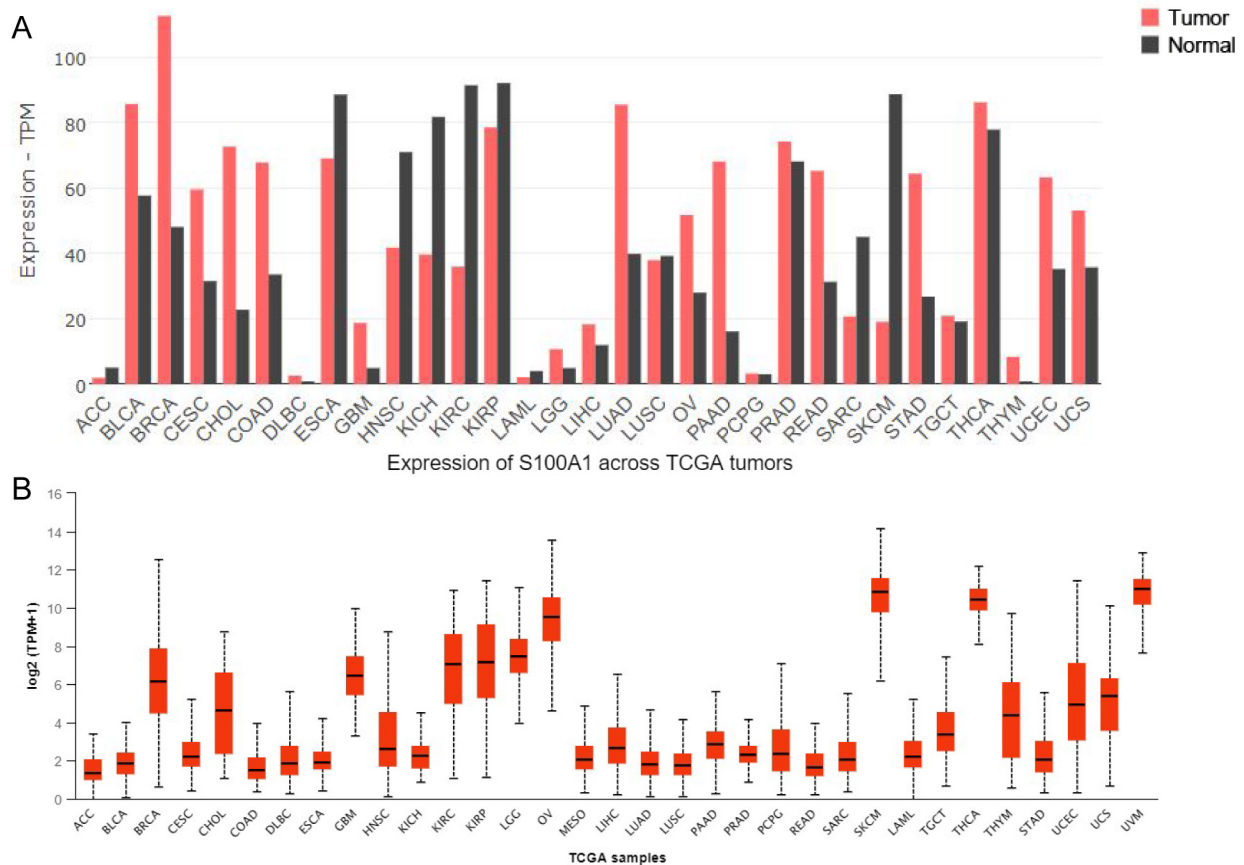


**Table S1** Antibody and dilution

Antibody	Biological source	Cat.	Dilution for Western blot	Company
S100A1	Rabbit	#5066	1:1,000	Cell Signaling Technology, MA
PCNA	Rabbit	#13110	1:1,000	Cell Signaling Technology, MA
Survivin	Rabbit	#2808	1:1,000	Cell Signaling Technology, MA
GPX4	Rabbit	ab125066	1:1,000	Abcam, Cambridge, MA
GAPDH	Mouse	ab8245	1:1,000	Abcam, Cambridge, MA



