# STUDY OF TUSC3 GENE CHANGES IN OVARIAN CANCER CELLS USING MASS SPECTROMETRY COUPLED WITH BIOSTATISTICAL METHODS

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Tumor Suppressor Candidate 3 (TUSC3) gene is a subunit of enzymatic complex (oligosaccharyltransferase) responsible for the N-glycosylation of proteins. Loss of TUSC3 expresion in ovarian cancer cells promotes aggressiveness of the disease (increase invasion and spreading) and limits survival of patients. In cultured cells, it induces profound phenotypical changes, most probably due to alterations in the glycoproteome. In vitro silencing TUSC3 gene causes possibility to study different ovarian cell types, expression proteins, and their post-translational modification. Changes in mass spectra profiles are reflecting changes in the inner cellular environment allowed discrimination using multivariate statistical methods or classification via self-learning approaches e.g. artificial neural networks (ANN) [1]. As model 2 human and 2 mouse ovarian cancer cell lines were selected. The mass spectra obtained from intact cells with or without TUSC3 silencing were post-processed and evaluated using the R Studio.

[1] Vaňhara P, Kučera L, Prokeš L, Jurečková L, Peña-Méndez EM, Havel J, Hampl A. Intact Cell Mass Spectrometry as a Quality Control Tool for Revealing Minute Phenotypic Changes of Cultured Human Embryonic Stem Cells. Stem Cells Transl. Med. 2018. 7(1):109-114. doi: 10.1002/sctm.17-0107