

- In-silico perturbation
  - Material
  - Methods
    - Gene chose
  - Result Visualization
    - PERK\_IRE1\_pMJ154
    - ATF6\_PERK\_pMJ150
    - ATF6\_IRE1\_pMJ152
    - ATF6\_PERK\_IRE1\_pMJ158
  - Gene
  - sveral genes concerning IRE1

# In-silico perturbation

## Material

NCBI dataset: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE90546>

Paper Adamson B, Norman TM, Jost M, Cho MY et al. A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. Cell 2016 Dec 15;167(7):1867-1882.e21. PMID: 27984733

## Methods

### Gene chose

I chose 3 genes which show difference between *ATF6\_IRE1\_pMJ152* and *PERK\_IRE1\_pMJ154* to evaluate whether using tfs to reconstruct the genes is reliable.

## Result Visualization

Test Dataset

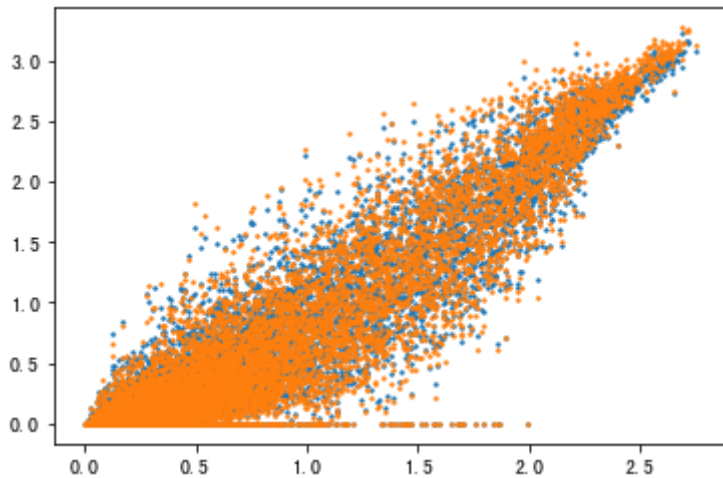
{'ATF6\_IRE1\_pMJ152',

'ATF6\_PERK\_IRE1\_pMJ158',

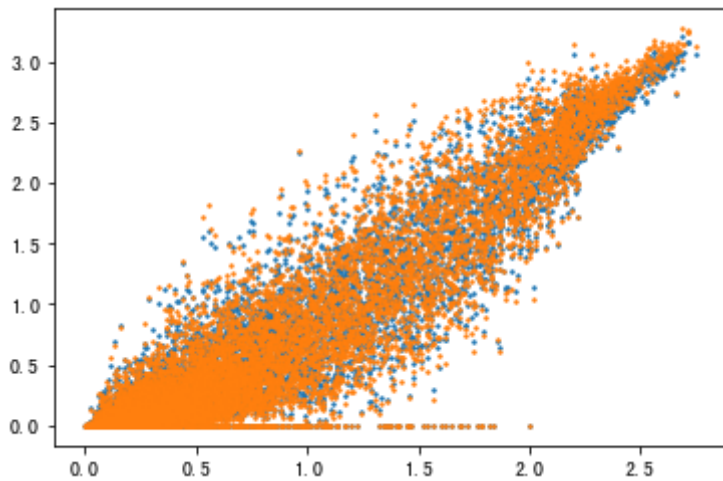
```
'ATF6_PERK_pMJ150',  
'PERK_IRE1_pMJ154'}
```

We show the reconstruction of genes by transcription factors in an in-silico perturbation dataset. Two visualizations are included, one comparing predicted genes with real genes (blue), and the other comparing other processed genes with real genes (orange).

