Reduced expression of SOX7 in ovarian cancer: a novel tumor suppressor through the Wnt/β-catenin signaling pathway

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Outline

- 1. Background
- 2. Research Goal
- 3. Data
- 4. Discussion

Conclusion,

Acknowledgements



Estimated New Cases

	All Sites	805,500	100%
	Ovary	22,240	3%
7	Pancreas	22,480	3%
1	Kidney & renal pelvis	24,720	3%
	Melanoma of the skin	31,630	4%
	Non-Hodgkin lymphoma	32,140	4%
	Thyroid	45,310	6%
	Uterine corpus	49,560	6%
	Colorectum	69,140	9%
	Lung & bronchus	110,110	14%
	Breast	232,340	29%



Estimated Deaths

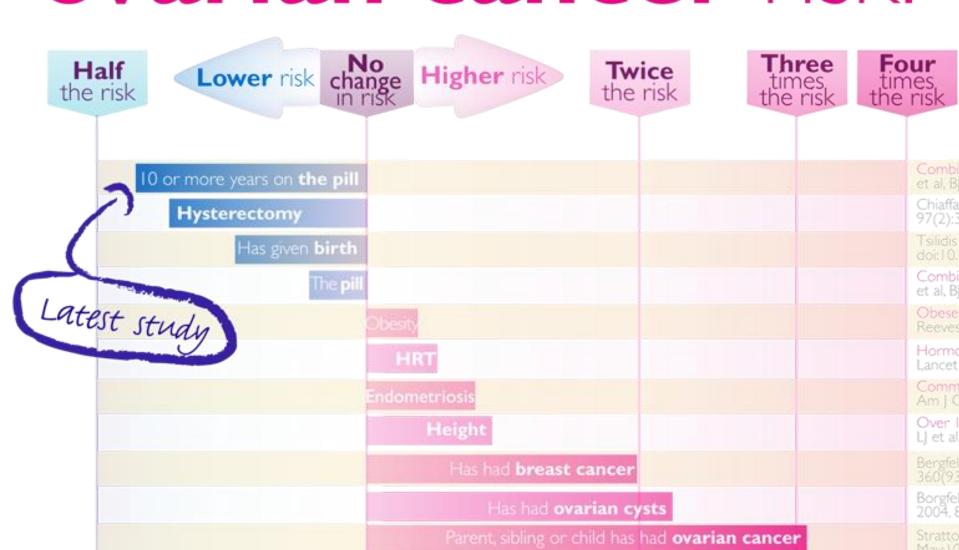
emales	3		
	Lung & bronchus	72,220	26%
	Breast	39,620	14%
	Colorectum	24,530	9%
	Pancreas	18,980	7%
	Ovary	14,030	5%
	Leukemia	10,060	4%
	Non-Hodgkin lymphoma	8,430	3%
1	Uterine corpus	8,190	3%
	Liver & intrahepatic bile duct	6,780	2%
	Brain & other nervous system	6,150	2%
	All Sites	273,430	100%

Late diagnosis results in poor survival

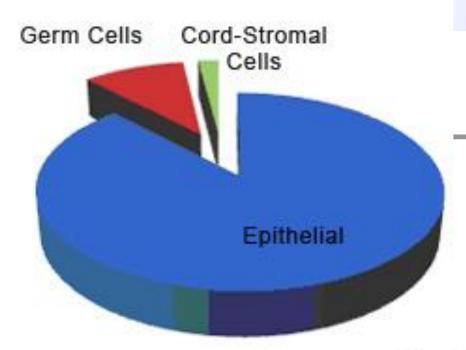
If diagnosed at the localised stage, the 5-year survival rate is 93%. However, only about 15% of all cases are diagnosed at this stage.

