

NanoAODs production packages comparison
for $B^0 \rightarrow K^{*0} \mu^+ \mu^-$ decay channel

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BPHNano

- CMS framework designed for the production of custom NanoAODs for B-physics analyses
- Developed to avoid each analysis reinventing the same reconstruction code
- Supports multiple decay channels simultaneously, all within the same output file
- New channels and variables can be added with minimal code changes
- Produces NanoAODs that contain standard NanoAOD content + BPH additional branches

Validation

- Our objective is to check whether BPHNano-produced NTuples (**BPH**) are equivalent to the standard private NTuple production in CMSSW (**Nano**)
- Since both methods of production apply pre-selection cuts in order to generate the NanoAOD outputs, we need to:
 - Identify, through both package codes, the equivalent branch names of NanoAOD outputs
 - Use them to apply the same cuts to both outputs
 - Compare plots of different physical variables after the cuts are equalized

Identification

- Embedded pre-selections, applied during generation, that cannot be removed (e.g. isLooseMuon)
- Not all variables from one package have a direct equivalent in the other (e.g. mumuDCA, svip2d)
 - Some of these are also used as pre-selection criteria for the final outputs
- Some branches represent the same physical concept, but are derived differently (e.g., muon pT)
- This means we can't fully equalize all pre-selections using only cuts on the available output branches, so some differences are expected



Dataset

0,1,...,7

Dataset: [/ParkingDoubleMuonLowMass0/Run2024C-PromptReco-v1/MINIAOD](#)

Dataset size: 4156631421735 (4.2TB) Number of blocks: 38 Number of events: 75262728 Number of files: 1288 Creation time: 2024-04-16 20:14:39

Release, [Blocks](#), [Files](#), [Runs](#), [Configs](#), [Parents](#), [Children](#), [Sites](#), [Physics Groups](#) [XSDB](#) Sources: [dbs3](#) [show](#)

nfill	nrun	nls	ncms	totdelivered(/fb)	totrecorded(/fb)
26	42	24254	24254	7.590384497	7.251968024

Integrated Luminosity for our dataset: $\approx 0.9 \text{ fb}^{-1}$

CMSSW version: CMSSW_15_0_13_patch2

Nano [github link](#)

BPHNano [github link](#)



Dataset

CMSSW version: CMSSW_15_0_13_patch2
Nano: [link](#) BPHNano: [link](#)

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BPH cuts

$4.5 < \text{"B_chosen_mass"} < 6.5$	$\text{BToTrkTrkMuMu_fit_trk1_pt, trk2_pt} > 0.72$
$\text{BPHMuon_pt1, pt2} > 3.96$	$0.99 < \text{BToTrkTrkMuMu_mll_fullfit} < 4.848$
$ \text{BPHMuon_eta1} , \text{BPHMuon_eta2} < 2.4$	$\text{MuMu_svprob} > 0.1$
$\text{Track_DCASig} > 0.8$	$\text{MuMu_l_xy} / \text{MuMu_l_xy_unc} > 3.0$
$\text{MuMu_pt} > 6.831$	$\text{MuMu_fit_cos2D} > 0.9$

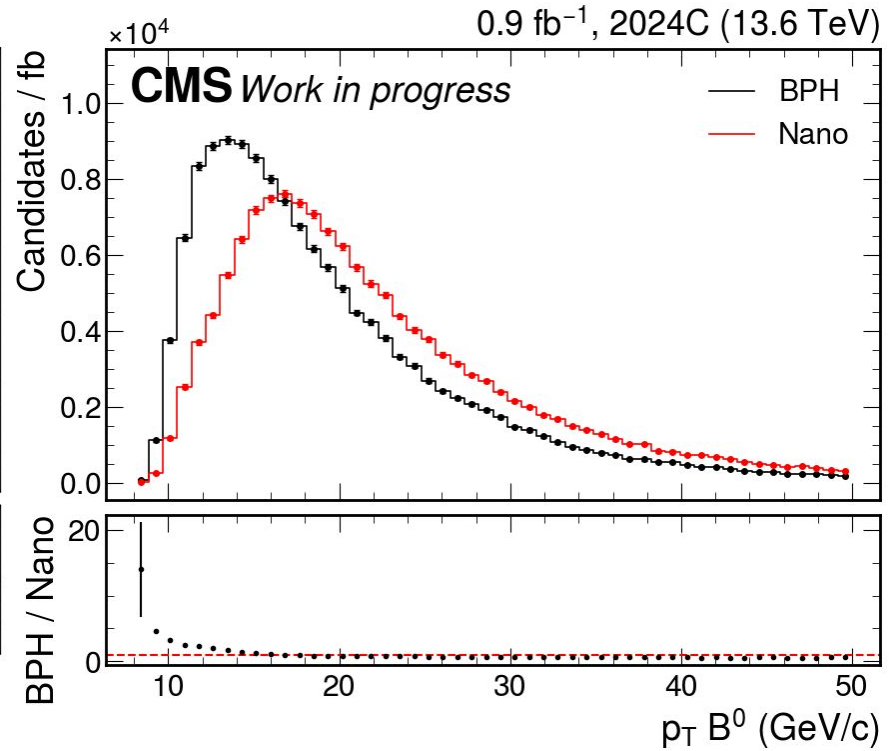
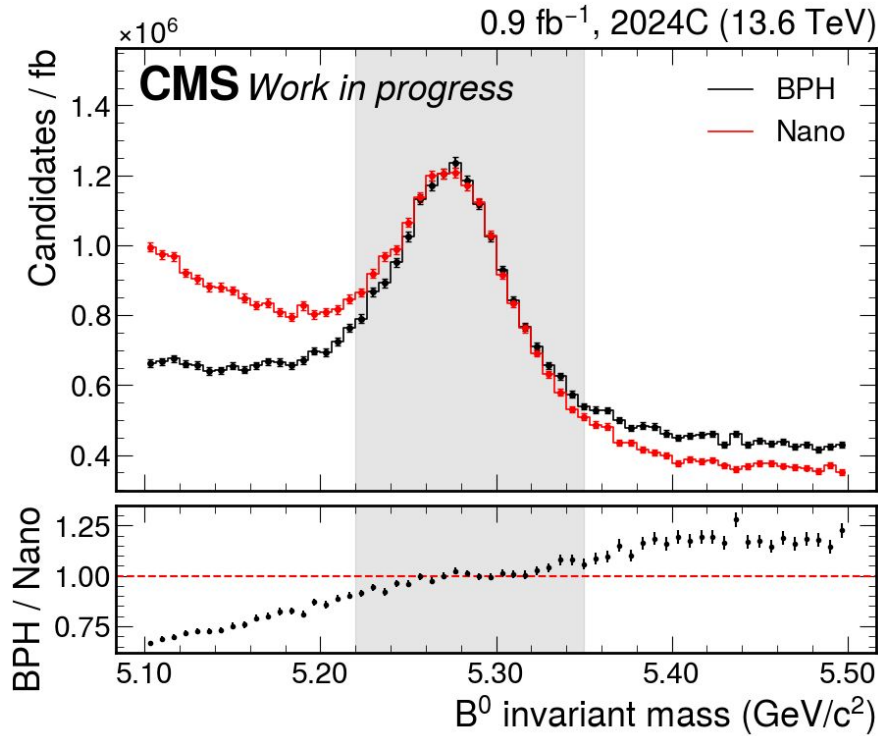
Nano cuts

