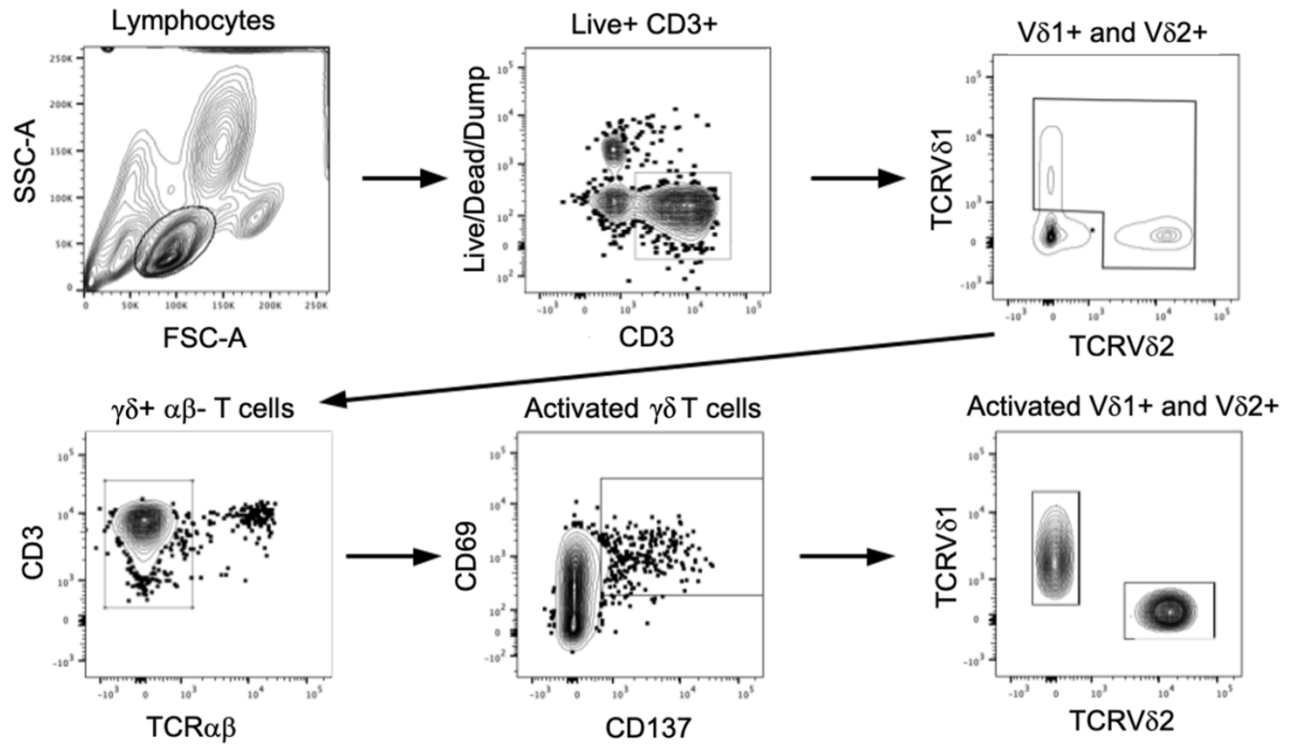
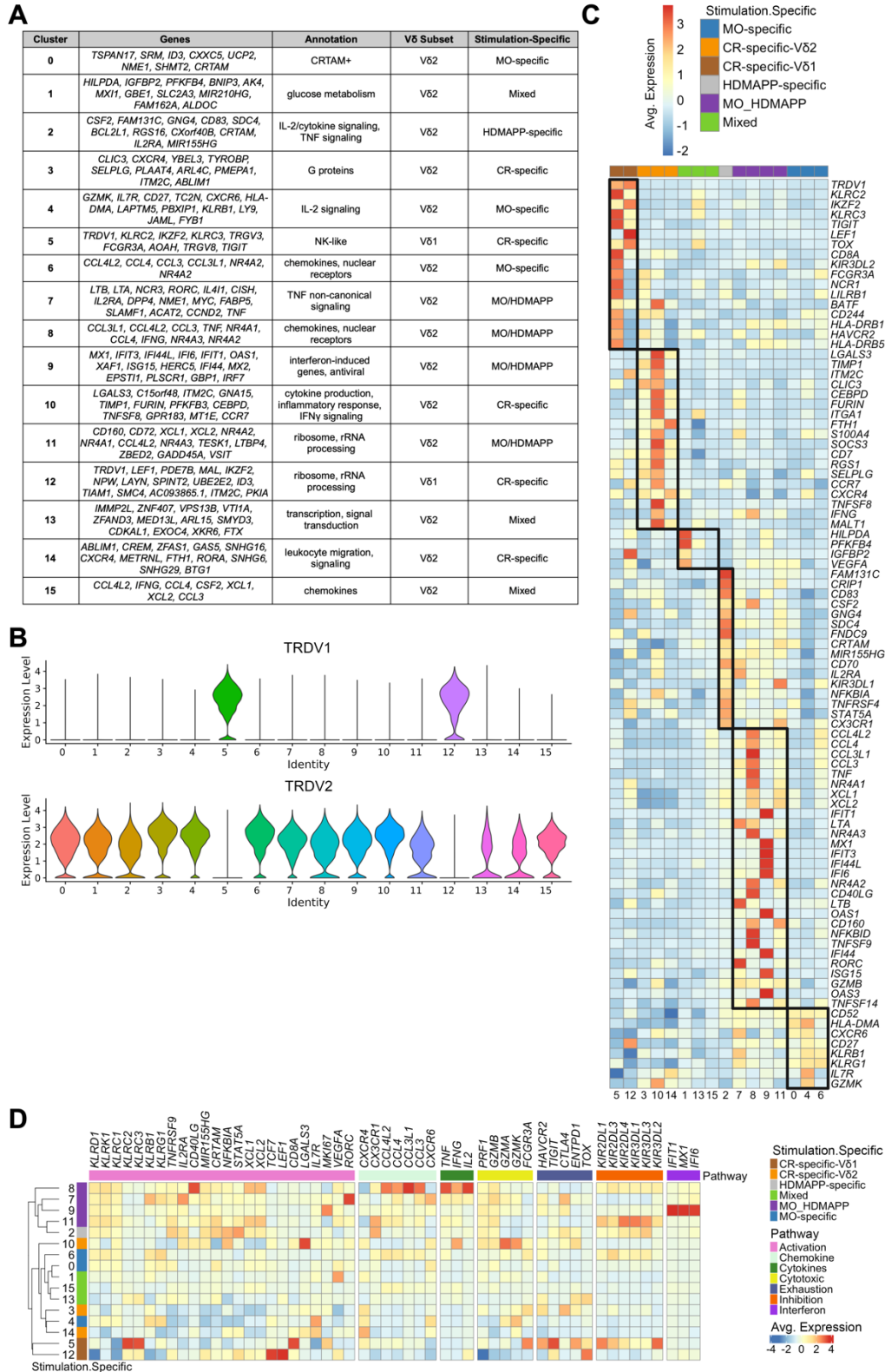


