***Supplementary Material***

**Supplementary file S1 – R Script.**

# Affymetrix

library(affy)

library(hgu133plus2cdf)

celfiles <- list.files("raw", full.names=TRUE)

affy.raw <- ReadAffy(filenames = celfiles)

print("CEL files loaded")

print(affy.raw)

##QC - Affy

library(simpleaffy)

library(annotation)

library(arrayQualityMetrics)

affy.raw <- ReadAffy(filenames = celfiles)

affy.qc <- qc(affy.raw)

plot(affy.qc)

library(arrayQualityMetrics)

affy.raw <- ReadAffy(filenames = celfiles)

arrayQualityMetrics(affy.raw, outdir = "qc")

##this wrote pdf report to "qc" directory

##CDF

affy.raw@cdfName <- "HG-U133\_Plus\_2"

library(simpleaffy)

library(annotation)

library(arrayQualityMetrics)

affy.qc.data <- ReadAffy(filenames = celfiles)

pdf(file=qc.file)

affy.qc <- qc(affy.qc.data)

plot(affy.qc)

qc.file <- "affy\_qc.pdf"

dev.off()

##GCRMA Normalization

library(gcrma)

affy.data <- gcrma(affy.raw)

print("GCRMA summarization finished")

print(affy.data)

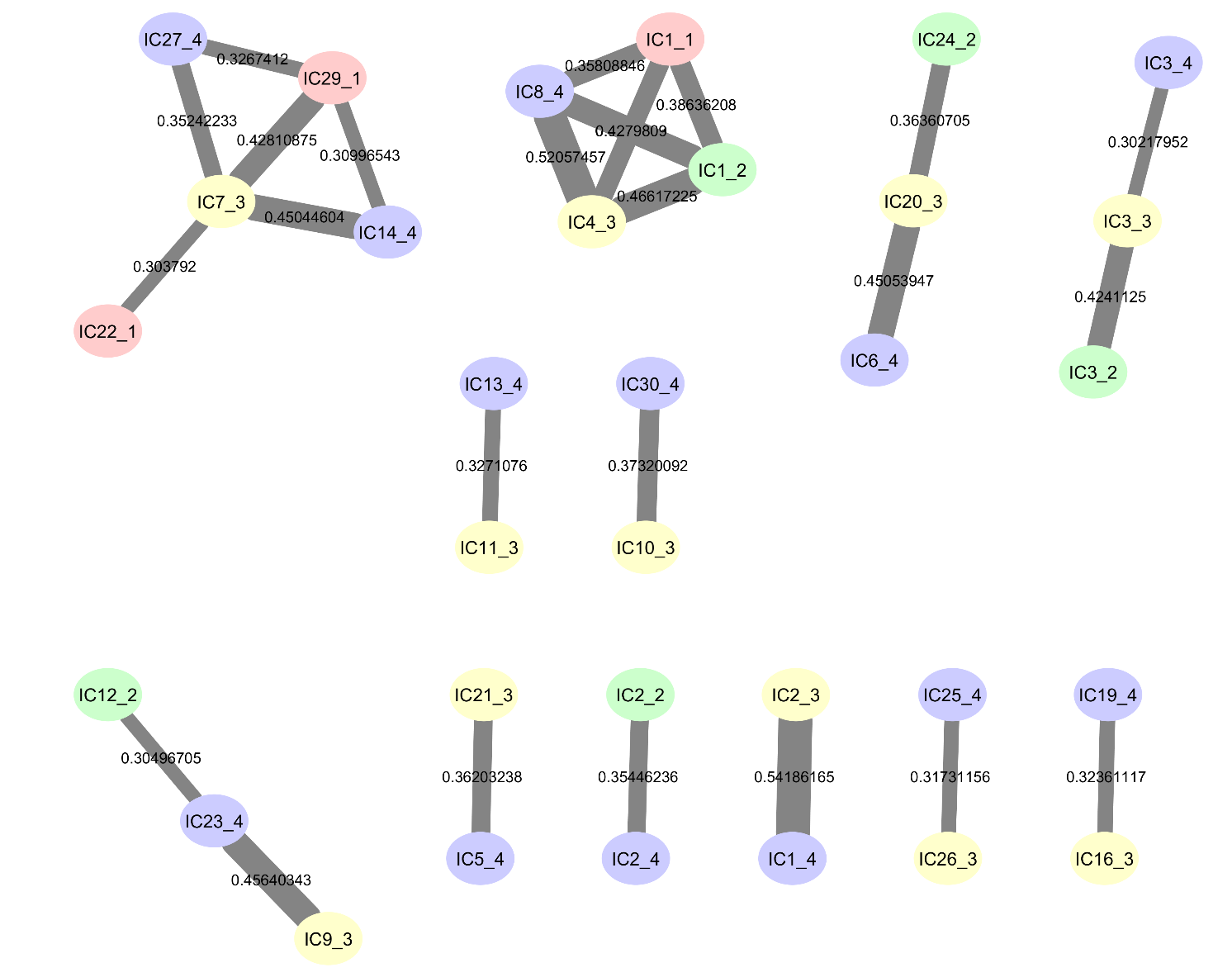
print(head(exprs(affy.data)))

write.exprs(affy.data, "affy\_gcrma.txt")

