



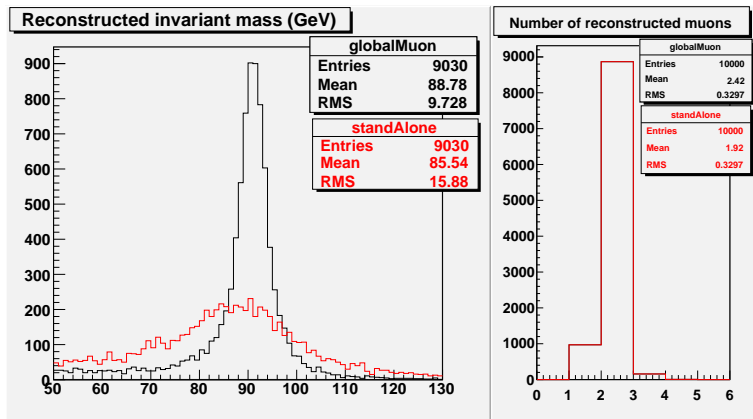
# Validation of CSA07 1\_6\_4 AICaRecoMu samples

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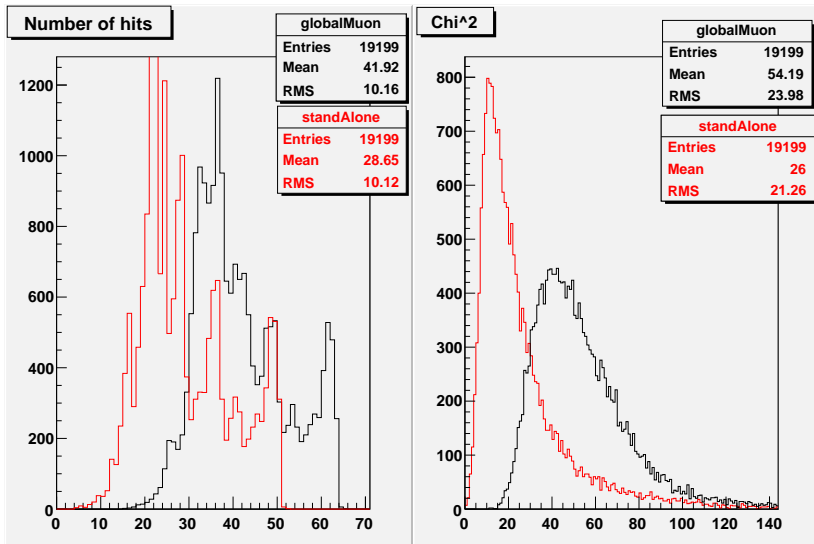
Texas A&M University

5 October, 2007

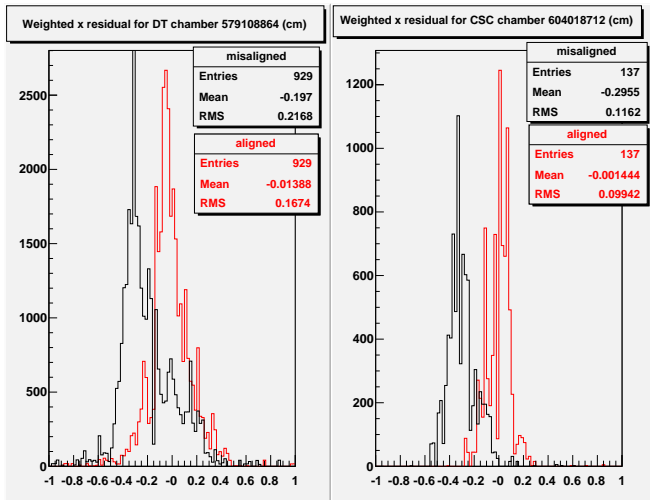
I'll get right to the plots!



These are all in 1\_6\_4: I could not compare with 1\_5\_4 because I couldn't access my personal CASTOR...?



Other than being selected for large initial misalignment, these two chambers are typical. Most chambers show internal (layer-by-layer) structure, presumably from miscalibration.



(Looking at chamber-by-chamber residuals is a small step removed from an iteration of HIP alignment. So why not?)

