Bone & Joint Research

Supplementary Material

10.1302/2046-3758.119.BJR-2022-0075.R1

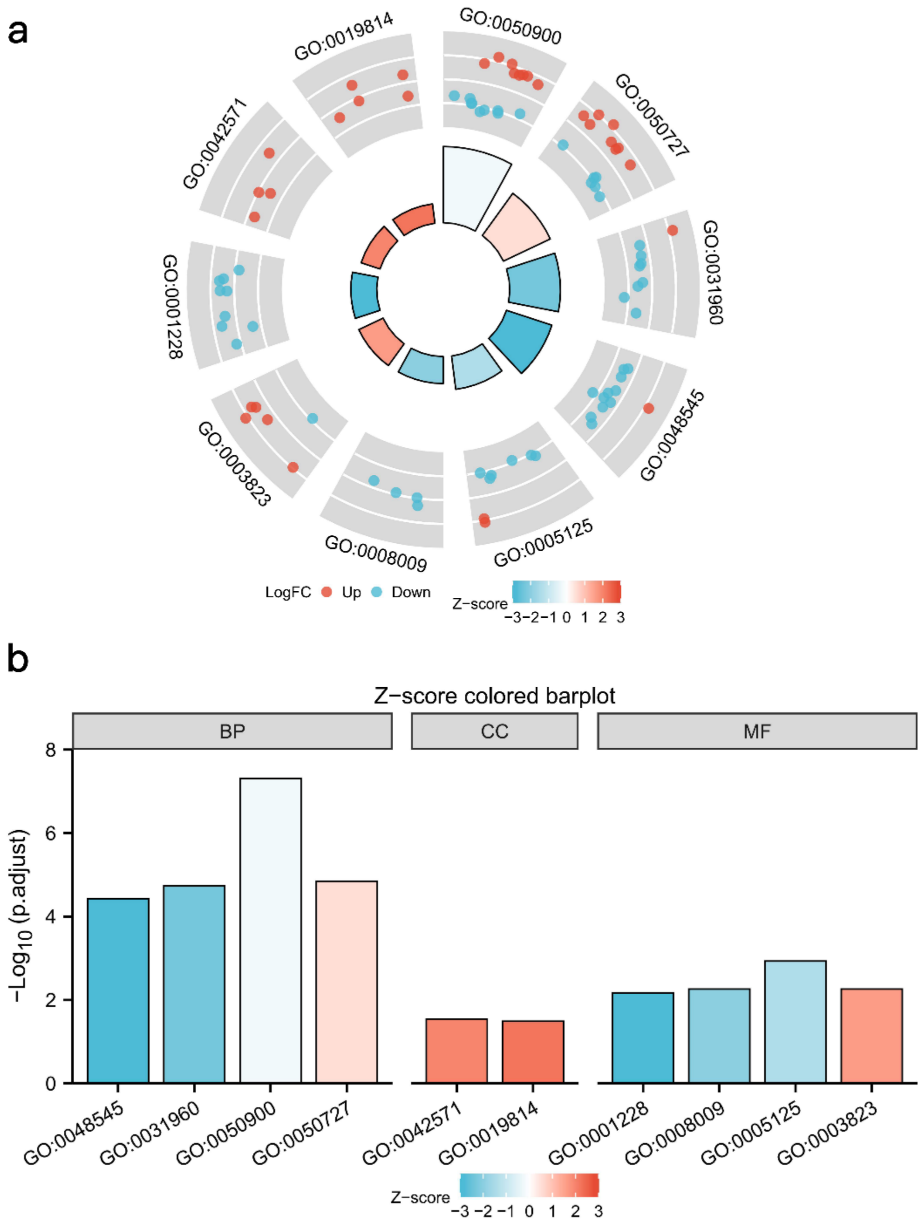

Fig a. a) The plot showing the gene ontology (GO) enrichment results for differentially expressed genes. b) The bar plot showing the Z-score results of the top ten GO terms. Z-scores were defined as follows: (upregulated genes – downregulated genes)/the square root of gene counts. BP, biological processes; CC, cell components; MF, molecular function.

