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Supplemental information

HLA-B*46 associates with rapid HIV disease progression in Asian cohorts and prominent differences in NK cell phenotype

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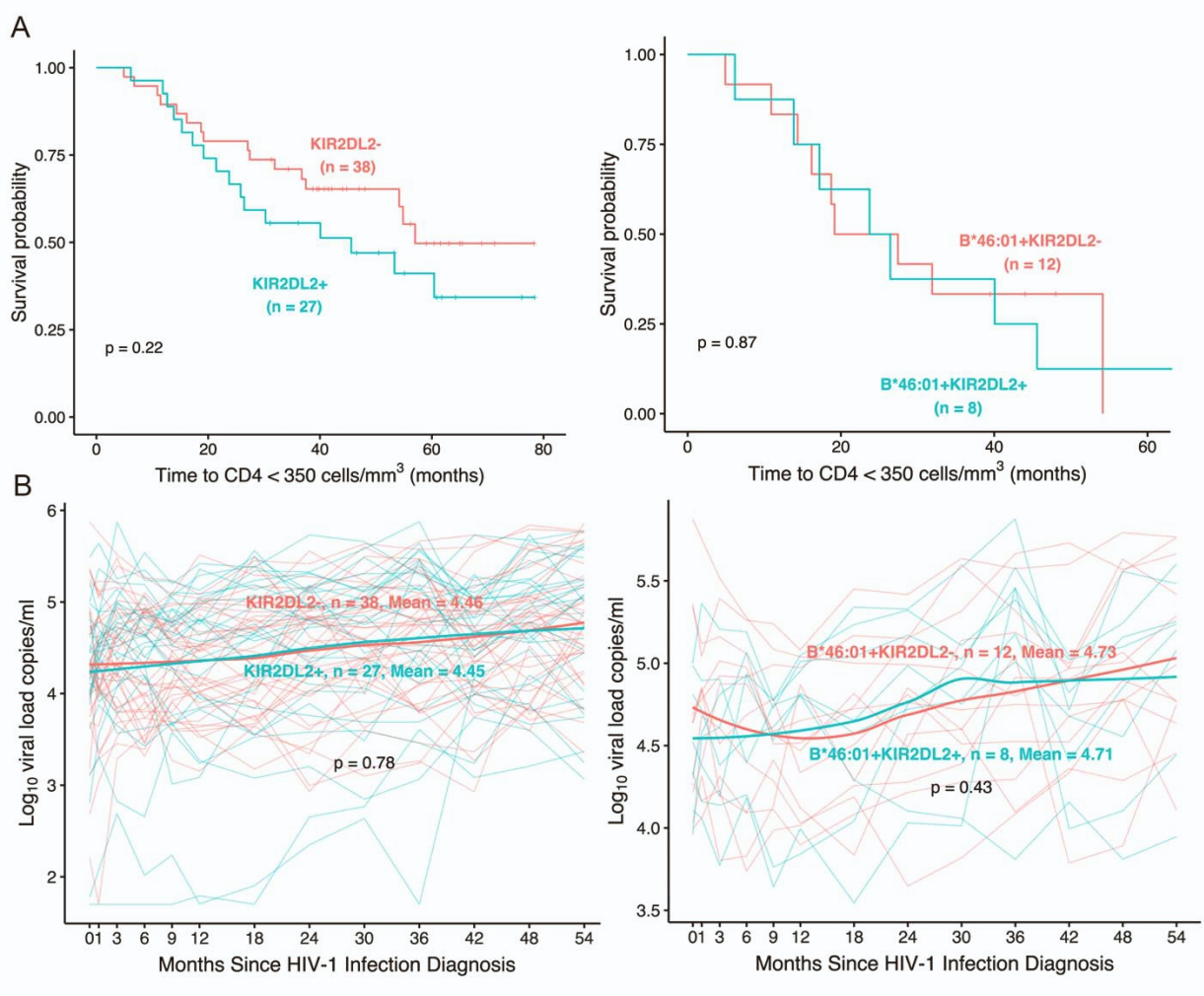

