

Bam Processing

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Create tsrexplorer object.

```
exp <- tsr_explorer()
```

Prepare sample sheet.

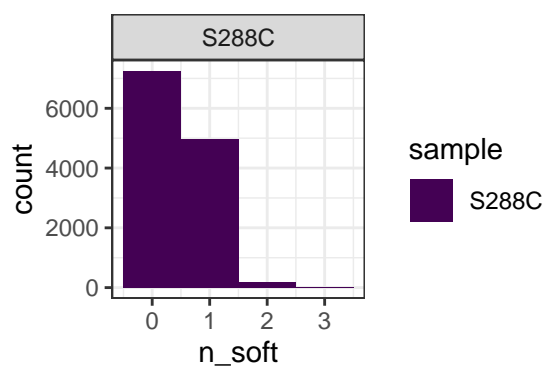
```
bam_file <- system.file("extdata", "S288C.bam", package="TSRexploreR")
samples <- data.frame(sample_name="S288C", file_1=bam_file)
```

Import BAMs.

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

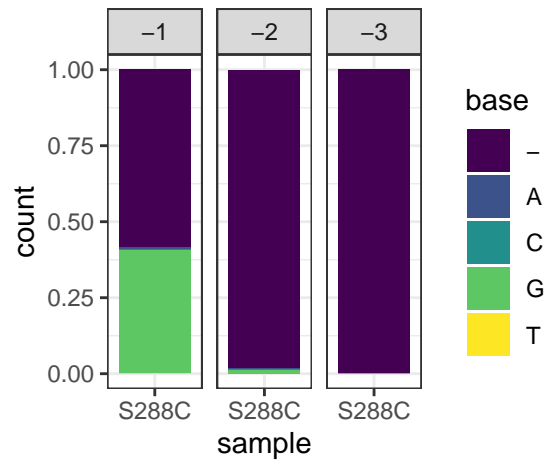
Plot soft-clipped histogram.

```
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.

```
assembly <- system.file("extdata", "S288C_Assembly.fasta", package="TSRexploreR")
exp <- G_correction(exp, assembly)
```

Aggregate TSSs by position.

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