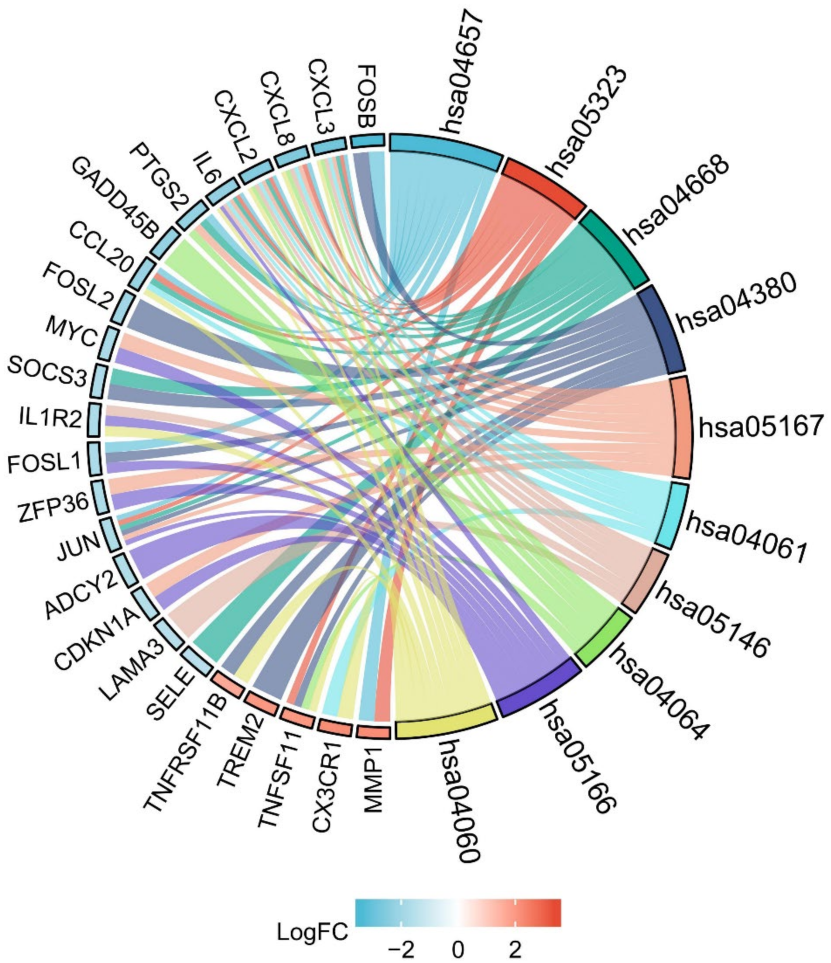

Fig b. The plot showing the relationships between differentially expressed genes and the top ten enriched Kyoto Encyclopedia of Genes and Genomes pathways.

