

GSI2021 analysis without tracking

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Cross section measurement

With available data total integrated and angle differential cross section are achievable (no kinetic energy)

$$\Delta\sigma(Z) = \int_{\beta_{\min}}^{\beta_{\max}} \int_0^{\theta_{\max}} \left(\frac{\partial^2 \sigma}{\partial \theta \partial \beta} \right) d\theta d\beta = \frac{Y(Z)}{N_{\text{prim}} \cdot N_{\text{TG}} \cdot \varepsilon(Z)}$$

Align FOOT detectors and estimate angular acceptance

Extract fragment yields from TW

Calculate MC efficiencies for fragments

Evaluate the beta range from data and put in MC for efficiency calculations

Cross section measurement

With available data total integrated and angle differential cross section are achievable (no kinetic energy)

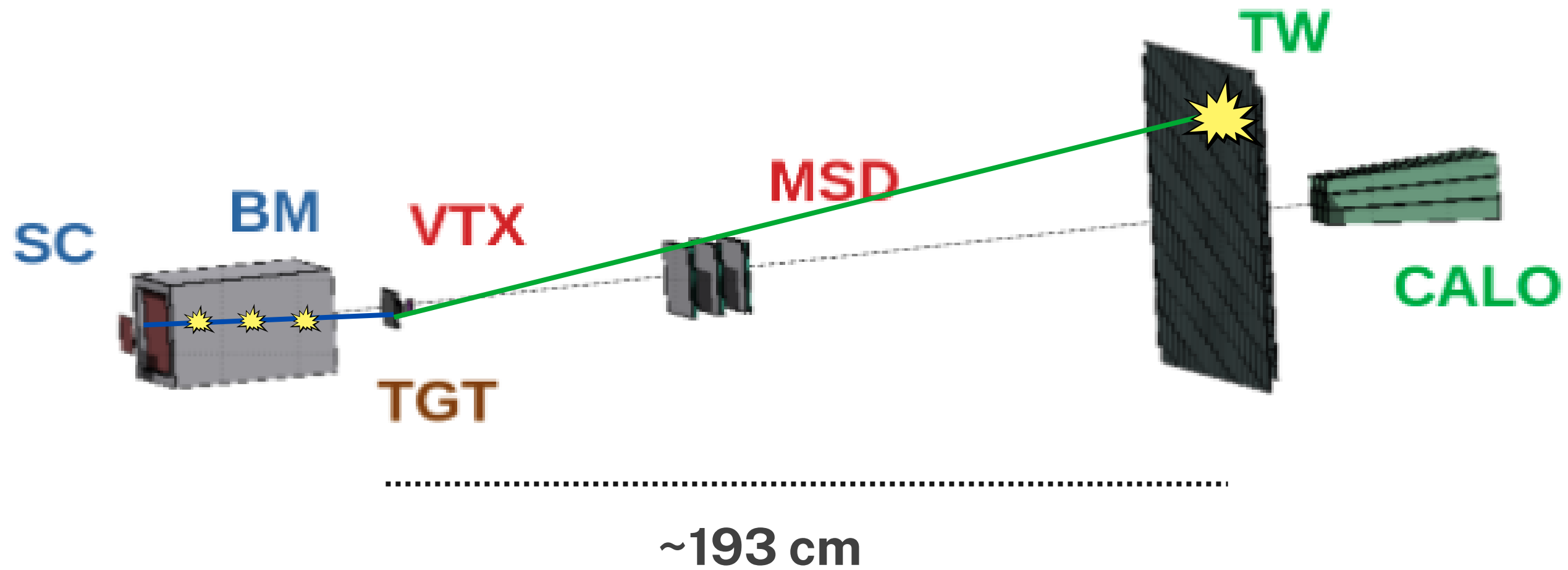
$$\frac{d\sigma}{d\theta}(Z) = \frac{Y(Z, \theta)}{N_{\text{prim}} \cdot N_{\text{TG}} \cdot \Delta\theta \cdot \varepsilon(Z, \theta)}$$

Align FOOT detectors and estimate angular acceptance

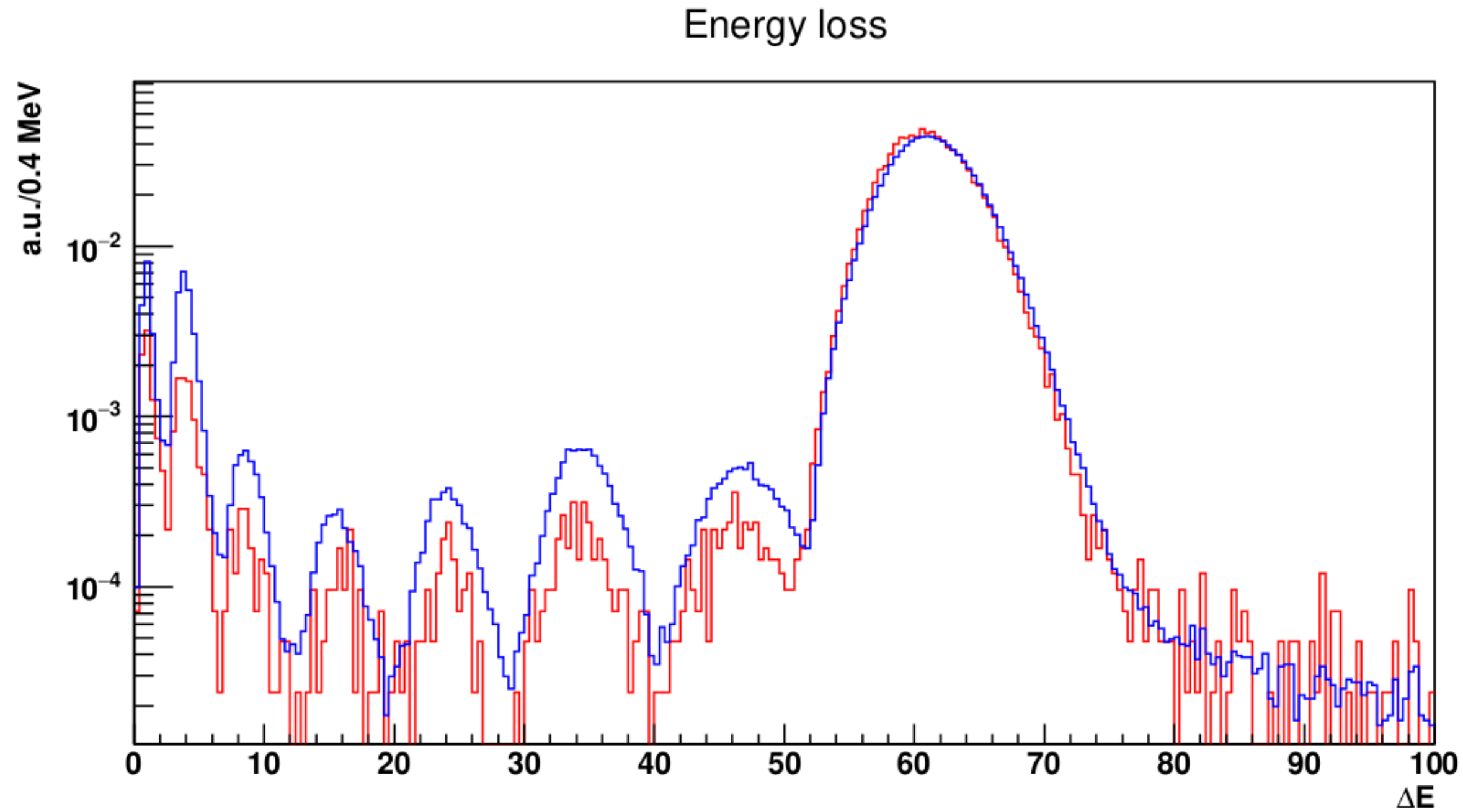
Extract fragment yields from TW

Calculate MC efficiencies for fragments

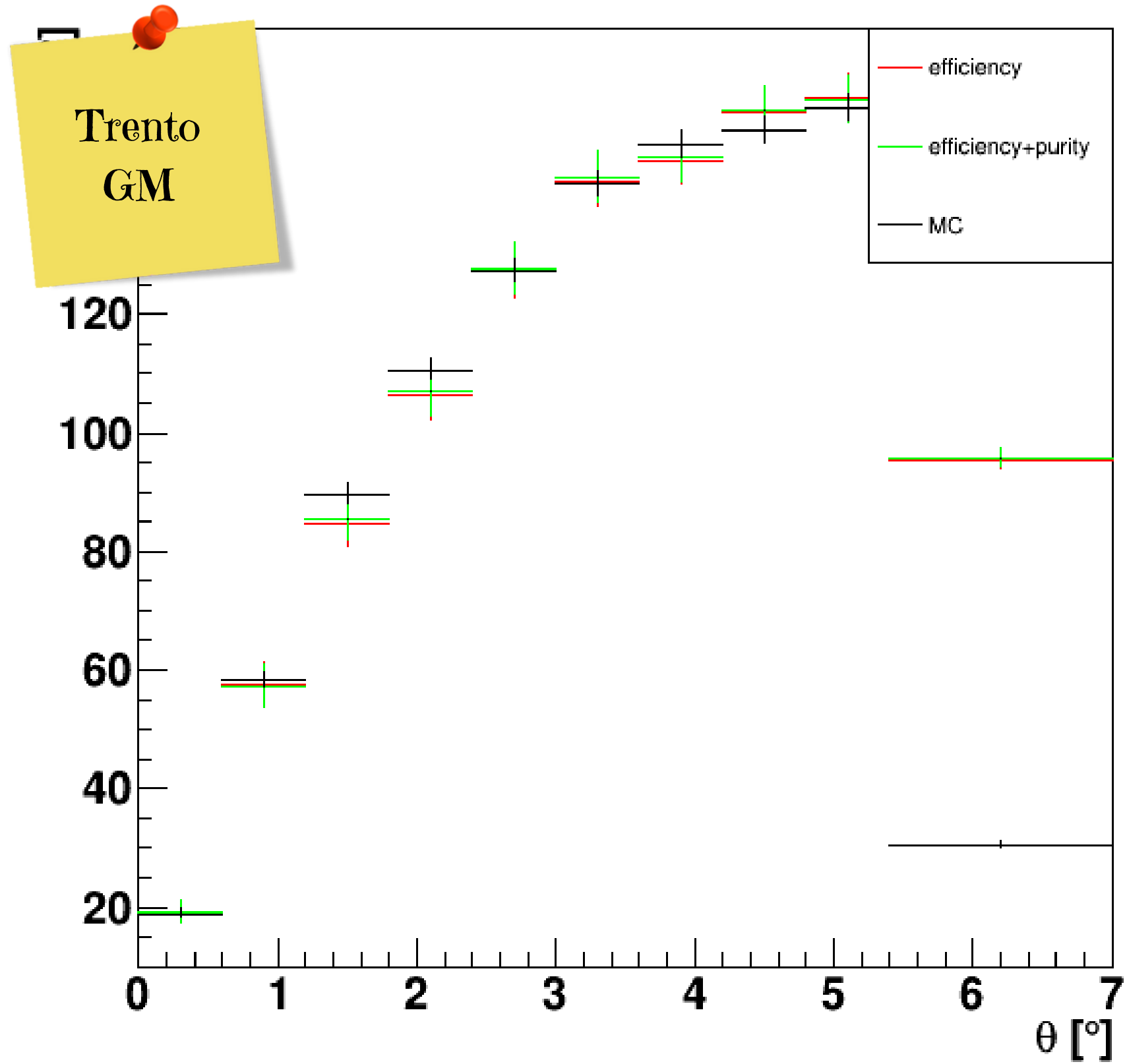
Angle measurement



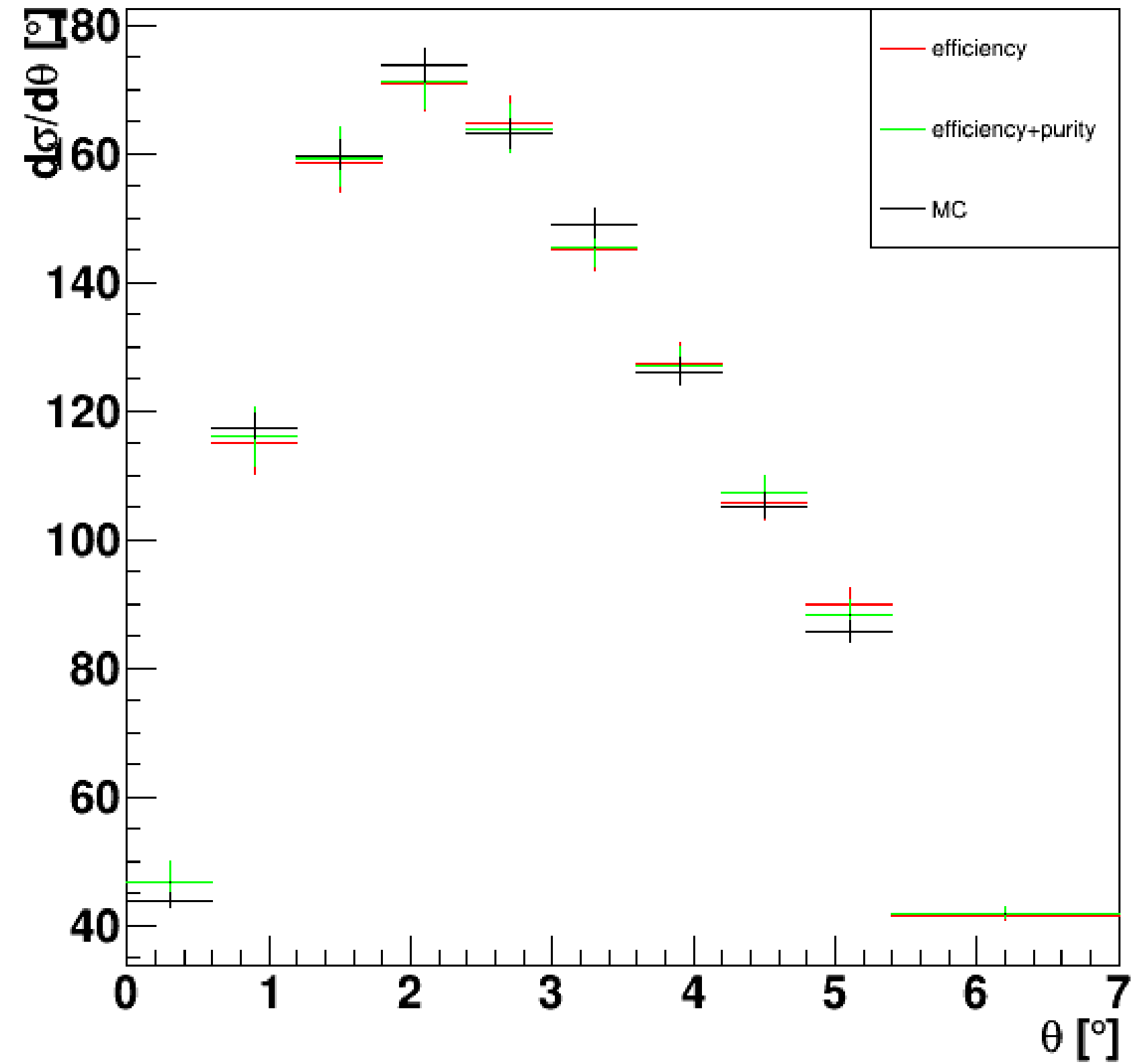
Why background subtraction?



