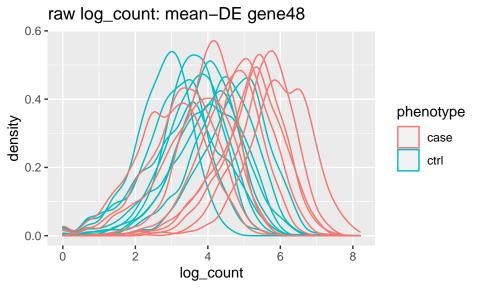
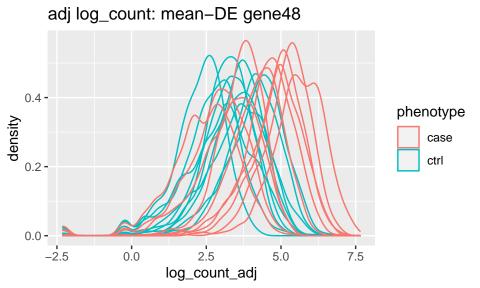
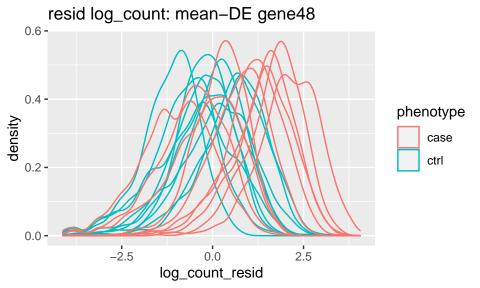


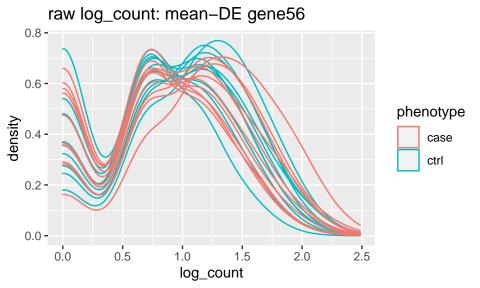
adj log_count: mean-DE gene40 0.75 phenotype density 0.50 case ctrl 0.25 -0.00 log_count_adj

resid log_count: mean-DE gene40 0.75 phenotype density case ctrl 0.25 -0.00 log_count_resid

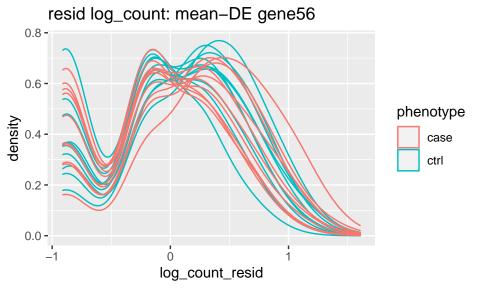








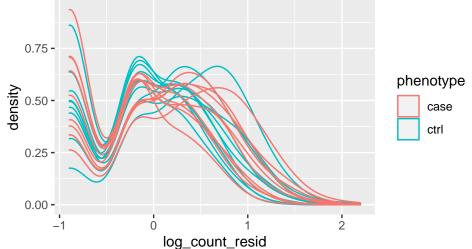
adj log_count: mean-DE gene56 0.6 phenotype density case ctrl 0.2 -0.0 log_count_adj



raw log_count: mean-DE gene59 0.75 phenotype density 0.50 case ctrl 0.25 -0.00 log_count

adj log_count: mean-DE gene59 0.75 phenotype density 0.50 case ctrl 0.25 -0.00 log_count_adj

resid log_count: mean-DE gene59

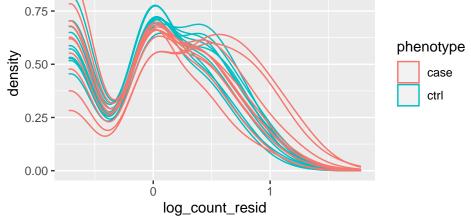


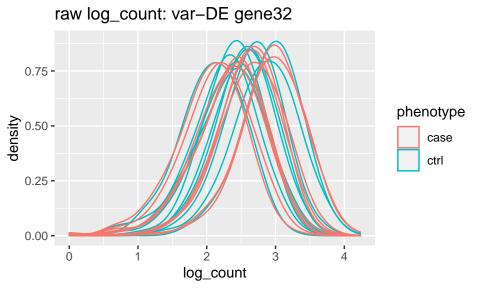
raw log_count: var-DE gene21 0.75 phenotype density 0.50 case ctrl 0.25 -0.00 -0.5 1.5 2.0 2.5 0.0 log_count

