

Research Article

A Five-Gene Signature Inferred from Transcriptome Profiling of Homologous Recombination-Mediated DNA Repair Predicts Clinical Outcome of Patients with Cancer

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Received: 10-08-2015

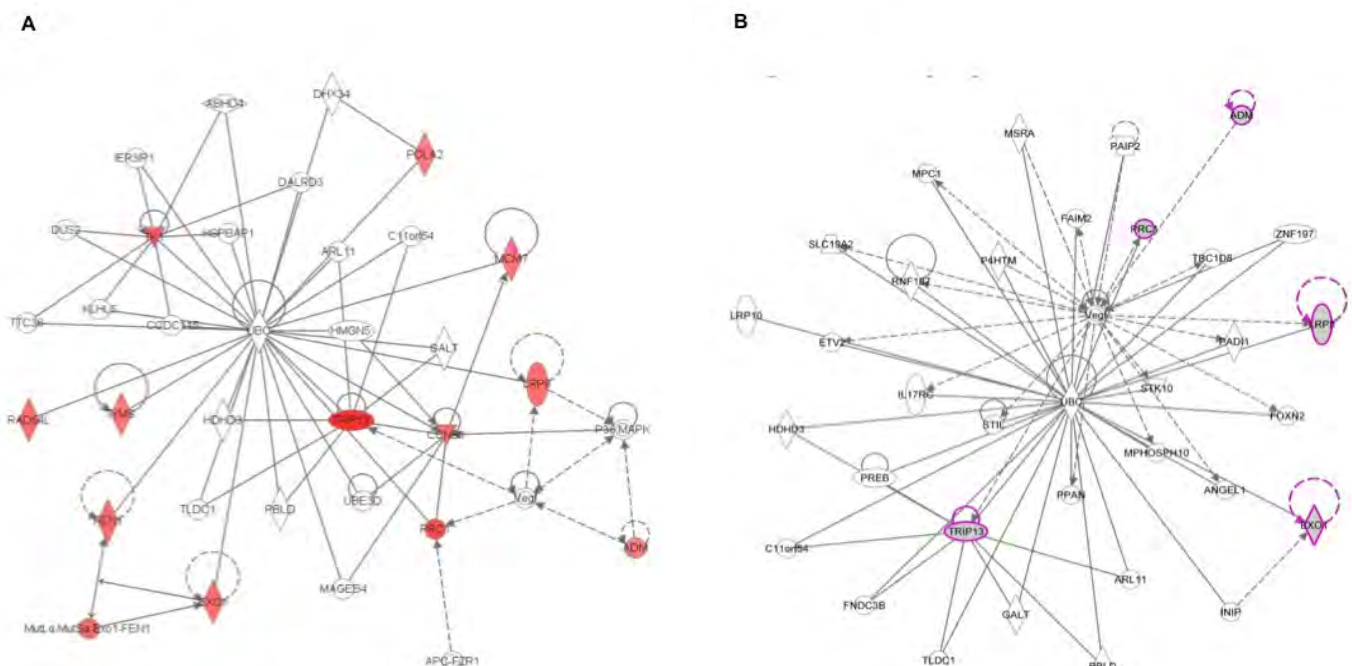
Accepted: 10-21-2015

Published: 12-10-2015

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Supplementary Figure 1

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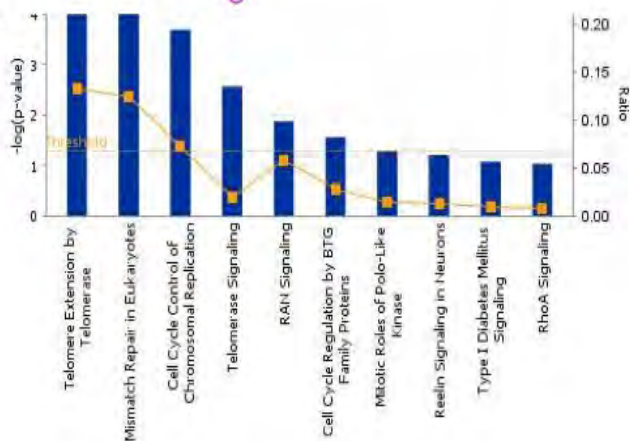
S1 Figure The networks of -13gene and -5gene signatures. (A) The networks in which the 13 genes are involved, according to analysis with Ingenuity Systems' IPA software. The networks included cell cycle G2/M DNA damage checkpoint regulation, nucleic acid metabolism, and cellular assembly and organization. (B) The networks in which the five genes are involved, according to analysis with Ingenuity Systems' IPA software.

Supplementary Figure 2

A



B



S2 Figure Recursion analysis identifies 15 genes most significantly associated with breast cancer survival. (A) The networks in which the 15 genes are involved, according to analysis with Ingenuity Systems' IPA software. The networks included cell cycle G2/M DNA damage checkpoint regulation, nucleic acid metabolism, and cellular assembly and organization. (B) Top 10 canonical pathways of the 15 genes using Ingenuity Systems' IPA software. The $-\log(p\text{ value})$ is obtained by the Ingenuity program using Fisher's exact test. The threshold for significance is $P=0.05$.