Figure S1. No significant association of KIR2DL2 (n = 65) or HLA-B*46+ KIR2DL2+ (n = 20) combination with HIV disease progression. Related to Figure 1. A) time to CD4 counts < 350 cells/mm^3 and B) VL copies/ml

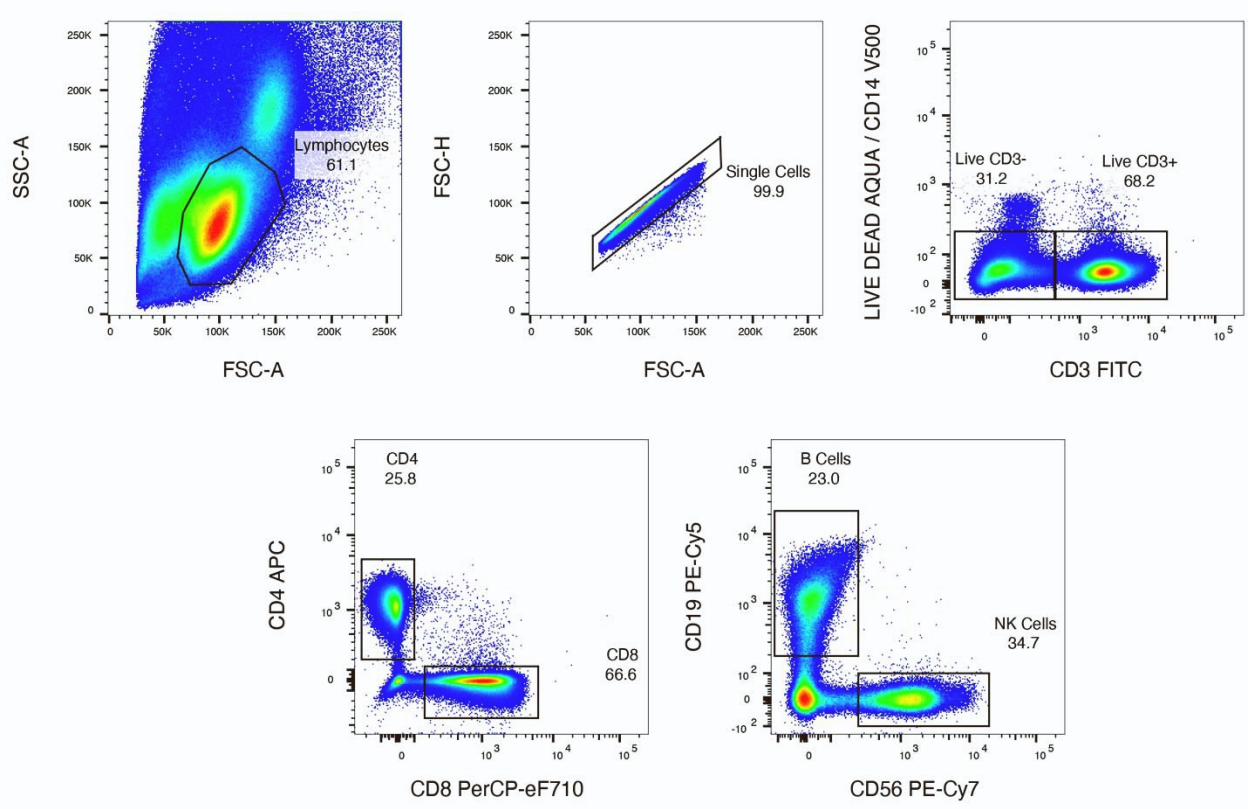

Figure S2. Gating strategy used for flow sorting lymphocyte populations in human samples during acute HIV infection from the RV217 study cohort. Related to Figure 3 and STAR Methods. RNA-Seq was performed in sorted lymphocyte populations from peripheral blood samples (n = 28).