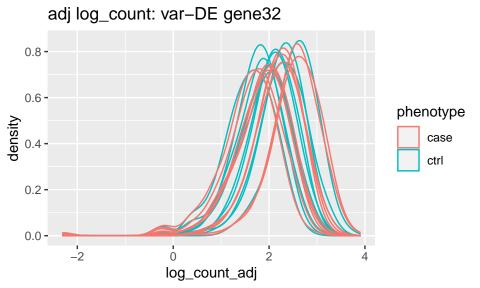
adj log_count: var-DE gene21 0.75 phenotype density o.50 case ctrl 0.25 -0.00 -

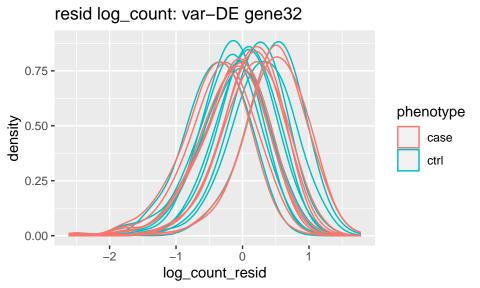
log_count_adj

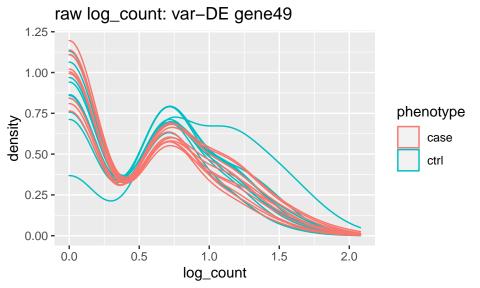
resid log_count: var-DE gene21 0.75 phenotype density 0.50 case ctrl 0.25 -

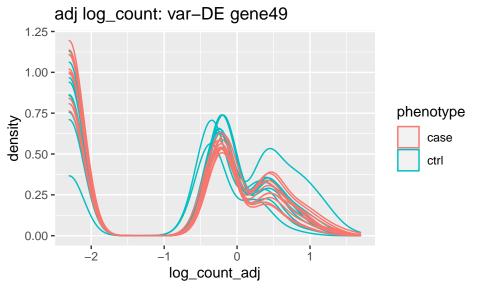


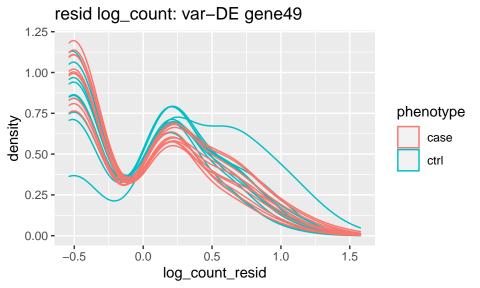




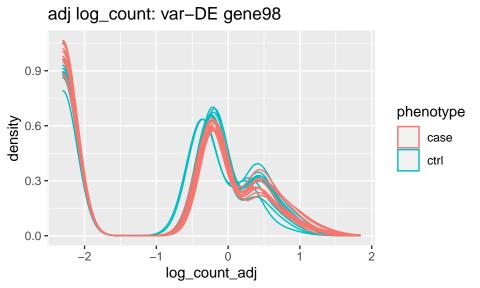


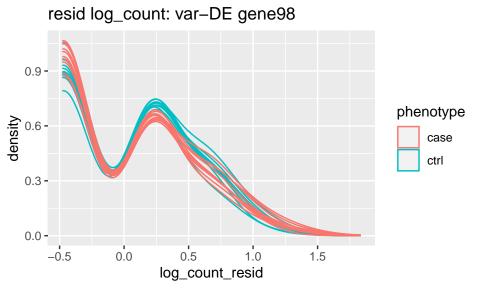


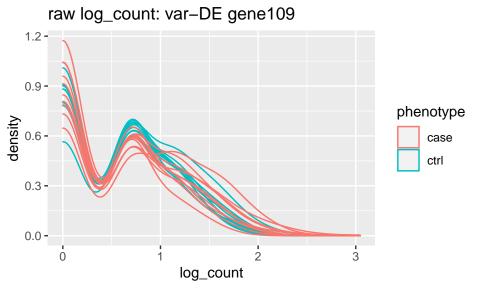


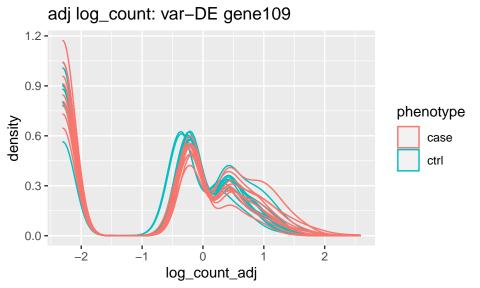


raw log_count: var-DE gene98 0.9 phenotype density case ctrl 0.3 -0.0 -0.5 1.0 2.0 log_count



