

The figure displays a large-scale gene co-expression network. Nodes are categorized by color based on their biological or clinical significance:

- Red nodes:** Primarily related to Kinesin-like family proteins.
- Orange nodes:** Associated with drugs, such as Aspirin and Fluorouracil.
- Green nodes:** Linked to diseases like Myeloid Leukemia, Chronic Liver carcinoma, Sepsis, and Septicemia.
- Blue nodes:** Represent molecular functions like nucleoside-triphosphatase activity and glucose binding.
- Yellow nodes:** Correspond to biological processes such as leukocyte mediated immunity, neutrophil activation, and granulocyte activation.
- Purple nodes:** Involved in the immune system, including myeloid leukemia-mediated immunity and neutrophil activation.
- Grey nodes:** Other genes and pathways not specifically highlighted by color.

The network illustrates how these genes interact and co-express, providing insights into the underlying biology of the studied conditions.

Supplementary Figure 1. Genes associated with BM derived CD11b+ cells by gene ontology. This figure was derived as in Figure 4. Genes directly associated with BM derived CD11b+ cells in the co-expression atlas category are shown highlighted in yellow, linked directly to the 5 co-expression categories (also in yellow).