**Model Training Results** 

Marginal Footprinting (2wk vs 8wk)

#### TFs we examined:

From motif\_to\_pwm.TF tsv file (image on right).

NRF1 GCGCATGCGC

AP1 CGATATGACTCATCCC

CTCF TTGGCCACTAGGGGGCGCTAT
ETS CCGAAAGCGGAAGTGAGAC
SP1 AAGGGGGCGGGGCCTAA
RUNX CCCTAACCACAGCCC

NFKB GCAAGGGAAATTCCCCAGG

GATA+TAL GGCTGGGGGGGCAGATAAGGCC

TAL GGCTGGG

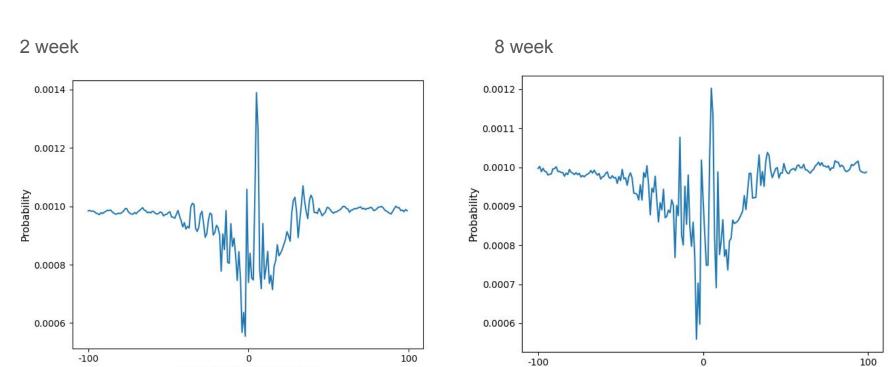
NFYB CCAGCCAATCAGAGC GABPA GAAACCGGAAGTGGCC

BACH1+MAFK AACTGCTGAGTCATCCCG

NRF1 CCCCGCGCATGCGCAGTGC HNF4G CCGTTGGACTTTGGACCCTG

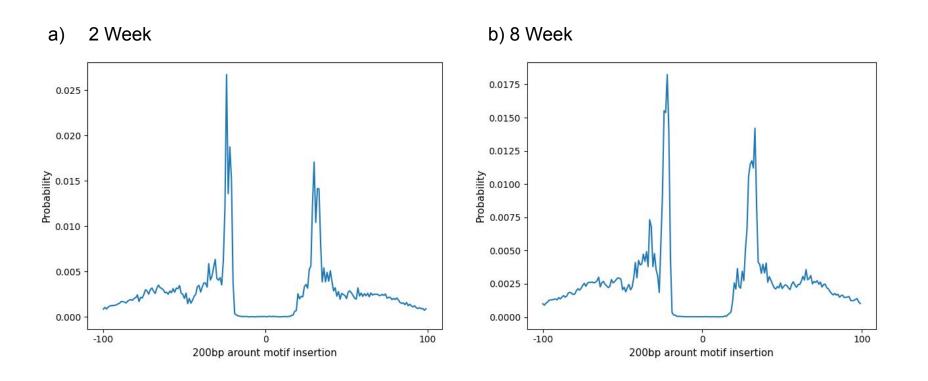
### AP1 footprint - similar.