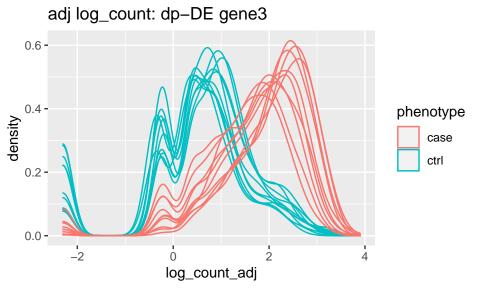


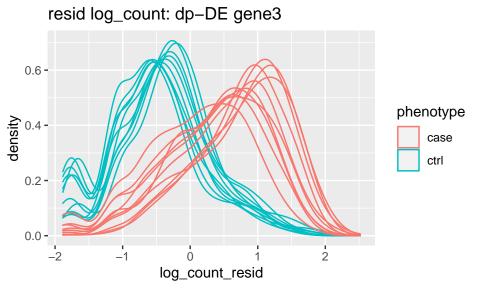




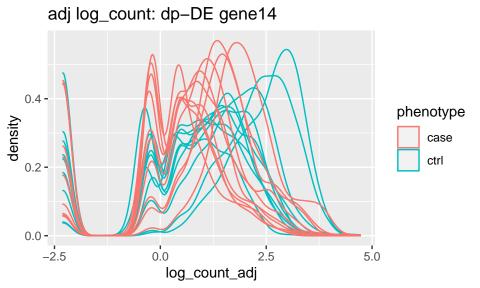
resid log_count: var-DE gene109 1.2 -0.9 phenotype density case ctrl 0.3 -0.0 log_count_resid

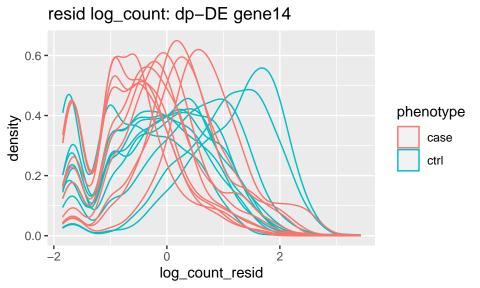
raw log_count: dp-DE gene3 0.6 phenotype density case ctrl 0.2 -0.0 log_count



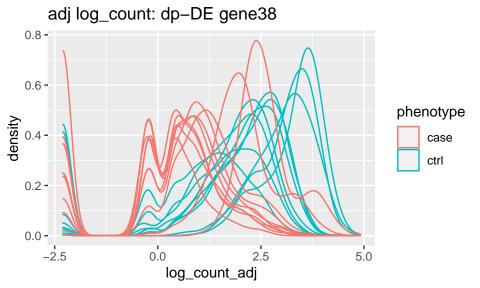


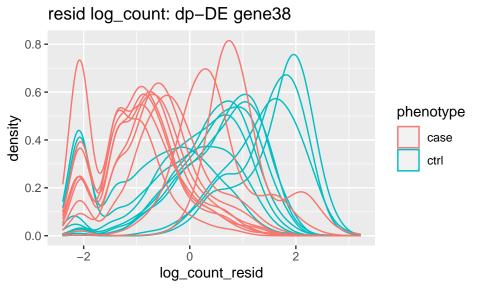
raw log_count: dp-DE gene14 0.6 density 0.4 phenotype case ctrl 0.2 -0.0 log_count

