4 - 68 An Integrative Model of miRNAs and mRNAs Expression Signature for Patients of Breast Invasive Carcinoma with Radiotherapy Prognosis

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Radiotherapy is widely used in cancer treatment. The radiotherapy for breast invasive carcinoma (BRCA) presents challenges due to the heterogeneous of patients. In this study, the clinical data and expression data (including miRNA and mRNA) were obtained from the database of The Cancer Genome Atlas (TCGA) to predict prognosis after radiotherapy. We selected the 73 patients with radiotherapy for further study. The results showed that four clinical factors (age, tumor status, estrogen receptor status and race) were not associated with patient survival after radiotherapy by log-rank test. Furthermore, the miRNAs and mRNAs expression have been as factors for analysis of the relationship between RNAs expression and patient survival time after radiotherapy. According to calculating weighted prognostic index (WPI) and hazard ratio (HR) from univariate Cox regression between RNAs expression and patient survival, we classified the patients with radiotherapy into low-risk and hig-risk groups(Fig. 1(a) and (b)). The result showed that 22 RNAs were closely associated with survival (Fig. 1(c)). Of these 22 RNAs, 9 mRNAs were considered as protective genes (HR<1; $P < 0.05$) and 5 miRNAs and 8 mRNAs were considered as high-risk genes (HR>1; $P < 0.05$). And the high-risk group defined by WPI has significantly shorter survial time comparison with low-risk group by log-rank test (P=0.046).

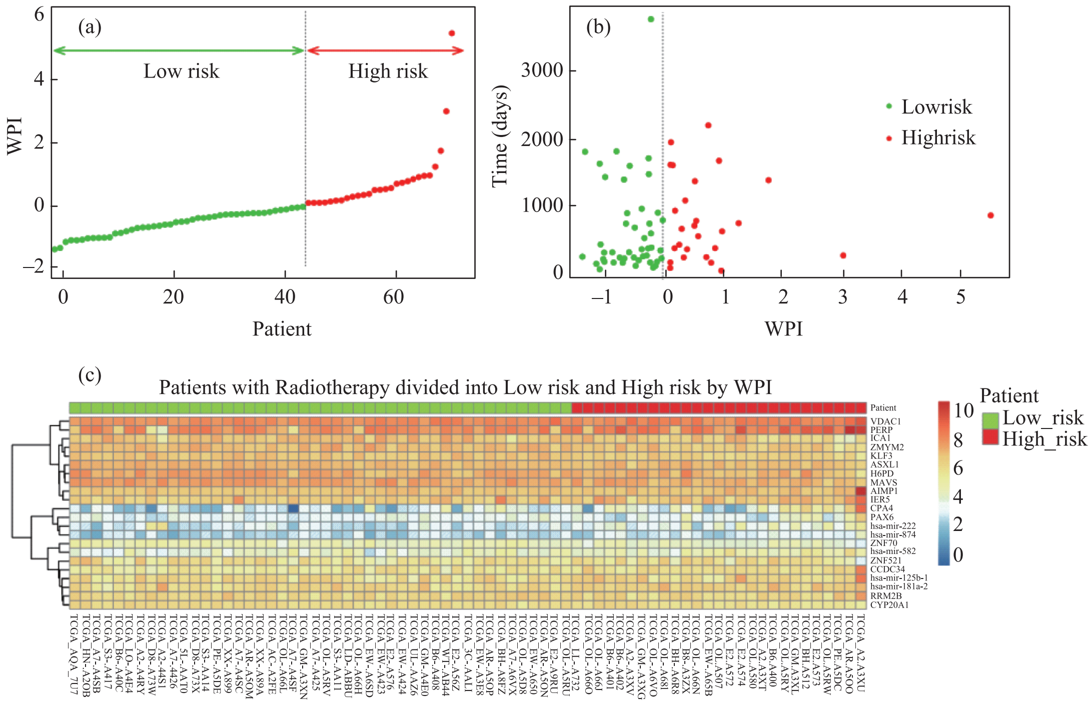

Fig. 1 (color online) The Low-risk and High-risk of 73 BRCA patients with radiotherapy analysis by 22 RNAs WPIs. (a) WPIs of RNAs distribution of the BRCA patients with radiotherapy. (b) Patient survival status along with WPIs. (c) Heat map of 22 RNAs expression profiles of BRCA patients; rows represent risky and protective RNAs, and columns represent the accession number of patients in TCGA.