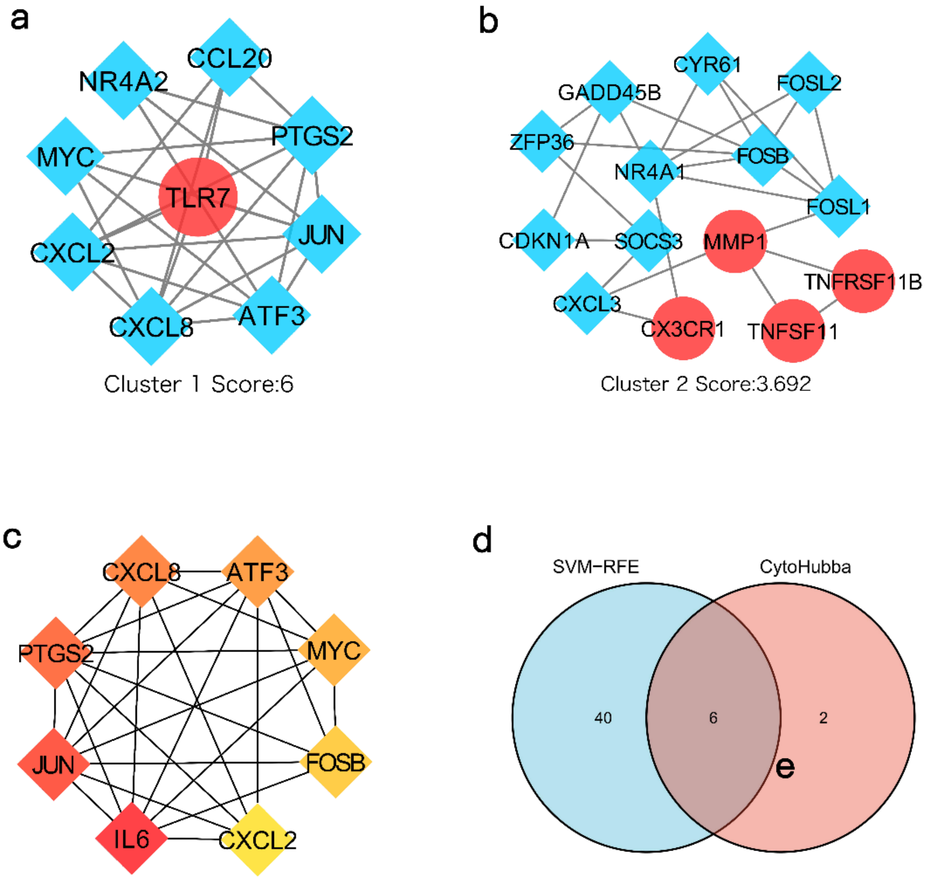

Fig c. a) The first cluster module extracted by MCODE which had the highest score (score: 6, 9, nodes and 24 edges). b) Second cluster (score: 3.692, 14 nodes and 24 edges). c) The top eight hub genes predicted by three algorithms (MCC, MNC, and Degree) of cytoHubba. d) Venn diagram shows the intersection of hub genes obtained by the two algorithms. ATF3, activating transcription factor 3; CDKN1A, cyclin dependent kinase inhibitor 1A; CXCL2, C-X-C motif ligand 2; CYR61, as known as CCN1, cellular communication network factor 1; IL6, interleukin-6; FOSB, FosB proto-oncogene, AP-1 transcription factor subunit; FOSL, FOS like, AP-1 transcription factor subunit; GADD45B, growth arrest and DNA damage inducible beta; JUN, Jun proto-oncogene, AP-1 transcription factor subunit; MMP1, matrix metalloproteinase 1; MYC, MYC proto-oncogene, bHLH transcription factor; NR4A1, nuclear receptor subfamily 4 group A member 1; PTGS2, prostaglandin-endoperoxide synthase 2; SOCS3, suppressor of cytokine signaling 3; SVM-RFE, support vector machine-recursive feature elimination; TLR7, toll like receptor 7; TNFSF11, TNF superfamily member 11; ZFP36, ZFP36 ring finger protein.