SUPPLEMENTAL MATERIALS

Supplemental Figures

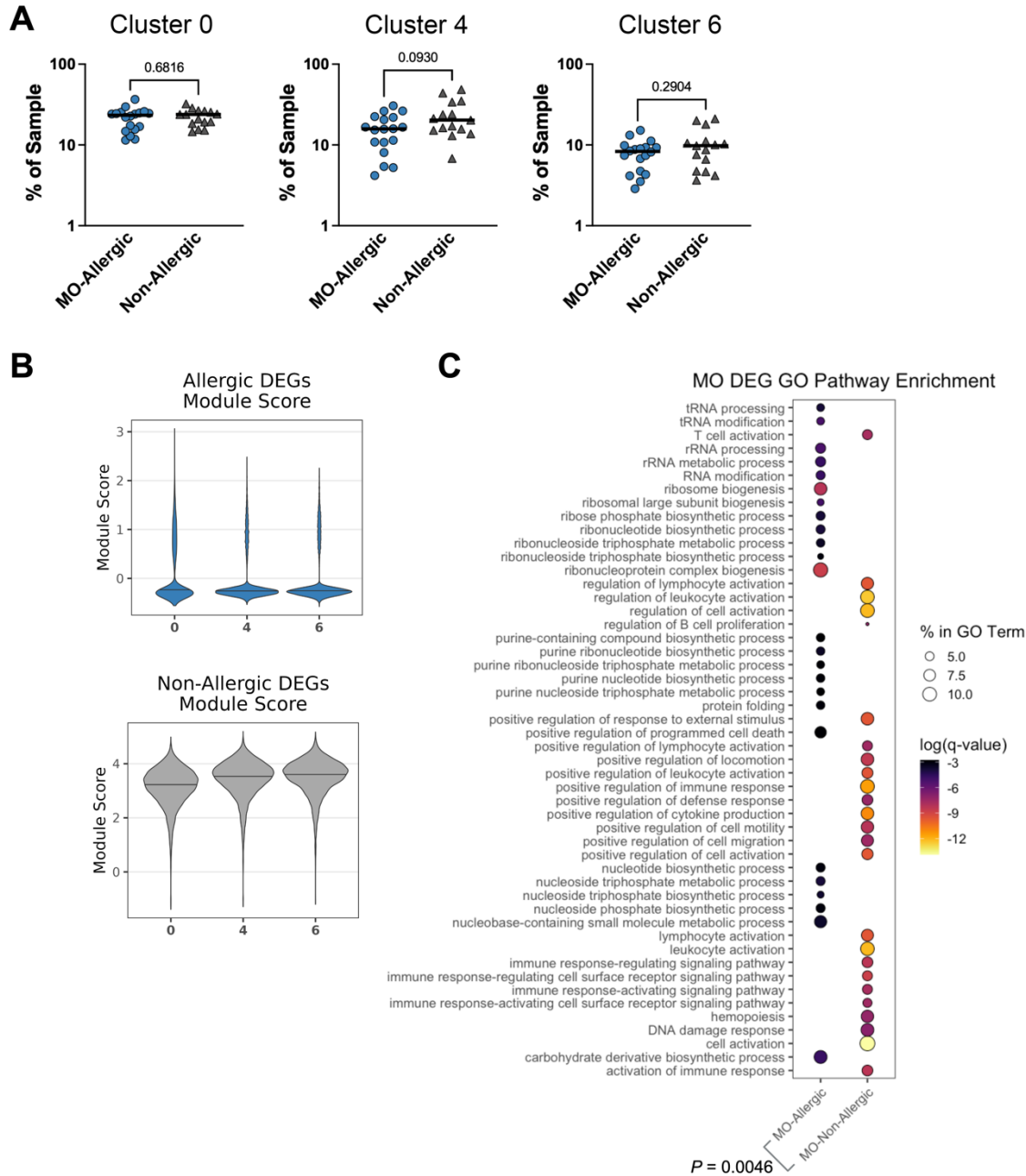


Supplemental Figure 1. Gating strategy, related to Figure 1. Representative gating strategy for sorting AIM+ Vδ1 and Vδ2 cells. Representative dotplots from a CR-stimulated sample is shown.

