# RBBP5 protein is associated with poor survival in breast invasive carcinoma through desregulation of DNA damage genes.

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**Background & Objectives**: In women, breast cancer is one of leading cancer-related cause of disease. Even when advance in detection and therapy have been development, still remains as most lethal cancer worldwide, therefore, it's urgent to identify new molecular target to increase patients survival.

**Method (s) and Results**: In order to study gene expression throughout the illness, we analized transcriptional levels associated at each cancer stages (T1 – T4), using cbioportal database. Our data show that levels of RBBP5 (Retinoblastoma-binding protein 5) signficantly increase as well the disease progresses. In arround 9% of patients (89 patients) RBBP5 gen was found amplified and 24% (238 patients) have high levels of the transcript. Interesly, high RBBP5 levels correlationed with a poor survival (Logrank P =0.0142). Functional protein association assay, using String database, reveled that RBBP5 interact with different member of Histone-lysine N-methyltransferase family (KMT2A, KMT2C, KMT2D) and MLL1/MLL complex (WDR5) to bound at differents DNA sites. Predict protein-DNA interaction assay (Chip-atlas database) showed 7633 RBBP5'targets genes, which are mostly enriched in DNA repair category (by ontology assay).

**Conclusions**: Our data suggest that RBBP5 interact with several methyltransferase to modulate DNA repair-associated genes expression, which drive an decrease in survival in patients with breast invasive carcinoma.

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**Keywords**: RBBP5, breast cancer, DNA damage, methyltransferase, predict genes expression.