

A randomized phase 2 clinical trial to treat moderate-to-severe plaque psoriasis patients with high-induction dosing of risankizumab

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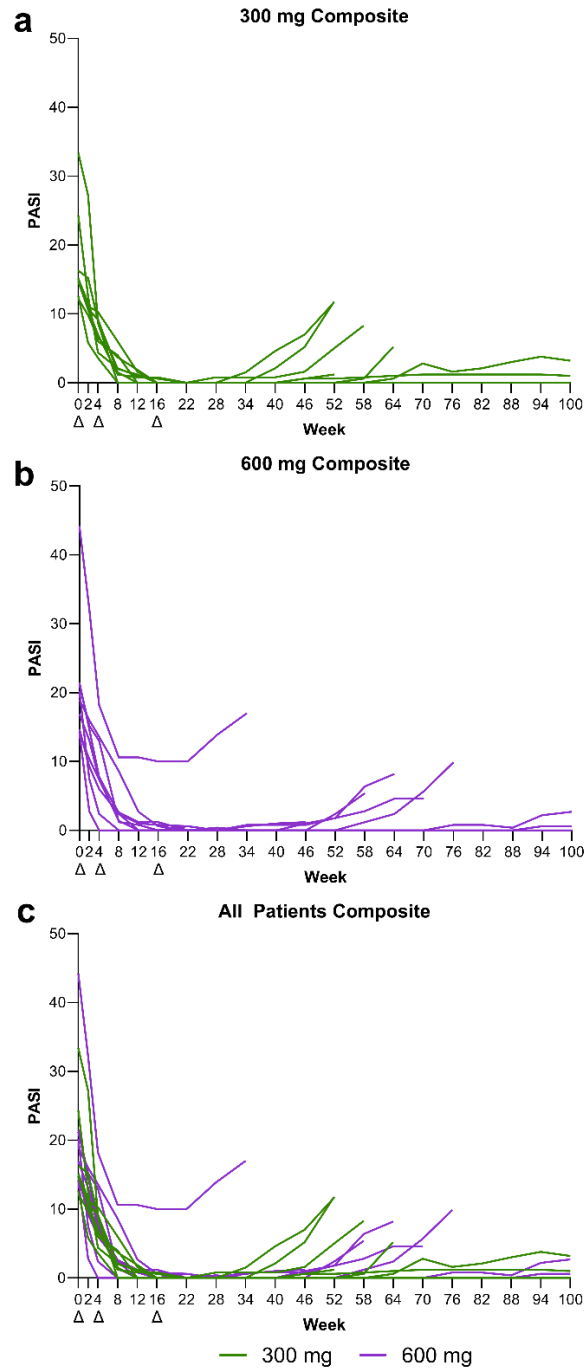
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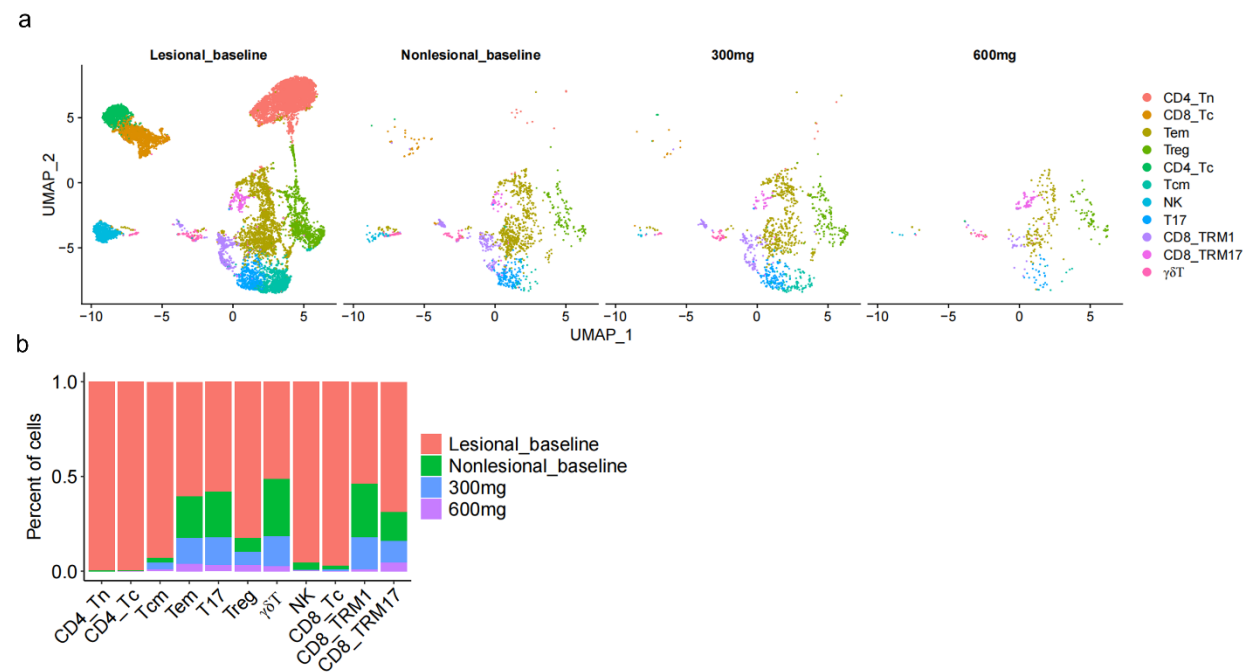
*equal contributions

