

Alignment of the VELO pixel detector

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Abstract

The LHCb experiment is designed to perform high precision measurements to study CP-violation and rare decays of beauty and charm hadrons. During LS2, prior to Run 3 of the LHC, the LHCb detector will go through a major upgrade. One of the sub-detectors that will be upgraded is the Vertex Locator (VELO) which after the upgrade will be capable of readout at 40 MHz at a luminosity of $2 \cdot 10^{33} \text{ cm}^{-2}\text{s}^{-1}$. VELO is a high precision detector designed to reconstruct and discriminate between primary and secondary vertices close to the interaction point. Due to safety of the detector, the VELO is divided into two retractable halves which prior to each fill into LHC are retracted from the beam-line, and closed once stable beam is declared. Best possible performance of the VELO requires the halves of the VELO, and the individual detector elements of it, to be aligned for correct reconstruction of tracks and vertices.

In this project the radial residual distribution is studied for different track selections for each and every module of the VELO detector using MC data. Also, the mean residual has been studied as a function of module number and η -angle.

1 Introduction

LHCb is one of the main experiments at the LHC, dedicated to the study of the matter-antimatter asymmetry and the search for rare decays of c - and b -hadrons. As the production of b -mesons is preferentially in the forward direction, the LHCb experiment detector is constructed as a single arm forward spectrometer covering a pseudorapidity range $2 < \eta < 5$. The detector is made up of layers of sub-detectors, all designed to meet different experimental requirements. One such requirement is the ability to discriminate between primary and secondary vertices of particle collisions. A primary vertex is due to the initial particle collision and a secondary one is due to the decay of a short-lived particle. For this purpose, and for the reconstruction of particle trajectories (tracks) close to the interaction point, the Vertex Locator (VELO) detector is constructed. The VELO surrounds the interaction point of the proton beams closest to the beam-line. Charged particles traversing the VELO are reconstructed as tracks by identification of their hit patterns in the detector. Primary and secondary vertices are reconstructed using the track information available from the event.

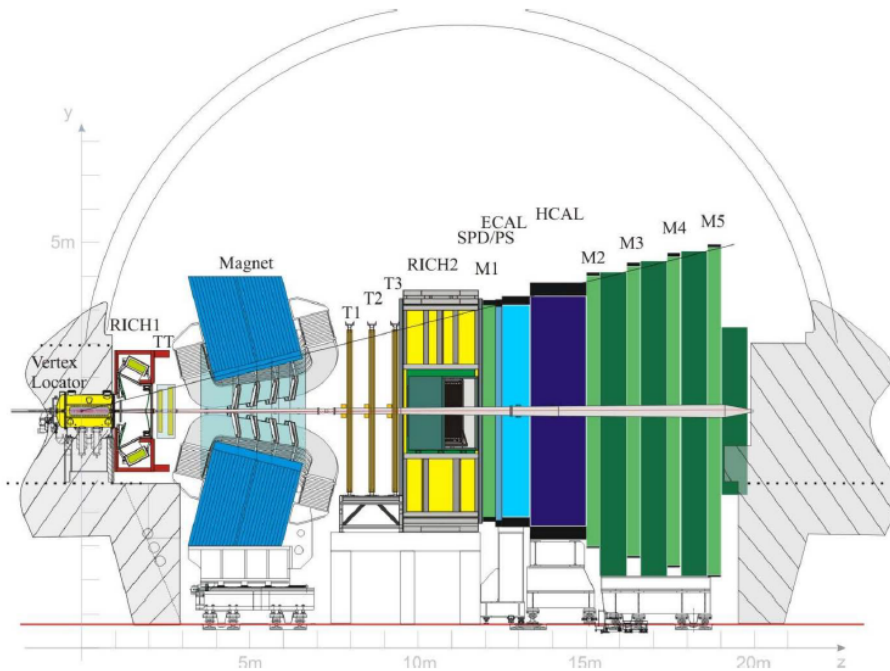


Figure 1: Schematic picture of the LHCb experiment detector

Except for VELO there are four other tracking detectors designed to reconstruct tracks and measure their momentum as they traverse the active material in the detectors. For this task charged particle trajectories are curved by a large dipole magnet enclosing the detectors. Particle identification is provided by the RICH (Rich Imaging Cherenkov) detectors using Cherenkov radiation. Triggering and reconstruction of neutral particles are enabled by the electromagnetic calorimeter (ECAL) and the hadron calorimeter (HCAL). The outermost part of the LHCb detector consists of a muon chamber designed to detect muons.

During long shutdown 2 (LS2), prior to Run 3, LHCb will go through an upgrade (planned to start at the end of 2018 [1]) to allow for an increased beam luminosity and to improve physics performance of the detector. During the upgrade the current VELO silicon micro strip detector will be upgraded to a lightweight hybrid pixel detector, capable of readout at 40 MHz at a luminosity of $2 \cdot 10^{33} \text{ cm}^{-2}\text{s}^{-1}$ [1].

2 The VERtEx LOcator (VELO) pixel detector

The upgraded VELO comprises a series of 52 silicon pixel modules positioned on varying distances from each other along the beam-line. To fulfill the requirements of high precision reconstruction of primary and secondary vertices the VELO modules are placed as close as possible to the beam-line. To ensure

safety of the detector the VELO is divided into two halves, one A side and one C side, where every second module is part of one of the respective sides. In the global LHCb frame of reference the A side is at positive x (toward the center of the LHC ring) and the C side is at negative x . Each half of the VELO is retractable from the beam-line so that the furthest distance between active VELO material and the beam-line is 3 cm during fill of the LHC, see Figure 2. When stable beam is declared VELO is closed and the closest distance between VELO pixels and the beam-line is 5.1 mm, see Figure 3. Once the VELO is closed there is a few millimeters overlap between the two modules comprising one pair of the A and C side.

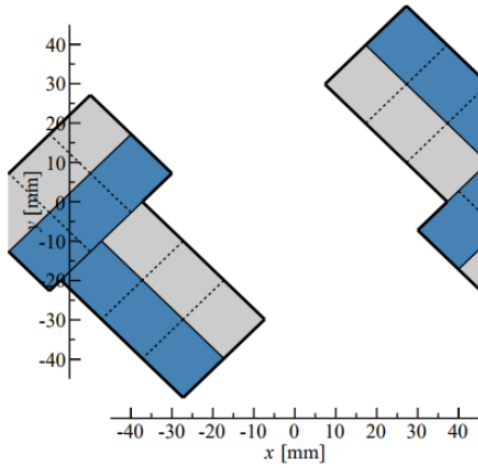


Figure 2: Open VELO as seen in a plane perpendicular to the beam-line

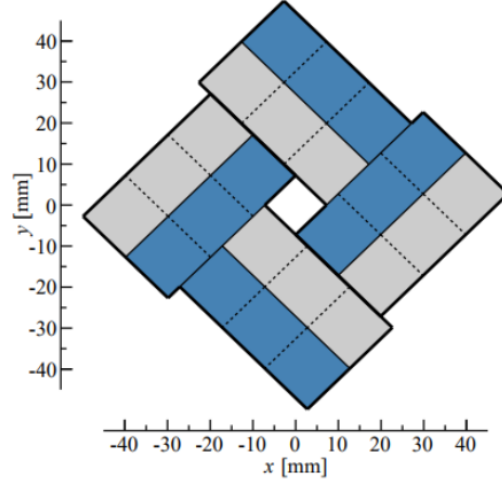


Figure 3: Closed VELO as seen in a plane perpendicular to the beam-line

Once VELO is closed an alignment procedure is performed in order to ensure optimal data taking and best possible performance of the detector. VELO is initially assembled and surveyed with high precision, which is further improved by a track-based software alignment procedure [2].

3 Alignment of the VELO

The spatial alignment of the VELO detector is essential for the discrimination between primary and secondary vertices. The aim of the alignment procedure is to estimate the misalignment of the modules with respect to their initial positions. This is done through a track-based alignment procedure and once the misalignment is parametrized it is compensated for in the reconstruction of tracks [3].

The principle behind the track-based alignment is illustrated in Figure 4a and 4b, where modules to be aligned are shown in black, the measured hits are shown in red and fitted tracks are represented by blue lines. This illustrates the situation where one module has in reality been dislocated from its design position. The misalignment of a module biases the reconstruction of tracks and the average distance between hits and reconstructed tracks are increased. This leads us to the definition of *residuals*, represented by orange arrows in Figure 4c and 4d.

For each hit of a track the residual is defined as the distance between the hit and the intersection between the fitted track and the detector element. The residual is unbiased if the hit under consideration is not taken into account for the track fit, see Figure 4c, whereas the biased residual is defined when the considered track is taken into account for the track fit, as seen in Figure 4d. Hence, there is a correlation between the size of the residuals and misaligned detector elements.

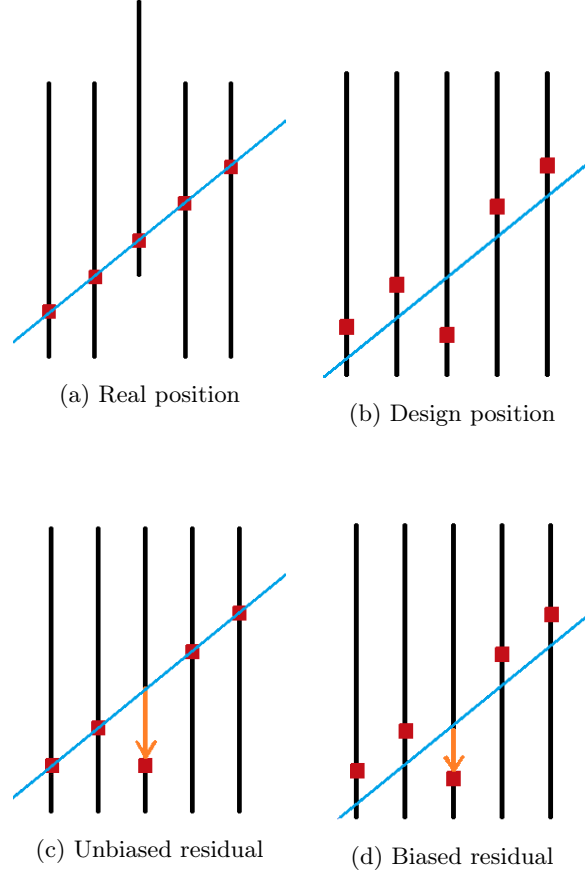


Figure 4: Schematic illustration of the scenario with one misaligned module in the real position, Figure 4a, as compared to the designed position of the modules, Figure 4b. The residuals are defined as the distance between the hits in the detector module and the intersection between the track fit and the detector module. An unbiased residual and a biased residual is defined as shown in 4c and 4d respectively.

Misalignments of each element are parametrized by six degrees of freedom: translational (T_x , T_y , T_z parametrized by Δ_x , Δ_y , Δ_z) and rotational (R_x , R_y , R_z , parametrized by Δ_α , Δ_β , Δ_γ). The parameters are referred to as *alignment constants*.

The alignment procedure is based on the minimization of residuals through a global χ^2 -method to produce alignment constants. An important component of the alignment procedure is the selection of track sample used, which should contain tracks from both primary and secondary vertices [2], as well as from beam gas events, which are tracks sensitive to different degrees of freedom.

In the case of no misalignment, the residual distribution is a Gaussian distribution centered at zero. A translational misalignment causes a shift in the residual distribution whereas a rotational misalignment causes a broadening of the residual distribution, which can be taken into account in the track fit. Special care must be taken to misaligned modules in configurations called *weak modes*. These type of configurations allow good track fits with residual distributions centered at zero. Examples of weak modes are a global translations and a rotation of all the modules. Weak modes are constrained via constraint equations, see [3].

4 Analysis

The aim of this project has been to study the residual distributions dependency on track selection and the effect on residual distributions due to a large misalignment of the modules which has been aligned using the alignment procedure. For this purpose the MC data used are reconstructed for an ideally aligned scenario and for a large misaligned scenario. The residuals are studied as functions of different variables

to study possible dependencies on the variables. Here the radial residual (r -residual) has been studied due to its sensitivity to z-misalignments which the VELO geometry is less sensitive to. The radial residual is defined as

$$r - \text{residual} = \sqrt{\text{track}_x^2 + \text{track}_y^2} - \sqrt{\text{hit}_x^2 + \text{hit}_y^2} \quad (1)$$

where track_x and track_y are the track fit in the x- and y-direction respectively, and hit_x and hit_y are the measured hit-positions in the x- and y-direction respectively. For the *reconstructed* r -residual the track_x and track_y are the reconstructed track-fits in x- and y- respectively and for the *Truth* r -residual the track_x and track_y are replaced by the Monte Carlo Truth simulated fitted tracks.

The r -residual depends on projected angle, number of hits on tracks, extrapolation of tracks, energy loss and multiple scattering effects. Some of these parameters are strongly correlated, such as the projected angle and the radius.

Long tracks are measured passing through the VELO in the forward direction, then passing through the tracking system outside of VELO in LHCb which enables identification of the particle momentum, see Figure 5. Backward tracks are tracks that are only detected in VELO (see VELO tracks in Figure 5), but then pass out through the detector in the backward direction, hence they are never possible to detect by any other part of the LHCb detector.

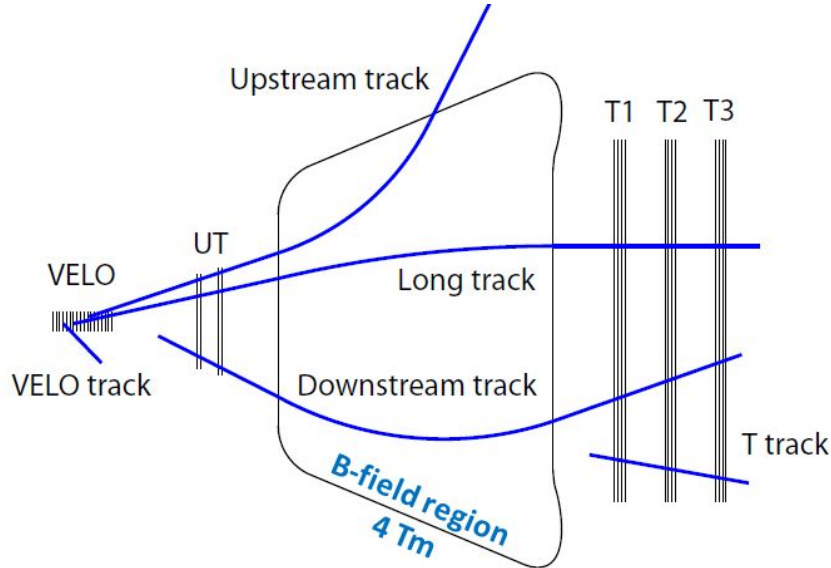


Figure 5: Schematic picture showing the definitions of different types of LHCb tracks. Long tracks pass through the VELO detector into the forward direction where it reaches the outer layers of the detector and the particle momentum can be identified. The backward tracks are VELO tracks that pass through VELO in the backward direction and never reach any other part of the LHCb detector.

A probability of so called ghost tracks exists for every particle track detected. Ghost tracks are misidentified tracks that have less than 70% of hits matching the hits of any final state Monte Carlo Particle. Ghost tracks are removed based on the *ghost probability* [4].

The data used are Monte Carlo simulations of random proton-proton collisions in upgrade conditions. An initial track selection on both long tracks and backward tracks included the rejection of tracks with hits in the overlap region of two modules and a cut on all tracks outside of the LHCb acceptance in pseudorapidity: $2 < \eta < 5$. Further the track selection was applied individually to long and backward tracks respectively. For long tracks the track selections used was: $p \geq 5$ GeV, $p_T > 200$ MeV, total number of hits in the VELO > 8 and total number of tracks in the event < 30 . For backward tracks the initial track selection used was: total number of hits in the velo > 5 and total number of tracks per event < 30 .

To further study the residual distributions dependency on the ghost probability and the χ^2 per degree of freedom two additional cuts were individually applied to both the long and the backward tracks:

- χ^2 per degree of freedom < 2
- ghost probability < 0.01

The residual distributions for reconstructed tracks and truth Monte Carlo was compared and shown to be equal. Further the reconstructed track residual distributions have been studied for all tracks, a track selection as above described, and with the additional cuts on χ^2 per degree of freedom and on the ghost probability. The residual distribution has been studied for both no misalignment and the large misalignment scenario for each module within the VELO detector. The first 16 modules (Module 0 to 15) are in the backward direction whereas the rest (Module 16 to 51) are in the forward direction of the LHCb detector with respect to the interaction point. The mean residual distribution has been studied as a function of module number and η for all track selections.

The large T_z misalignment scenario studied here corresponds to a large rotational misalignment (R_y) resulting in a translational misalignment of $1000 \mu\text{m}$ of every second module in the positive z -direction. The rotation is applied around the y -axis at the position of the cooling block, based on measurements of prototype modules. As a result of the rotation around y there is a displacement in z of a point 10 cm away, corresponding to the part of the module furthest from the supporting structure. The rotation around y can be thought of as a scenario due to a major mechanical failure.

5 Results

The residual distributions for reconstructed tracks and MC Truth were checked to correspond. In Figure 6 the truth r -residual distribution minus the reconstructed r -residual distribution is shown for Module 8, Module 13, Module 16, Module 26, Module 27, Module 29 and Module 33.

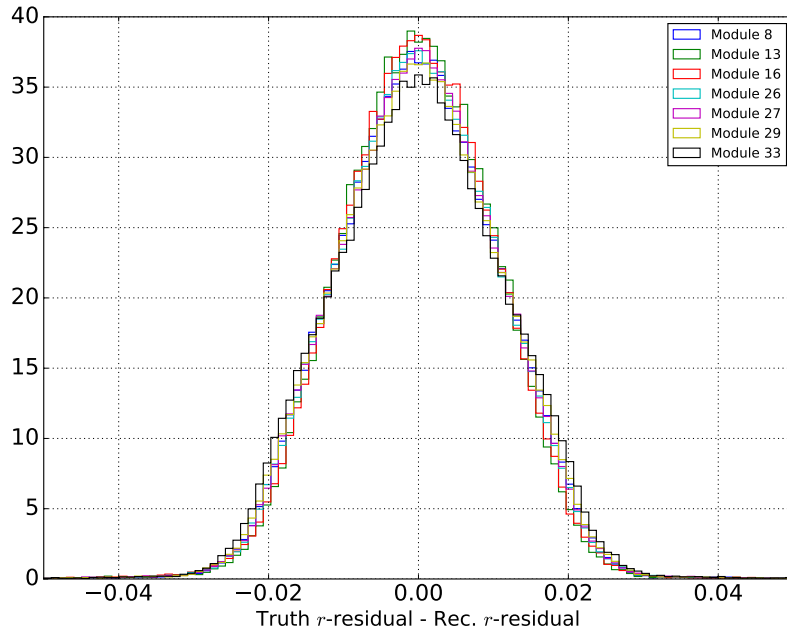


Figure 6: Truth residual distribution minus reconstructed residual distribution for 7 modules of the VELO

As seen in Table 1 the number of long tracks were in total reduced from 779911 tracks to 206739 by applying all the track cuts whereas the backward tracks were reduced from 850723 to 6198 tracks by applying all the cuts. In the table one can also see that the *ghost probability*-cut reduces the number of long tracks more than the cut on χ^2 per d.o.f.. In the case of backward tracks however, the cut on χ^2 per d.o.f. reduces the number of tracks more than the *ghost probability*-cut.

