PID framework – Trd: Hadron identification with TRD-dE/dx

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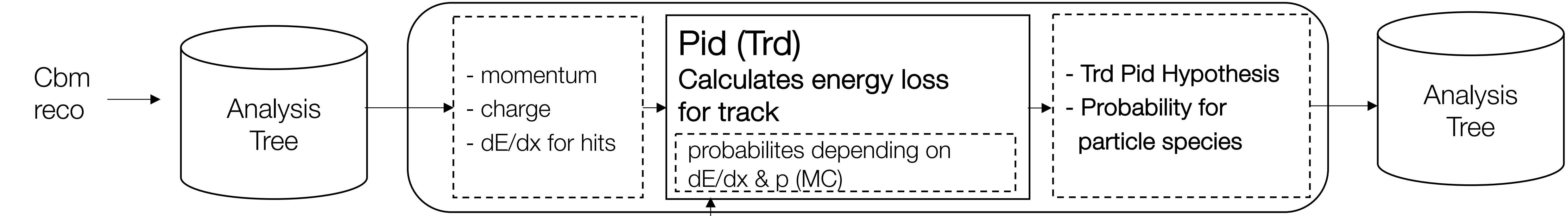
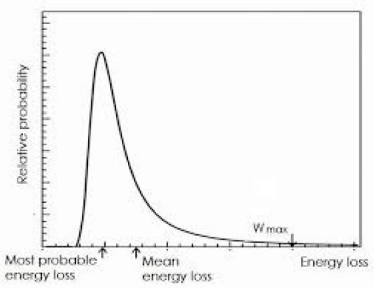
Pid (Trd)



User settings

Calculation of energy loss over N dector layers

1) Average: Energy loss averaged over all N detector layers
2) Truncation: Select hits to reduce fluctuations through Landau distribution



Calculation of probabilities

1) *Total probability*: Probability that a track with dE/dx-p-value is particle specie i (depends on multiplicities)

2) *likelihood*: Probability that a particle specie i with p-value has dE/dx-value

Number of minimum hits

Minium purity for pid hypothesis

```
Branch RecTracks
Floating fields:
Id           Name
...
48           prob_trd_bg
47           prob_trd_d
46           prob_trd_kaon
44           prob_trd_p
45           prob_trd_pion
Integer fields:
Id           Name
...
7            pid_trd
```

Identification options:
- highest probability
  => 1 pid for every track
- minimum probabiliy
  => 0, 1 or > 1 pids for every track possible

Methods for probability calculation

Probability

1) Total probability

calculation based on tracks

= ratio of particles i vs. all particles in dEdx-p-bin

$$prob_{track}(i, dEdx, p) = \frac{N^{i}_{tracks}\ in\ dEdx{-}p{-}bin}{N^{all}_{tracks}\ in\ dEdx{-}p{-}bin}$$

2) likelihood

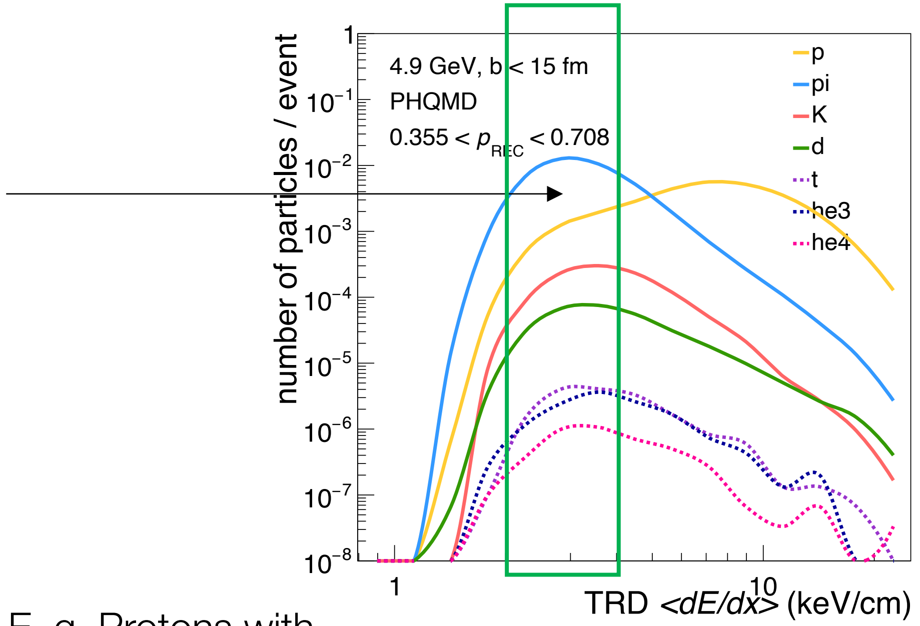
calculation based on hits

= ratio of particles i in dEdx-p-bin vs. particles i in p-slice (normalized over all particle species)

$$prob_{hit}(i, dEdx, p) = \frac{N^{i}_{hits}\ in\ dEdx{-}p{-}bin}{N^{i}_{hits}\ in\ p{-}slice}$$

$$prob_{track}(i, dEdx, p) = \prod_{i} p_{hit}(i, dEdx, p)$$

$$prob^{norm}_{track}(i, dEdx, p) = \frac{p_{track}(i, dEdx, p)}{\sum_i p_{track}(i, dEdx, p)}$$



E. g. Protons with
2.0 < <dE/dx> < 4.0 keV/cm
- high probability for (1)
- low probability for (2)

Pid (Trd): Steps

Creating MC input (only once):

Step 1:

Create MC-histograms

(Input from: atree MC)

Input: p_{REC}, dE/dx, q, mc-pdg

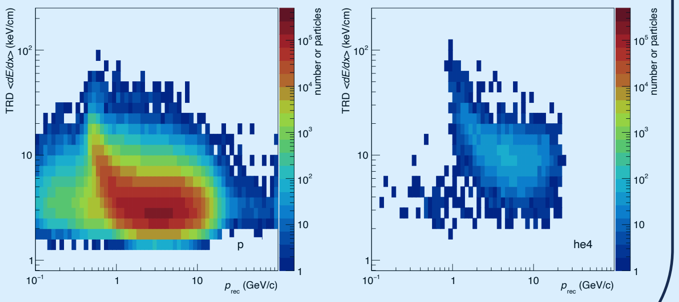
Output:

Number of entries in dE/dx vs. p_{REC}

- for all, p, π, K, d, he3, he4, e, μ
- for nhits trd = 1-4
- for truncation = 1-4 (including average)
- for tracks & hits

User options:

- p & dE/dx binning



Step 2:

Calculate MC-Probabilities

Input:

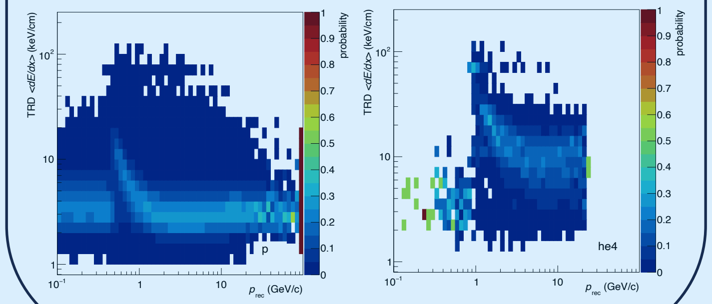
Number of entries in dE/dx vs. p_{REC}

for particle species i

Output:

Probabilities in dE/dx vs. p_{REC}

- for p, π, K, d, he3, he4, e, μ
- for nhits = 1-4
- for truncation = 1-4 (including average)
- for probability mode R & L



Executing:

Step 3:

Fill output tree

(Input from: atree REC; output to: atree PID)

Input: p_{REC}, dE/dx, q

Output:

- Probability that a track is particle specie i depending on p & dEdx
- Pid hypothesis (= highest probability)

User options:

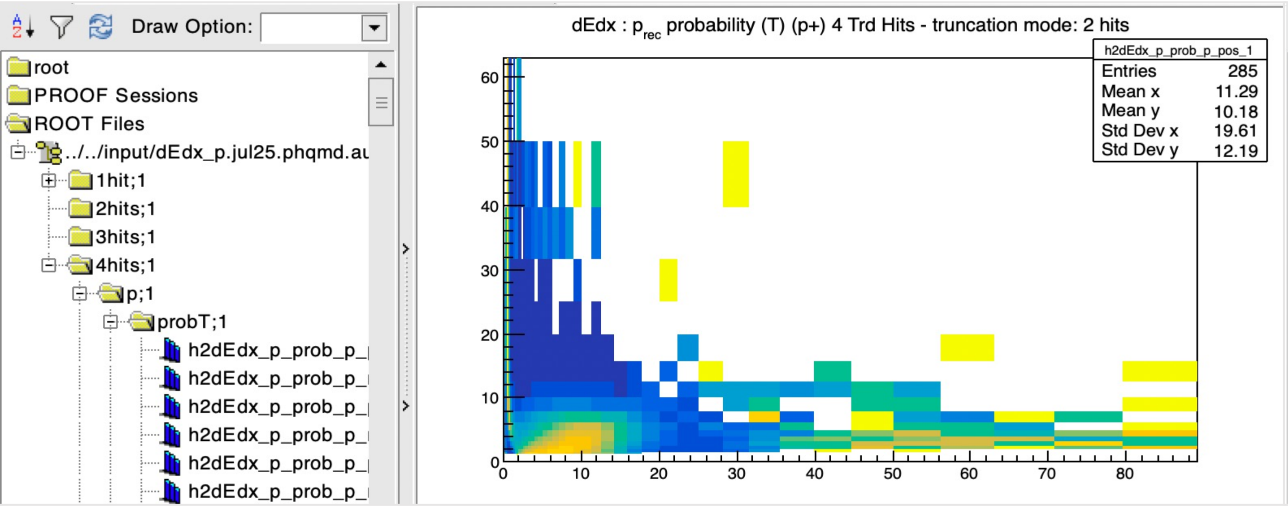
- min. Trd-hits
- truncation or average
- probability mode
- minimum purity for pid-hypothesis

Calculation of probabilities

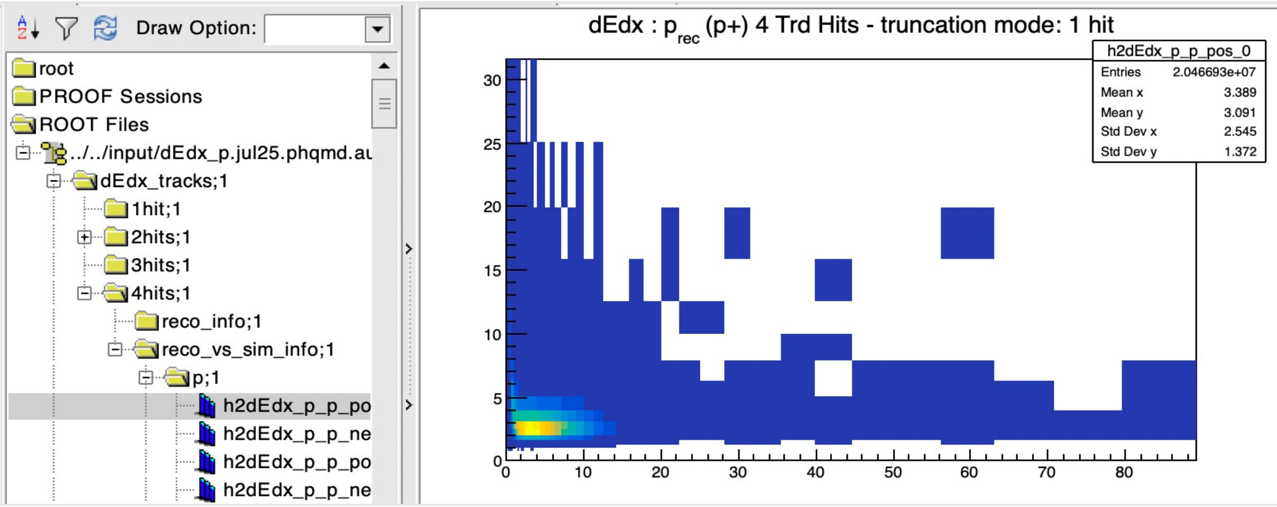
	Step 1: MC-histograms	Step 2: MC-Probabilities	Step 3: Fill output tree
total prob	For every track: 1) calculate dEdx with selected hits 2) fill histograms p vs. dEdx for all pdgs i	$prob_{track}(i, dEdx, p) = \frac{N^{i}_{tracks}\ in\ dEdx{-}p{-}bin}{N^{all}_{tracks}\ in\ dEdx{-}p{-}bin}$	1) calculate dEdx for track with selected hits 2) get probability for dEdx-p-bin for every pdg i $p_{track}(i, dEdx, p)$
likeli-hood	For every hit: 1) fill histograms p vs. dEdx for all pdgs i for selected hits	$prob_{hit}(i, dEdx, p) = \frac{N^{i}_{hits}\ in\ dEdx{-}p{-}bin}{N^{i}_{hits}\ in\ p{-}slice}$	1) get probability for dEdx-p-bin for selected hits for every pdg i $prob_{hit}(i, dEdx, p)$ 2) multiply probabilities over all hits for all pdgs i $prob_{track}(i, dEdx, p) = \prod_{i} prob_{hit}(i, dEdx, p)$ 3) normalize probabilities over all particle species $prob^{norm}_{track}(i, dEdx, p) = \frac{prob_{track}(i, dEdx, p)}{\sum_{i} prob_{track}(i, dEdx, p)}$

