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Methods: BM samples from 6 SLE patients and 5 healthy controls and 2 umbilical cord blood (CB) samples were used. CD34+ cells were isolated from BM and CB samples and single cell capture and RNA extraction were performed on Fluidigm C1 IFC. Libraries were prepared and 75bp or 150bp paired-end sequencing was performed. Cells were excluded if total reads were <25,000, alignment rate was <50%, the number of detected genes (at least 1 count) was <200 and >6,000 and the percentage of reads mapping to mitochondrial genes was >20%. The Seurat and harmony R packages were used for normalization, marker identification and graph-based clustering. Pseudobulk differential expression (DE) analysis was performed using edgeR R package. Enrichment analysis was performed using EnrichR.

Results: A total of 426 out of 836 genes and 24,473 genes were used in the analysis.

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