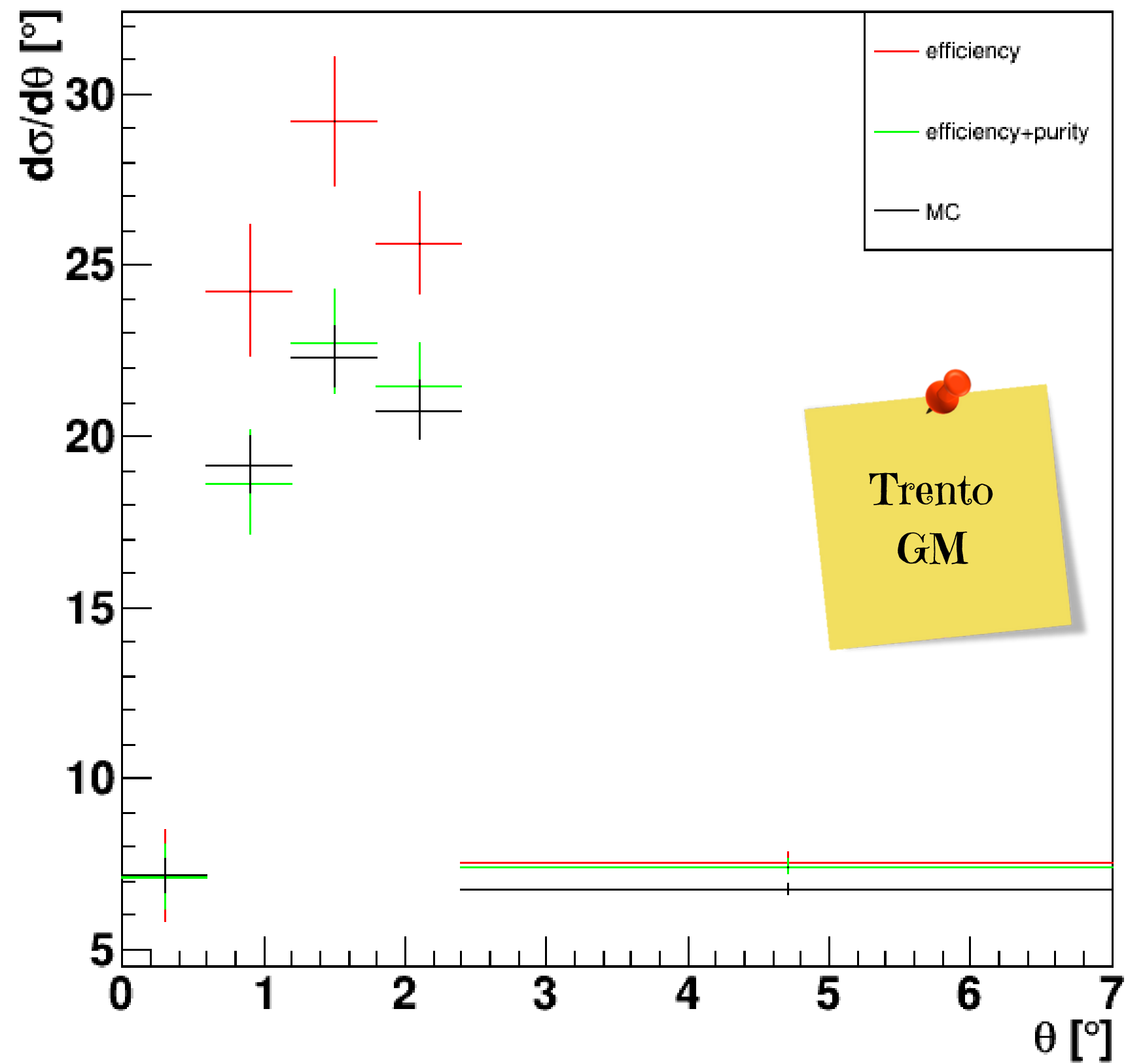
Angular cross section Z1



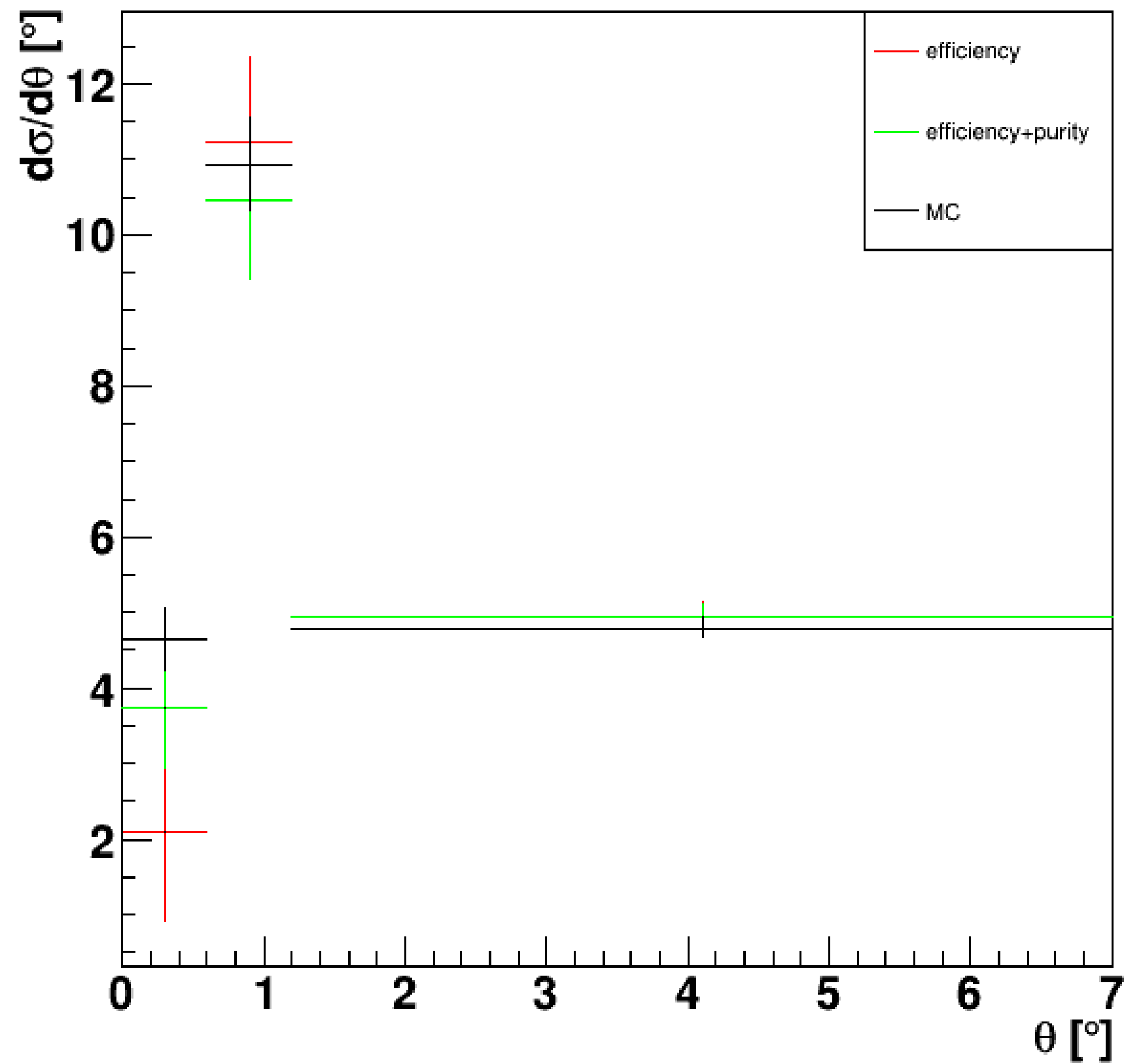
Angular cross section Z2



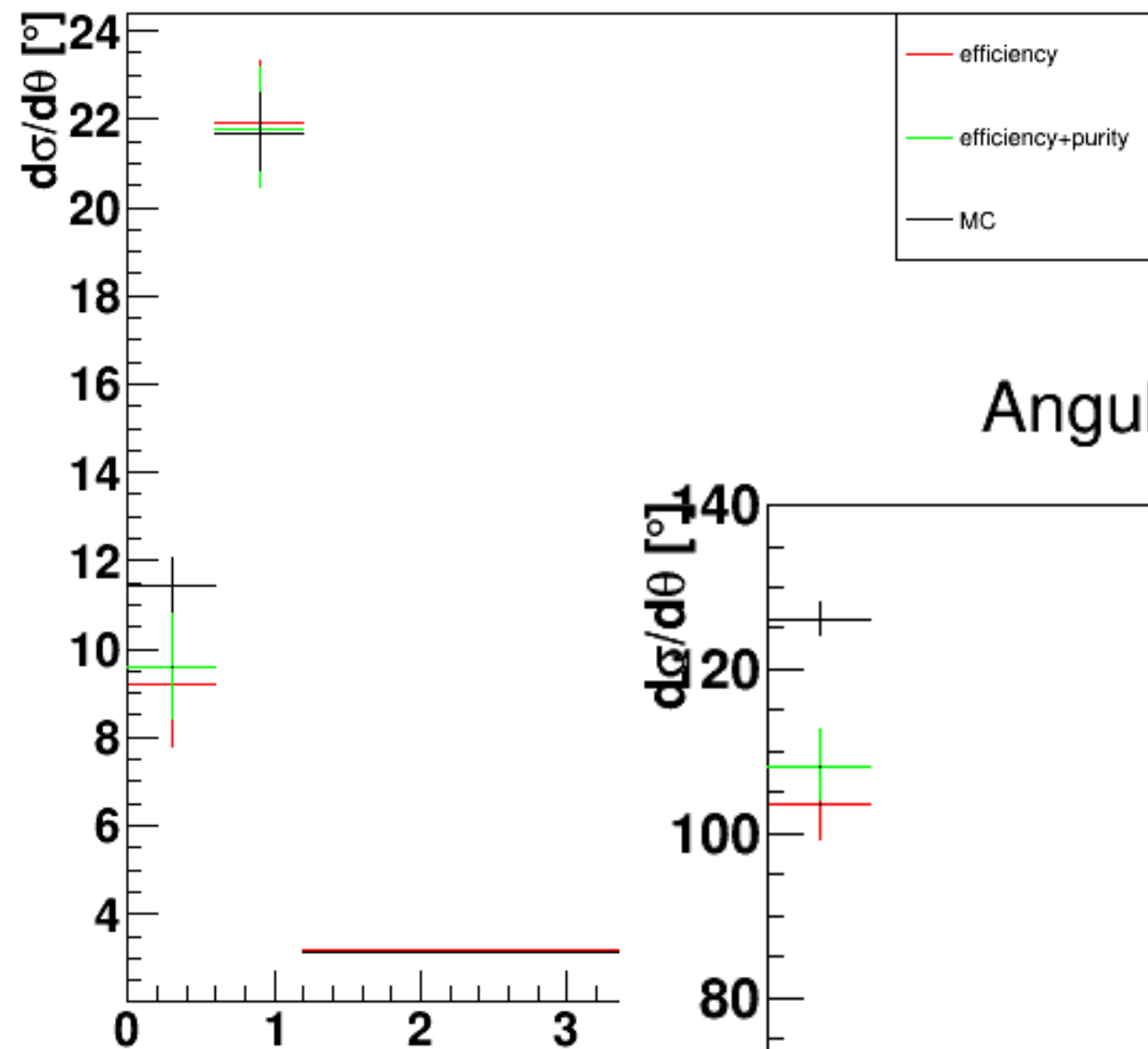
Angular cross section Z3



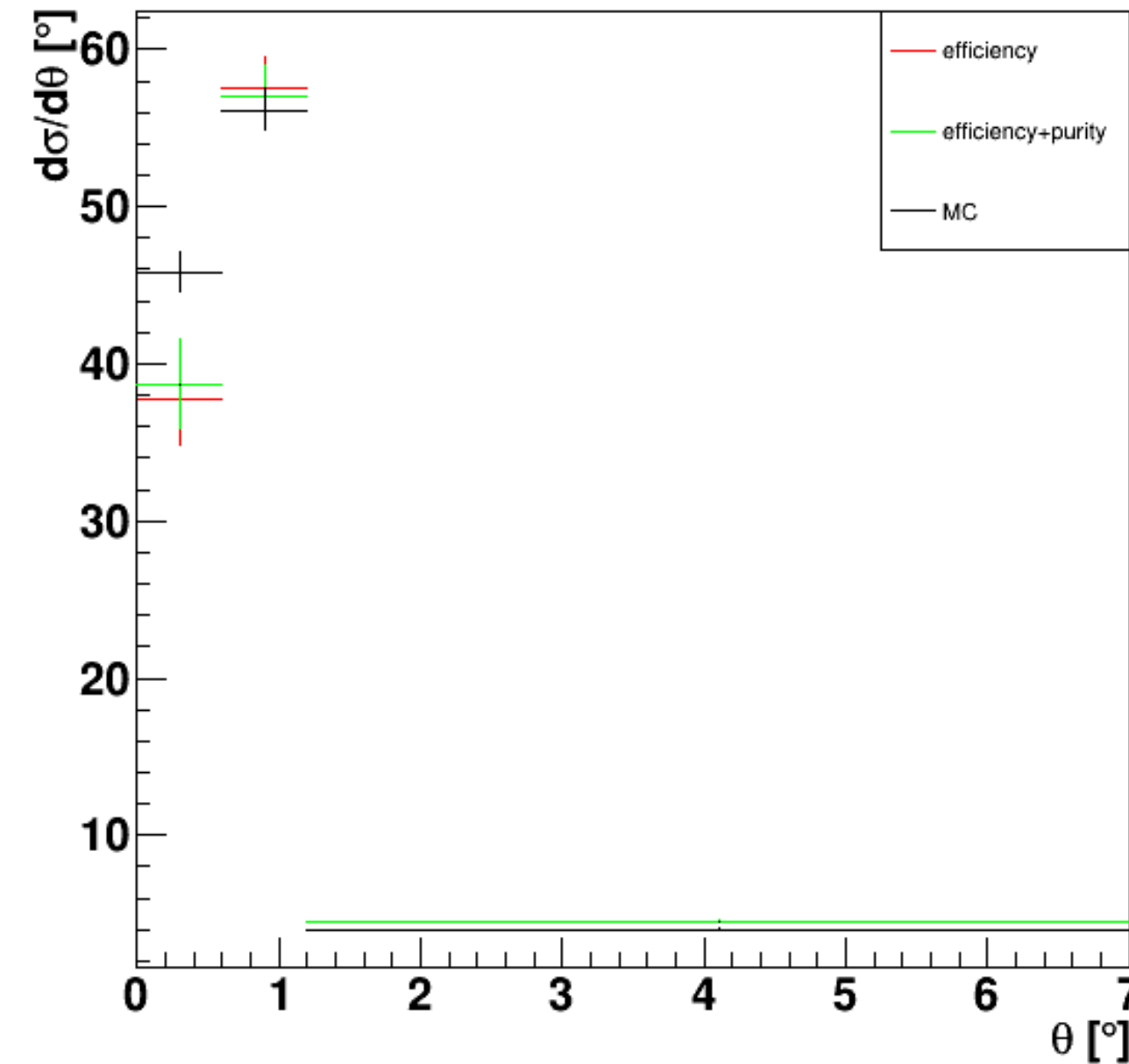
