TSS Shifting

Prepare Data

```
library("TSRexploreR")

TSSs <- system.file("extdata", "S288C_TSSs.RDS", package = "TSRexploreR")
TSSs <- readRDS(TSSs)

annotation <- system.file("extdata", "S288C_Annotation.gtf", package = "TSRexploreR")

samples <- data.frame(
  sample_name=c(sprintf("S288C_D_%s", seq_len(3)), sprintf("S288C_WT_%s", seq_len(3))),
  file_1=NA, file_2=NA,
  condition=c(rep("Diamide", 3), rep("Untreated", 3))
)
```

```
exp <- tsr_explorer(TSSs, genome_annotation=annotation, sample_sheet=samples) %>%
  format_counts(data_type = "tss") %>%
  tss_clustering(threshold=3) %>%
  merge_samples(data_type = "tss", merge_group="condition") %>%
  merge_samples(data_type = "tsr", merge_group="condition")
```

Calculate Shifting

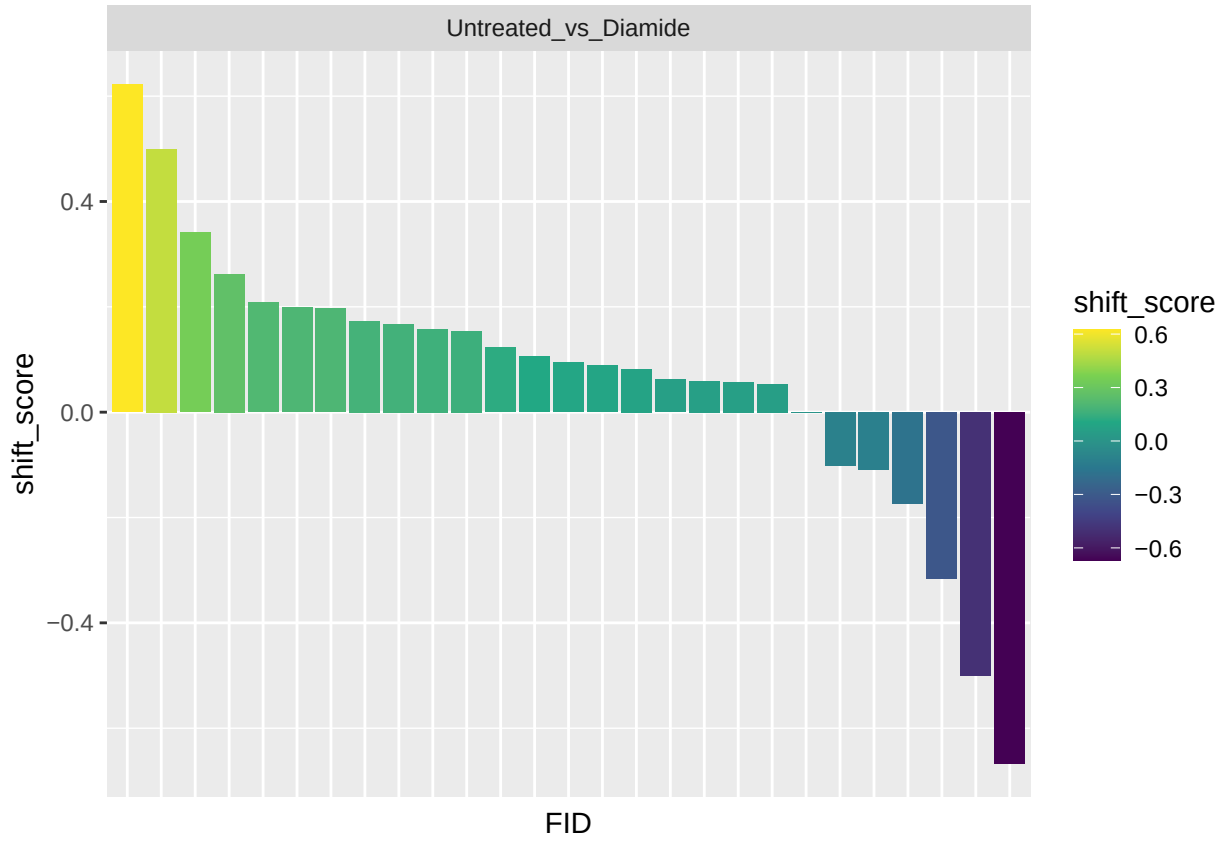
Calculate the shifting scores.

```
exp <- tss_shift(
  exp,
  sample_1=c(TSS="Untreated", TSR="Untreated"),
  sample_2=c(TSS="Diamide", TSR="Diamide"),
  comparison_name="Untreated_vs_Diamide",
  min_distance = 100, min_threshold = 10, n_resamples = 1000L
)
```

