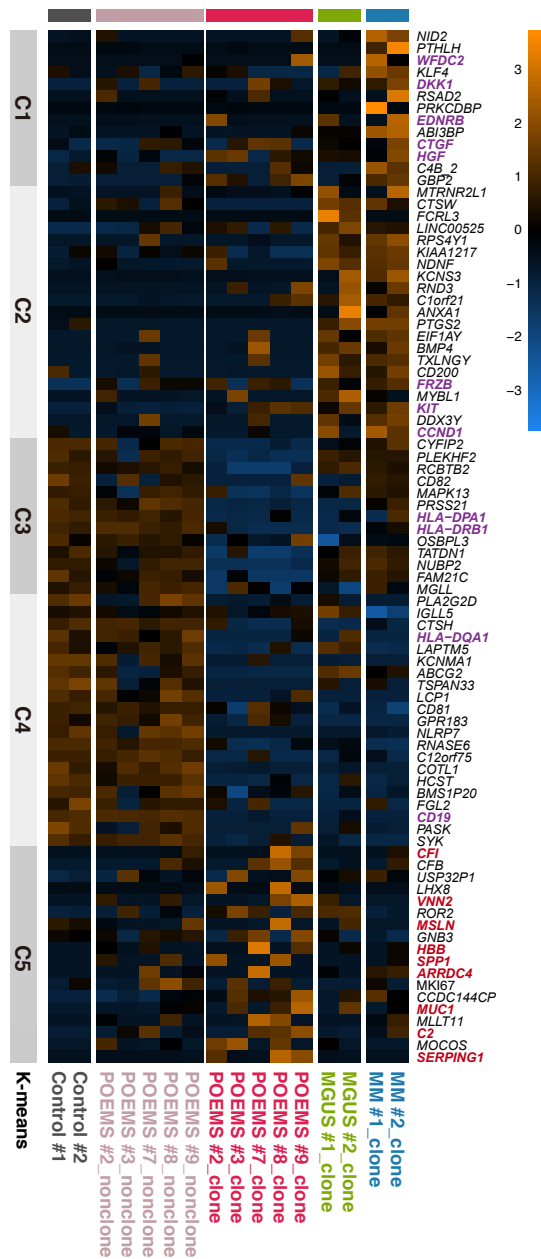
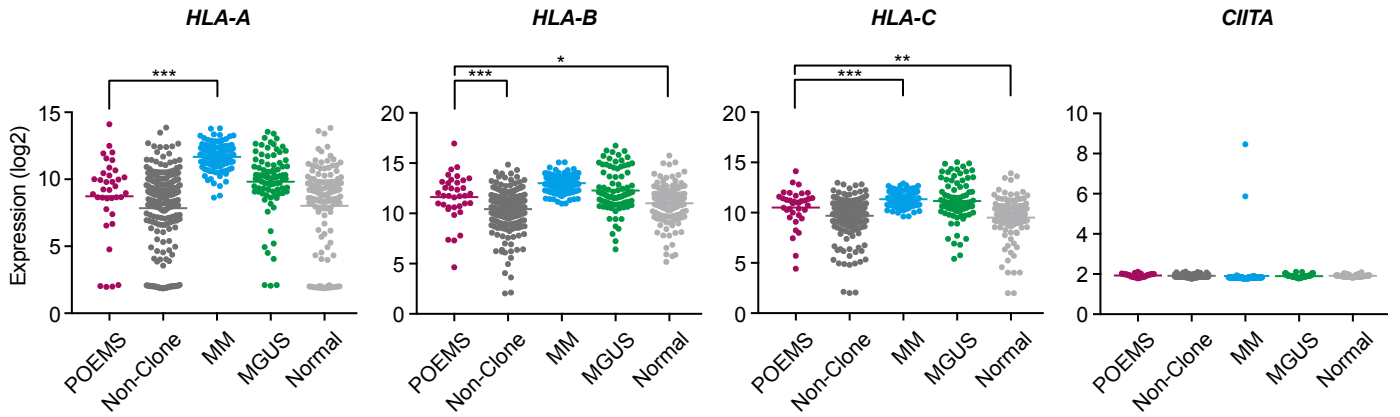


Supplemental Figure 1. Frequencies of POEMS-specific *IGL* sequences in POEMS 1, 4, 6, and 10
Frequencies of POEMS-specific *IGL* sequences in the RNA-seq of 200 plasma cells from POEMS 1, 4, 6, and 10 who did not have any candidate POEMS clones in the scRNA-seq analyses.

