Supplementary Material for
Time-series RNA-Seq and data-driven network inference unveil dynamics of cell activation, survival and crosstalk in Chronic Lymphocytic Leukaemia *in vitro* models

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Day 1

Day 4   macrophages

Day 8   macrophages
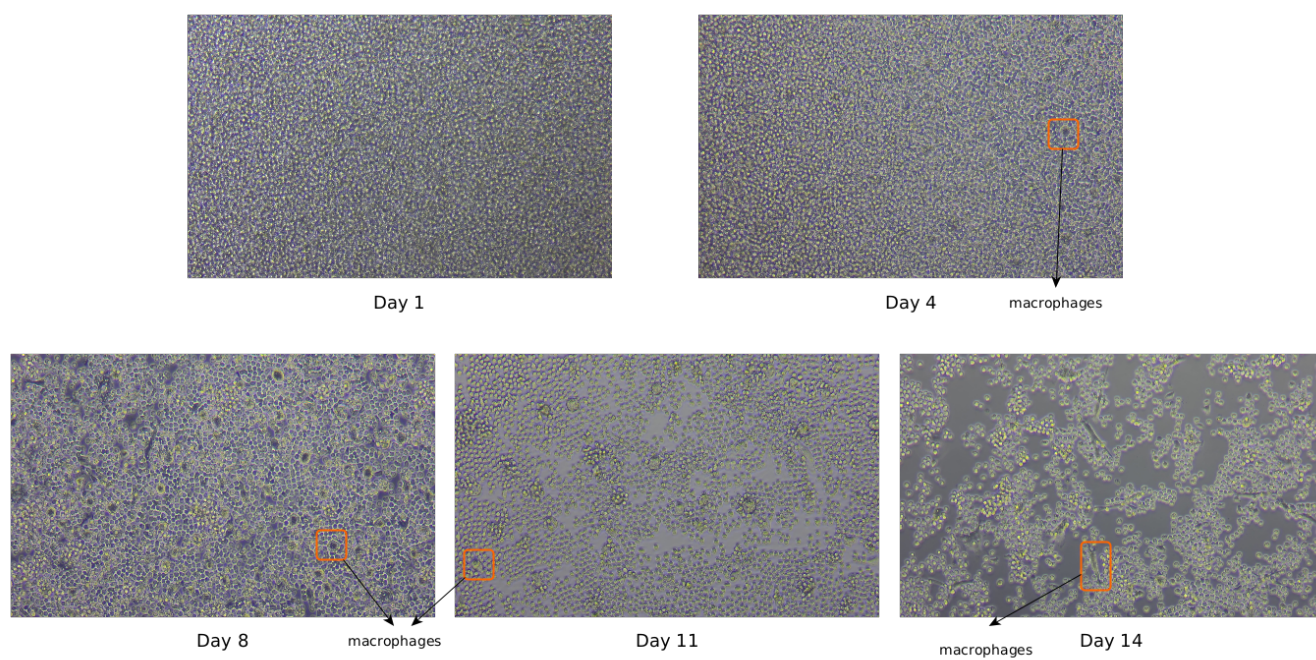
Day 11

macrophages   Day 14