200bp arount motif insertion



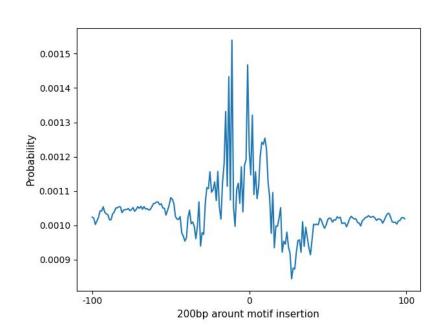
200bp arount motif insertion

### CTCF footprint - "largest" footprints in terms of probability

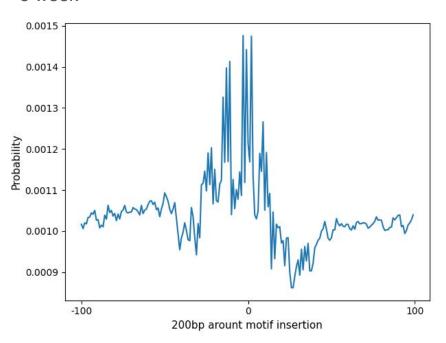


### ETS footprint - highly similar.

2 week

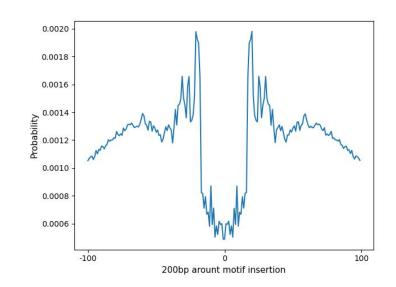


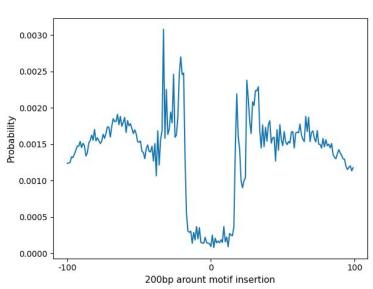




## NRF1 footprint - difference in 0.001 here

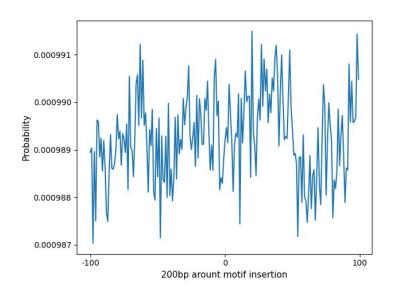
2 week 8 week



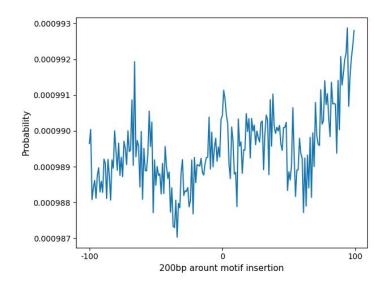


## Control footprint

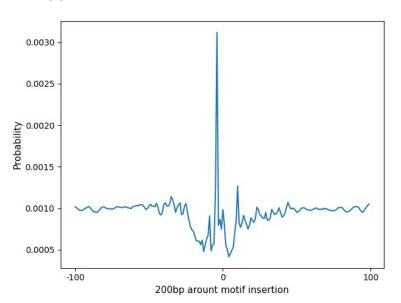
#### 2 week

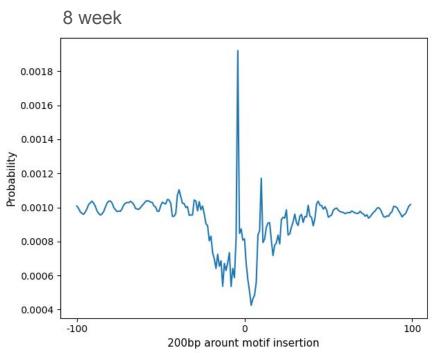


#### 8 week



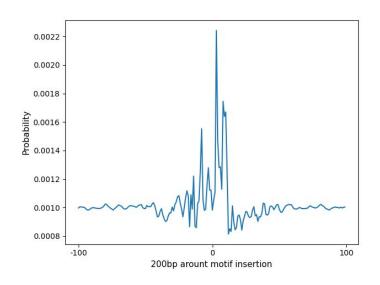
# GATA+TAL ...Additional Footprints (can add to overleaf) 0.001 difference here.