**Supplementary file S2 – Correlation values between ICs (R>0.3).**

|  |  |
| --- | --- |
| **IC interactions** | **Correlation Value** |
| IC22\_1\_\_IC7\_3 | 0.303792 |
| IC26\_3\_\_IC25\_4 | 0.31731156 |
| IC12\_2\_\_IC23\_4 | 0.30496705 |
| IC2\_4\_\_IC2\_2 | 0.35446236 |
| IC2\_4\_\_IC1\_3 | 0.5461127 |
| IC29\_1\_\_IC27\_4 | 0.3267412 |
| IC8\_4\_\_IC4\_3 | 0.52057457 |
| IC2\_3\_\_IC1\_4 | 0.54186165 |
| IC3\_3\_\_IC3\_4 | 0.30217952 |
| IC7\_3\_\_IC29\_1 | 0.42810875 |
| IC14\_4\_\_IC29\_1 | 0.30996543 |
| IC7\_3\_\_IC14\_4 | 0.45044604 |
| IC10\_3\_\_IC30\_4 | 0.37320092 |
| IC11\_3\_\_IC13\_4 | 0.3271076 |
| IC19\_4\_\_IC16\_3 | 0.32361117 |
| IC23\_4\_\_IC9\_3 | 0.45640343 |
| IC1\_1\_\_IC4\_3 | 0.3711783 |
| IC1\_1\_\_IC8\_4 | 0.35808846 |
| IC1\_2\_\_IC1\_1 | 0.38636208 |
| IC1\_2\_\_IC4\_3 | 0.46617225 |
| IC1\_2\_\_IC8\_4 | 0.4279809 |
| IC27\_4\_\_IC7\_3 | 0.35242233 |
| IC20\_3\_\_IC24\_2 | 0.36360705 |
| IC20\_3\_\_IC6\_4 | 0.45053947 |
| IC3\_2\_\_IC3\_3 | 0.4241125 |
| IC21\_3\_\_IC5\_4 | 0.36203238 |