Figure S1. Microscopy images of the *in vitro* culture. After D8, the formation of macrophages is complete.
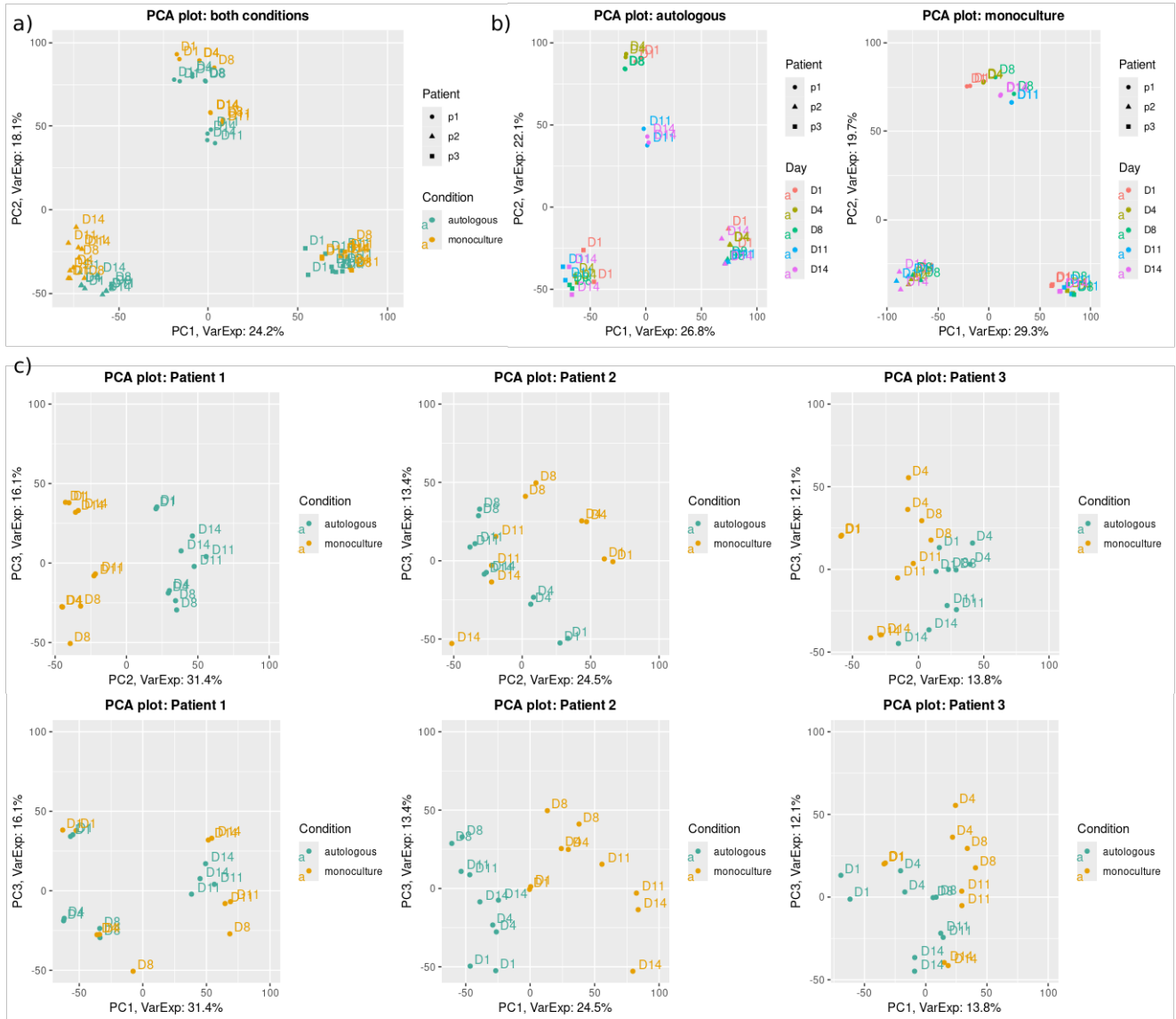
Figure S2. Principal Component Analysis of autologous and monoculture, showing