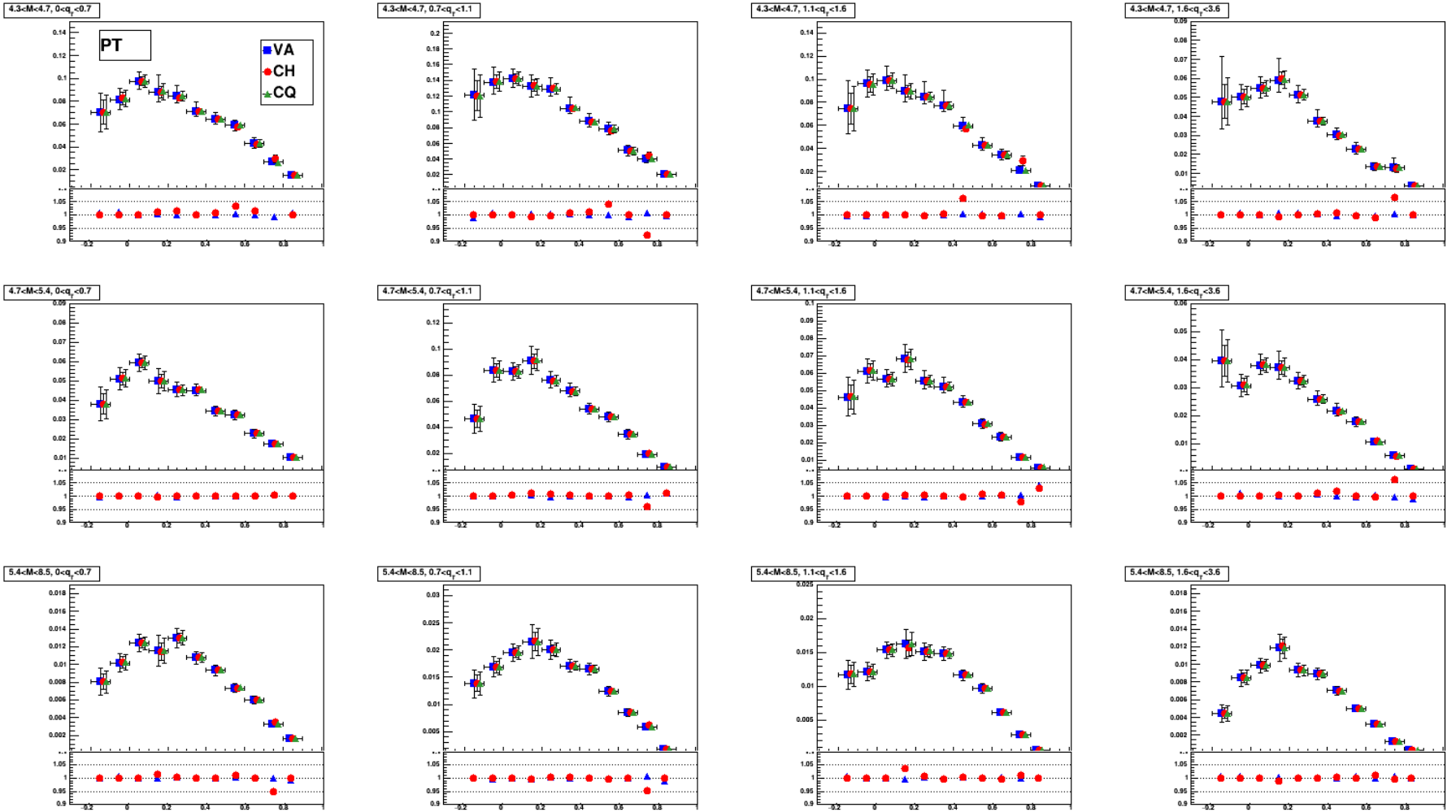
Comparisons between our cross-section results, as in the release from 2023.

E-mail exchange on 04-07-2024, based on the histograms provided by Chia-Yu
On 03-07-2024 (2D) and on 04-06-2024 (3D):
calSys_3D_cut295,6_[X]_m4.3.root
calSys_2D_COMPASS_xfpt_cut295_[X]_m4.3.root X={Al, NH3_1st2nd, W_1st2nd}