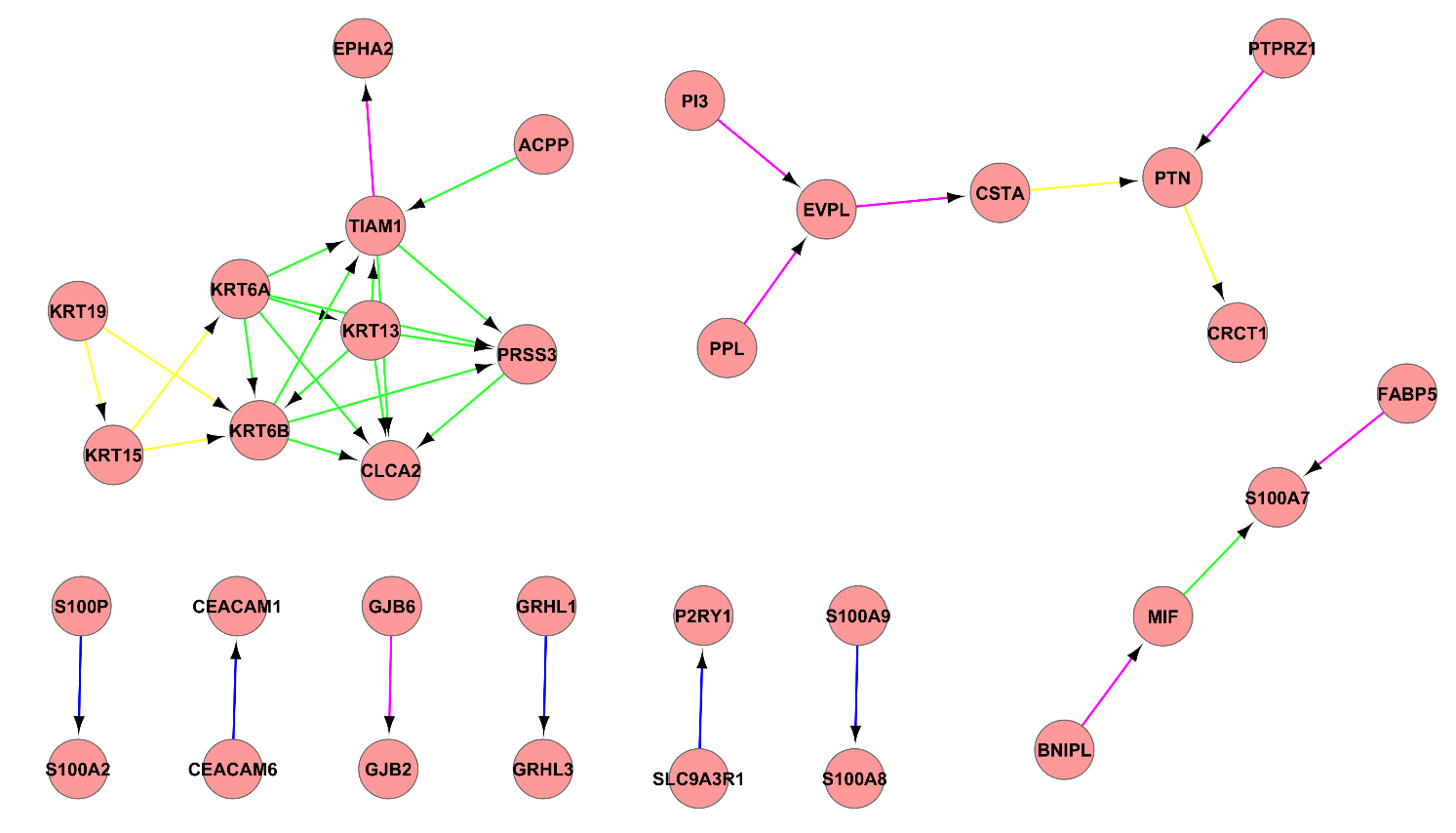
**Supplementary file S3 – Correlation graph**





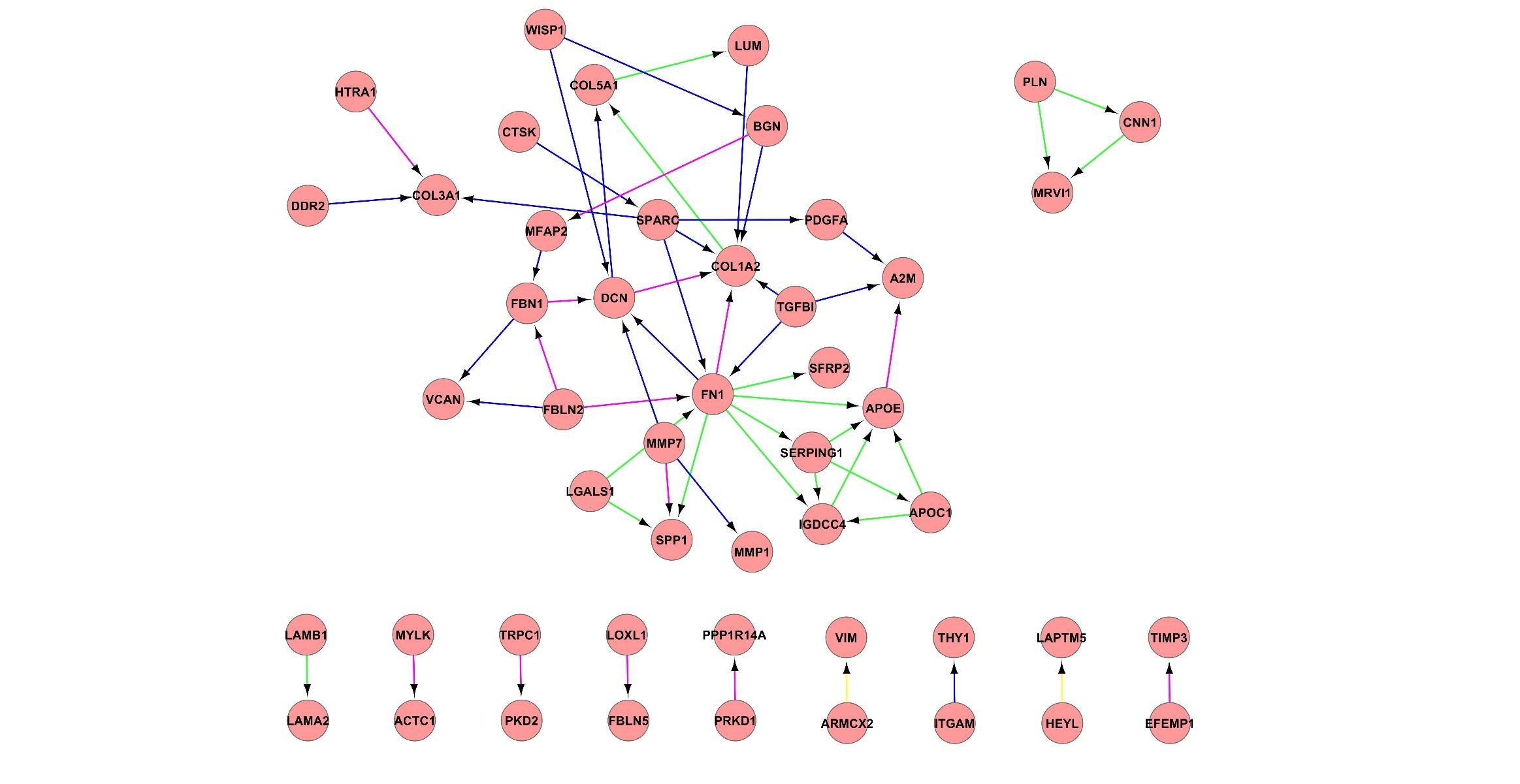
**The correlation graph between decompositions into 30 ICs was built with absolute correlation values exceeding 0.3.**