Angular cross section Z4



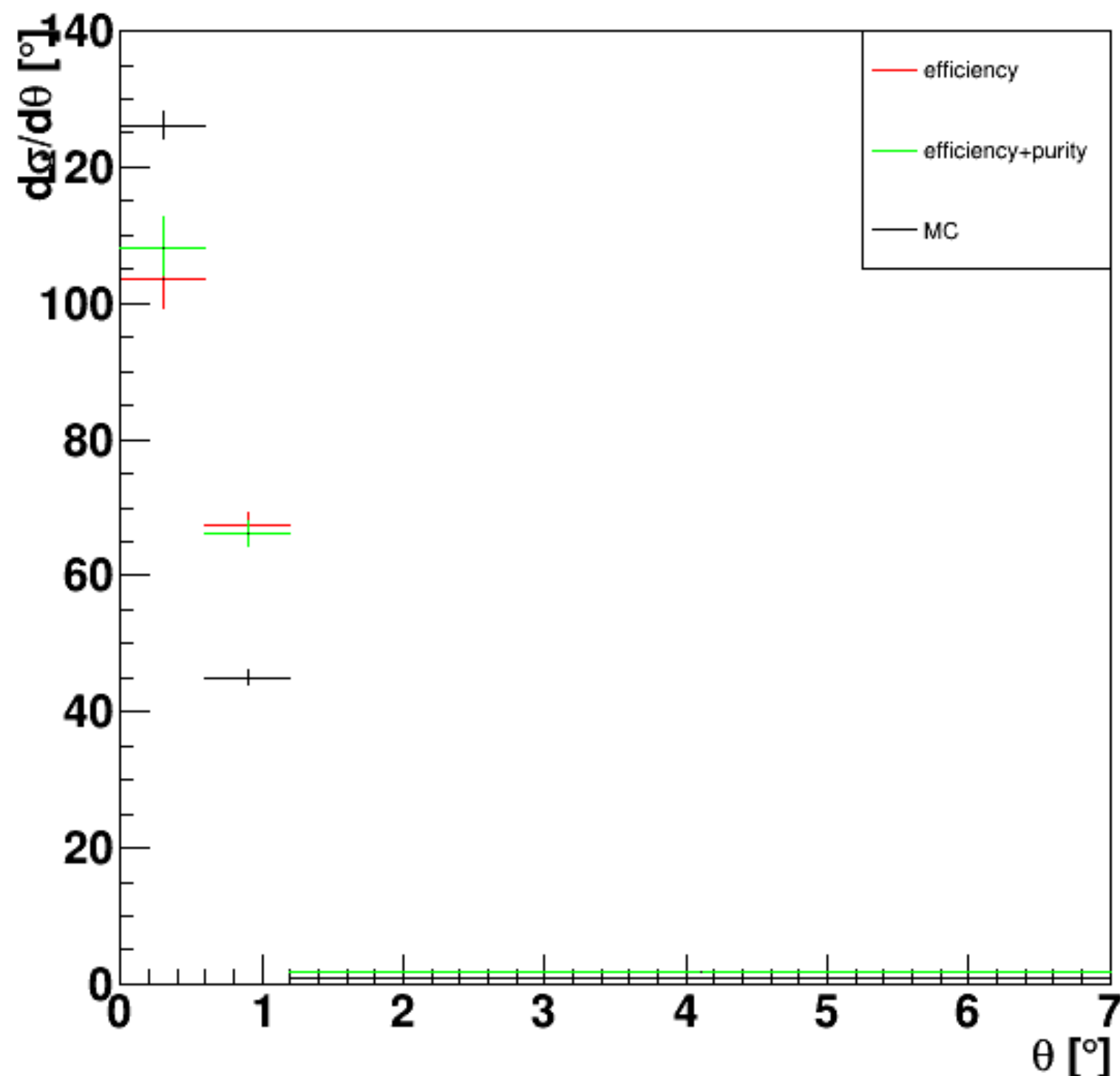
Angular cross section Z5

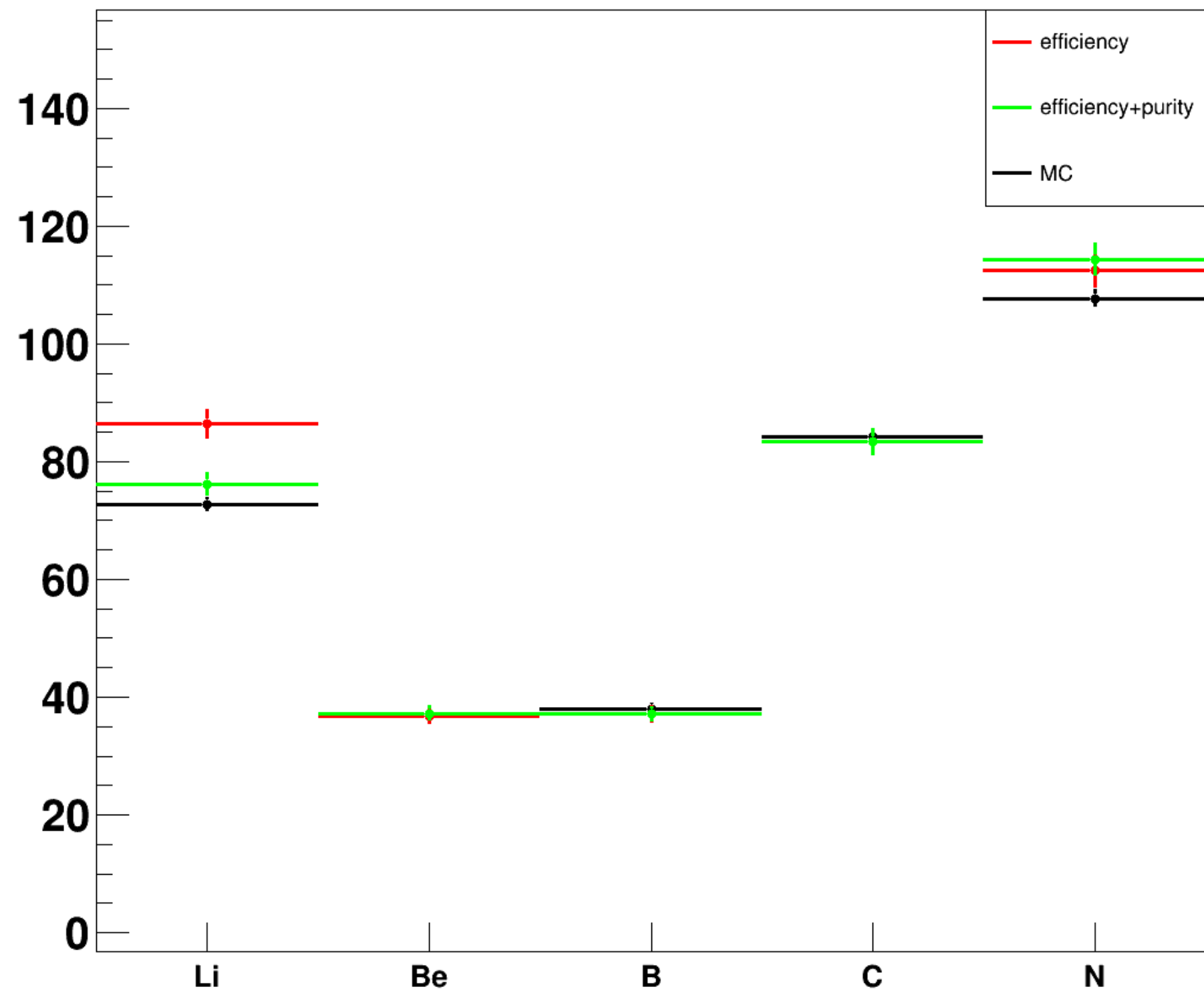
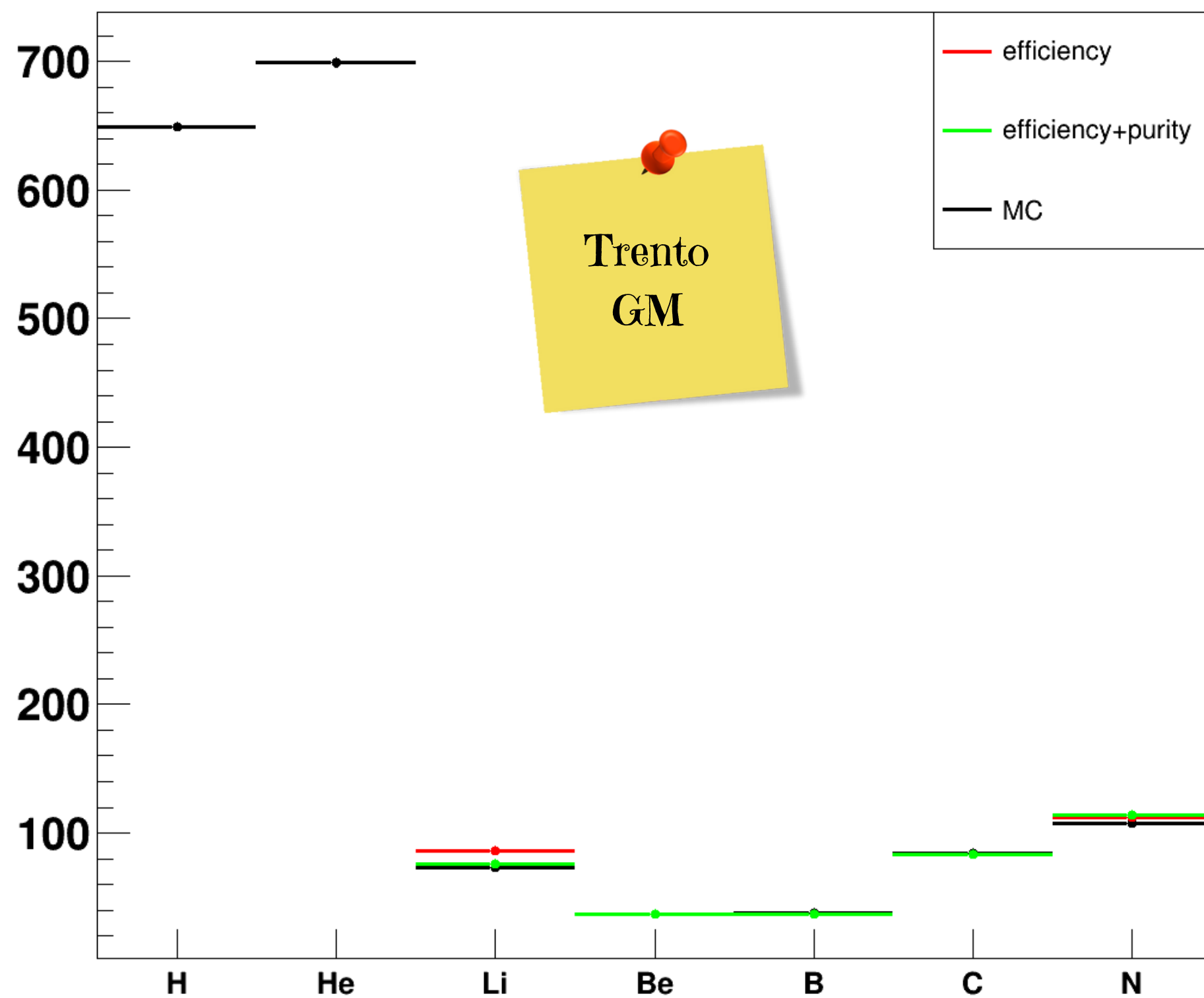


Angular cross section Z6



Angular cross section Z7





Some comments...