the high heterogeneity between patients.
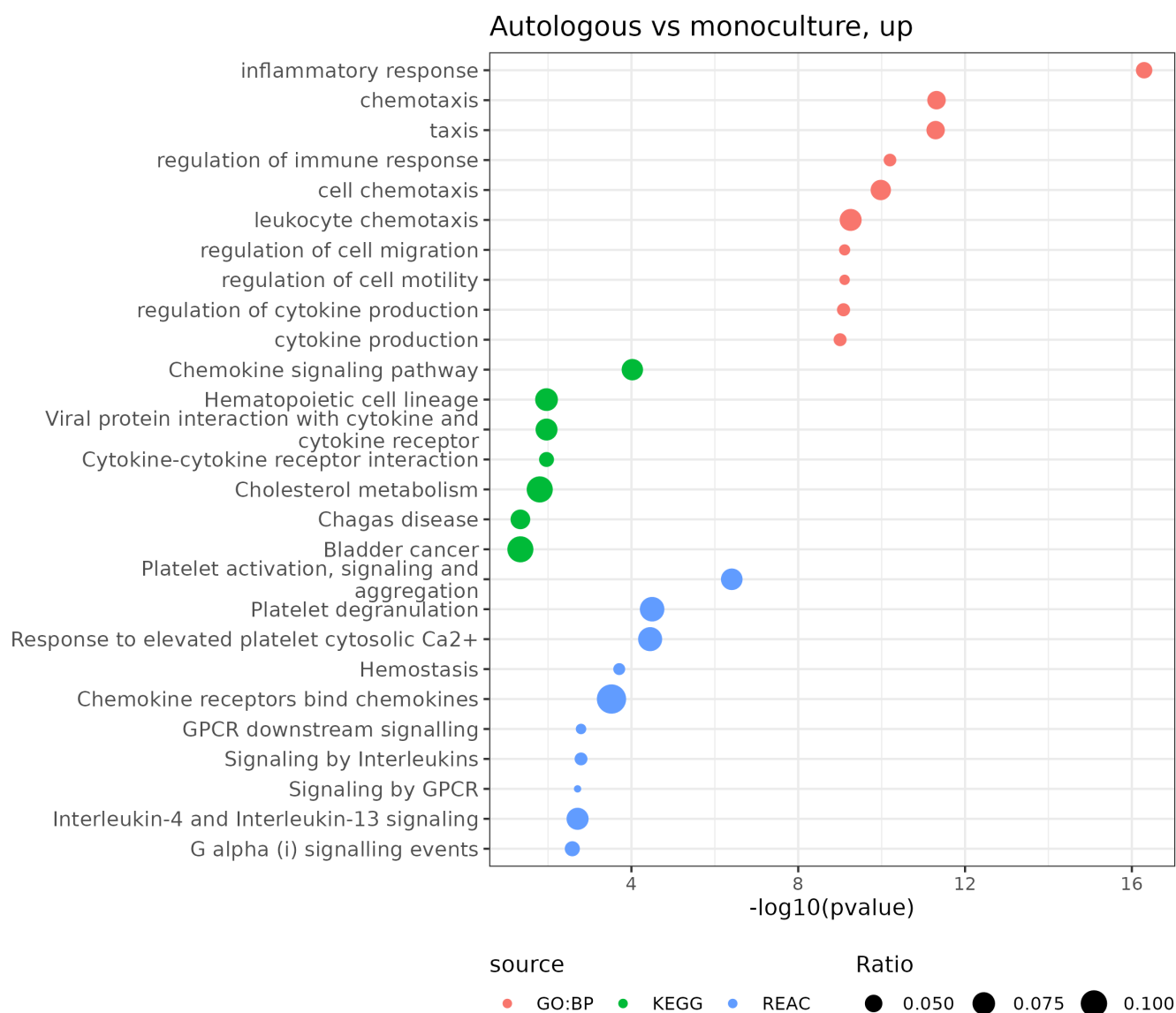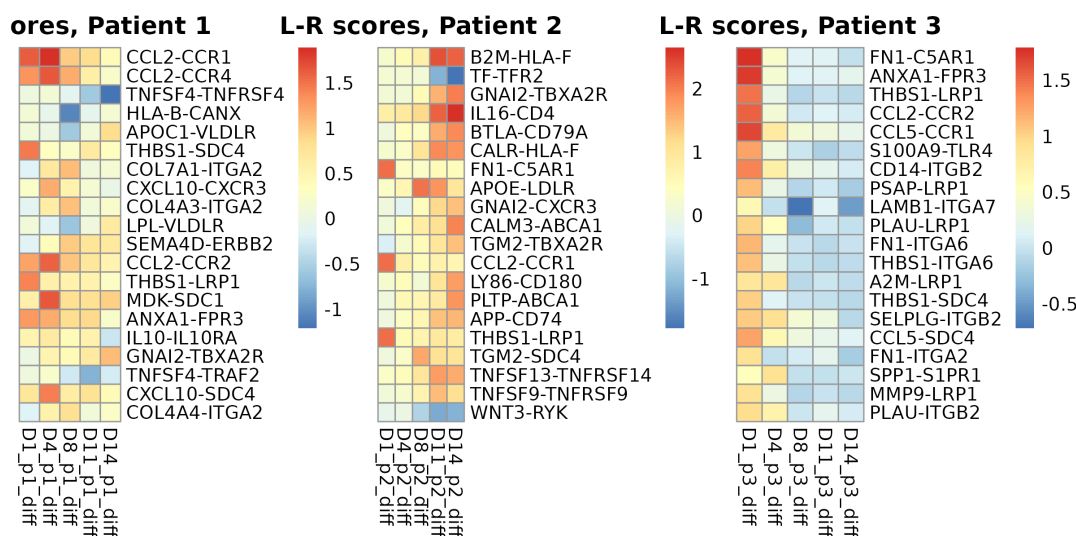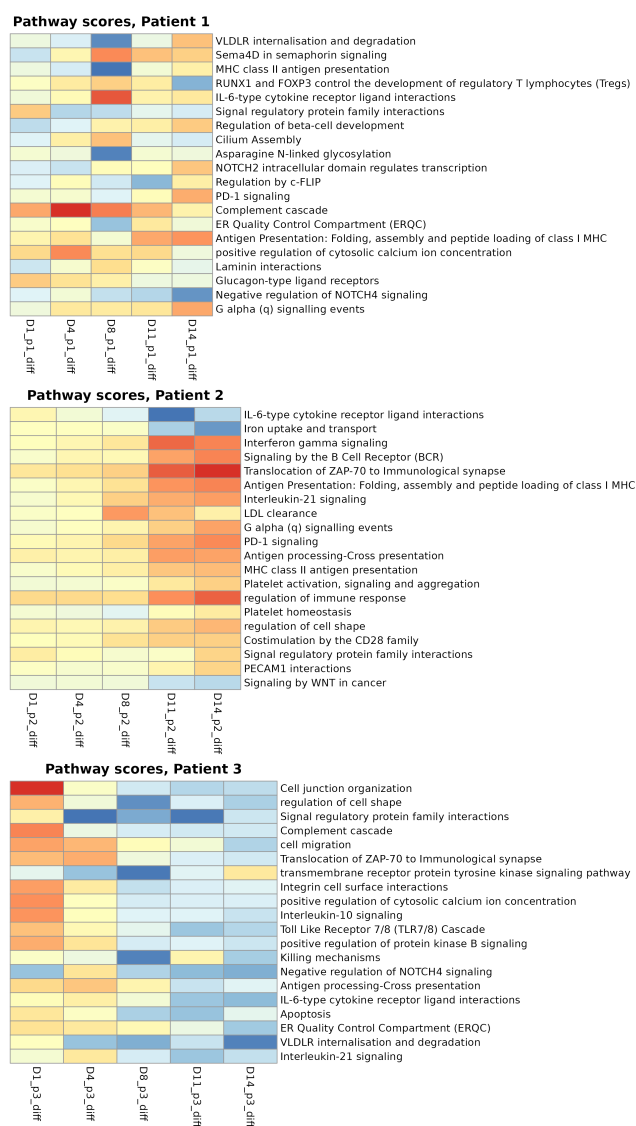
Autologous vs monoculture, up