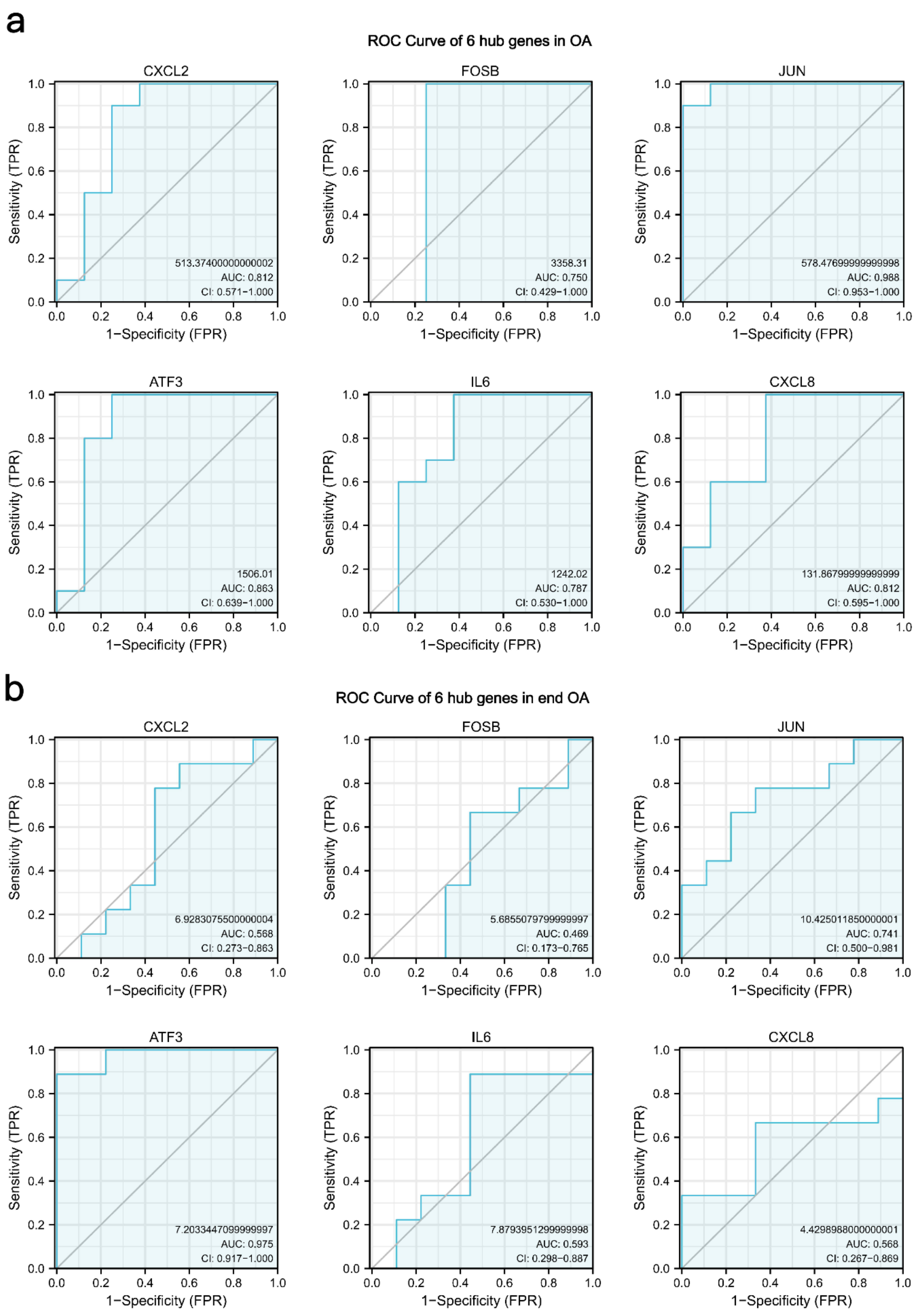

Fig d. Receiver operating characteristic (ROC) curve of six hub genes. a) ROC curve of six hub genes in osteoarthritis (OA) samples. b) ROC curve of six hub genes in end-stage OA samples. ATF3, activating transcription factor 3; AUC, area under the curve; CI, confidence interval; CXCL, C-X-C motif ligand; FOSB, FosB proto-oncogene, AP-1 transcription factor subunit; FPR, false positive rate; IL6, interleukin-6; JUN, Jun proto-oncogene, TPR, true positive rate.