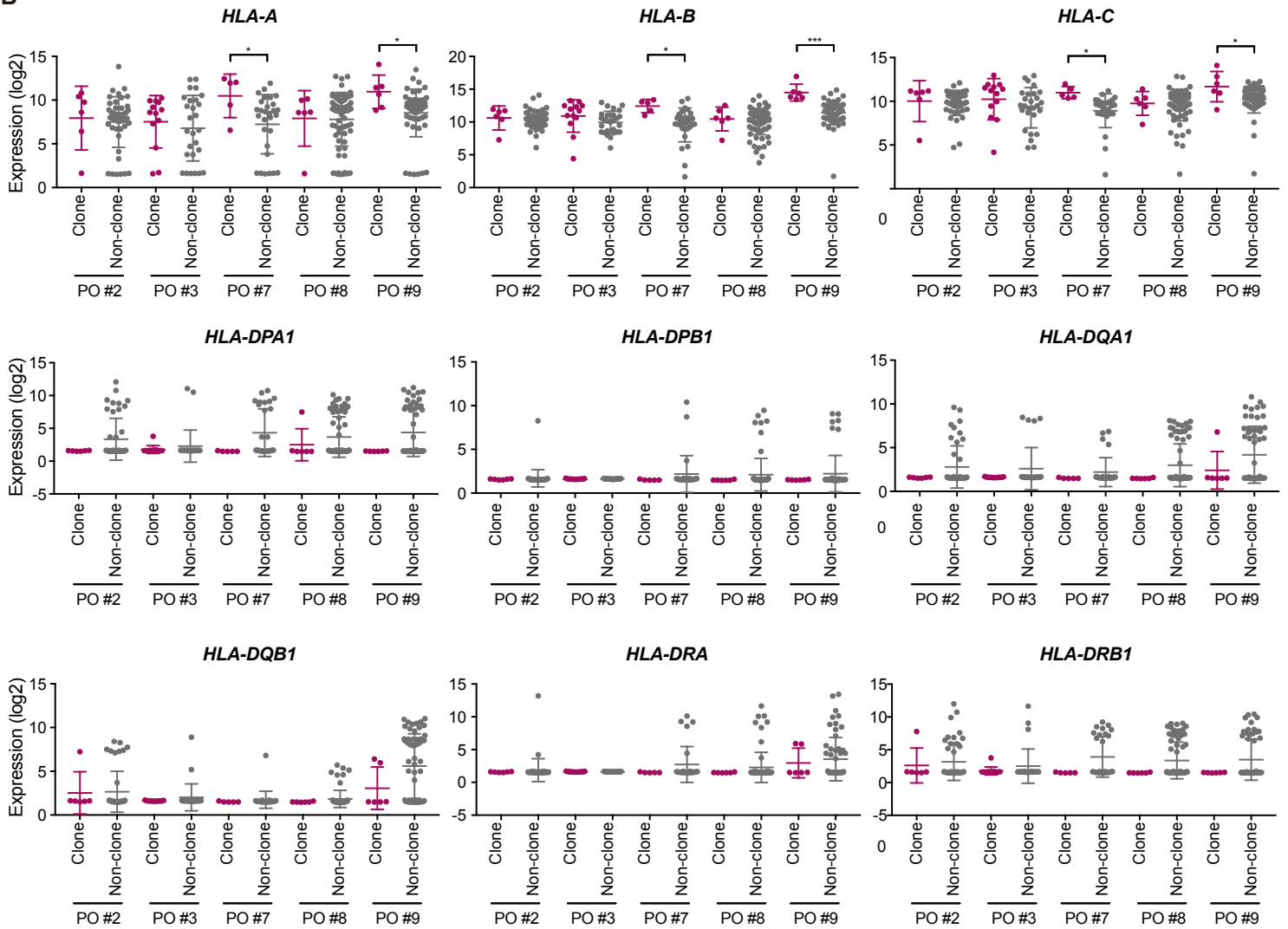


Supplemental Figure 2. Gene expression profiles of POEMS clones and non-clones.
 K-means clustering of scRNA-seq data. Normalized read counts (log2) were averaged within each group and transformed into z-scores. Heatmap of normalized expression levels were shown with same gene sets and order as shown in Figure 3A.

