Expression of mesenchyme-specific gene signatures by follicular dendritic cells: insights from the meta-analysis of microarray data from multiple mouse cell populations

Neil A. Mabbott, J. Kenneth Baillie, Atshushi Kobayashi, David S. Donaldson, Hitoshi Ohmori, Sunny Yoon, Arnold S. Freedman, Tom C. Freeman, Kim M. Summers

Supplementary Fig. 1: The average expression profile of the top 50 clusters over the 85 samples used in our analysis. (Pearson r = 0.85, MCL = 2.2). Samples are grouped according to cell type: **1**, mesenchyme-lineage cells, embryonic stem cells, neurones; **2**, bone marrow progenitor cells; **3**, splenic classical DC and plasmacytoid DC; **4**, phagocytes (bone marrow-derived, peritoneal, RAW-264, osteoclasts, microglia); **5**, granulocytes, NK cells and mast cells; **6**, B and T lymphocytes; **7**, tissues (bone marrow, spleen and lymph nodes); **8**, FDC.









