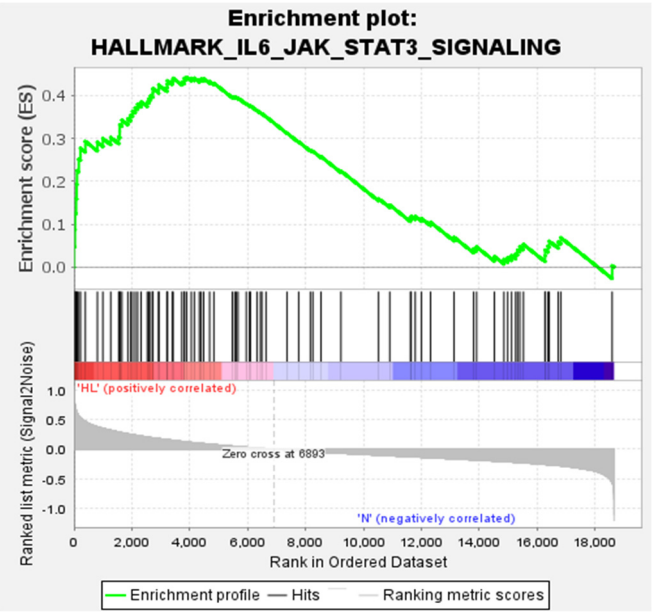
Supplementary materials

A



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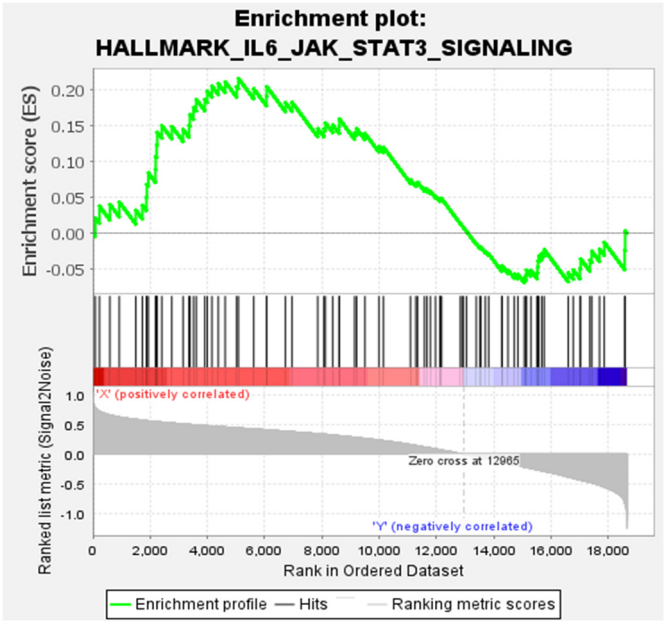

