Introduction:
Shock is a common complication of critical illness in patients in intensive care units (ICUs), who are undergoing major surgery. This condition is the most common cause of death in postsurgical ICUs. Nowadays, there are different ICU scoring systems for predicting the likelihood of mortality, such as APACHE or SOFA. Nevertheless, they are used rarely because they also depend on the reliability and predictions of physicians. In these sense, gene expression signatures can be used to evaluate the survival of patients with postsurgical shock.

Methods:
mRNA levels in the discovery cohort were evaluated by microarray to select the most differentially expressed genes (DEGs) between groups of those that survived and did not survive 30 days after their operation. Selected DEGs were evaluated by quantitative real time polymerase chain reactions (qPCR) for the validation cohort to determine the reliability of the expression data and compare their predictive capacity to that of established risk scales.

Results:
*IL1R2*, *CD177*, *RETN*, and *OLFM4* genes were upregulated in the non-survival group of the discovery cohort. Further confirmation of the predictive power of these genes was found in the validation cohort. Areas under the receiver operating characteristics curves (AUC) were 0.653 (0.535–0.771), 0.669 (0.544–0.794), 0.739 (0.628–0.850) and 0.782 (0.682–0.877) for *IL1R2*, *CD177*, *RETN*, and *OLFM4*, respectively. These values were more instructive than the classical mortality risk scores from the APACHE (0.647; 0.543–0.751) and SOFA (0.580; 0.456–0.705). Finally, a regression model was performed including gene expression values and different adjust variables, improving the AUC value up to 0.800 (0.693–0.906).

Conclusion:
This study offered new biomarkers based on transcriptional patterns for classifying patients with postsurgical shock as either at low or high risk of death. The results were more accurate than the other mortality risk scores APACHE and SOFA.