A

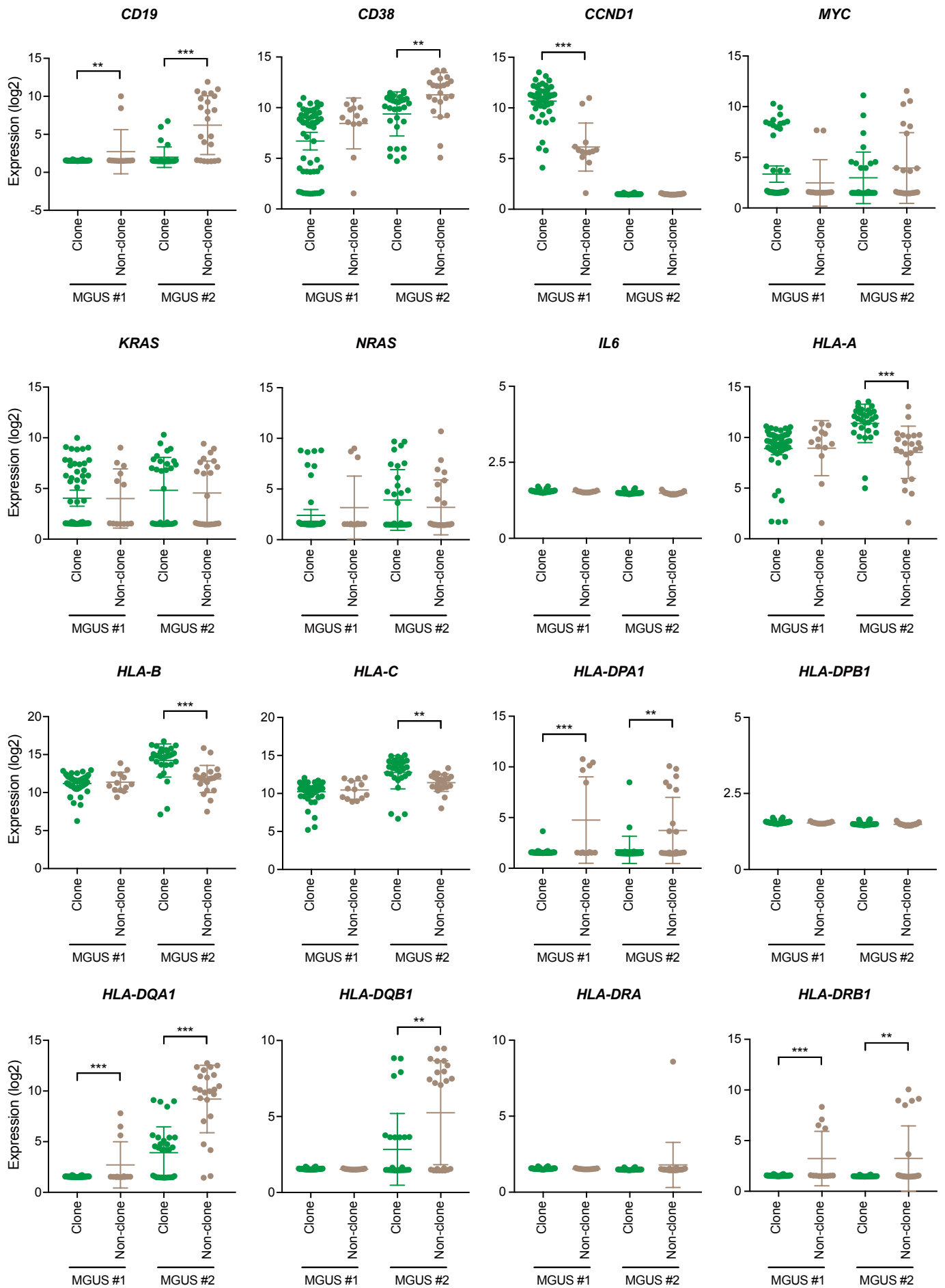


B



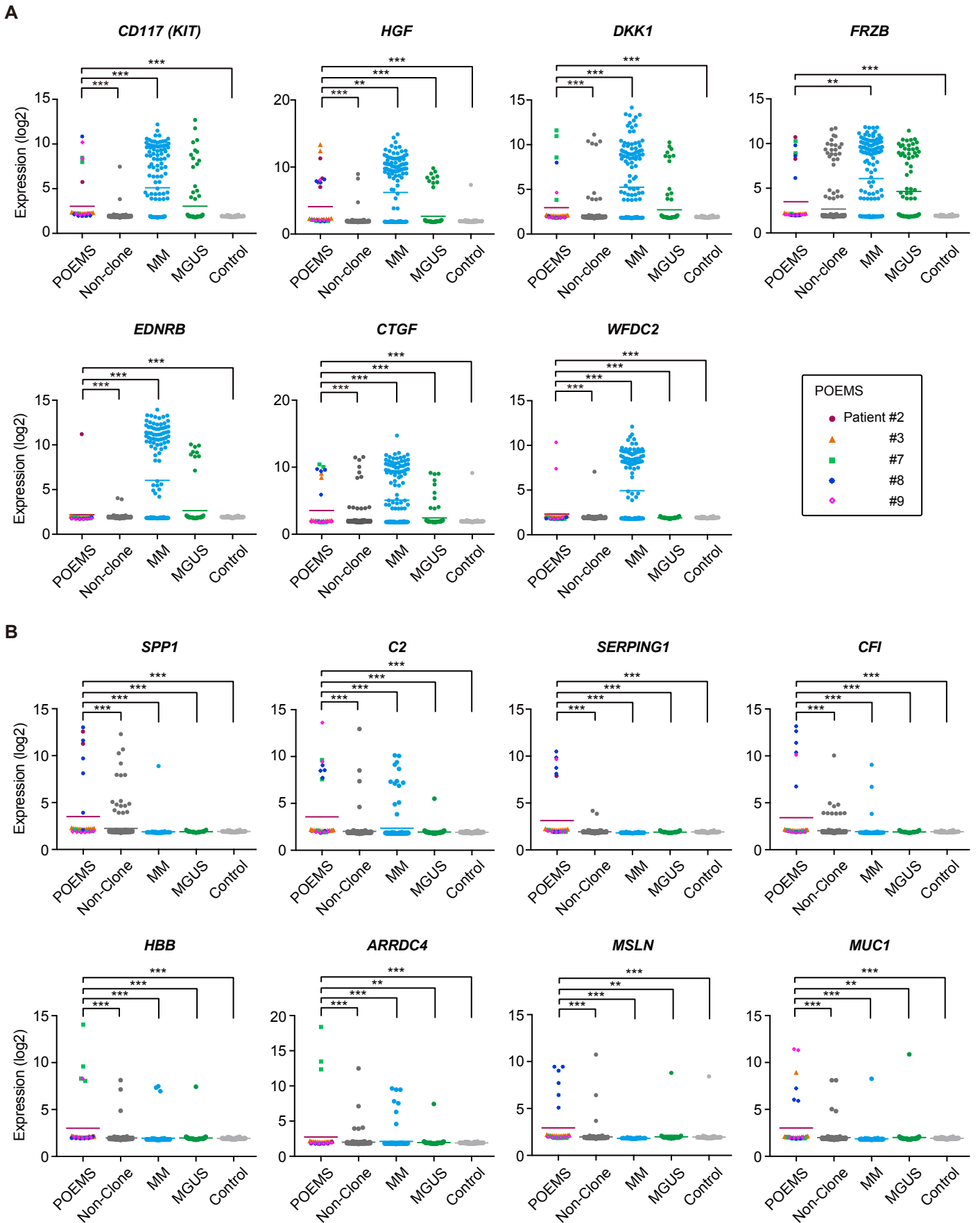
Supplemental Figure 3. Gene expression profiles of POEMS clones and non-clones.

