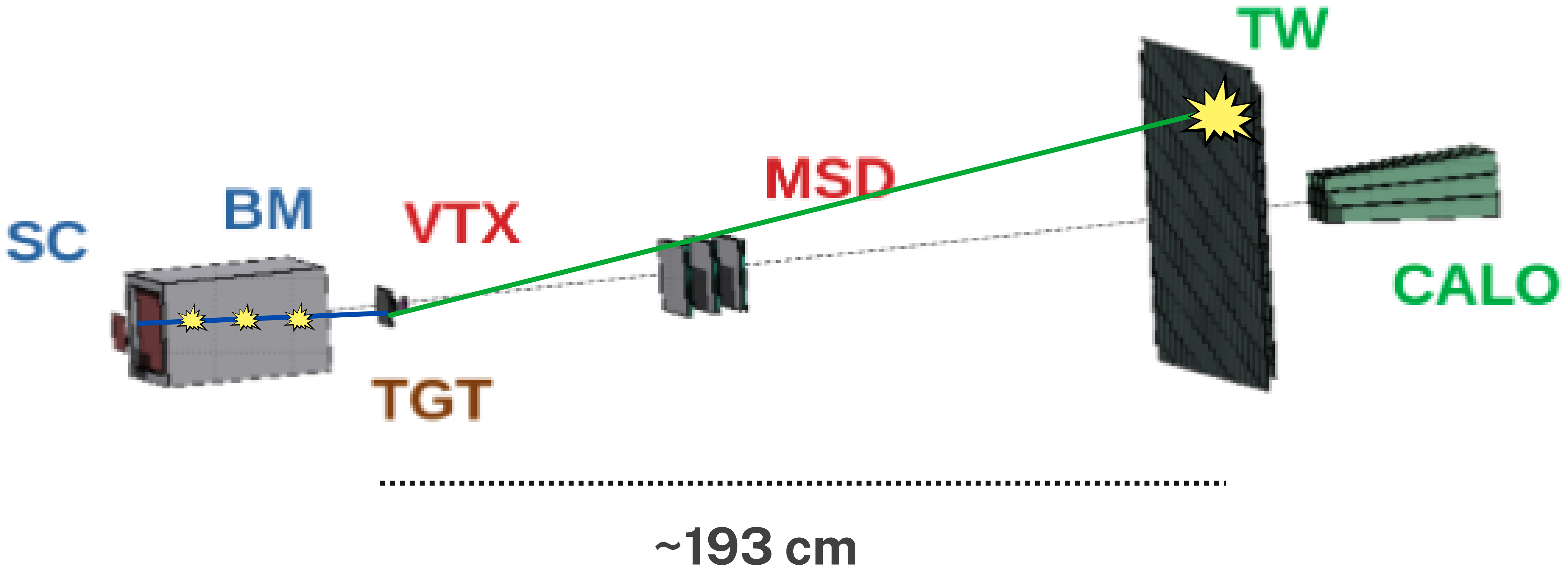
GSI2021 analysis without tracking

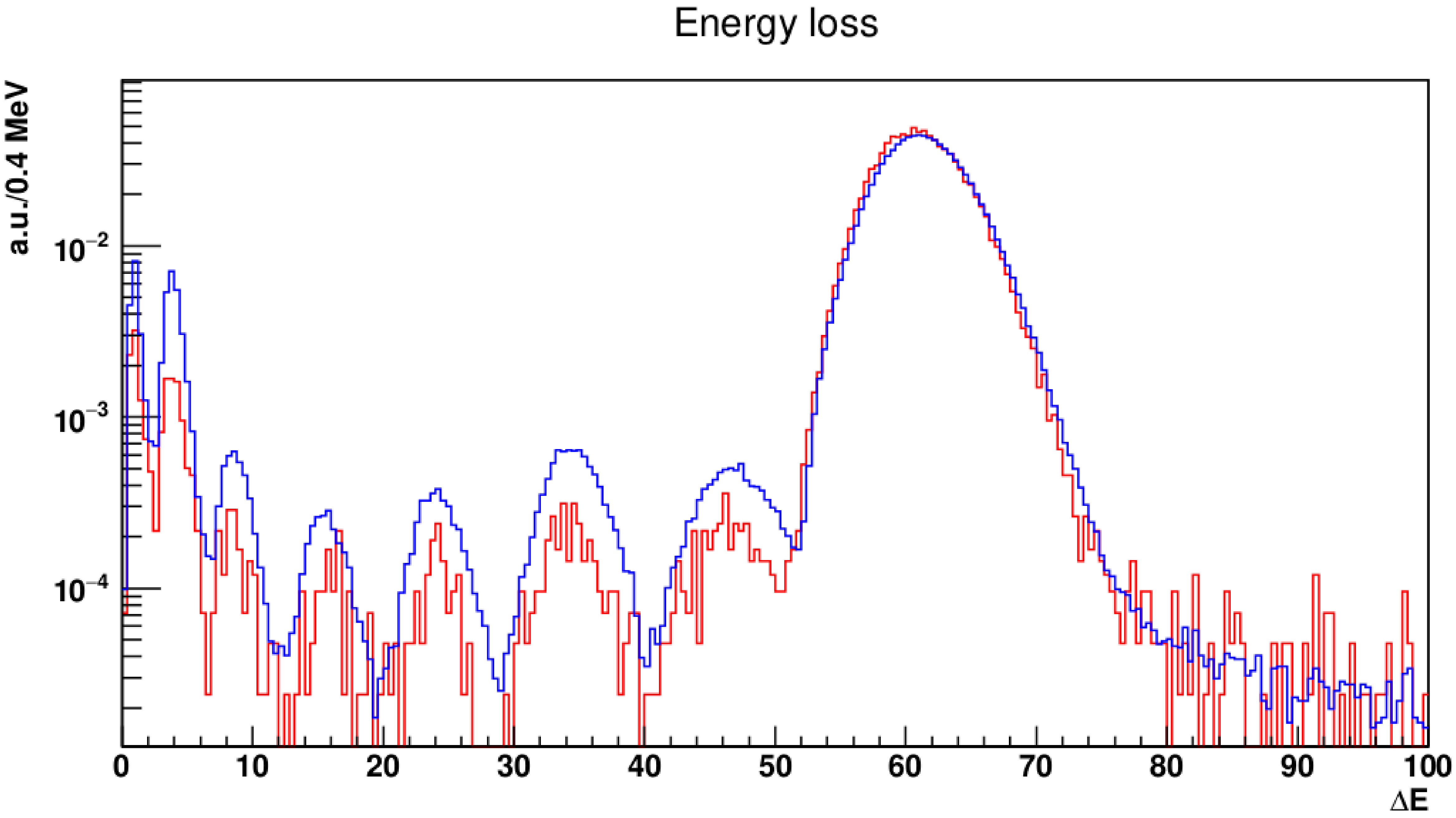
Riccardo Ridolfi

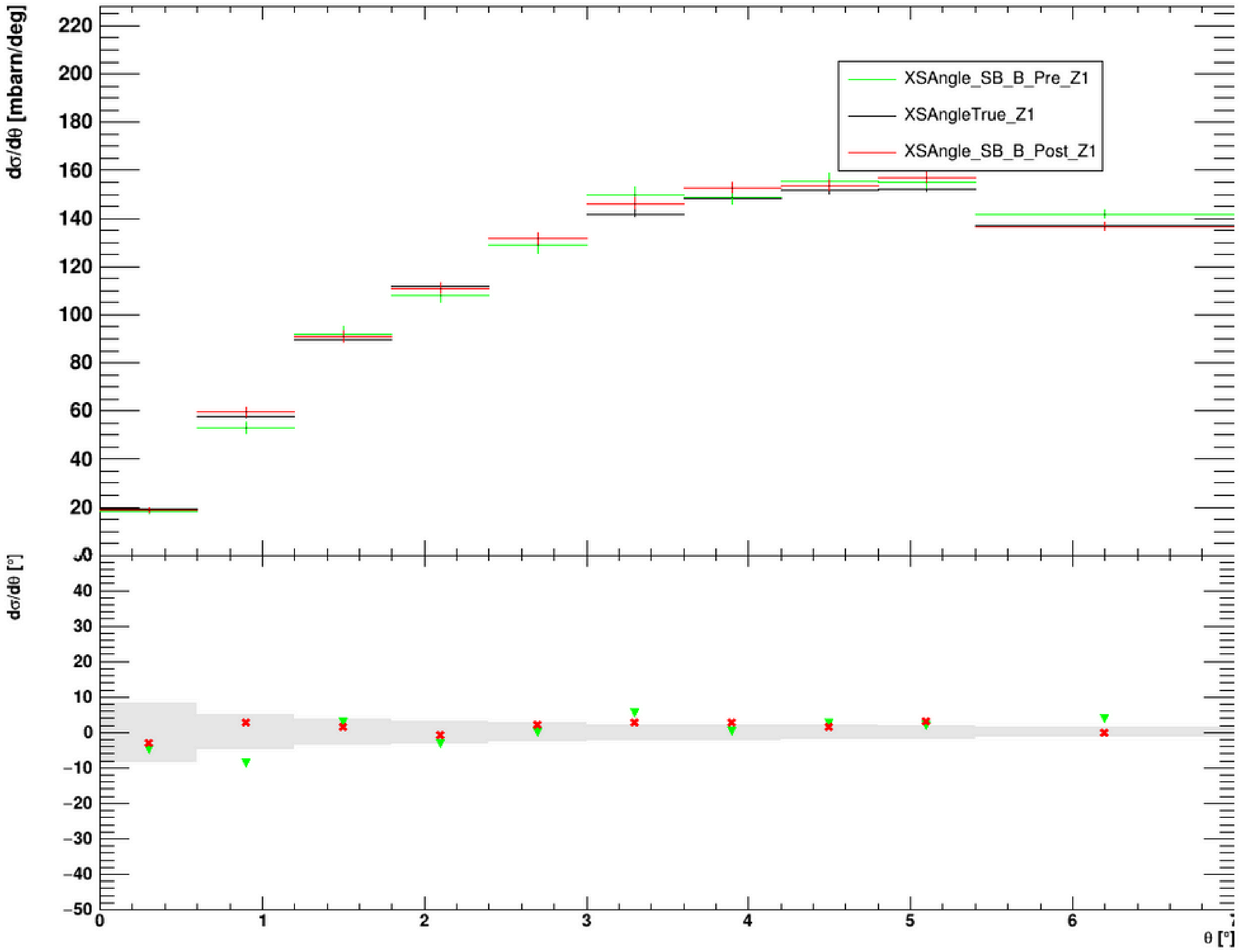
5 June 2024

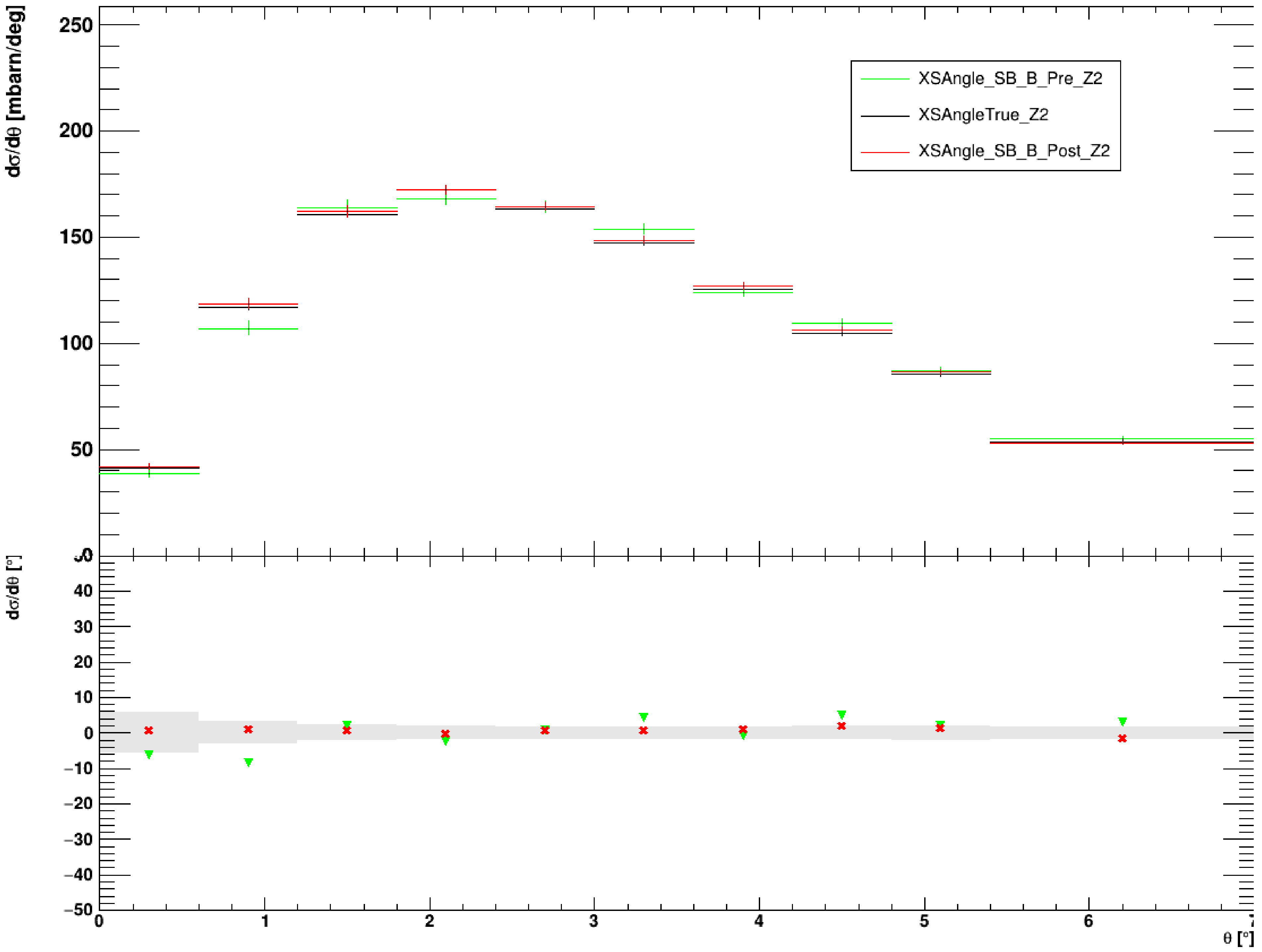
Angle measurement

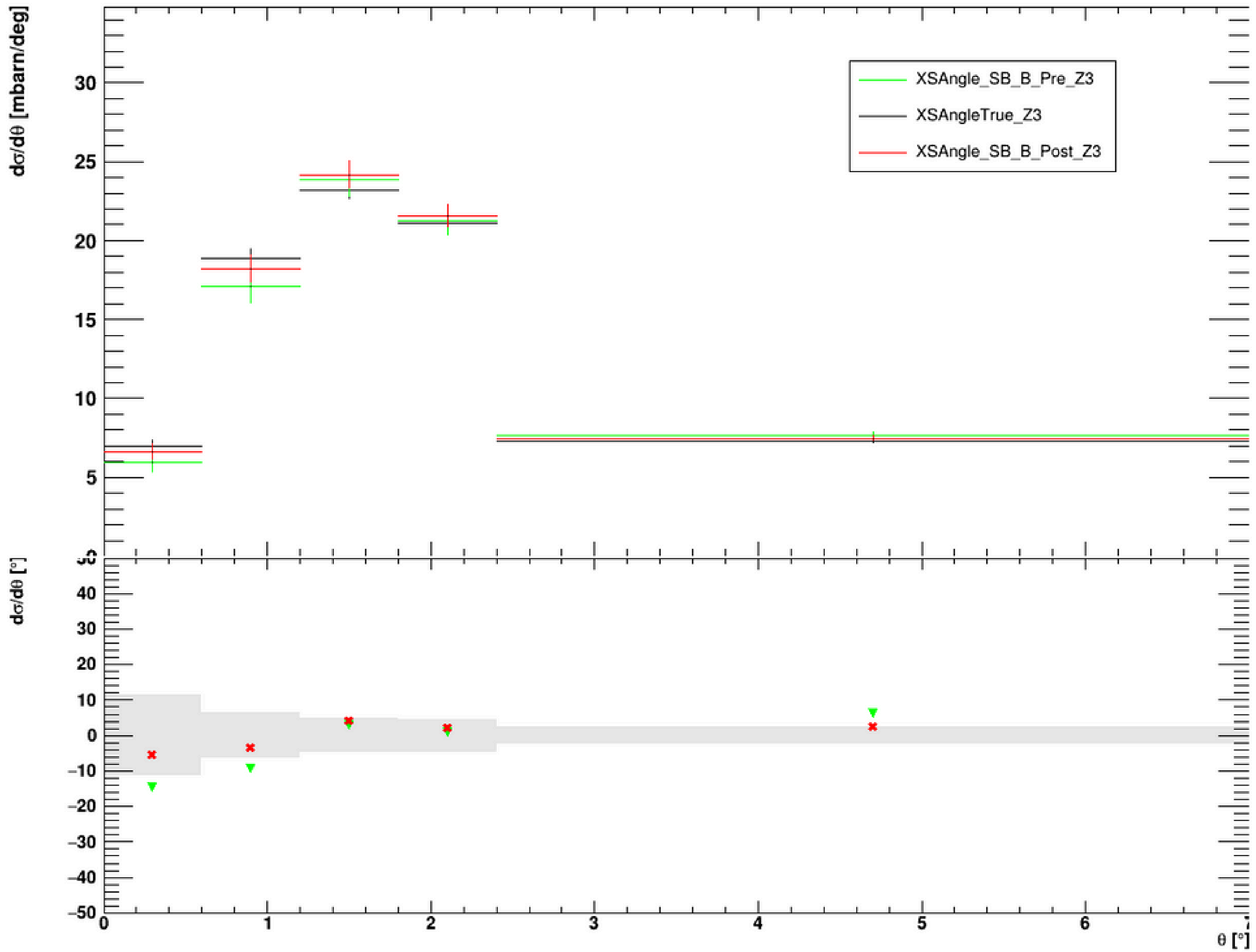


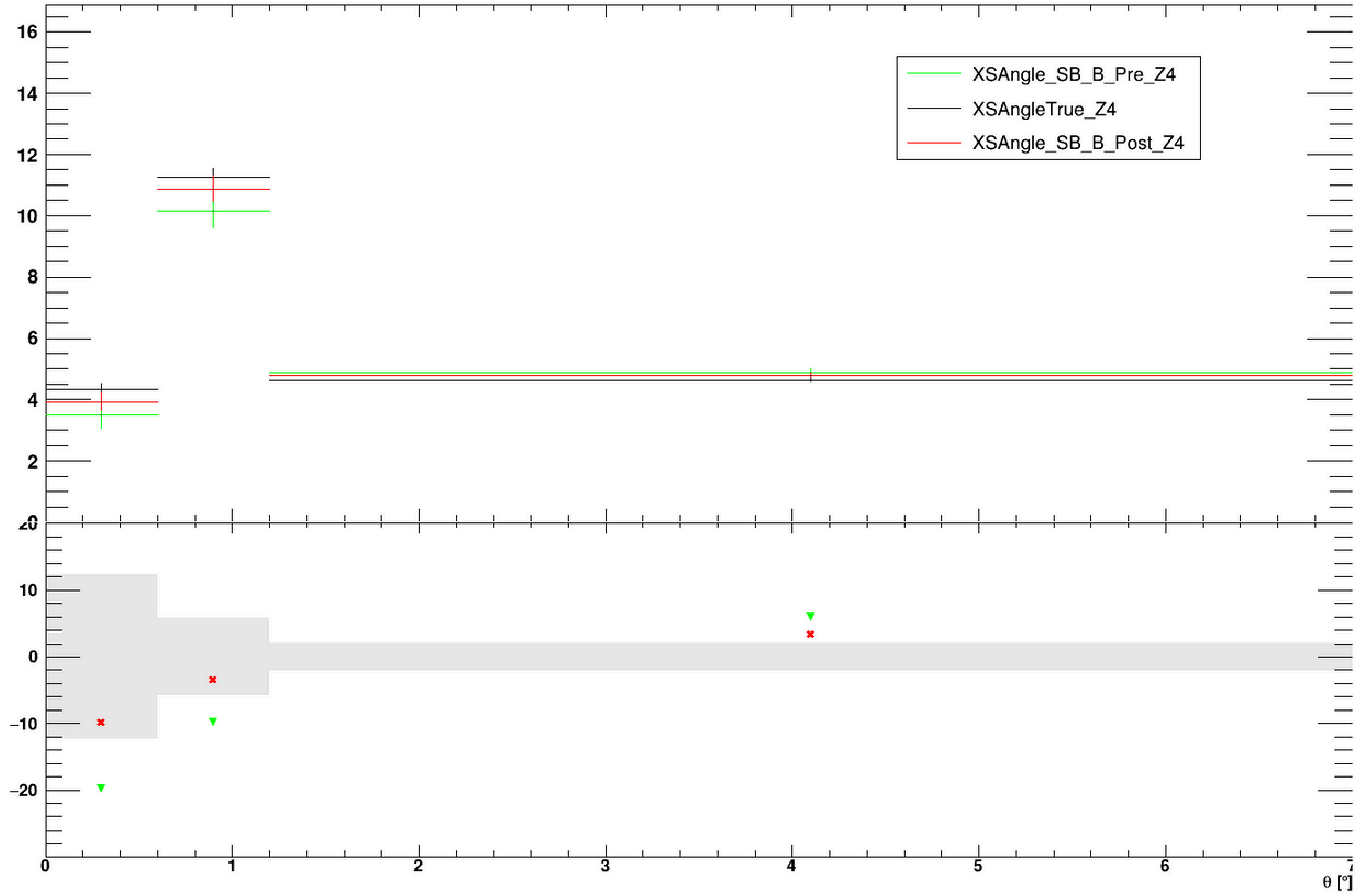
Why background subtraction?