Shifting Plots

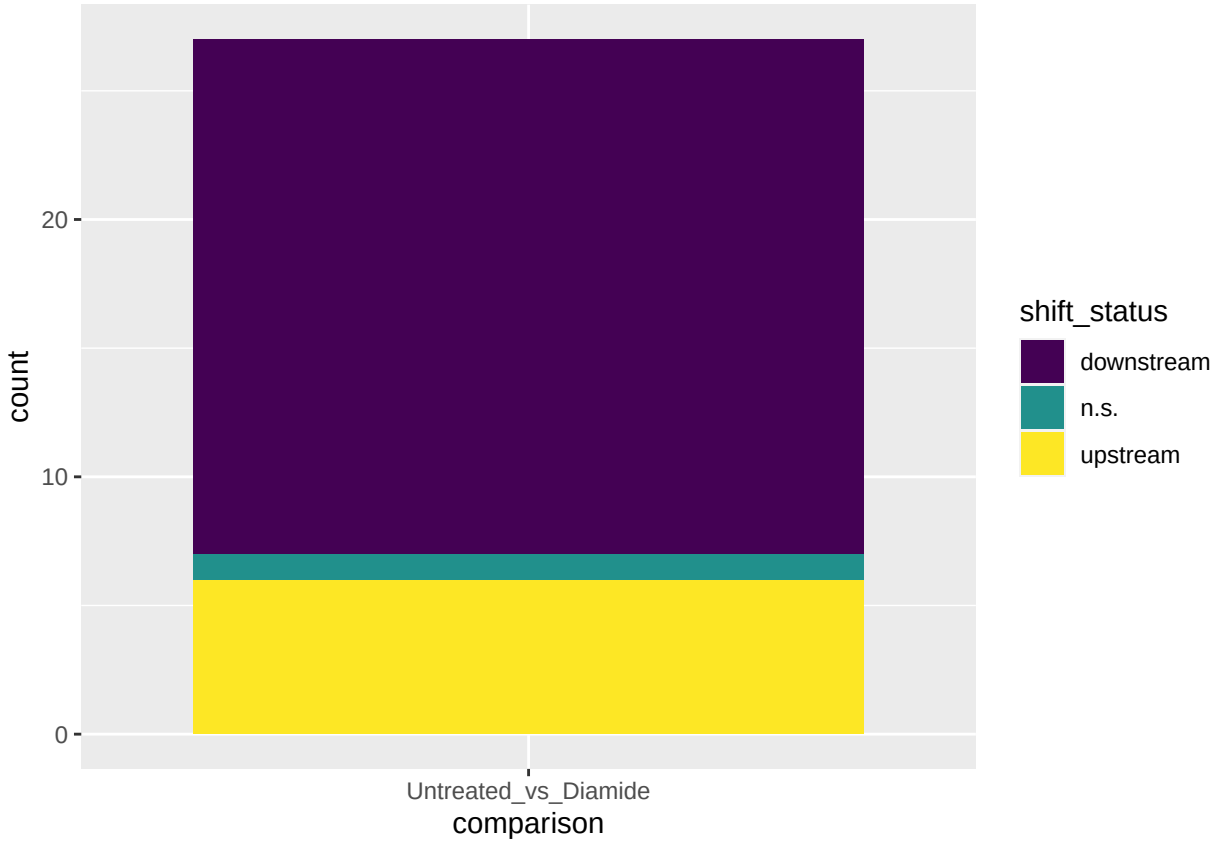
Create a shift score rank plot.

```
plot_shift_rank(exp) +
  scale_fill_viridis_c()
```