The correlation graph is a connected structure in the form of clicks or pseudo-clicks, the nodes of which are correlated independent components. Each color corresponds to a specific cancer dataset: pink – GSE26886, green – GSE69925, yellow – GSE32701, blue – GSE21293. In the correlation graph with correlation coefficients R>0.3 pseudo-clips were observed, which are characterized by multiple relationships with independent components from different sets. The thickness of the edges between the nodes of the clique depends on the correlation coefficient (the larger the coefficient, the greater the thickness of the edges). The 12 pseudo-clicks were selected for constructing signal pathways for gene interaction.

**Supplementary file S4. PPI network between the IC1\_2 and IC8\_4**

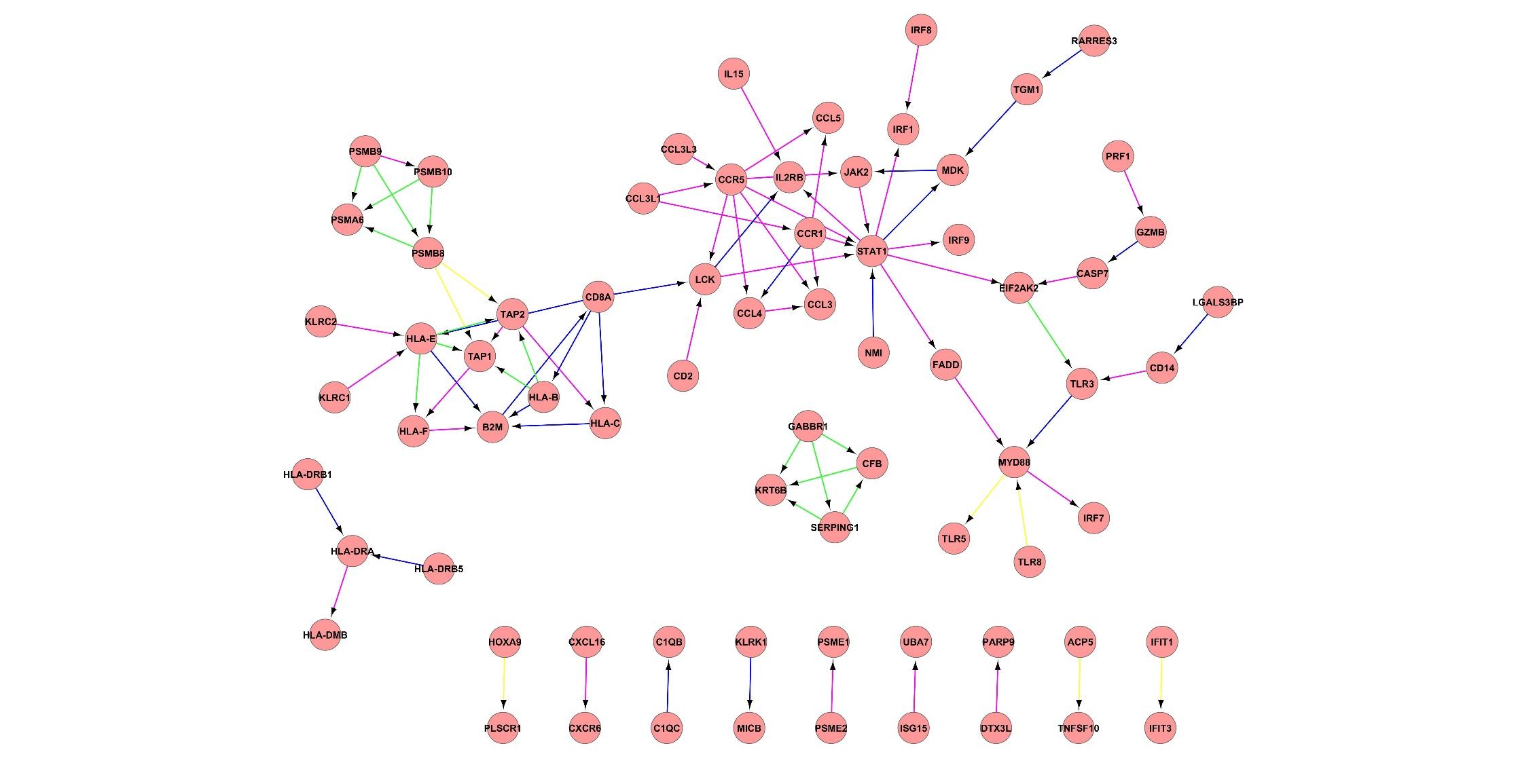
**PPI network between the IC1\_2 and IC8\_4.** Proteins are illustrated with circles and directed interactions are illustrated with edges. Color of the edges represents the type of experiments used in HPRD database: blue - in vitro, red – in vivo, green – Y2H. This representation was obtained using Cytoscape software according to the HPRD database.

