

**Single-cell and spatial transcriptomics reveal P4HA2-mediated  
radiotherapy resistance mechanisms in breast cancer**

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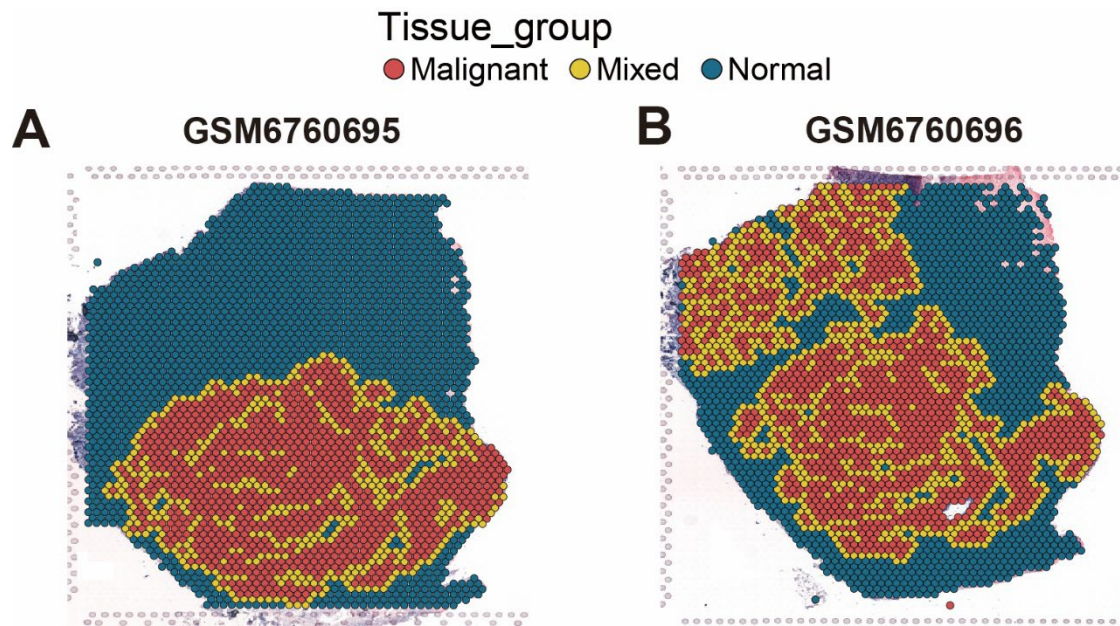