MC Input - example

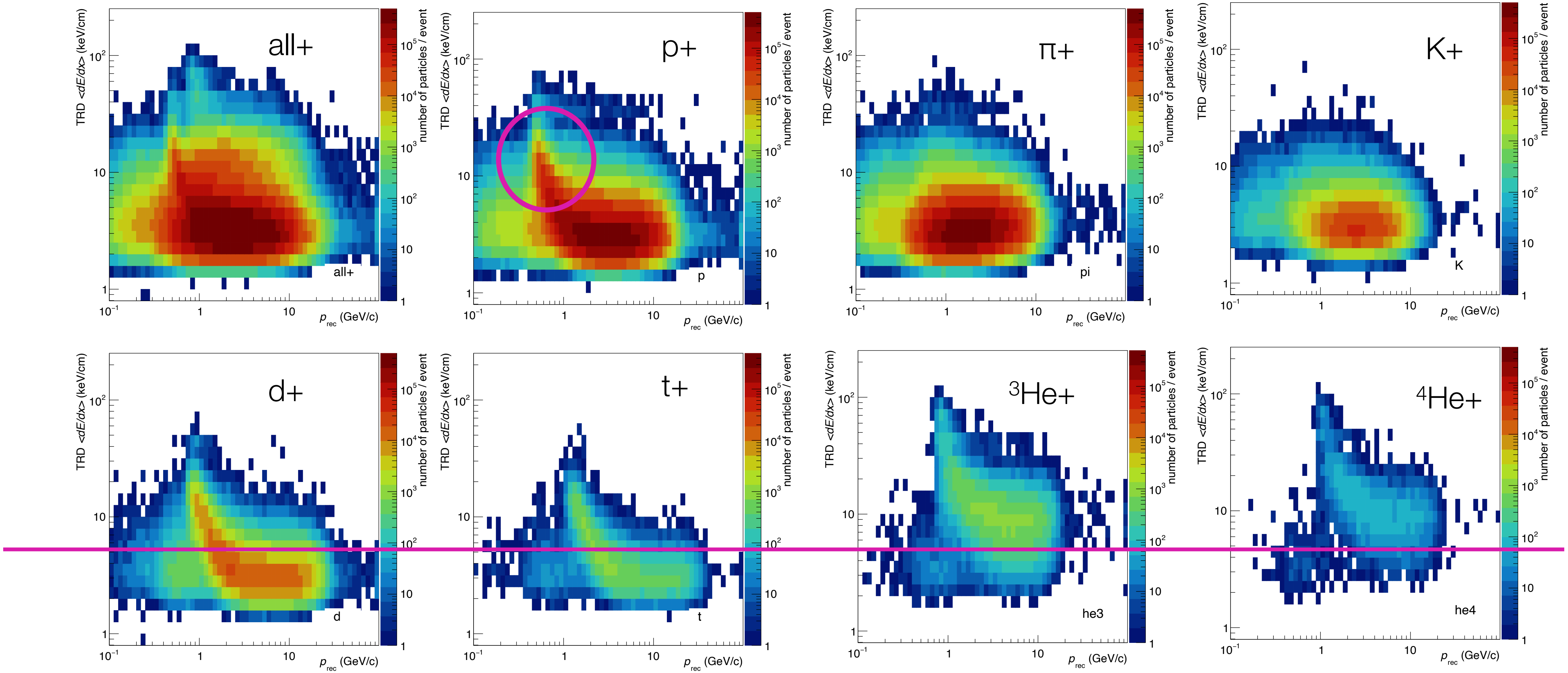
Step 1: MC-histograms



Step 2: MC-Probabilities



Number of tracks in dE/dx vs. p



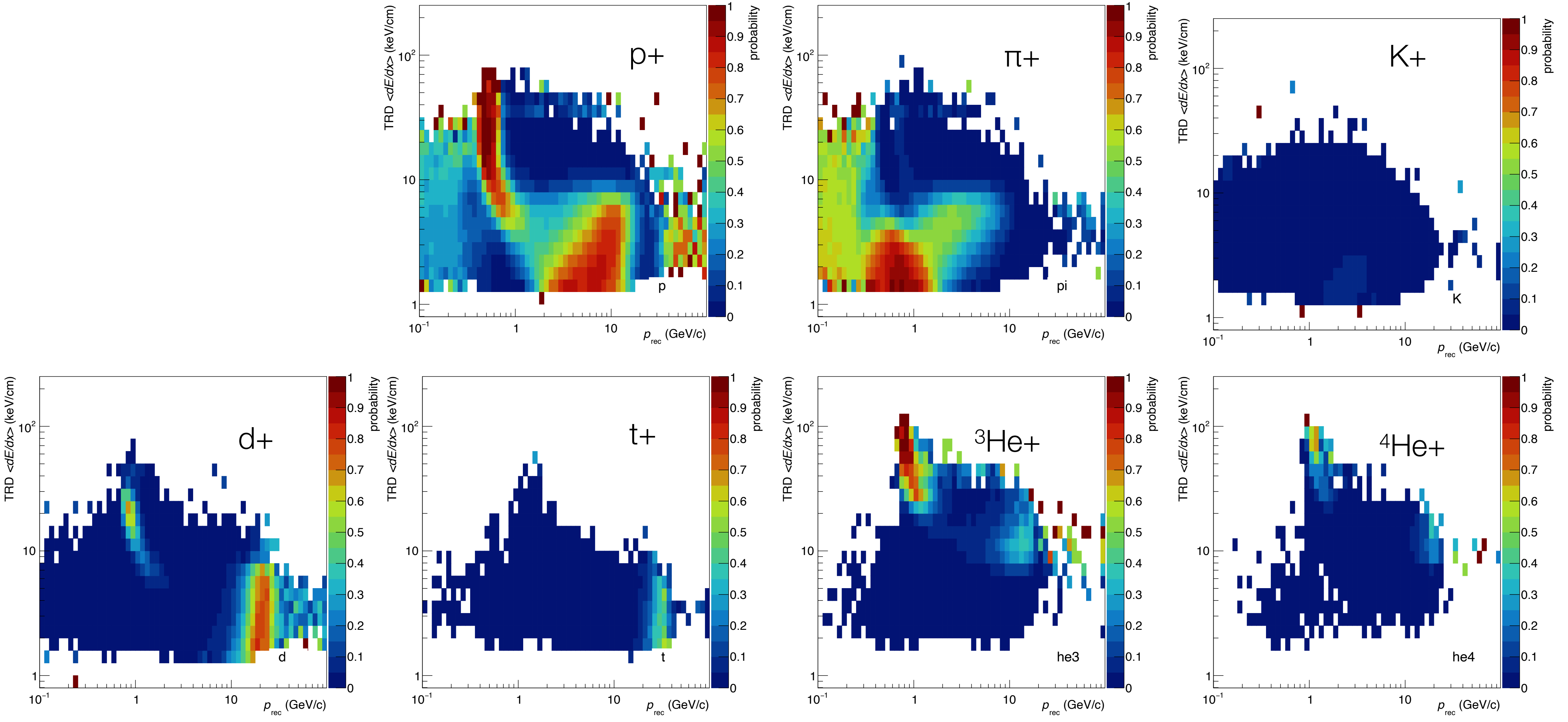
=> Separation of protons / pions for low momentum

