

SUPPLEMENTARY CODE

Please browse Full Text version to see the data of Supplementary Code.

Supplementary Code. (i) the code (Perl language) used to perform text mining in order to extract raw EMT related genes/proteins from Pubmed query xml results; (ii) the code (R language) for unsupervised clustering analysis based on expression levels of 756 EMT-related genes using multiple R packages; (iii) the code (Perl language) of our custom Perl functions to perform batch effect evaluation using MBatch v1.0 software; (iv) the code (Perl language) used to perform expression quantitative trait methylation (eQTM) and expression quantitative trait copy number alterations (eQTCN) analysis.