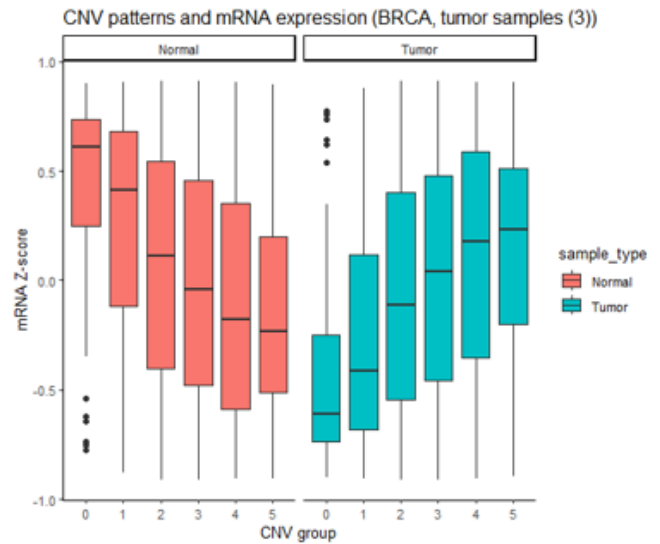
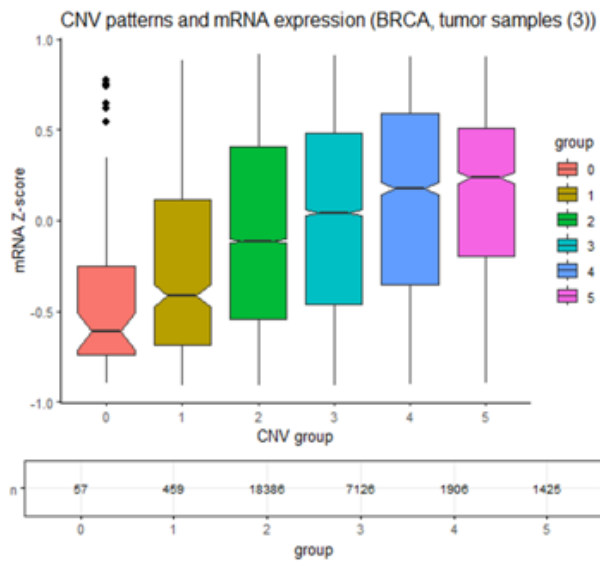
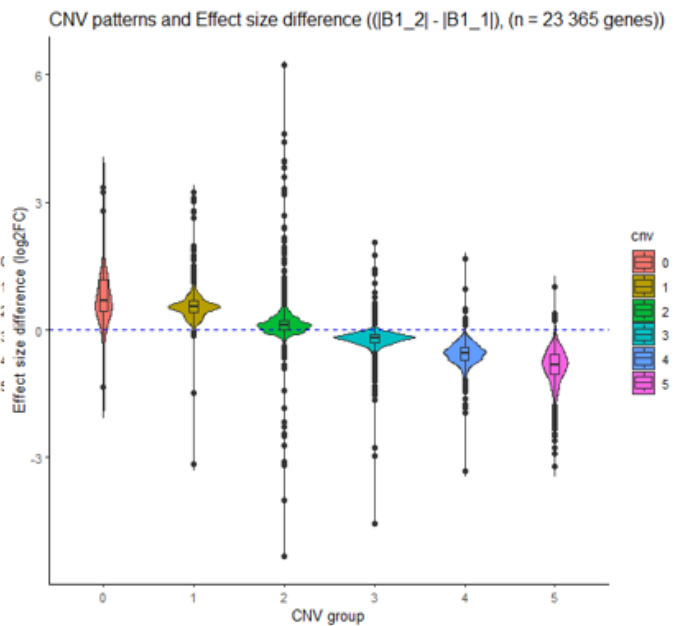
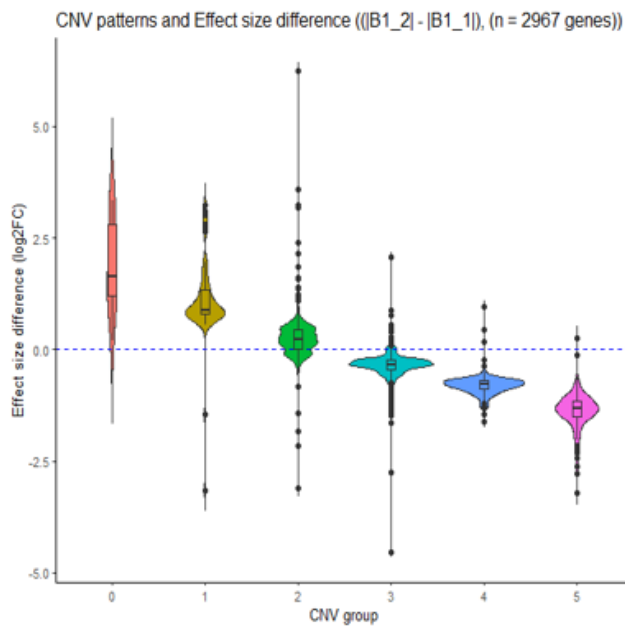


mRNA and CNVs relationship exploration (TCGA, BRCA)

