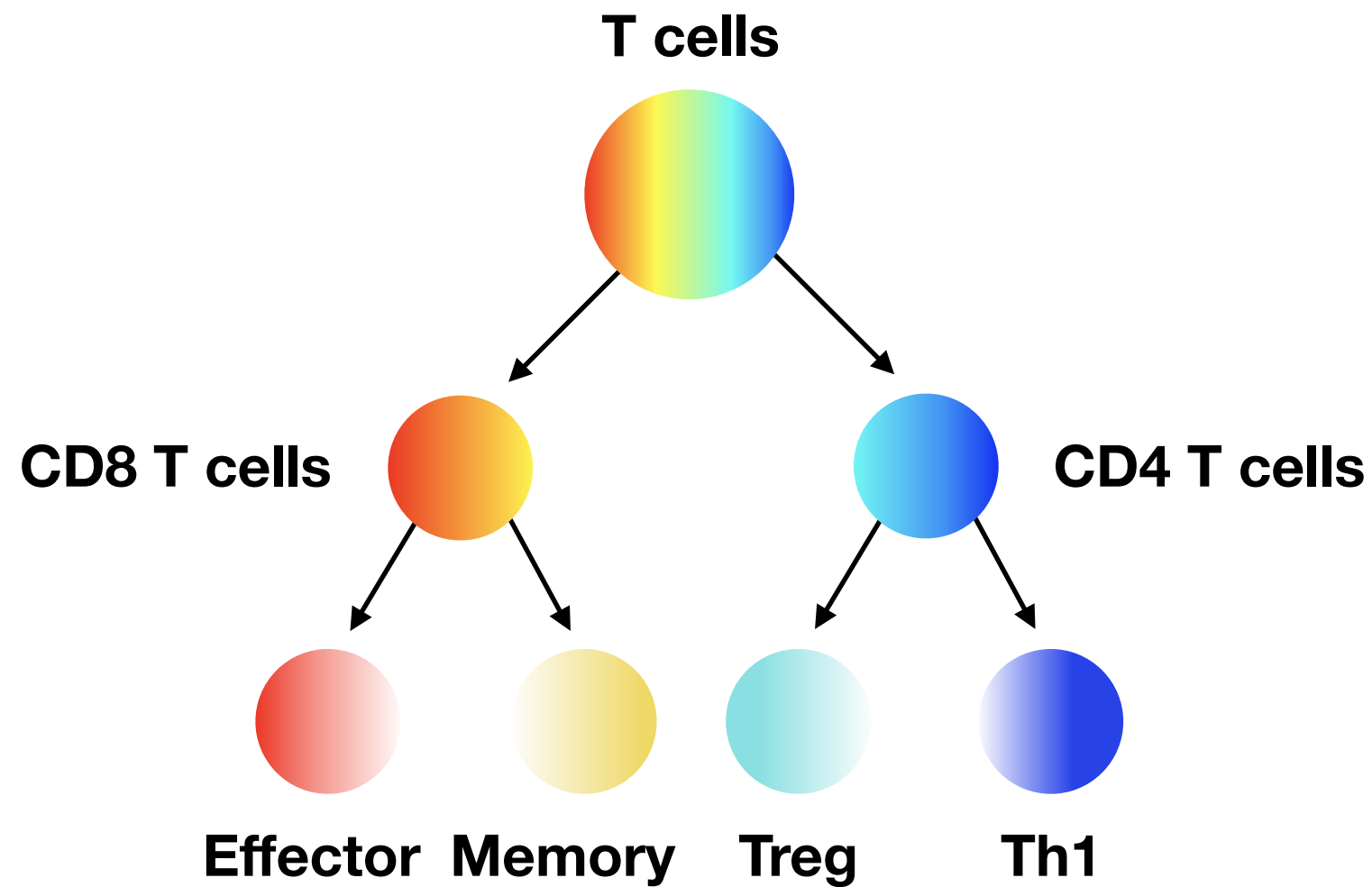


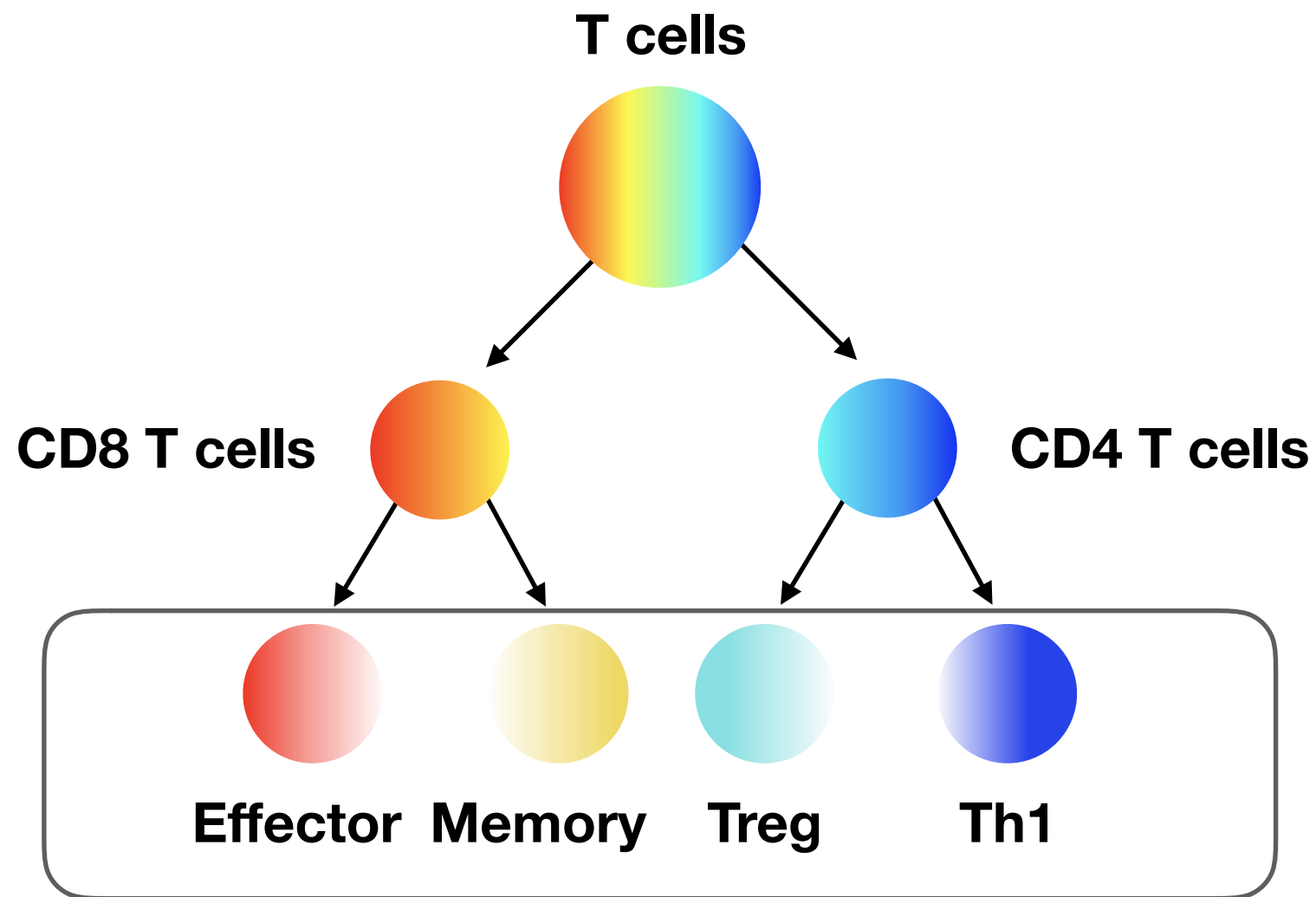
# Robust sub-population discovery using self-pruning decision trees

Claire Malley, Mamie Wang, Billy Kim,  
Amulya Shastry, Christopher Rhodes,  
Jonathan Badger, Assaf Magen

