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Using Big Data Approaches to Map Myocardial Infarction Signatures

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INTRODUCTION

- Myocardial infarction (MI) results in the loss of cardiomyocytes, which stimulates a wound healing response to stimulate scar tissue formation in the heart.
- Developing gene maps will help us find therapeutic targets for better MI outcomes.

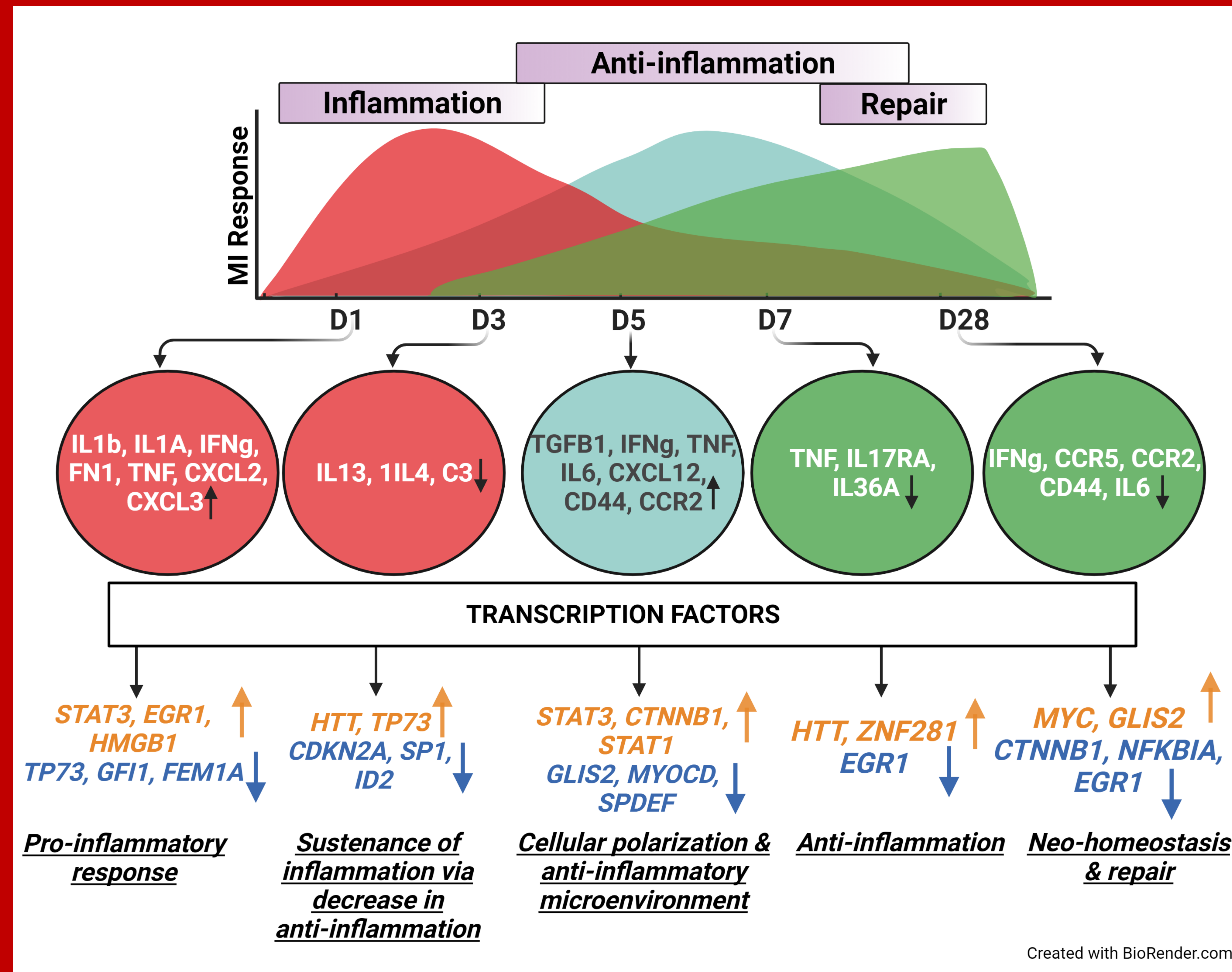
METHODS

- The mouse heart attack research tool (mHART) database was queried for retrospective analysis of gene expression data for 84 extracellular matrix genes (n=91) and 84 inflammatory genes (n=109) from the infarct region of C57/BL6J mice (3-9 months old). Data from D0-no MI mice were used as controls.
- Statistical evaluation and Ingenuity pathway analysis (IPA) were used for data visualization.

