Isolated photon analysis in pp collisions at 13 TeV analysis status

--- analysis further check

ranxu

LPSC regular meeting
17/12/2021

Last presentation

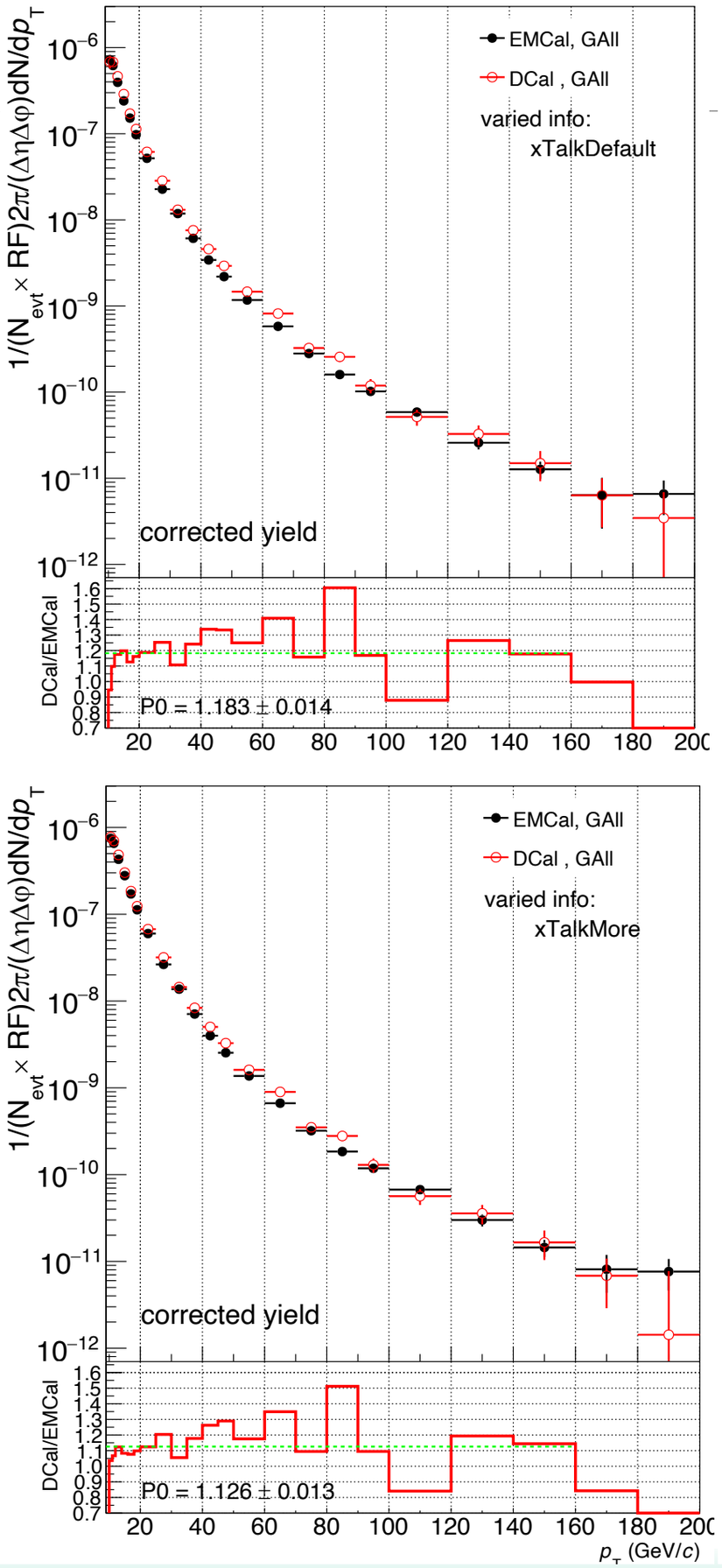
- comparing mainly analysis result between EMCal and DCal
  - → after acceptance normalization, combined spectrum ratio ~ 0.8 (DCal / EMCal).
  - → efficiency ratio around 0.7 which comes from reconstruct level.
- check distribution between EMCal and Dcal
  - → dead/bad regions mask: MC can reproduce data
  - → p_T^{iso}: MC can reproduce data
  - → effect of time cut: No large impact (~1% when decreasing to +-20 ns)
  - → shower shape cut for signal: not sensitive to shower shape parameter

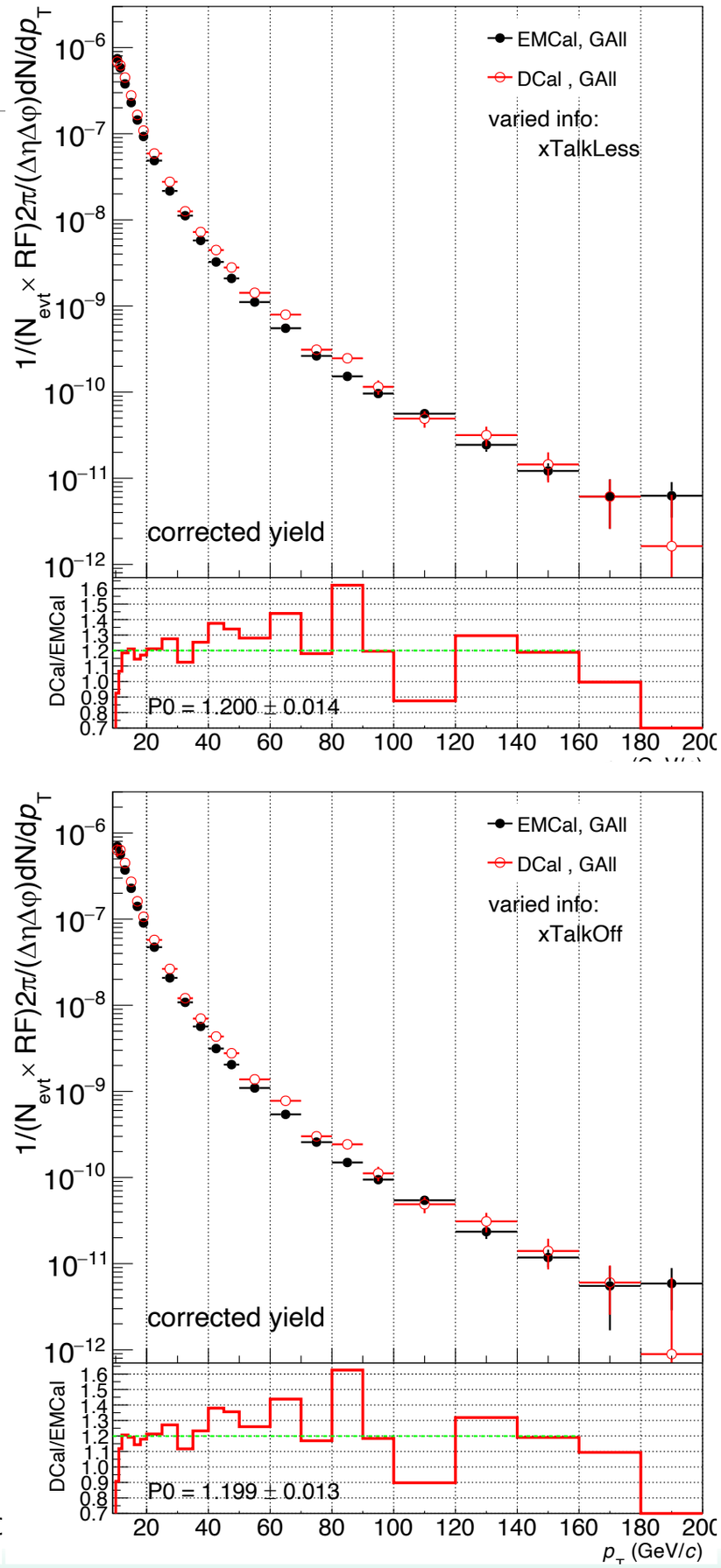
Outline

- Different XTalk
- Pi0 InvMass check

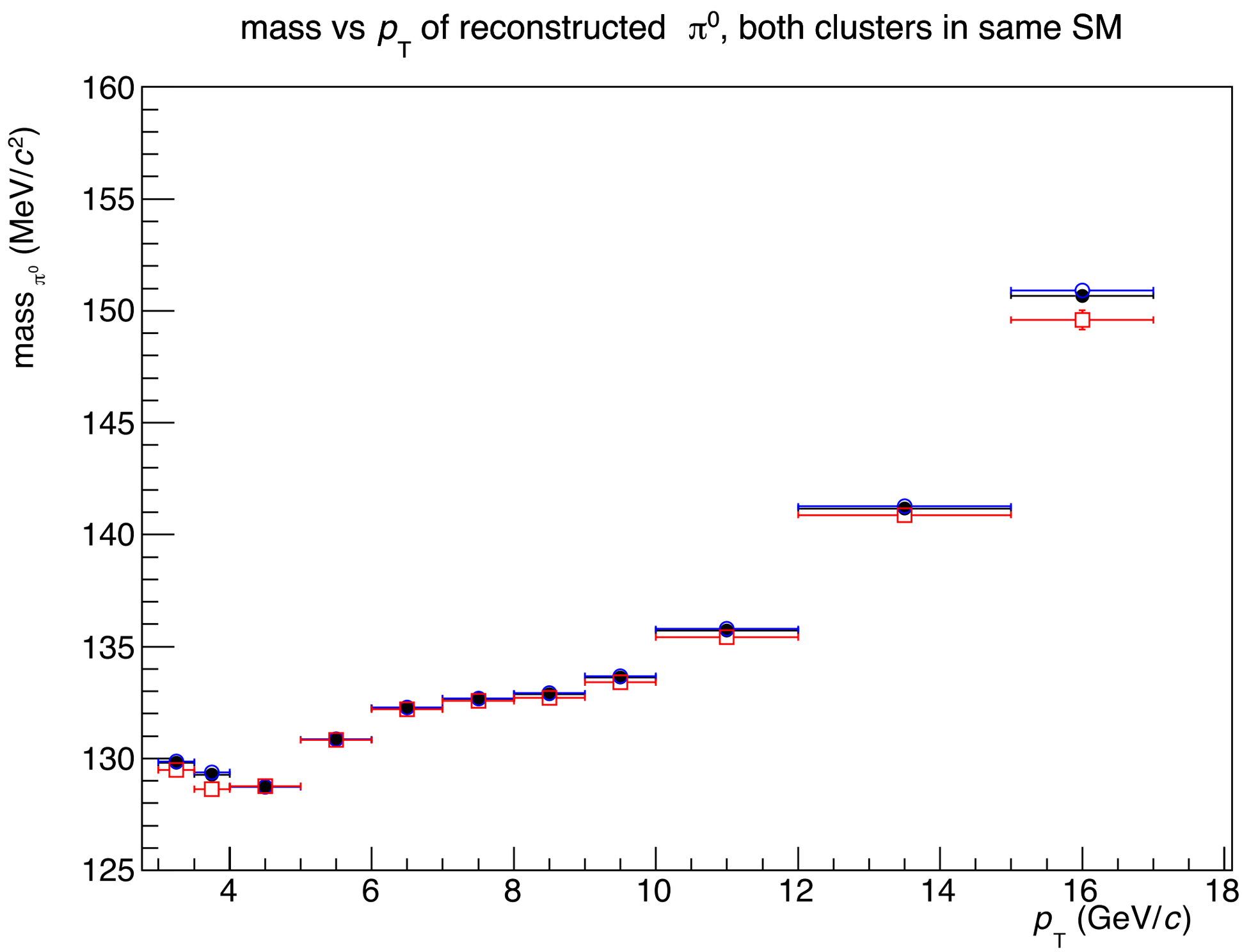
diff xTalk

xTalk	Pol0 fit value (DCal/EMCal)
Default	1.183 ± 0.014
More	1.126 ± 0.013
Less	1.200 ± 0.014
Off	1.199 ± 0.013





