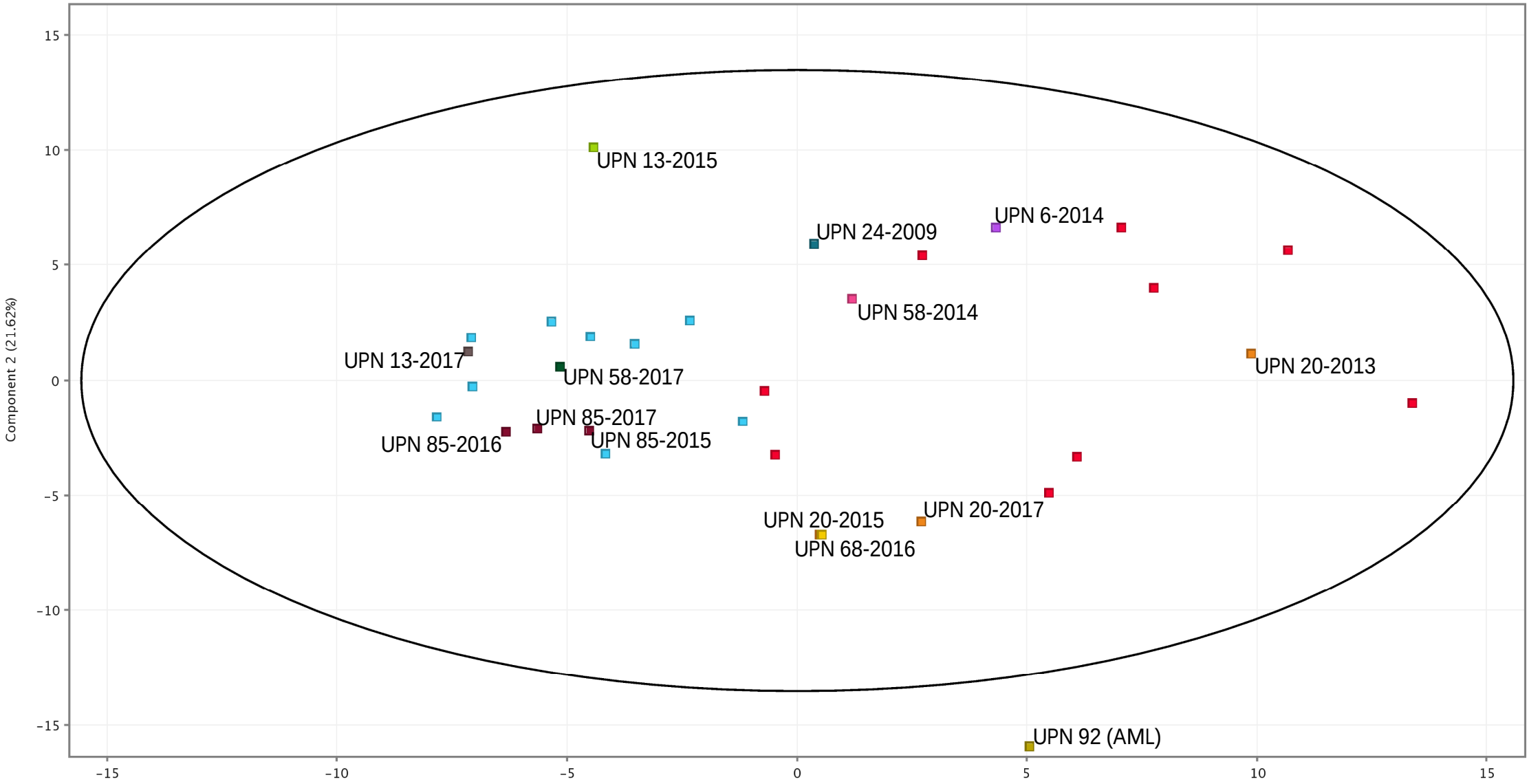