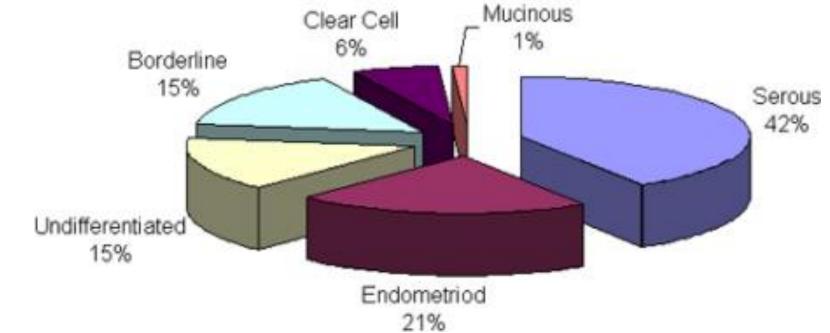


What affects ovarian cancer risk?

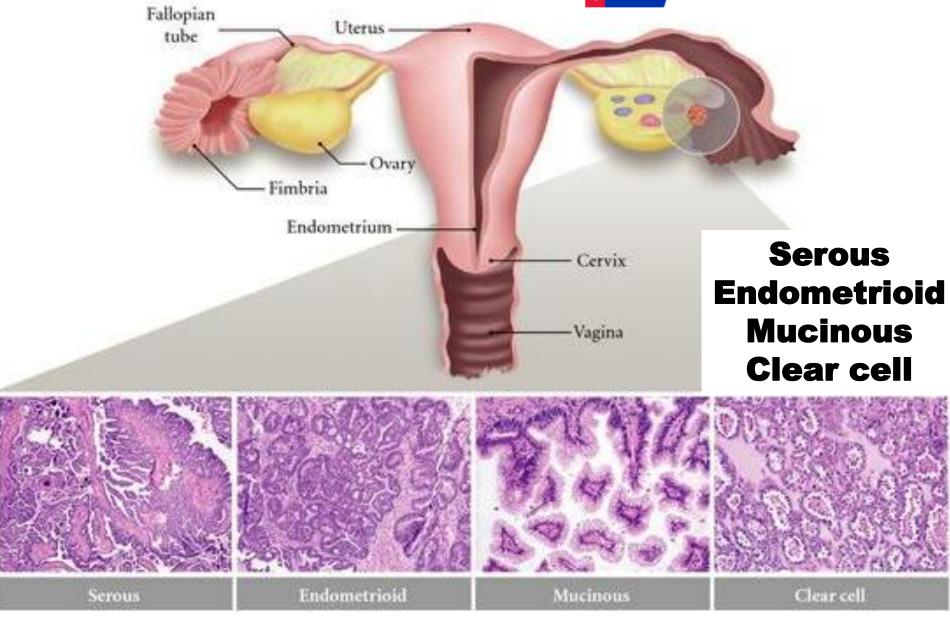










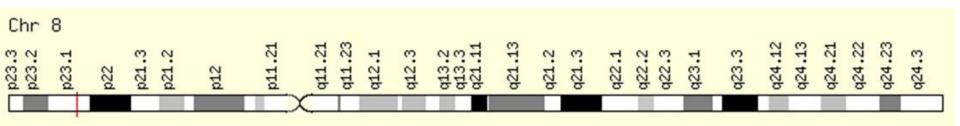




SOX7

SRY (sex determining region Y)-boxes

- SOX7, a member of subfamily SOX F along with SOX17 and SOX18, has been identified as a developmental regulator in hematopoiesis and cardiogenesis.
- Genomic location for SOX7 gene: 8p23.1