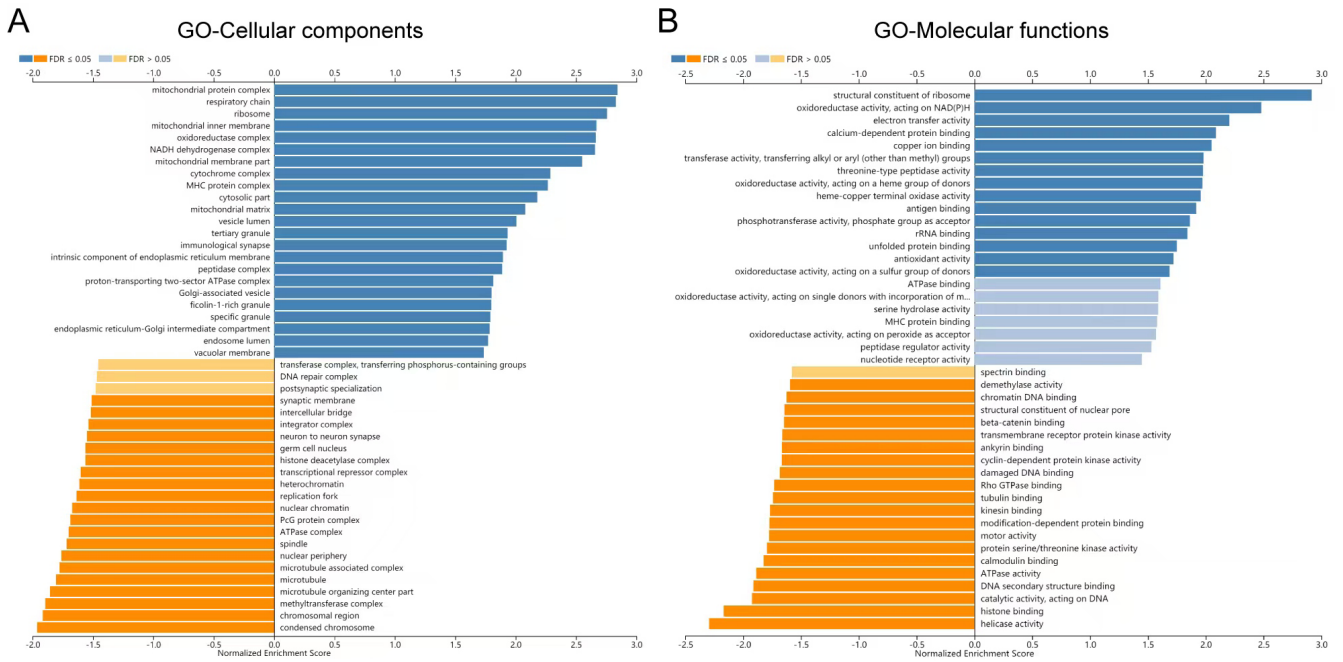
**Figure S1** S100A1 levels in different cancers. (A) GEPIA analysis. Bar heights indicate median expression levels. (B) UALCAN analysis. GEPIA, Gene Expression Profiling Interactive Analysis; UALCAN, University of Alberta-Lung Cancer Analysis.

