

Summary reports of non-classic function detection of : mESC_GSM1562337_CBX7

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1 Data description

Table 1 mainly describes the input files, parameters and options.

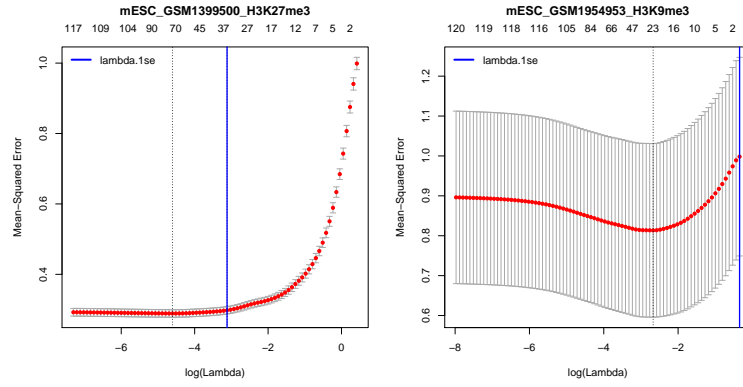
Table 1: parameter description

parameter	value
output name	mESC_GSM1562337_CBX7
HMRpeak(peak filename)	mESC_GSM1562337_CBX7.bed
HM signal(bw filename)	mESC_GSM1399500_H3K27me3 mESC_GSM1954953_H3K9me3
#coTF candidates	143
options	value
extend size	1000bp
Alpha (Elastic net)	0.5
Pvalue cutoff	0.001
topN cofactors	all

2 ElasticNet co-factor selection

In this step we use a feature selection (elastic-net. Zou, H. and Hastie T. (2005)) to select potential co-factors which corresponded to the non-classic function. Below shows the cross-validation curve for the decision of lambda in elastic-net for each histone modification substrate.

Figure 1: cross-validation curve for lambda decision



3 potential co-factors corresponded to non-classic function

In summary, 9 factors were predicted to potentially act as a co-factor of the non-classic function. The top9 co-factors were listed.

3.1 summary of co-factors

The corresponded histone modification substrate (HMsubstrate), empirical P-value, R-square (ordered) and the number of non-classic (NC) sites for each potential co-factor were listed below. The empirical P-value was calculated based on the comparison of foreground (observed) R-square and background R-square (distribution of random R-square generated from the 1,000 permutations of co-binding events) for each potential co-factor. The non-classic (NC) sites were defined by lower HMsubstrate signal (using Otus' method) and co-binding events of each potential co-factor.

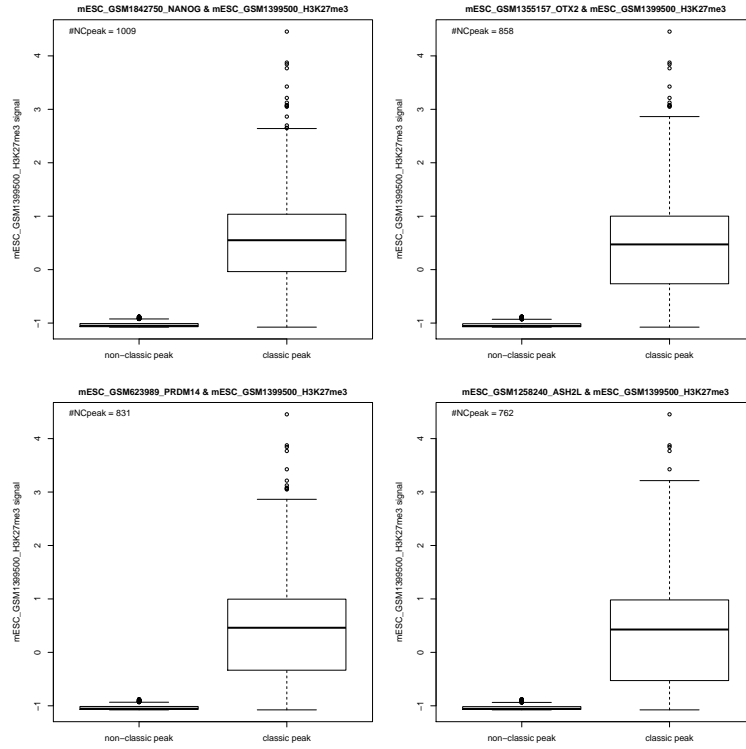
Table 2: cofactor summary

co-factor	HMsubstrate	Pval	Rsquare	NCsites
mESC_GSM1842750_NANOG	mESC_GSM1399500_H3K27me3	0.001	0.577	1009
mESC_GSM1355157_OTX2	mESC_GSM1399500_H3K27me3	0.001	0.44	858
mESC_GSM623989_PRDM14	mESC_GSM1399500_H3K27me3	0.001	0.391	831
mESC_GSM1258240_ASH2L	mESC_GSM1399500_H3K27me3	0.001	0.348	762
mESC_GSM1355154_POU5F1	mESC_GSM1399500_H3K27me3	0.001	0.288	861
mESC_GSM1406445_TRIM28	mESC_GSM1399500_H3K27me3	0.001	0.167	479
mESC_GSM1003807_ZNF384	mESC_GSM1399500_H3K27me3	0.001	0.134	382
mESC_GSM1003799_HCFC1	mESC_GSM1399500_H3K27me3	0.001	0.116	385
mESC_GSM1563242_RAD23B	mESC_GSM1399500_H3K27me3	0.001	0.11	662

3.2 Boxplot of HM on non-classic and classic sites

Boxplot was generated to compare the difference of the histone mark (HM) signal on either non-classic or classic sites(peak). The non-classic sites were defined by lower HM signal (using Otus' method) and co-binding events of each potential co-factor. The boxplot corresponded to top co-factors were displayed.

Figure 2: boxplot cofactor HMsignal



4 Output list

All the main output files were described in the following table

Table 3: output list

description	filename
summary table of non-classic (NC) function	summary/mESC_GSM1562337_CBX7_NCsummary.txt
summary report (this doc)	summary/mESC_GSM1562337_CBX7_summary.pdf
cobinding matrix on HMR peaks	tmpResults/mESC_GSM1562337_CBX7_peakov.bed
histone mark signal on HMR peaks	tmpResults/mESC_GSM1562337_CBX7_HMsig.bed