Today's meeting's summary

1 message

Davit Sargsyan <sargdavid@gmail.com> Thu, Aug 30, 2018 at 1:17 PM
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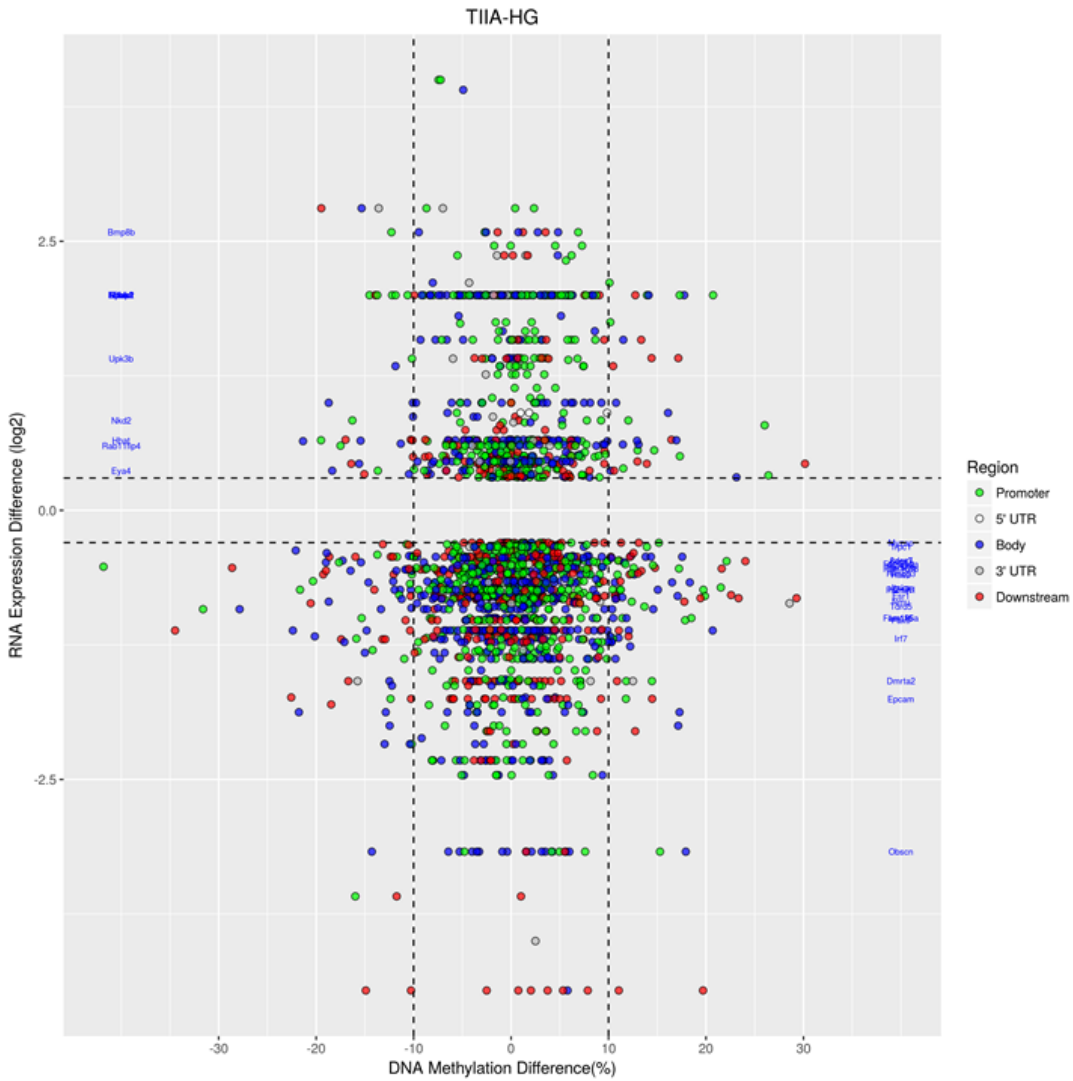
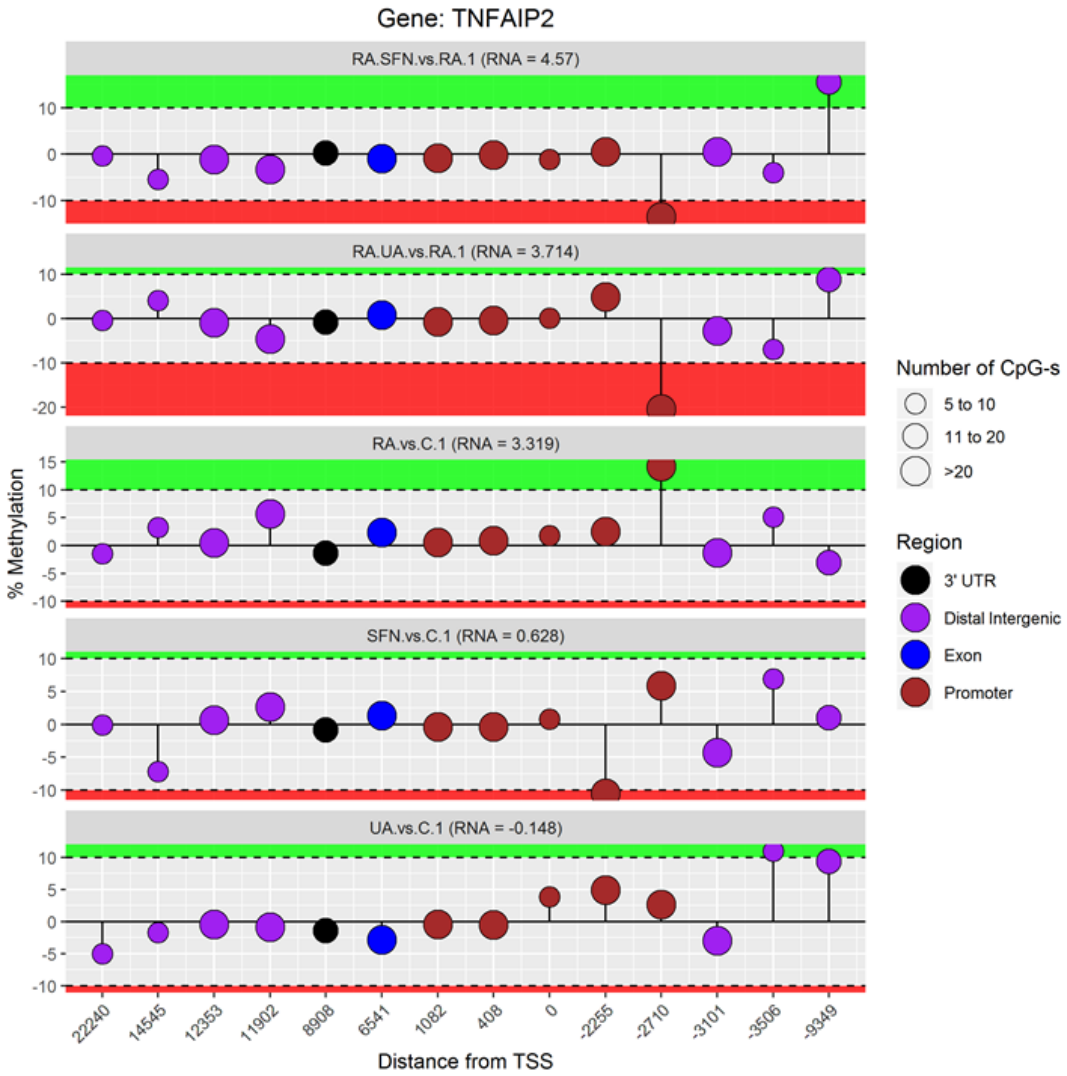
Dear Petruta,