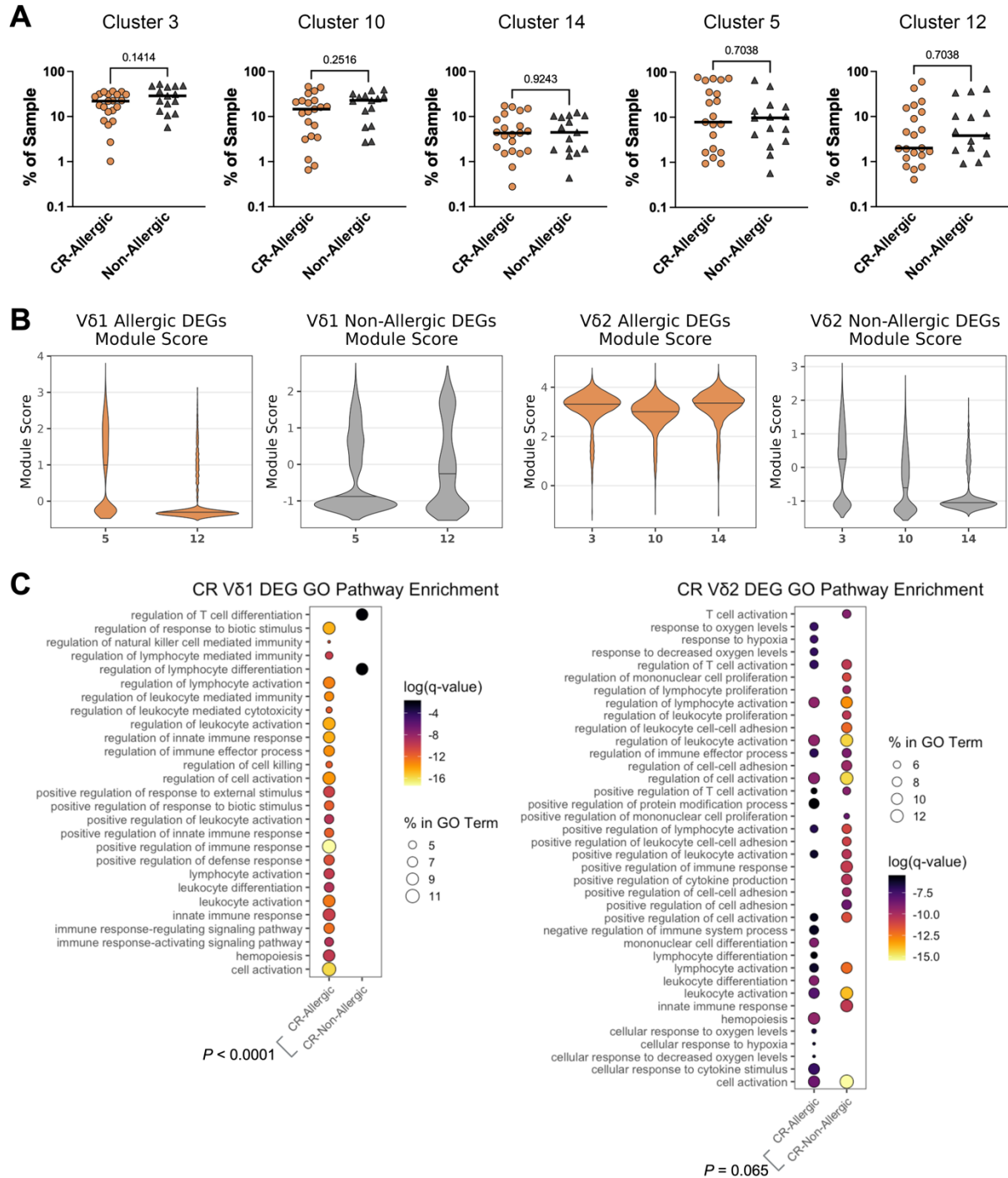


Supplemental Figure 2. Cluster profiling, related to Figure 2. A) List of top genes, Vδ subset, and stimulation-specific annotation per cluster. B) Expression levels of TRDV1 (top) and TRDV2 (bottom) per cluster. C) Average expression of top genes per cluster. D) Heatmap of averaged expression of selected genes grouped by associated pathway (x-axis) per cluster (y-axis).

Supplemental Figure 3. V γ 9V δ 2 dominance and diversity in MO- and CR-specific TCR clusters. A) Gini index for each cohort for the full dataset and the downsampled dataset. Wilcoxon matched-pairs signed rank test. P-values <0.05 considered statistically significant. B,C) Clonal expansion within each MO-specific (B, top) and CR-specific (C, top) cluster. Euler plot showing number of unique clones shared across MO-specific (B, bottom) and CR-specific (C, bottom) clusters. D,E) Proportion of shared clones (Tables 1, 2) within the cohort repertoire of each cluster for MO-specific (D) and CR-specific (E) clusters. Bars connected across cohorts represent the same gene present in both allergic and non-allergic cohorts. F,G) Clonal expansion of allergic vs. non-allergic repertoires in MO-specific (F) and CR-specific (G) clusters. H,I) Percent of each sample with specific TRGV/TRDV pairings separated by allergic status and TRDV gene for MO-specific (H) and CR-specific (I) samples. Only gene pairings found in at least three samples in at least one cohort are shown.