Pi0 Invmass comparison

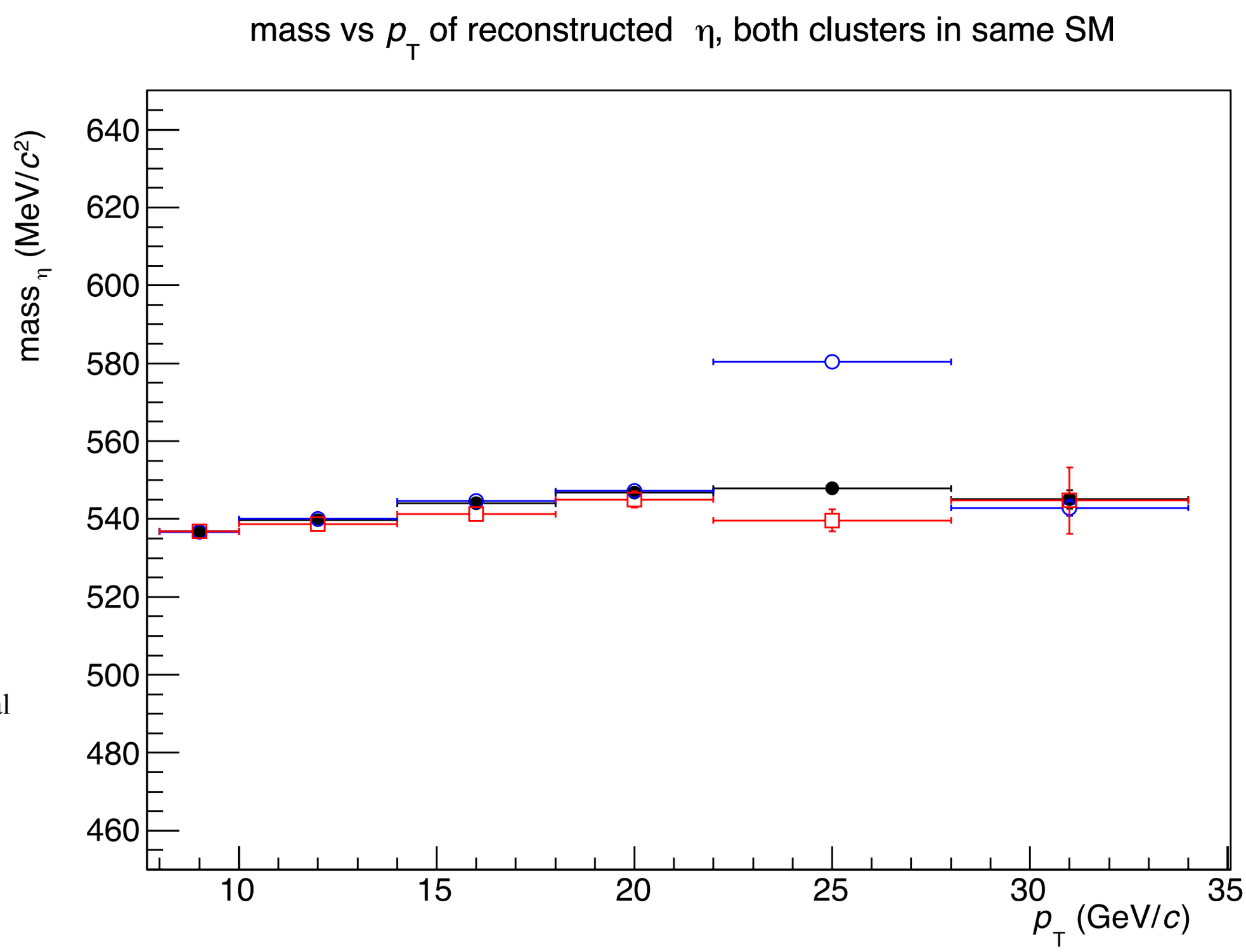


Red: Dcal

Blue: EMCal

Black: EMCal+DCal

Eta Invmass comparison



Red: Dcal

Blue: EMCal

Black: EMCal+DCal

Summary

✢ check distribution between EMCal and Dcal

→cross talk parameter: not sensitive to XTalk parameter

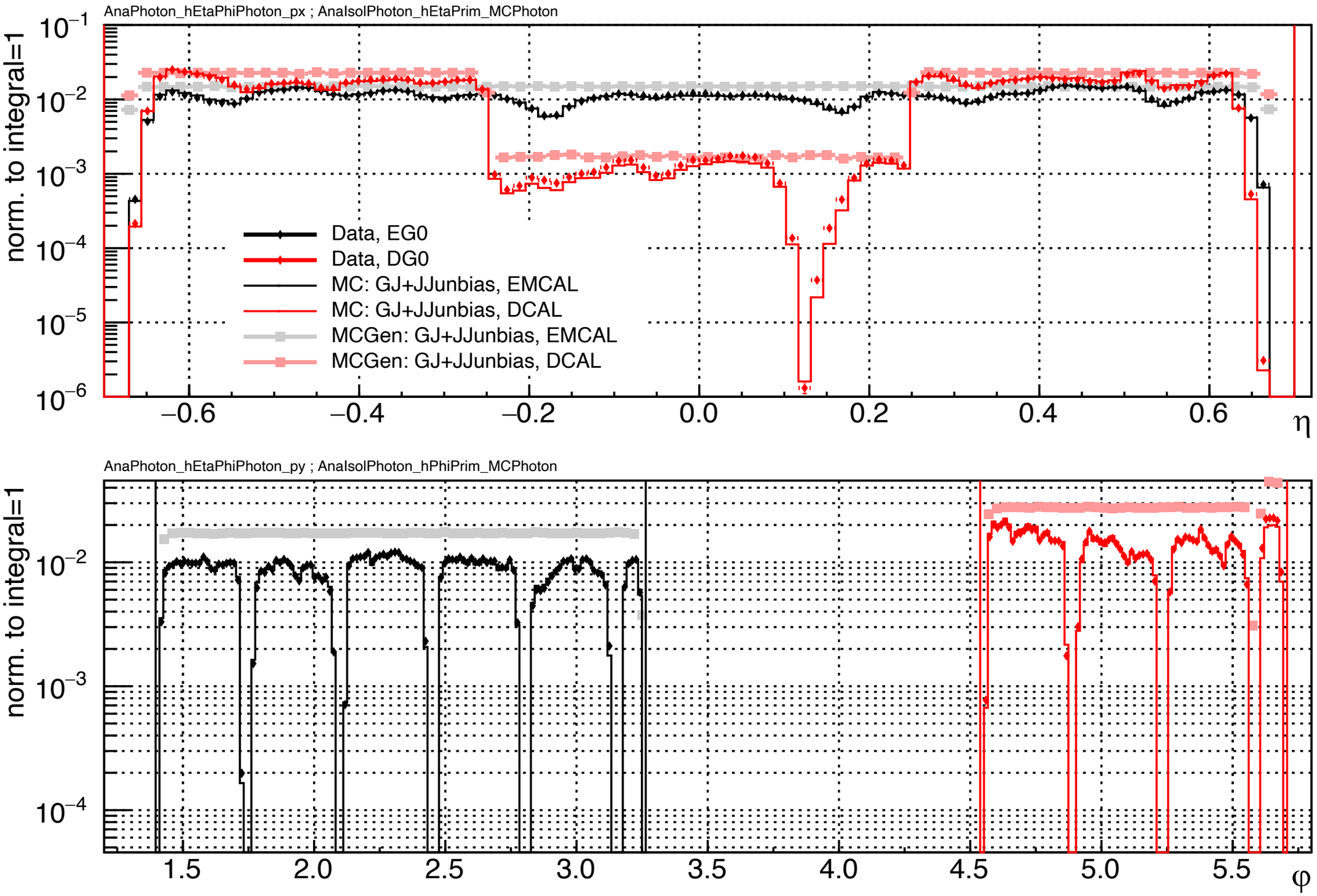
→ detector calibration: well for EMCal and DCal

Next step:

- check EMCal/DCal ratio with other cluster selection cut variations:
  - ▻ using different EMCal and DCal subregions
  - ▻ without distance to bad channel applied
  - ▻ with different track matching cuts
  - ▻ with different NLM cut
  - ▻ with different exoticity cut
  - ▻ …

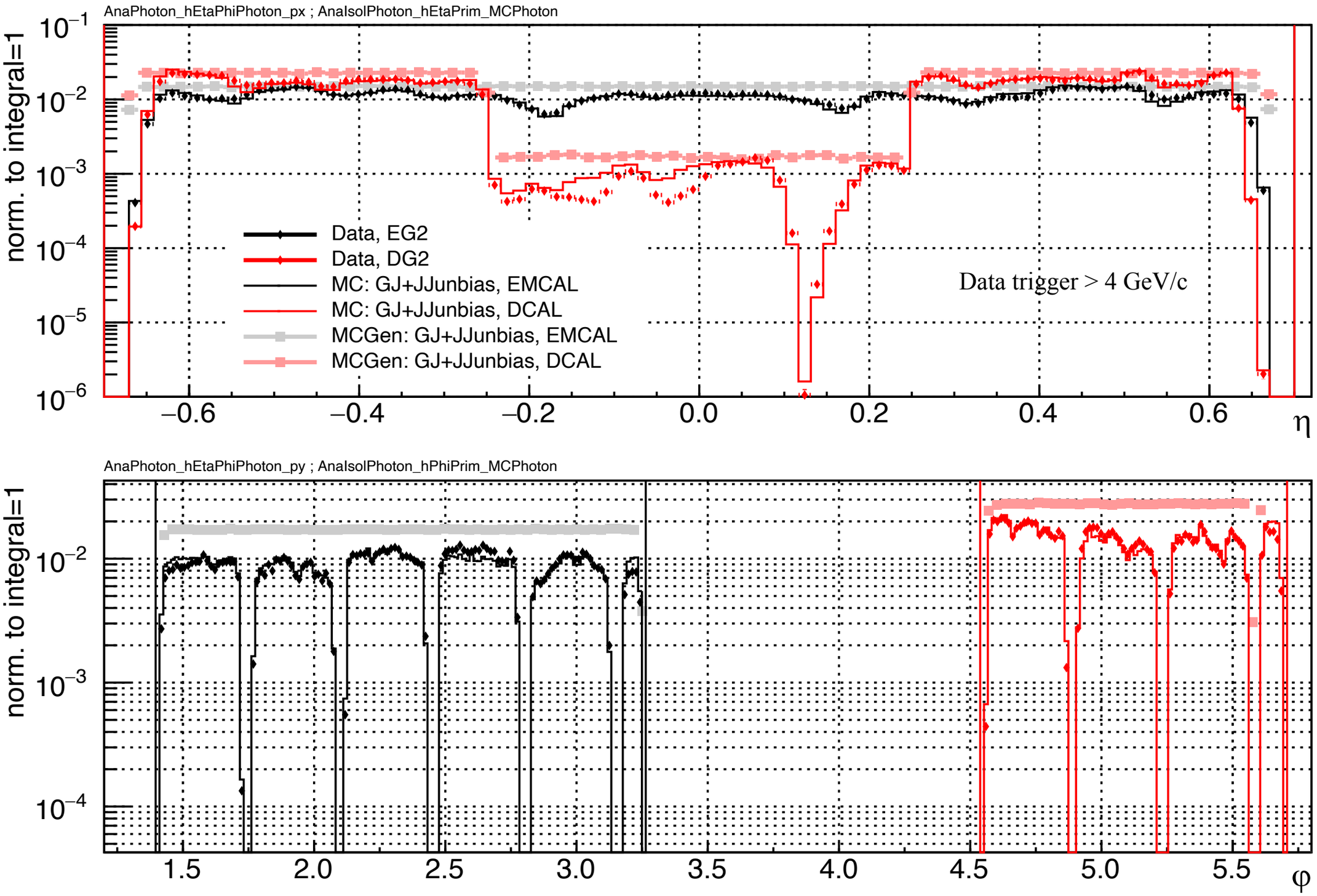
BACK UP

Eta(Phi) distribution, combined MB V.S. GJ+JJunb V.S. Gen



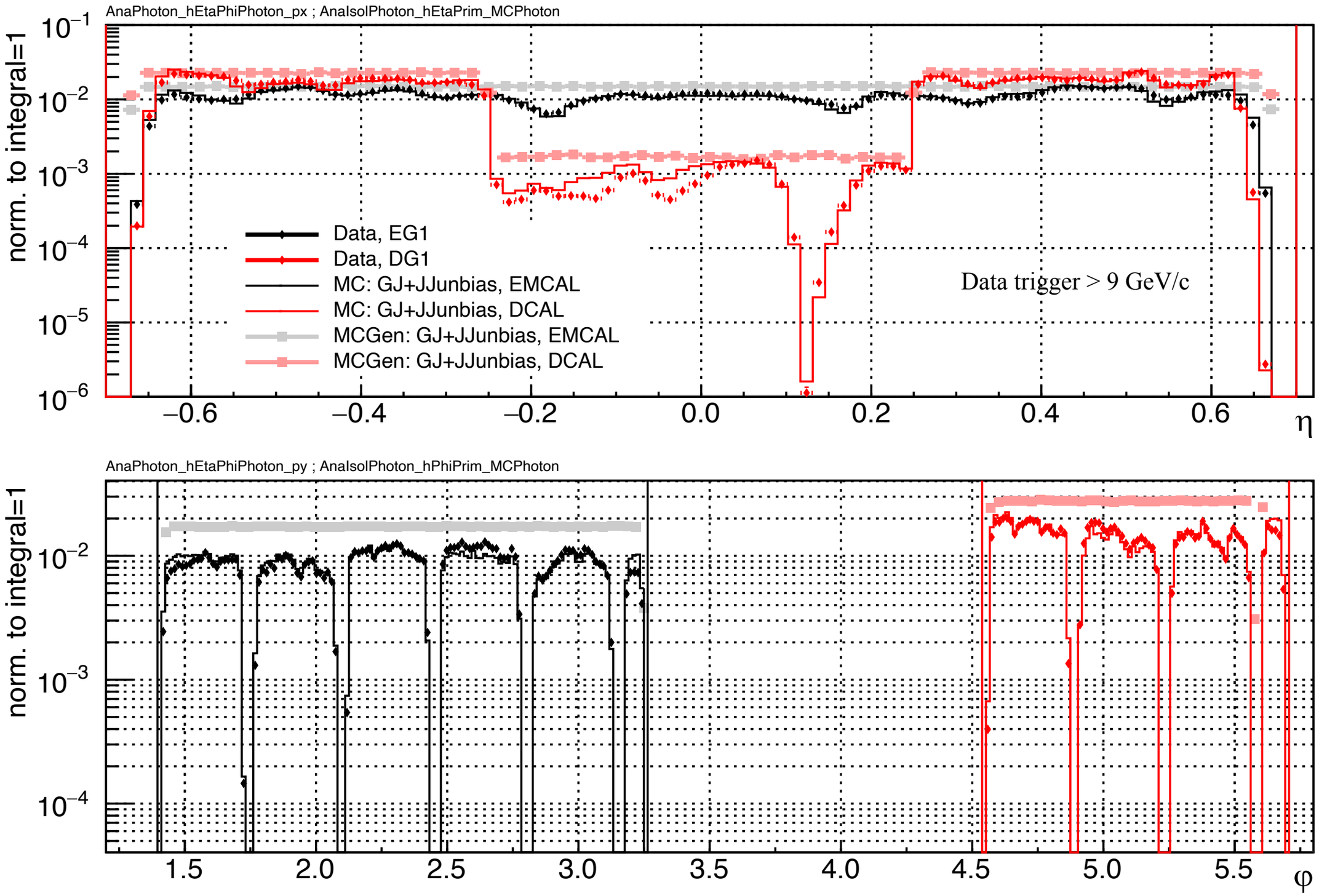
Gen level has similar distribution with data and MC rec level in η and φ distribution

Eta(Phi) distribution, combined G2 V.S. GJ+Jjunb V.S. Gen



Gen level has similar distribution with data and MC rec level in η and φ distribution

Eta(Phi) distribution, combined G1 V.S. GJ+Jjunb V.S. Gen



Gen level has similar distribution with data and MC rec level in η and φ distribution

Last presentation

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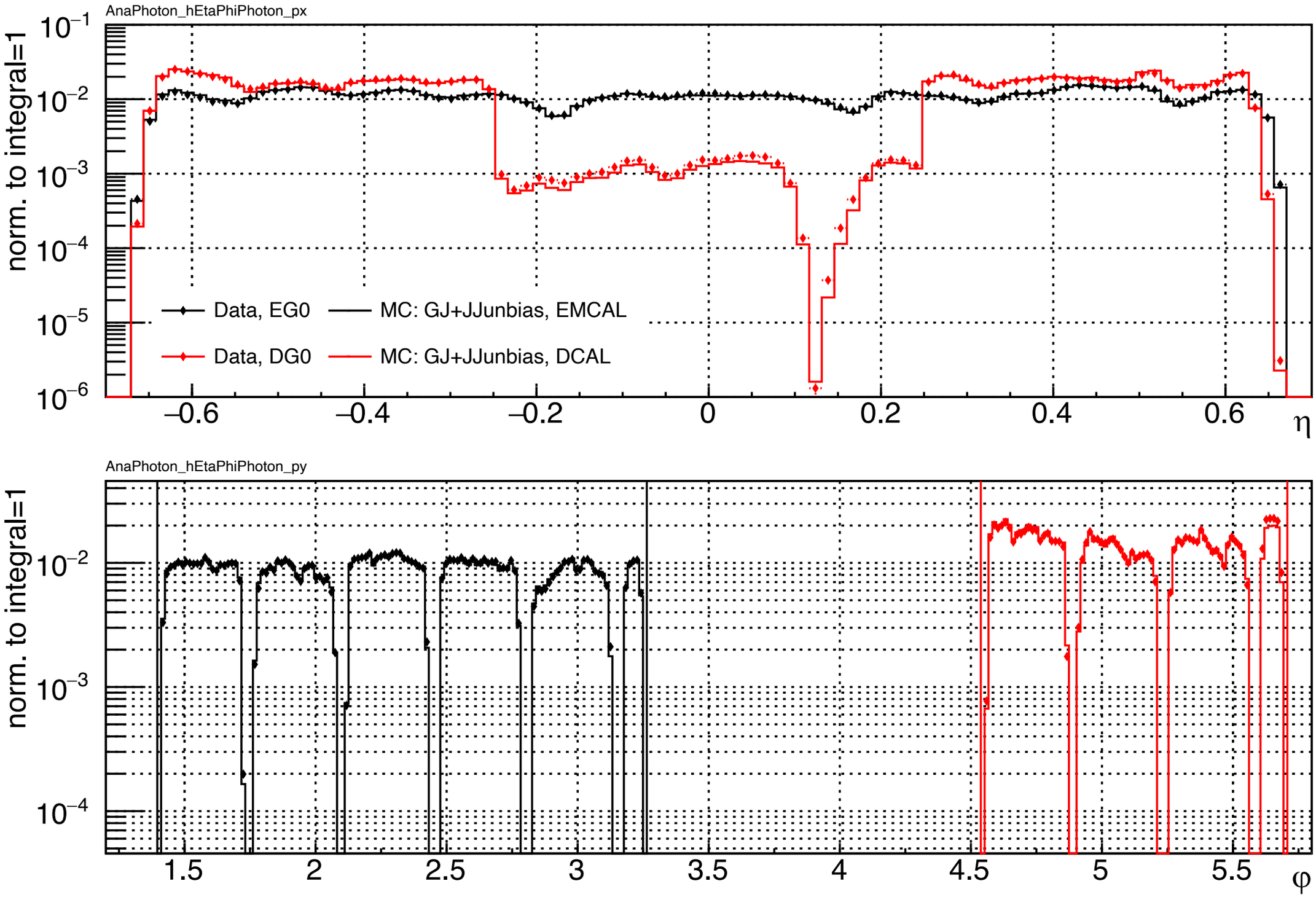
- comparing mainly analysis result between EMCal and DCal
  - → after acceptance normalization, combined spectrum ratio ~ 0.8 (DCal / EMCal).
  - → purity has similar distribution between EMCal and DCal.
  - → efficiency ratio around 0.7 which comes from reconstruct level.
  - → yield and cross section ratio around 1.17 which equal to ratios from each analysis procedures

Outline

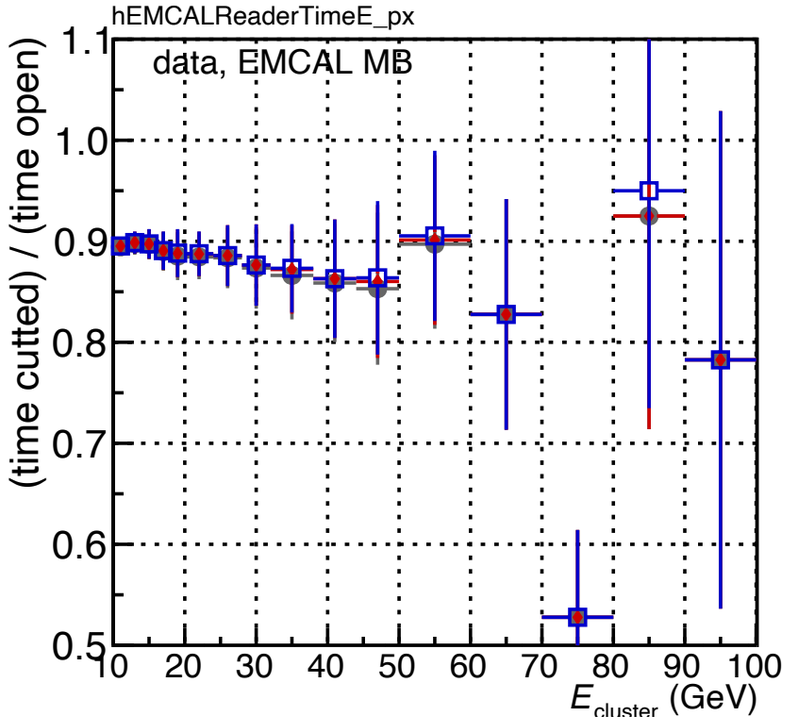
- dead/bad region mask
- effect of time cut
- Sum pt in isolation cone distribution
- Shower shape parameter for signal