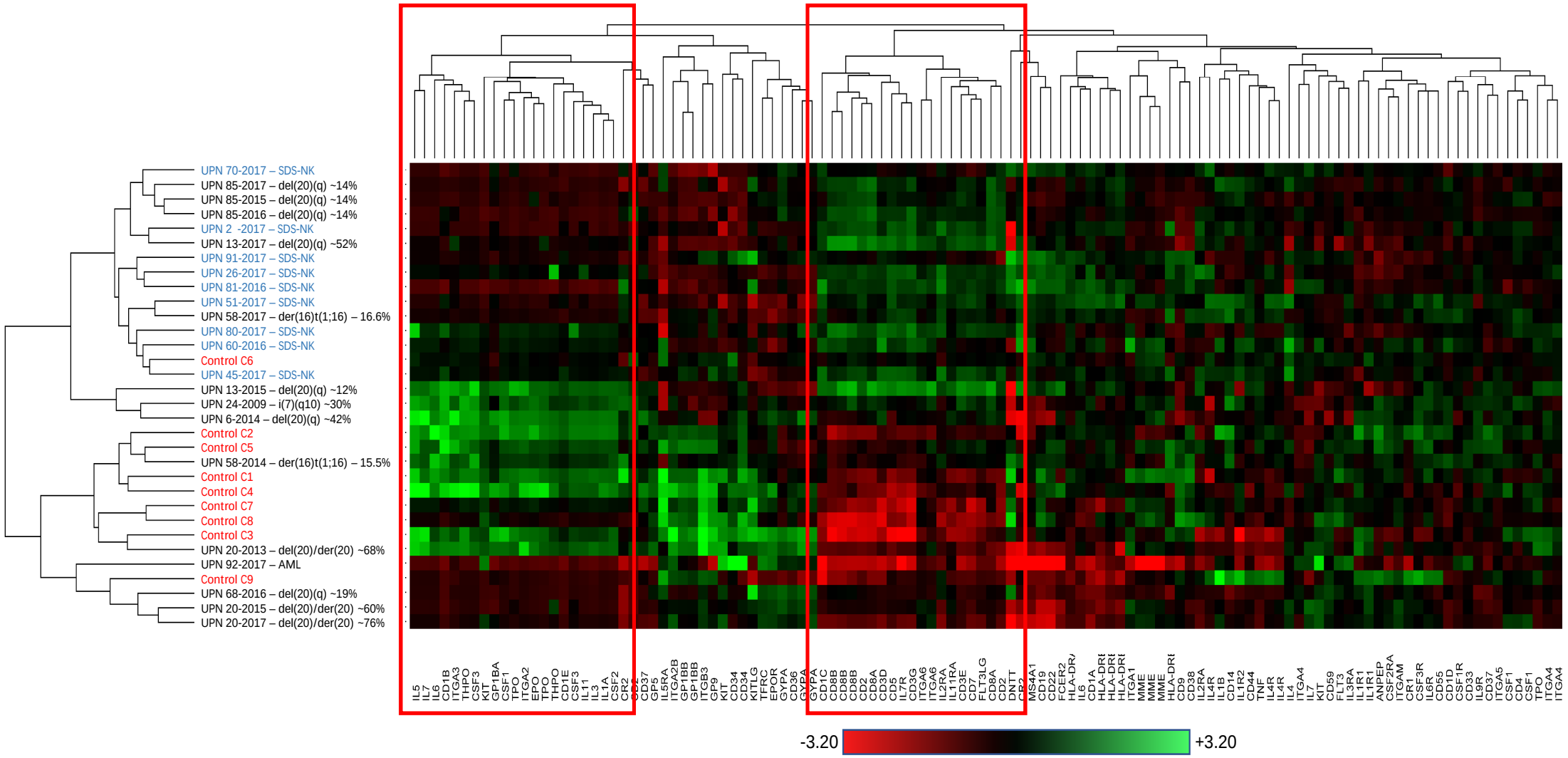


