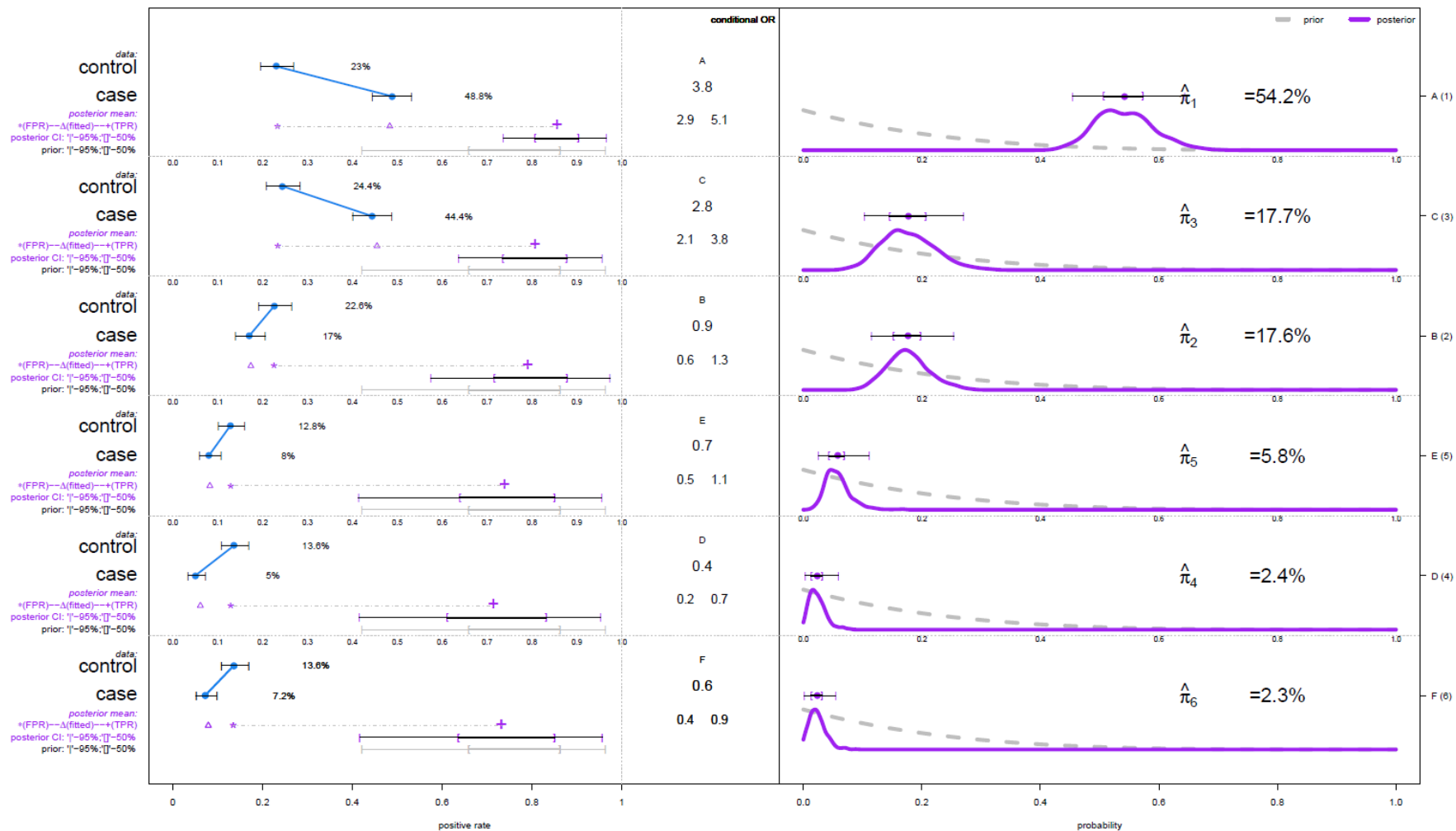