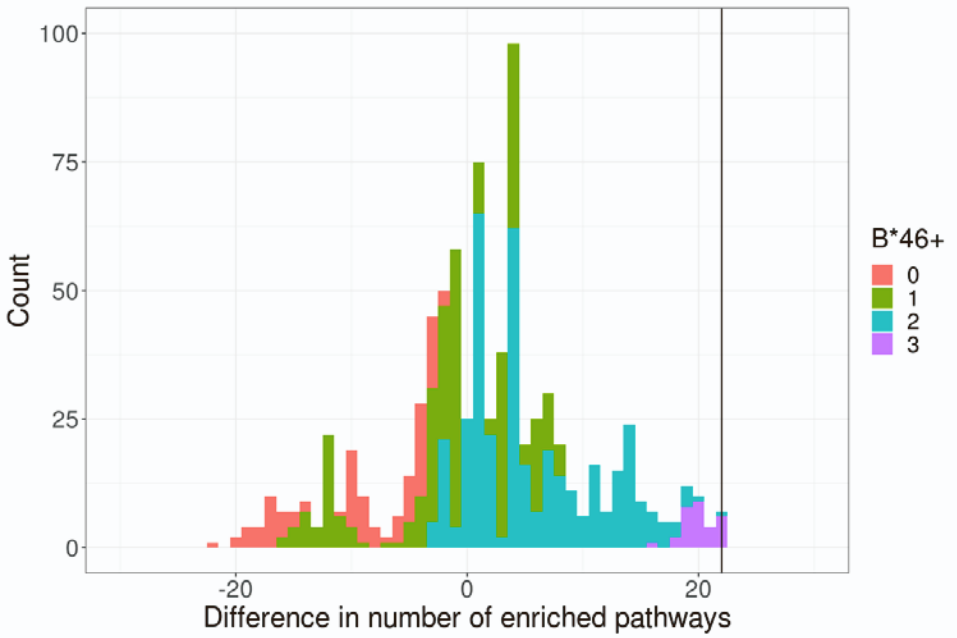

Figure S3. Distribution of difference in number of enriched pathways in NK cells based on the presence of B*46. Related to Figure 3. Permutation analyses of the sample labels with the B*46+ genotype shows the observed difference of 22 or more pathways occurred for fewer than 0.7% of iterations in NK cells (black line). The x axis is the difference of significant pathways between B*46- and + groupings and the y axis shows the number of occurrences.

