Abstract

Sense-Antisense Gene Pairs for Patient Stratification, Prognosis and Therapeutic Biomarkers Identification

The present invention relates to a method of identification of clinically and genetically distinct sub-groups of patients subject to a medical condition, particularly breast, lung, and colon cancer patients using a composition of respective gene expression values for certain gene pairs. Sense-antisense gene pairs (SAGPs) which are relevant for a medical condition and the disease prognosis are used by the method to generate statistical models based on the expression values of the SAGPs. SAGPs for which the statistical models are found to have high value in prognosis of the variation of medical condition and the diseases are selected and integrated in the prognostic signature including specified parameters (e.g. cut-off values) of the prognostic model. It further relates to using respective gene expression values for these genes to predict patient' risk groups (in context of patient's survival or/and disease progression) and to using the predicted groups for identification of patient risk, and specific and robust prognostic biomarkers with mechanistic interpretations of biological changes (associated with the gene signatures) appropriating for an implementation of therapeutic targeting.

[Figure to print with the abstract: Fig. 1]