=> Separation of deuterons / ^{4}He

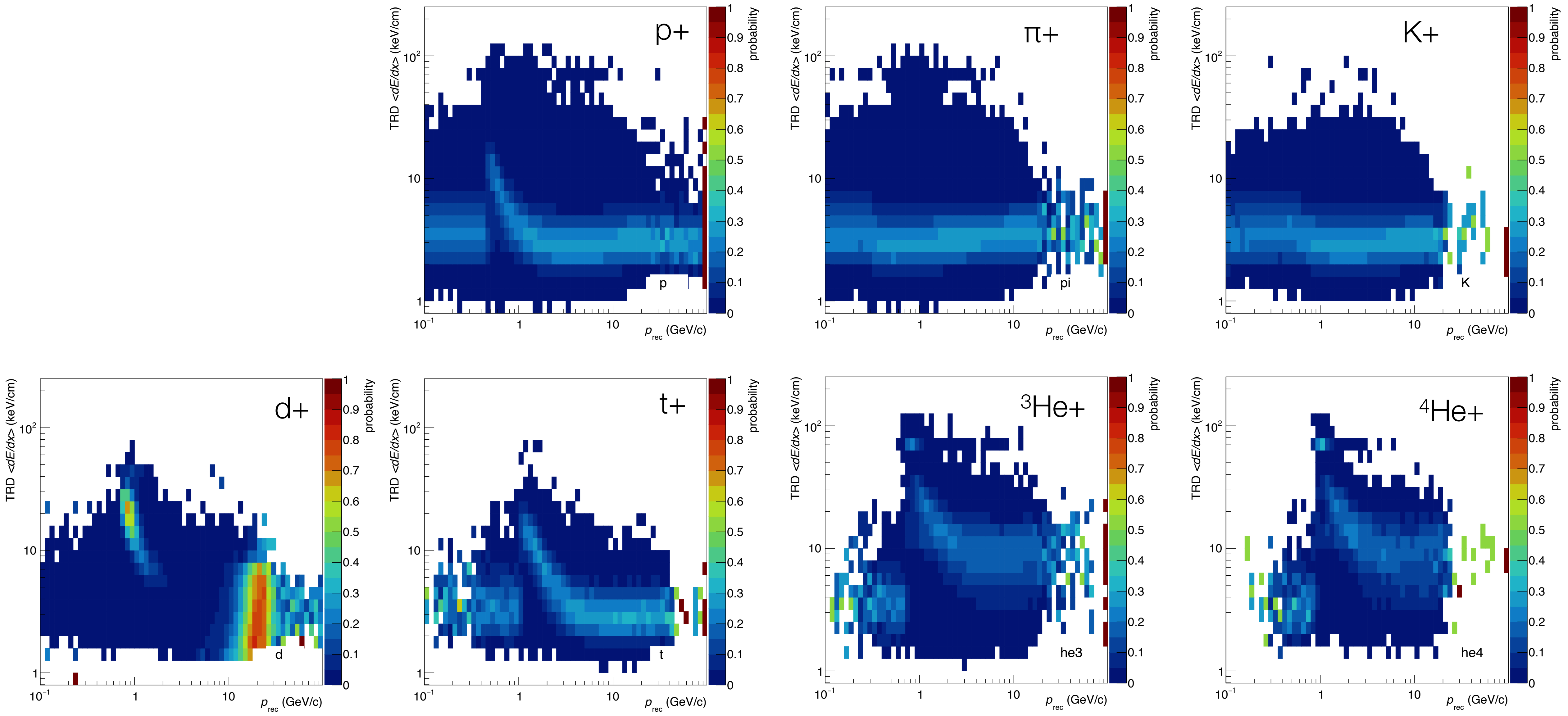
truncation mode: 1 hit

nhits = 4

MC probabilities total probability

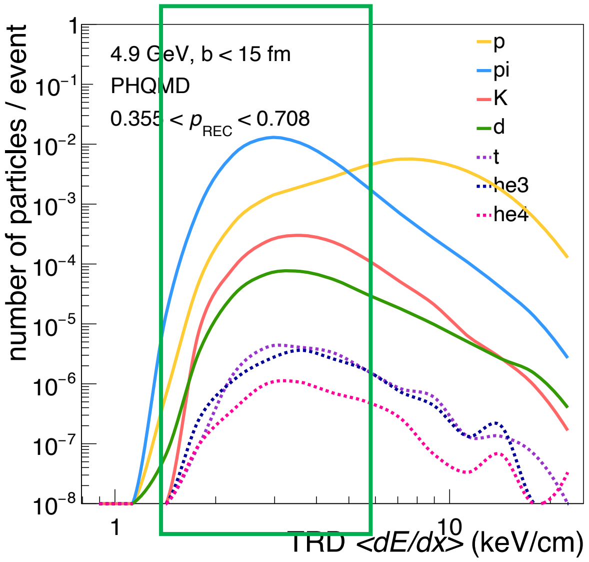


MC probabilities likelihood



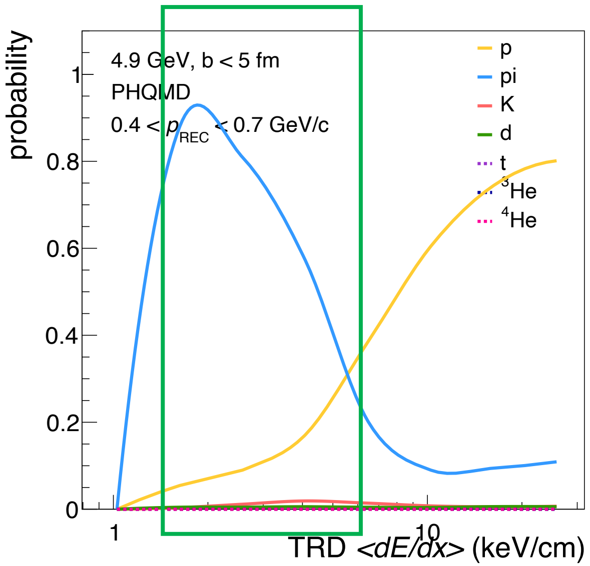
Pid (Trd) – comparison of different methods

Number of particles



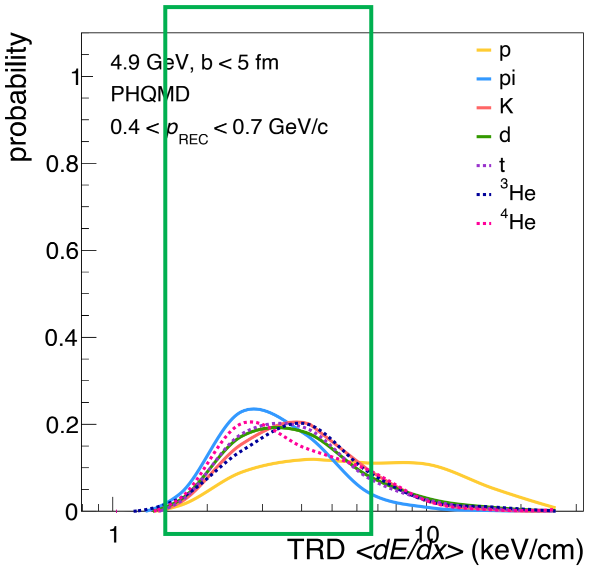
- for dEdx < 6 keV: more protons than K, d, t, he3, he4
- proton distribution is more flat

probabilities: total prob



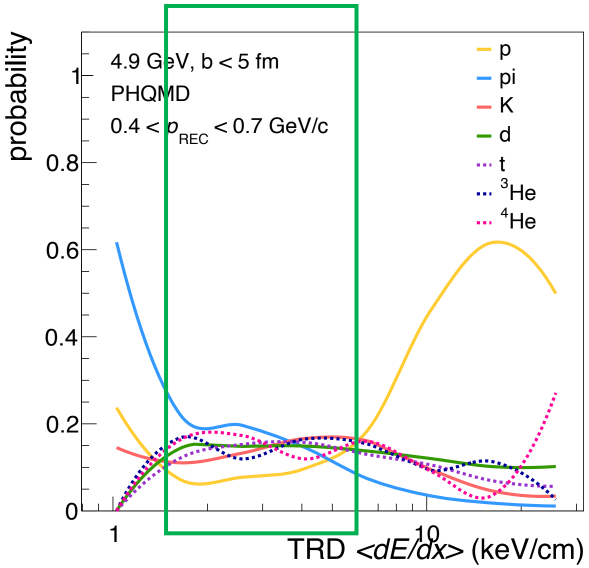
- for dEdx < 6 keV: high probability for protons

