

B meson R_{AA} status

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MC Generation

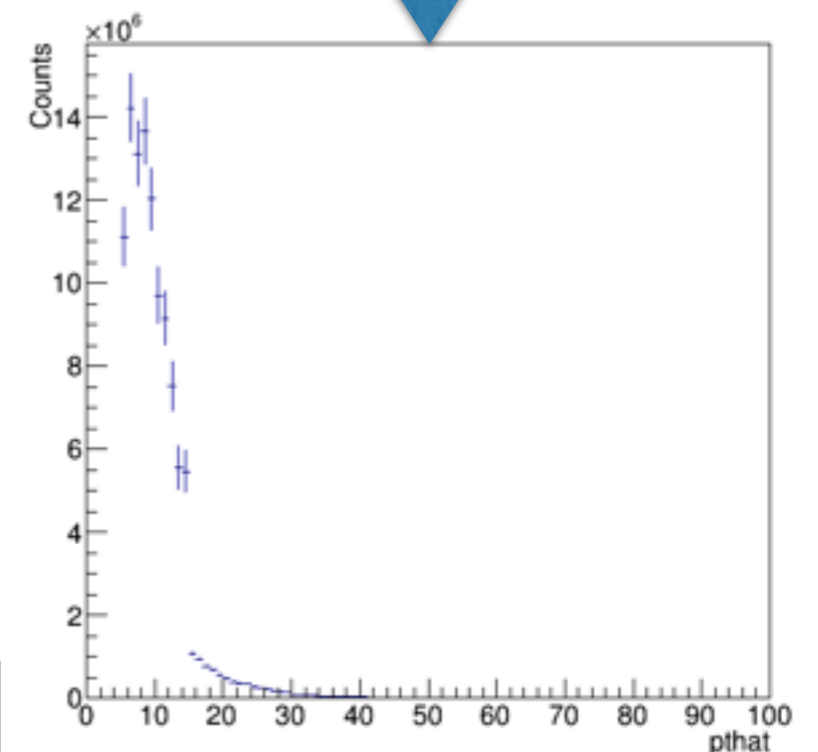
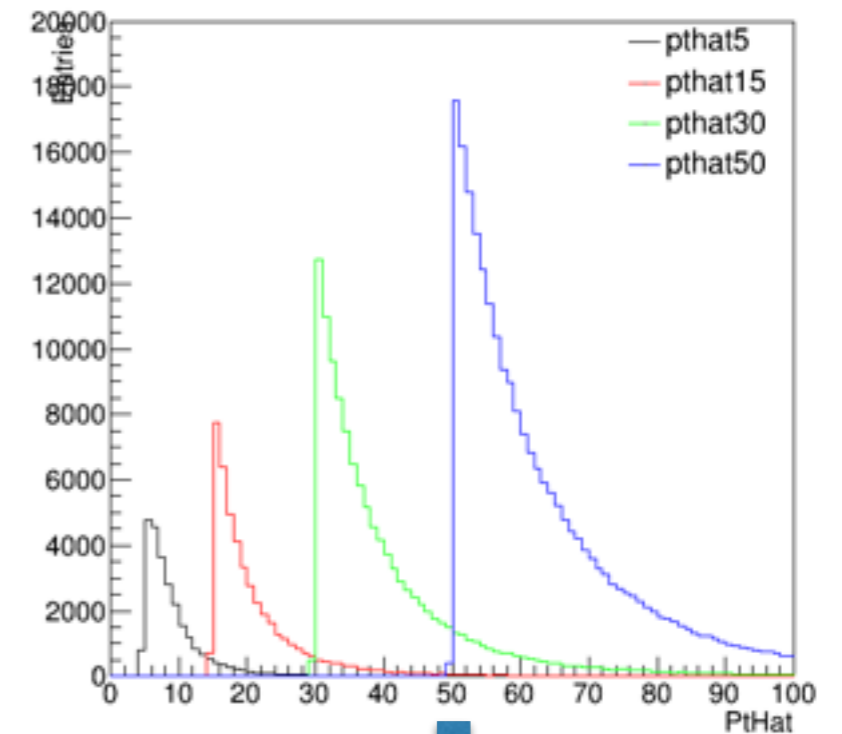
- 4 MC samples are generated based on pthat range
- Weight is applied to merge 4 samples

	pthat5	pthat15	pthat30	pthat50
range	5~∞	15~∞	30~∞	50~∞
Cross-Section(pb)	5.920×10^7 $\pm 9.724 \times 10$	5.622×10^6 $\pm 4.428 \times 10$	6.819×10^5 $\pm 3.928 \times 10$	9.782×10^4 $\pm 5.089 \times 10$

$$weight(i, i+1) = \frac{\sigma(i) - \sigma(i+1)}{N_{pthat}(i) - N_{pthat}(i+1)}$$

	pthat5~ pthat15	pthat15~ pthat30	pthat30~ pthat50	pthat50~ pthat10000
Events	2229	10758	39530	119482
Weight	24036.8	459.202	14.7756	0.818701

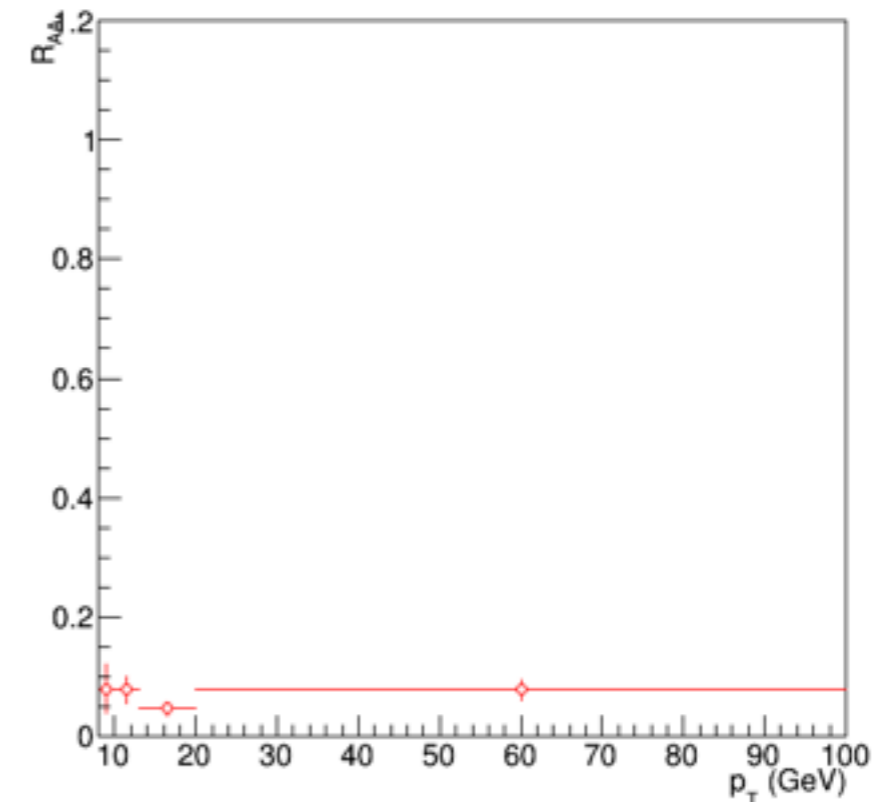
- Low pthat events have low statistics
- Weight is dominant for low pthat



Dataset status

Primary Dataset	Trigger Name
DoubleMu0A	HLT_HIL1DoubleMu0_v1
DoubleMu0B	HLT_HIL1DoubleMu0_part1_v1
DoubleMu0C	HLT_HIL1DoubleMu0_part2_v1
DoubleMu0D	HLT_HIL1DoubleMu0_part3_v1

Previous raw yield R_{AA}



- Previous R_{AA} result lost plenty of PbPb events due to wrong trigger name matching
- 30 % of DoubleMu0B PD files are failed at the skim level
 - Skim is ongoing by Geonhee again

Best Candidate Selection

previous

Event	B_Index	Onia_Index
1	1	1
1	2	1
1	3	1
1	4	2
1	5	2
1	6	2
1	7	3
1	8	3
2	9	1
2	10	1
2	11	2