Table 1: The table shows how the track selection and the two track cuts, χ^2 per d.o.f. <2 and *ghost probability* < 0.01 , cuts down the number of tracks for long tracks and backward tracks. The track selection-cut refers to the initial track selection made on long and backward tracks individually.

Cuts	Long tracks	Backward tracks
No cuts	779911	850723
Track selection	271723	7093
Track selection and χ^2 per d.o.f. <2	261914	6229
Track selection and Ghost probability <0.01	206786	7035
Track selection, χ^2 per d.o.f. <2 and ghost probability <0.01	206739	6198

Residual distributions for each module has been studied as function of the track selection reported in Table 1. Each module is on a different z-position along the beam-line, where the closest one to the interaction point are module 15 and 16. Lower module numbers than 15 are in the backward direction whereas higher modules numbers than 16 are in the forward direction. The residual distributions per module for long and backward tracks are reported in the Appendix.

5.1 No misalignment

Below, residual distributions for modules 23 and 44 for long tracks are shown. Module 23 is close to the interaction point whereas Module 44 is further away in the positive forward direction. The rightmost figures show the same distributions as the leftmost figures but with log scale on the y-axis where the tail of the distributions are more visible. Long track residuals without track selection is shown in grey and the selected tracks are shown in pink. The residual distributions of tracks with additional cuts χ^2 per d.o.f. <2 and *ghost probability* less than 0.01 are shown in black and blue respectively.

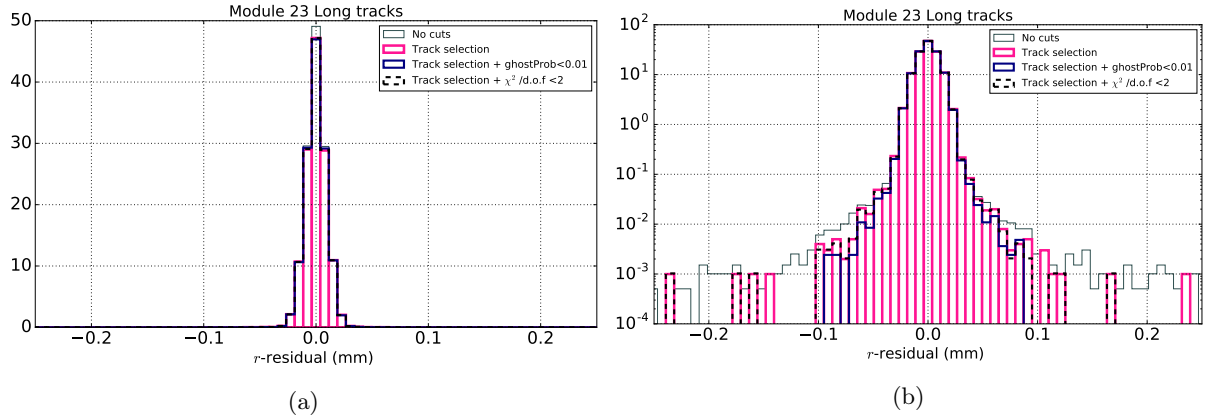


Figure 7: Long tracks r -residual distribution Module 23 without and with log scale on the y-axis in (a) and (b) respectively

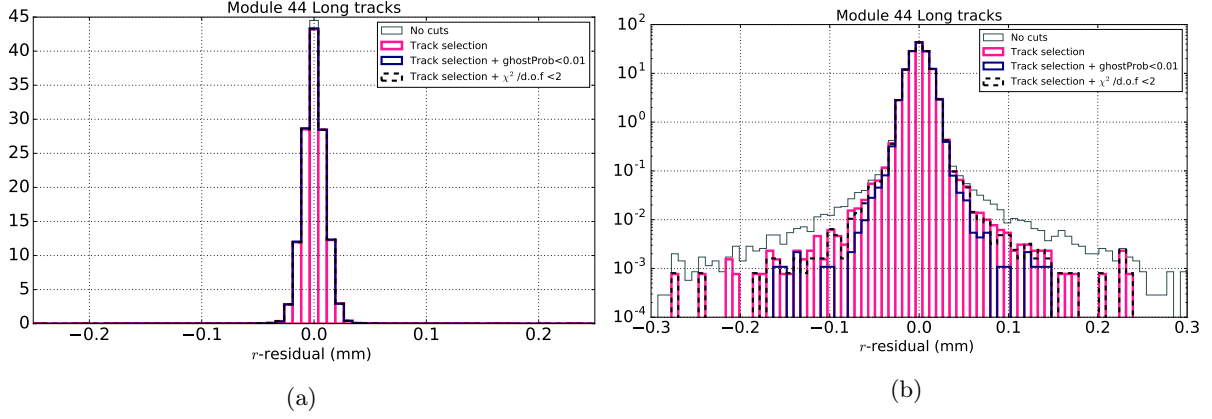


Figure 8: Long tracks r -residual distribution Module 44 without and with log scale on the y-axis in a and b respectively

As seen in Figure 7b and 8b the ghost probability cut effectively reduces the number of tracks that contributes to the tail of the residual distributions. All track selections here applied allows for the residual distribution form to stay the same and only the tail is cut off.

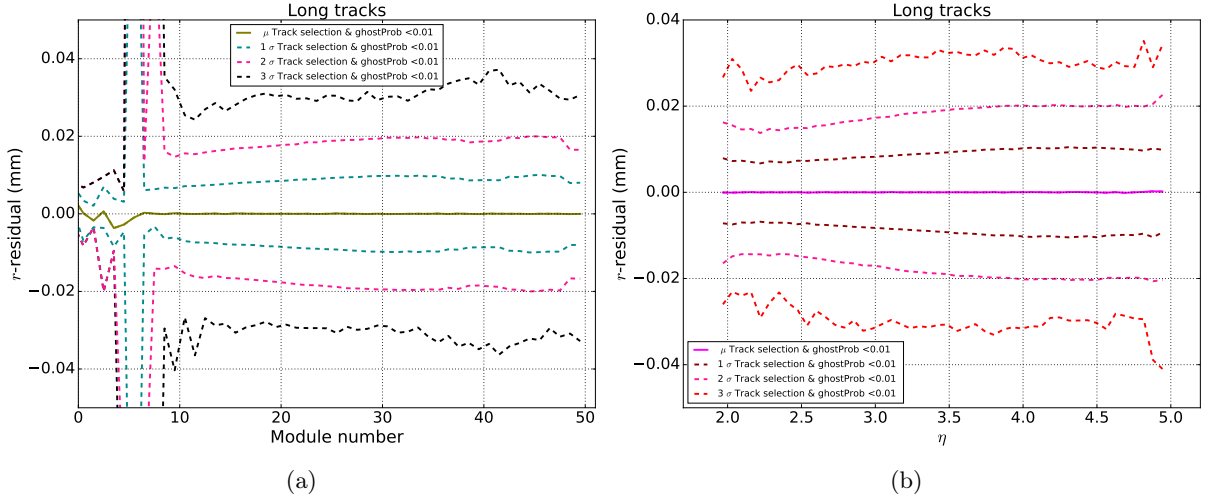


Figure 9: Long tracks mean r -residual as a function of module number (a) and η (b) with 1, 2 and 3 standard deviations (σ) indicated.

Figure 9 shows the mean residual as a function of Module number (a) and η angle (b). It can be seen in 9a that the mean residual is centered at zero but the resolution, indicated by the 1, 2 and 3 σ distributions varies with module number. The resolution is low in modules far away from the interaction point. The resolution of the silicon in the pixel detectors depends on the track angle which in turn depends on the module number. Also, as the modules are placed on varying distances from each other the detector geometry changes through-out the detector which also affects the resolution.

Figure 9b shows that the mean residual as a function of η -angle is centered at zero and the standard deviations indicate varying resolution for different η -values. The resolution depends on the projected angle (θ) which has a maximum value for low η values, hence the resolution is better for low η values and gets poorer for a higher η -value.

Below, residual distributions for modules 3 and 14 for backward tracks are shown. Backward track residuals without track selection is shown in green and the selected tracks are shown in pink. The residual distributions of tracks with applied cuts χ^2 per d.o.f. < 2 and *ghost probability* less than 0.01 are shown in black and blue respectively.

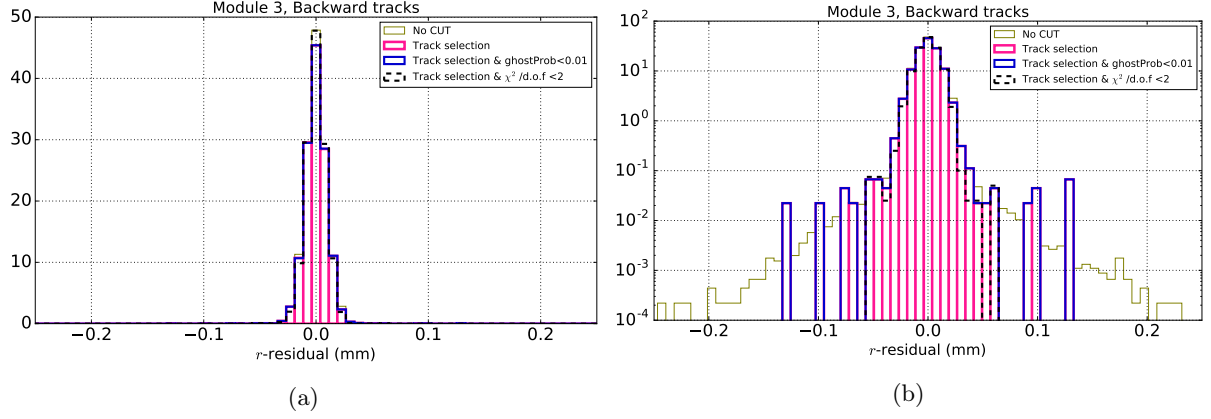


Figure 10: Backward tracks r -residual distribution Module 3 without and with log scale on the y-axis in *a* and *b* respectively

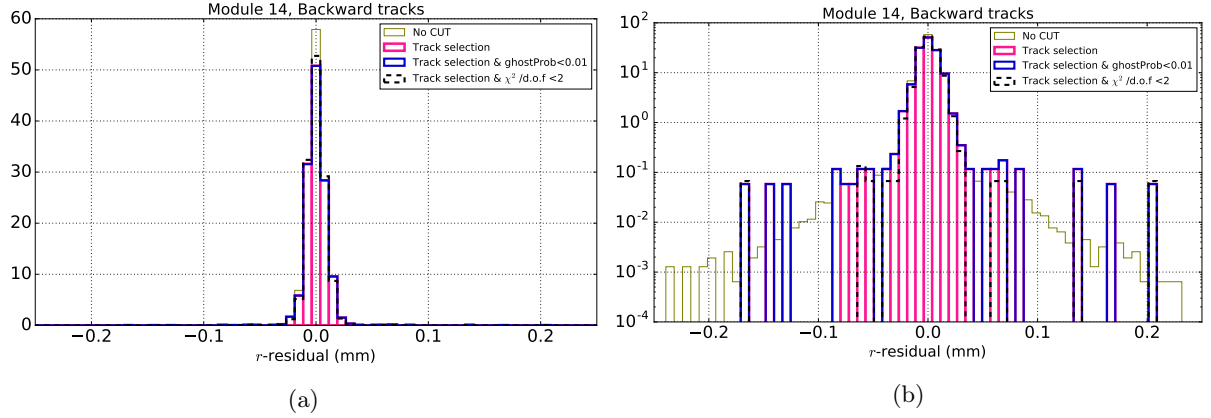


Figure 11: Backward tracks r -residual distribution Module 14 without and with log scale on the y-axis in *a* and *b* respectively

As seen in Figure 10b and 11b the ghost probability cut does not reduce the number of tracks contributing to the tail of the residual in the case of the backward tracks as effectively as in the case of long tracks. Here it shows that the two additional track cuts does not contribute much more than the initial track selection already has to cut of the residual distribution tails, as is also indicated by the cut on backward tracks in Table 1. All track selections here applied allows for the residual distribution form to stay the same an only the tail is cut off.

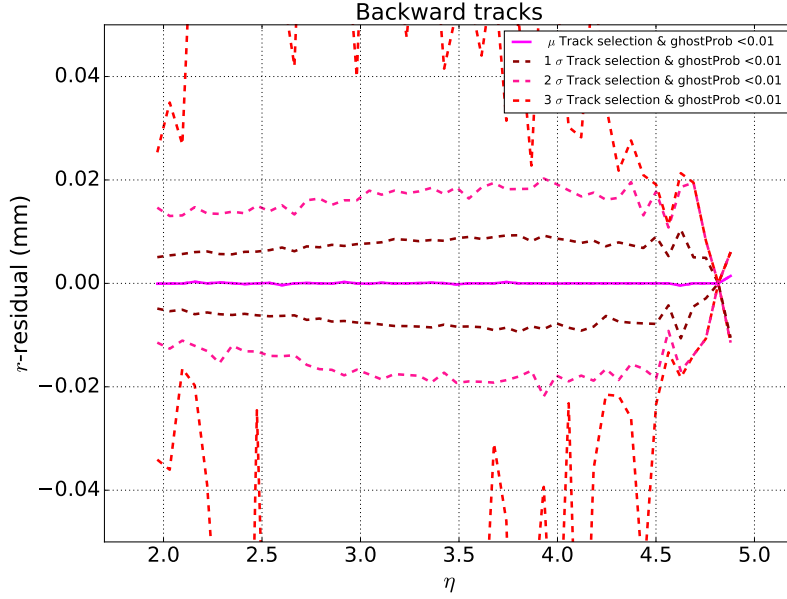


Figure 12: Backward tracks mean residual as a function of η with 1, 2 and 3 standard deviations (σ) indicated

The silicon detector resolution depends on the projected angle (θ), and as seen in Figure 12 the resolution is higher for low η -values but goes down with increasing η -values.

5.2 Large misalignment

Below, residual distributions for modules 29 and 44 for long tracks are shown in the case of a large misalignment as described in section 4. Module 29 is close to the interaction point whereas Module 44 is further away in the positive forward direction. Long track residuals without track selection are shown in grey and the selected tracks are shown in pink. The residual distributions of tracks with additional cuts χ^2 per d.o.f. < 2 and ghost probability less than 0.01 are shown in black and blue respectively.

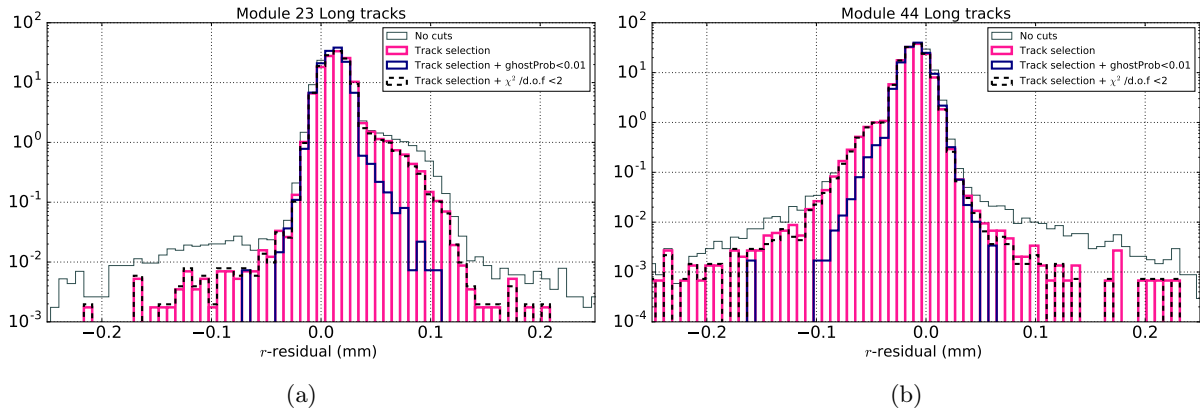


Figure 13: Long tracks r -residual distribution for Module 23 (a) and Module 44 (b) in the case of a large misalignment scenario with log scale on the y-axis

Below, residual distributions for modules 3 and 14 for backward tracks are shown in the case of a large misalignment scenario. Backward track residuals without track selection is shown in green and the selected tracks are shown in pink. The residual distributions of tracks with applied cuts χ^2 per d.o.f. < 2 and ghost probability less than 0.01 are shown in black and blue respectively.

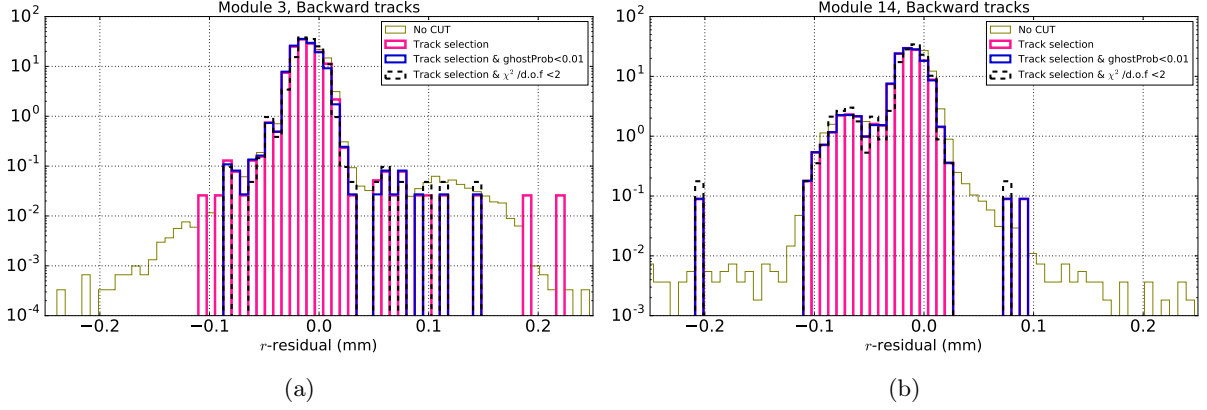


Figure 14: Backward tracks r -residual distribution for Module 3 (a) and Module 14 (b) in the case of a large misalignment scenario with log scale on the y-axis.

As expected the residual distributions seen in Figure 13 and 14 are broadened due to the large misalignment.

6 Conclusions

It has been shown that there are some unphysical tracks in the tails of the residual distributions, which the standard track selection does not reduce sufficiently in the case of long tracks. The contribution of non-physical tracks could cause the alignment procedure to be a sub-optimal alignment. On the other hand, a tighter selection should be avoided in the case of large misalignment that degrades the quality of the tracks a lot, as shown by the non gaussian residual distribution with very large tail.

It has been shown that by introducing a cut on the *ghost probability* and on the χ^2 per d.o.f. the number of unphysical tracks can be removed which potentially improves the alignment quality. To investigate further one could in the future look at the alignment performance with and without the track cuts here suggested on data generated with random misaligned scenarios.