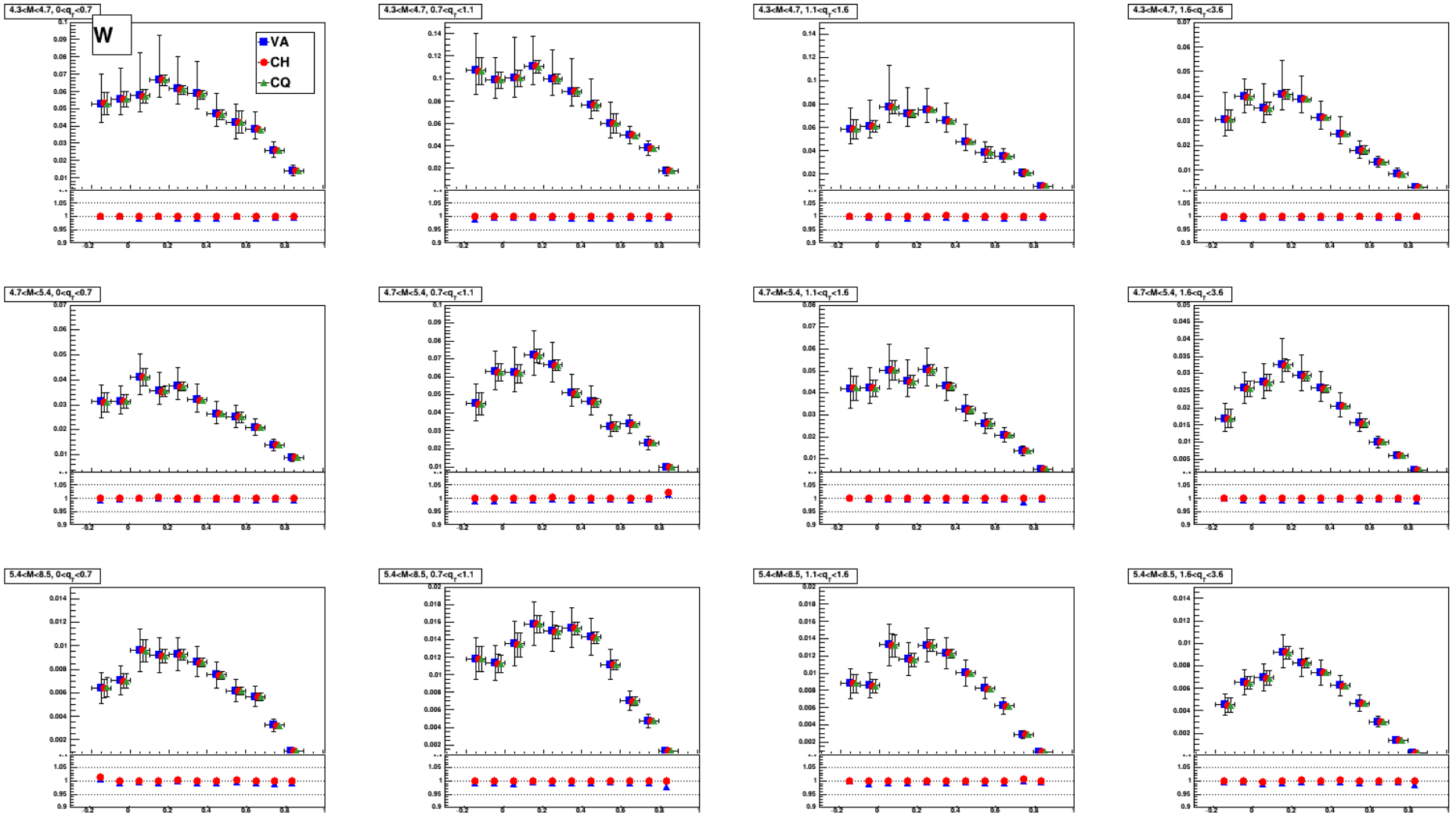
X-sec 3D (M, qT, xF): (NH3+He)