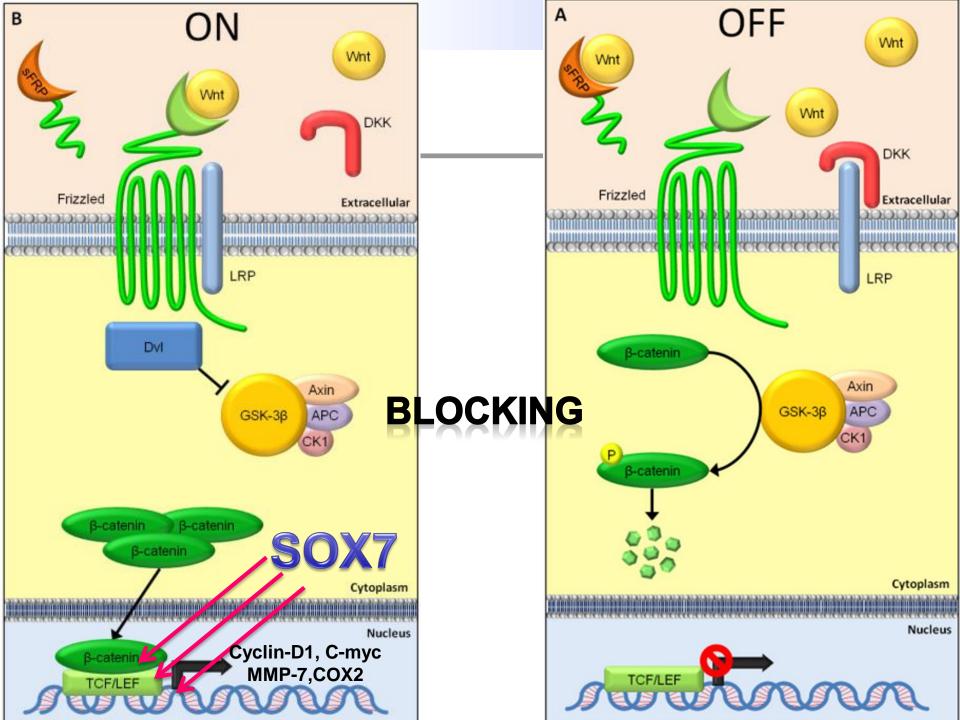




Wnt/β-catenin signal pathway

 It is reported that SOX7 can directly bind βcatenin and negatively regulate its activity.

 As SOX7 negatively regulates the Wnt/βcatenin signaling pathway by impeding the transcriptional machinery of βcatenin/TCF/LEF-1.



SOX7

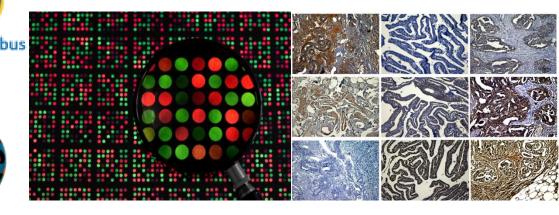
 SOX7 is frequently down-regulated in many human cancers, such as prostate, colon, lung and breast cancer, and its reduced expression often correlates with poor prognoses.



Research Goal

 We investigated the contributions and molecular mechanisms of SOX7 in ovarian cancer.







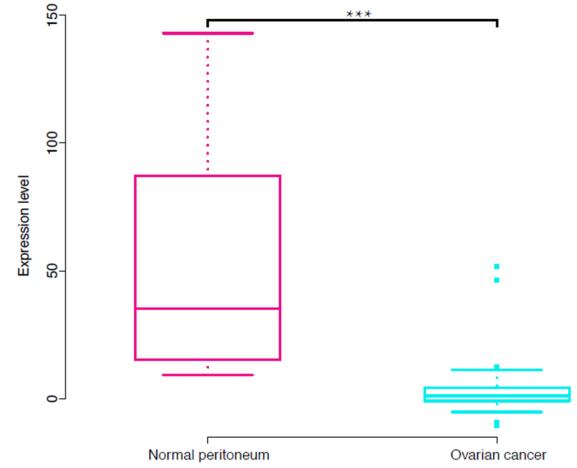
Materials & Methods

- Chemicals and antibodies
- Datasets and preprocessing
- Functional enrichment analysis
- Clinical specimens
- Immunohistochemistry
- Standard for evaluation
- Statistical analysis