Trento
GM

Purity correction goes always in the “right” direction

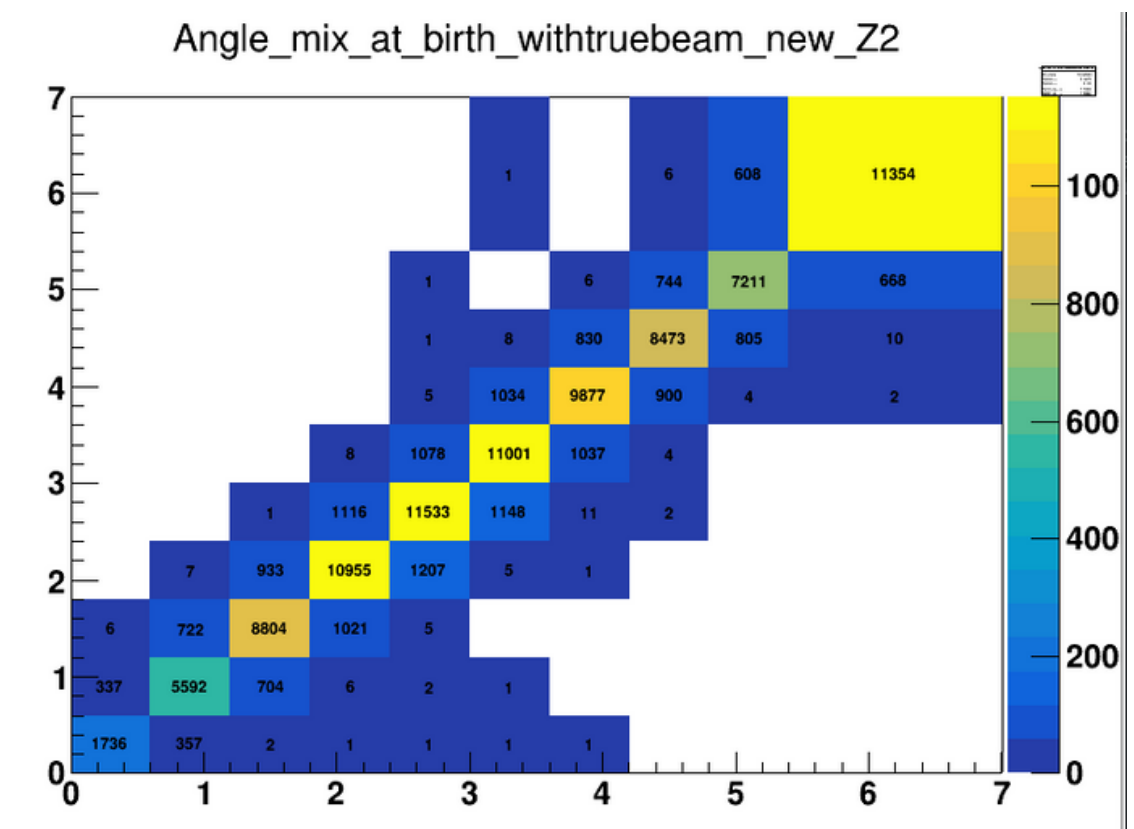
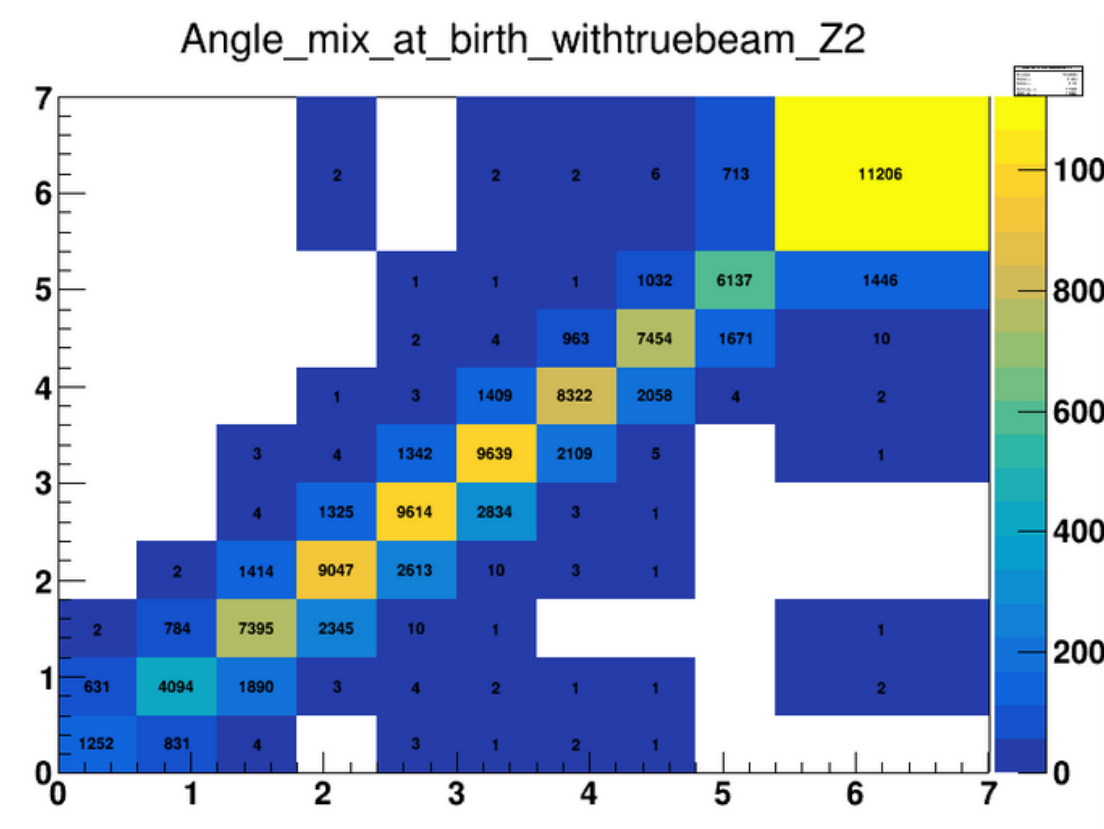
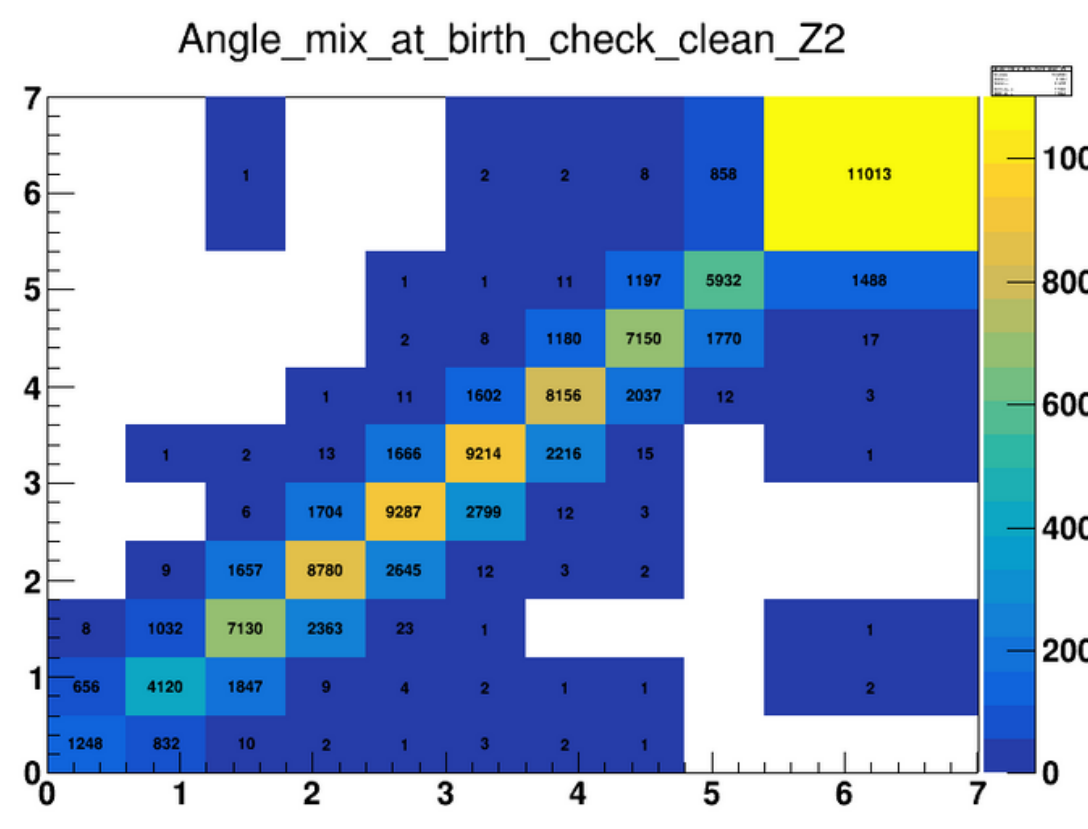
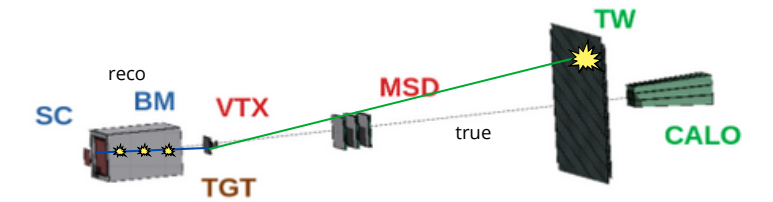
Huge contribution in Li (and Be) cross section as expected

Difference in C and N to be understood

Angle unfolding procedure will have an impact

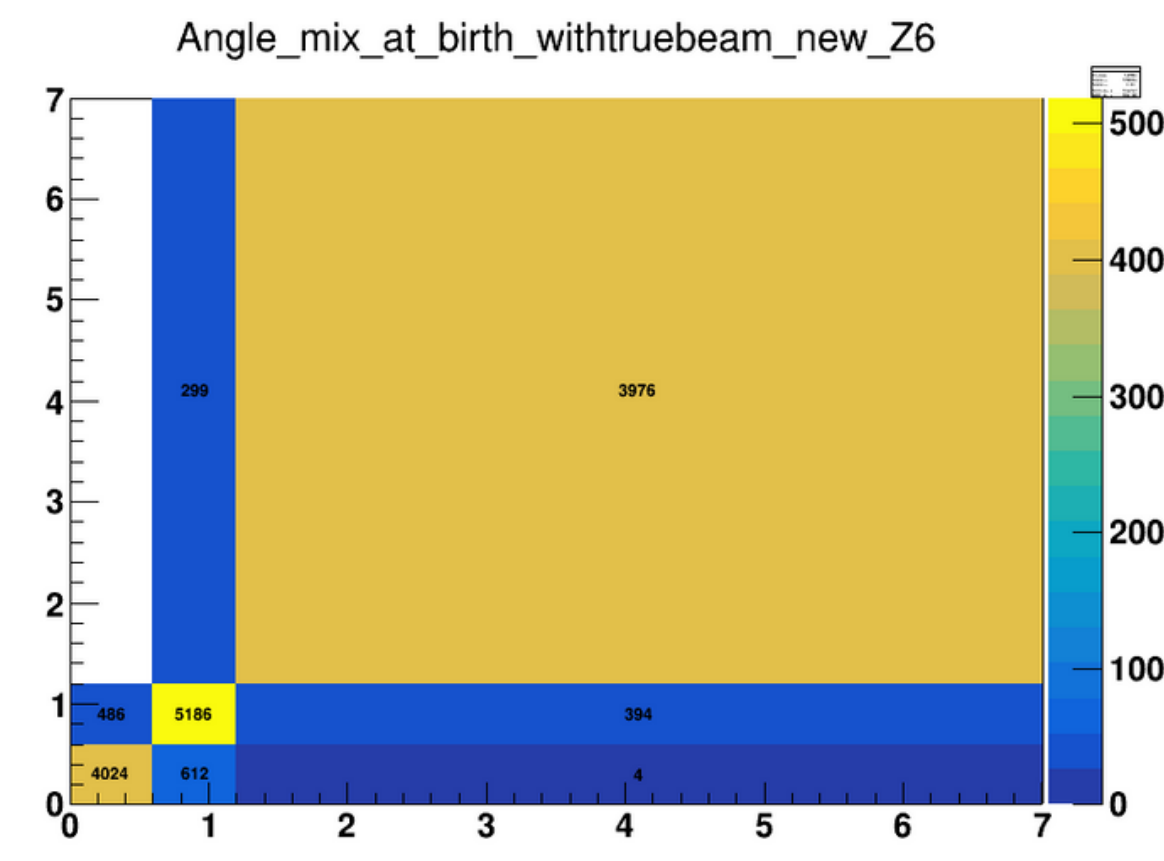
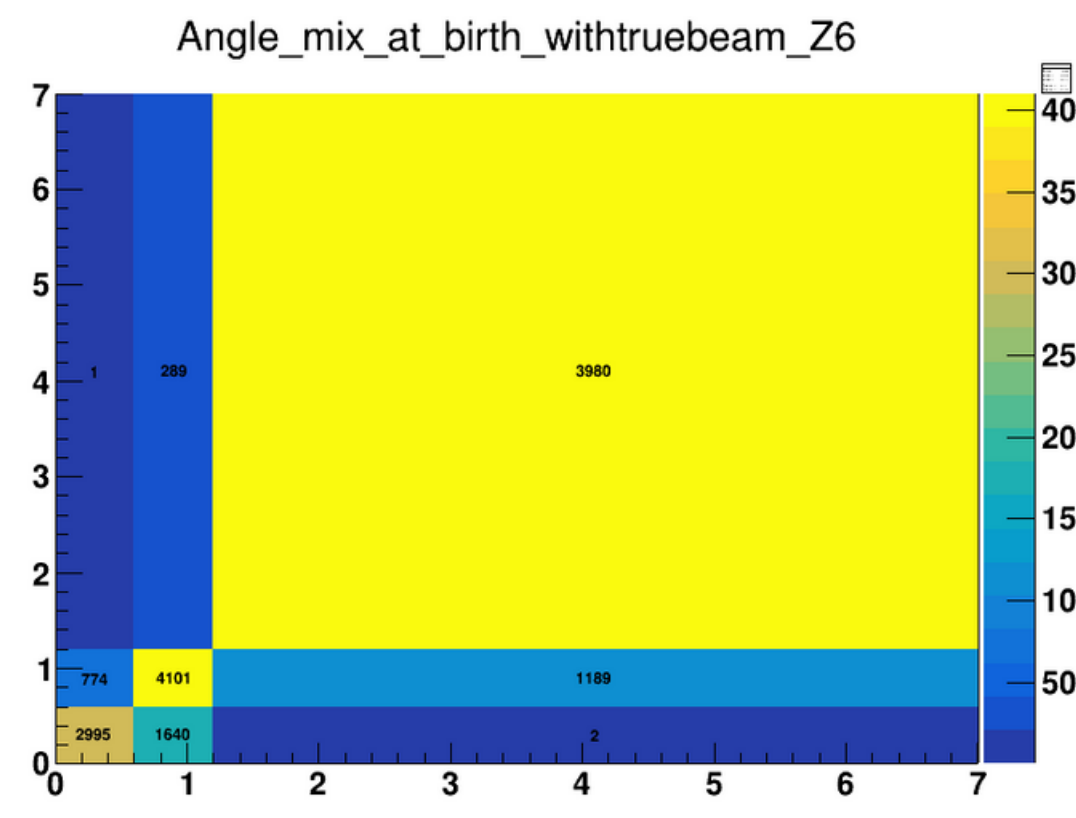
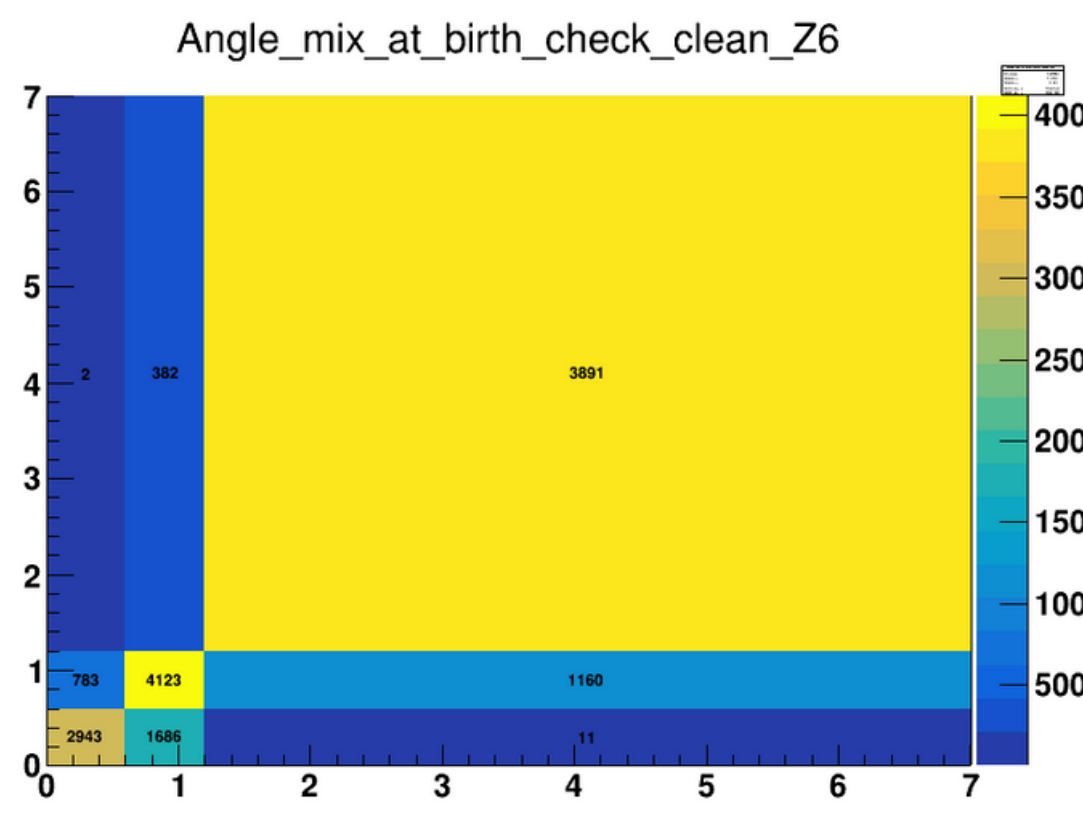
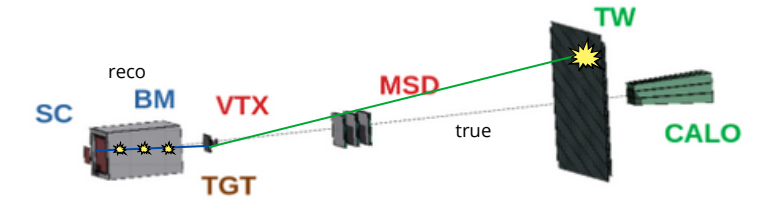
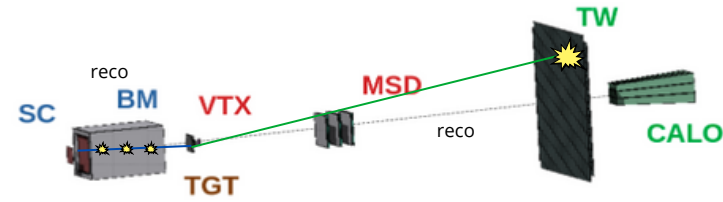
Why these differences?