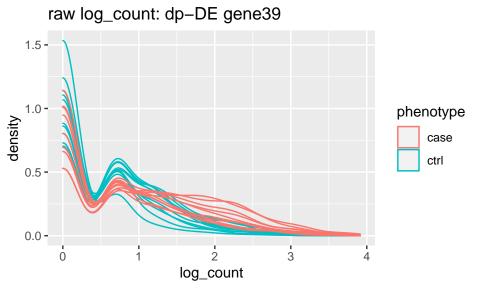


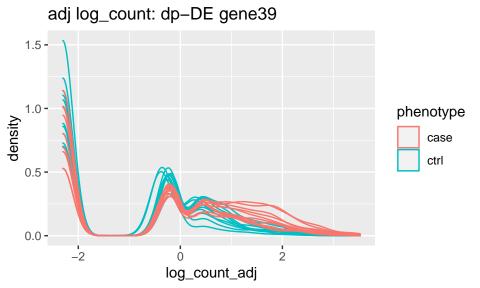


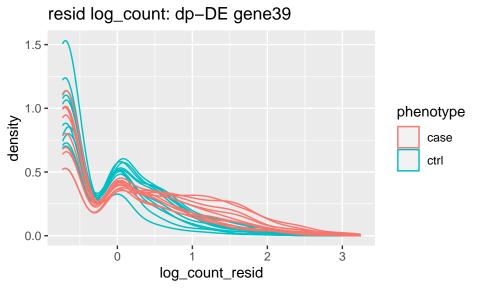
raw log_count: dp-DE gene38 0.8 -0.6 phenotype density case 0.4 ctrl 0.2 -0.0 log_count







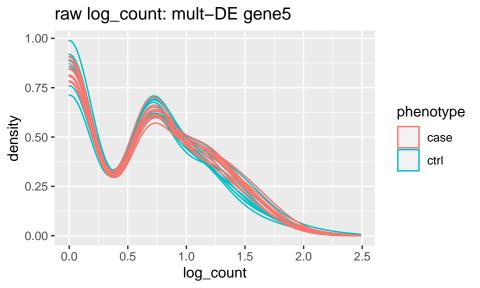




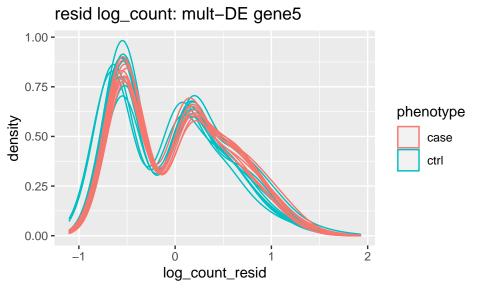
raw log_count: dp-DE gene42 1.25 -1.00 phenotype density 0.75 case ctrl 0.25 -0.00 log_count

adj log_count: dp-DE gene42 1.25 -1.00 phenotype density 0.75 case ctrl 0.25 -0.00 log_count_adj

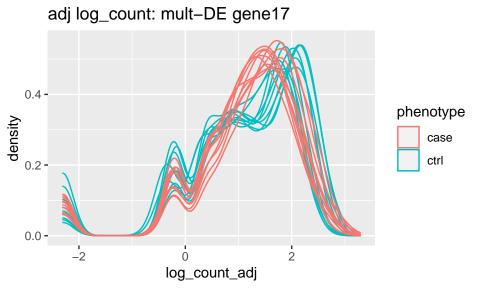
resid log_count: dp-DE gene42 1.25 -1.00 phenotype density 0.75 case ctrl 0.25 -0.00 log_count_resid

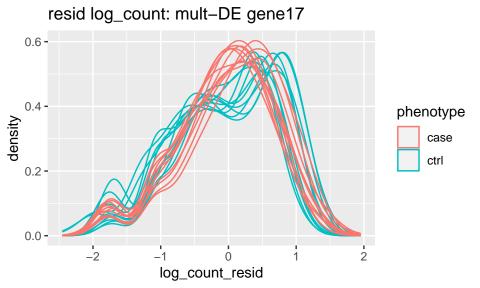


adj log_count: mult-DE gene5 1.00 -0.75 phenotype density case ctrl 0.25 -0.00 log_count_adj

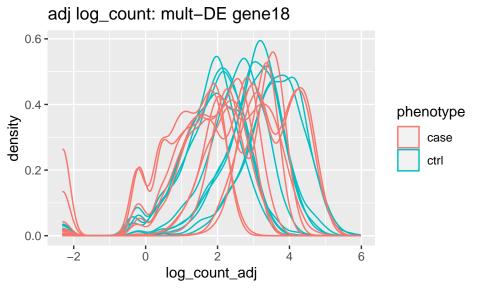


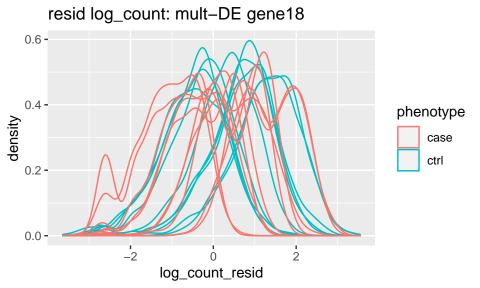
raw log_count: mult-DE gene17 0.6 -0.4 phenotype density case ctrl 0.2 -0.0 log_count