Supplementary Fig. 1.



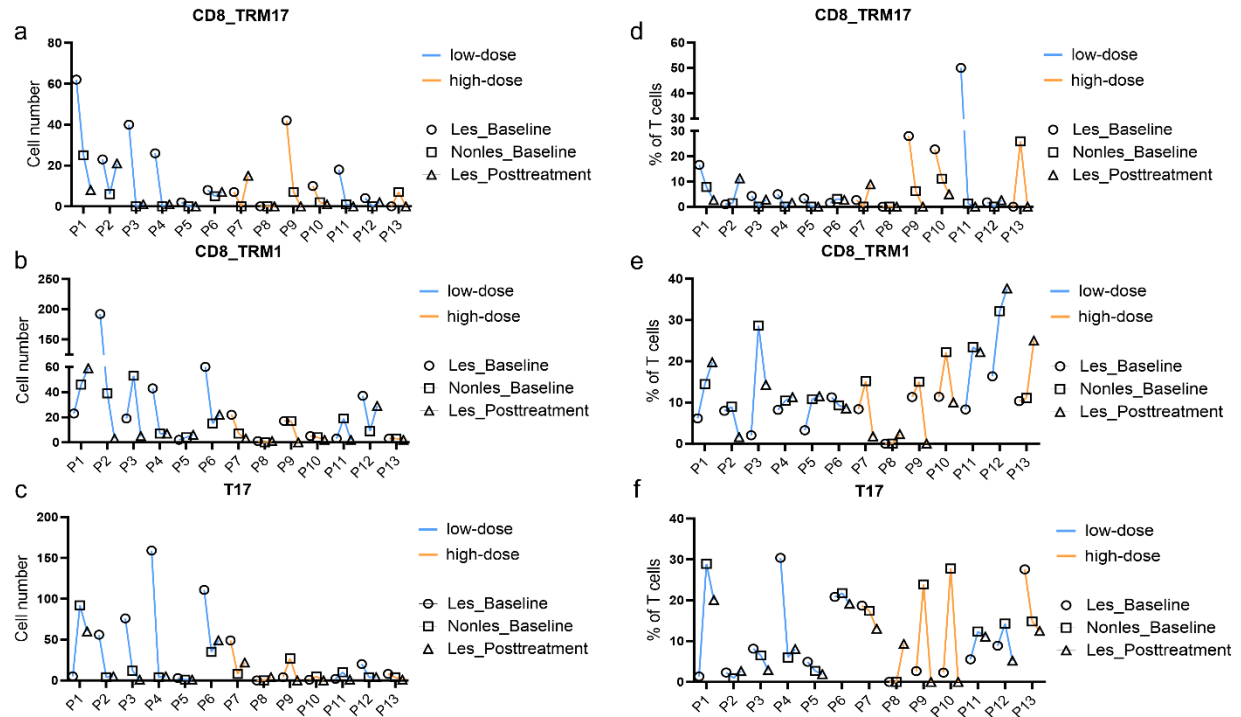
Individual patient PASI trajectories following high induction doses of risankizumab at Weeks 0, 4, and 16. a. 300 mg dose group. b. 600 mg dose group. c. Composite dose group.