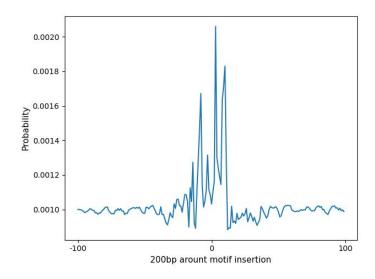




#### NFKB - rather similar.

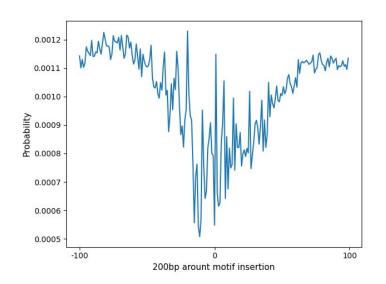
#### Week 2

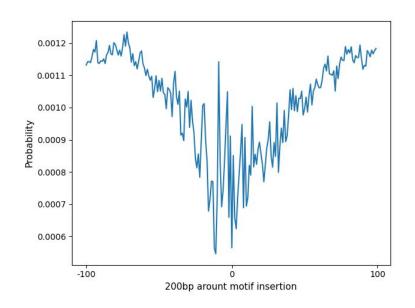




### NFYB - highly similar between the two.

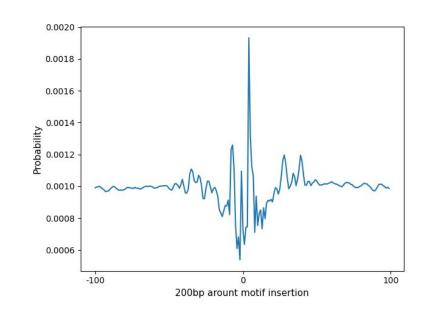
Week 2 Week 8

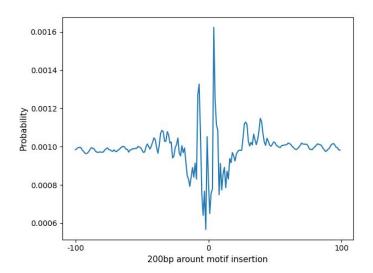




#### RUNX - rather similar.

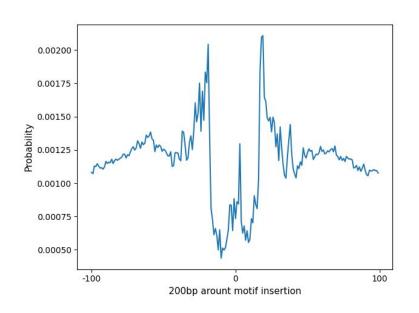
#### Week 2

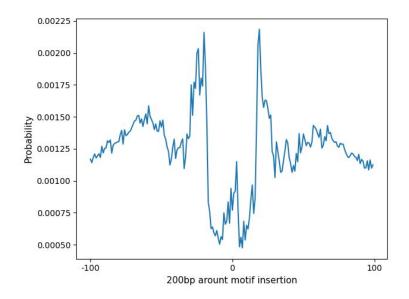




#### SP1 - rather similar.

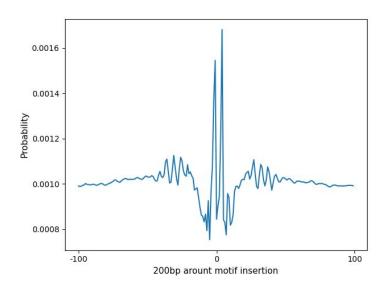
Week 2

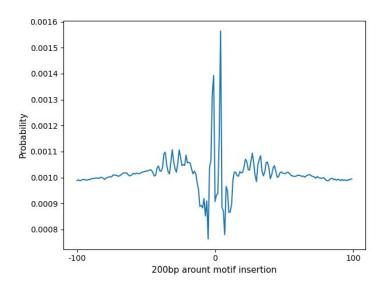




## TAL - highly similar 2 and 8.

#### 2 Week





2wk vs 8 wk SNP motifs

## SNPs we used in variant\_scoring and got shap scores for

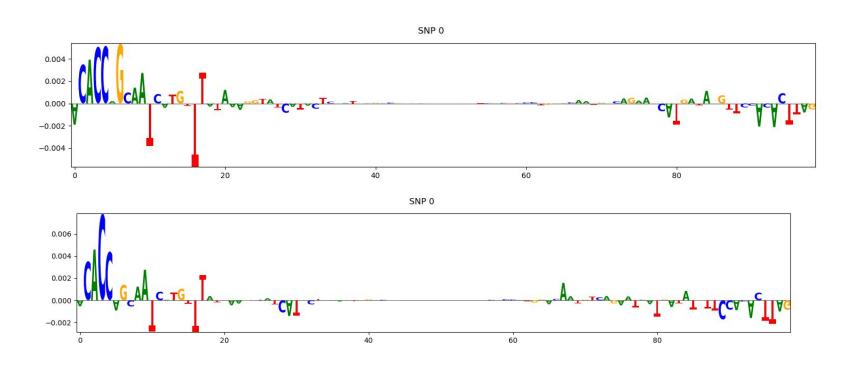
chr5	37859972	Α	С	8*10^-6
chr7	94075721	С	G	3*10^-6
chr7	94075721	С	Α	3*10^-6
chr15	22937754	Α	G	9*10^-6
chr15	22937754	Α	С	9*10^-6
chr15	57786063	Т	Α	2*10^-9
chr3	155998632	Α	G	9*10^-9
chr17	66282726	С	Т	4*10^-8
chr14	81144598	С	Т	9*10^-8
chr1	60952057	G	T	2*10^-6
chr16	7575790	Α	С	1*10^-5
chr16	7575790	Α	G	1*10^-5
chr16	7575790	Α	Т	1*10^-5
chr15	22927754	Α	G	9*10^-6
chr15	22927754	Α	С	9*10^-6
chr2	3170550	T	С	2*10^-6

2 vs 8 Week SNPs

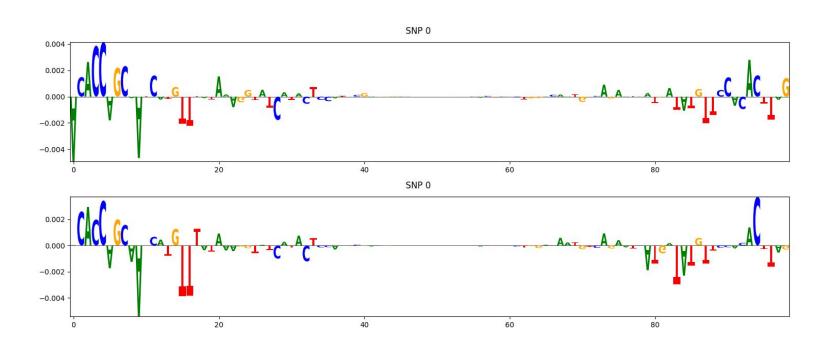
(Allele 1 normal vs. Allele 2 variant).

#### SNP 0 - 8 week

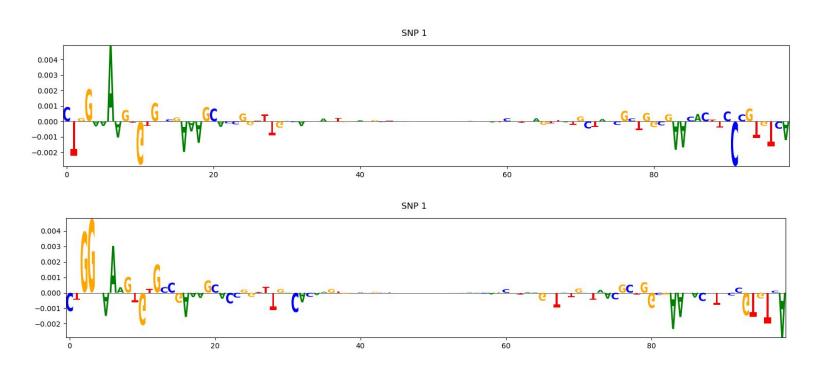
I.e. Index 0 so this is chr5 SNP in the chart on slide 11). Note: Allele 1 (top) vs 2 (variant allele - bottom) for all slides.



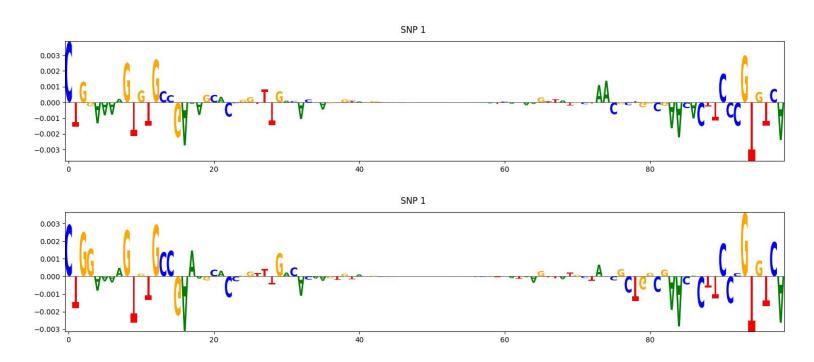
### SNP 0 - 2 week



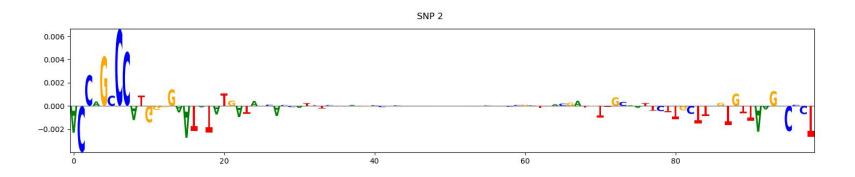
### SNP 1 - 8wk allele 1 (top) vs 2 (variant - bottom).