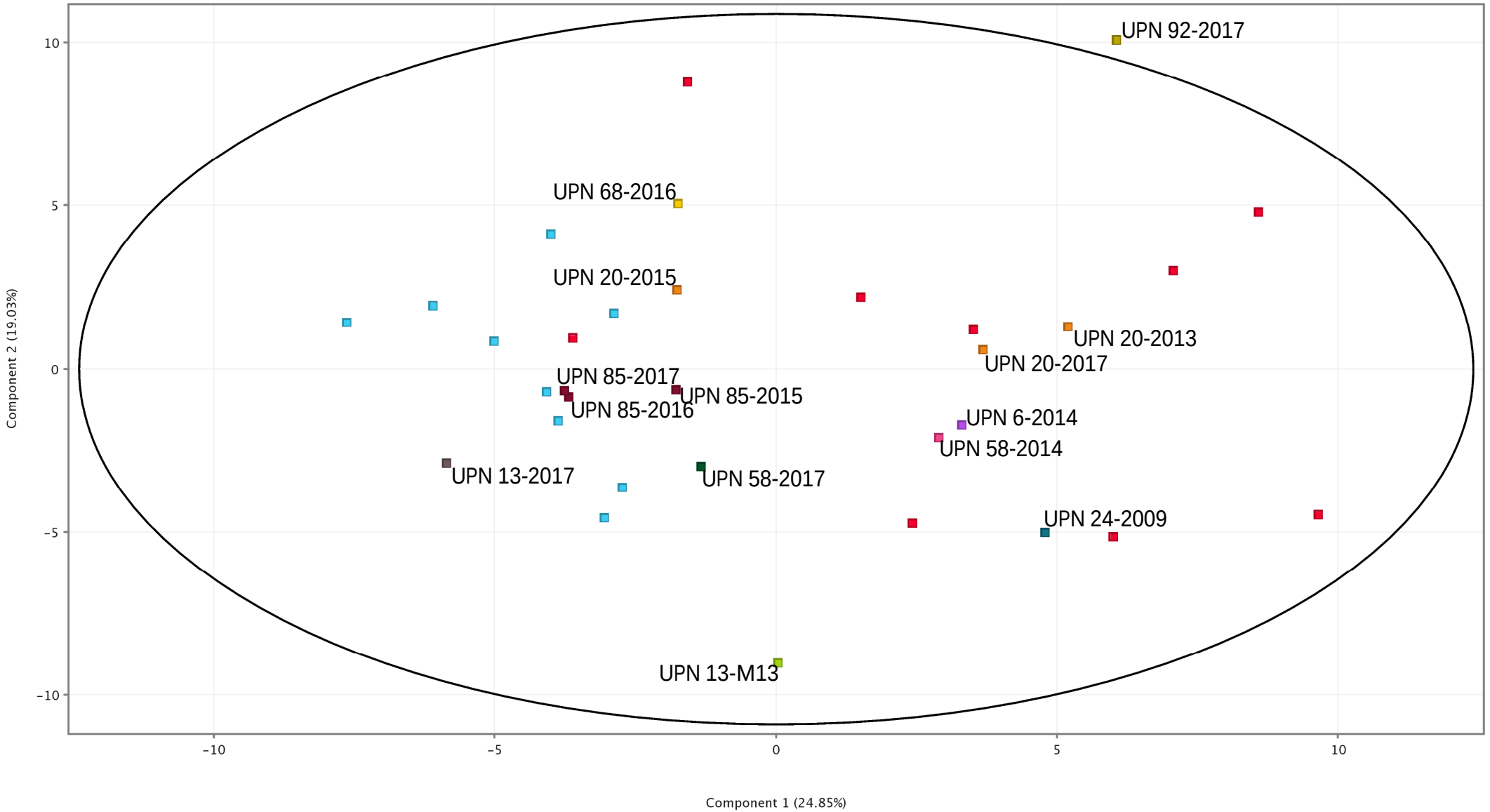
Supplemental Figure 1

Supplemental Fig. 1 Principal Component Analysis (PCA) plot for the Gene set 1 (KEGG Hematopoietic cell lineage). Healthy controls, SDS-NK patients, and patients with chromosome anomalies are identified as in Fig. 2 and in the text. Component 1 and 2 are indicated in the plot. The 95% confidence interval is shown by a black ellipse.