Supplementary Fig. 2.



Cell composition of T cell subtypes in 4 sample groups. a. UMAP plot showing the cells colored by T cell subtypes, split by different group. **b.** Bar plot showing the abundance composition across the groups for each subtype.

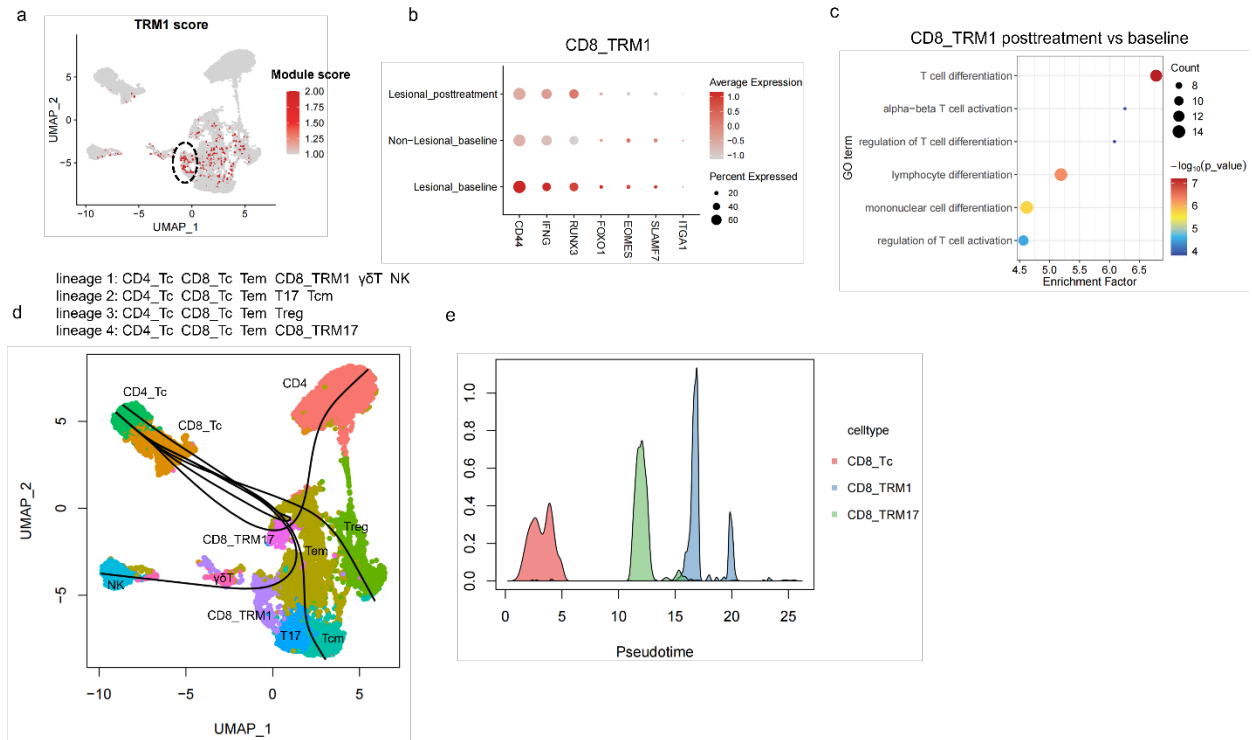
Supplementary Fig. 3.