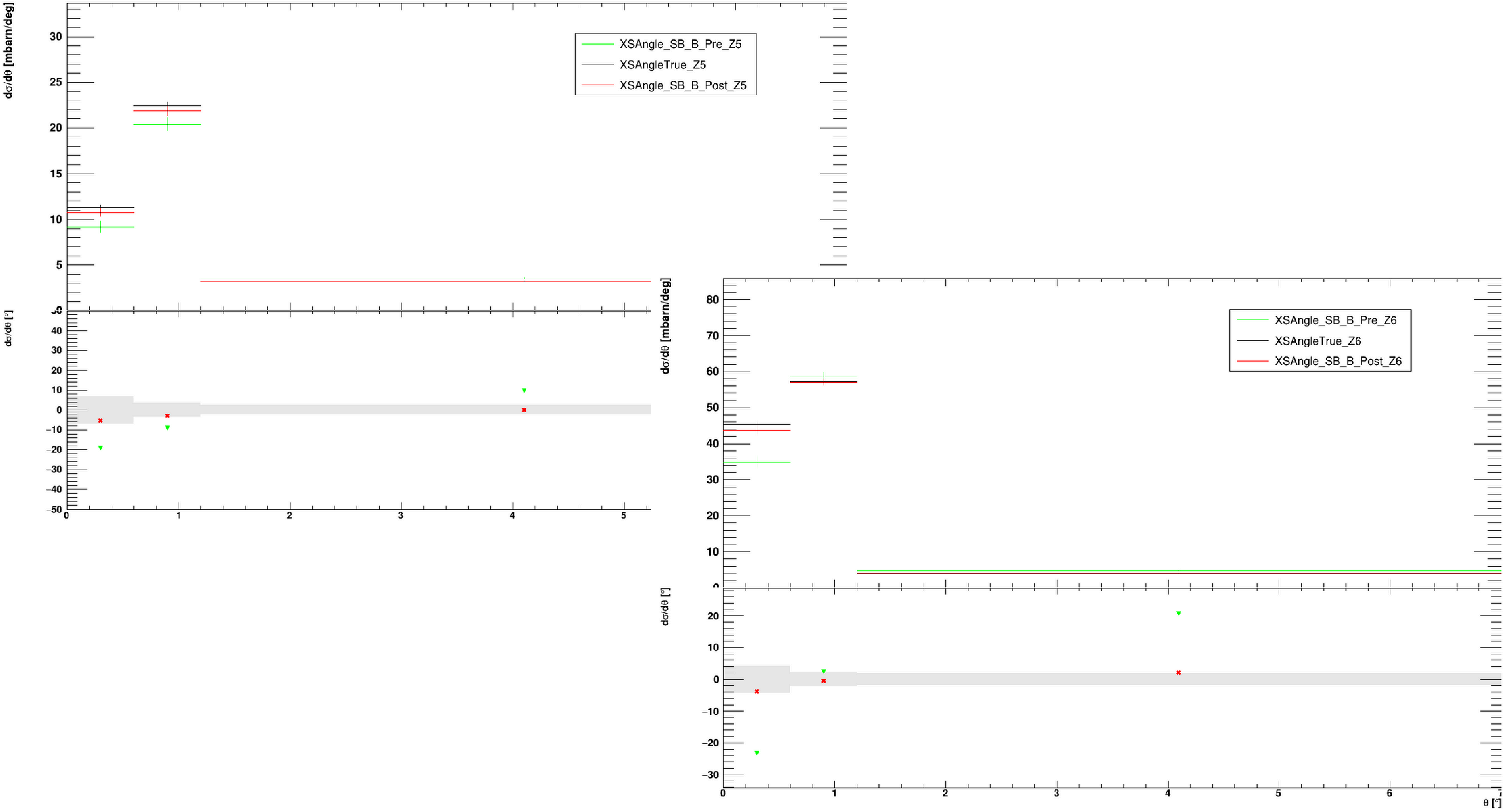


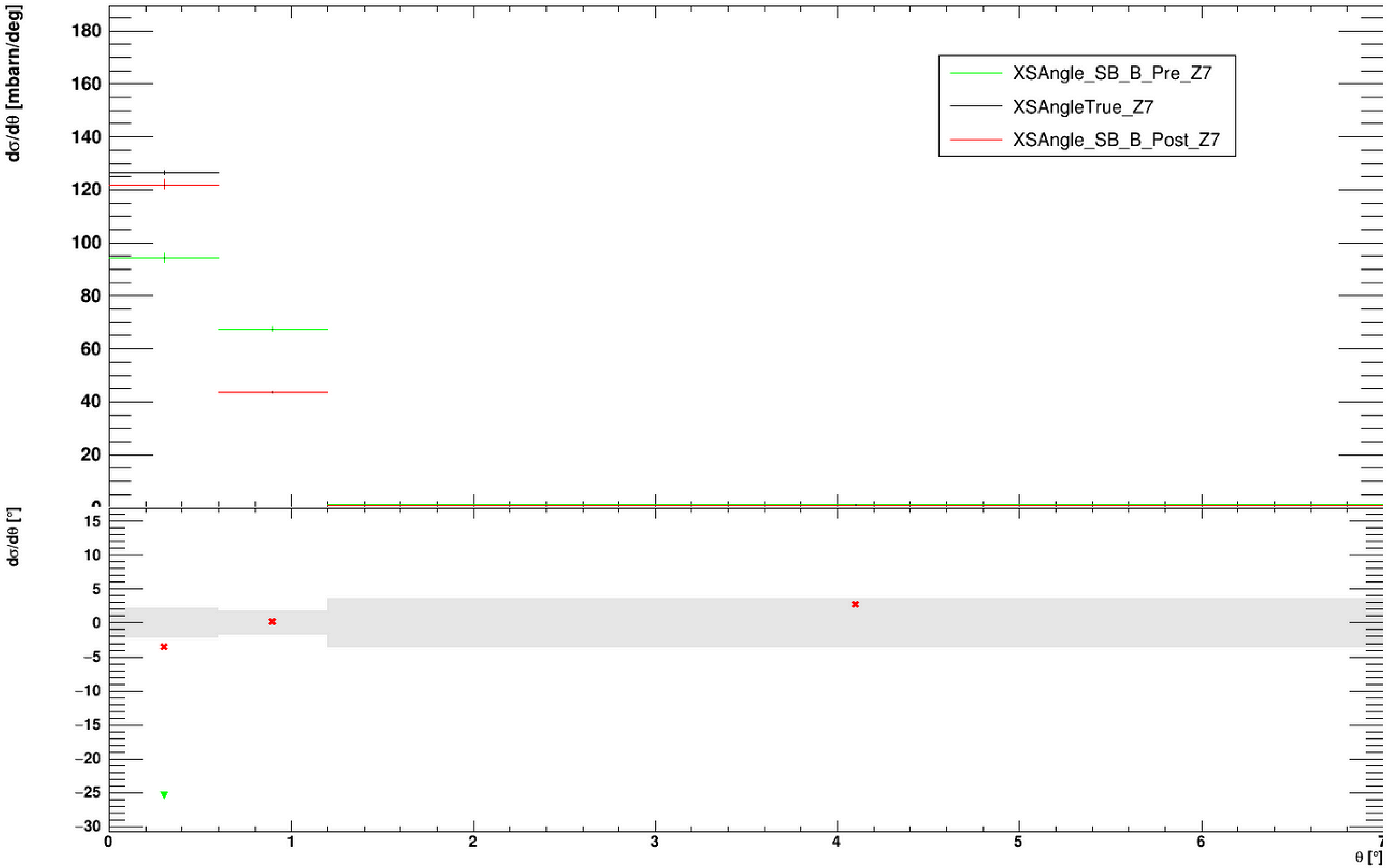

XSAngle_SB_B_Pre_Z1
XSAngleTrue_Z1
XSAngle_SB_B_Post_Z1
dσ/dθ [mbarn/deg]
220
200
180
160
140
120
100
80
60
40
20
0
dσ/dθ [°]
40
30
20
10
0
−10
−20
−30
−40
−50
0
1
2
3
4
5
6
θ [°]

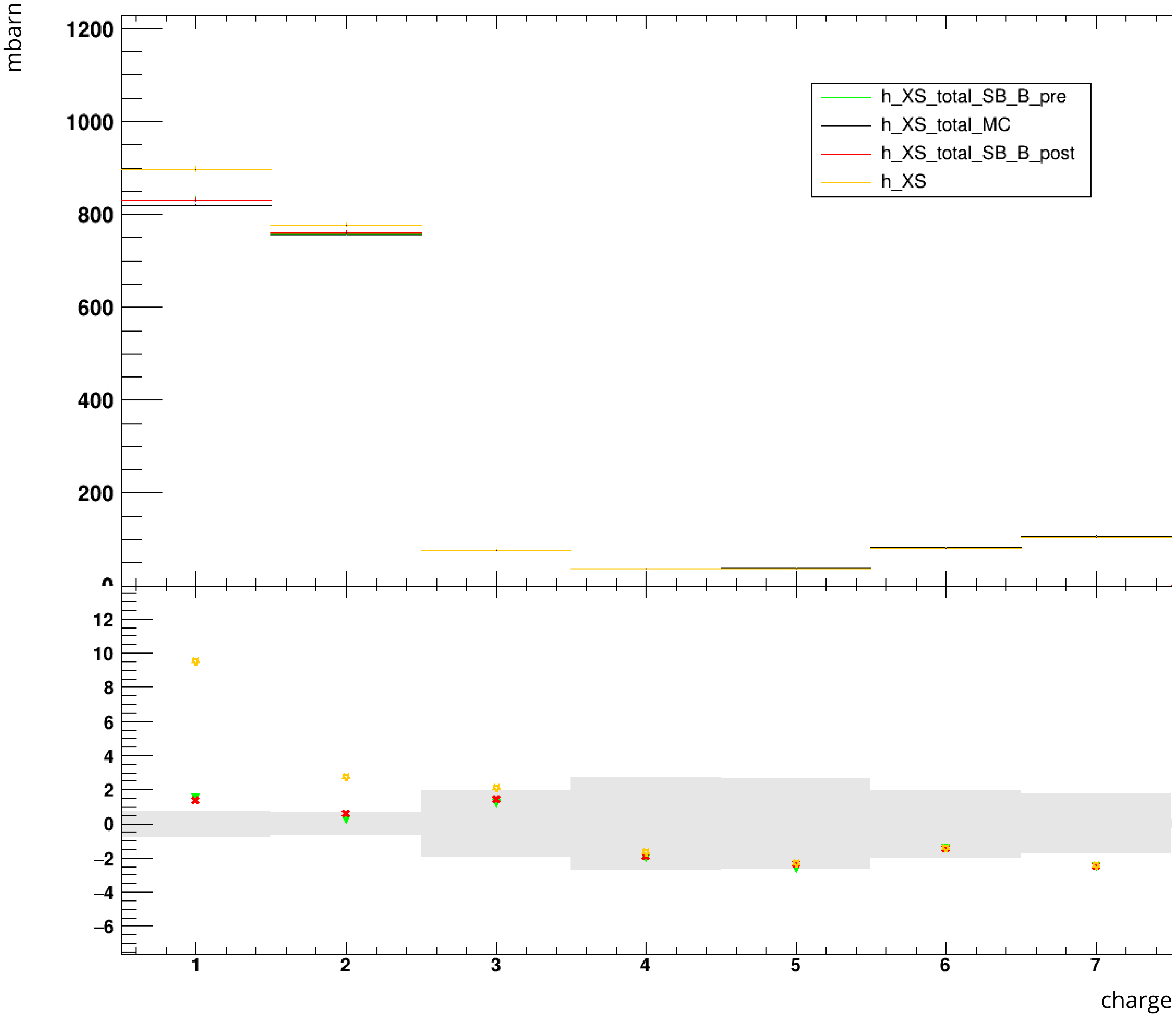

XSAngle_SB_B_Pre_Z2
XSAngleTrue_Z2
XSAngle_SB_B_Post_Z2
dσ/dθ [mbarn/deg]
250
200
150
100
50
0
dσ/dθ [°]
40
30
20
10
0
−10
−20
−30
−40
−50
0
1
2
3
4
5
6
θ [°]


XSAngle_SB_B_Pre_Z3
XSAngleTrue_Z3
XSAngle_SB_B_Post_Z3
dσ/dθ [mbarn/deg]
30
25
20
15
10
5
dσ/dθ [°]
40
30
20
10
0
−10
−20
−30
−40
−50
0
1
2
3
4
5
6
θ [°]


XSAngle_SB_B_Pre_Z4
XSAngleTrue_Z4
XSAngle_SB_B_Post_Z4
16
14
12
10
8
6
4
2
10
0
−10
−20
0
1
2
3
4
5
6
θ [°]


dσ/dθ [mbarn/deg]
XSAngle_SB_B_Pre_Z5
XSAngleTrue_Z5
XSAngle_SB_B_Post_Z5
30
25
20
15
10
5
0
dσ/dθ [°]
40
30
20
10
0
−10
−20
−30
−40
−50
0
1
2
3
4
5
dσ/dθ [mbarn/deg]
XSAngle_SB_B_Pre_Z6
XSAngleTrue_Z6
XSAngle_SB_B_Post_Z6
80
70
60
50
40
30
20
10
0
dσ/dθ [°]
20
10
0
−10
−20
−30
0
1
2
3
4
5
6
7
θ [°]


dσ/dθ [mbarn/deg]
180
160
140
120
100
80
60
40
20
0
XSAngle_SB_B_Pre_Z7
XSAngleTrue_Z7
XSAngle_SB_B_Post_Z7
dσ/dθ [°]
15
10
5
0
−5
−10
−15
−20
−25
−30
0
1
2
3
4
5
6
7
θ [°]

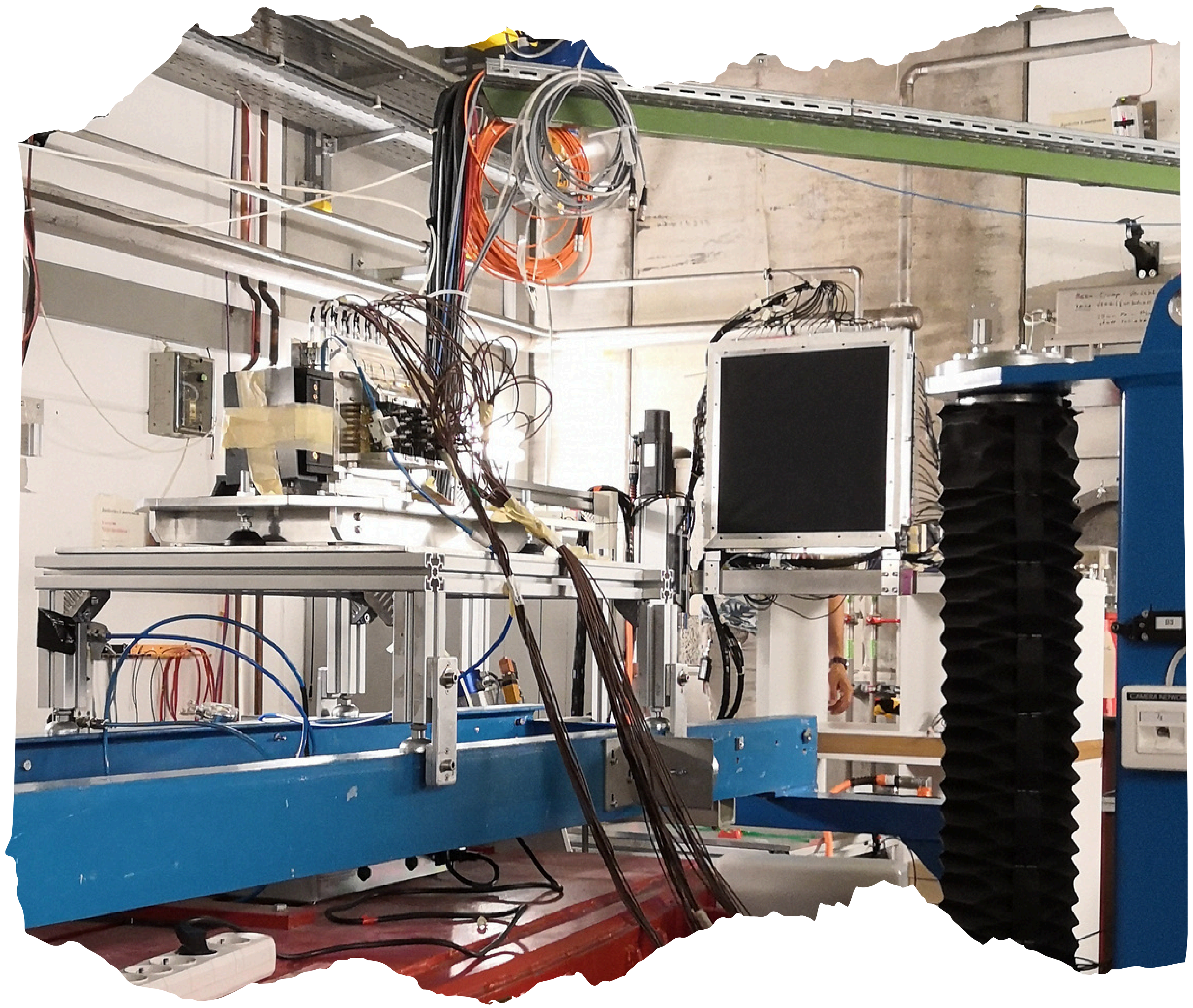

mbarn
1200
1000
800
600
400
200
0
h_XS_total_SB_B_pre
h_XS_total_MC
h_XS_total_SB_B_post
h_XS
12
10
8
6
4
2
0
−2
−4
−6
1
2
3
4
5
6
7
charge

Data analysis

Run on data with the same steps of MC analysis

400 MeV/u ^{16}O beam on 5mm Carbon target

Run	Trigger type	Target	Events
4305	MB	C	162102
4306	MB	C	577096
4307	MB	C	513370
4308	Frag + MB	C	510169
4309	Frag + MB	C	531812
4310	Frag + MB	C	1012099
4313	MB	no	57133



New analysis flow

Evaluate **efficiencies** and **purities**

Repeat for with and w/o target samples

Apply reconstruction cuts (SC, BM)

Normalize yields and **subtract** background

Apply efficiency and **purity** for fragmentation in target

Unfolding

Calculate angular **cross sections**

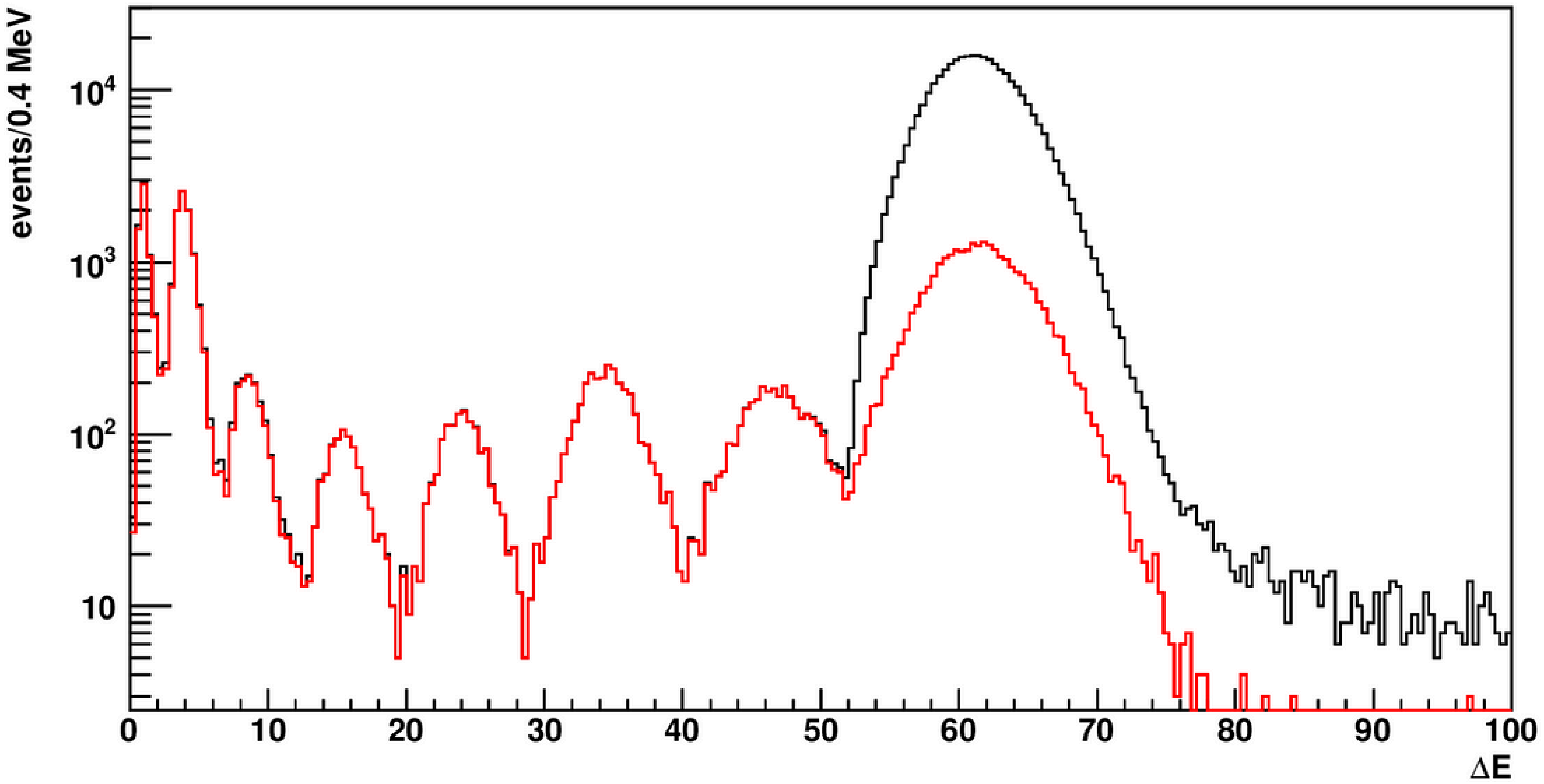
Add systematics uncertainties

Data analysis

In MB runs the number of primaries is the number of events passing selection cuts