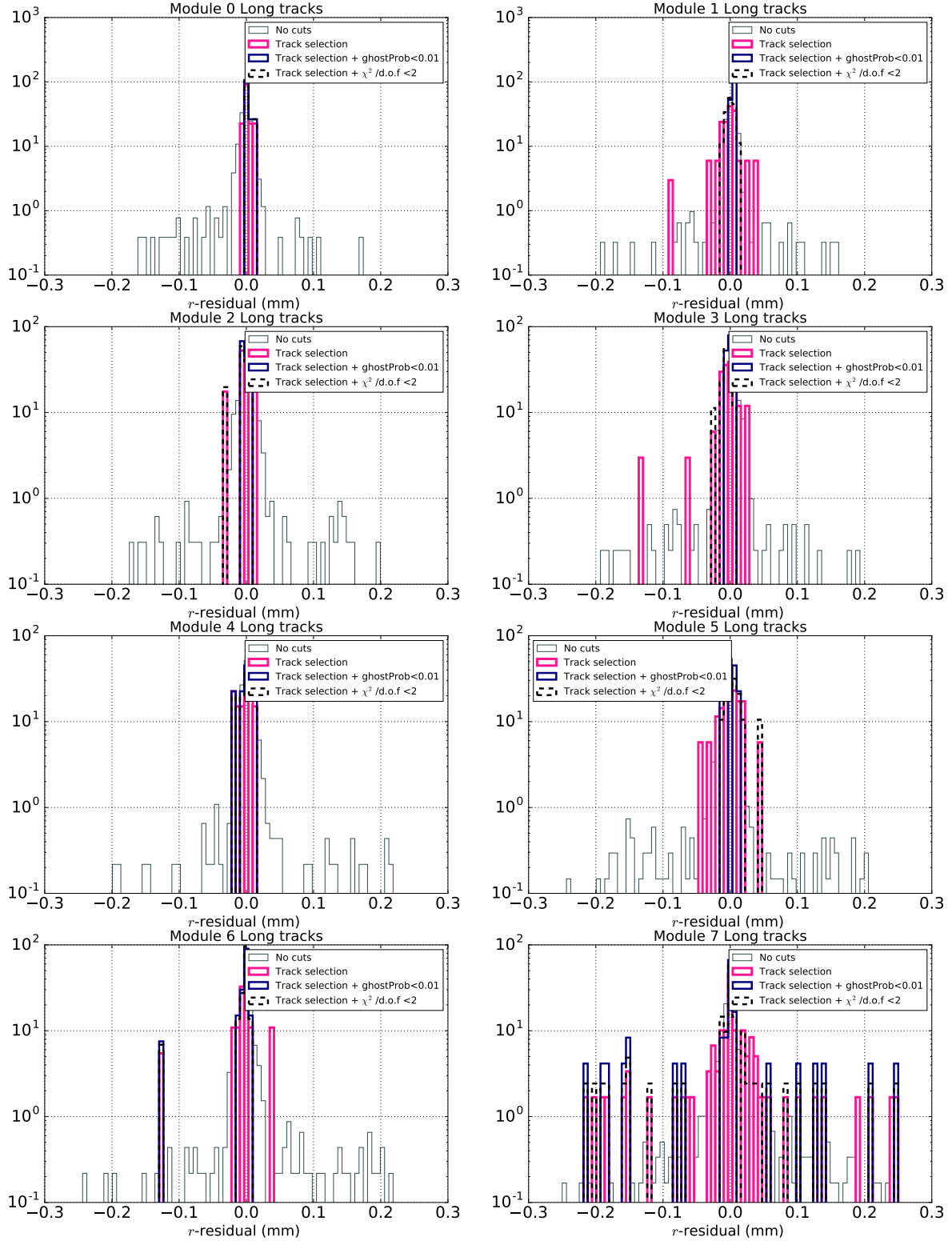
References

- [1] LHCb VELO Upgrade Technical Design Report; 2013-2017.
- [2] Viret S. Alignment strategy for the LHCb vertex locator; 2007.
- [3] Dujany G. Real-time alignment of the LHCb vertex detector and observation of charmless baryonic decays $B_c^0 \rightarrow p \bar{p} h^+ h^-$; 2017.
- [4] Perieanu A. Identification of Ghost Tracks using Neural Networks; 2007.