**Table S2** LinkedOmics was used to explore genes positively correlated with S100A1 in OC. The top 50 genes that were significantly positively correlated with S100A1 were performed

Query	Statistic	P value	FDR (BH)	Event_SD	Event_TD
S100A13	0.776504	2.49E-62	2.49E-58	303	303
SLPI	0.525189	7E-23	4.67E-19	303	303
S100A5	0.511494	1.33E-21	5.41E-18	303	302
S100A6	0.511435	1.35E-21	5.41E-18	303	303
RAB13	0.494298	4.5E-20	1.5E-16	303	303
CLU	0.470008	4.67E-18	1.34E-14	303	303
KLK6	0.435105	1.99E-15	2.85E-12	303	303
POLD4	0.433083	2.77E-15	3.47E-12	303	303
KRTCAP2	0.431999	3.31E-15	3.9E-12	303	303
CLTB	0.427613	6.7E-15	6.39E-12	303	303
S100A16	0.425865	8.85E-15	8.06E-12	303	303
LOC121838	0.422823	1.43E-14	1.12E-11	303	303
SLC48A1	0.419544	2.39E-14	1.77E-11	303	303
PMVK	0.417314	3.38E-14	2.26E-11	303	303
S100A14	0.416201	4.01E-14	2.59E-11	303	303
CP	0.415905	4.2E-14	2.63E-11	303	303
VAMP8	0.406553	1.73E-13	9.3E-11	303	303
S100A4	0.406409	1.77E-13	9.3E-11	303	303
GSTK1	0.405967	1.89E-13	9.45E-11	303	303
WBSCR26	0.403478	2.73E-13	1.33E-10	303	294
CYBA	0.398325	5.79E-13	2.56E-10	303	303
PHLDA3	0.398226	5.88E-13	2.56E-10	303	303
C6orf1	0.396845	7.17E-13	2.87E-10	303	303
RAG1AP1	0.396707	7.32E-13	2.87E-10	303	303
DUSP23	0.396583	7.45E-13	2.87E-10	303	303
C10orf11	0.395998	8.1E-13	2.98E-10	303	303
GPX3	0.395189	9.1E-13	3.22E-10	303	303
REEP5	0.395117	9.2E-13	3.22E-10	303	303
HAX1	0.39488	9.51E-13	3.22E-10	303	303
IFITM3	0.394499	1E-12	3.22E-10	303	303
UQCRB	0.392752	1.29E-12	3.85E-10	303	303
ROBLD3	0.391597	1.52E-12	4.41E-10	303	303
PLCD3	0.391217	1.6E-12	4.58E-10	303	303
PCBD1	0.391127	1.62E-12	4.58E-10	303	303
MRPL24	0.39017	1.86E-12	4.99E-10	303	303
RRAS	0.389961	1.91E-12	5.04E-10	303	303
KCNK15	0.387536	2.69E-12	6.91E-10	303	303
ZNF524	0.386786	2.99E-12	7.38E-10	303	303
S100A11	0.386523	3.1E-12	7.5E-10	303	303
TMEM61	0.386418	3.14E-12	7.5E-10	303	303
EFNA1	0.386259	3.21E-12	7.57E-10	303	303
TMEM219	0.385971	3.34E-12	7.7E-10	303	303
CYB5R1	0.385193	3.73E-12	8.39E-10	303	303
NDUFC1	0.384606	4.04E-12	9E-10	303	303
NMNAT2	0.381912	5.86E-12	1.23E-09	303	303
LEMD1	0.381508	6.19E-12	1.29E-09	303	303
SLC34A2	0.381156	6.5E-12	1.34E-09	303	303
RAPGEF3	0.380903	6.72E-12	1.36E-09	303	303
C19orf33	0.380634	6.98E-12	1.38E-09	303	303
ABHD11	0.380573	7.03E-12	1.38E-09	303	303

**Table S3** LinkedOmics was used to explore genes negatively correlated with S100A1 in OC. The top 50 genes that were significantly negatively correlated with S100A1 were performed

