYN	-	1			

Supplementary Table 3. Primer sequences for the indicated exons of *TP53*, *ERBB2* and *NRAS*

Gene	Exon	Forward Sequence	Reverse Sequence
<i>TP53</i>	2	5'-GGTTGGAAGTGTCTCATGCTGG-3'	5'-CCTGCCCTTCCAATGGATC-3'
<i>TP53</i>	3	5'-ATGGGACTGACTTTCTGCTCTTGTC-3'	5'-CCAGCCCAACCCTTGCCT-3'
<i>TP53</i>	4.1	5'-CCTCTGACTGCTCTTTTCACCCAT-3'	5'-CCGCCGGTGTAGGAGCTG-3'
<i>TP53</i>	4.2	5'-CCAGAATGCCAGAGGCTGCT-3'	5'-GGTAGGTTTTCTGGGAAGGGACA-3'
<i>TP53</i>	4.3	5'-CTGCACCAGCCCCCTCCT-3'	5'-GCCAGGCATTGAAGTCTCATGG-3'
<i>TP53</i>	9	5'-TTCACCTTTATCACCTTTCCTTGCCT-3'	5'-GAAACTTTCCACTTGATAAGAGGTC-3'
<i>TP53</i>	10	5'-TACTTCTCCCCCTCCTCTGTTGC-3'	5'-TGGAATCCTATGGCTTTCCAACC-3'
<i>TP53</i>	11	5'-TCTCACTCATGTGATGTCATCTCTCCT-3'	5'-GTGGGGAACAAGAAGTGGAGAATG-3'
<i>ERBB2</i>	20	5'- CGTACCCTTGTCGCCAGGAAG-3'	5' -GTGGATGTCAGGCAGATGCC-3'
<i>NRAS</i>	2	5'-CACTAGGGTTTTCATTTCCATTG-3'	5'-AATACAGAATATGGGTAAAGATGATCC-3'
<i>NRAS</i>	3	5'-CCCCAGGATTCTTACAGAAAA-3'	5'-TGTAGAGGTTAATATCCGCAAATG-3'

Supplementary Table 4. Clinico-pathologic characteristics of the subset of SBT-EOC used for molecular analysis compared to the entire SBT-EOC cohort

		SBT-EOC	SBT-EOC subset	p –values (SBT-EOC vs SBT-EOC subset)
No. Samples		102	58	
Age	Mean	55	57	NS
	Range	20-78	22-78	
Pre-treatment CA125 (U/ml)	Mean	831	977	NS
Grade	1	33 (32%)	19 (33%)	NS
	2	29 (28%)	15 (26%)	
	3	33 (32%)	21 (36%)	
	unknown	7 (7%)	3 (5%)	
Stage	I	12 (12%)	5 (9%)	NS
	II	8 (8%)	4 (7%)	
	III	77 (75%)	47 (81%)	
	IV	5 (5%)	2 (3%)	
Residual Disease	Nil	39 (38%)	23 (40%)	NS
	≤ 1 cm	27 (26%)	14 (24%)	
	> 1 cm	23 (23%)	15 (26%)	
	unknown	13 (13%)	6 (10%)	
PFS (months)	Median	27.2	20.8	NS
	95% CI	20.6-42.7	15.2-36.6	
OS (months)	Median	79.1	76.2	NS
	95% CI	58.4-123.7	45.8-82.3	

SBT-EOC, serous carcinoma with adjacent borderline regions; EOC, serous carcinoma (with no borderline regions); CI, confidence interval; PFS, progression-free survival; OS, overall survival

Supplementary Table 5A. Somatic mutations found in borderline and invasive ovarian tumors