$4.5 < \text{"B_chosen_mass"} < 6.5$	$\text{mumuCosAlphaBS} > 0.9$
$ \text{rawkstTrkmEta} , \text{rawkstTrkpEta} < 2.4$	$ \text{rawmumEta} , \text{rawmupEta} < 2.4$

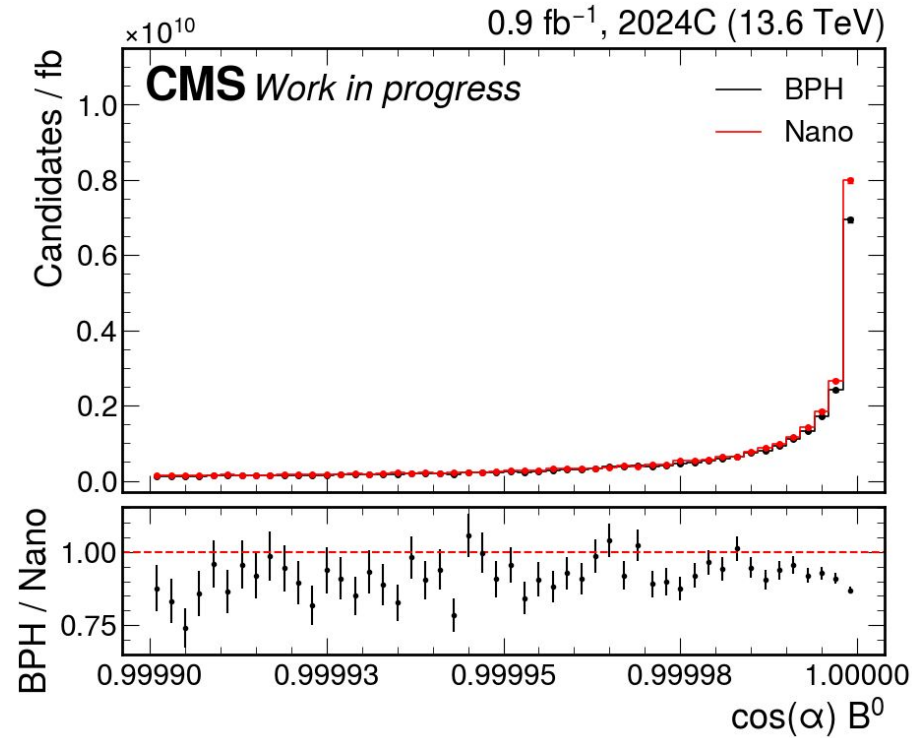
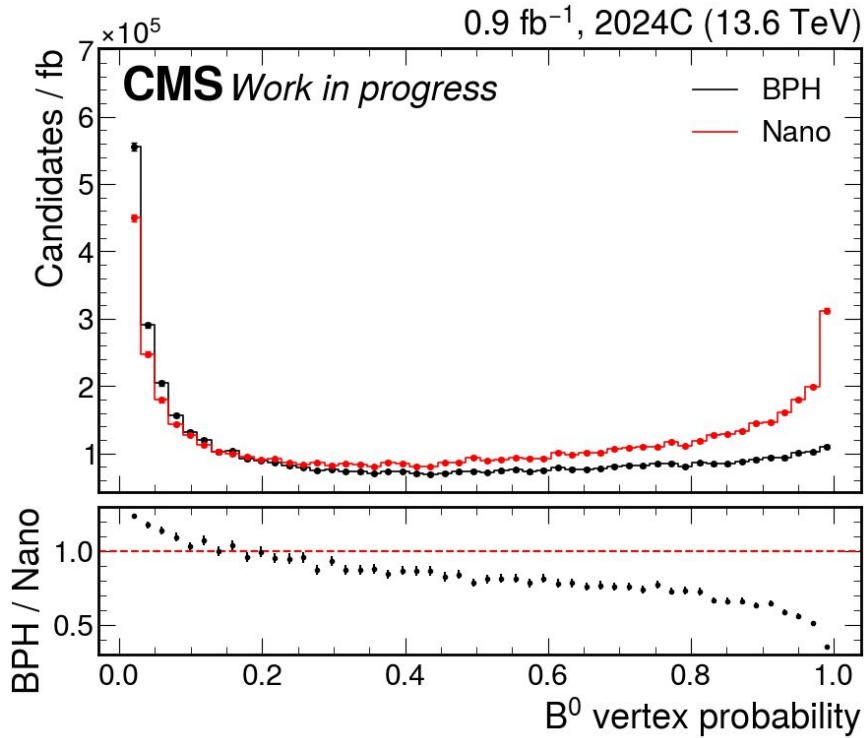
BPH: 31.083.532 candidates (295.3 GB) → 942.827 after cuts (3.03% efficiency), 49.1 GB
Nano: 1.910.666 candidates (12.1 GB) → 1.662.114 after cuts (86.99% efficiency), 11.3 GB