Query	Statistic	P value	FDR (BH)	Event_SD	Event_TD
TIMELESS	-0.45119	1.33E-16	3.34E-13	303	303
MURC	-0.44827	2.20E-16	4.90E-13	303	303
KIF7	-0.44223	6.13E-16	1.23E-12	303	303
GCN1L1	-0.43766	1.31E-15	2.38E-12	303	303
OTUD3	-0.4371	1.44E-15	2.40E-12	303	303
MCART6	-0.43573	1.80E-15	2.78E-12	303	303
SFRS13B	-0.4345	2.20E-15	2.94E-12	303	303
MSH6	-0.43072	4.07E-15	4.31E-12	303	303
FANCC	-0.4307	4.08E-15	4.31E-12	303	303
POLE	-0.43022	4.41E-15	4.42E-12	303	303
NINL	-0.42486	1.04E-14	9.05E-12	303	303
KLHL23	-0.42399	1.19E-14	9.94E-12	303	303
RAPGEF4	-0.42274	1.45E-14	1.12E-11	303	303
ZCCHC18	-0.41853	2.80E-14	2.00E-11	303	301
PHC1	-0.41799	3.04E-14	2.10E-11	303	303
EFS	-0.41521	4.67E-14	2.84E-11	303	303
SMO	-0.41399	5.63E-14	3.32E-11	303	303
MSI1	-0.41096	8.93E-14	5.11E-11	303	303
WHSC1	-0.40935	1.14E-13	6.33E-11	303	303
KDM2B	-0.40624	1.81E-13	9.30E-11	303	303
CDK5R1	-0.39981	4.67E-13	2.23E-10	303	303
DNMT3A	-0.39918	5.11E-13	2.38E-10	303	303
PAQR9	-0.39875	5.44E-13	2.48E-10	303	109
KIF18B	-0.39788	6.18E-13	2.63E-10	303	303
TET3	-0.39689	7.13E-13	2.87E-10	303	303
SNRNP200	-0.39682	7.20E-13	2.87E-10	303	303
PLCG1	-0.39619	7.88E-13	2.98E-10	303	303
ITPRIPL1	-0.39594	8.18E-13	2.98E-10	303	303
PLEKHG2	-0.39502	9.33E-13	3.22E-10	303	303
DENND2A	-0.39478	9.66E-13	3.22E-10	303	303
XKR5	-0.39461	9.89E-13	3.22E-10	303	303
MCAM	-0.39444	1.01E-12	3.22E-10	303	303
GFRA3	-0.39402	1.08E-12	3.37E-10	303	302
TMEM194A	-0.39371	1.12E-12	3.46E-10	303	303
HNF1A	-0.39319	1.21E-12	3.67E-10	303	303
NCAPD2	-0.39209	1.42E-12	4.17E-10	303	303
RHOBTB1	-0.391	1.65E-12	4.59E-10	303	303
MYO1B	-0.39092	1.67E-12	4.59E-10	303	303
CBX2	-0.39014	1.87E-12	4.99E-10	303	303
KIAA1549	-0.38789	2.56E-12	6.65E-10	303	303
DPF1	-0.38716	2.83E-12	7.19E-10	303	302
ZNF445	-0.387	2.90E-12	7.26E-10	303	303
PLAGL1	-0.38643	3.14E-12	7.50E-10	303	303
BRIP1	-0.38597	3.34E-12	7.70E-10	303	303
CDC25A	-0.38535	3.65E-12	8.30E-10	303	303
TRO	-0.38389	4.46E-12	9.82E-10	303	303
GPR98	-0.38303	5.02E-12	1.09E-09	303	298
TCEAL5	-0.38268	5.27E-12	1.13E-09	303	285
DPY19L2	-0.38204	5.76E-12	1.23E-09	303	303
TMEFF1	-0.38101	6.63E-12	1.36E-09	303	303



**Figure S2** GO annotations of genes co-expressed with S100A1 in OC, analyzed by GSEA. (A) Cellular components and (B) molecular functions. The Leading Edge Num and the FDR are shown in the blue and orange columns, respectively. GO, Gene Ontology; OC, ovarian cancer; GSEA, Gene Set Enrichment Analysis; FDR, false discovery rate.

