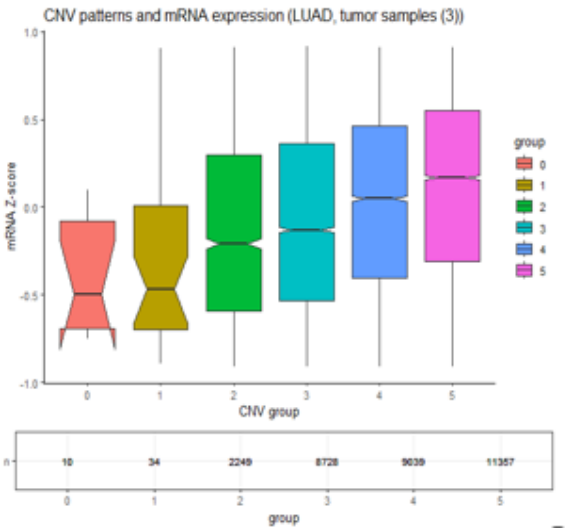
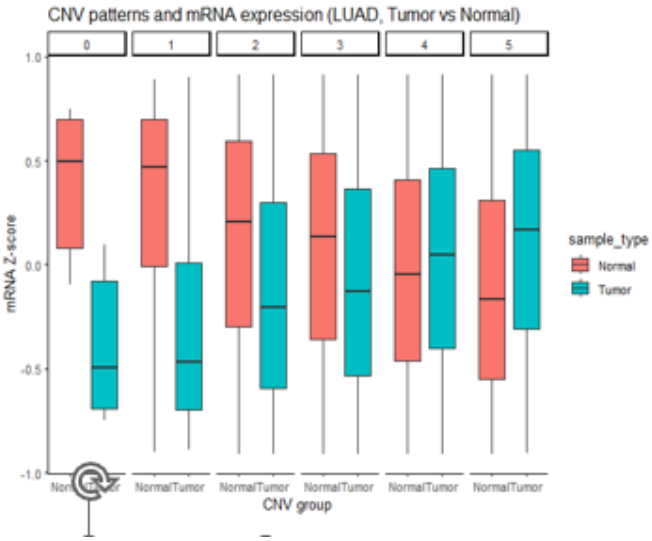
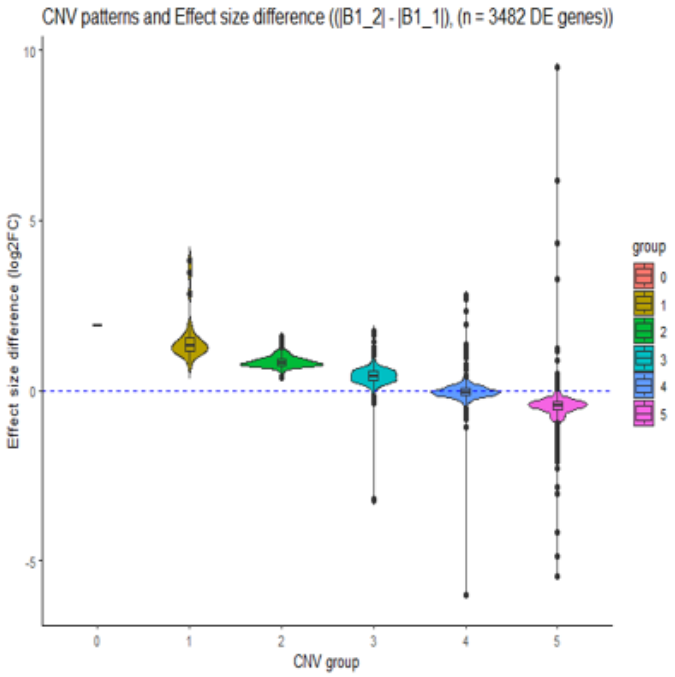
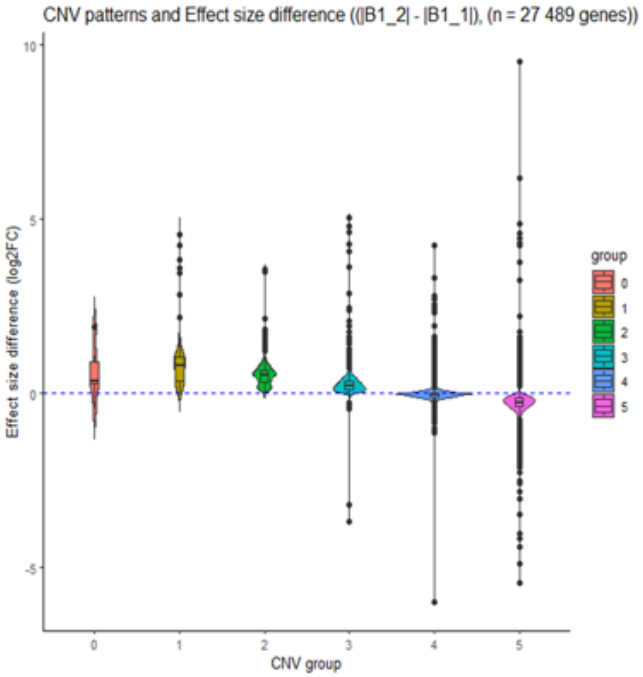
mRNA and CNVs relationship exploration (TCGA, LUAD)