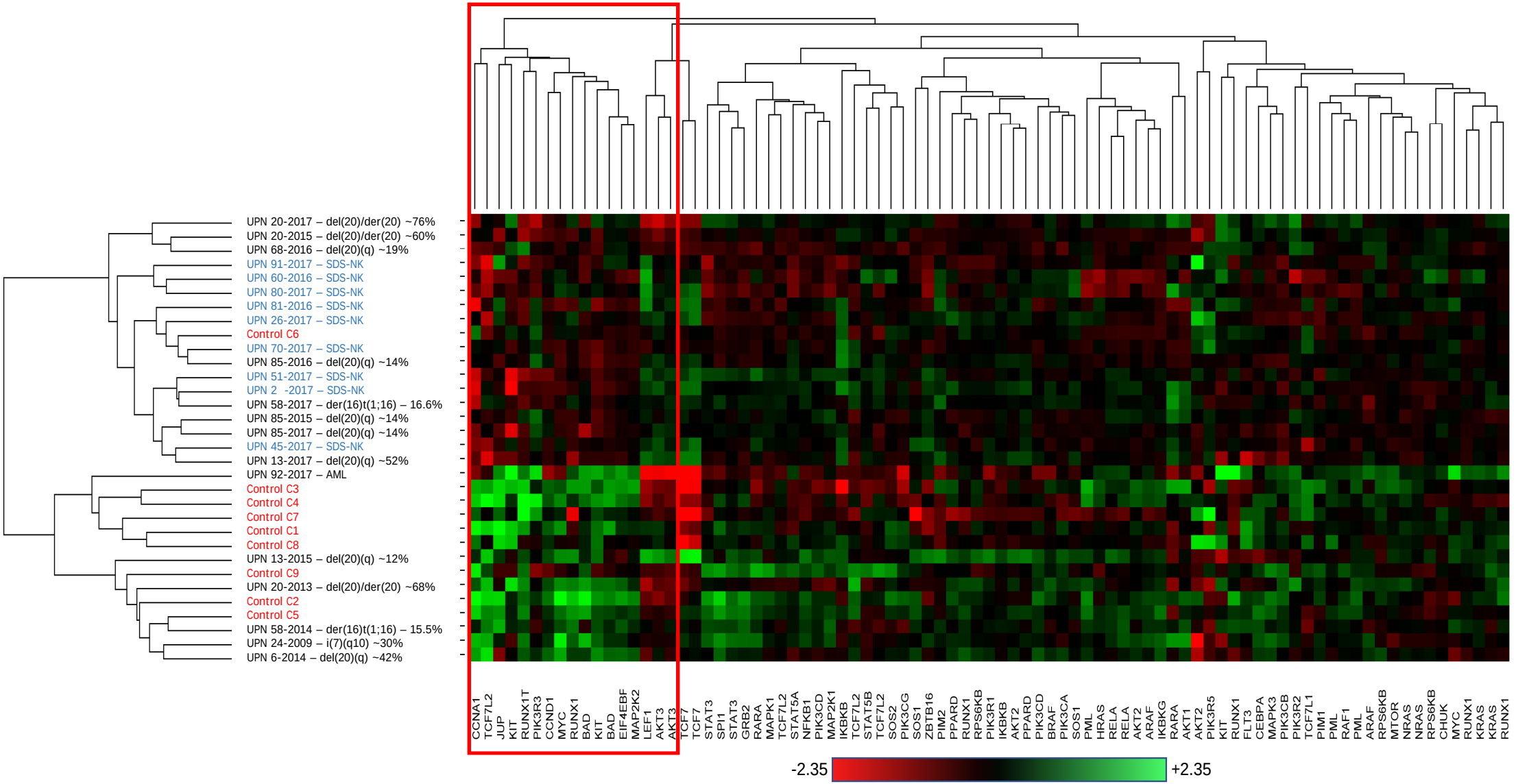
Supplemental Figure 2: KEGG Hematopoietic Cell Lineage

Supplemental Fig. 2 Heatmap and dendrogram of cluster analysis on both the axes for the Gene set 1 (KEGG Hematopoietic Cell Lineage). Healthy controls, SDS-NK and patients with chromosome anomalies are indicated near the dendrogram lines, with evidence of the sample (year), and the karyotype, as in Fig. 3 in the text. Two red boxes put in evidence genes with relevant differences of expression, related to the subgroups of controls and SDS-NK. Gene names and $\log_2$ color bar are under the heatmap.