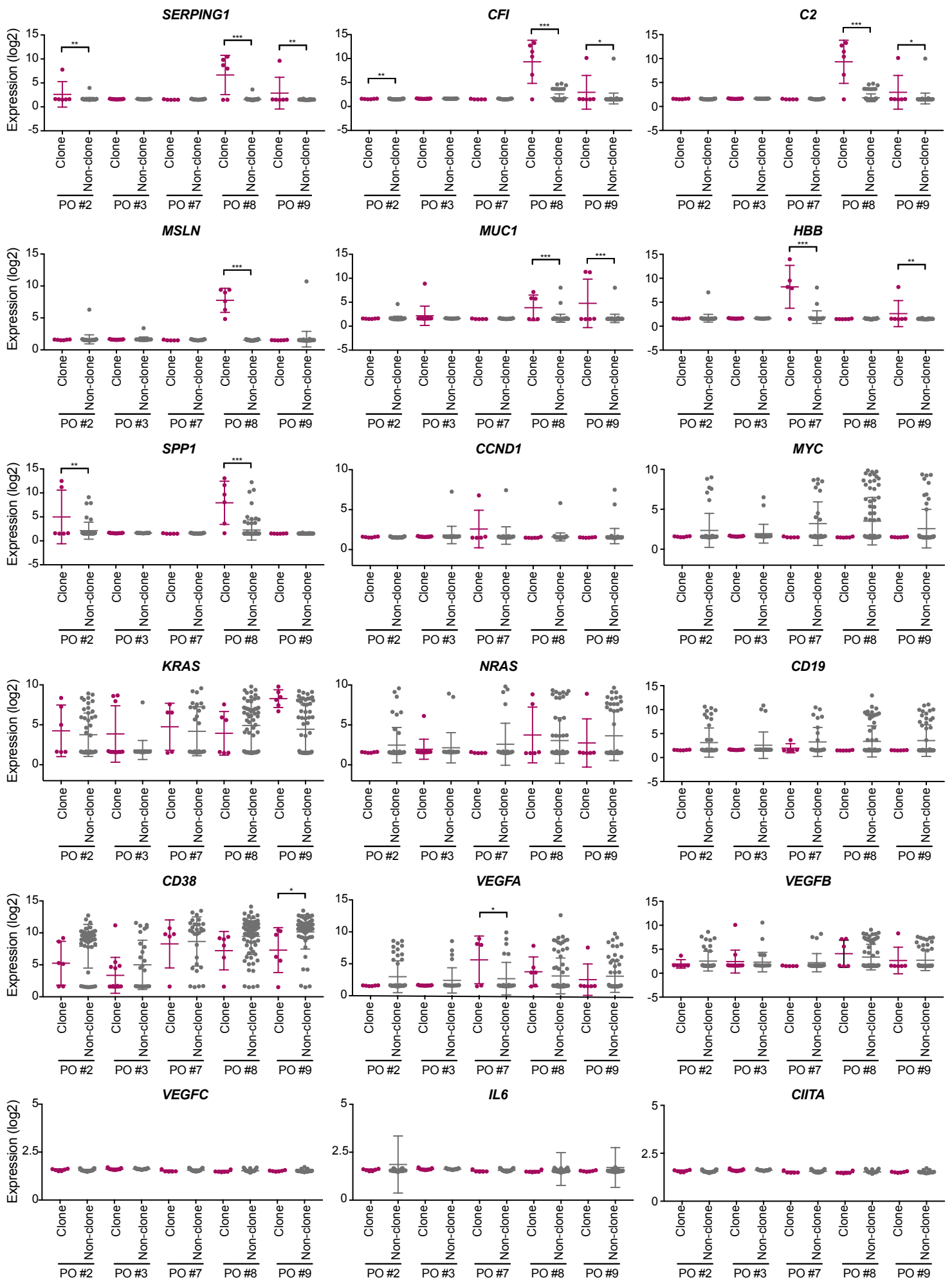
Expression of MHC class I and *CIITA* genes in normalized read counts of scRNA-seq data (log2) in POEMS clones and non-clones in total (A) and in each POEMS patient. Adjusted p values: *, p < 0.05; **, p < 0.01; ***, p < 0.001.