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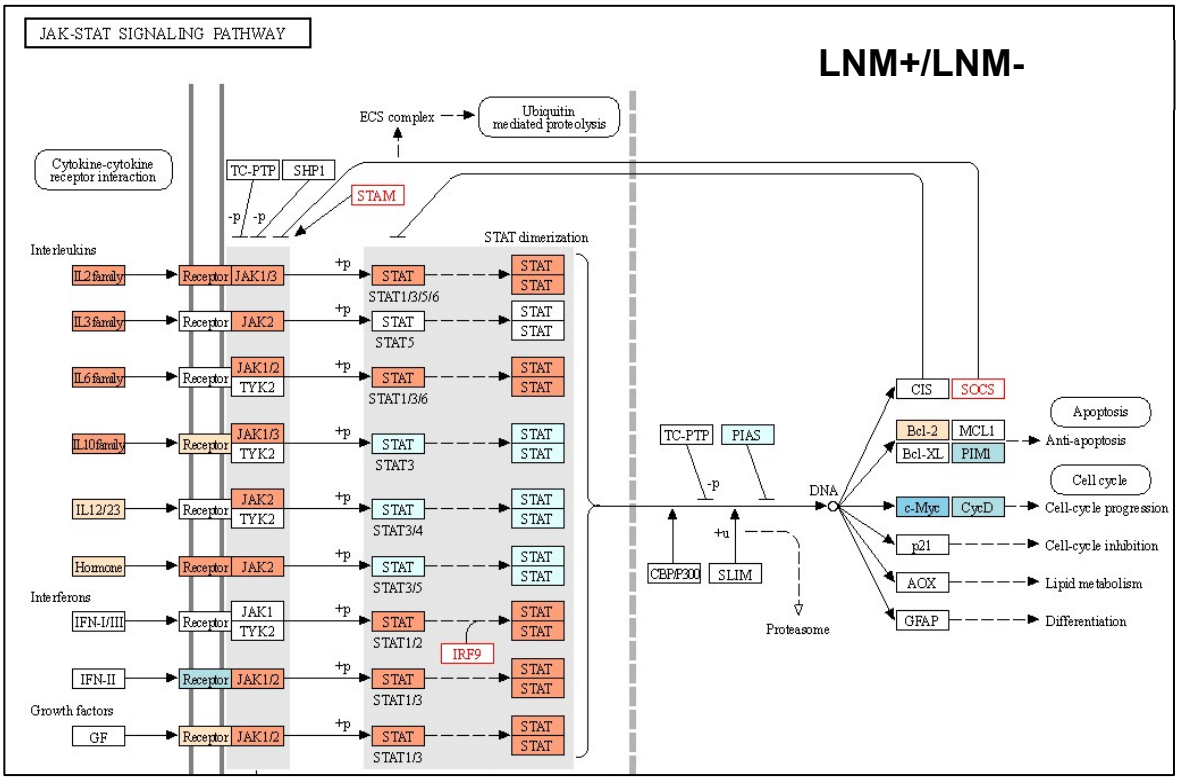

