

Identification of cellular senescence signatures for classifying senescence status based on machine learning approaches

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Cellular senescence is a permanent cell-cycle arrest which prevents damaged cells from unusual proliferation. By the secretion of senescence-associated secretory phenotype factors, senescent cells affect various age-related diseases including cancers. Selective elimination of senescent cells, named as 'senolysis', has emerged as a potential therapeutic method for various diseases. However, since senescent cells possess heterogeneous features according to cell types or senescence inducers, it was difficult to identify the senolysis markers. Therefore, we collected raw RNA-seq data (165 samples) of various fibroblast senescent samples by various inducers (e.g. replicative senescence, oncogene induced senescence, and therapy induced senescence) from different experiments to find out consensus features of cellular senescence regardless of inducer types. Meta-analysis and machine learning approaches such as LASSO and support vector machine were used for selecting representative features of cellular senescence and for construction of senescence classification model with selected features. The support vector machine model can discriminate senescent samples from non-senescent samples regardless of inducer types, with great performance. As a result, we offered these 15 signature genes as core characters of cellular senescence.