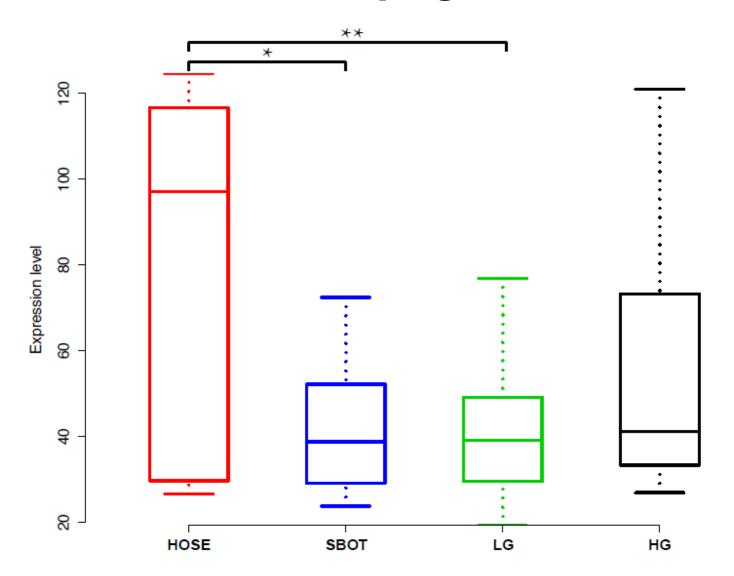


Results

Expression levels of SOX7 in ovarian cancer and normal tissues.



Correlation of reduced SOX7 expression with tumor progression





Correlation of reduced SOX7 expression with tumor progression

HOSE: Human ovarian surface epithelia

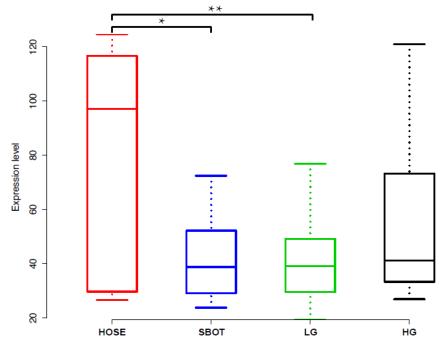
SBOT: Serous borderline ovarian tumors

LG: Low-grade serous ovarian carcinomas

HG: High-grade serous ovarian carcinomas

Malignant: LG>SBOT>HG>HOSE

SOX7: HOSE>HG>SBOT>LG





SOX7 as a negative regulator in Wnt/β-catenin pathway in ovarian cancer

To investigate the mechanism by which SOX7 is involved in the oncogenesis and progression of ovarian cancers,

We analyzed genes that were co-expressed with SOX7 and short-listed 7933 genes by Pearson correlation (FDR < 0.01) in GSE27651 (Additional file 1).

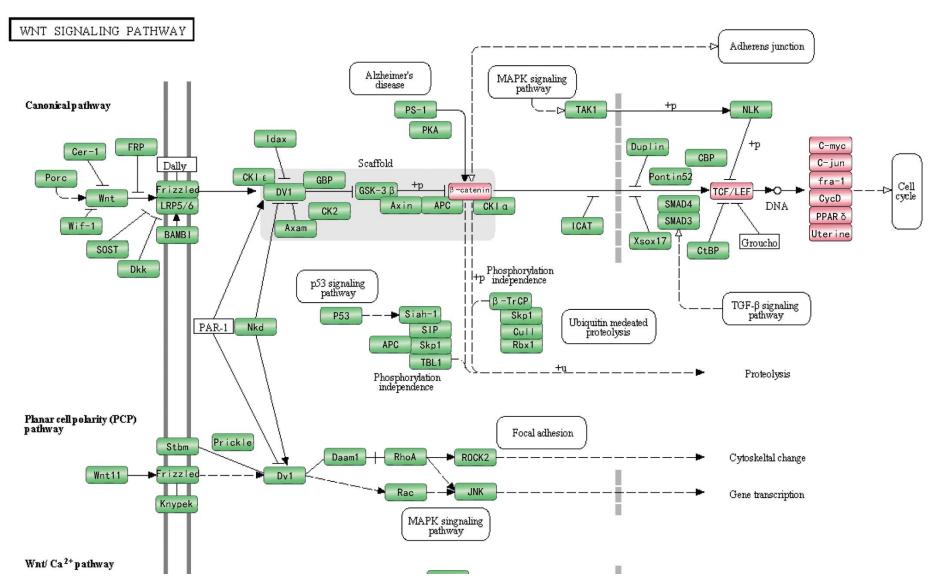
Short-listed 7933 genes were co-expressed with SOX7 by Pearson correlation (FDR < 0.01) in GSE27651