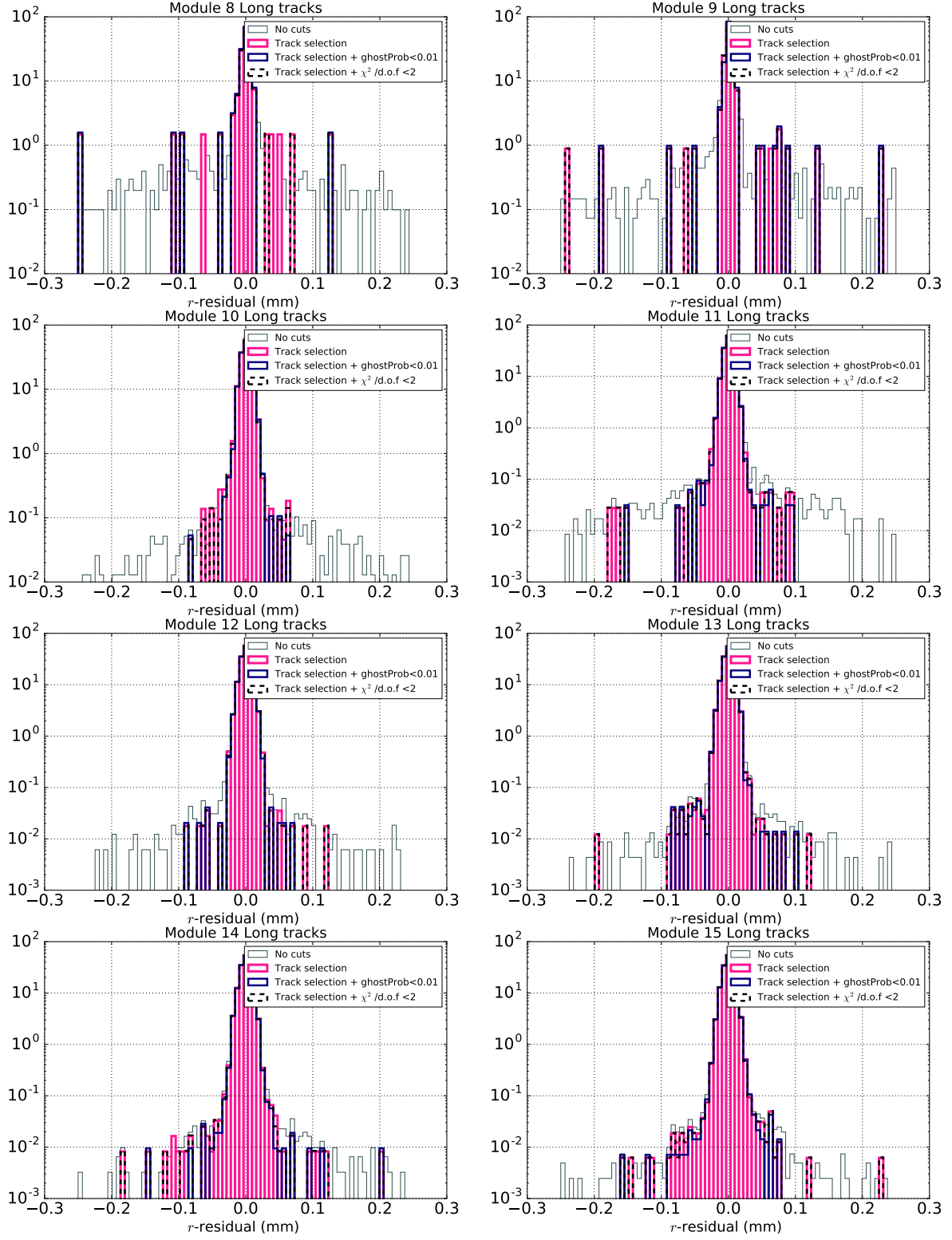
7 Appendix

No misalignment r -residual distributions

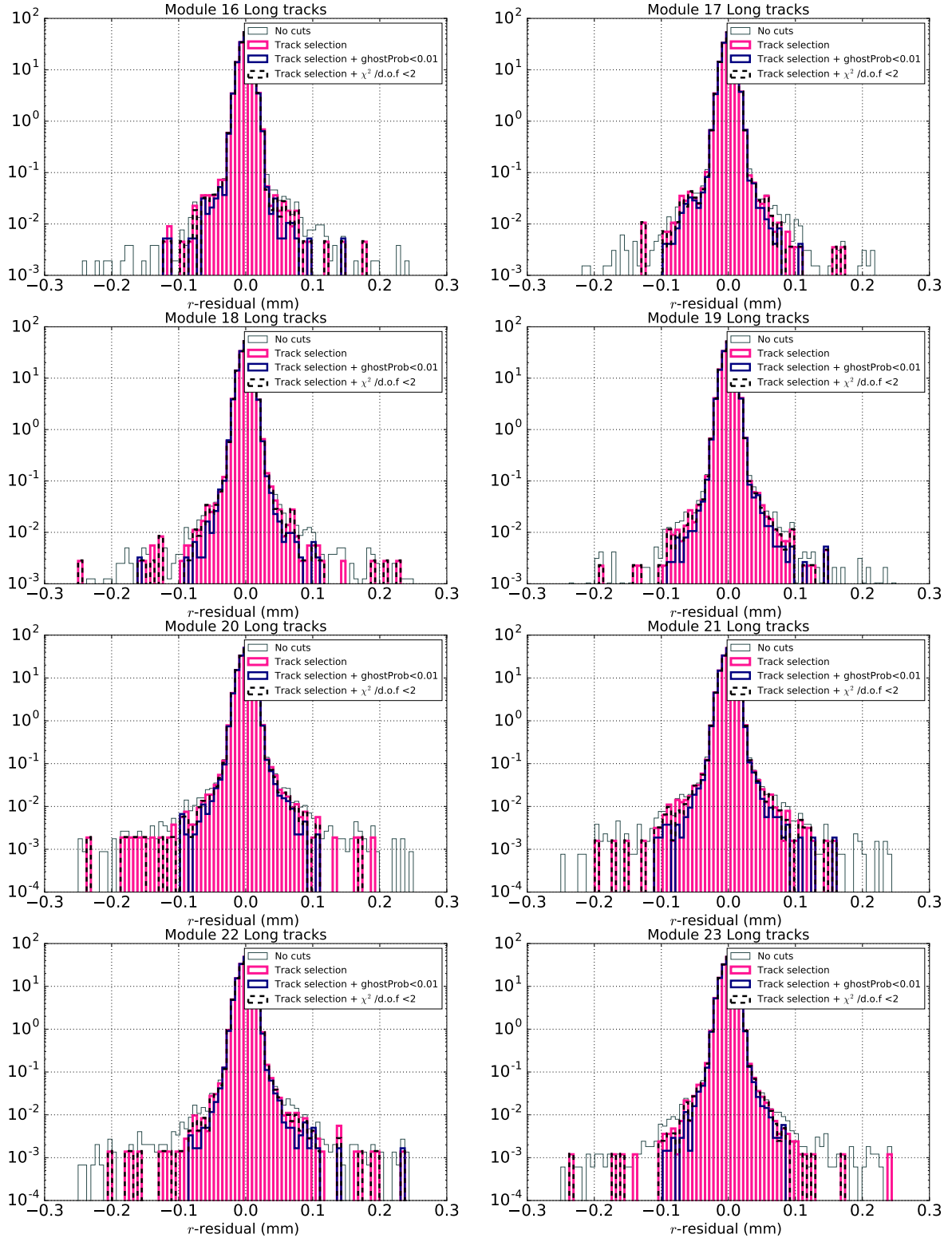
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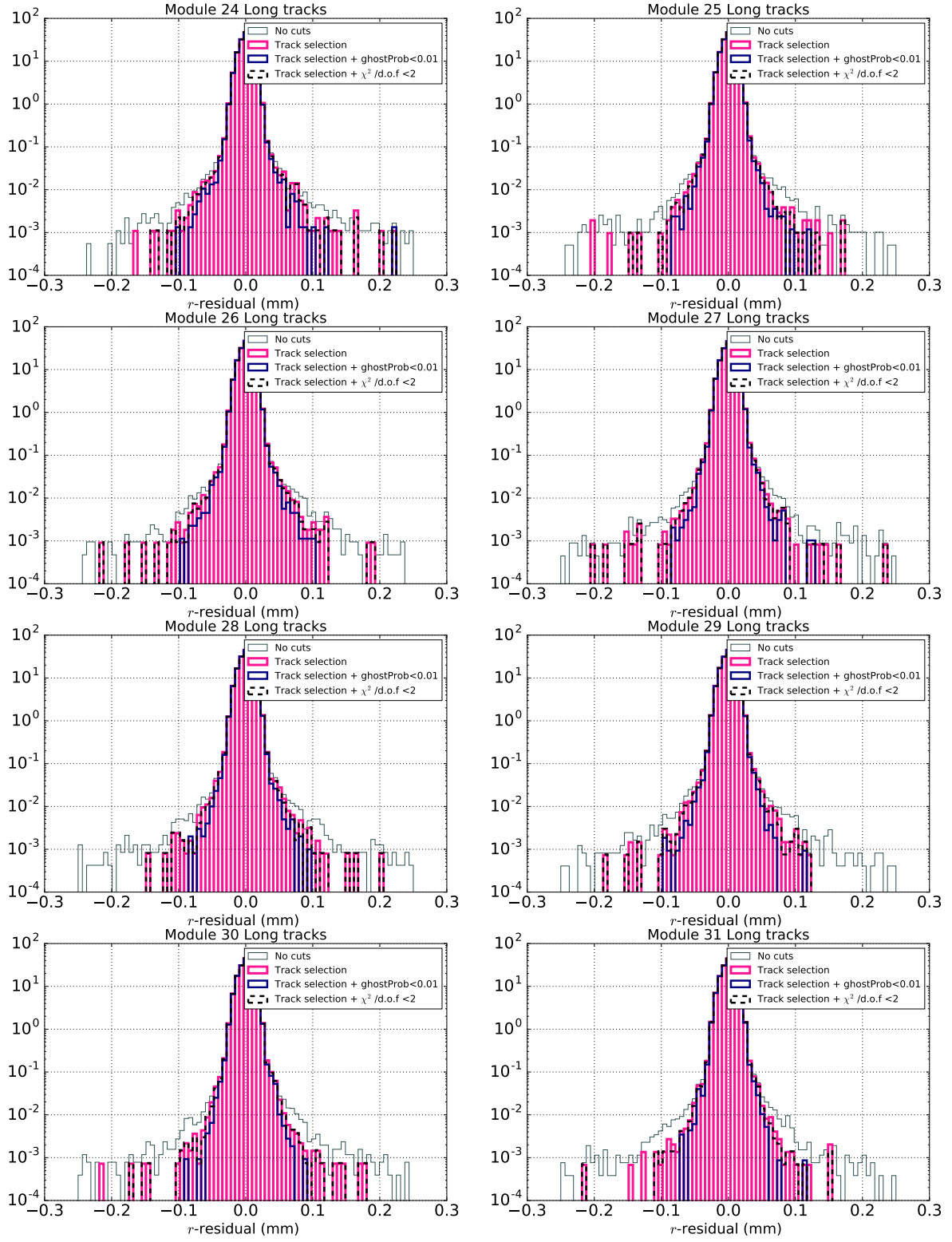
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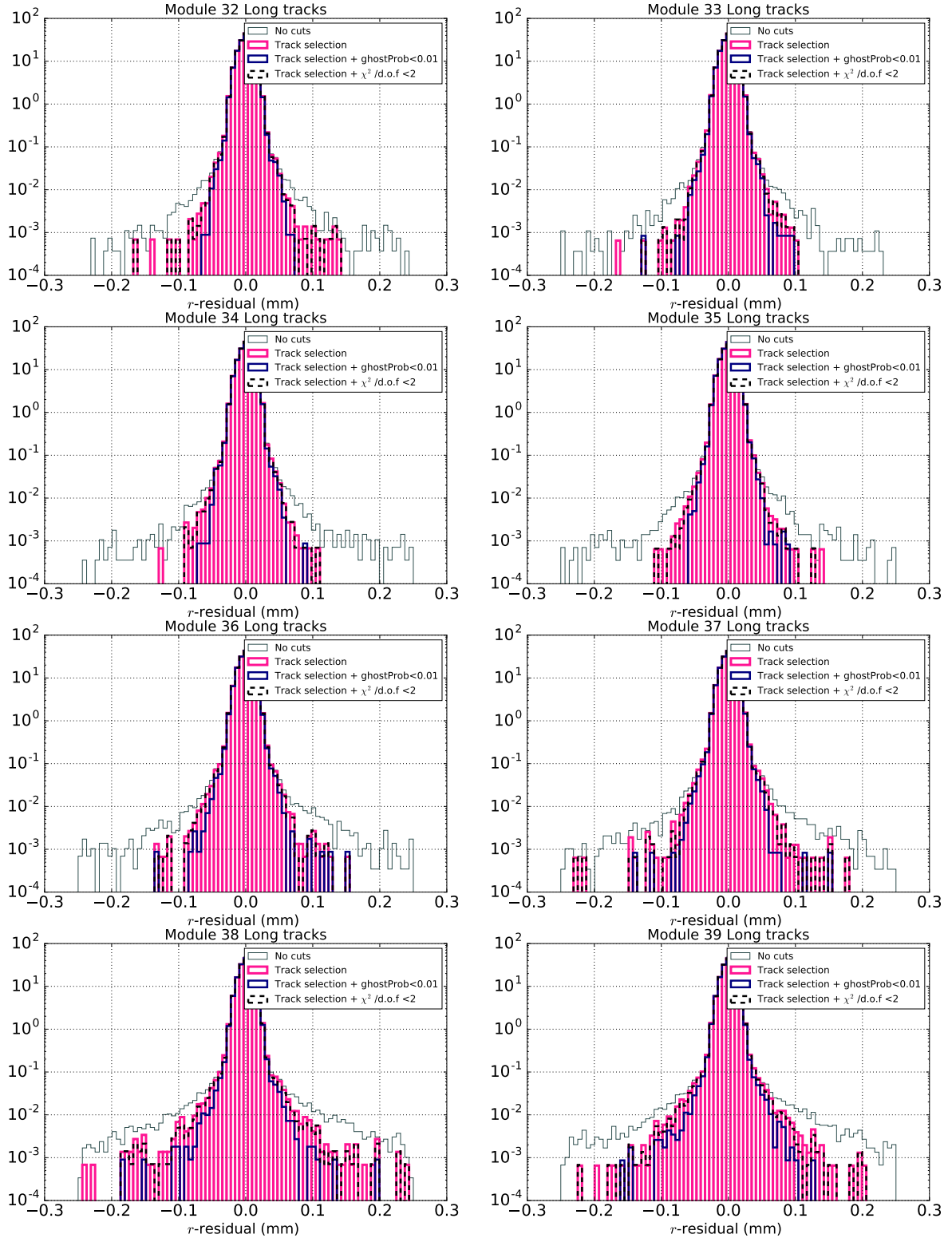
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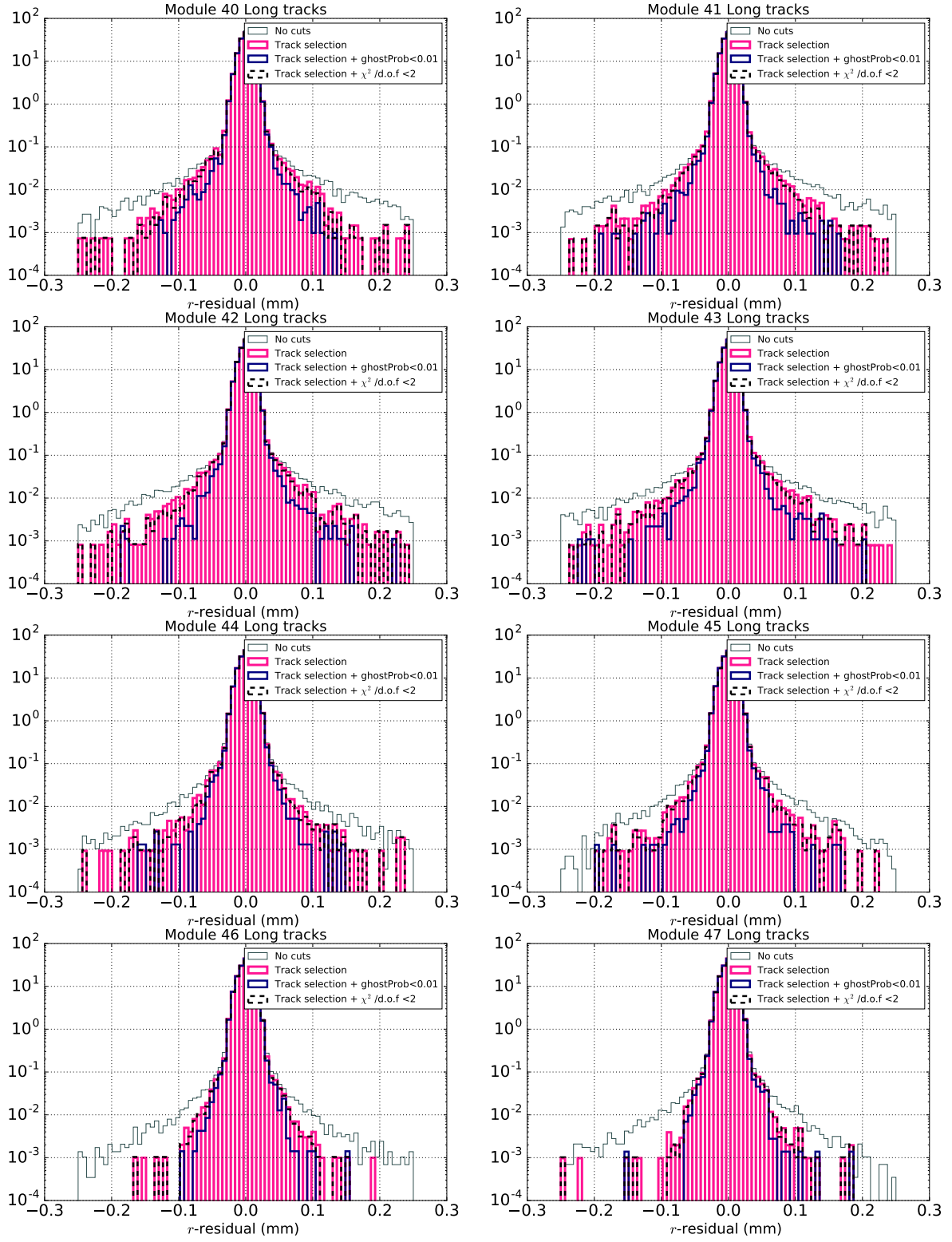
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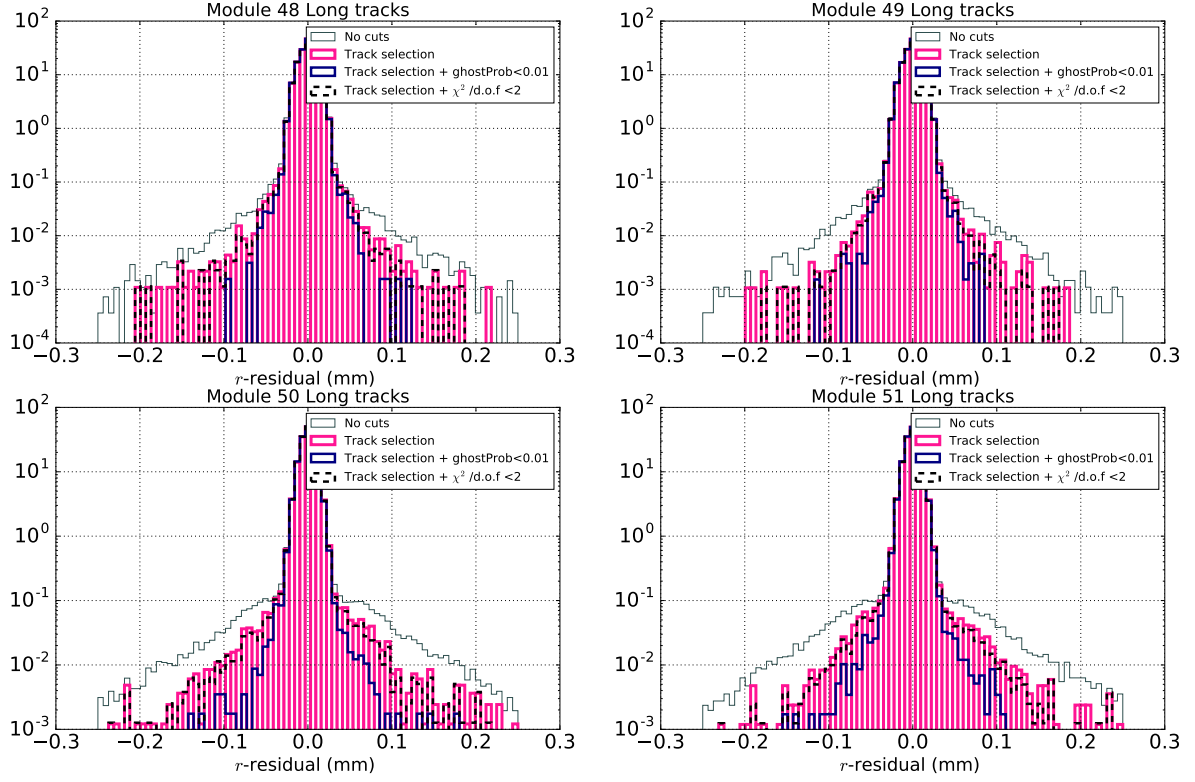
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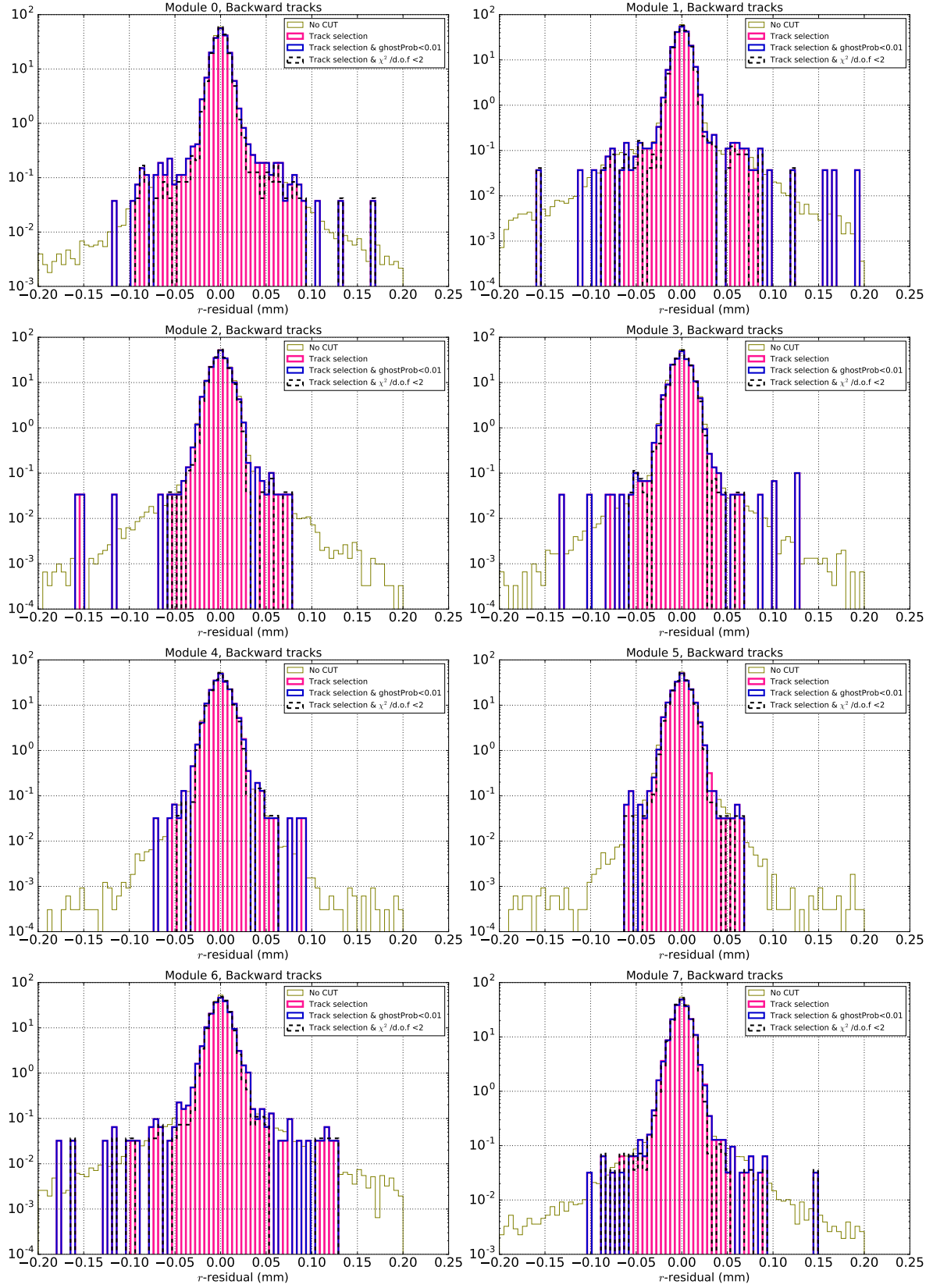