Supplemental Figure 4. MO-specific clusters details, related to Figure 3. A) Frequency of allergic and non-allergic samples within each MO-specific cluster. Mann-Whitney test. B) Module scores per cluster using DEGs associated with allergic (blue) or non-allergic (grey) cohorts depicted in Figure 3. Line at median. C) Top significantly enriched pathways of DEGs found upregulated in MO-specific clusters. The top 25 pathways ($\log(q\text{-value}) < -1.3$), then ranked by $\log(q\text{-value})$ and % in GO) per group are shown if the threshold of $\log(q\text{-value}) < -1.3$ was met. Wilcoxon matched-pairs signed rank test. P-values < 0.05 considered statistically significant.



Supplemental Figure 5. CR-specific clusters details, related to Figure 4. A) Frequency of allergic and non-allergic samples within each CR-specific cluster. Mann-Whitney test. B) Module scores per cluster using DEGs associated with allergic (orange) or non-allergic (grey) cohorts depicted in Figure 4. Line at median. C). Top significantly enriched pathways of DEGs found upregulated in Vδ1 (left) or in Vδ2 (right) clusters. The top 25 pathways ($\log(q\text{-value}) < -1.3$, then ranked by $\log(q\text{-value})$ and % in GO) per group are shown if the threshold of $\log(q\text{-value}) < -1.3$ was met. Wilcoxon matched-pairs signed rank test. P-values < 0.05 considered statistically significant.

Supplemental Table 1. Donor summary table.

Supplemental Table 2. Cluster markers.

Supplemental Table 3. TCR repertoire information.

Supplemental Table 4. MO-specific clusters DEG in allergic vs. non-allergic cohorts.

Supplemental Table 5. CR-specific clusters DEG in allergic vs. non-allergic cohorts.

Supplemental Table 6. Downsampled TCR repertoire data.