Populations of specific T cell subtypes before and after risankizumab treatment.

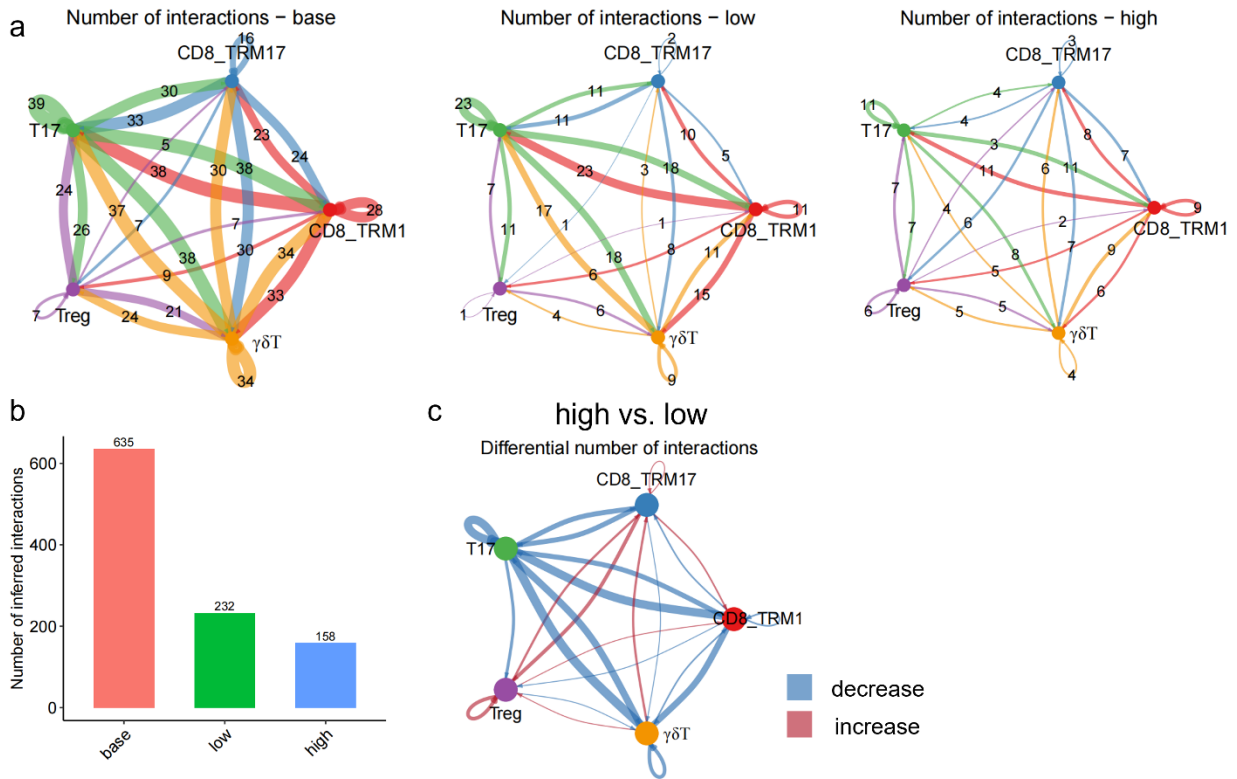
Absolute abundance of key immune cell types, including CD8+TRM17 (a), CD8+TRM1 (b), and T17 (c). Line color and shape represent treatment dose and sample groups, respectively. Relative proportions of key immune cell types, including CD8+TRM17 (d), CD8+TRM1 (e), and T17 (f). Line color and shape represent treatment dose and sample groups, respectively.

Supplementary Fig. 4.



