Off target effects

Amy Huang

2023-03-10

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))
```
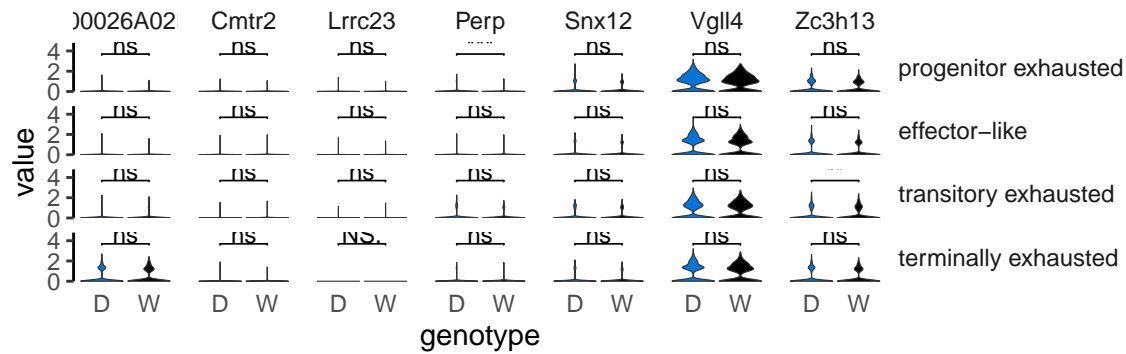
```
gene_expr_tidy %>%
  ggplot() +
  aes(genotype, value, fill = genotype) +
  geom_violin(scale = "width") +
  facet_grid(cluster_ids~name) +
  remove_x_spine() +
  theme(strip.background = element_blank(),
        strip.text.y = element_text(angle = 0, hjust = 0),
        legend.position = "none") +
  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)
```
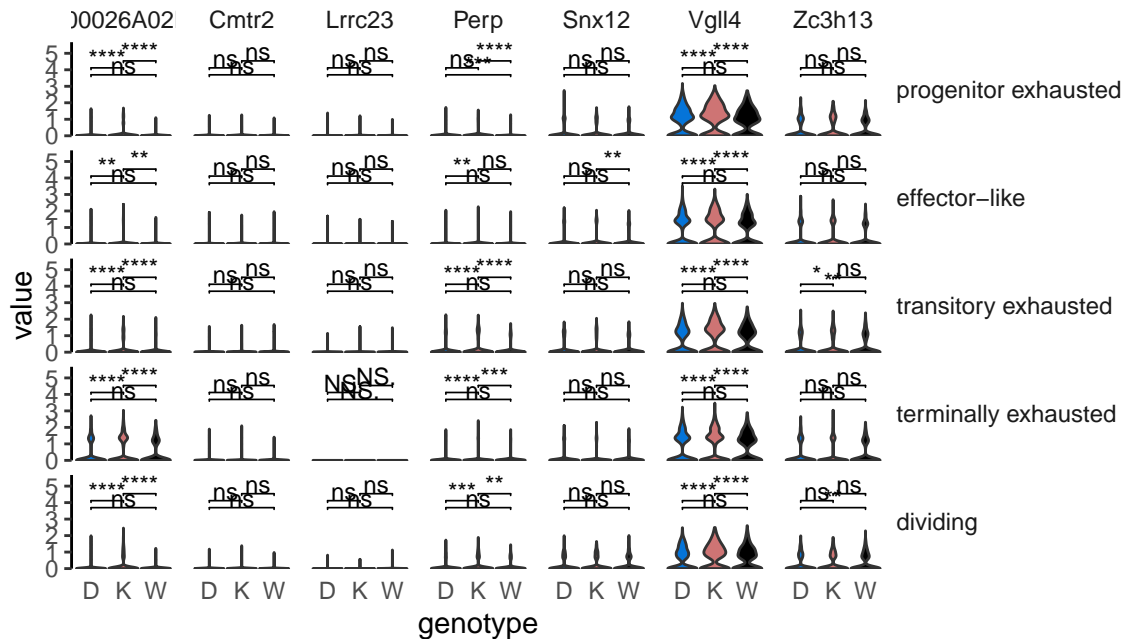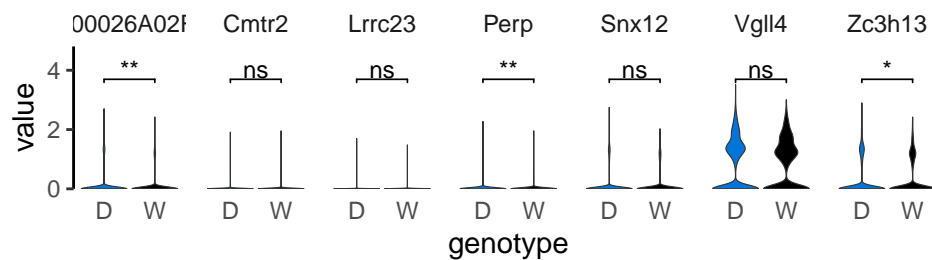


```
gene_expr_tidy %>%
  filter(genotype != "K") %>%
  filter(cluster_ids != "dividing") %>%
  ggplot() +
  aes(genotype, value, fill = genotype) +
  geom_violin(scale = "width", size = 0.2) +
  facet_grid(cluster_ids~name) +
  remove_x_spine() +
  theme(
    strip.background = element_blank(),
    legend.position = "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)
```

```
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(~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)
```


–>

(EnhDel)") –>

(EnhDel)") –>