probabilities: likelihood



- for dEdx < 6 keV: lowest probability for protons

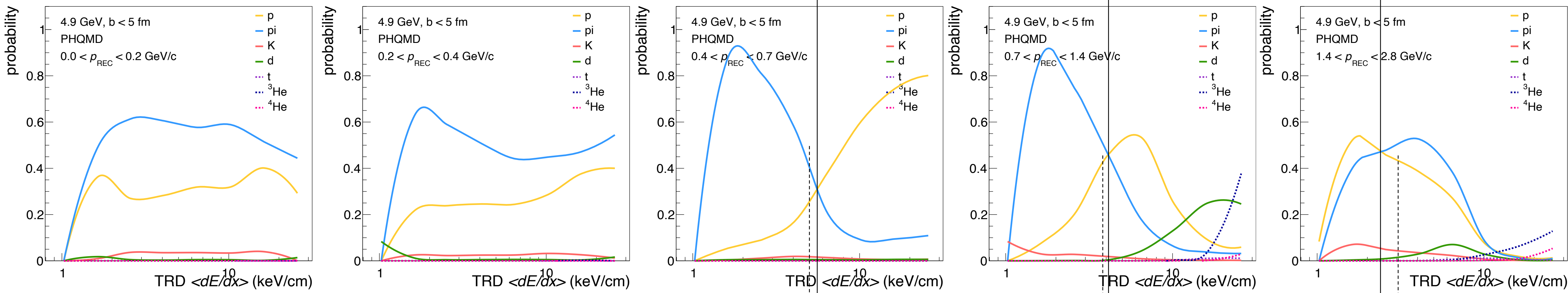
Probabilities: likelihood normalized



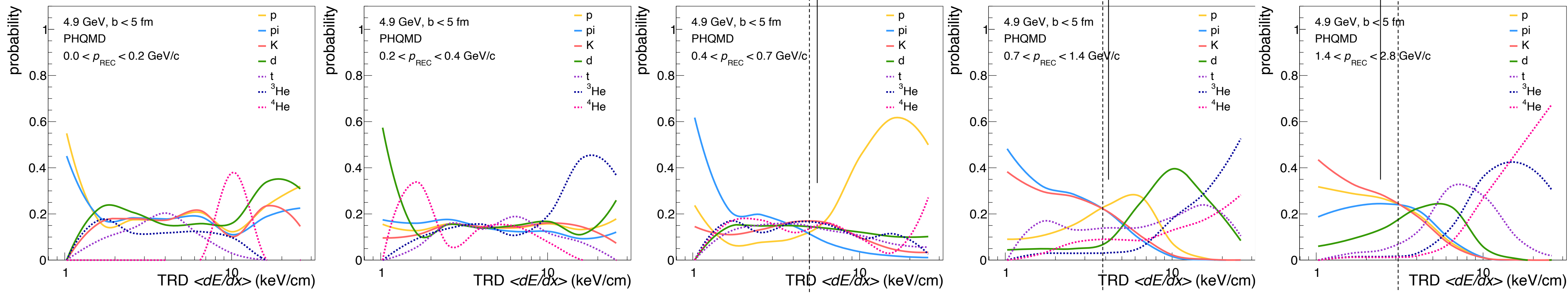
- for dEdx < 6 keV: lowest probability for protons

MC probabilities for p < 2.8 GeV/c – p/π separation

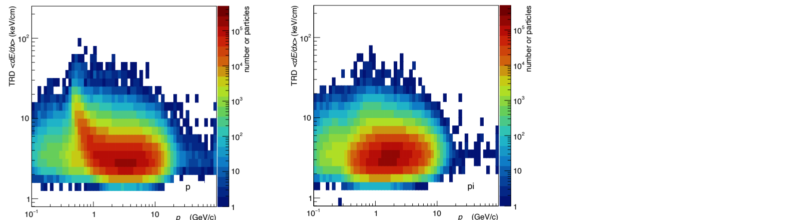
Total prob



Likelihood

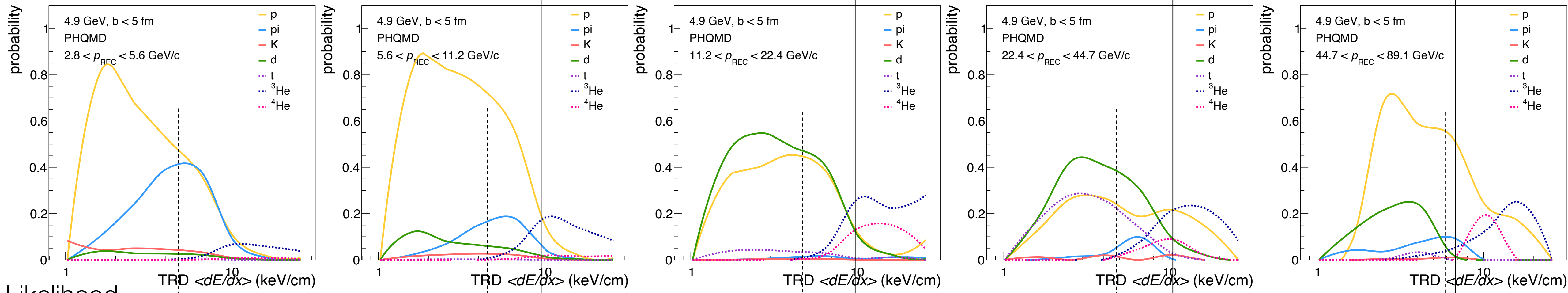


=> Sparation / identification of p/pi for 0.4 GeV/c < p < 2.8 GeV/c.

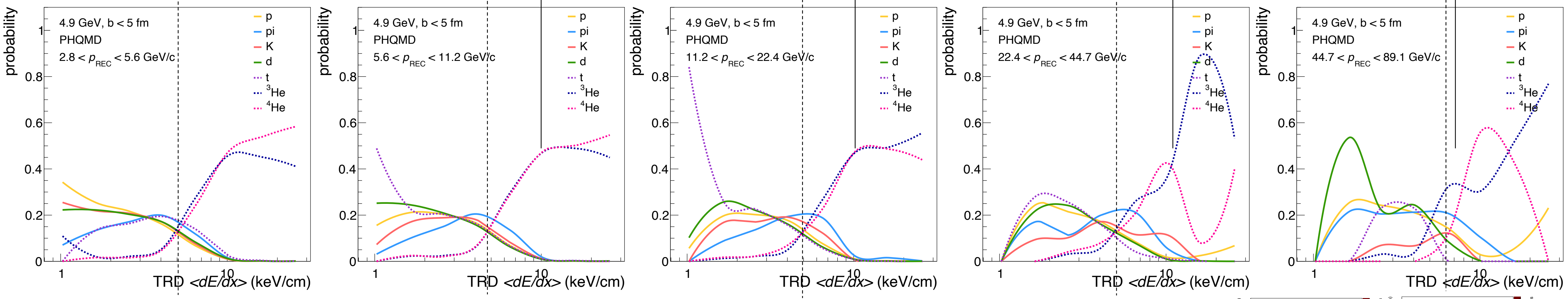


MC probabilities for $2.8 < p < 89.1$ GeV/c - ^{4}He/d separation

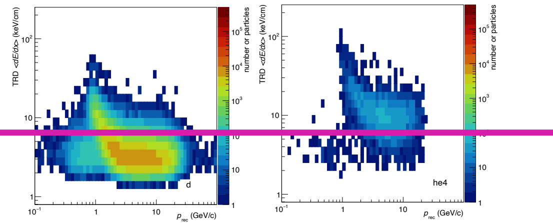
Total prob



Likelihood



=> Likelihood in favour of ^{4}He vs. d compared to ratio



Using probabilities for particle identification

Available information for every track after running Pid:

probability to be a p, π, K, d, t, ^{3}He, ^{4}He, e, μ, bg

This information can be used later on in the following ways (e.g. in PFSimple):