Plots

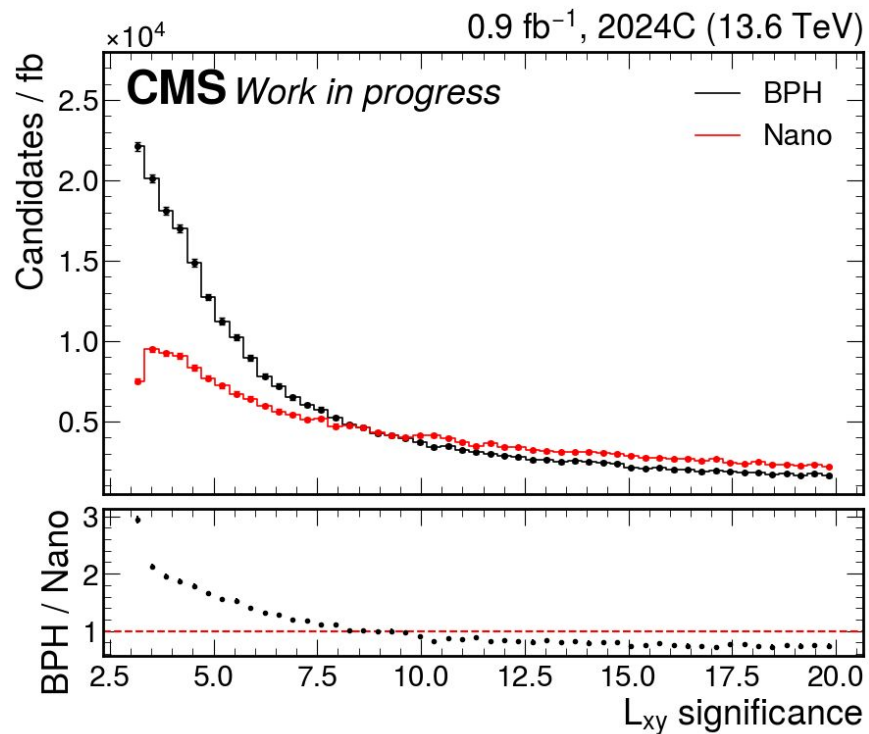
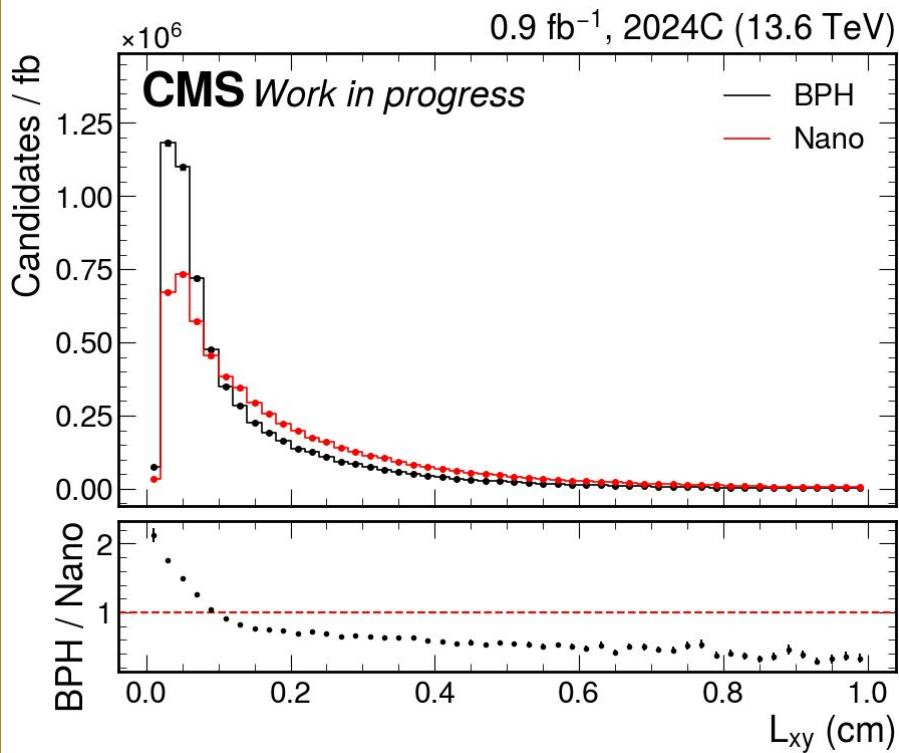
- * All normalized by integrated luminosity
- * No resonances removed



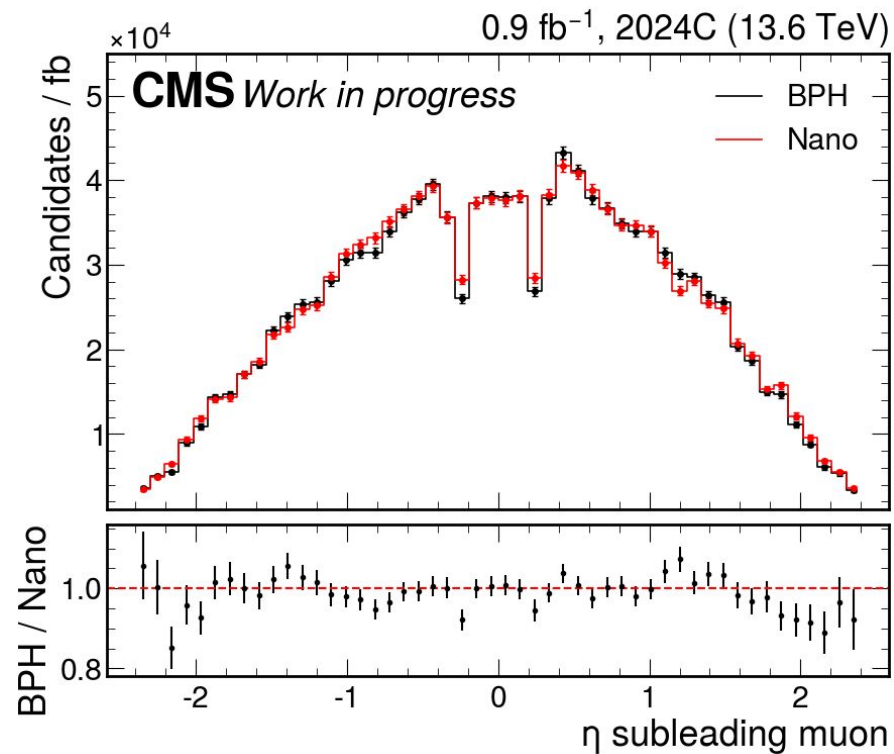
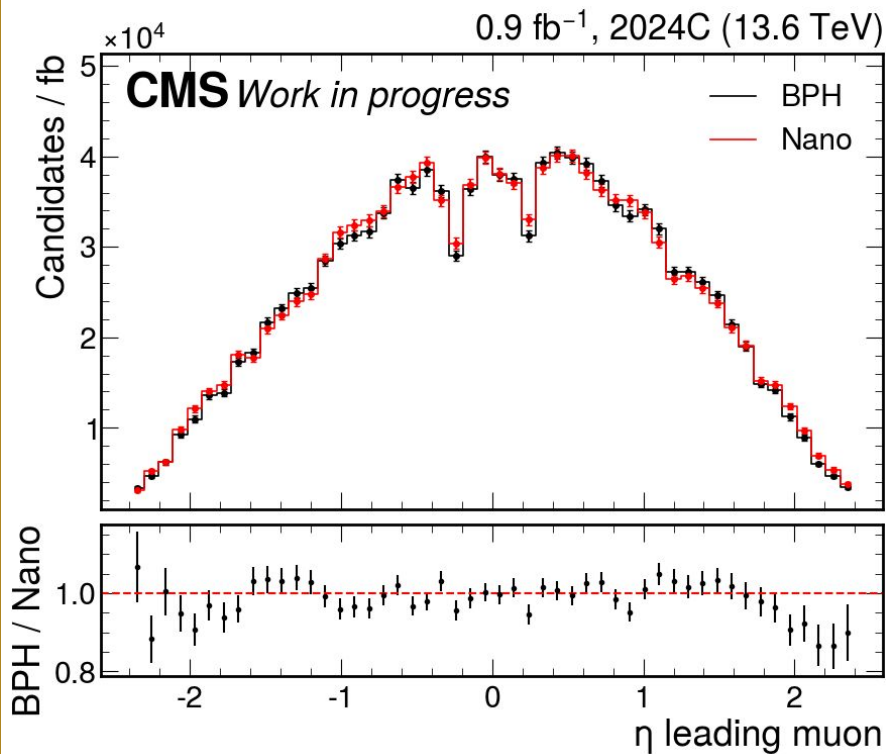
Plots