Supplemental Figure 4. Expression of genes in MGUS clones.

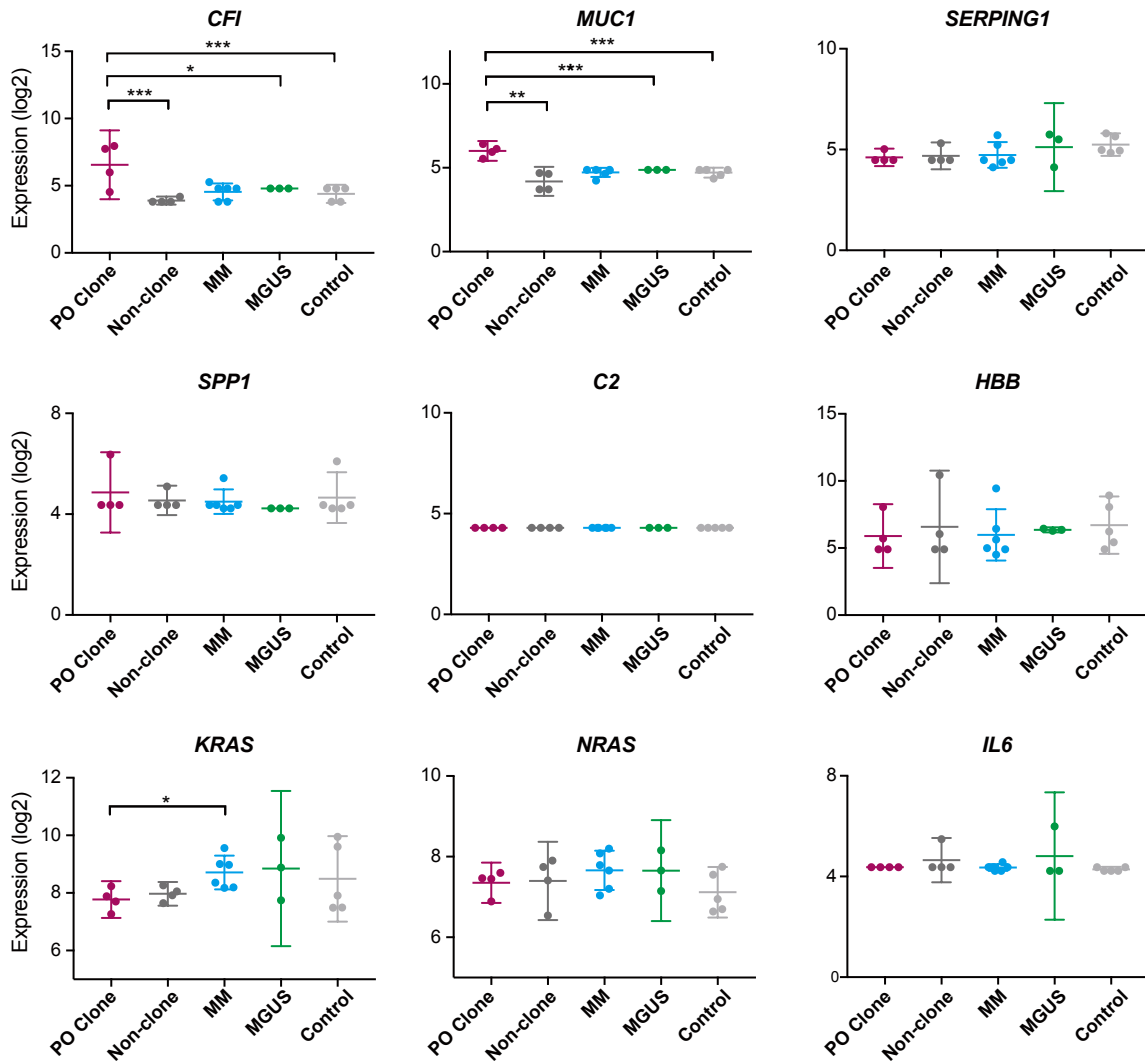
Expression of genes in plasma cells from MGUS patient #1 and #2. Normalized read counts of scRNA-seq data (log₂) are shown. Mean values are indicated by horizontal bars. *, p < 0.05; **, p < 0.01; ***, p < 0.001 by the Student's *t*-test.





