TSS Shifting

```
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 the shifting scores and return as table.

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

seqnames	start	end	strand	shift_score	pval	FDR
I	139567	141675	-	-0.0937736	0	0
I	225159	225159	+	0.0000000	0	0
II	105941	105941	-	0.5000000	0	0
II	13931	13931	-	-0.5000000	0	0
II	187315	187316	-	-0.5000000	0	0
II	29884	29884	+	0.0000000	0	0