Identification of Potential Key (Hub) Genes Associated with Prognosis of Triple-Negative Breast Cancer in Asian versus non-Asian Populations Based on Bioinformatics Analysis

<u>Rassanee Bissanum</u>[a], Raphatphorn Navakanitworakul[a], Suphawat Laohawiriyakamol[b], Piyanan Wangkulangkul[b], Ayako Nakatake[c],

Kazuhiro Morishita[c], Rawikant Kamolphiwong[a], and Kanyanatt Kanokwiroon[a, *]

[a]Department of Biomedical Sciences and Biomedical Engineering, Faculty of Medicine, Prince of Songkla University, Hat Yai, Songkhla, Thailand

[b]Department of Surgery, Faculty of Medicine, Prince of Songkla University, Hat Yai, Songkhla, Thailand

[c]Division of Tumor and Cellular Biochemistry, Department of Medical Sciences, University of Miyazaki, Miyazaki, Japan
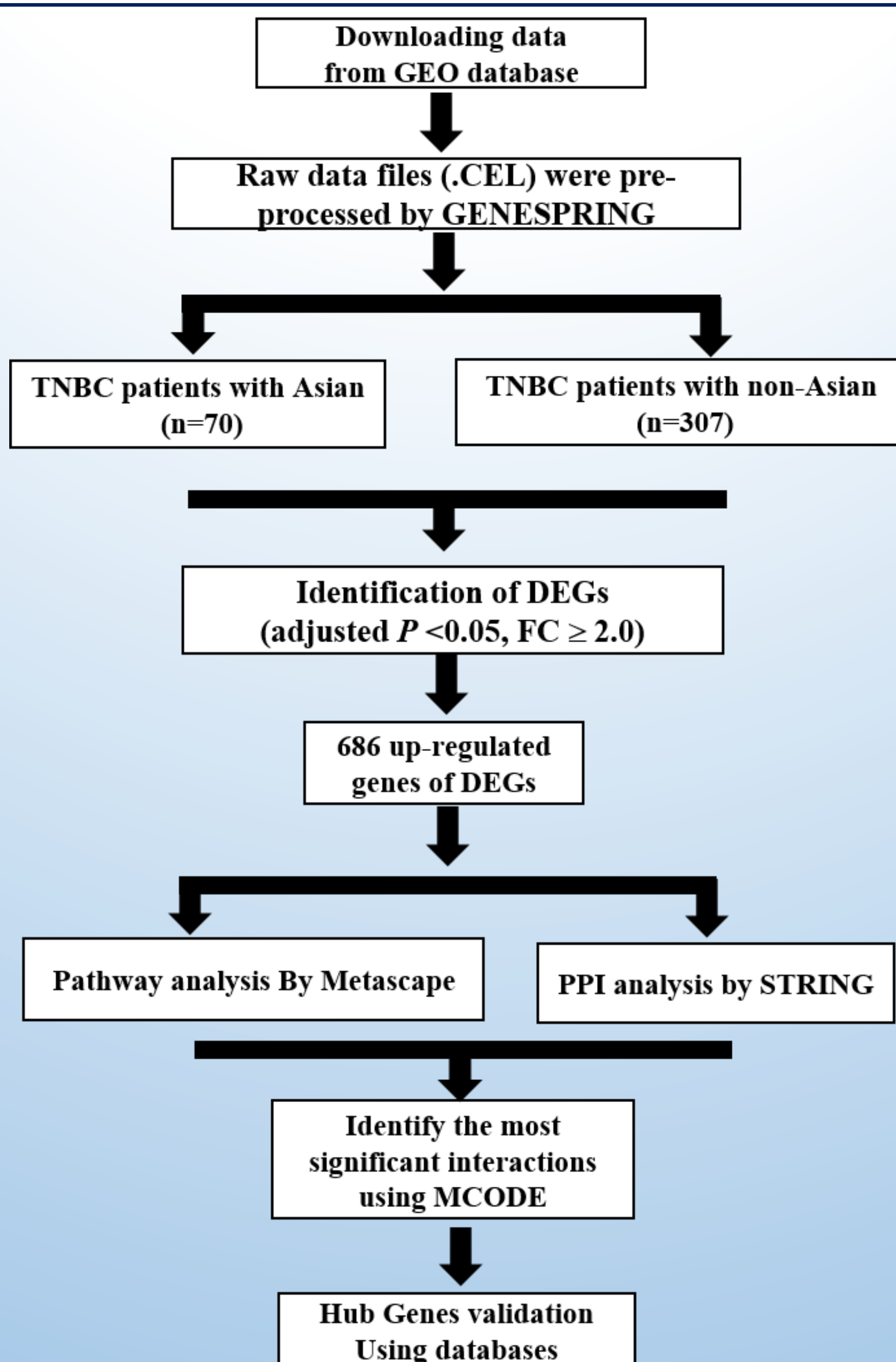
Abstract