Total genes tested: **29359**, number of samples: **3**

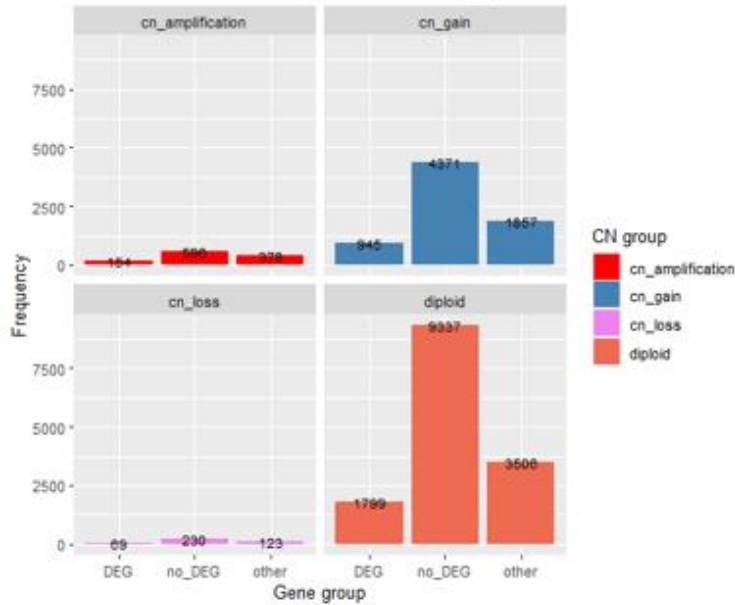


DEGs vs All tested genes, BRCA

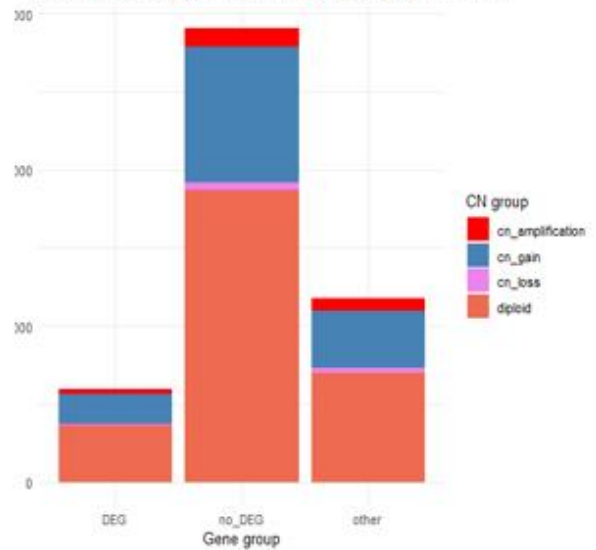


TCGA, BRCA

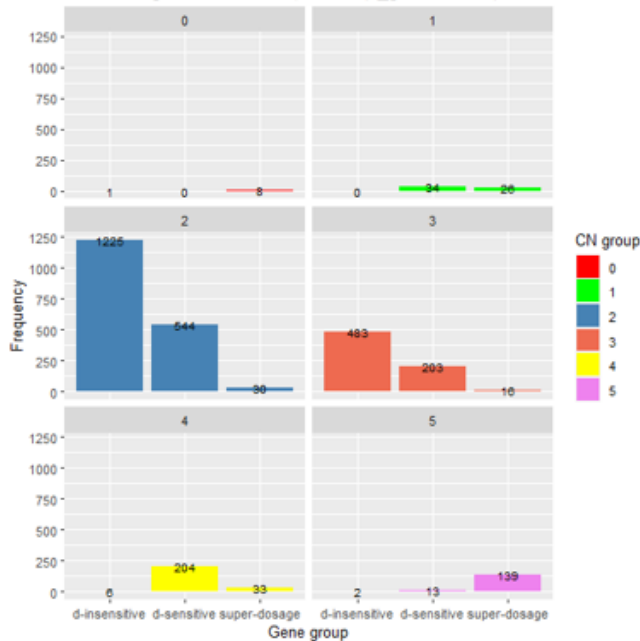
CNV informed Gene Expression, BRCA (n_genes=23365)



CNV informed Gene Expression, BRCA (n_genes=23365)

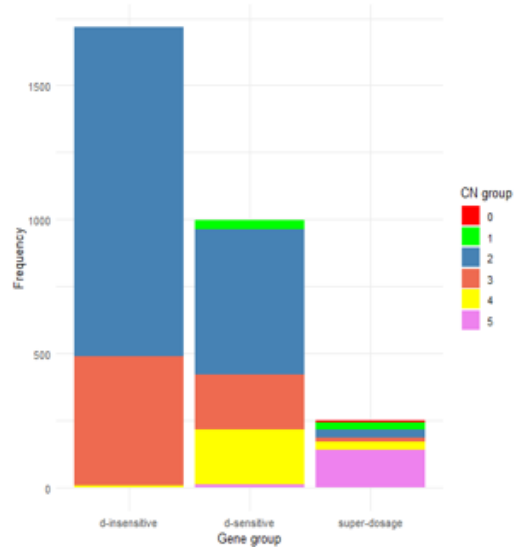


CNV dosage effect on DGE, BRCA (n_genes=2967)



about 42 % (1250) of DE genes are explained by the effect of CNV

CNV dosage effect on DGE, BRCA (n_genes=2967)



```
#Gene group facrorization based on Effect size difference
deg <- deg %>%
  mutate(gene_group = case_when(
    Difference <= -1.0 ~ "super-dosage",
    Difference >= 1.0 ~ "super-dosage",
    Difference > -1.0 & Difference < -0.4 ~ "dosage-sensitive",
    Difference < 1.0 & Difference > 0.4 ~ "dosage-sensitive",
    Difference >= -0.4 & Difference <= 0.4 ~ "dosage_insensitive"
  ))
```