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Systematic evaluation of collagen family gene transcripts: Implications for prognostic stratification in lung cancer patients

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Remodeling of the extracellular matrix (ECM) is expressed as one of the most powerful processes in the development of lung cancer (LC). Moreover, its alternative regulation showed significant relationship with a wide range of diseases and traits. Since the collagen family is one of the most important components of the ECM, in silico analyzes were performed to determine which collagen type among all collagens was significant for survival of lung cancer. Overall survival (OS) plots were generated for all collagen members and subsequently, the transcript levels of collagen members with significant OS values were examined using the GEPIA web tool. According to the survival graphs of 46 genes, the expressions of *COL6A4P2*, *COL6A6*, *COL7A1*, *COL11A1*, *COL19A1*, and *COL22A1* genes have a significant relationship with OS in Lung Adenocarcinoma (LUAD). *COL1A2*, *COL4A1*, *COL5A2*, *COL6A5*, and *COL28A1* genes have a significant relationship with OS for Lung Squamous Cell Carcinoma (LUSC) ($P \leq 0.05$). *COL6A6-001*, *COL6A6-002*, *COL11A1-001*, *COL11A1-007* transcripts for LUAD, and *COL1A2-002*, *COL1A2-004*, *COL1A2-005*, *COL1A2-007*, *COL1A2-008*, *COL1A2-011*, *COL4A1-004*, *COL6A5-003*, *COL6A5-004* transcripts for LUSC were found to be significant. *COL6A6-002*, *COL11A1-001*, *COL11A1-007* and *COL1A2-005* transcripts were also found to be significant for stratifying pathological stages.

Keywords: Collagen, Lung cancer, Transcriptome