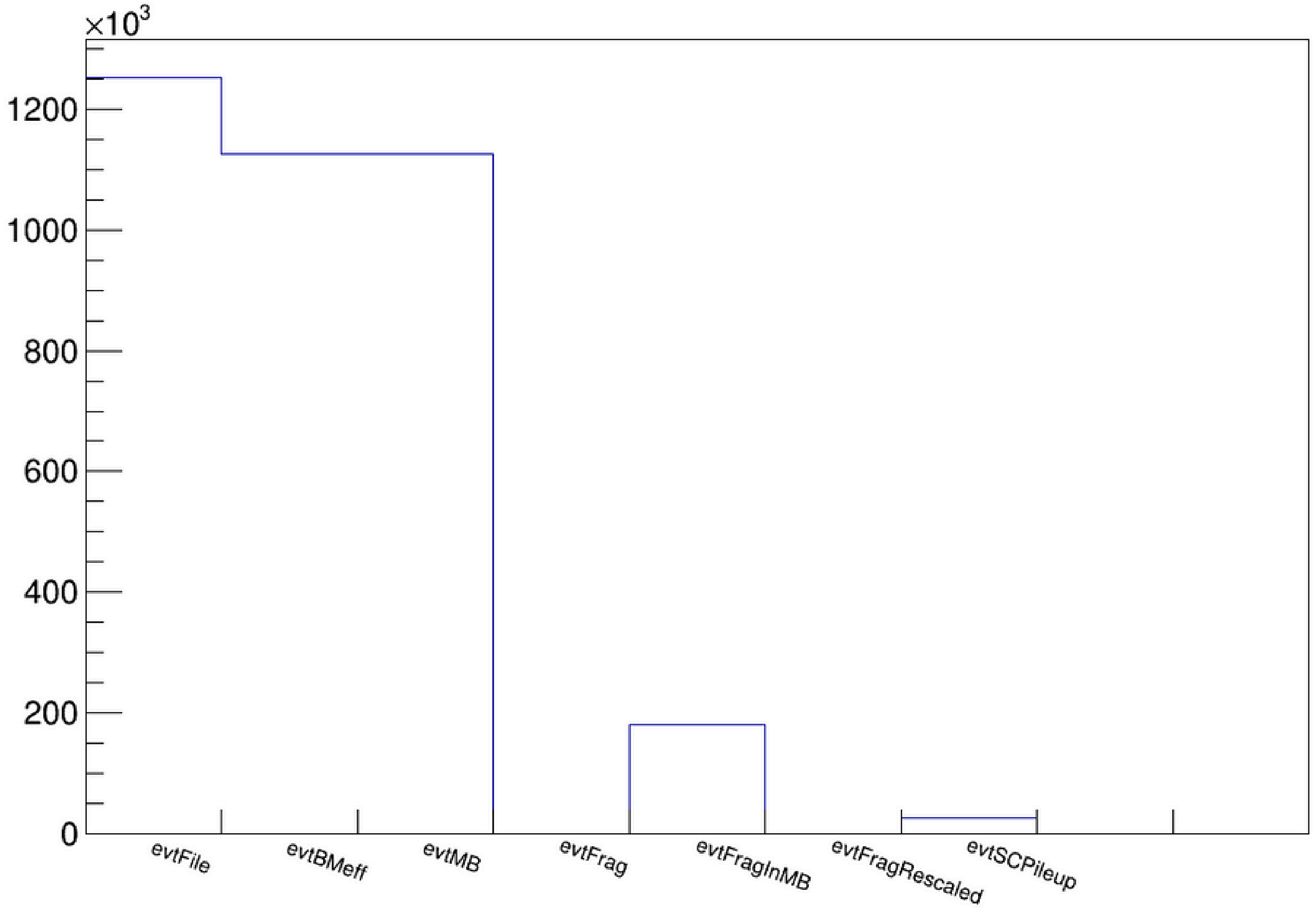
In fragmentation runs the number of primaries has to take into account the **trigger rejection factor**

It can be evaluated from MB runs (fragmentation flag: ON)

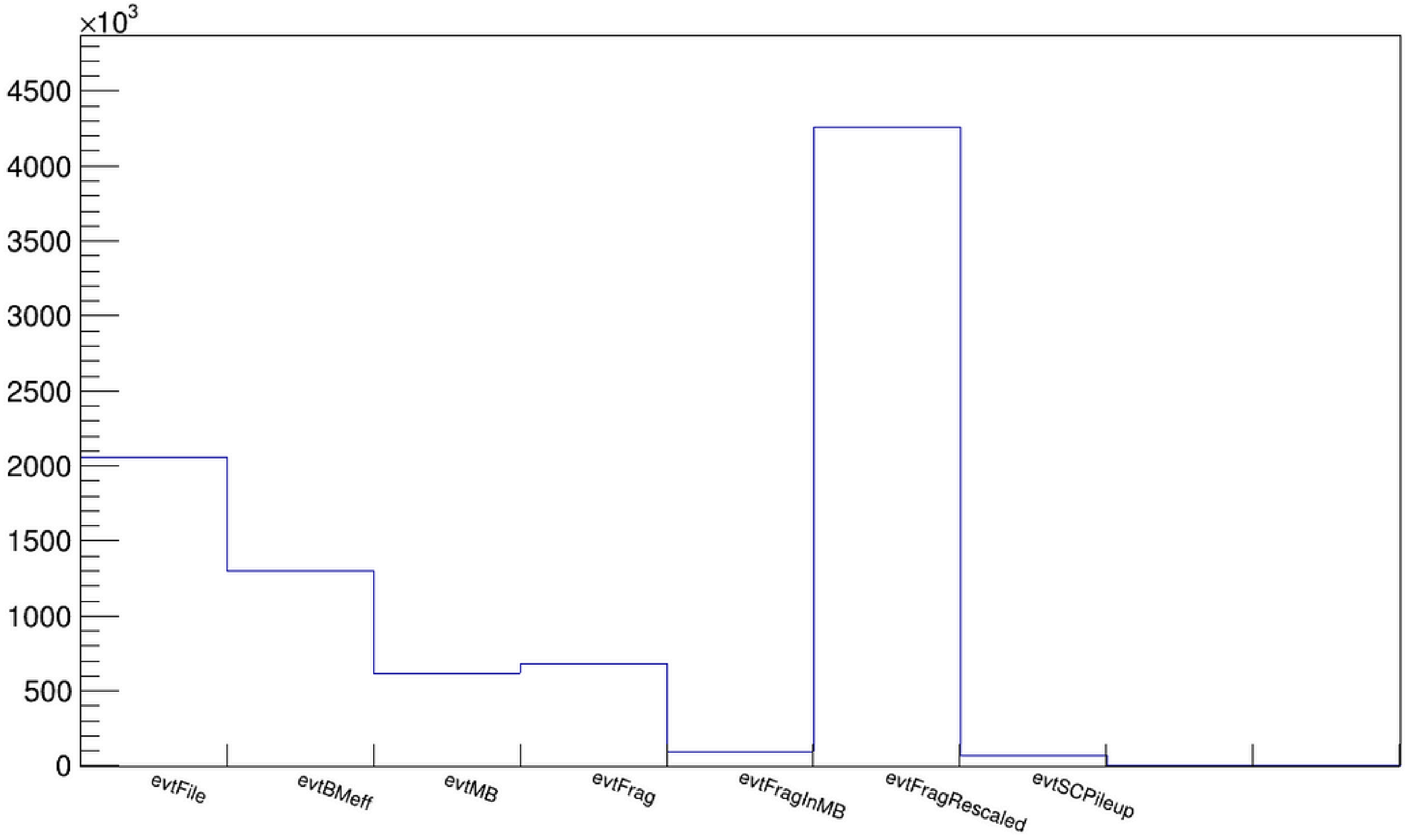


Number of events

Minimum bias (4305,4306,4307)

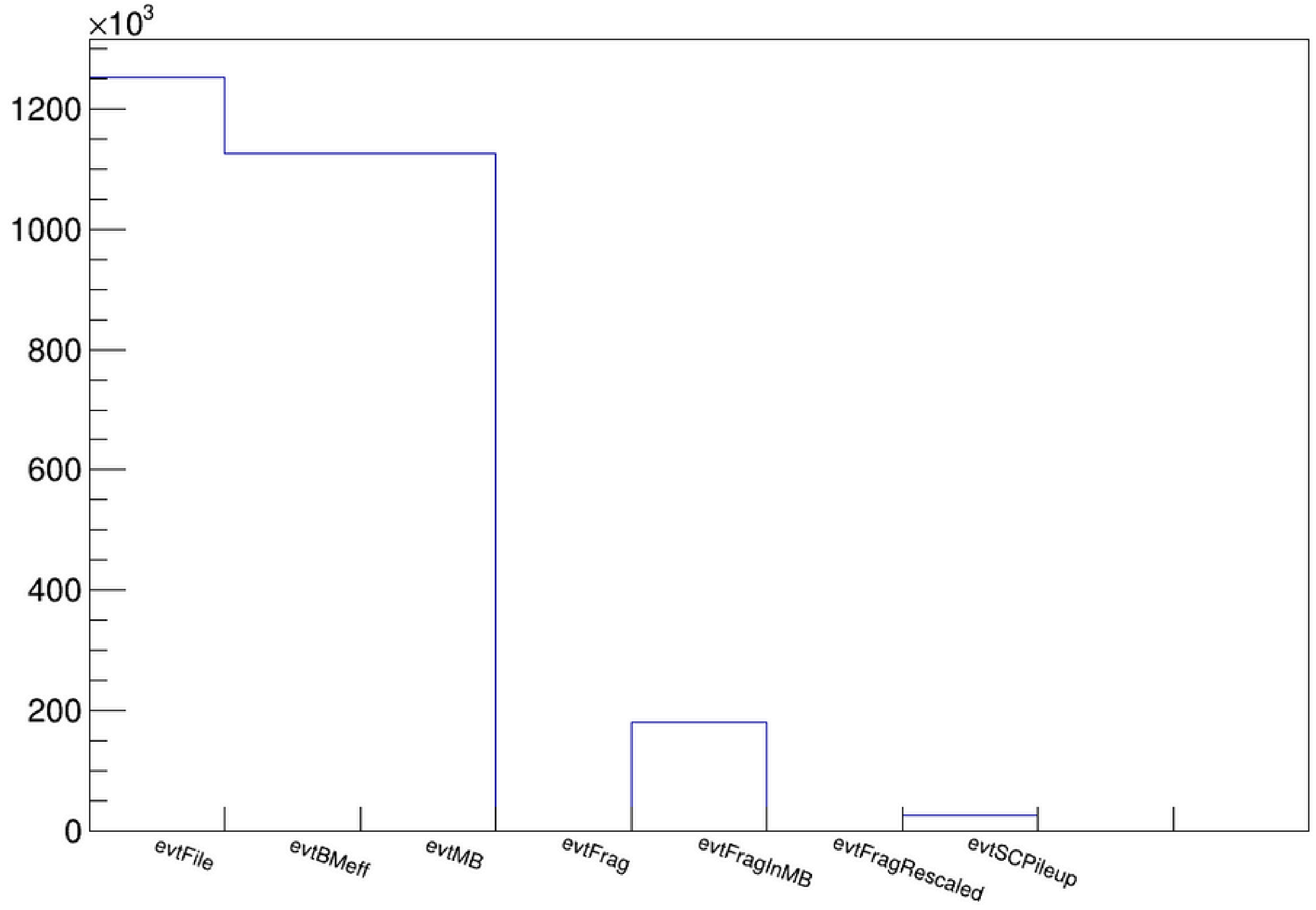


Fragmentation+MB (4308, 4309, 4310)

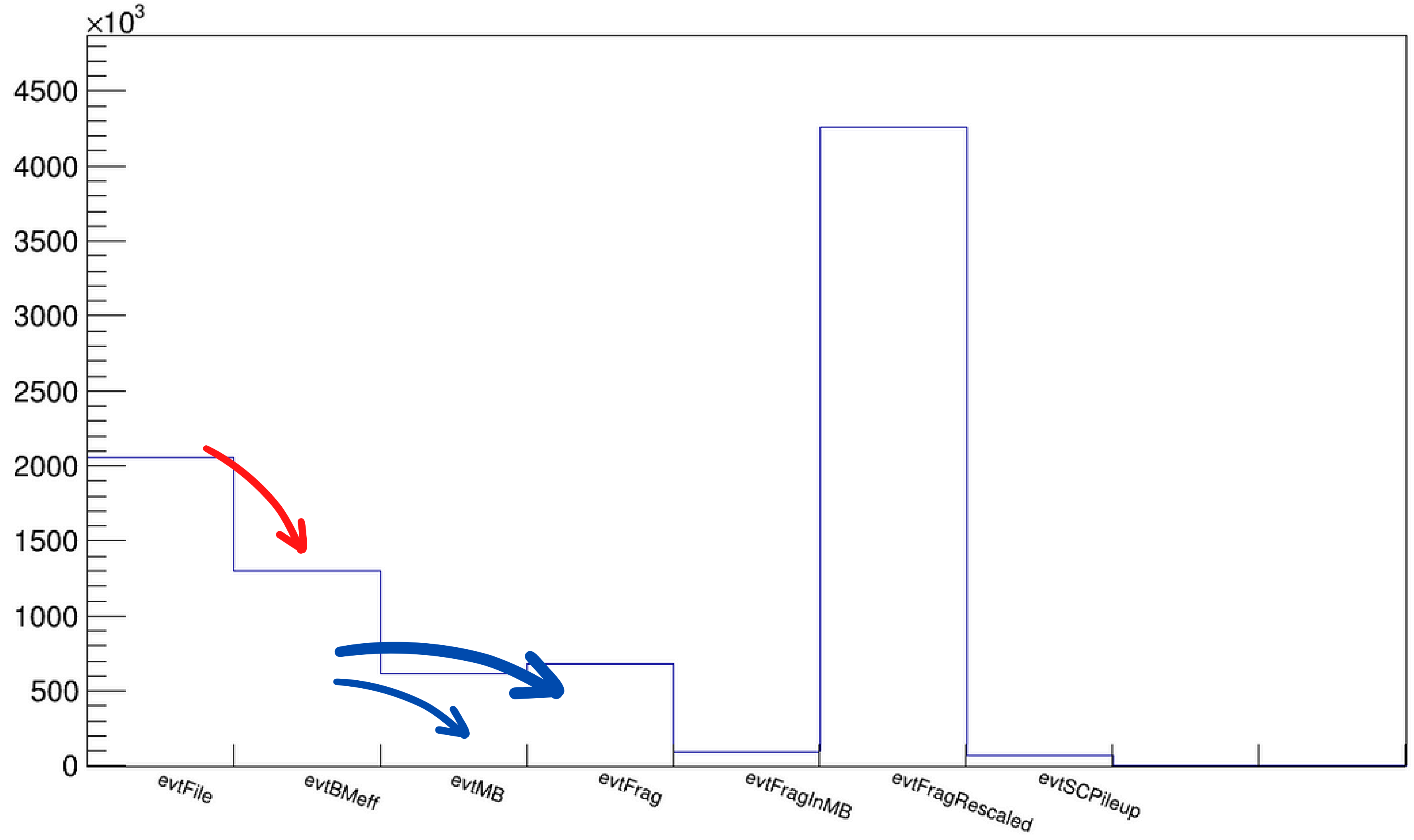


Number of events

Minimum bias (4305,4306,4307)

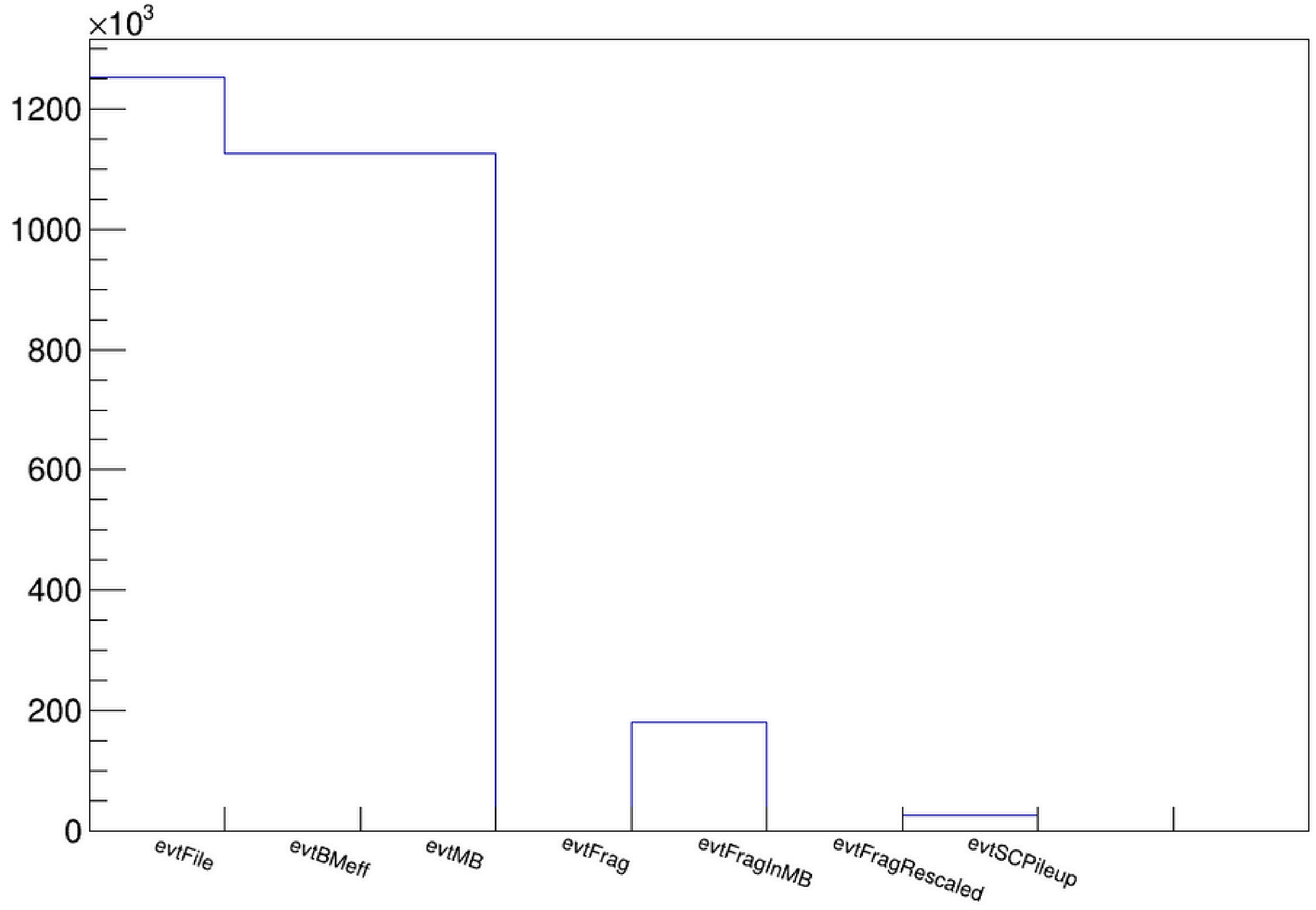


Fragmentation+MB (4308, 4309, 4310)