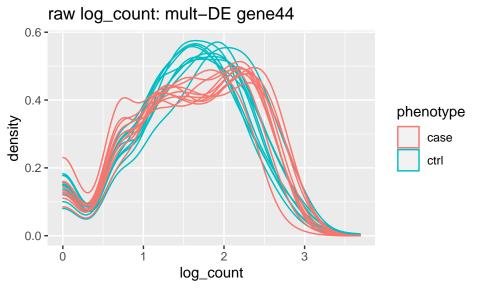


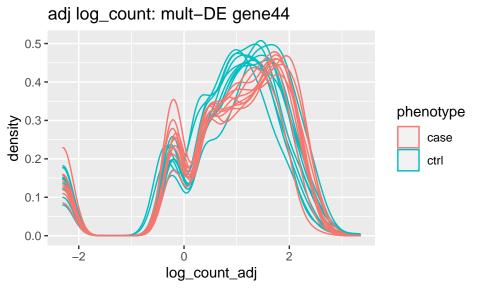


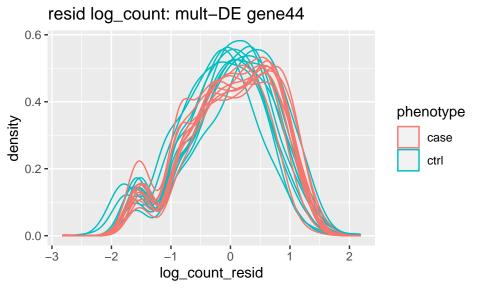
raw log_count: mult-DE gene18 0.6 -0.4 phenotype density case ctrl 0.2 -0.0 log_count



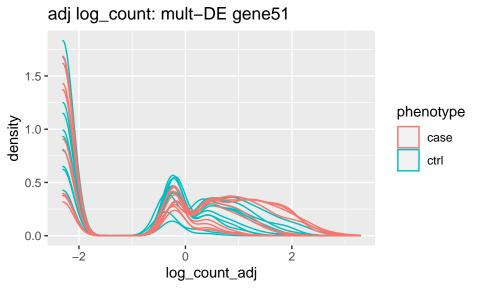


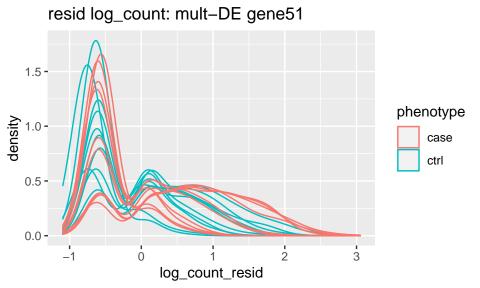


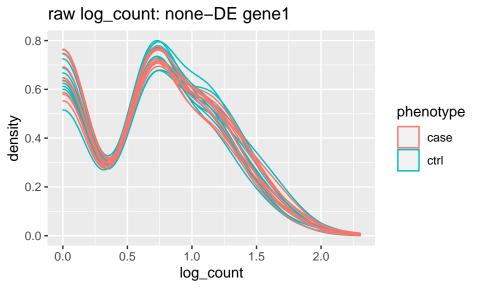


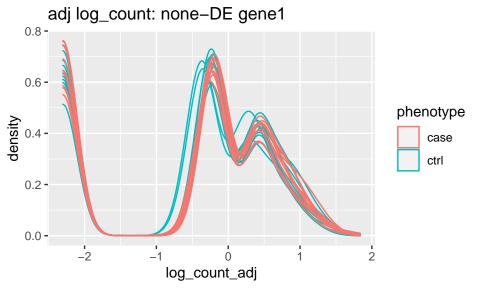


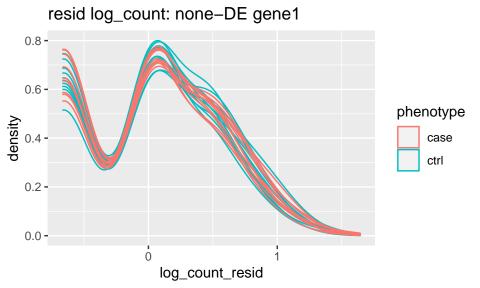
raw log_count: mult-DE gene51 1.5 phenotype density case ctrl 0.5 -0.0 log_count