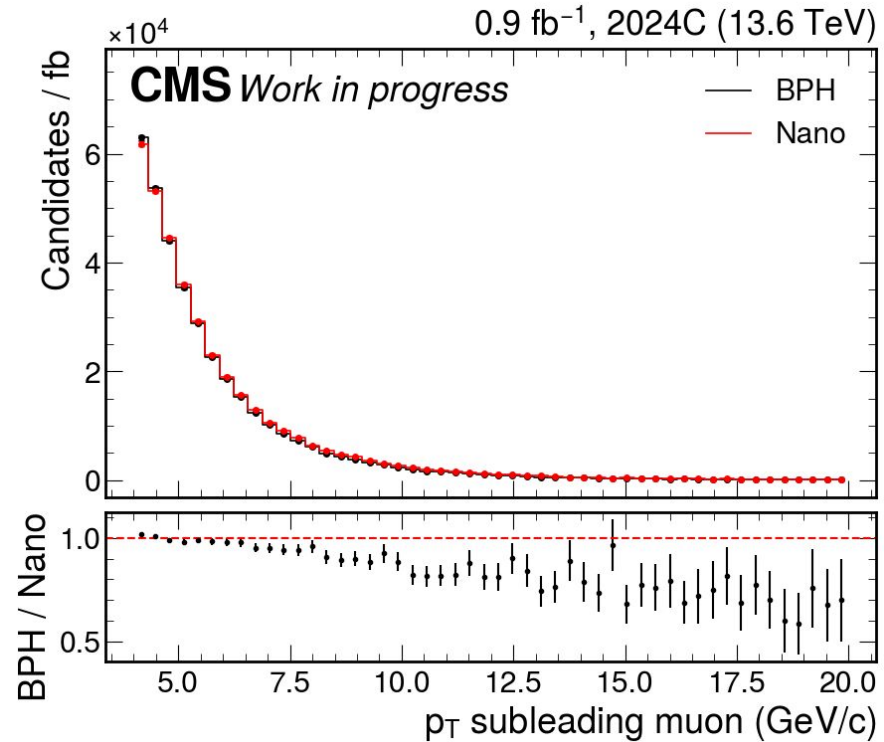
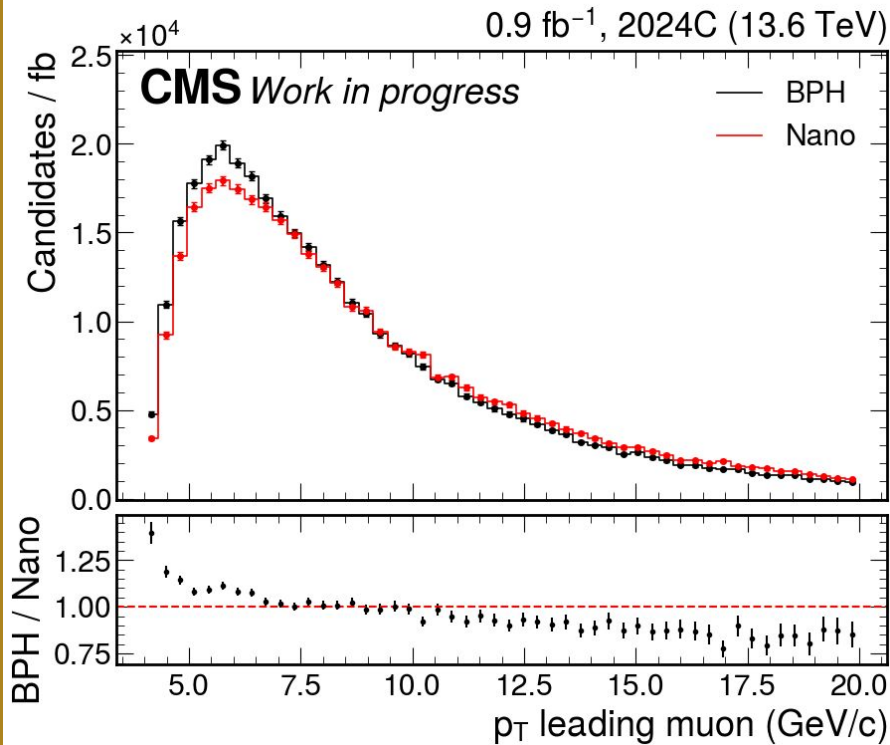
Plots



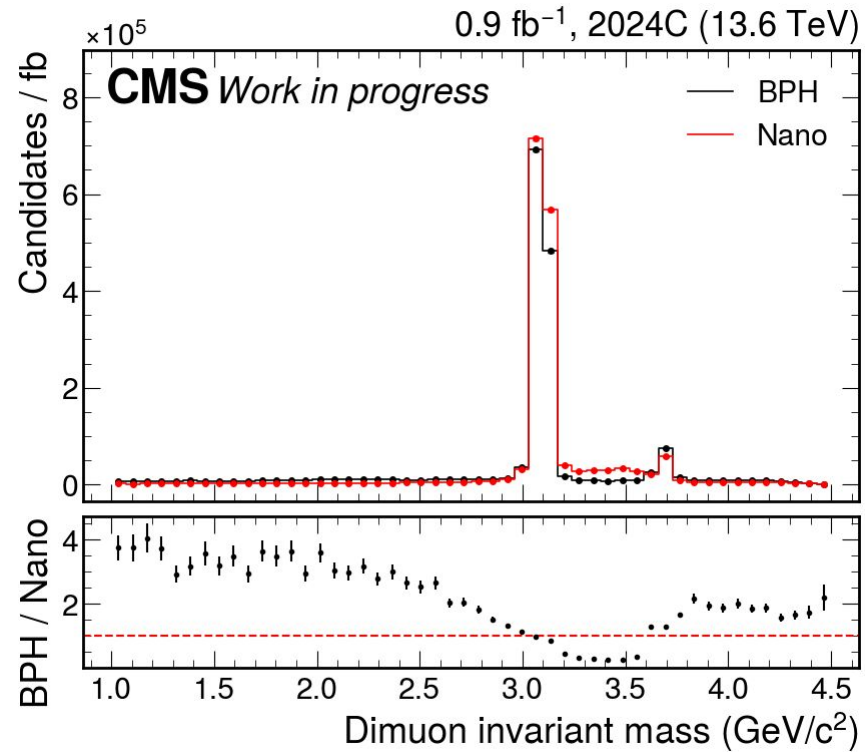
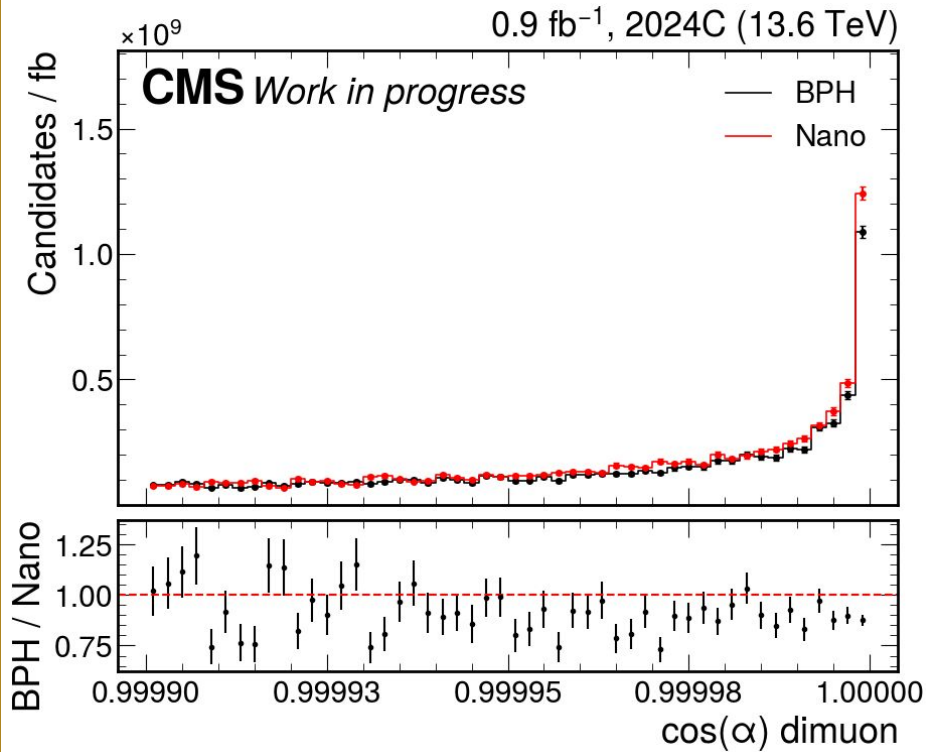
Plots