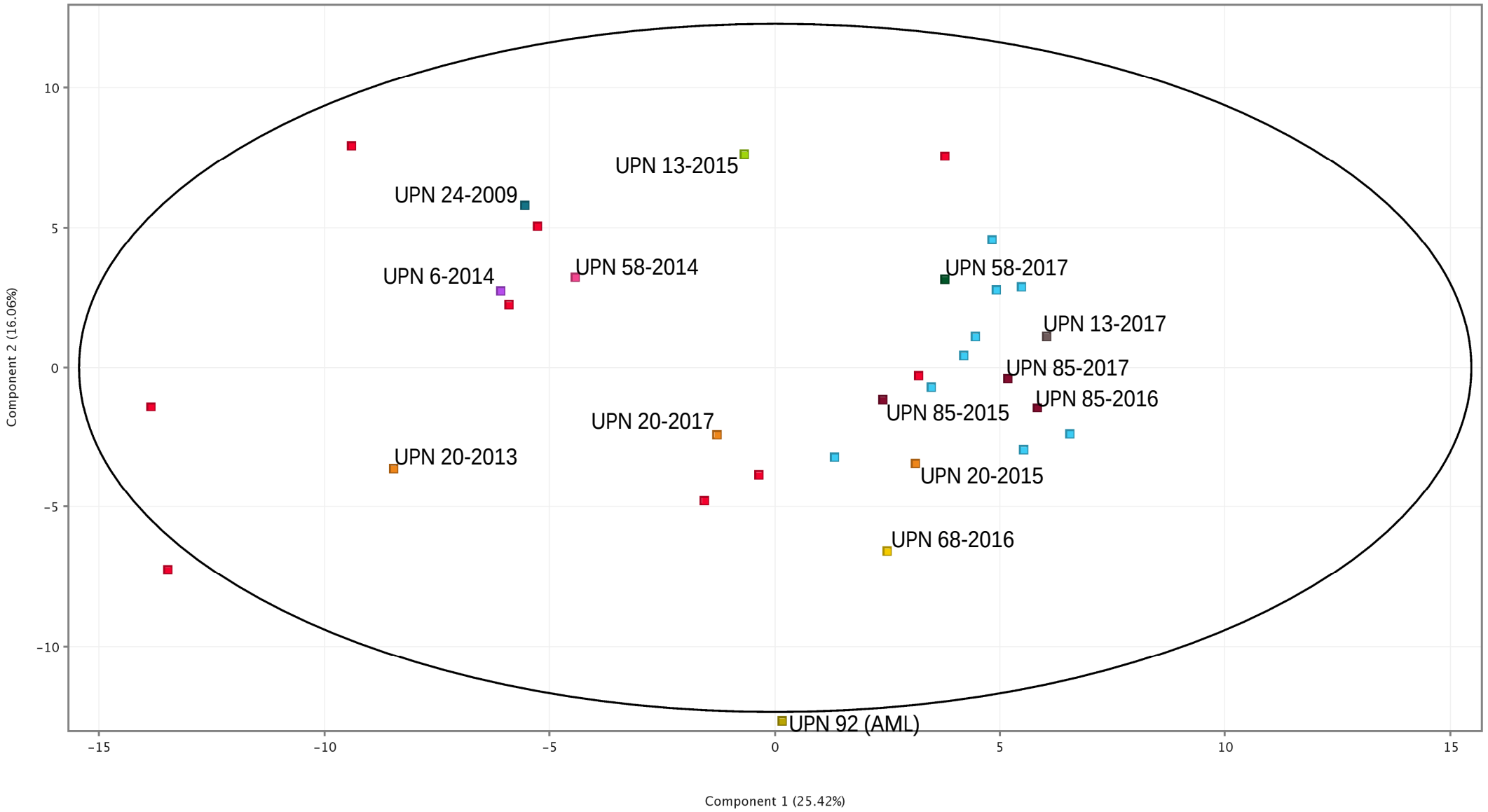
Supplemental Figure 3: KEGG Acute Myeloid Leukemia

Supplemental Fig. 3 Principal Component Analysis (PCA) plot for the Gene set 2 (KEGG Acute myeloid leukaemia). Healthy controls, SDS-NK patients, and patients with chromosome anomalies are identified as in Fig. 2 and in the text. Component 1 and 2 are indicated in the plot. The 95% confidence interval is shown by a black ellipse.