Angle mixing with this method is not negligible...



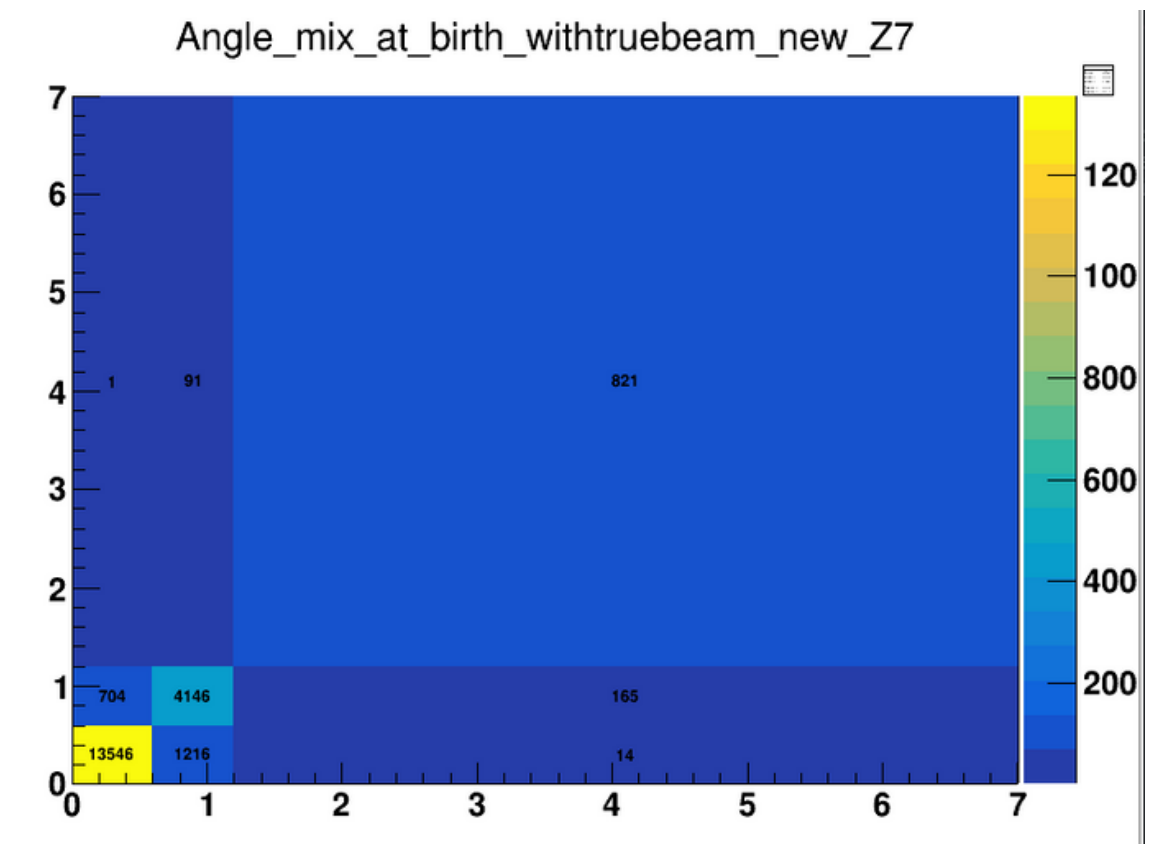
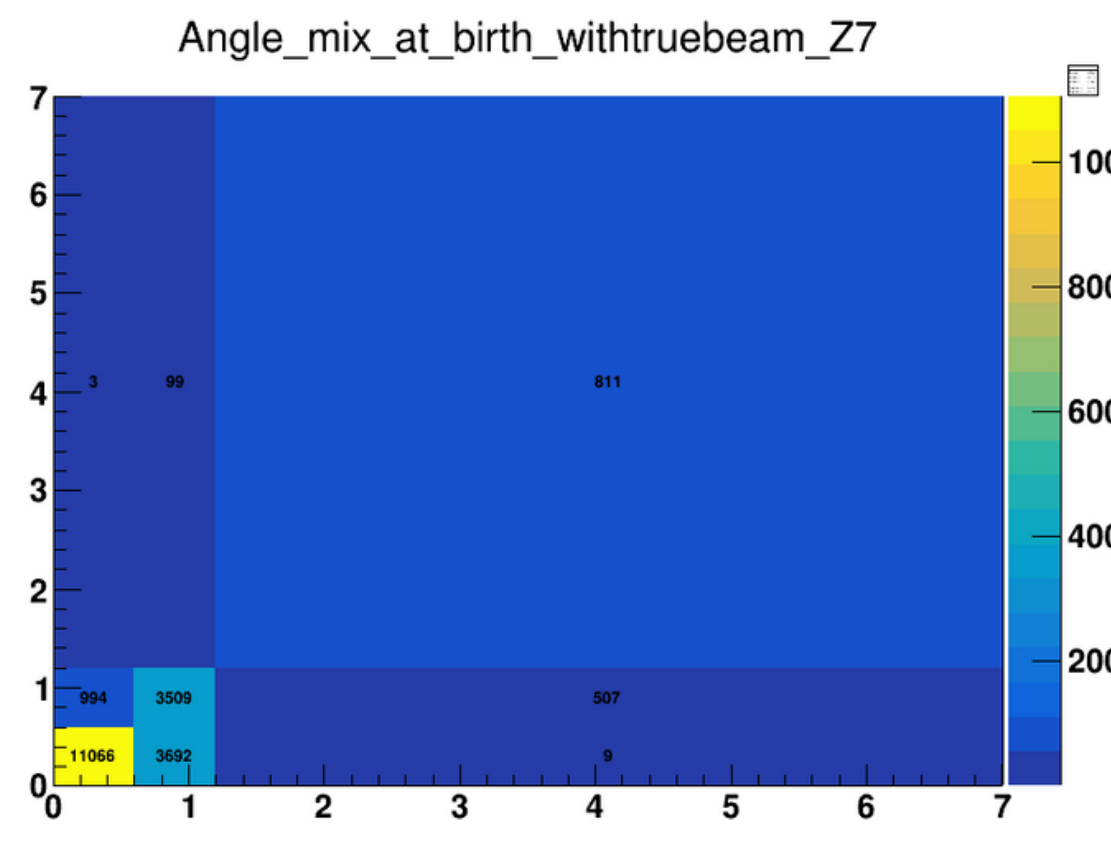
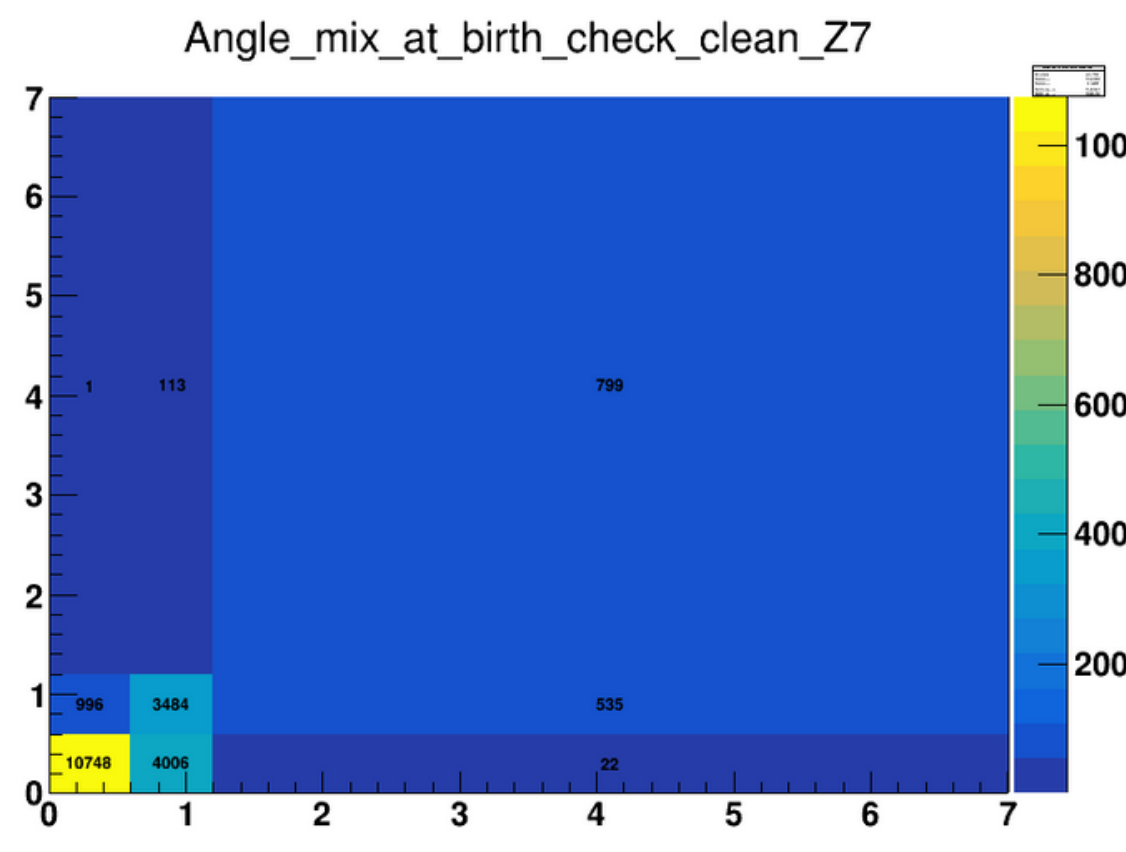
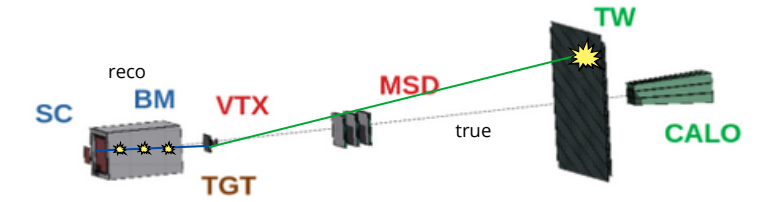
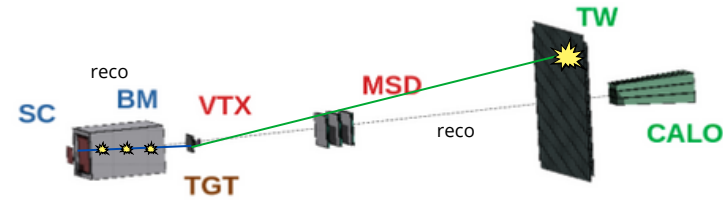
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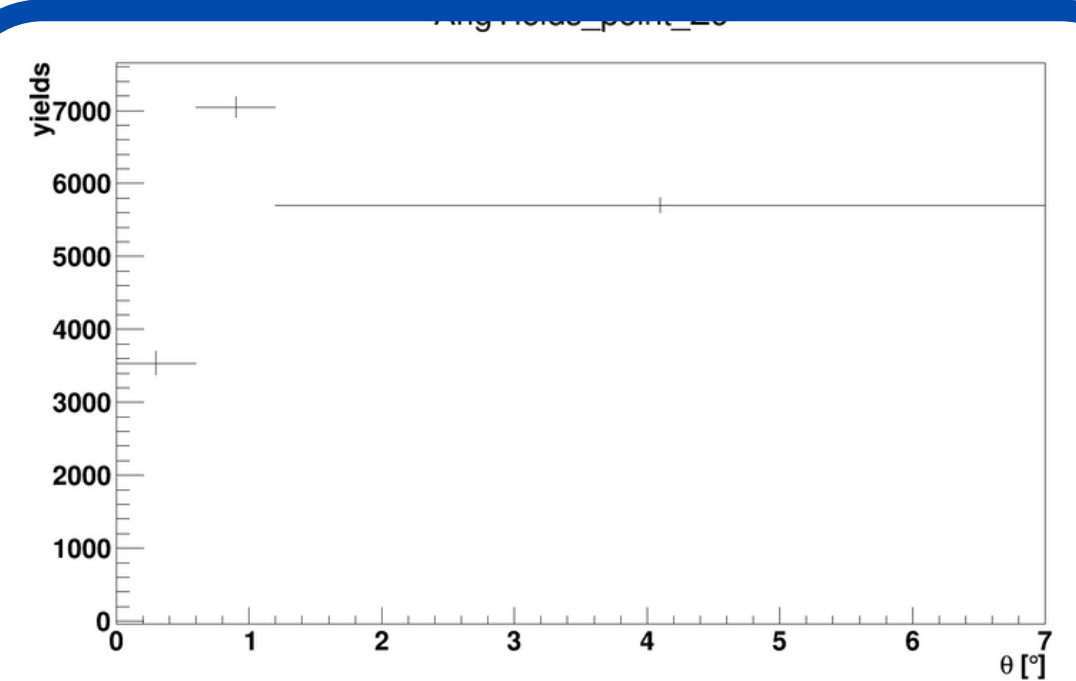
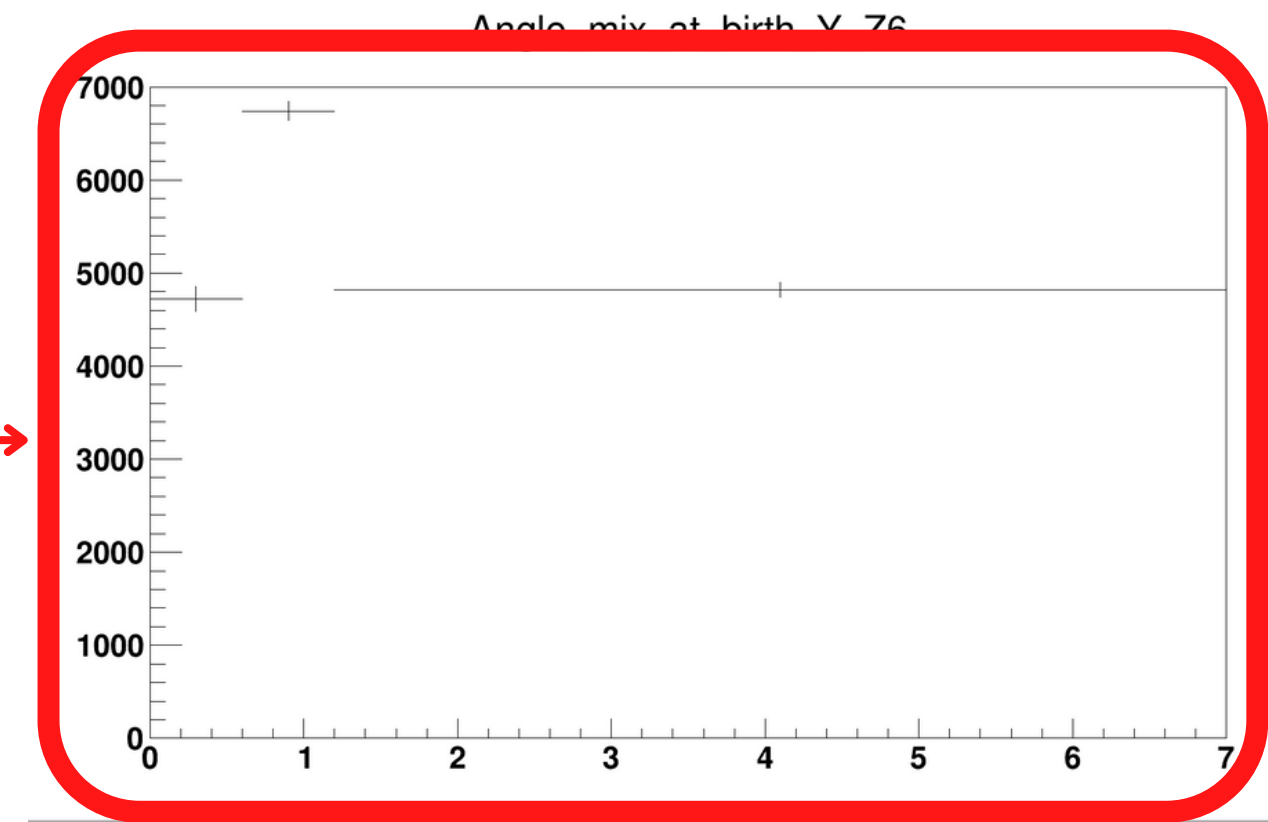
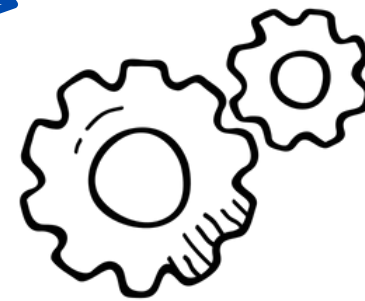
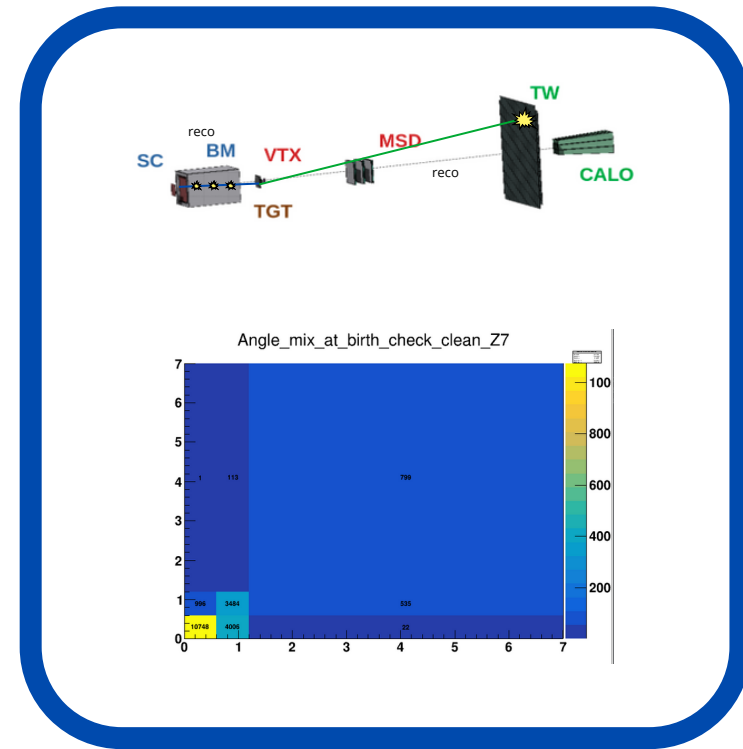
Why these differences?