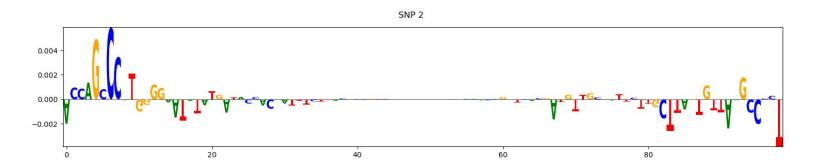


### SNP 1 - 2 week

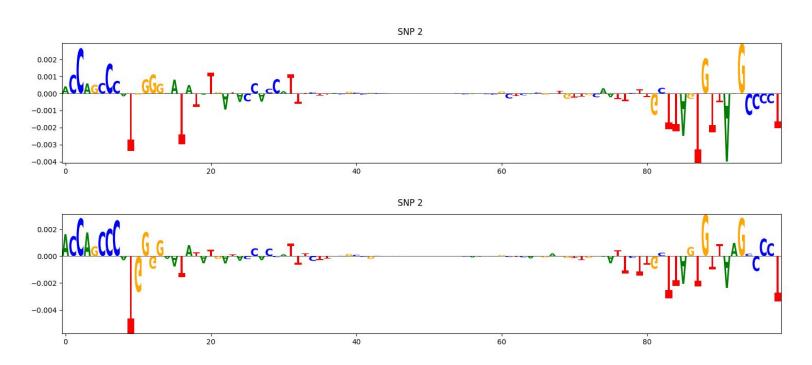


### SNP 2 - 8 week

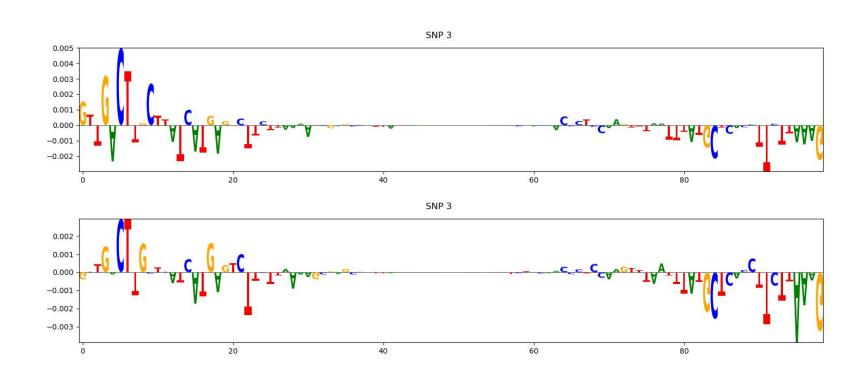




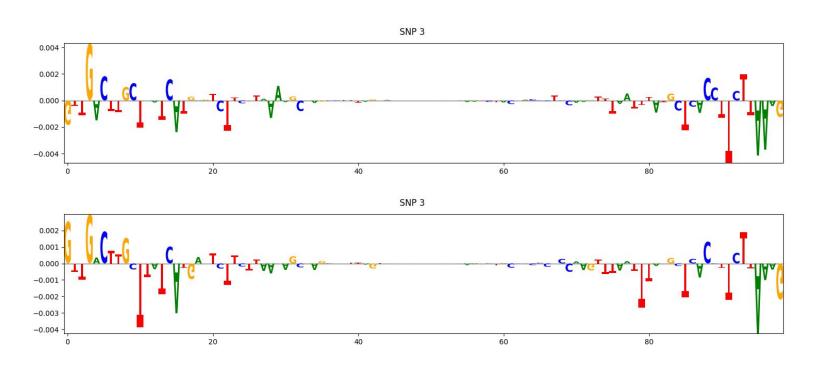
#### SNP 2 - 2 week



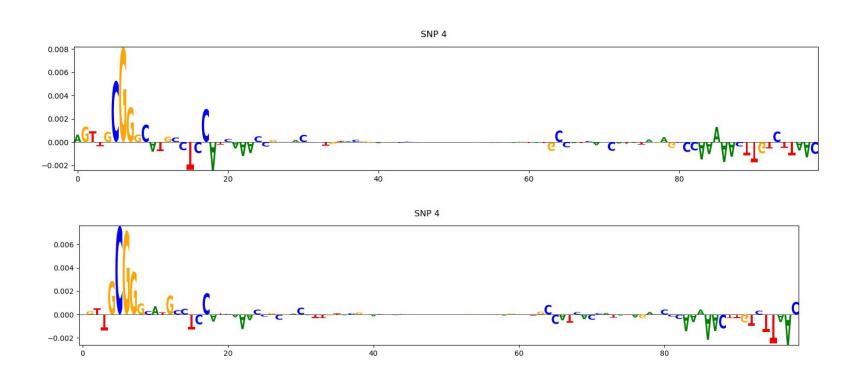
### SNP 3 - 8 week



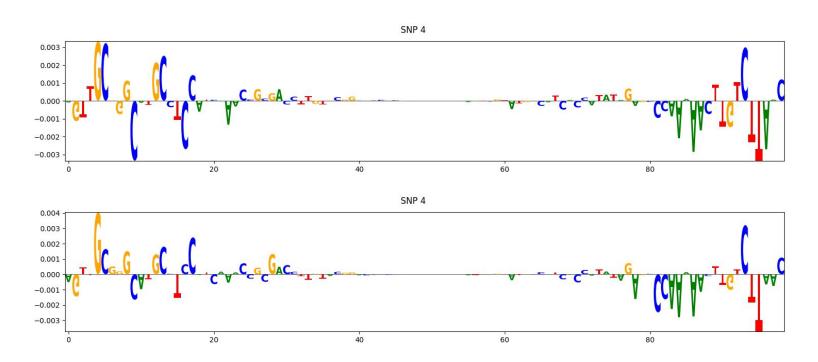