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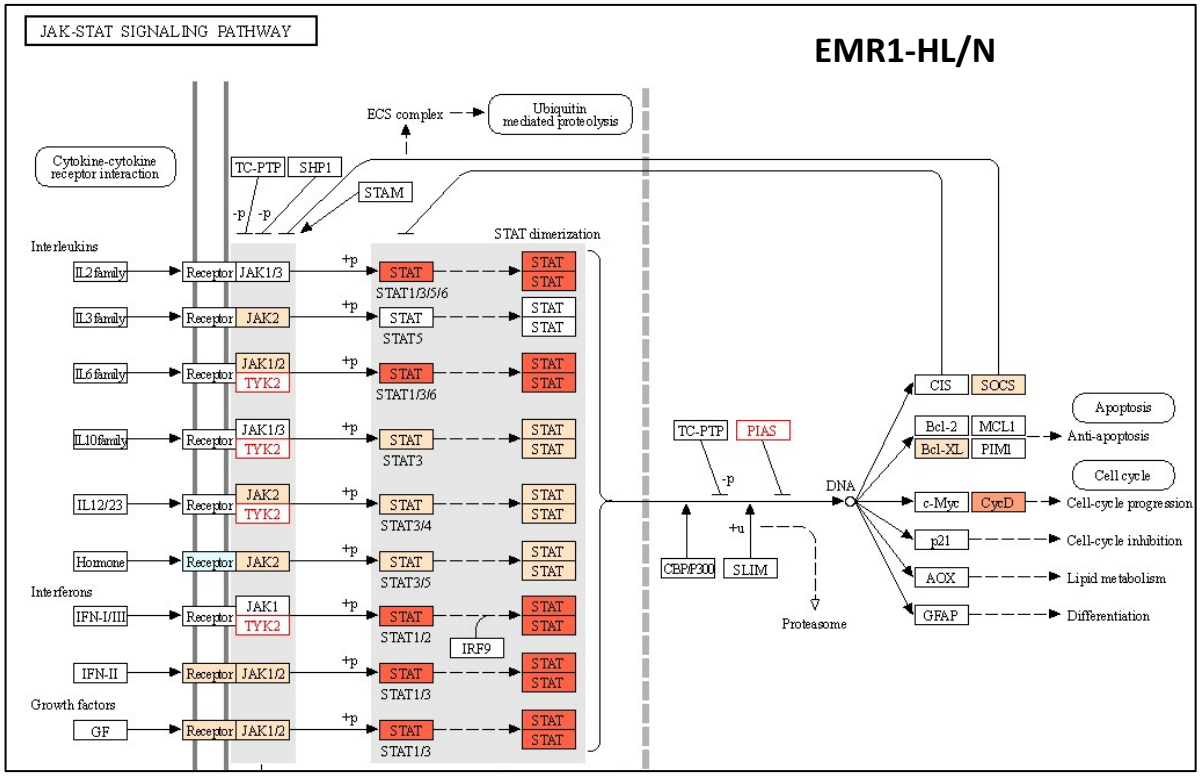