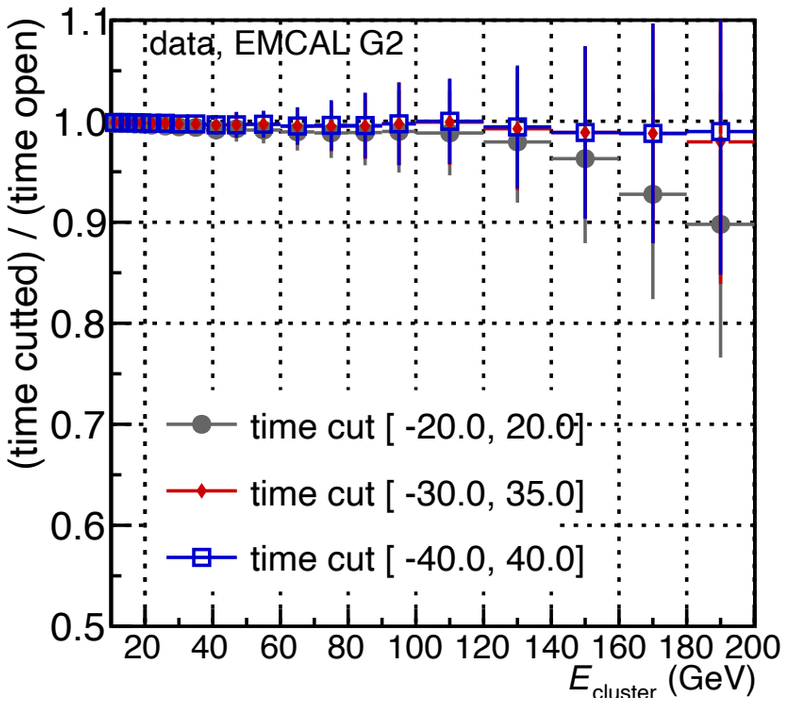
Eta(Phi) distribution, combined MB V.S. GJ+JJunb

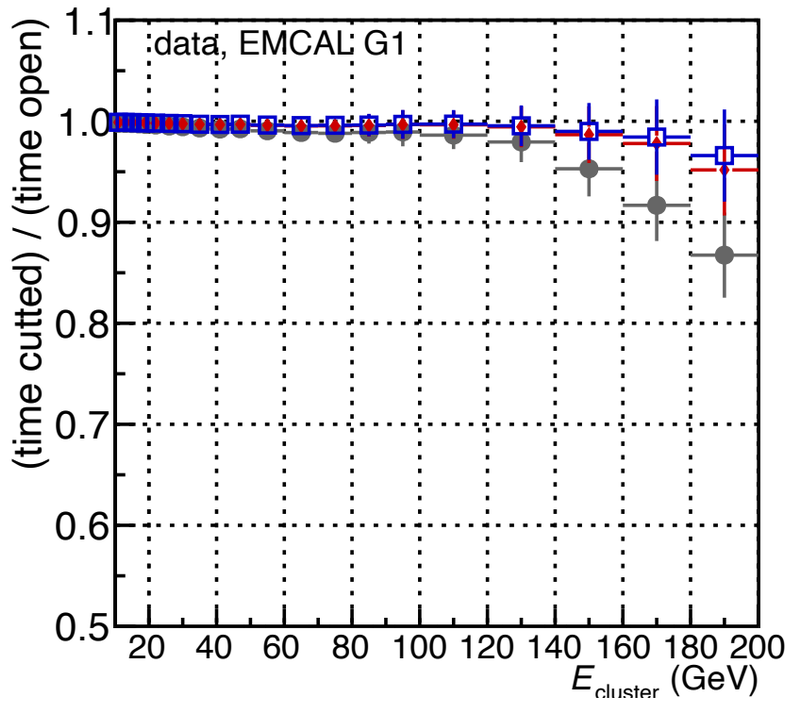


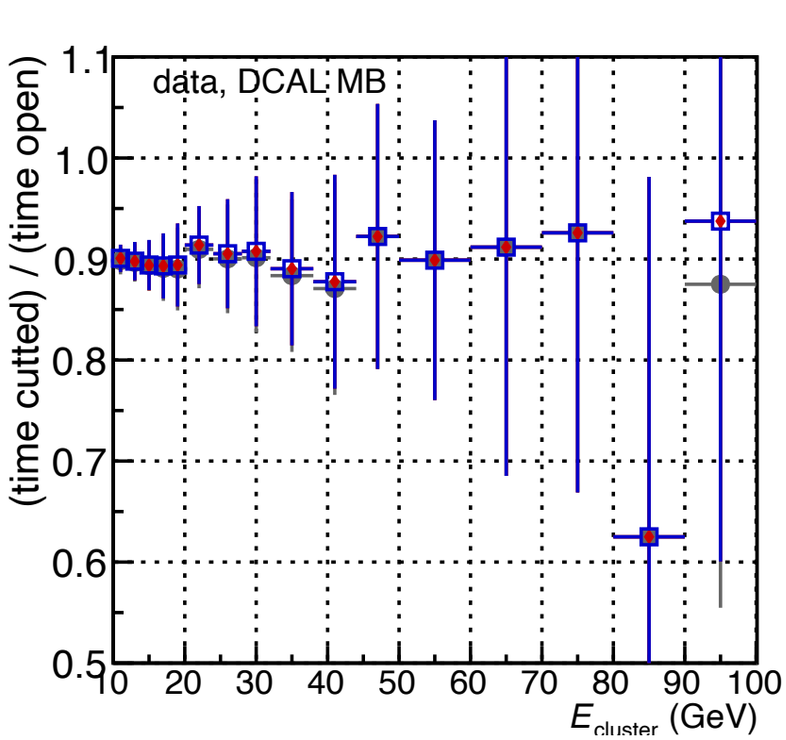
MC has similar distribution with data in η and φ distribution

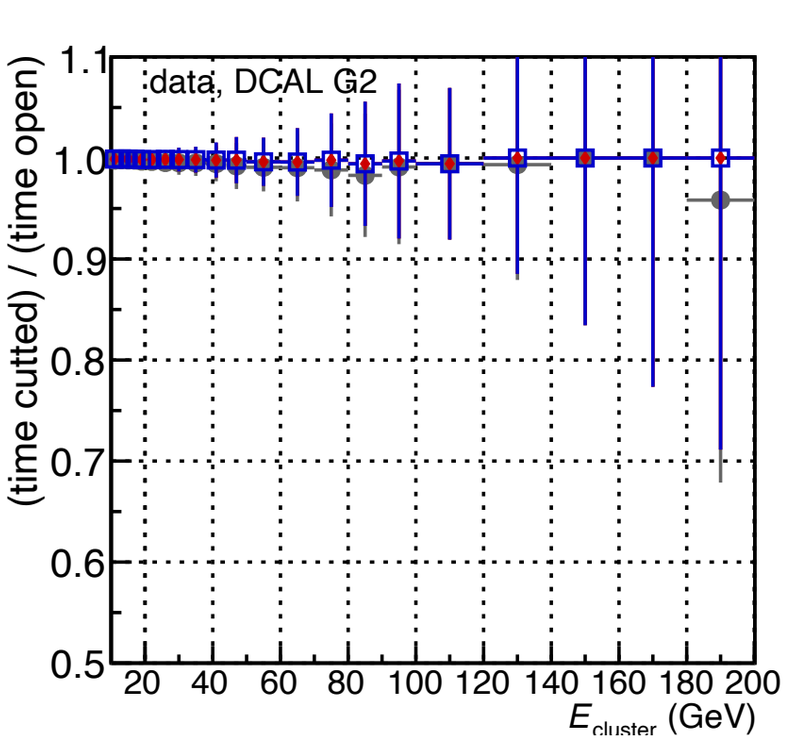
Time cut fraction

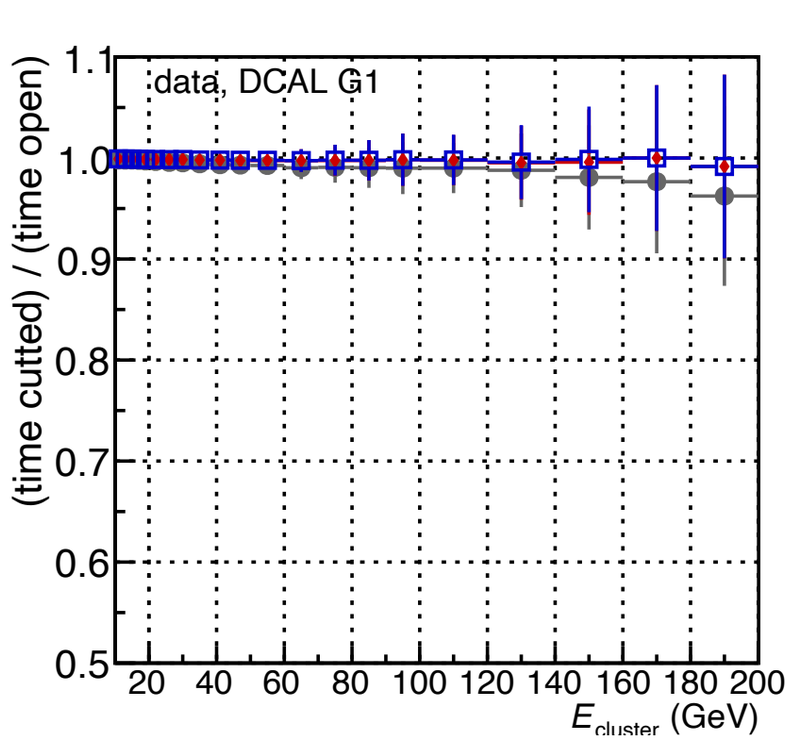








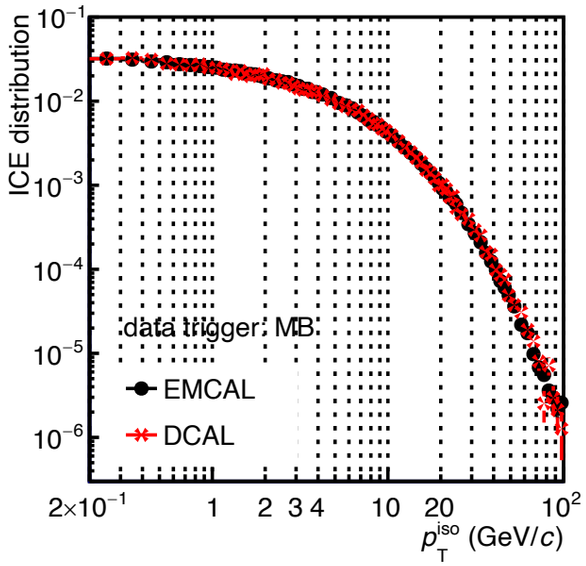




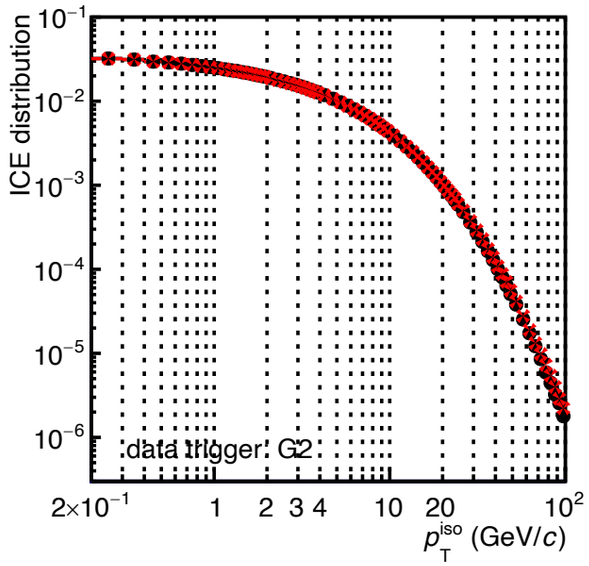
- No large impact (~1% when decreasing to +-20 ns), might need to open it at very high p_T (>100 GeV)