Create a shifting status count plot.

```
plot_shift_count(exp) +
  scale_fill_viridis_d()
```



Annotate Shifting

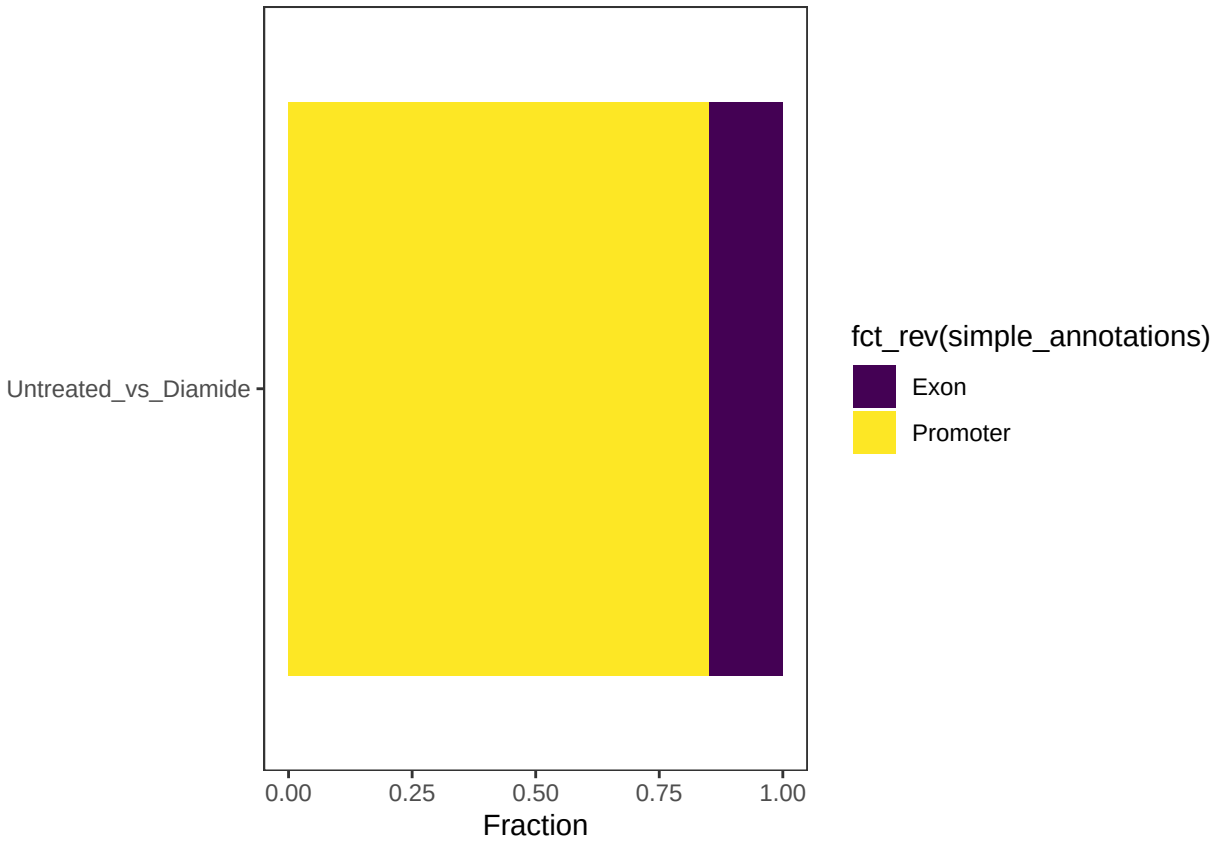
Annotate the shifted ranges.

```
exp <- annotate_features(exp, data_type="shift", feature_type="transcript")
```

```
## >> preparing features information...      2020-12-18 08:55:20 AM
## >> identifying nearest features...        2020-12-18 08:55:20 AM
## >> calculating distance from peak to TSS...   2020-12-18 08:55:20 AM
## >> assigning genomic annotation...        2020-12-18 08:55:20 AM
## >> assigning chromosome lengths           2020-12-18 08:55:21 AM
## >> done...                    2020-12-18 08:55:21 AM
```

Plot the genomic distribution.