RESULTS

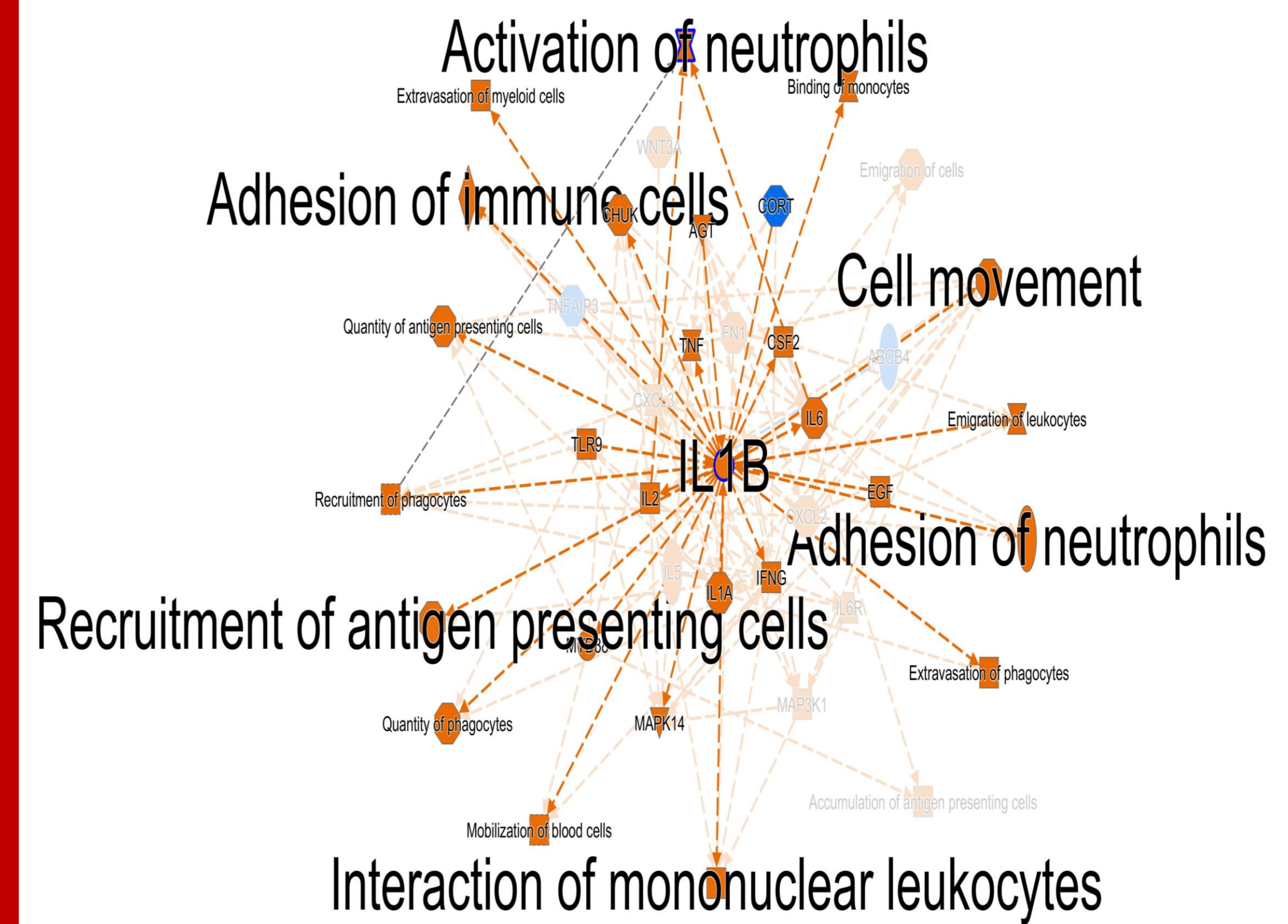
- D1 and D3 showed strong pro-inflammatory responses.
- D5 and D7 showed strong anti-inflammation responses linked to the inhibition of the pro-inflammatory genes.
- D28 showed a reparative phenotype with activation of tissue homeostasis genes.