#### SNP 3 - 2 week



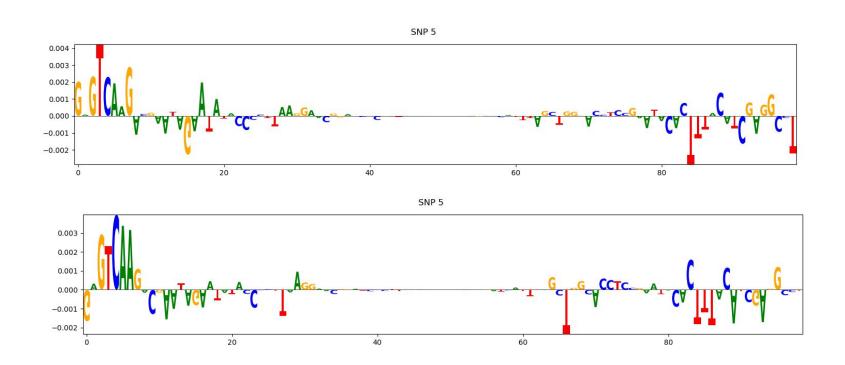
## SNP 4 - 8 week very similar



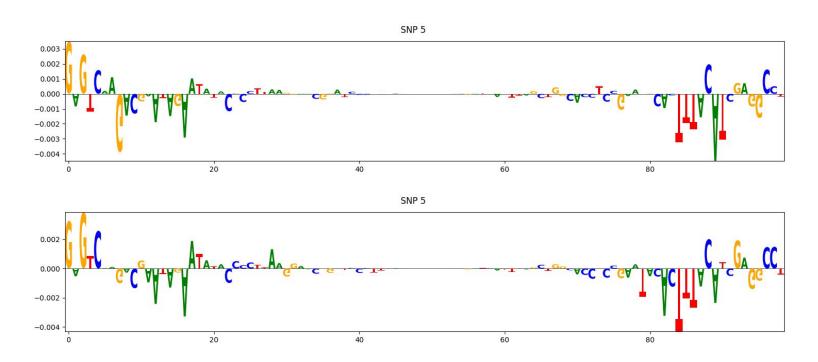
#### SNP 4 - 2 week



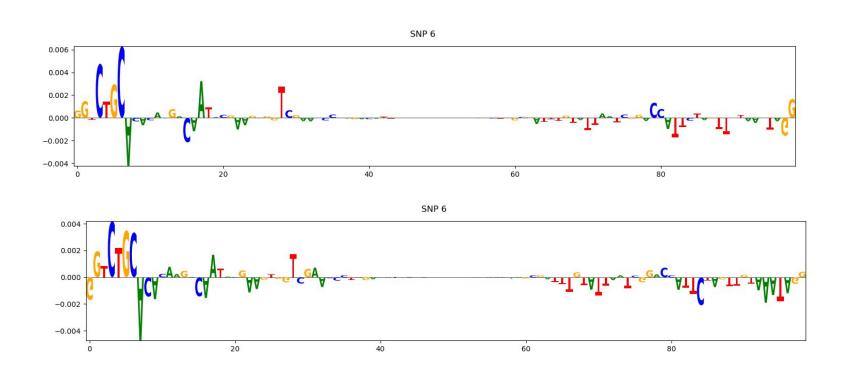
### SNP 5 - 8 week



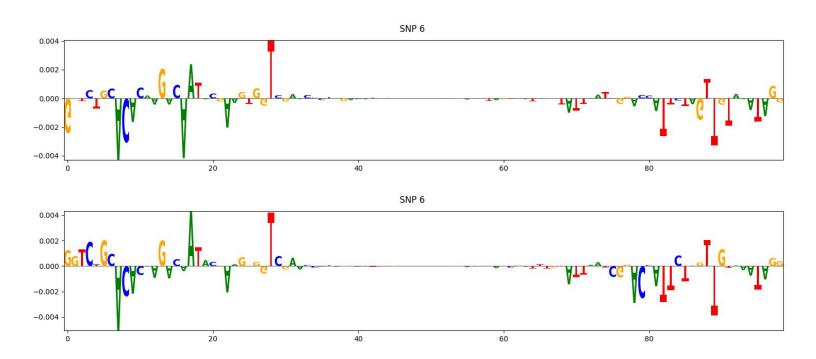
#### SNP 5 - 2 week



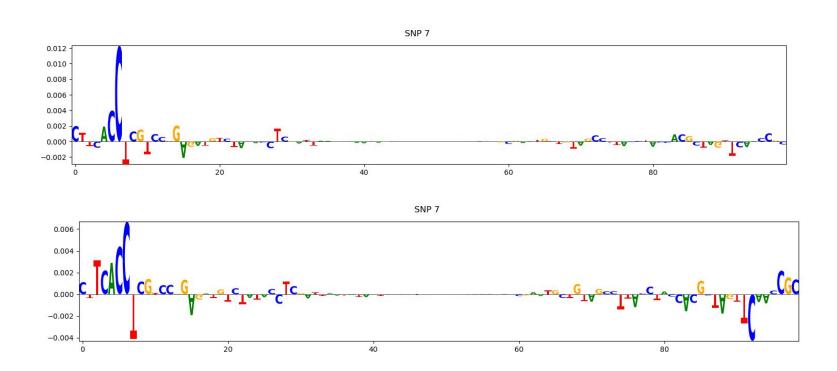
### SNP 6 - 8 week



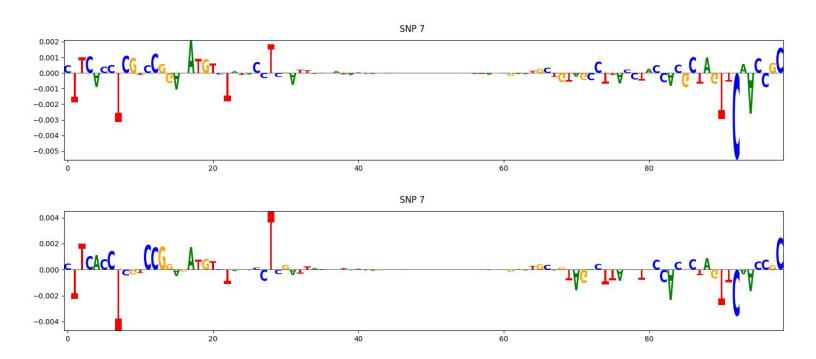
