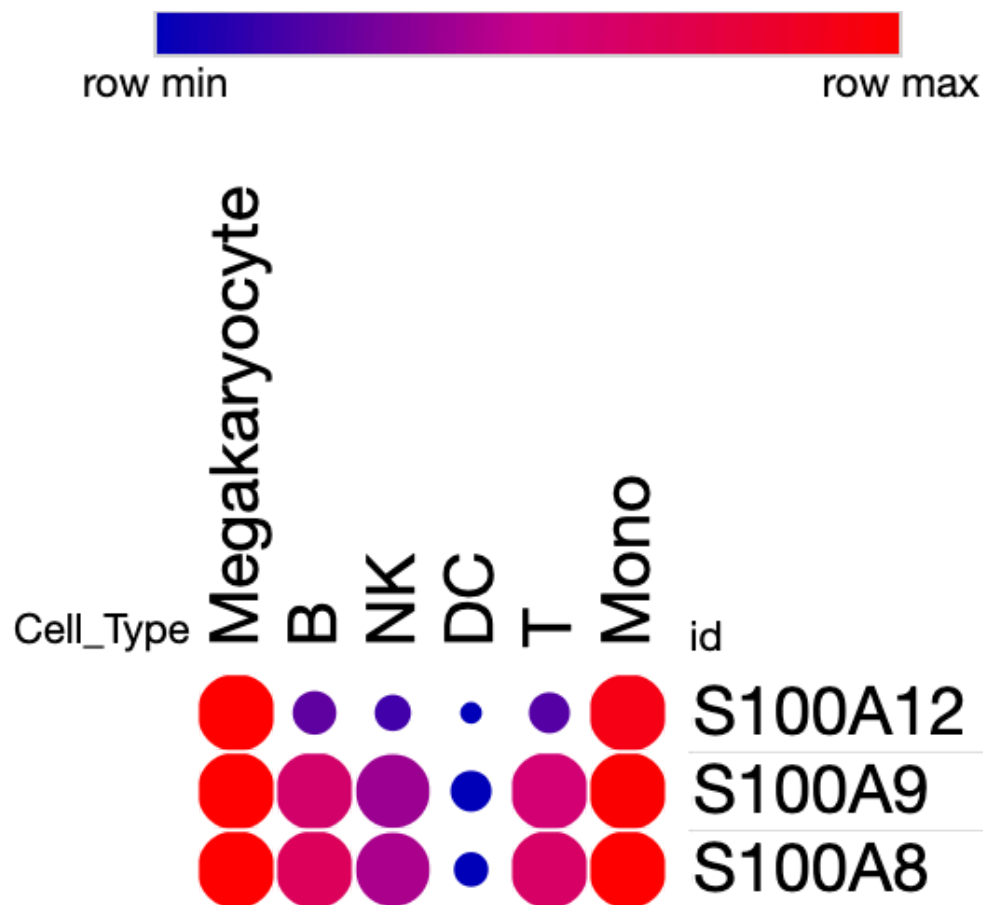


Results of analyzing the expression of three key inflammatory genes — **S100A12**, **S100A9**, and **S100A8** — across various immune cell types using single-cell RNA-seq data. These genes are part of the S100 protein family, well-known for their roles in inflammation, innate immunity, and particularly in conditions like sepsis.

The data is visualized using a dot plot heatmap, where:

- Color shows the average expression level (red = high, blue = low),
- Dot size shows the percentage of cells in each cell type expressing the gene.



- **Strong, consistent expression in Monocytes**
 - All three genes — S100A12, S100A9, and S100A8 — are highly expressed in monocytes
 - The dots are large and red, meaning:
 - Most monocytes express these genes.
 - They express them at a high level.

- This is biologically expected: monocytes are major players in the immune response and produce calgranulins like S100A8/A9/A12 during infections and inflammation, especially in sepsis.

- **Megakaryocytes show notable expression**

- Interestingly, megakaryocytes also show strong expression (large red dots).
- While their primary function is platelet production, they can also participate in inflammation and interact with immune cells, especially in septic environments.
- This suggests a role in immune activation or emergency hematopoiesis in response to infection.

- **T cells and B cells show moderate expression**

- For T cells and B cells, the dots are moderate in size and color intensity, especially for S100A8 and S100A9.
- This indicates that some subpopulations of T and B cells are expressing these genes — not all, and not at the highest levels.
- This might reflect inflammatory activation of these adaptive immune cells during sepsis, as they respond to innate immune signals.
- T and B cells are adaptive immune cells, and while they may express S100A12 in some rare or activated contexts, it's generally not a signature gene for them.

- **Natural Killer (NK) Cells**

S100A8 & S100A9: Dot Size: Large → A high percentage of NK cells are expressing these genes.
Color: Blueish → Low average expression level, but widely expressed.

S100A12: Dot Size: Small → Few NK cells express this gene. Color: blue → Very low expression overall.

Conclusion for NK: S100A8 and S100A9 are broadly expressed in NK cells, though not at high levels (widespread but weak expression). S100A12 is rarely expressed and very low in NK cells.

- **Dendritic Cells (DC):**

S100A8, S100A9, S100A12:

- Dot Size: Tiny to small → Only a small fraction of DCs express these genes.
- Color: Deep blue → Extremely low expression levels.

Conclusion for DCs: Very limited expression of all three genes, both in terms of how many cells express them and how strongly they are expressed.



Conclusion:

The dot plot analysis reveals distinct expression patterns of the S100A8, S100A9, and S100A12 genes across immune cell types. These genes are most abundantly and strongly expressed in monocytes and megakaryocytes, suggesting a key role in innate immune activation during bacterial sepsis. In contrast, dendritic cells (DCs) show minimal expression of all three genes, indicating limited involvement in S100-mediated responses.

Natural killer (NK) cells widely express S100A8 and S100A9, but at low per-cell expression levels, while S100A12 is scarcely expressed in NK cells. B and T cells show moderate dot sizes but relatively lower expression intensities, indicating minor contributions.

These findings highlight that monocytes are the dominant source of S100A-family gene expression in peripheral blood mononuclear cells (PBMCs), consistent with their role as early responders in the innate immune response to sepsis.