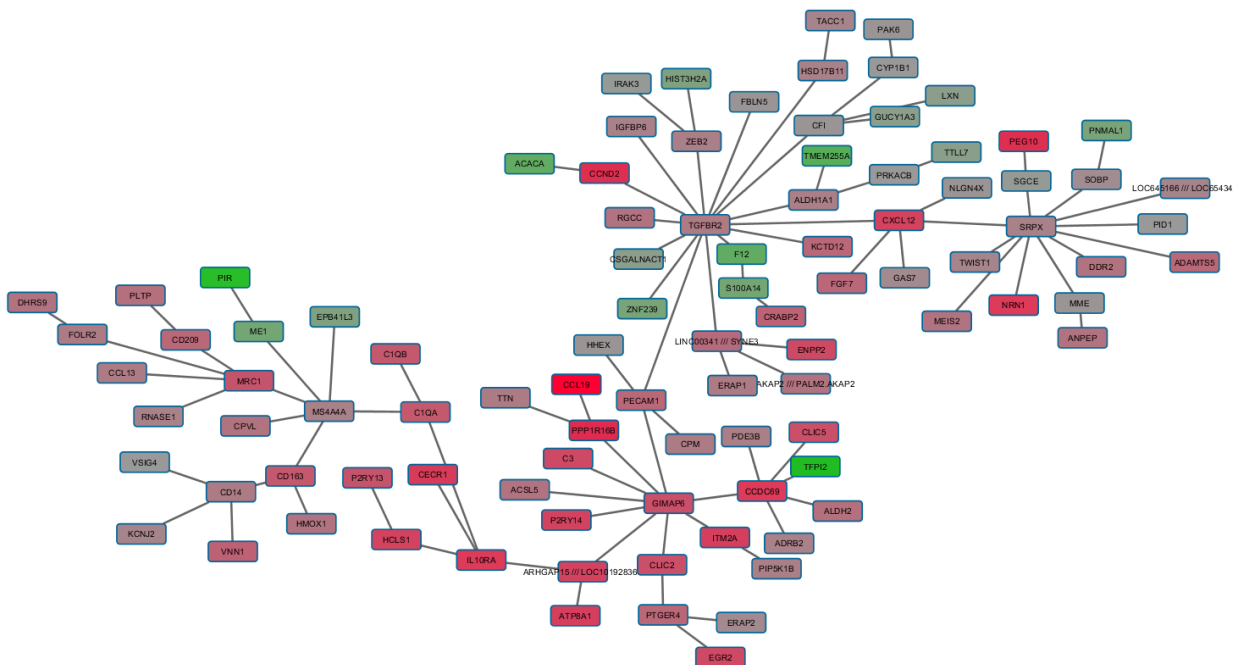
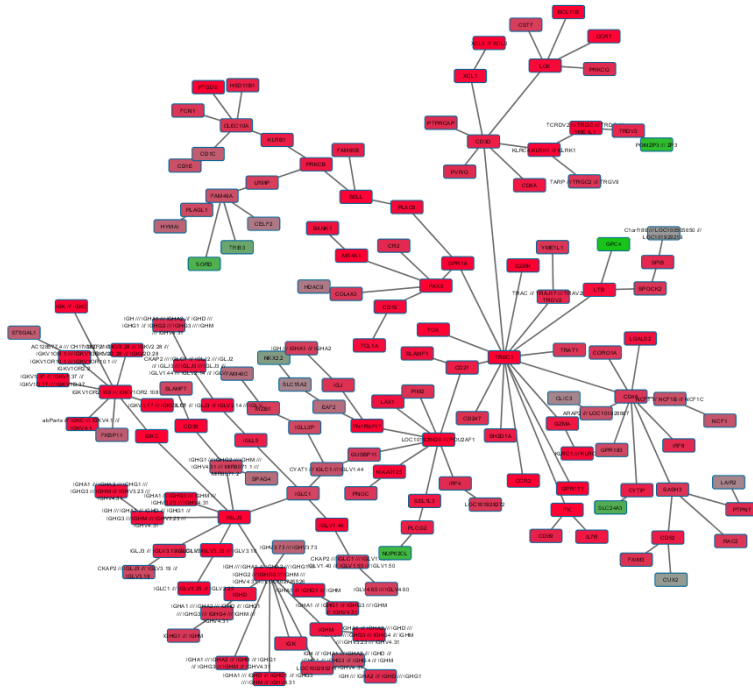