#### SNP 6 - 2 week



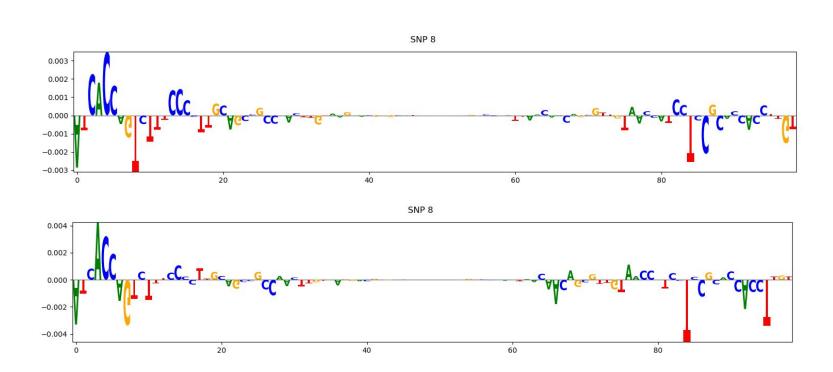
### SNP 7 - 8 week



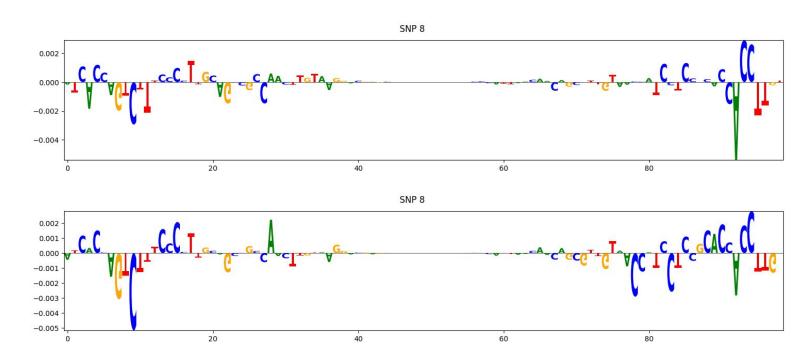
#### SNP 7 - 2 week



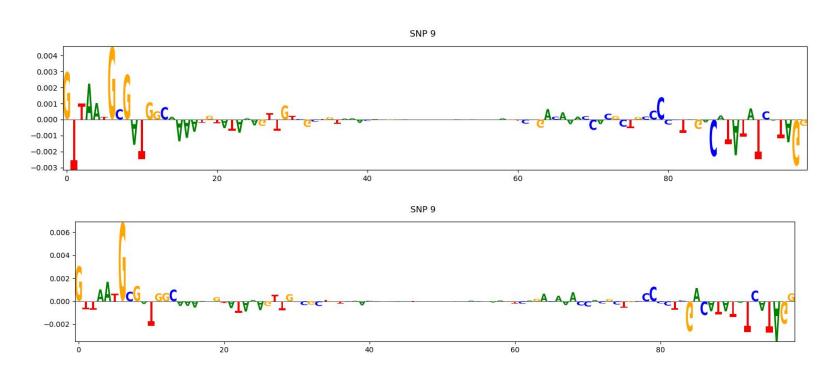
### SNP 8 - 8 week



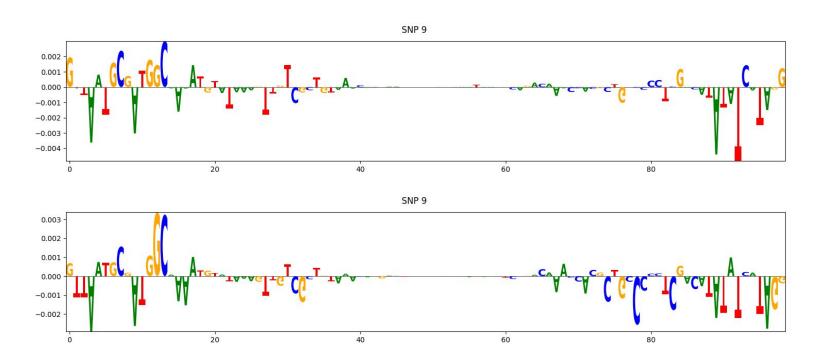
#### SNP 8 - 2 week



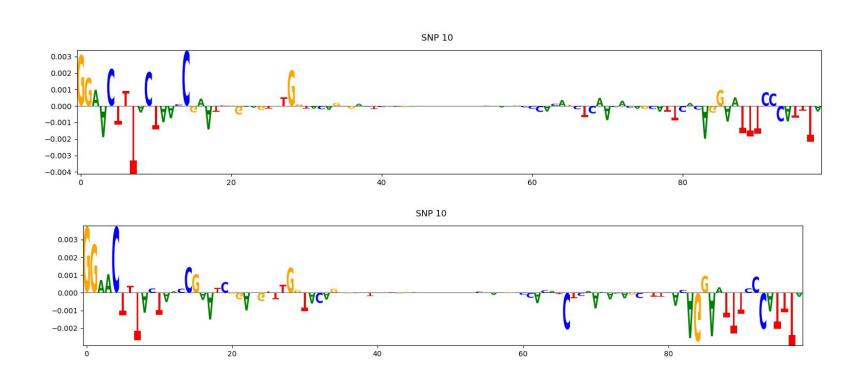
### SNP 9 - 8 week



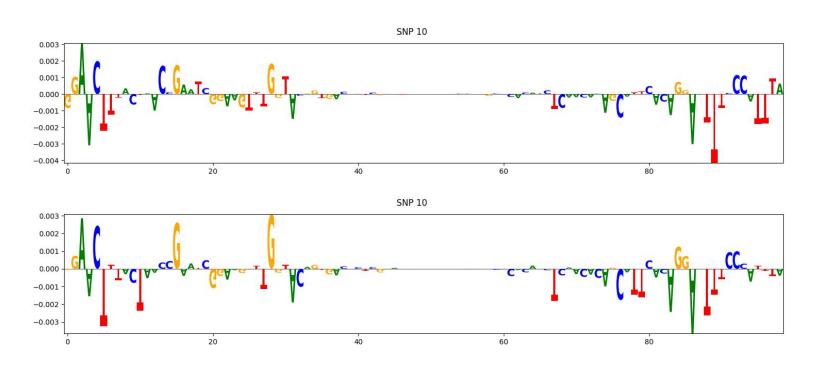
