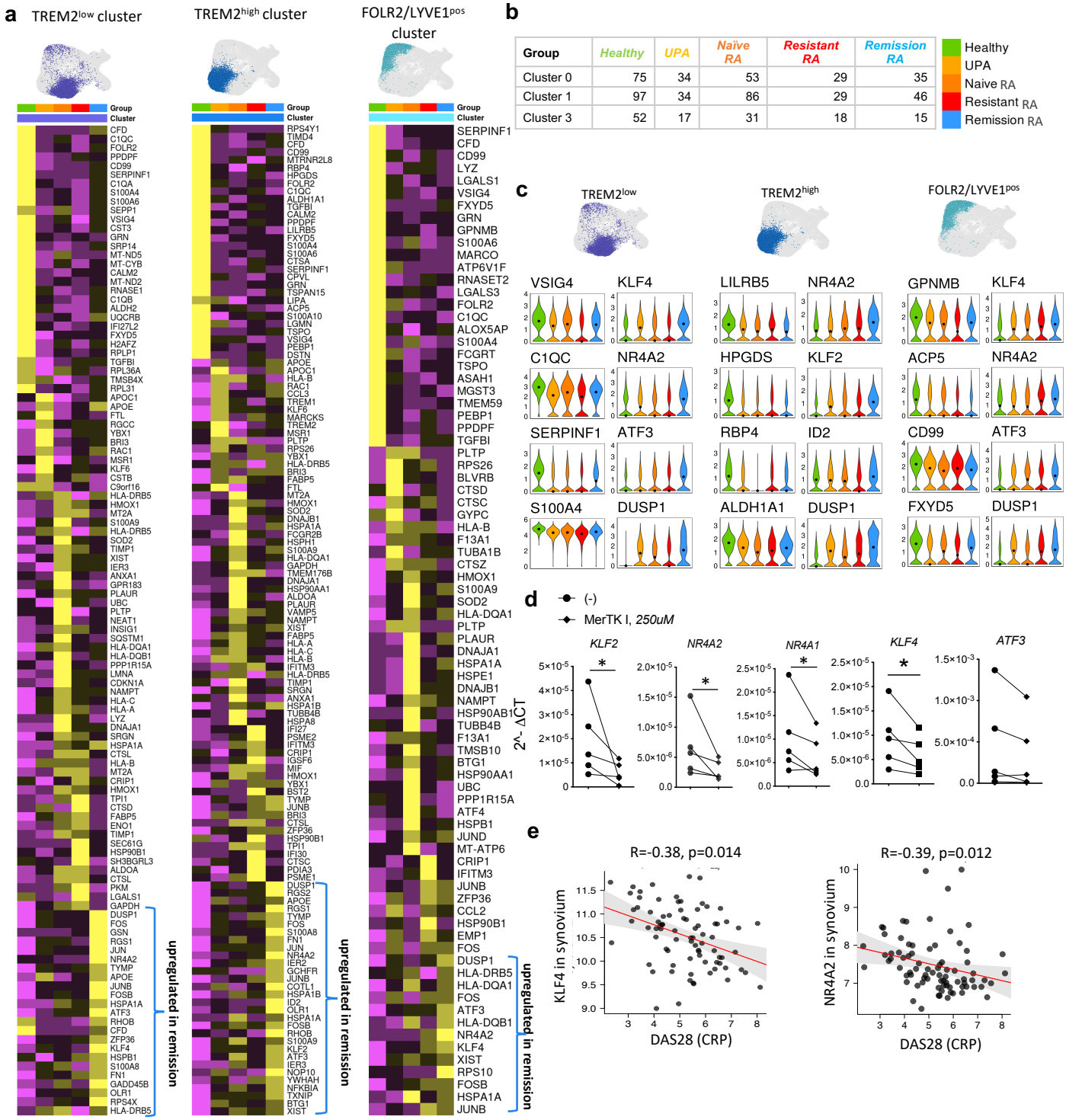

Group	Healthy	UPA	Naïve RA	Resistant RA	Remission RA
Cluster 0	75	34	53	29	35
Cluster 1	97	34	86	29	46
Cluster 3	52	17	31	18	15

Figure 4. TREM2pos and FOLR2pos clusters of MerTKpos STMs from RA patients in remission share a unique transcriptomic signature. (a) Heatmaps illustrating scaled expression of the top 30 marker genes of each condition within the TREM2low, TREM2high and FOLR2/LYVE1pos clusters. Rows are genes and columns show equal pseudo-bulk expression per condition within each cluster. All genes are expressed in at least 60% of cells in that condition, with an average log fold-change ≥0.25, ($p<0.05$ corrected for multiple comparisons. (b) The numbers of genes differentially expressed between conditions for each cluster. (c) Violin plots illustrating the expression of top marker genes of TREM2pos and FOLR2pos clusters unique for healthy or remission STMs. (d) Transcription factors identified in TREM2pos and FOLR2pos clusters in remission are inhibited in macrophages incubated with MerTK inhibitor, *$p<0.05$ paired t-test. (e) Synovial tissue expression of KLF4 and NRA42 in (PEAC cohort) negatively correlates with DAS28.