



## HMGB3 characterization in gastric cancer

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**ABSTRACT.** Gastric cancer is a major health problem worldwide; it is the second most common cause of cancer death in the world. Recent studies indicate that the high-mobility group (HMG) of chromosomal proteins is associated with cancer progression. However, HMGB3 has been little studied. We analyzed the co-expression network between HMGB3 and differentially-expressed genes in the GSE17187 database, identifying the relevant transcription factors, and the conserved domain of HMGB3 to understand the underlying regulation mechanisms involved in gastric cancer. Thirty-one relationships between 11 differentially-expressed genes were included in a co-expression network; many of these genes have been identified as related to cancer, including TBX5 and TFR2. Further analysis identified nine transcription factors, these being GATA3, MZF1, GATA1, GATA2, SRY, REL, NFYB, NFYC, and NFYA,

which could interact with HMGB3 to regulate target gene expression and consequently regulate gastric cancer cell proliferation, migration and invasion. The HMG-box domain was very similar in various species, with only a few amino acid changes, indicating conserved functions in HMG-box. This information helps to provide insight into the molecular mechanisms of HMGB3 in human gastric cancer.

**Key words:** HMGB3; Gastric cancer; HMG-box