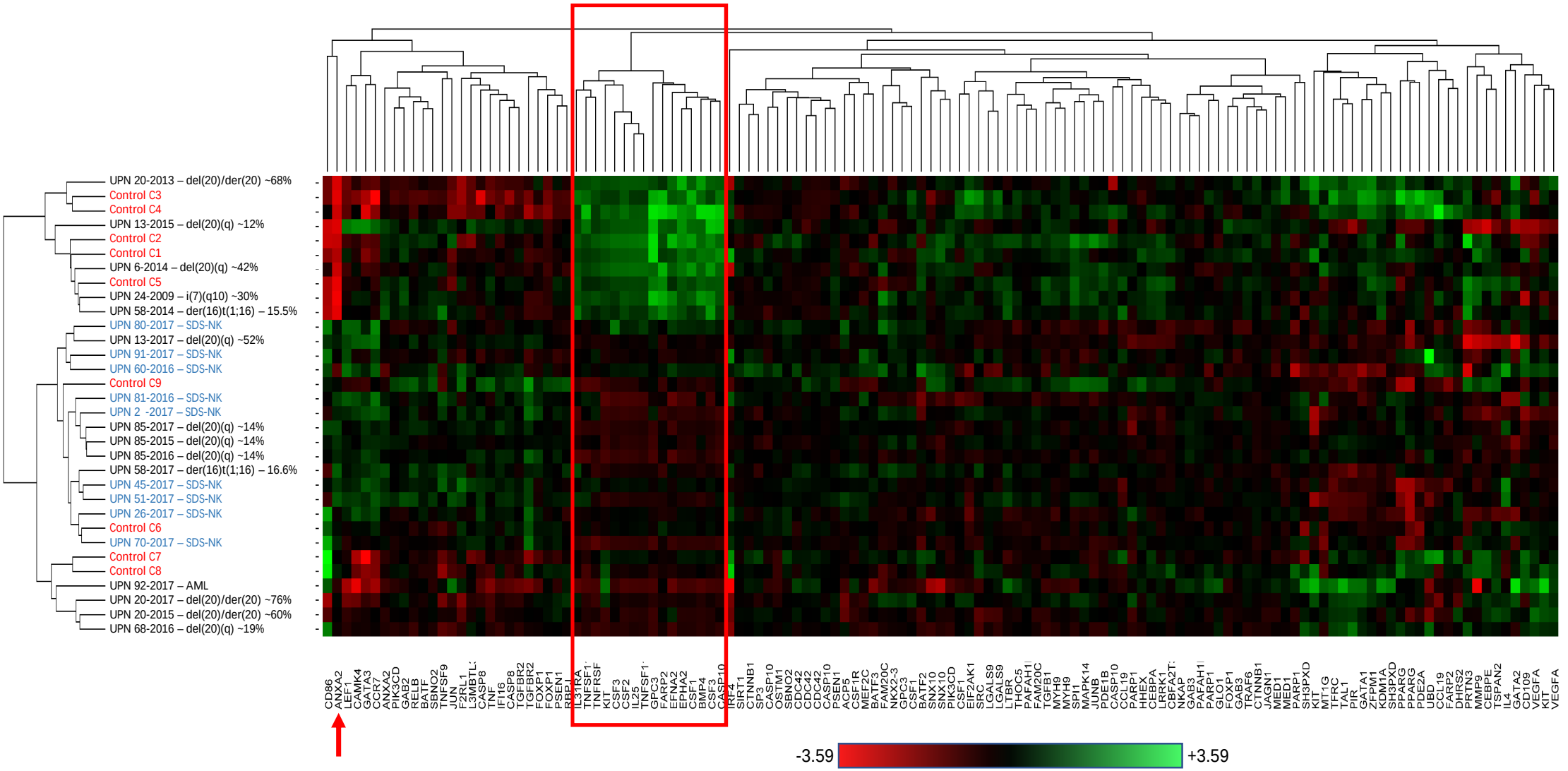
Supplemental Figure 4: KEGG Acute Myeloid Leukemia

Supplemental Fig. 4 Heatmap and dendrogram of cluster analysis on both the axes for the Gene set 2 (KEGG Acute myeloid leukaemia). Healthy controls, SDS-NK and patients with chromosome anomalies are indicated near the dendrogram lines, with evidence of the sample (year), and the karyotype, as in Fig. 3 in the text. A red box put in evidence genes particularly up/down-regulated, with difference in the groups of controls and SDS-NK. Gene names and $\log_2$ color bar are under the heatmap.



Supplemental Figure 5: Gene Onthology Myeloid Leukocyte Differentiation

Supplemental Fig. 5 Principal Component Analysis (PCA) plot for the Gene set 3 (Gene Ontology Myeloid Leukocyte Differentiation). Healthy controls, SDS-NK patients, and patients with chromosome anomalies are identified as in Fig. 2 and in the text. Component 1 and 2 are indicated in the plot. The 95% confidence interval is shown by a black ellipse.



Supplemental Figure 6: Gene Onthology Myeloid Leukocyte Differentiation

Supplemental Fig. 6 Heatmap and dendrogram of cluster analysis on both the axes for the Gene set 3 (Gene Ontology Myeloid Leukocyte Differentiation). Healthy controls, SDS-NK and patients with chromosome anomalies are indicated near the dendrogram lines, with evidence of the sample (year), and the karyotype, as in Fig. 3 in the text. A red arrow and a red box put in evidence genes particularly up/down-regulated, with difference in the groups of controls and SDS-NK. Gene names and $\log_2$ color bar are under the heatmap.