Number	Gene	EntrezGene	Fdr	Correlation Coefficient
1	NAT2	10	0.000513216	0.521953398
2	AAMP	14	0.002578854	-0.463809284
3	AANAT	15	4.50E-07	0.687615139
4	ABCA2	20	0.00033142	0.535889973
5	ABCB7	22	0.000125177	-0.56417787
6	ABCF1	23	4.98E-08	0.72395679
7	A TO CT A A	0.4	E /ED 07	0.692662042

 Using DAVID with a 5% FDR control, we found that the 7933 genes were significantly overrepresented in eleven GO-biological processes involved mainly in transcription activities (Table 1)

Table 1 Biological processes enriched with genes dysregulated to a larger extent in ovarian cancer

Accession	Term	P-Values	FDR
GO:0006414	translational elongation	4.692062542984977E-29	9.047961108371685E-26
GO:0006412	translation	2.04912911734554E-22	3.951447873919316E-19
GO:0006396	RNA processing	2.7244884076177707E-10	5.253780188674284E-7
GO:0022613	ribonucleoprotein complex biogenesis	1.3552603187281535E-9	2.6134227004703803E-6
GO:0016071	mRNA metabolic process	3.895055800131527E-8	7.51104669238778E-5
GO:0006397	mRNA processing	5.7556740309817435E-8	1.1098975527534805E-4
GO:0000375	RNA splicing, via transesterification reactions	3.5239047199996375E-7	6.795316527141715E-4
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	3.5239047199996375E-7	6.795316527141715E-4
GO:0000398	nuclear mRNA splicing, via spliceosome	3.5239047199996375E-7	6.795316527141715E-4
GO:0042254	ribosome biogenesis	5.134416394199803E-7	9.900929787476365E-4
GO:0008380	RNA splicing	1.103477760861063E-6	0.0021278751



We chose thirteen genes from KEGG that were annotated in the Wnt/β-catenin pathway as downstream or pivotal hub genes (Figure 3)



The Pearson correlation coefficients of expression levels between the 13 genes and SOX7

Table 2 The Pearson correlation coefficients between the expression levels of 13 genes and SOX7

Gene name	r	p
CCN-D1	-0.2753514639	0.0555052128
CCND2	-0.2083737906	0.1507783665
CCND3*	-0.3789749206	0.0072460704
CTNNB1	-0.2298744109	0.1120735508
JUN*	-0.328410818	0.0212317742
MMP7	-0.1436013727	0.3249317121
MYC*	-0.3794897149	0.0071609446
PPARD(NR1C2)	0.0113166546	0.9384851238
TCF7*	-0.4721329855	0.0006148219
TCF7L2*	-0.5079689459	0.00019461
FOSL1	0.1976706188	0.1733712192
LEF1*	-0.4230961749	0.0024547299
TCF7L1	0.014360968	0.9219826098

