Bam Processing

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Create tsrexplorer object.

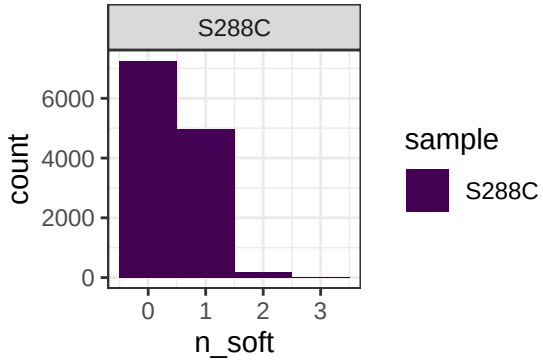
```
# BAM file.
bam_file <- system.file("extdata", "S288C.bam", package="TSRexploreR")

# Genome assembly.
assembly <- system.file("extdata", "S288C_Assembly.fasta", package="TSRexploreR")

# Sample sheet.
samples <- data.frame(sample_name="S288C", file_1=bam_file, file_2=NA)

exp <- tsr_explorer(sample_sheet=samples, genome_assembly=assembly)
```

Import BAMs.

```
exp <- import_bams(exp, paired=TRUE, proper_pair=TRUE)
```

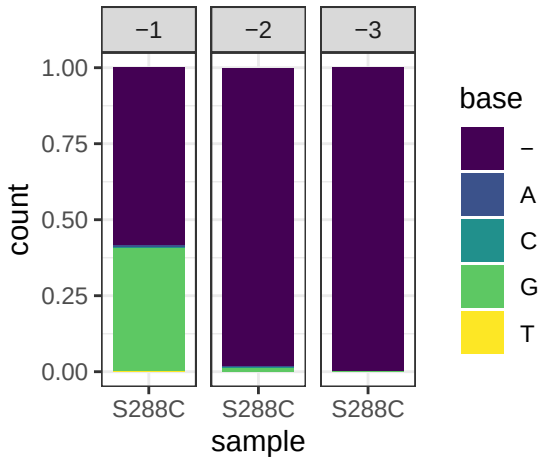
Plot soft-clipped histogram.

```
softclip_histogram(exp) +
  theme_bw() +
  scale_fill_viridis_d()
```



Plot softclipped base frequency.

```
softclip_composition(exp) +
  theme_bw() +
  scale_fill_viridis_d()
```



Correct for G content.

```
exp <- G_correction(exp)
```

Aggregate TSSs by position.

```
exp <- tss_aggregate(exp)
```