# SNP 9 - 2 week



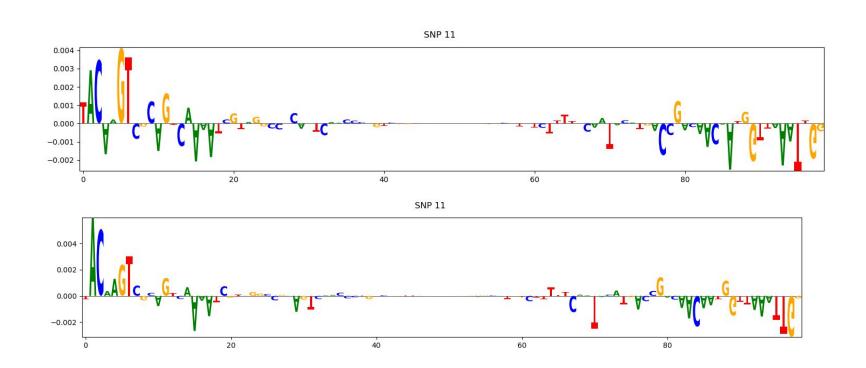
# **SNP 10 - 8 week**



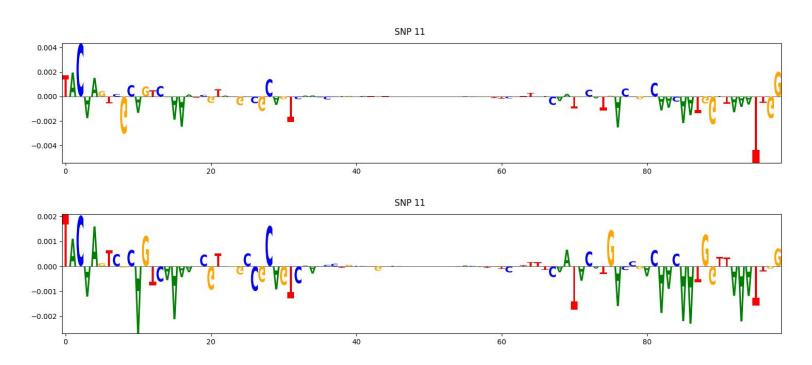
## **SNP 10 - 2 week**



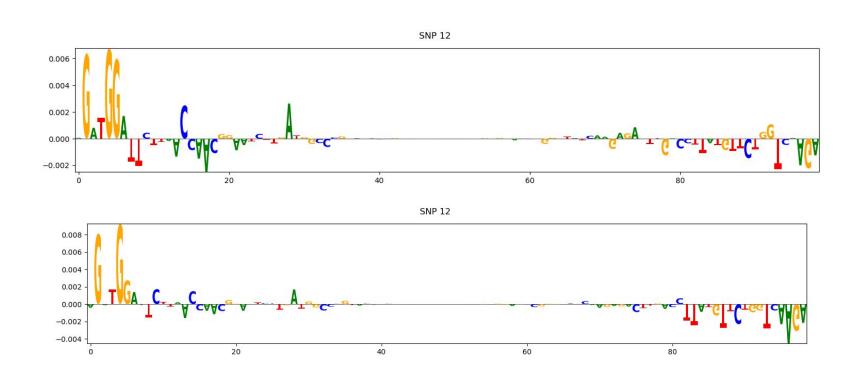
## SNP 11 - 8 week



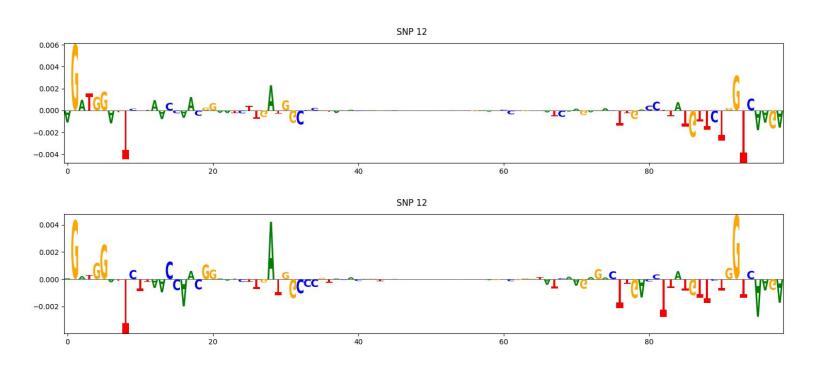
## **SNP 11 - 2 week**



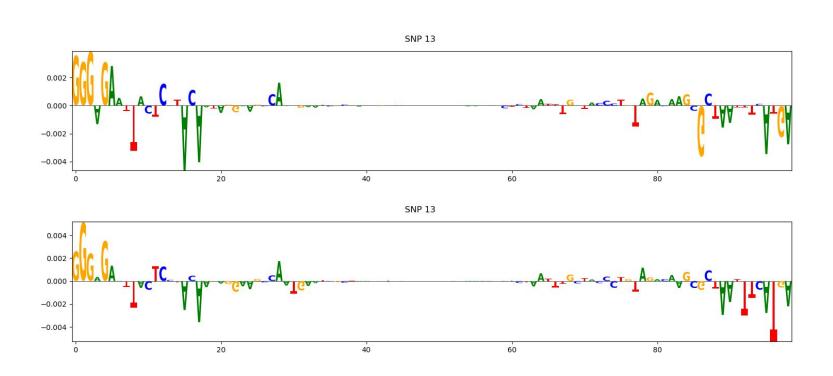