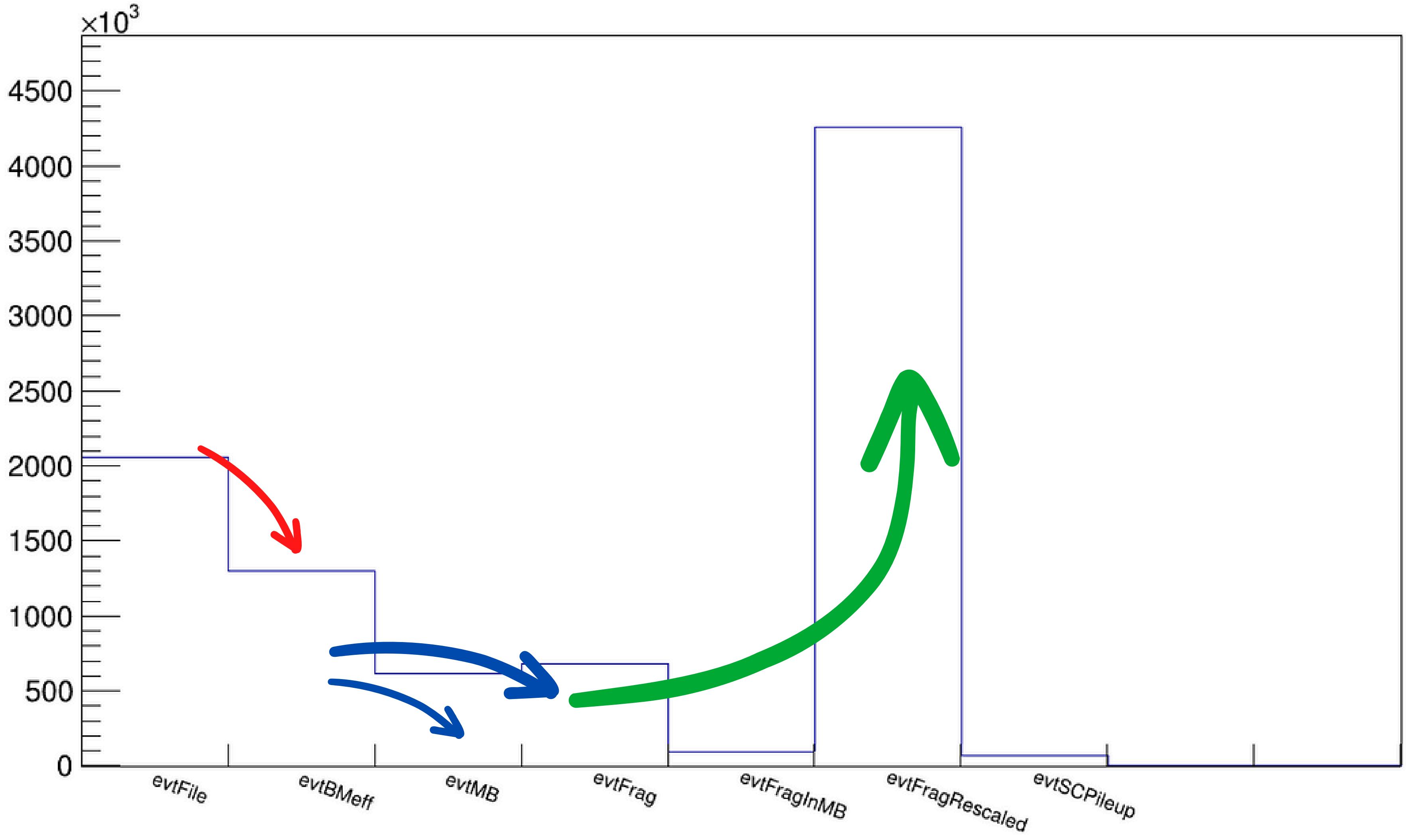


Number of events

Minimum bias (4305,4306,4307)



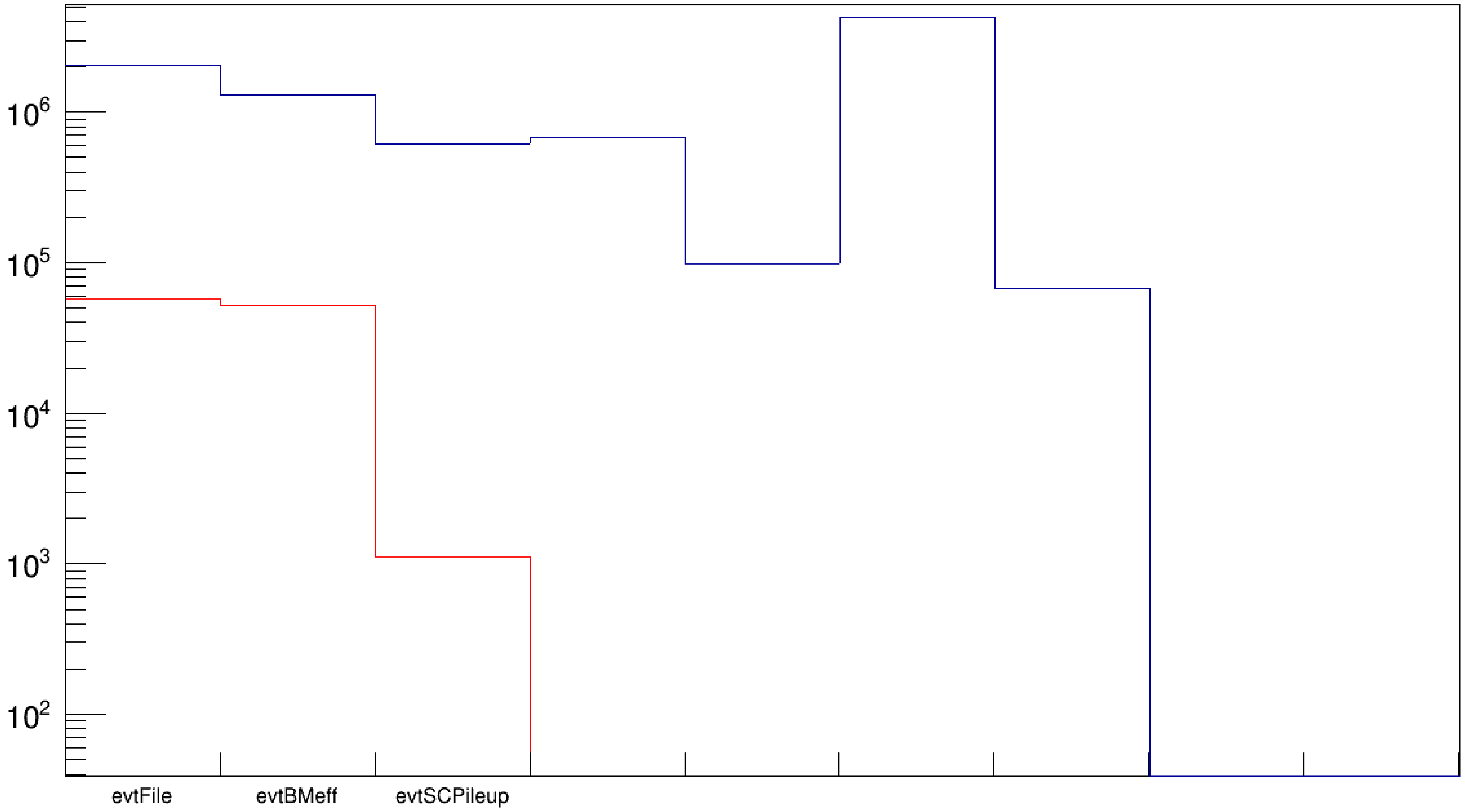
Fragmentation+MB (4308, 4309, 4310)



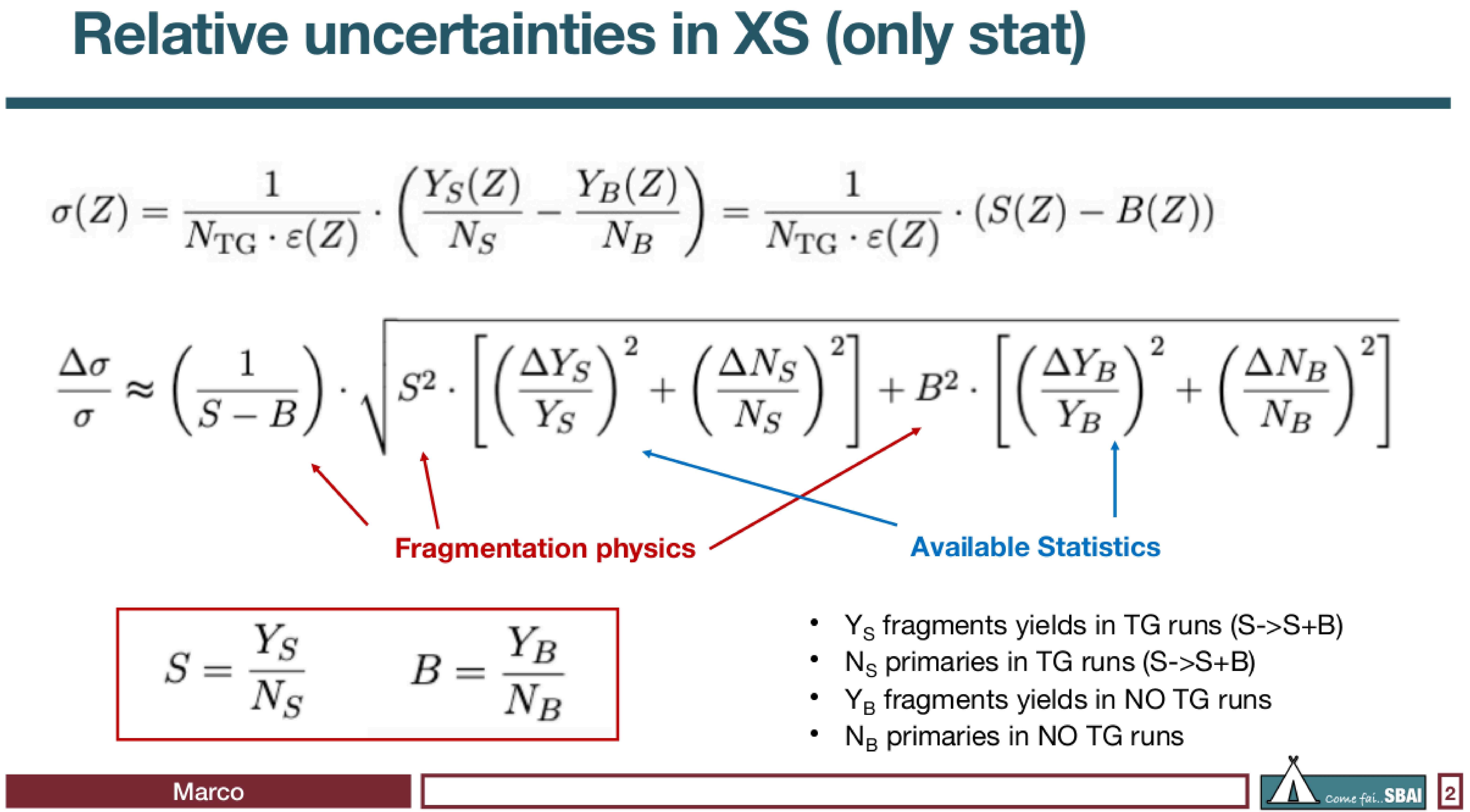
Number of events

Fragmentation+MB (4308, 4309, 4310)

Background MB (4313)



Impact of statistics on XS resolution



Relative uncertainties in XS (only stat)

$$\sigma(Z)=\frac{1}{N_{\mathrm{TG}}\cdot\varepsilon(Z)}\cdot\left(\frac{Y_S(Z)}{N_S}-\frac{Y_B(Z)}{N_B}\right)=\frac{1}{N_{\mathrm{TG}}\cdot\varepsilon(Z)}\cdot(S(Z)-B(Z))$$

$$\frac{\Delta\sigma}{\sigma}\approx\left(\frac{1}{S-B}\right)\cdot\sqrt{S^2\cdot\left[\left(\frac{\Delta Y_S}{Y_S}\right)^2+\left(\frac{\Delta N_S}{N_S}\right)^2\right]+B^2\cdot\left[\left(\frac{\Delta Y_B}{Y_B}\right)^2+\left(\frac{\Delta N_B}{N_B}\right)^2\right]}$$

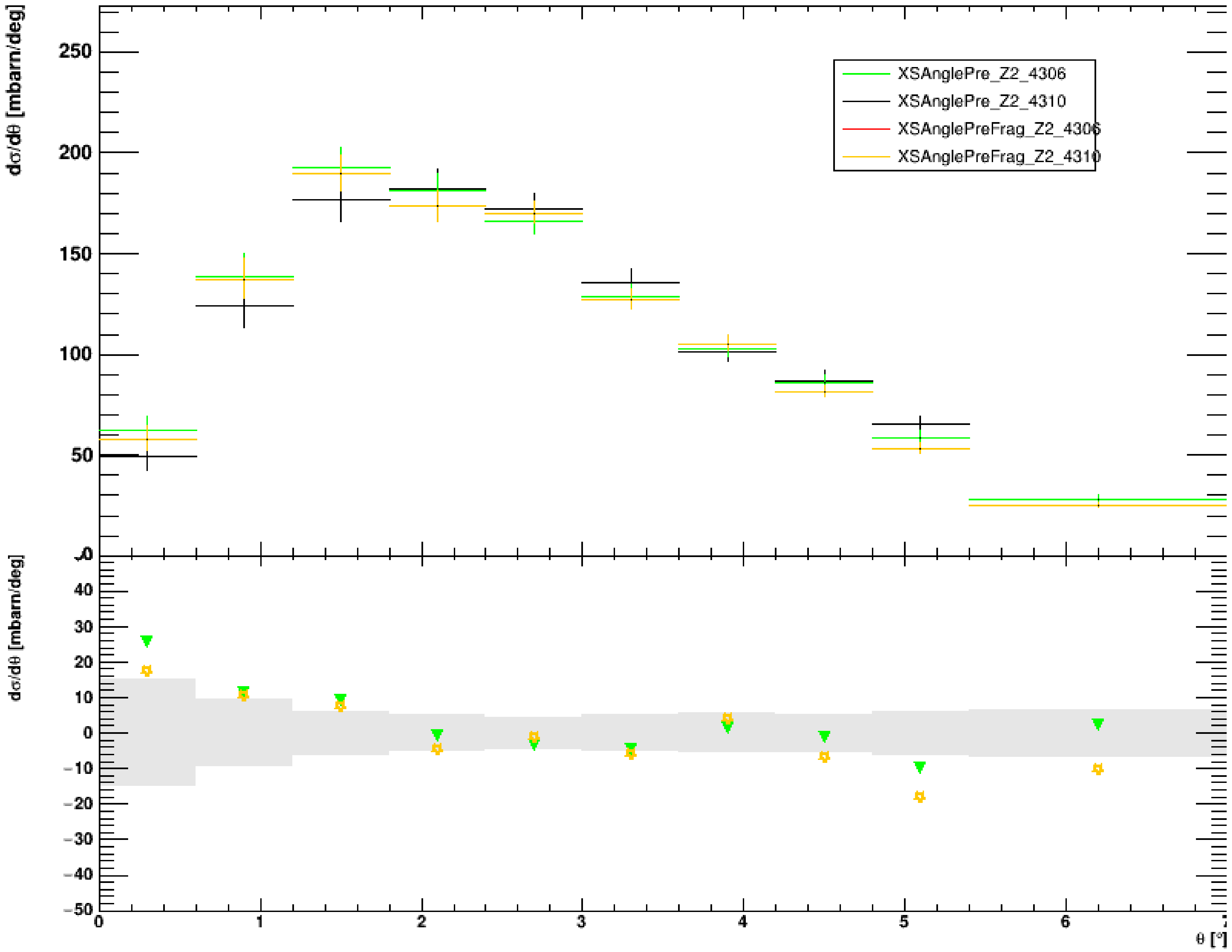
Fragmentation physics

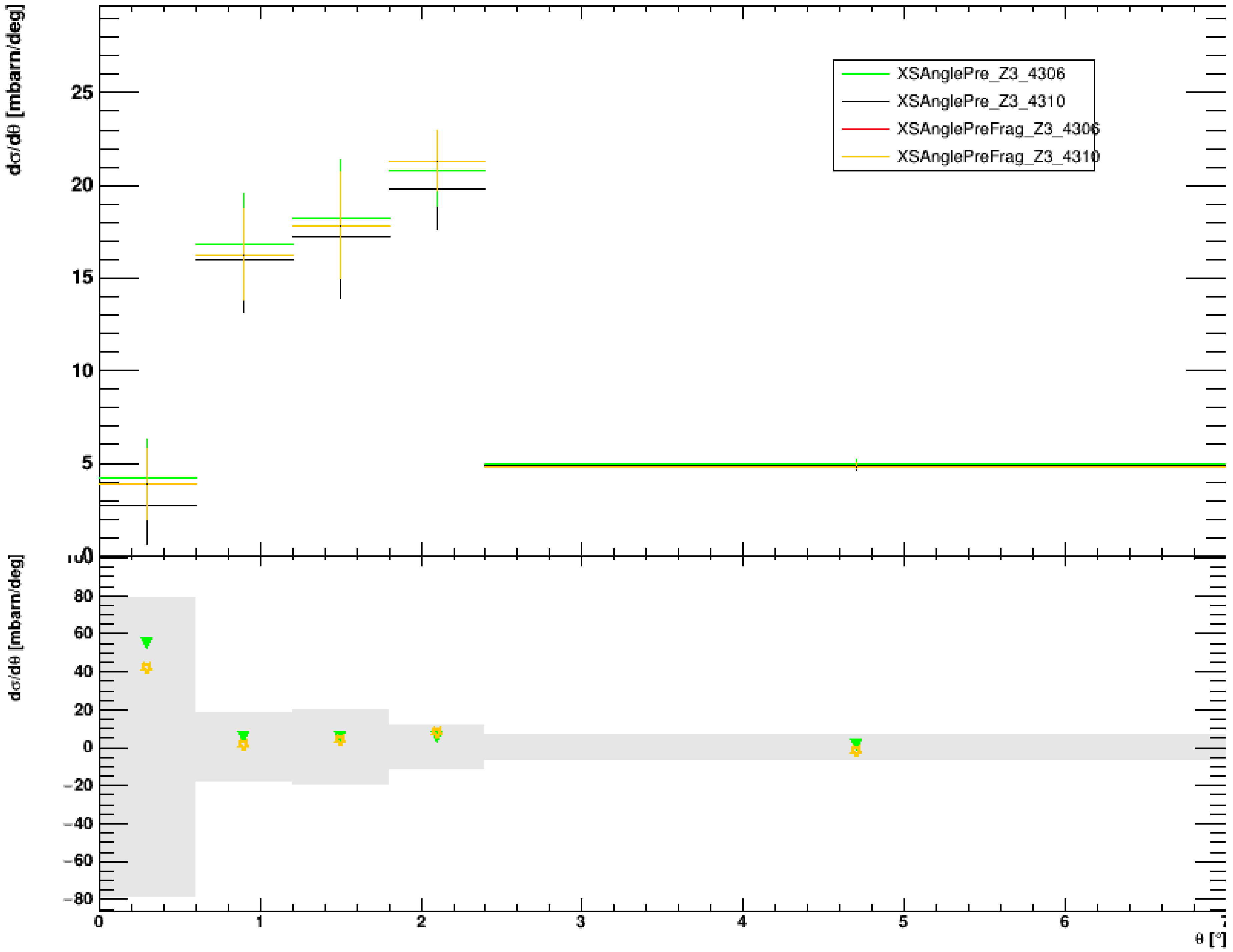
Available Statistics

$$\boxed{S=\frac{Y_S}{N_S}\qquad B=\frac{Y_B}{N_B}}$$

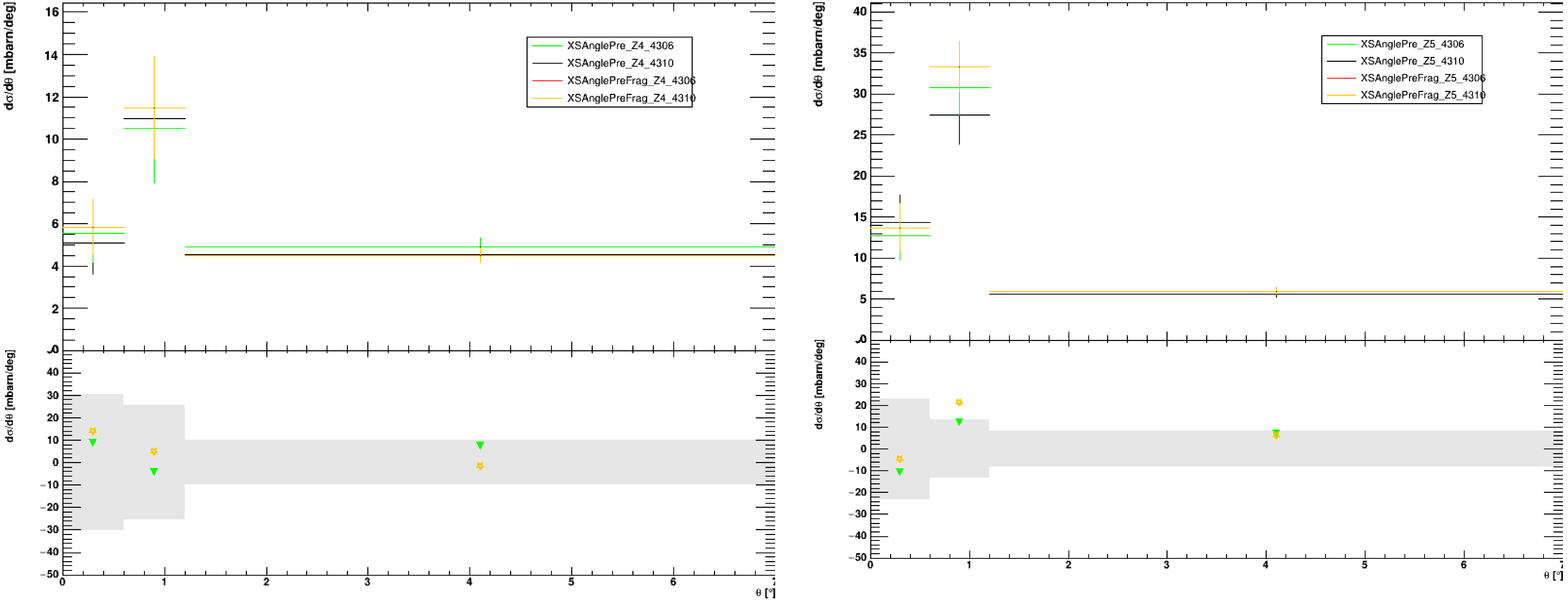
- Y_S fragments yields in TG runs (S->S+B)
- N_S primaries in TG runs (S->S+B)
- Y_B fragments yields in NO TG runs
- N_B primaries in NO TG runs