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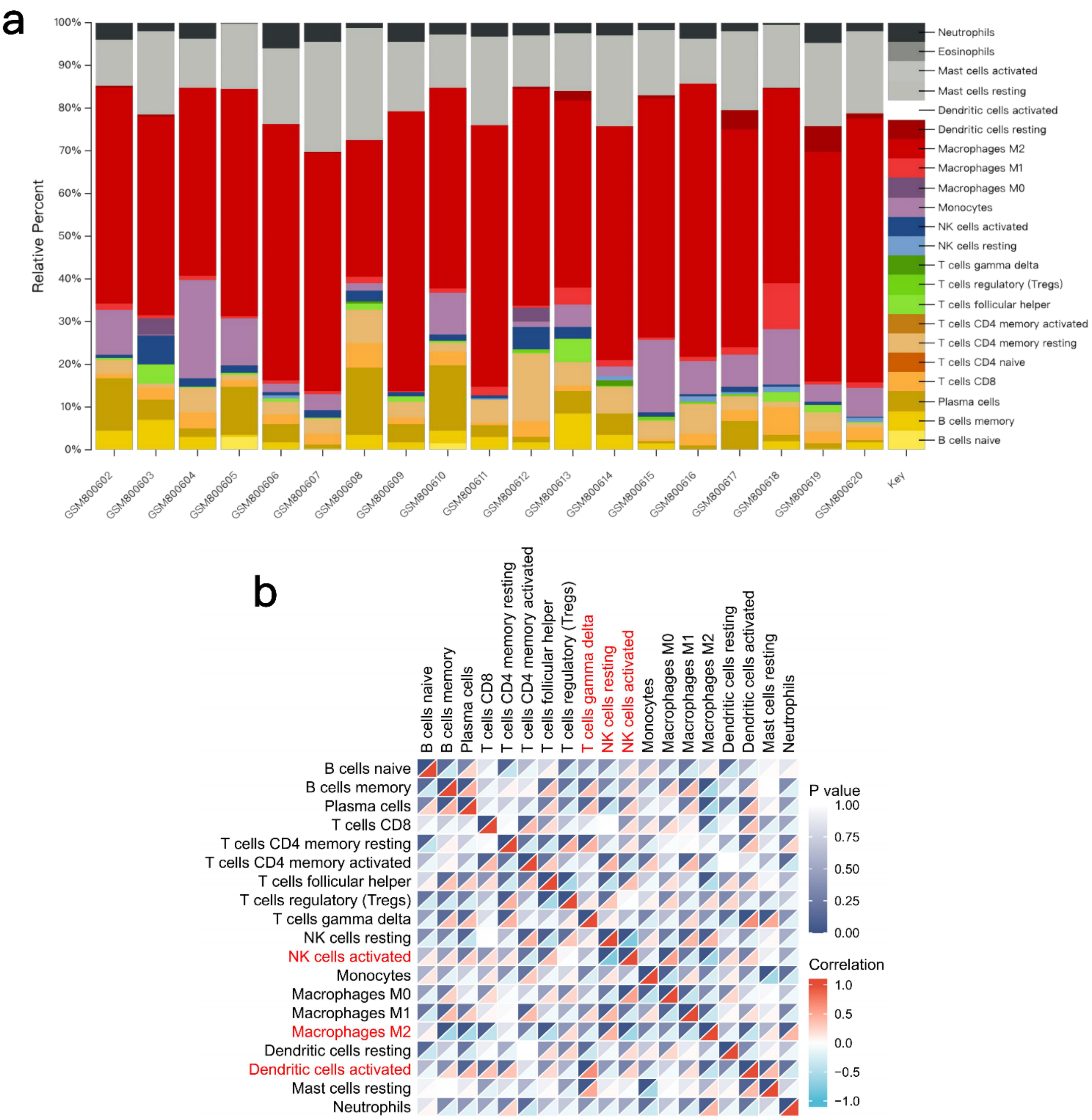

Fig e. Evaluation and visualization of the landscape of immune infiltration between early-stage osteoarthritis (OA) and end-stage OA. a) The relative percentage of the subpopulations of immune cells in 19 samples from GSE32317 datasets. b) Correlation heatmap of immune cells. Red represents a positive correlation and blue represents a negative correlation. The darker the colour, the stronger the correlation and the lower the p-value.