$\Sigma p_{T,incone}^{iso}$ distribution in data and MC

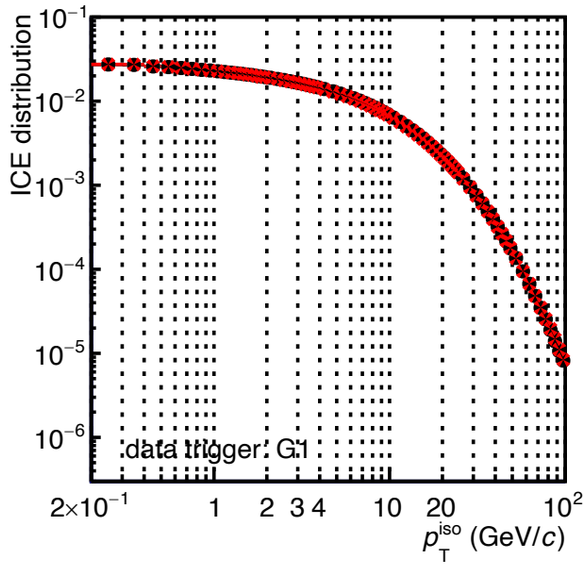
MB



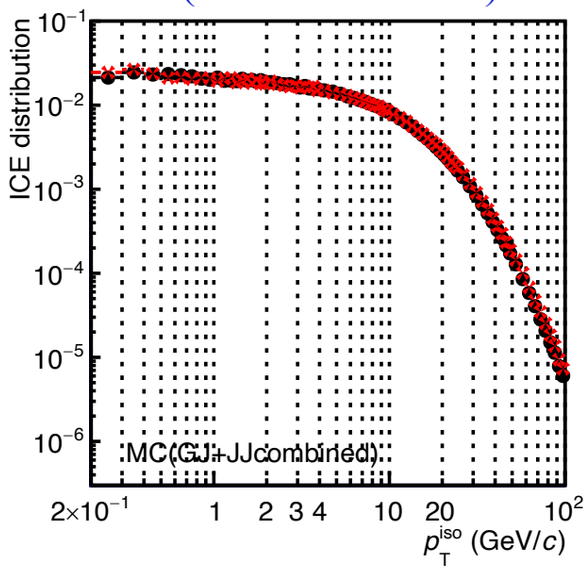
G2

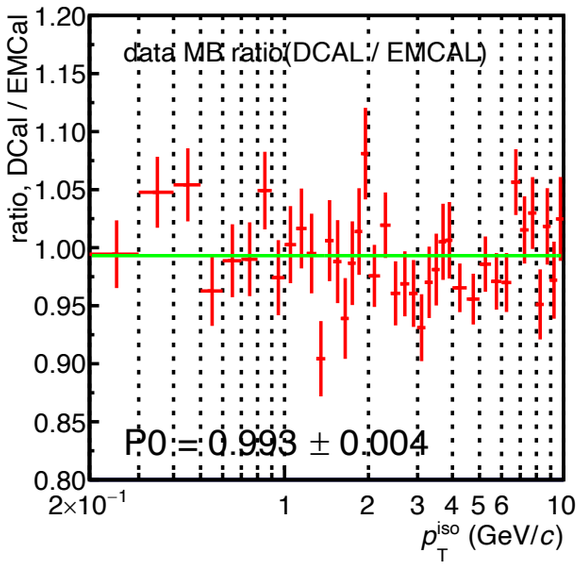


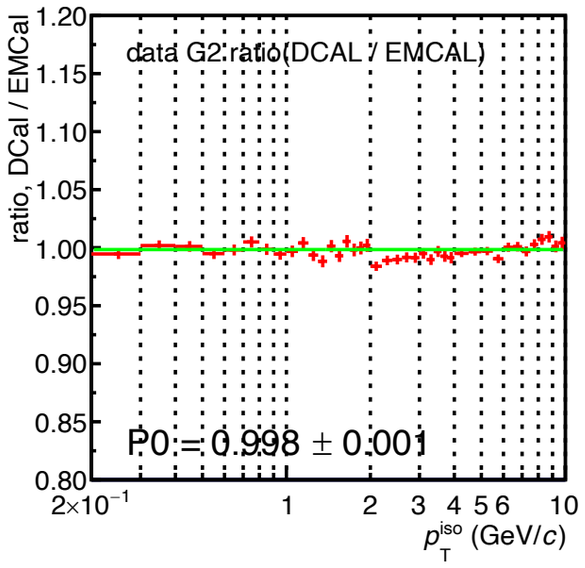
G1

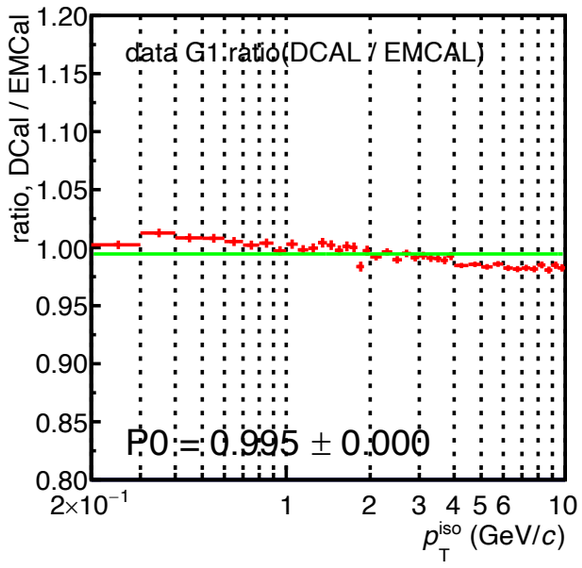


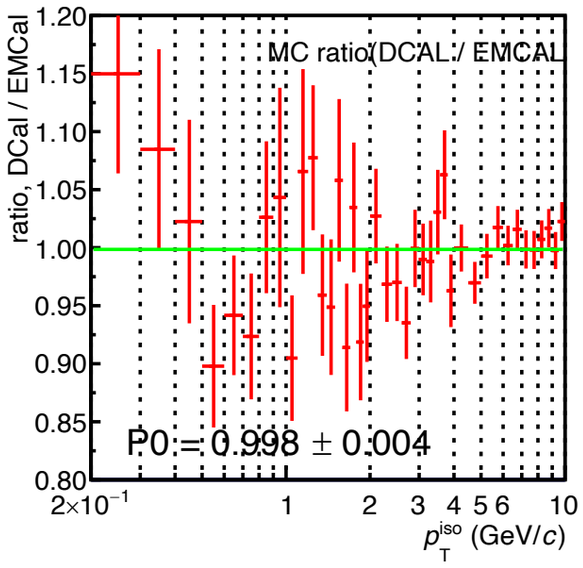
MC(GJ+JJcombined)







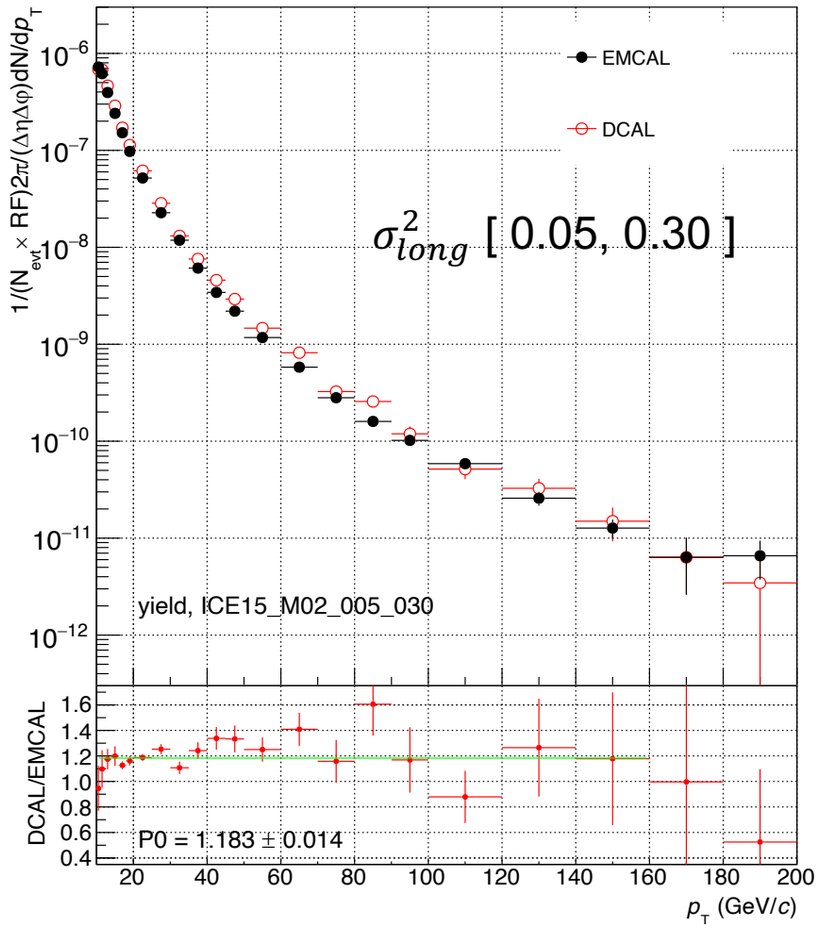


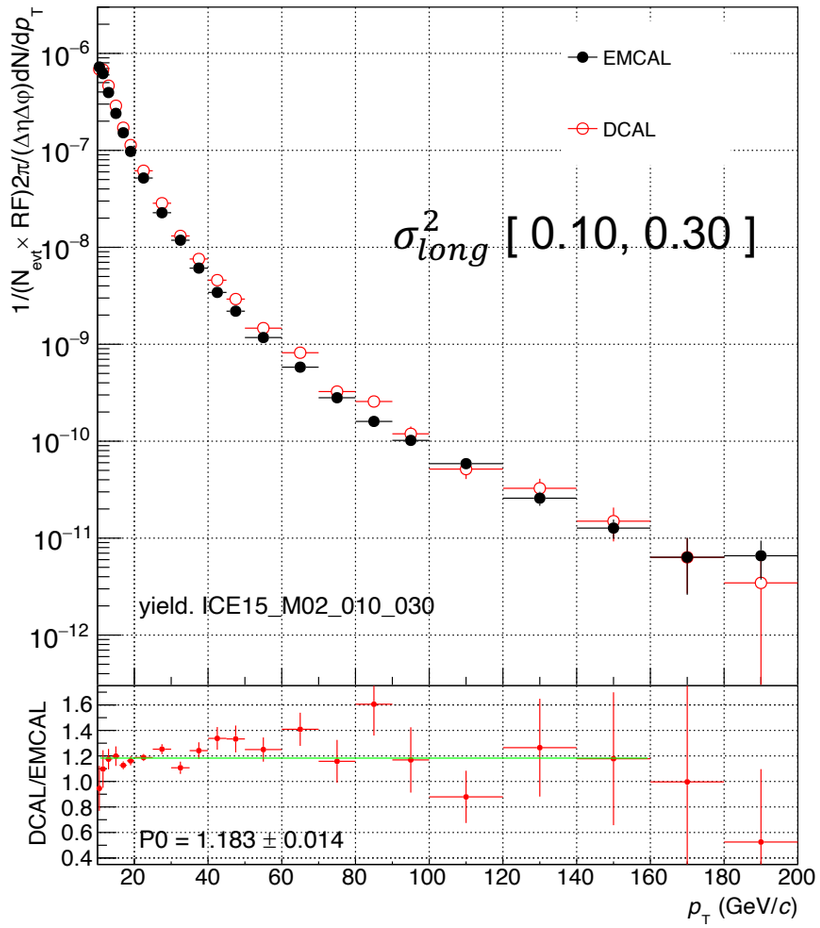


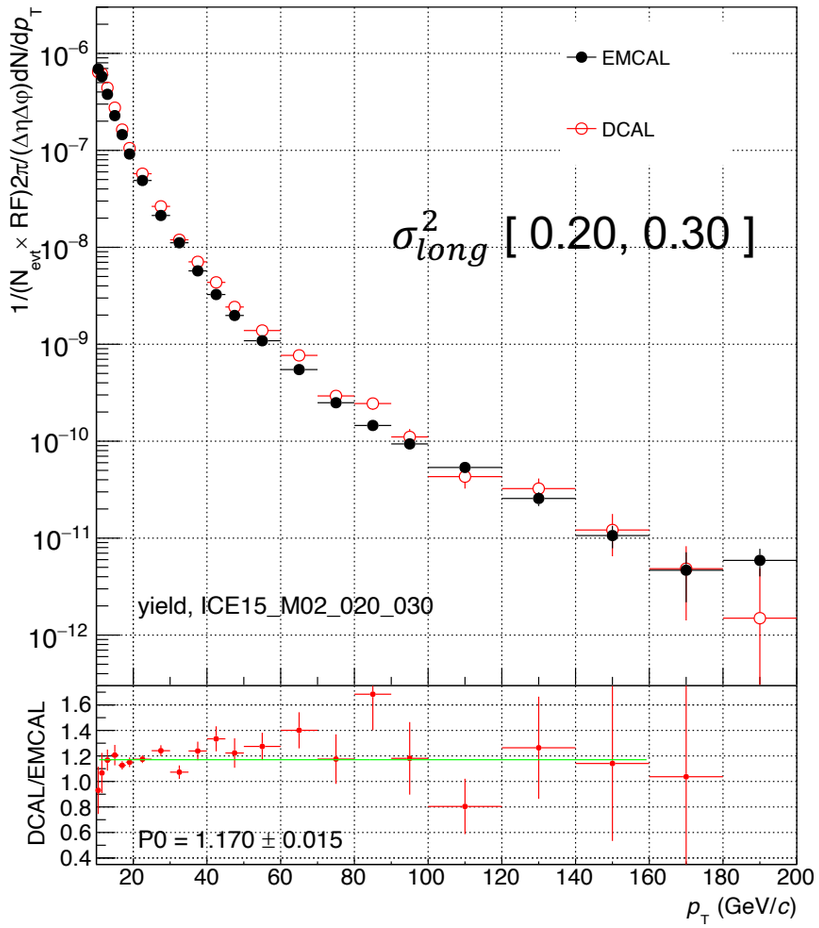
	MB	data(G2)	data(G2)	MC
Pol0	P0 = 0.993±0.004	P0 = 0.998±0.001	P0=0.995±0.000	P0=0.998±0.004

- MC and data have similar Σp_T distribution in isolation cone

Shower shape minimum cut variation



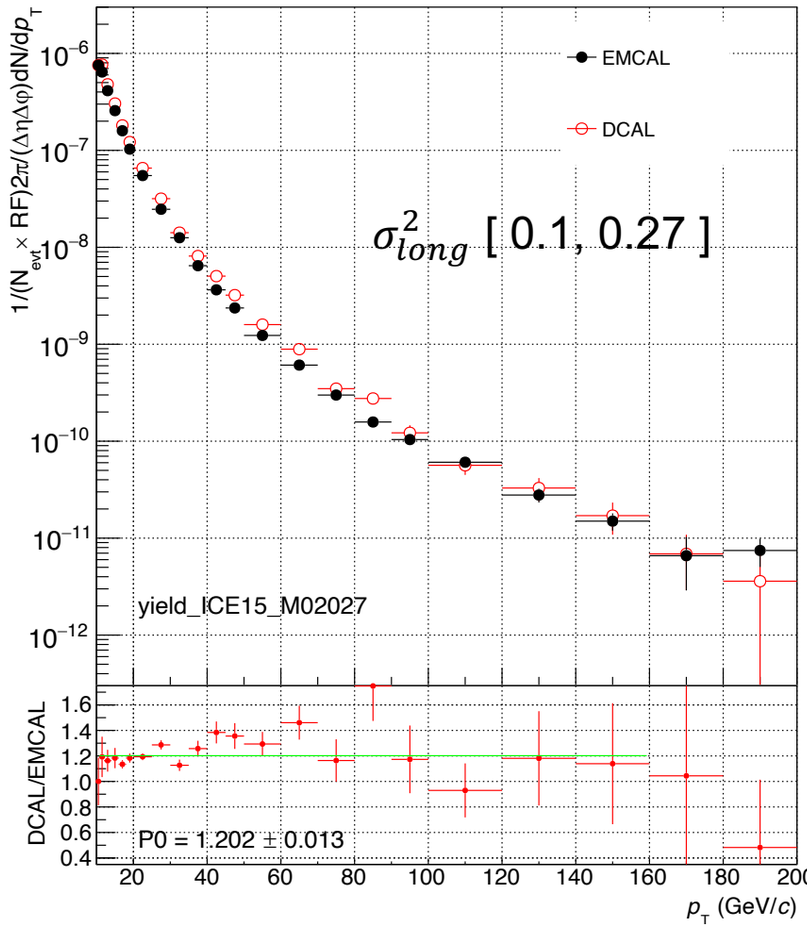


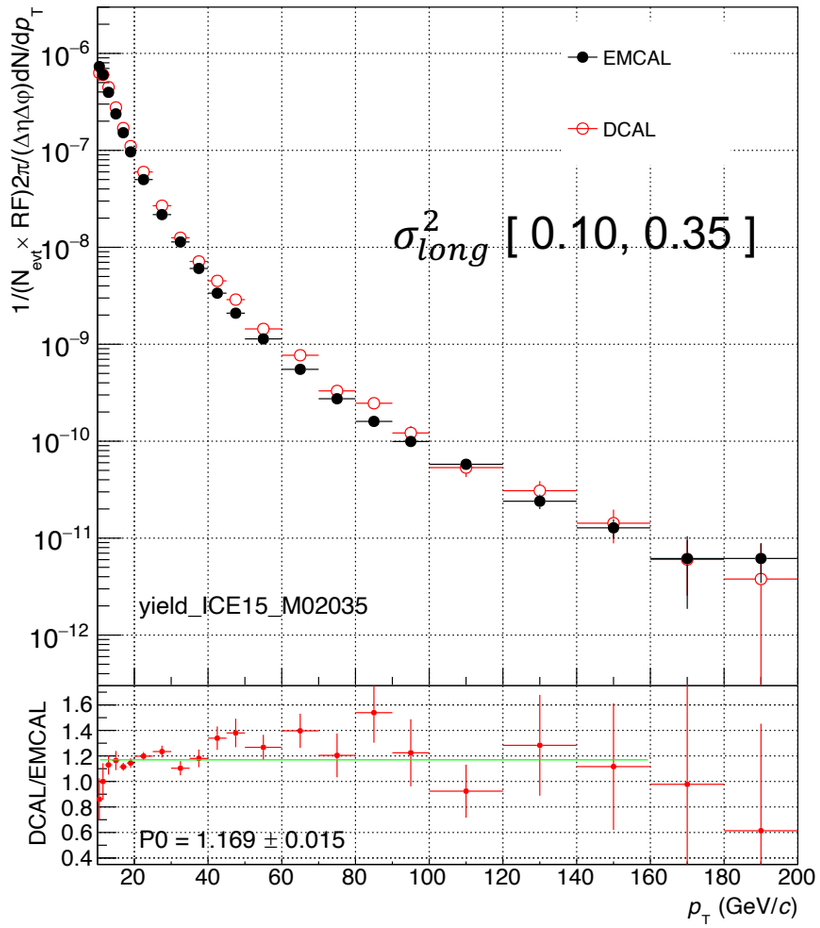


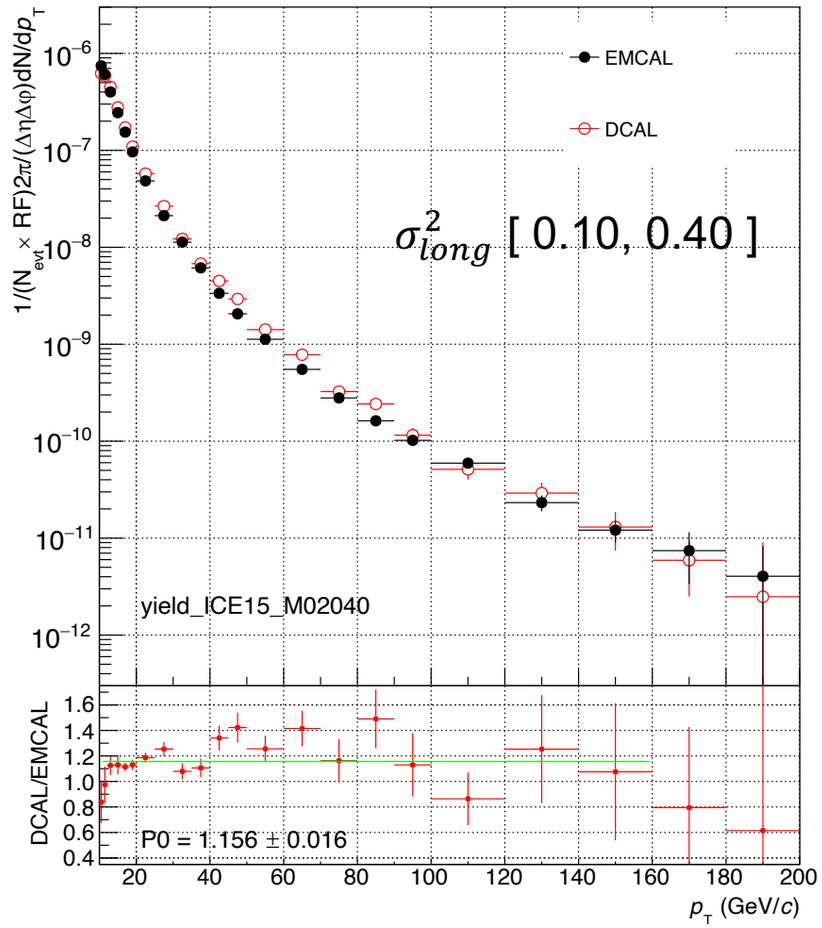
σ^2_{long}	[0.05, 0.30]	[0.1, 0.30]	[0.2, 0.30]
Pol0 fit value	1.183±0.014	1.183±0.014	1.17±0.015