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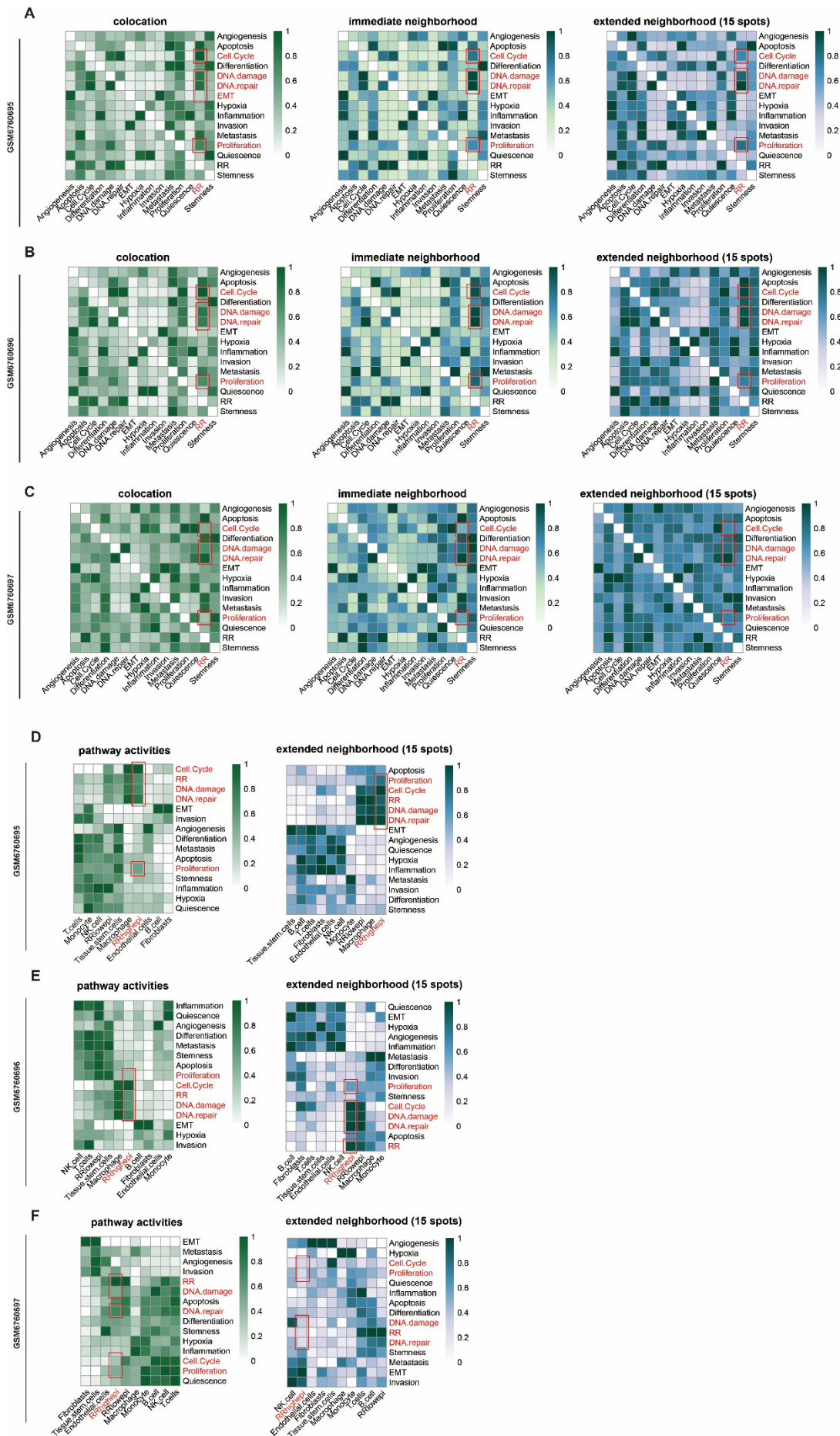
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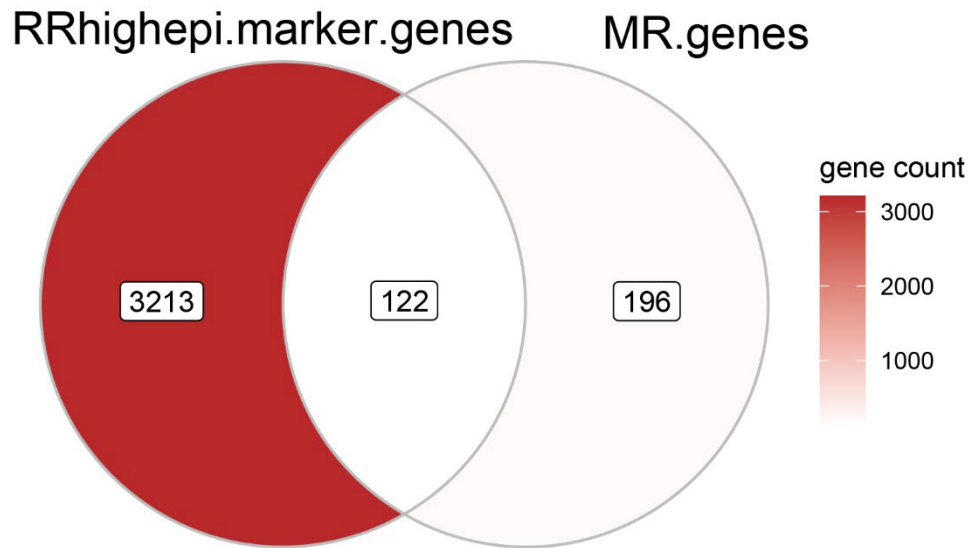
**Supplementary Materials Legends**