Consistency checks on data

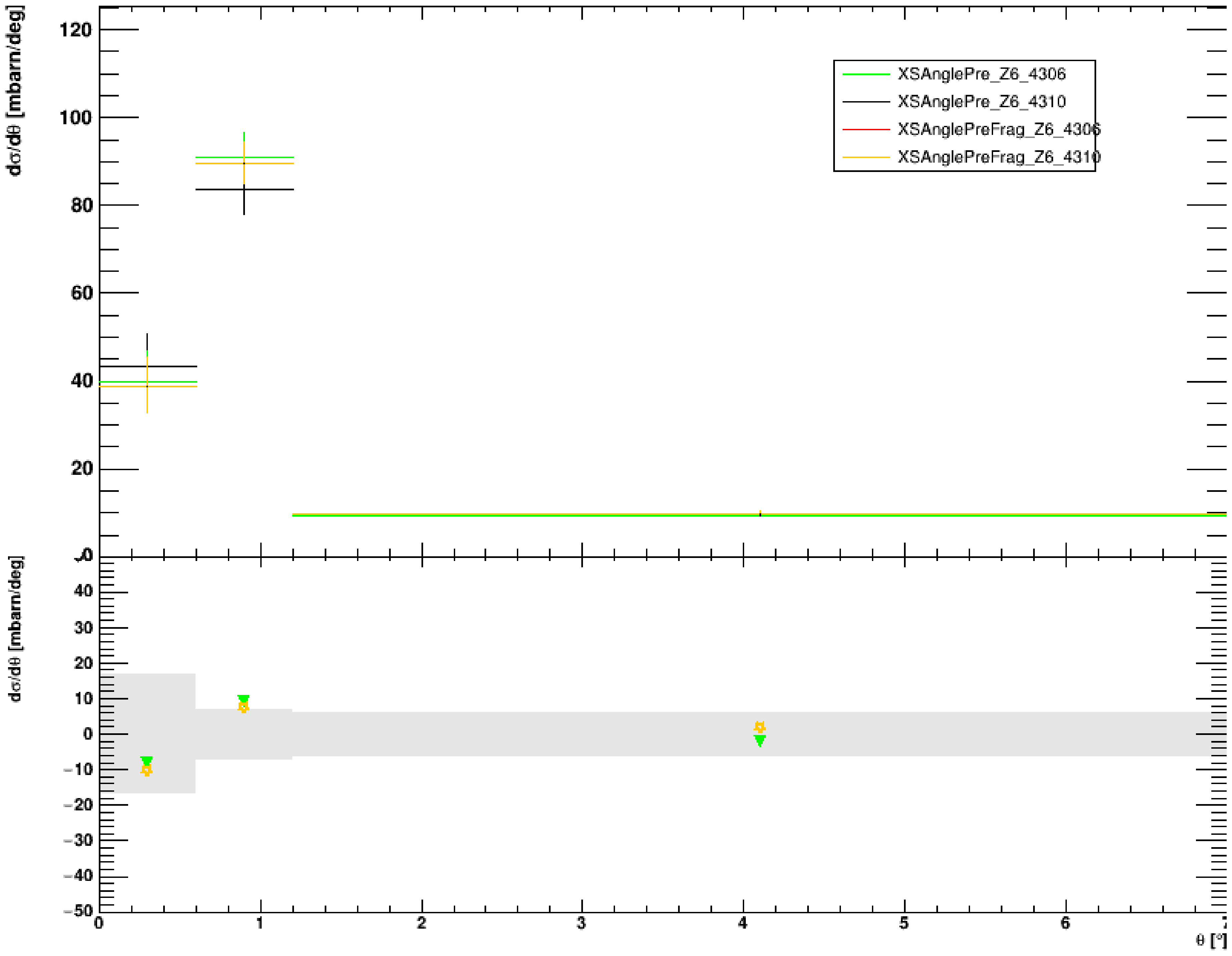


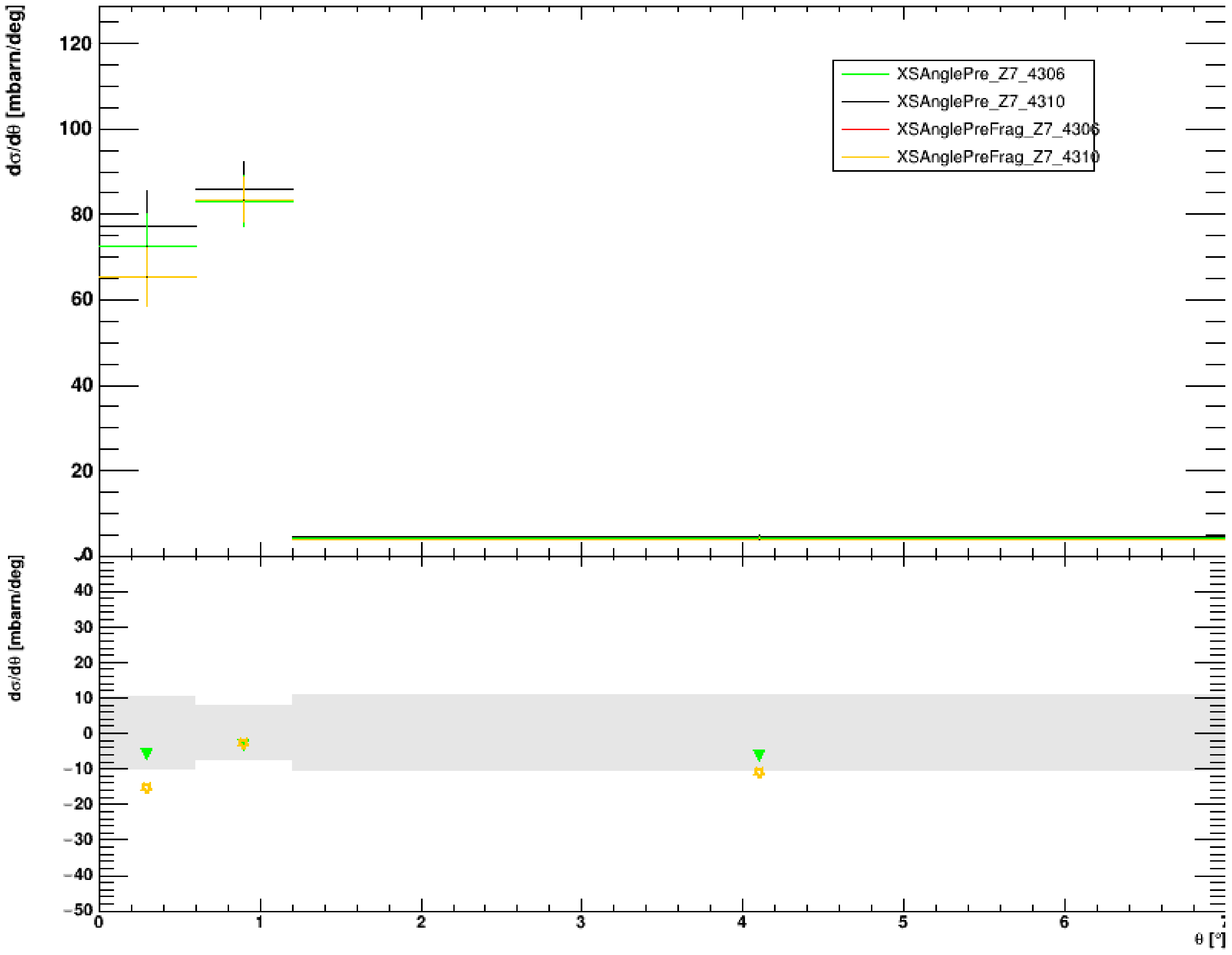


Consistency checks on data

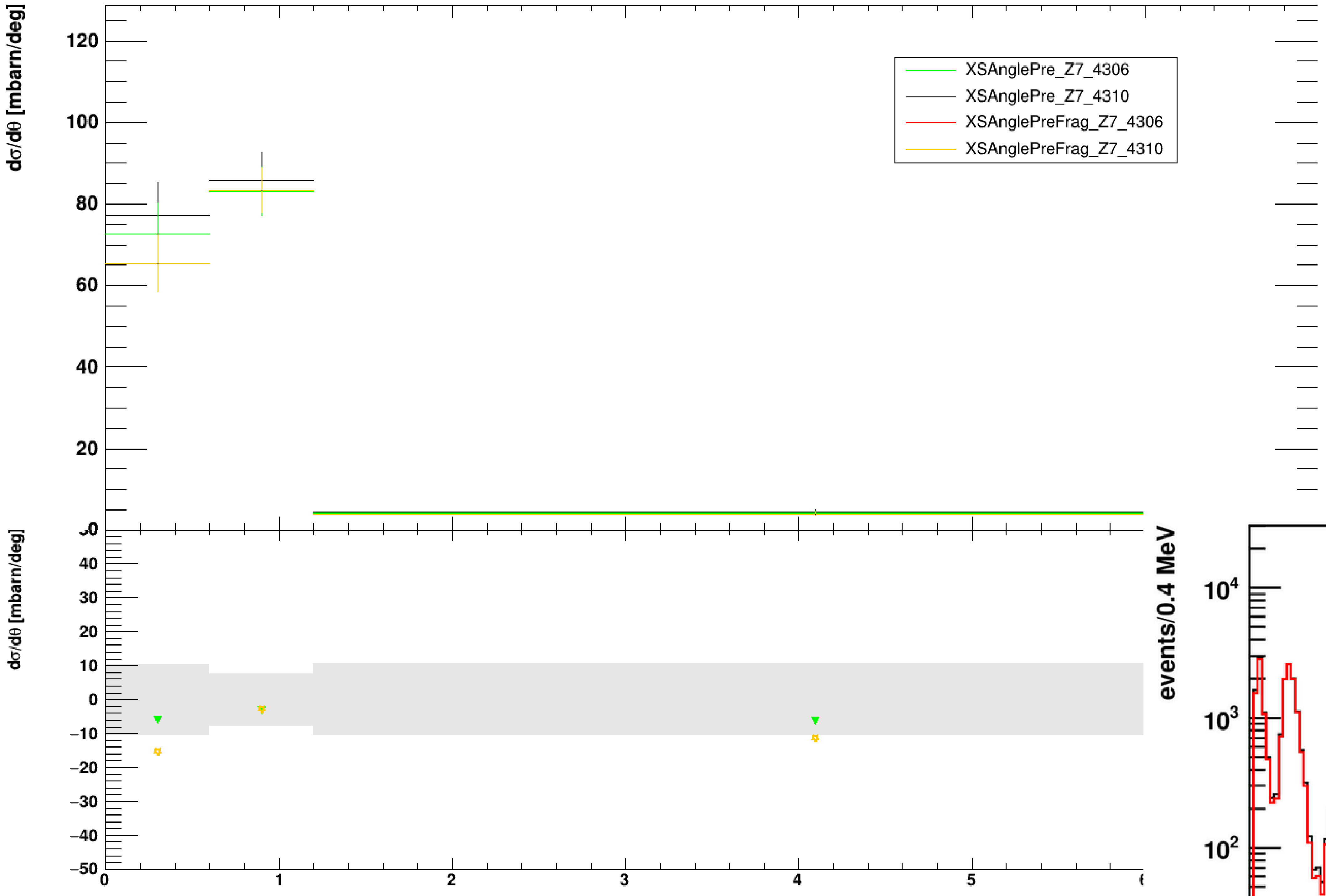


Consistency checks on data

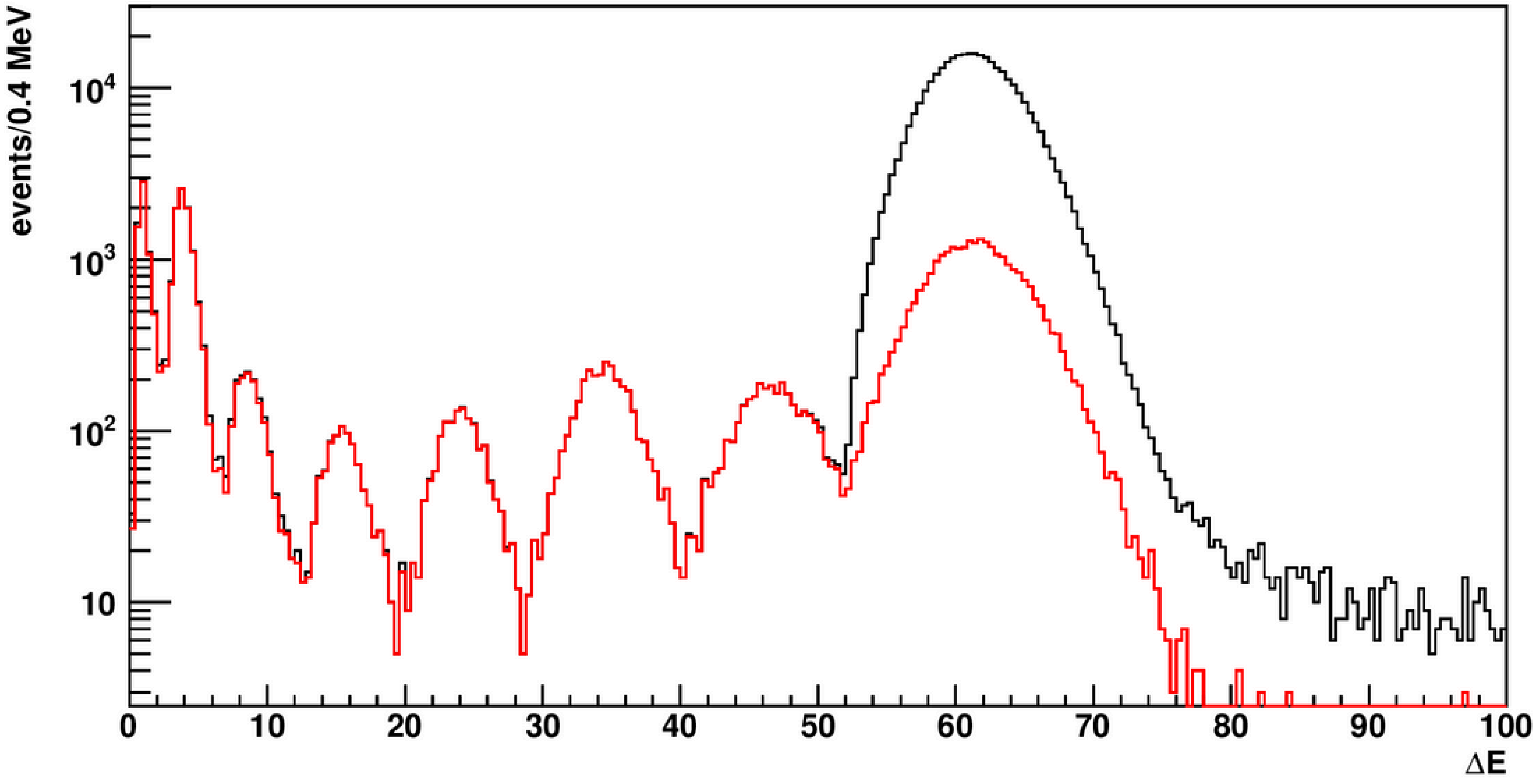




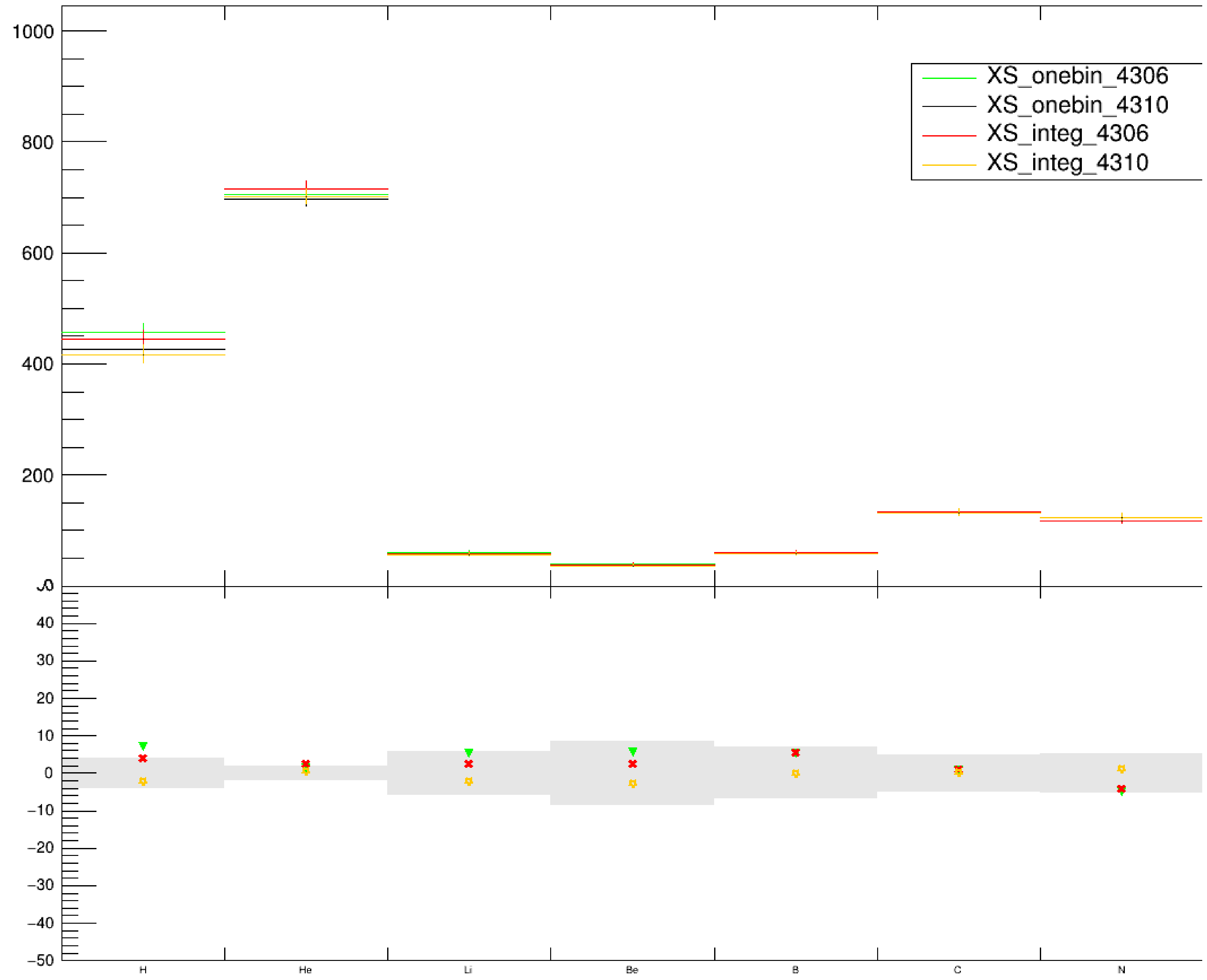
Consistency checks on data

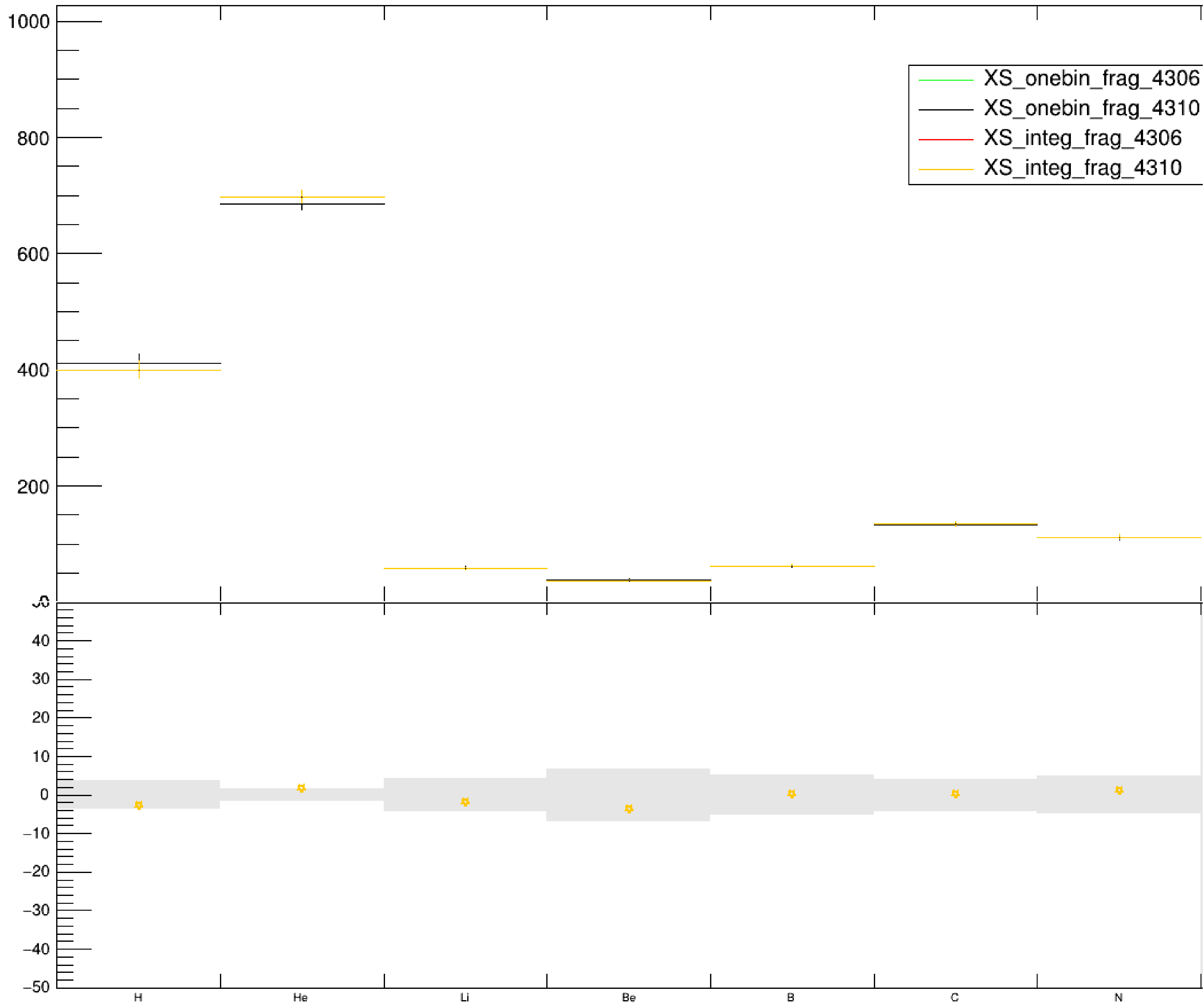


Fragment rescaling maybe useful for N if outside our uncertainties (it seems not)



