**The roadmap**

We propose the following roadmap for the research community:

1) For a gene of interest that is among the DEGs, one can search **Table S1** for relative gene expression across CD8+ T subsets, search **Table S3** to determine the histone modification states at the gene promoters, search **Tables S4** and **S5** to find a regulating enhancer(s) and its activities at different stages of CD8+ T cell responses. One can also search **Table S6** to determine if the gene is regulated by a super enhancer. In **Table S7**, one can find TF(s) predicted to regulate the expression of the gene of interest during CD8+ T cell responses.

2) For a gene of interest that is NOT among the DEGs, one can search **Table S4** and **S5** to find a regulating enhancer(s) and its activities at different stages of CD8+ T cell responses.

3) For a TF of interest, **Table S7** shows the enhancers it binds and corresponding target gene promoters across CD8+ T subsets, which can provide useful information for applying “reverse genetic” approaches to identify and characterize key protein factors that act *in trans* at the enhancers.

4) For an enhancer of interest, one can search **Tables S4** and **S5** for its genomic coordinates and potential target genes at different stages of CD8+ T cell responses, search **Table S6** to determine if it is part of a super enhancer, search **Table S7** to identify enriched TF motifs. With the advance of genome editing technologies, the contribution of a TF, an enhancer, and the TF-enhancer interaction can be experimentally dissected.