Case ID	Grade	Tumor type	Gene	Nucleotide ¹	Amino acid ¹	Reference ²
4953	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
1162	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
7315	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
8897	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
9795	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
8632	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	3
2615	L	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
4466	L	SBT	<i>ERBB2</i>	c.2313_2324dup	p.W772_A775dup	1
2989	L	SBT	<i>KRAS</i>	c.35G>A	p.G12D	1
2713	L	SBT	<i>KRAS</i>	c.35G>A	p.G12D	1
893	L	SBT	<i>KRAS</i>	c.35G>A	p.G12D	3
2072	L	SBT	<i>KRAS</i>	c.35G>T	p.G12V	1
1268	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
2006	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
2358	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
2359	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
3964	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
9341	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
9663	H	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
1277	H	SBT	<i>ERBB2</i>	c.2314_2325dup	p.W772_A775dup	1
4808	H	SBT	<i>ERBB2</i>	c.2311_2322dup	p.W772_A775dup	1
1848	H	SBT	<i>ERBB2</i>	c.2311_2322dup	p.W772_A775dup	1
1624	H	SBT	<i>KRAS</i>	c.35G>A	p.G12D	1
2007	NK	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
10115	NK	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	1
6176	NK	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	3
2244	NK	SBT	<i>BRAF</i>	c.1799T>A	p.V600E	3
3905	NK	SBT	<i>KRAS</i>	c.35G>A	p.G12D	1
4452	NK	SBT	<i>KRAS</i>	c.35G>A	p.G12D	1
8430	NK	SBT	<i>KRAS</i>	c.35G>A	p.G12D	3
1842	NK	SBT	<i>KRAS</i>	c.35G>A	p.G12D	1
8591	NK	SBT	<i>KRAS</i>	c.35G>T	p.G12V	1
1832	NK	SBT	<i>KRAS</i>	c.36_37delinsAC	p.G13R	3
2469	NK	SBT	<i>KRAS</i>	c.35G>A	p.G12D	3
7198	NK	SBT	<i>KRAS</i>	c.35G>T	p.G12V	1
10744	NK	SBT	<i>KRAS</i>	c.35G>C	p.G12A	3
11368	1	SBT-EOC	<i>BRAF</i>	c.1799T>A	p.V600E	
5711	1	SBT-EOC	<i>BRAF</i>	c.1799T>A	p.V600E	
15043	1	SBT-EOC	<i>KRAS</i>	c.35G>A	p.G12D	
65662	1	SBT-EOC	<i>KRAS</i>	c.35G>T	p.G12V	
65673	1	SBT-EOC	<i>KRAS</i>	c.35G>T	p.G12V	
65663	1	SBT-EOC	<i>KRAS</i> ³	c.35G>A	p.G12D	
8395	1	SBT-EOC	<i>KRAS</i>	c181C>A	p.Q61K	
6251	1	SBT-EOC	<i>KRAS</i>	c.35G>T	p.G12V	
9128	1	SBT-EOC	<i>NRAS</i>	c.182A>G	p.Q61R	
6582	1	SBT-EOC	<i>NRAS</i>	c.182A>G	p.Q61R	
7200	1	SBT-EOC	<i>NRAS</i>	c.182A>G	p.Q61R	
9125	2	SBT-EOC	<i>BRAF</i>	c.1799T>A	p.V600E	