1 B/1 evt

1 B/1 Onia



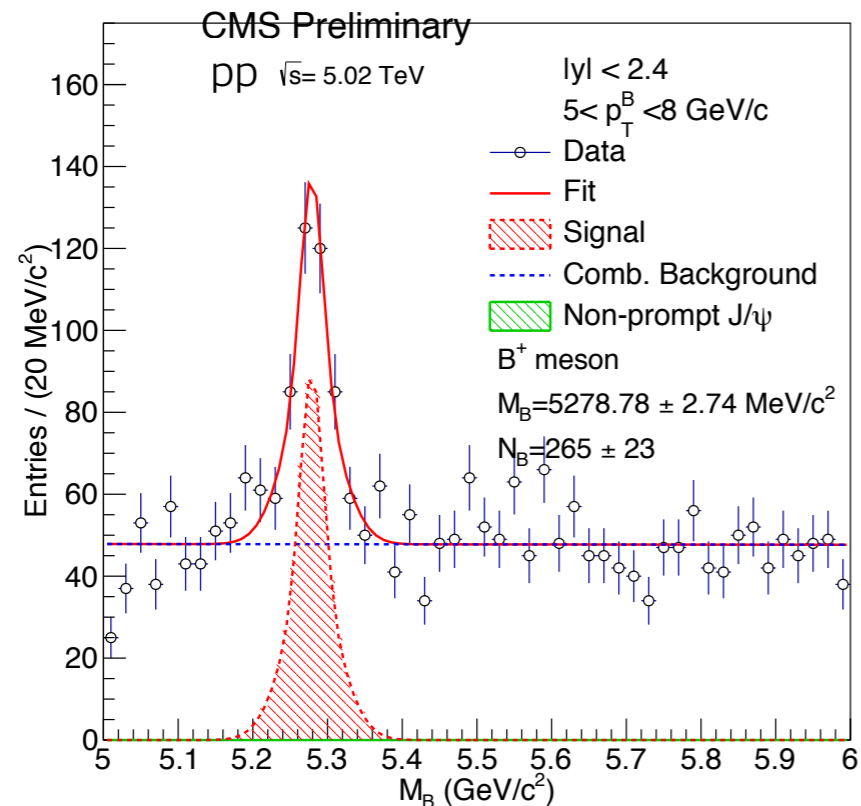
now

Event	B_Index	Onia_Index
1	1	1
1	2	1
1	3	1
1	4	2
1	5	2
1	6	2
1	7	3
1	8	3
2	9	1
2	10	1
2	11	2

- Selection algorithm is improved
- Previously selected one B candidate for one event
- Now select one B candidate for one onia candidate

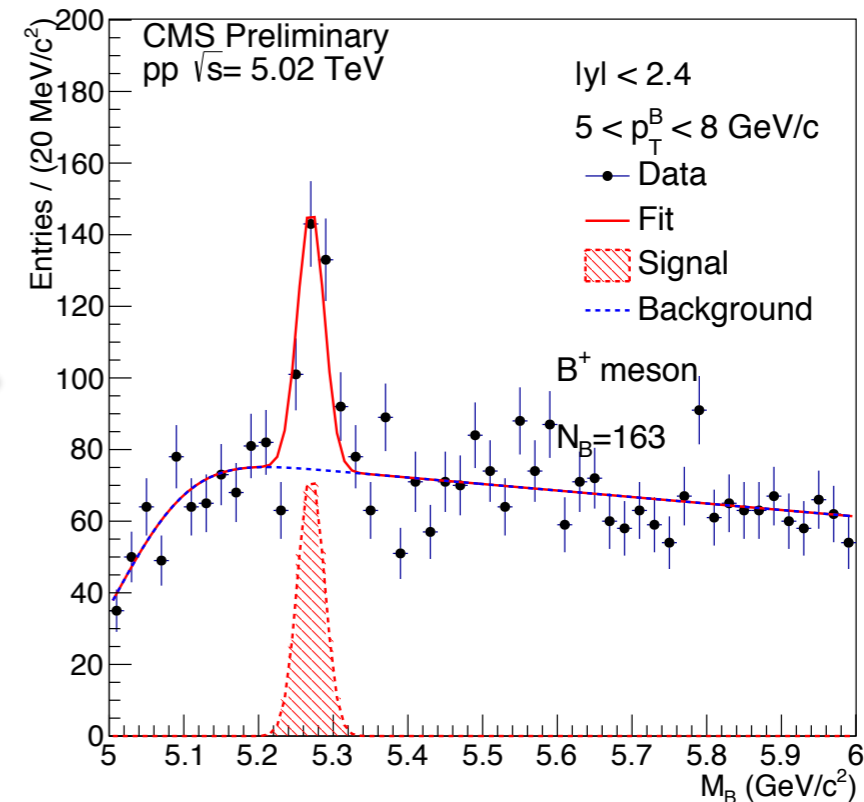
Mass fitting

previous



$$\text{Bkg} = (p_1x + p_2)$$

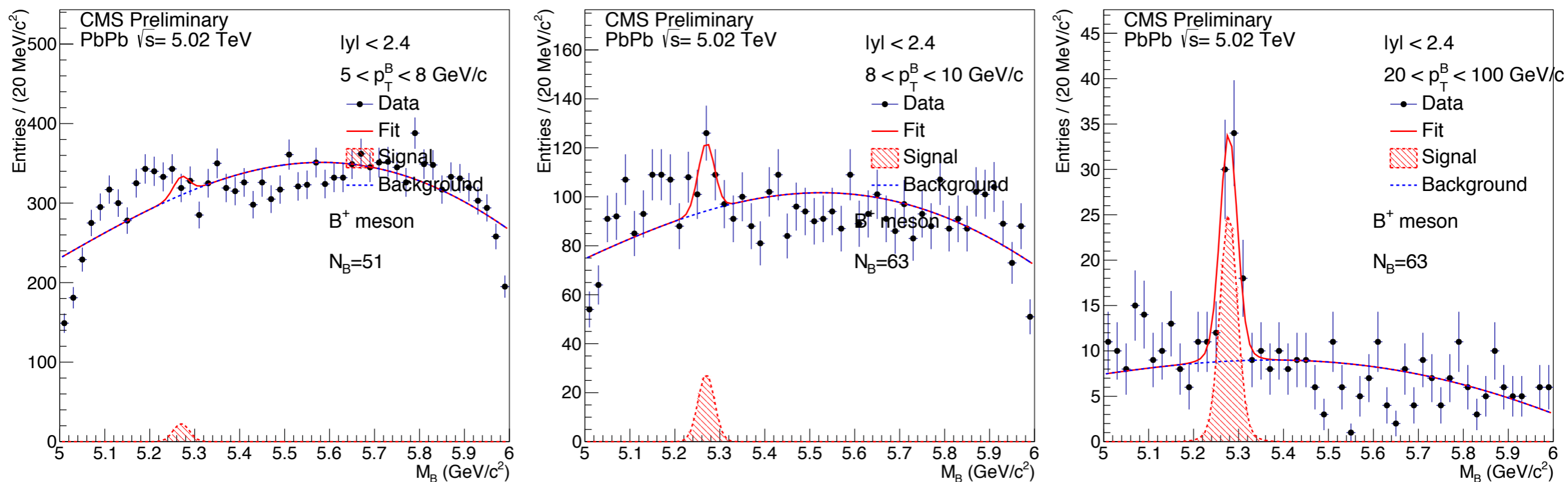
now



$$\text{Bkg} = (\text{Erf}((x-p_1)/p_2)+1)(p_3x+p_4)$$

- Previously fall down shape at low mass region was not described well
- Now background shape is multiplication of error function and 1st order polynomial
- Do we need function from other B or need to study it again?

PbPb mass fitting



- Parameters should be modified
- For the $5 < p_T < 8$ region, it is hard to find peak shape
- More tight track p_T study for PbPb is planned

Raw Yield R_{AA}

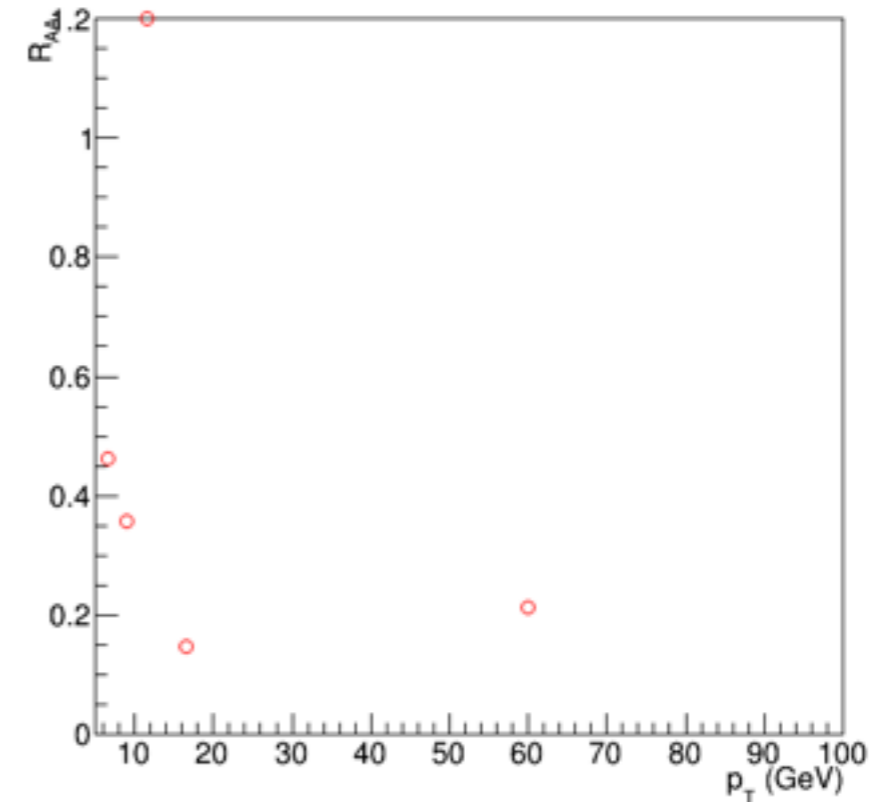
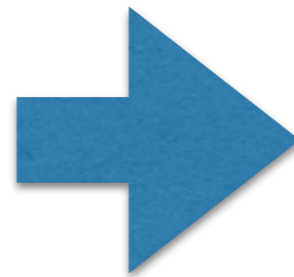
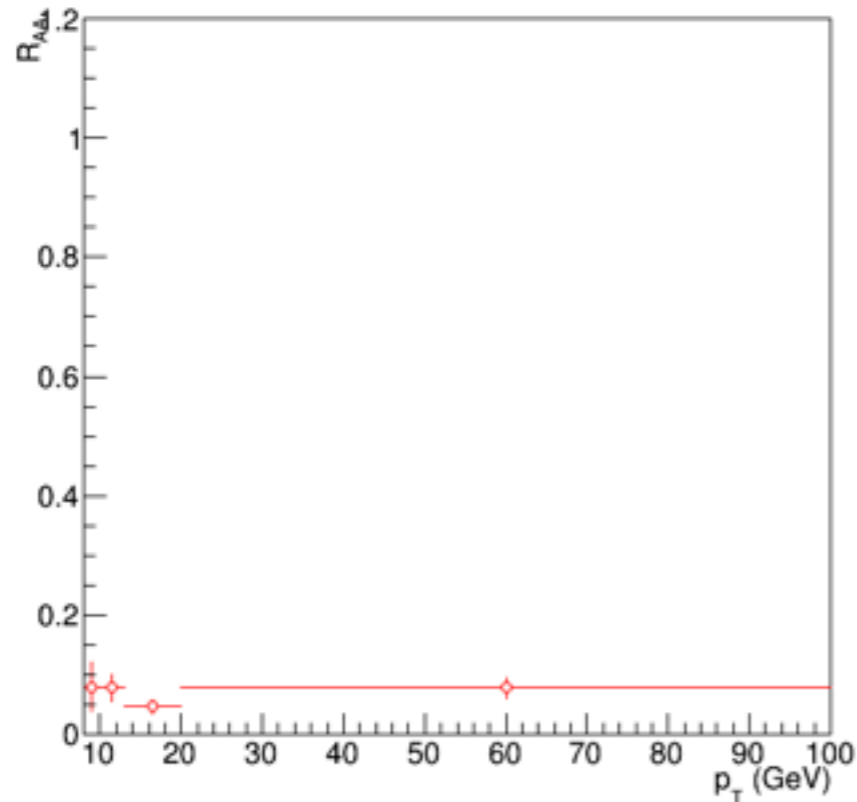
$$\frac{d\sigma(p_T)}{dp_T} = \frac{1}{2} \frac{1}{\Delta p_T} \frac{N(p_T)}{(Acc\mathcal{E})B\mathcal{L}}$$

$$R_{AA} = \frac{\left(\frac{d\sigma}{dp_T}\right)_{PbPb}}{AA\left(\frac{d\sigma}{dp_T}\right)_{pp}} = \frac{N_{PbPb}(p_T)\mathcal{L}_{pp}}{AAN_{pp}(p_T)\mathcal{L}_{PbPb}}$$

$$\begin{aligned} A: & \quad 208 \\ \mathcal{L}_{pp}: & \quad 25.8 \text{ pb}^{-1} \\ \mathcal{L}_{PbPb}: & \quad 404 \text{ } \mu\text{b}^{-1} \end{aligned}$$

previous

now



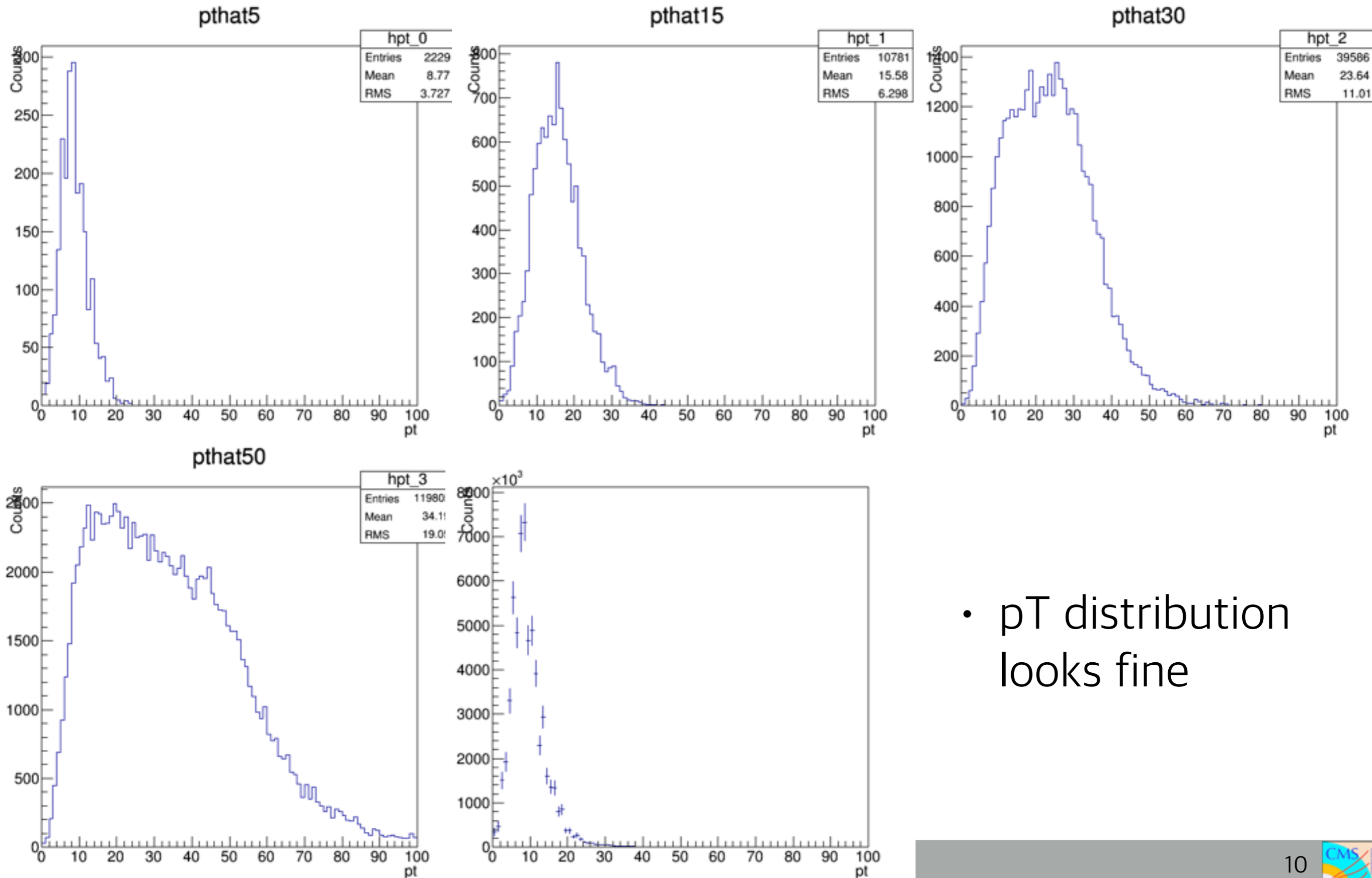
- Efficiency and Acceptance correction are not applied yet
- R_{AA} values are increased due to corrected trigger matching and improved selection

Summary

- 1. MC file is generated but low p_{t} events are not enough
 - Hyunchul is producing p_{t} 5, 15 again
- 2. Data file trigger matching corrected
 - Geonhee is reskimming Doublemu0B
- 3. Best candidate selection is improved
- 4. Using error function for low p_{t} pp is well matched but not for high p_{t}
- 5. Fitting function need to be improved

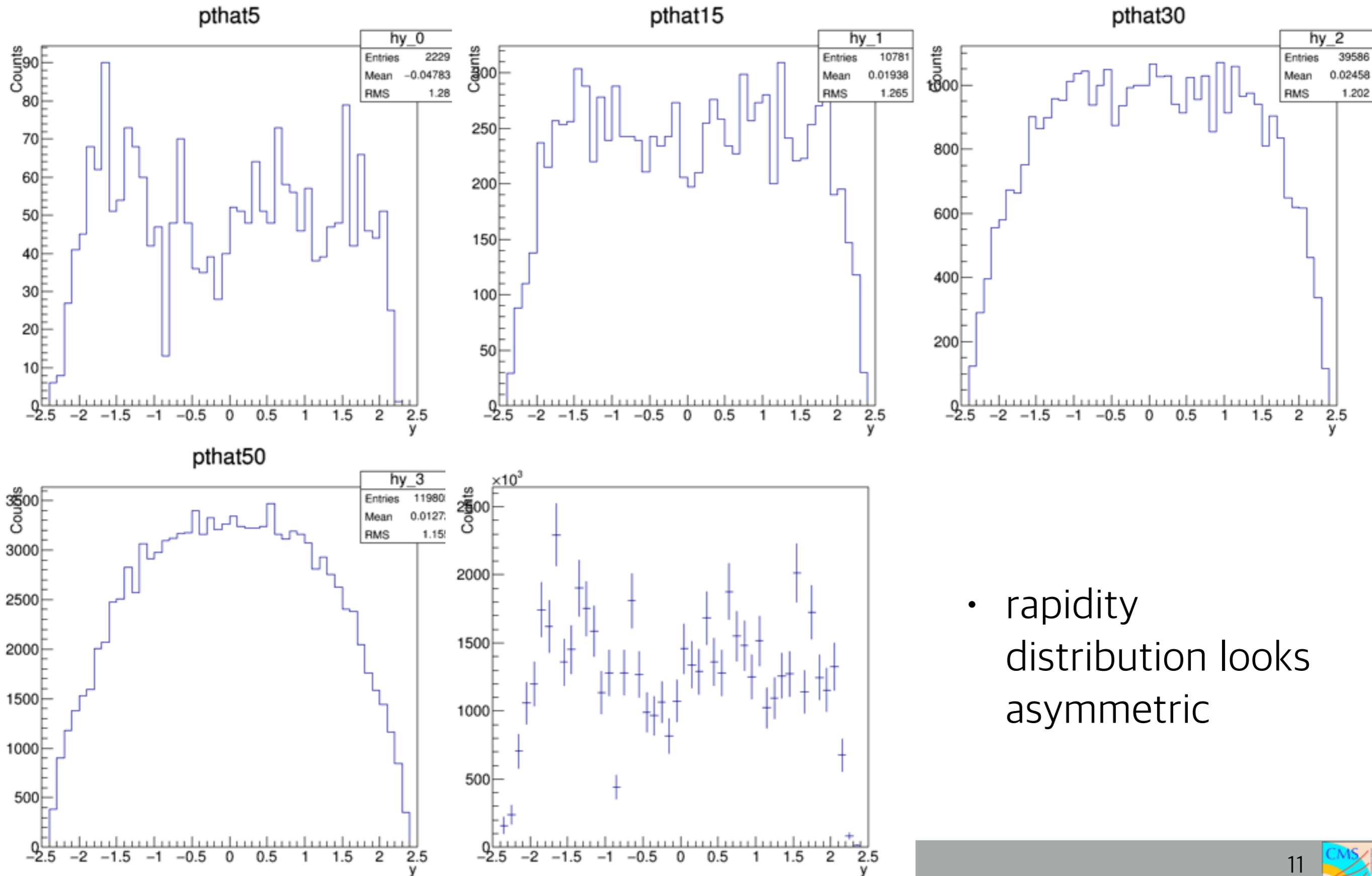
back up

Gen pT distribution



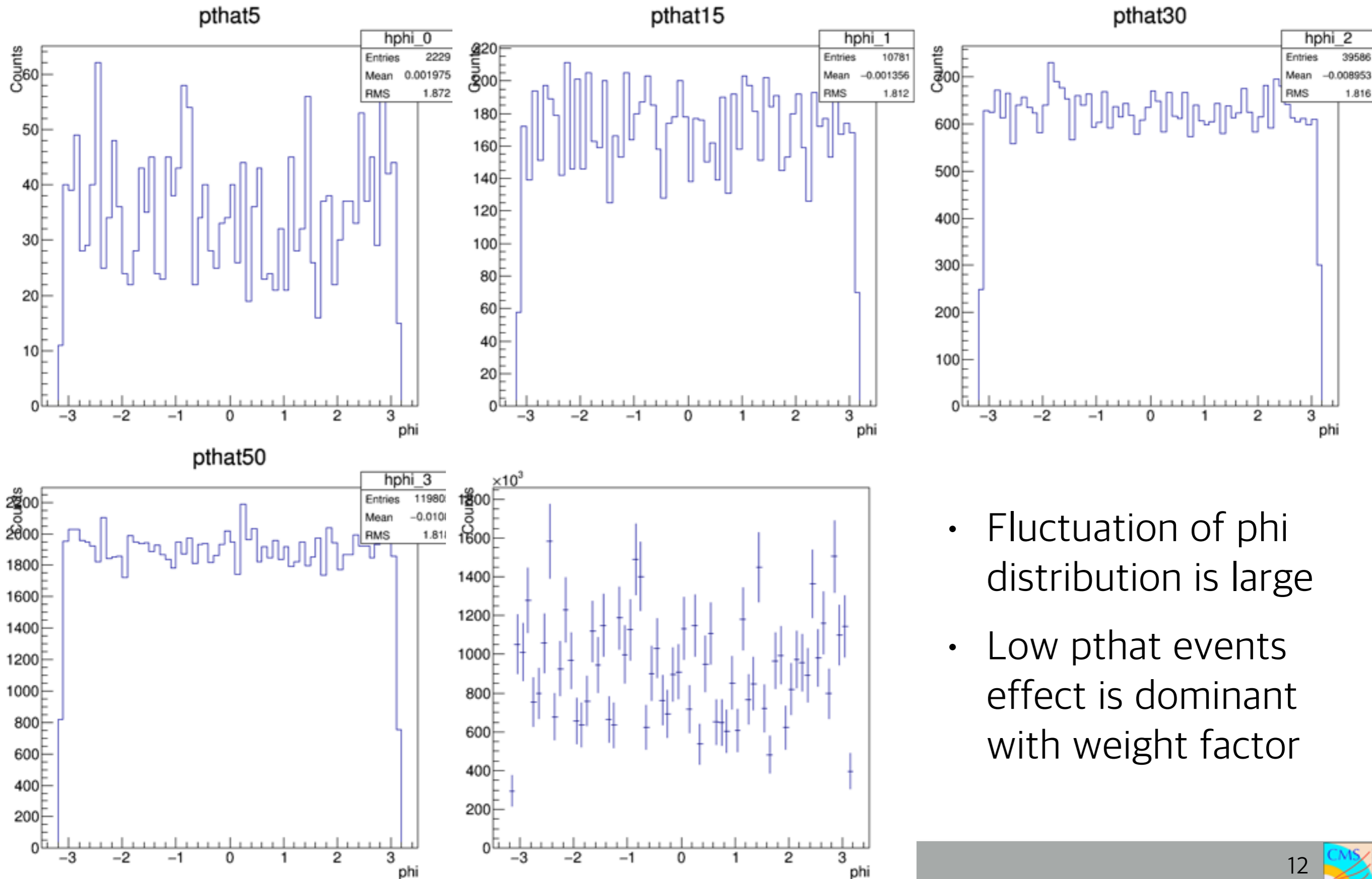
- pT distribution looks fine

Gen Rapidity distribution



- rapidity distribution looks asymmetric

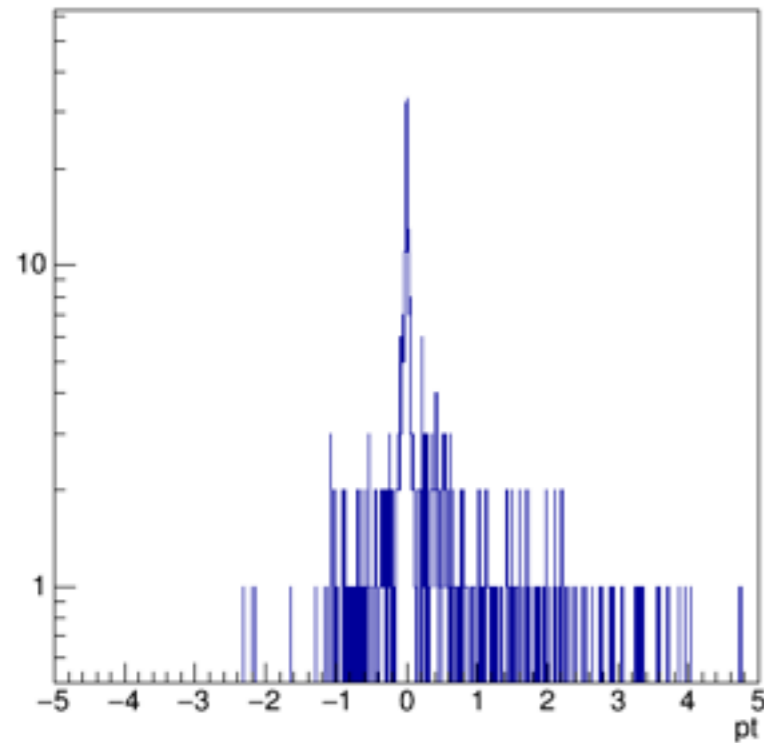
Gen Phi distribution



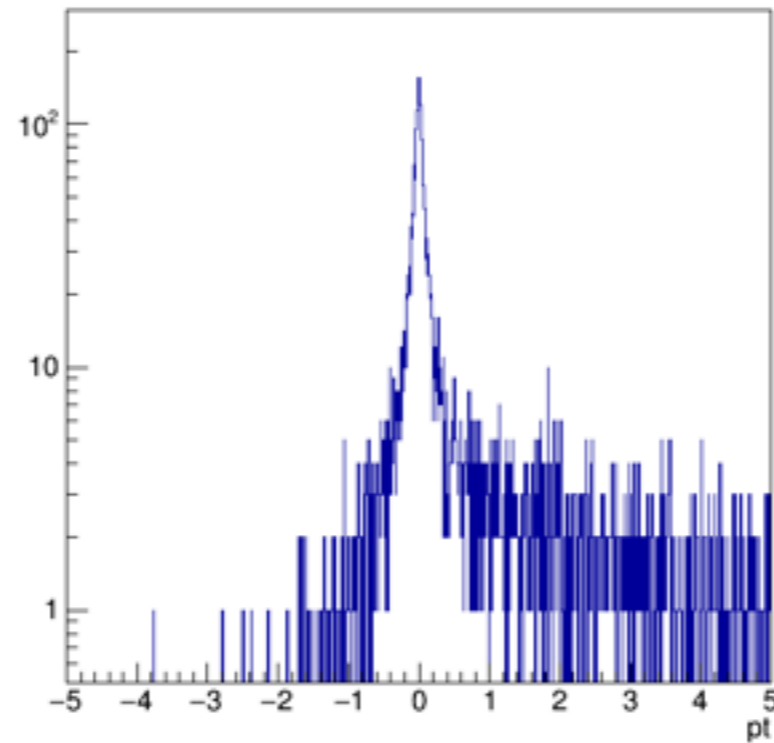
- Fluctuation of ϕ distribution is large
- Low p_{that} events effect is dominant with weight factor

MC Reco Gen matching study(pt)

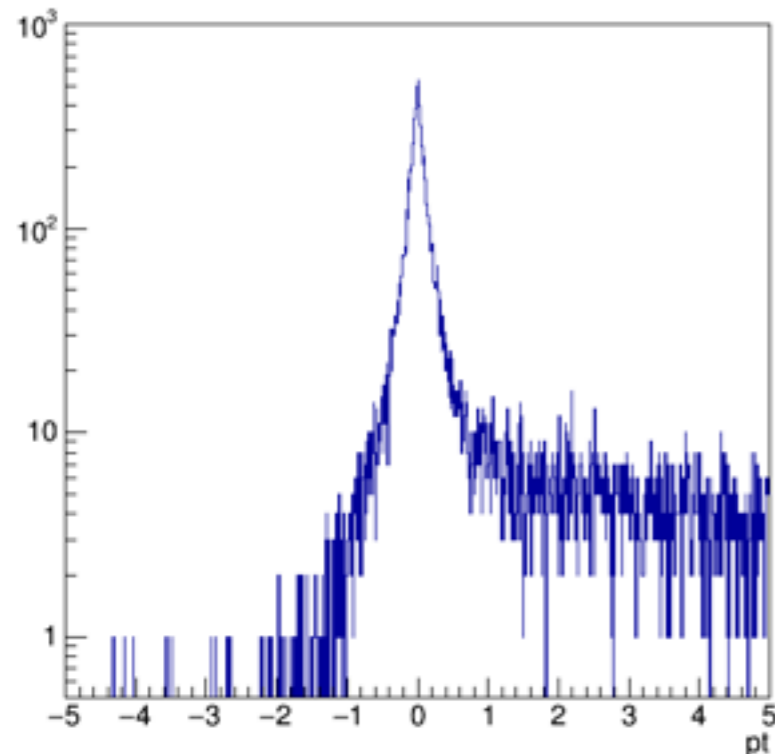
pthat5



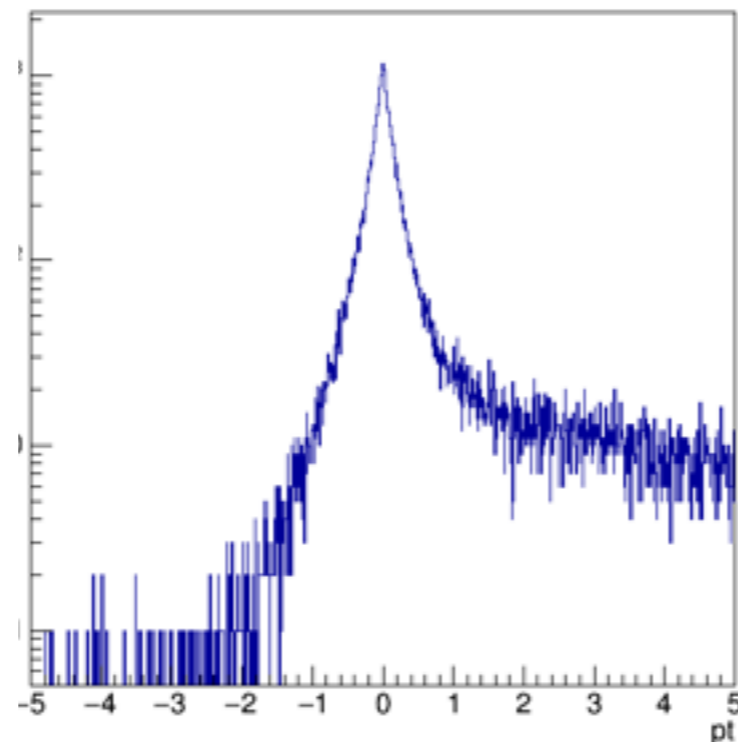
pthat15



pthat30



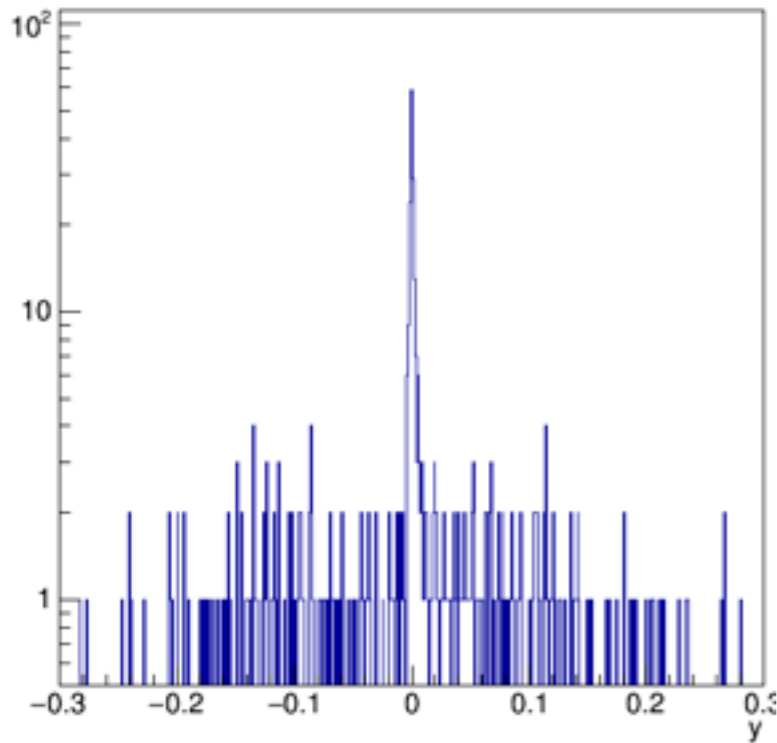
pthat50



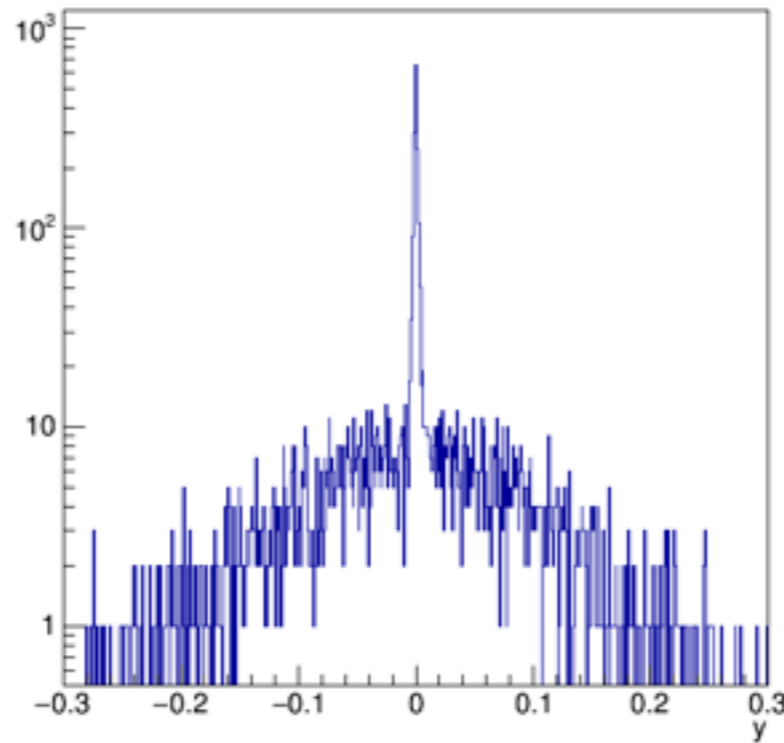
- We set the pt cut for Gen matching from Gen pt - Reco pt distribution
- $|\text{Gen pt} - \text{Reco pt}| < 1$

MC Reco Gen matching study(rapidity)

