



## Survey SOX2 ,SOX2OT-S1 and SOX2OT-S2 expression in breast cancer

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**Aim & Background** :Cancer is one of the leading causes of death worldwide. Breast cancer is the most frequently diagnosed cancer and the leading cause of cancer death among females in the world. Long non-coding RNAs (lncRNAs) are involved in multiple biological processes and can be used as a candidate for cancer diagnosis, prognosis and treatment. A multi-exon lncRNA, known as SOX2 overlapping transcript (SOX2OT) has been suspected to participate in regulation of SOX2 expression and other related processes.

**Material & Method** :To determine the expression of SOX2, SOX2OT-S1 and SOX2OT-S2 in Iranian patients with breast cancer, we collected a group of tissue biopsies from breast tumor samples and non-tumoral related tissues. RNA extraction, cDNA synthesis, RT-PCR and real time PCR were performed for all samples and the results were analyzed by SPSS software.

**Results** :We showed over expression of SOX2 gene, a master regulator of pluripotency, in breast tumor samples compared to the non-tumor tissues obtained from the margin of the same tumors. The results also indicated upregulation of the two splice variants SOX2OT-S1 and SOX2OT-S2 in breast tumor samples compared to the non-tumor related tissues.

**Conclusion** :To our knowledge, this is the first study investigating the expression of SOX2OT-S1 and SOX2OT-S2 in breast cancer. It showed a coregulation of SOX2OT and its splice variants, SOX2OT-S1 and SOX2OT-S2, with key stem cell pluripotency gene, SOX2. This correlation in expression patterns between SOX2 and SOX2OT-S1, SOX2OT-S2 advocates that lncRNA SOX2OT probably has a role in development of breast tumors. However, more samples are required to see potential use of these splice variants in diagnosis of breast cancer and also reveal the mechanisms involved in this process.: