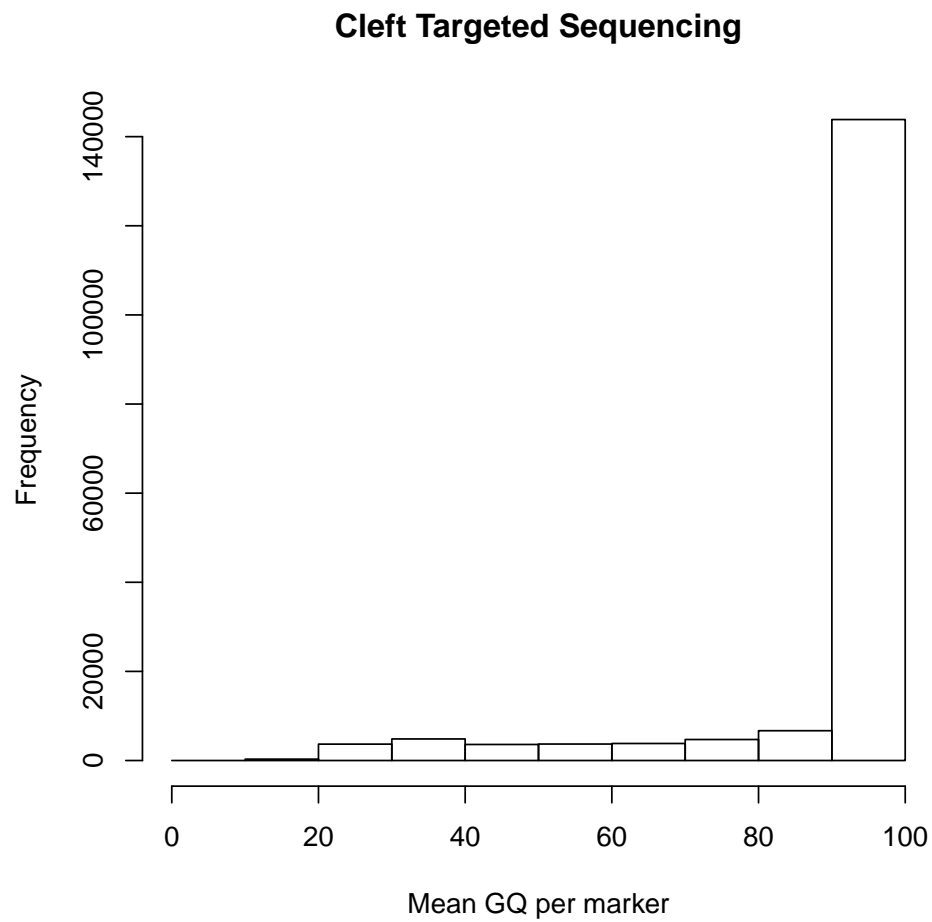```
> hist(gq.marker, xlab = "Mean GQ per marker", breaks = 10,
    xlim = c(0, 100), main = "Cleft Targeted Sequencing")
```

**Cleft Targeted Sequencing**



```
> data(gq.marker)

> summary(gq.marker)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  9.739  97.350  99.890  91.880  99.970 100.000
```

```
> F.marker <- ecdf(gq.marker)
> plot(x = x <- seq(0, 100, length.out = 10000), y = F.marker(x),
    type = "l", xlim = range(gq.marker), lwd = 2, main = "Cleft Targeted Sequencing",
    xlab = "Mean GQ per marker", ylab = "CDF")
```

Cleft Targeted Sequencing