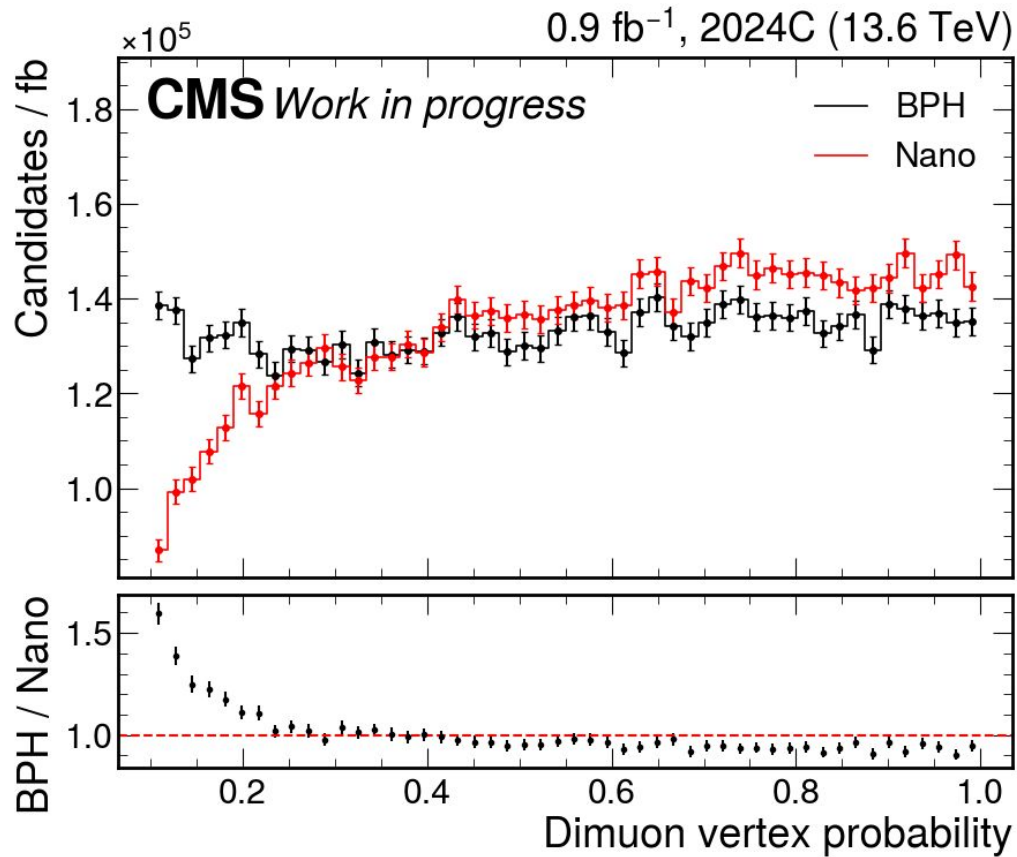
Plots



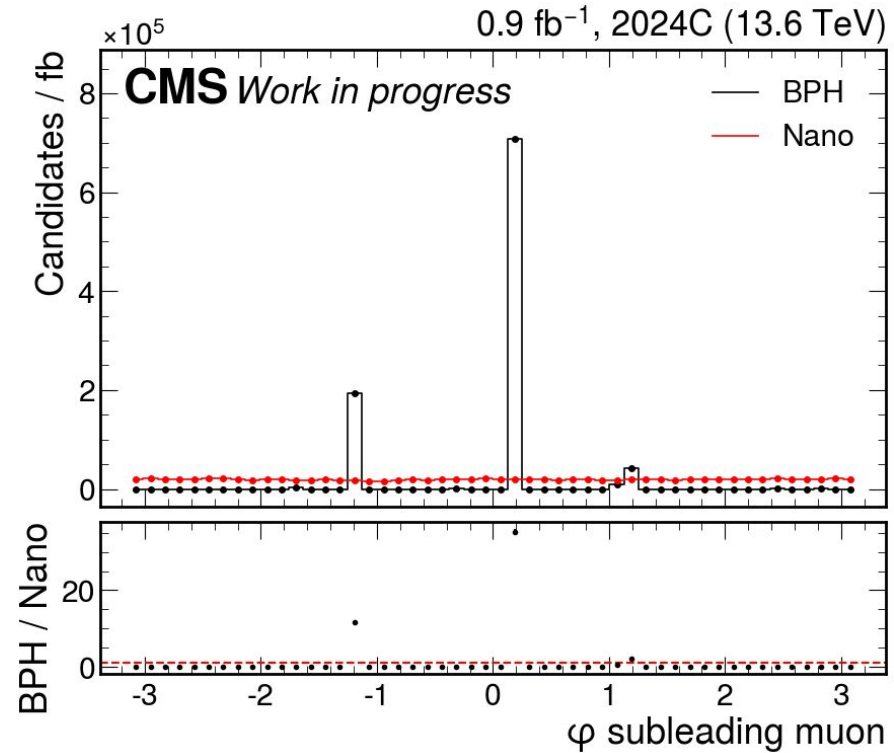
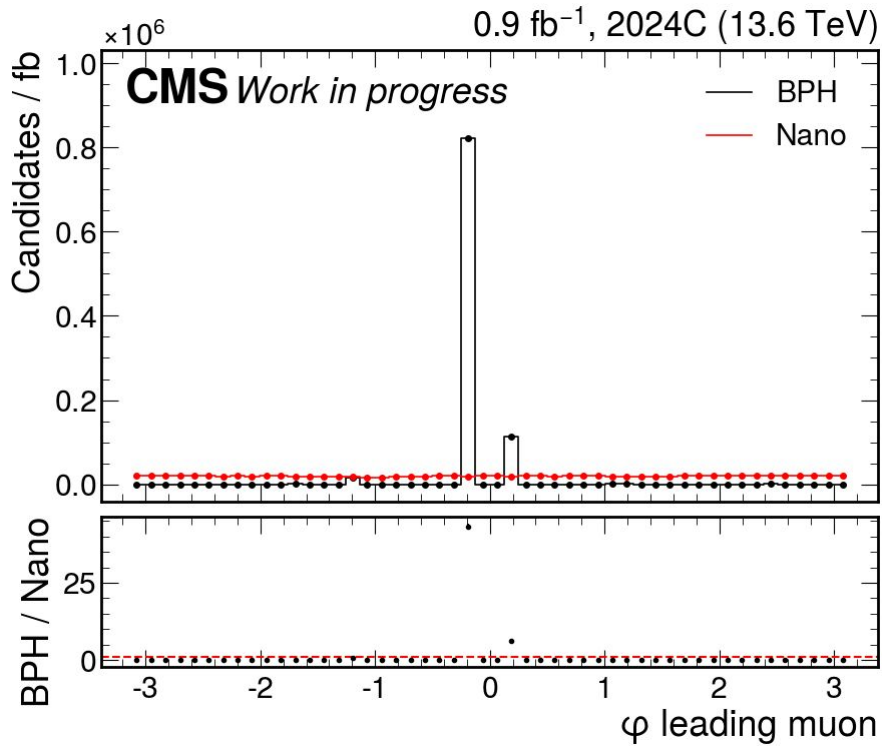
Plots