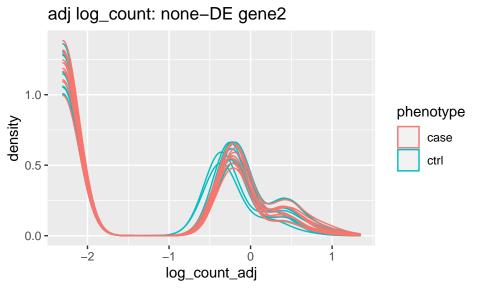


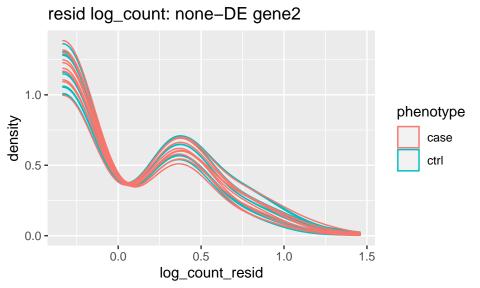


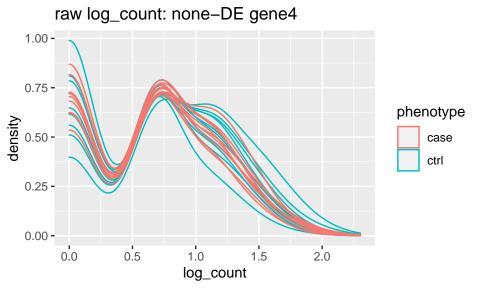


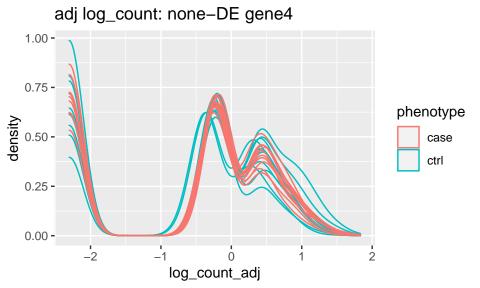


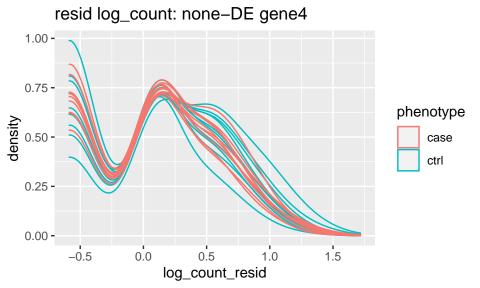
raw log_count: none-DE gene2 1.0 phenotype density case ctrl 0.0 -0.5 1.0 1.5 0.0 log_count



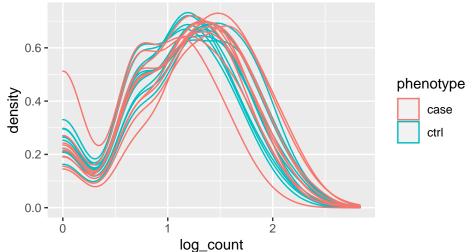


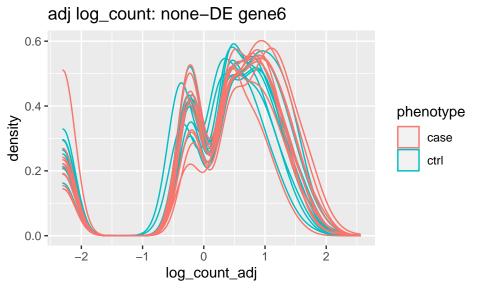




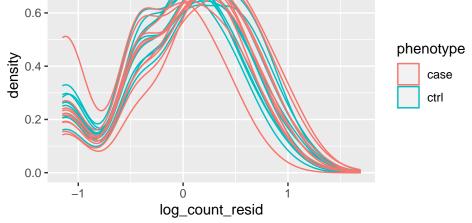


raw log_count: none-DE gene6





resid log_count: none-DE gene6 0.6 phenotype density - _{0.0} case ctrl



raw log_count: none-DE gene7 0.9 phenotype density case ctrl 0.3 -0.0 -0.5 1.0 1.5 2.0 0.0 log_count