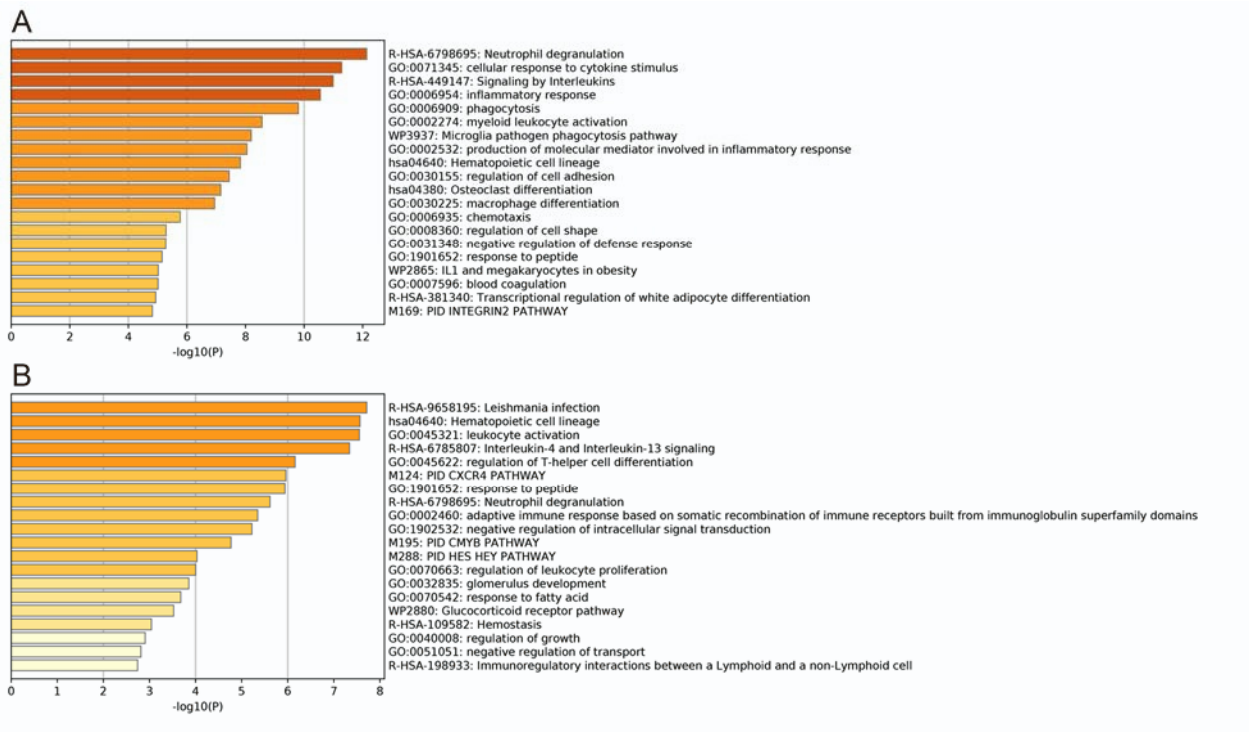

Figure S4. Higher gene expression of specific pathways in NK cells in the absence of the B*46 allele. Related to Figure 3. Functional pathway analyses of enriched genes from the top two modules A) M11.0 and B) M37.0 during VL setpoint that were enriched in the group without B*46.