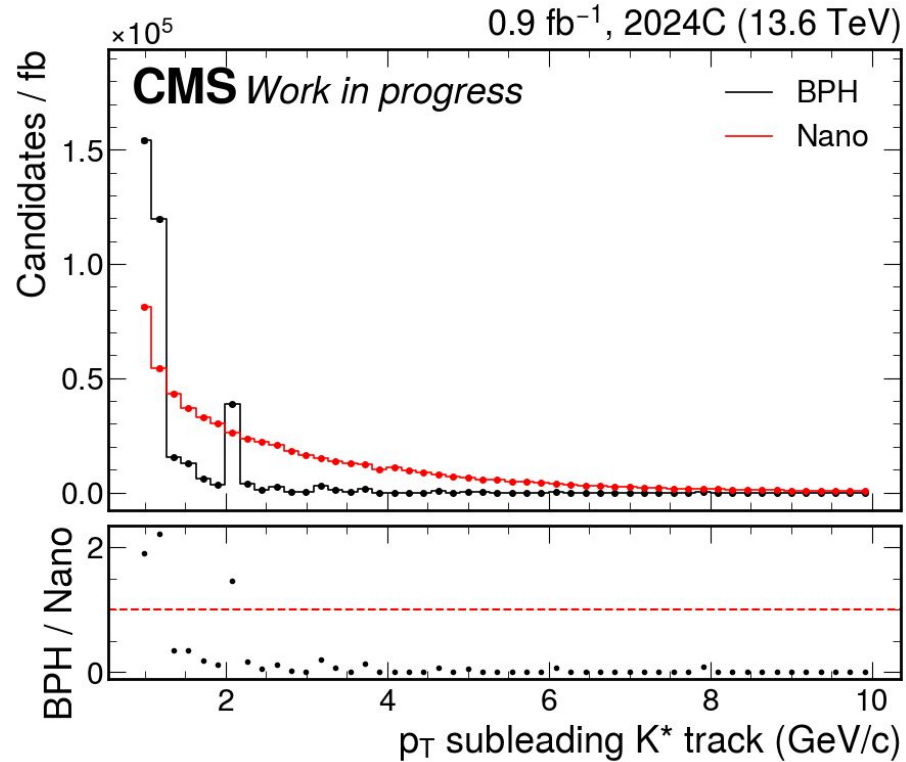
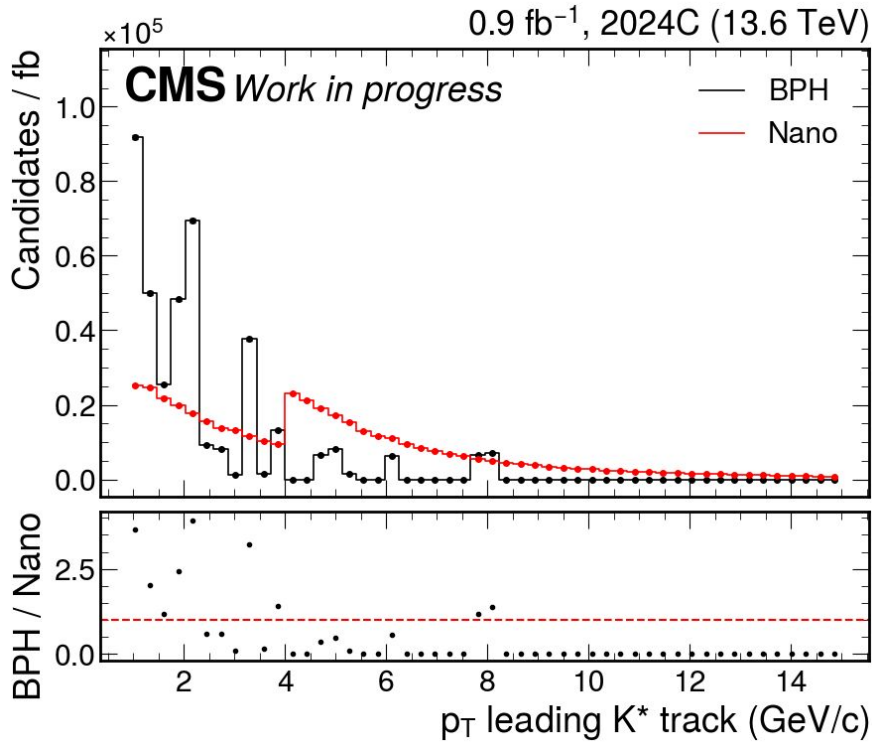
Plots



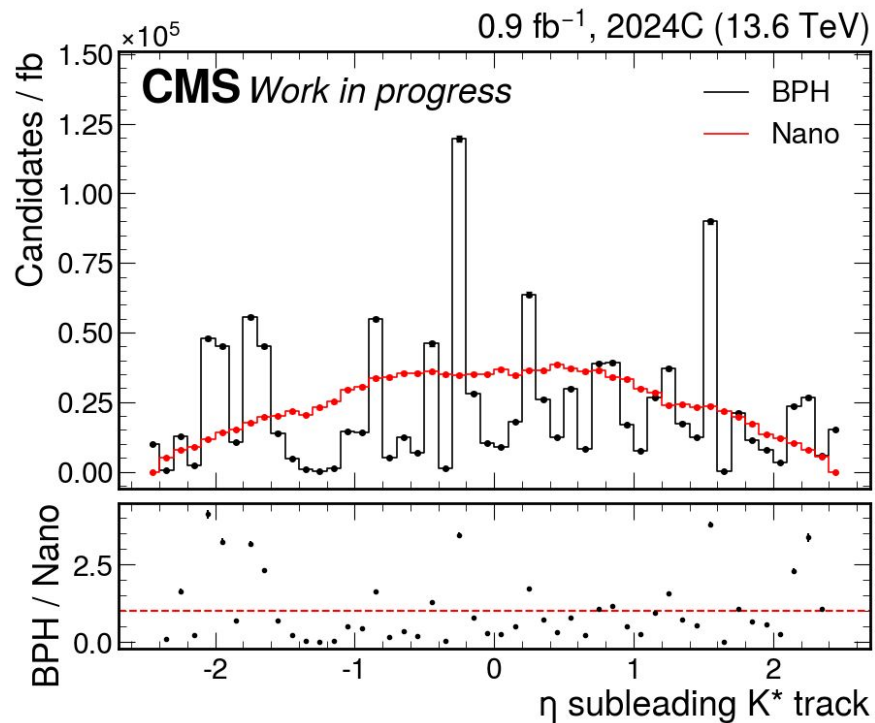
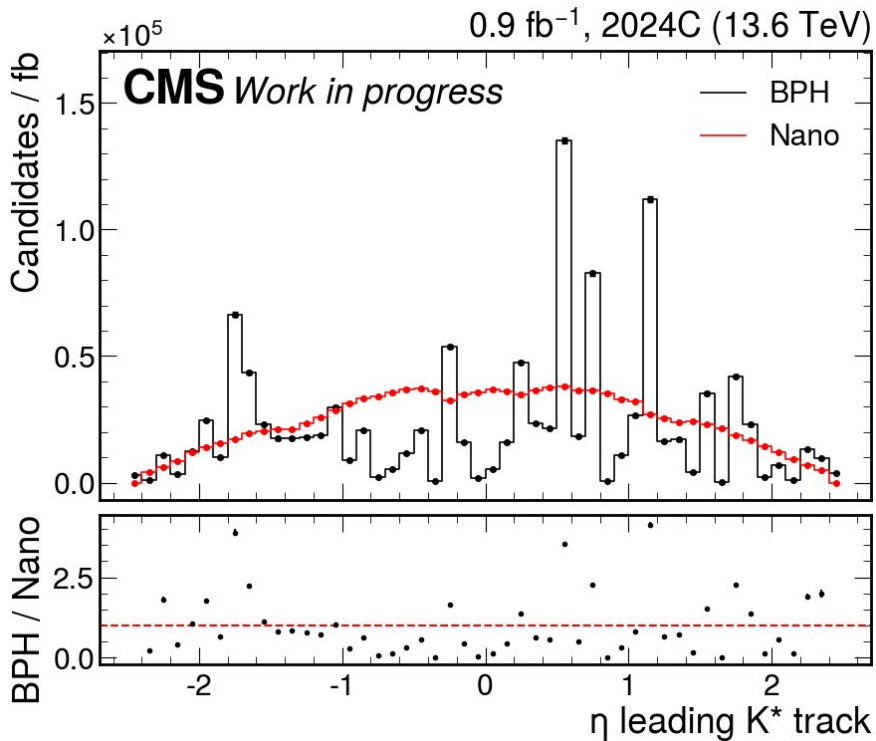
Plots



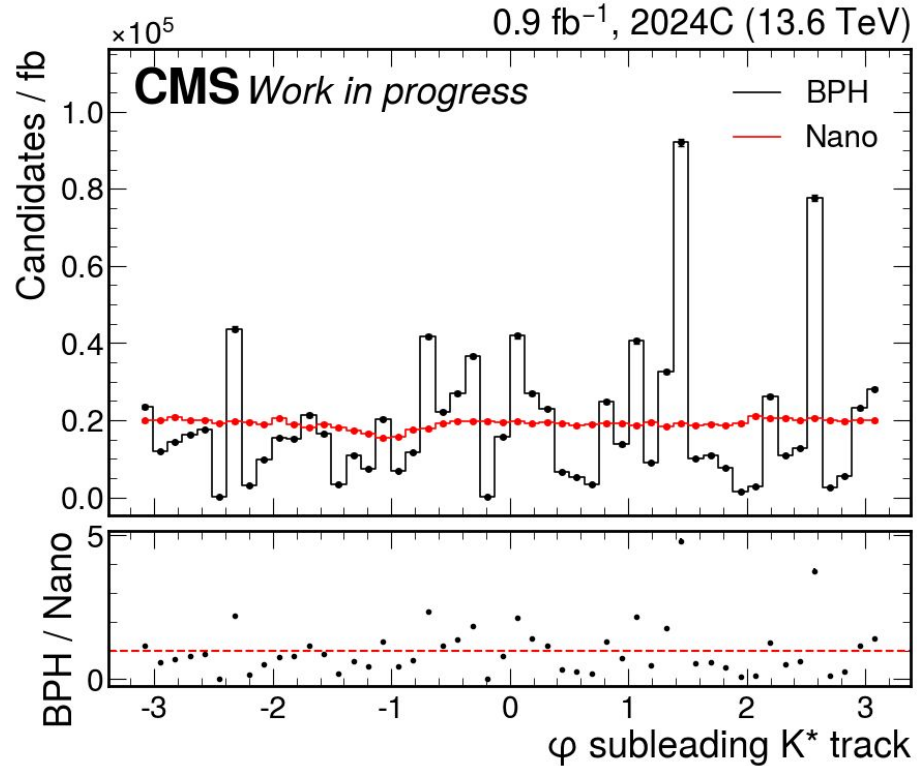
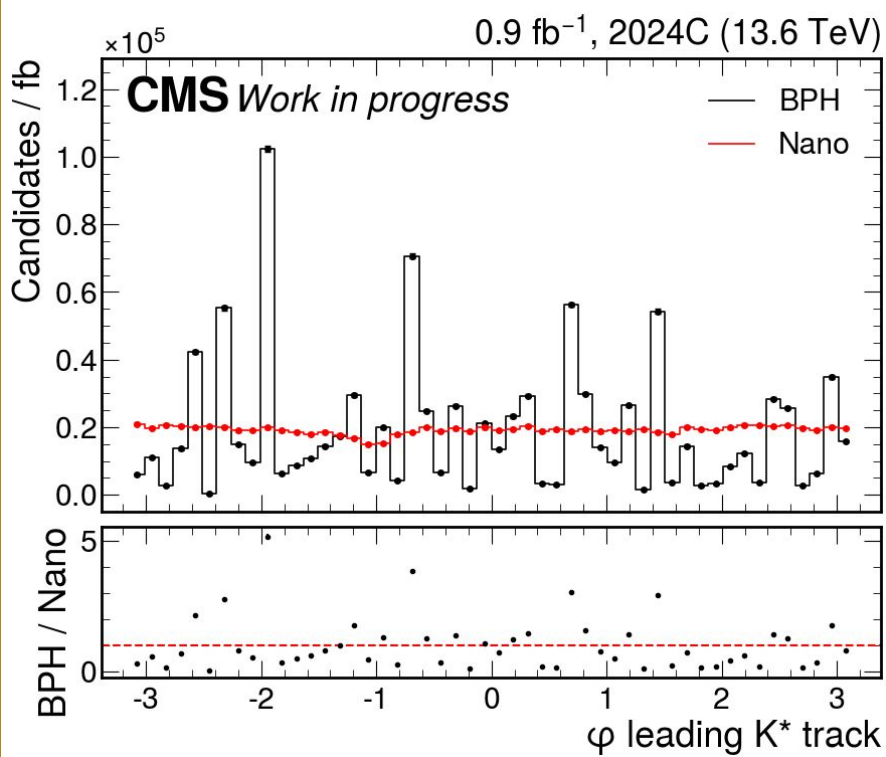
Plots



Plots



Plots



Conclusion

- Since the BPH and Nano do not yet share the same preselection, some differences were already expected. This is evident by the different number of candidates after cuts (BPH: 942.827, Nano: 1.662.114)
- Despite the difference in preselections, many of these variables show reasonable agreement, validating the comparison strategy
- Some anomalies are probably caused by the reordering of tracks by transverse momentum (BPH) instead of charge (Nano) and/or by the incorrect flattening of these variables
- Next steps include the correction of track variables and a better alignment of the preselection cuts

Thank you

Backup

Variable	Branch BPH	Branch Nano	BPH cuts (file:row)	Nano cuts (file:row)	Best Cut
pT muon	BPHMuon_pt	rawmumPt, rawmupPt (pre-fit)	BPHMuon_pt>3.0	rawmumPt > 4.0, rawmupPt > 4.0 (eff: > 3.96) (miniKstarMuMu.cc:316,345; _cfg.py:103)	Nano
Eta muon	BPHMuon_eta	rawmumEta, rawmupEta (pre-fit)	BPHMuon_eta <2.4	rawmumEta < 2.4, rawmupEta < 2.4 (eff: <2.424) (miniKstarMuMu.cc:316,345; _cfg.py:104)	BPH
muon quality (highPurity)	?	mumHighPurity, mupHighPurity	None	mumHighPurity, mupHighPurity (miniKstarMuMu.cc:1060,1097)	No branch for BPH
DCA muon to Beam Spot	?	mumDCABS, mupDCABS	None	abs(mumDCABS) < 2.0, abs(mupDCABS) < 2.0 (miniKstarMuMu.cc:129-131,161-163; cfg:101).	No branch for BPH
DCA sig. hadron to BS	Track_DCASig	kstTrkmDCABS/kstTrkmDCABSE, kstTrkpDCABS/kstTrkpDCABSE	None	kstTrkmDCABS/kstTrkmDCABSE > 0.8, kstTrkpDCABS/kstTrkpDCABSE > 0.8	Nano
DCA muon-muon	?	mumuDCA	None	mumuDCA < 0.5 (miniKstarMuMu.cc:388; cfg:100)	No branch for BPH
pT dimuon system	MuMu_pt	sqrt(mumuPx^2 + mumuPy^2)	None	mumuPt > 6.9 (miniKstarMuMu.cc:388; cfg:105)	Nano
invariant mass dimuon	BToTrkTrkMuMu_mll_fullfit	mumuMass	0 < fitted_mass < 15.0 (MuMu_cff.py:23)	1.0 < mumuMass < 4.8 (eff: 0.99 & 4.848) (miniKstarMuMu.cc:402; cfg:106,107)	Nano
vertex probability dimuon	MuMu_svprob	mumuVtxCL	sv_prob > 0.001 (MuMu_cff.py:18)	mumuVtxCL > 0.1 (miniKstarMuMu.cc:431; cfg:98)	Nano
decay length sig.dimuon (L/σ)	MuMu_l_xy / MuMu_l_xy_unc	mumuLBS / mumuLBSE	None	mumuLBS/mumuLBSE > 3.0 (miniKstarMuMu.cc:451; cfg:99)	Nano
cosa dimuon	MuMu_fit_cos2D	mumuCosAlphaBS	None	mumuCosAlphaBS > 0.9 (miniKstarMuMu.cc:468, cfg:102)	Nano
cosa B°	BToTrkTrkMuMu_fit_cos2D	bCosAlphaBS	fitted_cos_theta_2D >= 0.90 (BToTrkTrkLL_cff.py:15)	None	Both post-fit.
pT (K/π)	Track_pt	rawkstTrkmPt, rawkstTrkpPt	Track_pt > 0.7	Both > 0.8 (eff: > 0.72) (miniKstarMuMu.cc:493; cfg:114)	Nano
Eta (K/π)	Track_eta	rawkstTrkmEta, rawkstTrkpEta	Track_eta < 2.4	Both < 3.0	BPH
hadron quality (highPurity)	?	kstTrkmHighPurity, kstTrkpHighPurity	None	kstTrkmHighPurity == 1, kstTrkpHighPurity == 1 *	No branch for BPH
Mass K* ⁰ (hyp: π ⁺ K ⁻)	BToTrkTrkMuMu_fit_ditrack_mass_Kpi	kstMass	[4.5,6.0] FOR BEST HYP. B MASS (BToTrkTrkLL_cff.py:14)	[0.746, 1.046] FOR BEST HYP. K* MASS (miniKstarMuMu.cc:595)	Fit all on best hypothesis
Mass K* ⁰ (hyp: K ⁺ π ⁻)	BToTrkTrkMuMu_fit_ditrack_mass_piK	kstBarMass	[4.5,6.0] FOR BEST HYP. B MASS (BToTrkTrkLL_cff.py:14)	[0.746, 1.046] FOR BEST HYP. K* MASS (miniKstarMuMu.cc:595)	Fit all on best hypothesis
Mass B ⁰ (hyp: K* ⁰)	BToTrkTrkMuMu_fit_mass_Kpi	bMass	[4.5,6.0] FOR BEST HYP. B MASS (BToTrkTrkLL_cff.py:14)	4.5 < bMass < 6.5 (miniKstarMuMu.cc:865; cfg:109,110).	Fit all on best hypothesis
Vertex probability B ⁰	BToTrkTrkMuMu_svprob	bVtxCL	sv_prob > 0.001 (BToTrkTrkLL_cff.py:15)	Mini: Corte bVtxCL > 0.01 (miniKstarMuMu.cc:558; cfg:98).	Nano
2D IP: hadrons:dimuon vertex	BToTrkTrkMuMu_trk1_svip2d BToTrkTrkMuMu_trk2_svip2d	?	Both < 0.045 (BToTrkTrkLL_cff.py:15)	None	No branch for Nano

Definitions

- B invariant mass reconstruction (“B_chosen_mass”):
 - 1- Evaluates the ditrack masses from both hypothesis ($K^+\pi^-$ and $K^-\pi^+$ hypothesis)
 - 2- Select the hypothesis whose ditrack mass is closest to K^* mass
 - 3- Define “B_chosen_mass” as either bMass ($K^+\pi^-$) or bBarMass ($K^-\pi^+$)

- Flattening

The entire analysis was carried out in a Python + uproot environment
Data processing relies on columnar analysis and multiprocessing
Arrays must have the same length to be used together, but many arrays are jagged — different events contain a different number of entries (e.g., muons, tracks).
Flattening is the process of converting these jagged arrays into flat, one-dimensional arrays of equal length, so they can be combined with other variables.