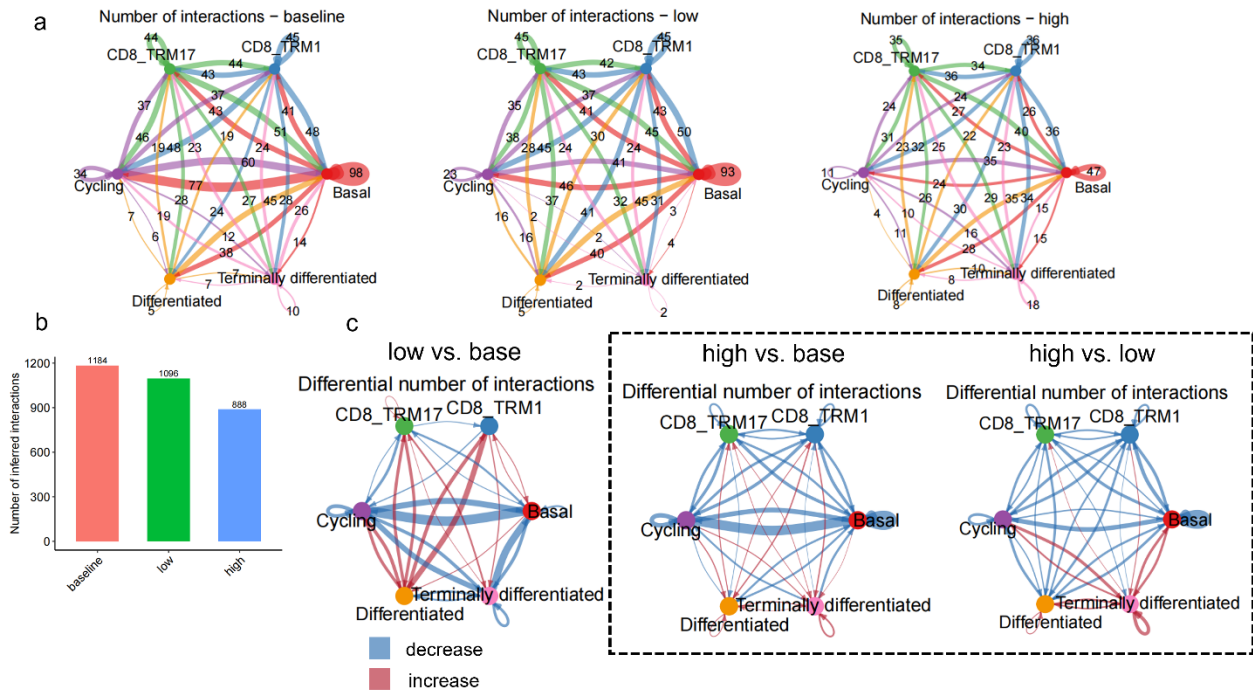
Differential expression analysis in CD8+TRM1 cells. a. UMAP visualization of T cells, showing the module score of TRM1 markers observed in each subtype. **b.** Risankizumab-induced downregulation of genes in CD8+TRM1 cells. **c.** Dot plot showing the top Gene Ontology (GO) pathway enrichment using DEGs comparing post-treatment (300 mg and 600 mg) to baseline in CD8+TRM1. **d.** Pseudotime analysis projected onto UMAP plot. Curves represent inferred trajectories. **e.** T cell subsets distribution density along pseudotime.

Supplementary Fig. 5.