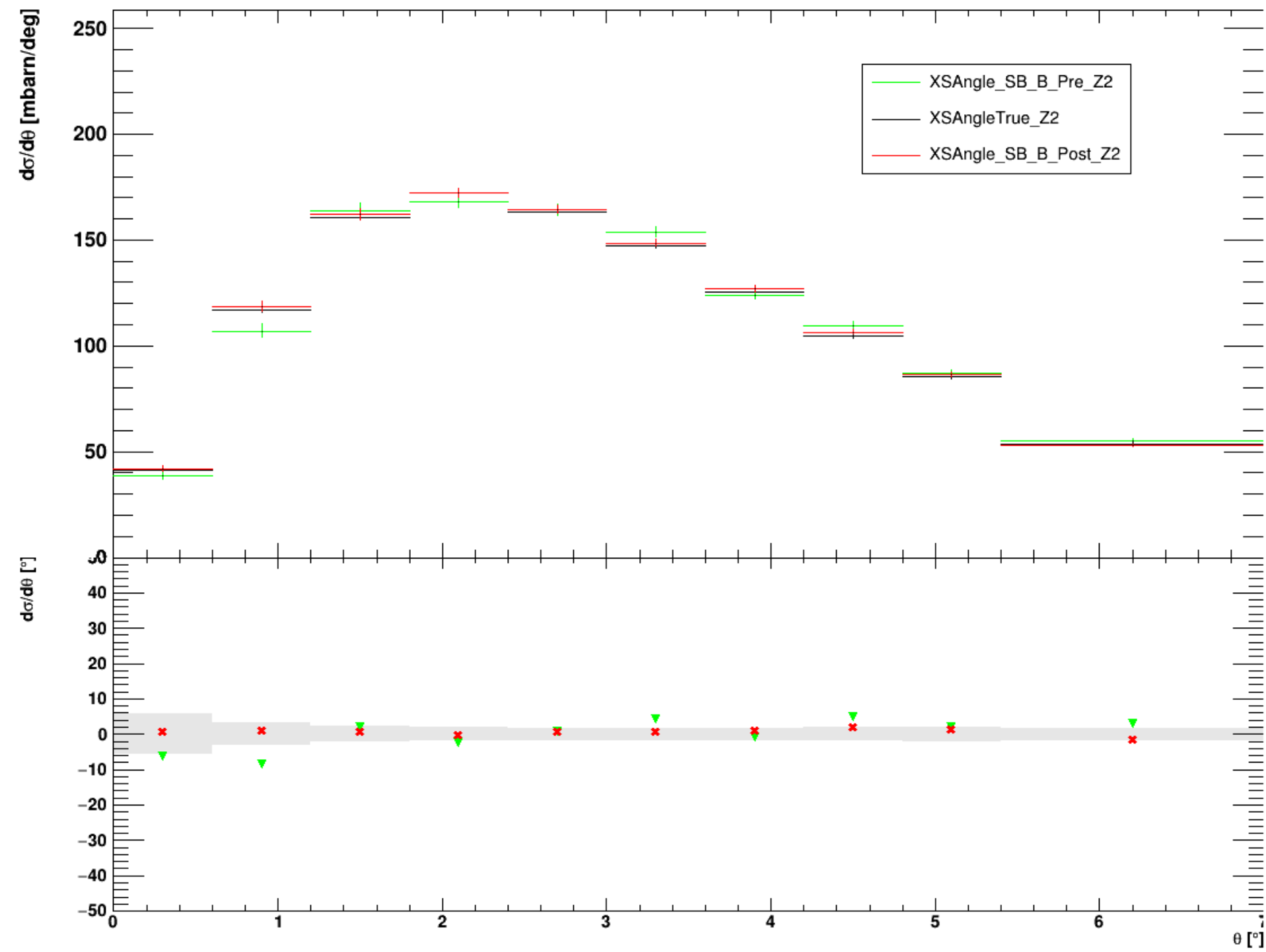
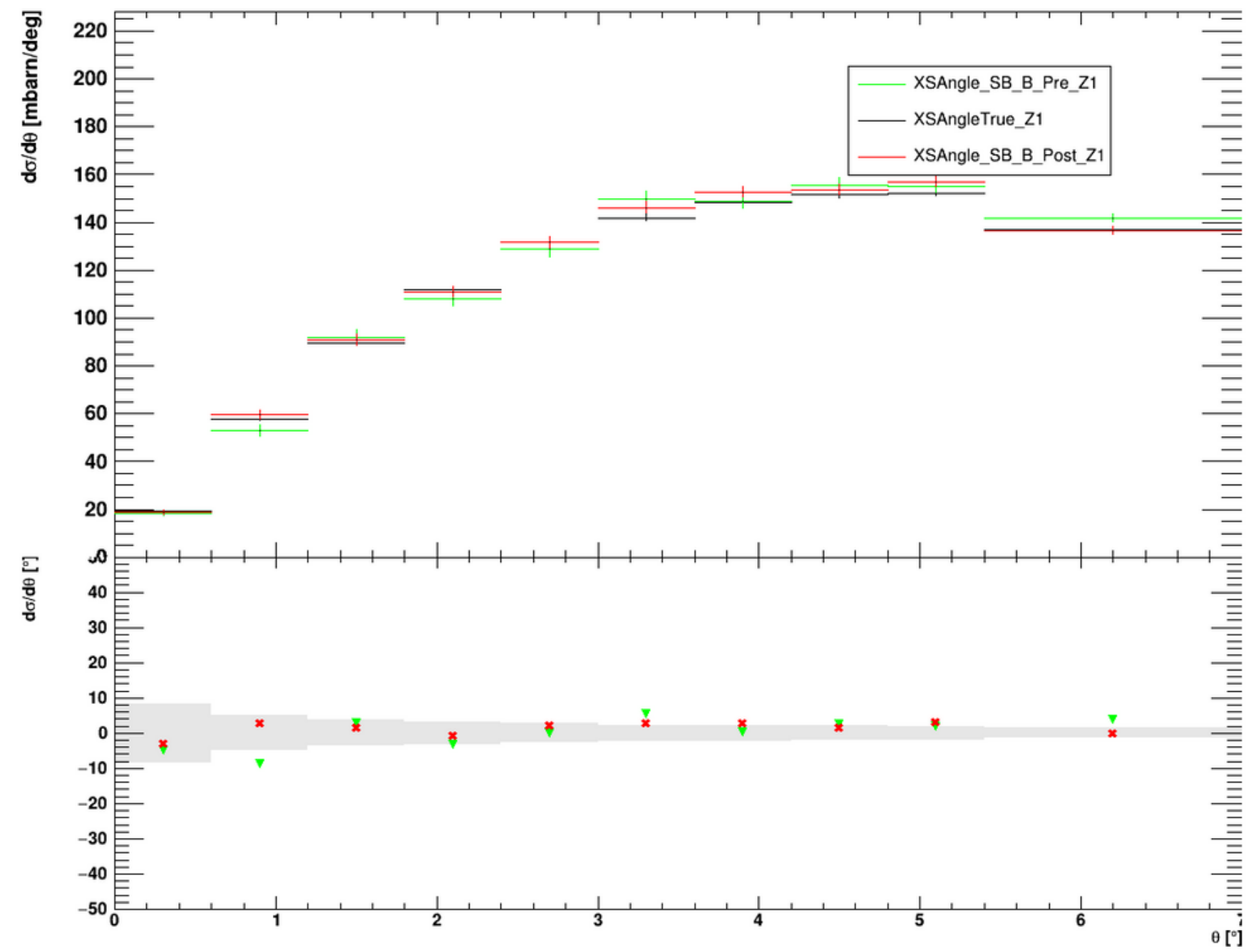
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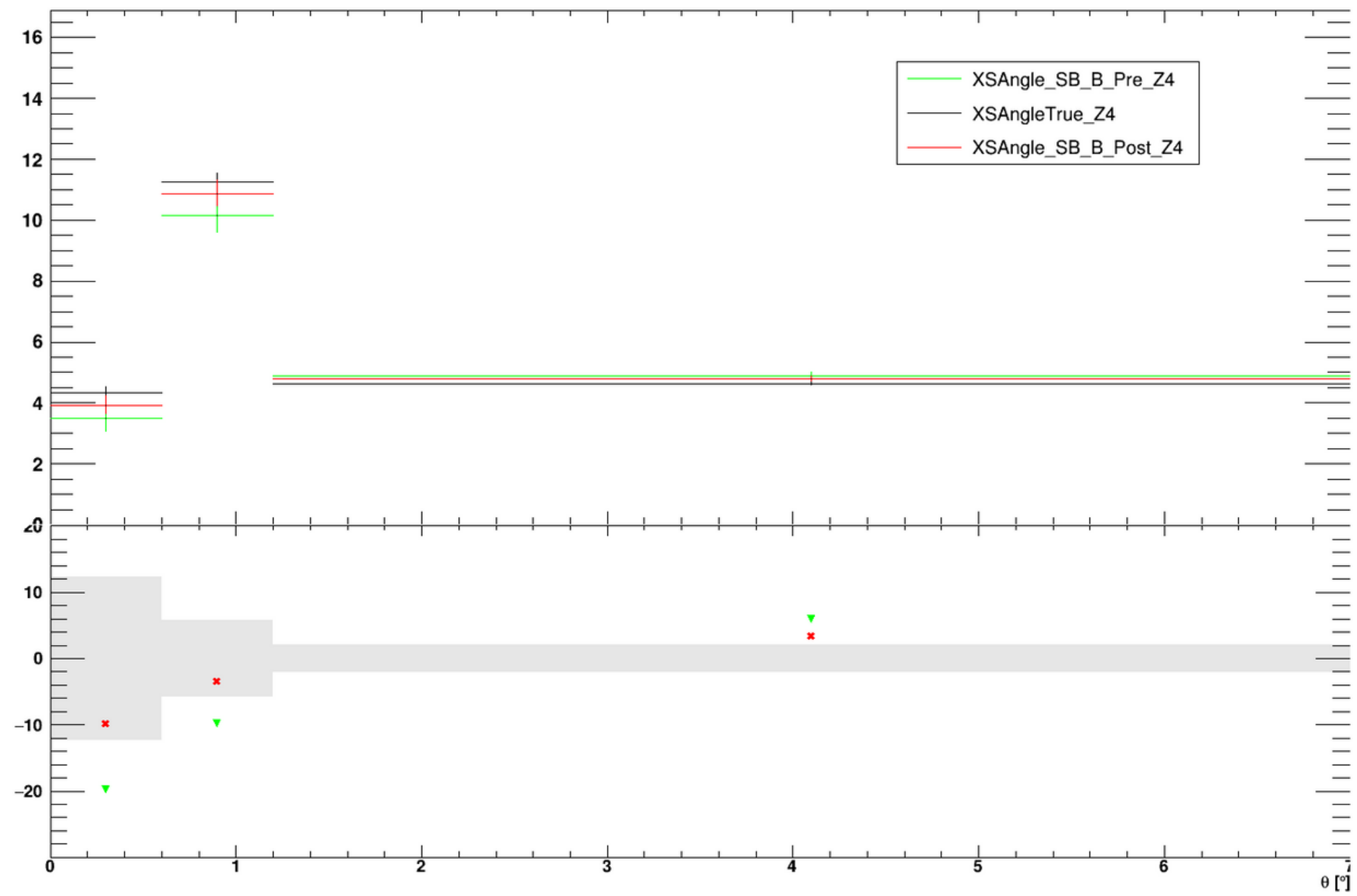
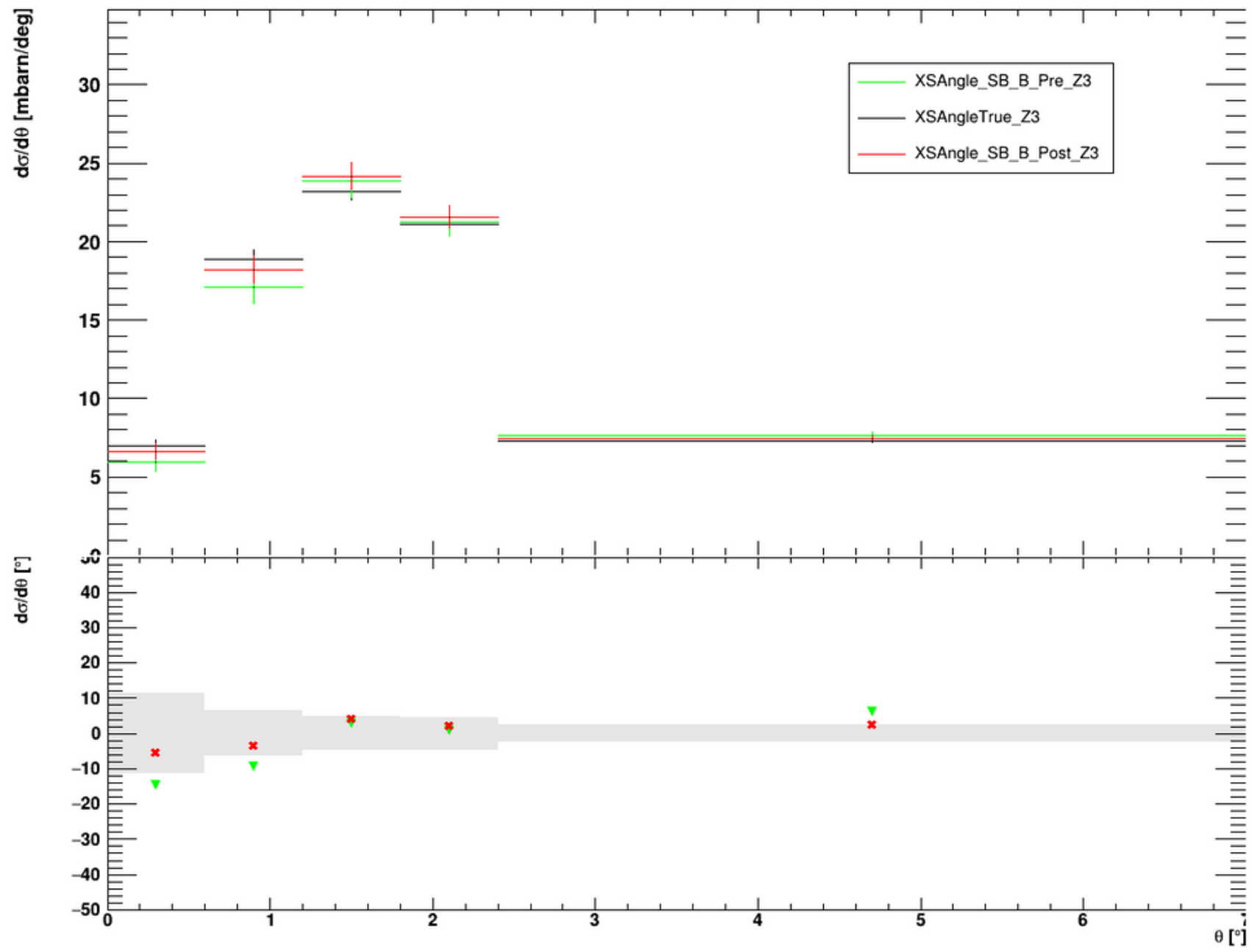