Figure S3. Pathway enrichment analysis of the up-regulated genes in the autologous vs monoculture.

(a) Top 20 LR pairs for each patient, selected based on the variance of LR scores.

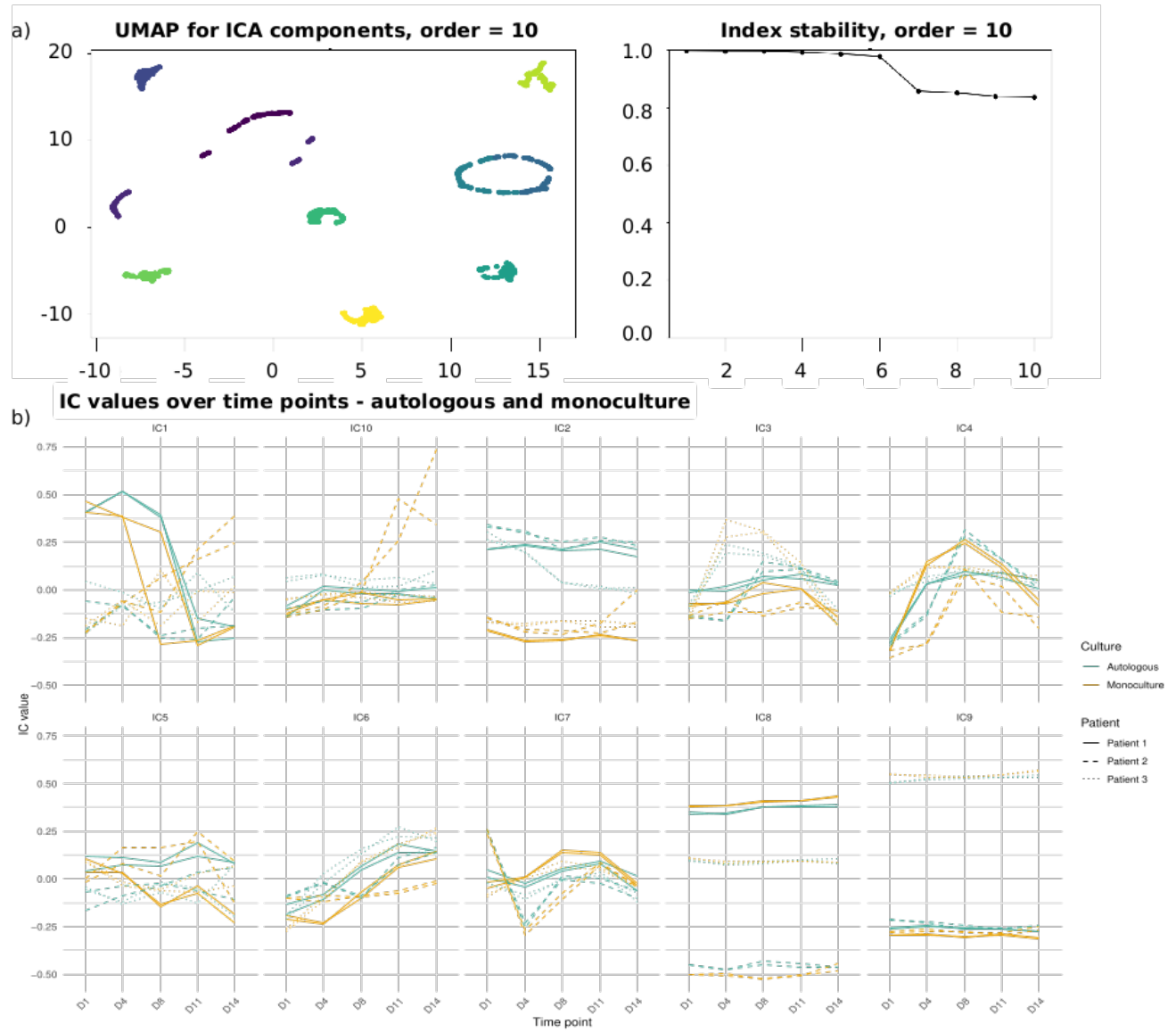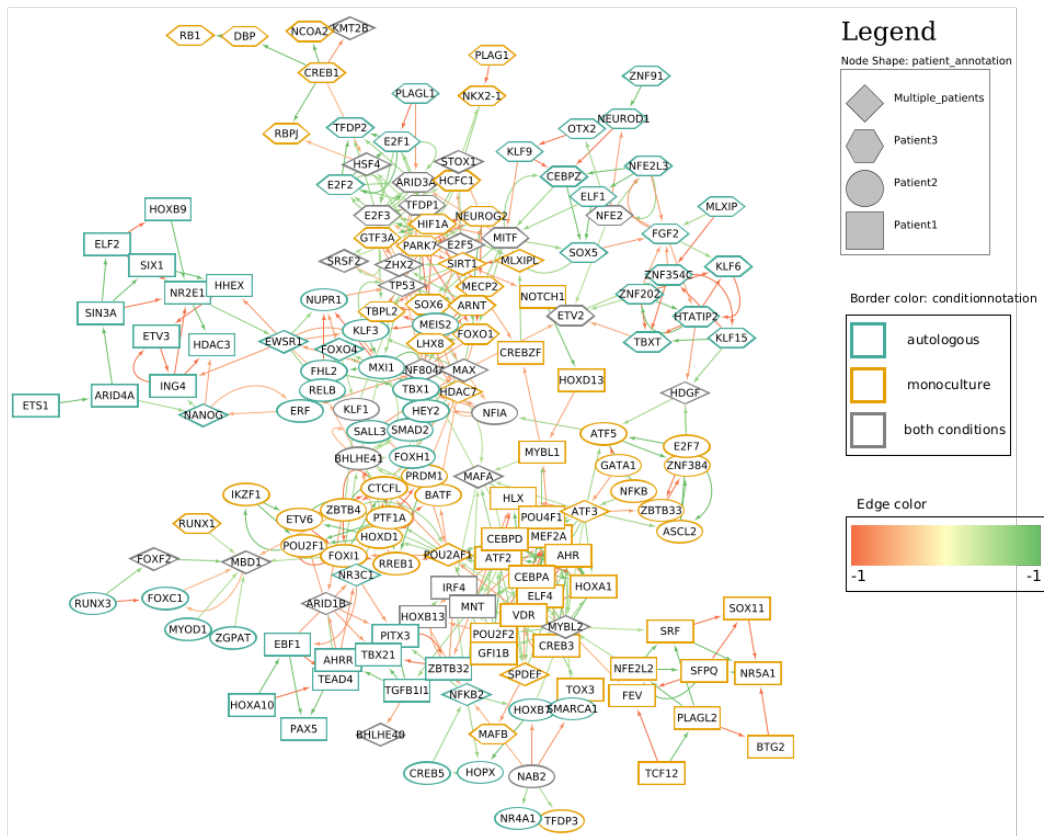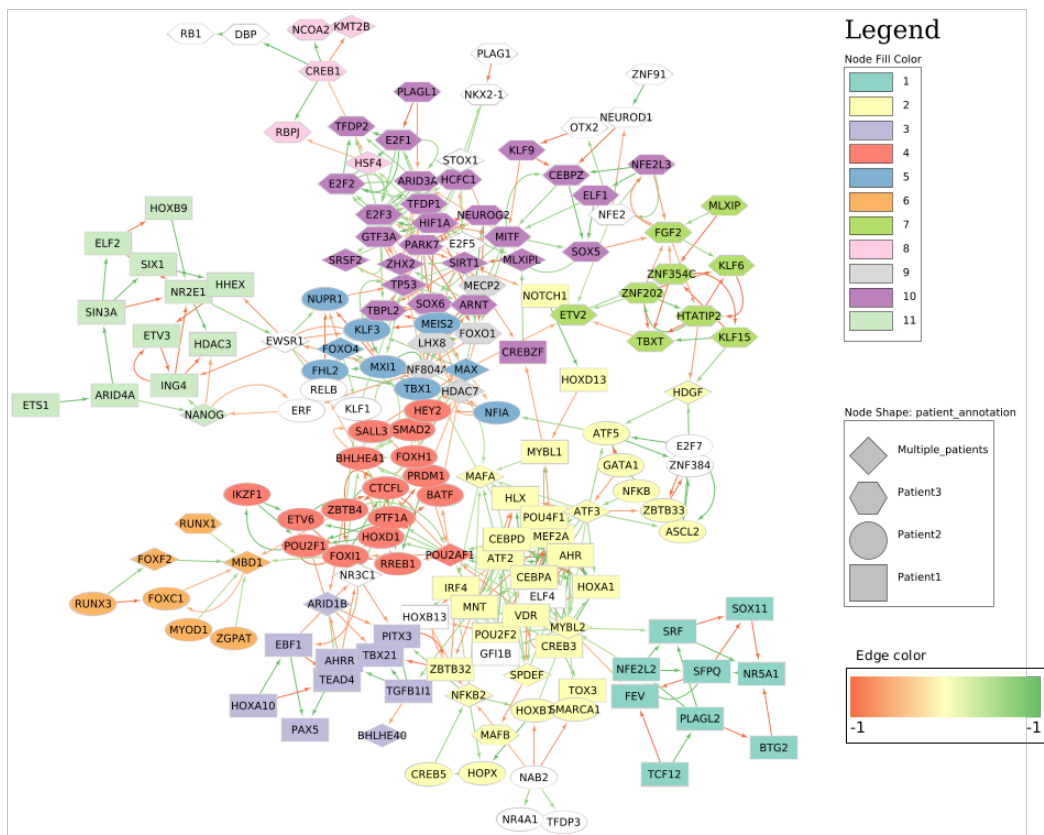**(b)** Top 20 pathways for each patient, selected based on the variance of pathway scores.