11/13 genes Negative

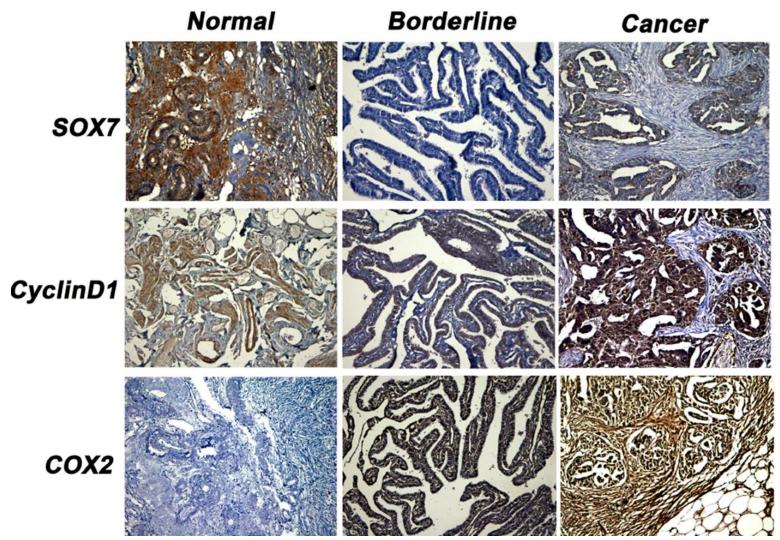
SOX7
Negative regulator

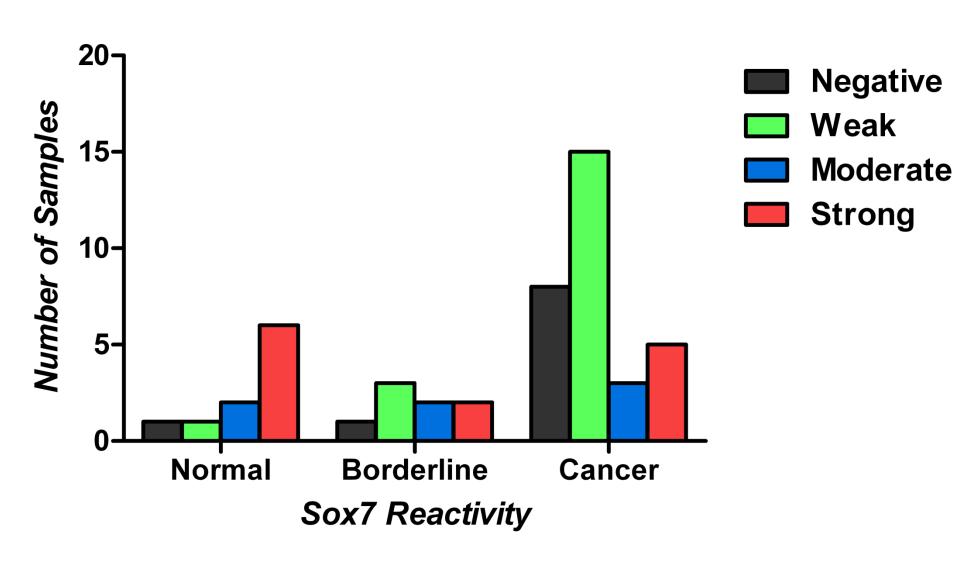
Bold front denotes downstream genes in wnt signal pathway list in KEGG.

^{*}Presents significant correlation.



• Expression of SOX7, cyclin-D1 and COX2 proteins in normal ovarian tissues, borderline ovarian tumors and ovarian cancer.