USING BIG DATA APPROACHES TO MAP MYOCARDIAL INFARCTION SIGNATURES

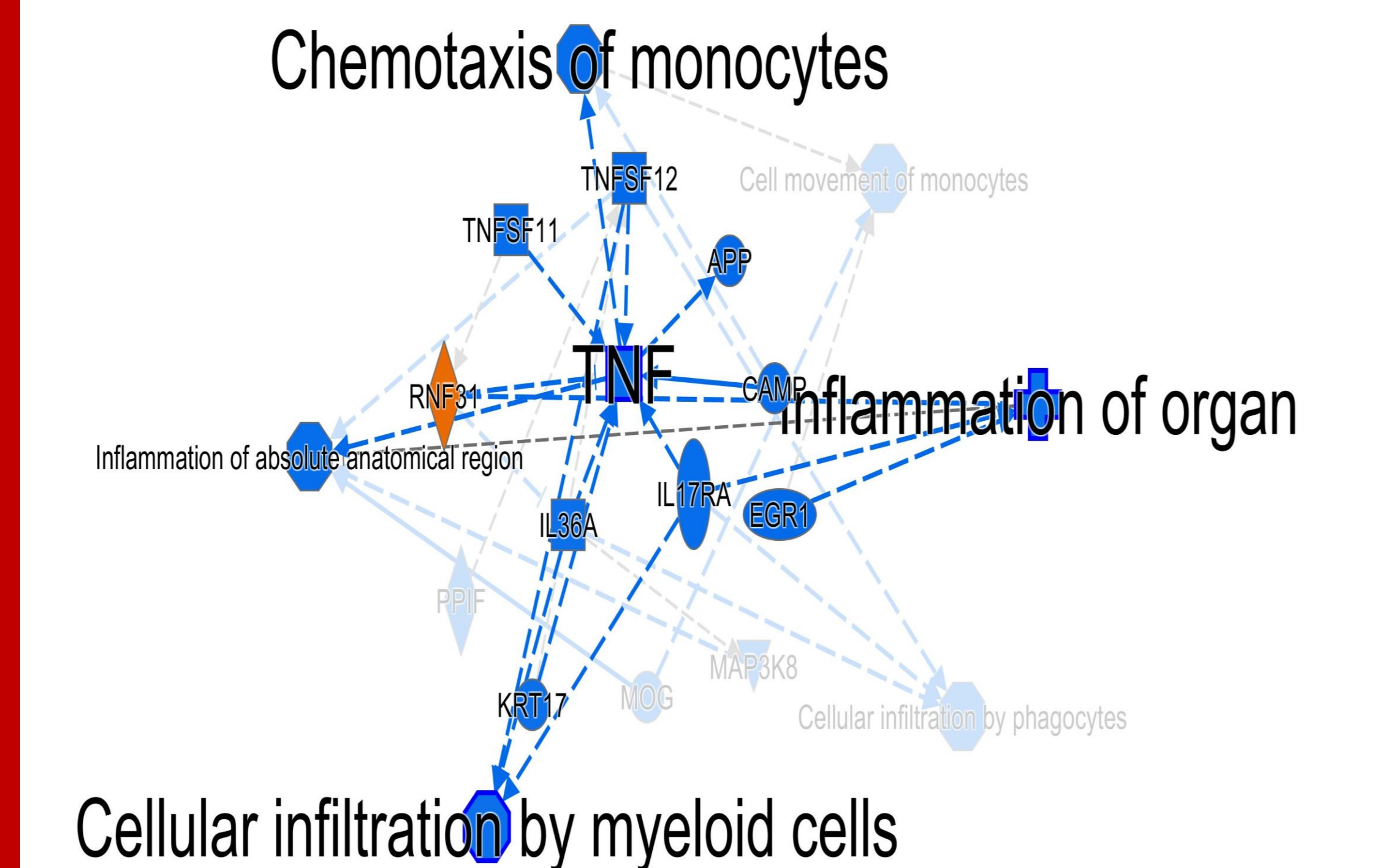


There is a gradual shift in signaling from early inflammation to resolution and repair over the course of MI.

1) D0 to D1: Early inflammation



2) D5 to D7: Anti-inflammation



3) D7 to D28: Tissue homeostasis and Repair