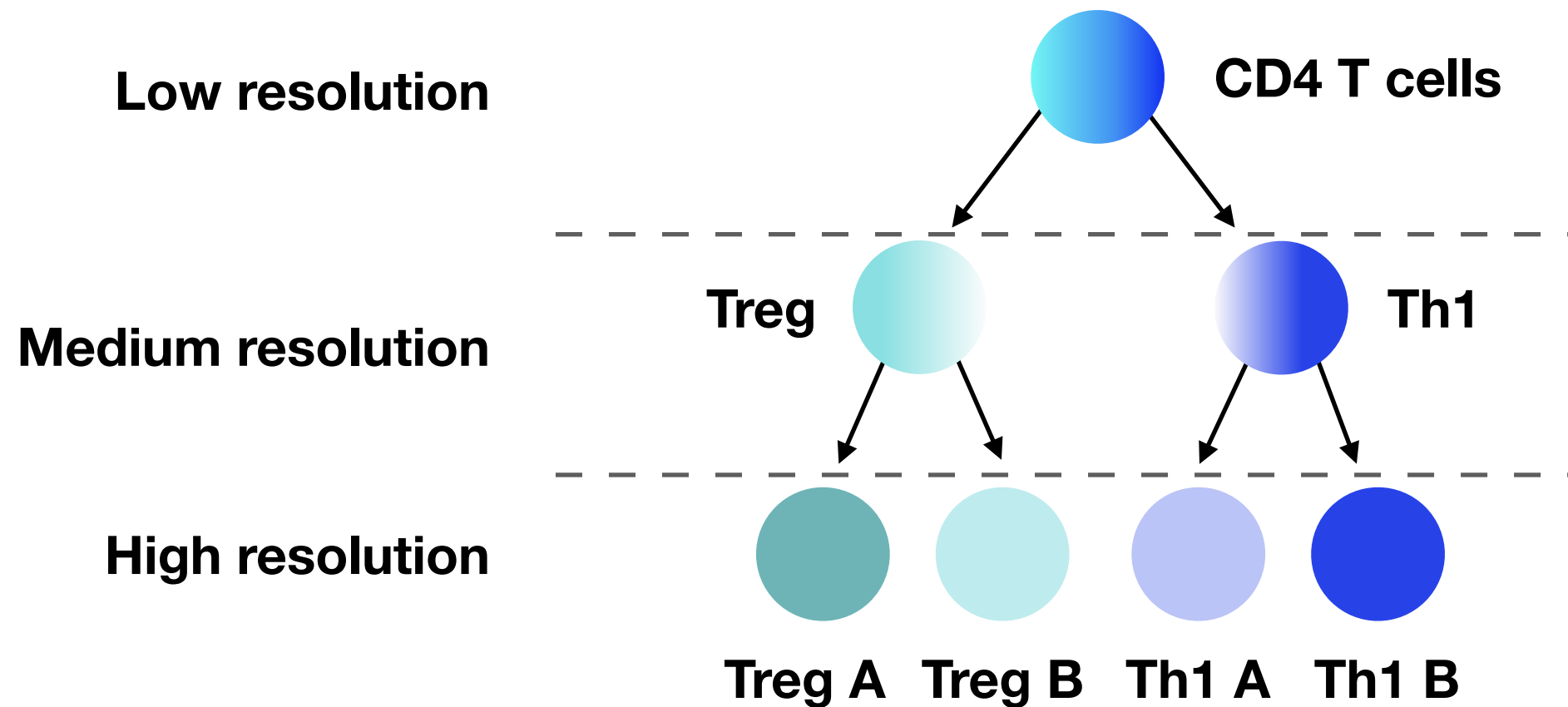
scRNAseq can be used to characterize  
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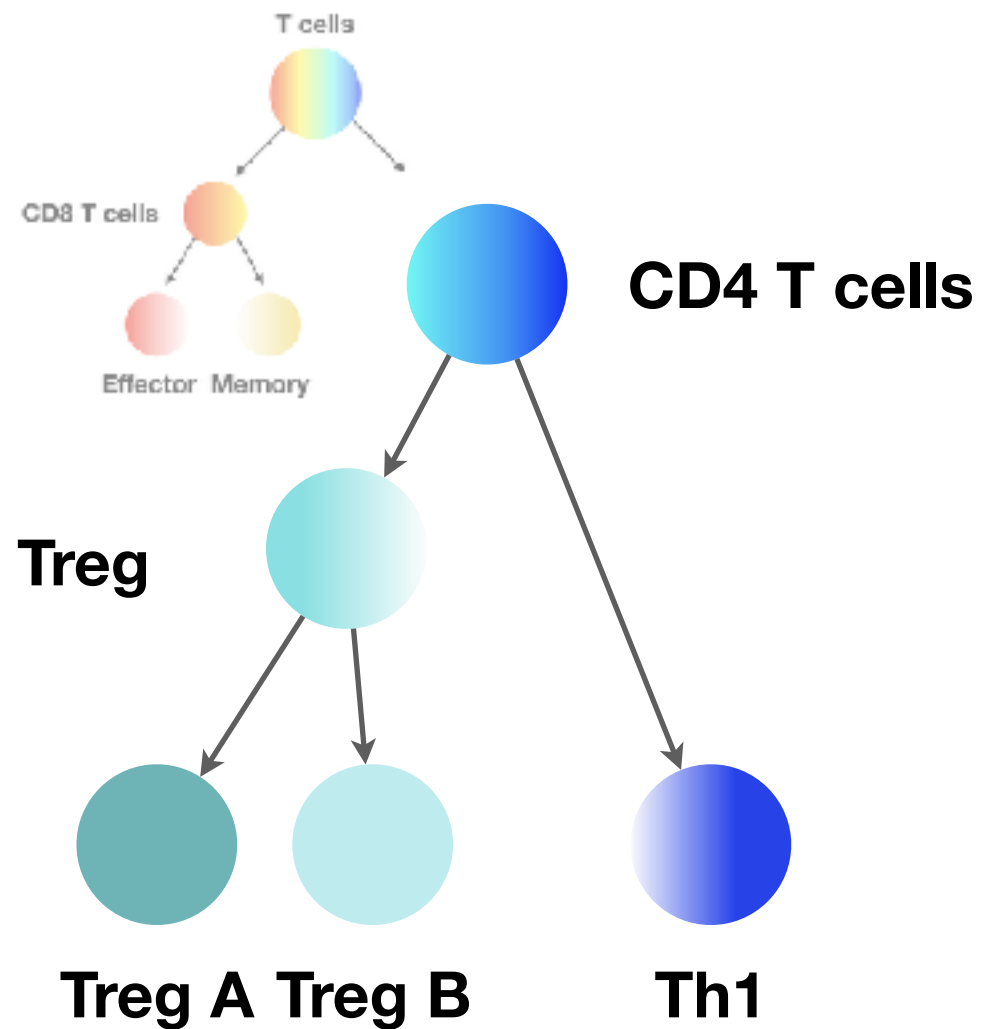