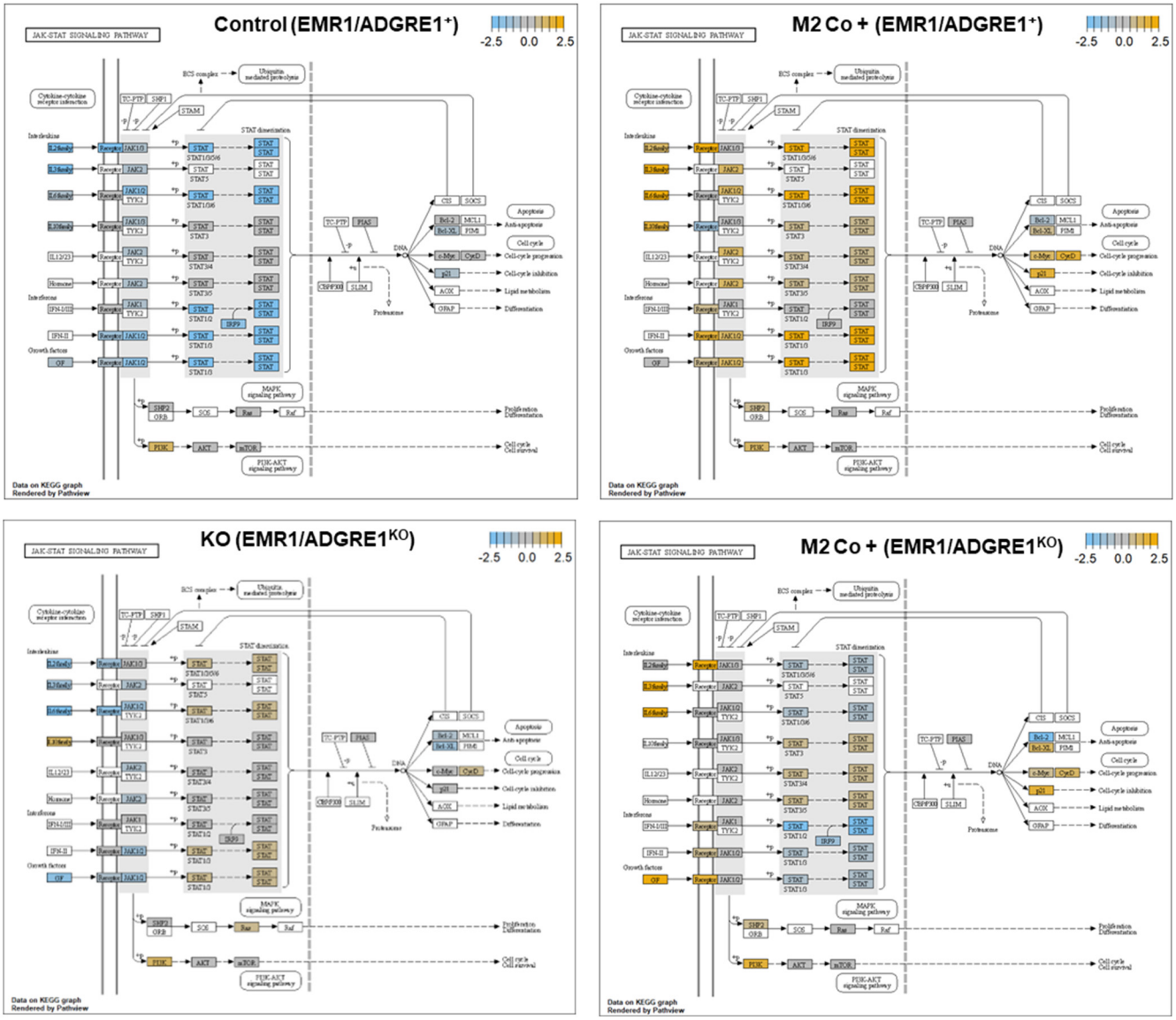
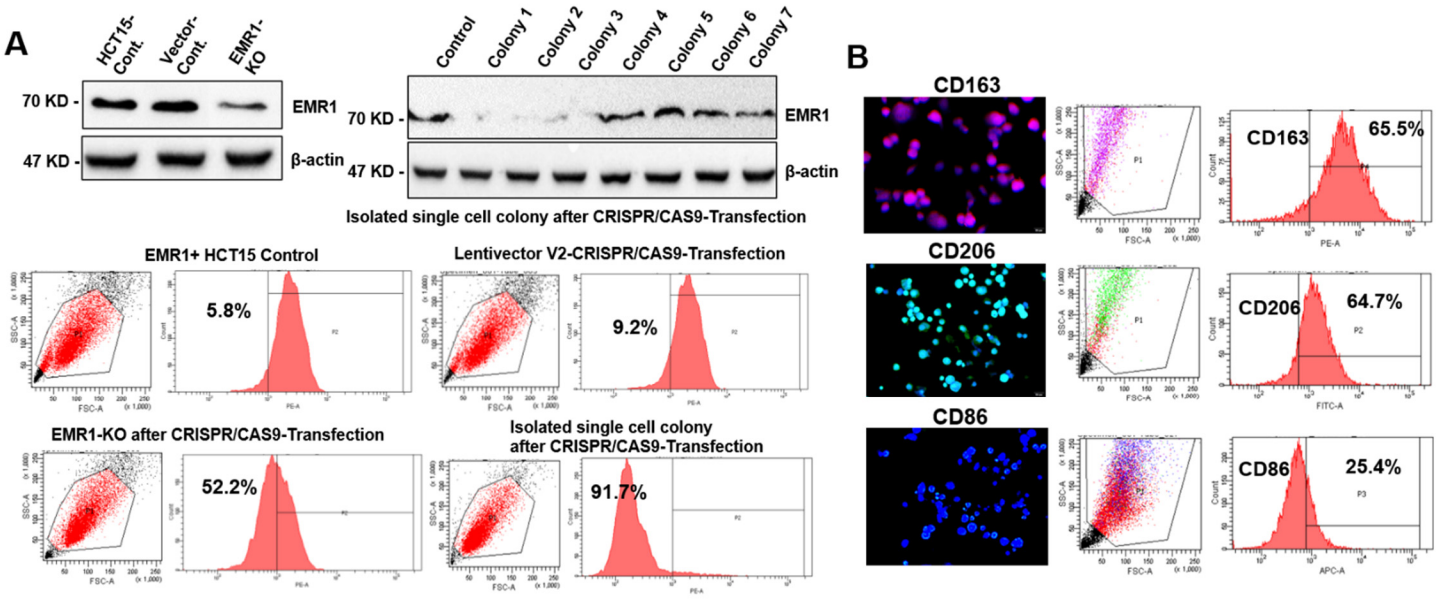


