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HOXA4, a regulator from homeobox family, has been noted to be disrupted in human colorectal cancer. Still, the function, co-expression profile, and clinicopathologic significance of HOXA4 in colorectal cancer progression are not well elucidated in the literature. So, in this study, we systematically explore HOXA4 expression as well as its clinical outcome in colorectal cancer using widely accessible cancer microarray datasets and patient survival data through numerous online platforms. To observe the variations in HOXA4 mRNA expression level between colorectal cancer tissues and their normal counterparts, which showing the upregulation in colorectal cancer. The HOXA4 showed the 24 mutations profiles and their associated 33 co-expression genes in colorectal cancer. The functional enrichments were investigated by the associated co-expressed genes through PANTHER web, which result shown involved ubiquitin proteasome pathway. The survival curve displayed a marked correlation between HOXA4 upregulation and poor patient survival. Also, show is the interaction of miRNAs, TFs, with HOXA4 and the miR-196b showing lowly expression in colorectal cancer. In conclusions, as a result, HOXA4 might be used as an oncogene and a prognostic biomarker and miR-196b is associated with HOXA4 in human colorectal cancer.