Case ID	Grade	Tumor type	Gene	Nucleotide ¹	Amino acid ¹	Reference ²
2044	2	SBT-EOC	NRAS	c.181C>A	p.Q61K	
5899	2	SBT-EOC	NRAS	c.182A>G	p.Q61R	
15018	2	SBT-EOC	TP53	c.473_478dup	p.A159_M160insSA	
15046	2	SBT-EOC	TP53	c.487T>G	p.Y163D	
15071	2	SBT-EOC	TP53	c.272G>A	p.Wp91*	
5349	2	SBT-EOC	TP53	c.919+1G>C	No protein change but disrupts splicing	
8390	2	SBT-EOC	TP53	c.818G>A	p.R273H	
3960	2	SBT-EOC	TP53	c.715_721del	p.N239Pfs*6	
8633	2	SBT-EOC	TP53	c.524G>A	p.R175H	
12237	2	SBT-EOC	TP53 (unclassified variant)	c.375+5G>T	No protein change but disrupts splicing	
6328	3	SBT-EOC	KRAS	c.35G>T	p.G12V	
65664	3	SBT-EOC	TP53	c.976G>T	p.E326*	
15060	3	SBT-EOC	TP53	c.716A>C	p.N239T	
65665	3	SBT-EOC	TP53	c.709A>G	p.M237V	
65666	3	SBT-EOC	TP53	c.569del	p.P190Lfs*57	
65667	3	SBT-EOC	TP53	c.428T>G	p.V143G	
65675	3	SBT-EOC	TP53	c.743G>A	p.R248Q	
65677	3	SBT-EOC	TP53	POLY- c.639A>G	p.R213R	
65679	3	SBT-EOC	TP53	c.742C>T	p.R248W	
65680	3	SBT-EOC	TP53	c.818G>A	p.R273H	
2110	3	SBT-EOC	TP53	c.742C>T	p.R248W	
9221	3	SBT-EOC	TP53	c.524G>A	p.R175H	
11266	3	SBT-EOC	TP53	c.581T>G	p.L194R	
9579	3	SBT-EOC	TP53	c.917_918dup	p.A307Efx*39	
11766	3	SBT-EOC	TP53	c.523C>G	p.R175G	
3958	3	SBT-EOC	TP53	c.395del	p.K132Rfs*38	
4723	3	SBT-EOC	TP53	c.536A>G	p.H179R	
7716	3	SBT-EOC	TP53	c.578A>C	p.H193P	
65668	3	SBT-EOC	TP53	c.524G>A	p.R175H	
3539	3	SBT-EOC	TP53 (synonymous variant)	c.297C>A	p.S99S	
4956	3	SBT-EOC	TP53	c.856G>A	p.E286K	2
15079	NK	SBT-EOC	KRAS	c.35G>T	p.G12V	1
1072	NK	SBT-EOC	KRAS	c.35G>A	p.G12D	
65672	NK	SBT-EOC	BRAF	c.1799T>A	p.V600E	
4489	1	EOC	KRAS	c.35G>T	p.G12V	1
7688	2	EOC	KRAS	c.35G>T	p.G12V	1
2476	2	EOC	TP53	c.493C>T	p.Q165*	2
4557	2	EOC	TP53	c.731_738del8	p.G244Efs*17	2
1203	2	EOC	TP53	c.746G>T	p.R249M	2
435	2	EOC	TP53	c.258_270del	p.P87Gfs*32	2
1033	2	EOC	TP53	c.590del	p.V197Gfs*50	2
1251	2	EOC	TP53	c.733G>A	p.G245S	2
1819	3	EOC	TP53	c.916C>T	p.R306*	2
2039	3	EOC	TP53	c.377A>G	p.Y126C	2
5120	3	EOC	TP53	c.887_888delinsT	p.H296Lfs*49	2
3142	3	EOC	TP53	c.659A>G	p.Y220C	2

Case ID	Grade	Tumor type	Gene	Nucleotide ¹	Amino acid ¹	Reference ²
4396	3	EOC	<i>TP53</i>	c.722C>A	p.5241Y	2
7486	3	EOC	<i>TP53</i>	c.993+1G>T	No protein change but disrupts splicing	2
3333	3	EOC	<i>TP53</i>	c.376-1G>T	splice site mutation-probable truncation	2
3334	3	EOC	<i>TP53</i>	c.584T>C	mutation	2
7514	3	EOC	<i>TP53</i>	c.742C>G	p.I195T	2
2738	3	EOC	<i>TP53</i>	c.584T>C	p.R248G	2
4065	3	EOC	<i>TP53</i>	c.97-2A>G	p.I195T	2
4675	3	EOC	<i>TP53</i>	c.469G>T	No protein change but disrupts splicing	2
5309	3	EOC	<i>TP53</i>	c.286del	p.V157F	2
7936	3	EOC	<i>TP53</i>	c.820G>T	p.S96Lfs*27	2
10516	3	EOC	<i>TP53</i>	c.817C>T	p.V274F	2
1946	3	EOC	<i>TP53</i>	c.389T>A	p.R273C	2
3843	3	EOC	<i>TP53</i>	c.294_297del	p.L130H	2
4799	3	EOC	<i>TP53</i>	c.832C>T	p.S99Rfs*23	2
386	3	EOC	<i>TP53</i>	c.701A>G	p.P278S	2
1096	3	EOC	<i>TP53</i>	c.772G>A	p.Y234C	2
6897	3	EOC	<i>TP53</i>	c.713G>A	p.E258K	2
4985	3	EOC	<i>TP53</i>	c.658T>C	p.C238Y	2
5504	3	EOC	<i>TP53</i>	c.542_559+6del	p.Y220H	2
1456	3	EOC	<i>TP53</i>	c.920-1G>A	p.C182G187del	2
					No protein change but disrupts splicing	2