Figure S4

Figure S5. (a) Index stability - autologous and monoculture. **(b)** Heatmap of the metasample matrix from ICA. **(c)** ICA - TF activity score.

Figure S6. Gene set enrichment analysis on the independent components.

(a) TF-TF network with nodes coloured by condition.

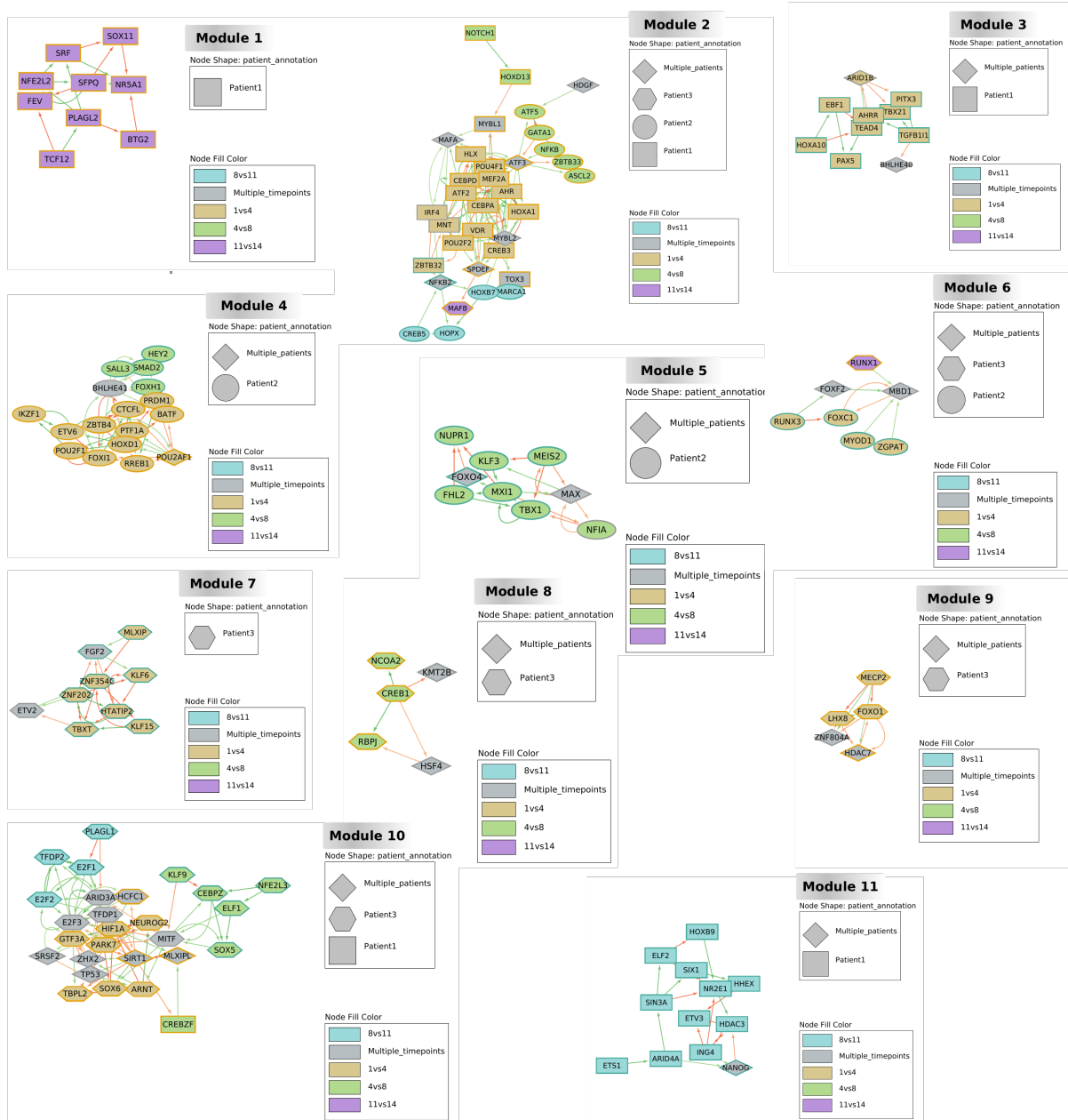**(b)** TF-TF network with nodes coloured by module.

Figure S7

Figure S8. Annotation of modules with nodes' features.

Figure S9. Pathway enrichment analysis of each cluster of TFs (including their targets).