Triple negative breast cancer (TNBC) is a heterogeneous disease associated with advanced stage and high metastatic rates. The prognosis of TNBC varies by race/ethnicity and genetic diversity. This study aimed to identify the potential key genes and their association with the prognosis of Asian TNBC patients through bioinformatics methods. Differentially expressed genes (DEGs) between TNBC patients in Asian and non-Asian population were analyzed. 686 up-regulated genes were identified in Asian population. The upregulated DEGs were mainly enriched in pathways including vesicle-mediated transport and membrane trafficking, apoptotic signaling and T cell activation. Our study found that high expression levels of *SEC61G*, *MRPL13* and *LSM5* gene were significantly associated with poor overall survival. Thus, these genes might be candidates for developing essential prognostic markers for Asian TNBC patients. (**Keywords** *:* Prognosis marker, triple negative breast cancer, bioinformatics analysis)

Introduction

- TNBC comprises 10-20% of all breast cancers depending on race and ethnicity. TNBC is characterized by the absence of estrogen receptor (ER) and progesterone receptor (PR) expression and without amplification of human epidermal growth factor receptor 2 (HER2) gene (Bianchini et al., 2016).
- A previous study summarized the list of genes involved in progression of TNBC using gene expression profiling in different geographic regions. They found that different genes were involved in the pathogenesis of TNBC in different ethnic backgrounds (Gupta et al., 2019).
- In the current study, we aimed to investigate and compare key pathways and hub genes of TNBC patients between Asian and non-Asian populations to provide additional prognostic markers.