Consistency checks on data

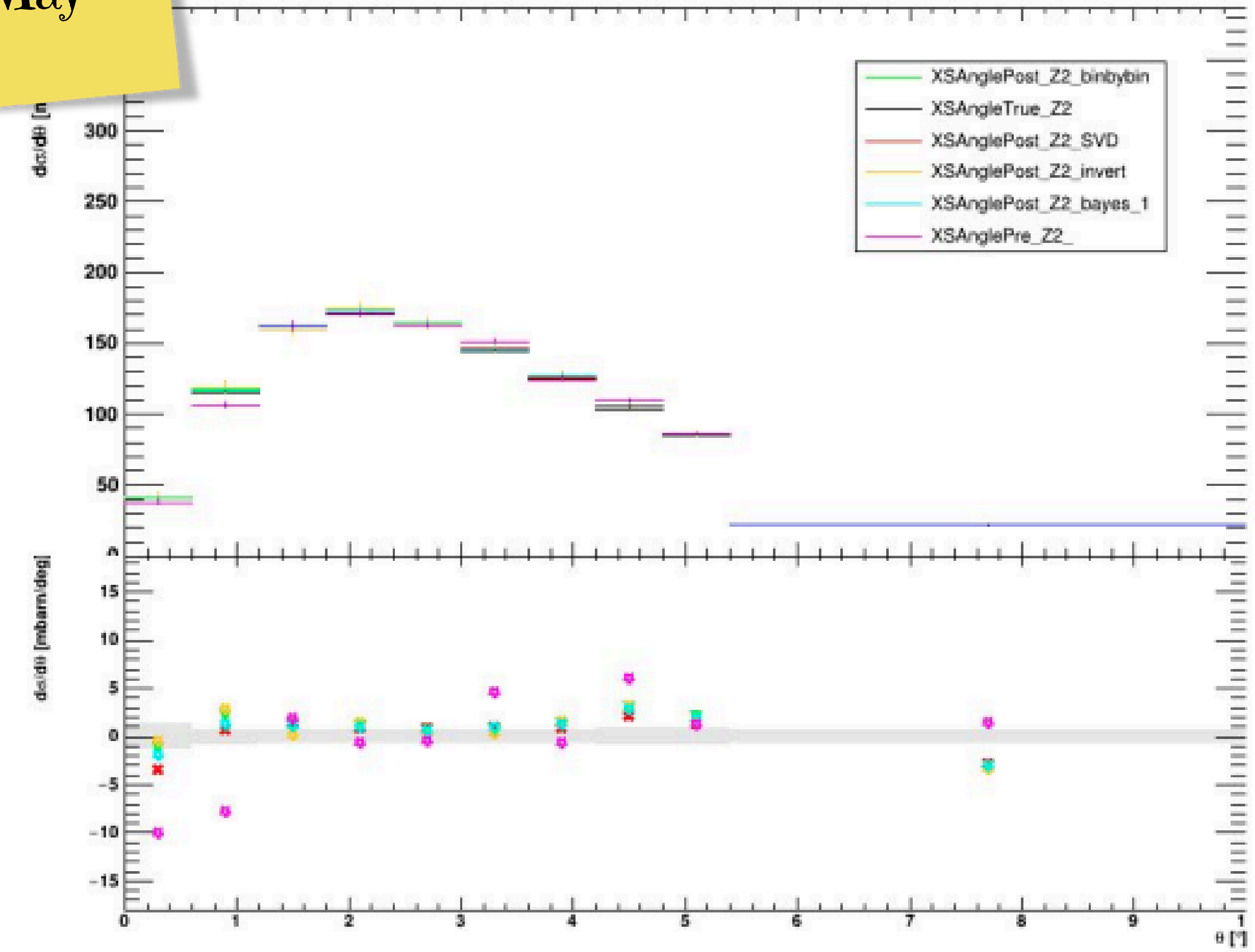




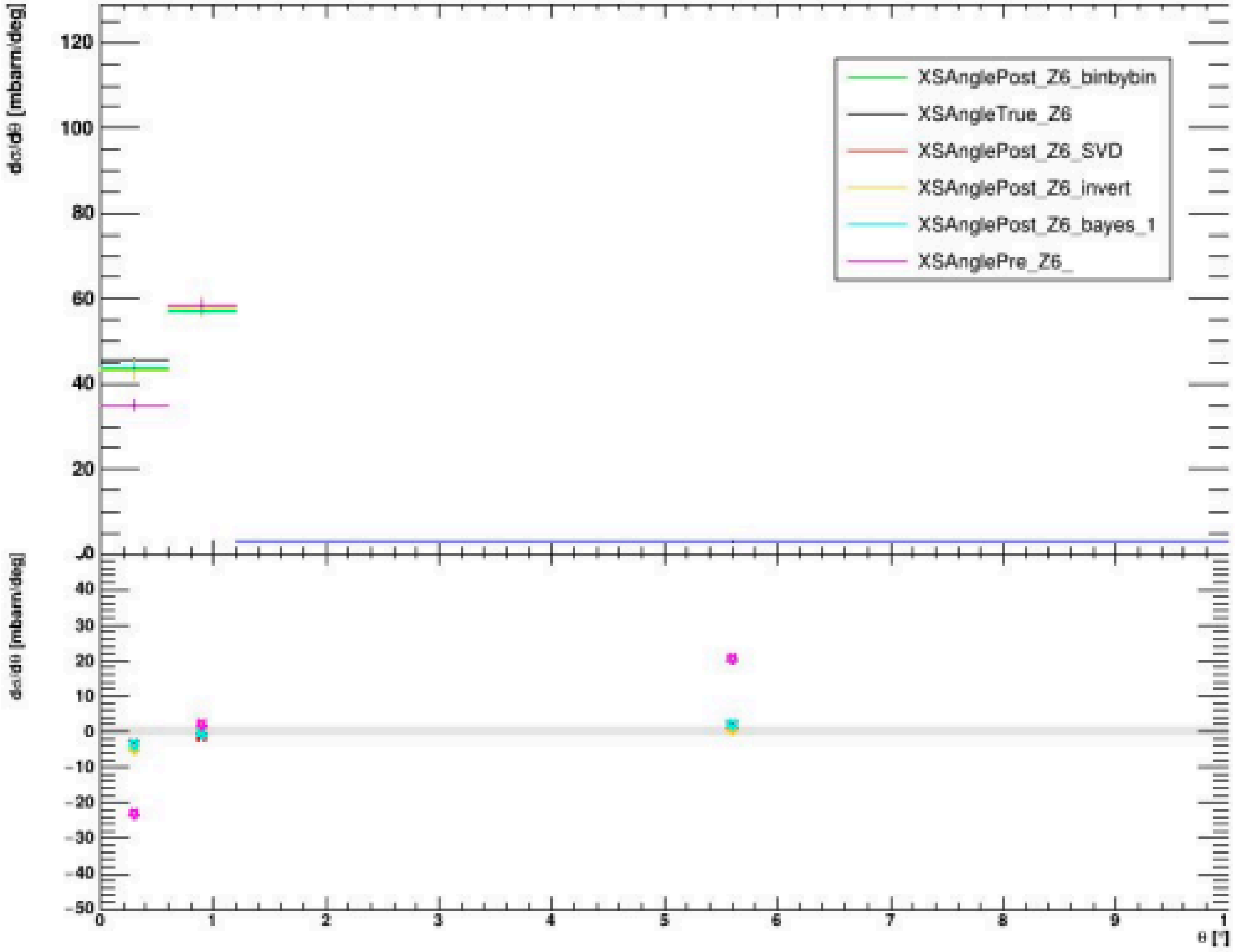
Unfolding Method Comparison

Alberto
21 May

Z=2



Z=6



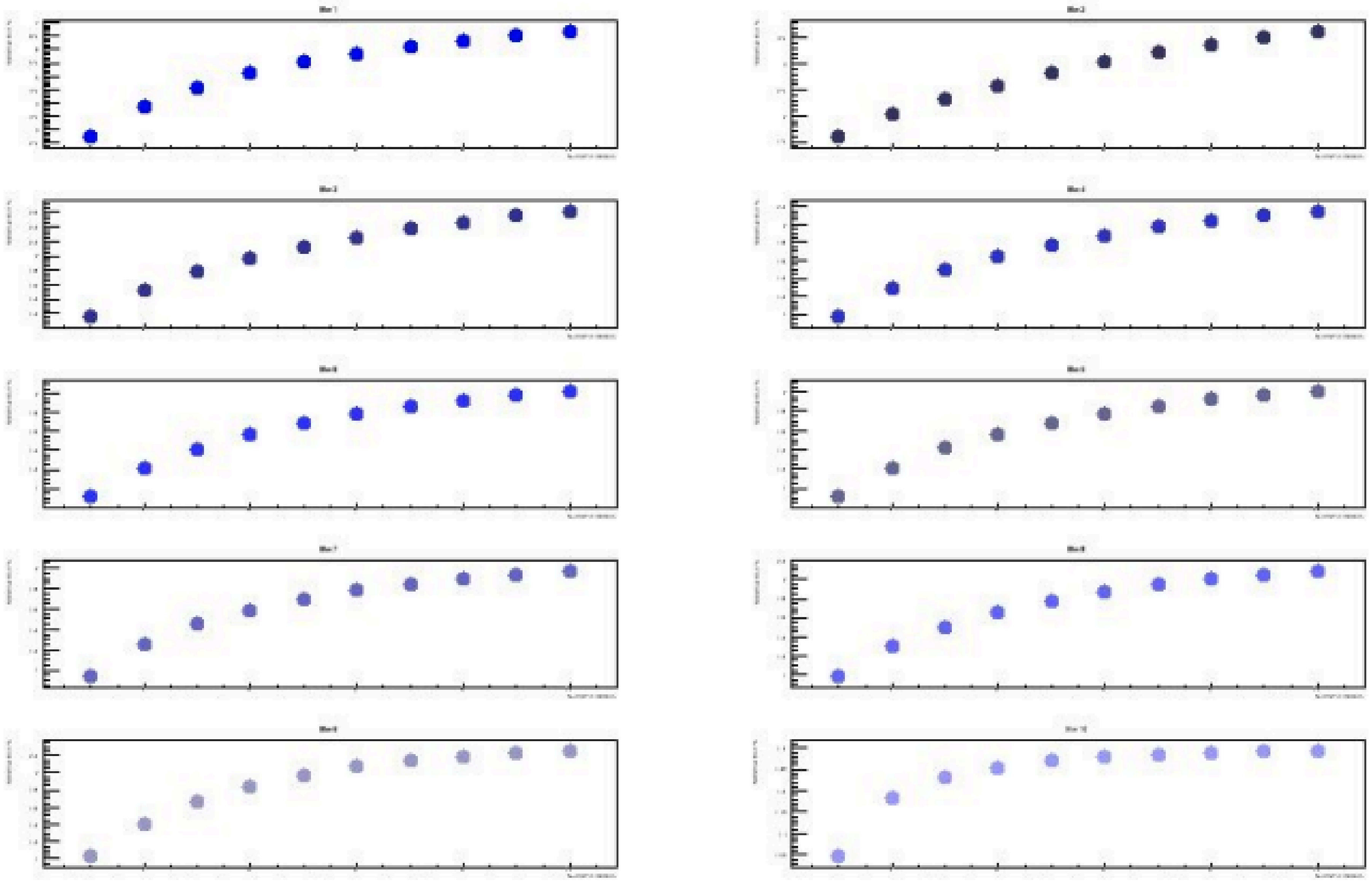
Different methods behave the same way → Bayes Iterative method chosen

Alberto
21 May

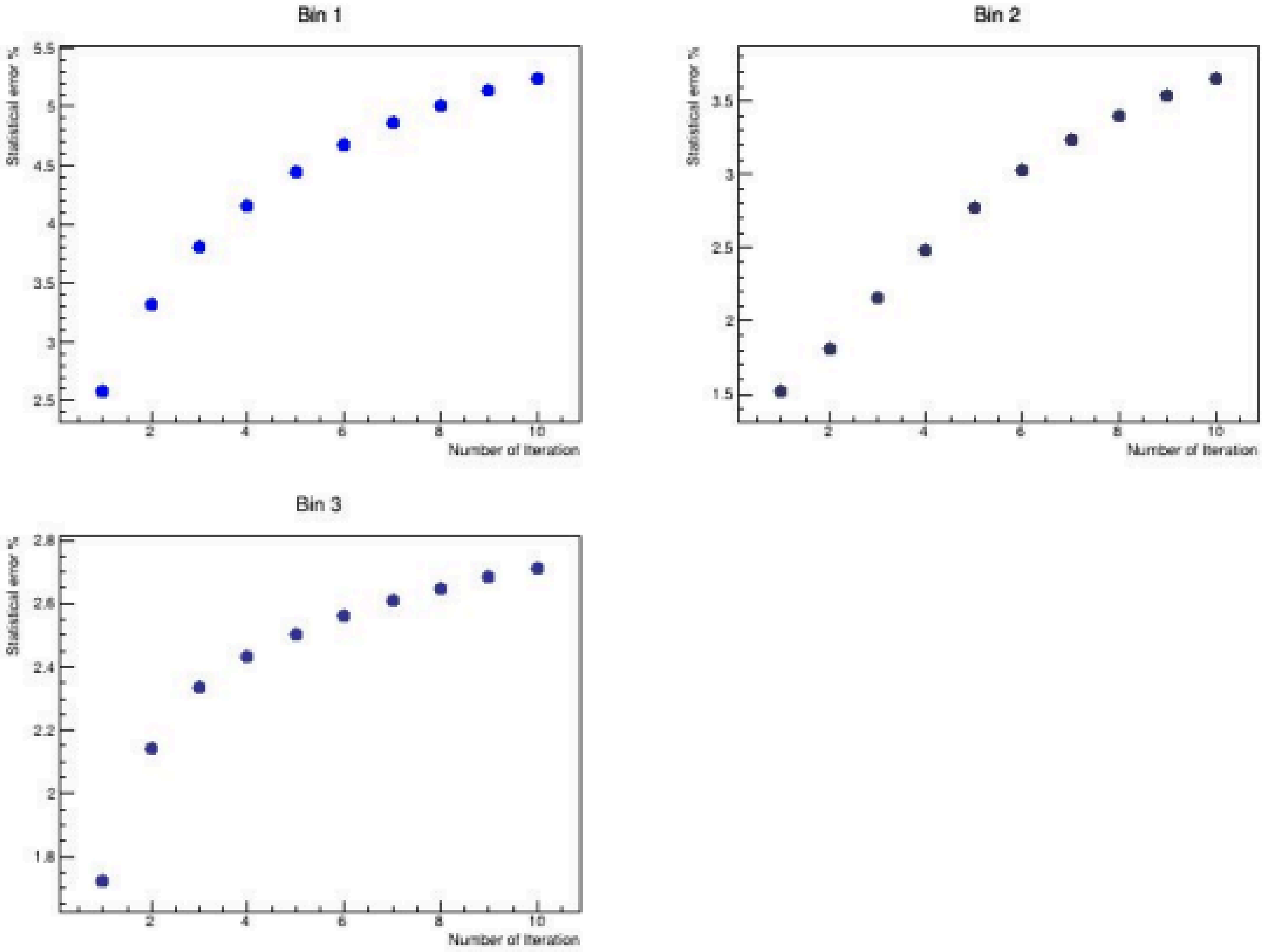
Studies on the number of iterations: Statistical uncertainty

The degree of convergence of the iterative procedure is checked by comparing each iteration to the previous one. In particular, the parameters taken into account are the bin-wise statistical error (it increases with the number of iterations, reaching a sort of plateau)

Z=2



Z=6

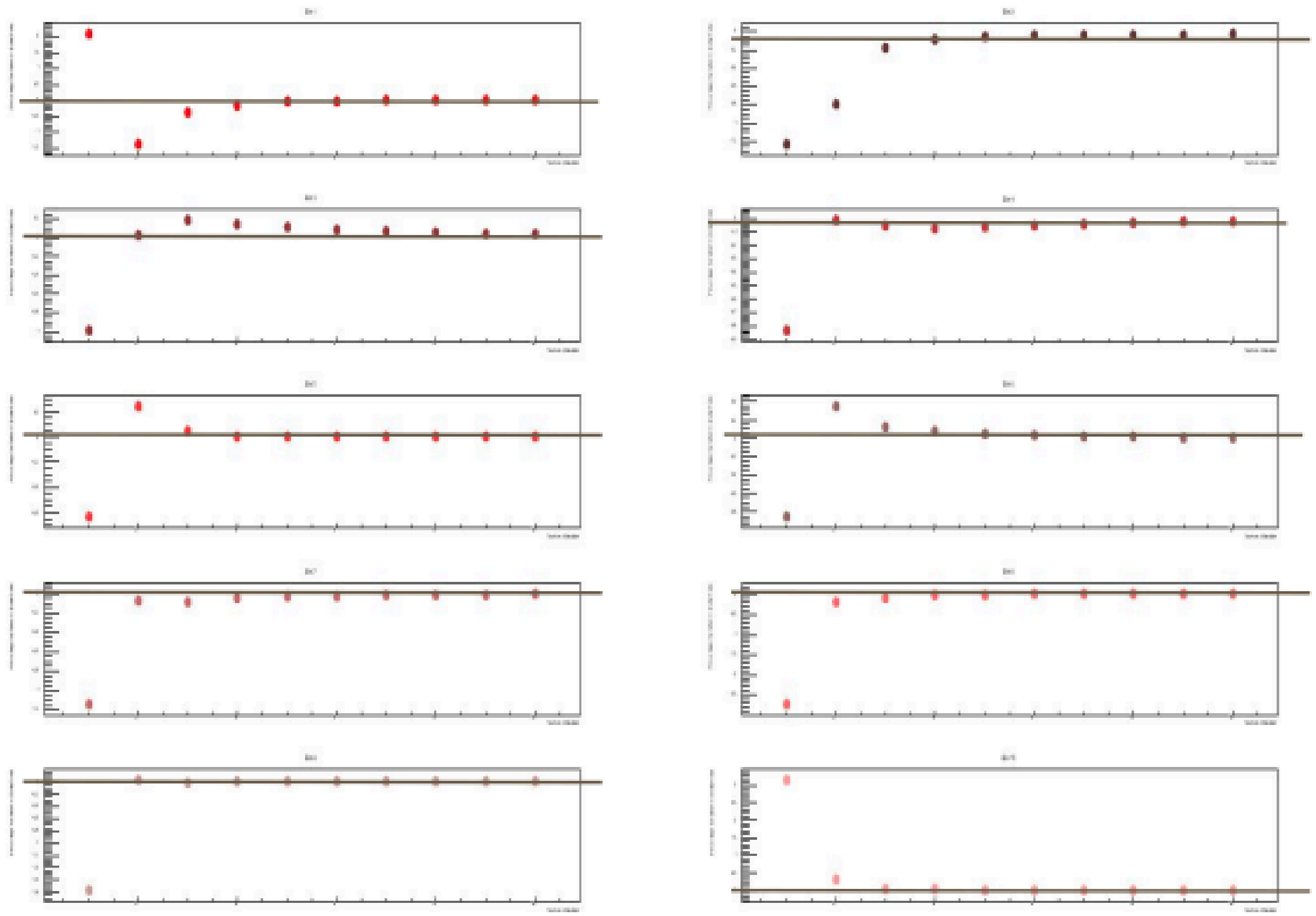


Alberto
21 May

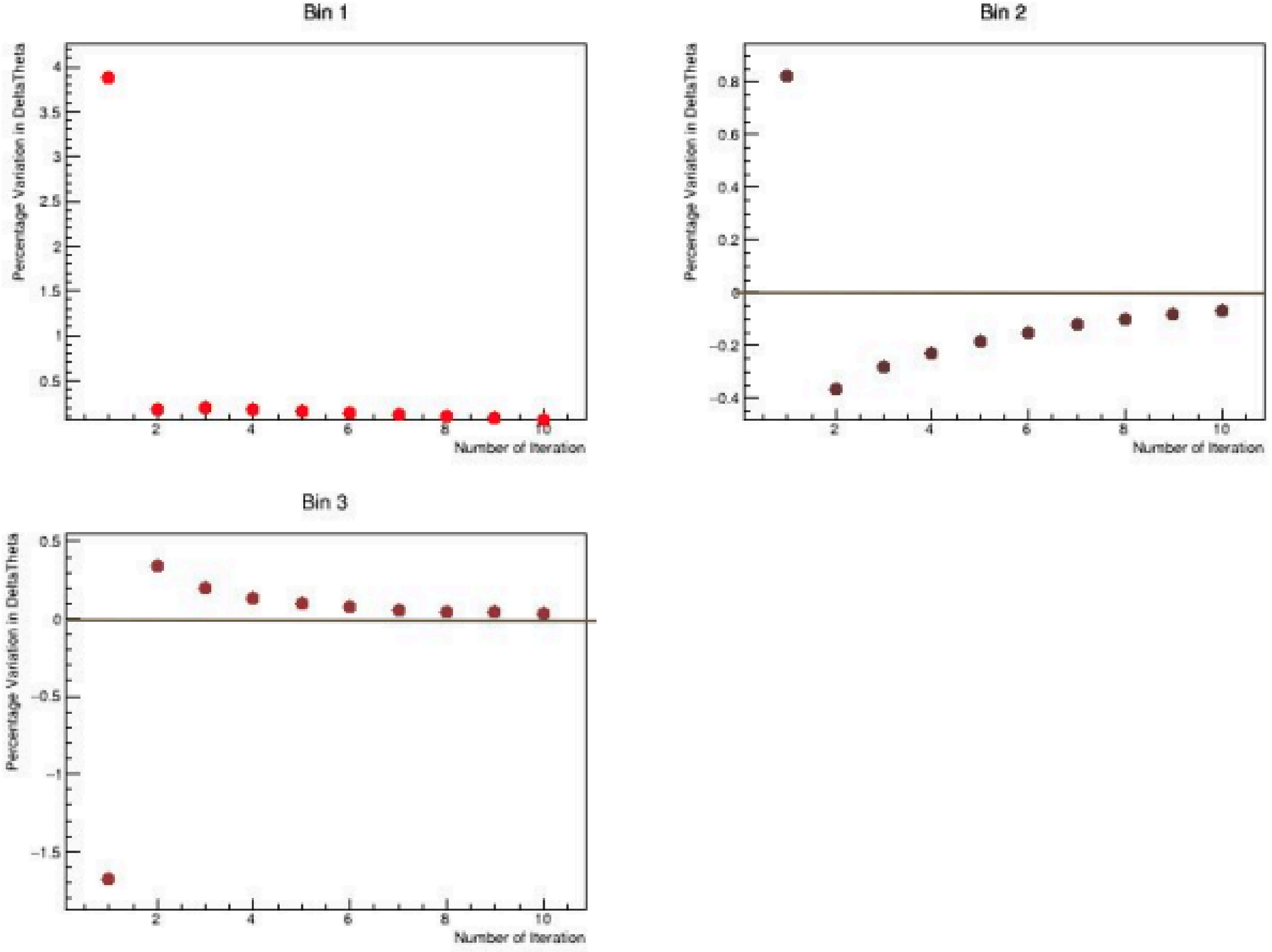
Studies on the number of iterations: bin residuals