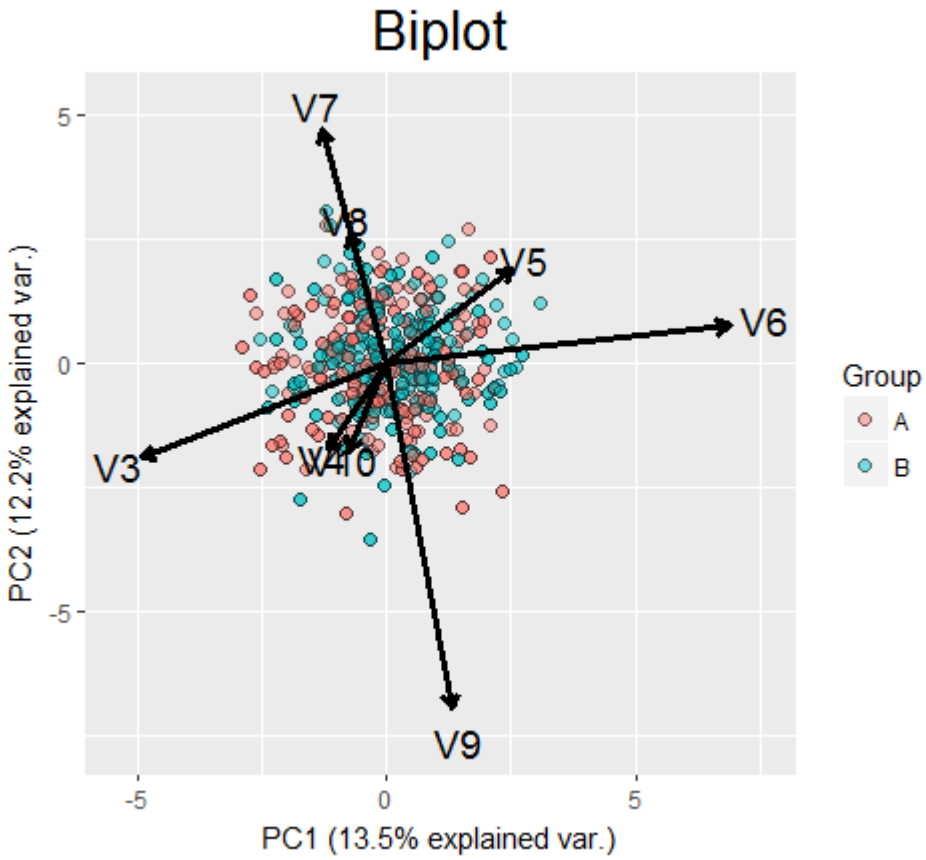
Below is the summary of our meeting.