¹ The mutations in the nucleotide sequence have been experimentally determined by Sanger sequencing. All identified mutations were reported according to HGVS (Human Genome Variation Society) recommendations (www.HGVS.org) and were determined using the Alumut program (Interactive Biosoftware). *Mutations are given based on National Center for Biotechnology Information Reference Sequence Accession numbers: NM_033360.2 (KRAS), NM_004333.4. (BRAF), NM_002524.4 (NRAS), NM_004448.2, (ERBB2) and NM_000546.4 (TP53).

² The reference is indicated where data was obtained from previously published work

1. Anglesio *et al.* Mutation of ERBB2 provides a novel alternative mechanism for the ubiquitous activation of RAS-MAPK in ovarian serous low malignant potential tumors. *Mol Cancer Res* 2008; **6**: 1678-1690.
2. Ahmed *et al.* Driver mutations in TP53 are ubiquitous in high grade serous carcinoma of the ovary. *J Pathol* 2010; **221**: 49-56.
3. Hunter *et al.* Copy number aberrations in benign serous ovarian tumors: a case for reclassification? *Clin Cancer Res* 2011; **17**: 7273

³ KRAS in LMP only, Inv was negative

SBT, serous borderline tumor; SBT-EOC, serous carcinoma with adjacent borderline regions; EOC, serous carcinoma (with no borderline regions); L, low grade SBT; H, high grade SBT; NK, Not Known

Supplementary Table 5B. Genes in which somatic mutations were found according to grade and co-existing serous borderline regions

	Grade 1 ²		Grade 2		Grade 3	
	SBT-EOC	EOC	SBT-EOC	EOC	SBT-EOC	EOC
n	19	1	15	7	21	26
<i>BRAF</i>	2 (11%)		1 (7%)			
<i>KRAS</i>	6 (32%)	1 (100%)		1 (14%)	1 (5%)	
<i>NRAS</i>	3 (16%)		2 (13%)			
<i>TP53</i>			7 (47%)	6 (86%)	18 (86%)	24 (92%)
<i>TP53 variant</i> ¹			1 (7%)		1 (5%)	
WT	8 (42%)		4 (27%)		1 (5%)	2 (8%)

¹One synonymous and one putative splice variant

²Cases where grade was not known are not included.

Supplementary Table 6. Genes differentially expressed between paired borderline and invasive regions of SBT-EOC (p<0.01, not corrected for multiple comparison).

