# Normal quantile plots

# The normal quantile plot

- see that normal distributions of data (or being normal enough) important
- only tools we have to assess this are histograms and maybe boxplots
- a better tool is **normal quantile plot**:
  - plot data against what you expect if data actually normal
  - look for points to follow a straight line, at least approx
- `ggplot` code: `aes` `sample`; geoms `stat_qq` and `stat_qq_line`

# Packages

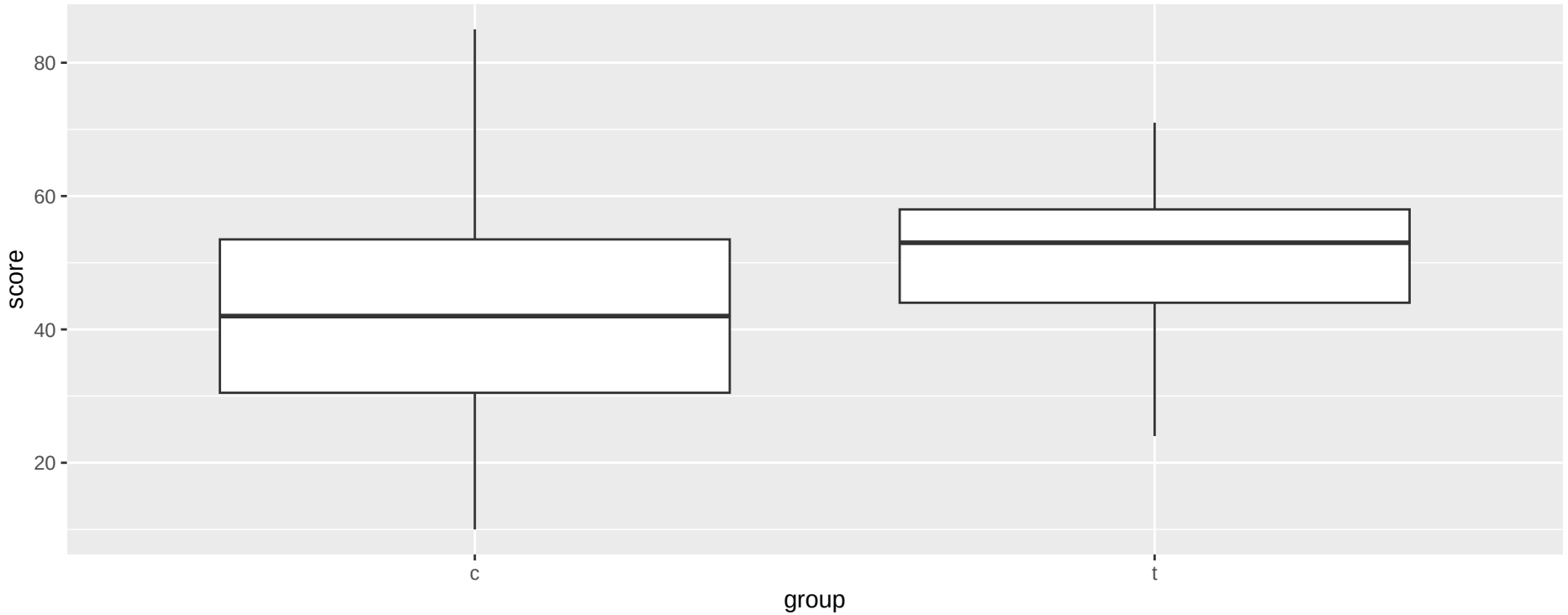
The usual:

```
library(tidyverse)
```

# Kids learning to read

```
Rows: 44
Columns: 2
$ group <chr> "t", "t", "t", "t", "t", "t", "t", "t", "t", "t"
$ score <dbl> 24, 61, 59, 46, 43, 44, 52, 43, 58, 67, 62, 57,
```

```
ggplot(kids, aes(x = group, y = score)) + geom_boxplot()
```