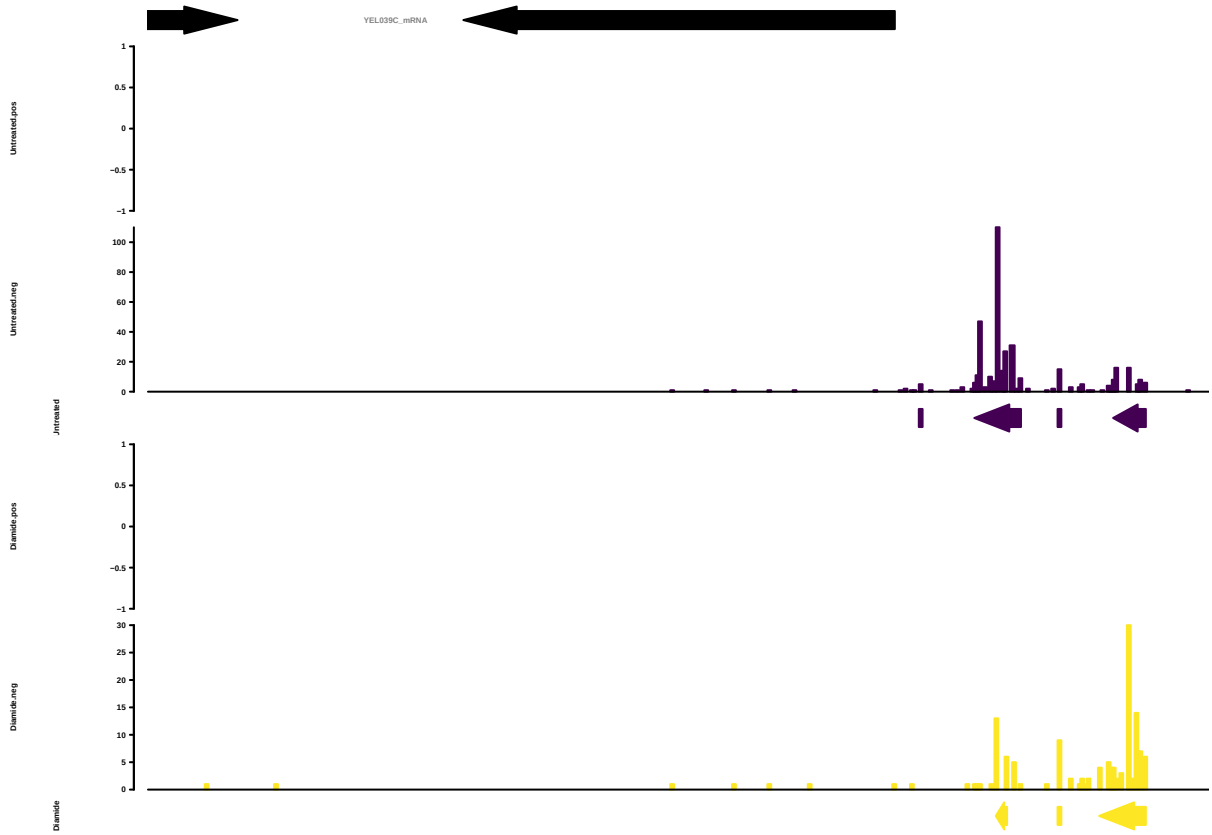
```
distribution <- genomic_distribution(exp, data_type="shift")

plot_genomic_distribution(distribution) +
  scale_fill_viridis_d()
```



Gene Tracks

Gene track of an example result.

```
gene_tracks(
  exp, feature_name="YEL039C",
  samples=c(
    TSS="Untreated", TSR="Untreated",
    TSS="Diamide", TSR="Diamide"
  ),
  tss_colors=viridis::viridis(2),
  tsr_colors=viridis::viridis(2)
)
```


YEL039C_mRNA
Untreated.pos
Untreated.neg
Untreated
Diamide.pos
Diamide.neg
Diamide