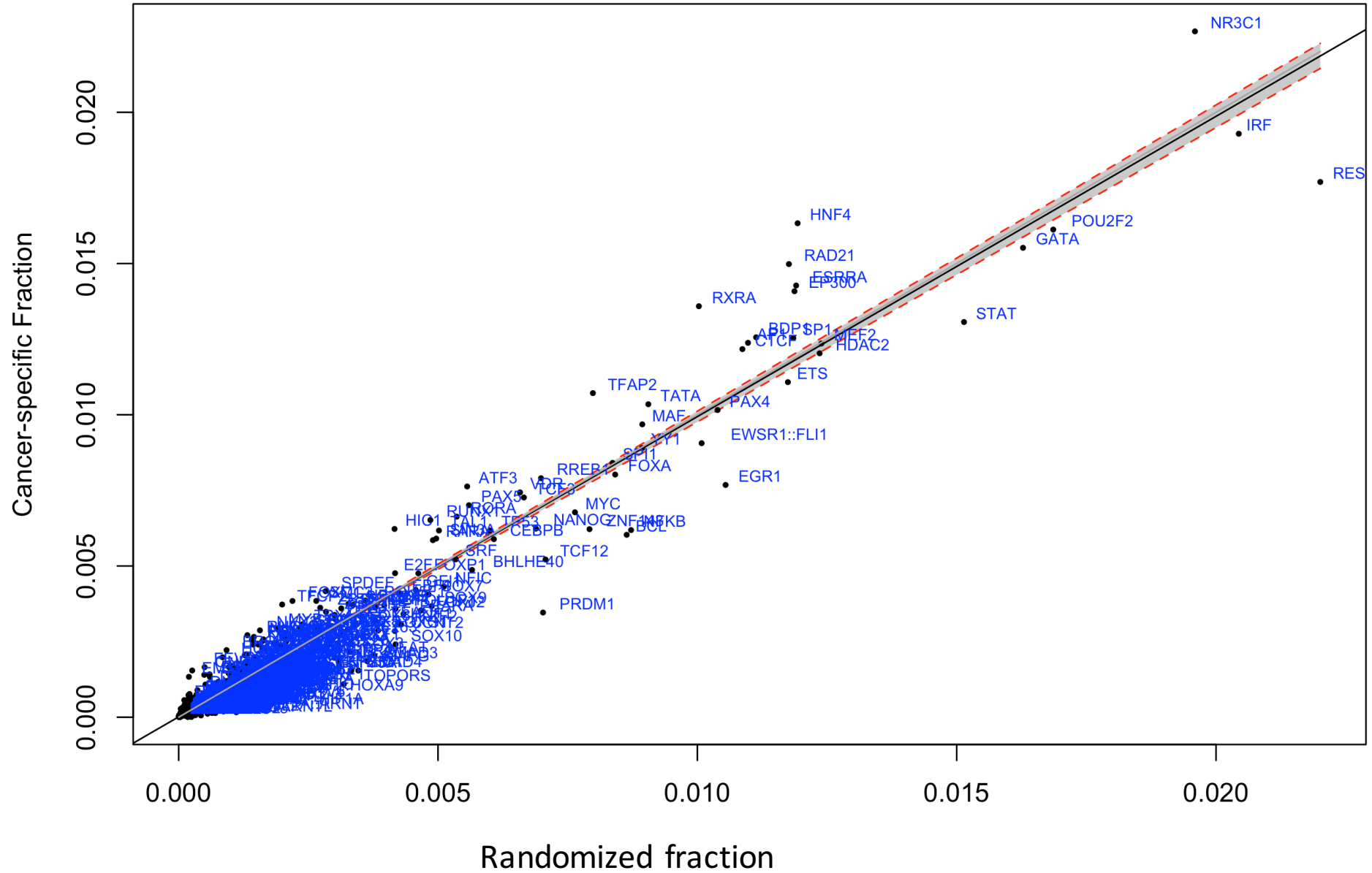# Paper E discussion

12/13/2016

Comparison of Motif Break Events in Lung-AdenoCA

Gene expression comparison workflow

For a given TF (***example : NR3C1***)with high fraction of SNVs leading to motif breaking event

Case :
1) Identify the regulated genes (Gi) and their expression level in the tumor sample with motif breaking event in NR3C1.