bin-wise residuals (the bin-by-bin difference between the unfolded distribution at the *i*-th iteration and the unfolded distribution at the *i* − 1-th iteration, which must converge to 0).

Z=2



Z=6



Alberto
21 May

Studies on the number of iterations: Average correlation

An optimal choice of the regularization parameter is the one that minimizes the average correlation factor:

$$\rho_{\text{avg}} \quad = \quad \frac{1}{M_x}\sum_{j=1}^{M_x}\rho_j \, .$$

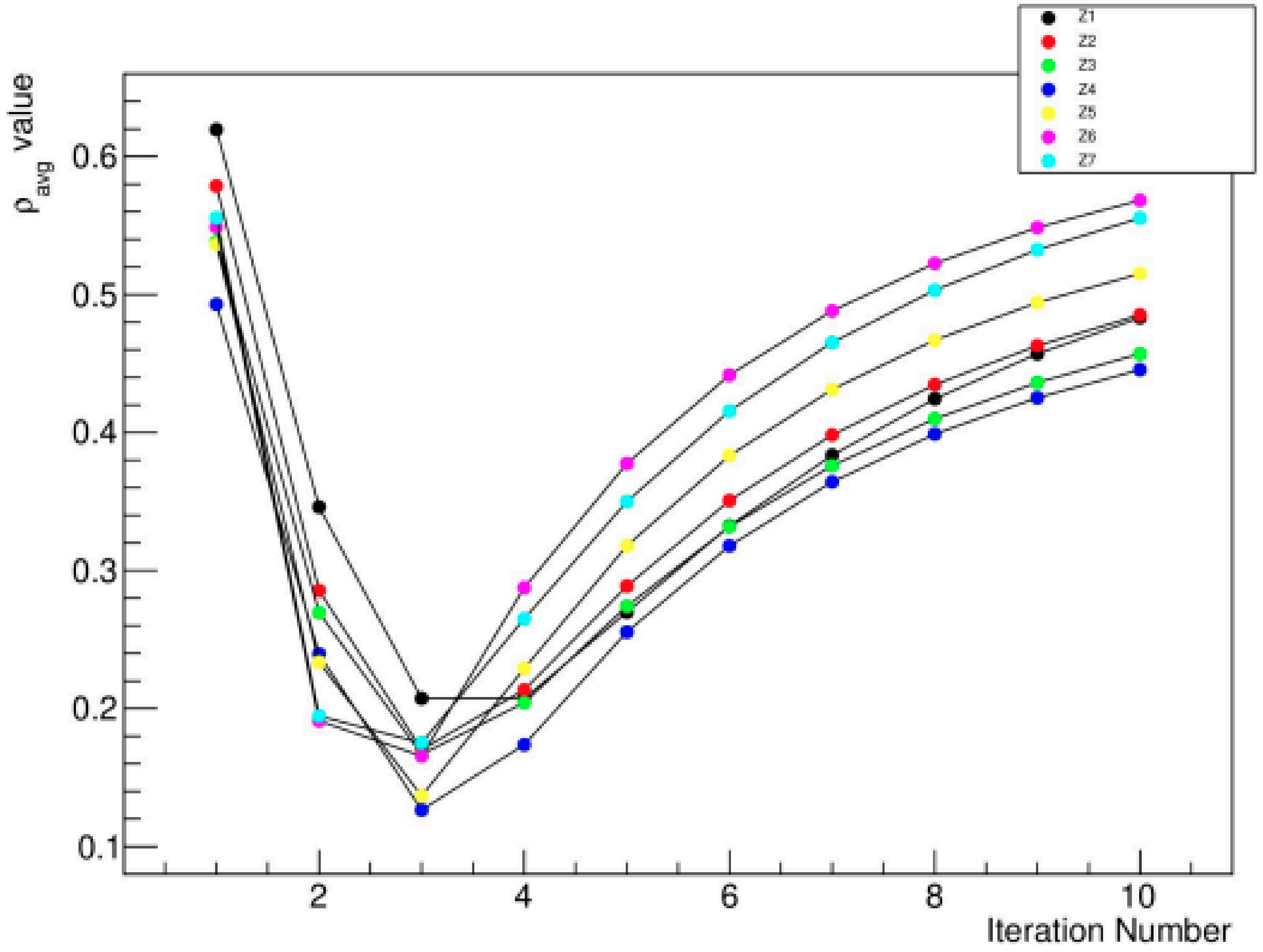
where ρ_j global correlation coefficient of bin j is defined as

$$\rho_j \quad = \quad \sqrt{1-\left((\boldsymbol{V_{xx}})_{jj}\left(\boldsymbol{V_{xx}}^{-1}\right)_{jj}\right)^{-1}} \, .$$

M_x : ndof ; V_{xx} : Cov. matrix

$$\rho_{\text{avg}} = \frac{1}{N_{\text{bins}}}\sum_{i=1}^{N_{\text{bins}}}\rho_i \qquad \rho_i = \sqrt{1-\left[C_{ii}\left(C^{-1}\right)_{ii}\right]^{-1}} \, .$$

S. Schmitt, Data Unfolding Methods in High Energy Physics, EPJ Web Conf. 137 (2017) 11008, ed. by Y. Foka, N. Brambilla and V. Kovalenko, arXiv: 1611.01927

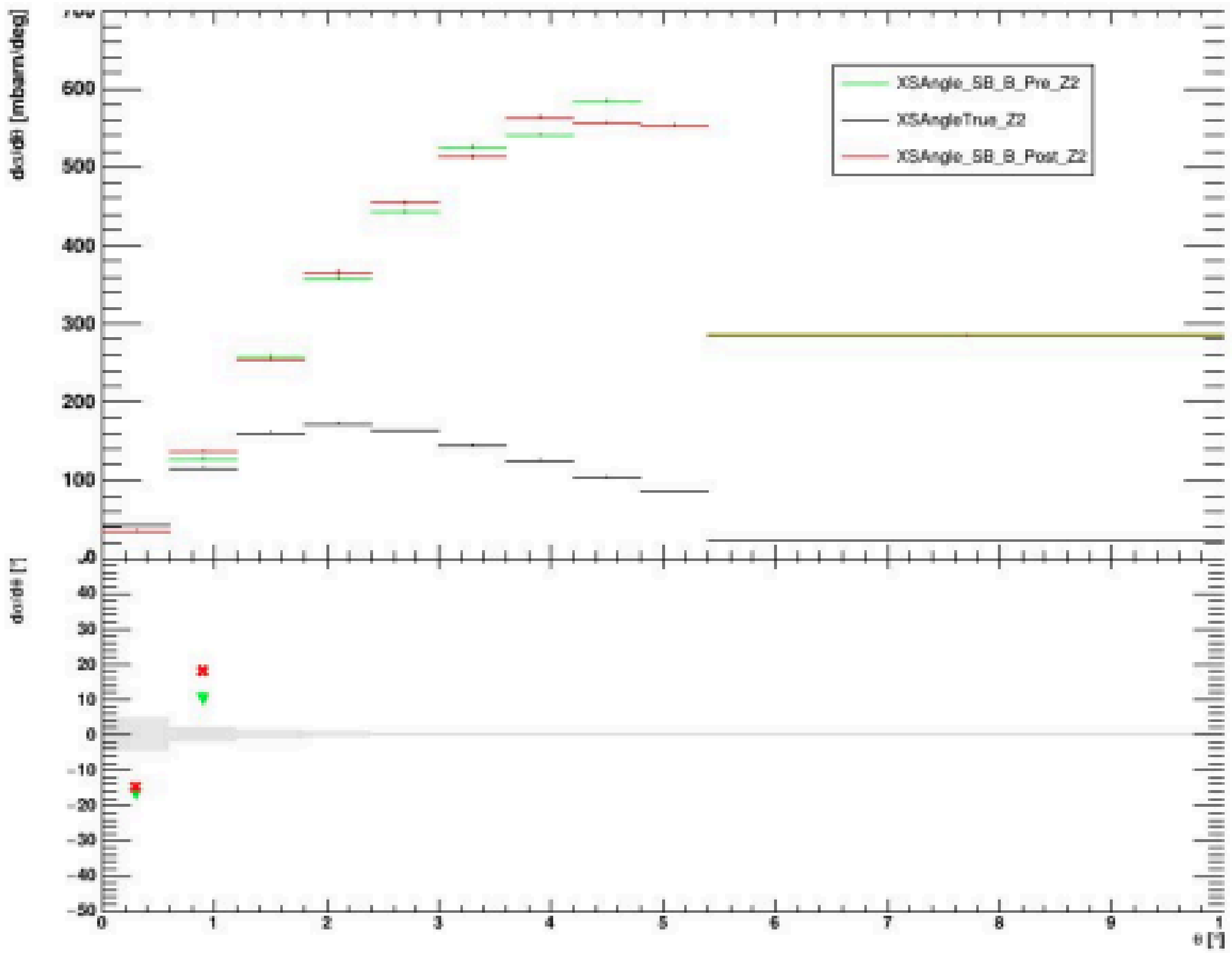


Alberto
21 May

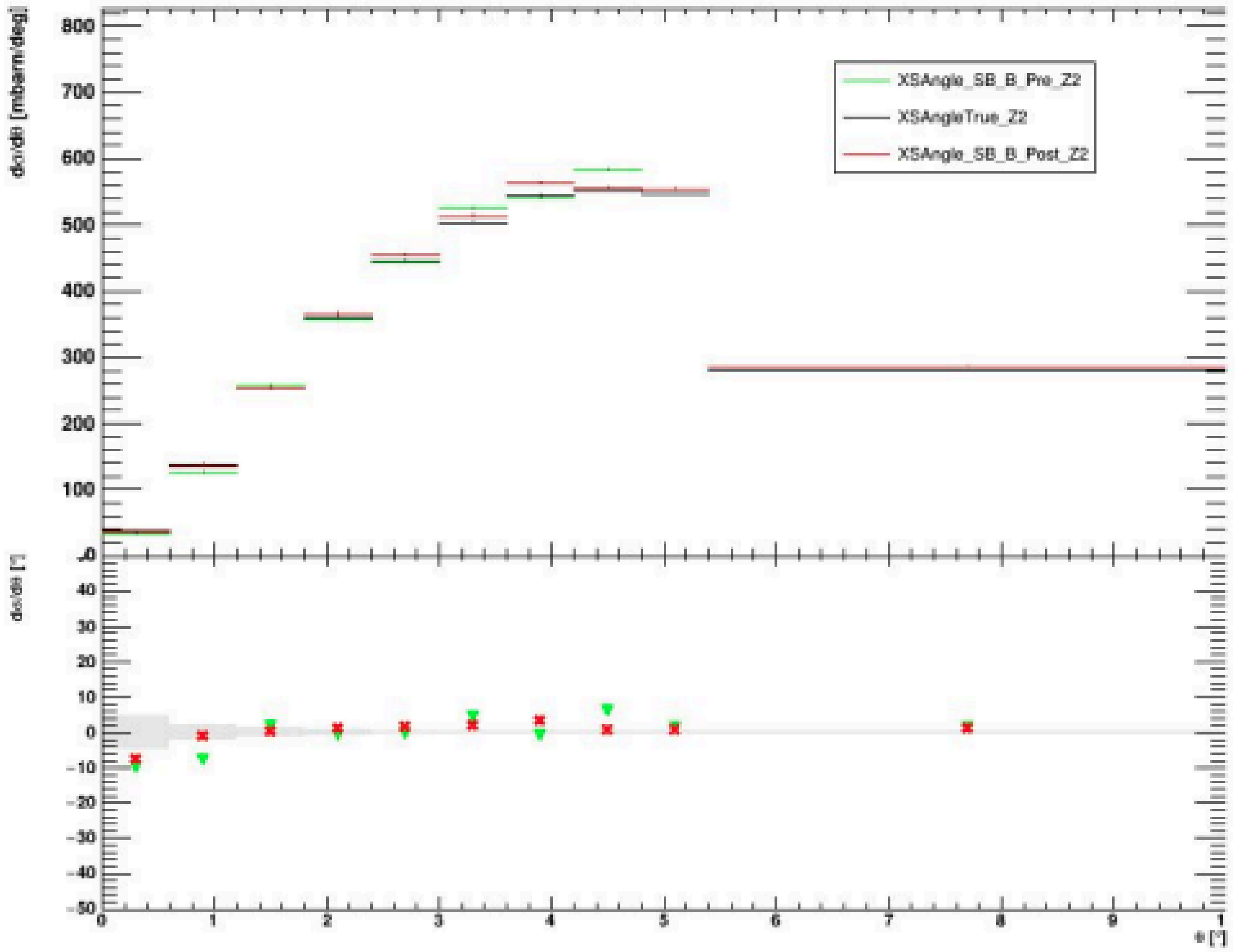
Stress tests

Due to the specific choice of the Monte Carlo sample for the training of the unfolding, it is necessary to check whether this choice could introduce a bias via the unfolding. To do this check the MC reweighting is required, in order to change the shapes of the distributions and get a varied distribution used as pseudo-data.