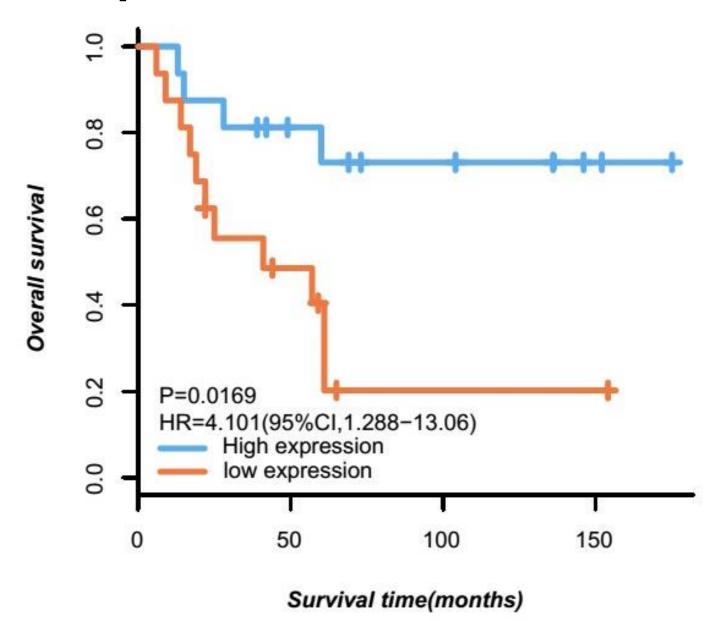


Relations between SOX7 and clinical or pathological characteristics in patients with epithelial ovarian carcinoma

- The down-regulation of SOX7 was significantly associated with the advanced stages (III-IV; 14/31, p = 0.037).
- The negative correlation of SOX7 with COX2 and cyclinD1 indicates a trend of inverse expression pattern of SOX7 to COX2 and cyclin D1.

Characteristic	Total	SOX7 expression		P
Characteristic	Iotai	Over-expression	Low-exeression	r
All cases	31			
Pathology type				NS
Serous	26	7	19	
Mucinous	2	0	2	
Endometrioid	3	1	2	
FIGO stage				0.037
Early(I-II)	16	7	9	
Advance(III-IV)	15	1	14	
Pathology grade				NS
Low(1)	4	1	3	
High(2+3)	27	7	20	
Age (years)				NS
≦ 60	21	5	16	
≧60	10	3	7	
COX2				r _s =-0.618,p<0.001
Over-expression	27	5	22	
Low-exeression	4	3	1	
CyclinD1				r _s =-0.583,p<0.001
Over-expression	26	8	18	
Low-exeression	5	0	5	

Expression of SOX7 v.s. Overall survival





Discussion

 In this study, we chose ovarian cancer to work on due to that relatively little has been done on SOX7 in ovarian cancer.

 Our results obtained from different platforms indicate that the expression levels of SOX7 were significantly reduced in all types of ovarian cancers studied here. Our results demonstrated that the expression levels of SOX7 and its targets, COX-2 and cyclin D1, have an inverse relationship.

• Further supporting our hypothesis that SOX7 is a negative regulator in the Wnt/ β -catenin signaling pathway in ovarian cancer.

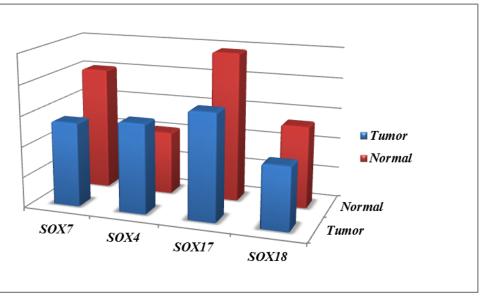
Conclusions

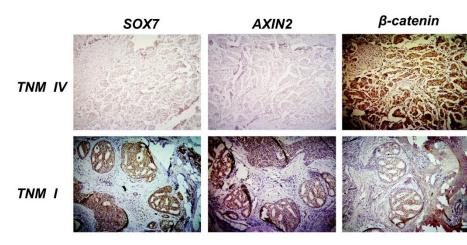
- Our work reported here suggests, for the first time, that SOX7 may play an important role as a tumor suppressor in ovarian cancer progression.
- Our results also revealed SOX7 as a negative regulator in the Wnt/β-catenin signaling pathway in ovarian cancer.
- Our result demonstrates the suppressive function of SOX7 in the carcinogenic process of ovarian cancer.



Future Direction

 Current data showed that the expression of SOX7 was significantly reduced in breast cancer and this effect might be positively correlated with AXIN2.





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