# Many questions remain unanswered

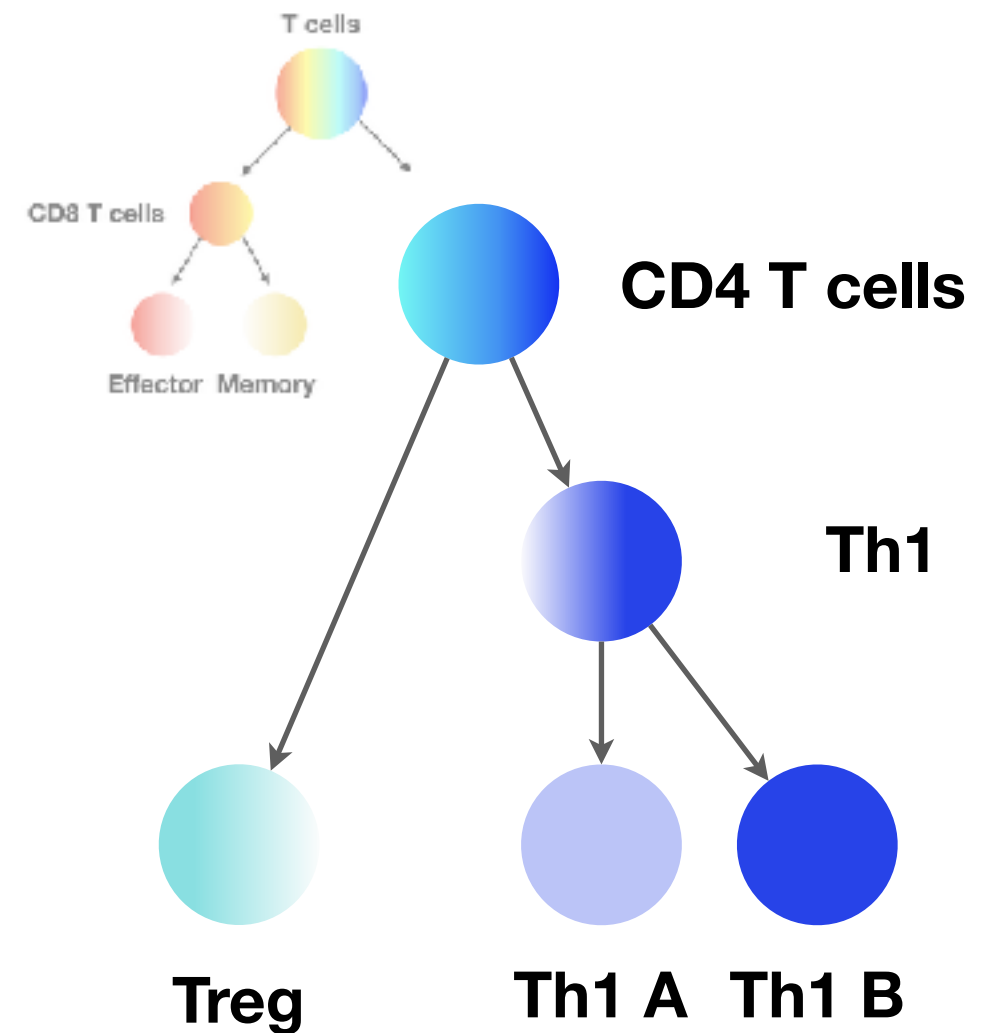


# Independent experiments can provide the solution

## Experiment I