- No obvious change when signal σ^2_{long} minimum parameter change

Shower shape maximum cut variation







σ^2_{long}	[0.1, 0.27]	[0.1, 0.30]	[0.1, 0.35]	[0.1, 0.40]
Pol0 fit value	1.202 $\pm$0.013	1.183$\pm$0.014	1.169 $\pm$0.015	1.156 $\pm$0.016

- No obvious change when signal σ^2_{long} maximum parameter change

Summary

✢ check distribution between EMCal and Dcal

→dead/bad regions mask: MC can reproduce data

→ $\Sigma p_{T,incone}^{iso}$: MC can reproduce data

→effect of time cut: No large impact (~1% when decreasing to +-20 ns), might need to open it at very high p_T (>100 GeV)

→shower shape cut for signal: not sensitive to shower shape parameter

Next step:

- check EMCal/DCal ratio with other cluster selection cut variations:
  - ▻ using different cross talk parameters
  - ▻ using different EMCal and DCal subregions
  - ▻ without distance to bad channel applied
  - ▻ with different track matching cuts
  - ▻ with different NLM cut
  - ▻ with different exoticity cut
  - ▻ …

Mainly ana results presentation

Data set and analysis mainly cut

Analysis dataset:

- Data: ALICE data taken from 2016,17,18
  - MB: EMCAL ~ 1023.9M / 1066.6M ; DCAL ~ 1027.0M / 1066.7M
  - G2 : EMCAL ~ 79.0M / 204.3M ; DCAL ~ 36.6M / 204.3M
  - G1 : EMCAL ~ 54.7M / 204.3M ; DCAL ~ 26.7M / 204.3M
- Simulation: Gamma-Jet event + Jet-Jet events

Cluster selection: (clusterizer V1)

- Ncells/cluster >= 2
- distance to bad channel > 2 cell
- time cut: [-30, 30]ns
- cells energy: Eseed = 500 MeV , Ecell = 100 MeV
- NLM <= 2
- Trackmactch: : p_T dependent
- Emulation of cross-talk T-Card in MC applied

Photon selection:

- Showershape: $\sigma^2_{long} < 0.3$

Isolation criterion:

- particle in cone: charg+neutral
- track p_T in lsolation cone: p_T,track > 0.2 GeV
- $|\eta| < 0.52$, φ (1.57,3.11)
- isolation crite: R = 0.4

$$p_T^{iso} \equiv \Sigma p_{T,track} < E_T^{th} = 1.5 GeV/c$$

$$p_T^{\overline{iso}} \equiv \Sigma p_{T,track} > E_T^{th} = 2.5 GeV/c$$

Cluster rejection factor

- $RF = \left(\frac{1}{N_{evt}}\frac{dN_{cluster}}{dP_T}\right)_{trigger} \Big/ \left(\frac{1}{N_{evt}}\frac{dN_{cluster}}{dP_T}\right)_{MB}$
- Trigger sample normalize:

$$\left(\frac{1}{N_{evt}}\frac{dN}{dp_T}\right)_{norm.} = \left(\frac{dN}{dp_T}\right)_{trigger} / \left(N_{evt,trig} * RF\right)$$

	EMCAL	DCAL
G2/MB	629.89±6.48	1280.87±9.24
G1/G2	12.64±0.71	12.04±0.69
G1/MB	7962.73	15427.31

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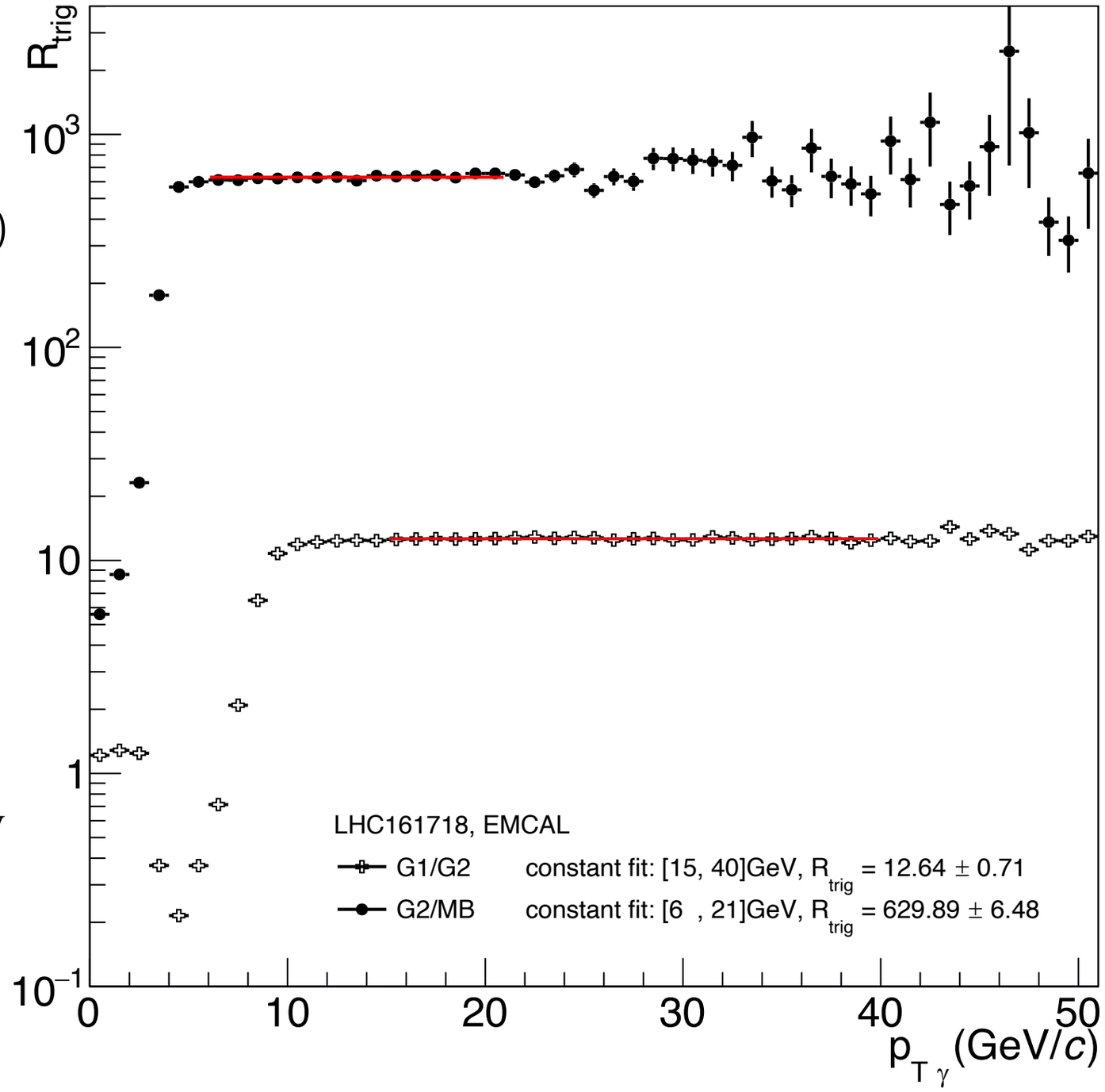


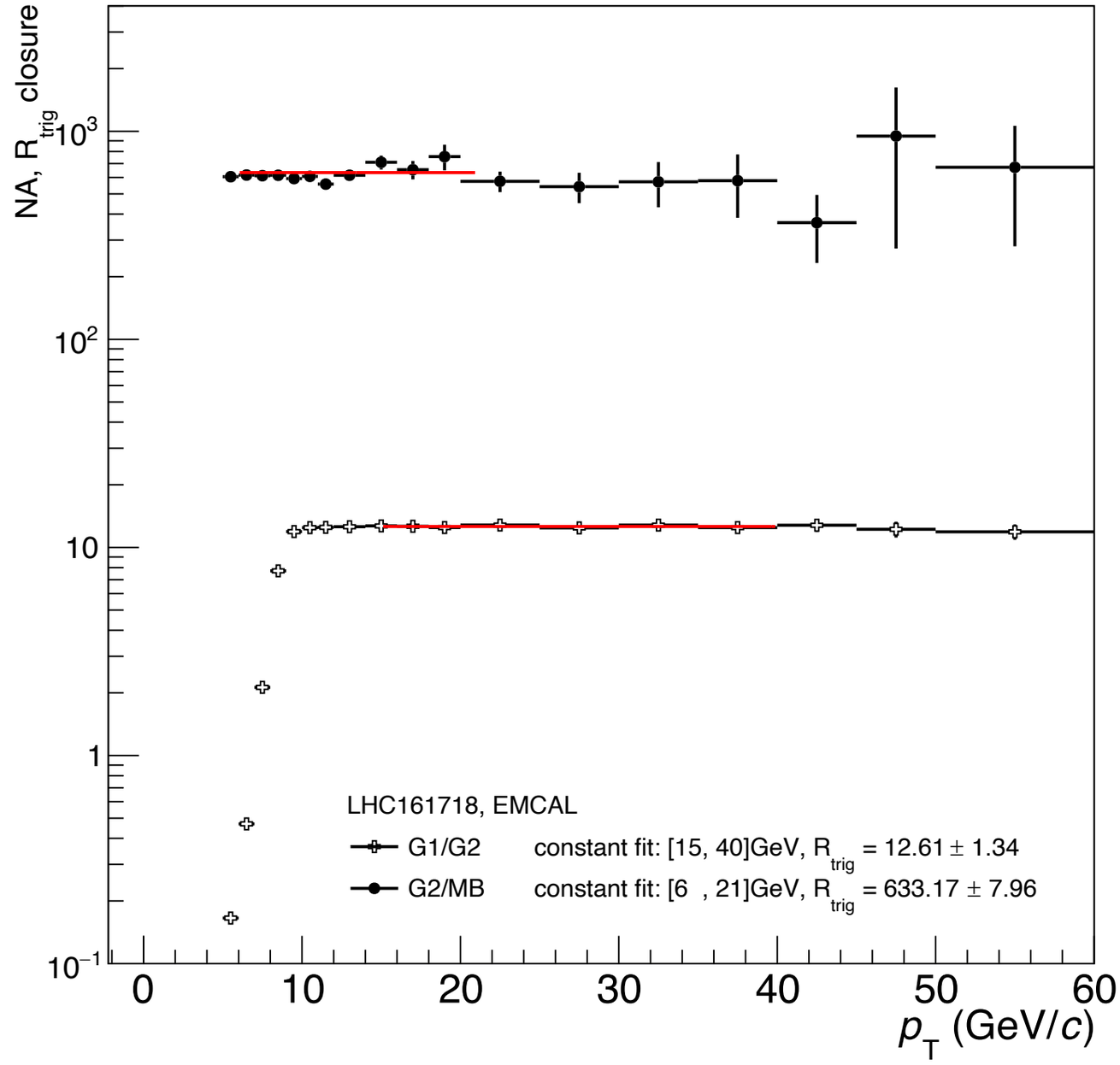
DCal RF plots in backup

Isolated photon rejection factor

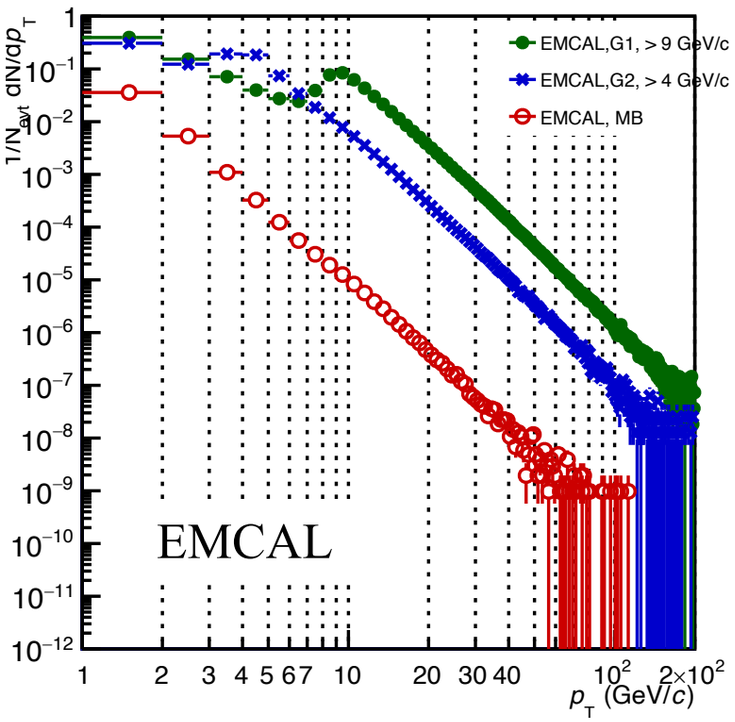
$$RF = \left(\frac{1}{N_{evt}}\frac{dN}{dP_T}\right)_{trigger} \Big/ \left(\frac{1}{N_{evt}}\frac{dN}{dP_T}\right)_{MB}$$

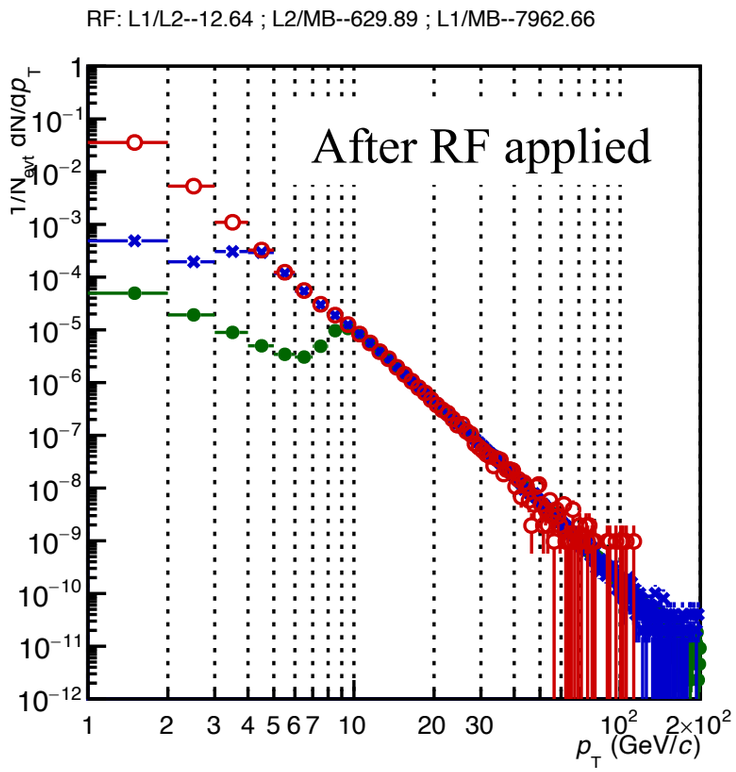
		cluster RF	Iso photon RF	Cluster/ IsoPhoton
EMCAL	G1 / G2	12.64±0.71	12.61±1.34	1.002
	G2 / MB	629.89±6.48	633.17±7.96	0.995
	G1 / MB	7962.73		
DCAL	G1 / G2	12.04±0.69	12.49±1.34	0.964
	G2 / MB	1280.87±9.24	1229.58±11.09	1.042
	G1 / MB	15427.31		