**Figure S1. Identification and characterization of benign and malignant regions in spatial transcriptomics based on R package Cottrazm. (A-B) Delineation of benign and malignant regions in spatial transcriptomics.**



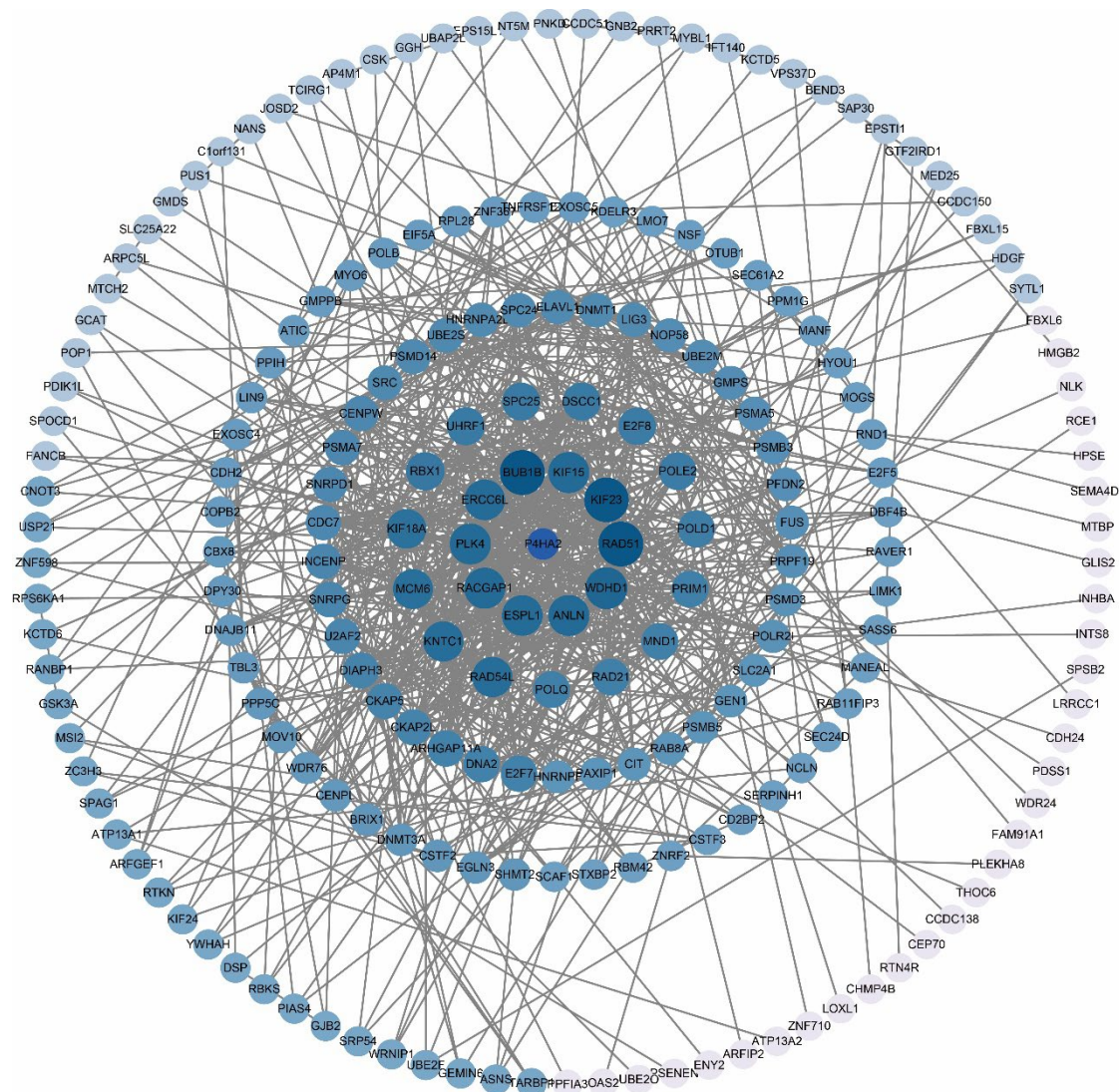
25 **Figure S2. Cell and pathway dependency analysis in spatial transcriptomics.** (A-  
26 C) Heatmap showing pathway-pathway dependency analysis in spatial transcriptomics  
27 colocation, immediate neighborhood, and extended neighborhood (15 spots) regions.  
28 (D-F) Heatmap showing cell-pathway dependency analysis in spatial transcriptomics  
29 intra and para regions.



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31 **Figure S3. Intersection of RRhighhepi genes and genes filtered by Mendelian**  
32 **randomization to obtain genes for establishing prognostic model (ML.genes).**





**Figure S4. Interaction between P4HA2 and the radiation resistance gene panel.**

### **Supplementary Tables:**

**Table S1. Differentially Expressed Genes in TCGA and GSE120798 and Antibody Information.**

**Table S2. The gene panel derived from Radiotherapy resistance.**

**Table S3. Mendelian randomization analysis of genes and their corresponding GWAS queue information related to the causal relationship between Radiotherapy resistance genomic panel and breast cancer.**

**Table S4. The marker gene of RRhighpi.**

43 **Table S5. Intersection of RRhighhepi and Genes Filtered by Mendelian**  
44 **Randomization for Prognostic Model Construction (ML.genes).**

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