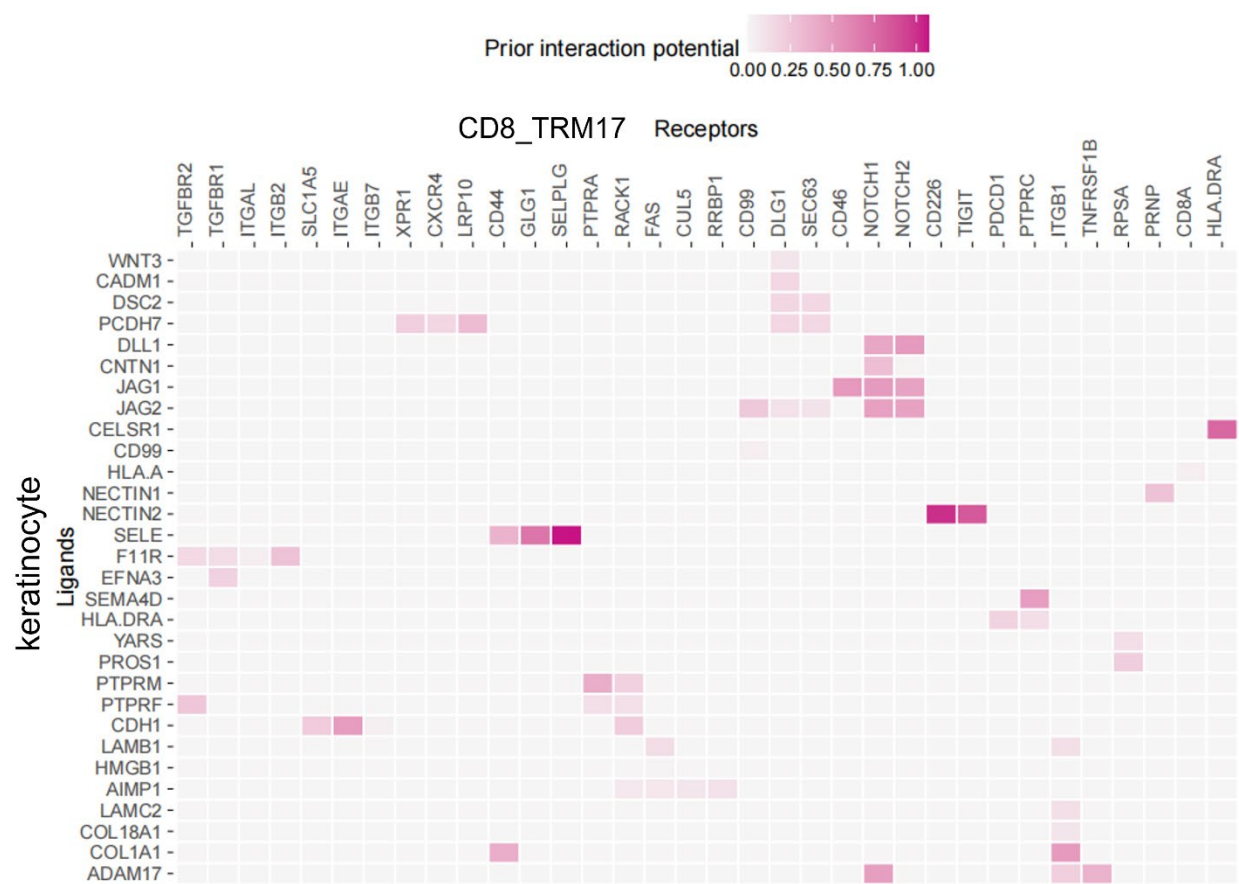
Cellular interactions between T cell subtypes. a. Network analysis showing communication between specific T cell subtypes. **b.** Bar plot showing the number of inferred interactions among T cell subtypes in different groups. **c.** Network analysis showing up-regulated or down-regulated interactions between specific T cell subtypes in the 300 mg and 600 mg dose groups. Blue represents decreases and red represents increases.

Supplementary Fig. 6.



Cellular interactions between keratinocytes and CD8⁺ T_{RM}. **a.** Network analysis showing communication between keratinocyte subtypes, CD8⁺TRM1, and CD8⁺TRM17. **b.** Bar plot showing the number of inferred interactions among keratinocyte subtypes and CD8⁺ T_{RM} cells in different groups. **c.** Network analysis showing up-regulated or down-regulated interactions under several comparisons. Blue represents decreases and red represents increases.

Supplementary Fig. 7



NicheNet ligand activity prediction for the communication between keratinocytes and CD8+TRM17. Matrix showing the potential targets of the top ranked ligands from keratinocytes and their potential receptors in CD8+TRM17.