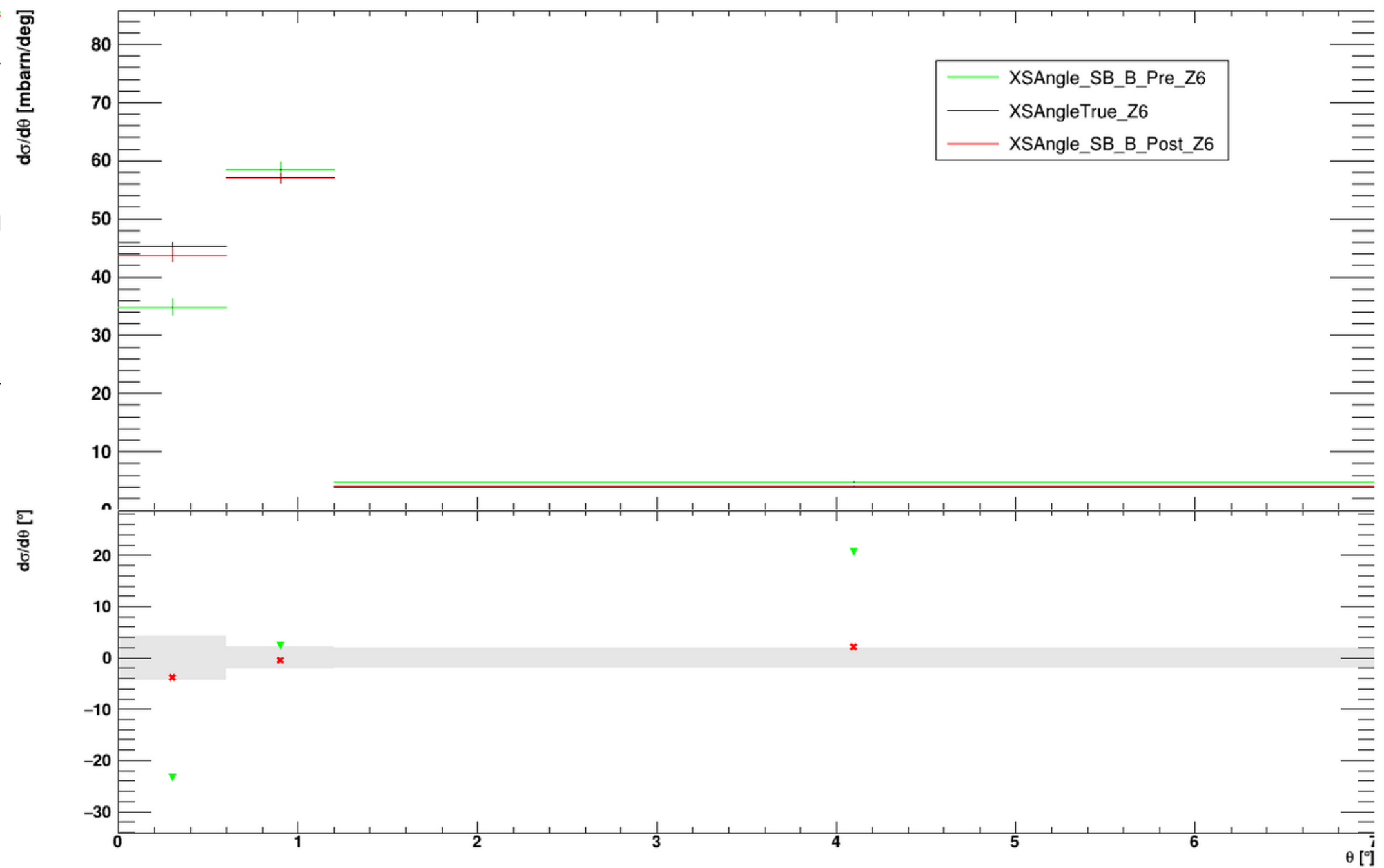
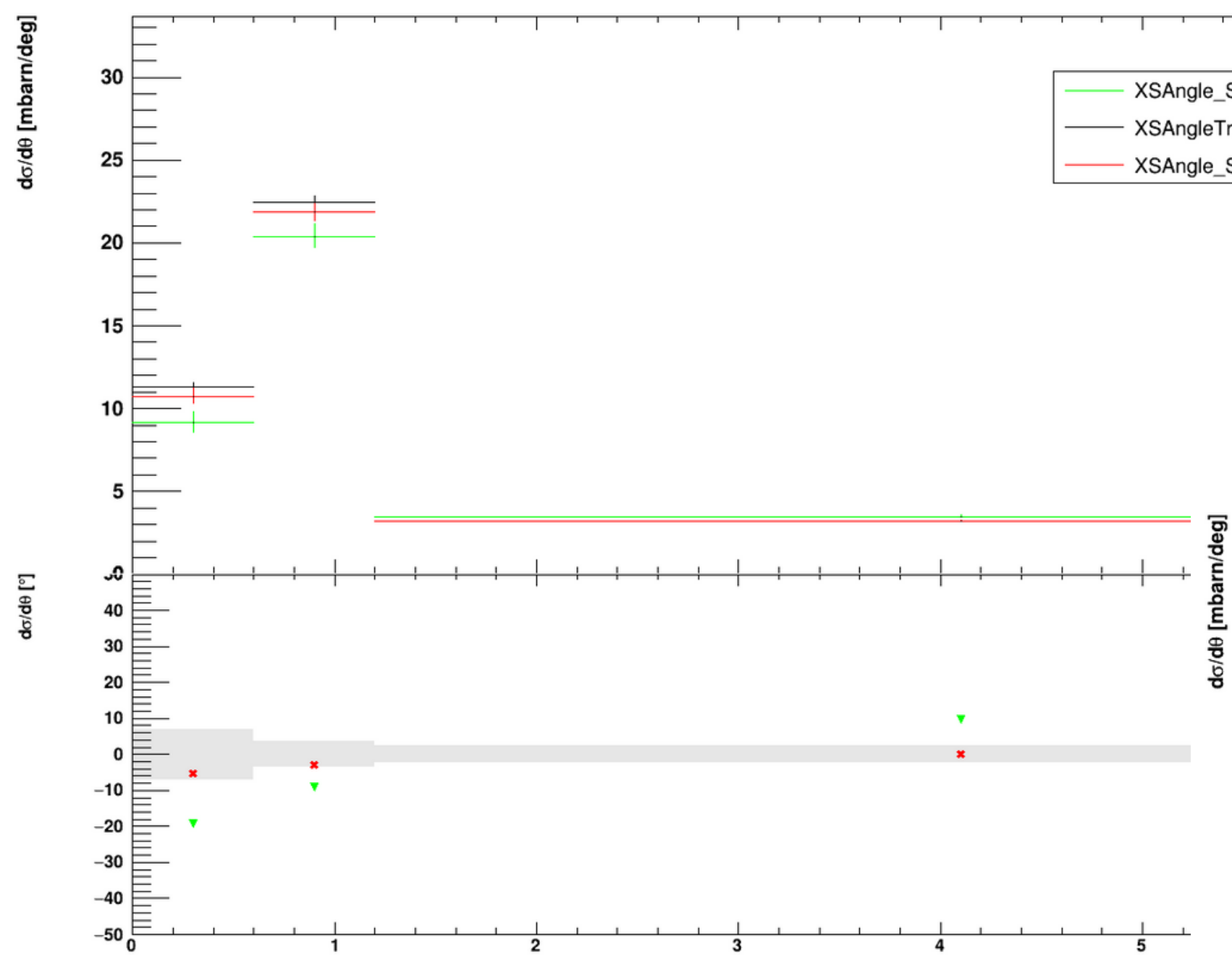
Angular unfolding