Supplementary Figure S1. Spatial transcriptomic analysis of CC according to EMR1 expression and LNM. A, B. GSEA enrichment plots showing JAK-STAT signaling pathway was enriched in the LNM+ vs LNM- group as well as EMR1-HL vs EMR1-N group. **C, D.** Map of the KEGG pathway "JAK-STAT SIGNALING PATHWAY" displaying genes with differentially expressed mRNA fragments in the LNM+ vs LNM- group as well as EMR1-HL vs EMR1-N group. The red color indicates upregulated and the blue color indicates downregulated mRNA. Here, X=LNM+, Y= LNM-. **Abbreviations:** LNM, lymph node metastasis; L=Low, H= High, N=Negative

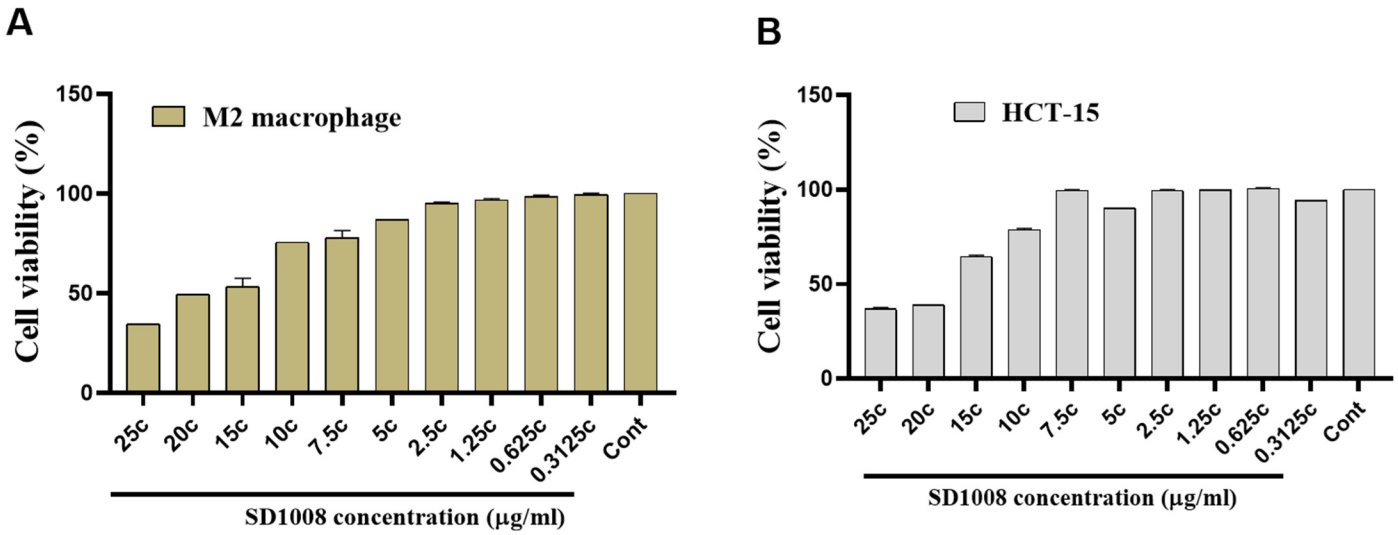
A



Supplementary Figure S2. Molecular changes between EMR1^{+} and EMR1^{KO} CC cells after coculture with macrophages in vitro. A. Map of the KEGG pathway "JAK-STAT SIGNALING PATHWAY" displaying genes with differentially expressed mRNA fragments. The yellow color indicates upregulated genes and the sky-blue color indicates downregulated genes.



Supplementary Figure S3. EMR1 knockout and macrophage polarization validation results. A. Validation of CRISPR/Cas9-mediated EMR1 knockout by western blot and flow cytometry analysis**. B.** Validation of THP1-derived macrophage polarization by immunofluorescence and flow cytometry analysis. Abbreviations: CRISPR/Cas9.



Supplementary Figure S4. Toxicity of JAK2/STAT3 inhibitor (SD1008) in macrophage and CC cells (HCT15). (**A-B**) The cells were treated with different concentrations of the SD1008 inhibitor for 48 h and toxicity was detected using a WST-1 reagent. Graphs represent data as means ± SD.