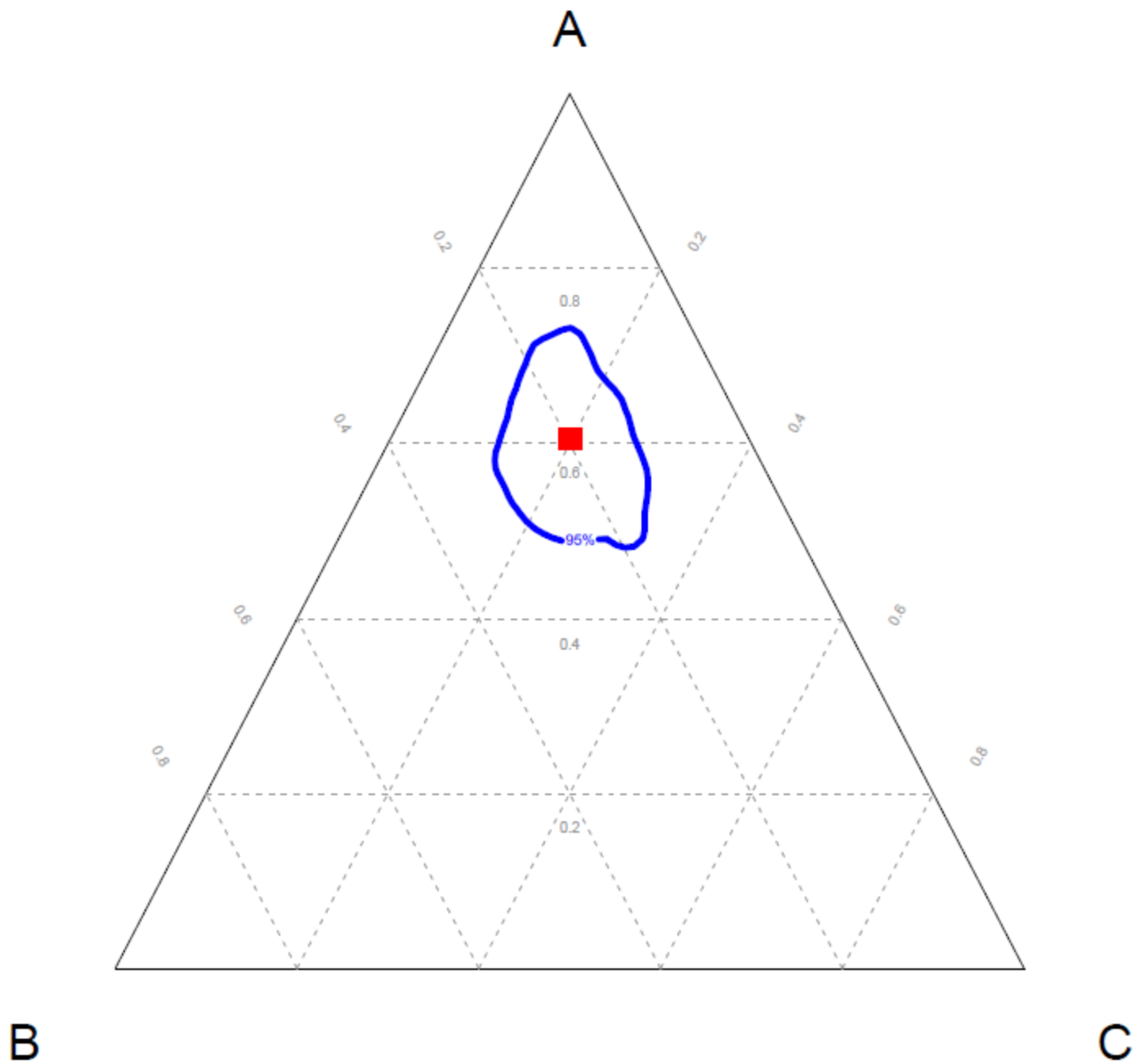