Methods

Results

Figure 1 : (A) Protein-protein interaction (PPI) network and (B) module analysis.
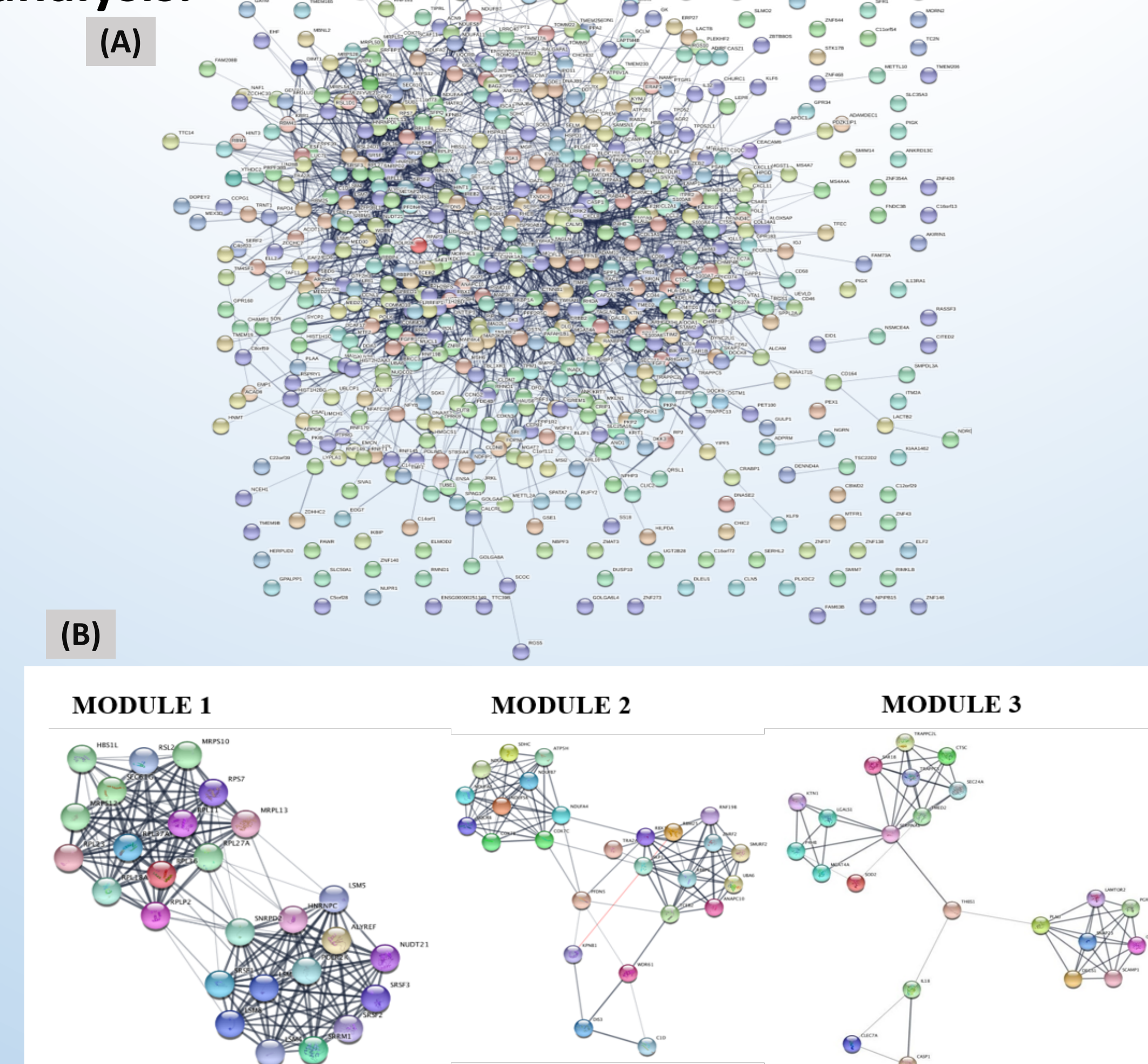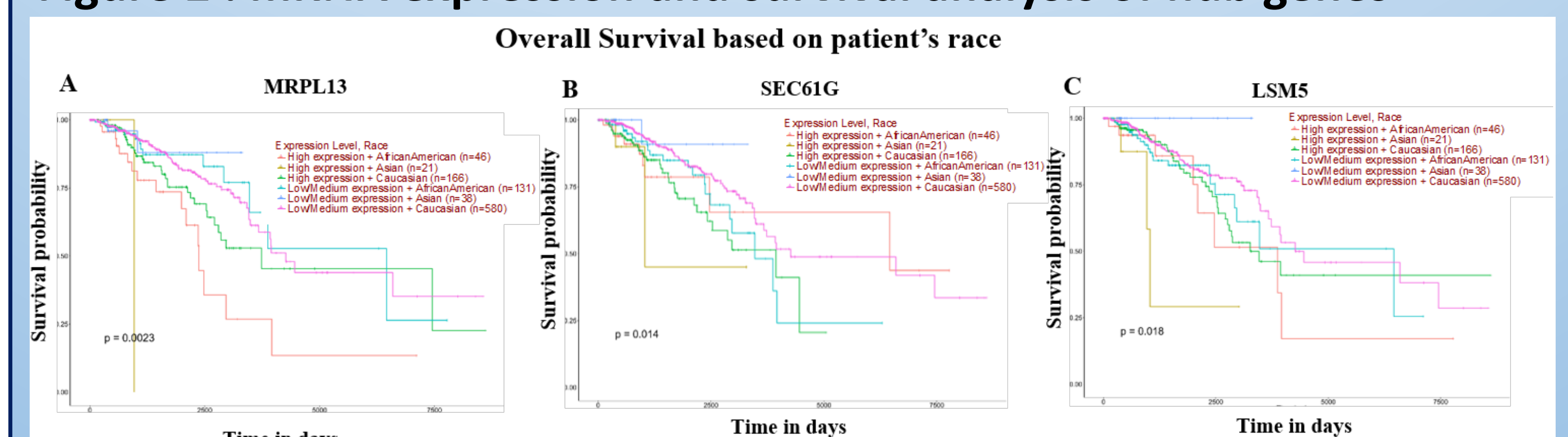

Figure 2 : mRNA expression and survival analysis of hub genes

Conclusion & Discussion

- In this study, we identified hub genes and related pathways through bioinformatics analysis of DEGs between TNBC in Asian and non-Asian populations.
- The survival analysis of the three hub genes suggests that SEC61G, MRPL13 and LSM5 might have some prognostic value for BC in Asian patients.
- Future *in vitro* and *in vivo* studies are needed to further elucidate the functions of these genes specifically in relation to TNBC tumorigenesis and prognosis.

References

Bianchini, G., Balko, J. M., Mayer, I. A., Sanders, M. E., & Gianni, L. (2016). Triple-negative breast cancer: challenges and opportunities of a heterogeneous disease. Nature reviews. Clinical oncology, 13(11), 674–690. https://doi.org/10.1038/nrclinonc.2016.66

Gupta, I., Sareyeldin, R. M., Al-Hashimi, I., Al-Thawadi, H. A., Al Farsi, H., Vranic, S., & Al Moustafa, A. E. (2019). Triple Negative Breast Cancer Profile, from Gene to microRNA, in Relation to Ethnicity. Cancers, 11(3), 363. https://doi.org/10.3390/cancers11030363

Jack, R. H., Davies, E. A., Renshaw, C., Tutt, A., Grocock, M. J., Coupland, V. H., & Møller, H. (2013). Differences in breast cancer hormone receptor status in ethnic groups: a London population. European journal of cancer (Oxford, England : 1990), 49(3), 696–702. https://doi.org/10.1016/j.ejca.2012.09.012