Total genes tested: **31417, number of samples: 3**

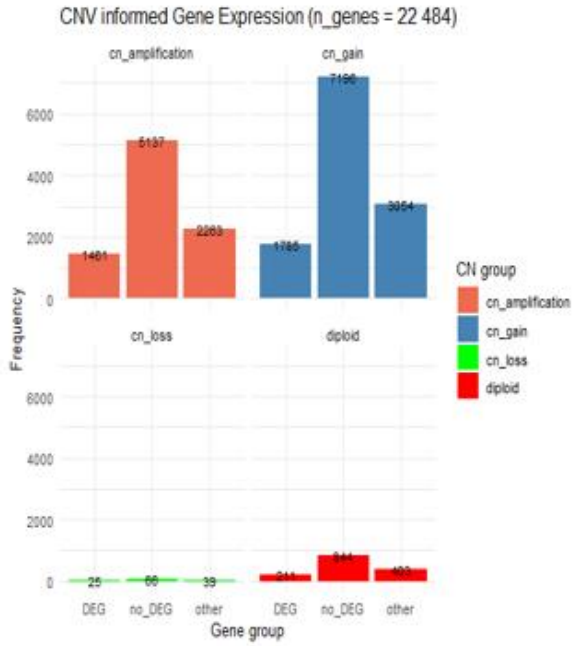


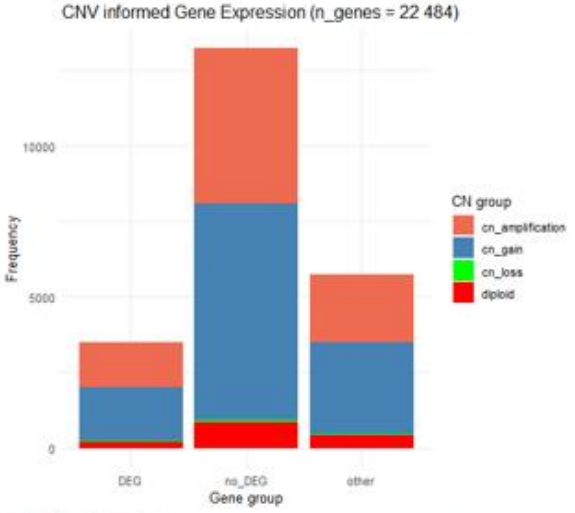






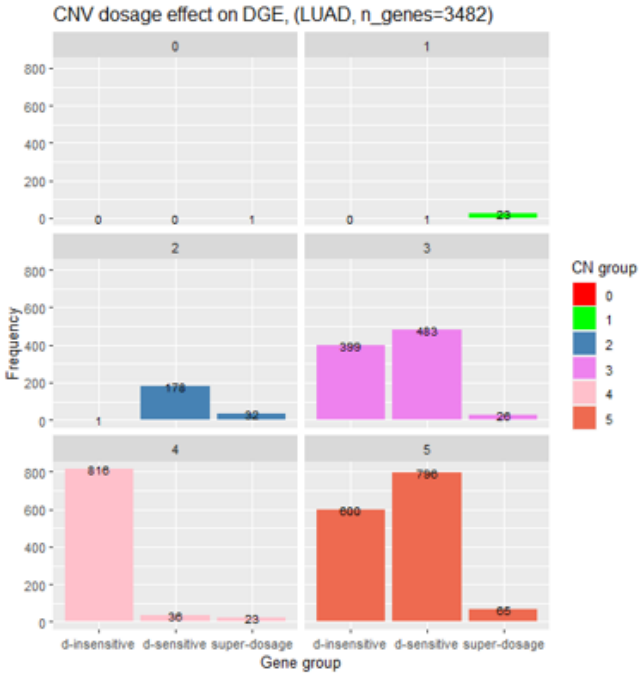
TCGA, LUAD

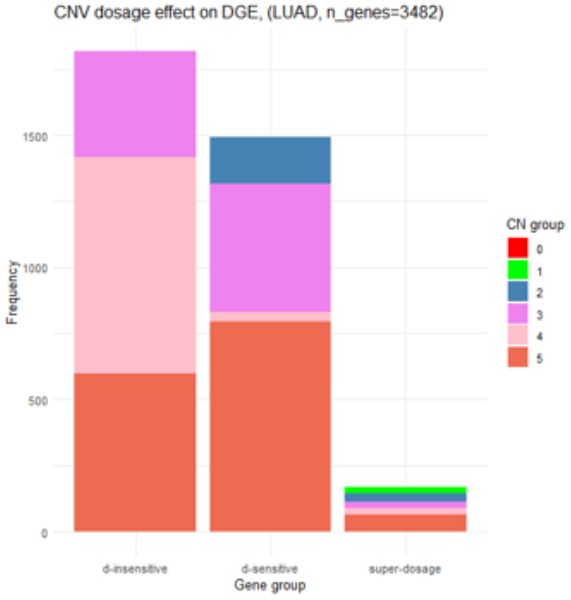





```
#gene group factorization
res_allGenes <- res_allGenes %>%
  mutate(gene_group = case_when(
    B1_1 < -0.5 & padj <= 0.05 ~ "DEG",
    B1_1 > 0.5 & padj <= 0.05 ~ "DEG",
    B1_1 <= 0.5 & B1_1 >= -0.5 ~ "no_DEG",
    B1_1 >= 0.5 & padj > 0.05 ~ "other",
    B1_1 <= -0.5 & padj > 0.05 ~ "other"))
```

```
# CN factorization
res_allGenes <- res_allGenes %>%
  mutate(cn_group = case_when(
    cnv == "2" ~ "Diploid",
    cnv == "0" ~ "cn_loss",
    cnv == "1" ~ "cn_loss",
    cnv == "3" ~ "cn_gain",
    cnv == "4" ~ "cn_gain",
    cnv == "5" ~ "cn_amplification"))
```





about **47 % (1664)** of DE genes are explained by the effect of CNV

```
#gene group factorization
deg_merged <- deg_merged %>%
  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 ~ "not_explained"
    ))
```