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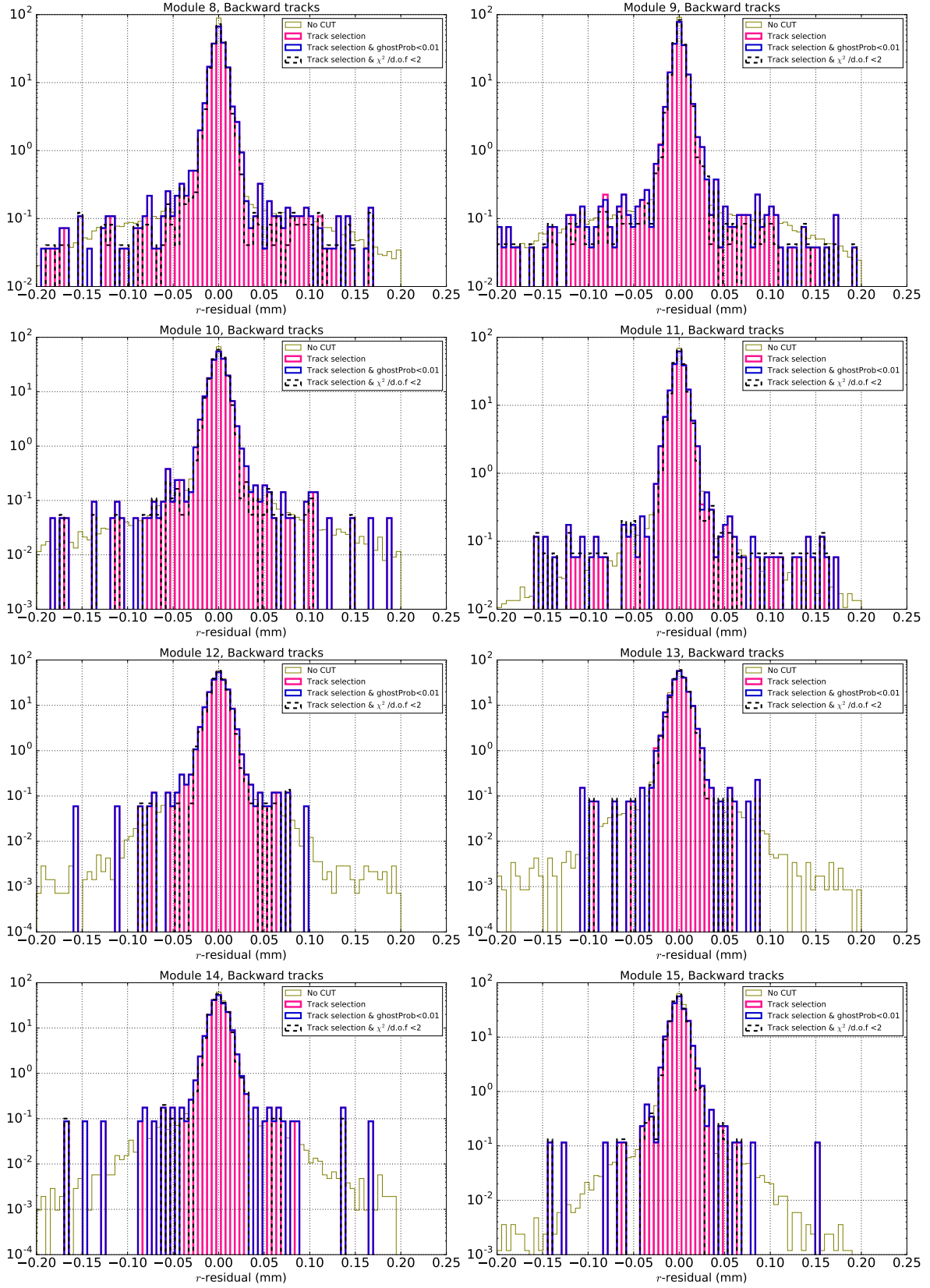
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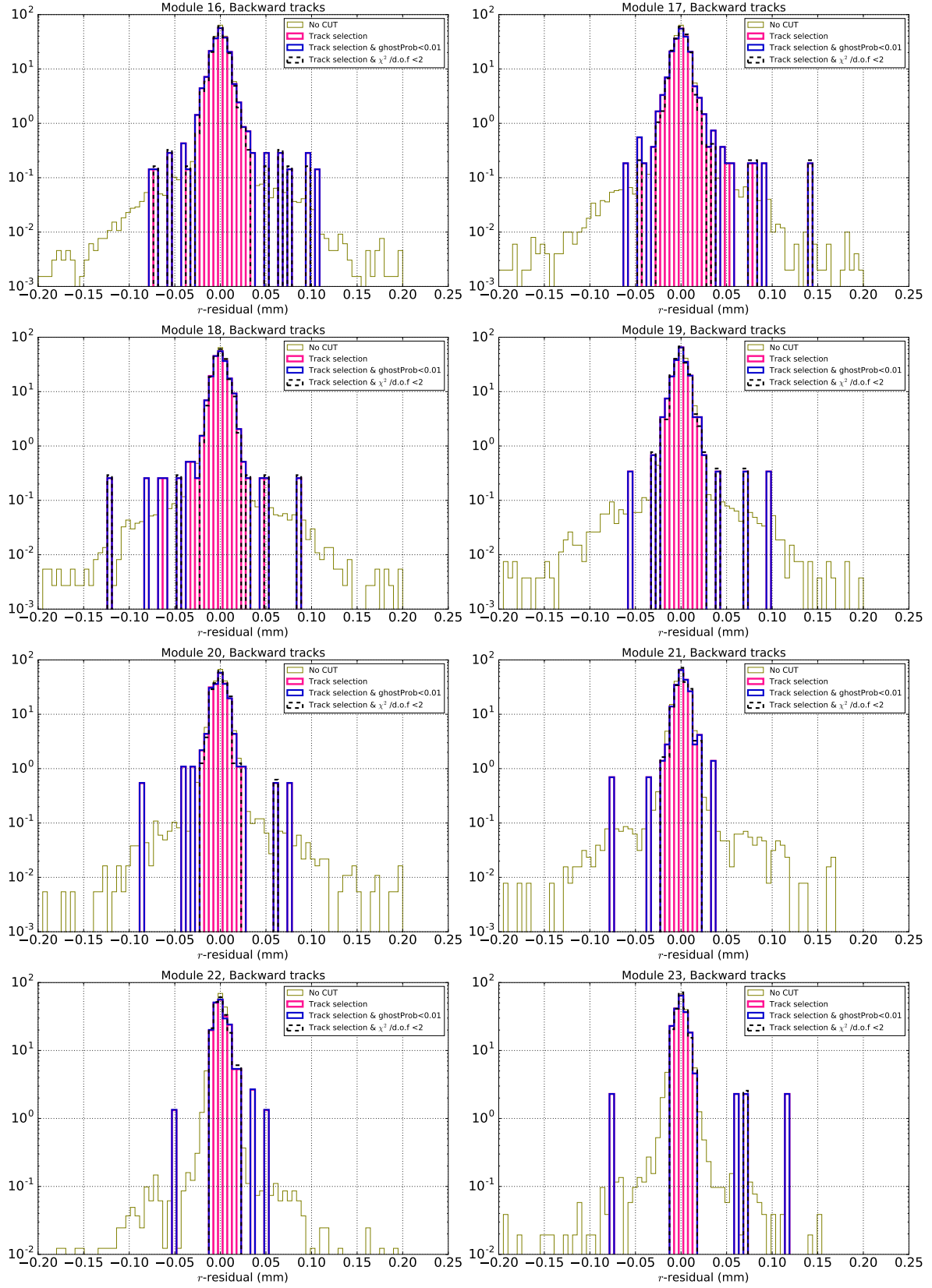
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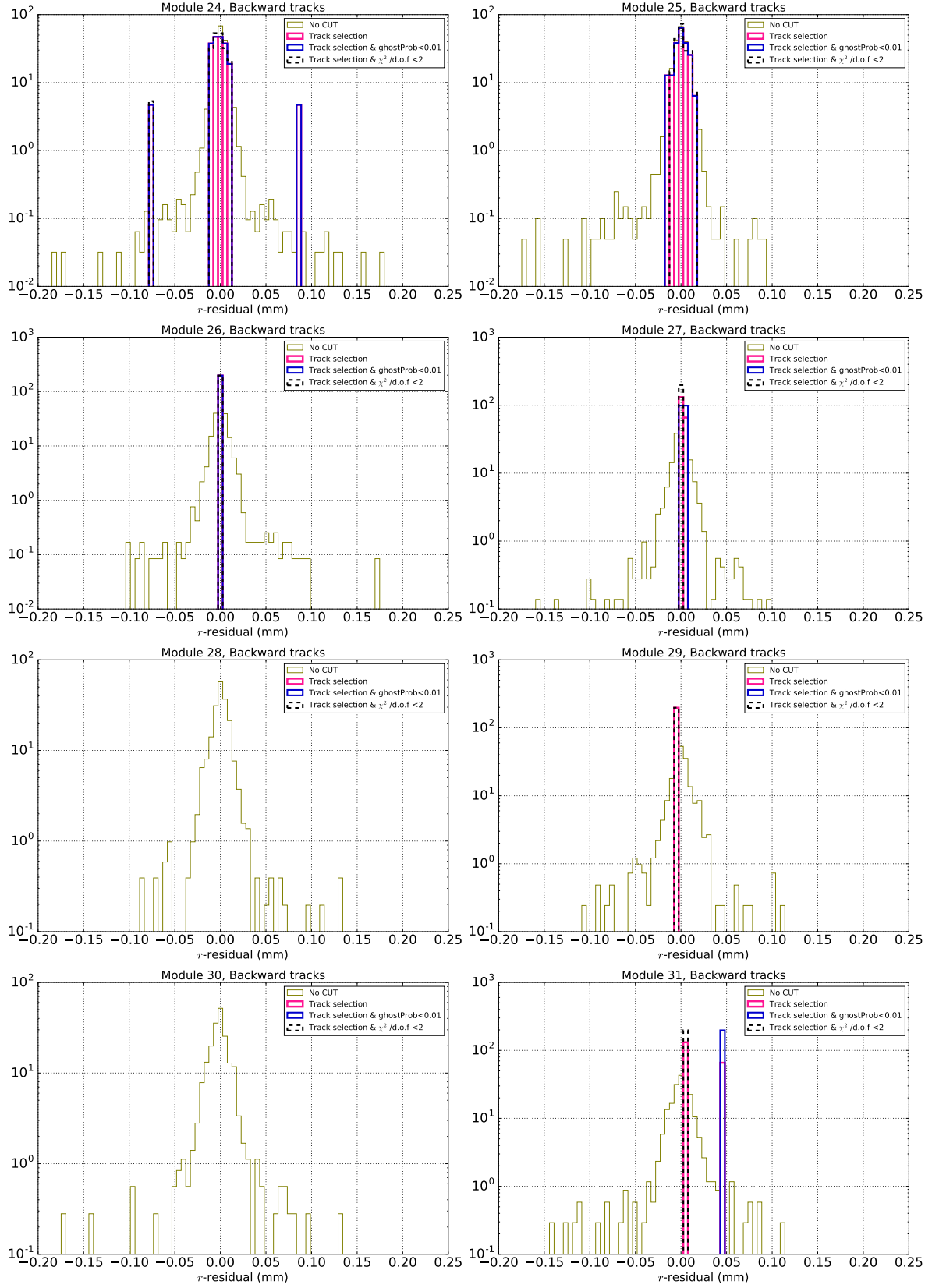
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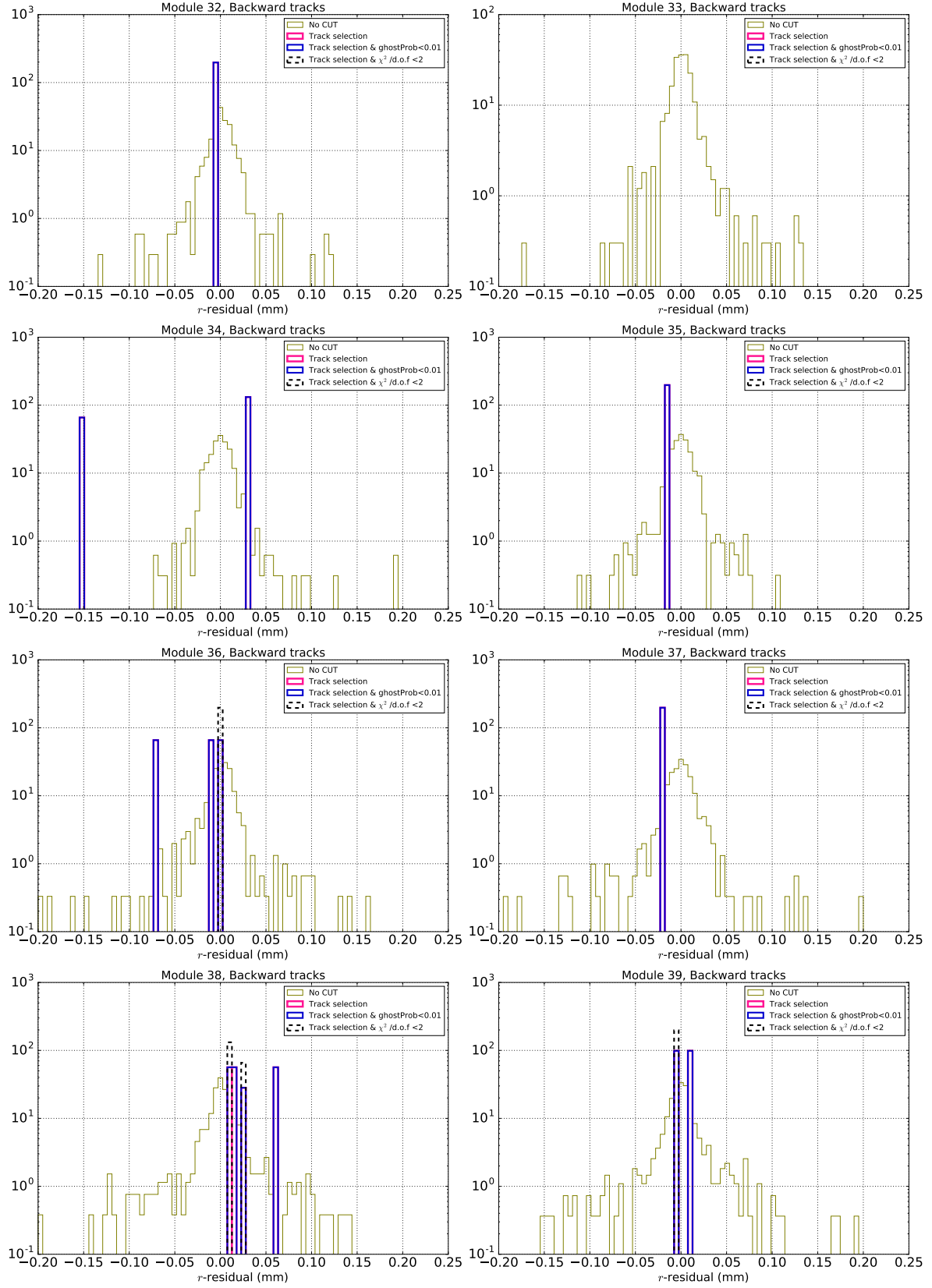
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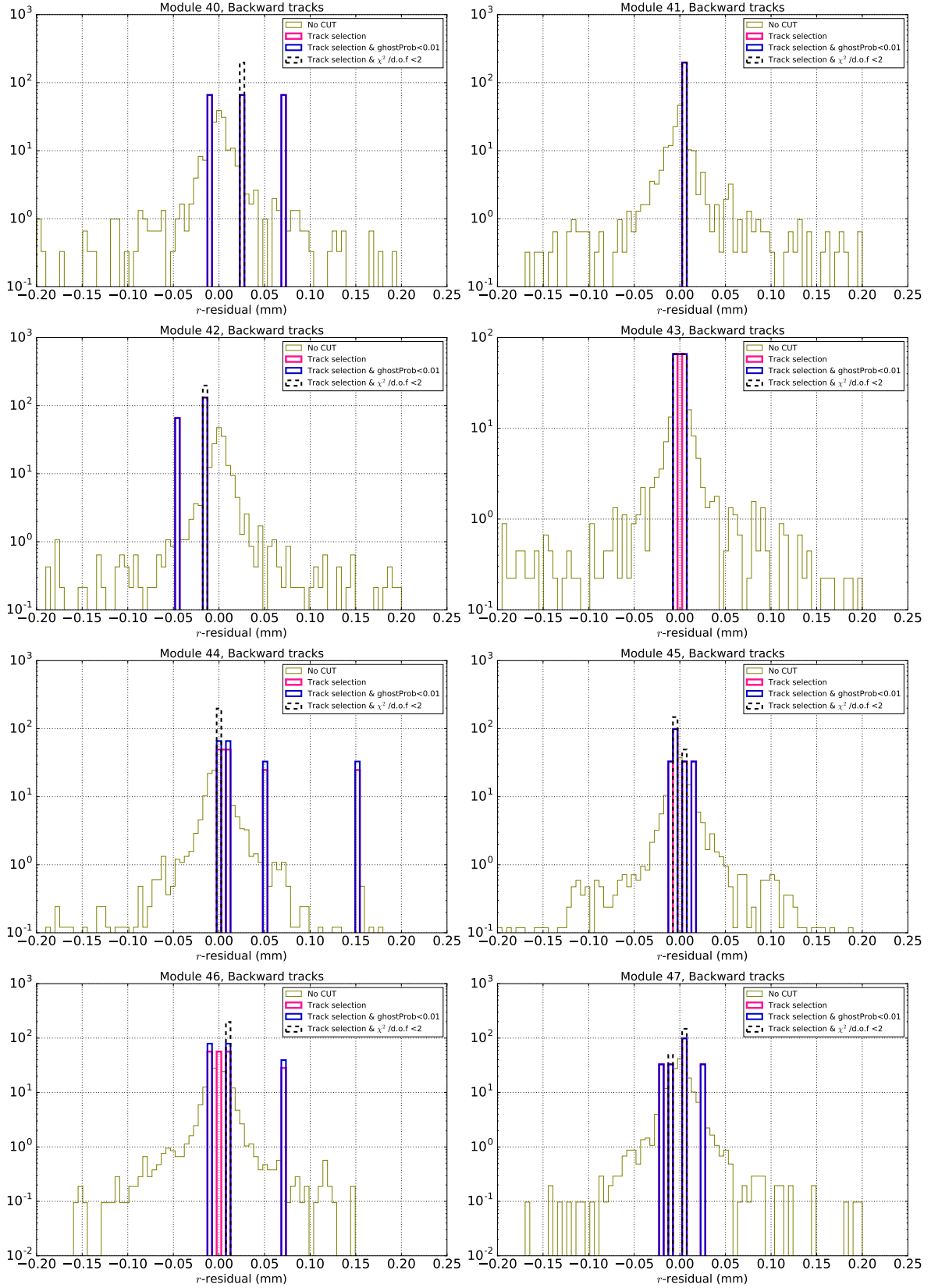
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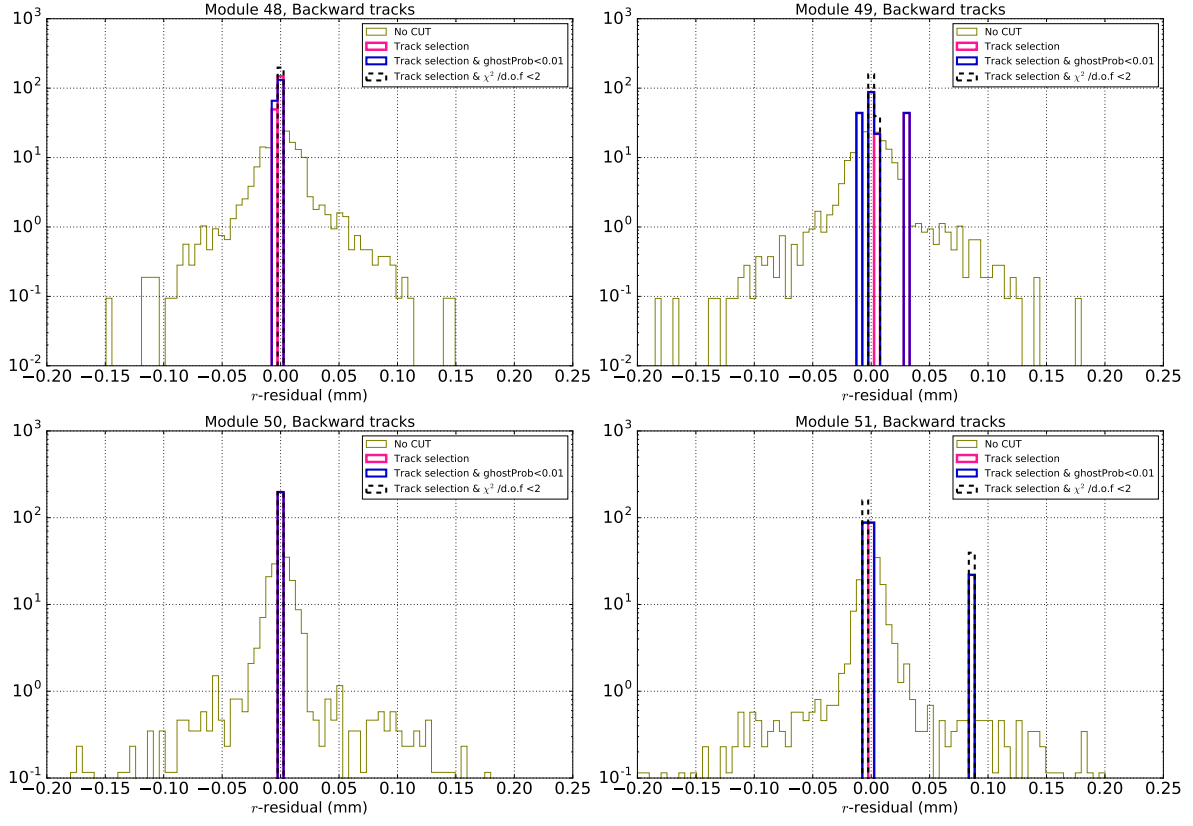
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Backward tracks r -residual distributions no misalignment, Modules 40 to 47:

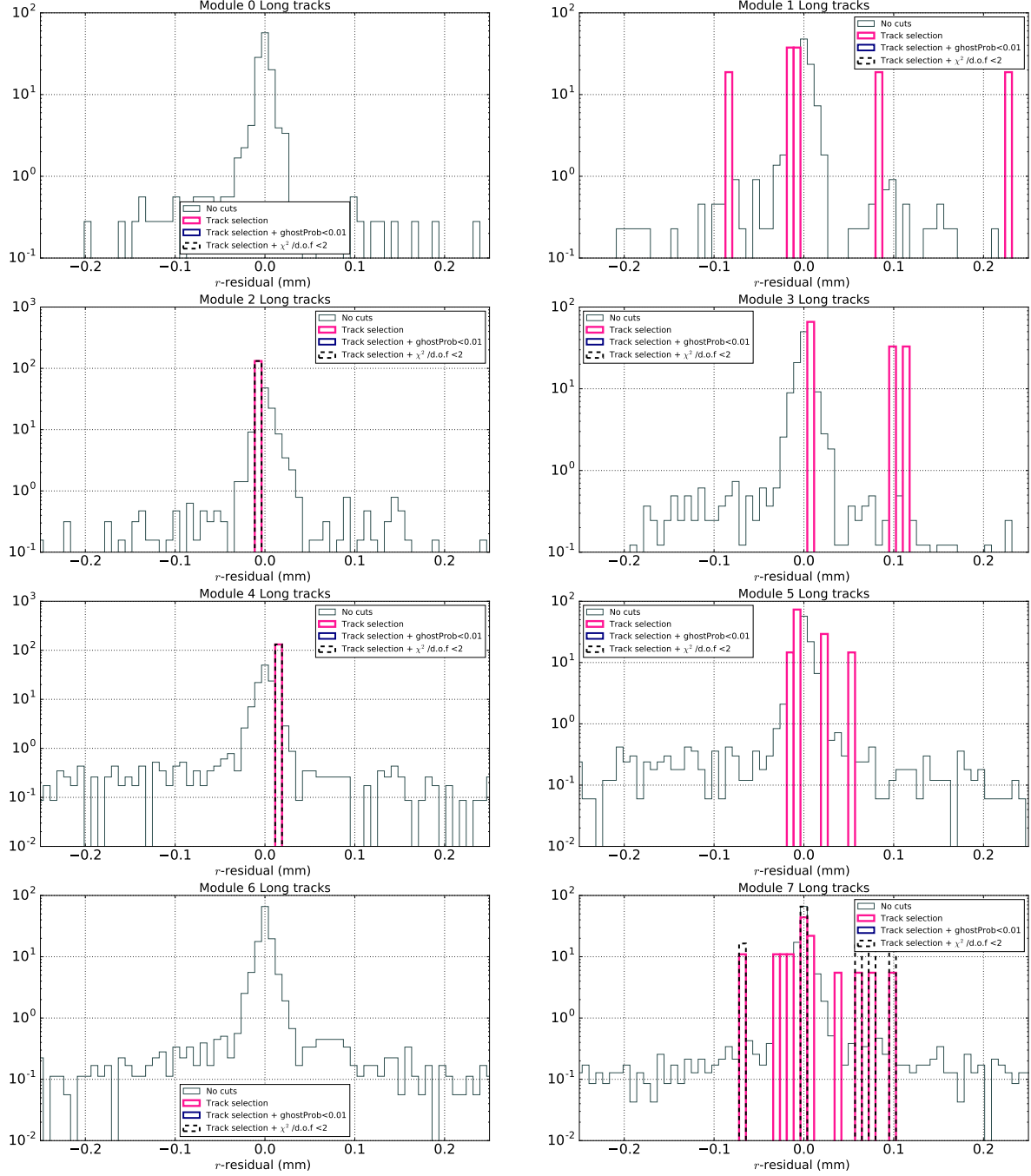


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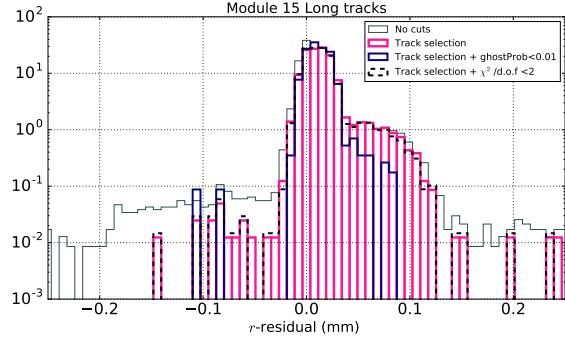
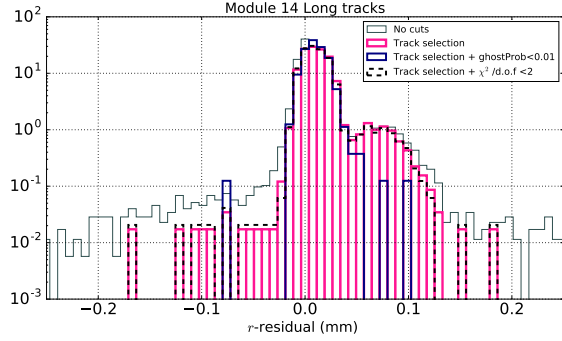
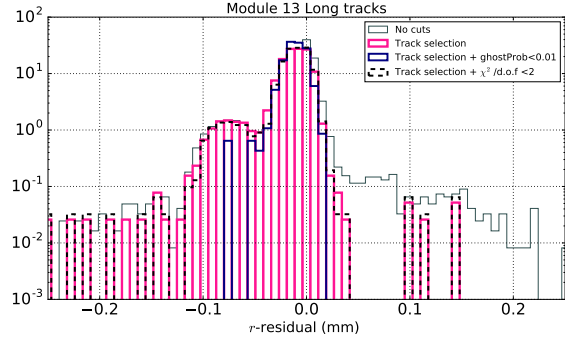
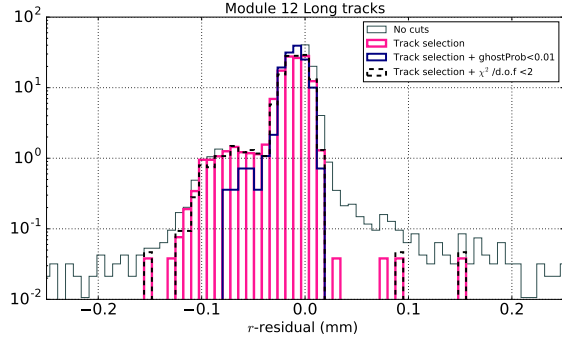
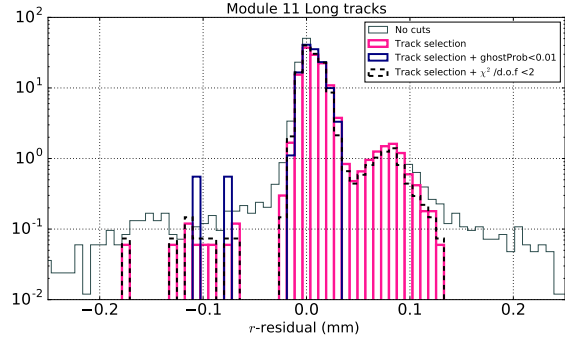
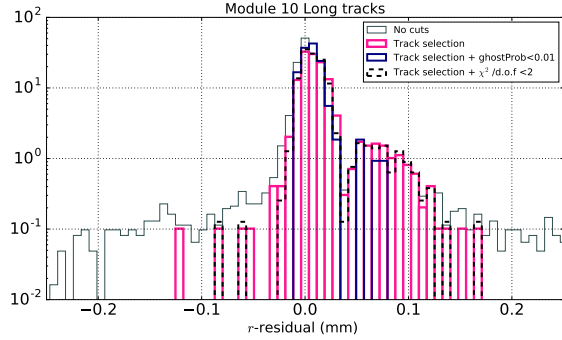
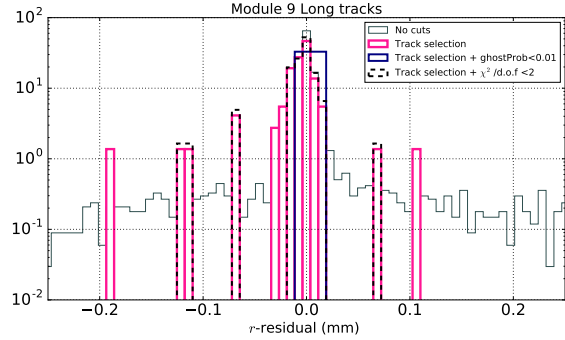
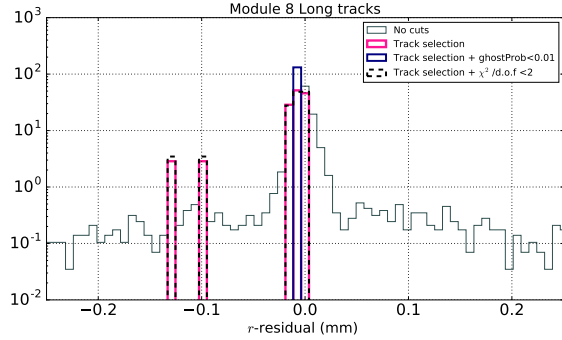


Large misalignment r -residual distributions

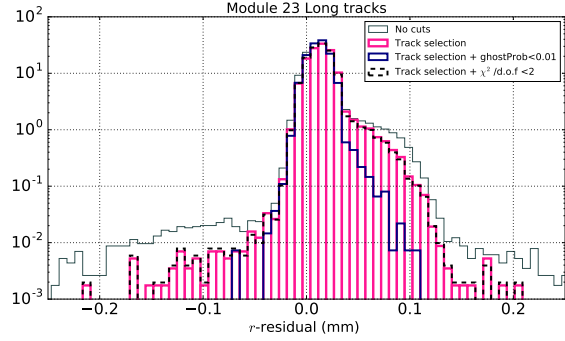
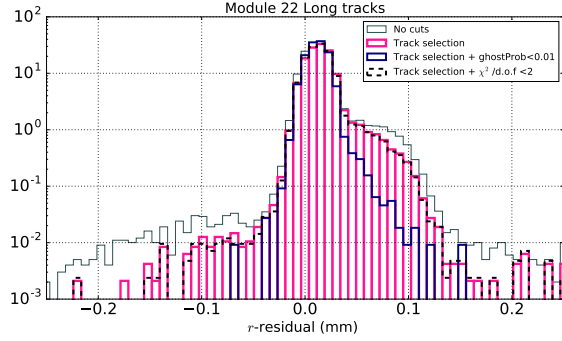
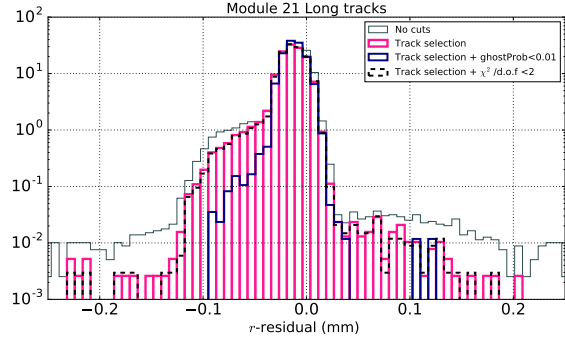
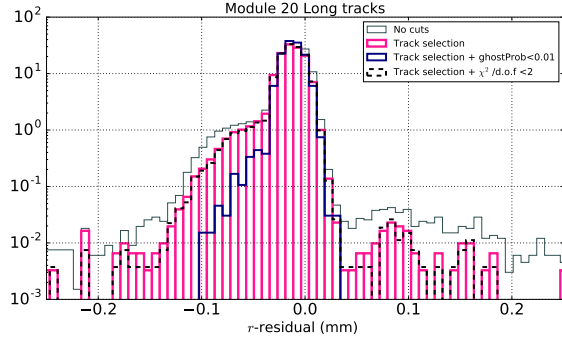
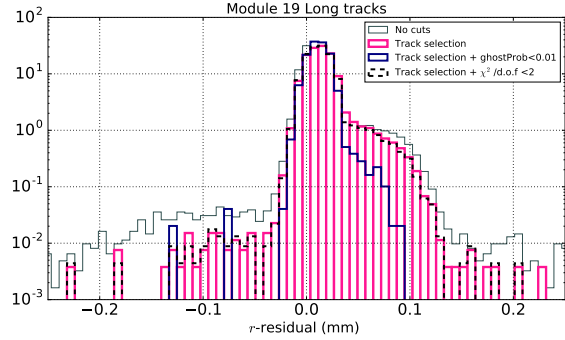
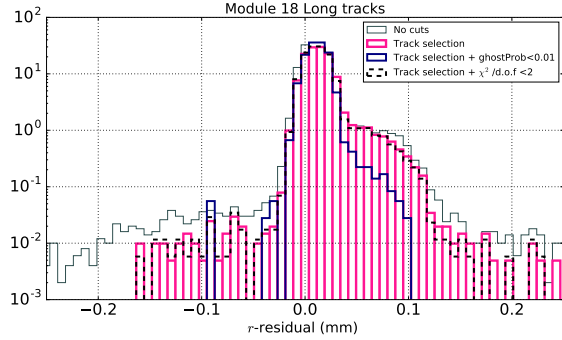
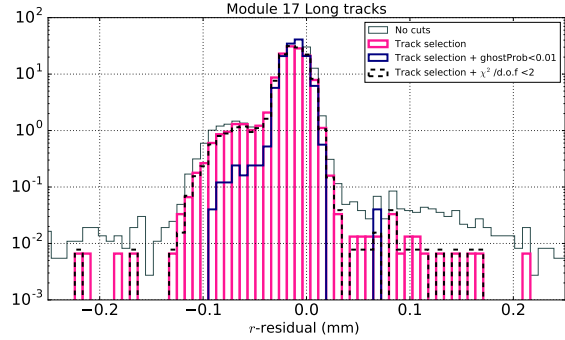
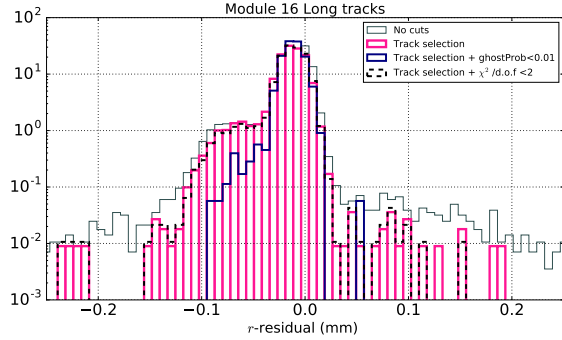
Long tracks r -residual distributions large misalignment,
Modules 0 to 7:



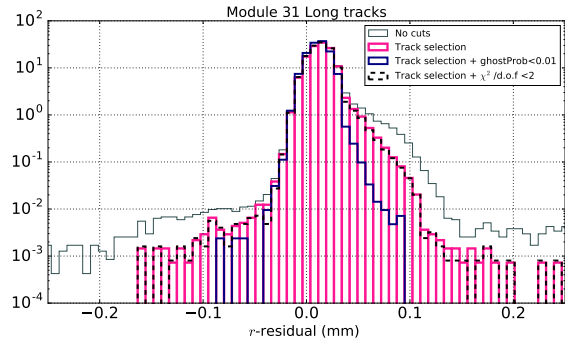
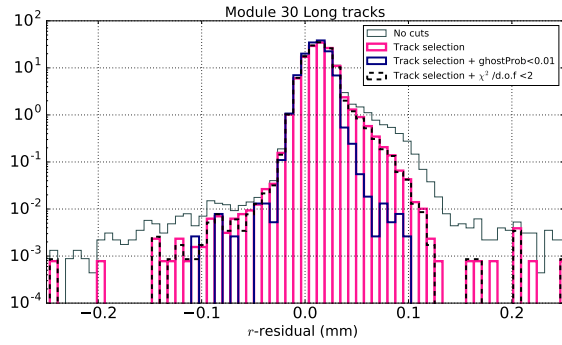
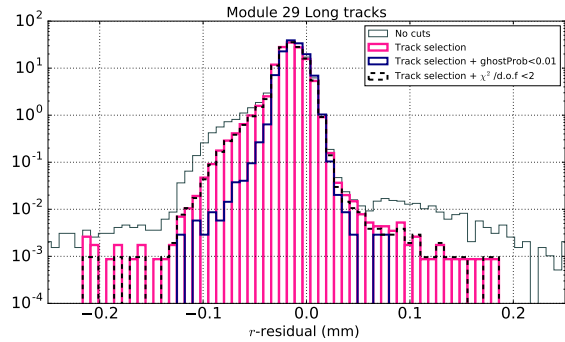
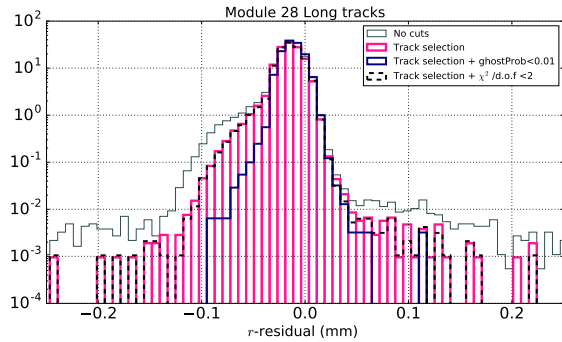
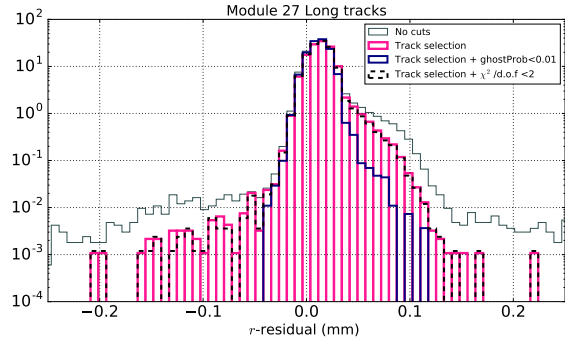
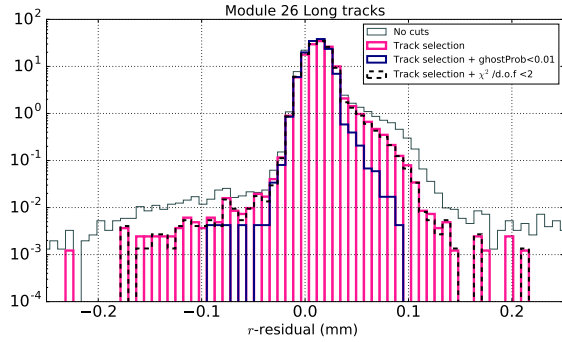
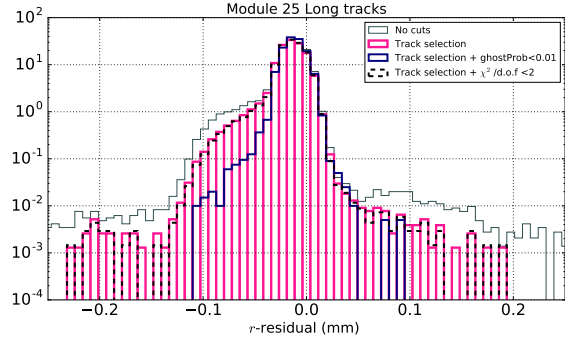
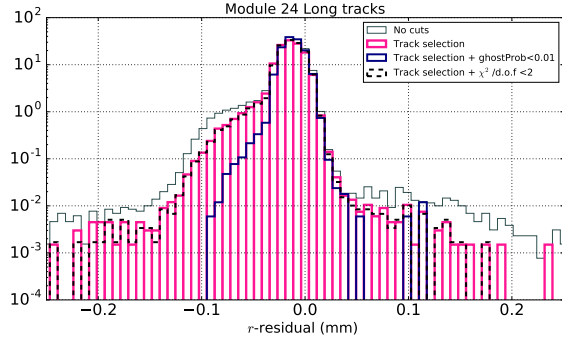
Long tracks r -residual distributions large misalignment, Modules 8 to 15:



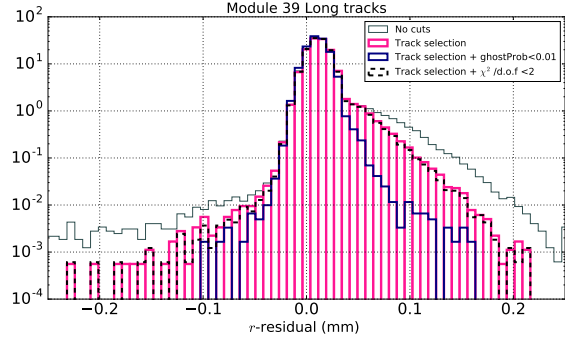
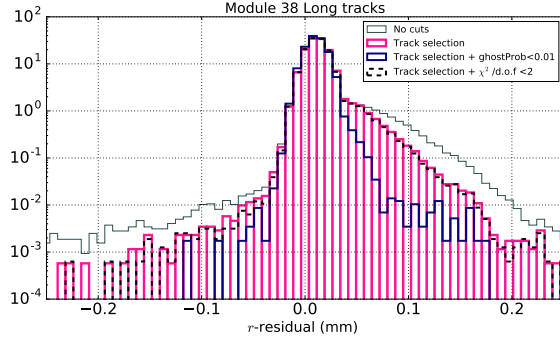
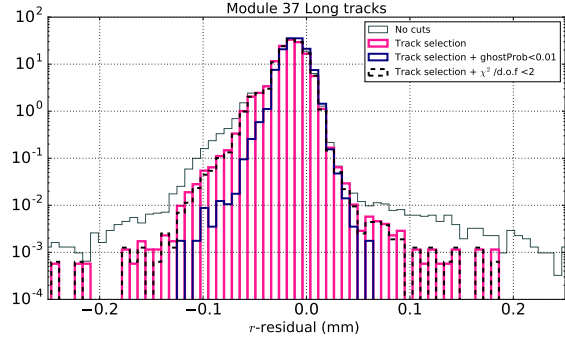
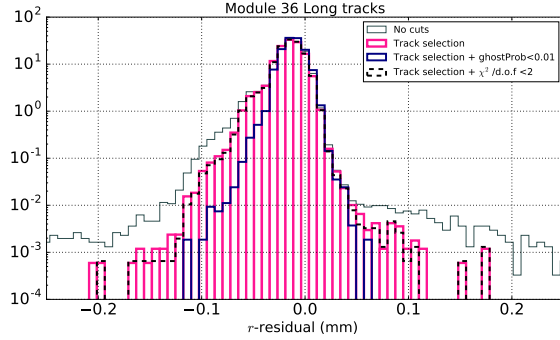
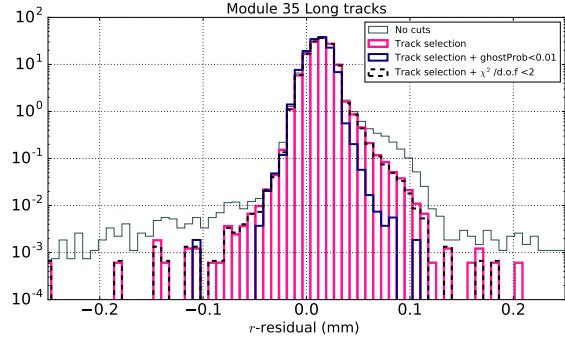
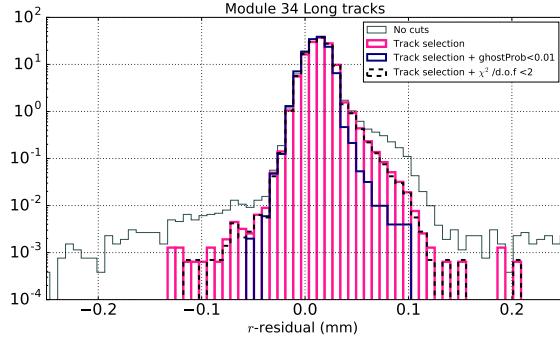
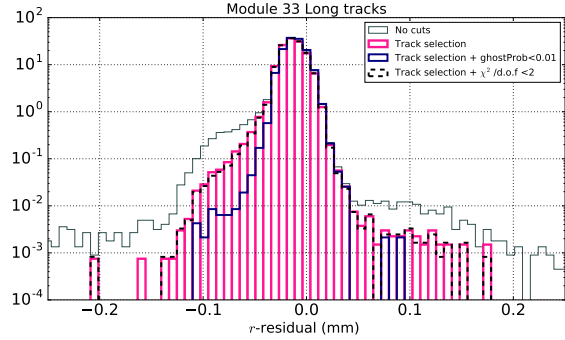
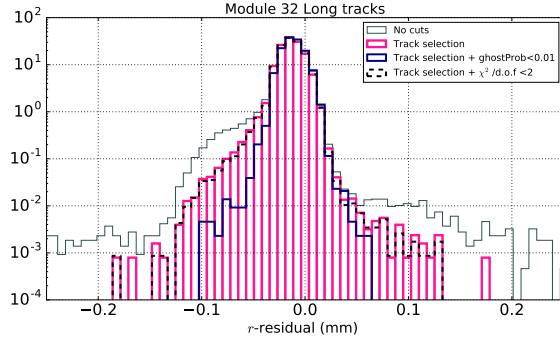
Long tracks r -residual distributions large misalignment, Modules 16 to 23:



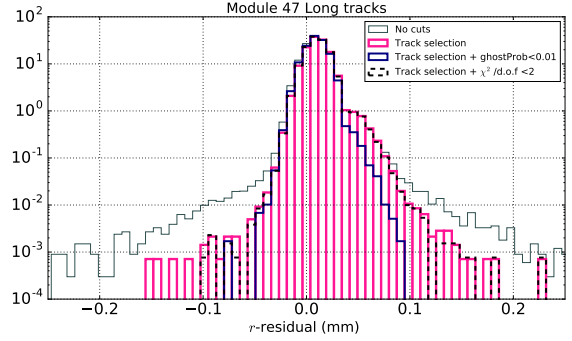
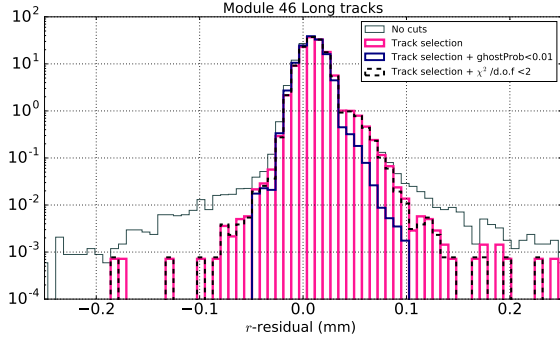
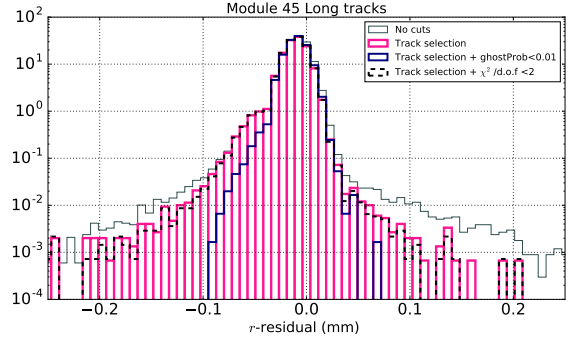
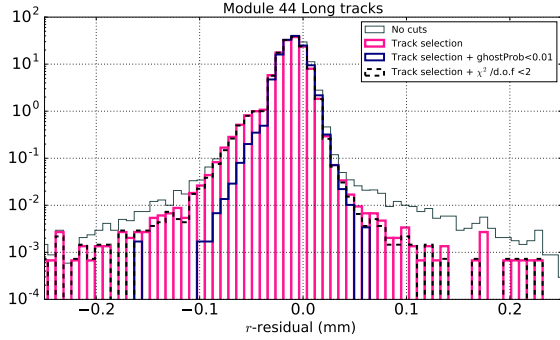
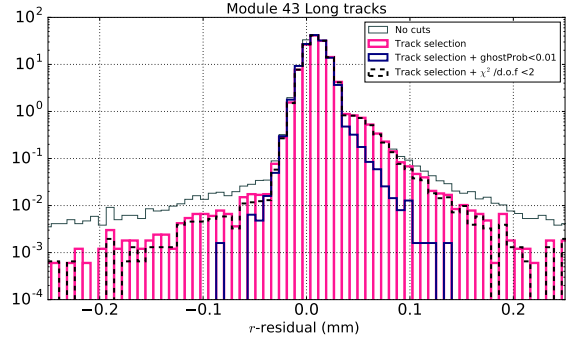
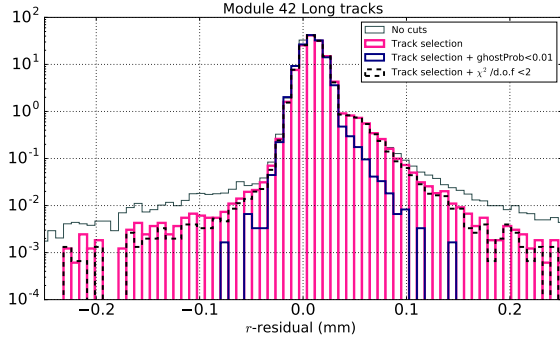
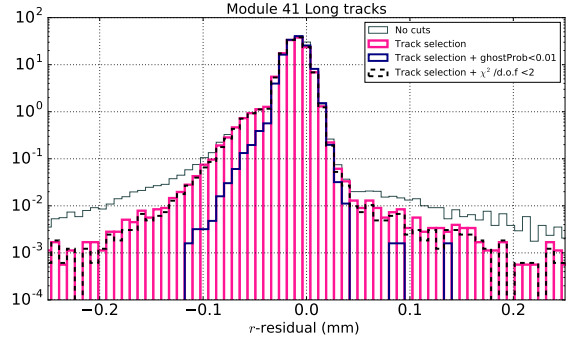
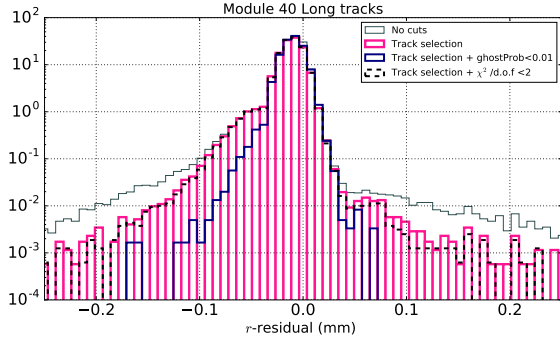
Long tracks r -residual distributions large misalignment, Modules 24 to 31:



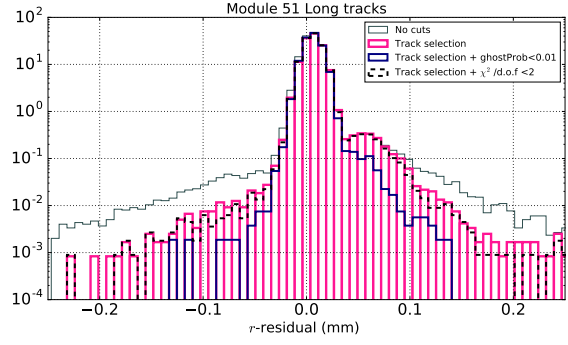
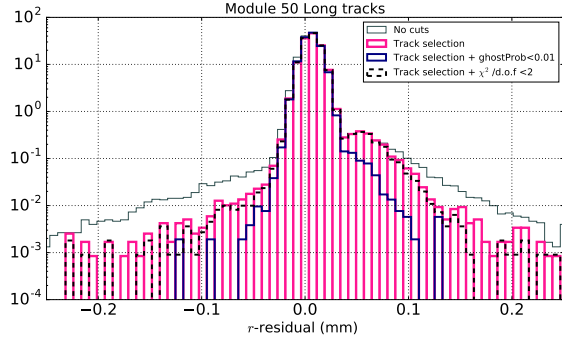
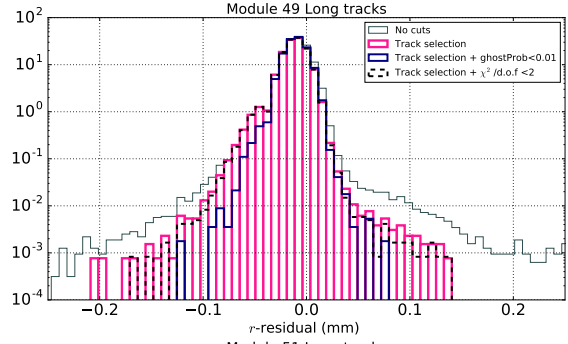
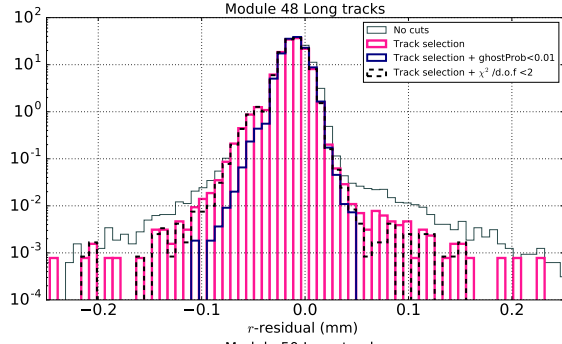
Long tracks r -residual distributions large misalignment, Modules 32 to 39:



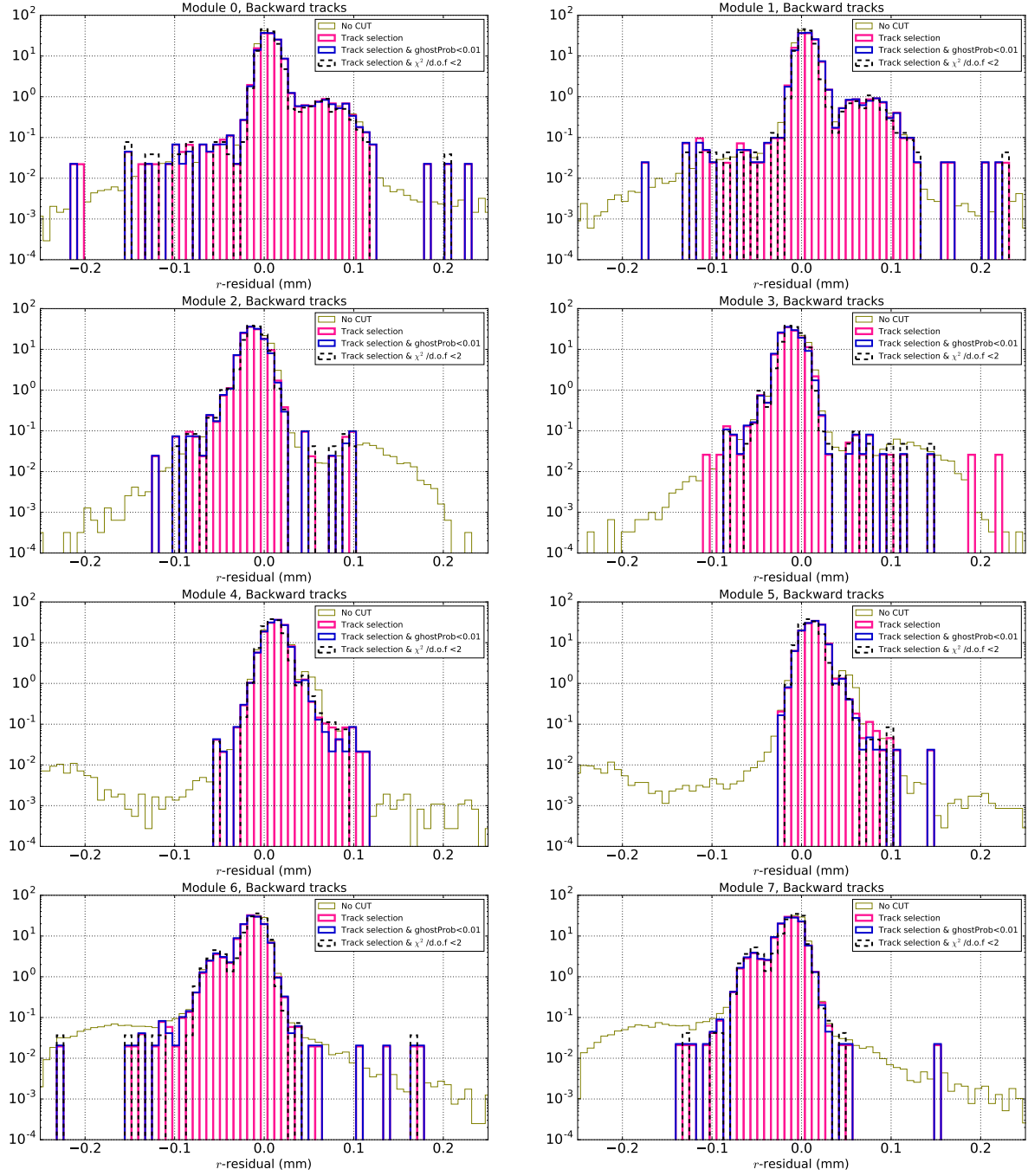
Long tracks r -residual distributions large misalignment, Modules 40 to 47:



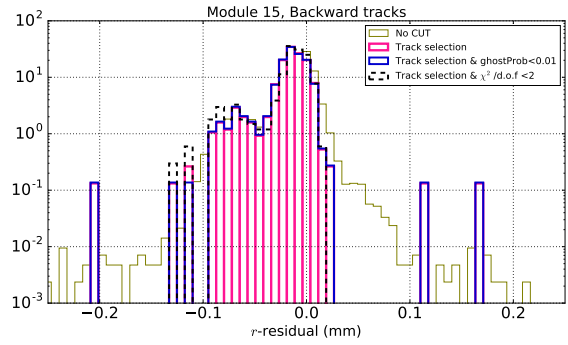
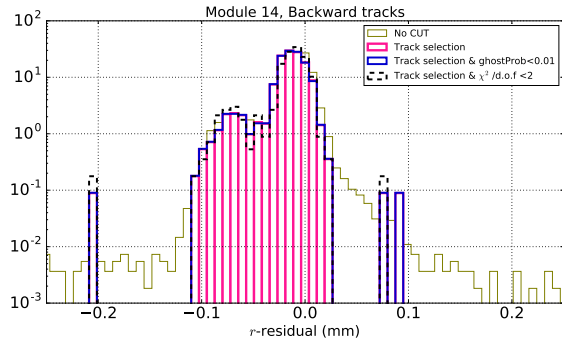
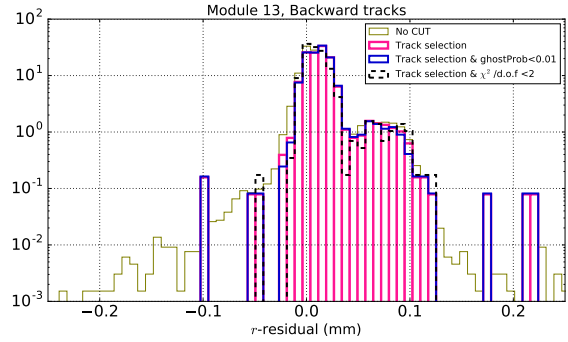
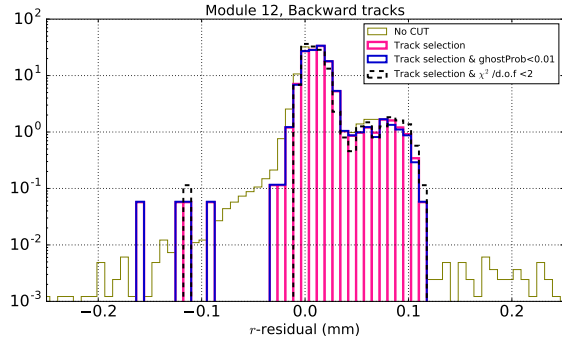
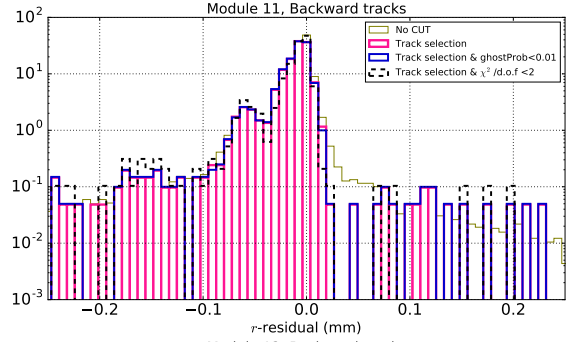
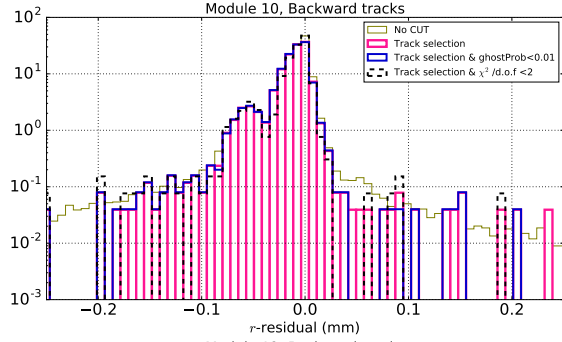
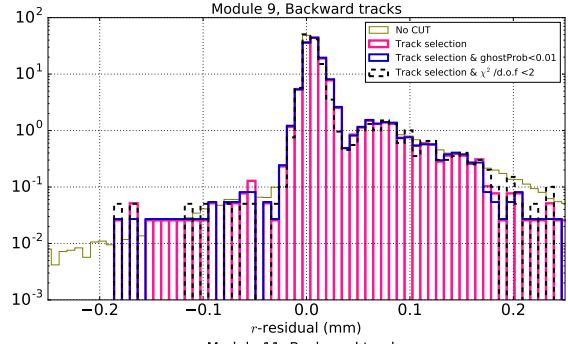
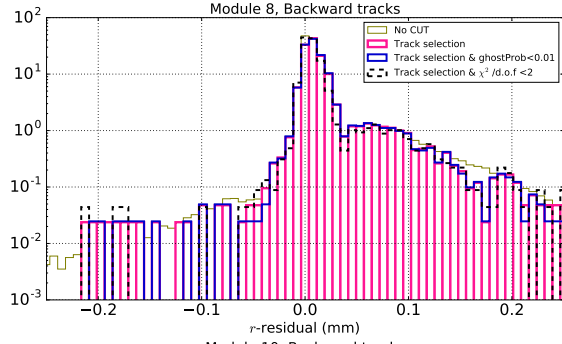
Long tracks r -residual distributions large misalignment, Modules 48 to 51:



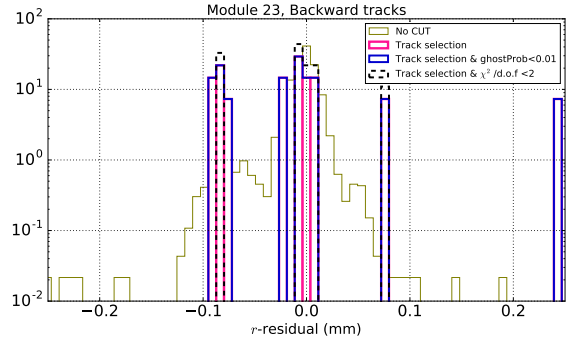
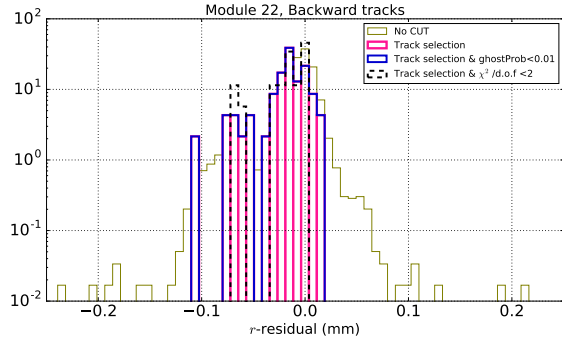
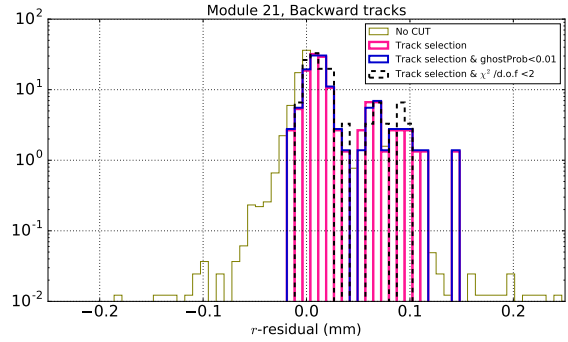
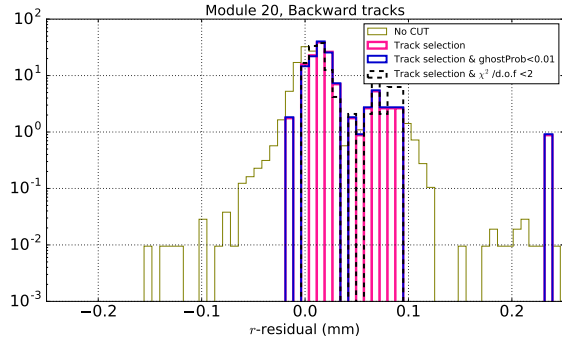
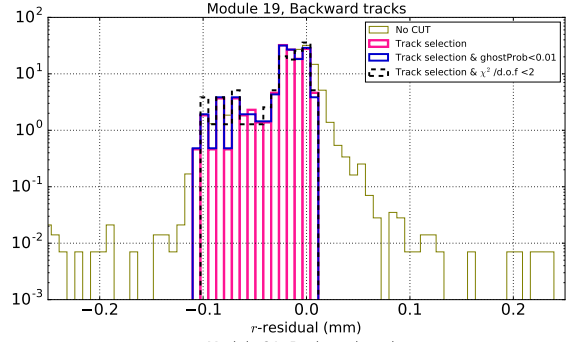
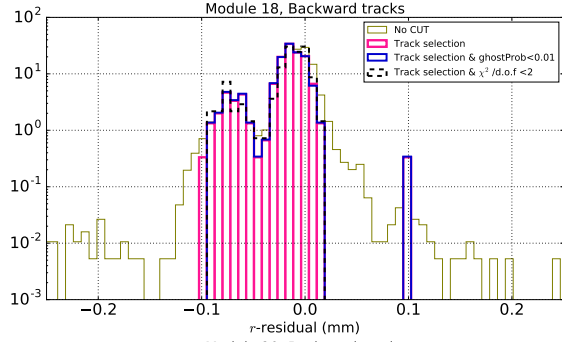
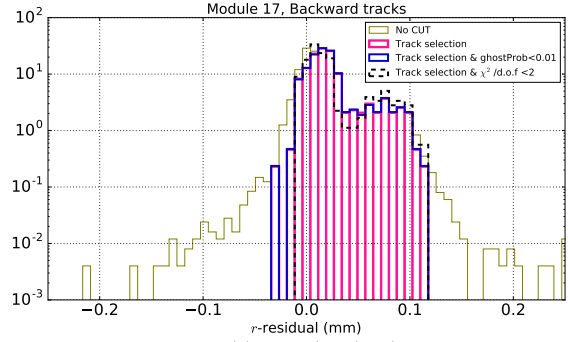
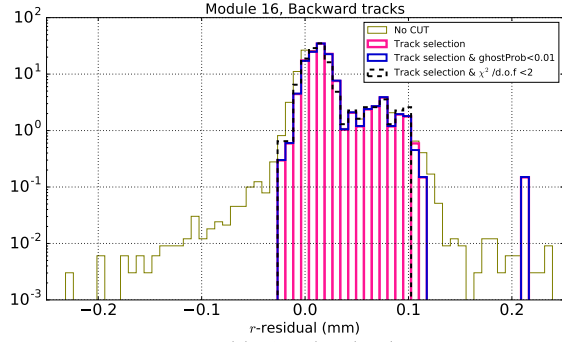
Backward tracks r -residual distributions large misalignment, Modules 0 to 7:



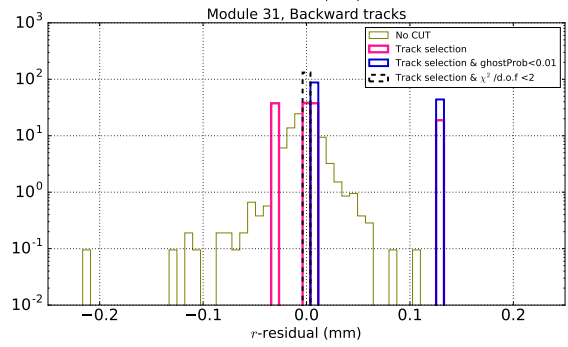
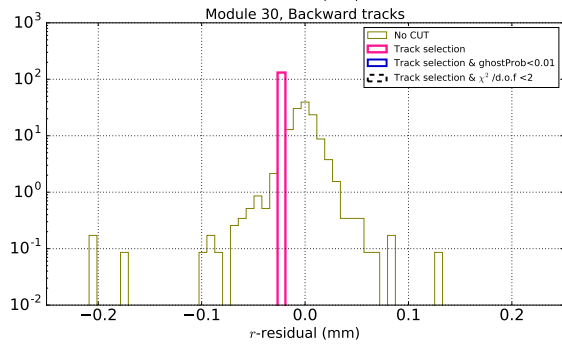
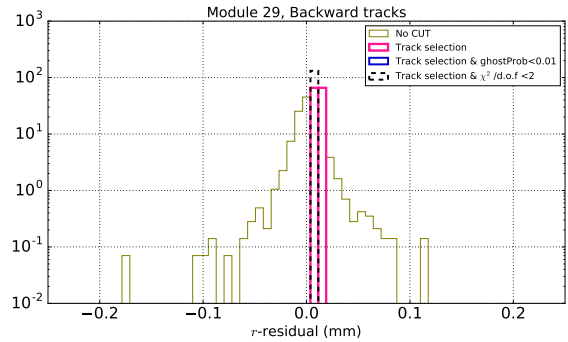
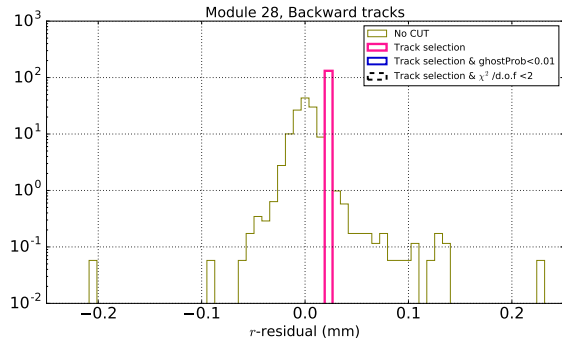
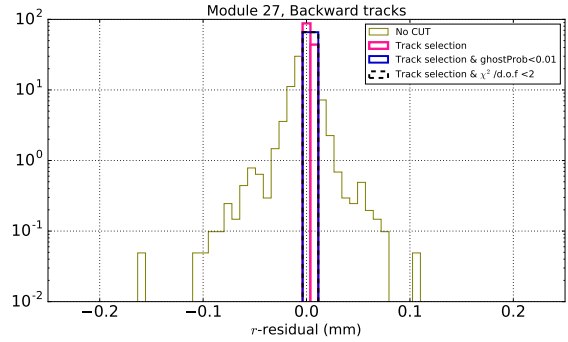
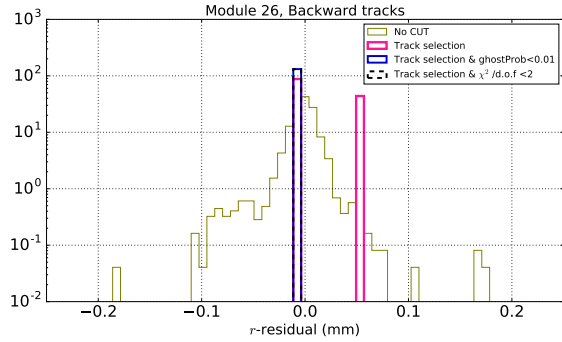
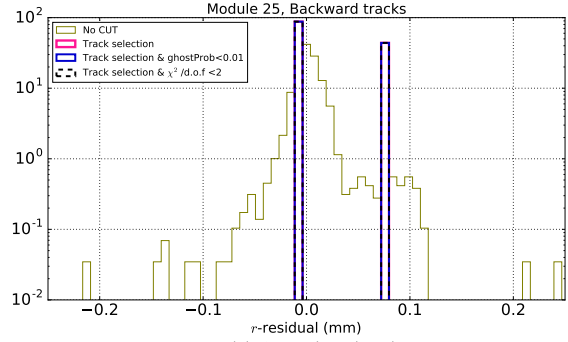
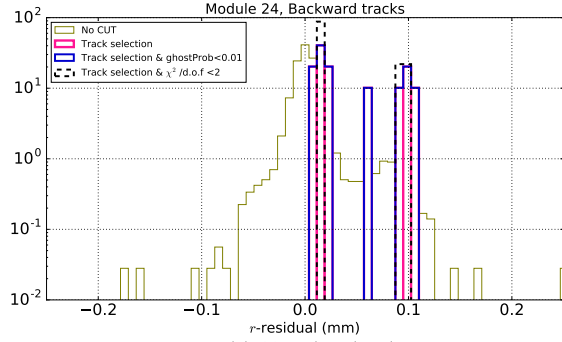
Backward tracks r -residual distributions large misalignment, Modules 8 to 15:



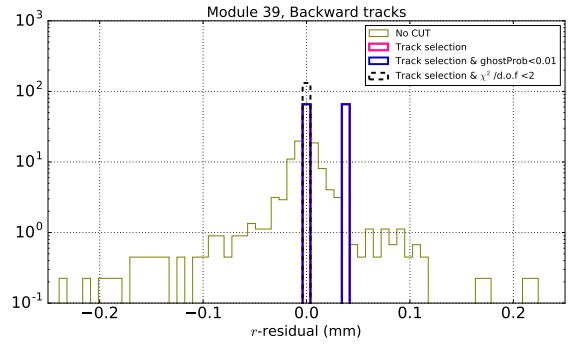
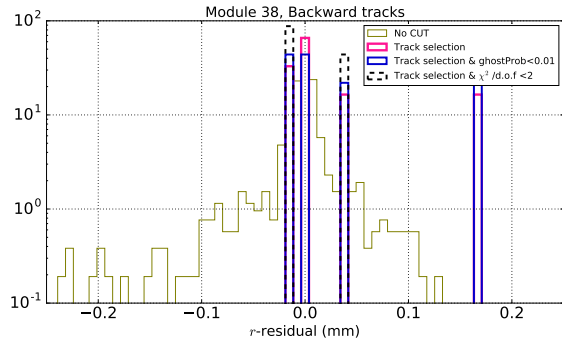
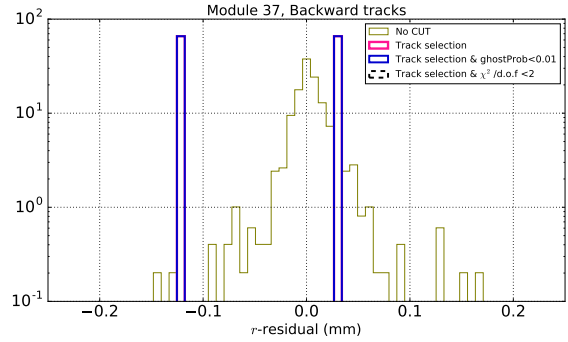
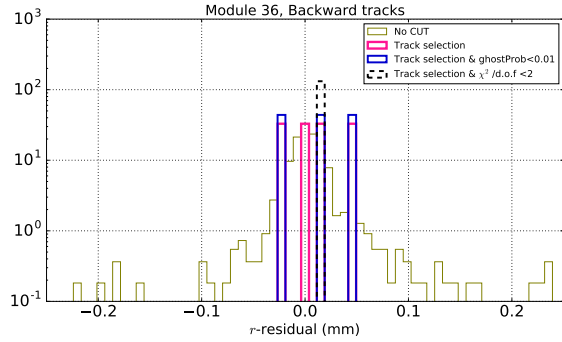
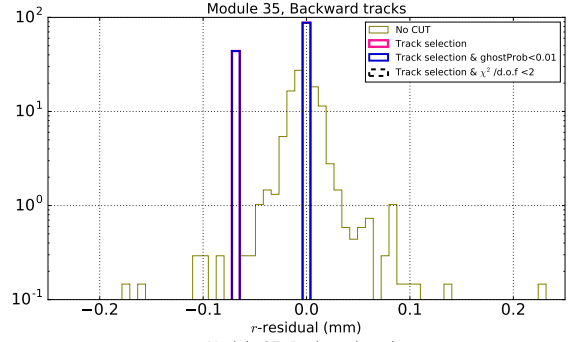
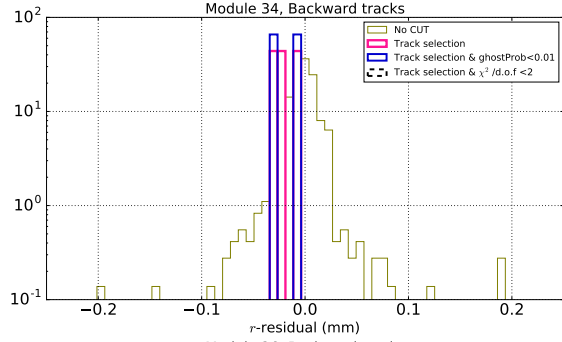
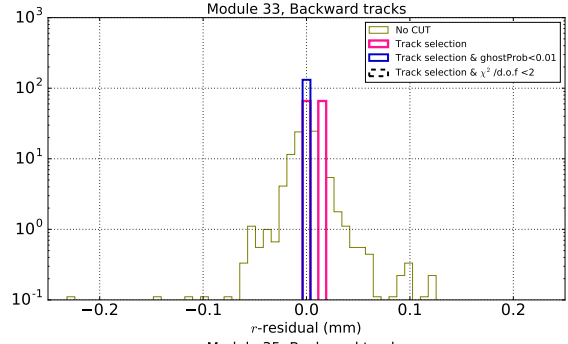
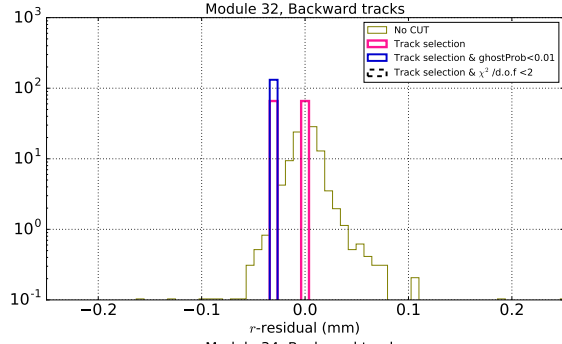
Backward tracks r -residual distributions large misalignment, Modules 16 to 23:



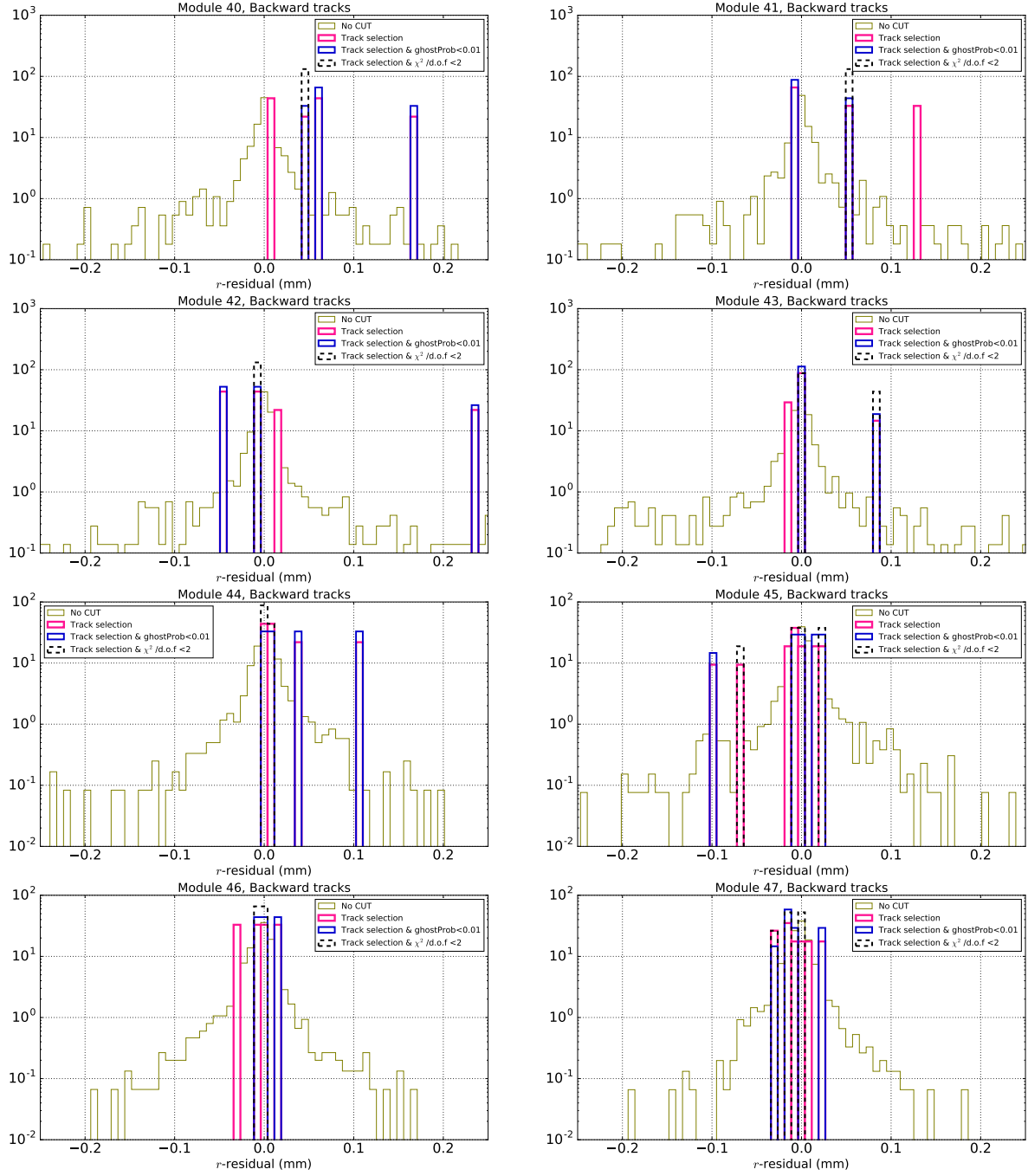
Backward tracks r -residual distributions large misalignment, Modules 24 to 31:



Backward tracks r -residual distributions large misalignment, Modules 32 to 39:



Backward tracks r -esidual distributions large misalignment, Modules 40 to 47:



Backward tracks r -residual distributions large misalignment, Modules 48 to 51:

