

Epigenetic investigation for immunotherapy related genes

ICR Pathways: GZMA GZMB PRF1 GNLY HLA molecules HLA-A HLA-B HLA-C HLA-E HLA-F HLA-G HLA-H HLA-DMA HLA-DMB HLA-DOA HLA-DOB HLA-DPA1 HLA-DPB1 HLA-DQA1 HLA-DQA2 HLA-DQB1 HLA-DRA HLA-DRB1 IFN-g pathway genes IFNG IFNGR1 IFNGR2 IRF1 STAT1 PSMB9 chemokines CCR5 CCL3 CCL4 CCL5 CXCL9 CXCL10 CXCL11 adhesion molecules ICAM1 ICAM2 ICAM3 ICAM4 ICAM5 VCAM1

Input genes for cbioportal query: IFNG IFNGR1 IFNGR2 IRF1 STAT1 PSMB9 ICAM1 ICAM2 ICAM3 ICAM4 ICAM5 VCAM1 CCR5 CCL3 CCL4 CCL5 CXCL9 CXCL10 CXCL11 GZMA GZMB PRF1 GNLY HLA-A HLA-B HLA-C HLA-E HLA-F HLA-G HLA-H HLA-DMA HLA-DMB HLA-DOA HLA-DOB HLA-DPA1 HLA-DPB1 HLA-DQA1 HLA-DQA2 HLA-DQB1 HLA-DRA HLA-DRB1 (41 genes) Case query: Skin cancer(melanoma) from TCGA provision (471 cases)

```
In [106]: # data source: http://www.cbioportal.org/index.do?session_id=59dbf8f6498e5df2e29663ab&show_samples=false&clinicalList=NO_CONTEXT_MUTATION_SIGNATURE,AJCC_TUM OR_PATHOLOGIC_PT,ICD_10&
# filename ifng
import pandas as pd
import numpy as np
import random
import math
%matplotlib inline
#%matplotlib notebook
import matplotlib.pyplot as plt
```

Exploratory: check HLA-B mRNA expression vs IFNG methylation

```
In [107]: data = pd.read_table('./plots-hlab-ifng.txt', index_col=False)
data.shape
```

```
Out[107]: (471, 4)
```

In [108]: `data.head(5)`

Out[108]:

	Sample Id	IFNG, Methylation (HM450)	HLA-B, mRNA expression (RNA Seq V2 RSEM)	Mutations
0	TCGA-YD-A9TB-06	0.328013	57170.5428	NaN
1	TCGA-XV-AAZY-01	0.444676	69591.2139	NaN
2	TCGA-XV-AAZW-01	0.757459	9246.8939	NaN
3	TCGA-XV-AAZV-01	0.627704	131417.7147	NaN
4	TCGA-W3-AA1V-06	0.622964	65417.2806	NaN

In [109]: `mask = data['Mutations'].isnull()
single = (data['Mutations'].str.count(':') == 1)
mut = data[~mask & single]
mut.shape`

Out[109]: (10, 4)

Check Pearson and Spearman correlation coefficient

we threshold at > 0.5 or < -0.5 to say it is significant

for mutated genes, HLA-B mRNA expression is significantly correlated with IFNG methylation

In [110]: `mut.corr(method='pearson')`

Out[110]:

	IFNG, Methylation (HM450)	HLA-B, mRNA expression (RNA Seq V2 RSEM)
IFNG, Methylation (HM450)	1.000000	0.642069
HLA-B, mRNA expression (RNA Seq V2 RSEM)	0.642069	1.000000

```
In [111]: mut.corr(method='spearman')
```

Out[111]:

	IFNG, Methylation (HM450)	HLA-B, mRNA expression (RNA Seq V2 RSEM)
IFNG, Methylation (HM450)	1.000000	0.951515
HLA-B, mRNA expression (RNA Seq V2 RSEM)	0.951515	1.000000

Plot best fit lines of data and mutated genes

Also show spearman and pearson correlation

```
In [112]: # plot best fit line & scatter plot
# add spearman and pearson correlation coeff
def methplotXY (df, axis, log, label, scatter, corr, color) :
    X = df.iloc[:,1]
    if (log) :
        Y = df.iloc[:,2].apply(np.log)
    else :
        Y = df.iloc[:,2]
    # best fit line for df
    z = np.polyfit(X, Y, deg=1)
    p = np.poly1d(z)

    if (scatter) :
        axis.scatter(X, Y, label="", color=color)
    if (corr) :
        Scorr = df.corr(method='pearson').iloc[0,1]
        Pcorr = df.corr(method='spearman').iloc[0,1]
        label = label+'(fit)'+"\ns:%.3f"%(Scorr,) + "\nnp:%.3f"%(Pcorr,)

    _ = plt.plot(X, p(X), '-' + color, label=label)

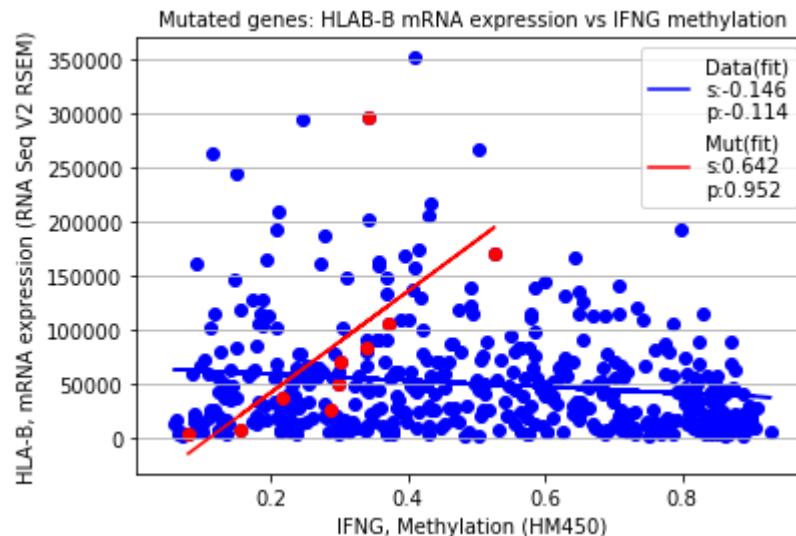
# plot best fit lines for df and mut using
# col 2(numerical or log) vs col 1 with title
def methplot(df, mut, log, scatter, title) :
    fig, axis = plt.subplots()
    # Grid Lines, Xticks, Xlabel, Ylabel
    axis.yaxis.grid(True)
    axis.set_title(title, fontsize=10)
    axis.set_xlabel(mut.columns.values[1], fontsize=10)
    if (log) :
        axis.set_ylabel(mut.columns.values[2] + '(log)', fontsize=10)
    else :
        axis.set_ylabel(mut.columns.values[2], fontsize=10)

    # best fit line and corr for df
    methplotXY(df, axis, log, "Data", scatter, 1, 'b')

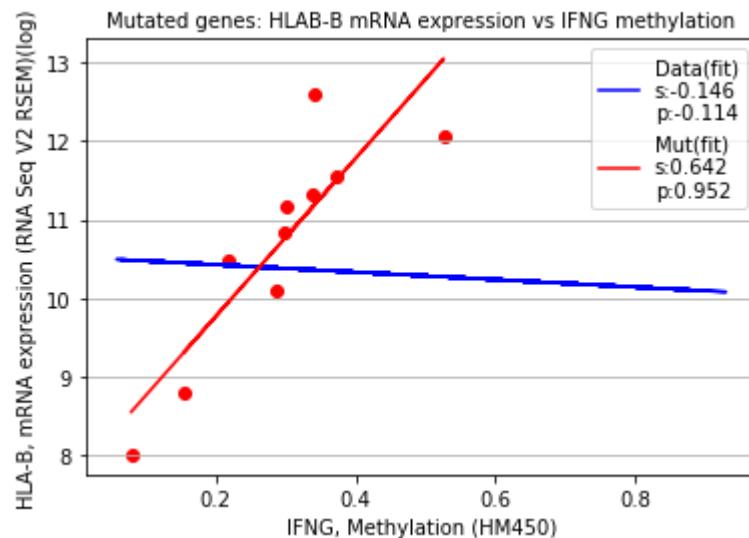
    # scatter plot, best fit line, corr for mut
    methplotXY(mut, axis, log, "Mut", 1, 1, 'r')

    # set Legend values
    plt.legend(loc='best')
    plt.show()
```

```
In [113]: methplot(data, mut, 0, 1, 'Mutated genes: HLAB-B mRNA expression vs IFNG methylation')
```



```
In [114]: methplot(data, mut, 1, 0, 'Mutated genes: HLAB-B mRNA expression vs IFNG methylation')
```

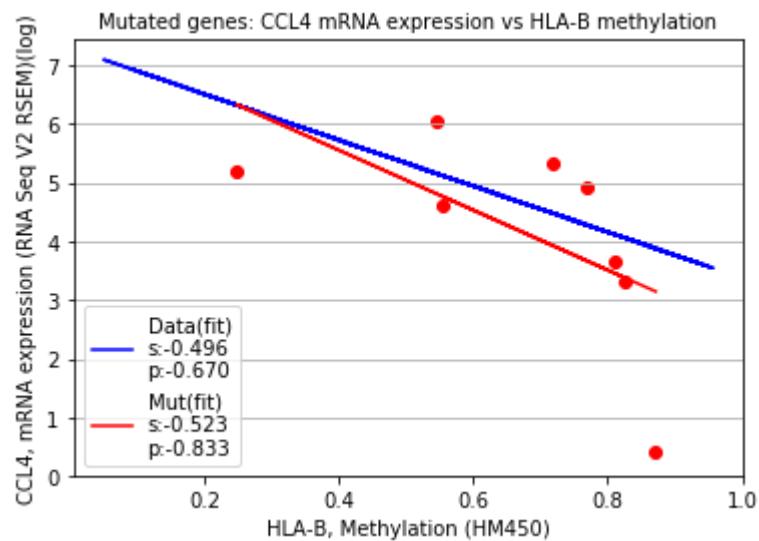
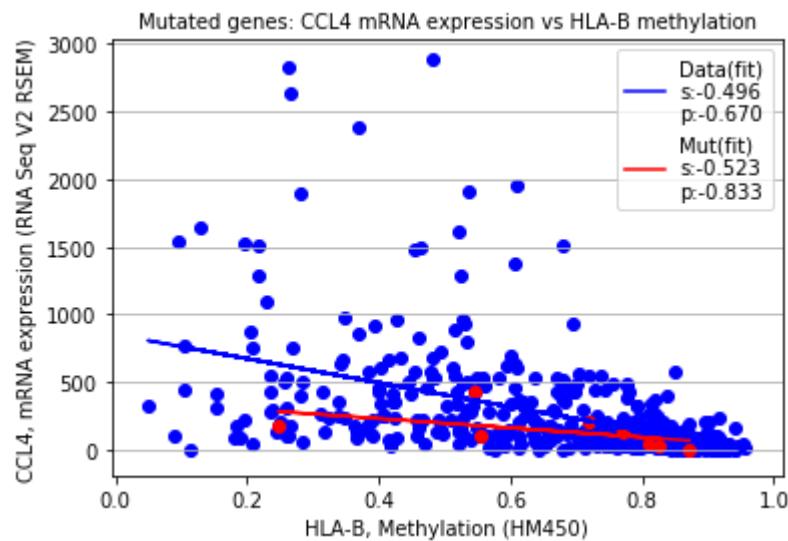


Plot mRNA expression vs methylation

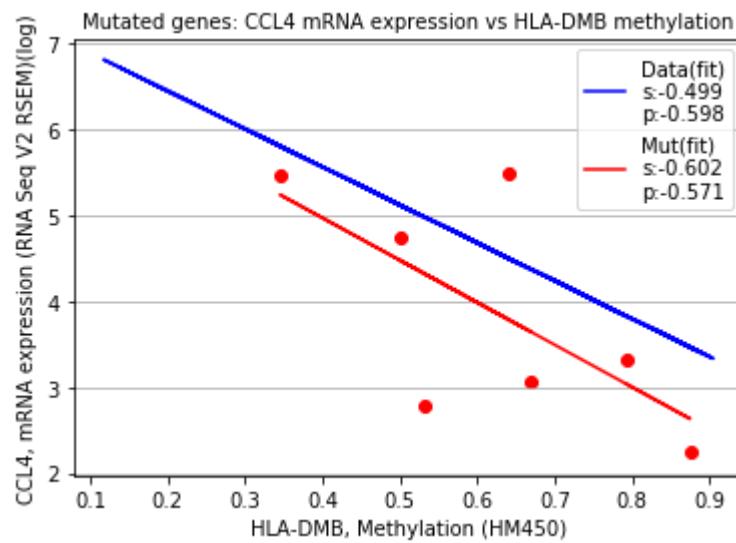
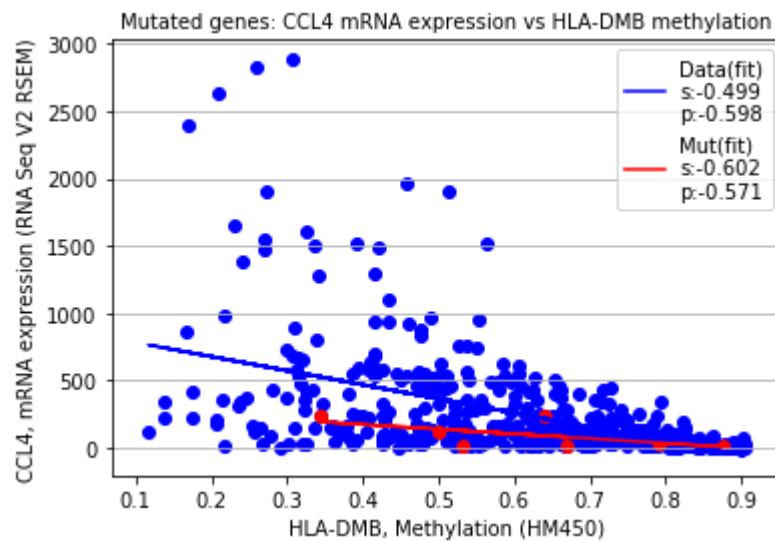
Criteria is pearson and spearman correlation are significant. Significant is either > 0.5 or < -0.5 . Also selecting cases where there are at least 5 cases of mutations

```
In [115]: def mutReadPlot(file, title) :
    data = pd.read_table(file, index_col=False)
    mask = data['Mutations'].isnull()
    single = (data['Mutations'].str.count('::') == 1)
    mut = data[~mask & single]
    methplot(data, mut, 0, 1, title)
    methplot(data, mut, 1, 0, title)
```

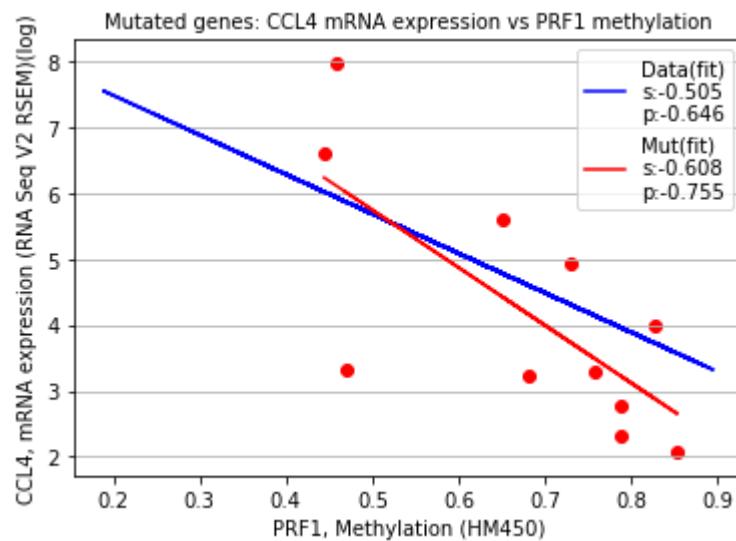
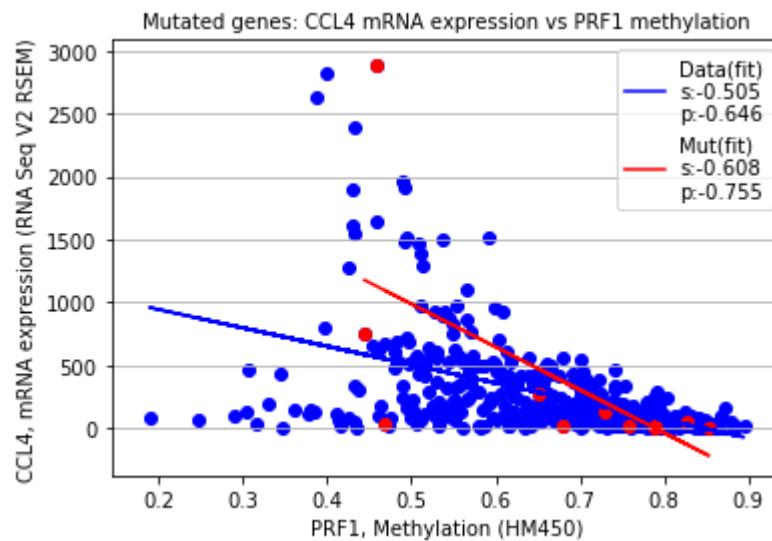
```
In [116]: mutReadPlot('./plots-ccl4-hlab.txt', 'Mutated genes: CCL4 mRNA expression vs HLA-B methylation')
```



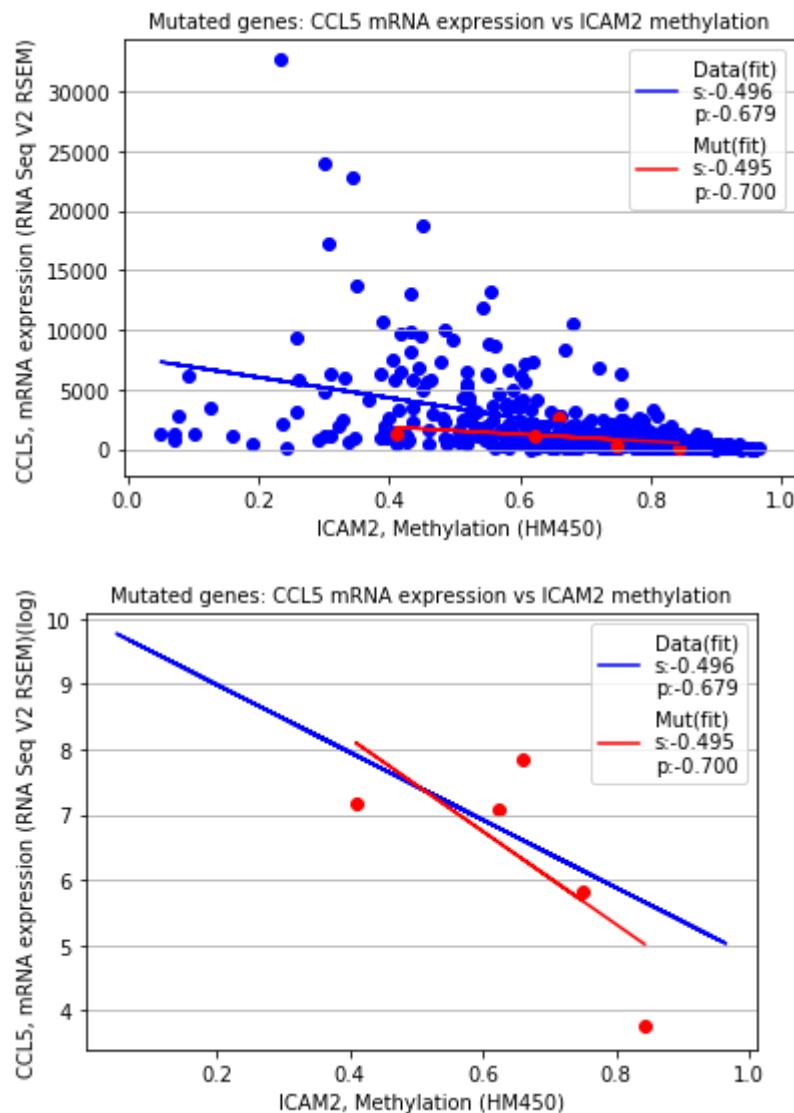
```
In [117]: mutReadPlot('./plots-ccl4-hladmb.txt', 'Mutated genes: CCL4 mRNA expression vs HLA-DMB methylation')
```



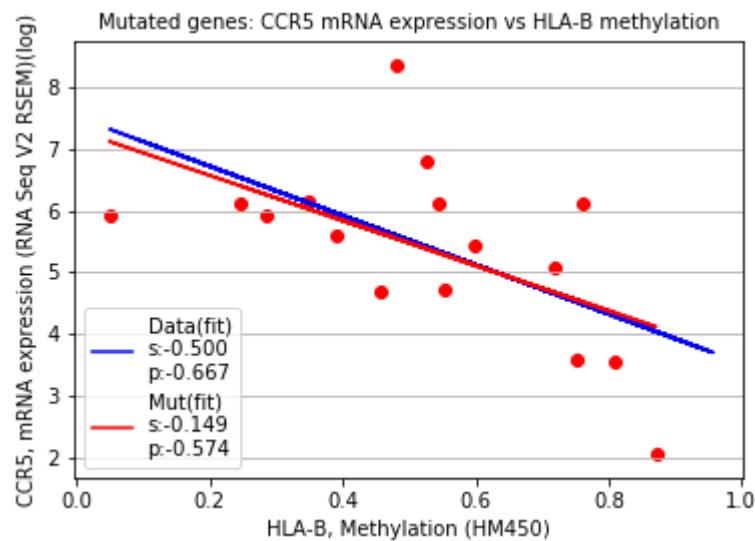
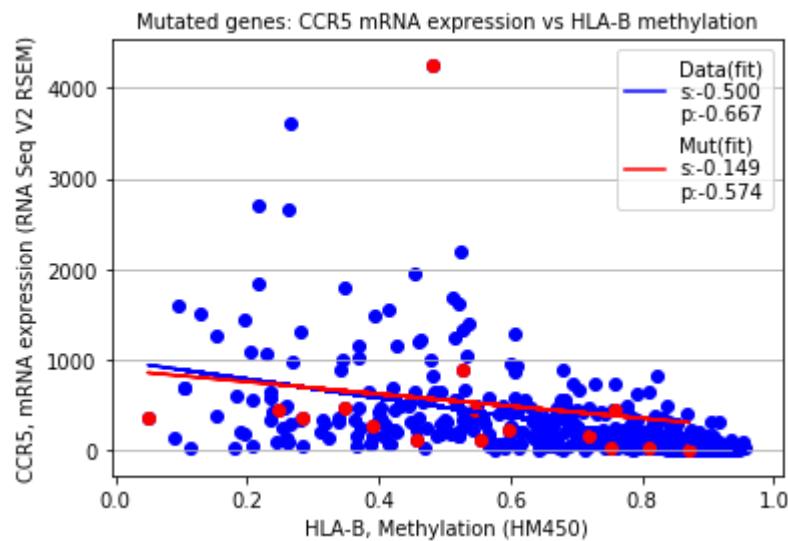
```
In [118]: mutReadPlot('./plots-ccl4-prf1.txt', 'Mutated genes: CCL4 mRNA expression vs P  
RF1 methylation')
```



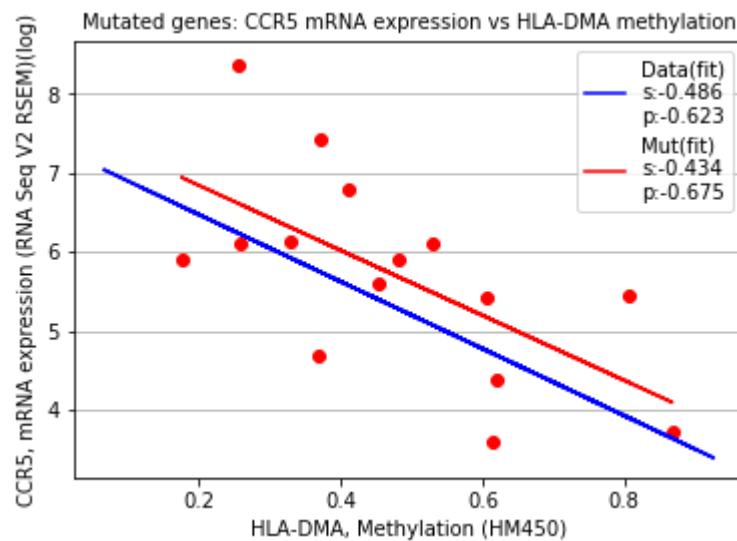
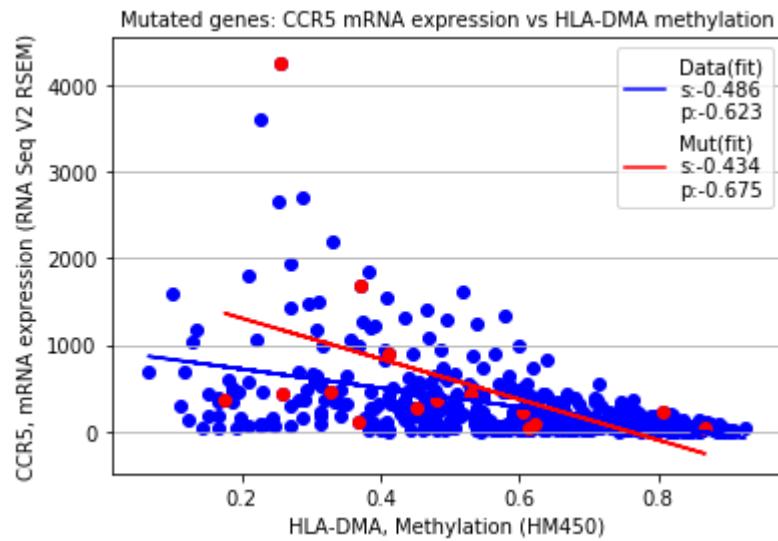
```
In [119]: mutReadPlot('./plots-ccl5-icam2.txt', 'Mutated genes: CCL5 mRNA expression vs ICAM2 methylation')
```



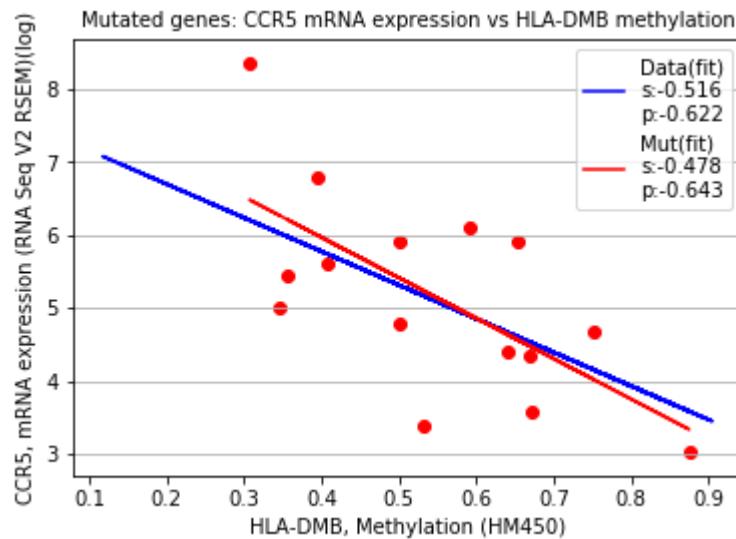
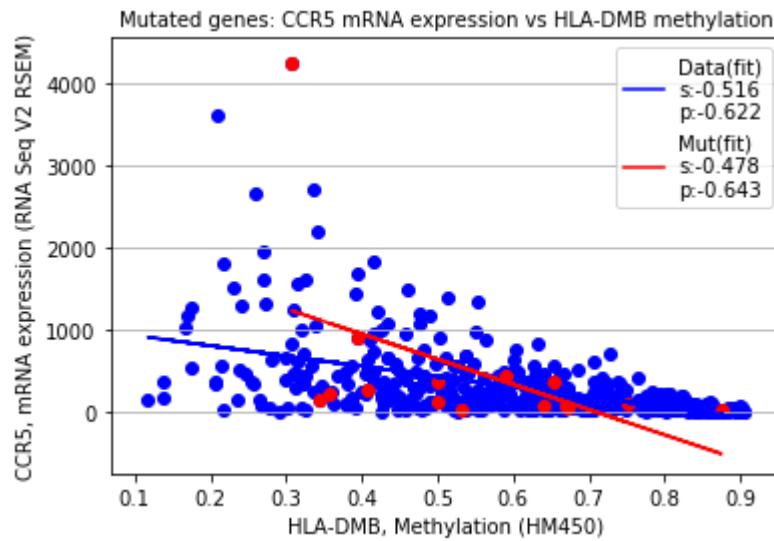
```
In [120]: mutReadPlot('./plots-ccr5-hlab.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-B methylation')
```



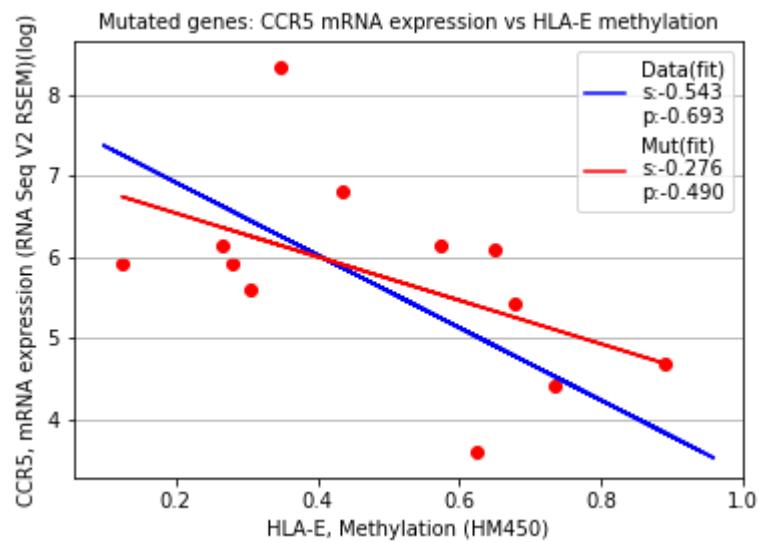
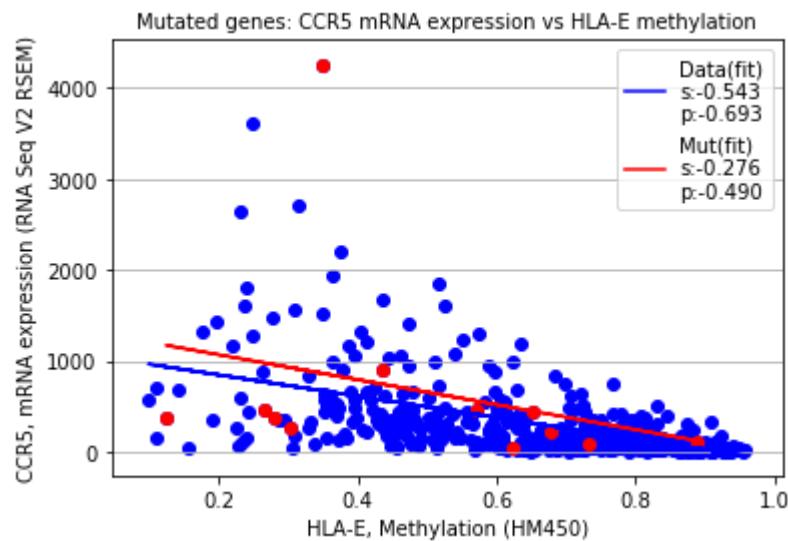
```
In [121]: mutReadPlot('./plots-ccr5-hladma.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-DMA methylation')
```



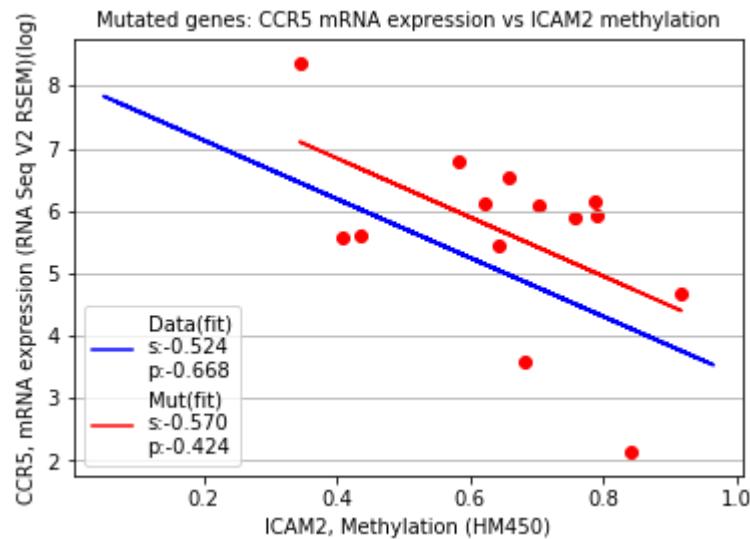
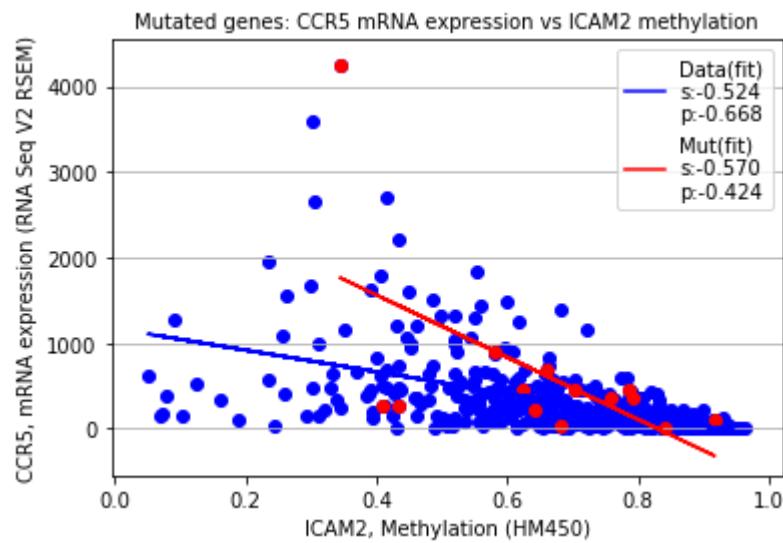
```
In [122]: mutReadPlot('./plots-ccr5-hladmb.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-DMB methylation')
```



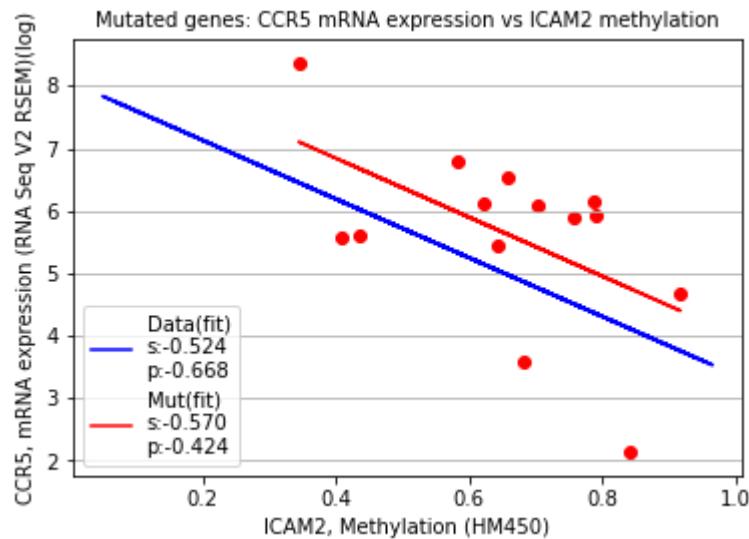
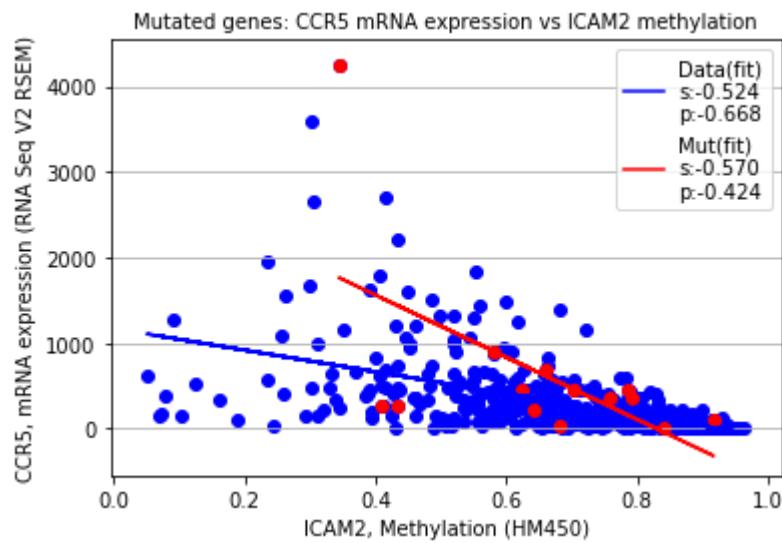
```
In [123]: mutReadPlot('./plots-ccr5-hlae.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-E methylation')
```



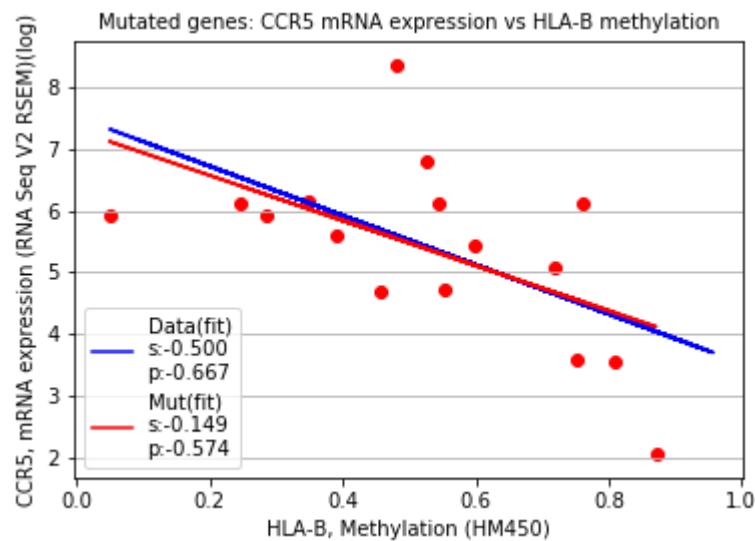
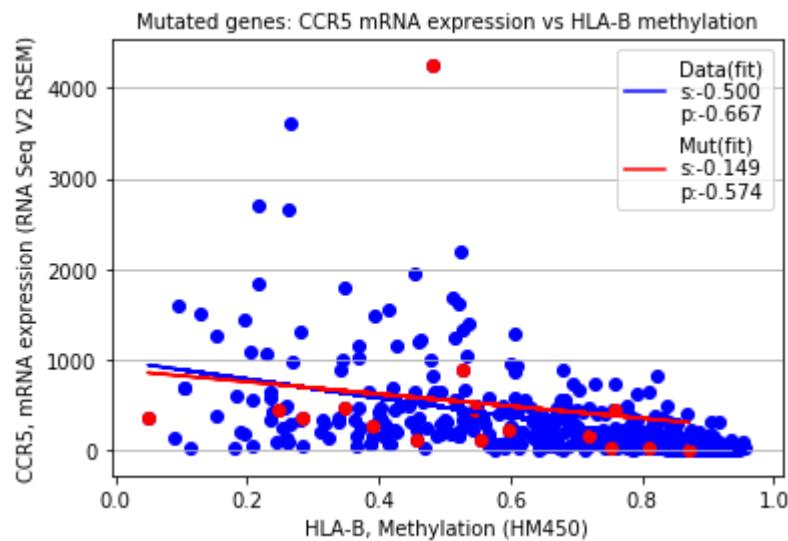
```
In [124]: mutReadPlot('./plots-ccr5-icam2.txt', 'Mutated genes: CCR5 mRNA expression vs ICAM2 methylation')
```



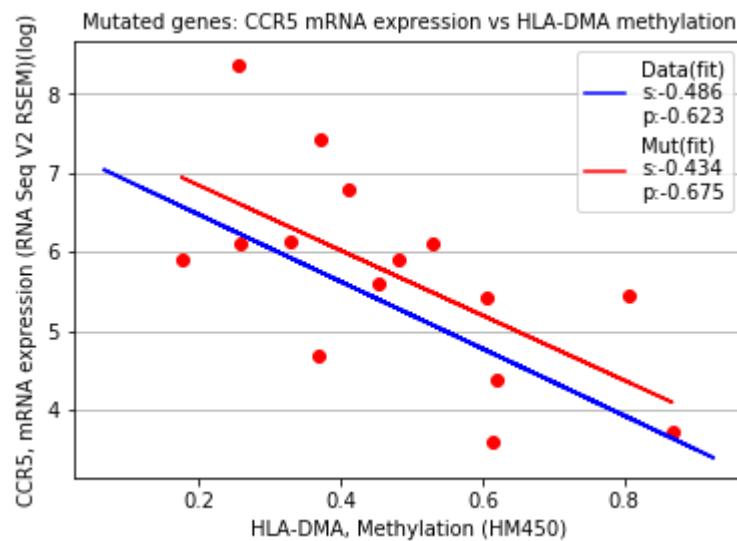
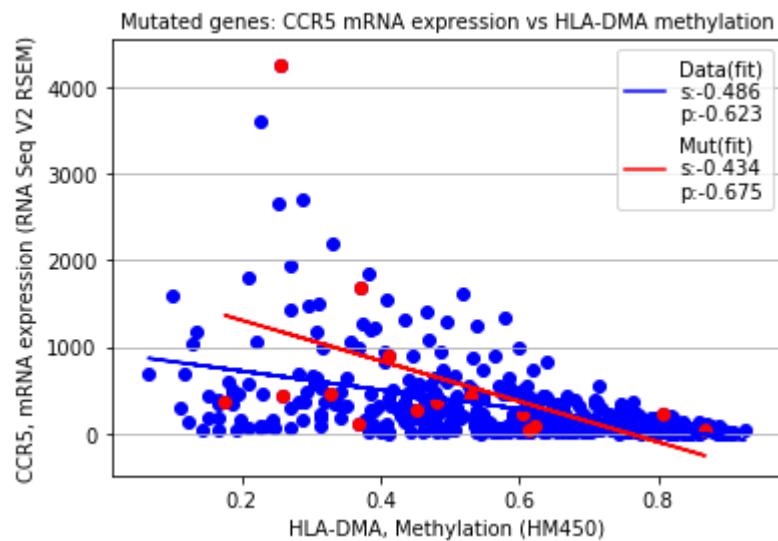
```
In [125]: mutReadPlot('./plots-ccr5-icam2.txt', 'Mutated genes: CCR5 mRNA expression vs ICAM2 methylation')
```



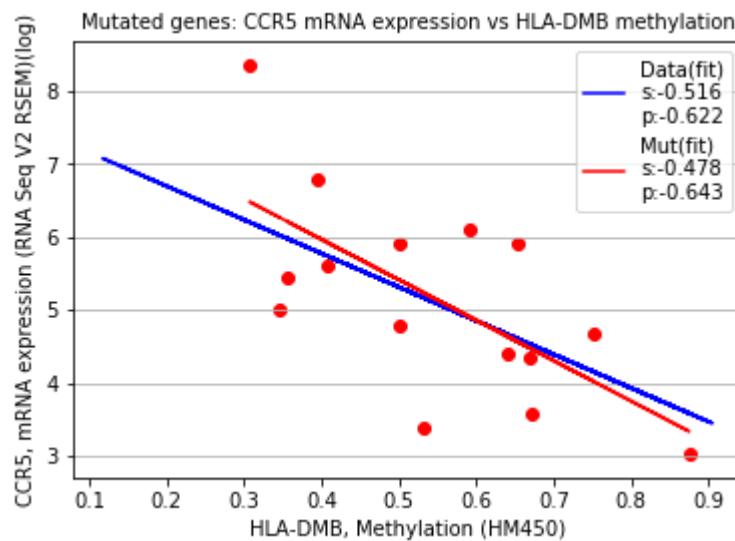
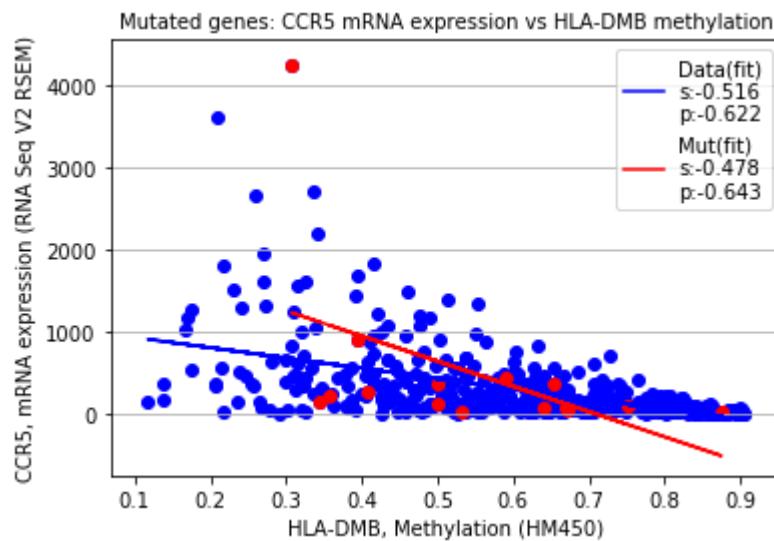
```
In [126]: mutReadPlot('./plots-ccr5-hlab.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-B methylation')
```



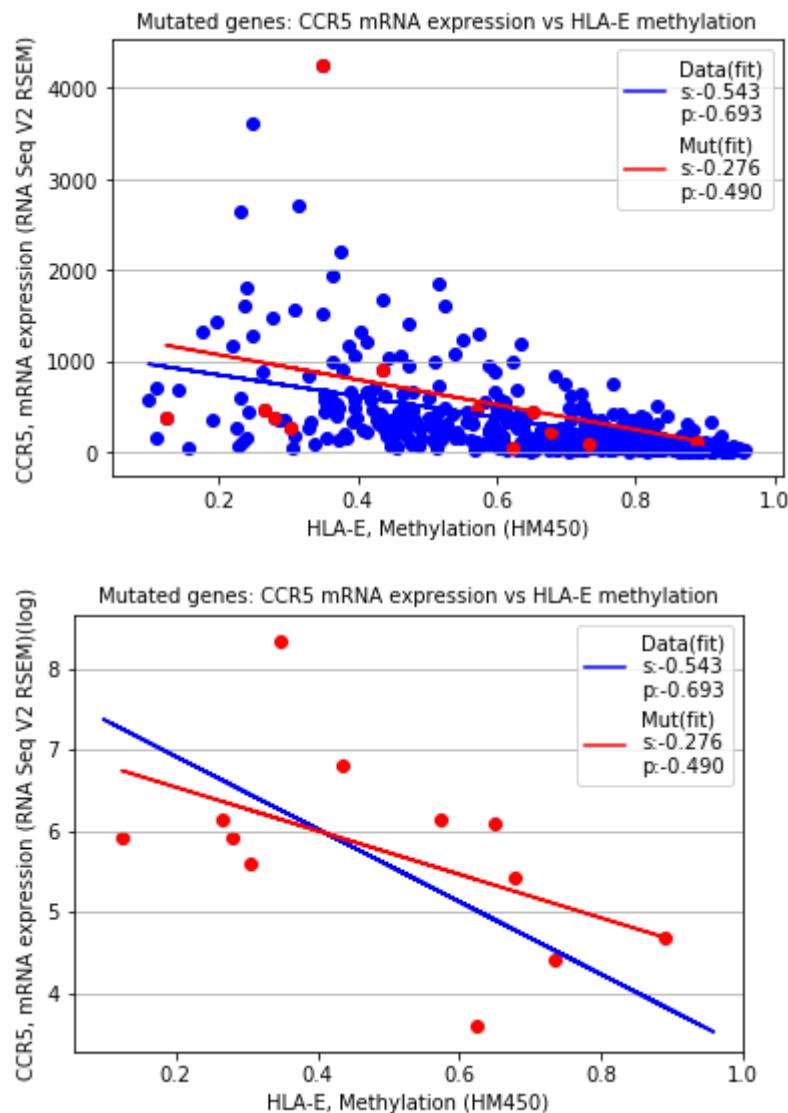
```
In [127]: mutReadPlot('./plots-ccr5-hladma.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-DMA methylation')
```



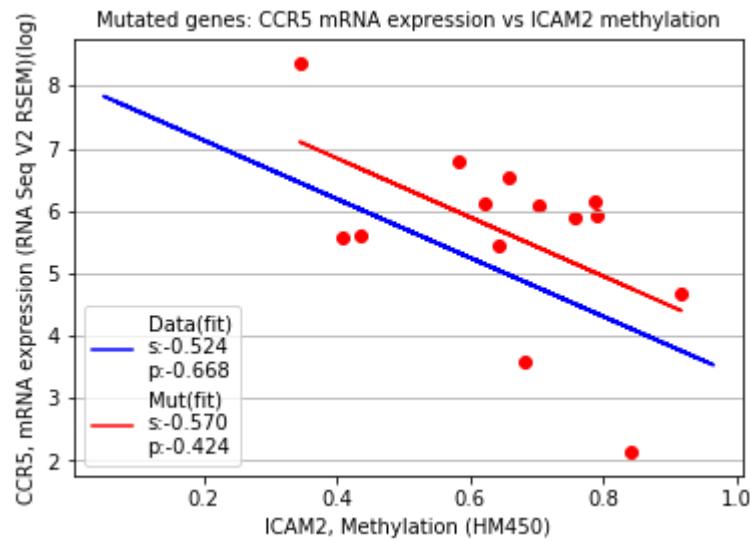
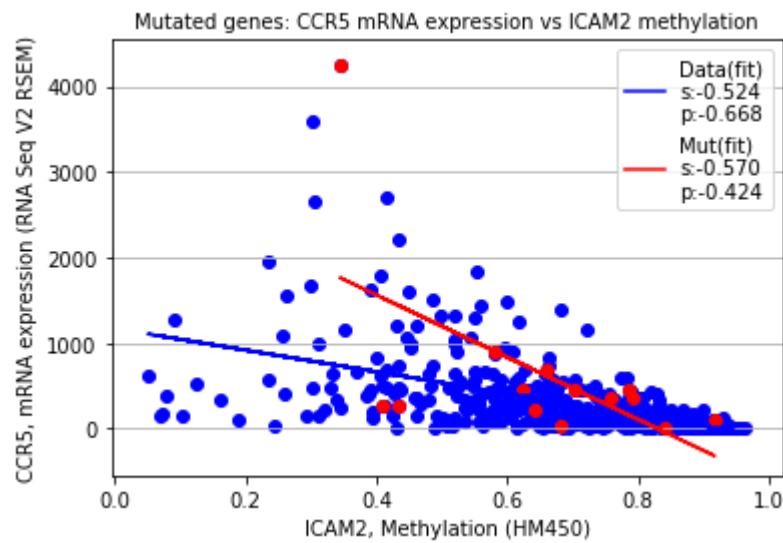
```
In [128]: mutReadPlot('./plots-ccr5-hladmb.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-DMB methylation')
```



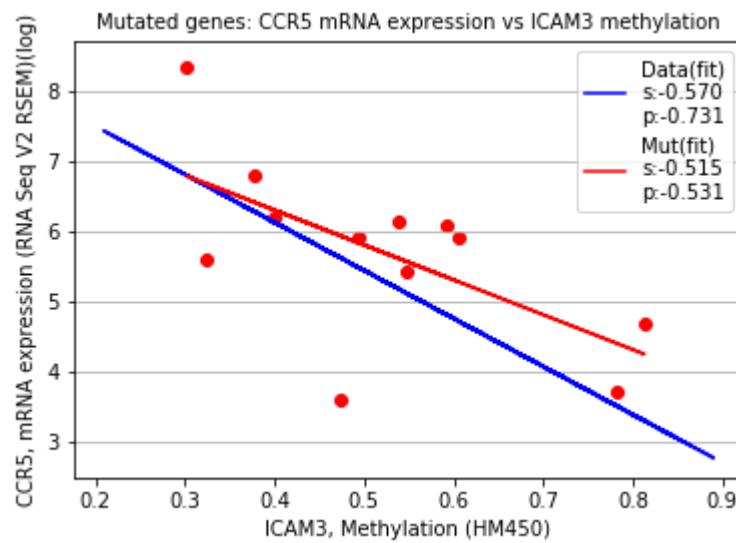
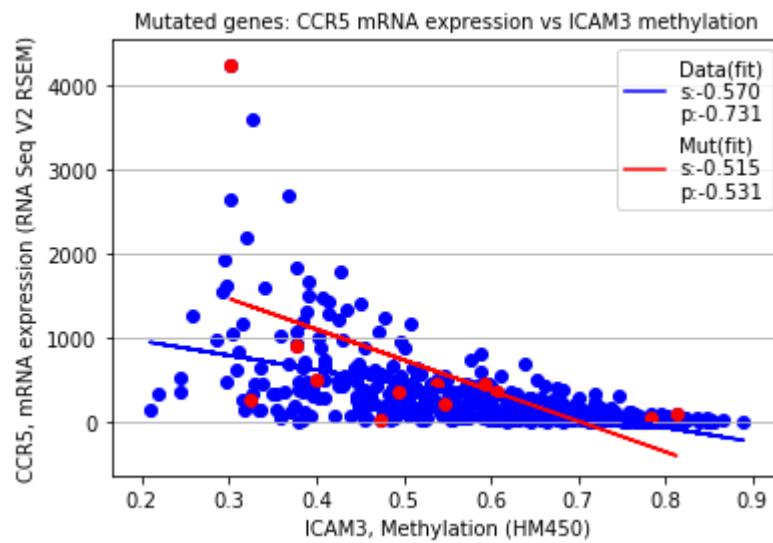
```
In [129]: mutReadPlot('./plots-ccr5-hlae.txt', 'Mutated genes: CCR5 mRNA expression vs HLA-E methylation')
```



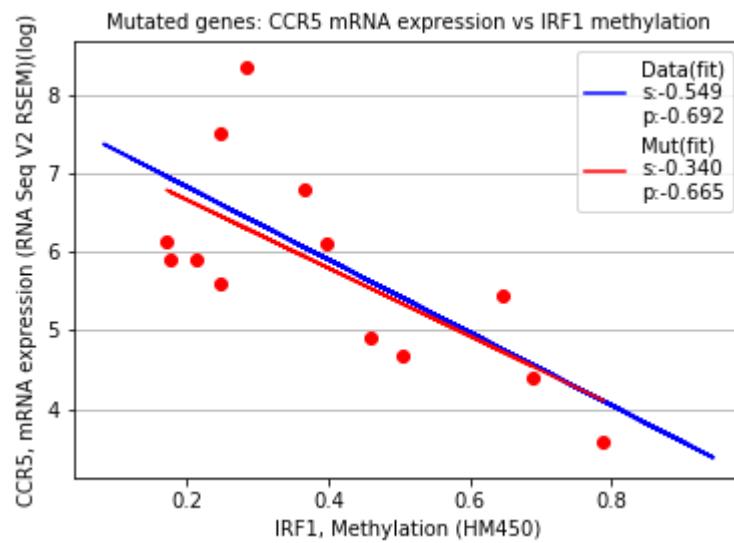
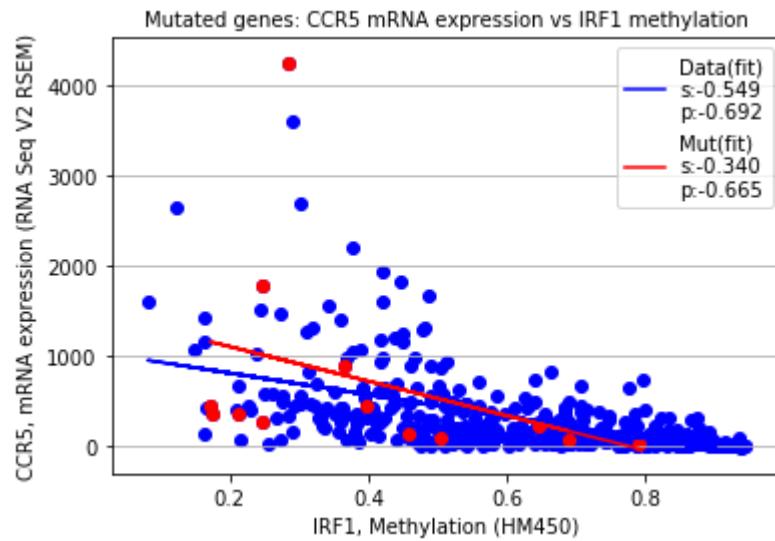
```
In [130]: mutReadPlot('./plots-ccr5-icam2.txt', 'Mutated genes: CCR5 mRNA expression vs ICAM2 methylation')
```



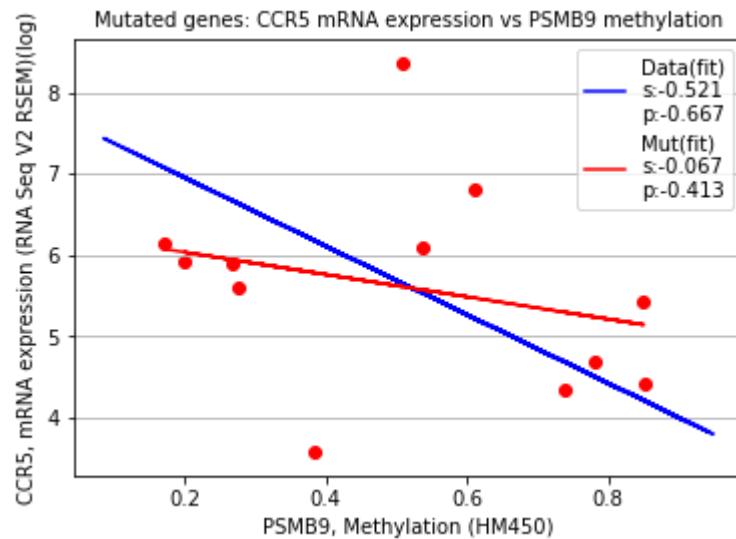
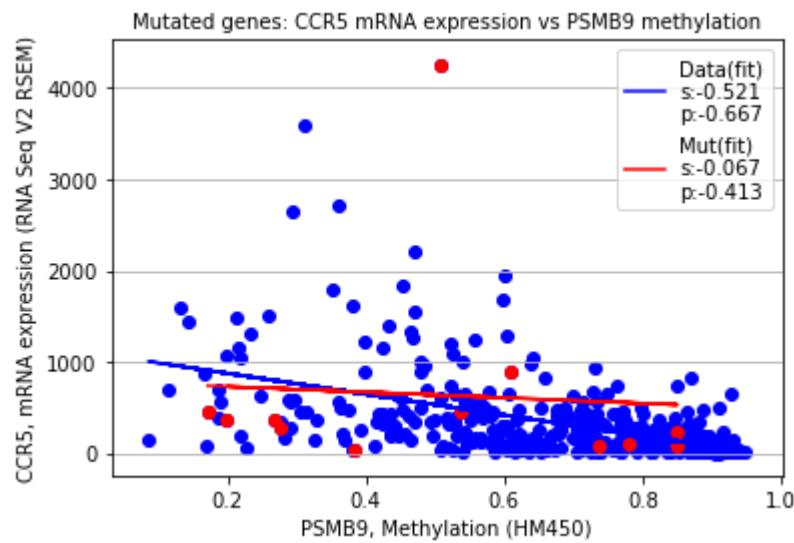
```
In [131]: mutReadPlot('./plots-ccr5-icam3.txt', 'Mutated genes: CCR5 mRNA expression vs ICAM3 methylation')
```



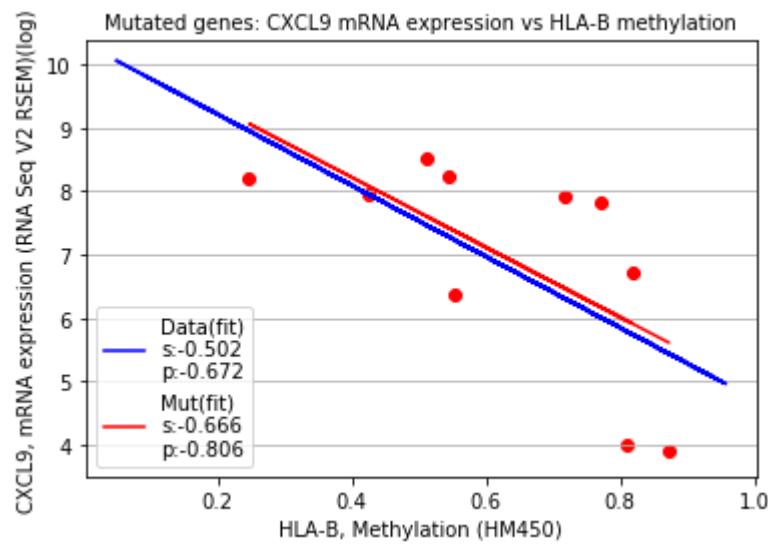
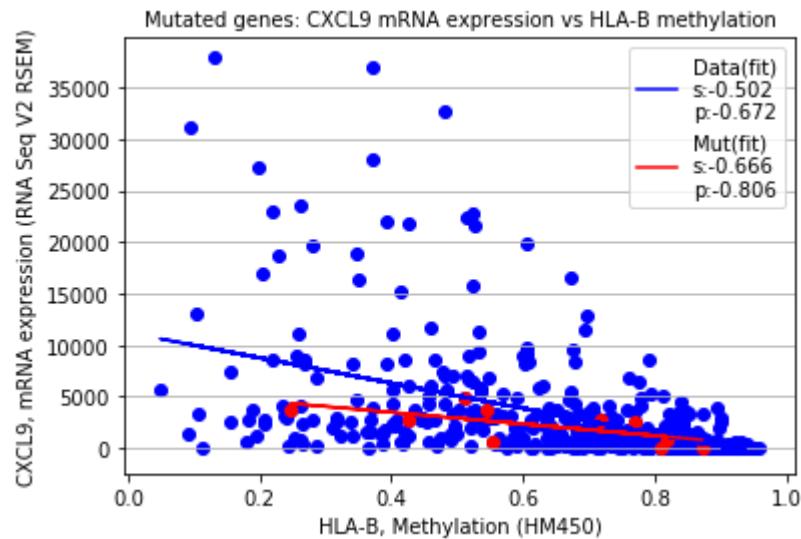
```
In [132]: mutReadPlot('./plots-ccr5-ifrl1.txt', 'Mutated genes: CCR5 mRNA expression vs I  
RF1 methylation')
```



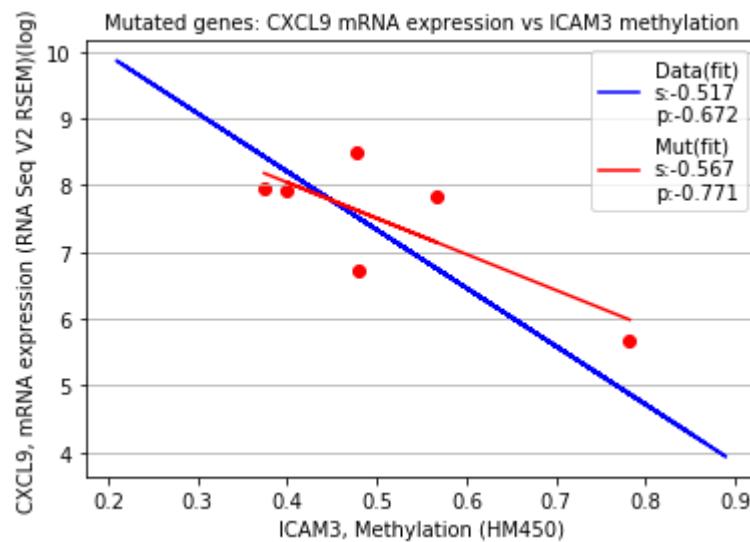
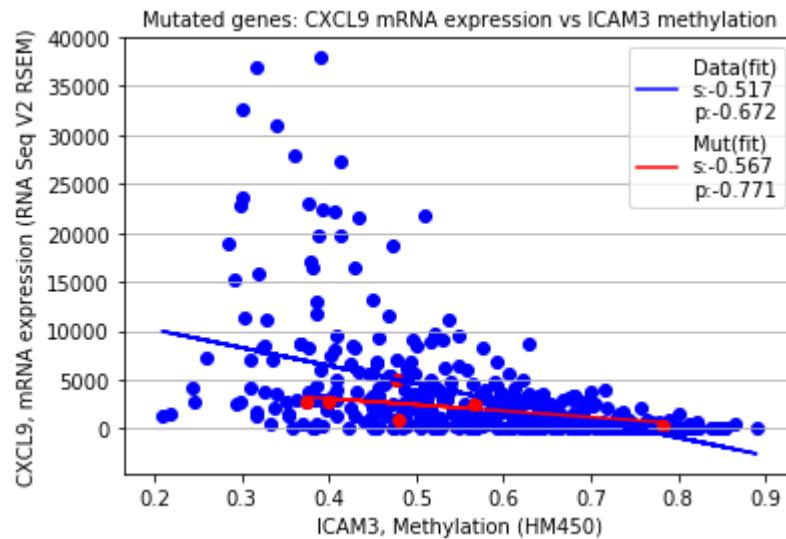
```
In [133]: mutReadPlot('./plots-ccr5-psmb9.txt', 'Mutated genes: CCR5 mRNA expression vs PSMB9 methylation')
```



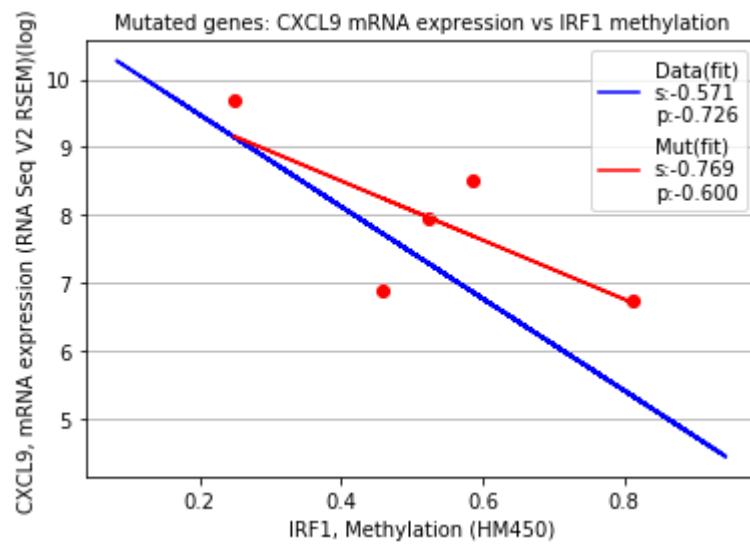
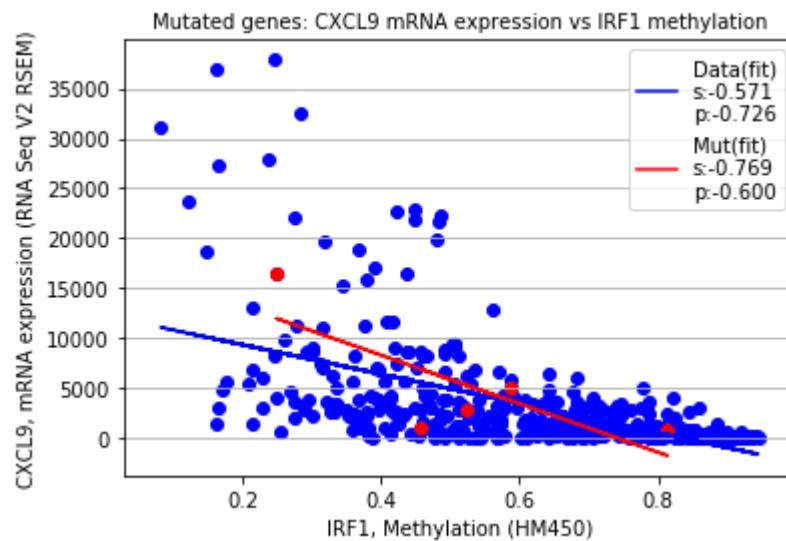
```
In [134]: mutReadPlot('./plots-cxcl9-hlab.txt', 'Mutated genes: CXCL9 mRNA expression vs HLA-B methylation')
```



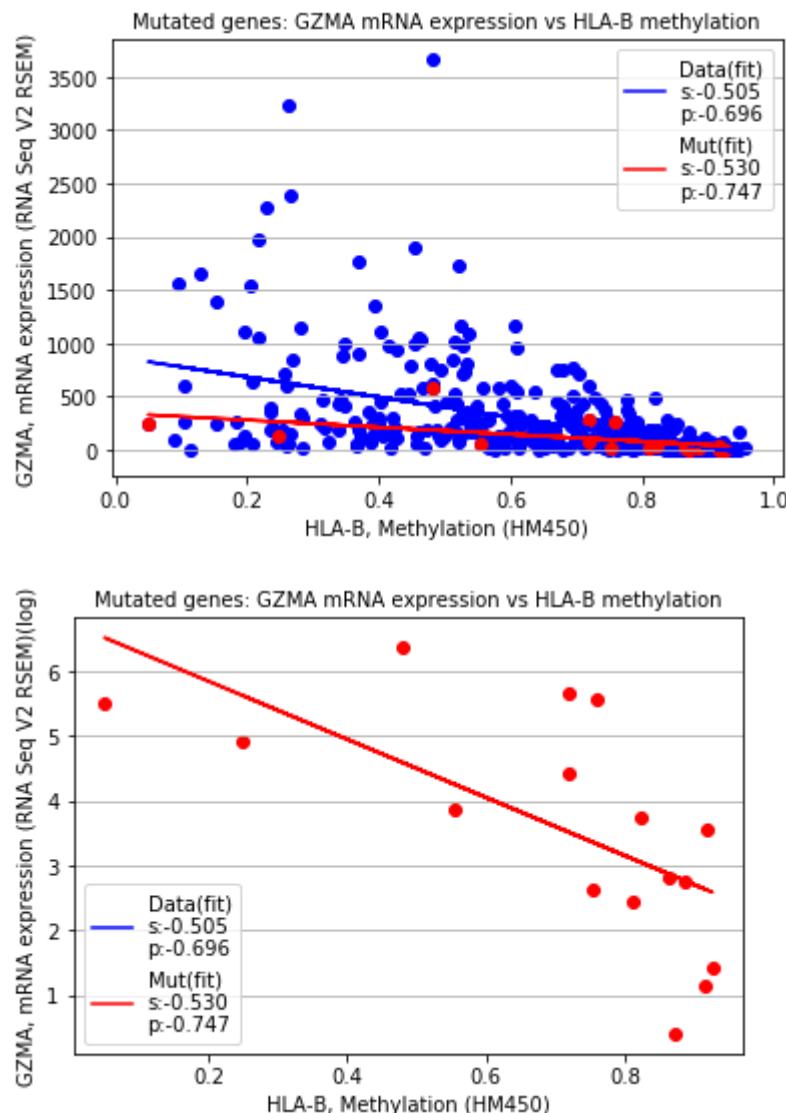
```
In [135]: mutReadPlot('./plots-cxcl9-icam3.txt', 'Mutated genes: CXCL9 mRNA expression v  
s ICAM3 methylation')
```



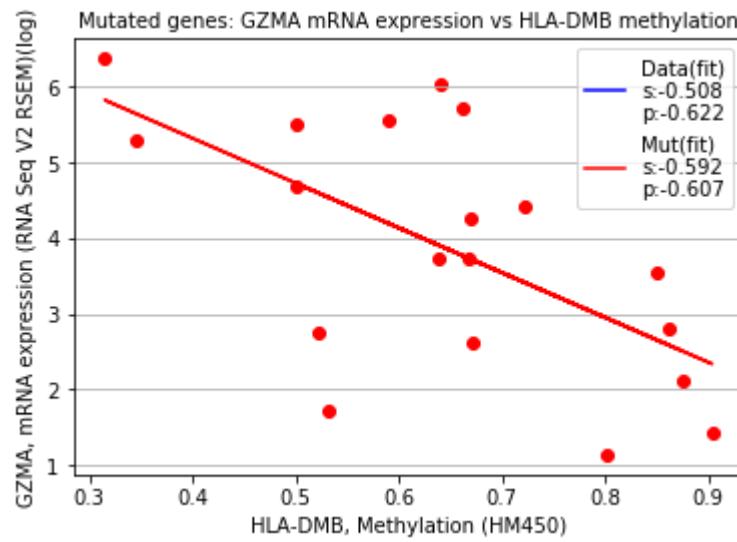
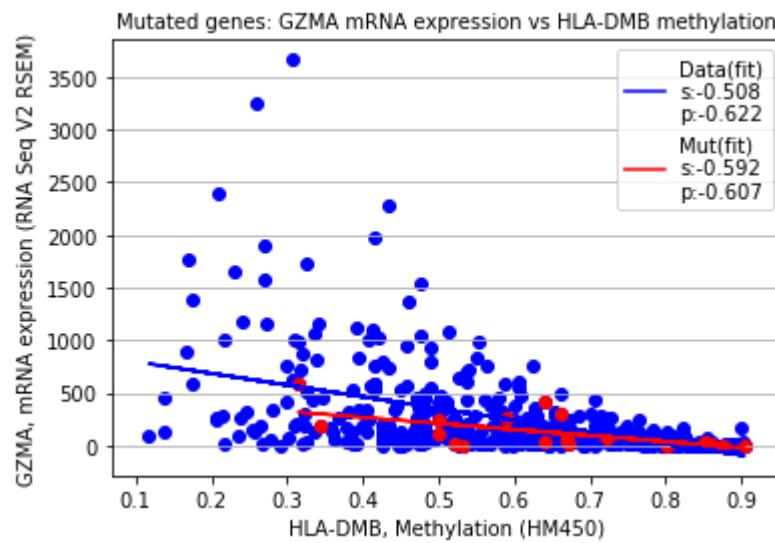
```
In [136]: mutReadPlot('./plots-cxcl9-ifn1.txt', 'Mutated genes: CXCL9 mRNA expression vs IRF1 methylation')
```



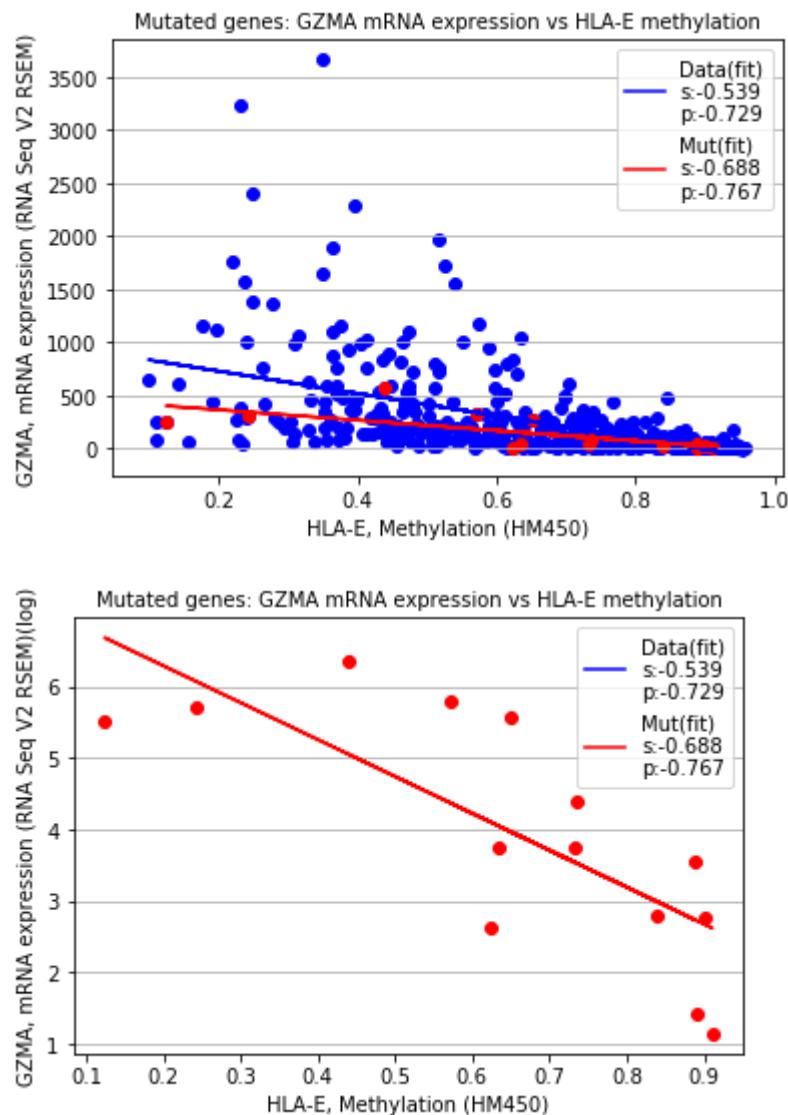
```
In [137]: mutReadPlot('./plots-gzma-hlab.txt', 'Mutated genes: GZMA mRNA expression vs HLA-B methylation')
```



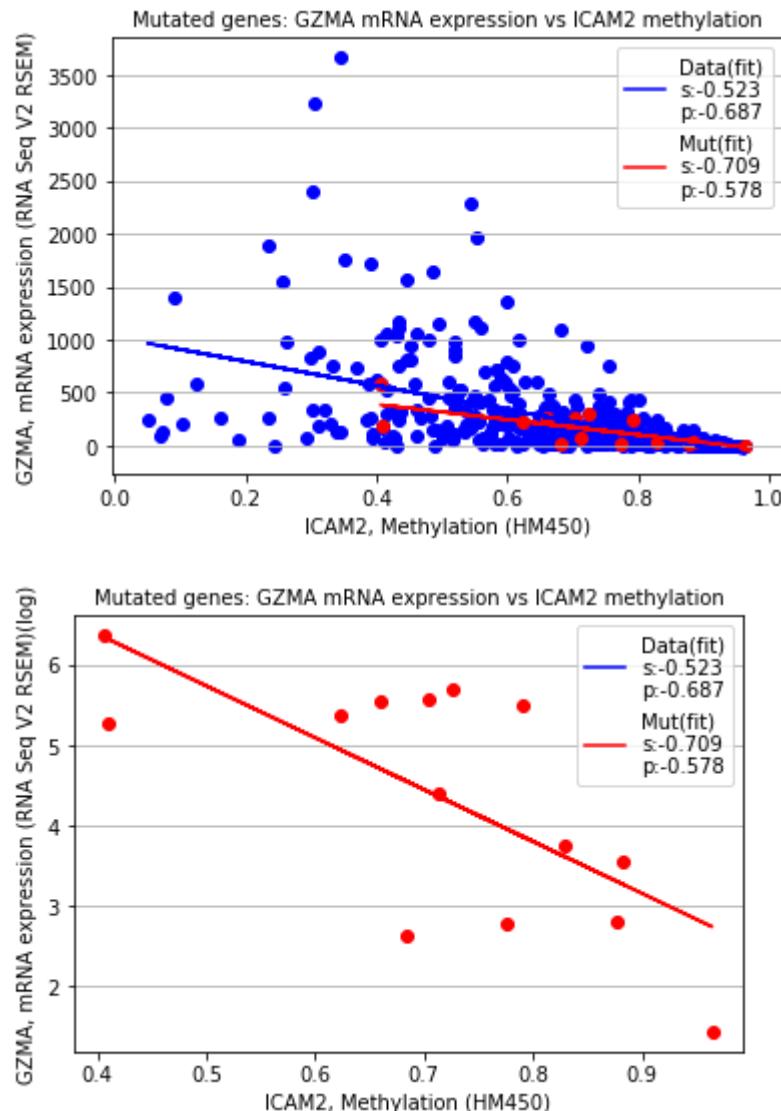
```
In [138]: mutReadPlot('./plots-gzma-hladmb.txt', 'Mutated genes: GZMA mRNA expression vs HLA-DMB methylation')
```



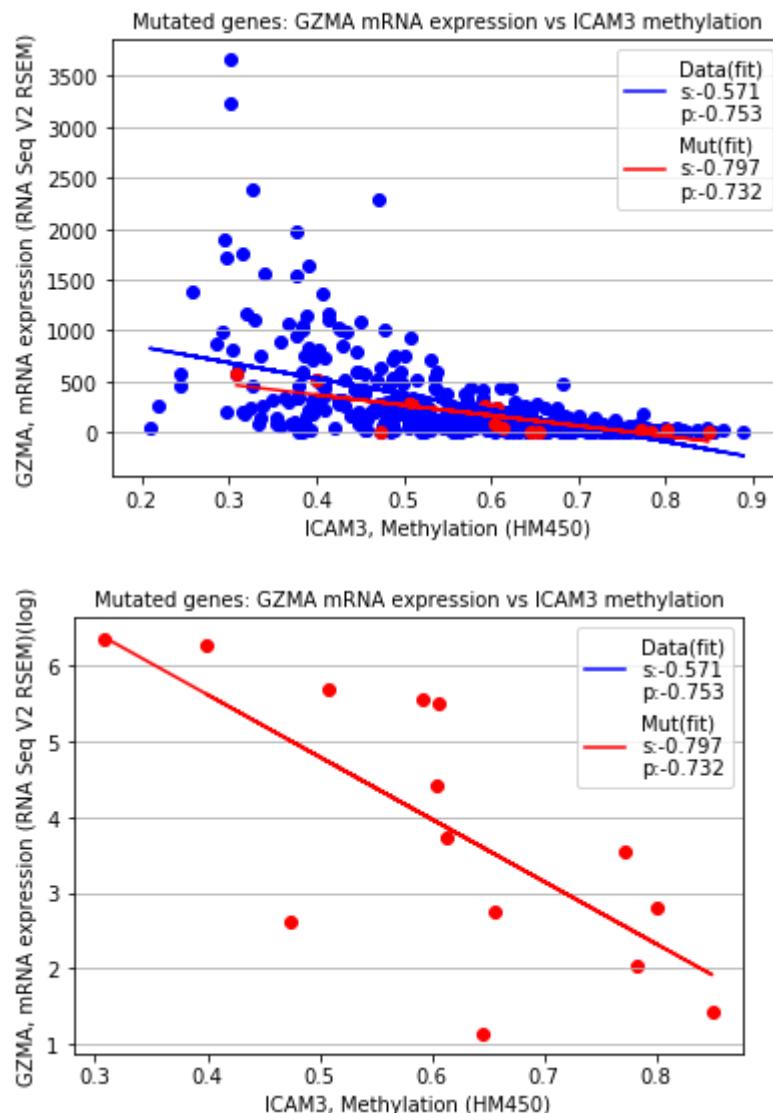
```
In [139]: mutReadPlot('./plots-gzma-hlae.txt', 'Mutated genes: GZMA mRNA expression vs HLA-E methylation')
```



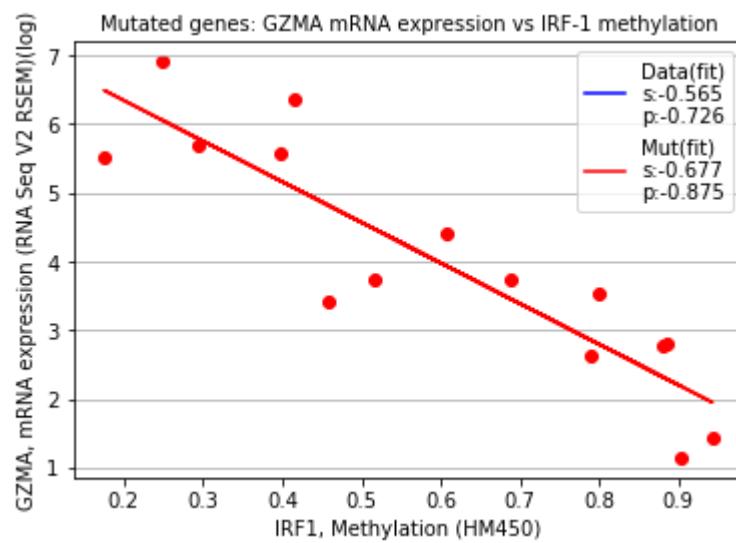
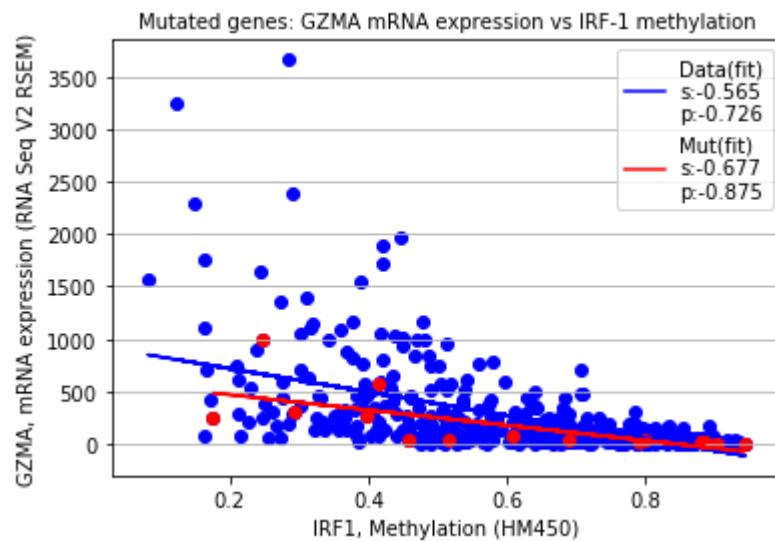
```
In [140]: mutReadPlot('./plots-gzma-icam2.txt', 'Mutated genes: GZMA mRNA expression vs ICAM2 methylation')
```



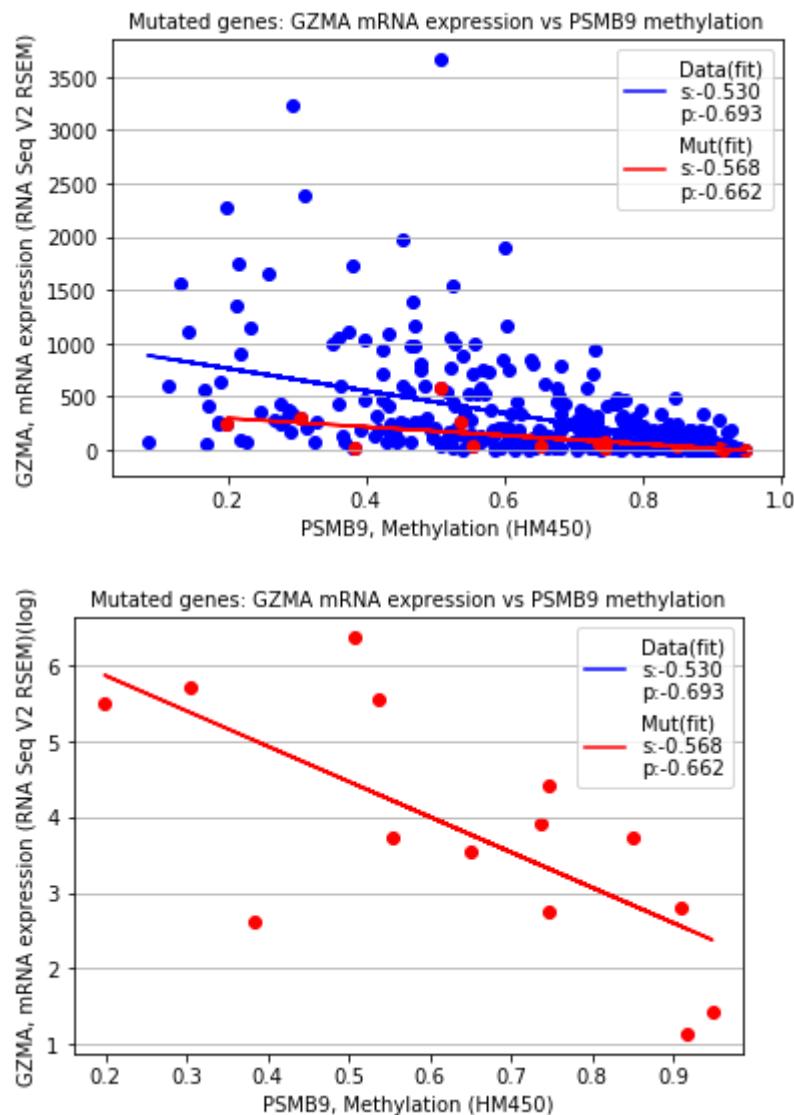
```
In [141]: mutReadPlot('./plots-gzma-icam3.txt', 'Mutated genes: GZMA mRNA expression vs ICAM3 methylation')
```



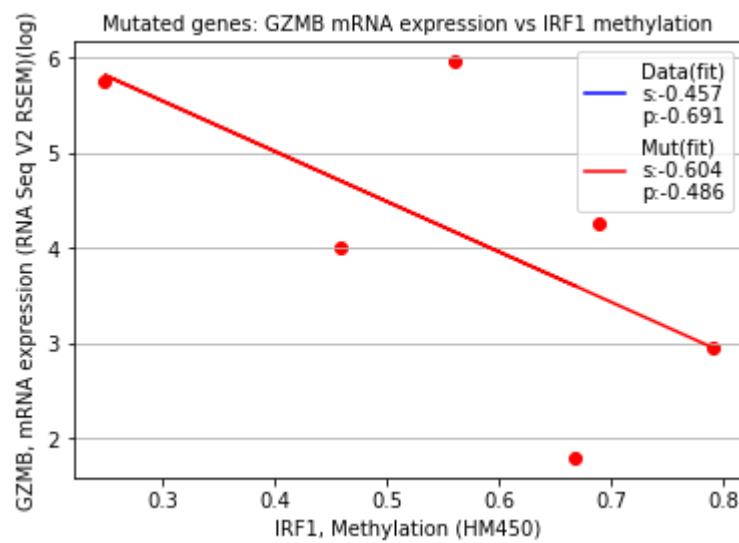
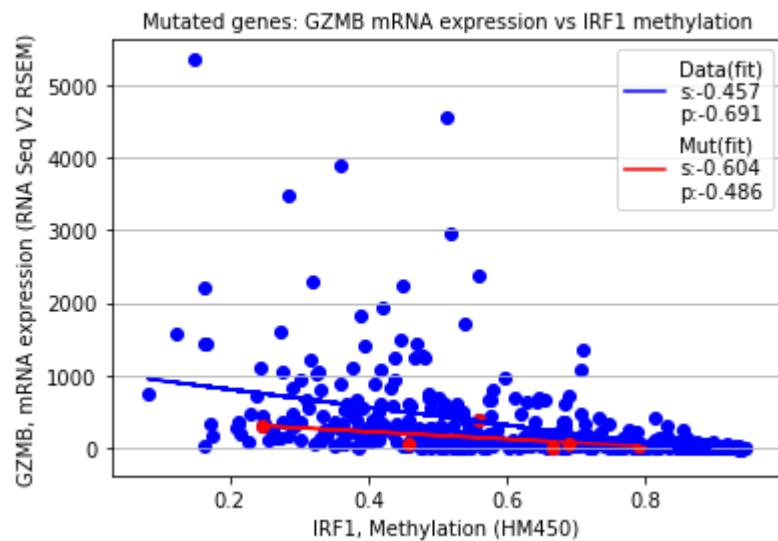
```
In [142]: mutReadPlot('./plots-gzma-irf1.txt', 'Mutated genes: GZMA mRNA expression vs I  
RF-1 methylation')
```



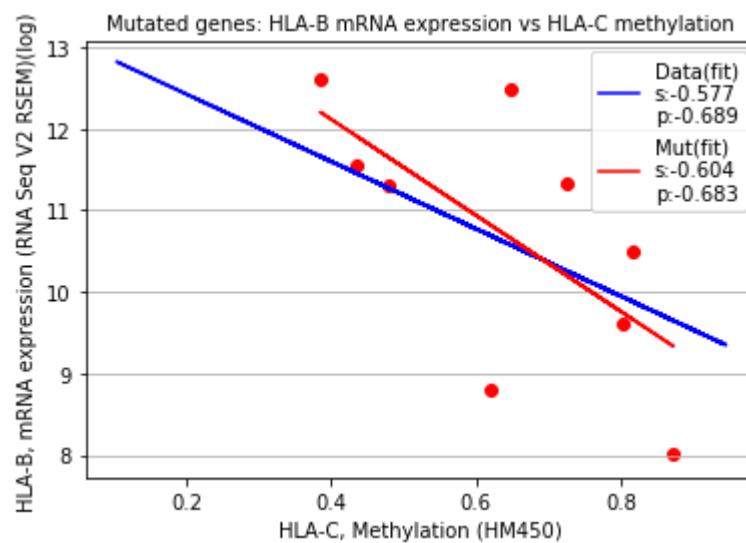
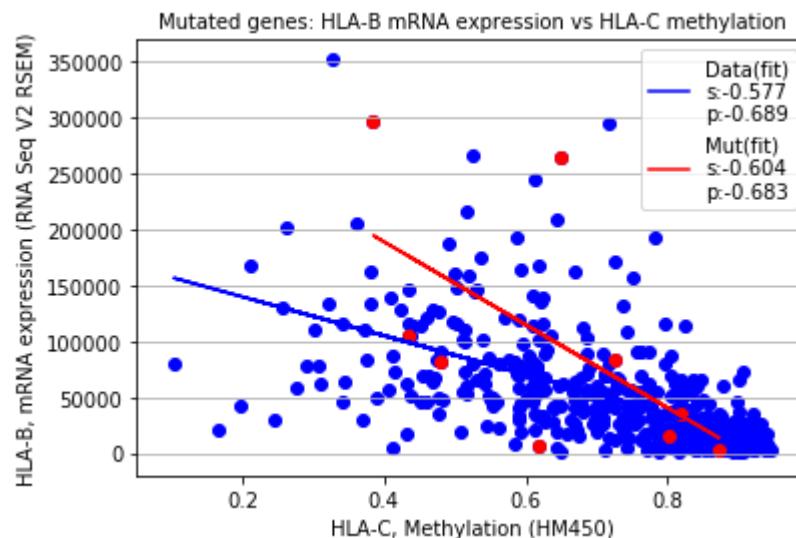
```
In [143]: mutReadPlot('./plots-gzma-psmb9.txt', 'Mutated genes: GZMA mRNA expression vs PSMB9 methylation')
```



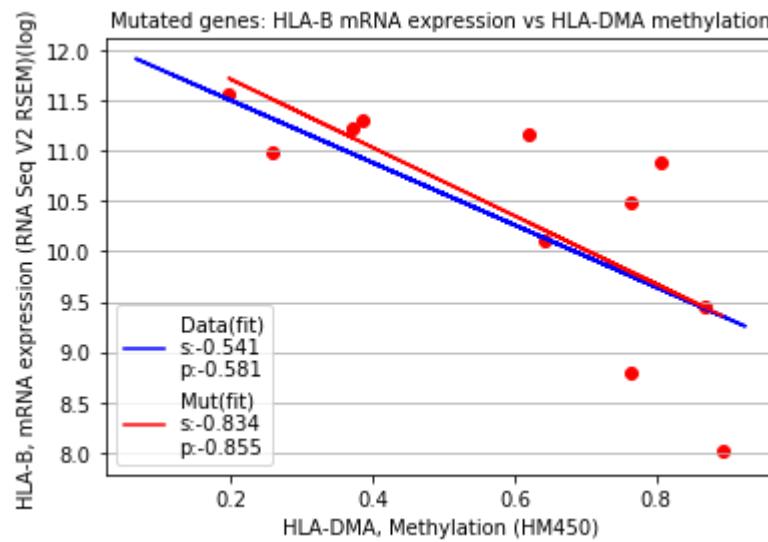
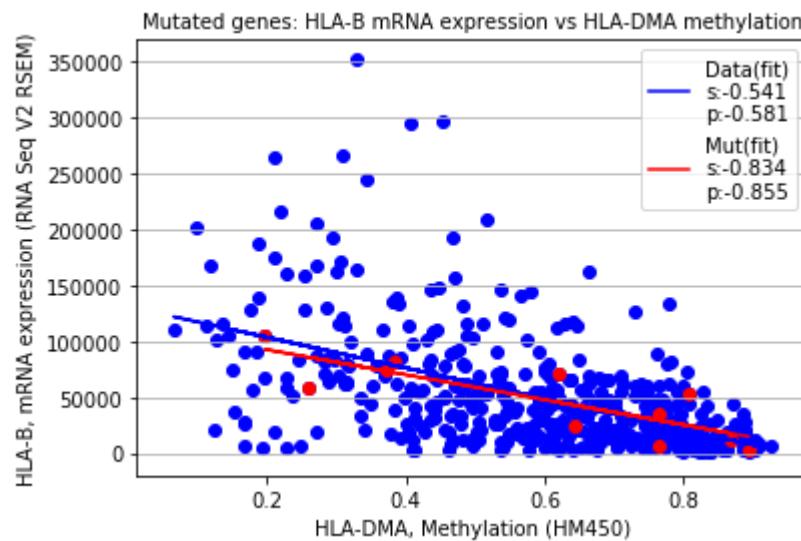
```
In [144]: mutReadPlot('./plots-gzmb-irf1.txt', 'Mutated genes: GZMB mRNA expression vs I  
RF1 methylation')
```



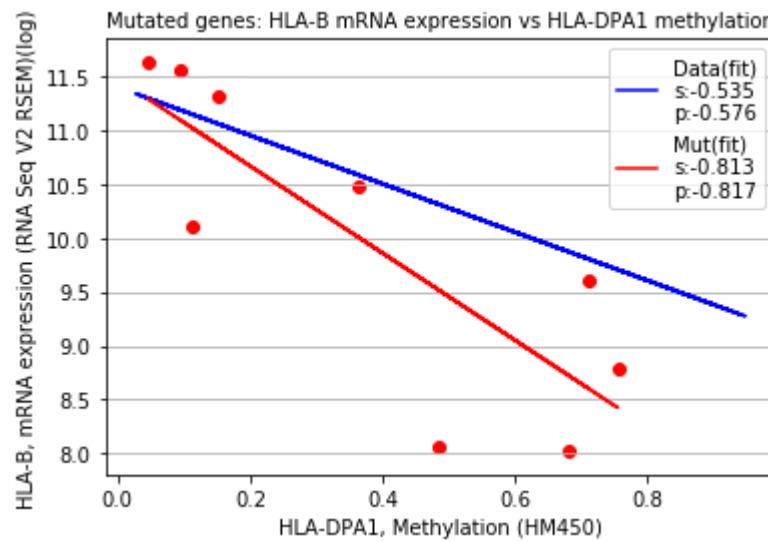
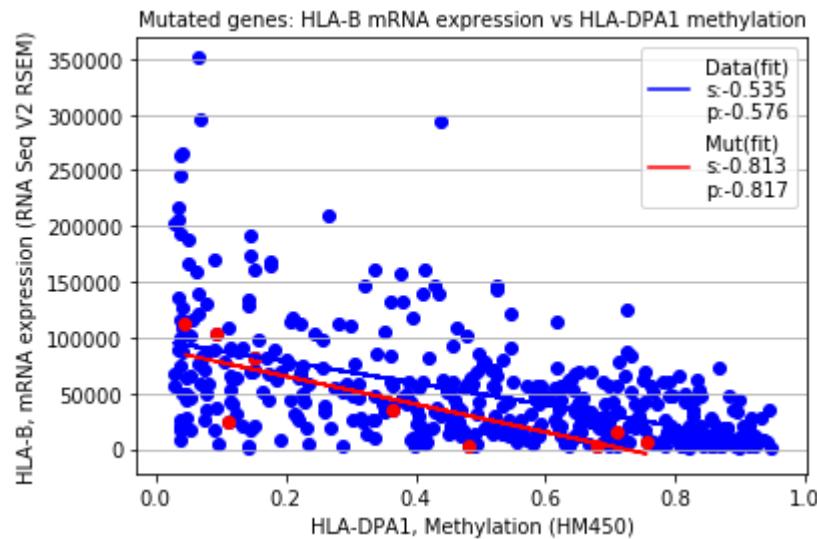
```
In [145]: mutReadPlot('./plots-hlab-hlac.txt', 'Mutated genes: HLA-B mRNA expression vs HLA-C methylation')
```



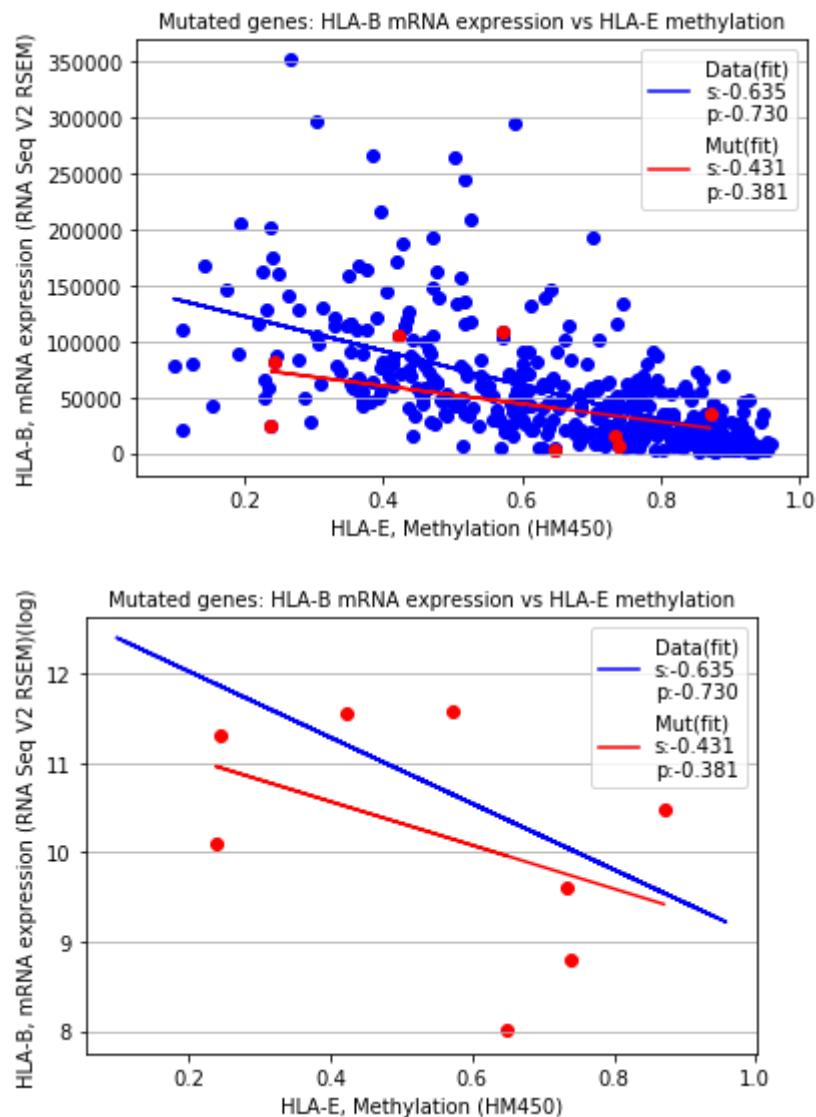
```
In [146]: mutReadPlot('./plots-hlab-hladma.txt', 'Mutated genes: HLA-B mRNA expression vs HLA-DMA methylation')
```



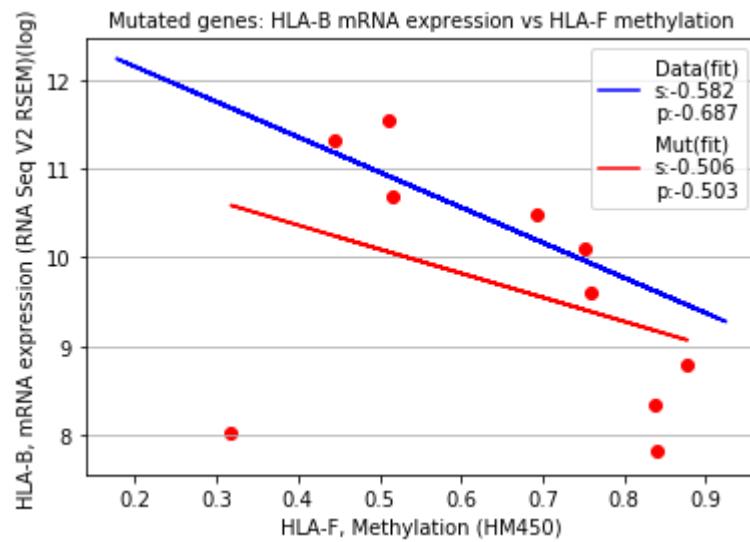
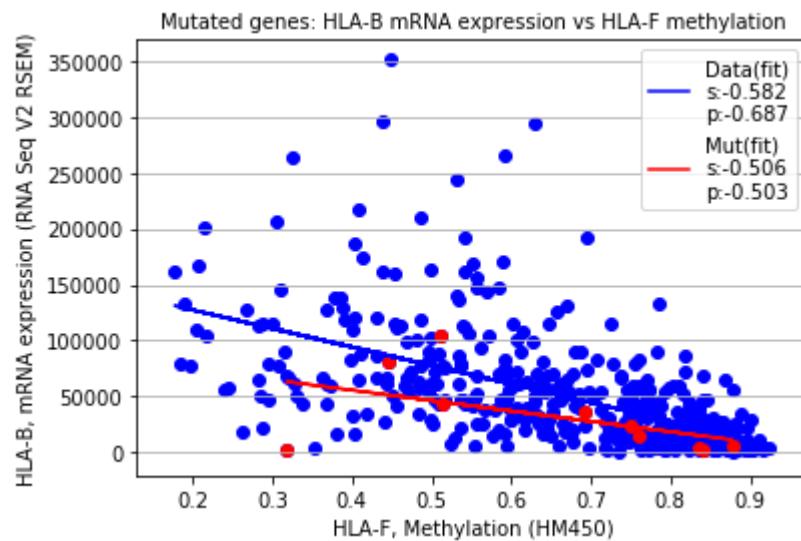
```
In [147]: mutReadPlot('./plots-hlab-hladpa1.txt', 'Mutated genes: HLA-B mRNA expression vs HLA-DPA1 methylation')
```



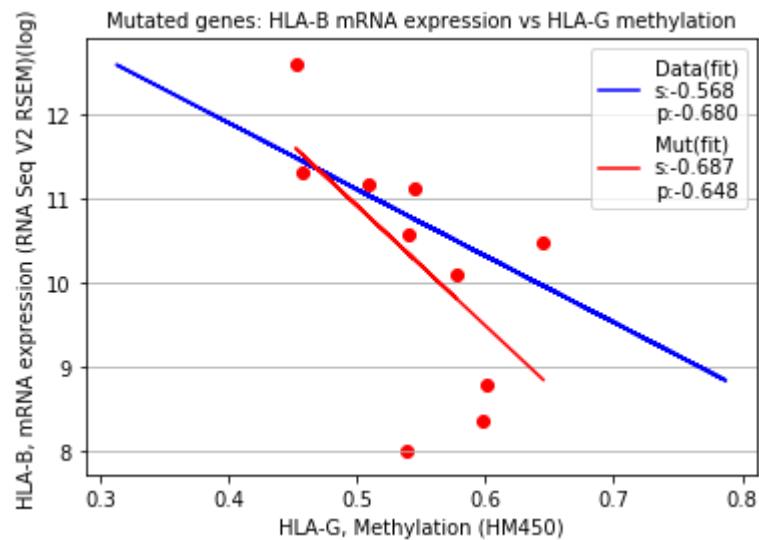
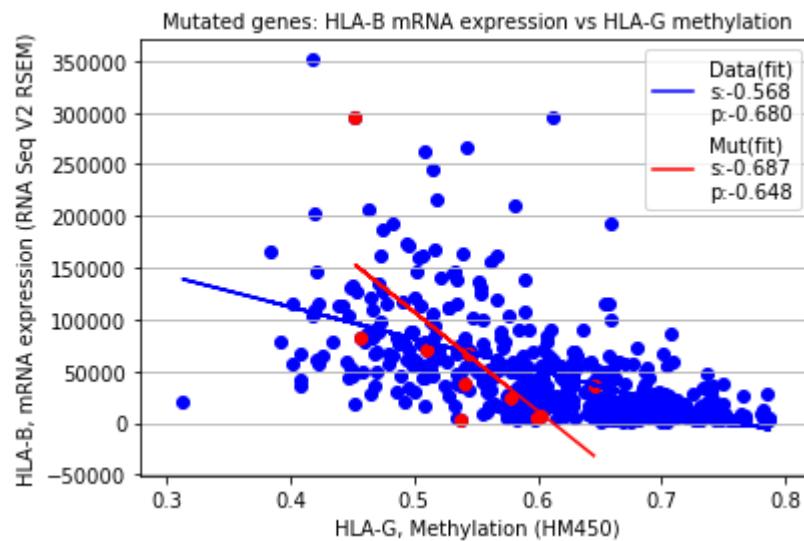
```
In [148]: mutReadPlot('./plots-hlab-hlae.txt', 'Mutated genes: HLA-B mRNA expression vs HLA-E methylation')
```



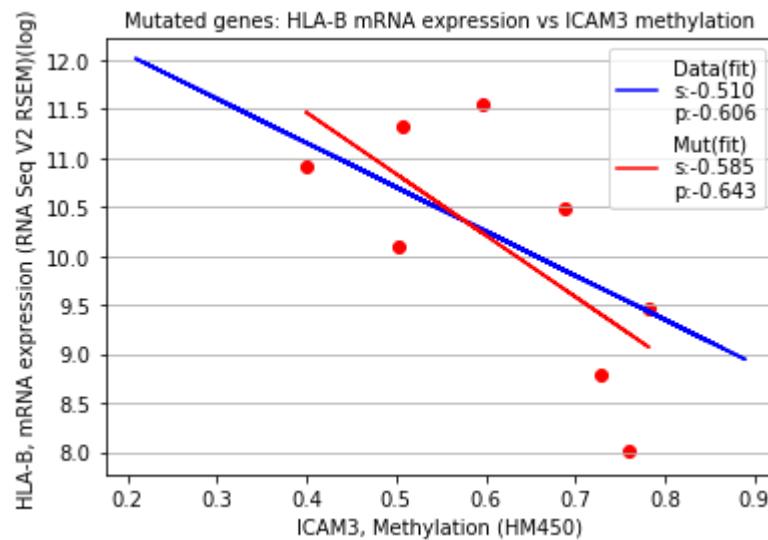
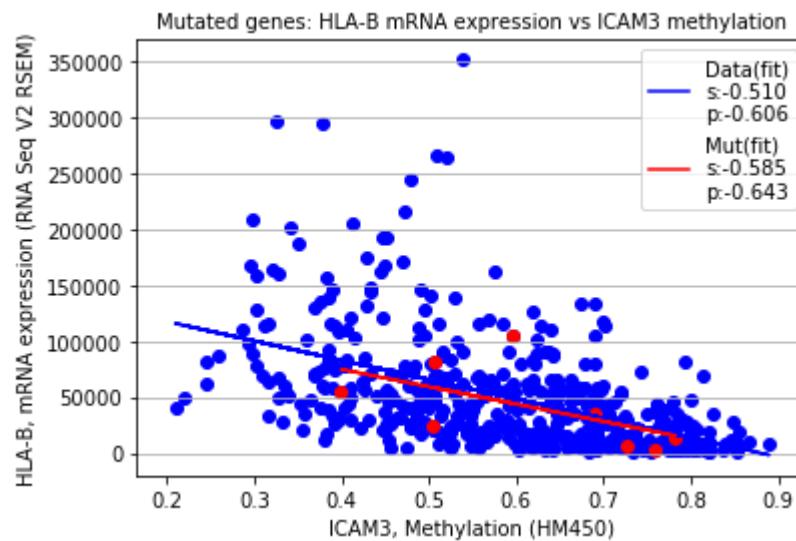
```
In [149]: mutReadPlot('./plots-hlab-hlaf.txt', 'Mutated genes: HLA-B mRNA expression vs HLA-F methylation')
```



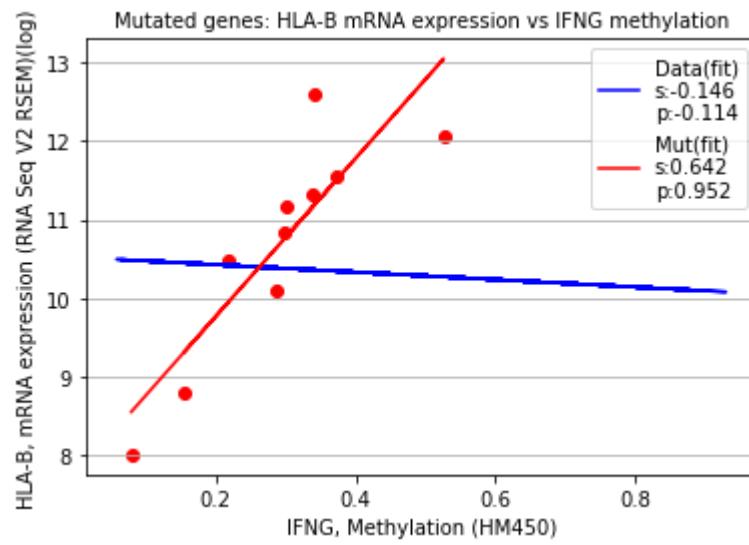
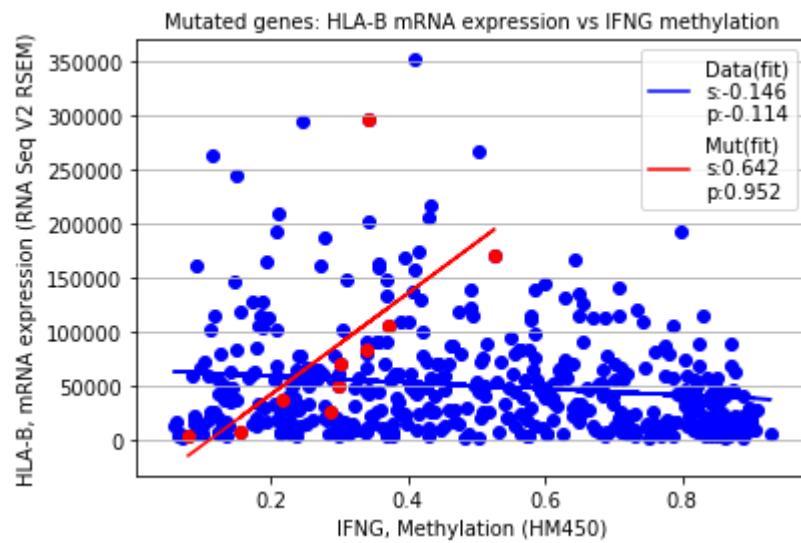
```
In [150]: mutReadPlot('./plots-hlab-hlag.txt', 'Mutated genes: HLA-B mRNA expression vs HLA-G methylation')
```



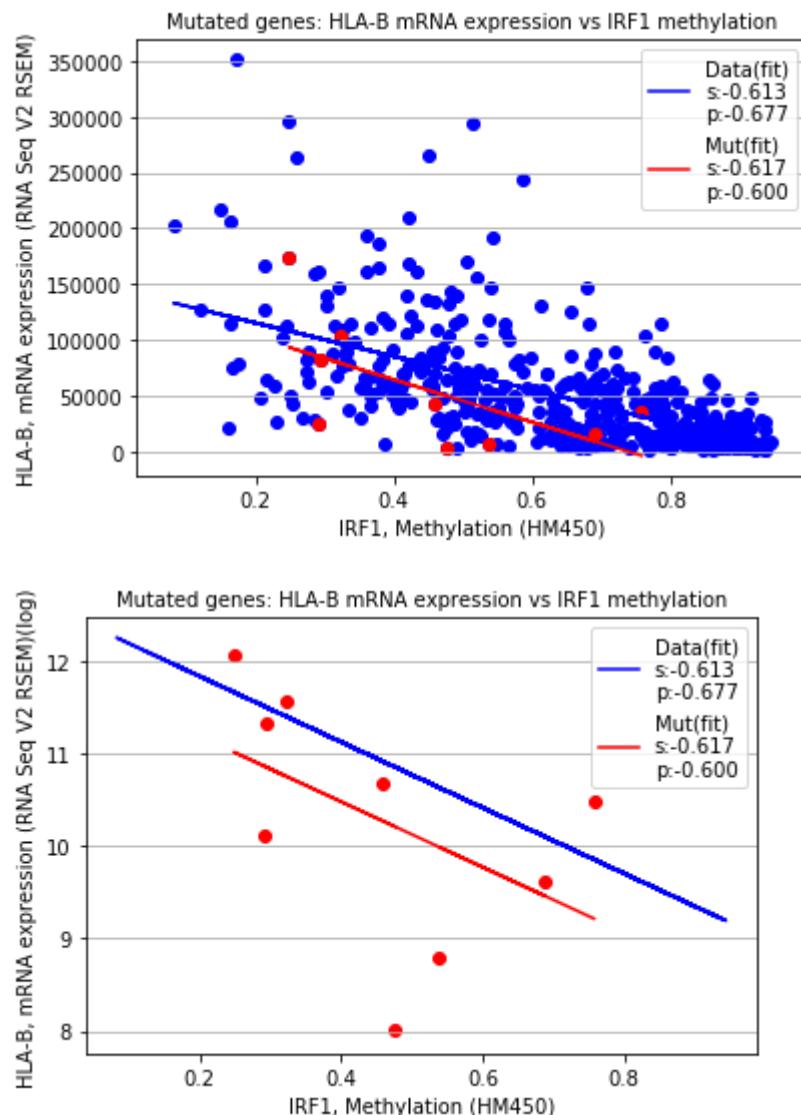
```
In [151]: mutReadPlot('./plots-hlab-icam3.txt', 'Mutated genes: HLA-B mRNA expression vs ICAM3 methylation')
```



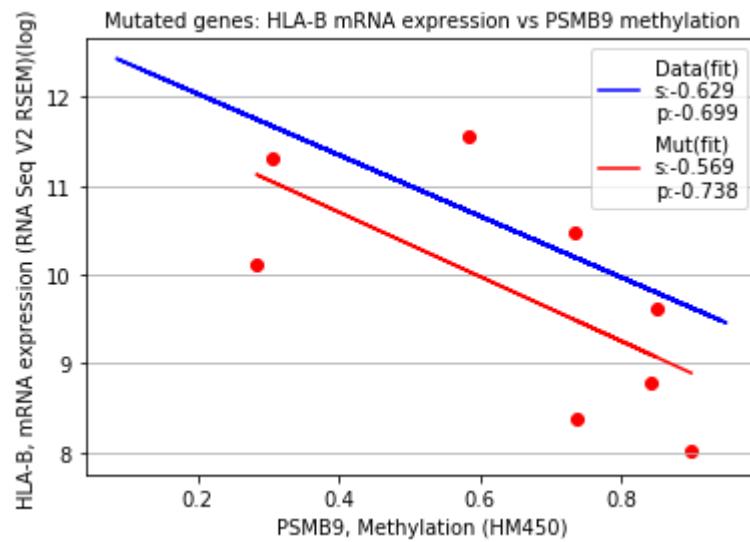
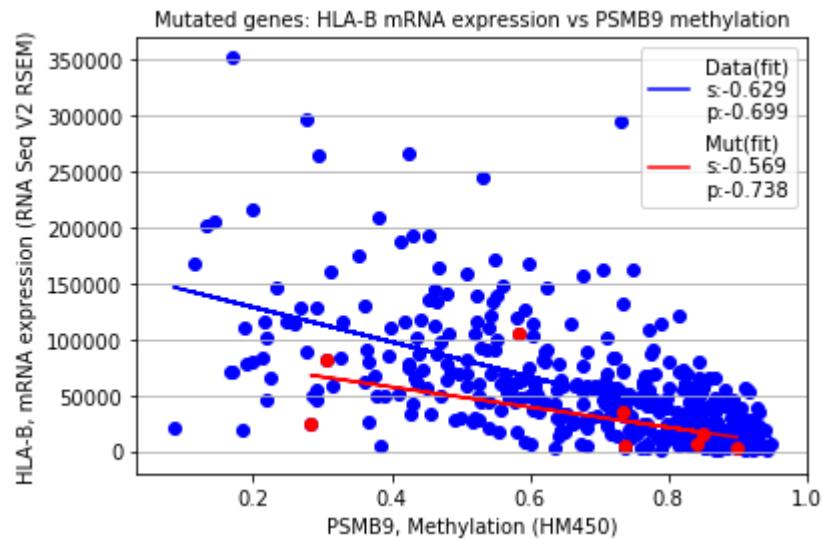
```
In [152]: mutReadPlot('./plots-hlab-ifng.txt', 'Mutated genes: HLA-B mRNA expression vs IFNG methylation')
```



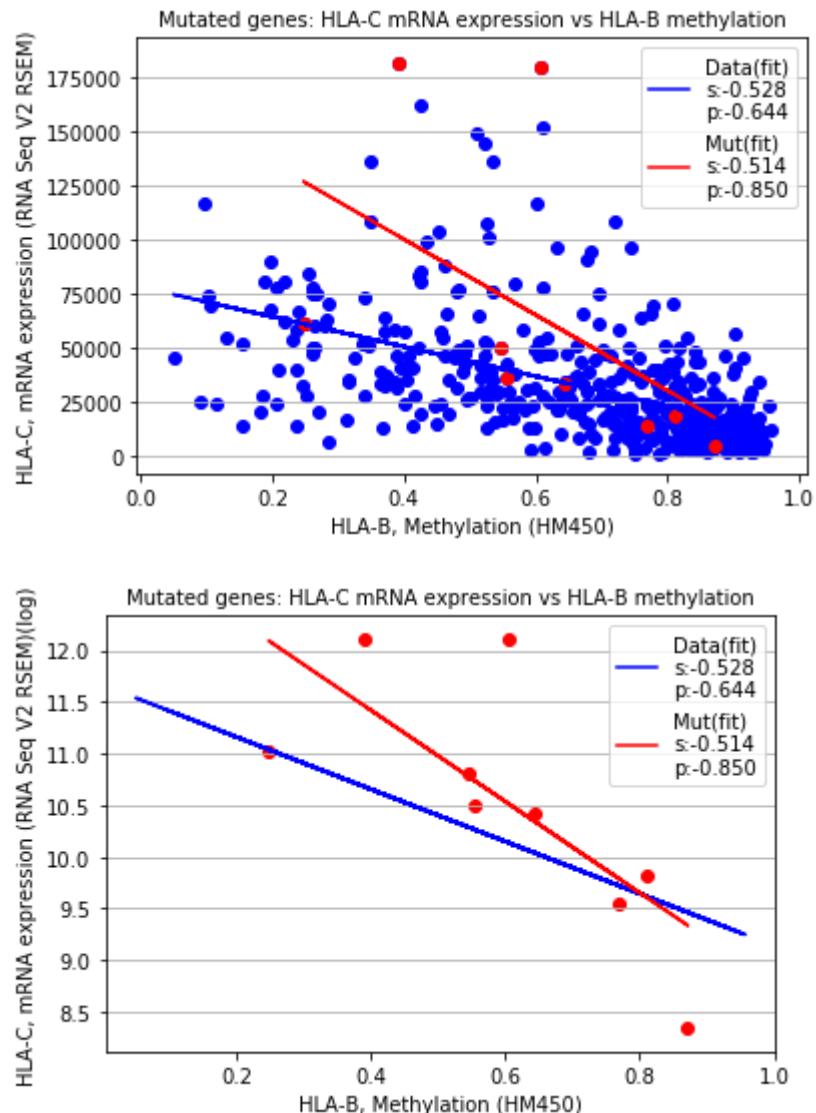
```
In [153]: mutReadPlot('./plots-hlab-irf1.txt', 'Mutated genes: HLA-B mRNA expression vs IRF1 methylation')
```



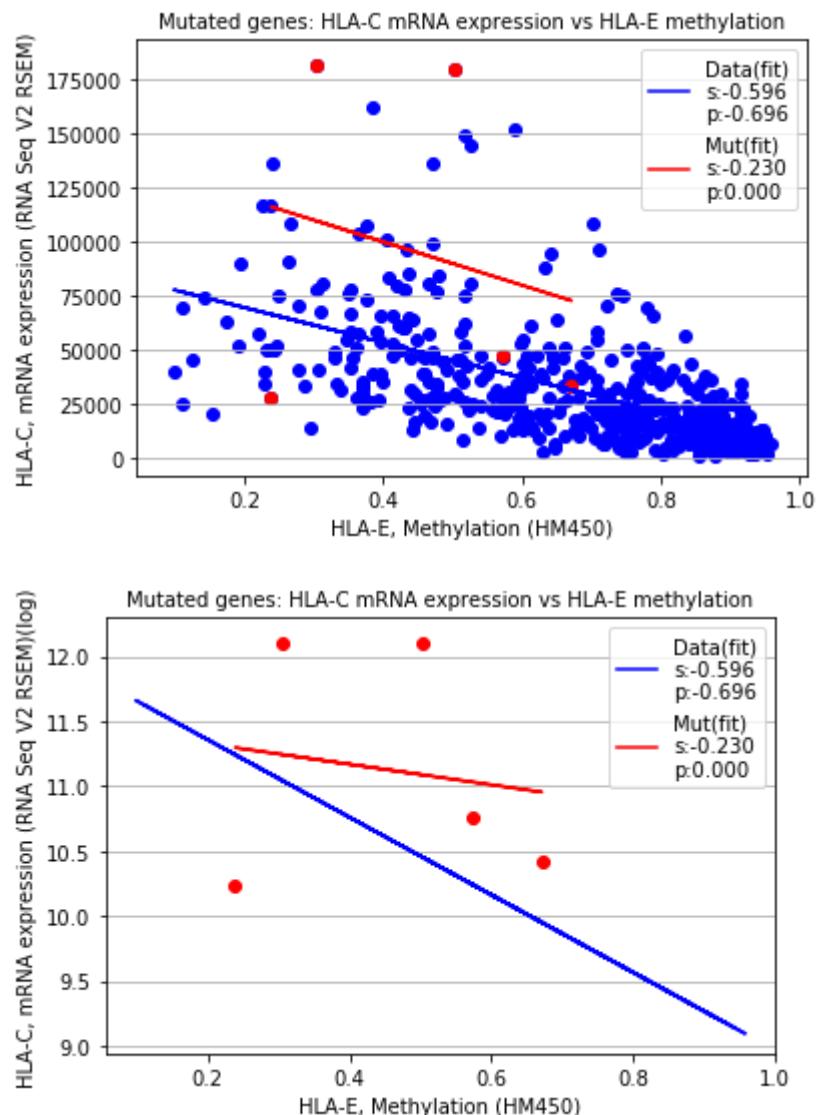
```
In [154]: mutReadPlot('./plots-hlab-psmb9.txt', 'Mutated genes: HLA-B mRNA expression vs PSMB9 methylation')
```



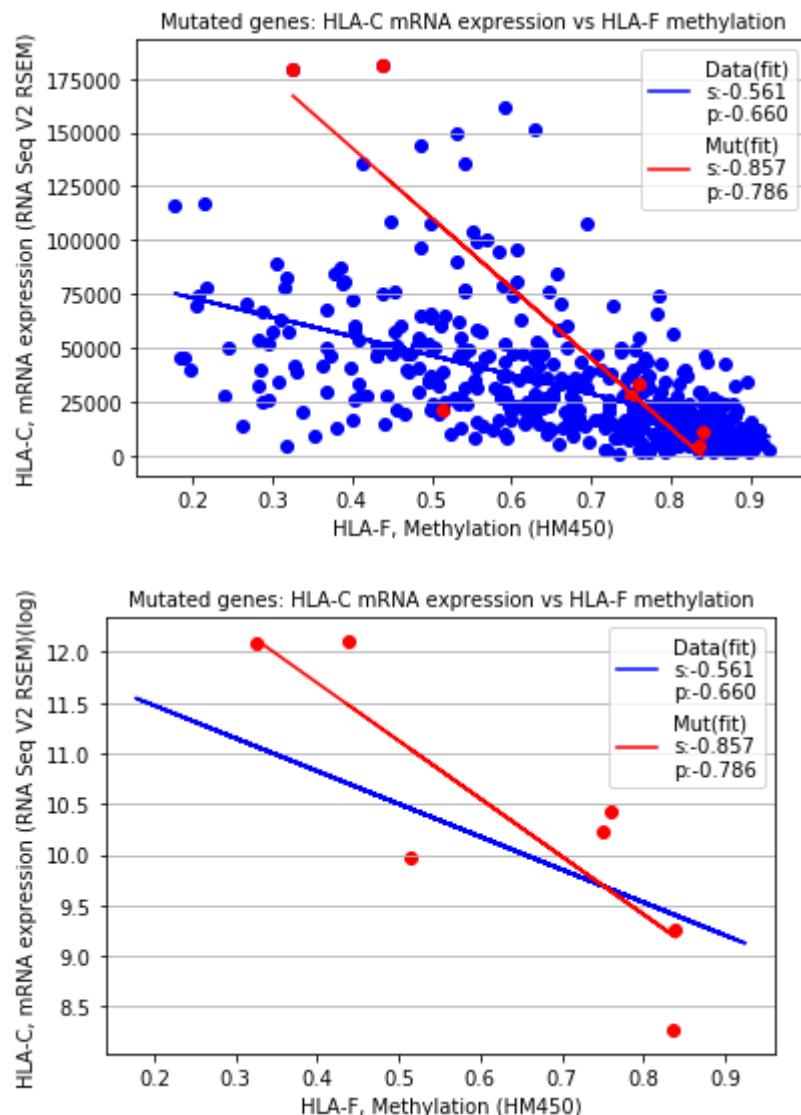
```
In [155]: mutReadPlot('./plots-hlac-hlab.txt', 'Mutated genes: HLA-C mRNA expression vs HLA-B methylation')
```



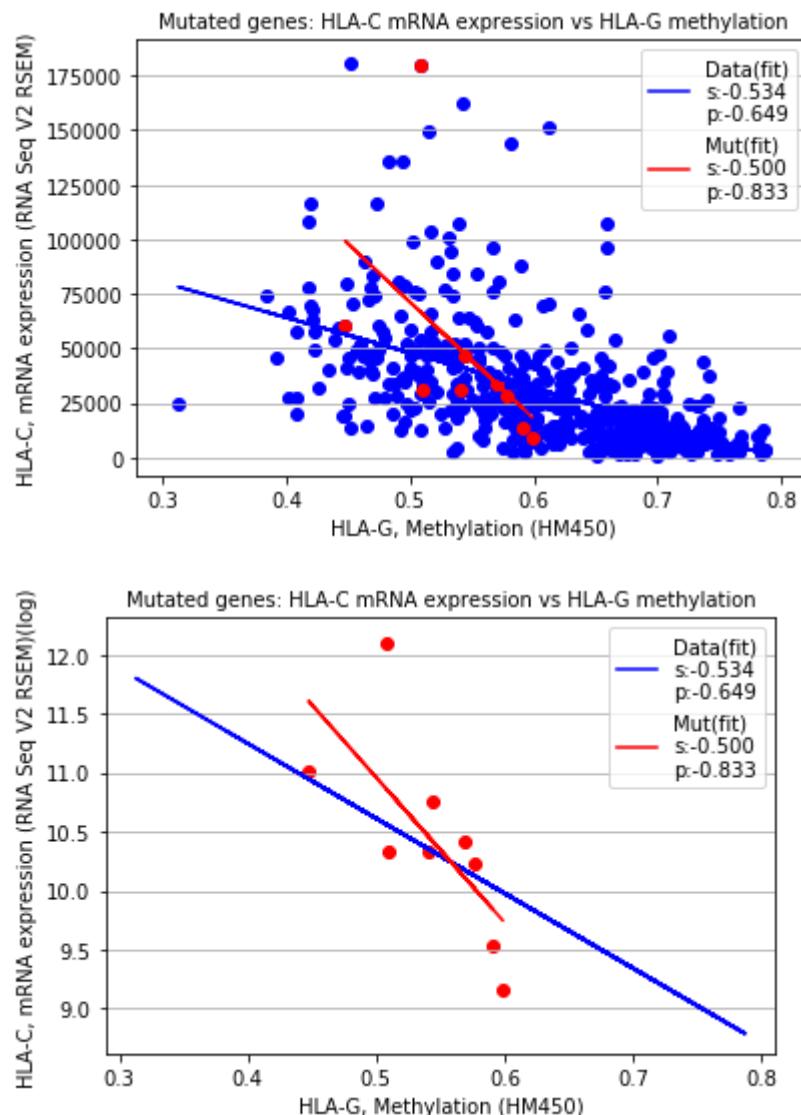
```
In [156]: mutReadPlot('./plots-hlac-hlae.txt', 'Mutated genes: HLA-C mRNA expression vs HLA-E methylation')
```



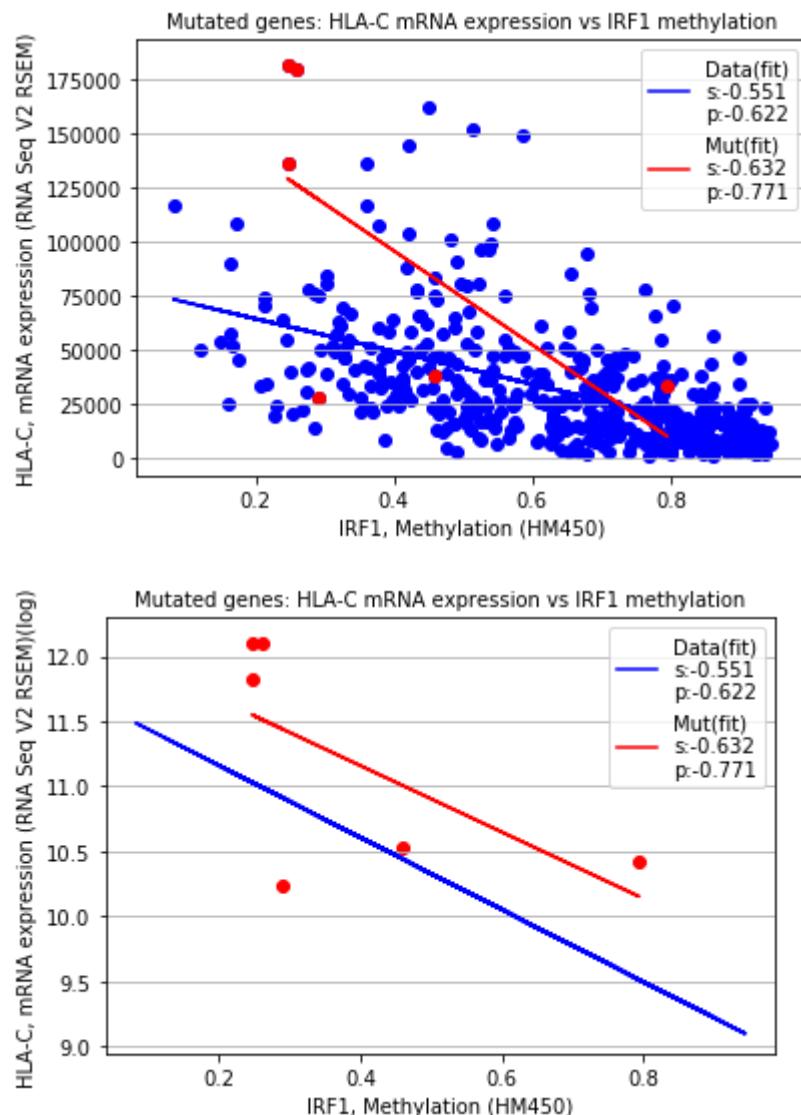
```
In [157]: mutReadPlot('./plots-hlac-hlaf.txt', 'Mutated genes: HLA-C mRNA expression vs HLA-F methylation')
```



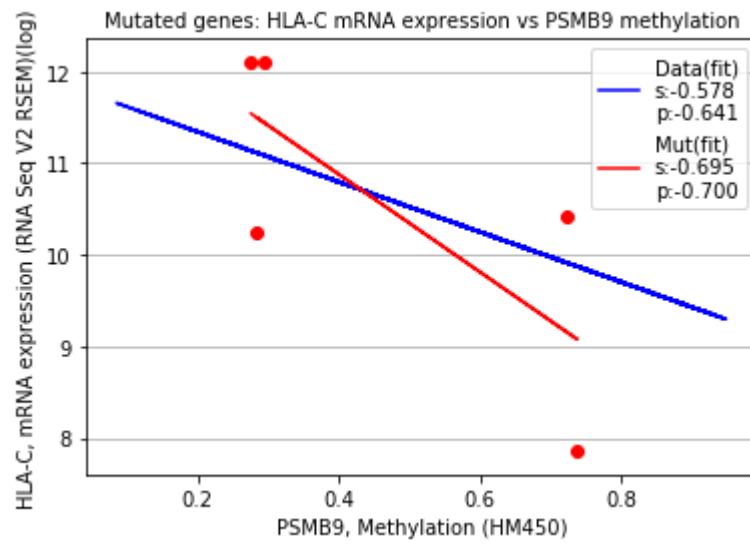
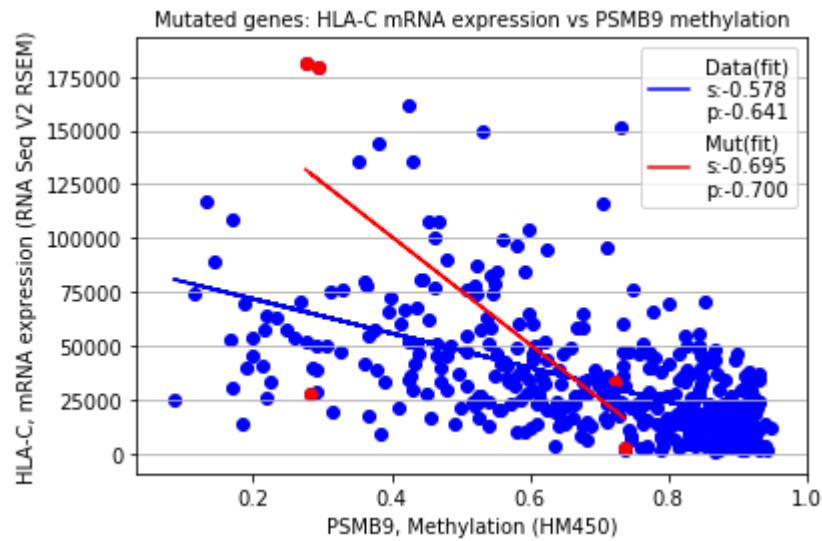
```
In [158]: mutReadPlot('./plots-hlac-hlag.txt', 'Mutated genes: HLA-C mRNA expression vs HLA-G methylation')
```



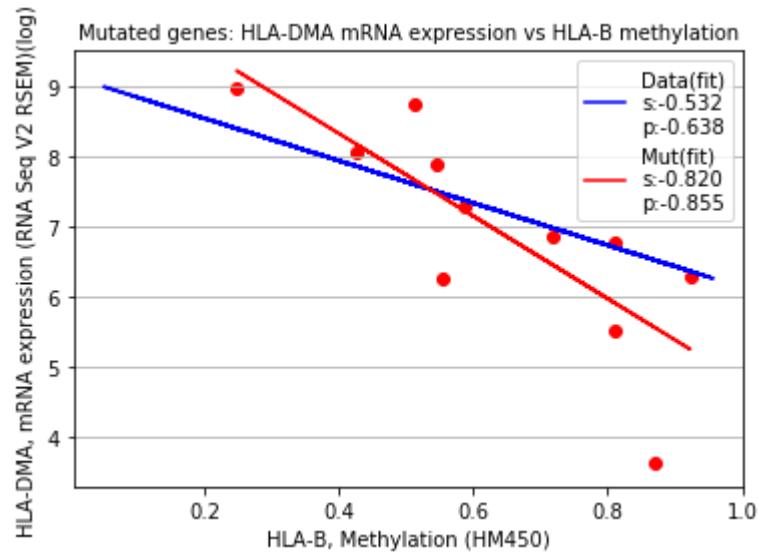
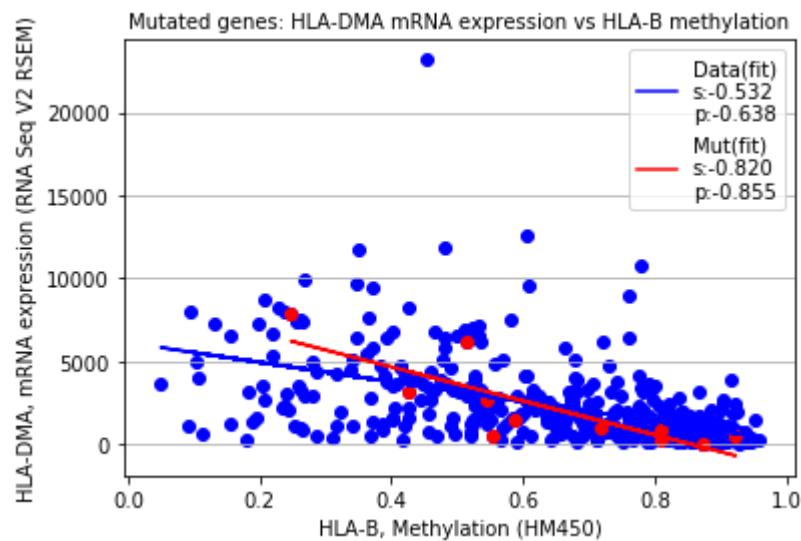
```
In [159]: mutReadPlot('./plots-hlac-irf1.txt', 'Mutated genes: HLA-C mRNA expression vs IRF1 methylation')
```



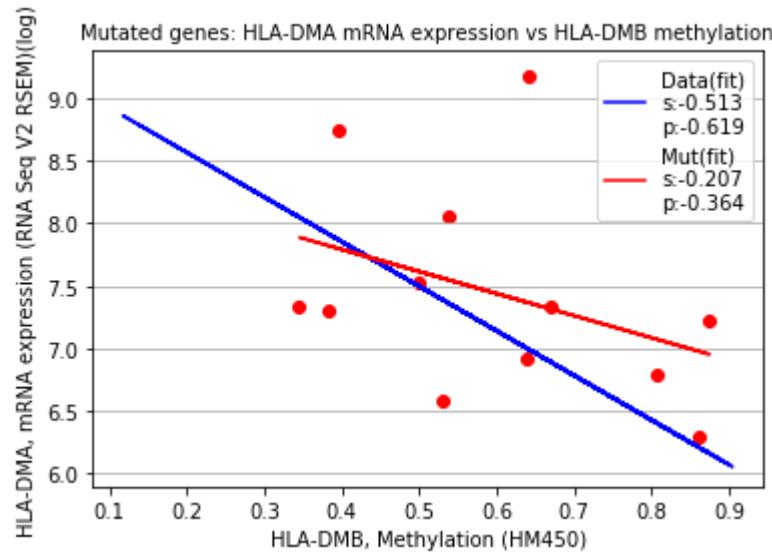
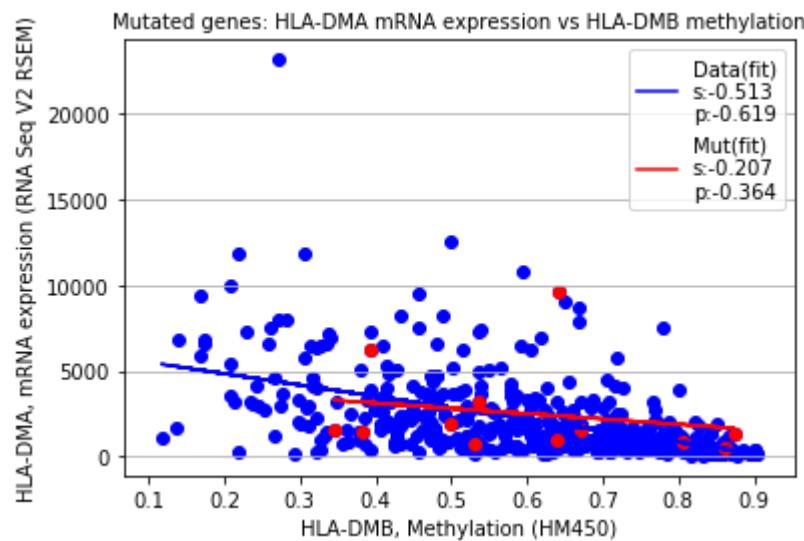
```
In [160]: mutReadPlot('./plots-hlac-psmb9.txt', 'Mutated genes: HLA-C mRNA expression vs PSMB9 methylation')
```



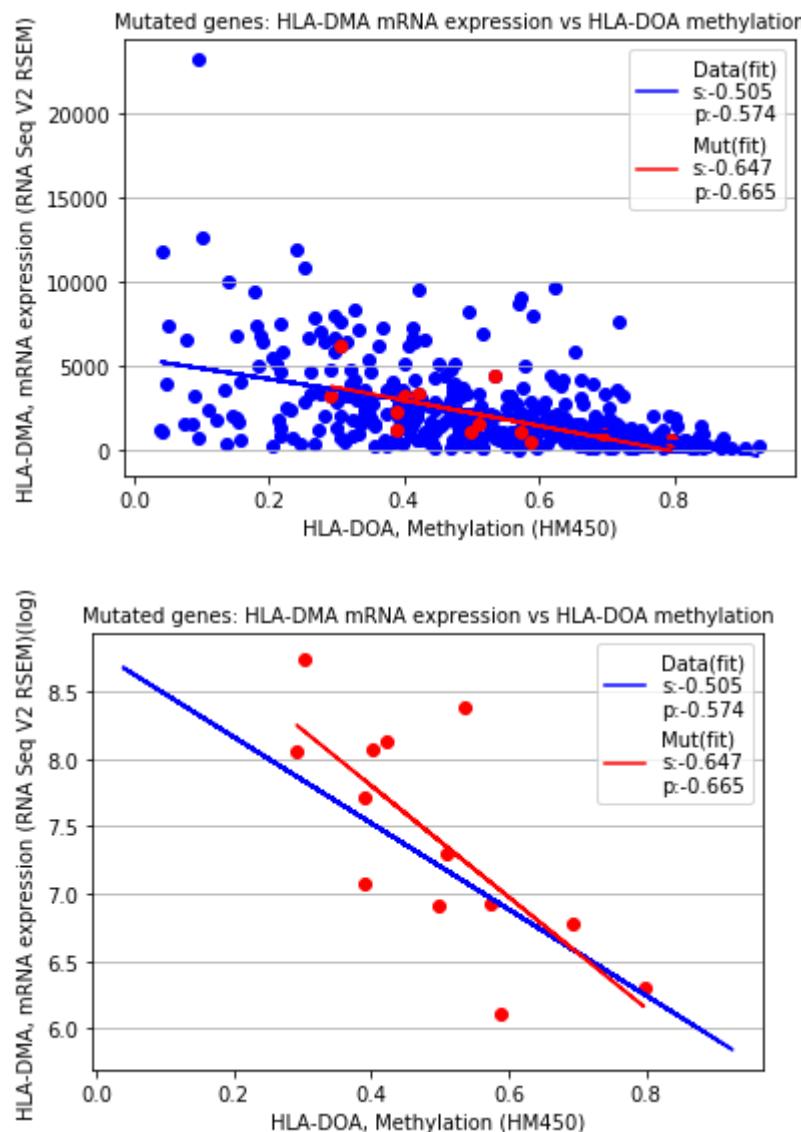
```
In [161]: mutReadPlot('./plots-hladma-hlab.txt', 'Mutated genes: HLA-DMA mRNA expression vs HLA-B methylation')
```



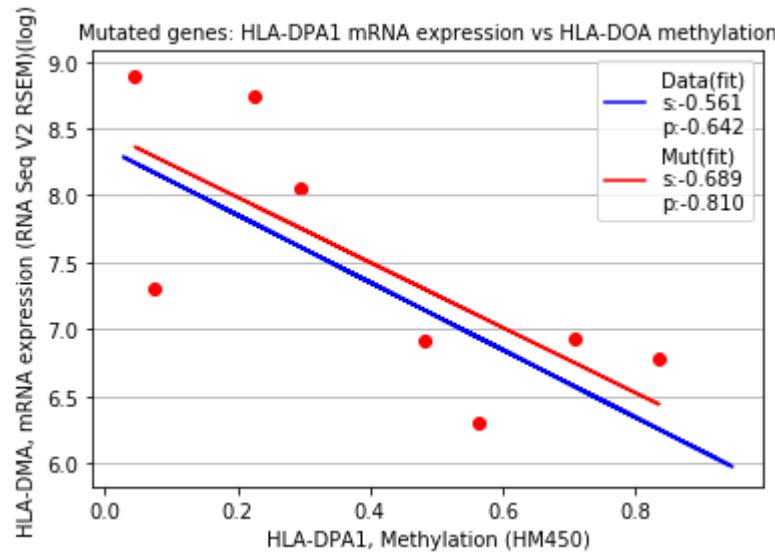
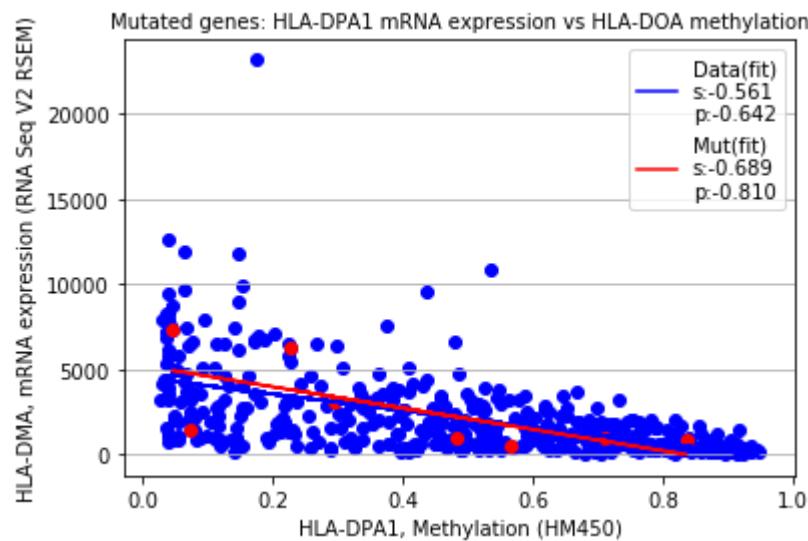
```
In [162]: mutReadPlot('./plots-hladma-hladmb.txt', 'Mutated genes: HLA-DMA mRNA expression vs HLA-DMB methylation')
```



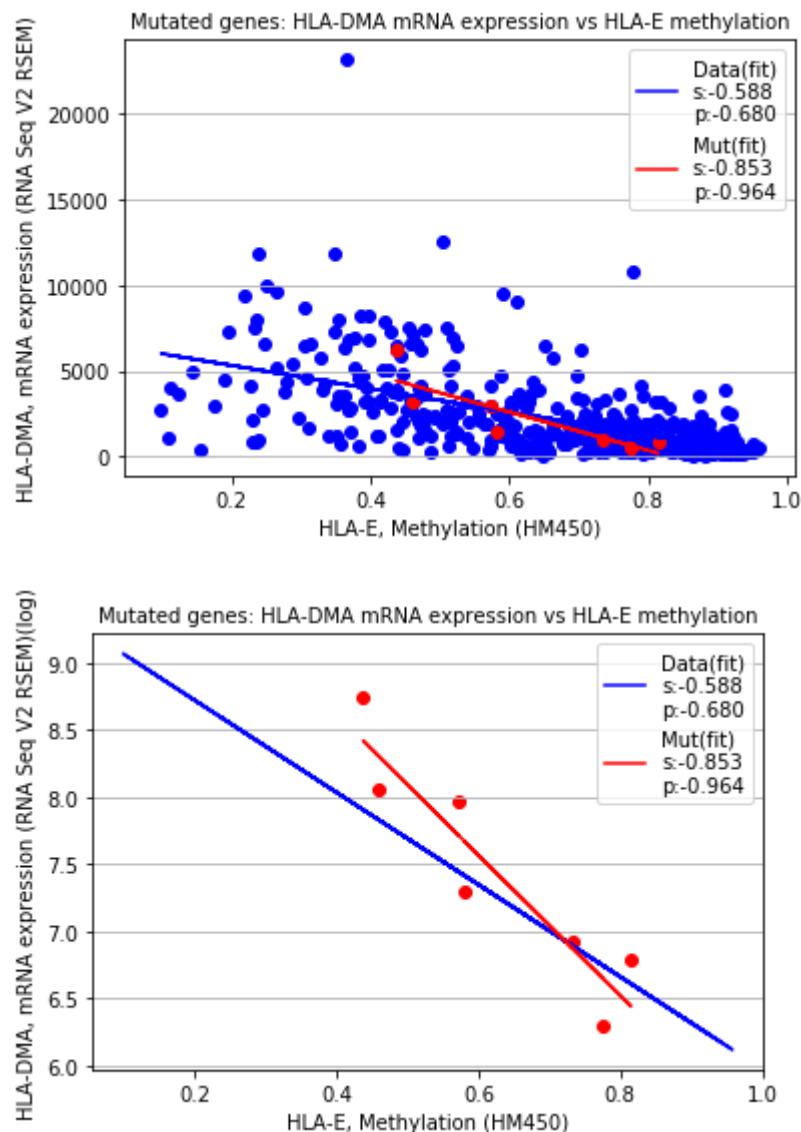
```
In [163]: mutReadPlot('./plots-hladma-hladoa.txt', 'Mutated genes: HLA-DMA mRNA expression vs HLA-DOA methylation')
```



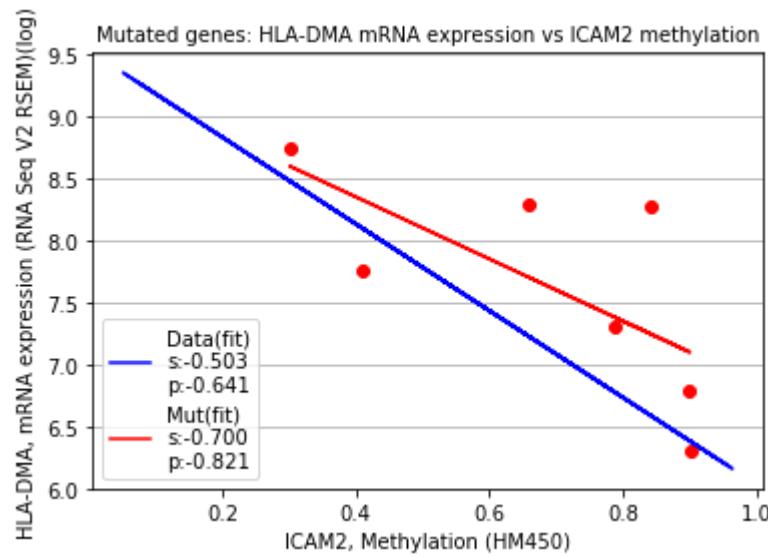
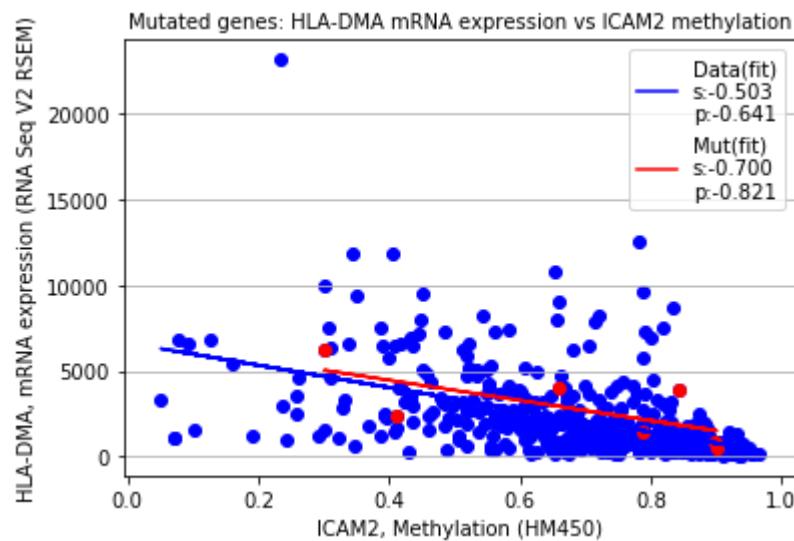
```
In [164]: mutReadPlot('./plots-hladma-hladpa1.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs HLA-DPA1 methylation')
```



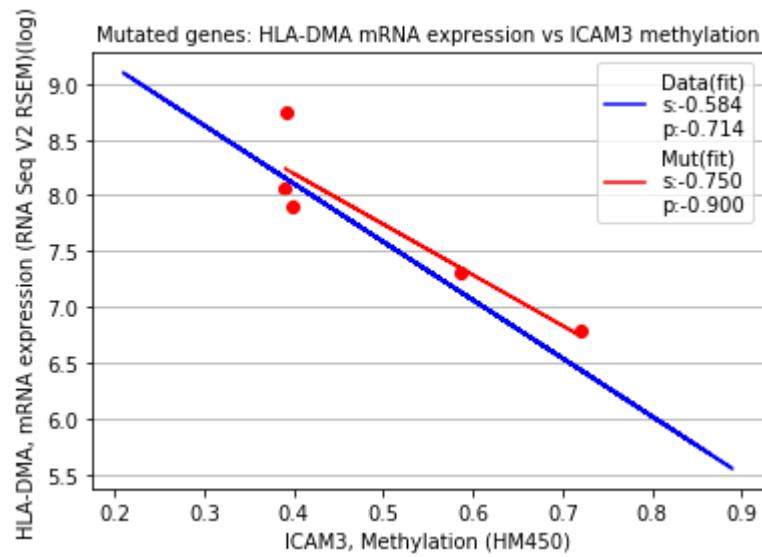
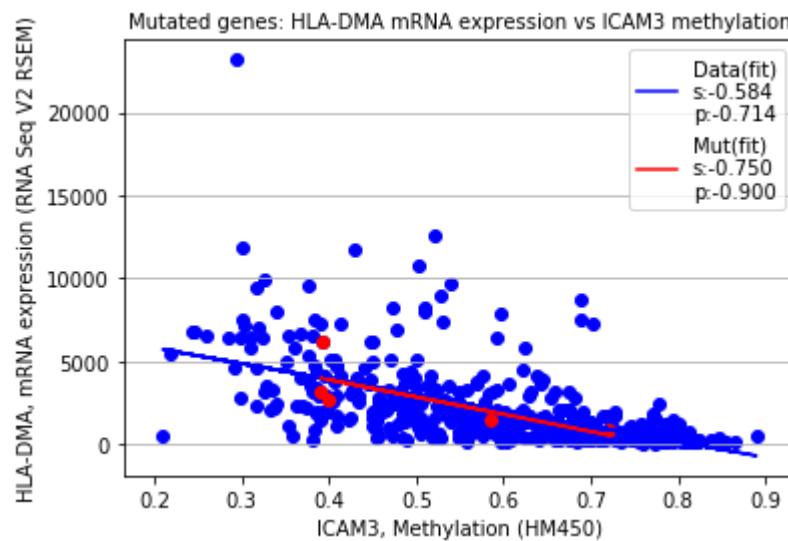
```
In [165]: mutReadPlot('./plots-hladma-hlae.txt', 'Mutated genes: HLA-DMA mRNA expression vs HLA-E methylation')
```



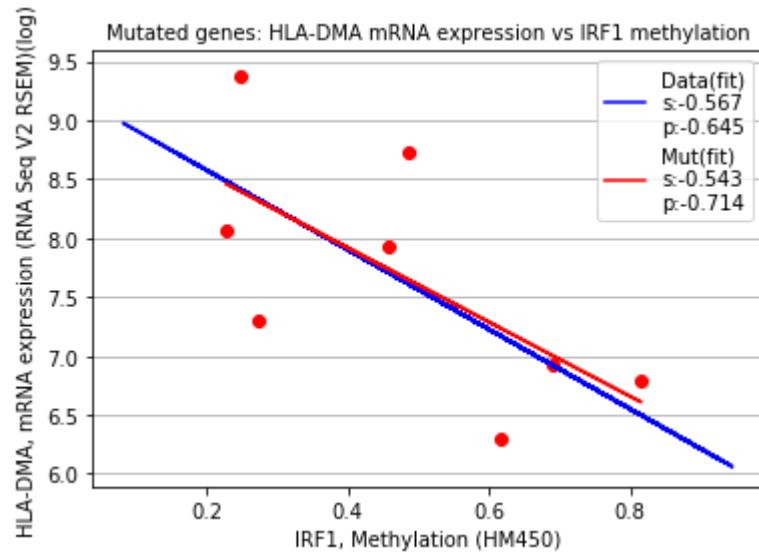
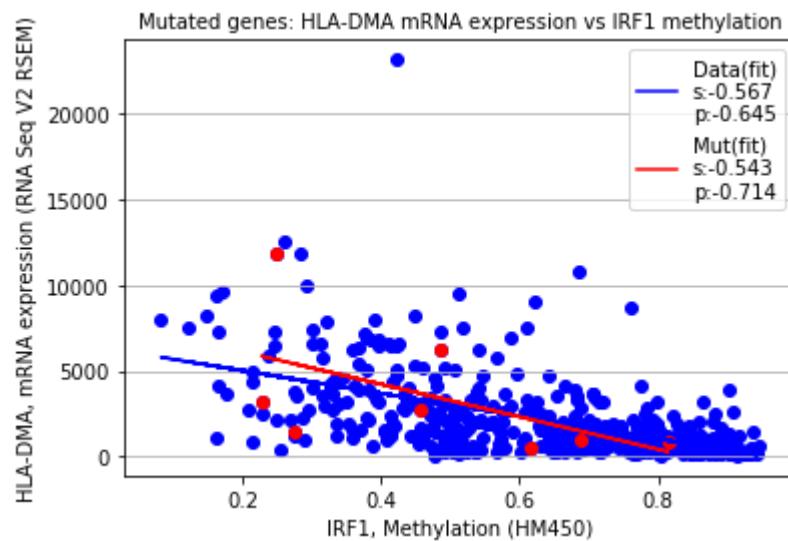
```
In [166]: mutReadPlot('./plots-hladma-icam2.txt', 'Mutated genes: HLA-DMA mRNA expression vs ICAM2 methylation')
```



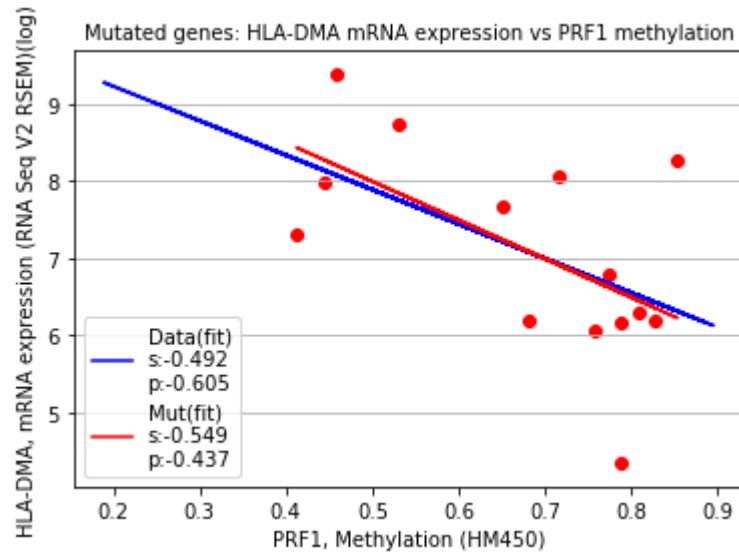
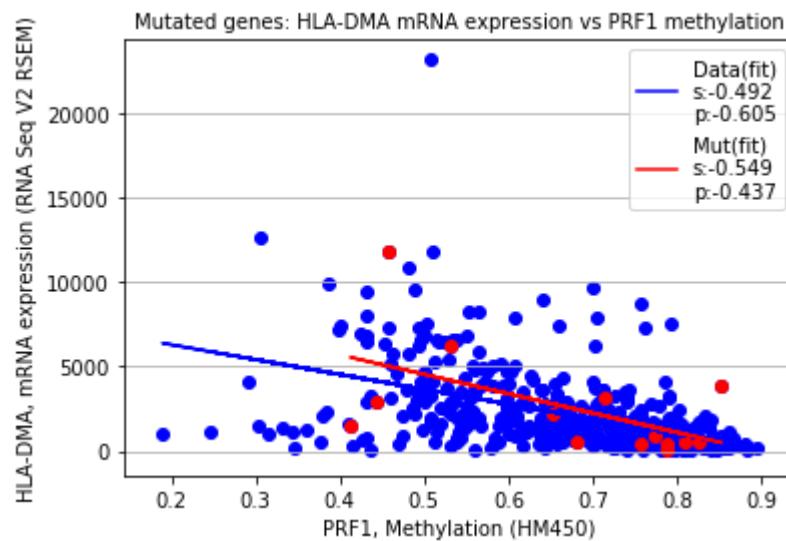
```
In [167]: mutReadPlot('./plots-hladma-icam3.txt', 'Mutated genes: HLA-DMA mRNA expression vs ICAM3 methylation')
```



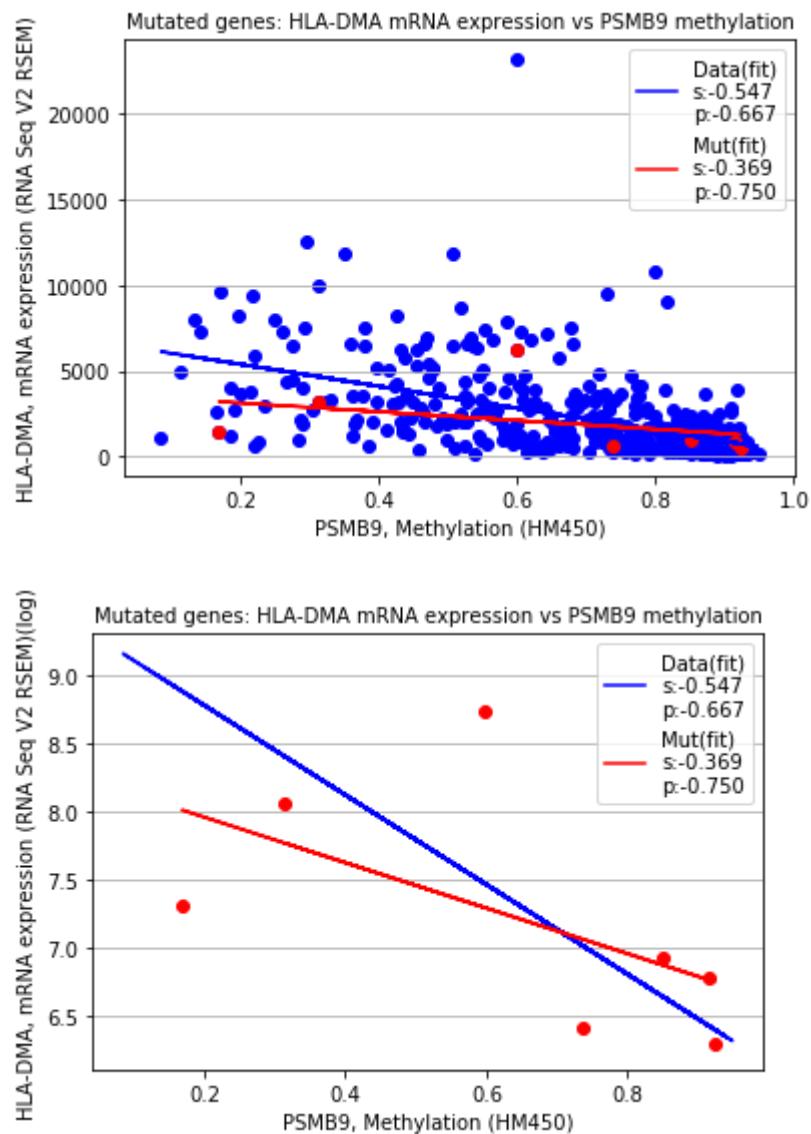
```
In [168]: mutReadPlot('./plots-hladma-irf1.txt', 'Mutated genes: HLA-DMA mRNA expression vs IRF1 methylation')
```



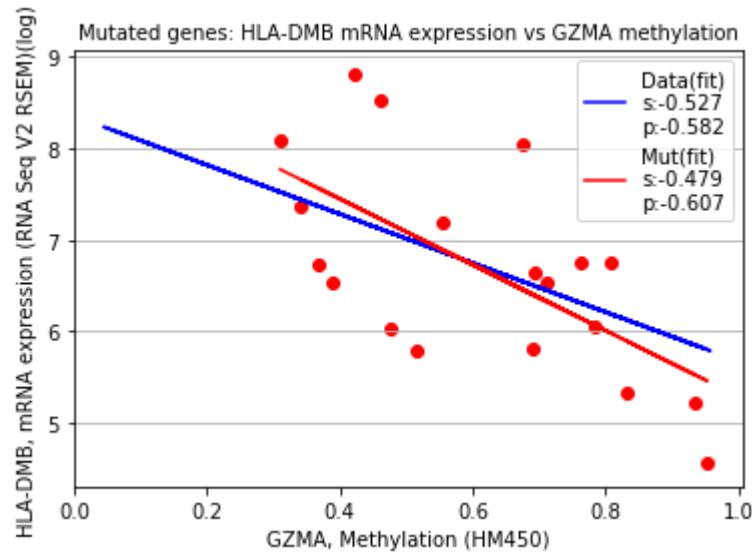
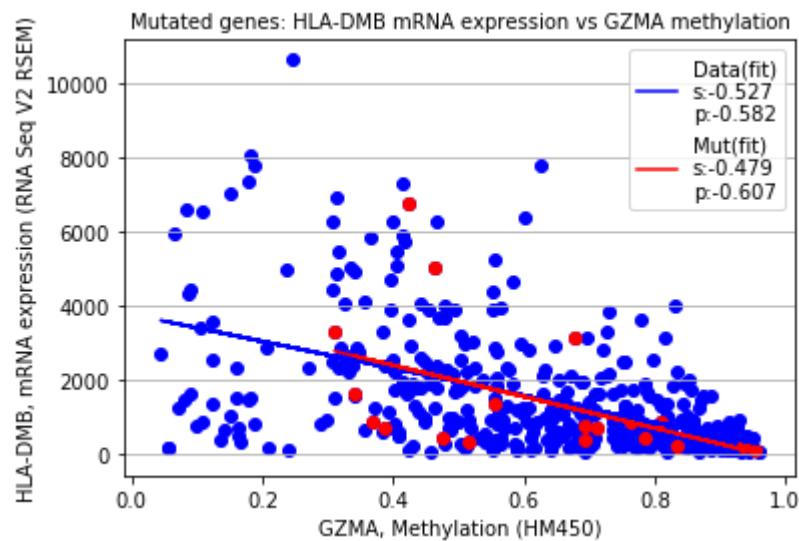
```
In [169]: mutReadPlot('./plots-hladma-prf1.txt', 'Mutated genes: HLA-DMA mRNA expression vs PRF1 methylation')
```



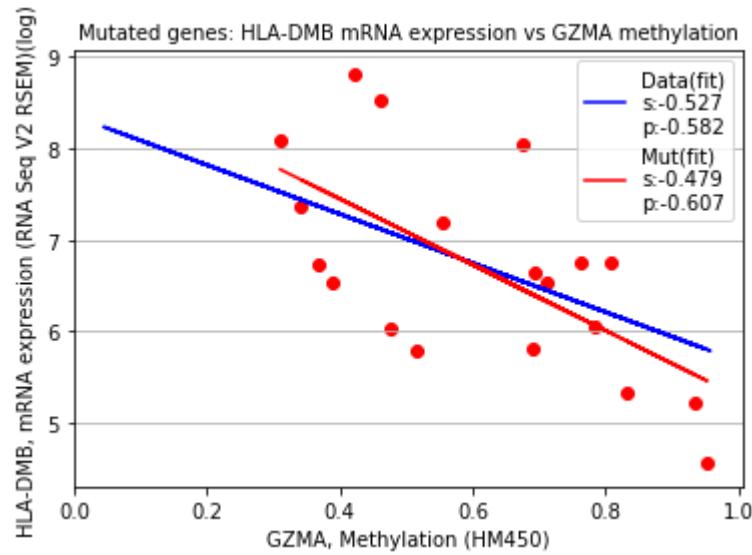
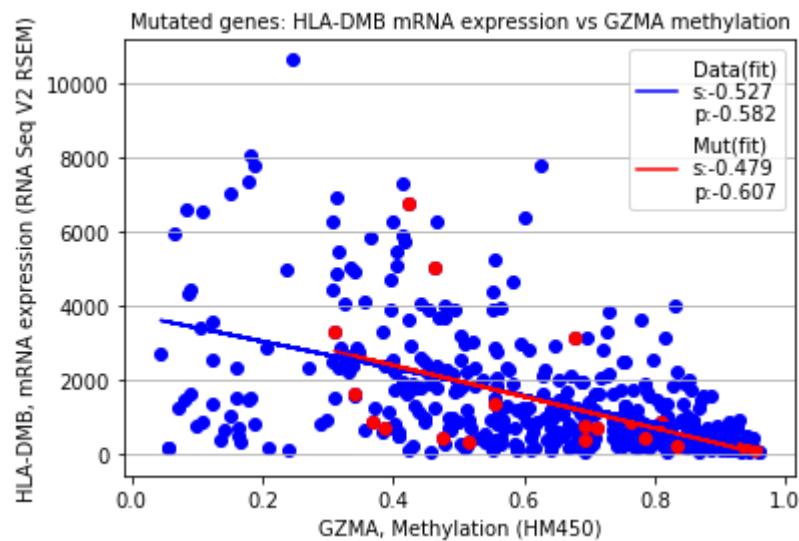
```
In [170]: mutReadPlot('./plots-hladma-psmb9.txt', 'Mutated genes: HLA-DMA mRNA expression vs PSMB9 methylation')
```



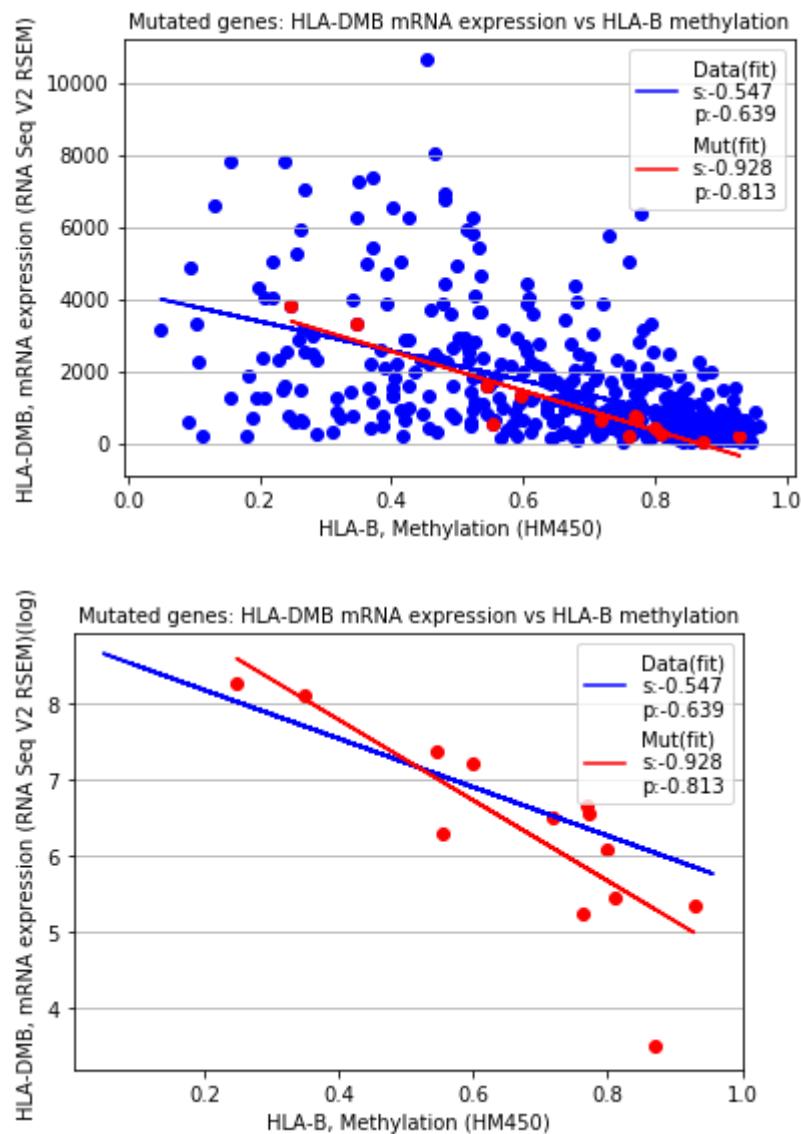
```
In [171]: mutReadPlot('./plots-hladmb-gzma.txt', 'Mutated genes: HLA-DMB mRNA expression vs GZMA methylation')
```



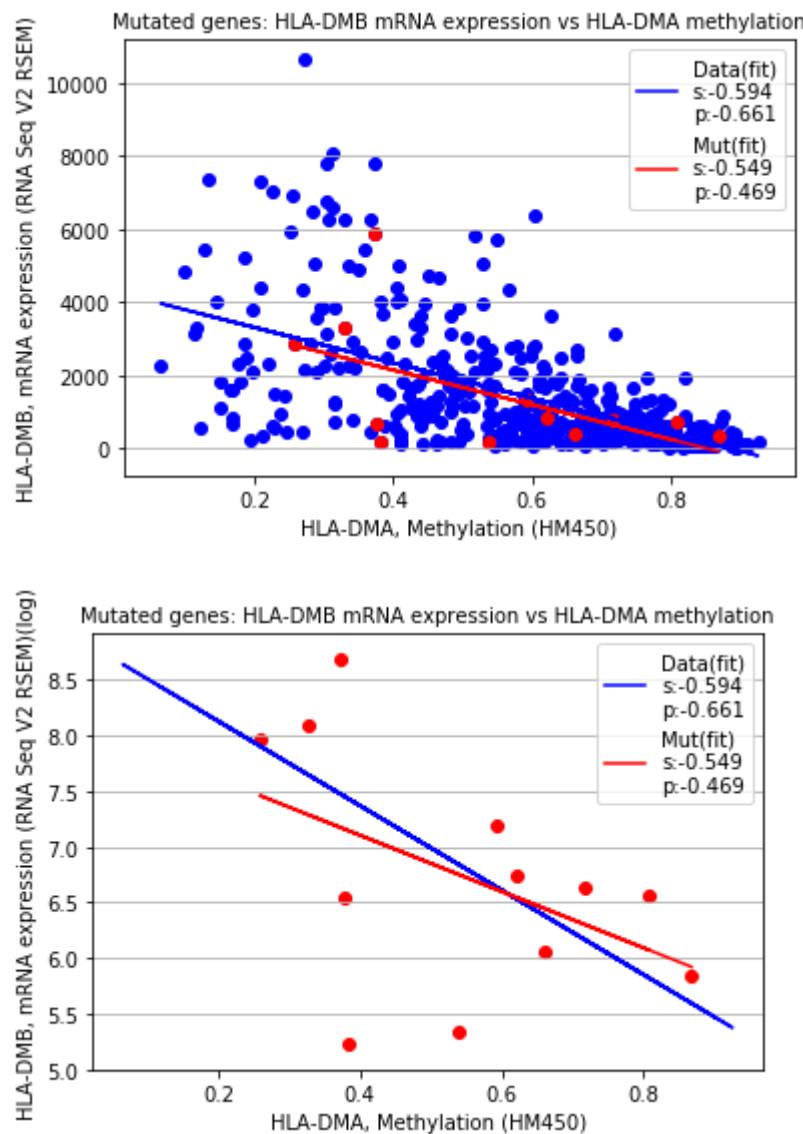
```
In [172]: mutReadPlot('./plots-hladmb-gzma.txt', 'Mutated genes: HLA-DMB mRNA expression vs GZMA methylation')
```



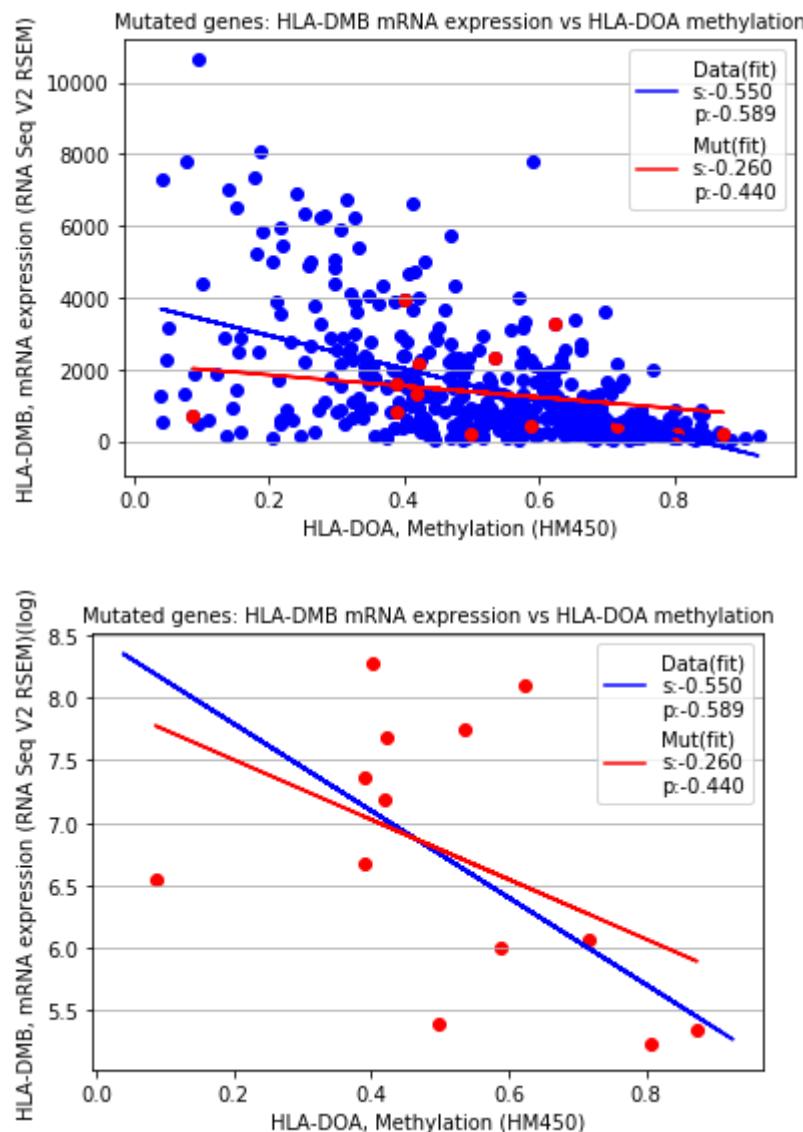
```
In [173]: mutReadPlot('./plots-hladmb-hlab.txt', 'Mutated genes: HLA-DMB mRNA expression vs HLA-B methylation')
```



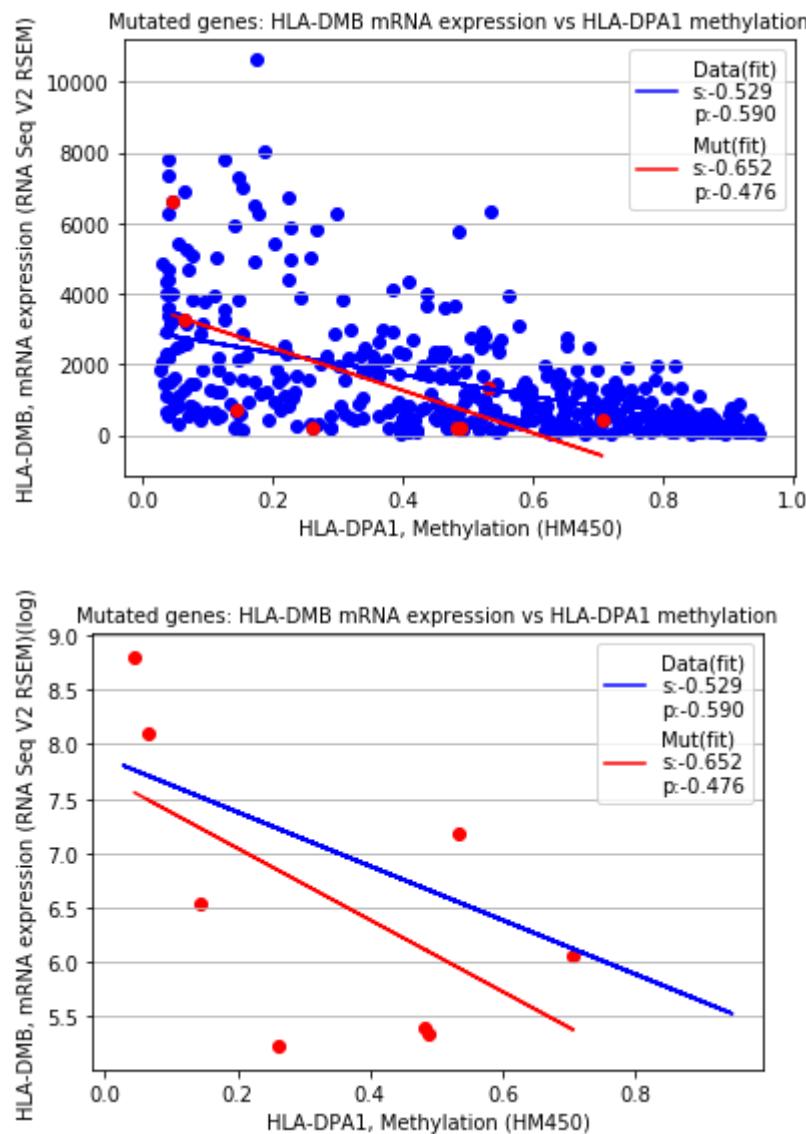
```
In [174]: mutReadPlot('./plots-hladmb-hladma.txt', 'Mutated genes: HLA-DMB mRNA expression vs HLA-DMA methylation')
```



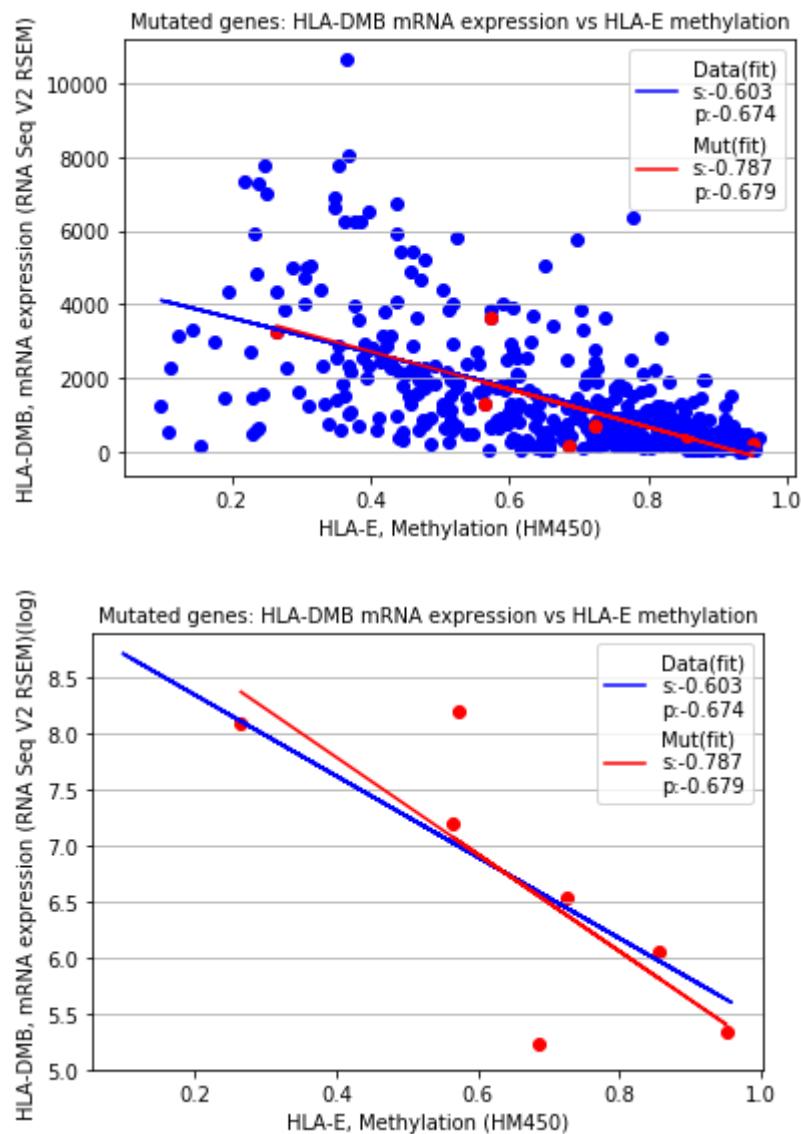
```
In [175]: mutReadPlot('./plots-hladmb-hladoa.txt', 'Mutated genes: HLA-DMB mRNA expression vs HLA-DOA methylation')
```



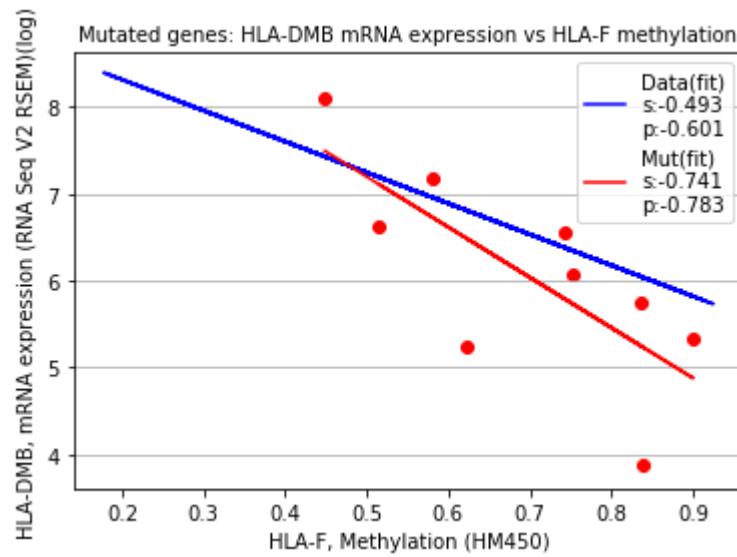
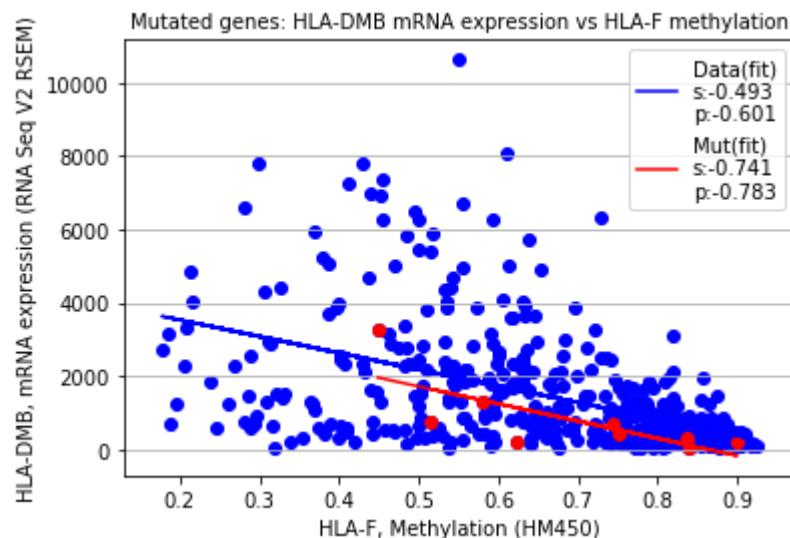
```
In [176]: mutReadPlot('./plots-hladmb-hladpa1.txt', 'Mutated genes: HLA-DMB mRNA expression vs HLA-DPA1 methylation')
```



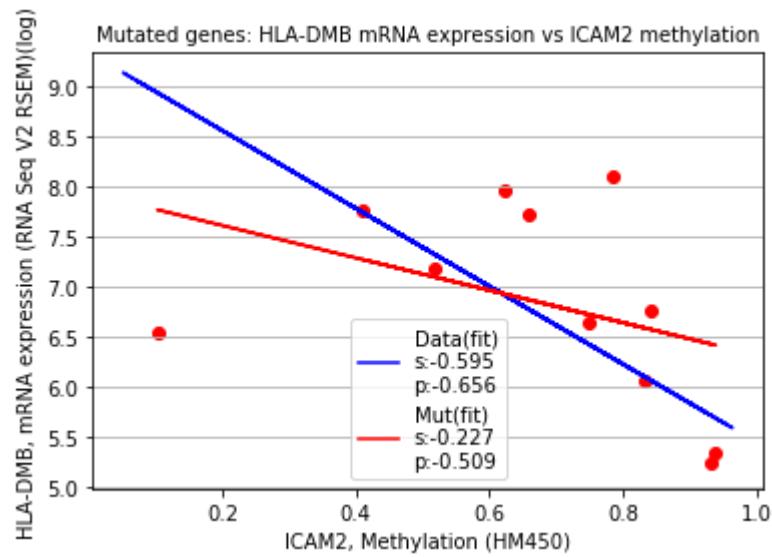
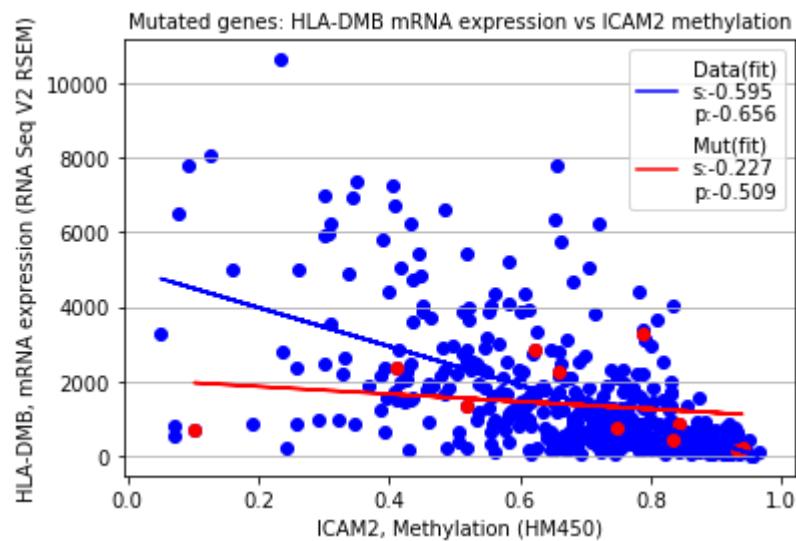
```
In [177]: mutReadPlot('./plots-hladmb-hlae.txt', 'Mutated genes: HLA-DMB mRNA expression vs HLA-E methylation')
```



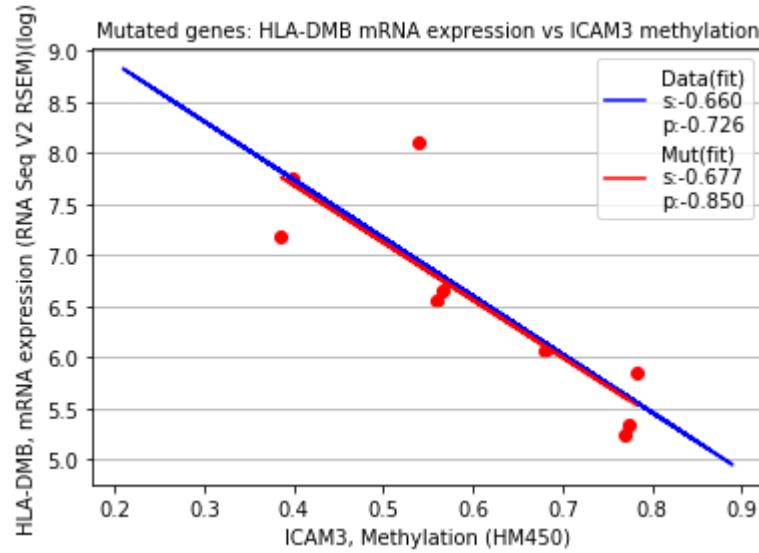
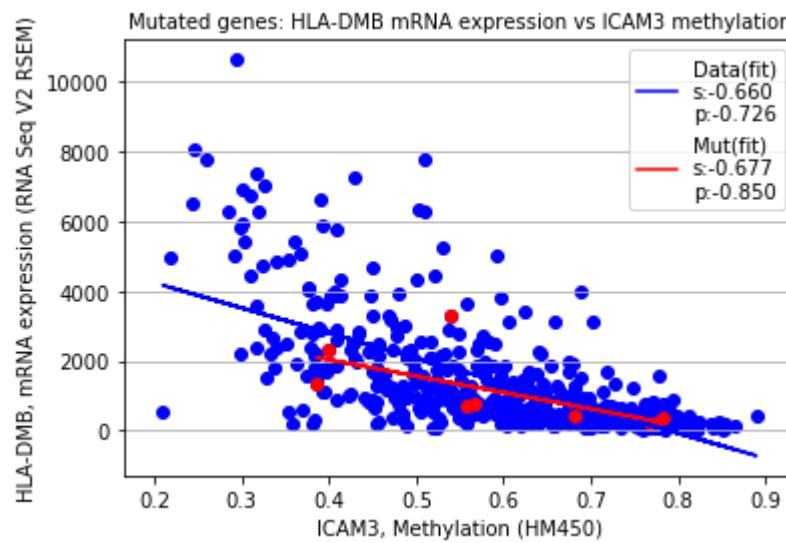
```
In [178]: mutReadPlot('./plots-hladmb-hlaf.txt', 'Mutated genes: HLA-DMB mRNA expression vs HLA-F methylation')
```



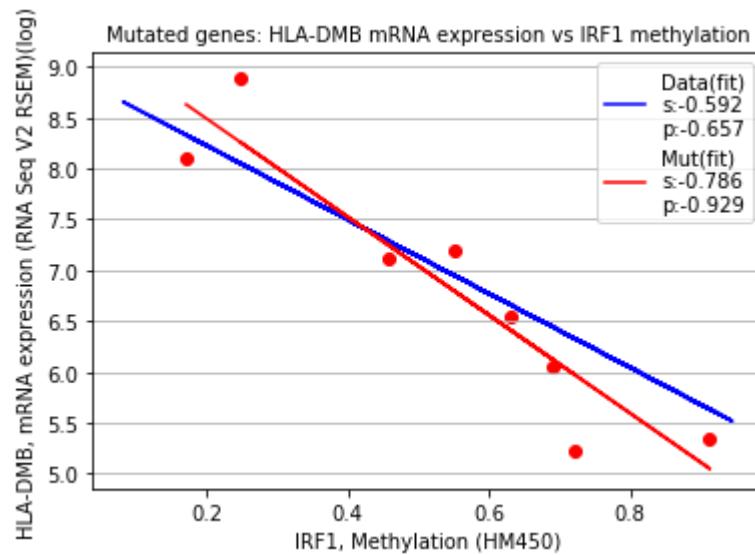
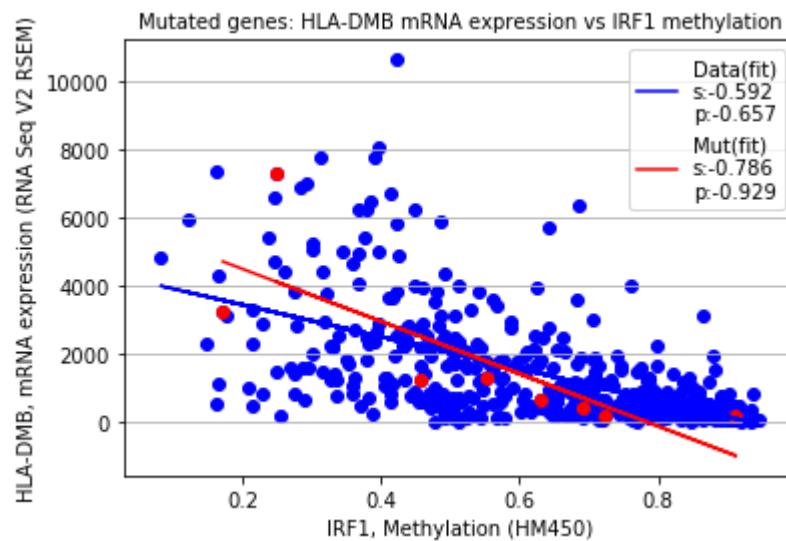
```
In [179]: mutReadPlot('./plots-hladmb-icam2.txt', 'Mutated genes: HLA-DMB mRNA expression vs ICAM2 methylation')
```



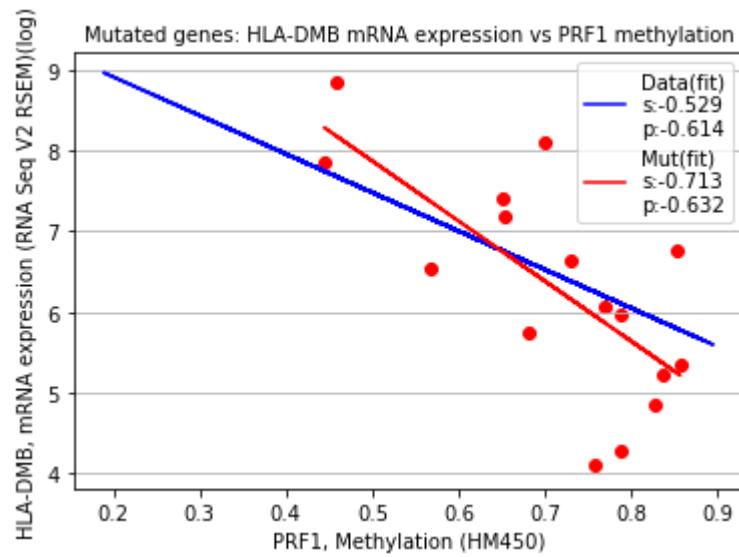
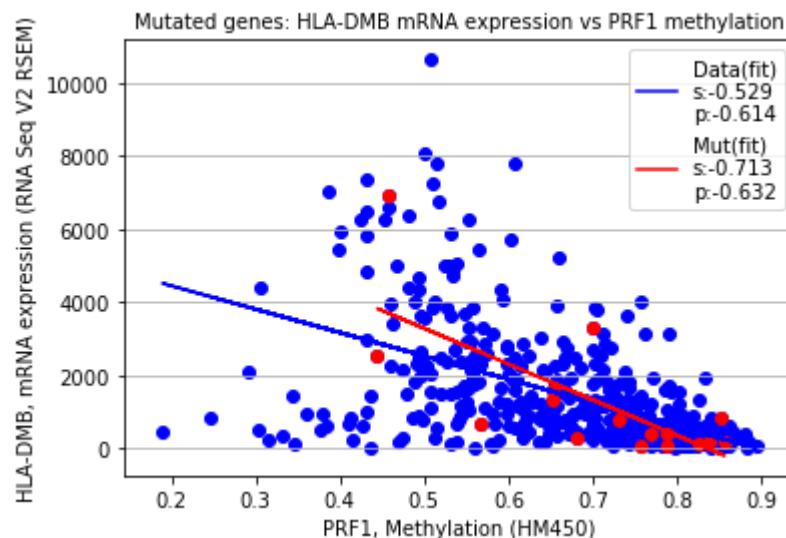
```
In [180]: mutReadPlot('./plots-hladmb-icam3.txt', 'Mutated genes: HLA-DMB mRNA expression vs ICAM3 methylation')
```



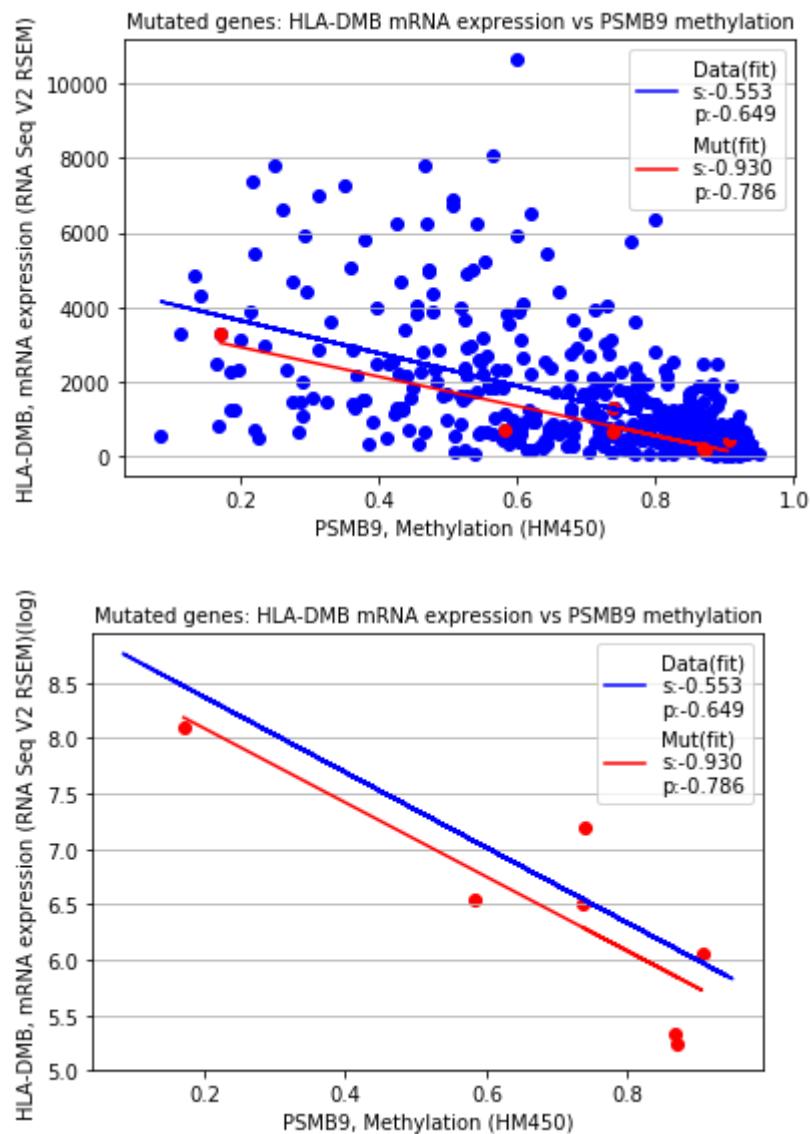
```
In [181]: mutReadPlot('./plots-hladmb-irf1.txt', 'Mutated genes: HLA-DMB mRNA expression vs IRF1 methylation')
```



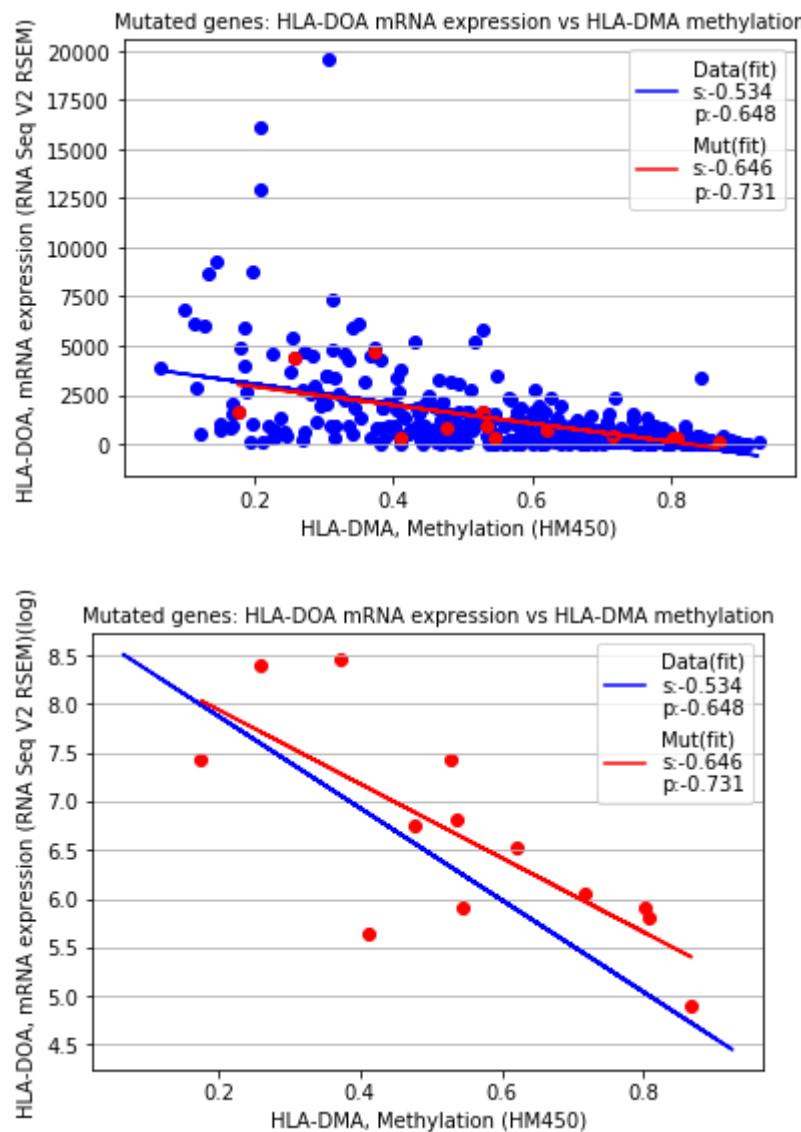
```
In [182]: mutReadPlot('./plots-hladmb-prf1.txt', 'Mutated genes: HLA-DMB mRNA expression vs PRF1 methylation')
```



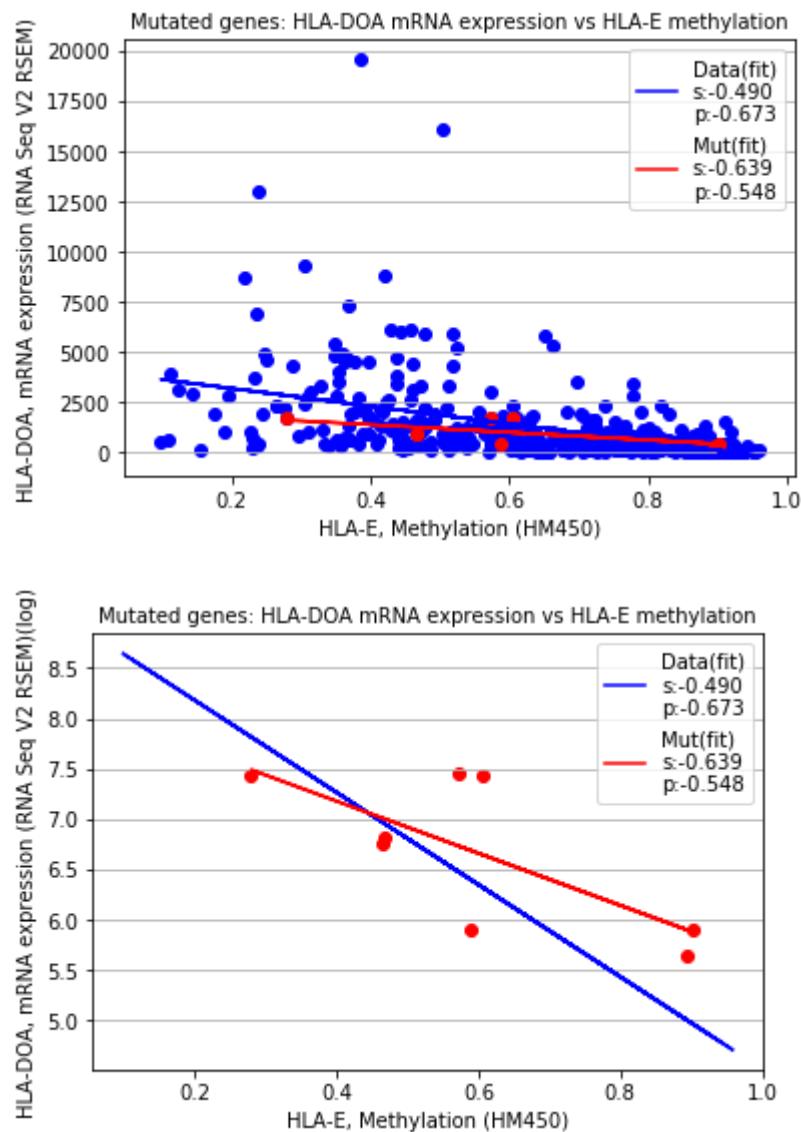
```
In [183]: mutReadPlot('./plots-hladmb-psmb9.txt', 'Mutated genes: HLA-DMB mRNA expression vs PSMB9 methylation')
```



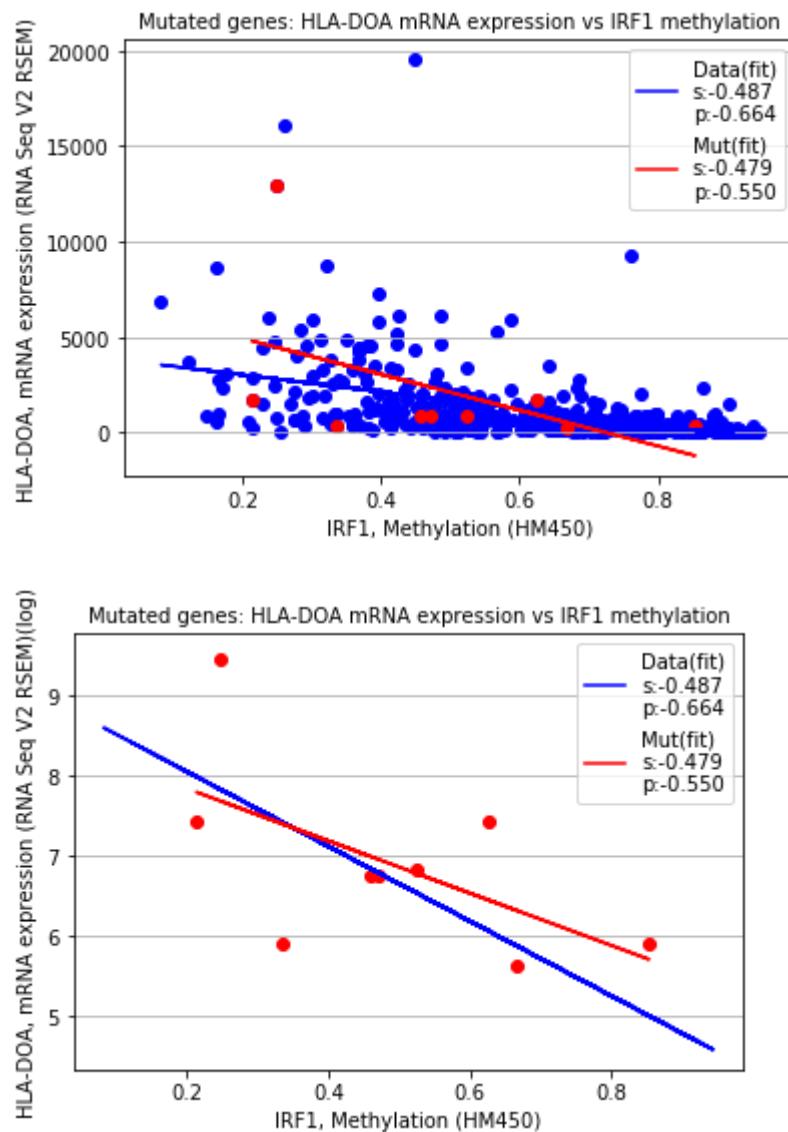
```
In [184]: mutReadPlot('./plots-hladoa-hladma.txt', 'Mutated genes: HLA-DOA mRNA expression vs HLA-DMA methylation')
```



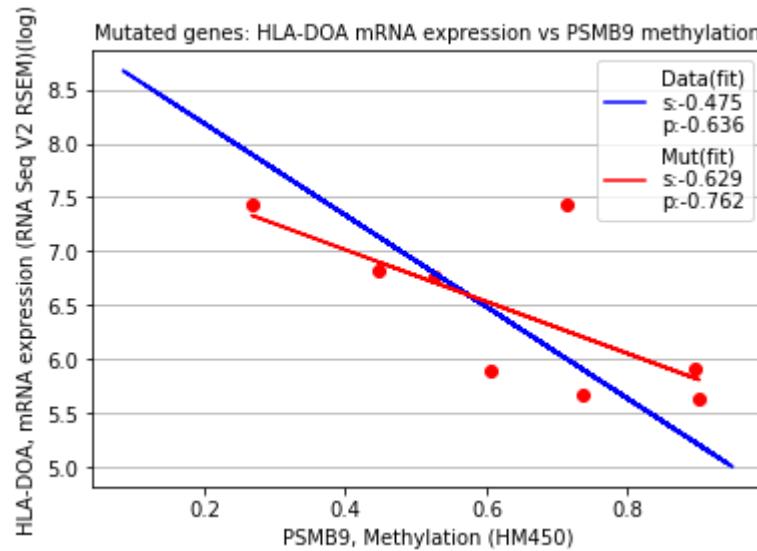
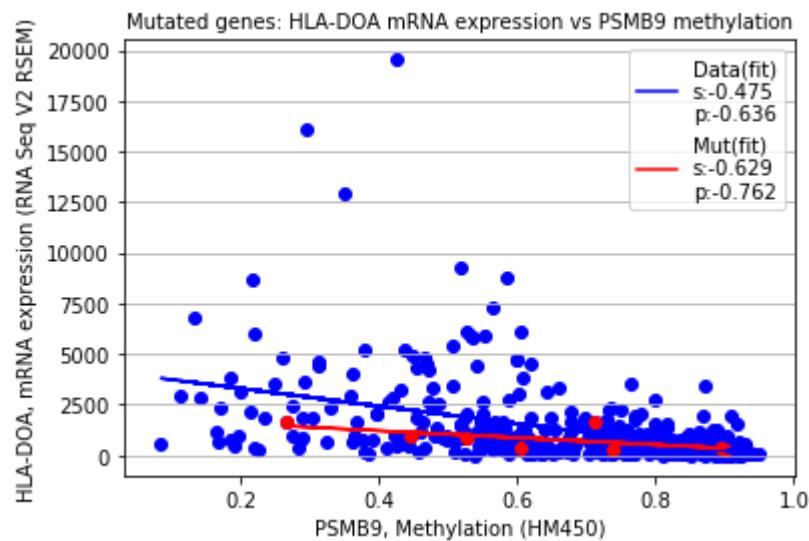
```
In [185]: mutReadPlot('./plots-hladoa-hlae.txt', 'Mutated genes: HLA-DOA mRNA expression vs HLA-E methylation')
```



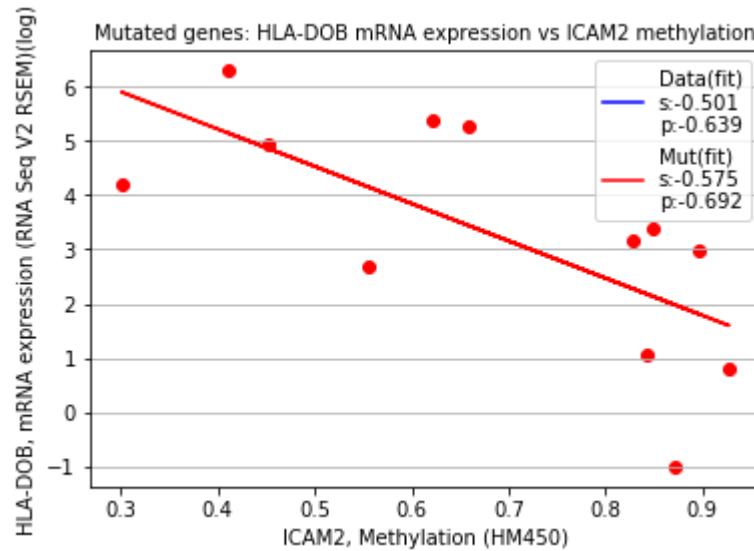
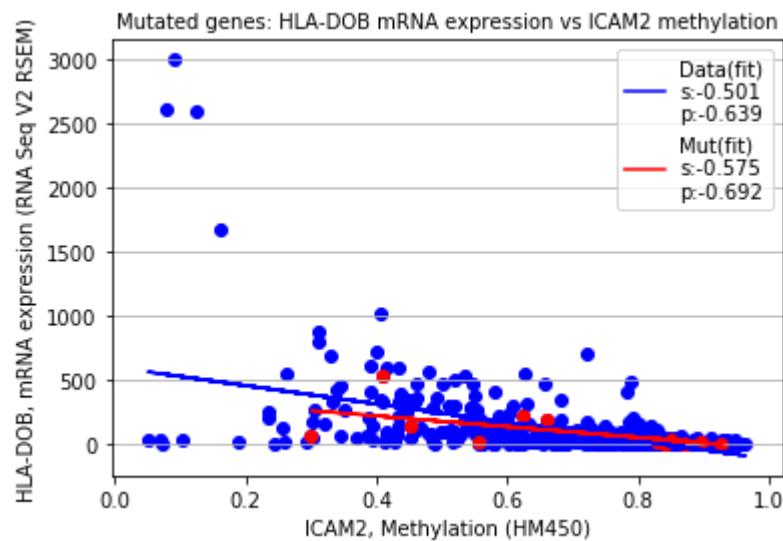
```
In [186]: mutReadPlot('./plots-hladoa-irf1.txt', 'Mutated genes: HLA-DOA mRNA expression vs IRF1 methylation')
```



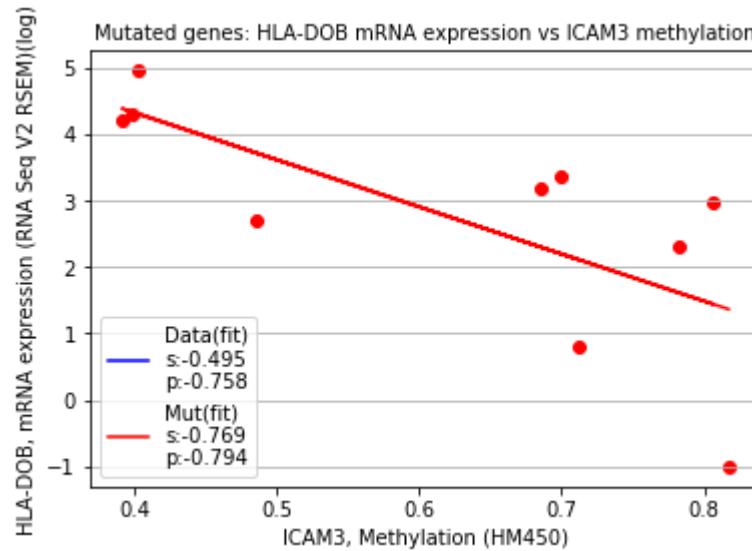
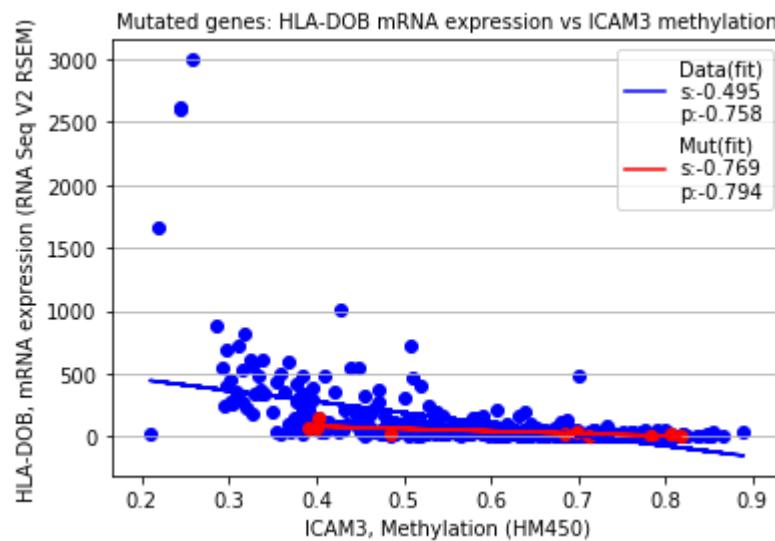
```
In [187]: mutReadPlot('./plots-hladoa-psmb9.txt', 'Mutated genes: HLA-DOA mRNA expression vs PSMB9 methylation')
```



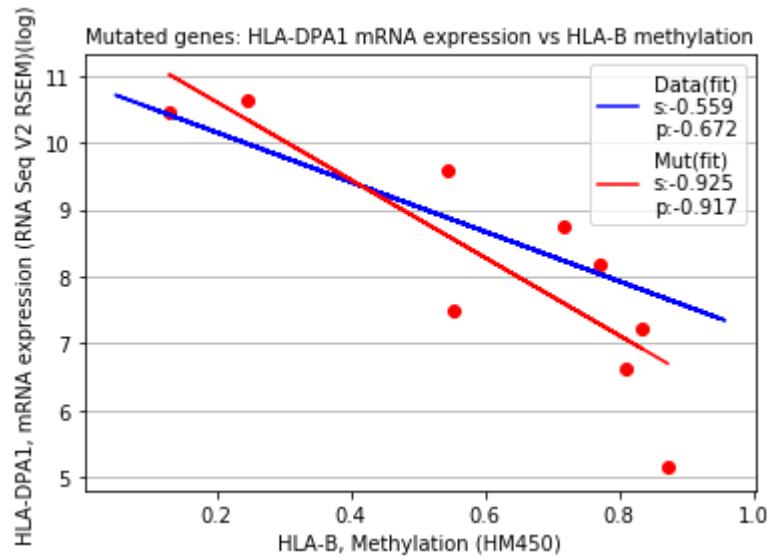
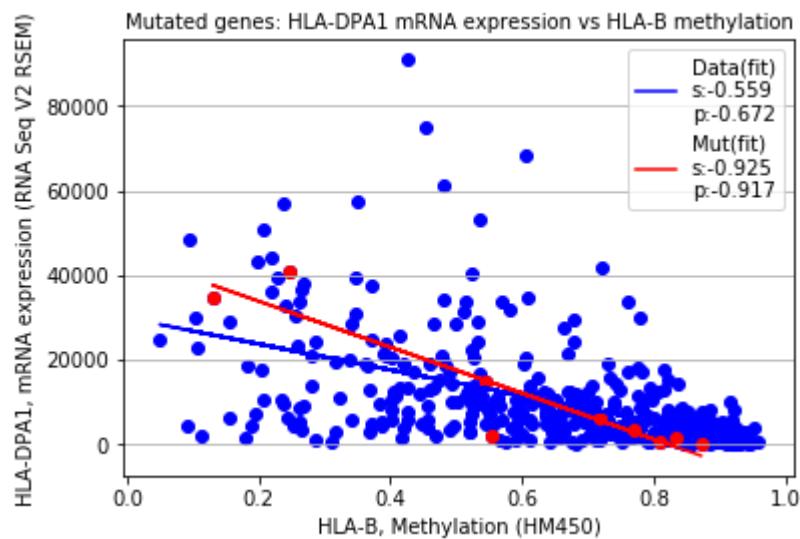
```
In [188]: mutReadPlot('./plots-hladob-icam2.txt', 'Mutated genes: HLA-DOB mRNA expression vs ICAM2 methylation')
```



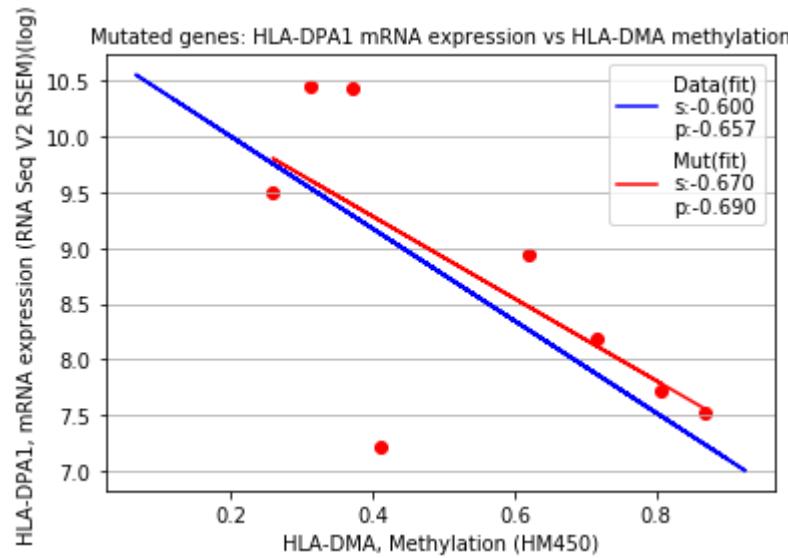
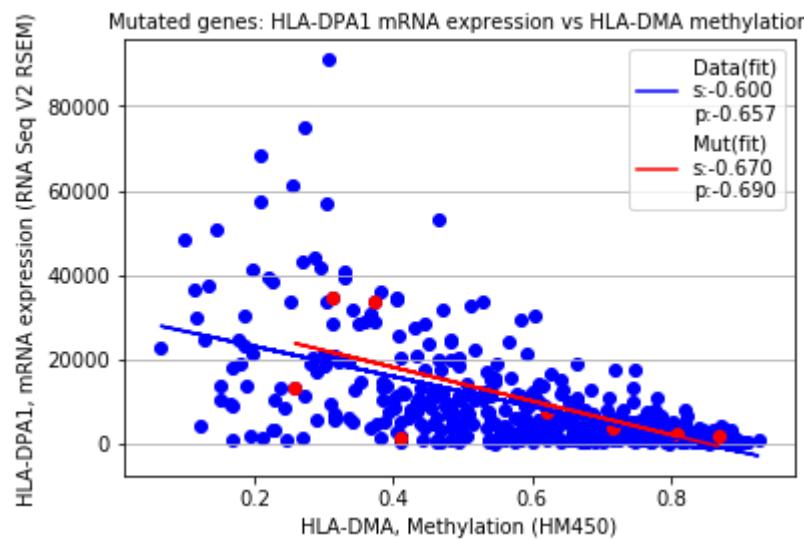
```
In [189]: mutReadPlot('./plots-hladob-icam3.txt', 'Mutated genes: HLA-DOB mRNA expression vs ICAM3 methylation')
```



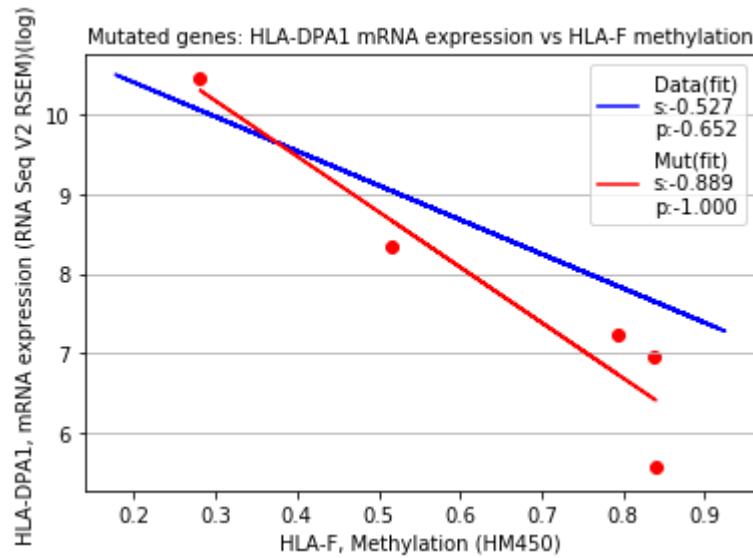
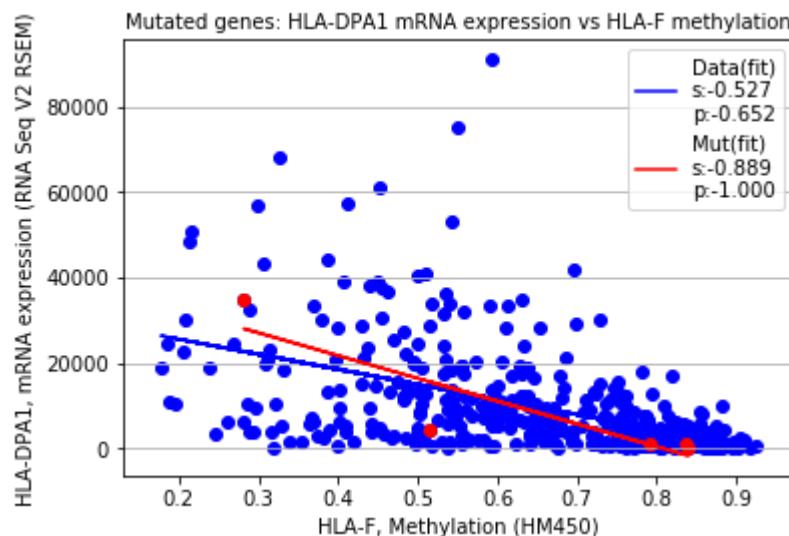
```
In [193]: mutReadPlot('./plots-hladpa1-hlab.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs HLA-B methylation')
```



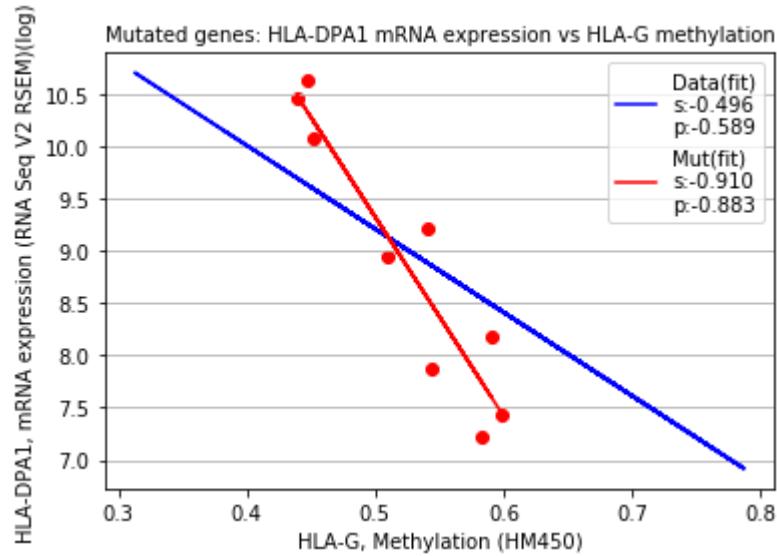
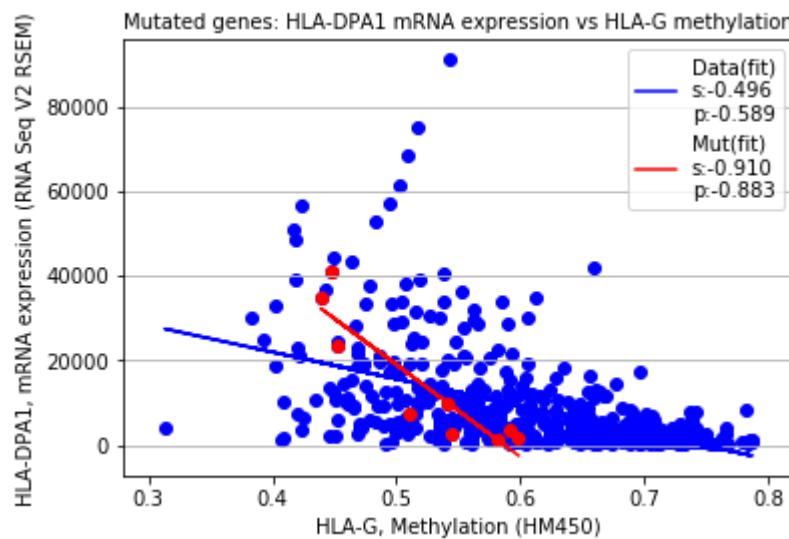
```
In [194]: mutReadPlot('./plots-hladpa1-hladma.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs HLA-DMA methylation')
```



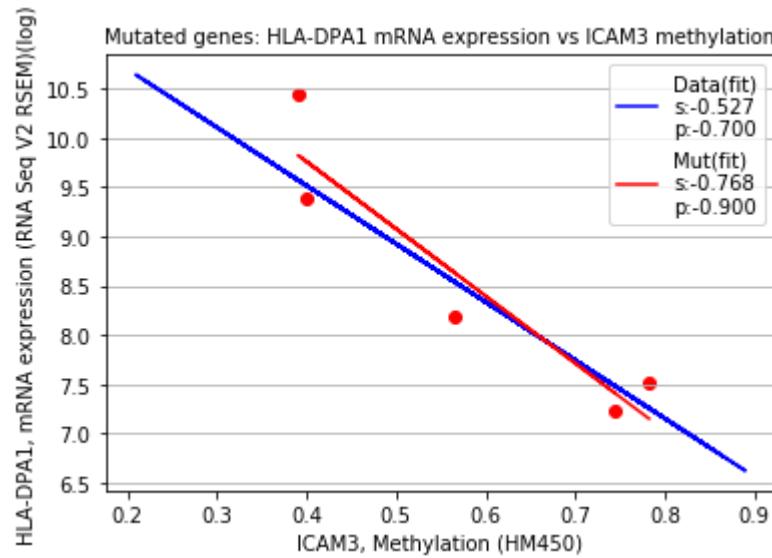
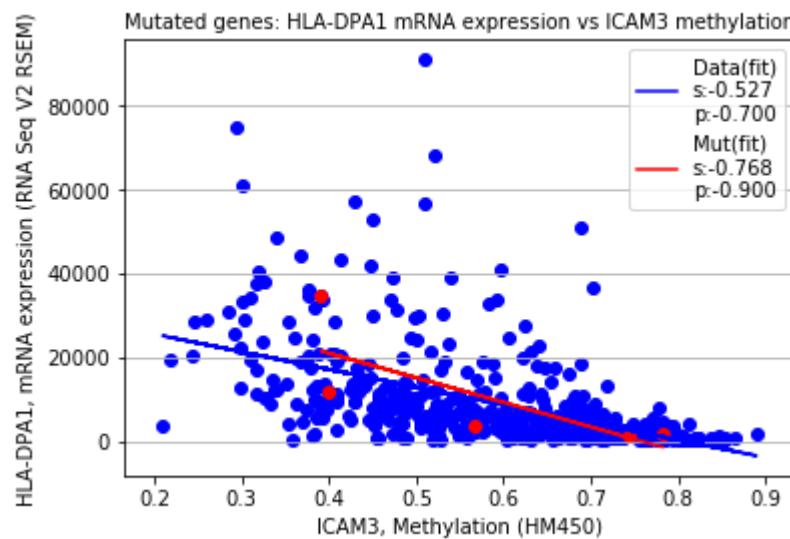
```
In [195]: mutReadPlot('./plots-hladpa1-hlaf.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs HLA-F methylation')
```



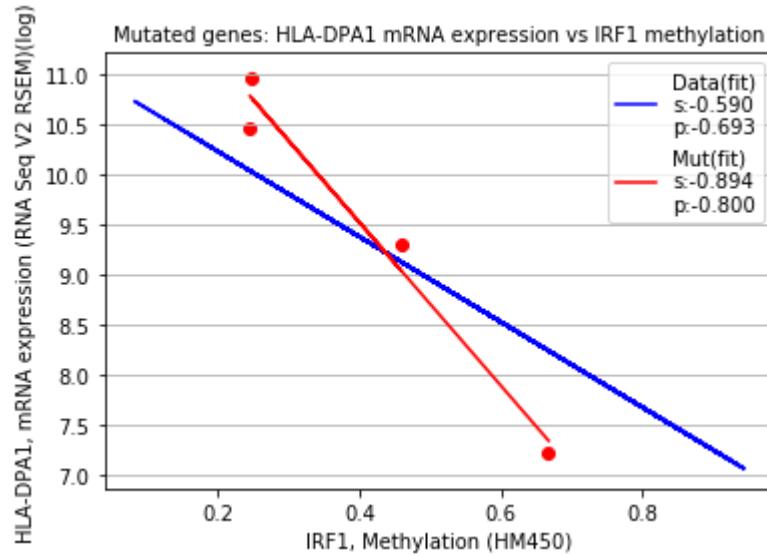
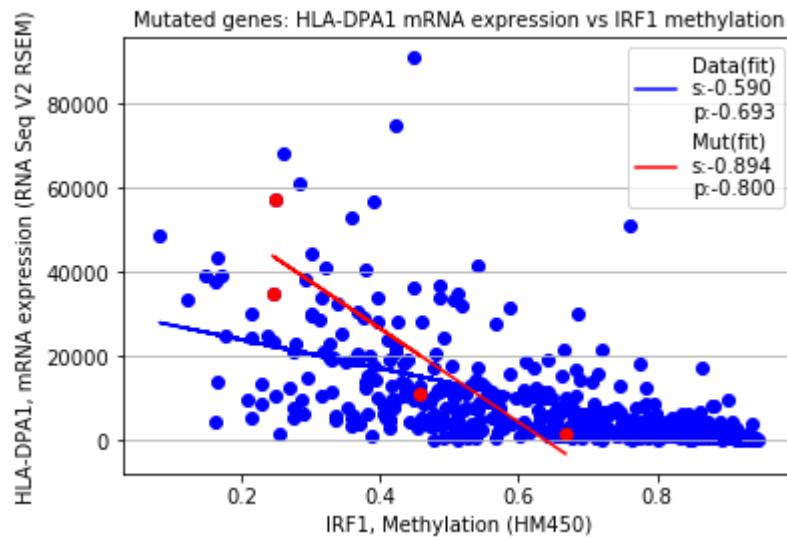
```
In [196]: mutReadPlot('./plots-hladpa1-hlag.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs HLA-G methylation')
```



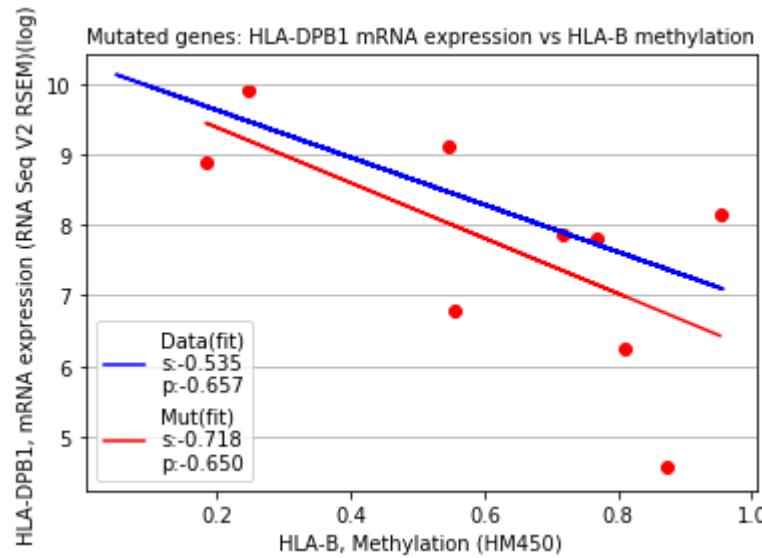
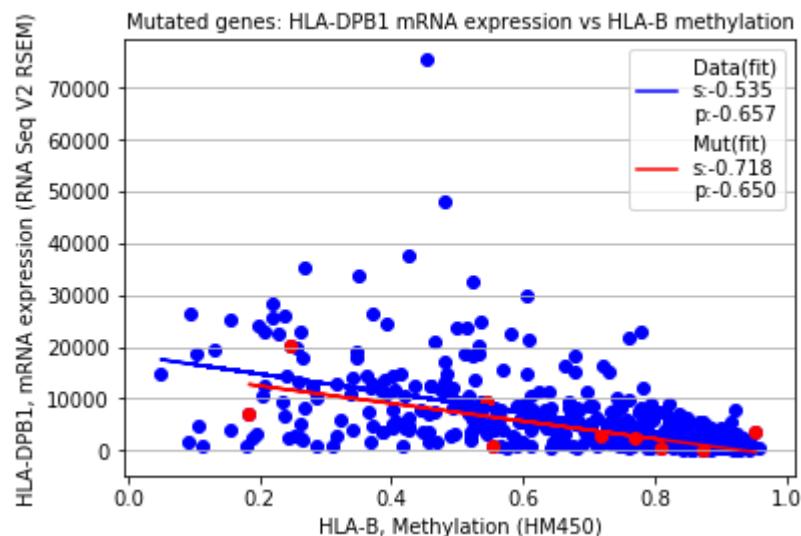
```
In [197]: mutReadPlot('./plots-hladpa1-icam3.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs ICAM3 methylation')
```



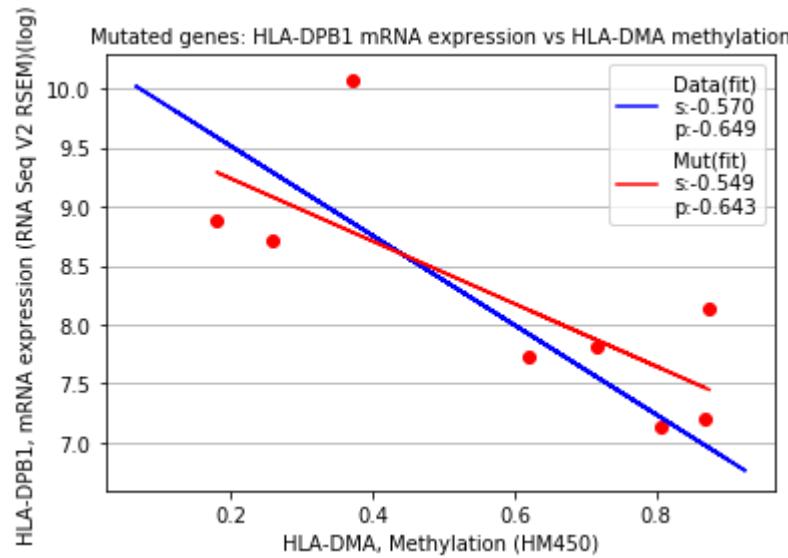
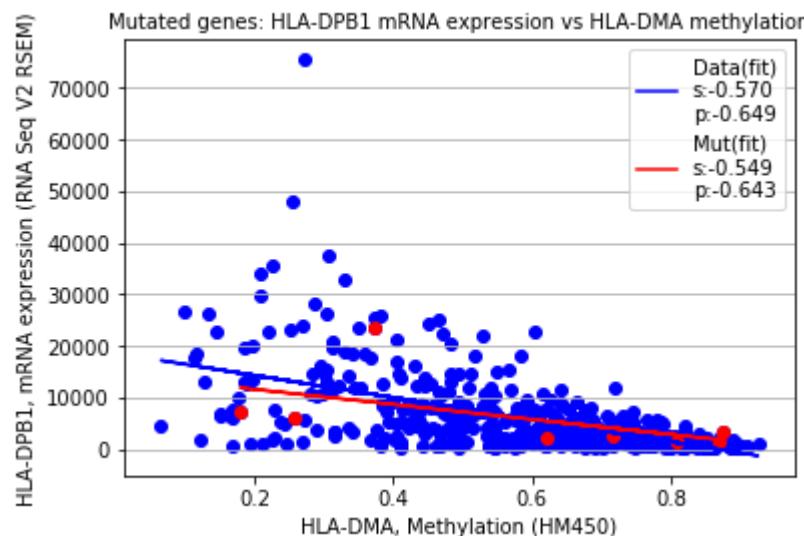
```
In [198]: mutReadPlot('./plots-hladpa1-irf1.txt', 'Mutated genes: HLA-DPA1 mRNA expression vs IRF1 methylation')
```



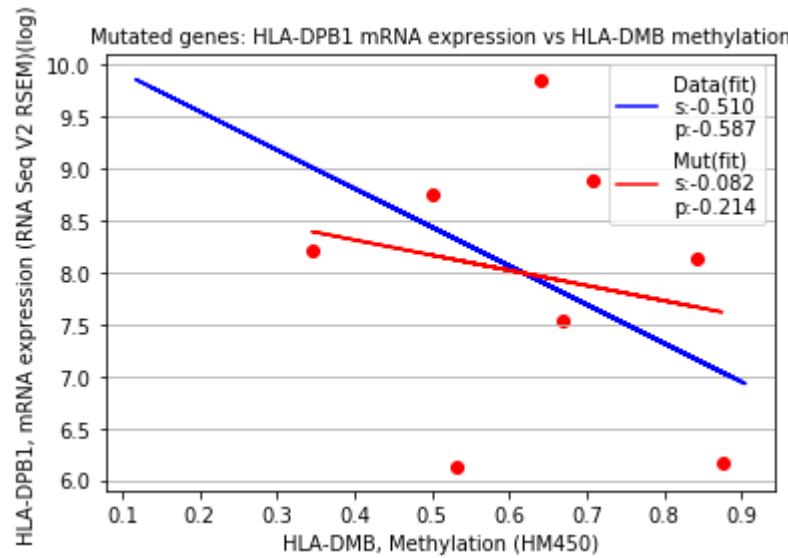
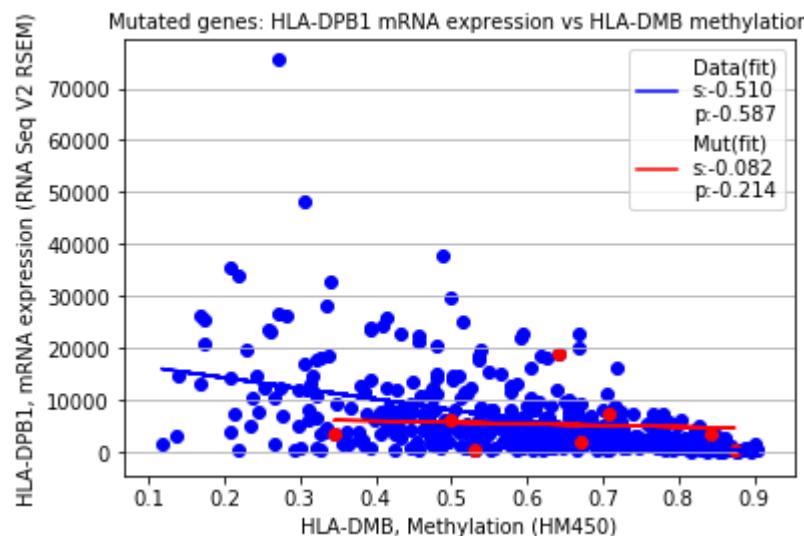
```
In [199]: mutReadPlot('./plots-hladpb1-hlab.txt', 'Mutated genes: HLA-DPB1 mRNA expression vs HLA-B methylation')
```



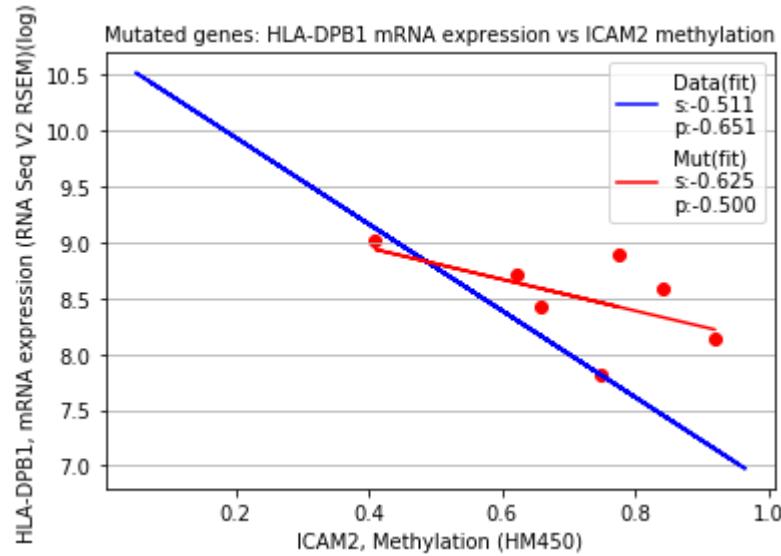
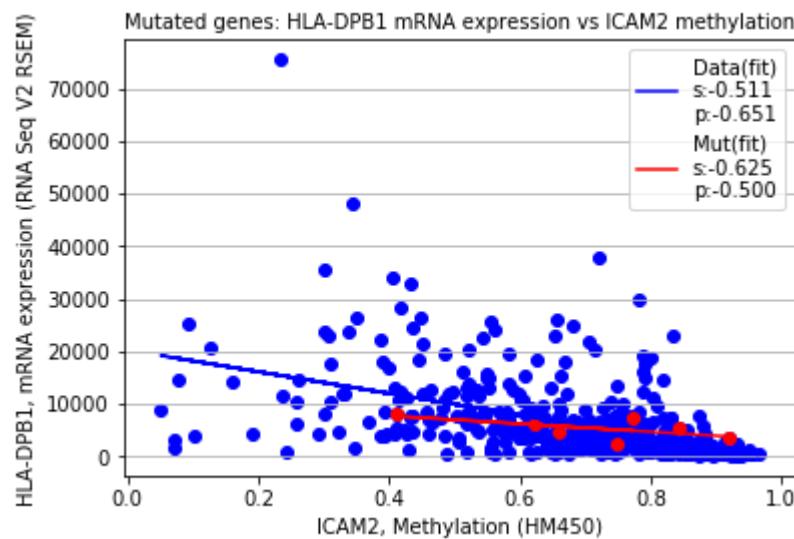
```
In [200]: mutReadPlot('./plots-hladpb1-hladma.txt', 'Mutated genes: HLA-DPB1 mRNA expression vs HLA-DMA methylation')
```



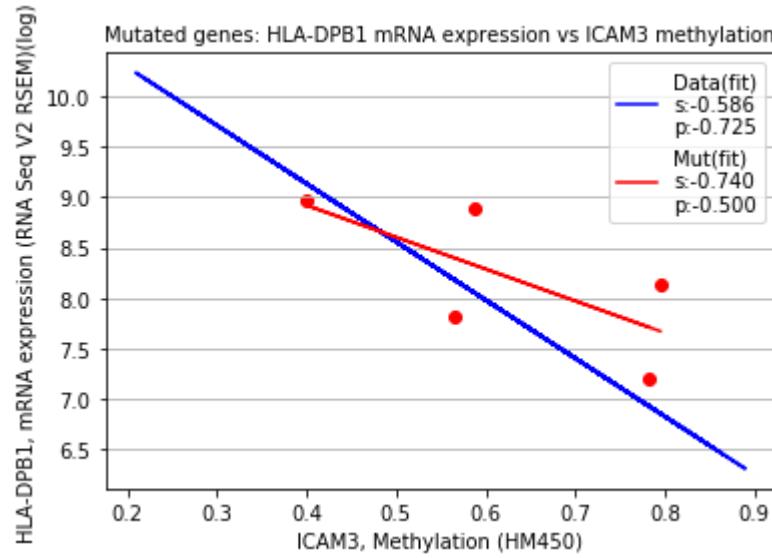
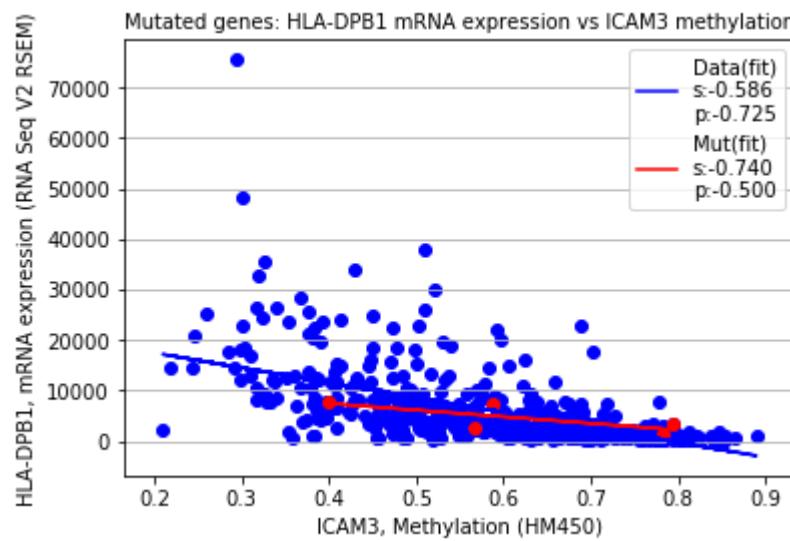
```
In [201]: mutReadPlot('./plots-hladpb1-hladmb.txt', 'Mutated genes: HLA-DPB1 mRNA expression vs HLA-DMB methylation')
```



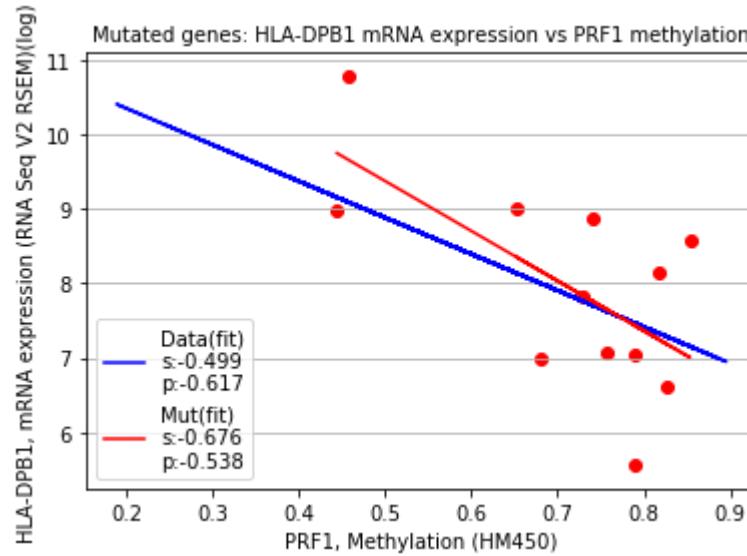
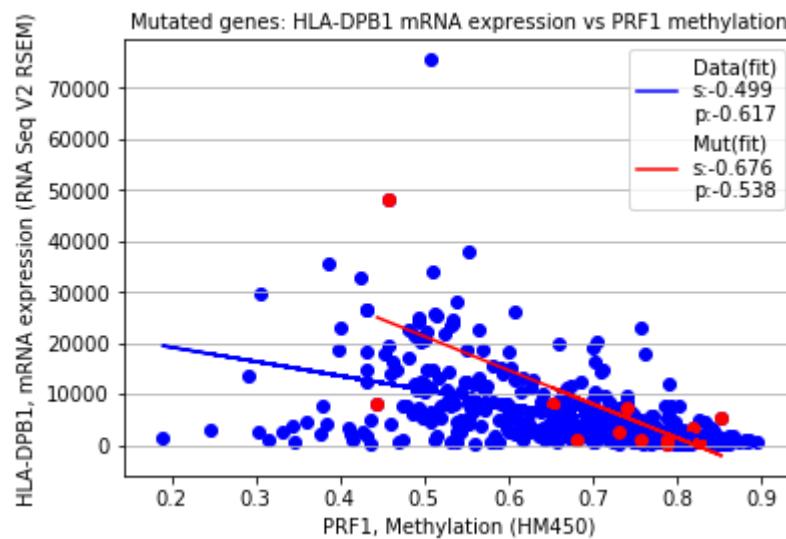
```
In [202]: mutReadPlot('./plots-hladpb1-icam2.txt', 'Mutated genes: HLA-DPB1 mRNA expression vs ICAM2 methylation')
```



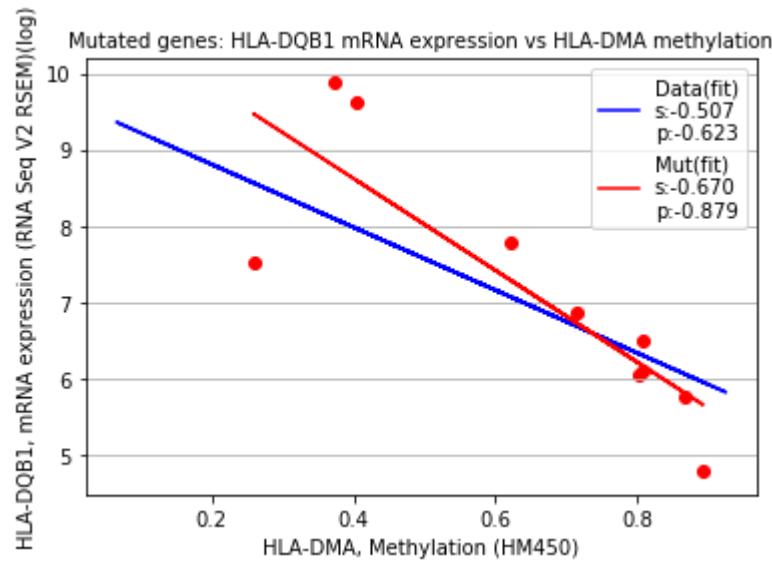
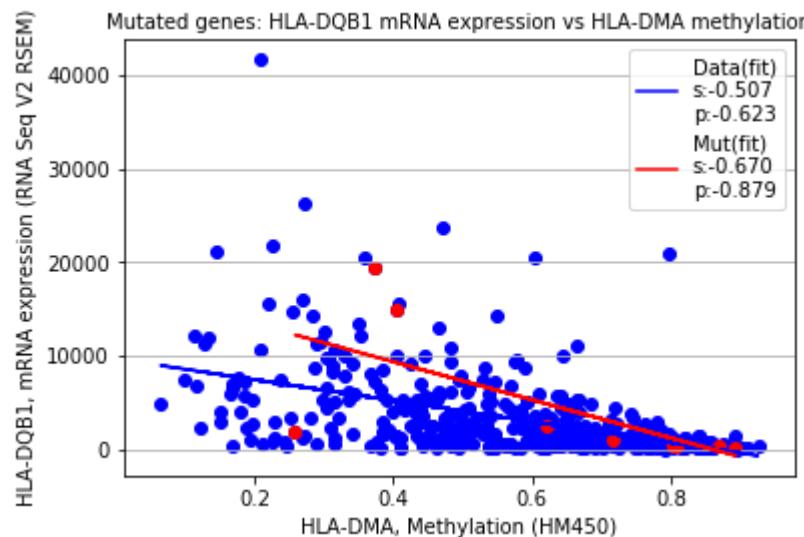
```
In [203]: mutReadPlot('./plots-hladpb1-icam3.txt', 'Mutated genes: HLA-DPB1 mRNA expression vs ICAM3 methylation')
```



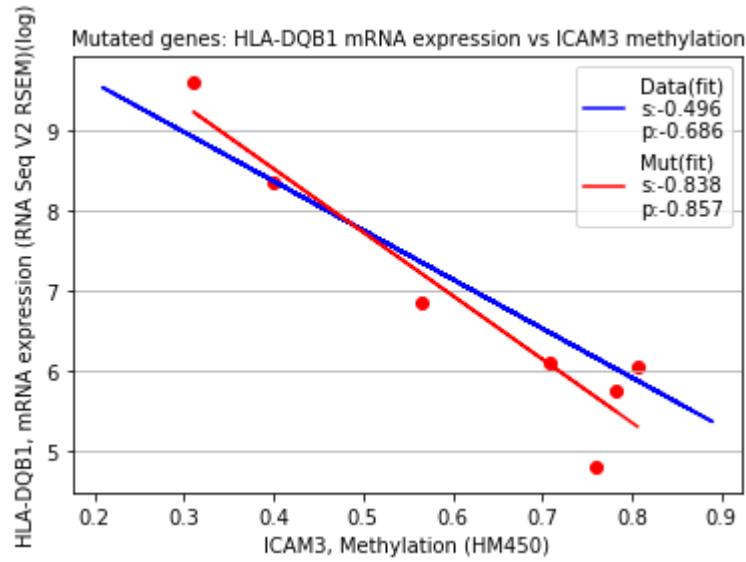
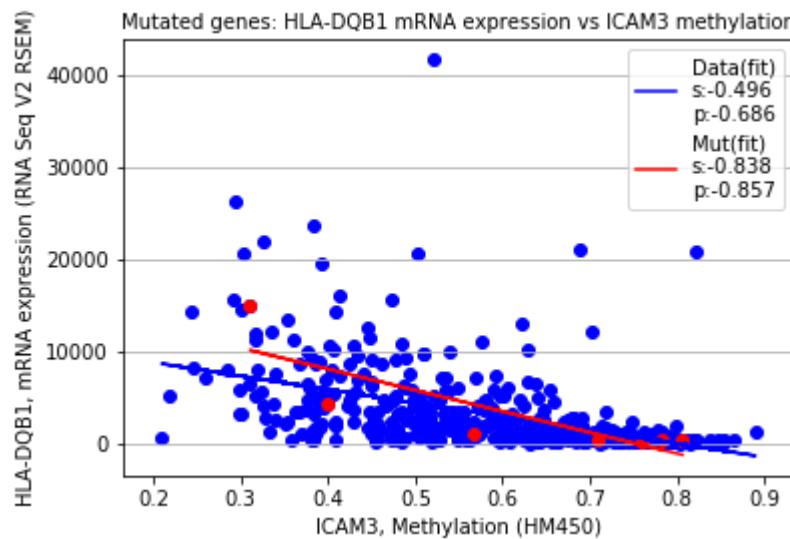
```
In [205]: mutReadPlot('./plots-hladpb1-prf1.txt', 'Mutated genes: HLA-DPB1 mRNA expression vs PRF1 methylation')
```



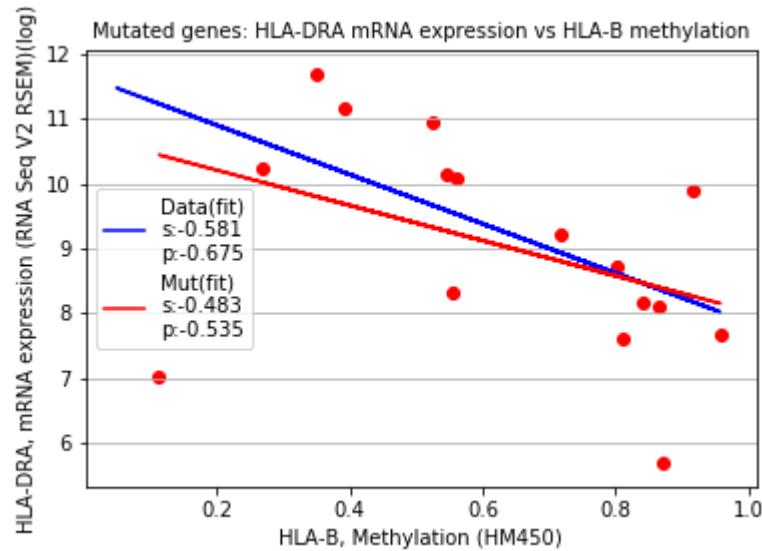
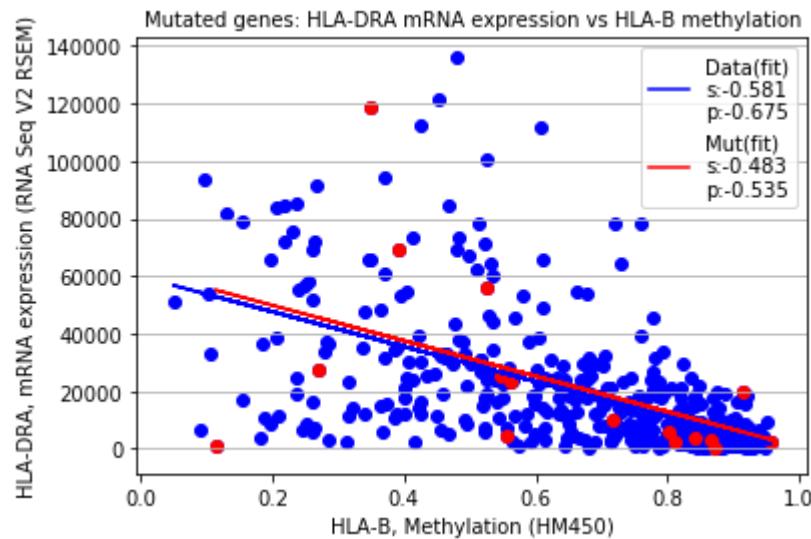
```
In [206]: mutReadPlot('./plots-hladqb1-hladma.txt', 'Mutated genes: HLA-DQB1 mRNA expression vs HLA-DMA methylation')
```



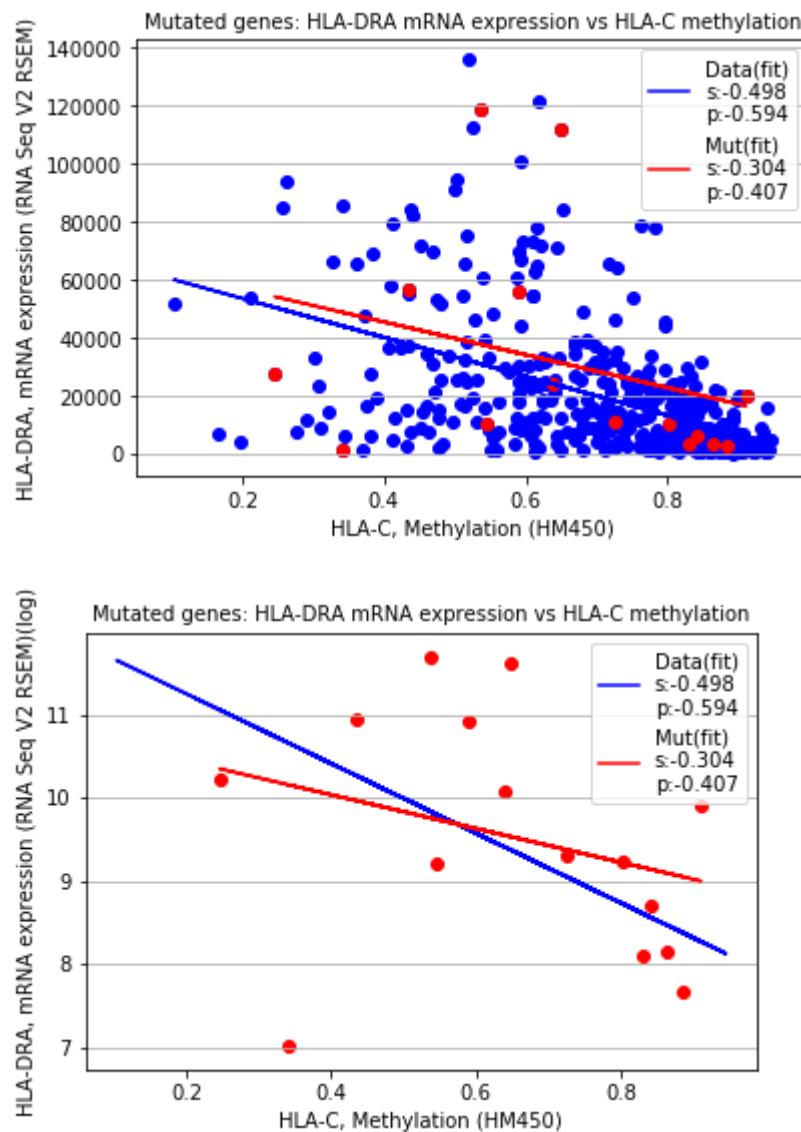
```
In [207]: mutReadPlot('./plots-hladqb1-icam3.txt', 'Mutated genes: HLA-DQB1 mRNA expression vs ICAM3 methylation')
```



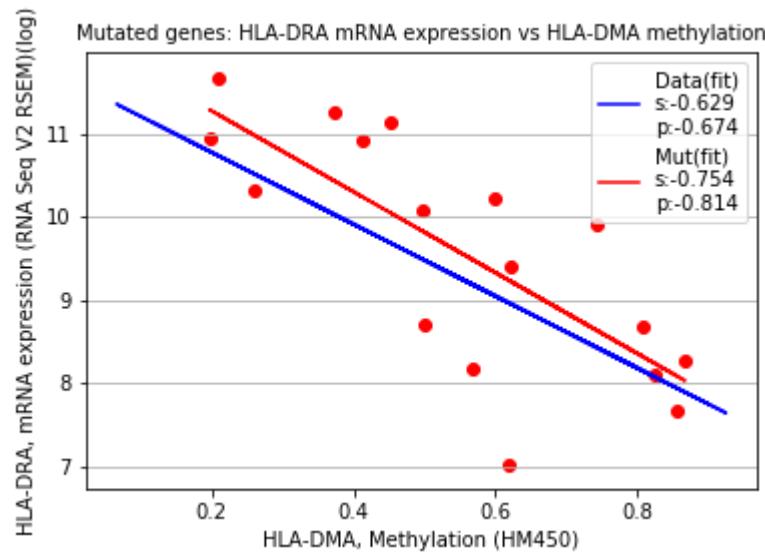
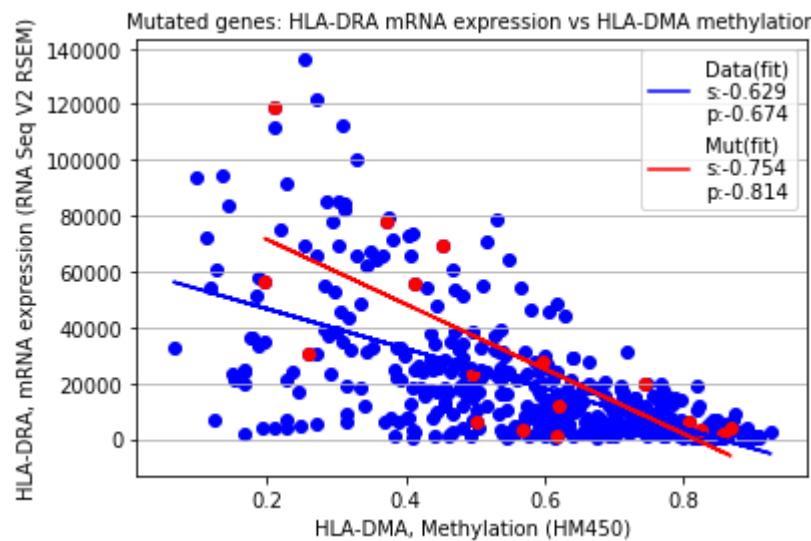
```
In [208]: mutReadPlot('./plots-hladra-hlab.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-B methylation')
```



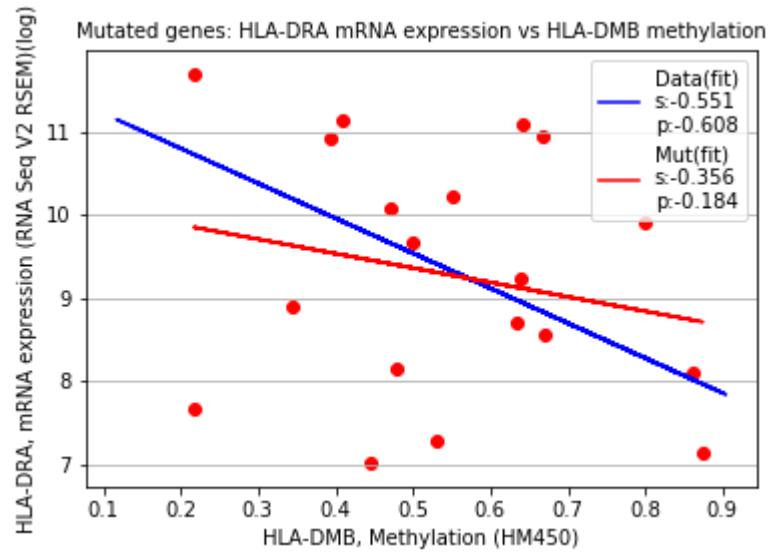
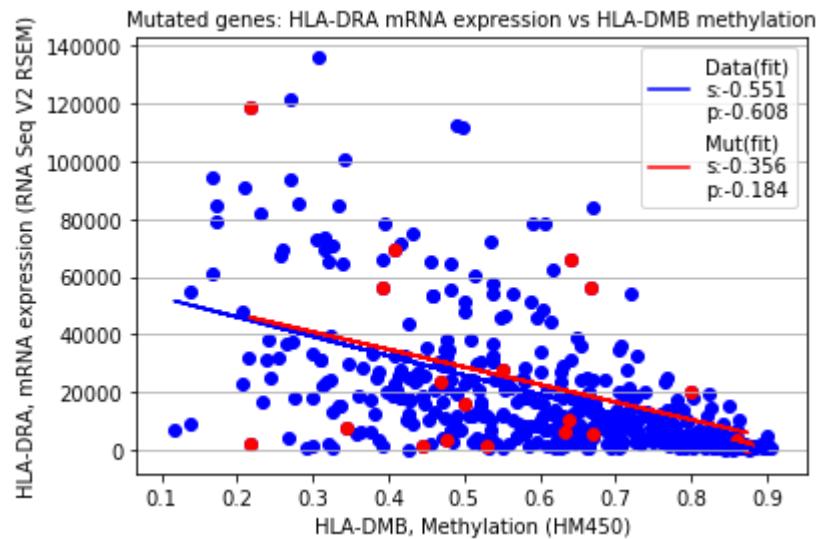
```
In [209]: mutReadPlot('./plots-hladra-hlac.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-C methylation')
```



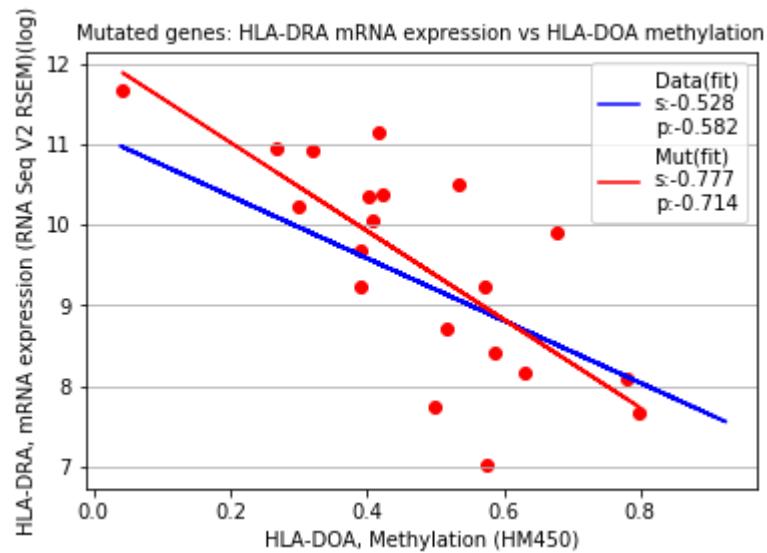
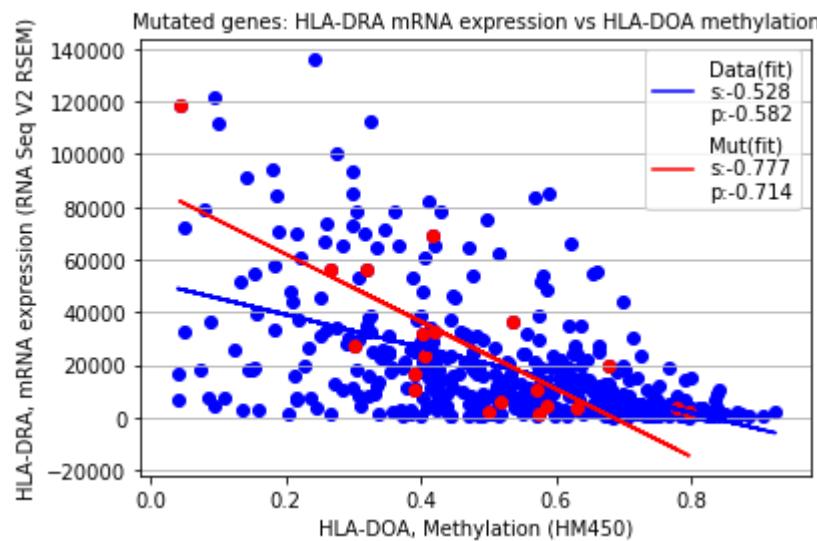
```
In [210]: mutReadPlot('./plots-hladra-hladma.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-DMA methylation')
```



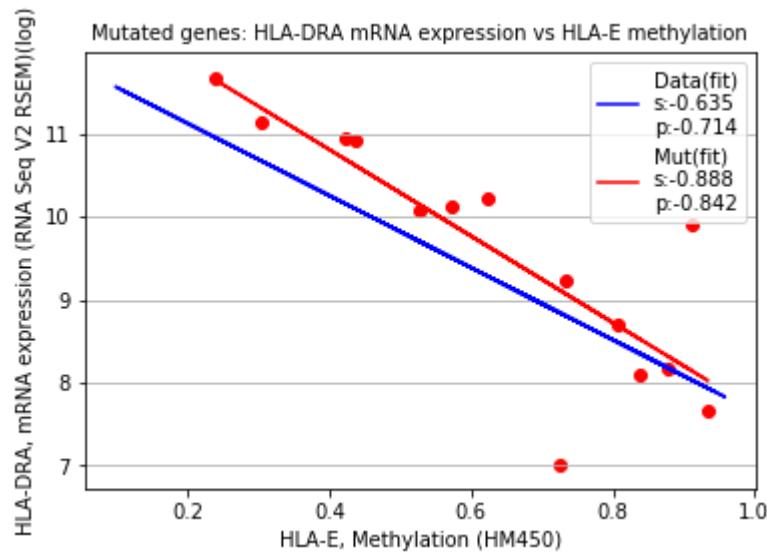
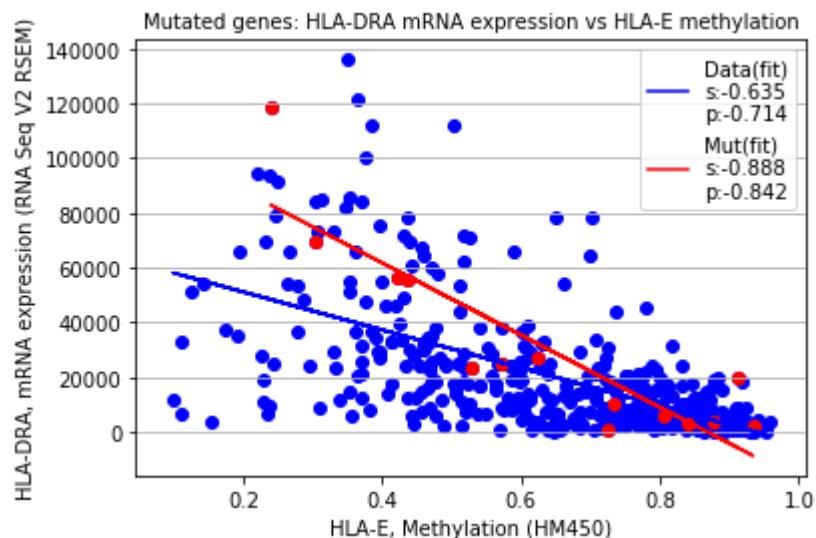
```
In [211]: mutReadPlot('./plots-hladra-hladmb.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-DMB methylation')
```



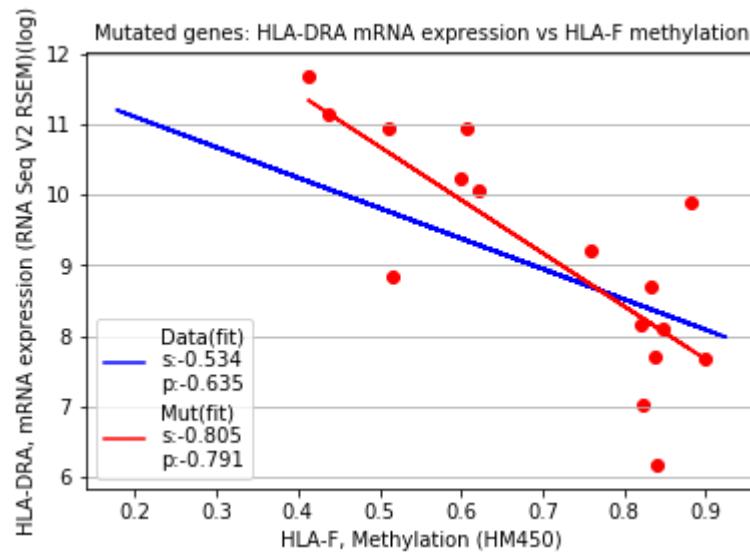
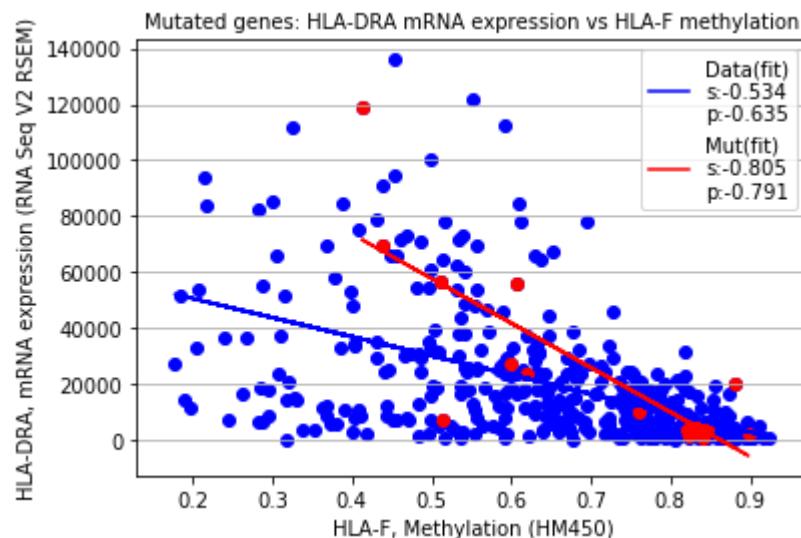
```
In [212]: mutReadPlot('./plots-hladra-hladoa.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-DOA methylation')
```



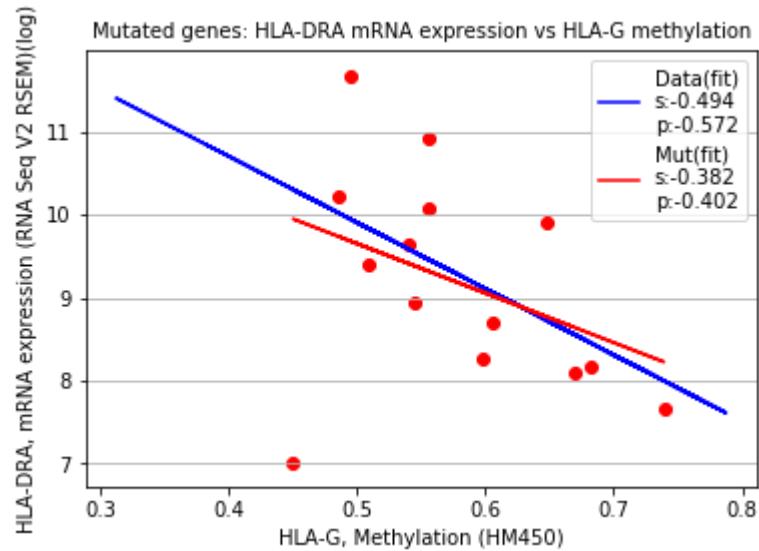
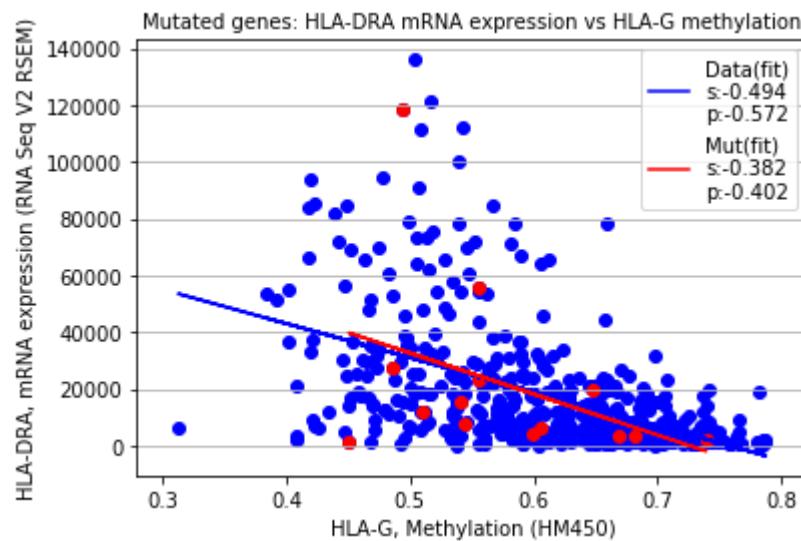
```
In [213]: mutReadPlot('./plots-hladra-hlae.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-E methylation')
```



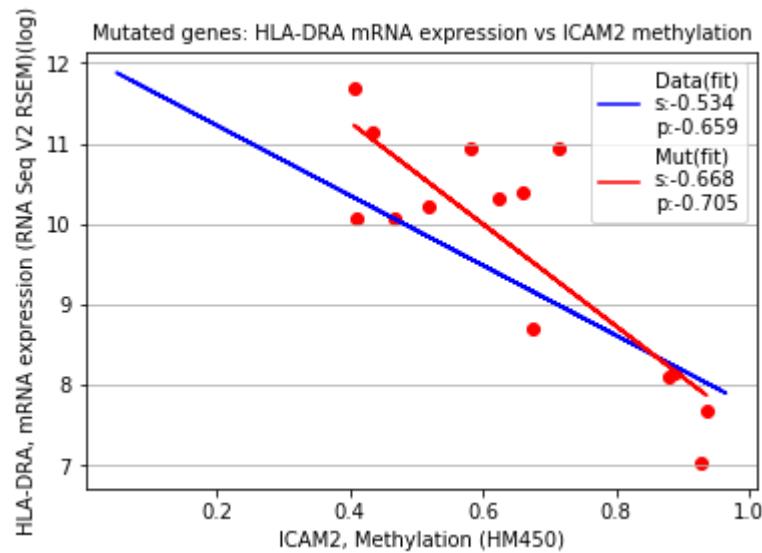
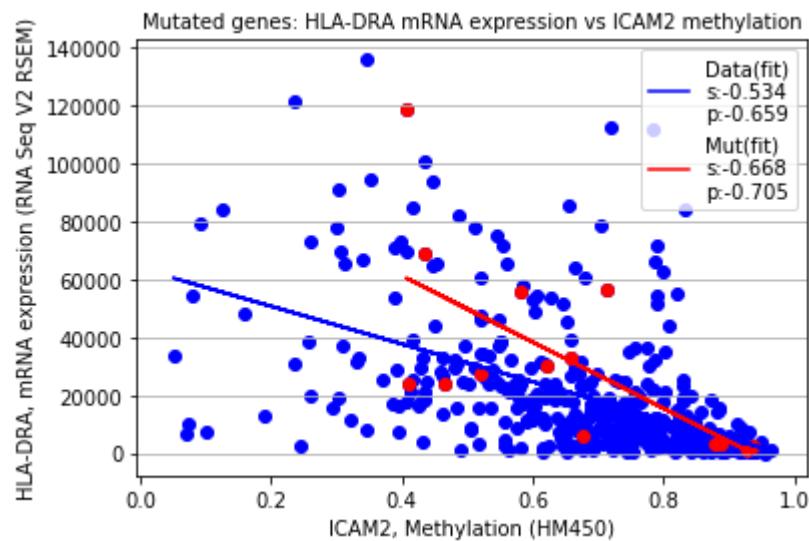
```
In [214]: mutReadPlot('./plots-hladra-hlaf.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-F methylation')
```



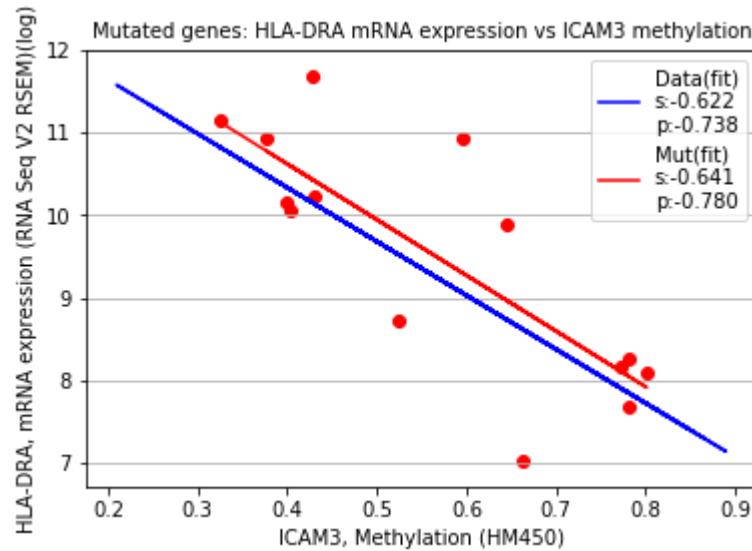
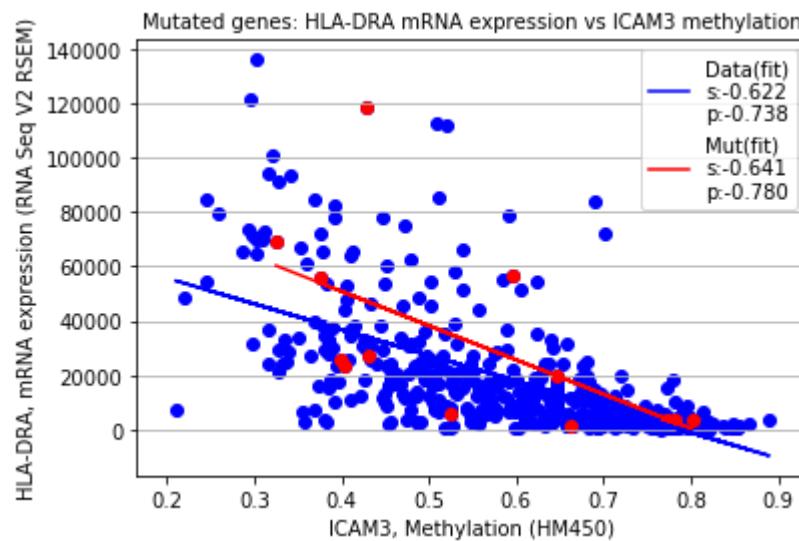
```
In [215]: mutReadPlot('./plots-hladra-hlag.txt', 'Mutated genes: HLA-DRA mRNA expression vs HLA-G methylation')
```



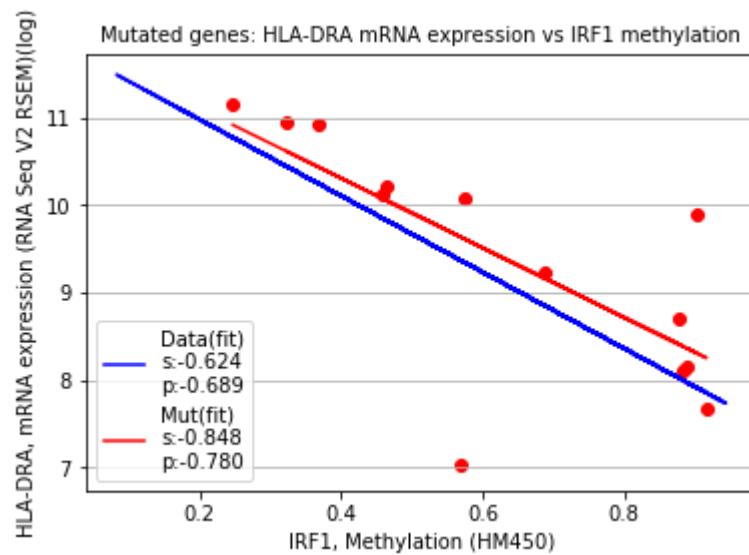
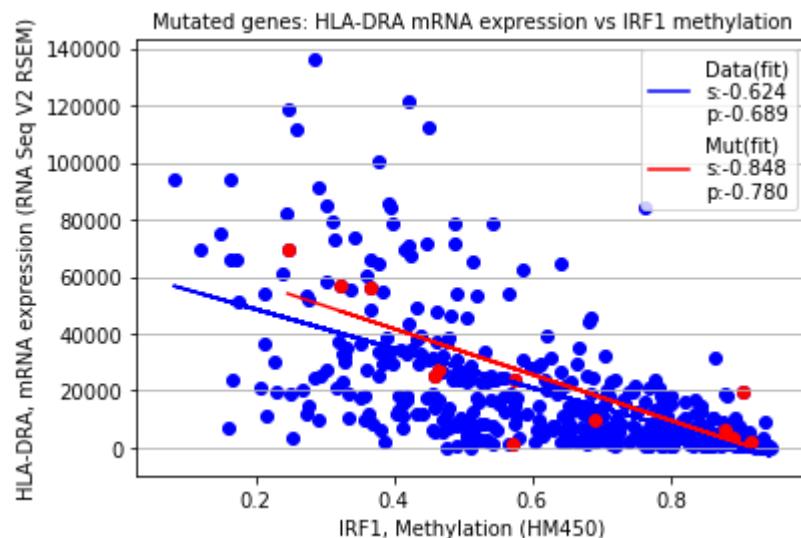
```
In [216]: mutReadPlot('./plots-hladra-icam2.txt', 'Mutated genes: HLA-DRA mRNA expression vs ICAM2 methylation')
```



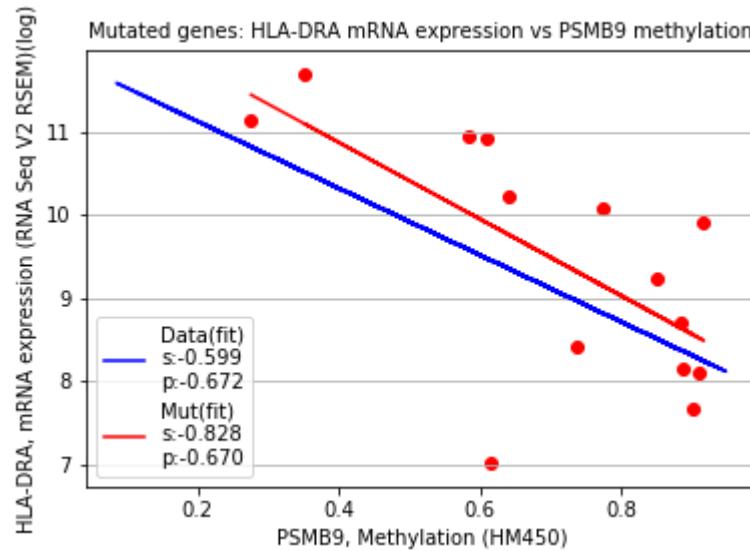
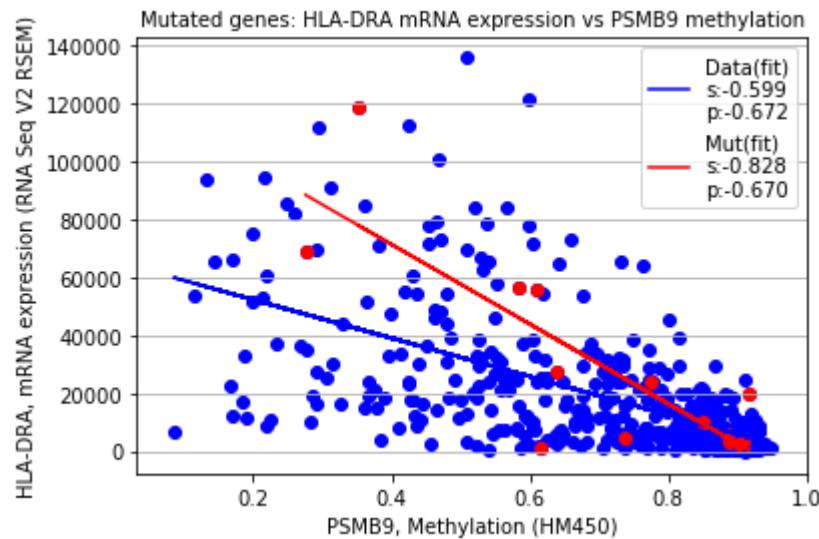
```
In [217]: mutReadPlot('./plots-hladra-icam3.txt', 'Mutated genes: HLA-DRA mRNA expression vs ICAM3 methylation')
```



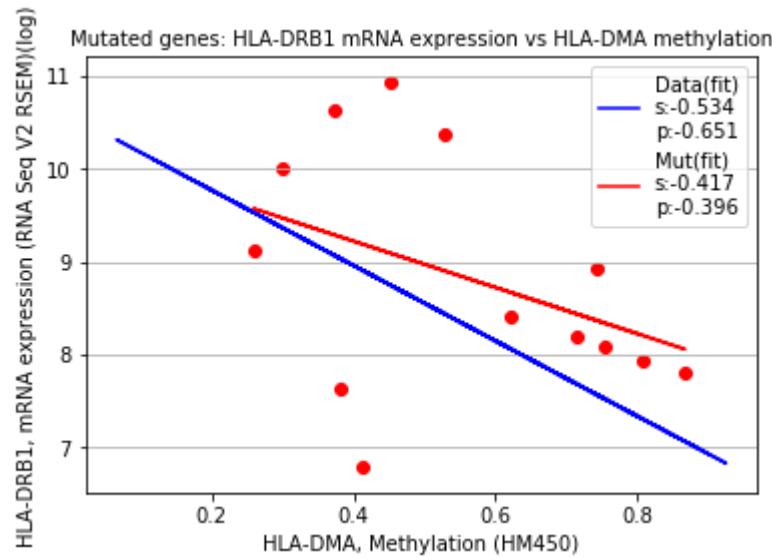
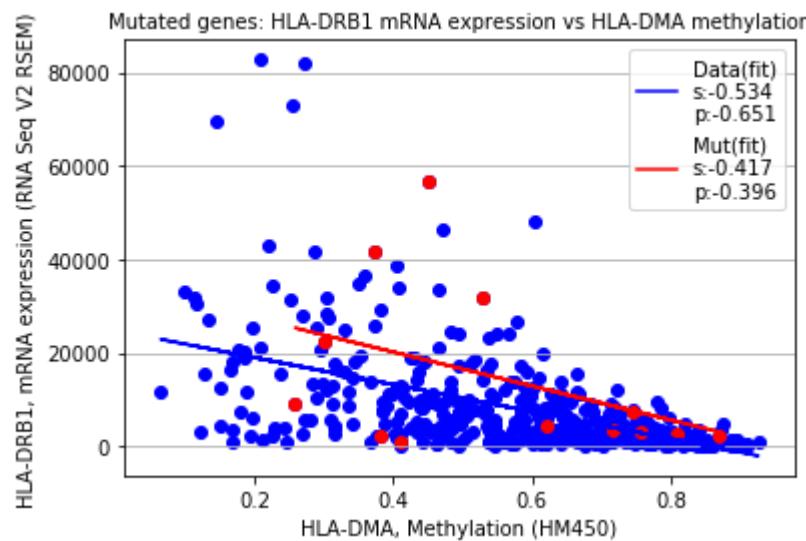
```
In [218]: mutReadPlot('./plots-hladra-irf1.txt', 'Mutated genes: HLA-DRA mRNA expression vs IRF1 methylation')
```



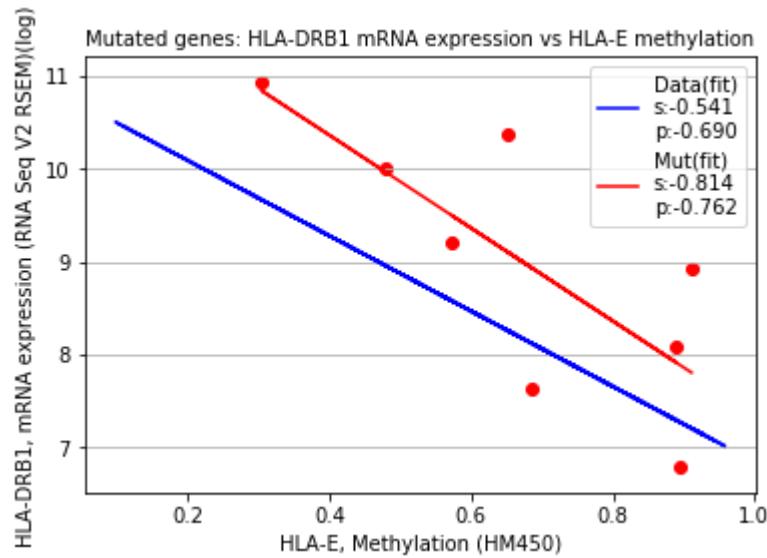
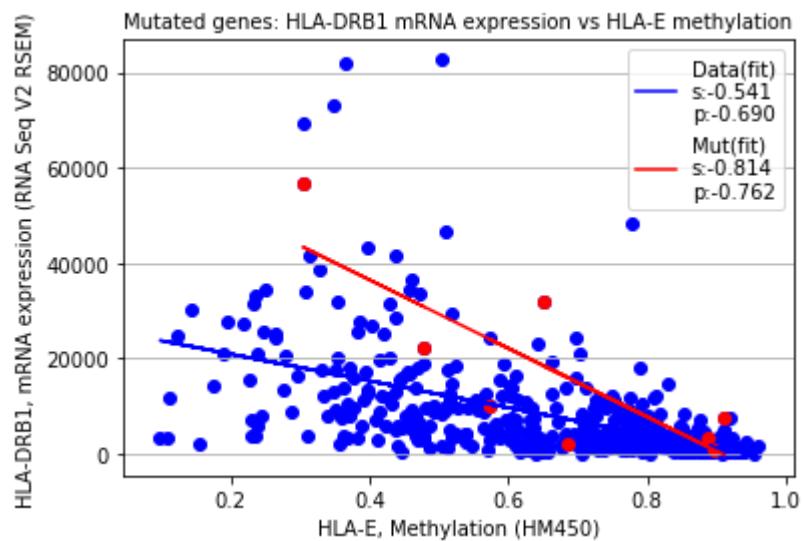
```
In [219]: mutReadPlot('./plots-hladra-psmb9.txt', 'Mutated genes: HLA-DRA mRNA expression vs PSMB9 methylation')
```



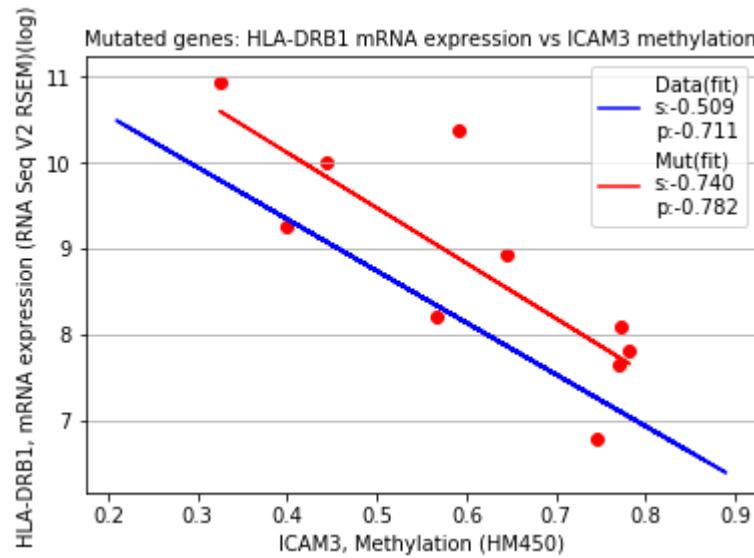
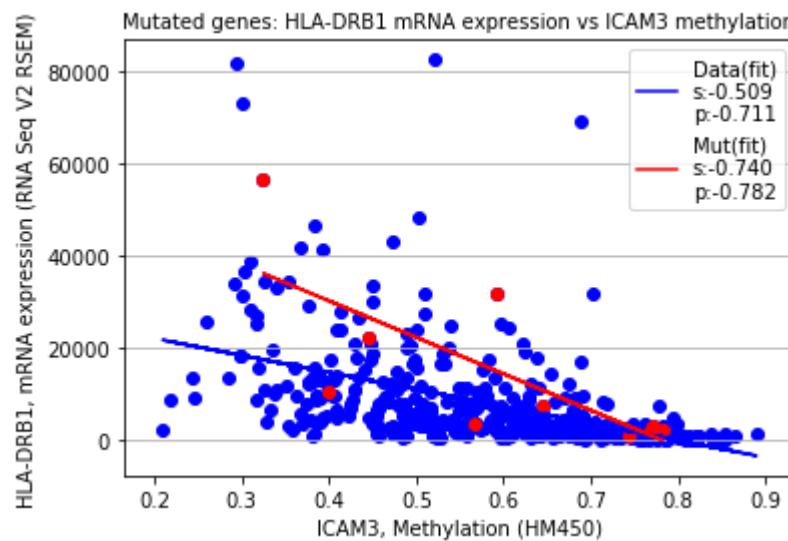
```
In [220]: mutReadPlot('./plots-hladrb1-hladma.txt', 'Mutated genes: HLA-DRB1 mRNA expression vs HLA-DMA methylation')
```



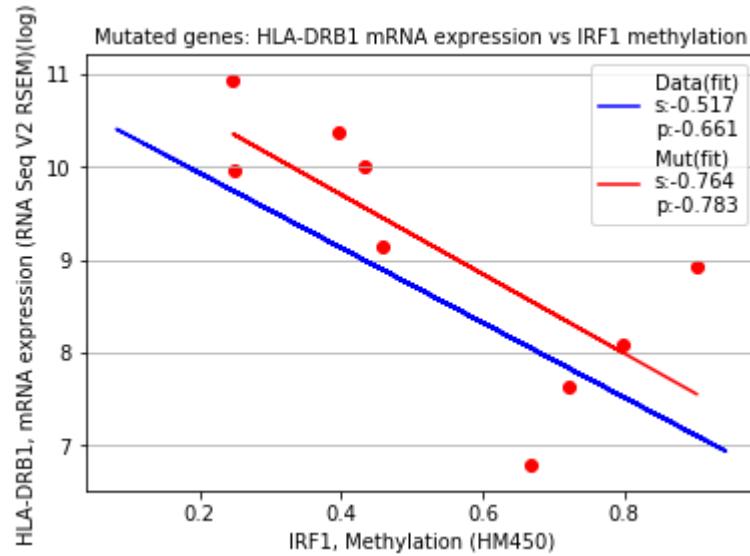
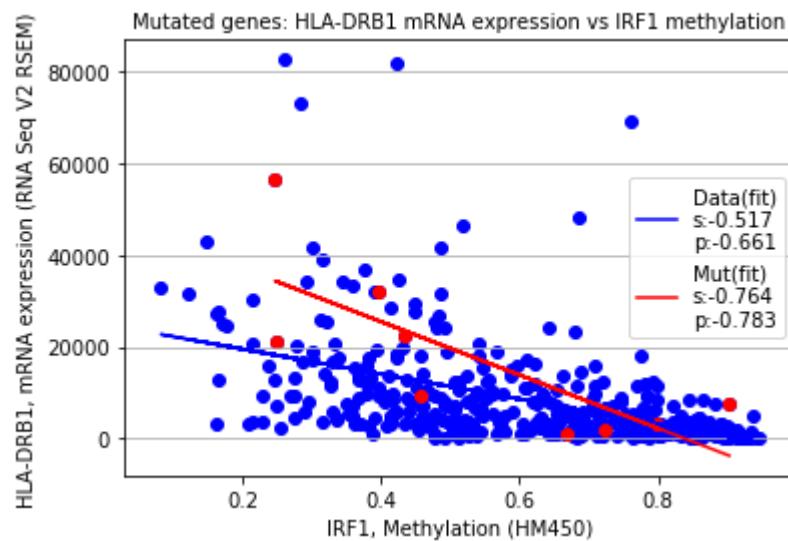
```
In [223]: mutReadPlot('./plots-hladrb1-hlae.txt', 'Mutated genes: HLA-DRB1 mRNA expression vs HLA-E methylation')
```



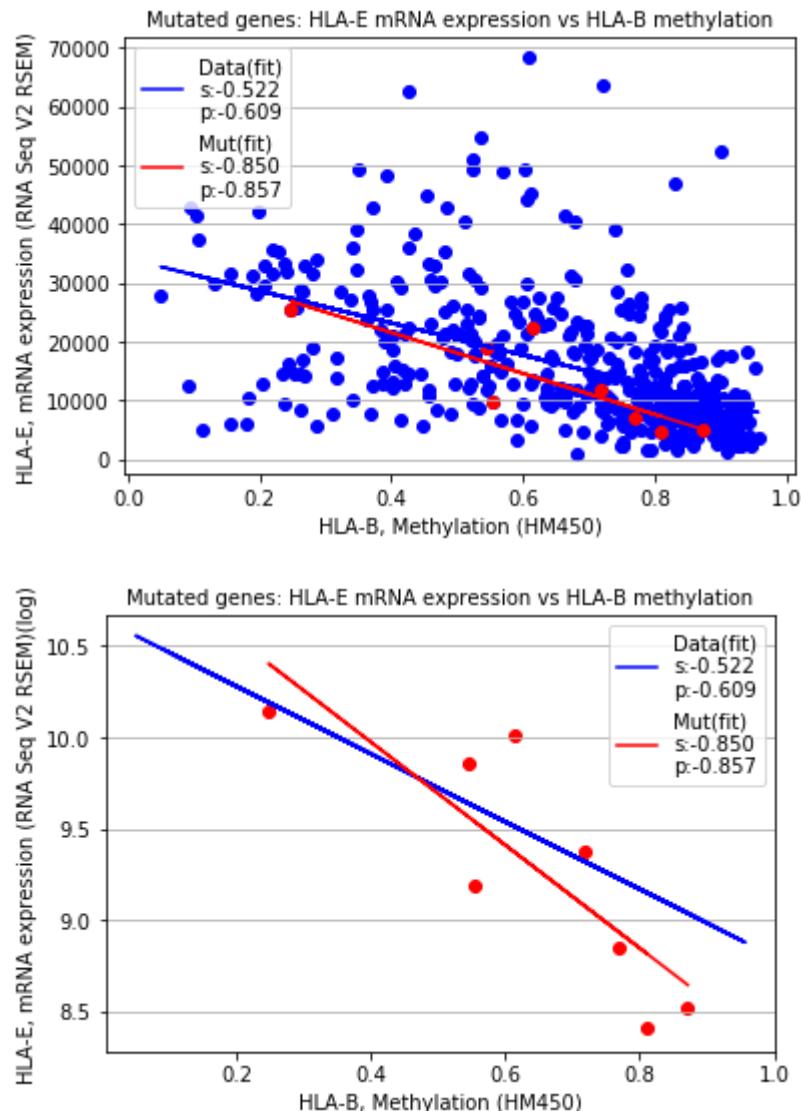
```
In [221]: mutReadPlot('./plots-hladrb1-icam3.txt', 'Mutated genes: HLA-DRB1 mRNA expression vs ICAM3 methylation')
```



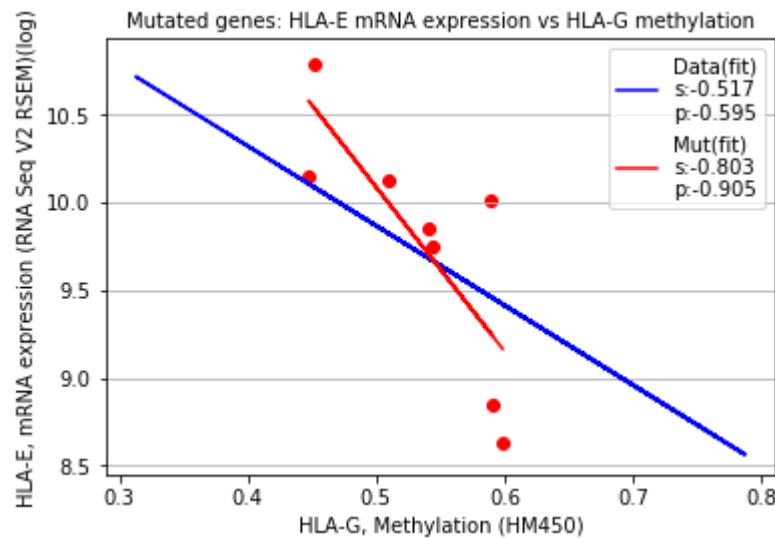
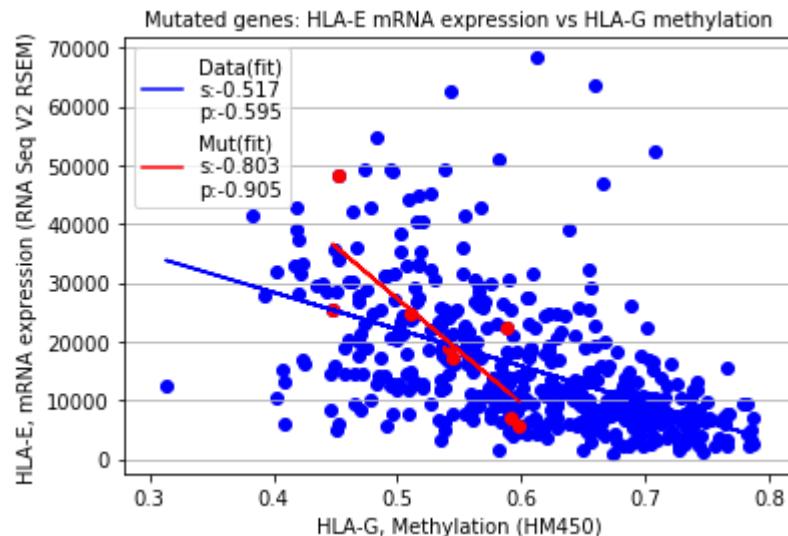
```
In [222]: mutReadPlot('./plots-hladrb1-irf1.txt', 'Mutated genes: HLA-DRB1 mRNA expression vs IRF1 methylation')
```



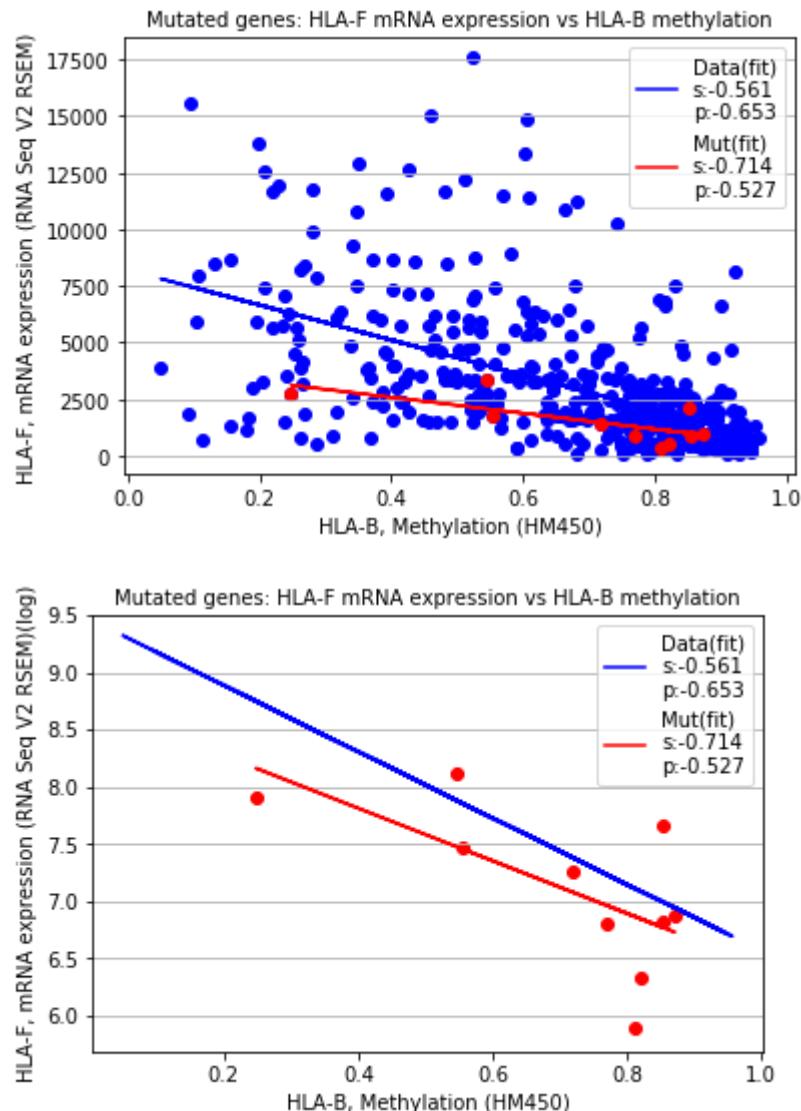
```
In [224]: mutReadPlot('./plots-hlae-hlab.txt', 'Mutated genes: HLA-E mRNA expression vs HLA-B methylation')
```



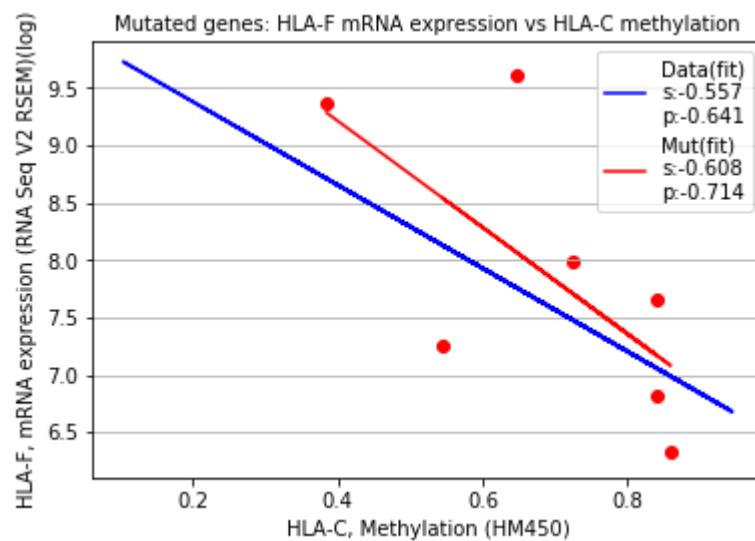
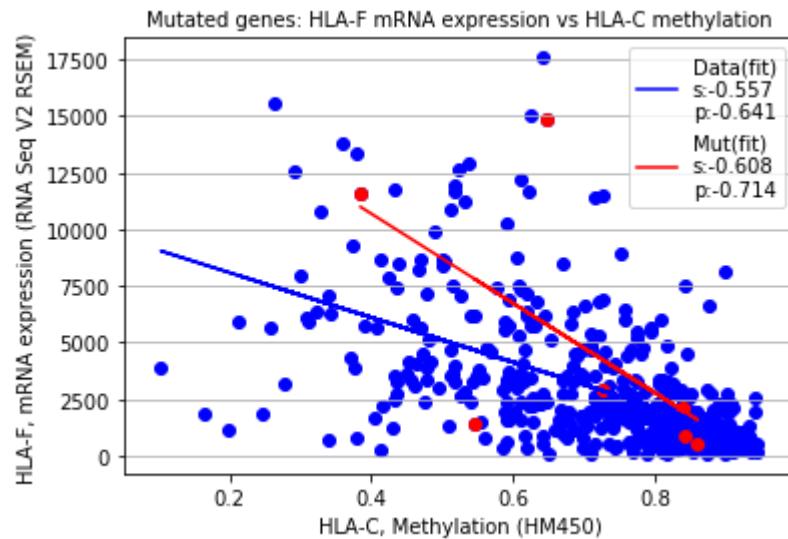
```
In [225]: mutReadPlot('./plots-hlae-hlag.txt', 'Mutated genes: HLA-E mRNA expression vs HLA-G methylation')
```



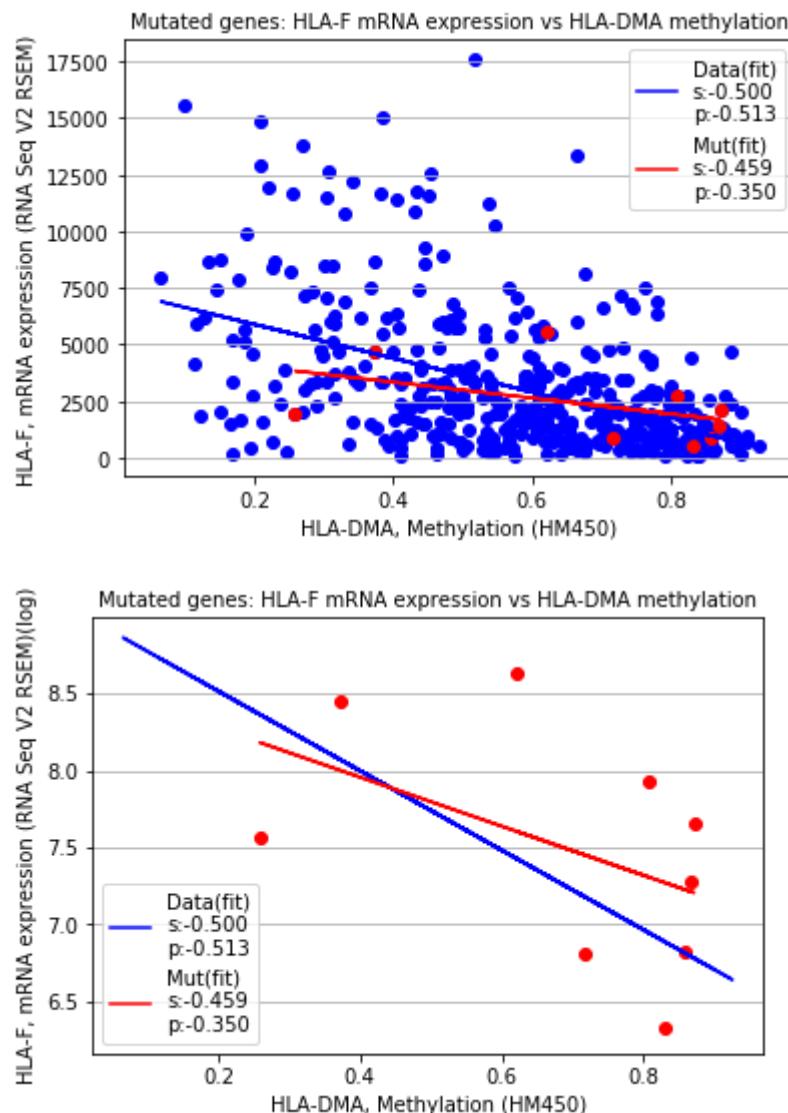
```
In [226]: mutReadPlot('./plots-hlaf-hlab.txt', 'Mutated genes: HLA-F mRNA expression vs HLA-B methylation')
```



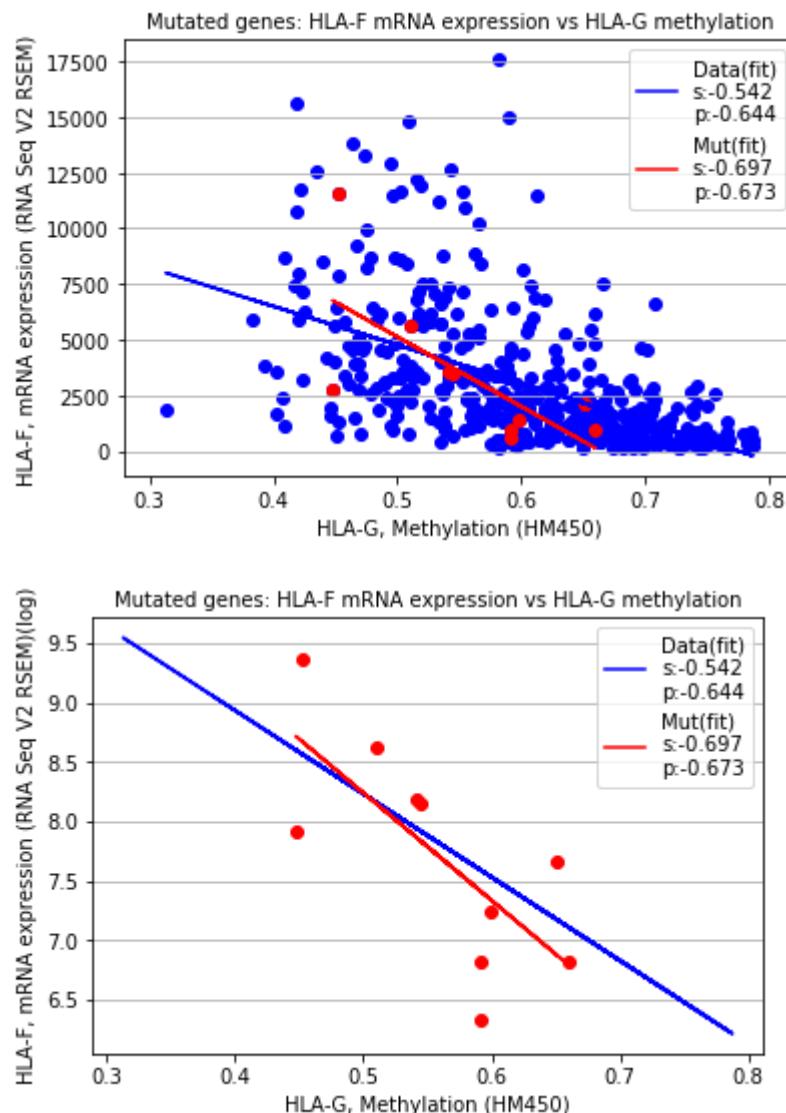
```
In [227]: mutReadPlot('./plots-hlaf-hlac.txt', 'Mutated genes: HLA-F mRNA expression vs HLA-C methylation')
```



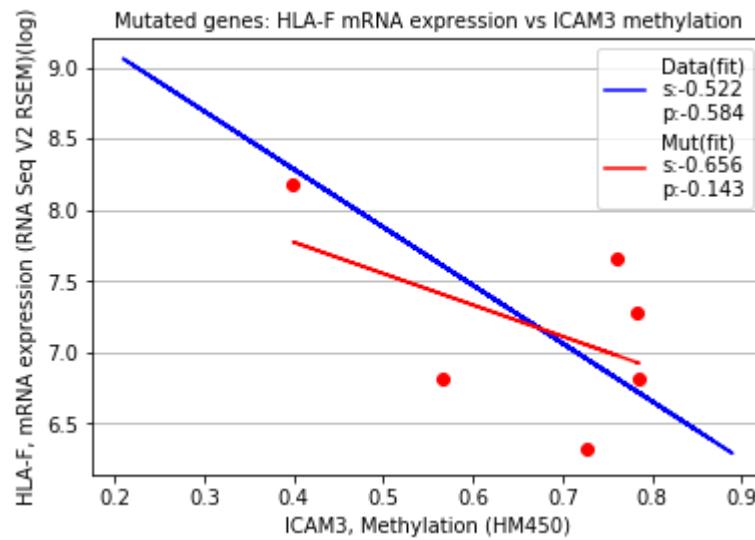
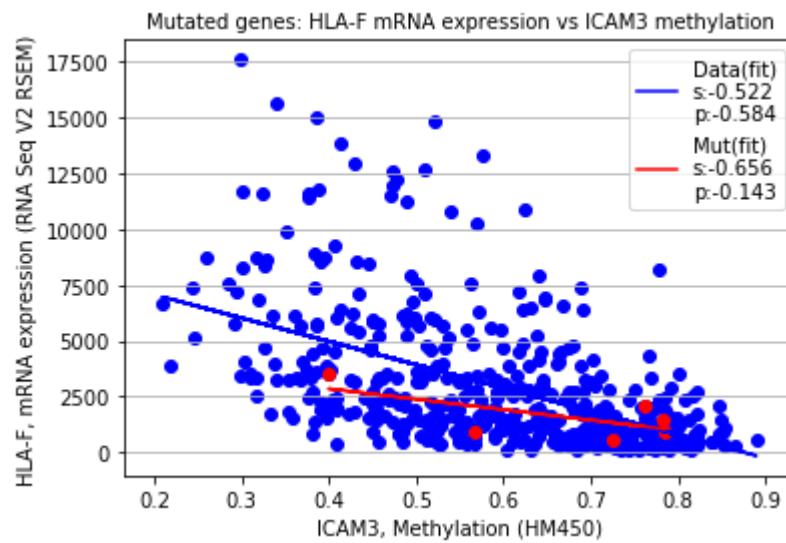
```
In [228]: mutReadPlot('./plots-hlaf-hladma.txt', 'Mutated genes: HLA-F mRNA expression vs HLA-DMA methylation')
```



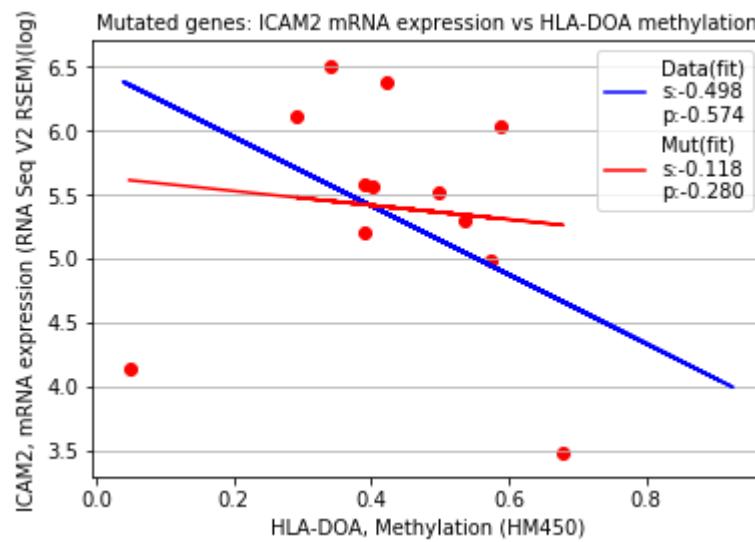
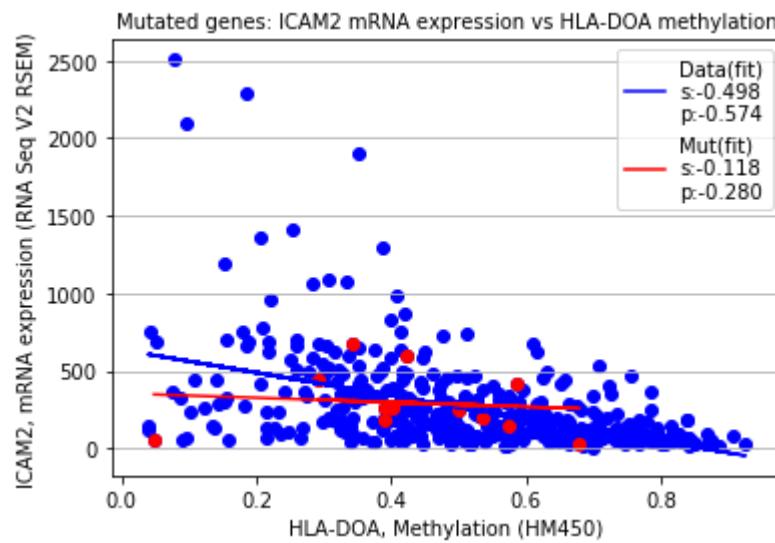
```
In [229]: mutReadPlot('./plots-hlaf-hlag.txt', 'Mutated genes: HLA-F mRNA expression vs HLA-G methylation')
```



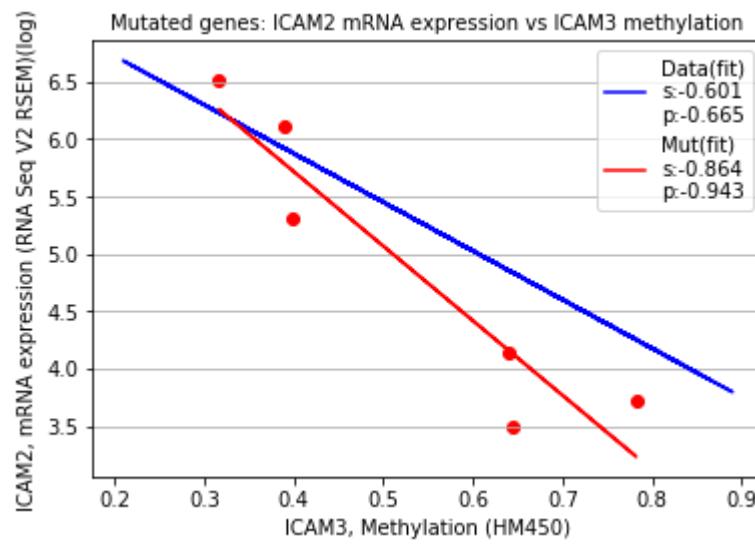
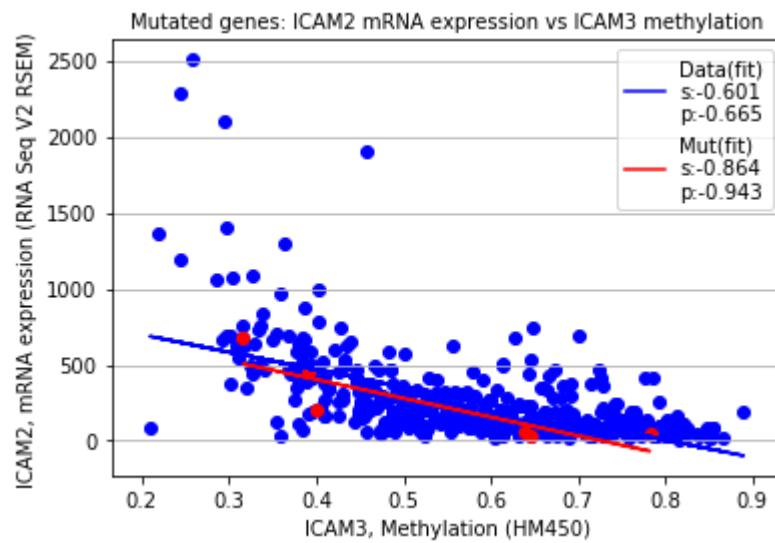
```
In [230]: mutReadPlot('./plots-hlaf-icam3.txt', 'Mutated genes: HLA-F mRNA expression vs ICAM3 methylation')
```



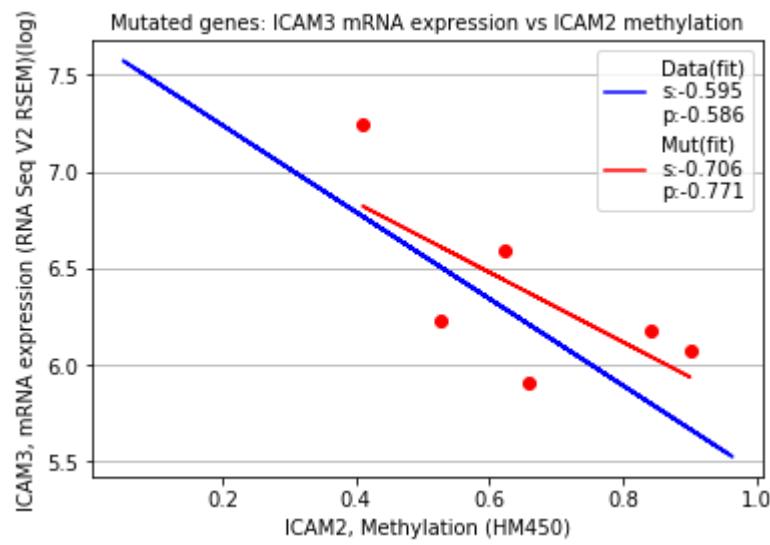
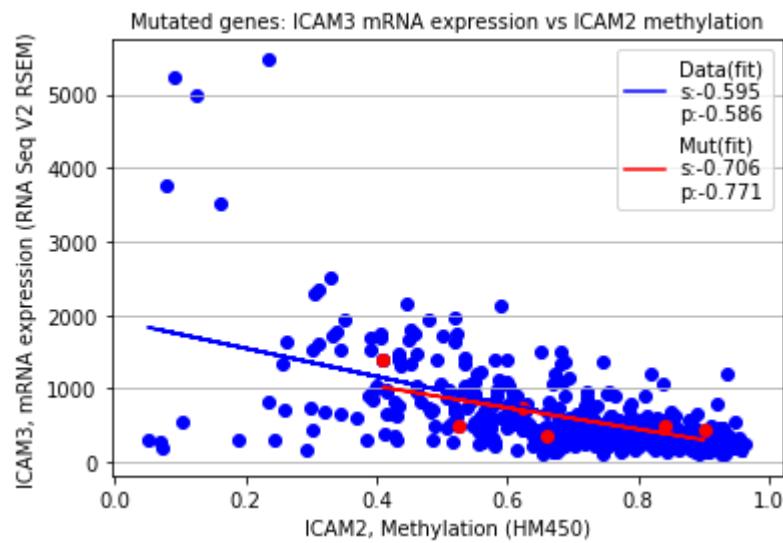
```
In [231]: mutReadPlot('./plots-icam2-hladoa.txt', 'Mutated genes: ICAM2 mRNA expression vs HLA-DOA methylation')
```



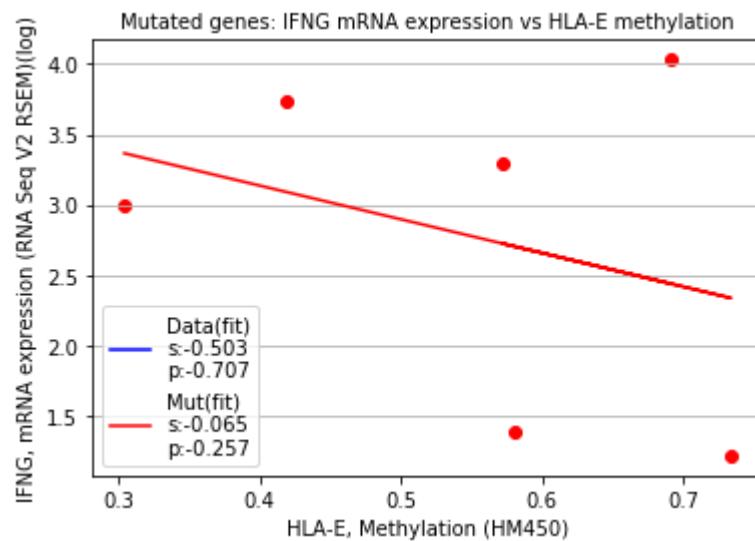
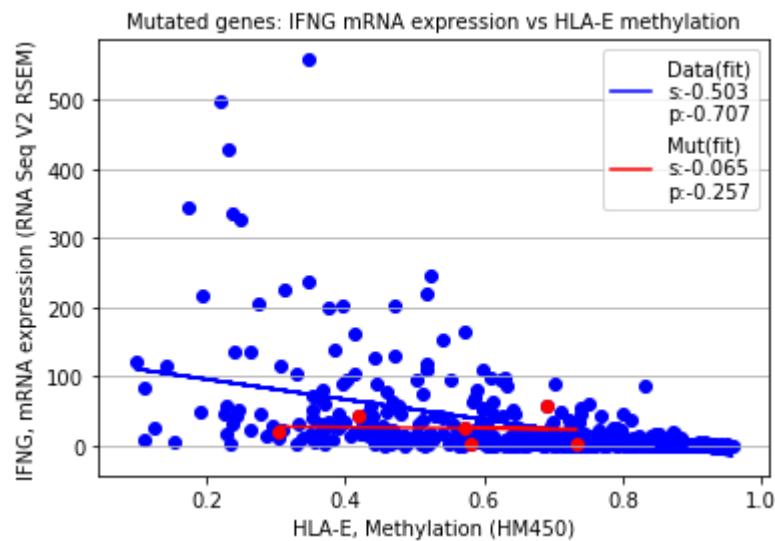
```
In [232]: mutReadPlot('./plots-icam2-icam3.txt', 'Mutated genes: ICAM2 mRNA expression v  
s ICAM3 methylation')
```



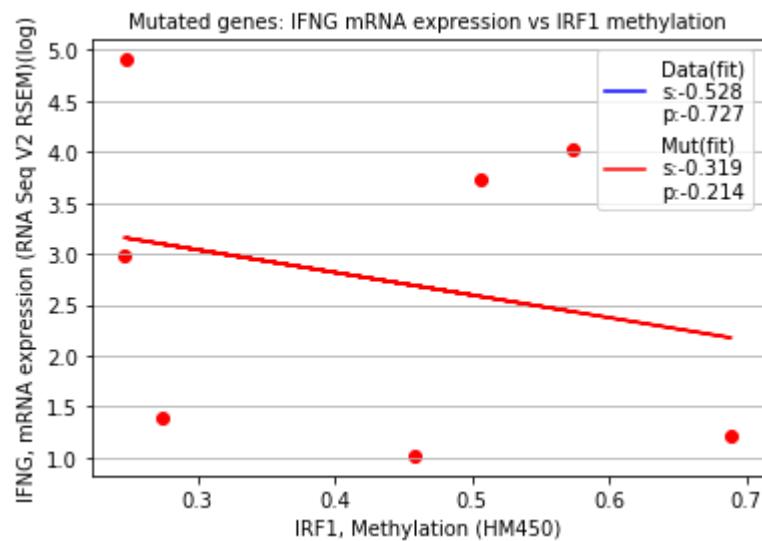
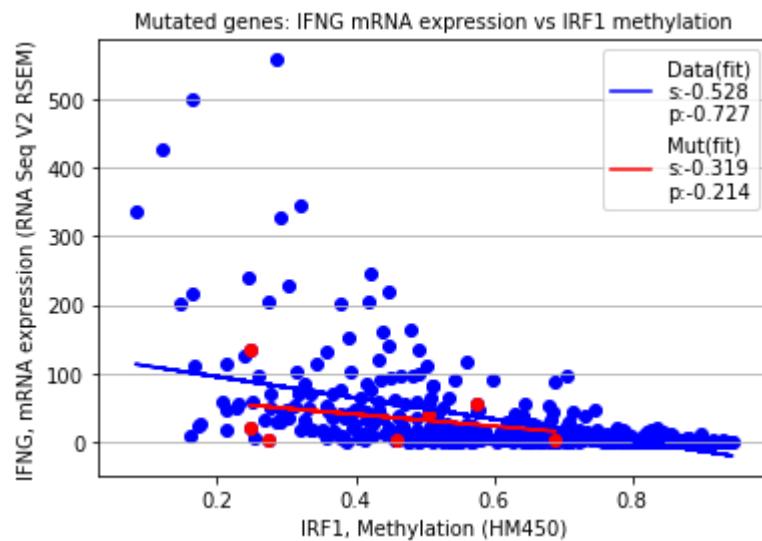
```
In [233]: mutReadPlot('./plots-icam3-icam2.txt', 'Mutated genes: ICAM3 mRNA expression v  
s ICAM2 methylation')
```



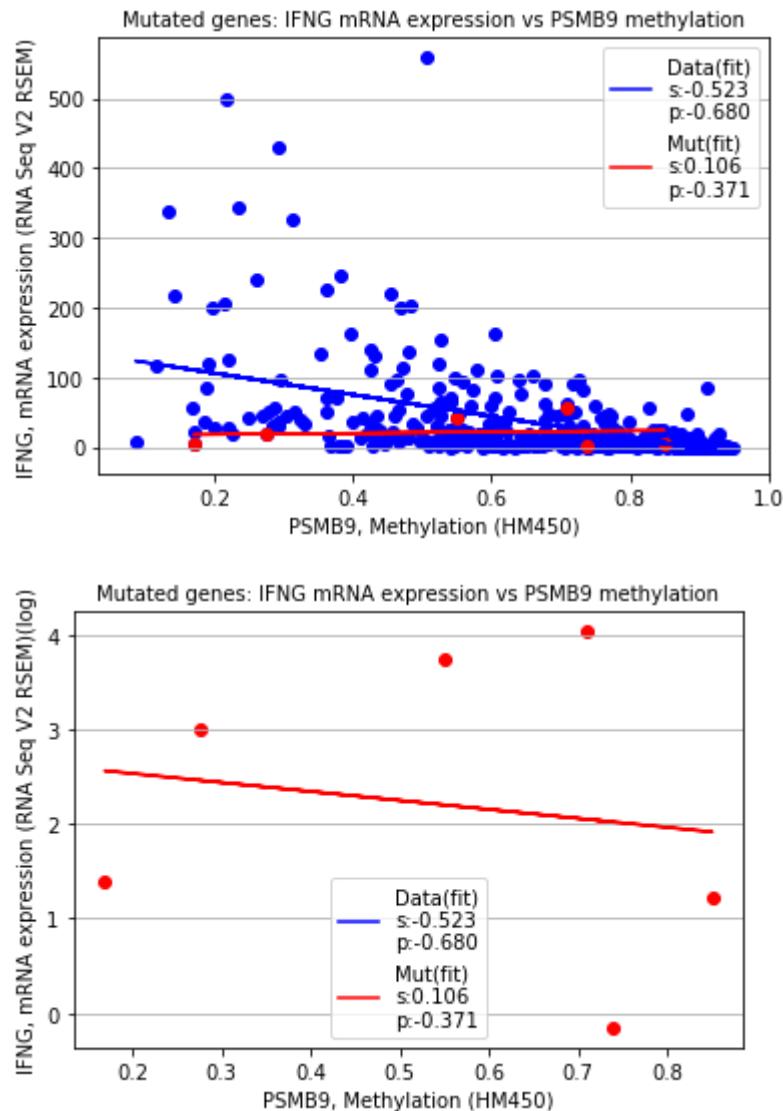
```
In [234]: mutReadPlot('./plots-ifng-hlae.txt', 'Mutated genes: IFNG mRNA expression vs HLA-E methylation')
```



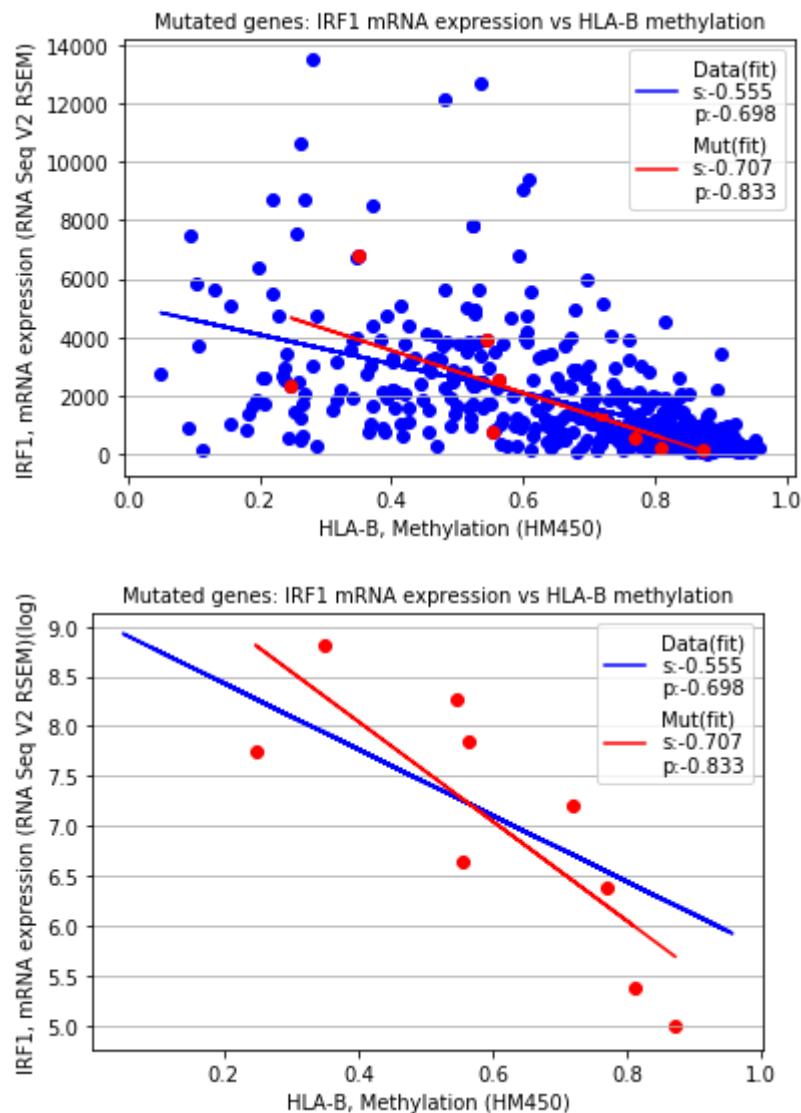
```
In [235]: mutReadPlot('./plots-ifng-ifr1.txt', 'Mutated genes: IFNG mRNA expression vs I  
RF1 methylation')
```



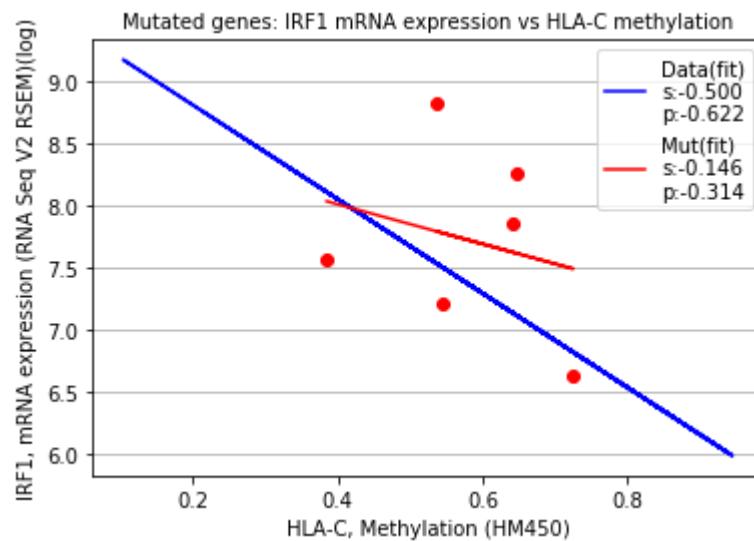
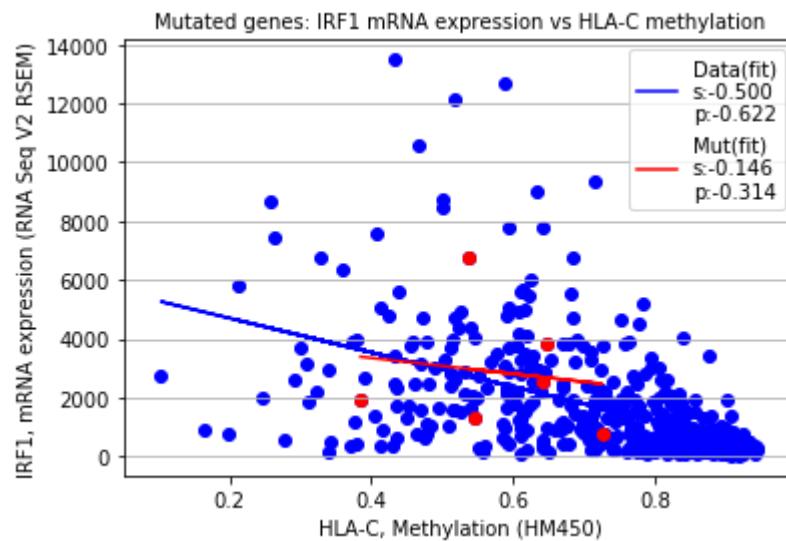
```
In [236]: mutReadPlot('./plots-ifng-psmb9.txt', 'Mutated genes: IFNG mRNA expression vs PSMB9 methylation')
```



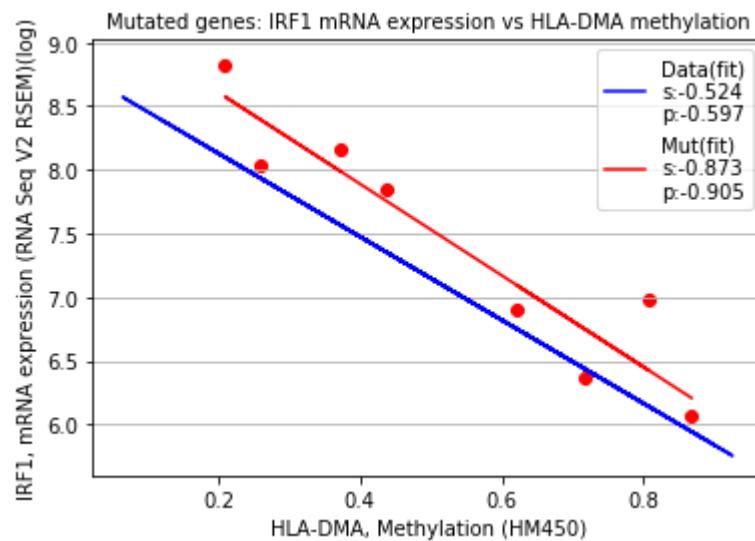
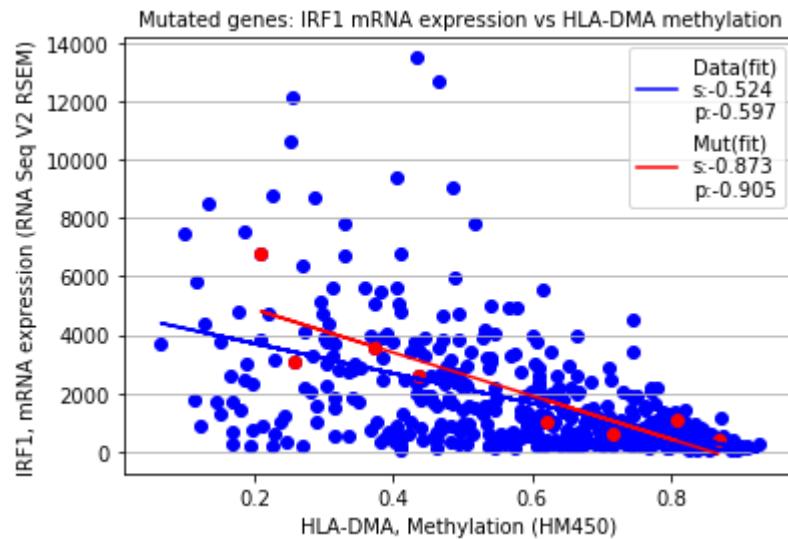
```
In [237]: mutReadPlot('./plots-if1-hlab.txt', 'Mutated genes: IRF1 mRNA expression vs HLA-B methylation')
```



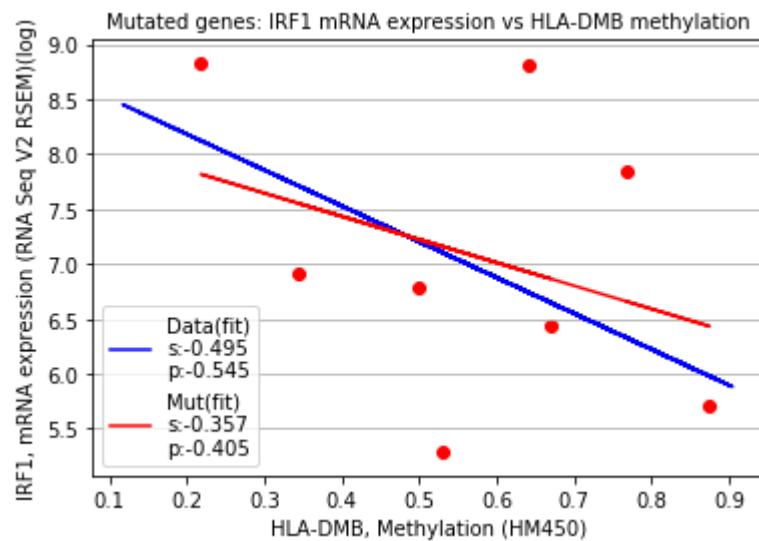
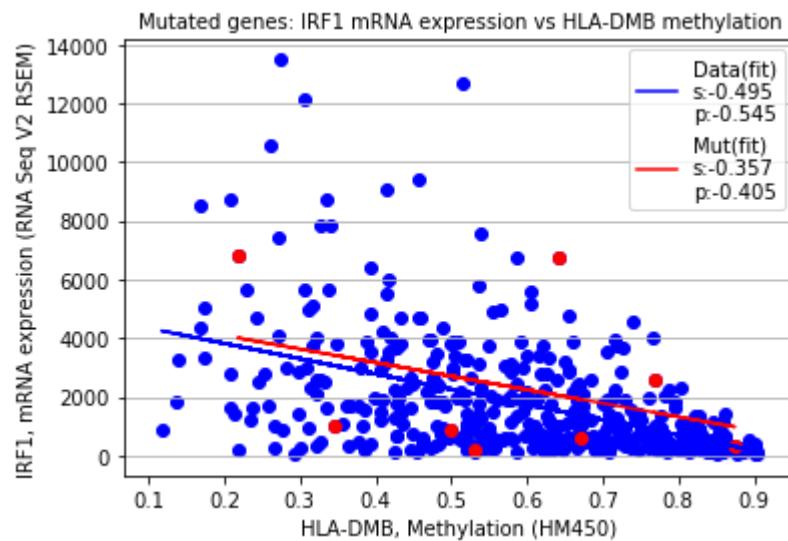
```
In [238]: mutReadPlot('./plots-if1-hlac.txt', 'Mutated genes: IRF1 mRNA expression vs HLA-C methylation')
```



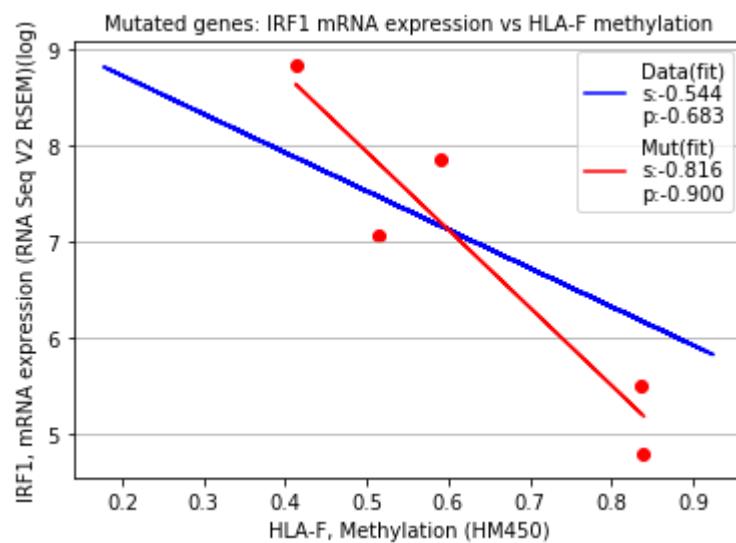
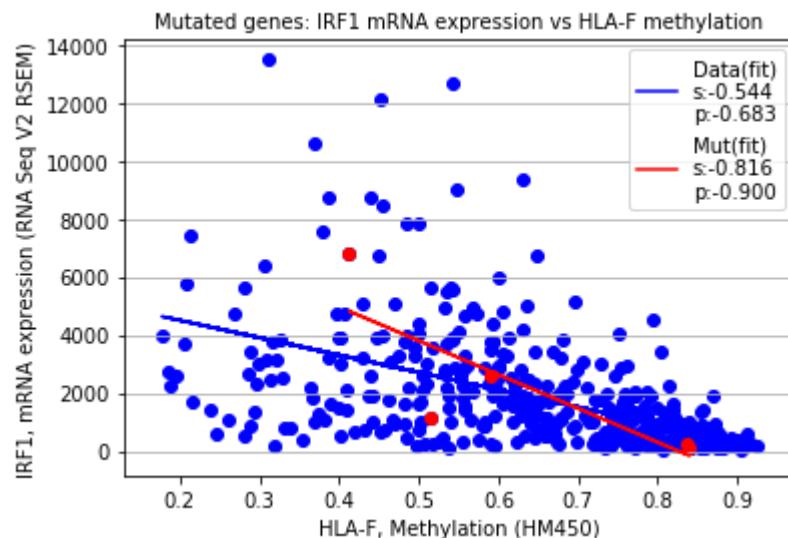
```
In [239]: mutReadPlot('./plots-ifng-hladma.txt', 'Mutated genes: IRF1 mRNA expression vs HLA-DMA methylation')
```



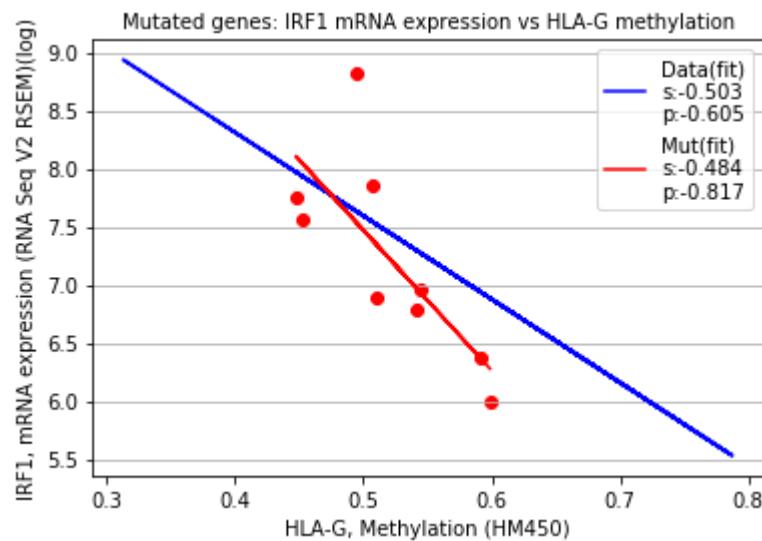
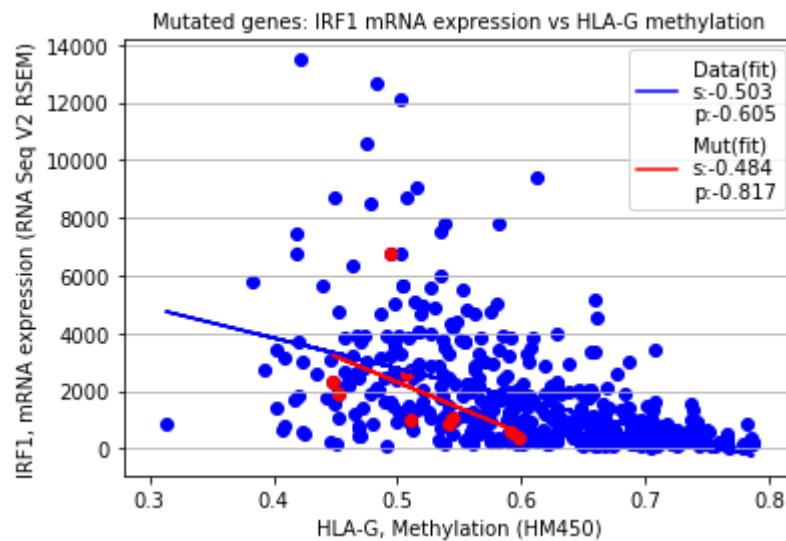
```
In [240]: mutReadPlot('./plots-ifr1-hladmb.txt', 'Mutated genes: IRF1 mRNA expression vs HLA-DMB methylation')
```



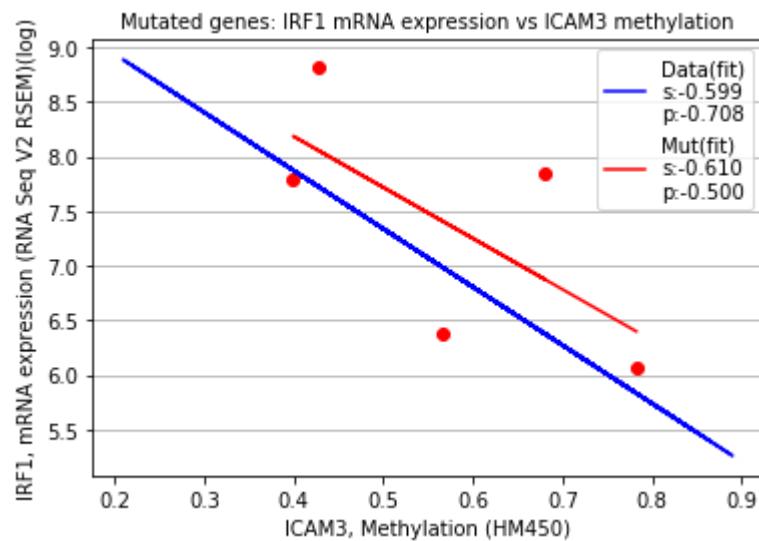
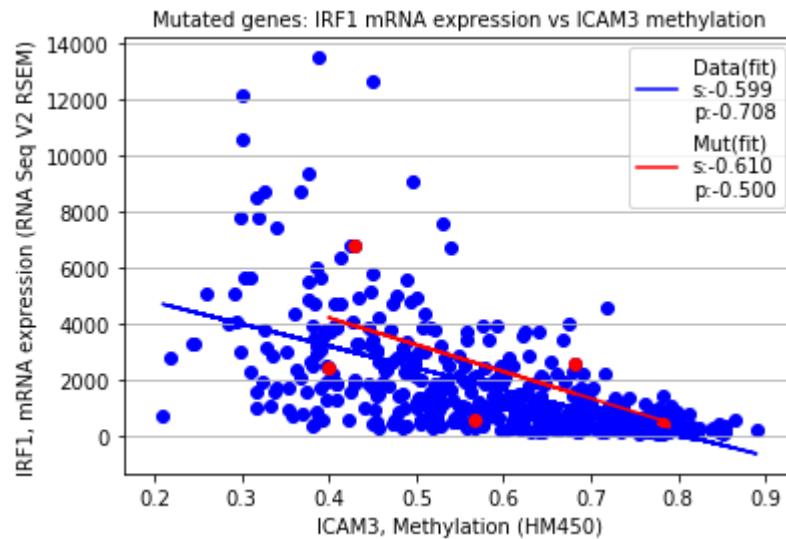
```
In [241]: mutReadPlot('./plots-ifng-hlaf.txt', 'Mutated genes: IRF1 mRNA expression vs HLA-F methylation')
```



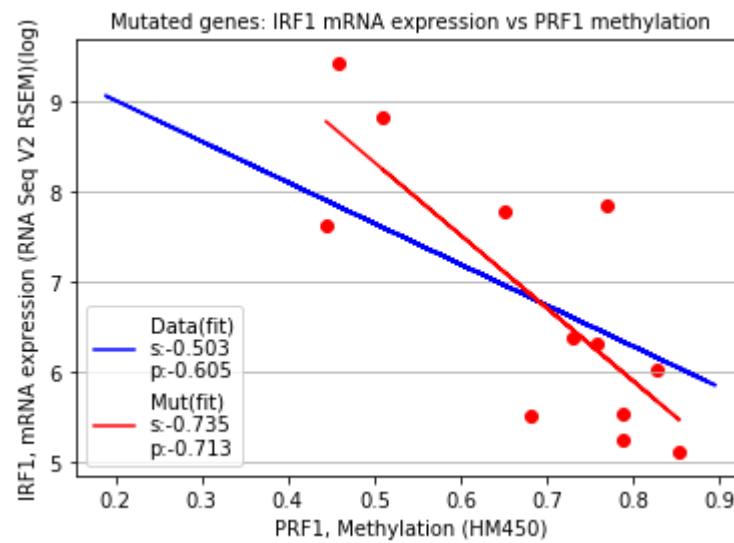
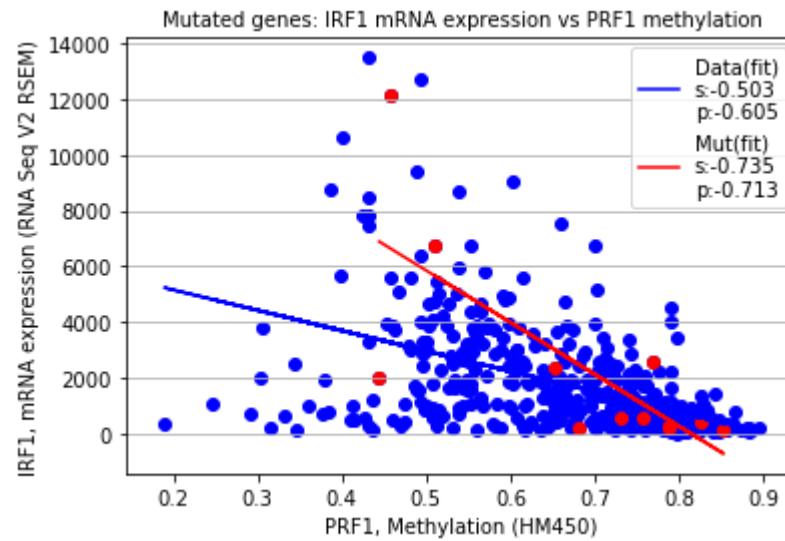
```
In [242]: mutReadPlot('./plots-if1-hlag.txt', 'Mutated genes: IRF1 mRNA expression vs HLA-G methylation')
```



