

# Off target effects

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## Purpose

To answer the question, “What are the off-target effects of the CRISPR editing?”

## Set up

To start, read in the Seurat object.

```
so <-  
  readRDS(here(  
    "scRNAseq",  
    "data",  
    "processed_data_objects",  
    "00_seurat_workflow.so.rds"  
  ))
```

## Final Analysis

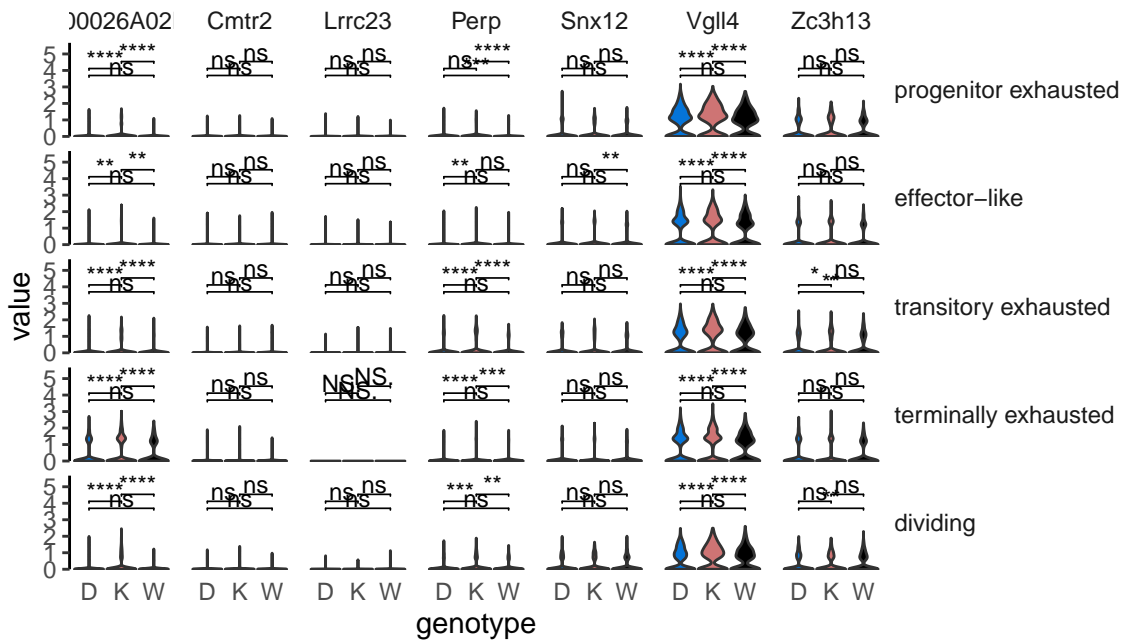
```
off_target_genes <- c("2900026A02Rik",  
                      "Cmtr2",  
                      "Lrrc23",  
                      "Perp",  
                      "Snx12",  
                      "Vgll4",  
                      "Zc3h13")  
  
gene_expr_tidy <-  
  get_metadata_from_so(so, genes = off_target_genes) %>%  
  pivot_longer(cols = all_of(off_target_genes))
```

```
gene_expr_tidy %>%  
  ggplot() +  
  aes(genotype, value, fill = genotype) +  
  geom_violin(scale = "width") +  
  facet_grid(cluster_ids~name) +  
  remove_x_spine() +  
  theme(strip.background = element_blank(),
```

```

strip.text.y = element_text(angle = 0, hjust = 0),
legend.position = "none") +
scale_fill_manual(values = palette_genotype) +
scale_y_continuous(expand = c(0, 0),
                    limits = ~c(..1[1], ..1[2]*1.25)) +
stat_compare_means(comparison = list(c("D", "W"),
                                     c("D", "K"),
                                     c("W", "K")),
                  label = "p.signif",
                  size = 3)

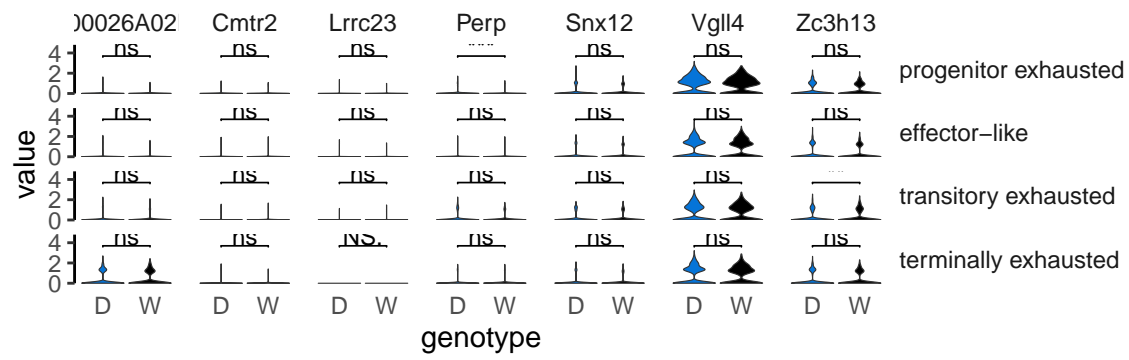
```



```

gene_expr_tidy %>%
  filter(genotype != "K") %>%
  filter(cluster_ids != "dividing") %>%
  ggplot() +
  aes(genotype, value, fill = genotype) +
  geom_violin(scale = "width", size = 0.2) +
  facet_grid(cluster_ids~name) +
  remove_x_spine() +
  theme(
    strip.background = element_blank(),
    legend.position = "none",
    strip.text.y = element_text(angle = 0, hjust = 0)
  ) +
  scale_fill_manual(values = palette_genotype) +
  scale_y_continuous(expand = c(0, 0),
                    limits = ~c(..1[1], ..1[2]*1.3),
                    breaks = c(0, 2, 4)) +
  stat_compare_means(comparison = list(c("D", "W")),
                    label = "p.signif",
                    size = 3)

```



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