1. We discussed the figures I sent you earlier this week. I also showed you a DNA vs. RNA plot (aka '"starburst" plot, see below) from another project (MES13). You want me to draw this plot first and then concentrate on the genes that were hypermethylated and downregulated (lower right quadrant). We can then examine these genes more closely using the plots I sent you.


TIIA-HG
RNA Expression Difference (log2)
DNA Methylation Difference(%)
2.5
0.0
-2.5
-30
-20
-10
0
10
20
30
Bmp8b
Upk3b
Nkd2
Rab11fip4
Eya4
Irf7
Dmrta2
Epcam
Obscn
Region
Promoter
5' UTR
Body
3' UTR
Downstream



2. RNA expressions Principal Component ANAlysis (PCA). Even though there are only 5 samples, we will draw a Byplot to see how samples and genes are clustered. Here is an example of a byplot (points will be samples, and arrows - genes):



Another possibility is to do PCA of CpG clusters (promoter only).

3. Petruta will send me her code for RNA-seq based gene selection as well as the full table of gene expressions. I will subset the genes based on p-values+fold-change and reanalyze.

4. Pathway analysis using Reactome and/or KEGG in R, and possibly IPA.

I will work on it from Sep 10 on as I need to catch up on our lab's data this and next week.

Thank you,

Davit