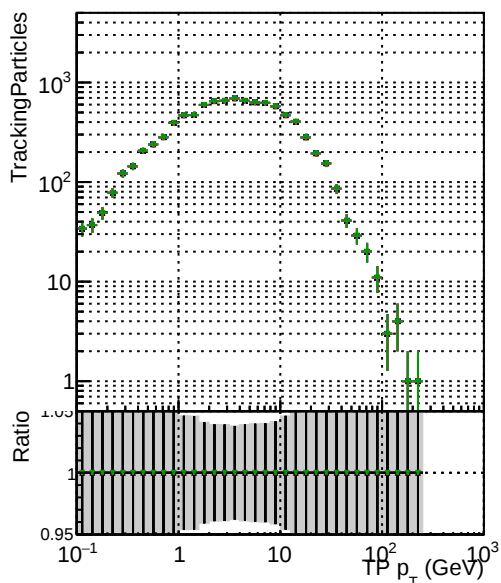


N of simulated tracks vs pT



N of associated tracks (simToReco) vs pT

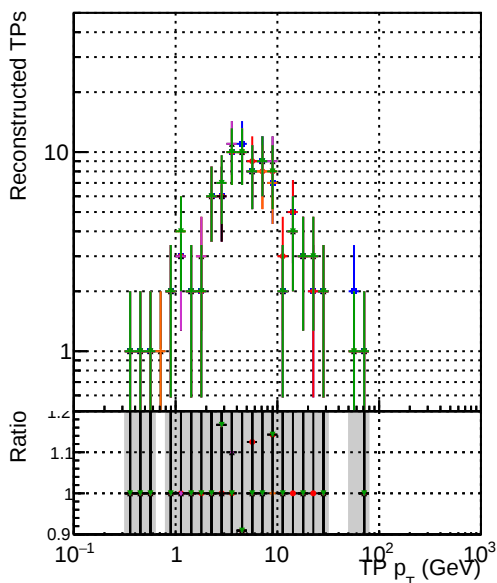
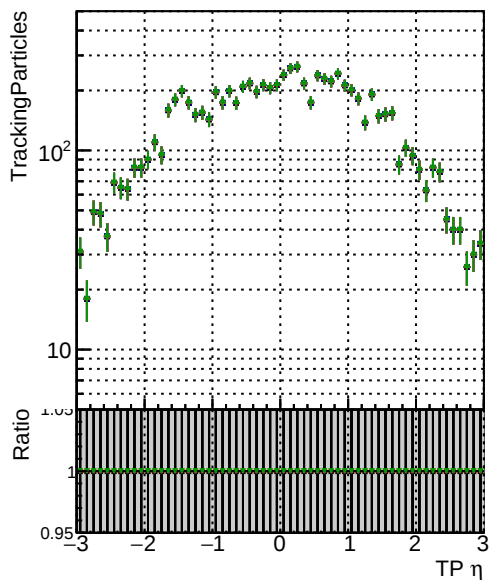
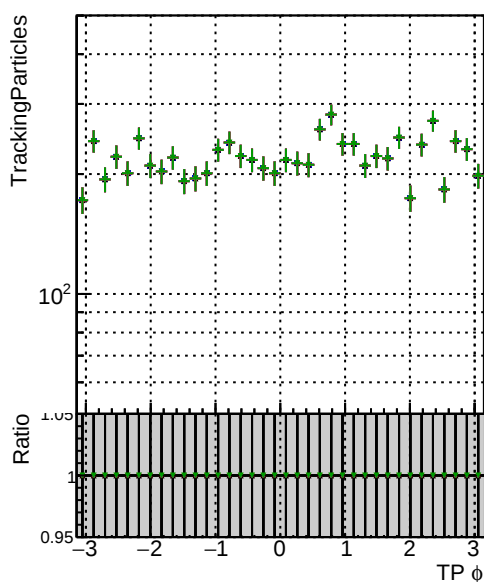


Figure 1 displays a grid of 180 small plots, organized by 'step' (1, 2, 3) and 'tbar-phase' (1, 2, 3). The rows represent different 'newgeom' values (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20). The columns represent different 'tbar-phase' values (1, 2, 3). The plots show the distribution of significant genes for different 'step' values (1, 2, 3) and 'tbar-phase' values (1, 2, 3). The legend indicates the 'N of significant genes' for each step and tbar-phase combination.



N of simulated tracks vs phi



N of associated tracks (simToReco) vs phi