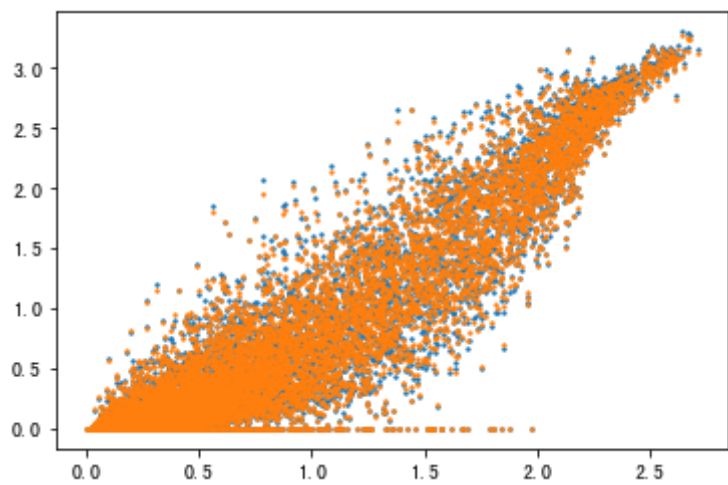
## PERK\_IRE1\_pMJ154



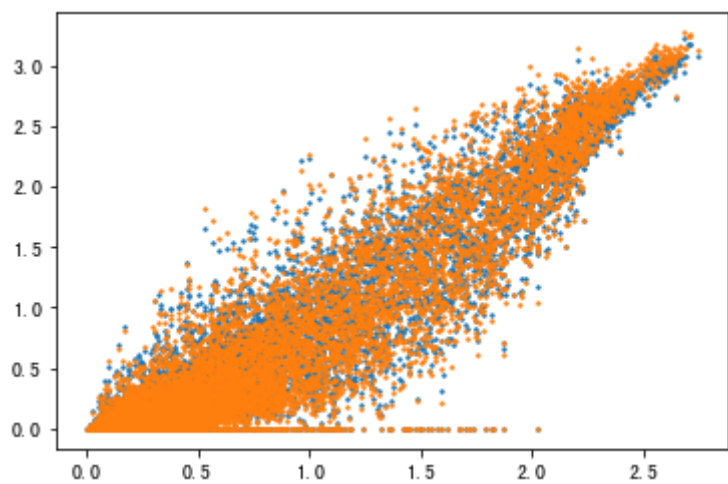
## ATF6\_PERK\_pMJ150



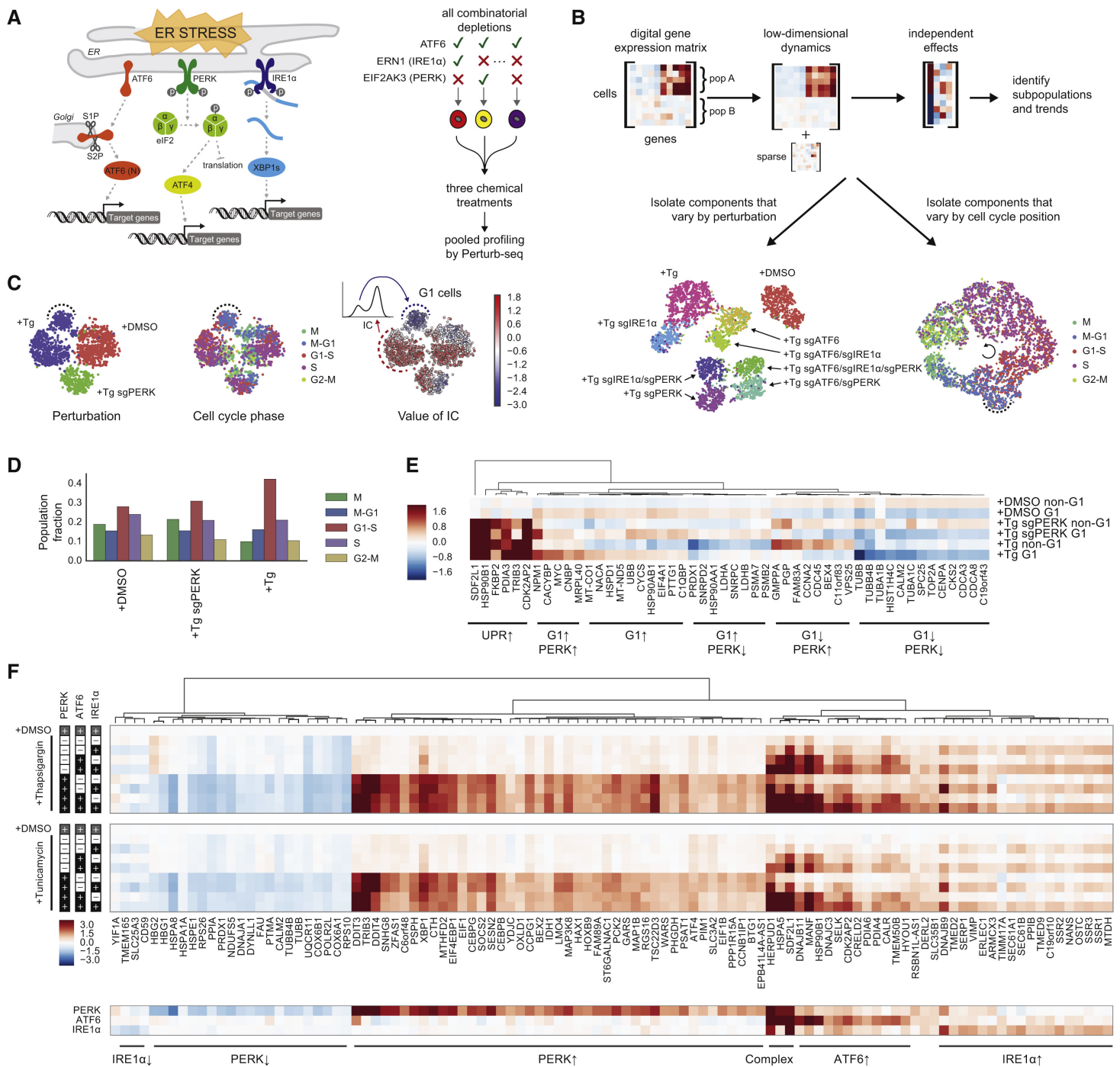
## ATF6\_IRE1\_pMJ152



**ATF6\_PERK\_IRE1\_pMJ158**



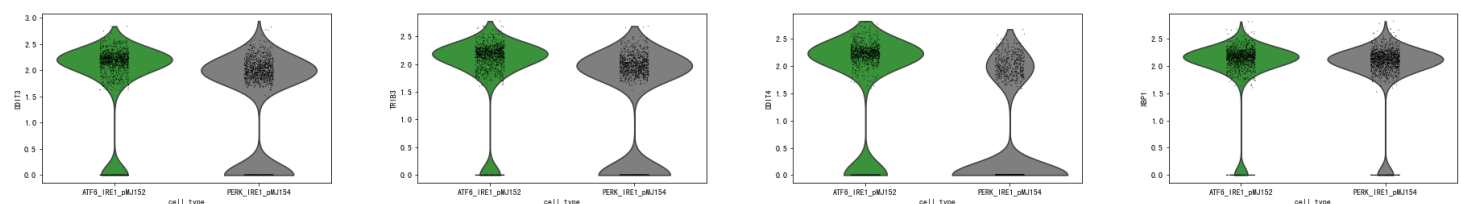
**Gene**



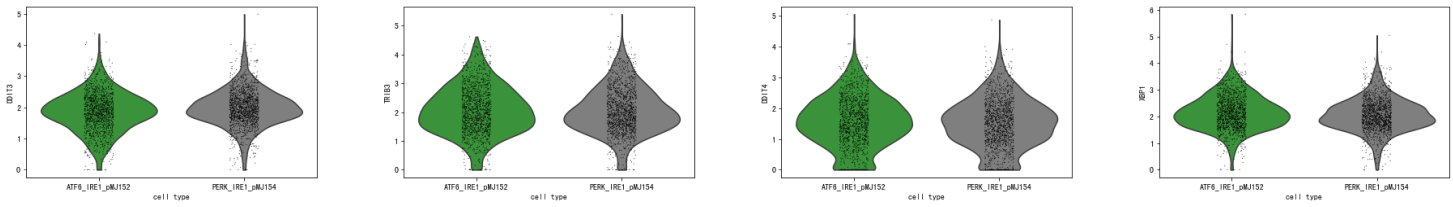
In this paper, the author indicated that some of the genes experienced significantly change.

I chose ATF6\_IRE1\_pMJ152, PERK\_IRE1\_pMJ154 groups to find out whether the difference genes will be reconstructed.

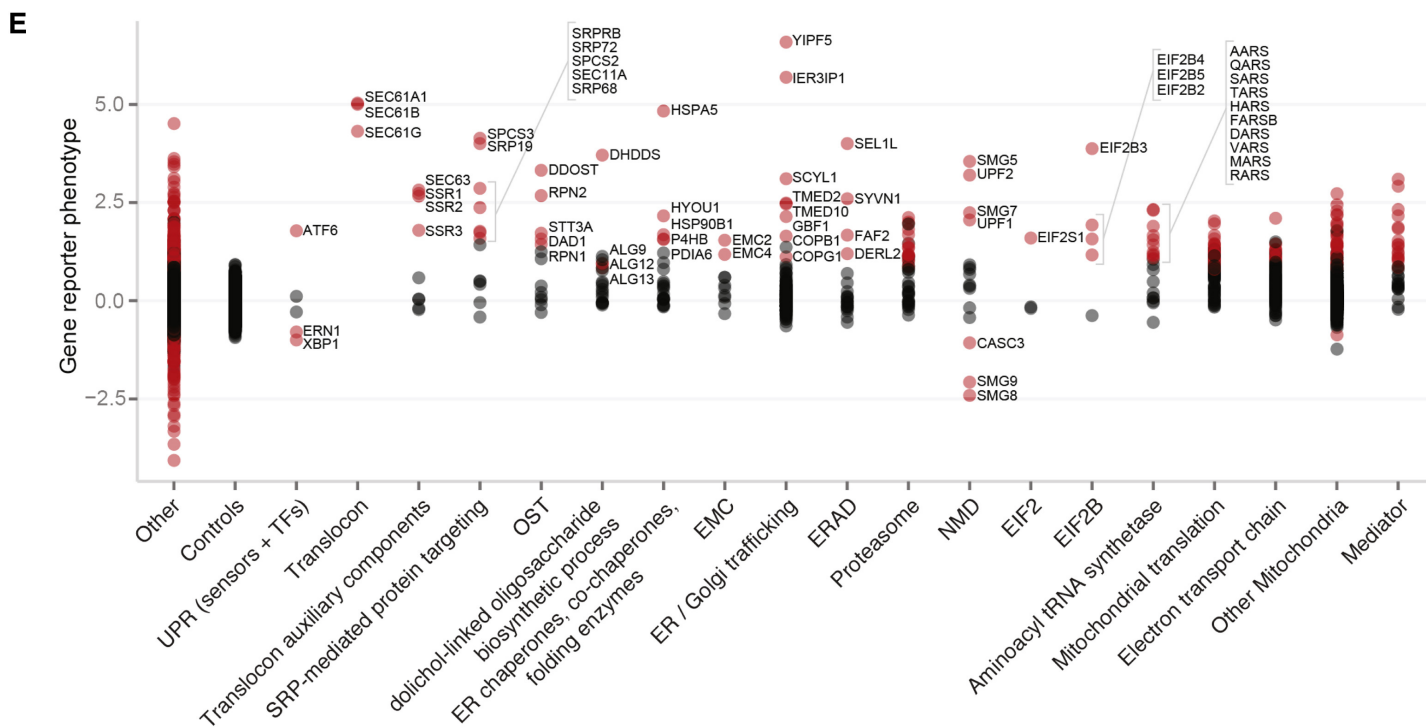
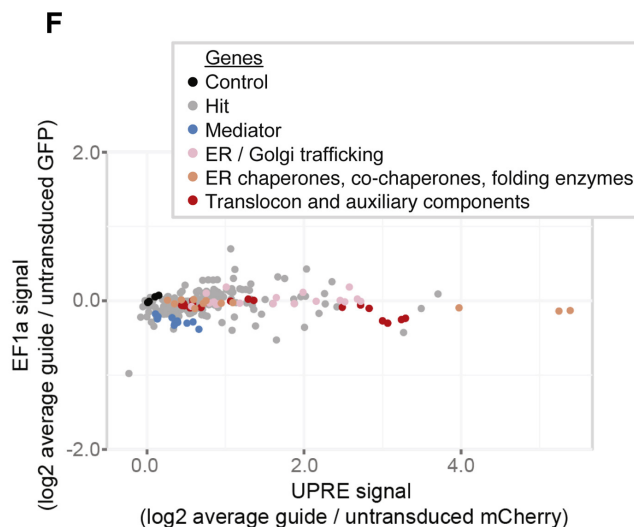
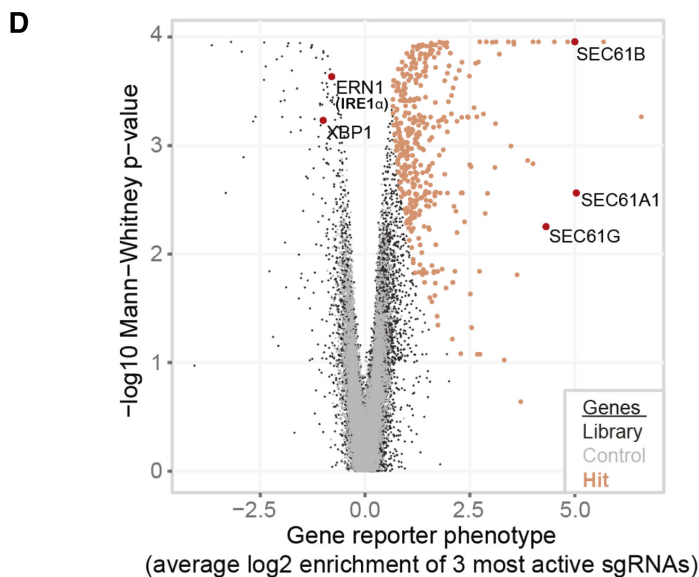
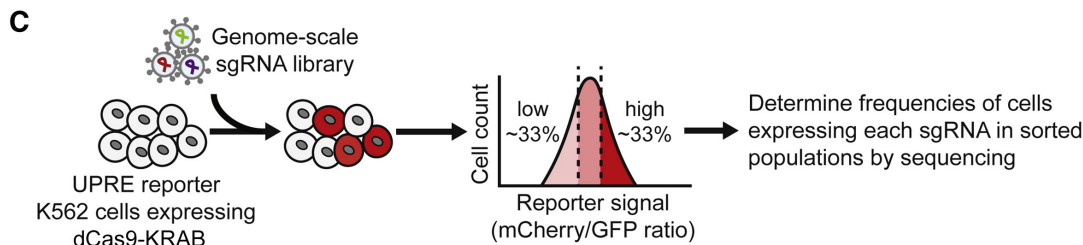
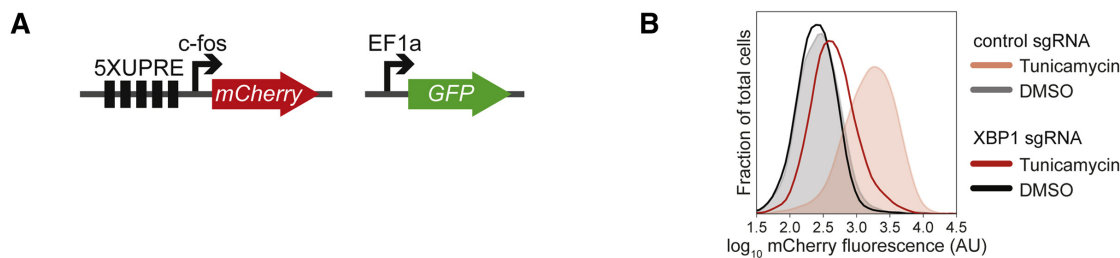
## Original



**Predicted**



**several genes concerning IRE1**



In the paper it said when the IRE1 was perturbed 3 main genes (**SEC61B SEC61A1 SEC61G**) will be suppressed, however it is not very obvious when I used the original data to construct the tsne map.