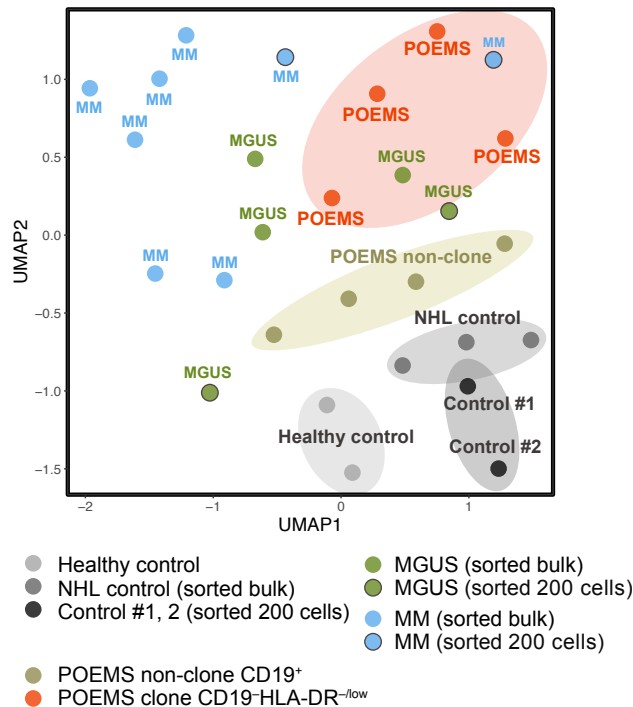
Supplemental Figure 6. Gene expression profiles of POEMS clones and non-clones

Expression of genes in plasma cells from each POEMS clone and non-clone. Normalized read counts of scRNA-seq data (log₂) are shown. Mean values are indicated by horizontal bars. *, p < 0.05; **, p < 0.01; ***, p < 0.001 by the Student's *t*-test.



Supplemental Figure 7. Gene expression profiles of enriched CD19-HLA-DR^{lo} POEMS clones by cell sorting
 Expression of genes in CD138⁺CD19-HLA-DR^{low} (POEMS clones-enriched) and CD138⁺CD19⁺ (POEMS non-clone enriched) plasma cells and CD138⁺ MGUS and MM plasma cells. Normalized read counts of RNA-seq data (log₂) are shown. Data are shown as the mean ± SEM. MGUS data was retrieved from Nagao et al., *Leukemia* 33:1723-1735, 2019. Adjusted p value: *, p < 0.05; **, p < 0.01; ***, p < 0.001.

**DEG 1260 genes :
POEMS, MGUS or MM vs. Controls**



Supplemental Figure 8. Gene expression profiles of control plasma cells

UMAP plots illustrating the transcriptomic profiles of Control, POMES clone and non-clone, MGUS, and MM plasma cells. Bulk RNA-seq data of CD138⁺CD19⁺HLA-DR^{low} (POEMS clone-enriched) and CD138⁺CD19⁺ (POEMS non-clone-enriched) plasma cells, CD138⁺ MGUS and MM plasma cells, 200 plasma cells from Controls (#1 and #2), MGUS (#1 and #2), and MM (#1 and #2) in Figure 1B were normalized and removed batch effects, then differential expression analysis of read counts were performed. A total of 1,260 DEGs between POEMS, MGUS, or MM compared with healthy BM plasma cells were obtained using the cutoff value $q < 0.0001$. UMAP analysis was performed using DEGs. Data of 3 NHL BM control plasma cells, 3 MGUS plasma cells, and 3 MM plasma cells were retrieved from Ref. 16 (Nagao et al., Leukemia 33:1723-1735, 2019).