2)Aggregate statistics over each sample in the cohort with motif breaking event for NR3C1.

Control :
1)Obtain the gene expression level for gene set(Gi) for individuals belonging to the particular cohort, where we do not observe motif breaking event in NR3C1.

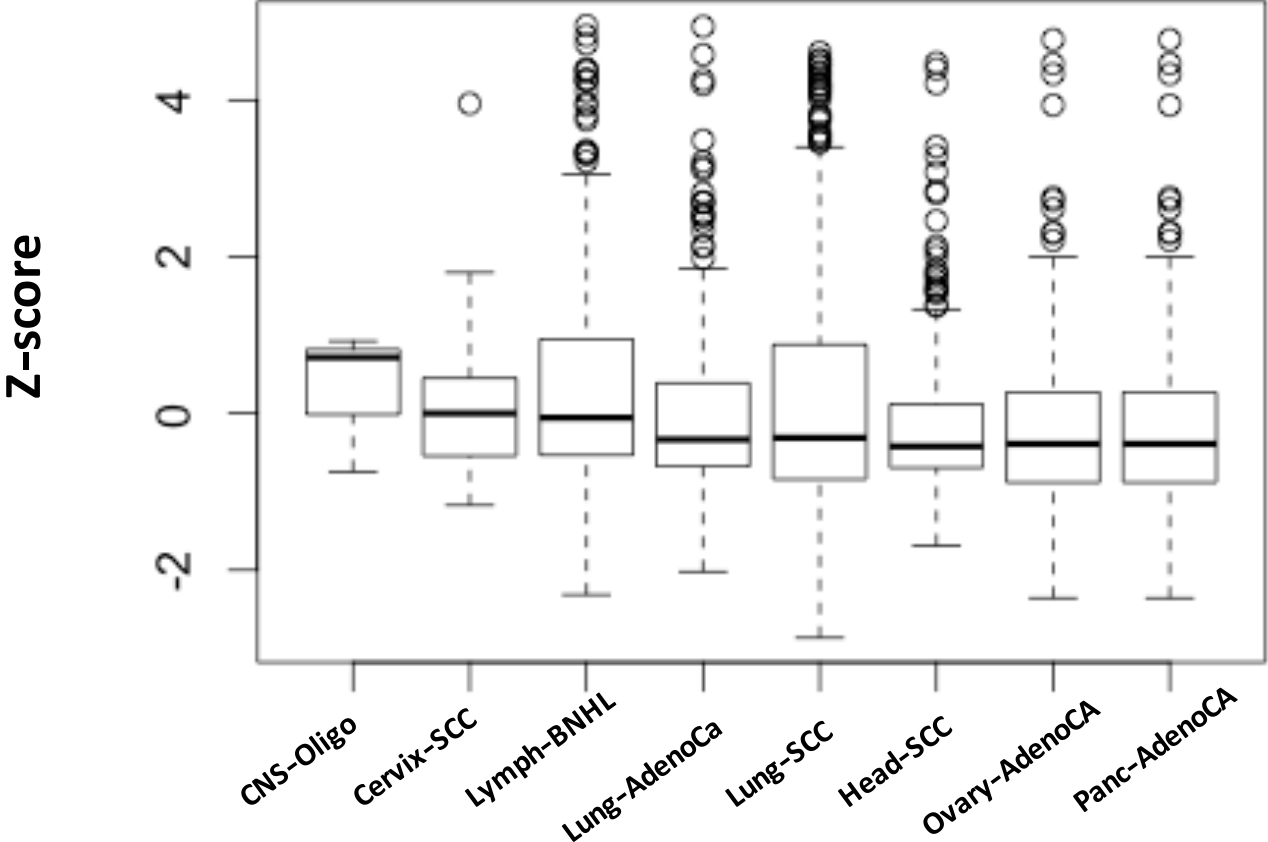2) Aggregate statistics over each sample in the cohort without motif breaking event for NR3C1.

