

### **Supplementary Information:**

**Figure S1.** The heatmap represents the association between genes and metastasis-related processes. Red (1) and white (0) cells in the matrix represent positive and neutral correlation values in the matrix.

**Figure S2.** Gene-gene association. The row similarity matrix represents a correlation between genes. Red (1), white (0), and blue (-1) represents positive, neutral, and negative correlation (measured as  $1 - \text{cosine-distance of association}$ ).

**Figure S3.** GeneMania network 185 non-redundant unique genes, presenting interactions between genes. Different network colors represent different associations, such as physical interaction, co-expression, genetic interaction, predicted association, co-localization, shared pathway, and shared protein domain homology.

**Figure S4.** Example of GeneMania network 185 non-redundant unique genes, highlighting interactions between Rac1 with other genes.

**Figure S5.** GeneMania network 77 candidate hub genes, presenting interactions between genes. Different network colors represent different associations, such as physical interaction, co-expression, genetic interaction, predicted association, co-localization, shared pathway, and shared protein domain homology.

**Table S1:** Text-mining results for association between human genes and metastasis related biological processes, and, cancer-specific filtered text-mining results.

**Table S2:** Correlation analysis of cancer metastasis related genes and biological processes using Clustergrammer.

**Table S3:** Gene ontology and pathway analysis results of cancer-specific unique genes.

**Table S4:** List of manually validated pre-clinical drugs to target hub genes.

**Table S5:** List of FDA approved/pre-clinical drugs, also validated on cancer-cell lines (CMap Score) for drug repurposing against hub genes.