Probabilistic graphical models relate immune status with response to neoadjuvant chemotherapy in breast cancer

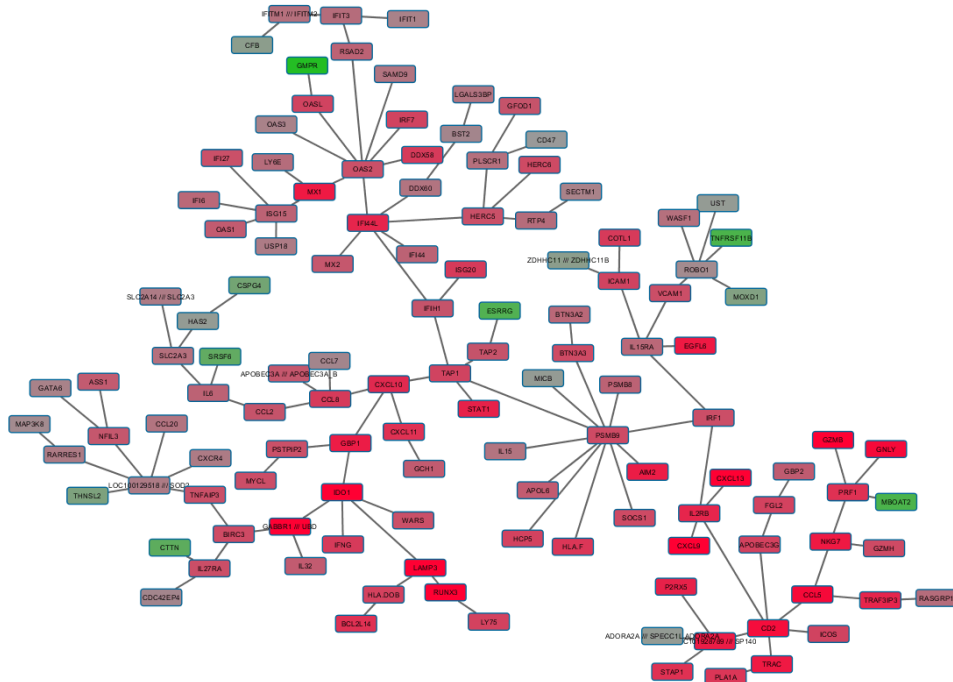
SUPPLEMENTARY MATERIALS



Supplementary Figure 1: Detail of “Immune response (MHCII)” (node 9) in Complete Response tumors. Genes with an expression below 0 were represented in green; genes with an expression around 0 were represented in grey and genes with an expression above zero were represented in red.



Supplementary Figure 2: Detail of “Immune response (B cell)” (node 11) in Complete Response tumors. Genes with an expression below 0 were represented in green; genes with an expression around 0 were represented in grey and genes with an expression above zero were represented in red.



Supplementary Figure 3: Detail of “Immune response (Interferon)” (node 12) in Complete Response tumors. Genes with an expression below 0 were represented in green; genes with an expression around 0 were represented in grey and genes with an expression above zero were represented in red.



Supplementary Figure 4: Detail of “Cell Cycle 1” (node 17) in Progressive Disease tumors. Genes with an expression below 0 were represented in green; genes with an expression around 0 were represented in grey and genes with an expression above zero were represented in red.



Supplementary Figure 5: Detail of “Cell Cycle 2 (node 18) in Progressive Disease tumors. Genes with an expression below 0 were represented in green; genes with an expression around 0 were represented in grey and genes with an expression above zero were represented in red.