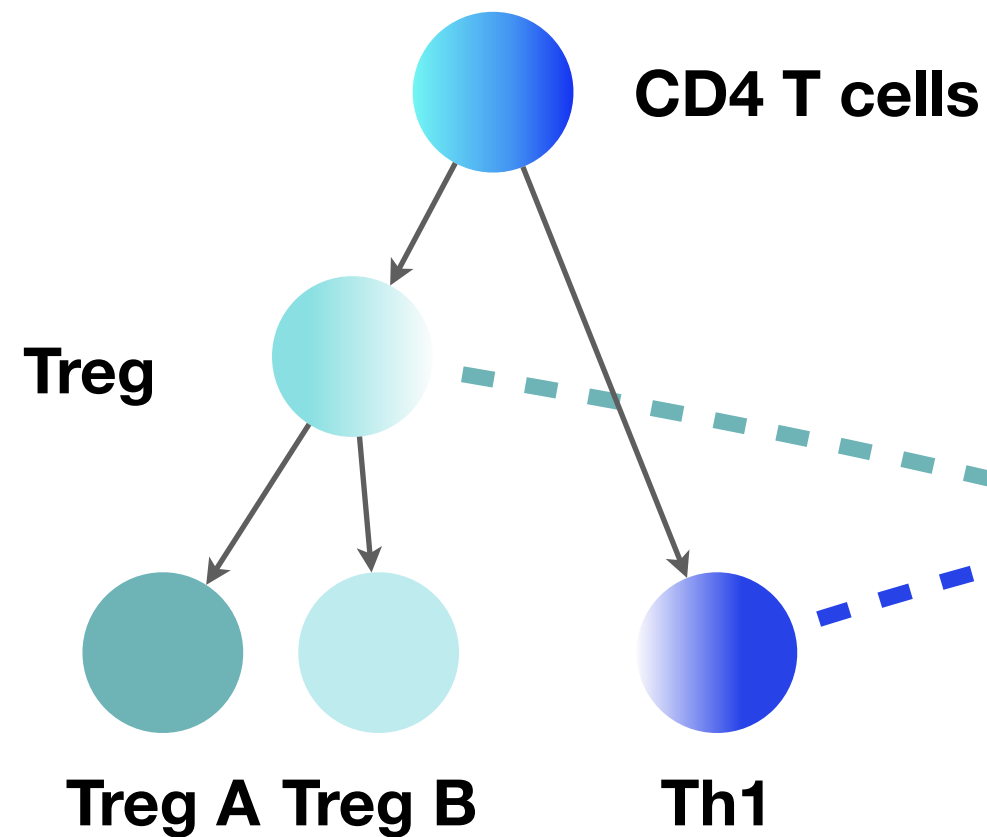


## Experiment II

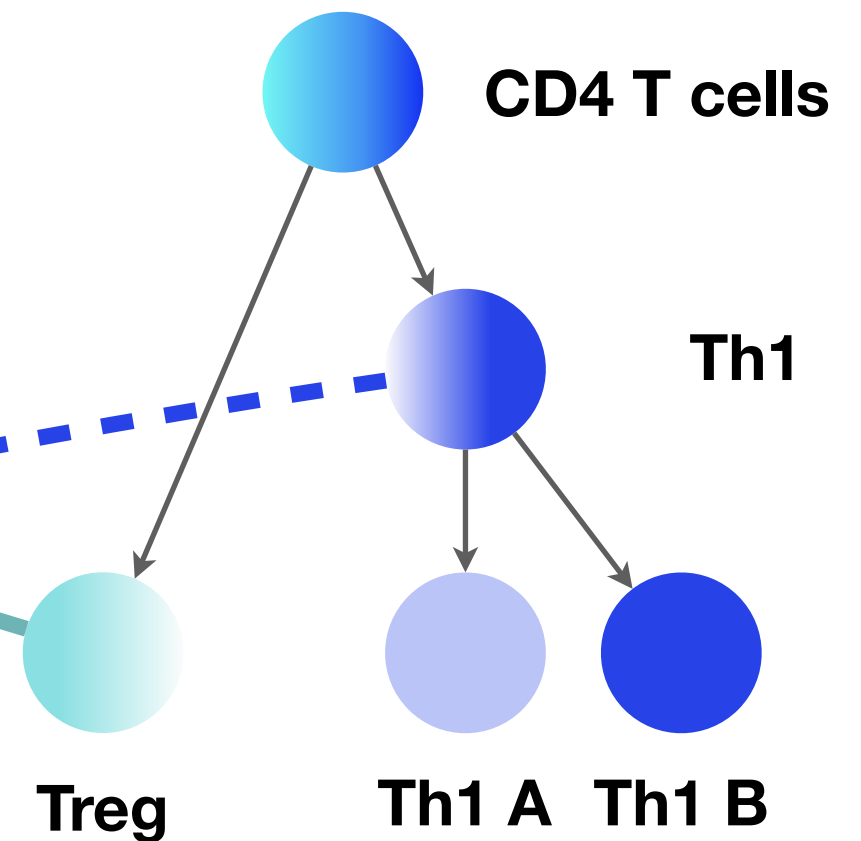


# Reproducibility analysis across experiments

## Experiment I