BrS: MBS1

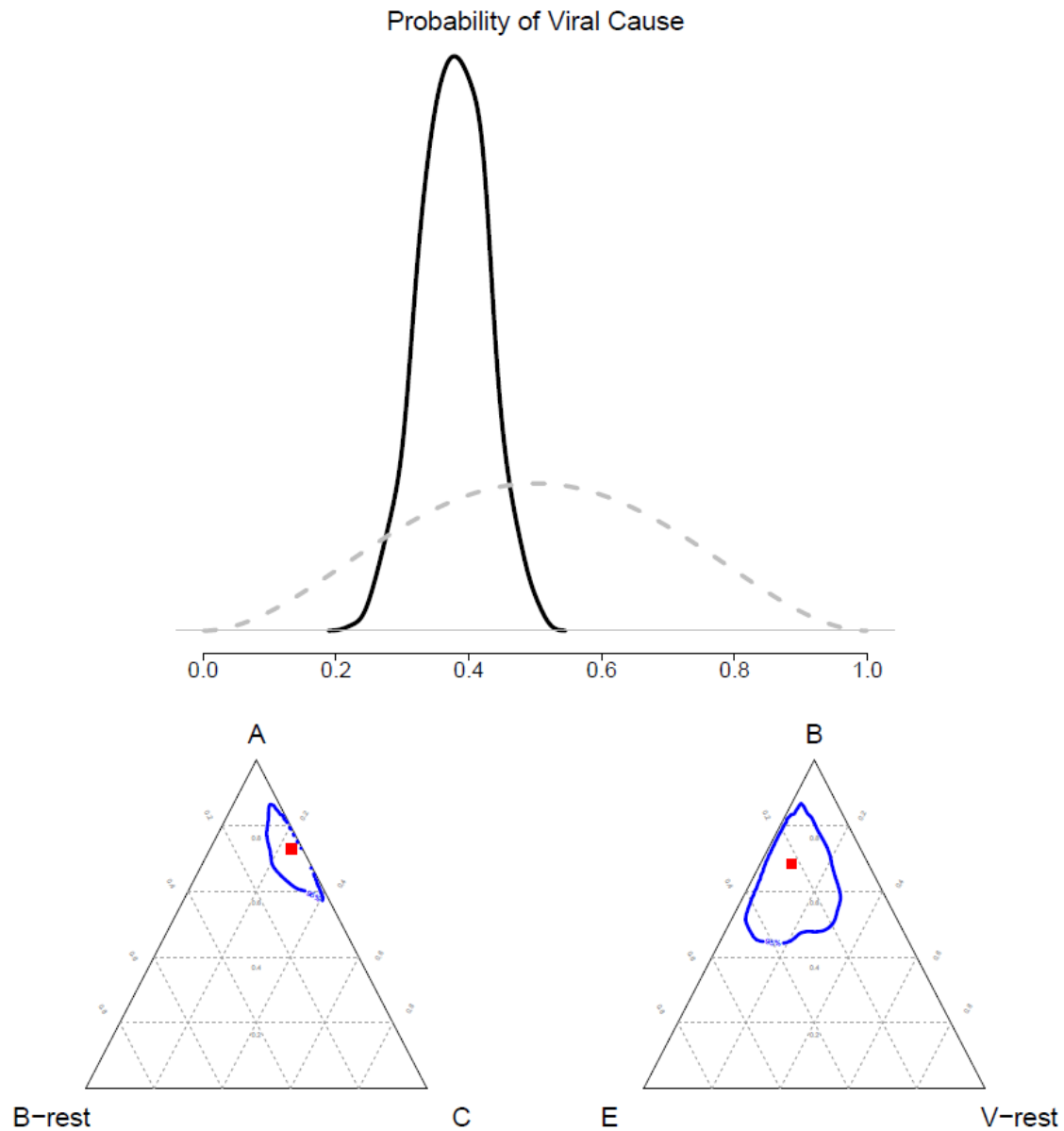
$\frac{\Lambda}{\pi}$



plot_panels(result_folder,bg_color=NULL)