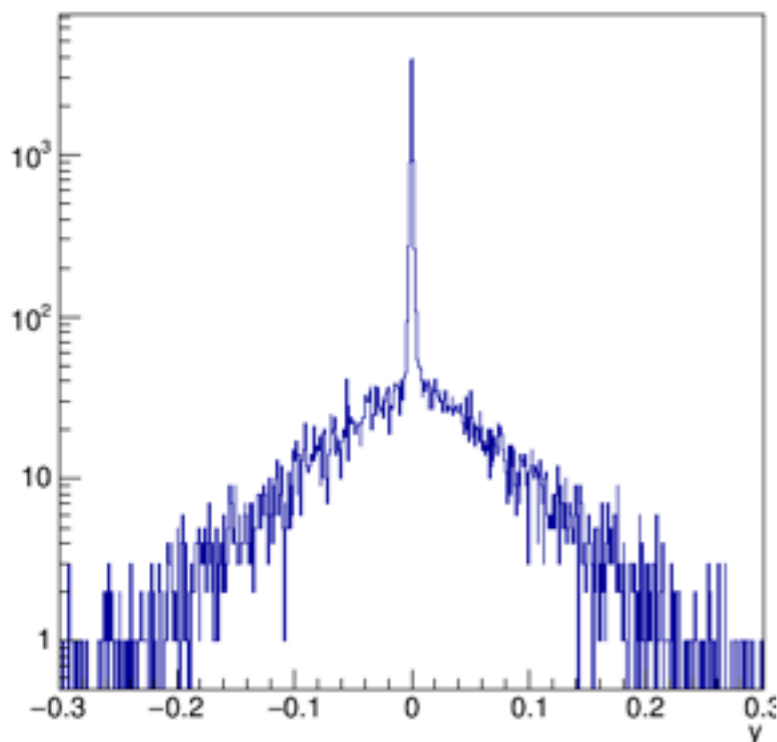
pthat5



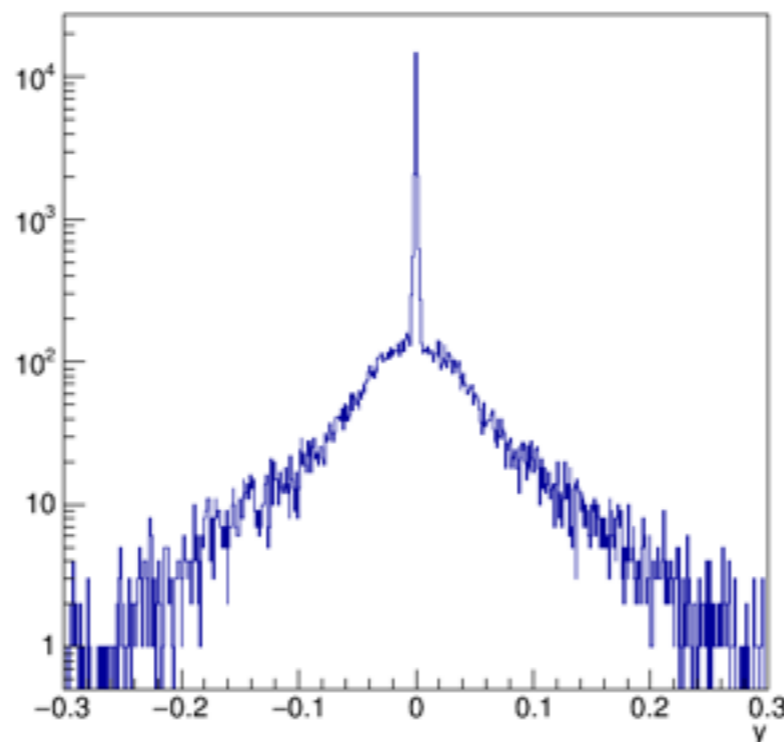
pthat15



pthat30



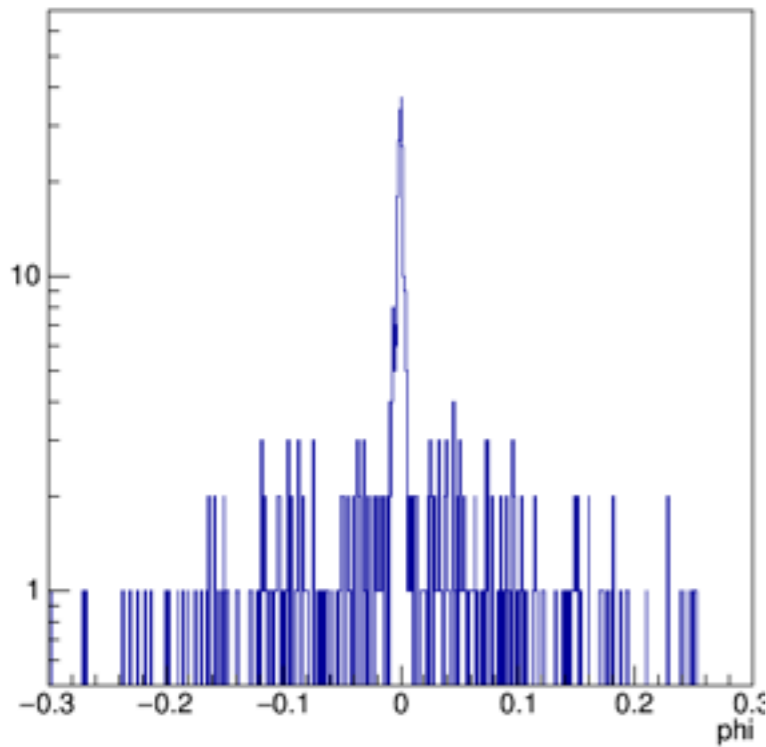
pthat50



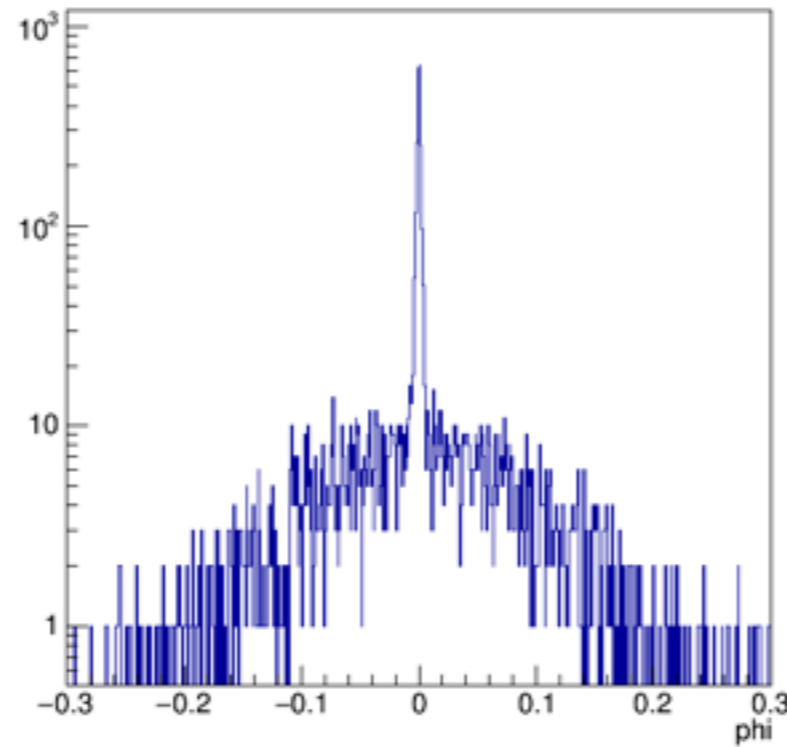
- We set the y cut for Gen matching from Gen y - Reco y distribution
- $|\text{Gen } y - \text{Reco } y| < 0.01$

MC Reco Gen matching study(phi)

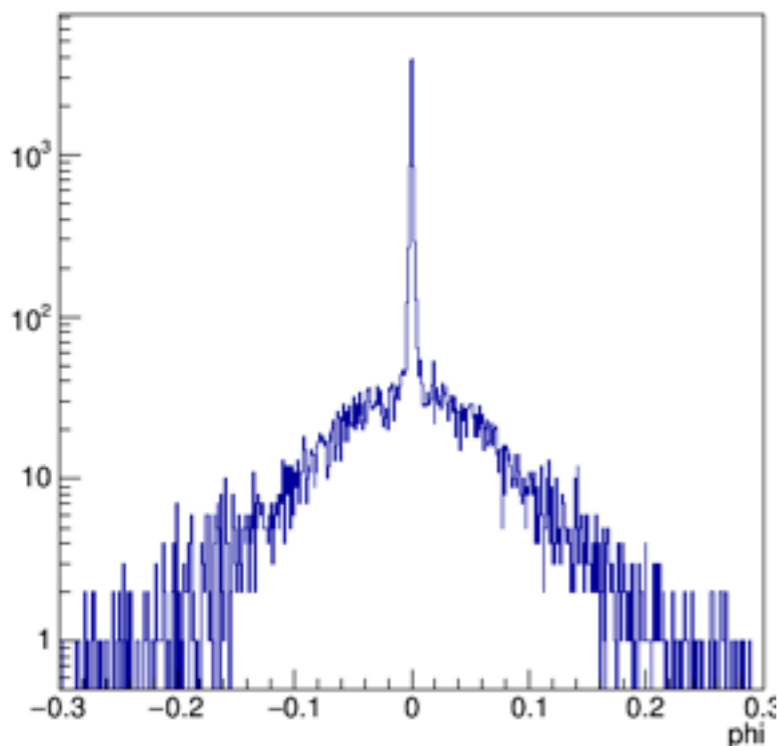
pthat5



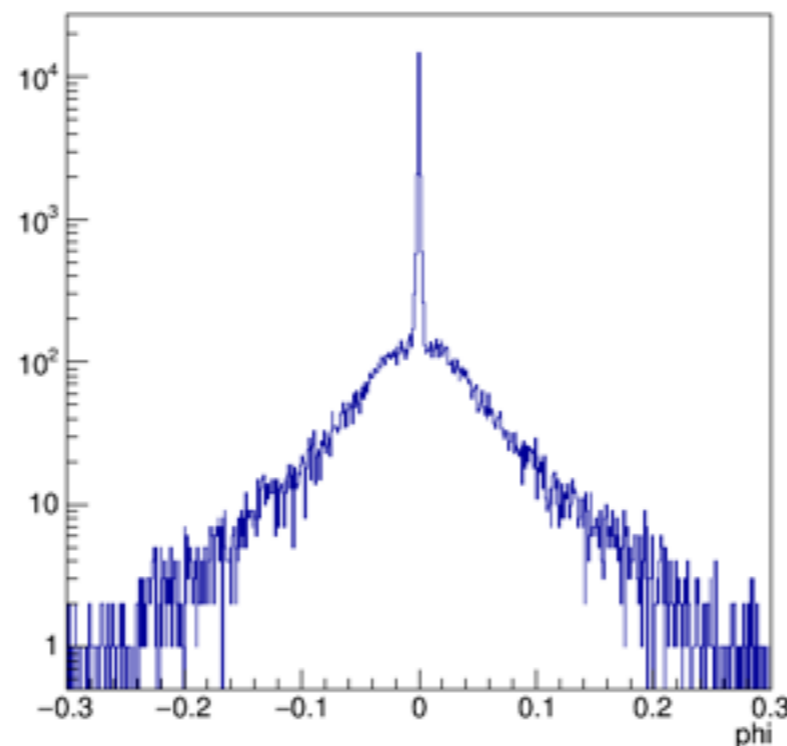
pthat15



pthat30