Only pseudo-data reweighted

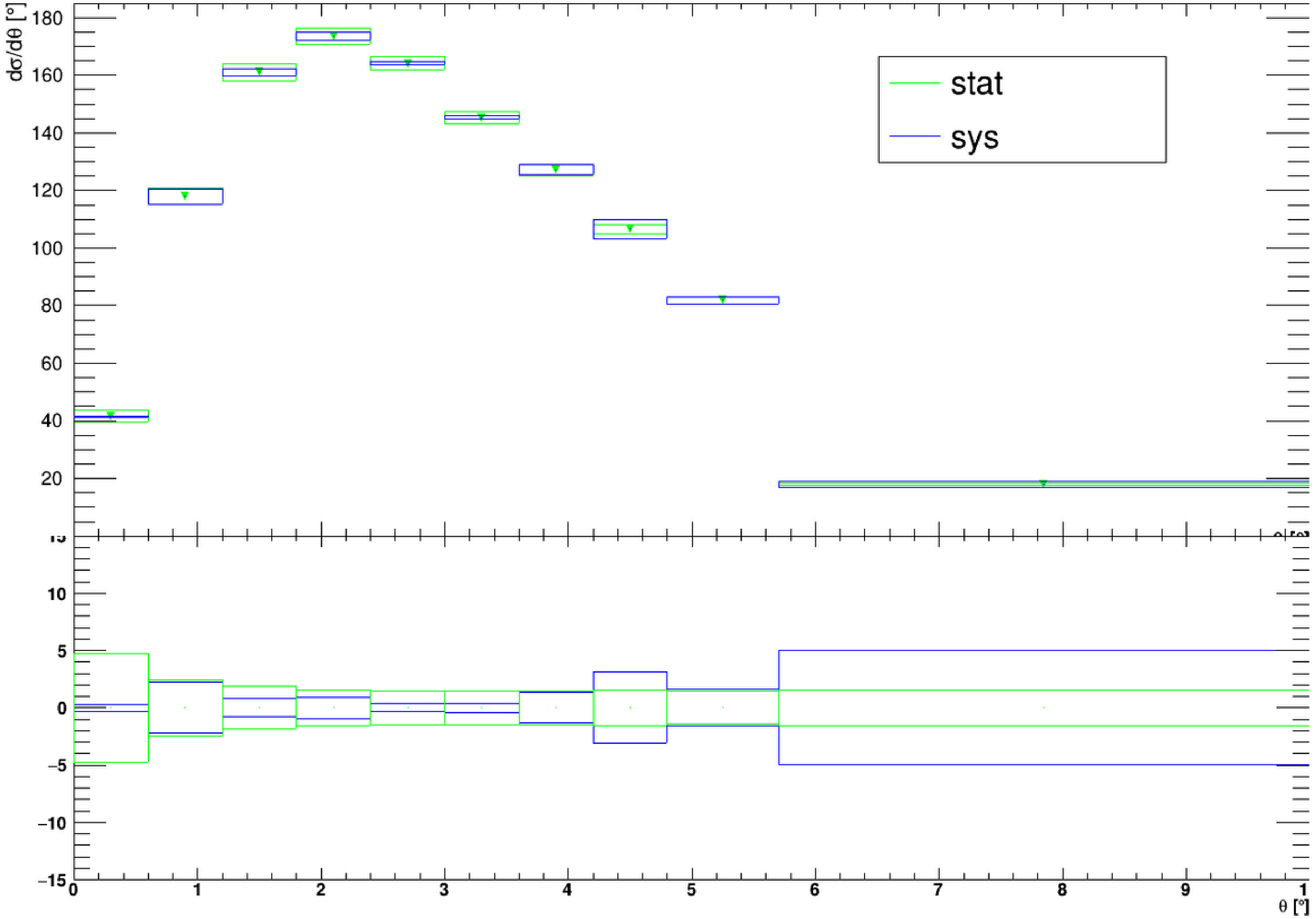


Both pseudo-data and truth reweighted

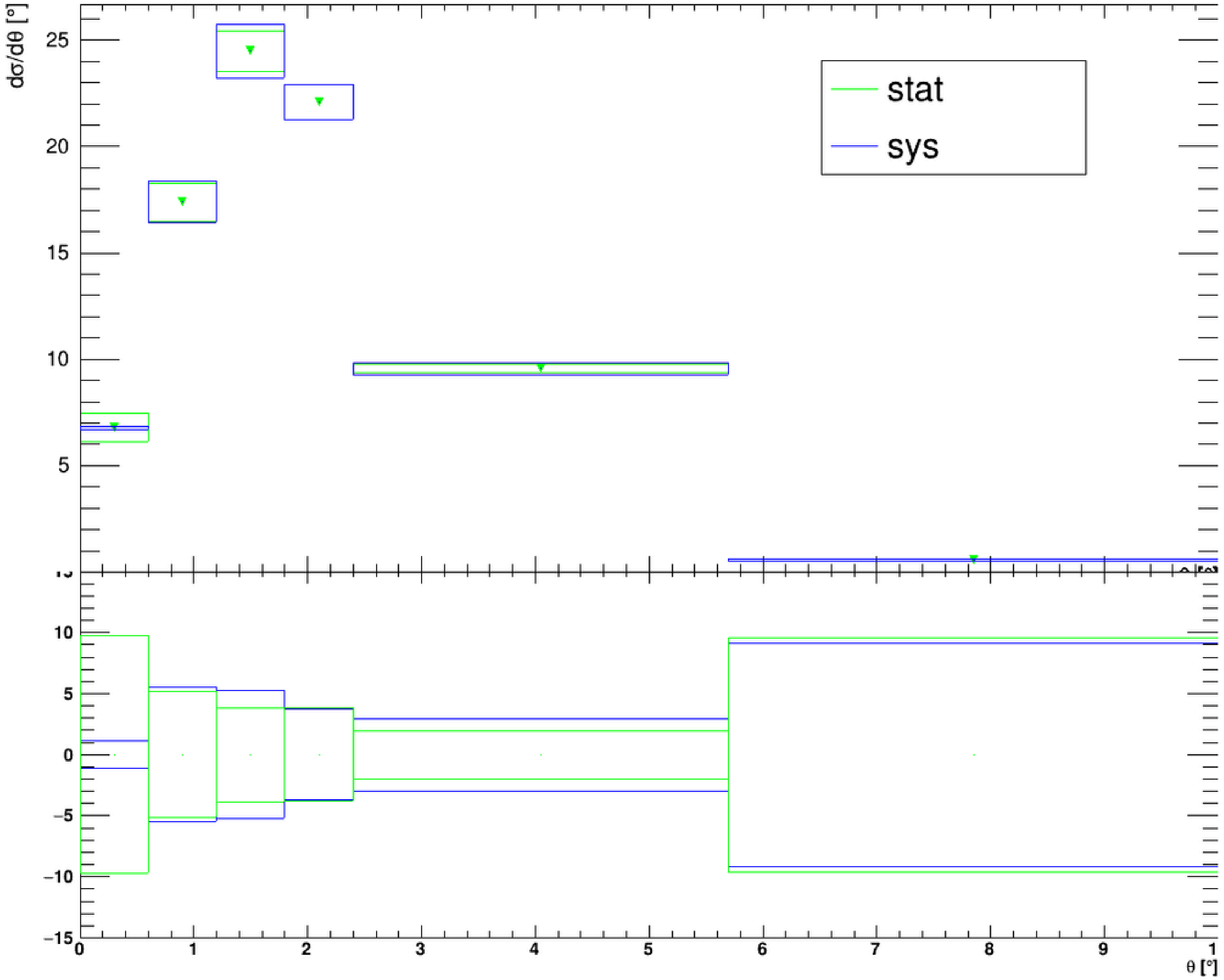


Merge all statistics

Z=2

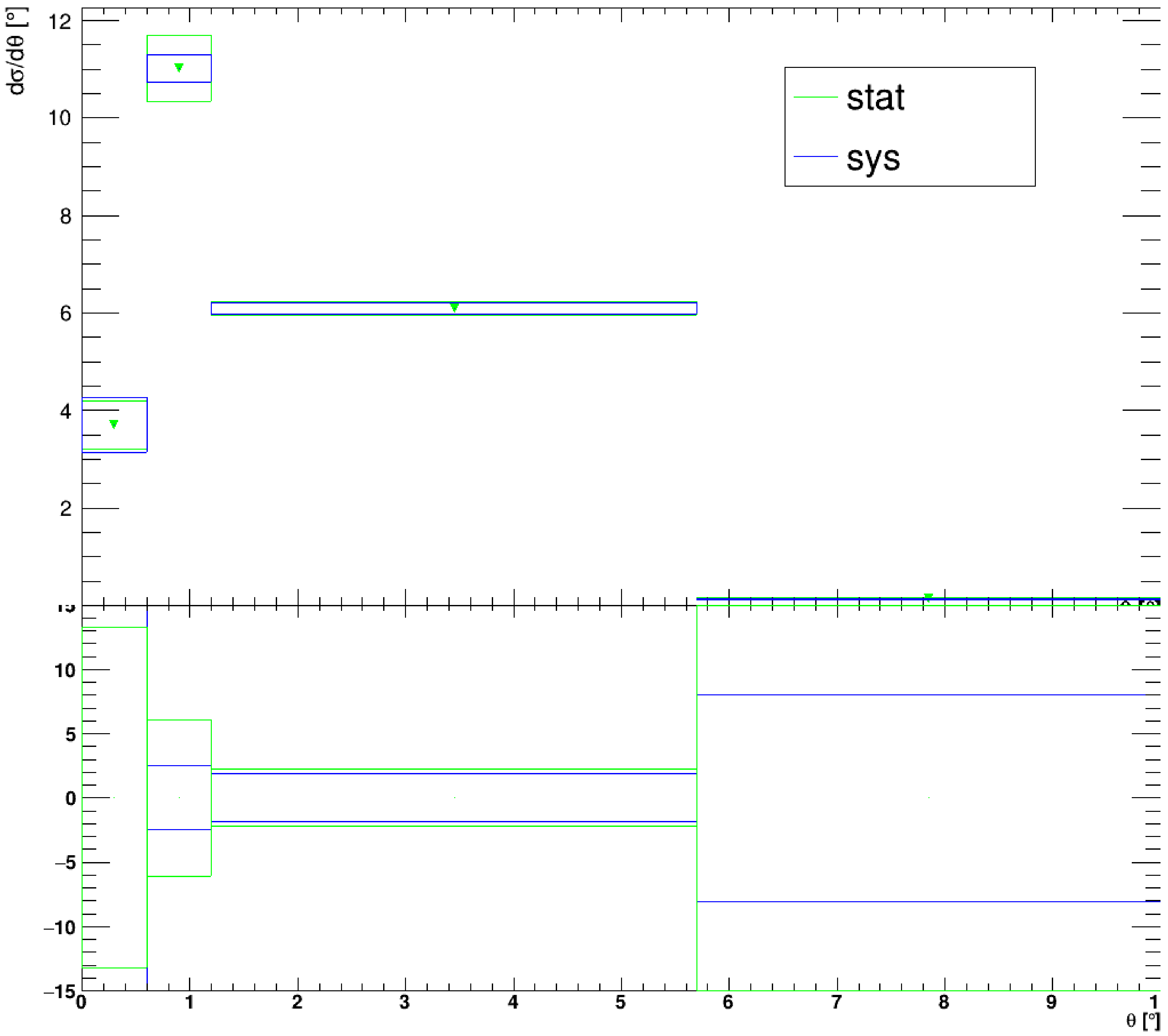


Z=3

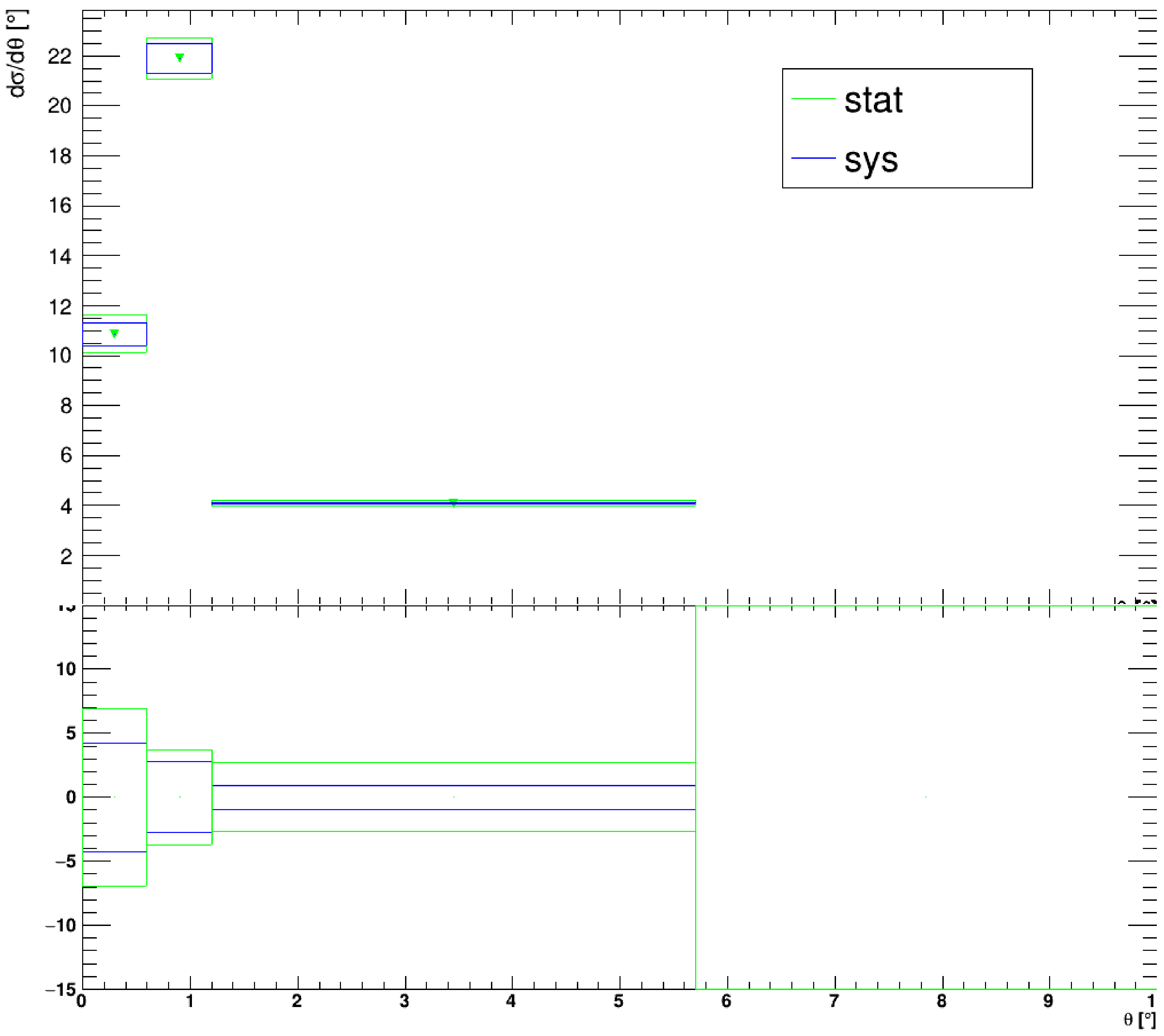


Merge all statistics

Z=4

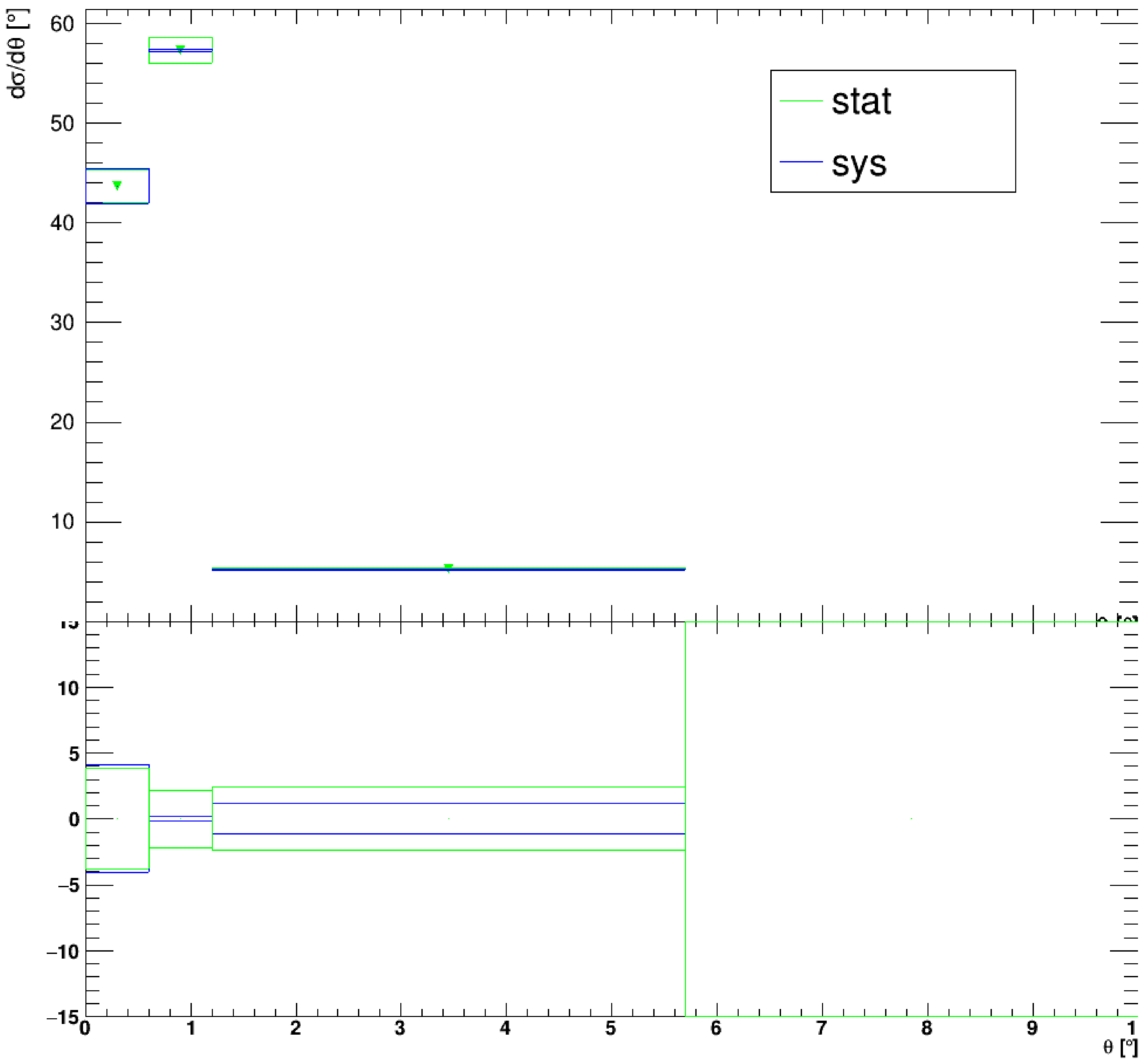


Z=5

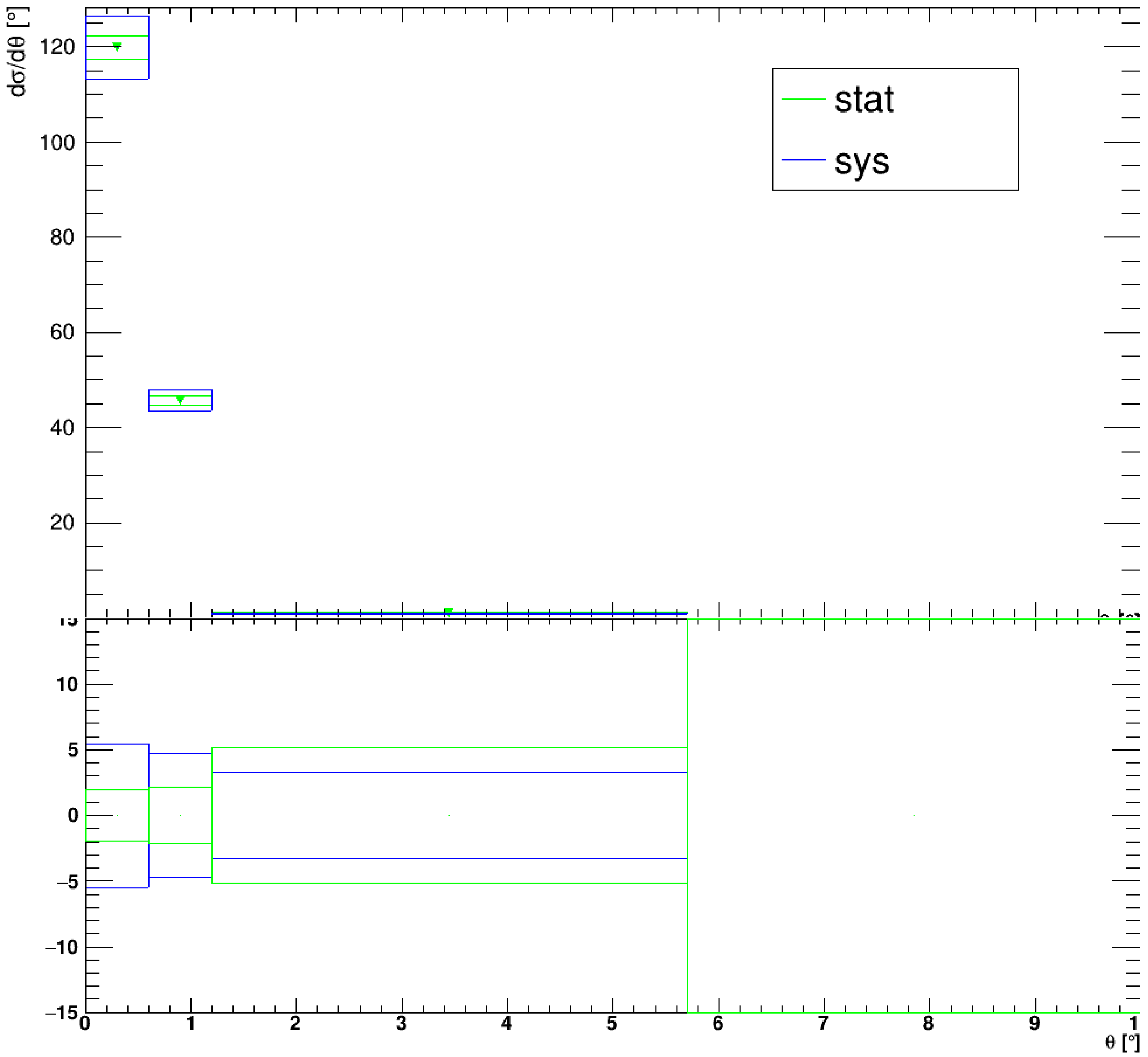


Merge all statistics

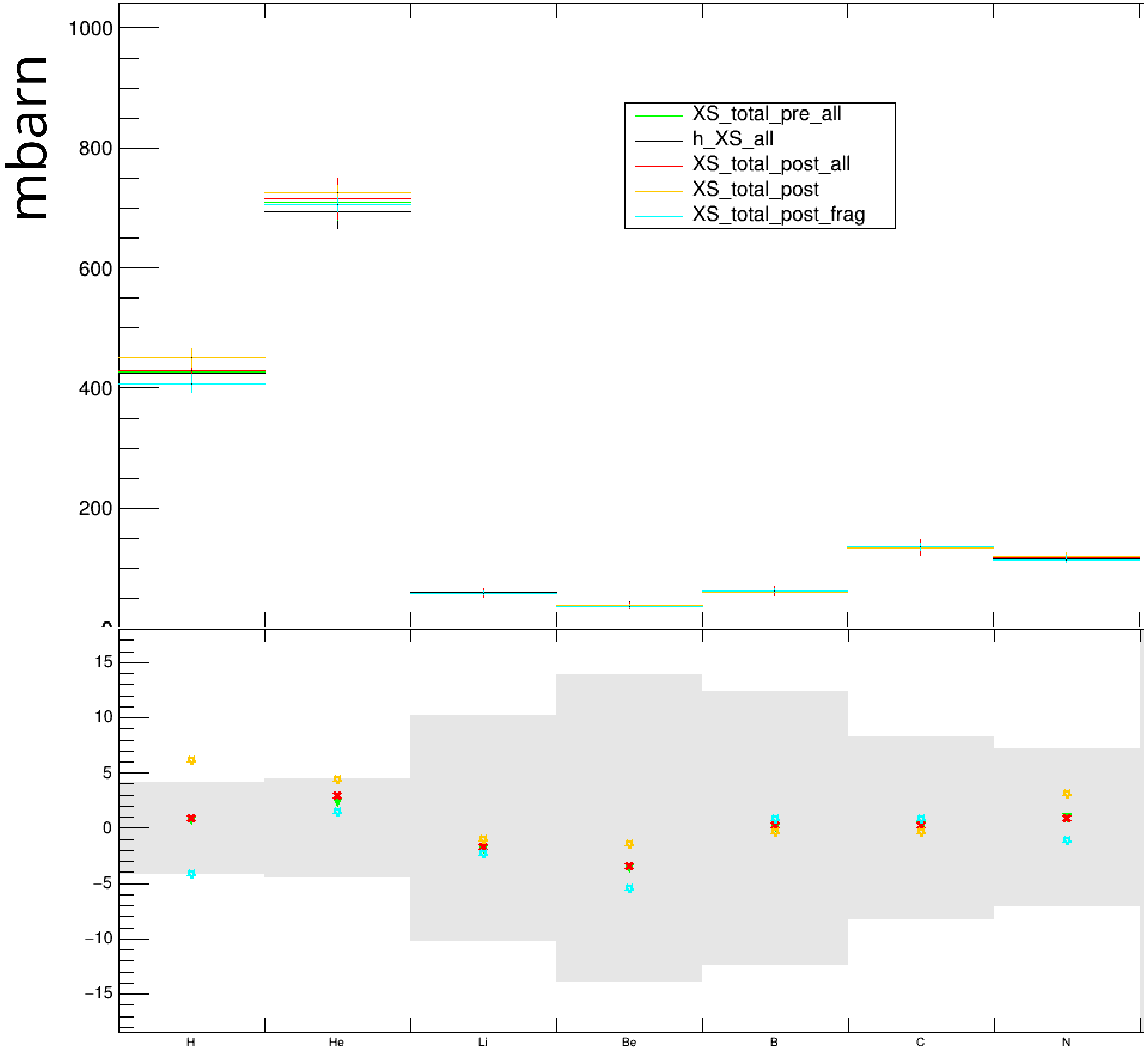
Z=6



Z=7



Merge all statistics



Next steps

Data seem to agree among runs

Merged all the statistics with target

Added systematics of the subtraction method

Bayes selected as unfolding method, others in systematics

Geometric efficiency to add for Z=2

We can start writing!

Thanks for listening!