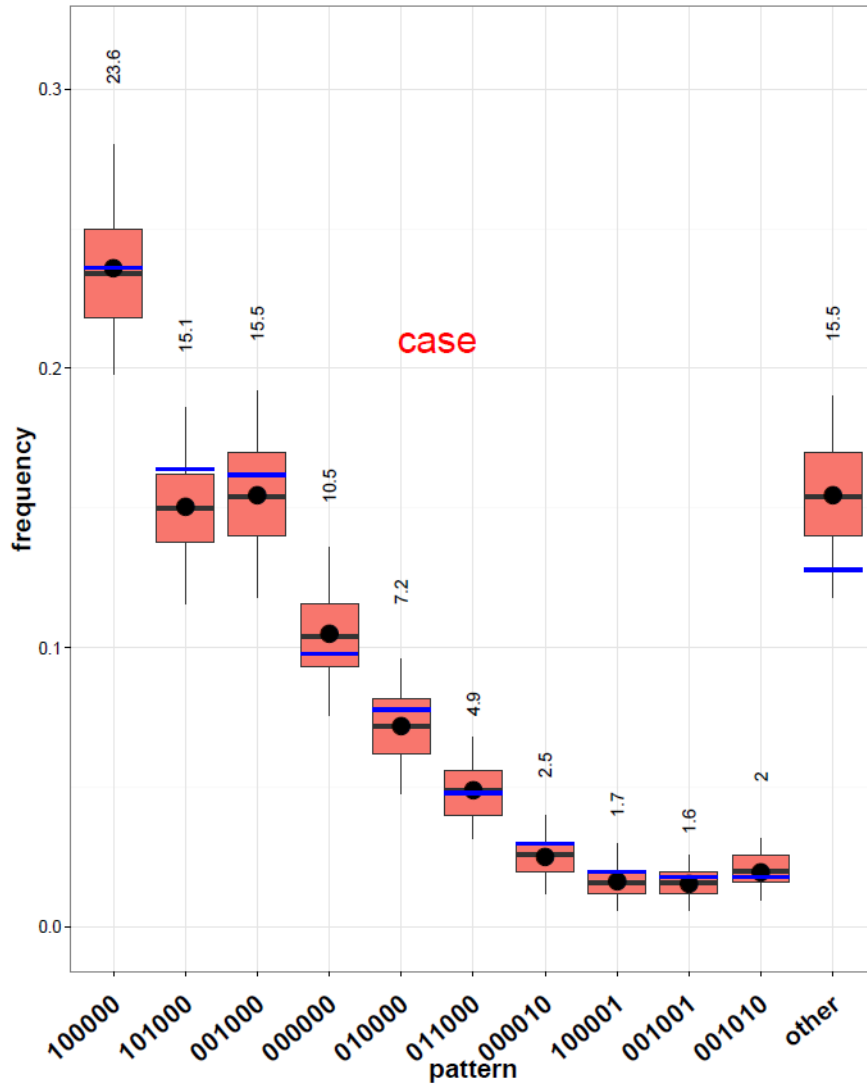


`plot_selected_etiology(selected = c("A","B","C"), result_folder, 1, 5)`

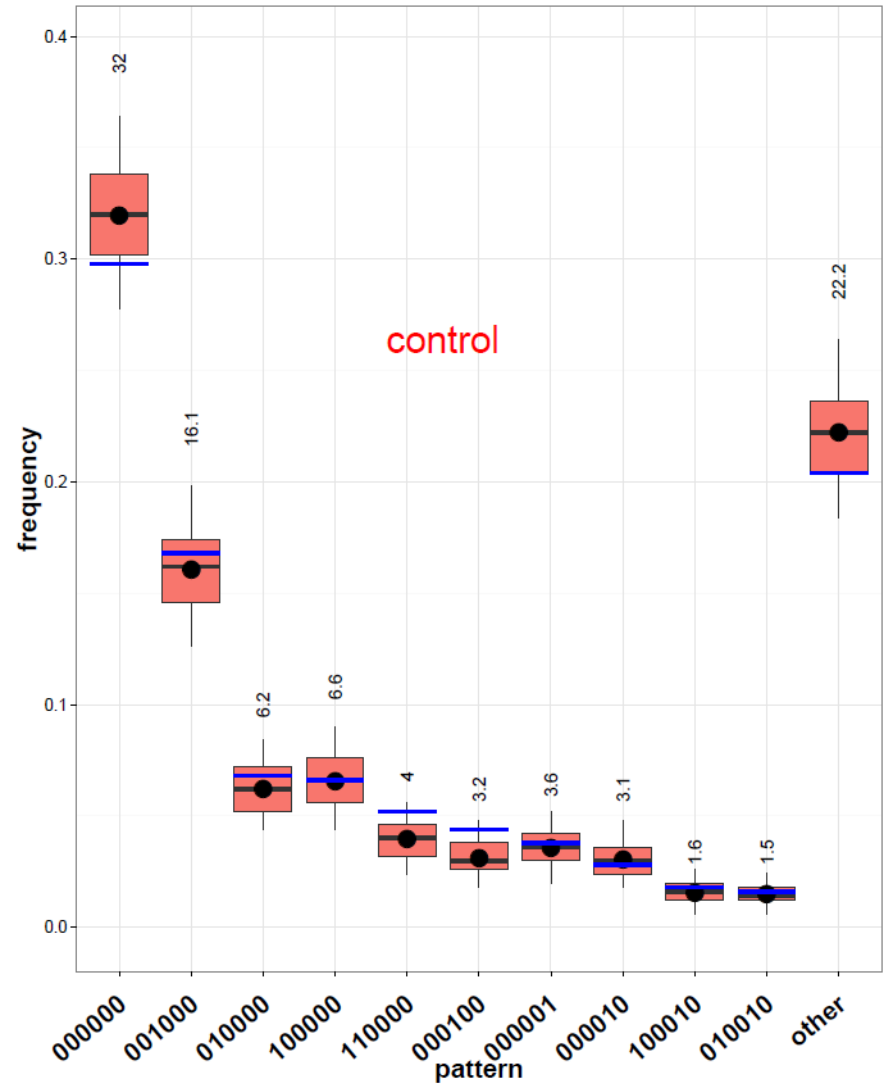


```
plot_group_etiology(result_folder,dir_taxo = file.path(working_dir,  
"pathogen_category_simulation.csv"))
```

Model  rep_1_kfit_2



Model  rep_1_kfit_2



plot_check_common_pattern(dir_list,slice_vec =c(1,1))