pthat50



- We set the pt cut for Gen matching from Gen pt - Reco pt distribution
- $|\text{Gen pt} - \text{Reco pt}| < 0.01$

Gen Matching cut

pthat5

pthat15

pthat30

pthat50

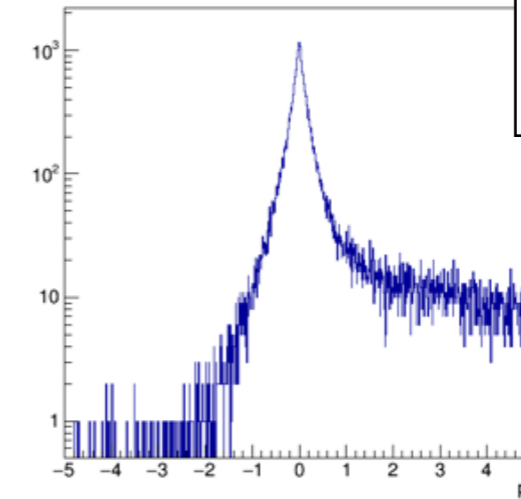
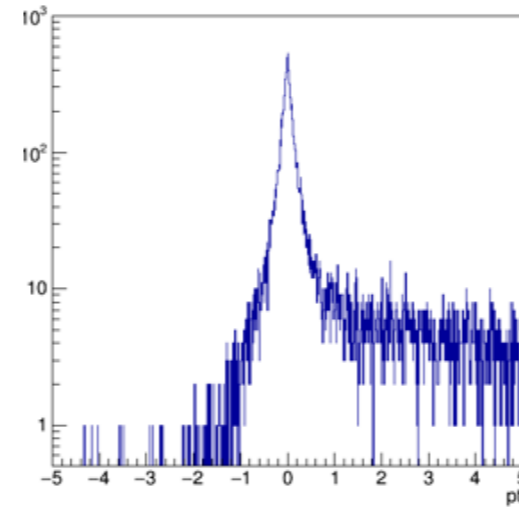
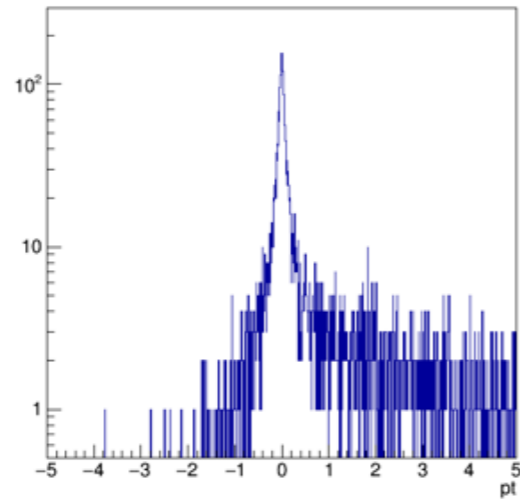
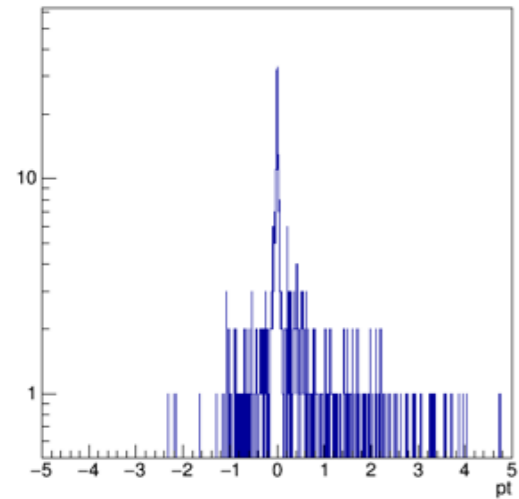
$$\begin{aligned} |p_T^{GEN} - p_T^{RECO}| < 1 \\ |y^{GEN} - y^{RECO}| < 0.01 \\ |\phi^{GEN} - \phi^{RECO}| < 0.01 \end{aligned}$$