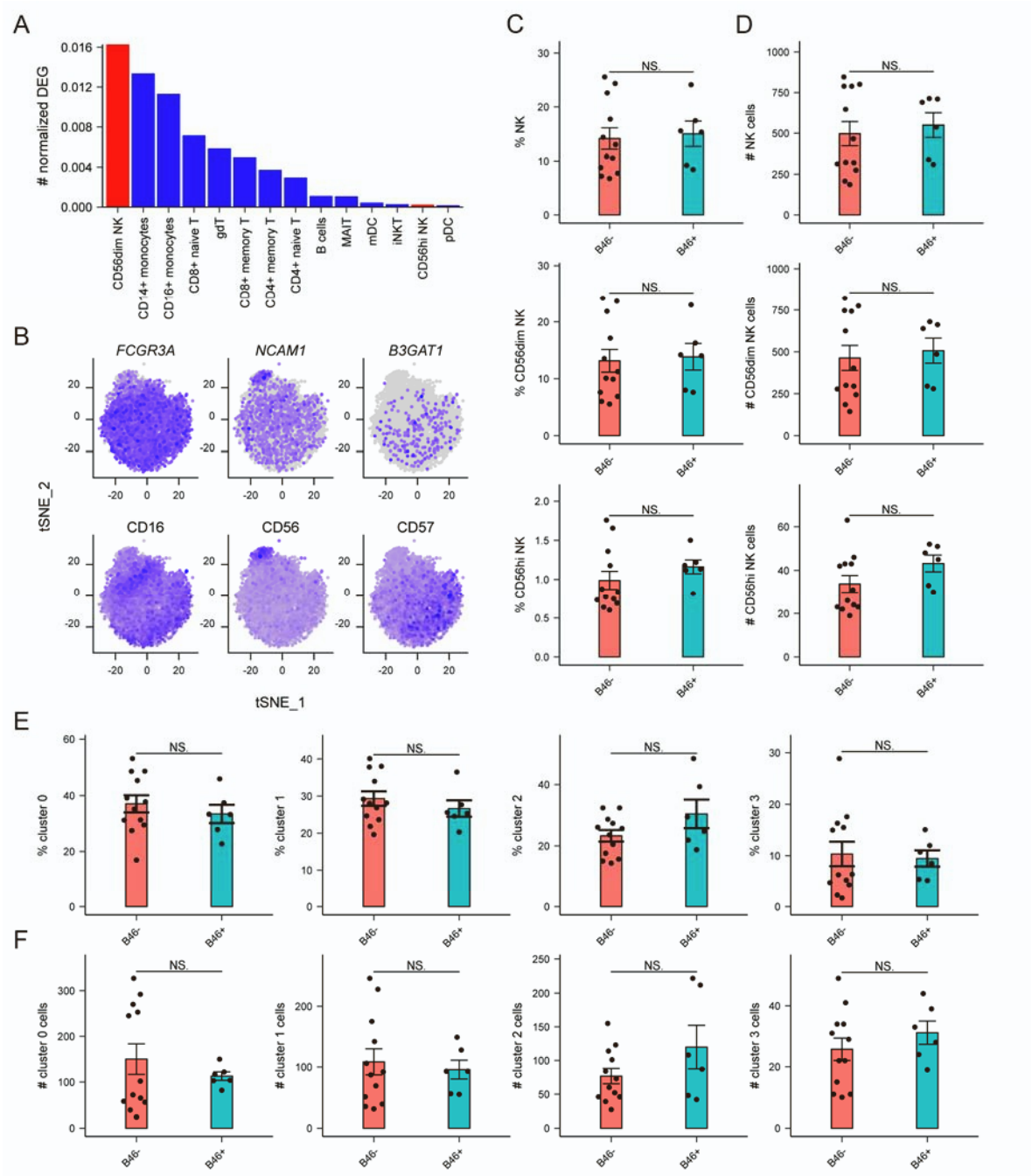

Figure S5. Single cell CITE-seq data shows NK cells as one of the top significant cell subsets associating with presence of HLA-B*46. Related to Figure 4. A) CITE-seq data from treated PLWH (n = 18) identified top cell populations with DEGs comparing B*46+ versus - groups. NK clusters are further defined by CD56 protein. B) Known protein and gene lineage markers that differentiate NK cell clusters. No significant differences in NK frequency C) percentage or D) absolute number when comparing the B*46+ and - groups in bulk NK cells, $CD56^{dim}$ NK cells, or $CD56^{hi}$ NK cells. Significant differences were not observed in NK cell frequency E) percentage or F) absolute number when further clustering into four subpopulations based on all proteins used in the assay.

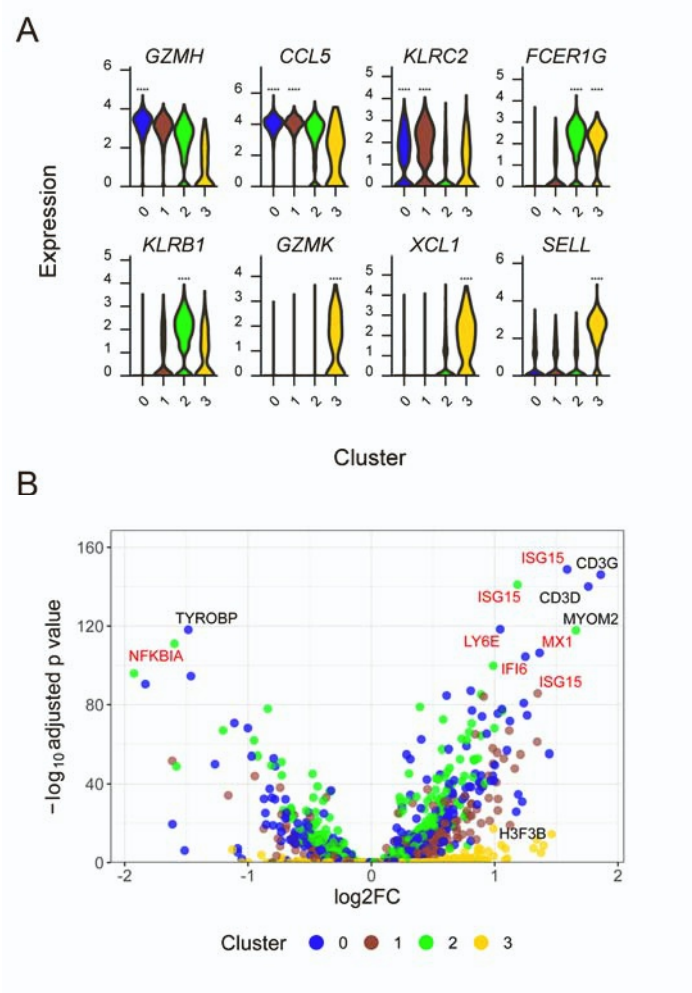

Figure S6. Single cell RNA-seq data from acute HIV infection. Related to Figure 4. A) HLA-B*46-associated cluster markers identified at the acute time point. B) Interferon stimulated genes, not *HLA-B*, are highly expressed during HIV infection when grouped by B*46 genotype. n = 6, **** $p<0.0001$.