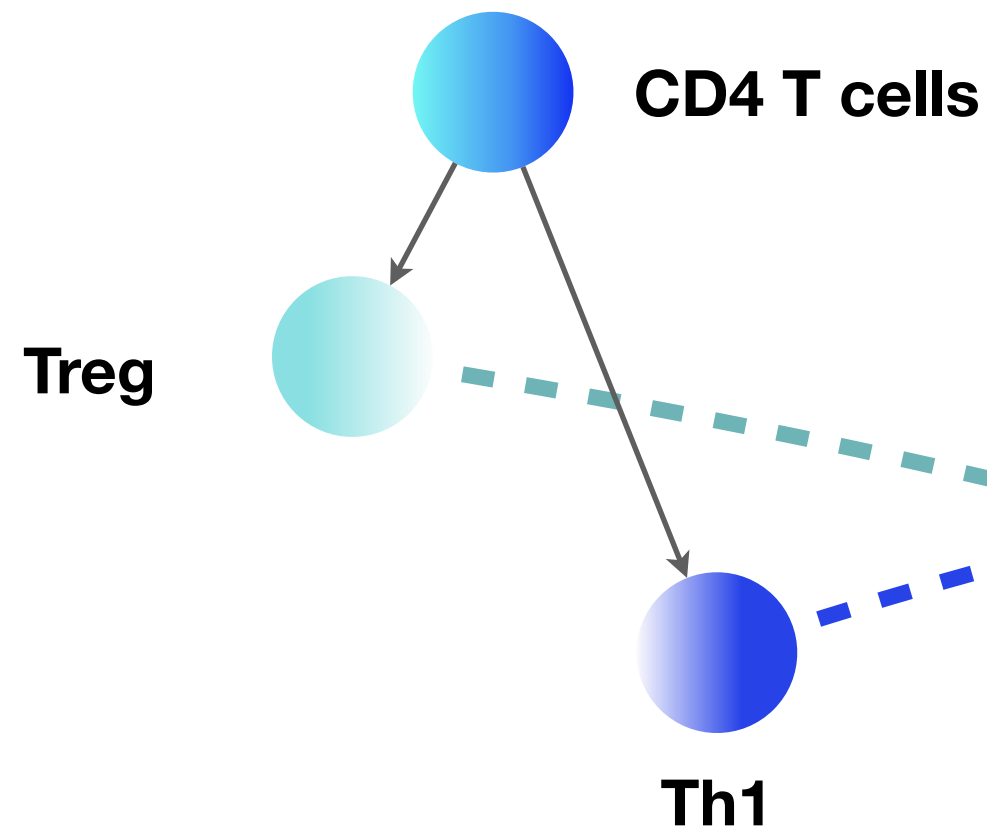


## Experiment II

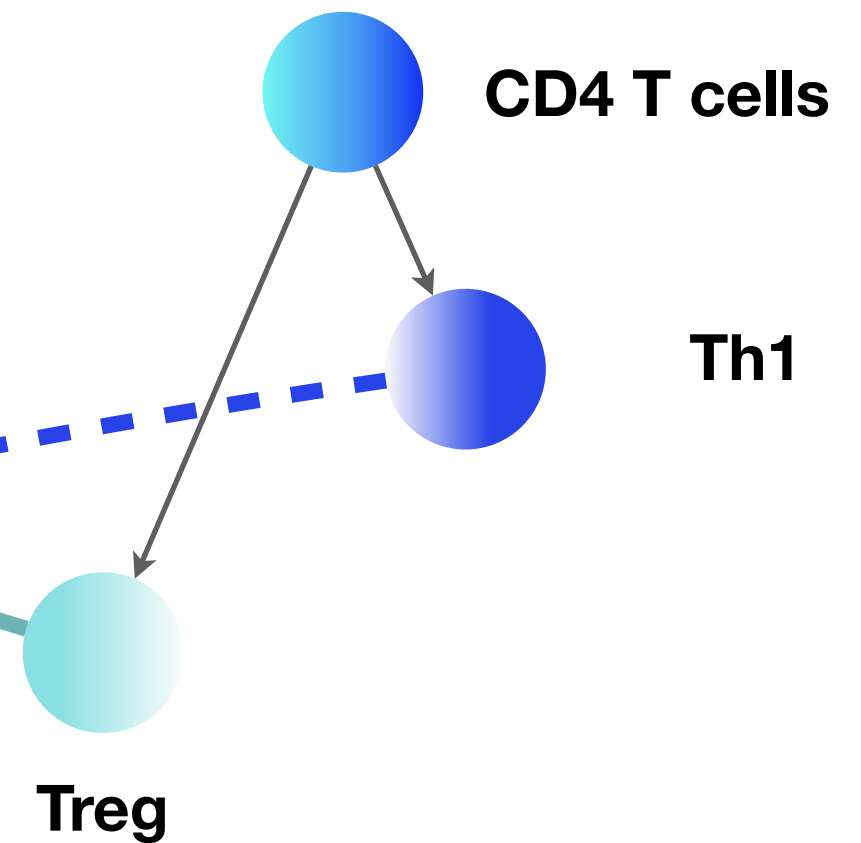


# Retain the reproducible hierarchy components

## Experiment I