Gen pt - Reco pt

Gen pt - Reco pt

Gen pt - Reco pt

Gen pt - Reco pt

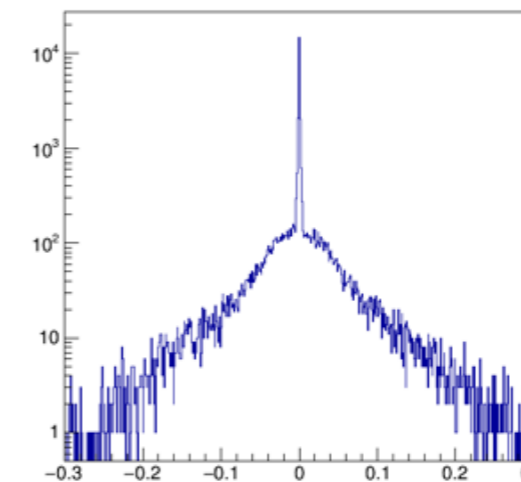
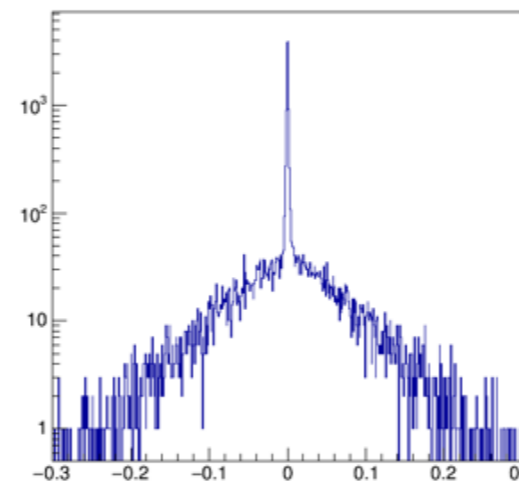
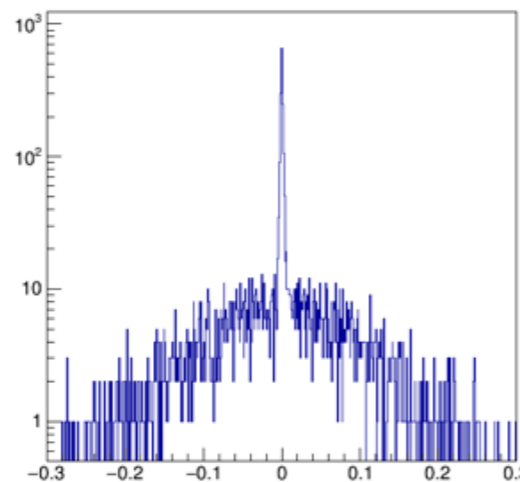
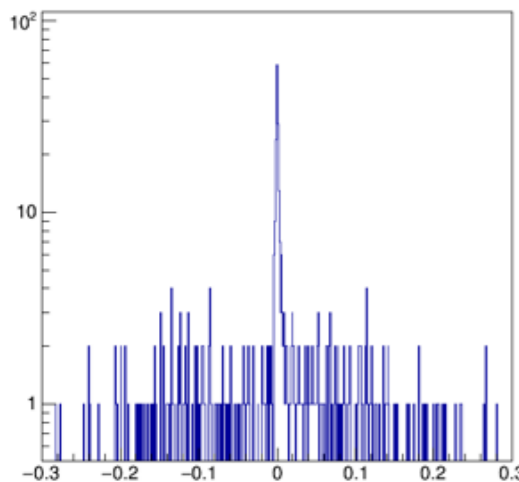


Gen y - Reco y

Gen y - Reco y

Gen y - Reco y

Gen y - Reco y

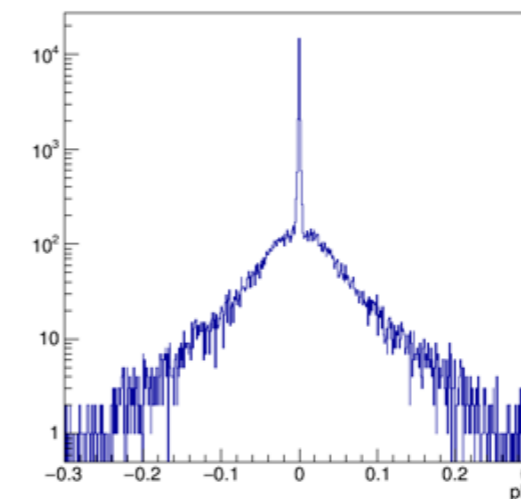
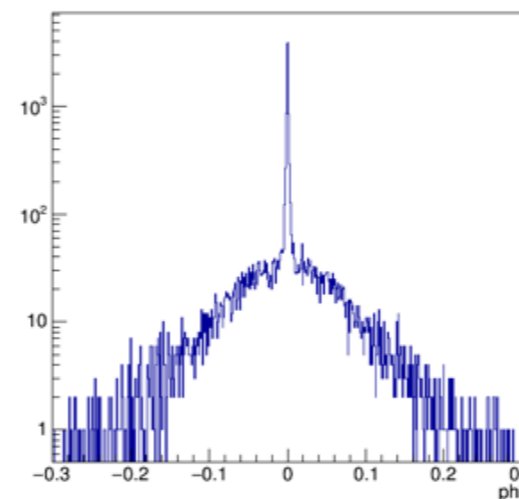
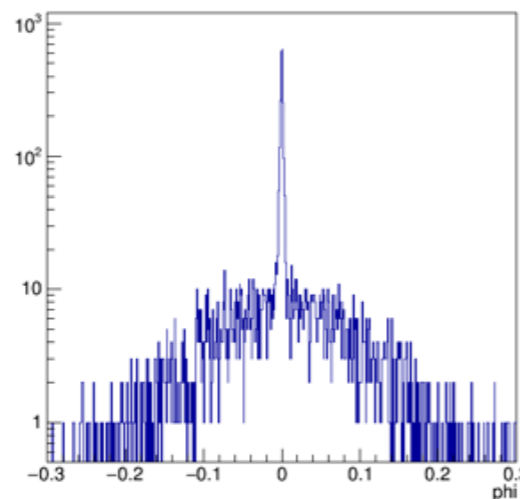
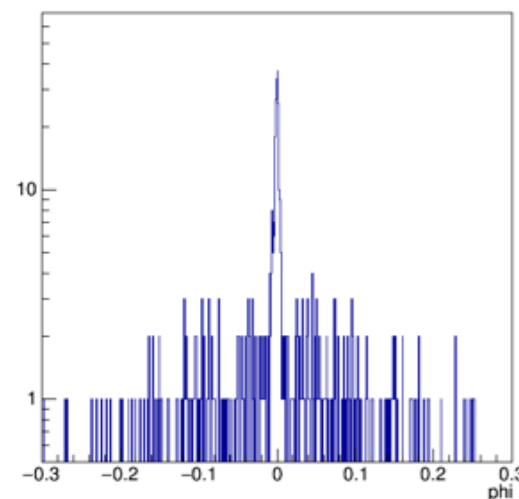


Gen phi - Reco phi

Gen phi - Reco phi

Gen phi - Reco phi

Gen phi - Reco phi



pp mass fitting