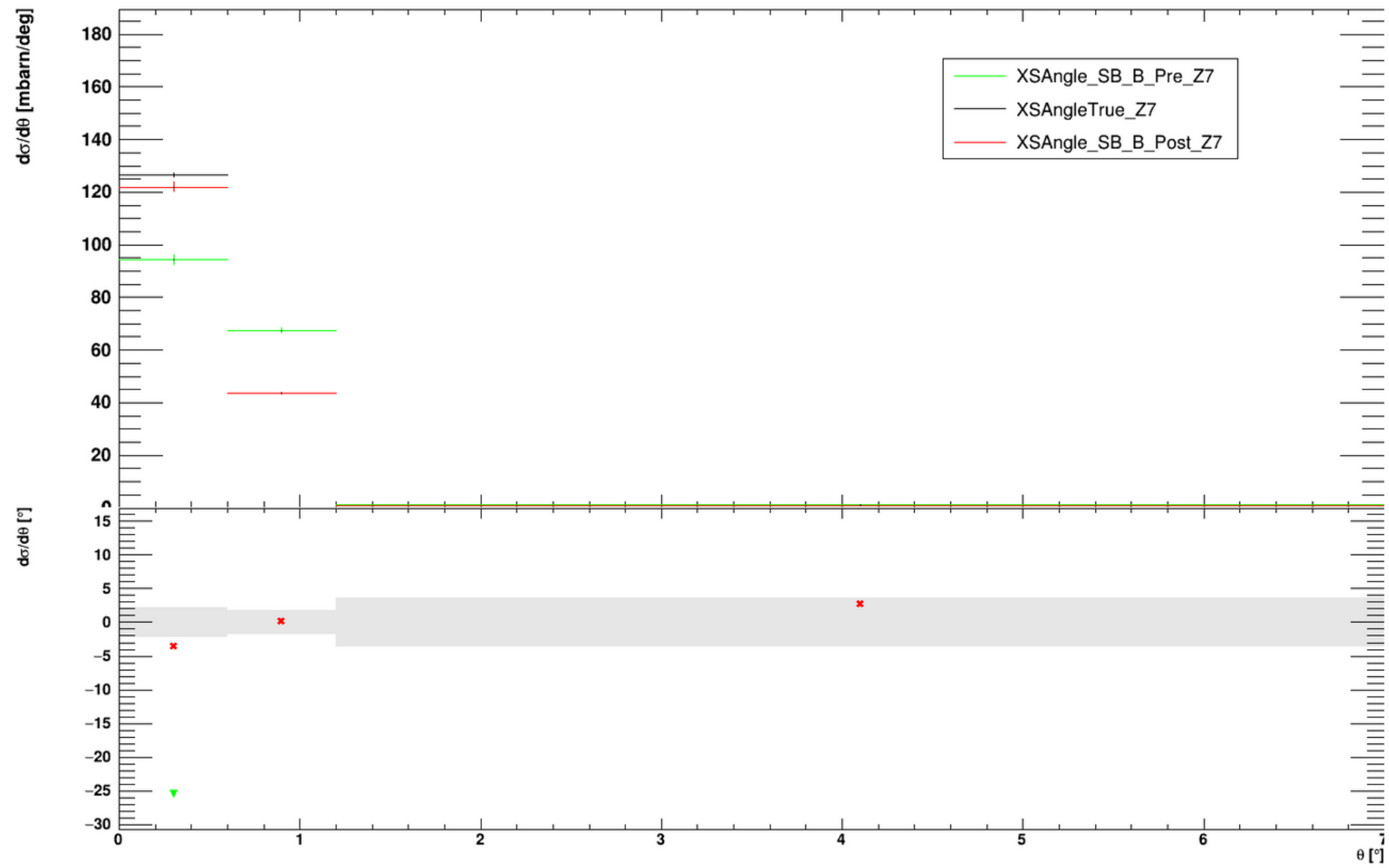
Several unfolding routines implemented (TUnfold, TUnfoldSVD, RooUnfold package)

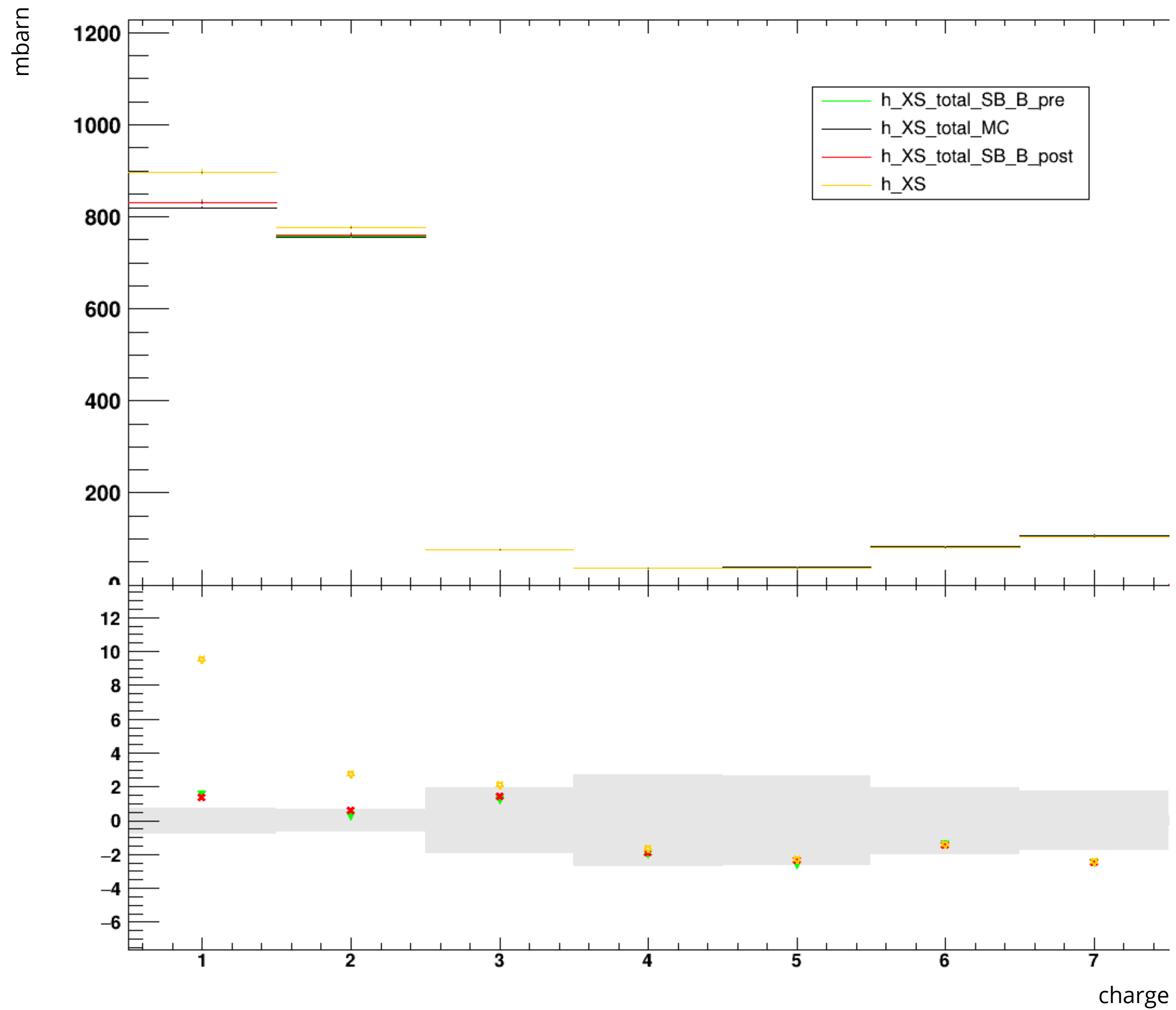












New analysis flow

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

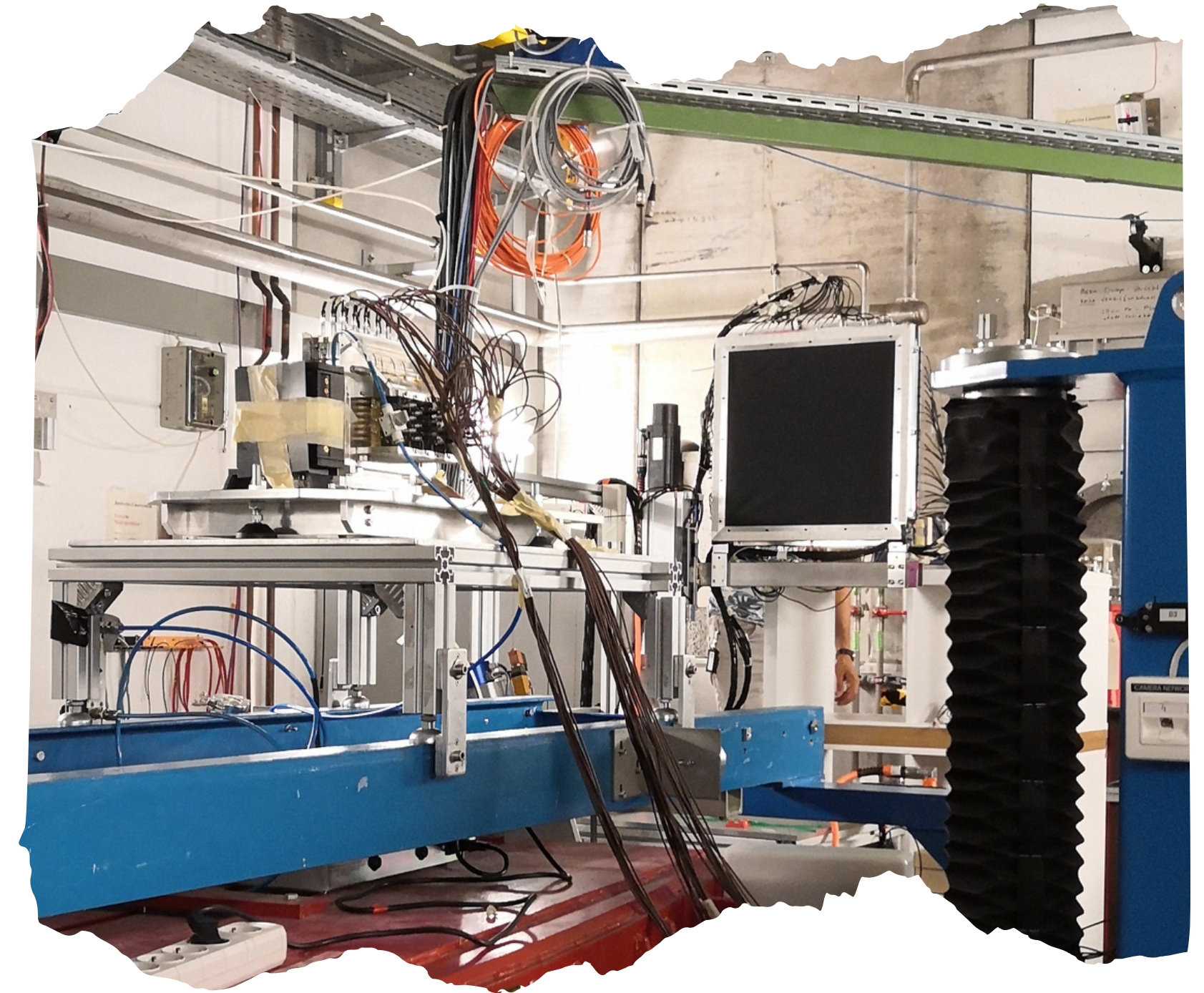
Calculate angular cross sections

Compare with MC

Next steps

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

Next update soon!

Thanks for listening!