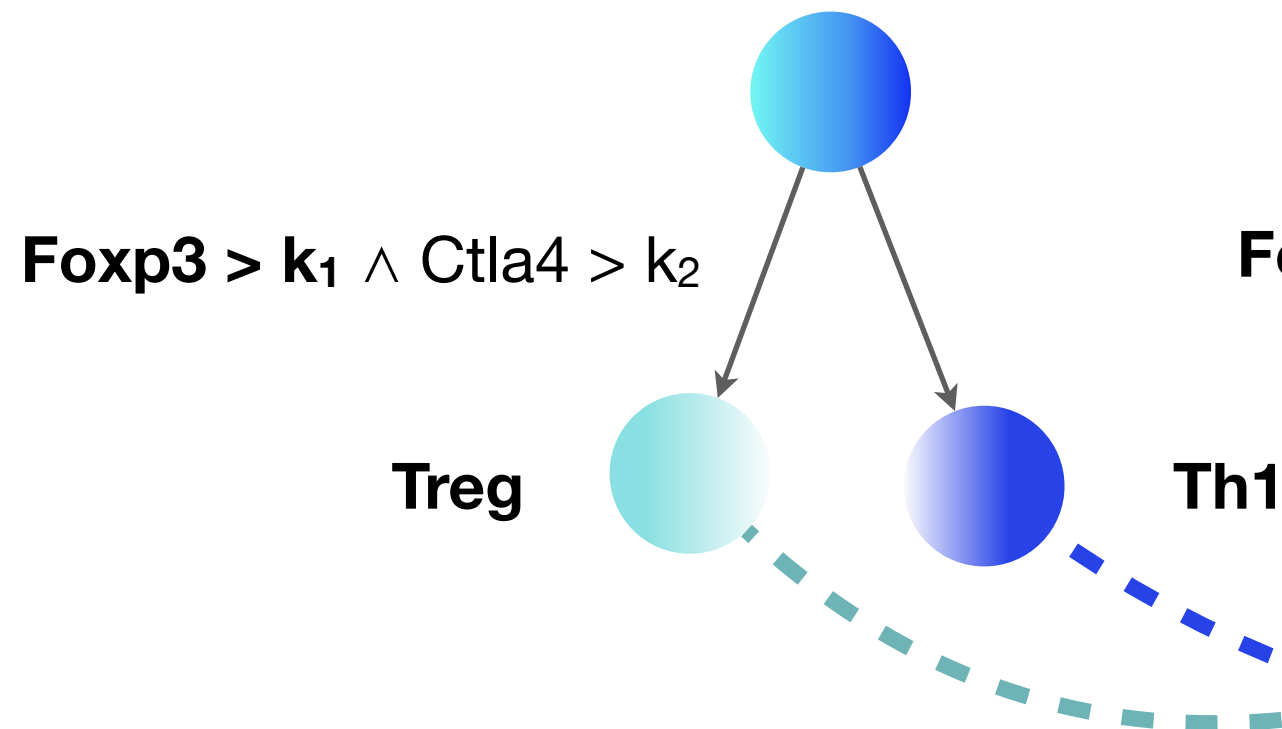


## Experiment II

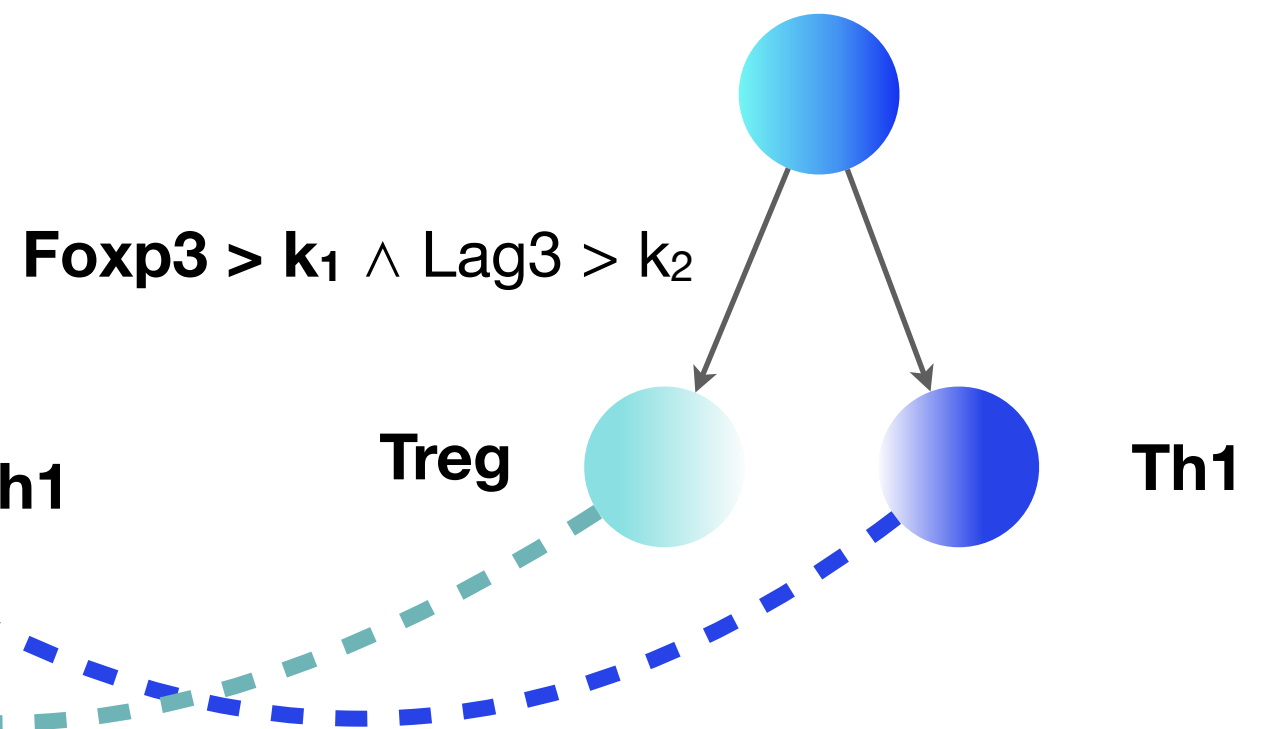


# Contrast differential expression between subtrees