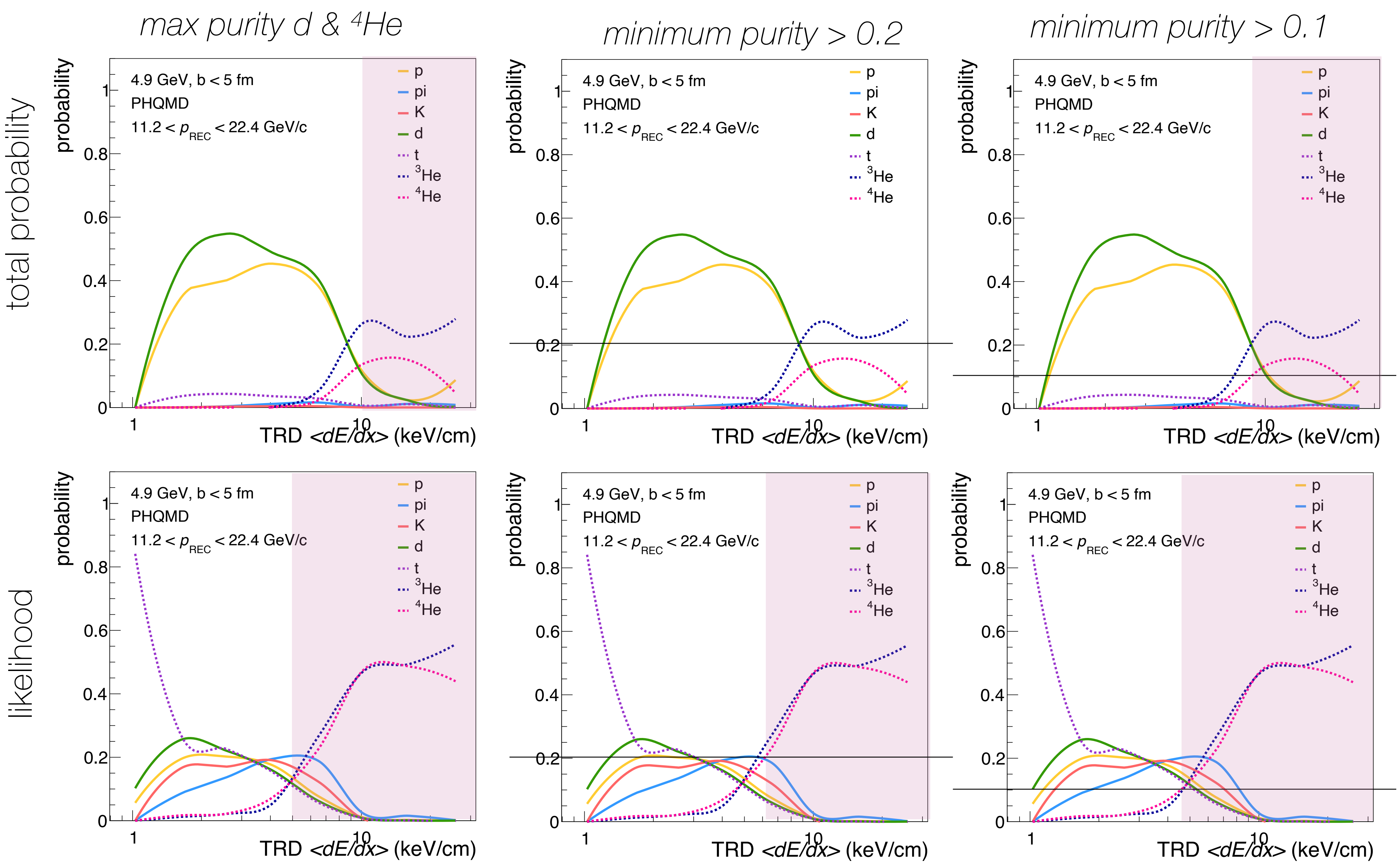
Pid selection for tracks:

- Maximum purity: choose species with maximum purity
- Minimum purities: select minimum purity for a track to be considered as specie i (one track can be considered several species or none)
- Maximum probability d/^{4}He

Application of Trd-cut:

- on top of Tof-cut to include tracks or to exclude tracks
- on tracks without Tof-id
- to separate d/^{4}He

^{4}He identification – Comparing maximum and minimum purities



In this example:

max purity d/^{4}He identifies more ^{4}He than *min purity > 0.2*

min purity > 0.1 identifies slighlly more ^{4}He than *max purity d/^{4}He*

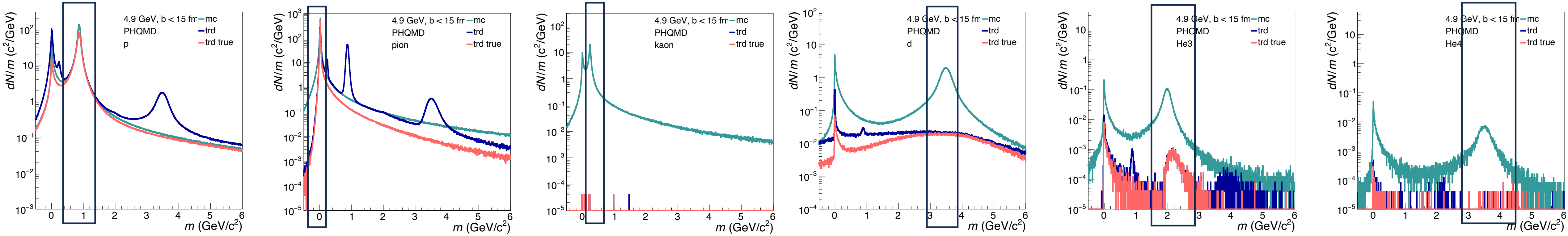
for both probability methods

MASS spectra

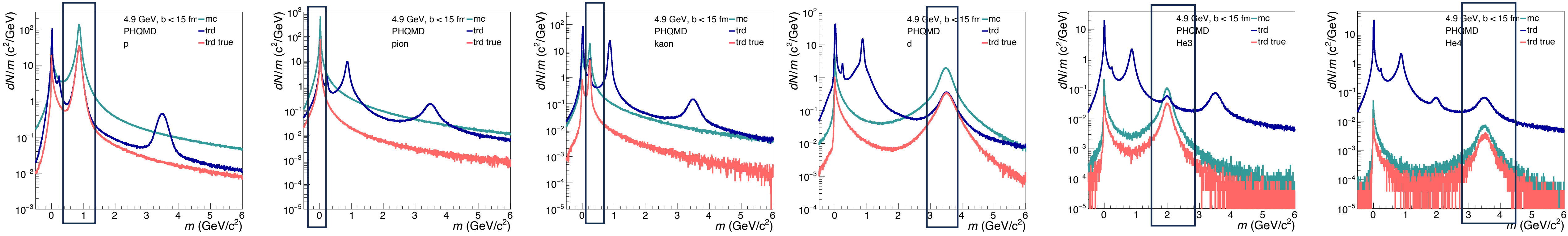
Mass spectra of reconstructed tracks – probability methods

Pid selection: Maximum purity

Total prob p π K d ^{3}He ^{4}He



Likelihood



Total probability works better for particles with high multiplicities.