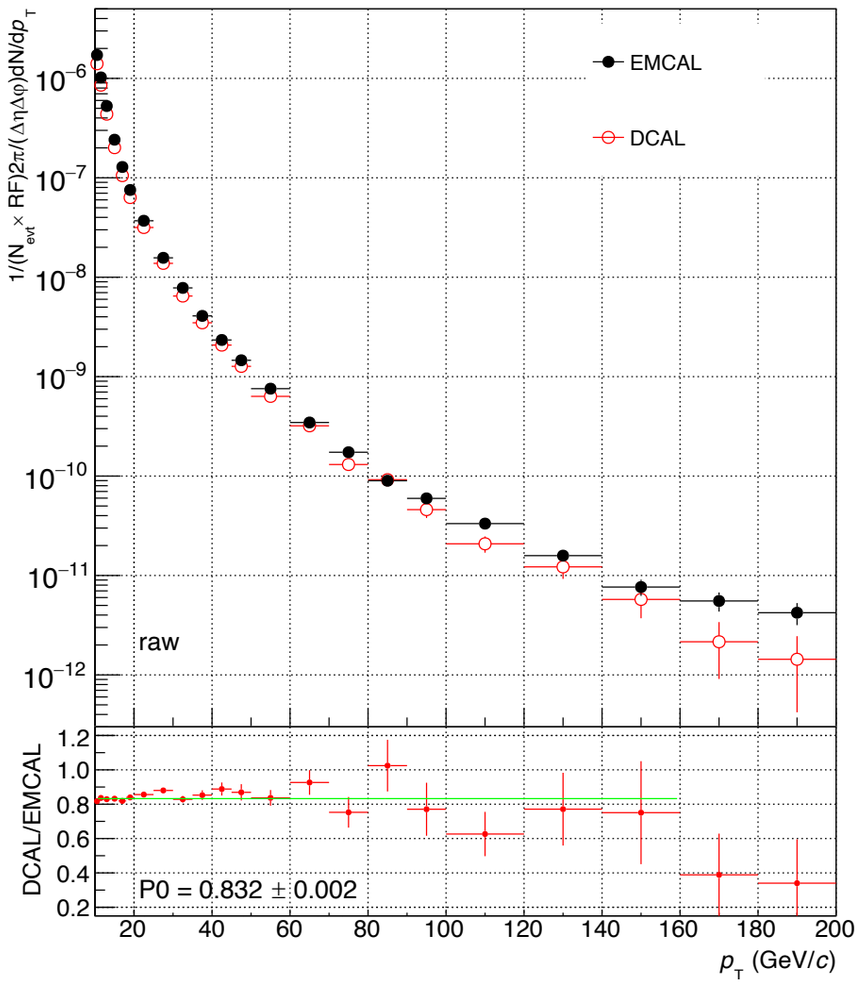
The rejection factor works equivalent in cluster and isolated photon.

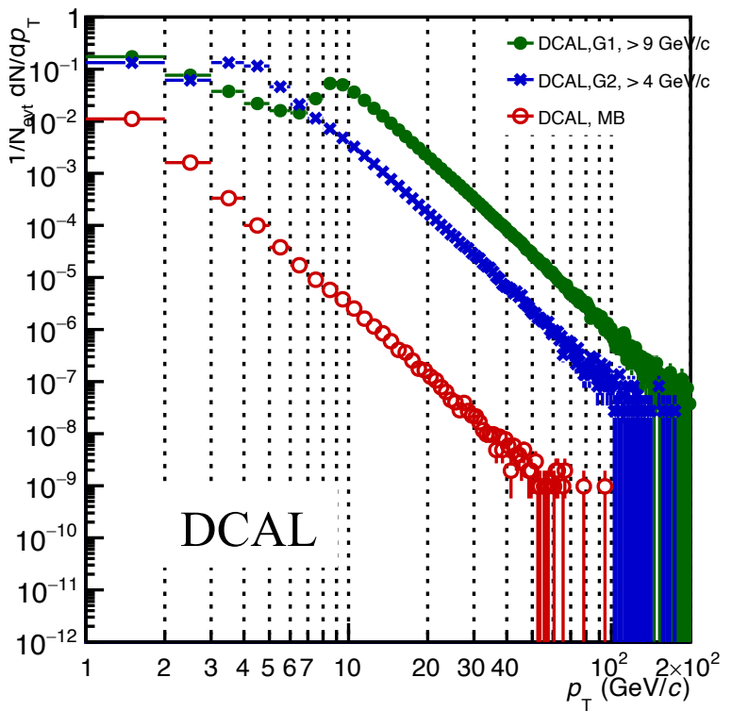


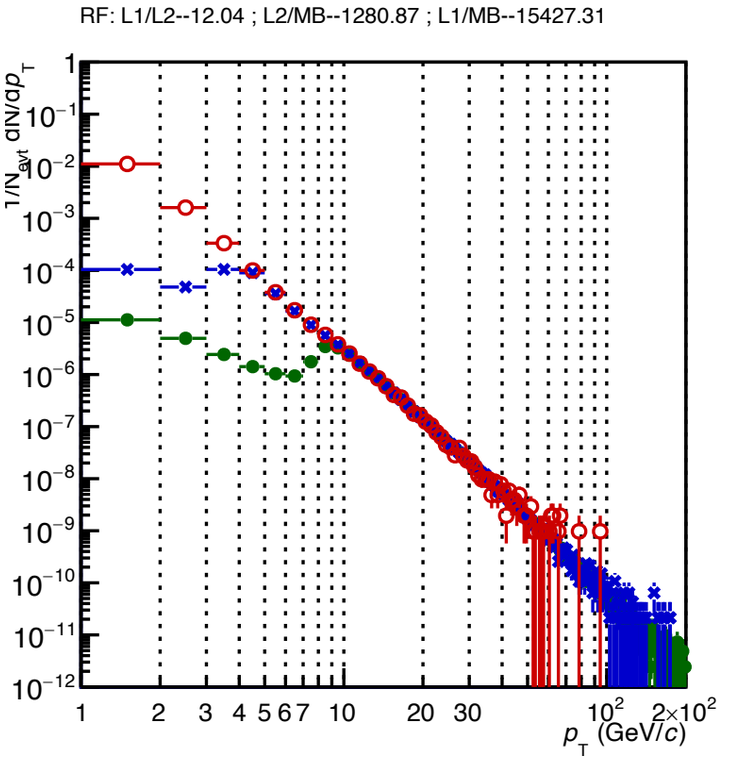
Isolated photon pt distribution





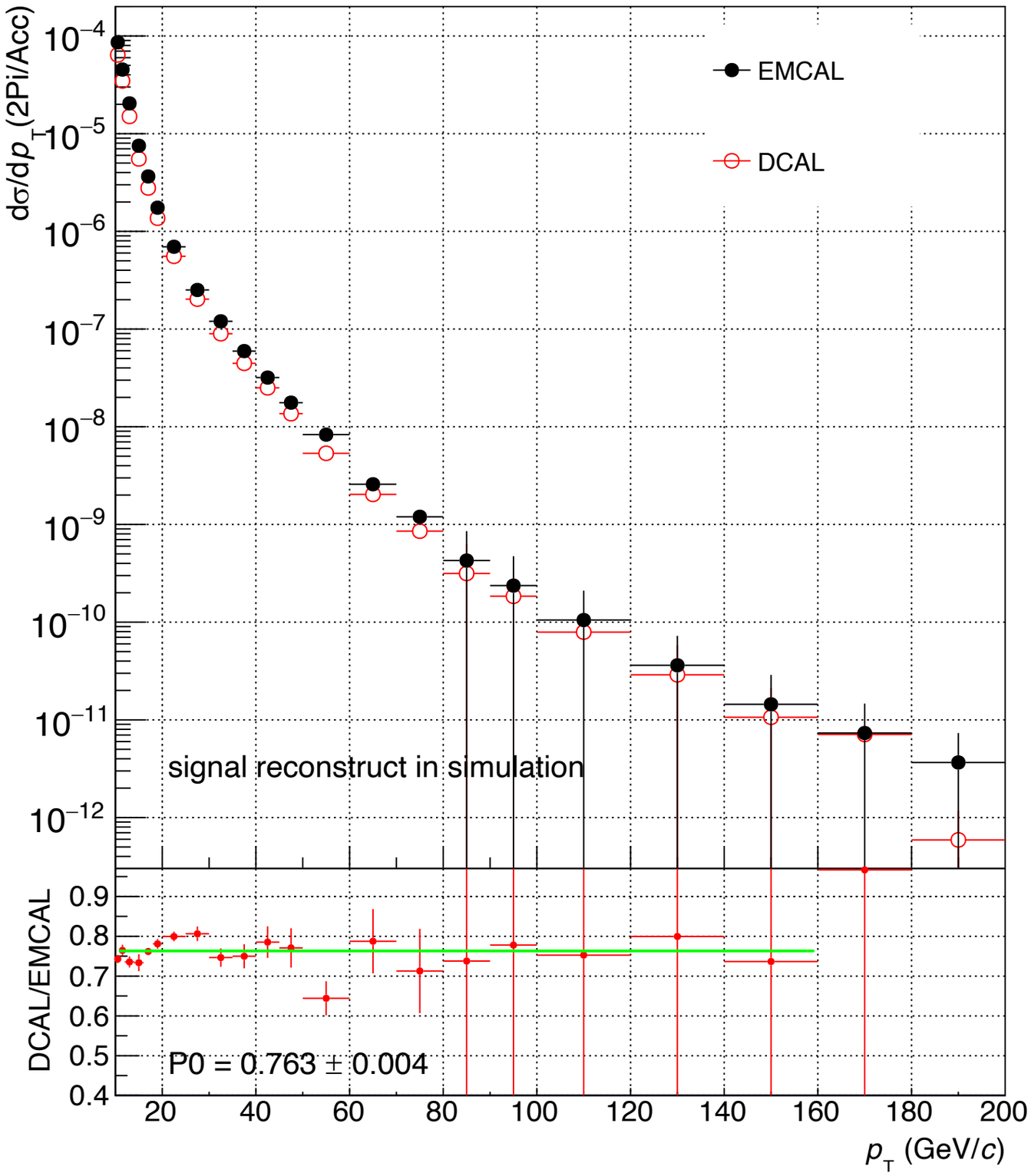






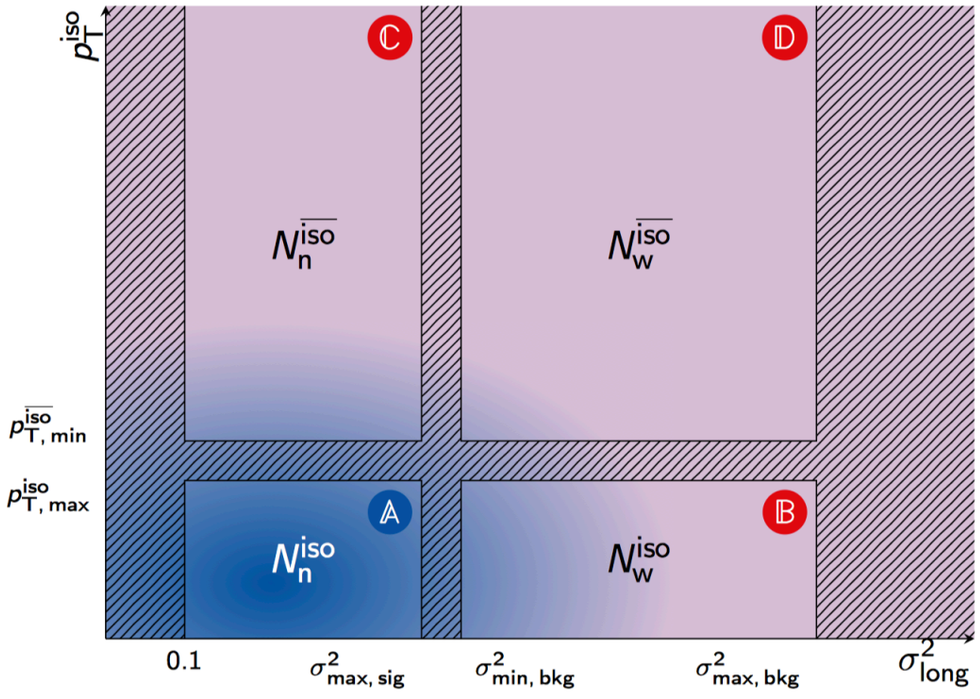
- After the cluster rejection factor applied, different samples similar to each other.
- Combined sample after acceptance normalized, DCAL/EMCAL around 0.83. because different masked regions not considered in acceptance correction factor.

Isolated photon pt distribution in MC



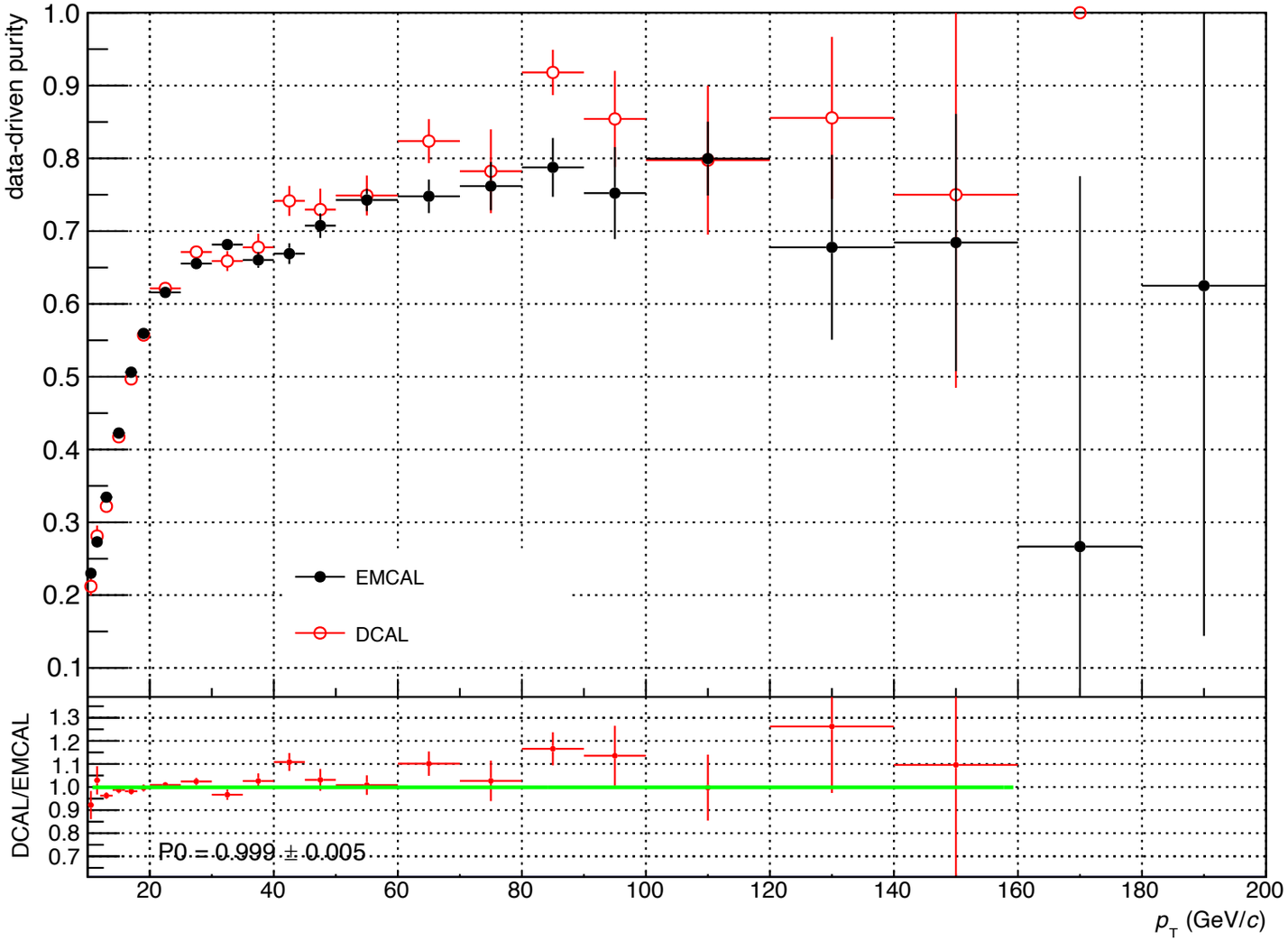
- In MC, the reconstructed signal in different calorimeters are close to each other after acceptance Combined sample after acceptance normalized.
- Ratio, DCAL/EMCAL is 0.76 in GJ but in data is 0.83.

Data driven purity in different detector



$$purity = \left[1 - \left(\frac{N_c/N_A}{N_D/N_B}\right)_{data}\right] \times \left(\frac{B_A/N_C}{N_B/N_D}\right)_{M}$$

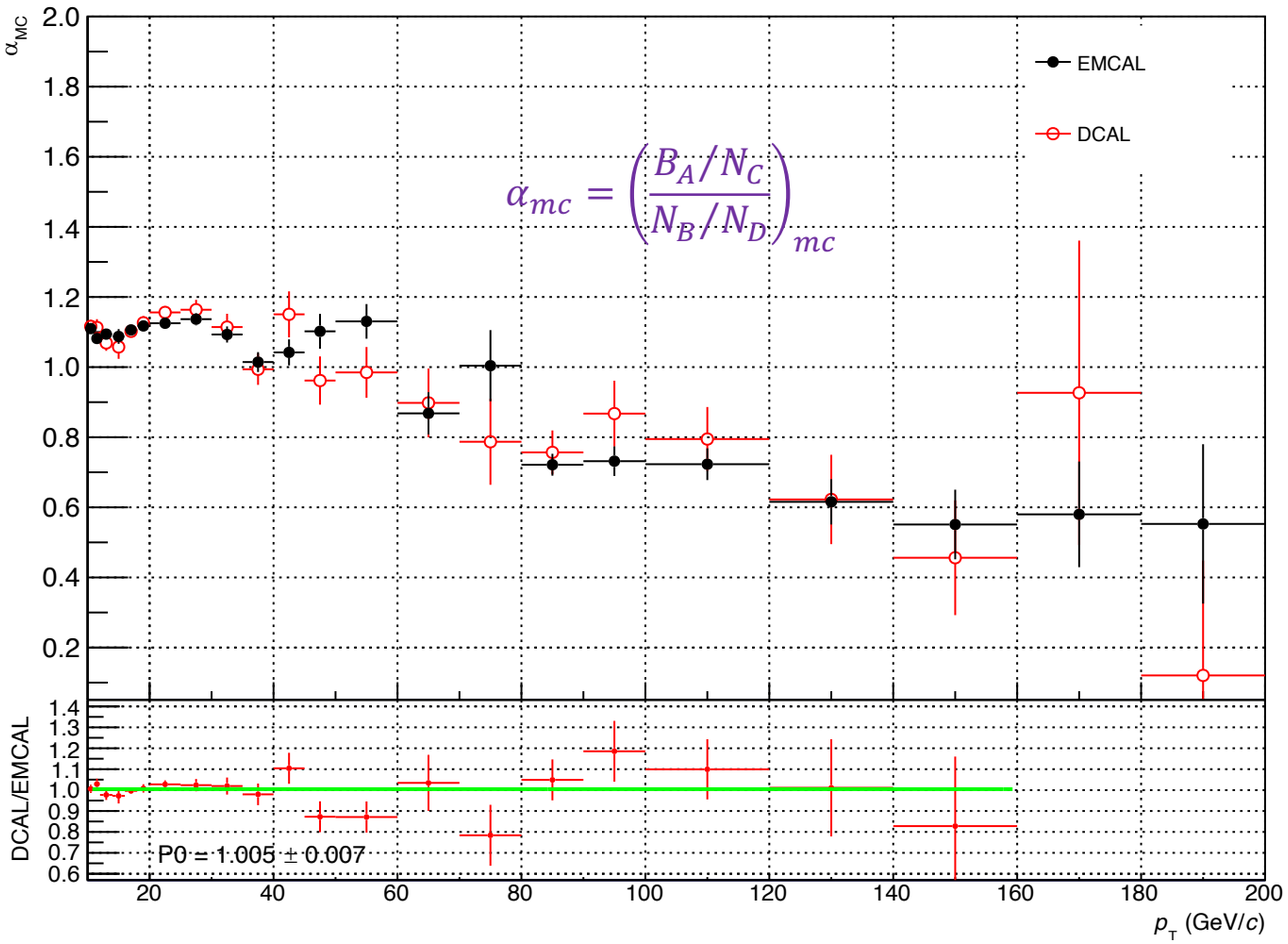
purity by data-driven

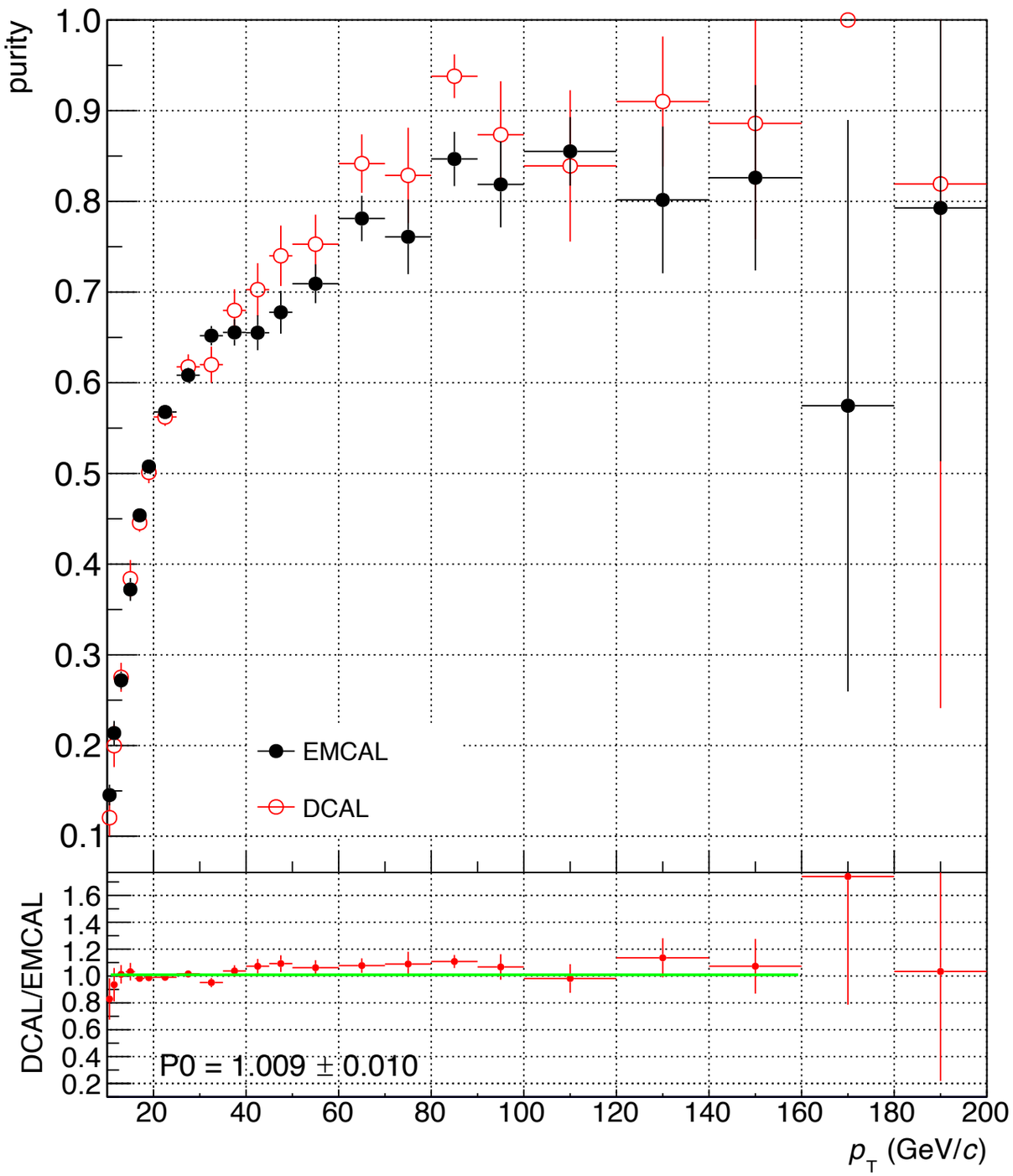


✢ Data-driven purity is equivalent between EMCal and DCal.

✢ Data-driven purity DCAL/EMCAL pol0 fit value: 0.999 ± 0.006.

MC correction factor and final purity



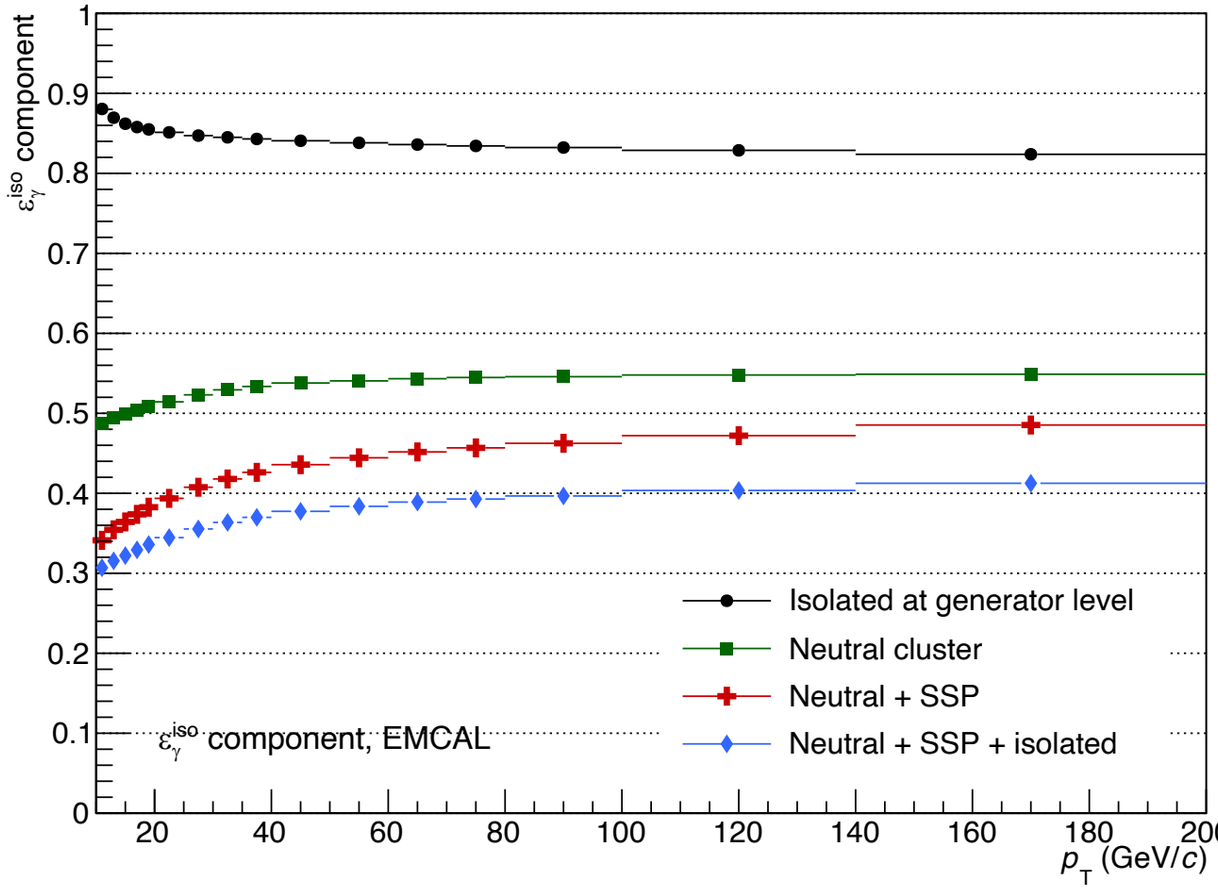


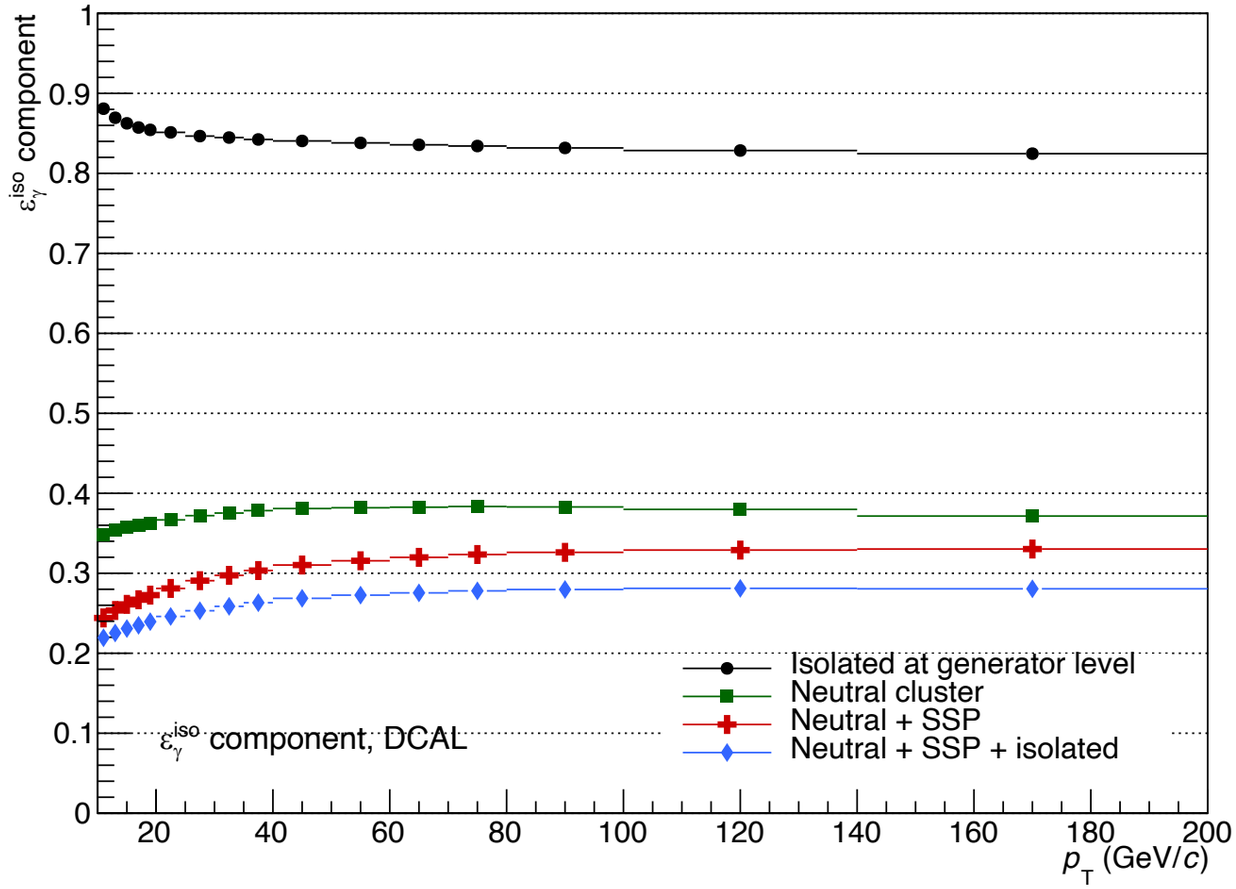
$$purity = 1 - \left(\frac{N_c/N_A}{N_D/N_B}\right)_{data} \times \left(\frac{B_A/N_C}{N_B/N_D}\right)_{mc} \alpha_{mc}$$

✢ MC correction factor is similar between EMCal and DCal. Pol0 fit: 1.005 ± 0.007

✢ Purity ~1 after 160 GeV/c in DCal due to data having less statistic.

Efficiency component





- Less neutral cluster can be reconstructed in DCal, because the different masked regions

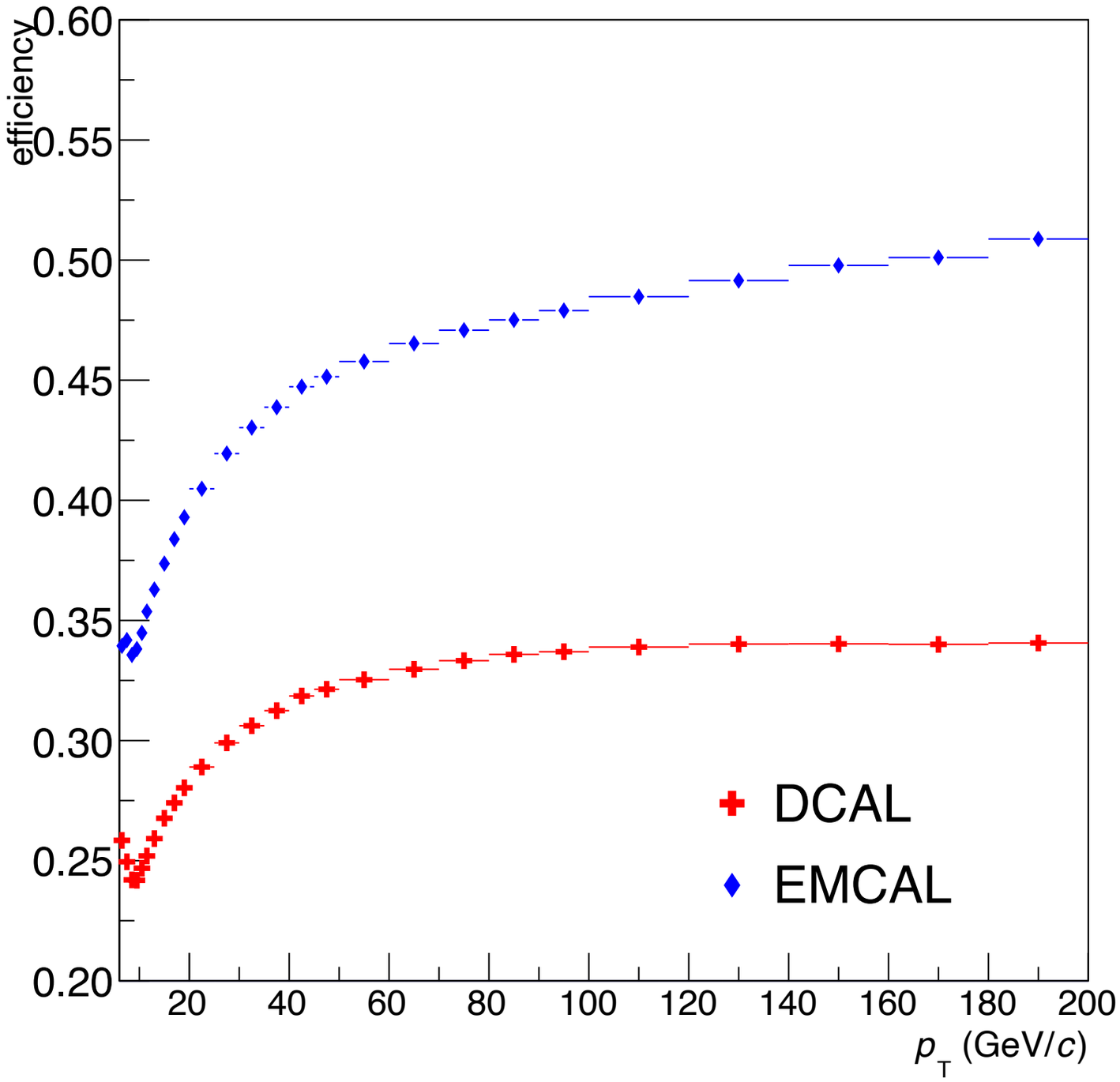
Efficiency comparison

- Efficiency correction:

$$\varepsilon_{\gamma}^{iso}(p_T) = \frac{dN_{\gamma_{iso}}^{reco}}{dp_T^{gen}} \Big/ \frac{dN_{\gamma_{iso}}^{gen}}{dp_T^{gen}}$$

Photon reconstruction, identification and isolation.

- Efficiency on EMCal is around 0.5 and DCal is 0.35.
  - — due to the less neutral cluster can be reconstructed in DCal.



Cross section comparison

cross section =

$$\sigma_{total} \times \frac{2\pi}{\Delta\eta\Delta\phi} \cdot \frac{1}{\sum(N_{evt,i} \times RF_i)} \sum \frac{dN}{dp_T} \times \frac{purity}{efficienc}$$

– $\frac{2\pi}{\Delta\eta\Delta\phi} \cdot \frac{1}{\sum(N_{evt,i} \times RF_i)} \sum \frac{dN}{dp_T}$ is raw spectrum

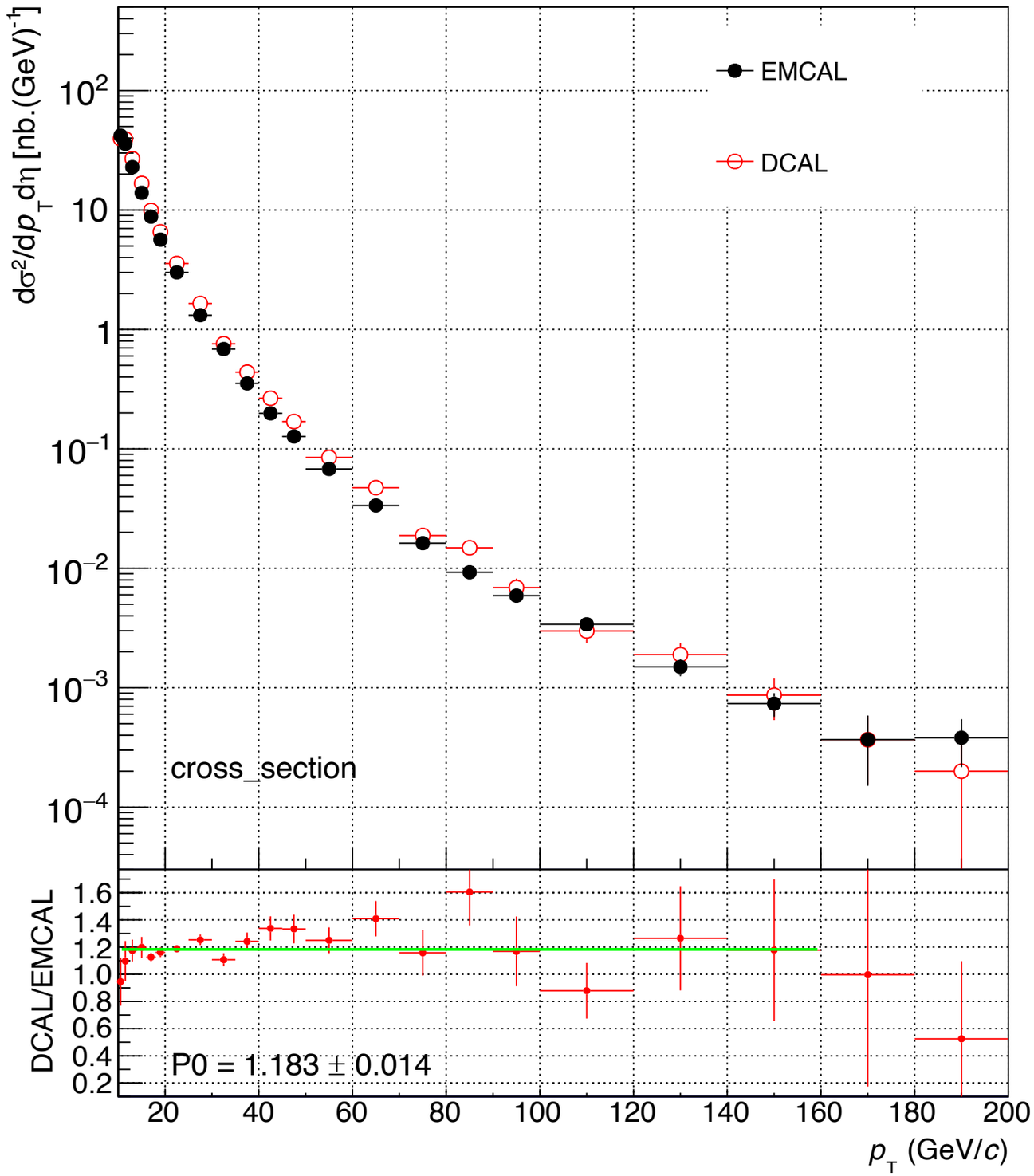
- Ratio DCAL / EMCAL around 1.18

  ratio fit information:

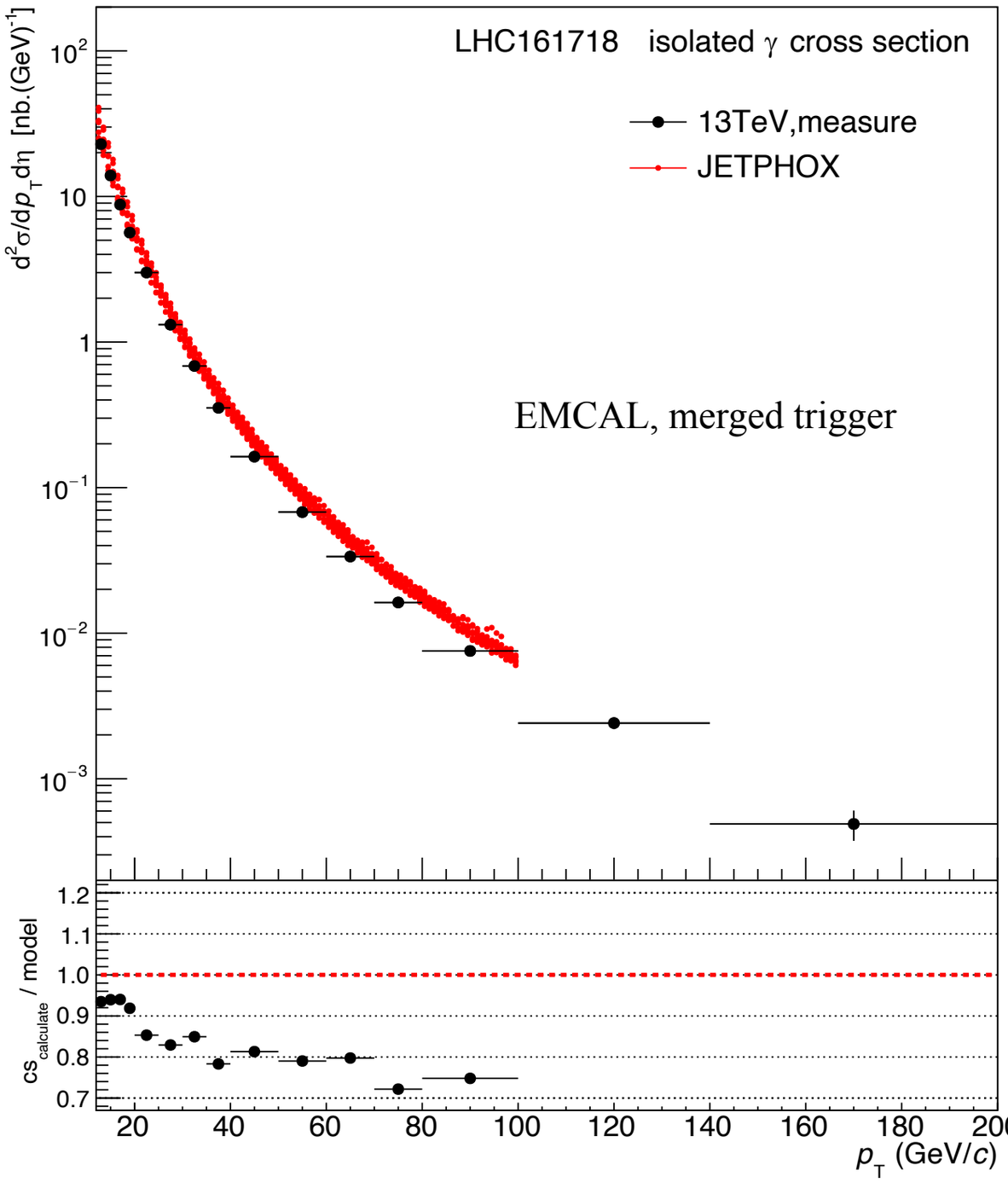
  -- fit function: pol0

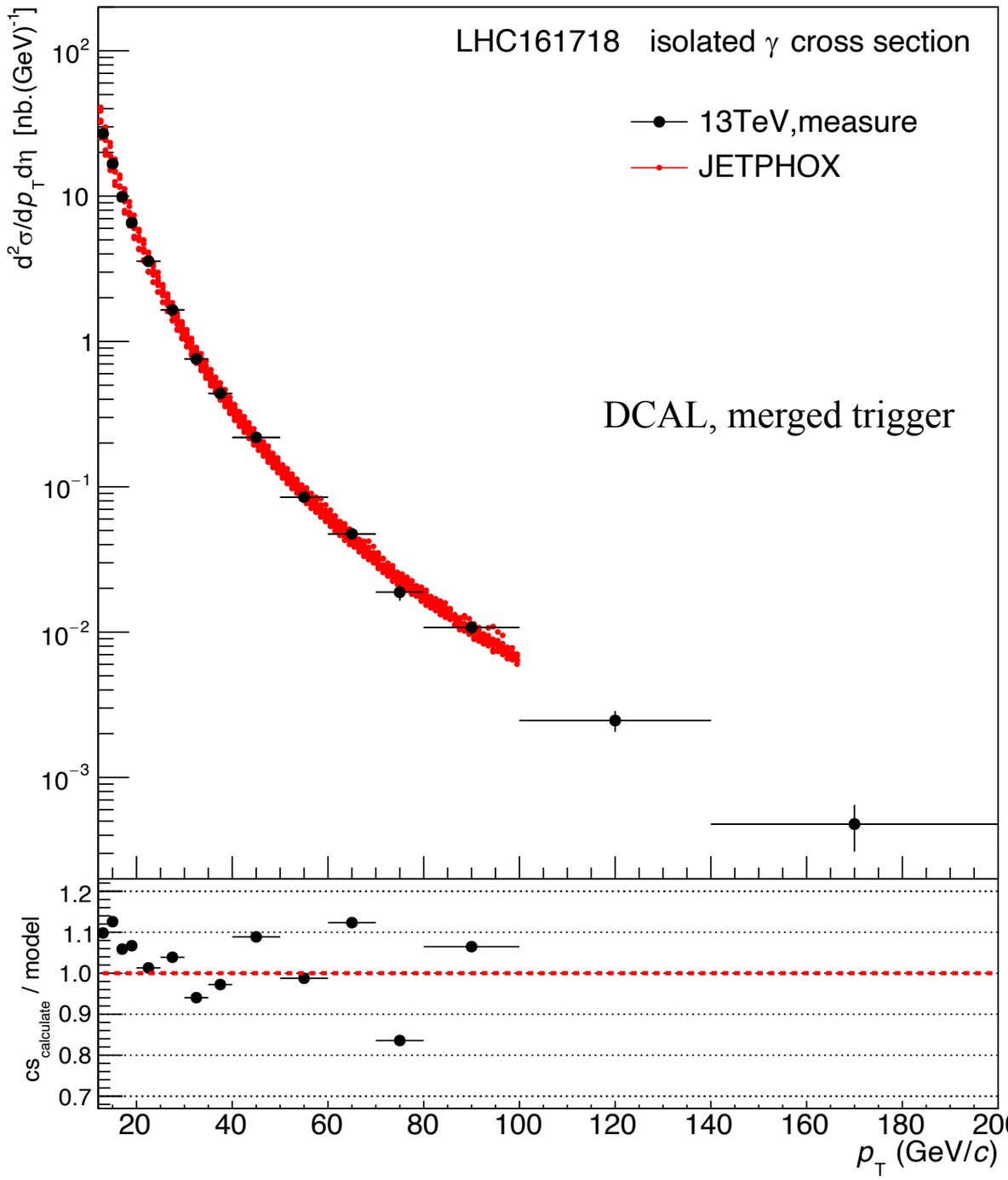
  -- fit range: [10. , 160.]

  -- fitted para: 1.183±0.014.



Cross section, EMCAL && DCAL





- Not sure the settings of the jetphox configuration settings, I will try to run jetphox and produce the theory points

Summary

✢ comparing mainly analysis result between EMCal and Dcal

→ after acceptance normalization, combined spectrum ratio ~ 0.8 (DCal / EMCal).

→ purity has similar distribution between EMCal and DCal.

→ efficiency ratio around 0.7 which comes from reconstruct level.

→ yield and cross section ratio around 1.17 which equal to ratios from each analysis procedures

$$\text{cross section} = \sigma_{total} \times \underbrace{\underbrace{\frac{2\pi}{\Delta\eta\Delta\phi} \cdot \frac{1}{\sum(N_{evt,i} \times RF_i)} \sum \frac{dN}{dp_T}}_{\text{raw, ratio} \sim 0.8} \times \frac{purity}{efficiency}}_{\text{yield, ratio} \sim 1.17} \begin{array}{l} \longleftarrow \text{ratio} \sim 1.0 \\ \longleftarrow \text{ratio} \sim 0.7 \end{array}$$

Next step:

1. check closely all the steps of the analysis to understand difference between EMCal and DCal
2. obtain theory curve running jetphox
3. prepare analysis note