Very good agreement



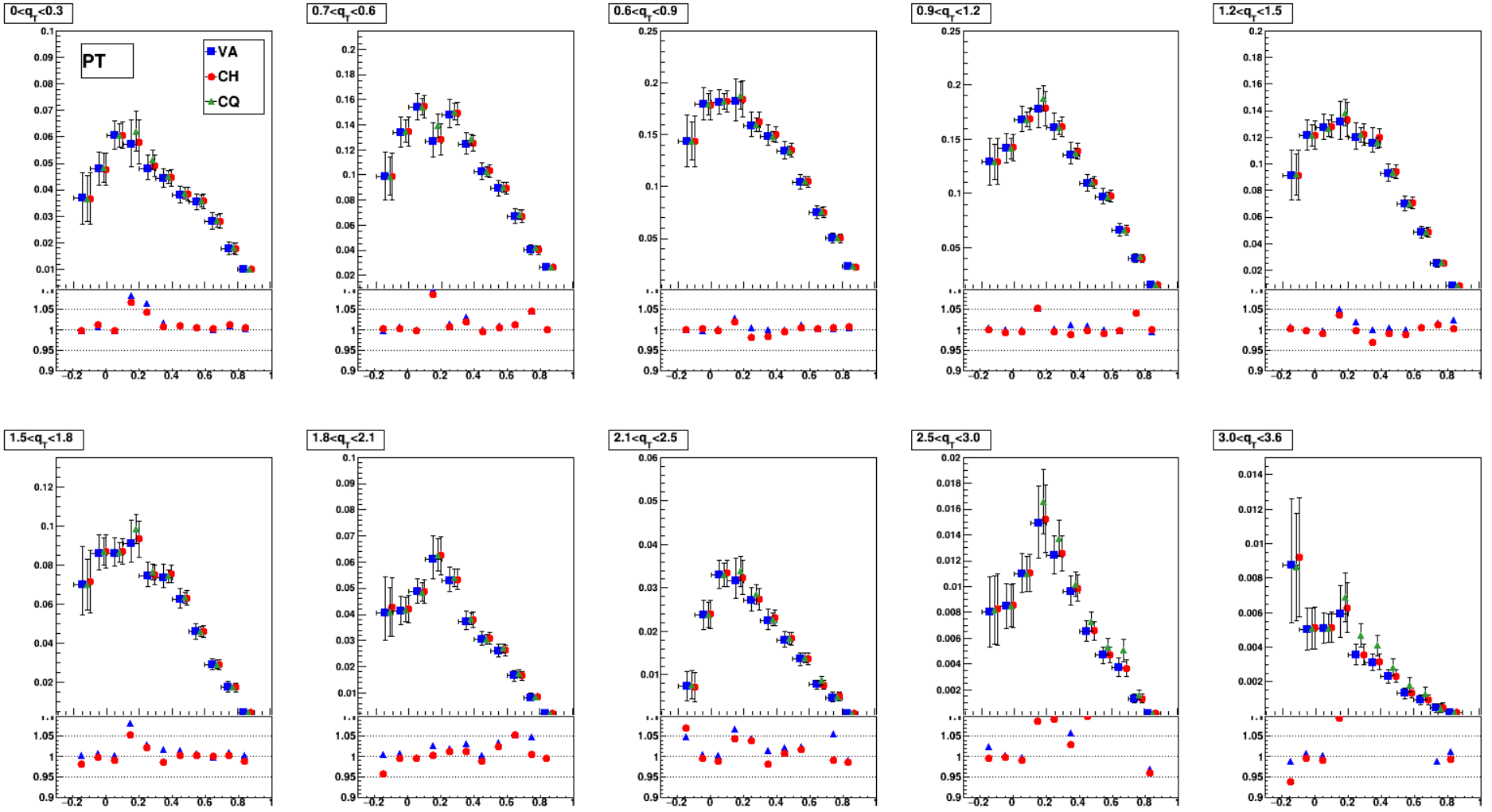
X-sec 3D (M, qT, xF): W

Very good agreement



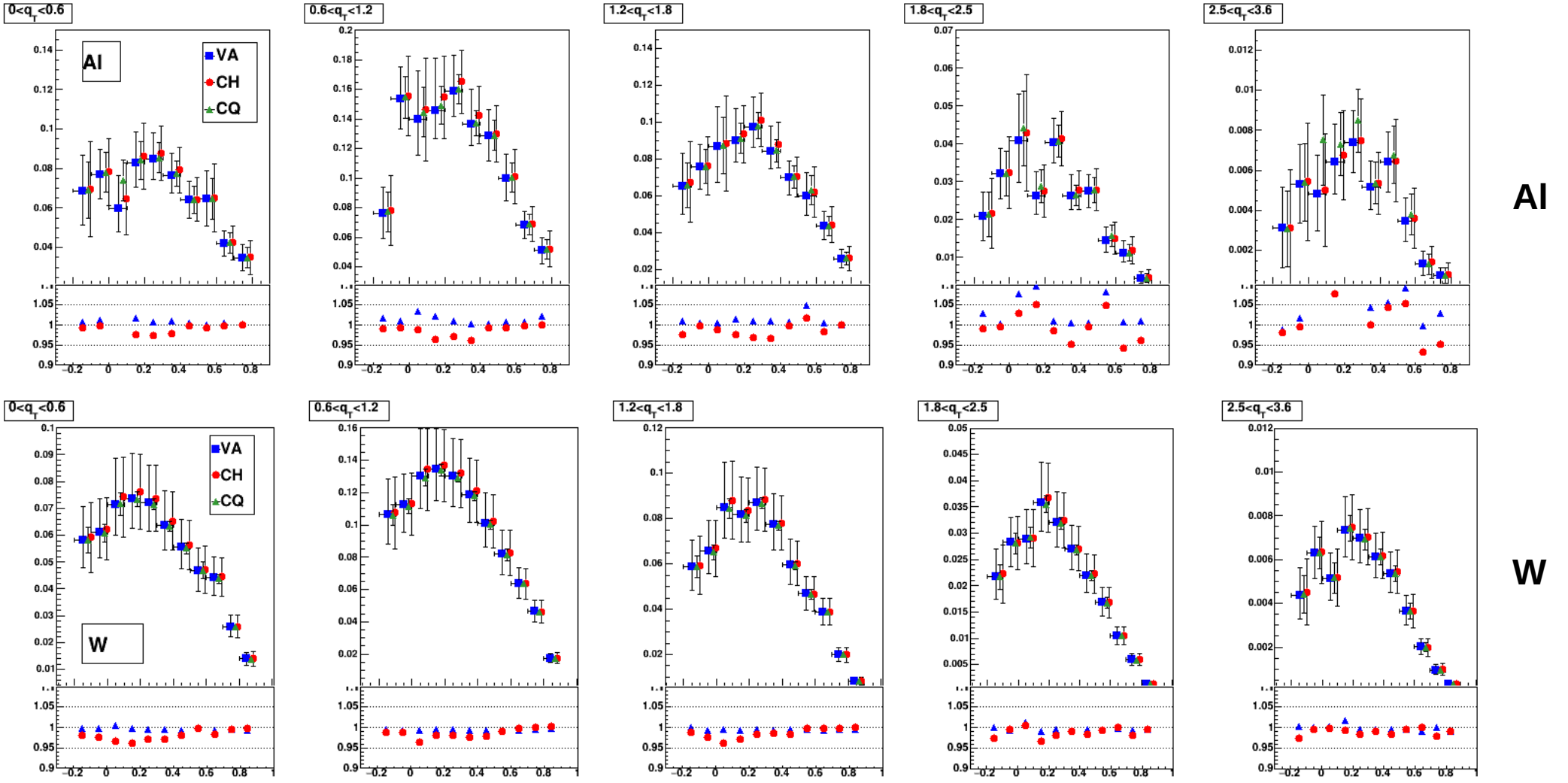
X-sec 2D (qT, xF): (NH3+He)

CQ in disagreement



X-sec 2D (qT, xF)

all in disagreement at low qT



About purity: difference between cocktail method and simple method

There is a tendency for the purity to be higher with simple method than with cocktail (but it is not true for all the bins, sometimes it goes smaller). The relative differences can go up to 35% at the lowest masses in W, up to 15% at lowest masses in PT.

I also tried to extract the purity by bootstrapping between the 2 methods, according to a uniform distribution (“new purities”). The ratio between these new purities and the released ones (from Vincent) tends to differ by less than 10% in the vast majority of the 2016 mass bins (4.3-8.5=> 42 bins*4*12=2016)

Vincent did this exercise in 01-2024, but I do not have his values to compare.

How close we are to publish: 3D

We agree in the cross-sections extracted.

We agree that, contrary to what we did in the 2023 release, the purity should be obtained by a sort of “average” between the two methods, simple and cocktail. Use the bootstrapping method varying uniformly between the two extremes to evaluate the new values of purity to use, and the “systematic on x-section due to purity extraction”.

The fact that, in both the simple method and in the cocktail, we fit the purity with a smoothing function (sigmoid) introduces a correlation between mass bins (the bins of 100 MeV), that results in error propagation when we integrate in mass (to get the 3 mass bins [4.3, 4.7], [4.7, 5.4] and [5.4, 8.5] GeV).

Thus, in the 3D results, the systematic error of the x-section points is a quadratic sum of statistic error + systematic on luminosity (normalization. Fully correlated point-to-point) + systematic on acceptance (44% uncorrelated, 89% correlated point-to-point) + systematic on trigger scaling (70% correlated = sqrt(2)/2 when combining LL and LO results) + systematic on purity (error propagation of the sigmoid fit params when integrating over mass, for each point).

To do for 3D:

Compare the results of purity obtained by bootstrapping by Vincent and Catarina.

Compare the resulting 3D cross-sections.

Propagate the systematic errorsaffecting the cross section

To do for 2D:

Compare the results and understand the discrepancies in the cross-section values
I compared my x-section 2D (M, xF) with Vincent, and got good agreement (for PT and W). These seem to be the same values Chia-Yu was using for comparisons In 2D (M, xF) also.