Likelihood works better for particles with low multiplicities.

truncation mode: 1 hit with lowest dE/dx

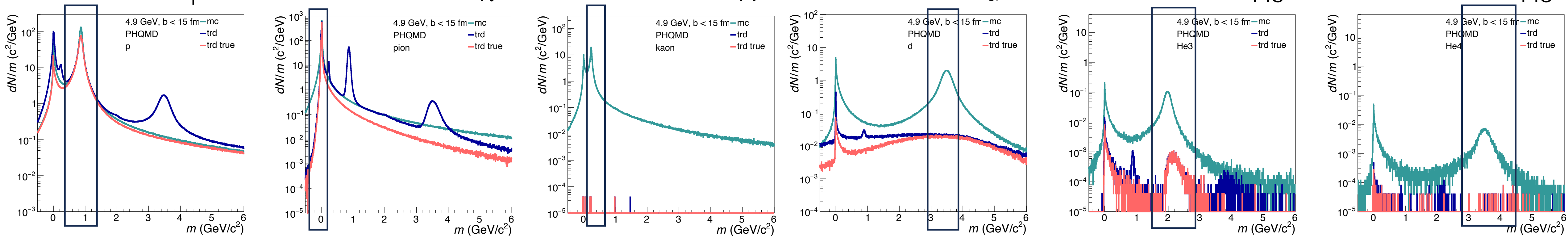
min trd hits: 1

Mass spectra of reconstructed tracks – pid selection methods

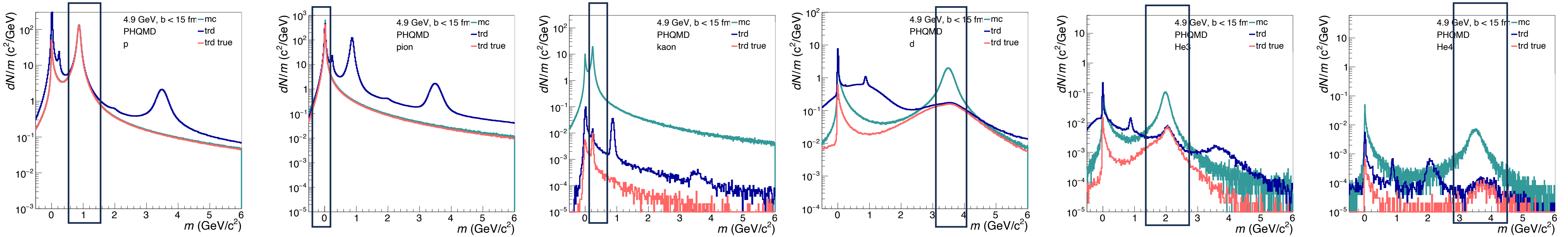
Probability method: total probability

Pid selection: max purity

p π K d ^{3}He ^{4}He



Pid selection: purity > 0.1.



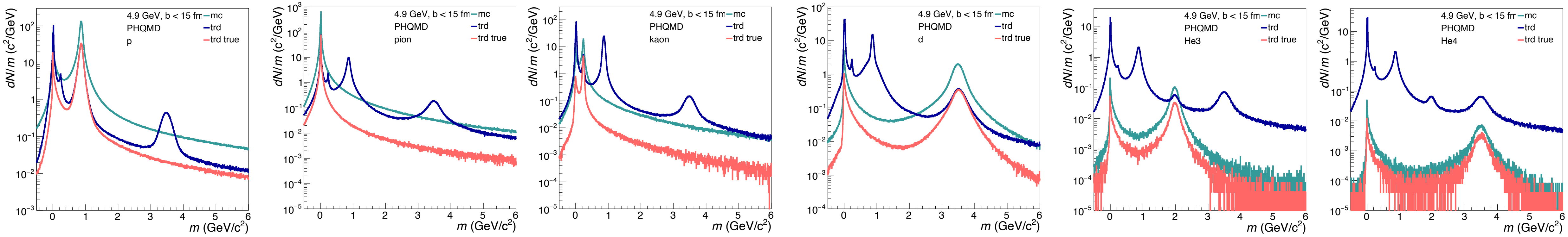
=> *purity > 0.1* increases number of reconstructed particles and works better for particles with low multiplicities compared to *max purity*.

Mass spectra of reconstructed tracks – pid selection methods

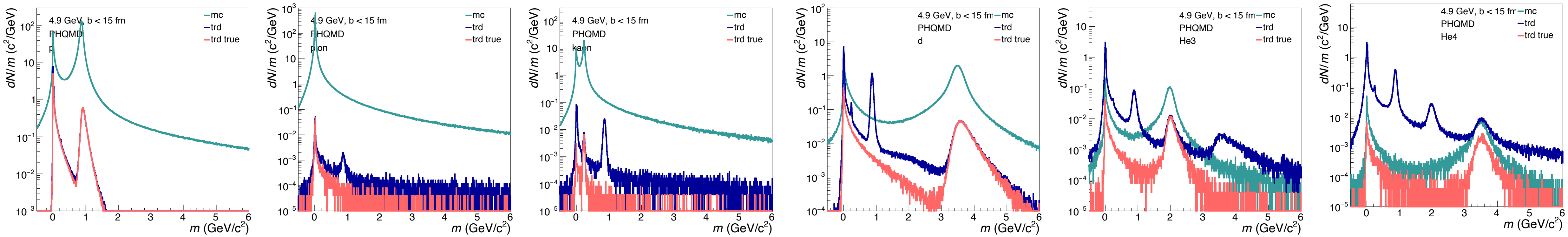
Probability method: likelhood

Pid selection: max purtiy

p π K d ^{3}He ^{4}He



Pid selection: purity > 0.4



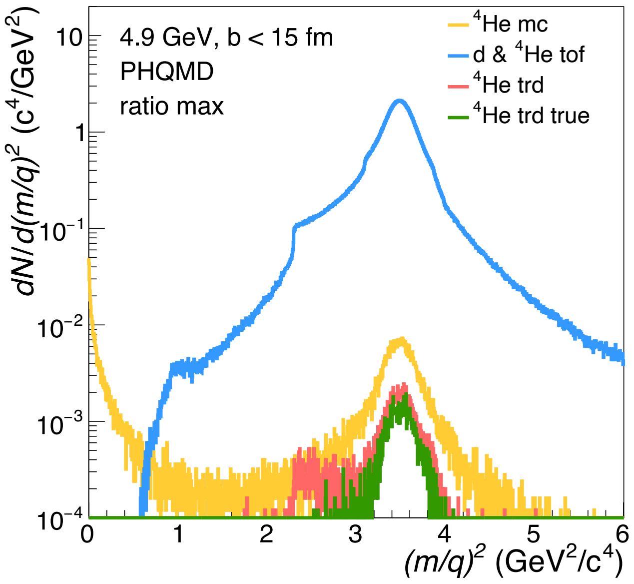
purity > 0.4 decreases the number of reconstructed particles and improves the S/B ratio compared *max purity*.