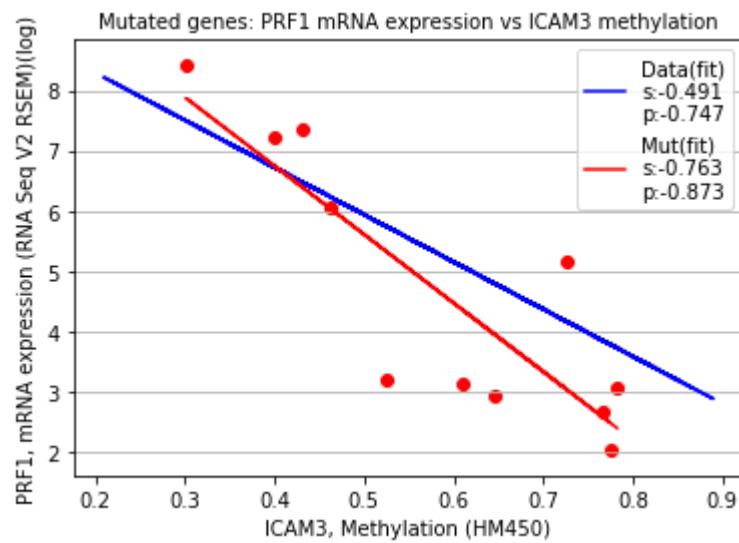
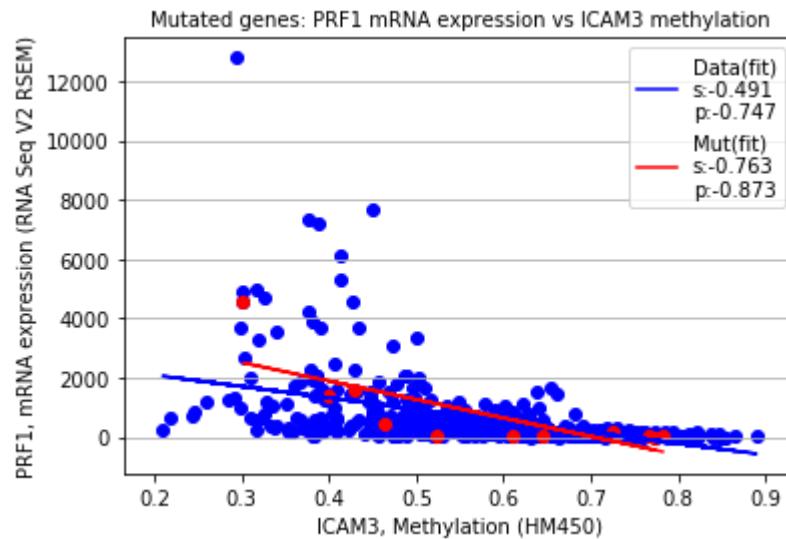
```
In [243]: mutReadPlot('./plots-ifr1-icam3.txt', 'Mutated genes: IRF1 mRNA expression vs ICAM3 methylation')
```



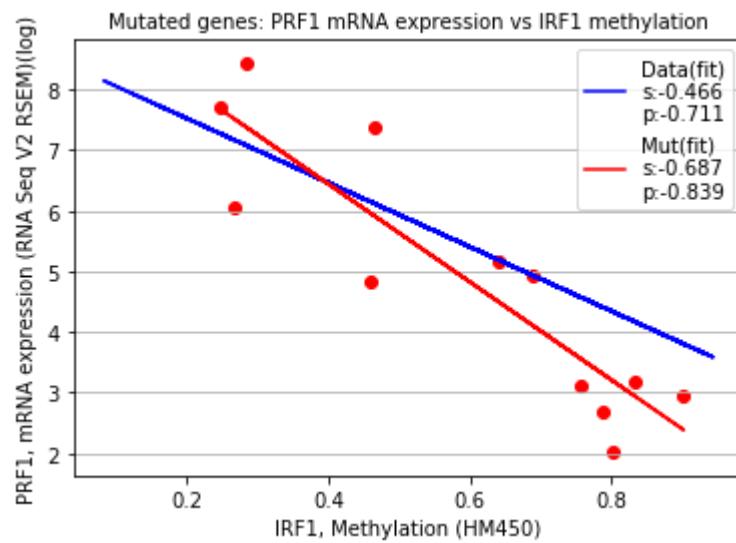
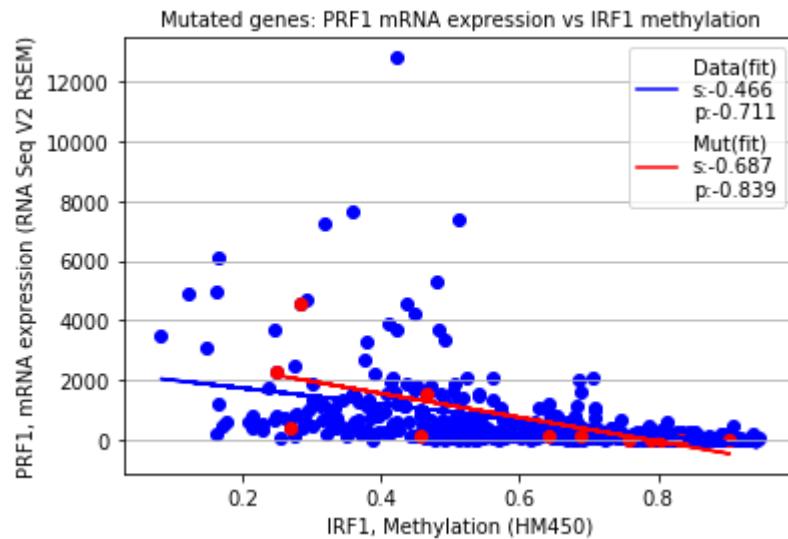
```
In [244]: mutReadPlot('./plots-ifng-prf1.txt', 'Mutated genes: IRF1 mRNA expression vs PRF1 methylation')
```



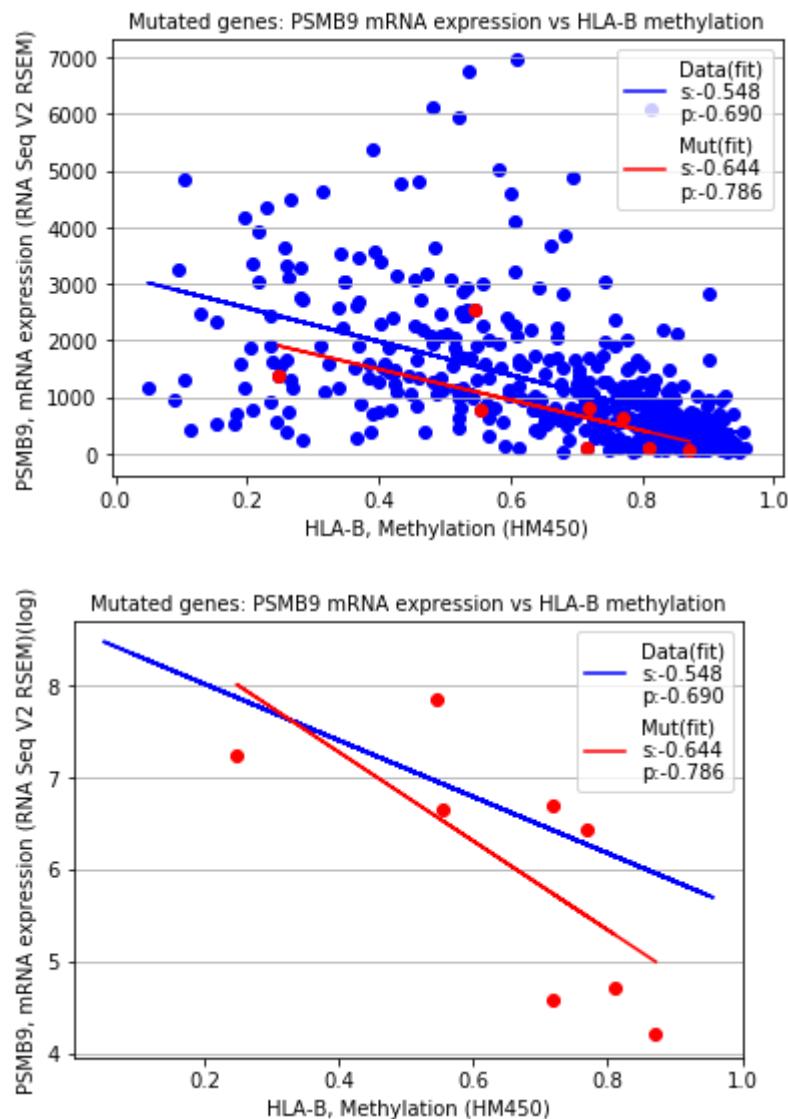
```
In [245]: mutReadPlot('./plots-prf1-icam3.txt', 'Mutated genes: PRF1 mRNA expression vs ICAM3 methylation')
```



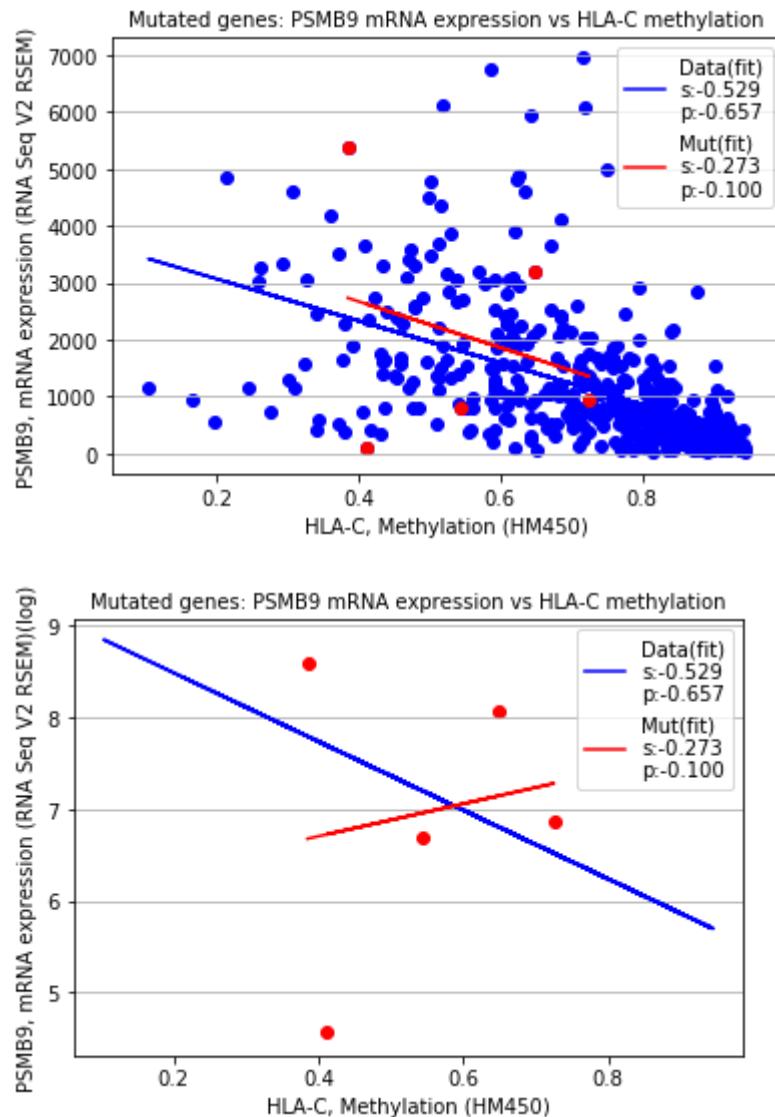
```
In [246]: mutReadPlot('./plots-prf1-irf1.txt', 'Mutated genes: PRF1 mRNA expression vs I  
RF1 methylation')
```



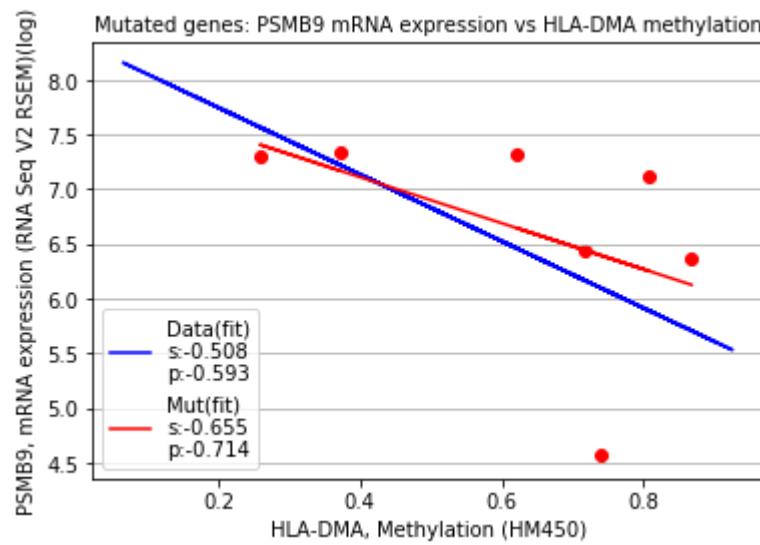
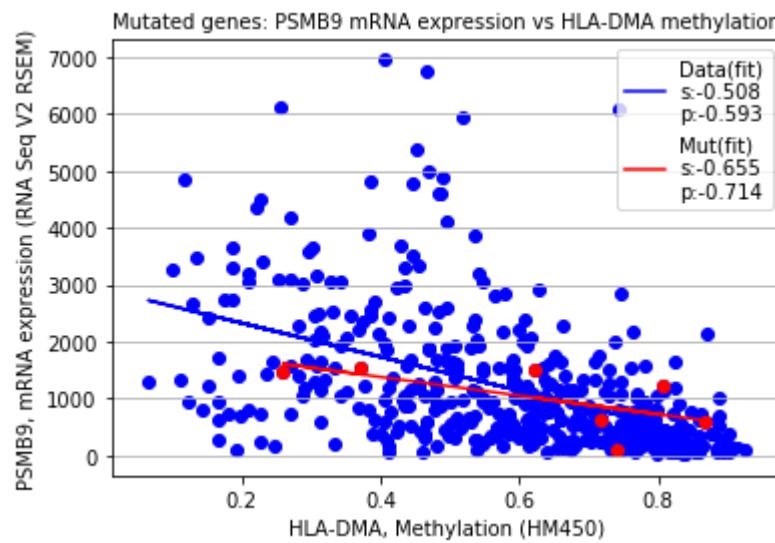
```
In [247]: mutReadPlot('./plots-psmb9-hlab.txt', 'Mutated genes: PSMB9 mRNA expression vs HLA-B methylation')
```



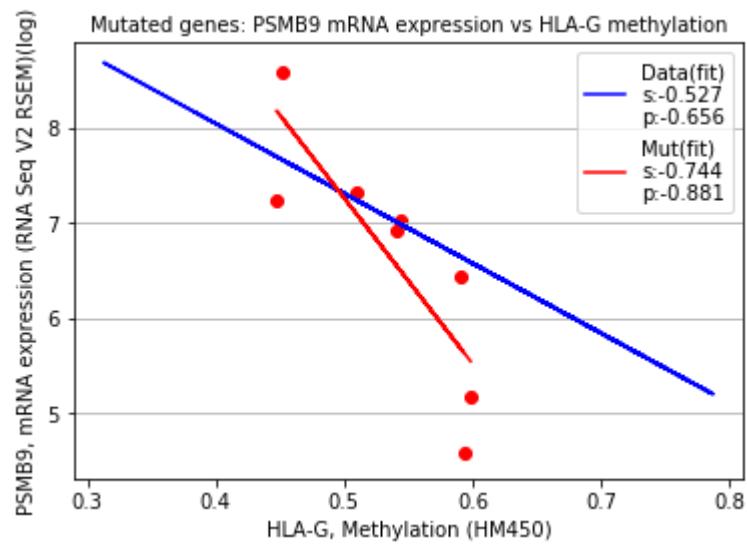
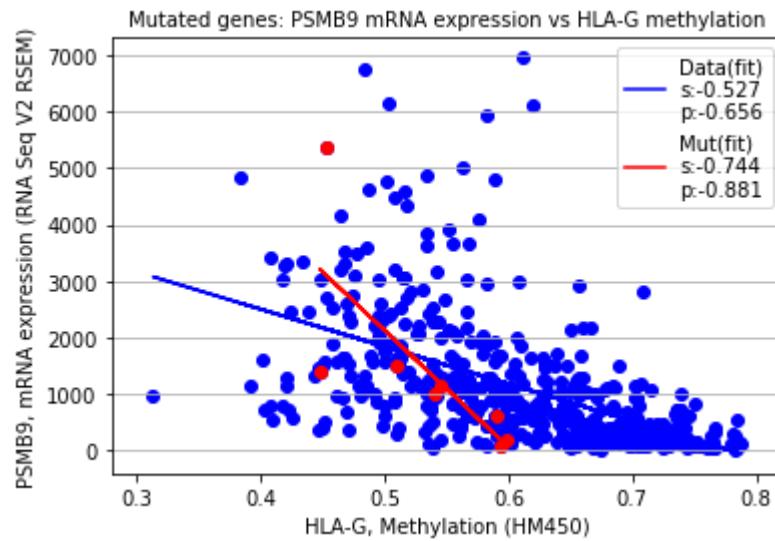
```
In [248]: mutReadPlot('./plots-psmb9-hlac.txt', 'Mutated genes: PSMB9 mRNA expression vs HLA-C methylation')
```



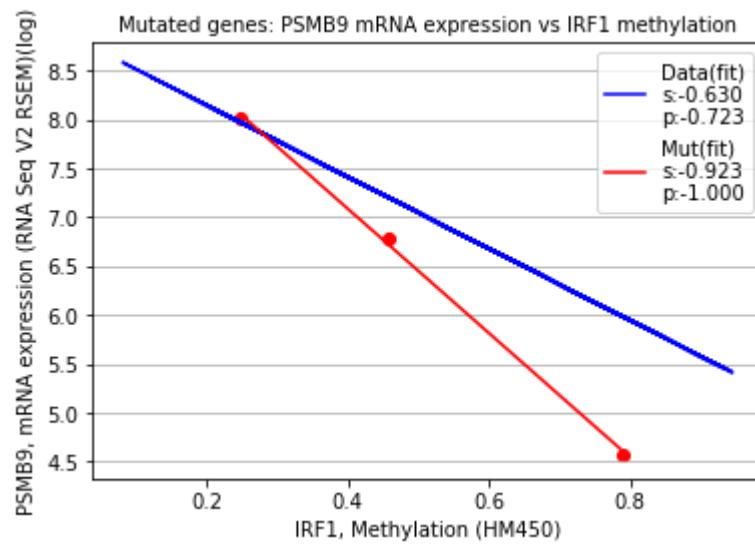
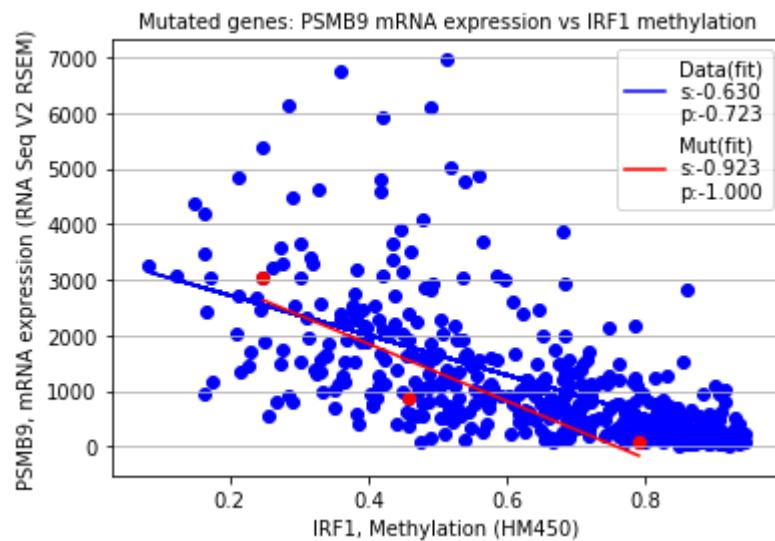
```
In [249]: mutReadPlot('./plots-psmb9-hladma.txt', 'Mutated genes: PSMB9 mRNA expression vs HLA-DMA methylation')
```



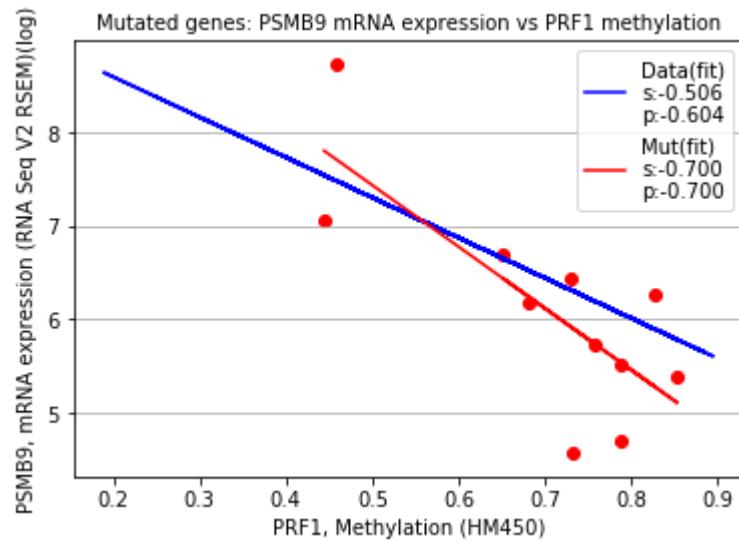
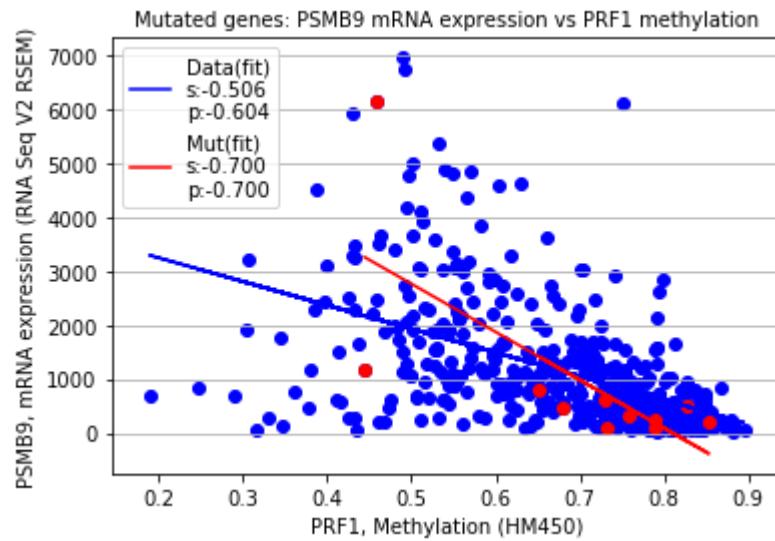
```
In [250]: mutReadPlot('./plots-psmb9-hlag.txt', 'Mutated genes: PSMB9 mRNA expression vs HLA-G methylation')
```



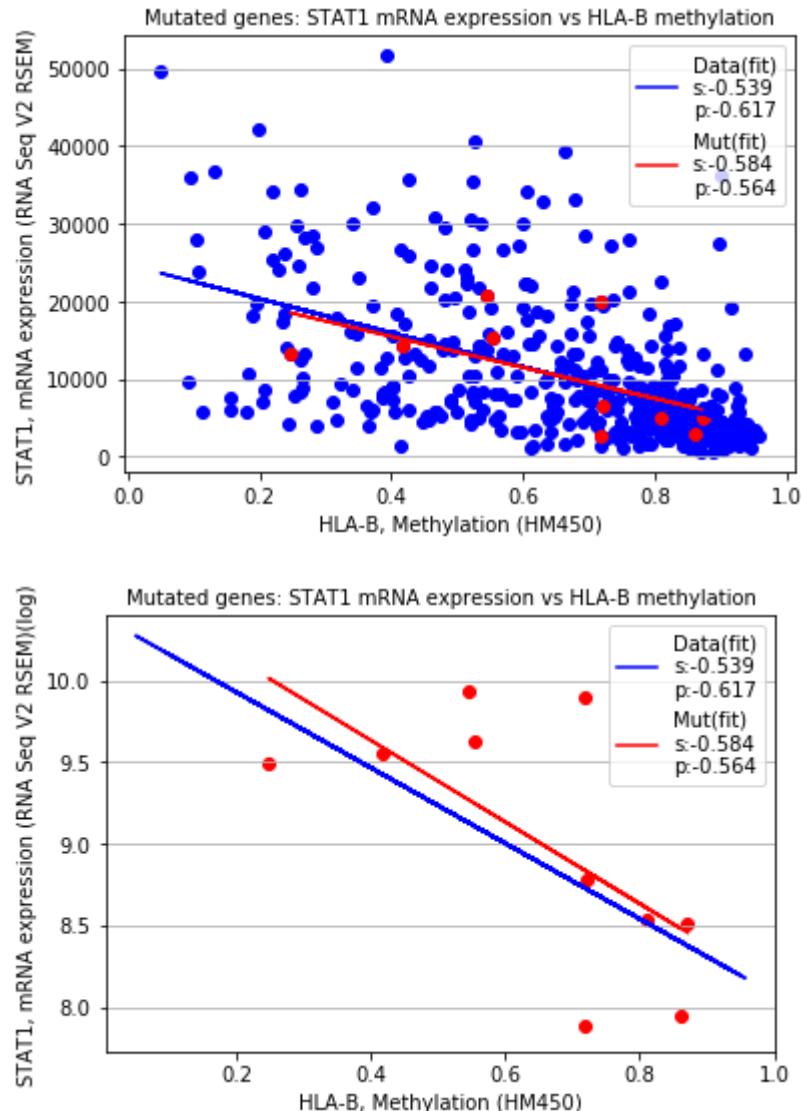
```
In [251]: mutReadPlot('./plots-psmb9-irf1.txt', 'Mutated genes: PSMB9 mRNA expression vs IRF1 methylation')
```



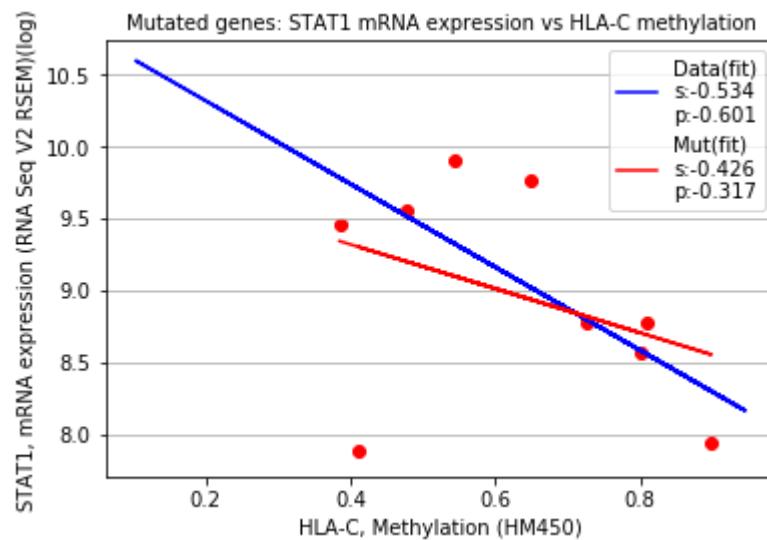
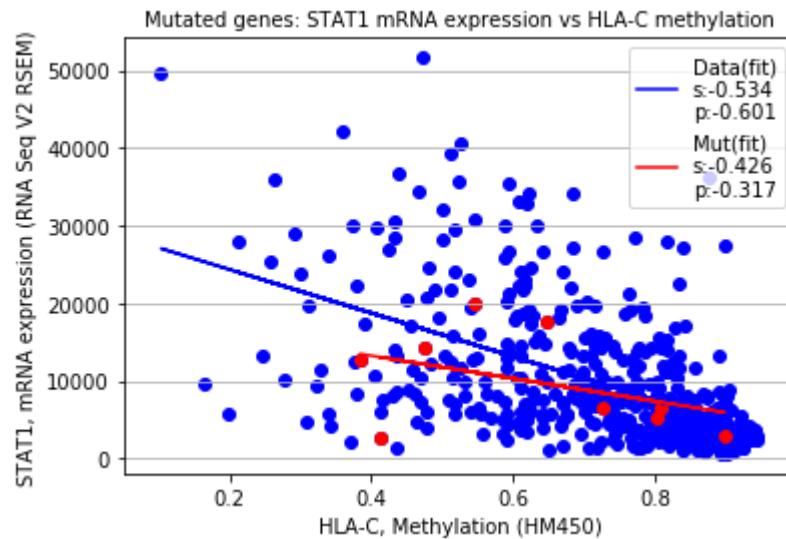
```
In [252]: mutReadPlot('./plots-psmb9-prf1.txt', 'Mutated genes: PSMB9 mRNA expression vs PRF1 methylation')
```



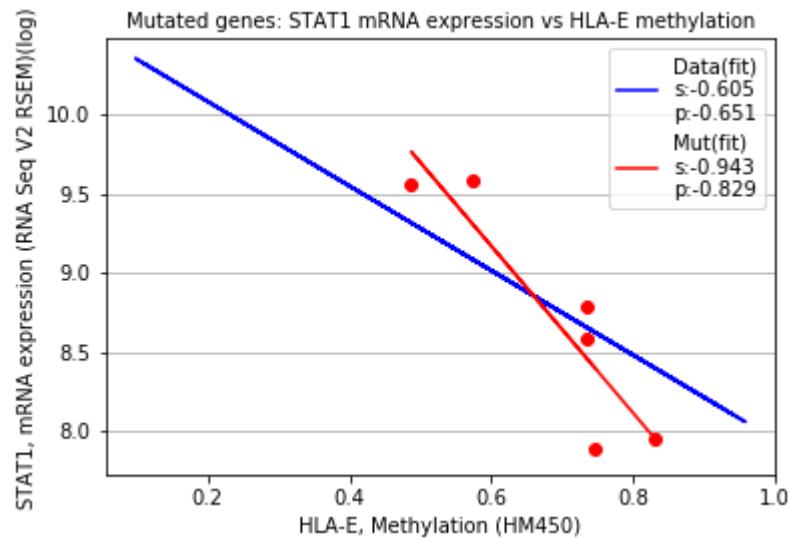
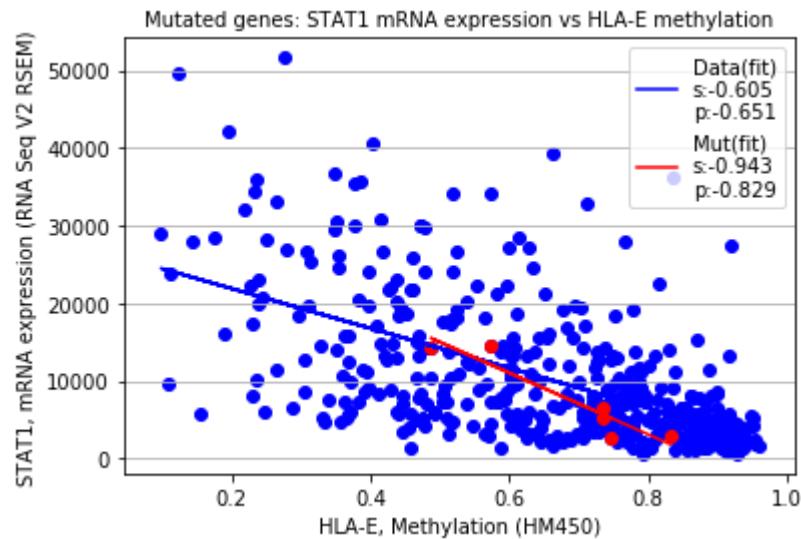
```
In [253]: mutReadPlot('./plots-stat1-hlab.txt', 'Mutated genes: STAT1 mRNA expression vs HLA-B methylation')
```



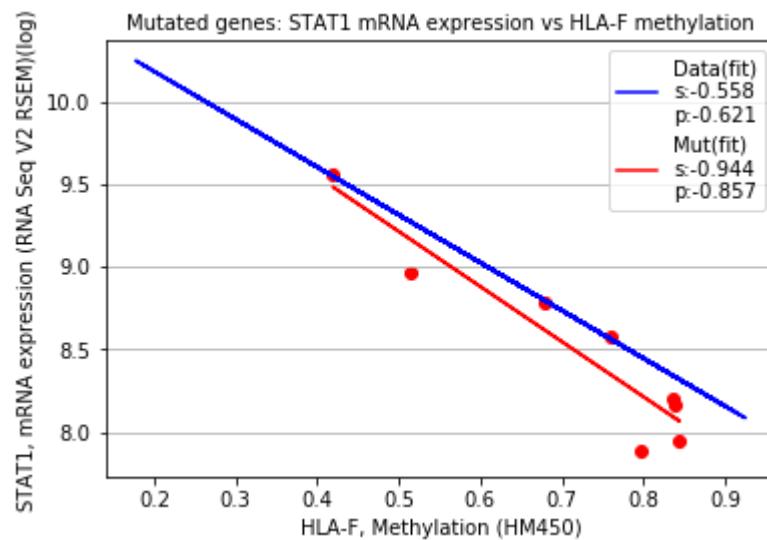
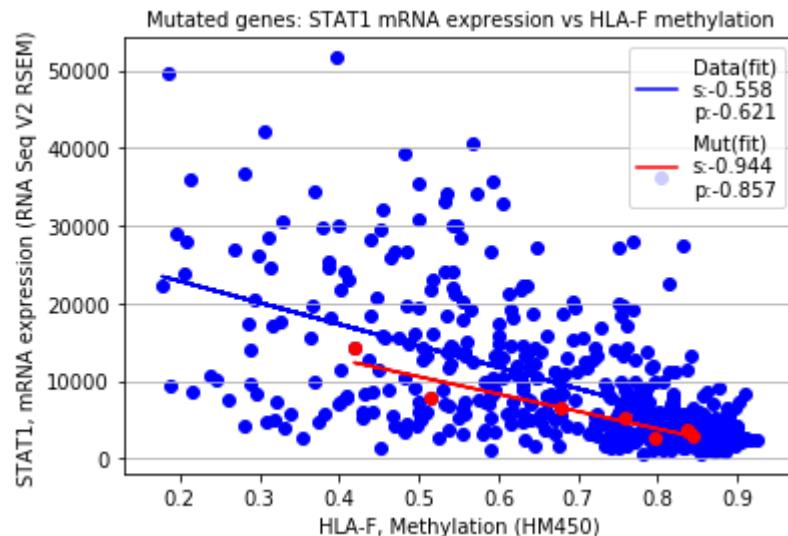
```
In [254]: mutReadPlot('./plots-stat1-hlac.txt', 'Mutated genes: STAT1 mRNA expression vs HLA-C methylation')
```



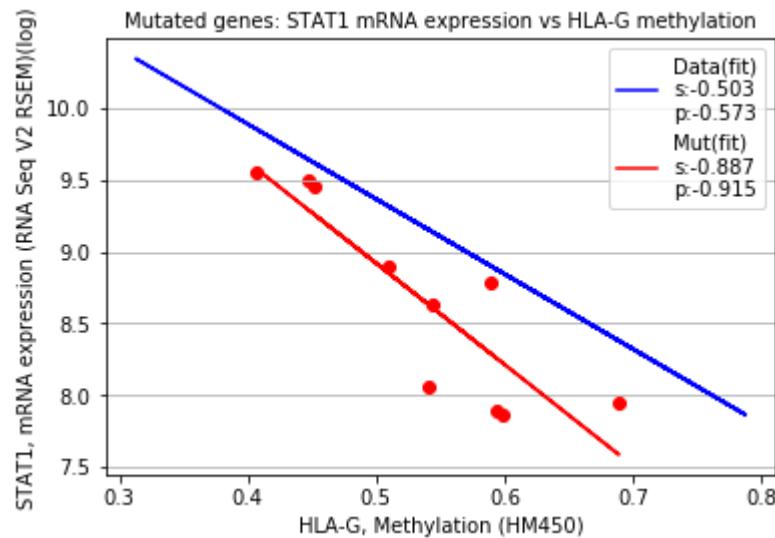
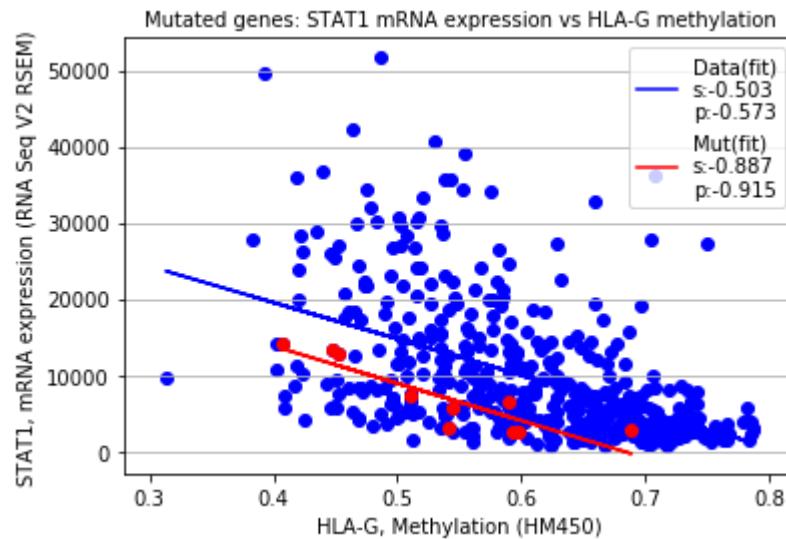
```
In [255]: mutReadPlot('./plots-stat1-hlae.txt', 'Mutated genes: STAT1 mRNA expression vs HLA-E methylation')
```



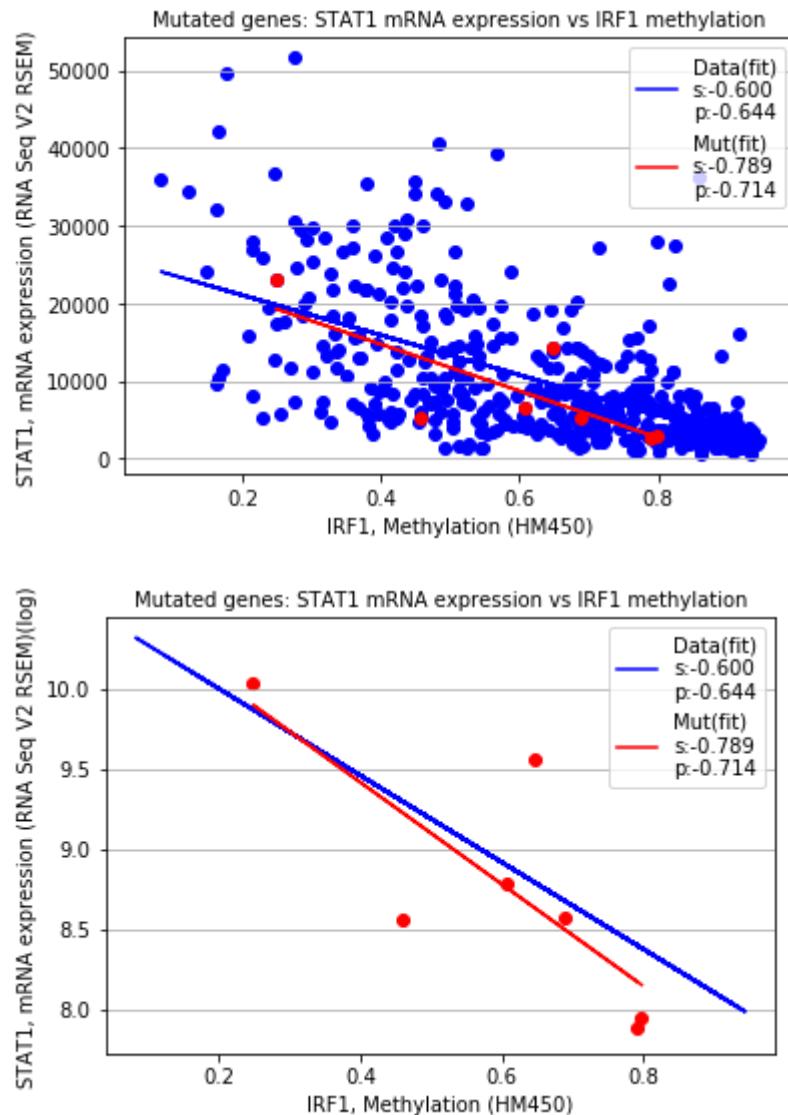
```
In [256]: mutReadPlot('./plots-stat1-hlaf.txt', 'Mutated genes: STAT1 mRNA expression vs HLA-F methylation')
```



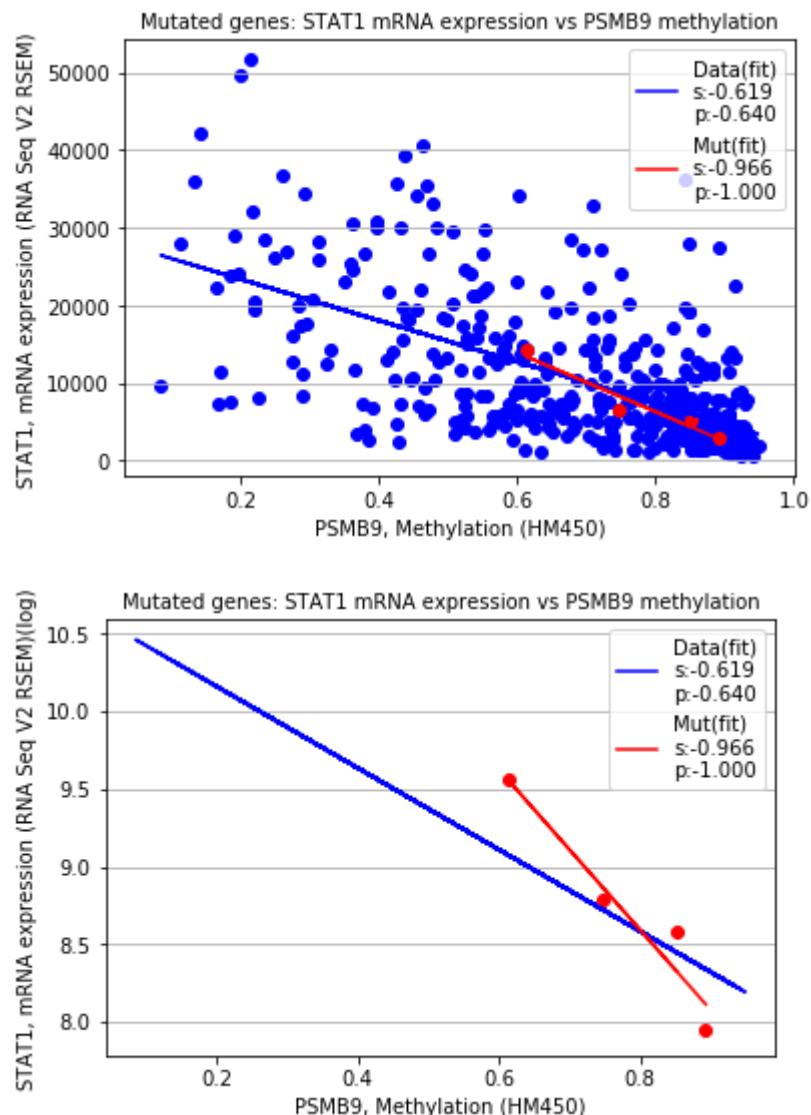
```
In [257]: mutReadPlot('./plots-stat1-hlag.txt', 'Mutated genes: STAT1 mRNA expression vs HLA-G methylation')
```



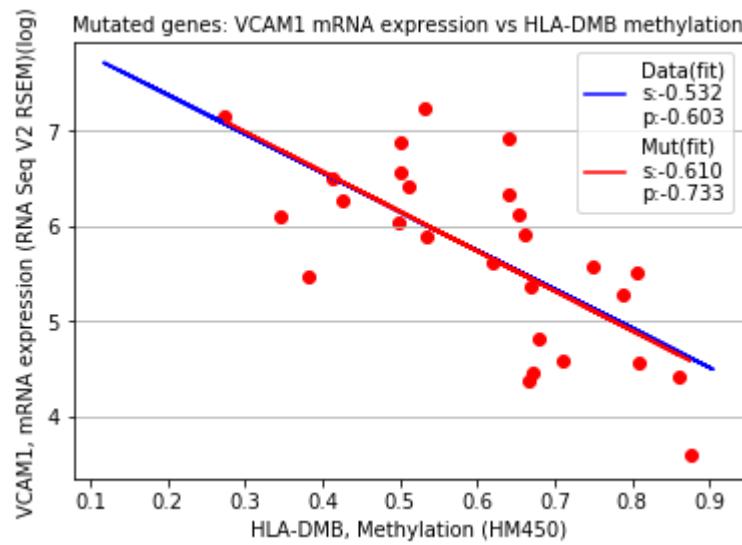
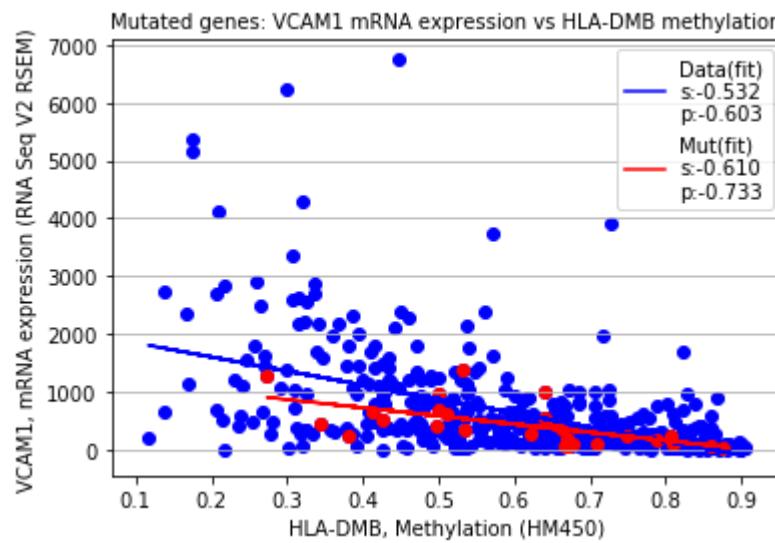
```
In [258]: mutReadPlot('./plots-stat1-irf1.txt', 'Mutated genes: STAT1 mRNA expression vs IRF1 methylation')
```



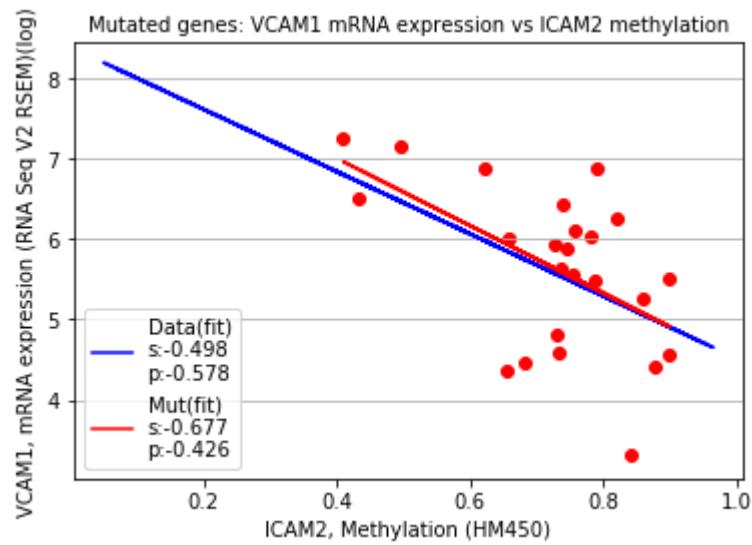
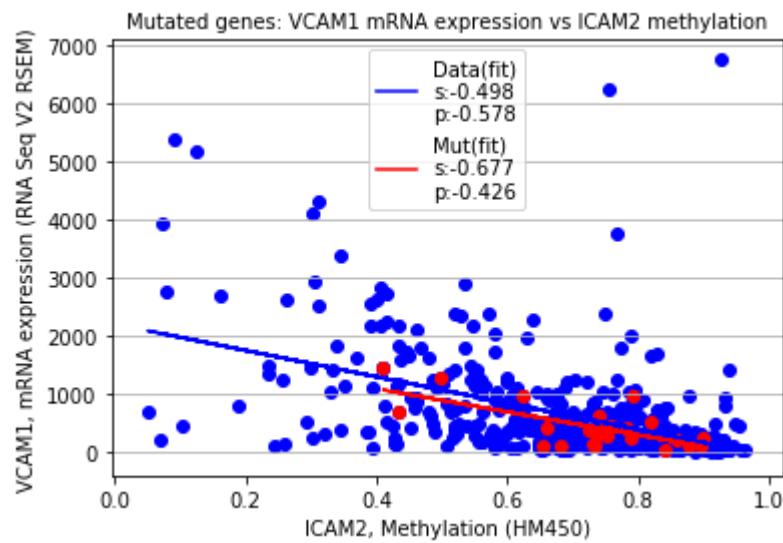
```
In [259]: mutReadPlot('./plots-stat1-psmb9.txt', 'Mutated genes: STAT1 mRNA expression v  
s PSMB9 methylation')
```



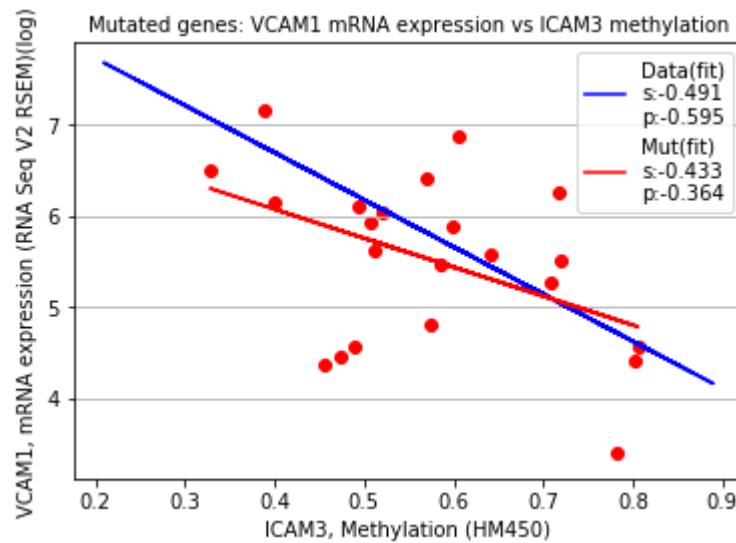
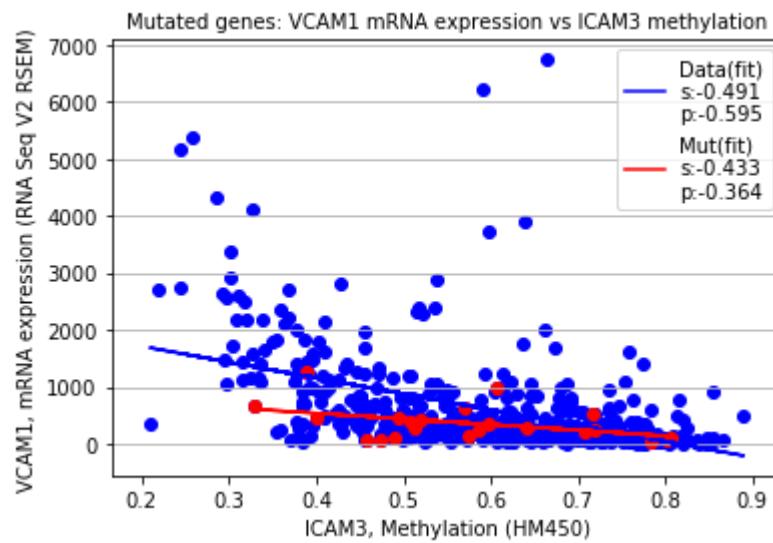
```
In [260]: mutReadPlot('./plots-vcam1-hladmb.txt', 'Mutated genes: VCAM1 mRNA expression vs HLA-DMB methylation')
```



```
In [261]: mutReadPlot('./plots-vcam1-icam2.txt', 'Mutated genes: VCAM1 mRNA expression v  
s ICAM2 methylation')
```



```
In [262]: mutReadPlot('./plots-vcam1-icam3.txt', 'Mutated genes: VCAM1 mRNA expression v  
s ICAM3 methylation')
```



```
In [ ]:
```