Gene	Average fold Change (borderline to invasive)	p	Gene	Average fold Change (borderline to invasive)	p
PGR	2.118	0.009	CAMLG	1.249	0.006
SLC7A2	1.949	0.007	SLC30A5	1.246	0.009
LPAR3	1.844	0.009	ZNF781	1.238	0.005
KIAA1324	1.794	0.008	BRP44L	1.237	0.006
PITPNC1	1.564	0.002	OR2M7	1.236	0.007
TYW3	1.507	0.005	ZNF90	1.236	0.006
KLHL13	1.489	0.009	MRPL37	1.235	0.008
PLAC8	1.484	0.002	DFFA	1.235	0.005
KLHL23	1.463	0.004	HLA-L	1.232	0.005
ITGB3BP	1.438	0.006	LGALS1	1.232	0.010
KBTBD12	1.429	0.001	LINC00339	1.227	0.008
PIGK	1.420	0.002	TRIM61	1.220	0.009
ME1	1.414	0.008	HAT1	1.214	0.009
SLC4A4	1.402	0.007	CMTM4	1.212	0.008
TPRKB	1.402	0.001	F8	1.209	0.009
CTPS	1.397	0.007	SLC9A6	1.205	0.005
ABCC9	1.394	0.007	ZFP106	1.205	0.009
SRD5A2	1.389	0.008	CCDC141	1.201	0.007
ICA1	1.389	0.009	POLR3H	1.200	0.009
ANKRD45	1.387	0.001	ZNF189	1.199	0.005
EIF3M	1.377	0.008	ZDBF2	1.198	0.008
GPR63	1.370	0.005	UBE2J1	1.188	0.009
PRKACB	1.364	0.008	PLXNA3	0.852	0.009
CCNG1	1.362	0.009	GRM6	0.834	0.010
POGLUT1	1.351	0.003	ZNF847P	0.828	0.006
ERAP1	1.349	0.003	GSN	0.817	0.007
CCNL2	1.346	0.007	NCCRP1	0.813	0.003
CCBE1	1.346	0.009	PRKCDBP	0.811	0.005
TMEM50A	1.341	0.006	CDC20	0.804	0.007
ANK2	1.338	0.004	LOC100506422	0.804	0.004
POTEG	1.335	0.006	EPPK1	0.798	0.004
SNORD114-6	1.322	0.008	HIST1H2BF	0.785	0.002
RNFT1	1.321	0.002	RASGRP3	0.774	0.010
ODC1	1.320	0.005	IFITM10	0.773	0.003
IMPDH2	1.317	0.009	SLC1A3	0.766	0.006
SNORD30	1.316	0.004	KIF5C	0.762	0.006
SACS	1.313	0.007	MEOX1	0.762	0.008
ZNF584	1.311	0.002	MXD1	0.757	0.005
GCA	1.311	0.008	JUB	0.756	0.008
NDUFAF4	1.311	0.005	C11orf80	0.754	0.002
BAG2	1.309	0.009	KCNT2	0.742	0.008
COX18	1.306	0.008	PSTPIP2	0.741	0.007
SLC9B2	1.305	0.003	EMP2	0.736	0.002
HPRT1	1.305	0.004	ESM1	0.707	0.001
C9orf21	1.304	0.007	ST6GALNAC2	0.703	0.008
CTH	1.304	0.001	TGM1	0.689	0.007
ASB13	1.291	0.001	TMEM130	0.686	0.002
MSMO1	1.290	0.004	LGR6	0.678	0.002
PRDM9	1.289	0.004	LMO7	0.677	0.001
AMN1	1.284	0.004	OR5P2	0.672	0.006
ZNF684	1.283	0.001	KRT17	0.670	0.004
IDH3A	1.282	0.009	OR2J3	0.669	0.003
ISOC1	1.275	0.007	KIR3DL1	0.654	0.001
KTI12	1.273	0.003	INF2	0.640	0.002
PIGV	1.272	0.001	KRT7	0.634	0.000
CLNS1A	1.272	0.009	PCDHB8	0.618	0.002
ECH1	1.270	0.003	ALS2CL	0.584	0.002
AMD1	1.268	0.009	IL1RN	0.584	0.006
SLC25A20	1.265	0.003	KLK6	0.579	0.007
FSIP1	1.264	0.008	SPTSSB	0.552	0.009
PPM1H	1.259	0.004	DDIT4	0.542	0.002
CXorf41	1.256	0.008	COL12A1	0.532	0.010
LOC100288884	1.255	0.009	FAM153C	0.438	0.004
CYP51A1	1.253	0.008			

SBT-EOC, serous carcinoma with adjacent borderline regions;

Supplementary Table 7. Clinico-pathological characteristics of SBT-EOC cases used for progesterone receptor (PGR) immunostaining

		Cases stained for PGR expression
No. Samples		10
Age	Mean	59
	Range	38-78
Pre-treatment CA125 (U/ml)	Mean	1445.4
Grade	1	3 (30%)
	2	3 (30%)
	3	4 (40%)
Stage	I	0%
	II	1 (10%)
	III	9 (90%)
Residual Disease	Nil	5 (50%)
	≤ 1 cm	2 (20%)
	> 1 cm	3 (30%)
PFS (months)	Median	28.6
	95% CI	5.8 - 51.4
OS (months)	Median	72.5
	95% CI	56.4 - 88.6

SBT-EOC, serous carcinoma with adjacent borderline regions; PFS, progression-free survival; OS, overall survival; CI, confidence interval