**Supplementary file S5. PPI network between the IC20\_3, IC24\_2 and IC6\_4**

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**PPI network between the IC20\_3, IC24\_2, and IC6\_4.** Proteins are illustrated with circles and directed interactions are illustrated with edges. Color of the edges represents the type of experiments used in HPRD database: blue - in vitro, red – in vivo, green – Y2H. This representation was obtained using Cytoscape software according to the HPRD database.

**Supplementary file S6. PPI network between the IC5\_4 and IC21\_3**

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**PPI network between the IC5\_4 and IC21\_3.** Proteins are illustrated with circles and directed interactions are illustrated with edges. Color of the edges represents the type of experiments used in HPRD database: blue - in vitro, red – in vivo, green – Y2H. This representation was obtained using Cytoscape software according to the HPRD database.

**Supplementary file S7. GSEA and ToppGene analysis results**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Clique | Components | GSEA | ToppGene | | |
| BP | MF | CC |
| 1 | IC3\_2, IC3\_3, and IC3\_4 | HALLMARK\_COMPLEMENT, HALLMARK\_INTERFERON\_GAMMA\_RESPONSE, HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION | [humoral immune response](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0006959), [immune response-activating cell surface receptor signaling pathway](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0002429), cornified envelope assembly | [Immunoglobulin receptor binding](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0034987), [antigen binding](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0003823), [protein-glutamine gamma-glutamyltransferase activity](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0003810) | [immunoglobulin complex](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0019814), [cornified envelope](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0001533) |
| 2 | IC7\_3 and IC14\_4 | HALLMARK\_G2M\_CHECKPOINT,  HALLMARK\_MITOTIC\_SPINDLE | [chromosome segregation](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0007059) | [receptor ligand activity](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0048018) | [mitochondrial protein complex](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0098798), [neutrophil migration](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:1990266) |
| 3 | IC1\_2 and IC8\_4 | HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION,  HALLMARK\_ESTROGEN\_RESPONSE\_LATE | [snRNA 3'-end processing](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0034472) |  | [integrator complex](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0032039) |
| 4 | IC20\_3, IC24\_2 and IC6\_4 | HALLMARK\_INTERFERON\_GAMMA\_RESPONSE, HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION, HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB | [extracellular matrix organization](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0030198), [defense response to virus](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0051607) | [extracellular matrix structural constituent](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0005201) | [collagen-containing extracellular matrix](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0062023) |
| 5 | IC5\_4 and IC21\_3 | HALLMARK\_INTERFERON\_ALPHA\_RESPONSE,  HALLMARK\_INFLAMMATORY\_RESPONSE, HALLMARK\_COMPLEMEN, HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION, HALLMARK\_KRAS\_SIGNALING\_UP | [type I interferon signaling pathway](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0060337), [defense response to virus](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0051607) | [chemokine receptor binding](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0042379) | [MHC protein complex](http://www.ebi.ac.uk/ego/DisplayGoTerm?id=GO:0042611) |