d/^{4}He

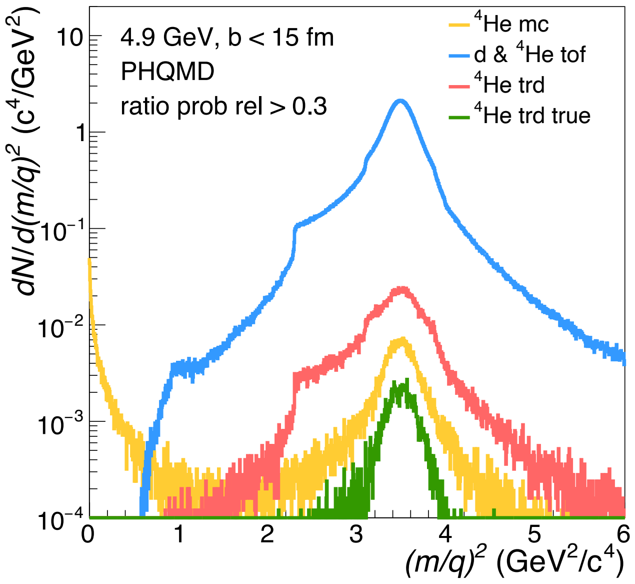
^{4}He separation* – different methods

total probability

max d/^{4}He

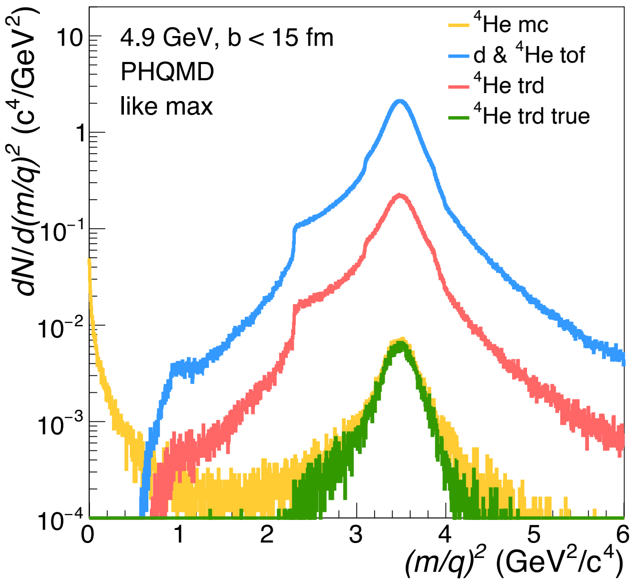


purity rel. > 0.3**

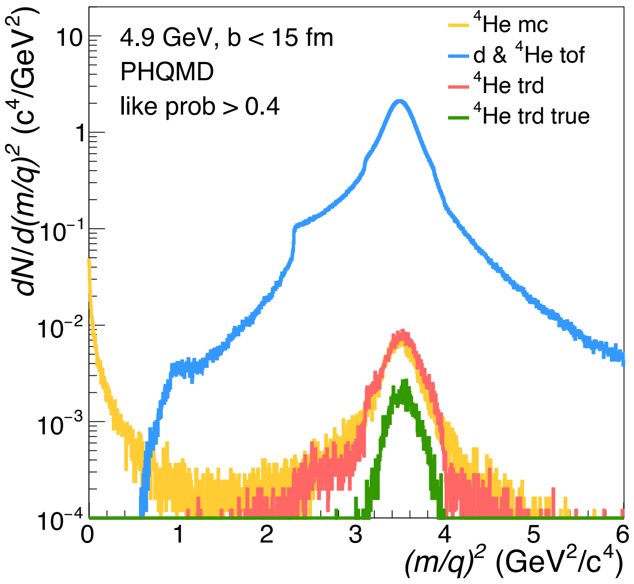


likelihood

max d/^{4}He



purity > 0.4

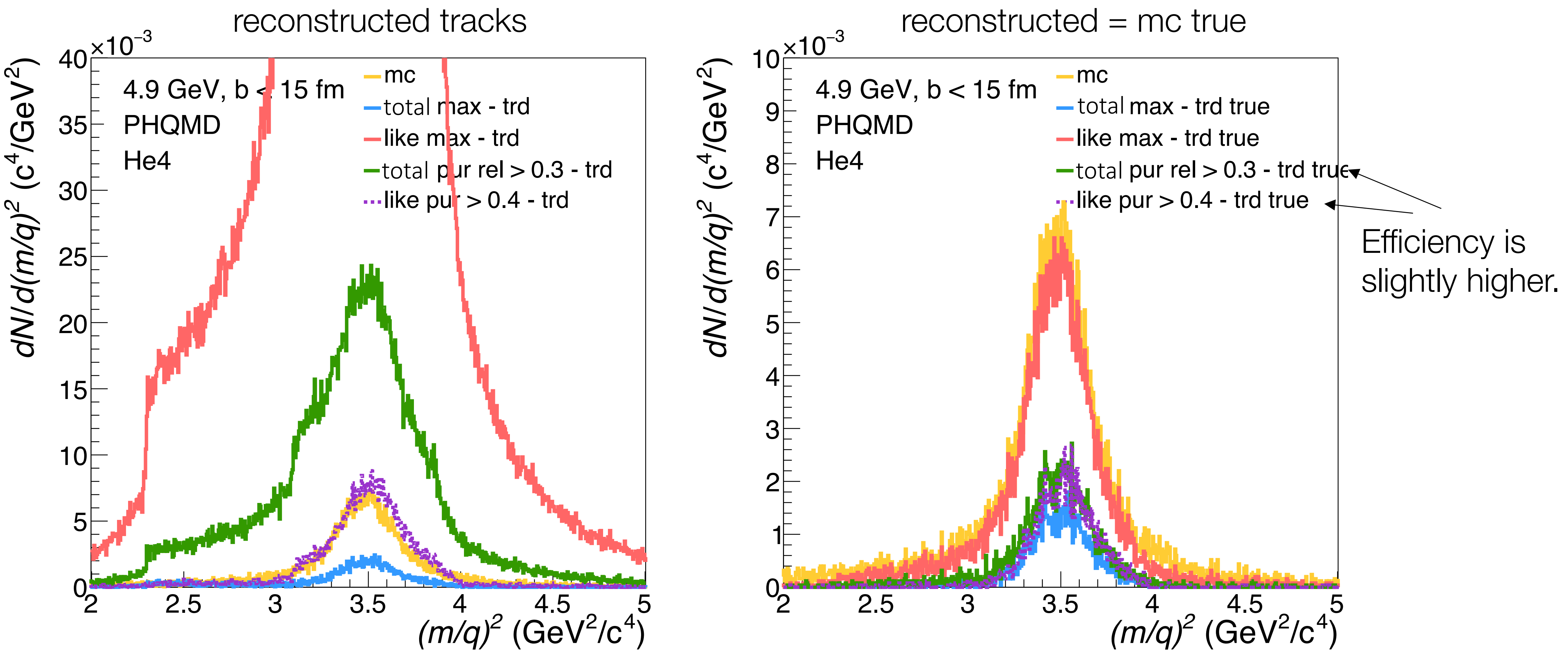


best S/B ratio

best efficiency, but very low S/B

*Tof-cut is included
** relative purity of d & He4

^{4}He separation* – comparison of efficiencies



*Tof-cut is included

=> Likelihood with *max purity* gives highst efficiencies, but S/B ratio is very low.

=> Likelihood with purity > 0.4 gives the best combination of efficiency and S/B ratio.