## Experiment I



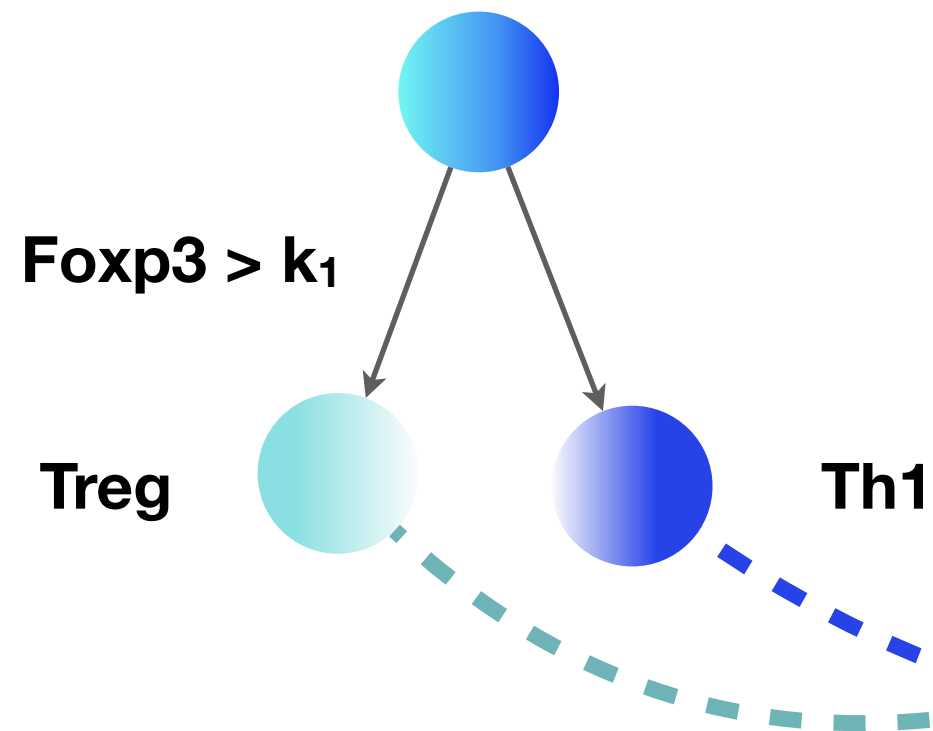
## Experiment II





# Identify robust population defining genes

## Experiment I



## Experiment II