Additional constraints

a. SNV falling in promoter region
b. Motif breaking score <= -0.1

Gene expression comparison for NR3C1
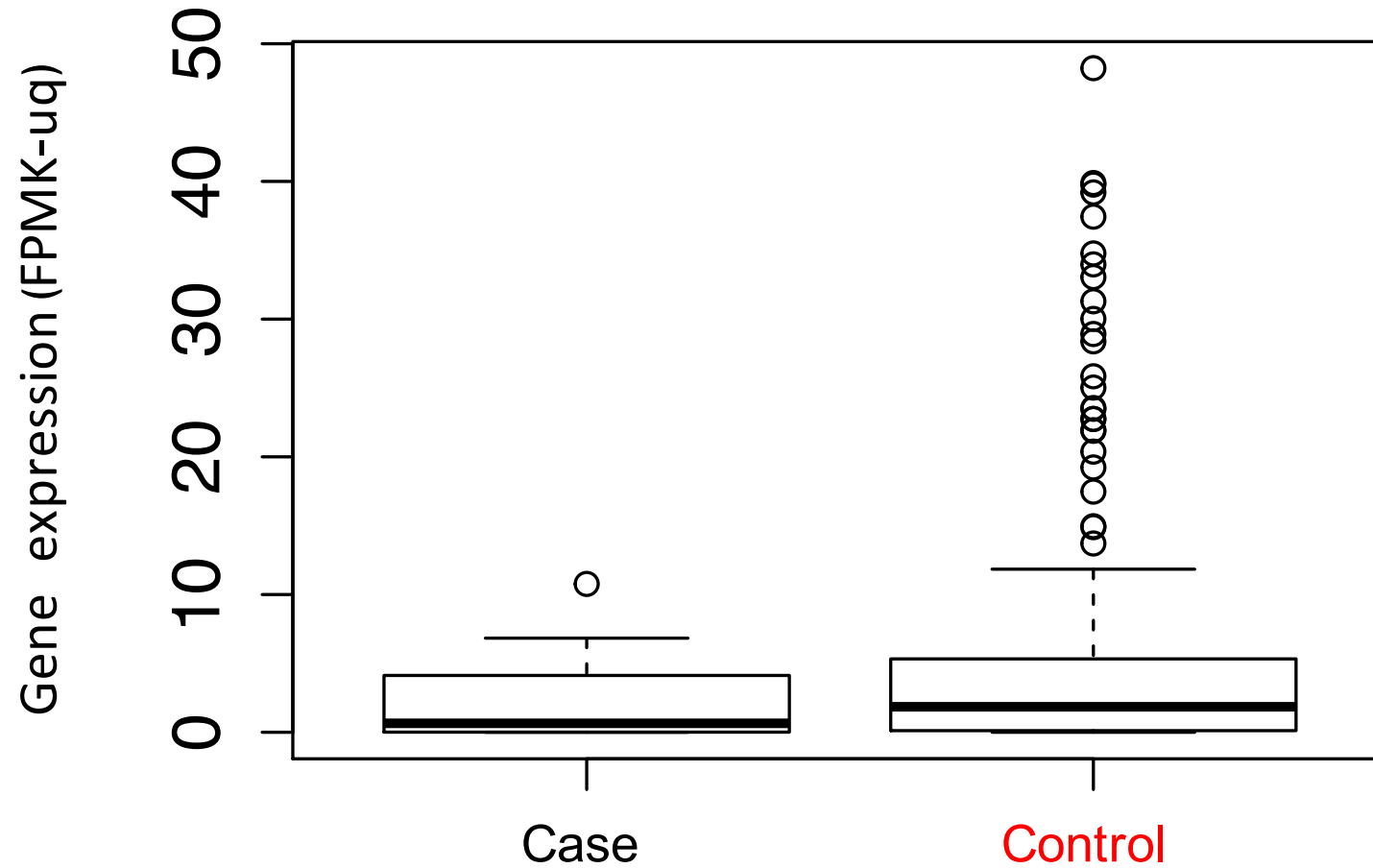
NR3C1 Motif Breaking

$$\text{Z-score} = G(i) - \langle G(i|mut=0) \rangle / stdv(G(i| mut=0)$$