### SNP 12 - 8 week



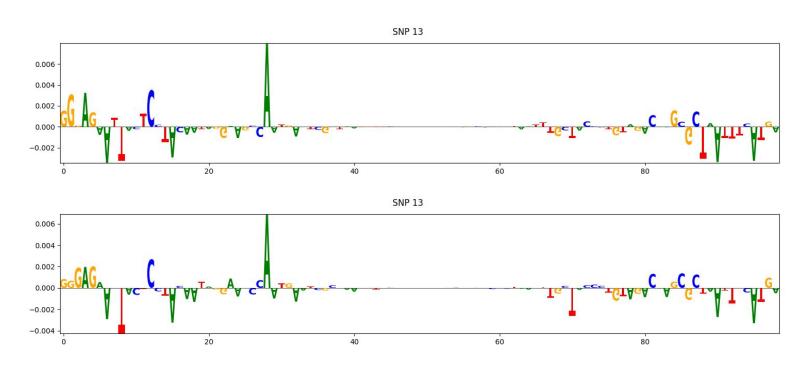
## **SNP 12 - 2 week**



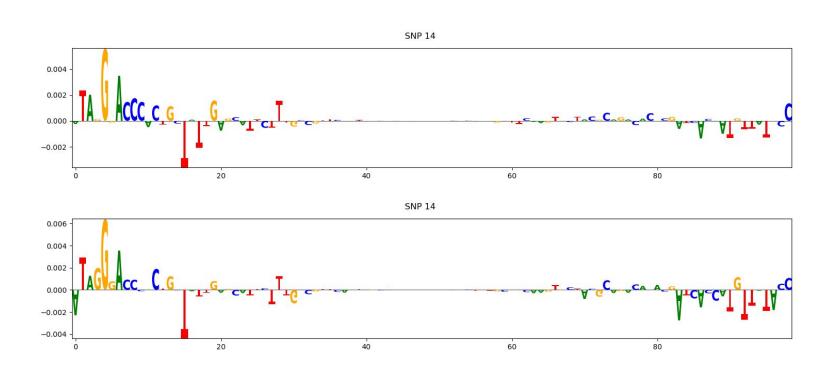
### **SNP 13 - 8 week**



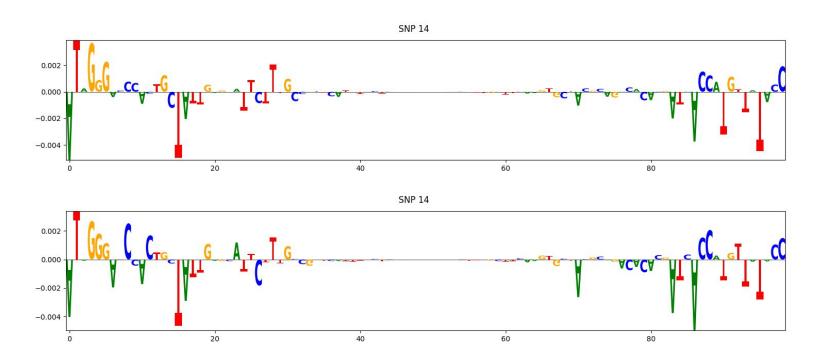
## **SNP 13 - 2 week**



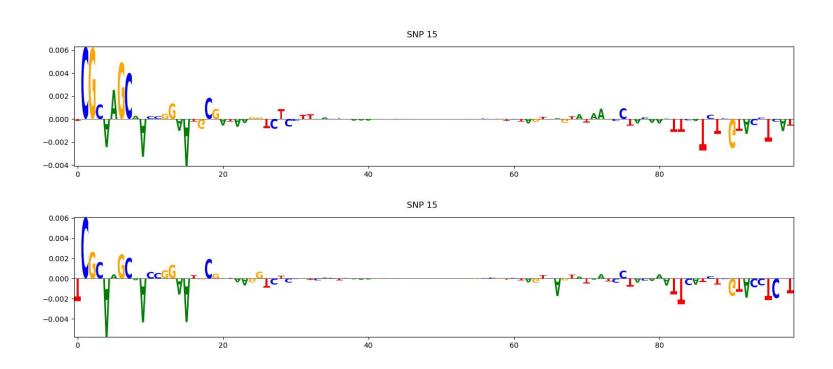
## **SNP 14 - 8 week**



## **SNP 14 - 2 week**



### **SNP 15 - 8 week**



## **SNP 15 - 2 week**