# Get the groups separately

```
kids %>% filter(group == "t") -> treatment
kids %>% filter(group == "c") -> control
```

to check

```
treatment %>% count(group)
```

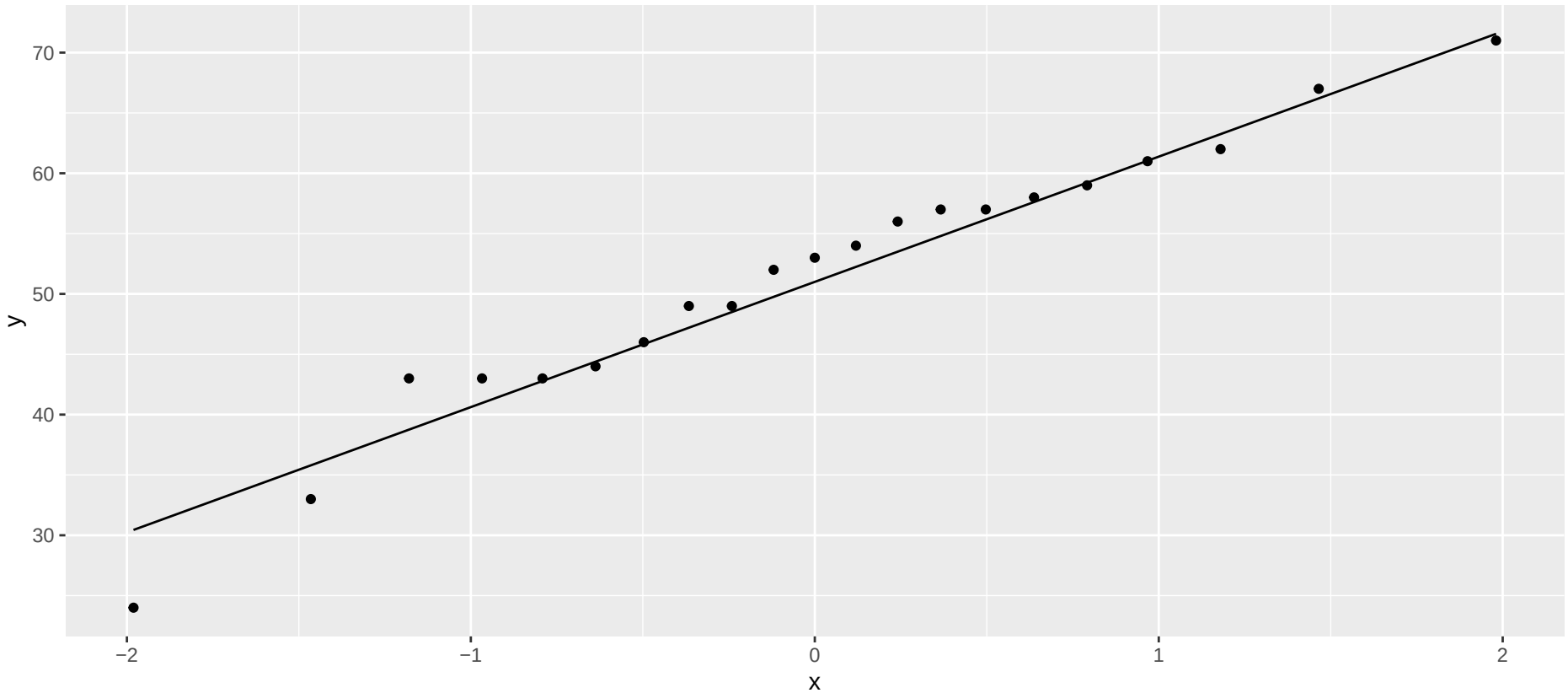
```
# A tibble: 1 x 2
  group     n
  <chr> <int>
1 t        21
```

```
control %>% count(group)
```

```
# A tibble: 1 x 2
  group     n
  <chr> <int>
1 c        23
```

# The treatment group

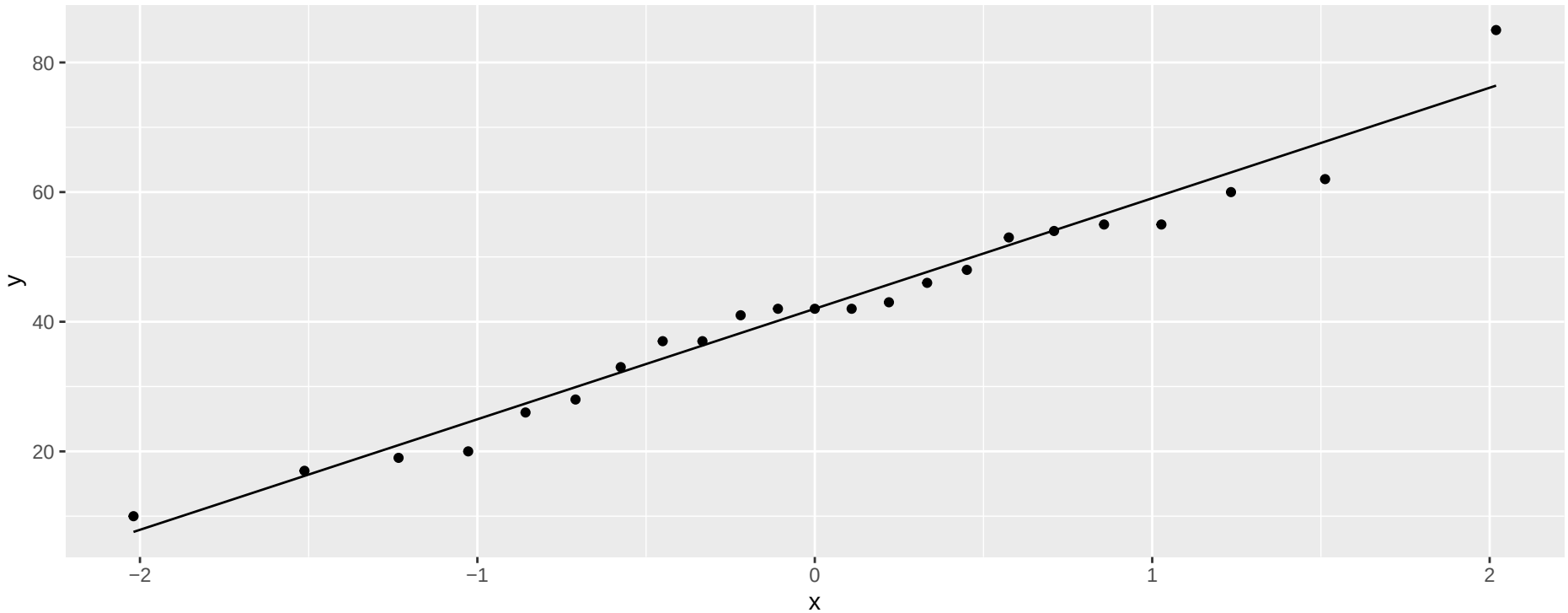
```
ggplot(treatment, aes(sample = score)) +
  stat_qq() + stat_qq_line()
```




only problem here is lowest value a little too low (mild outlier).

# Control group

```
ggplot(control, aes(sample = score)) +
  stat_qq() + stat_qq_line()
```

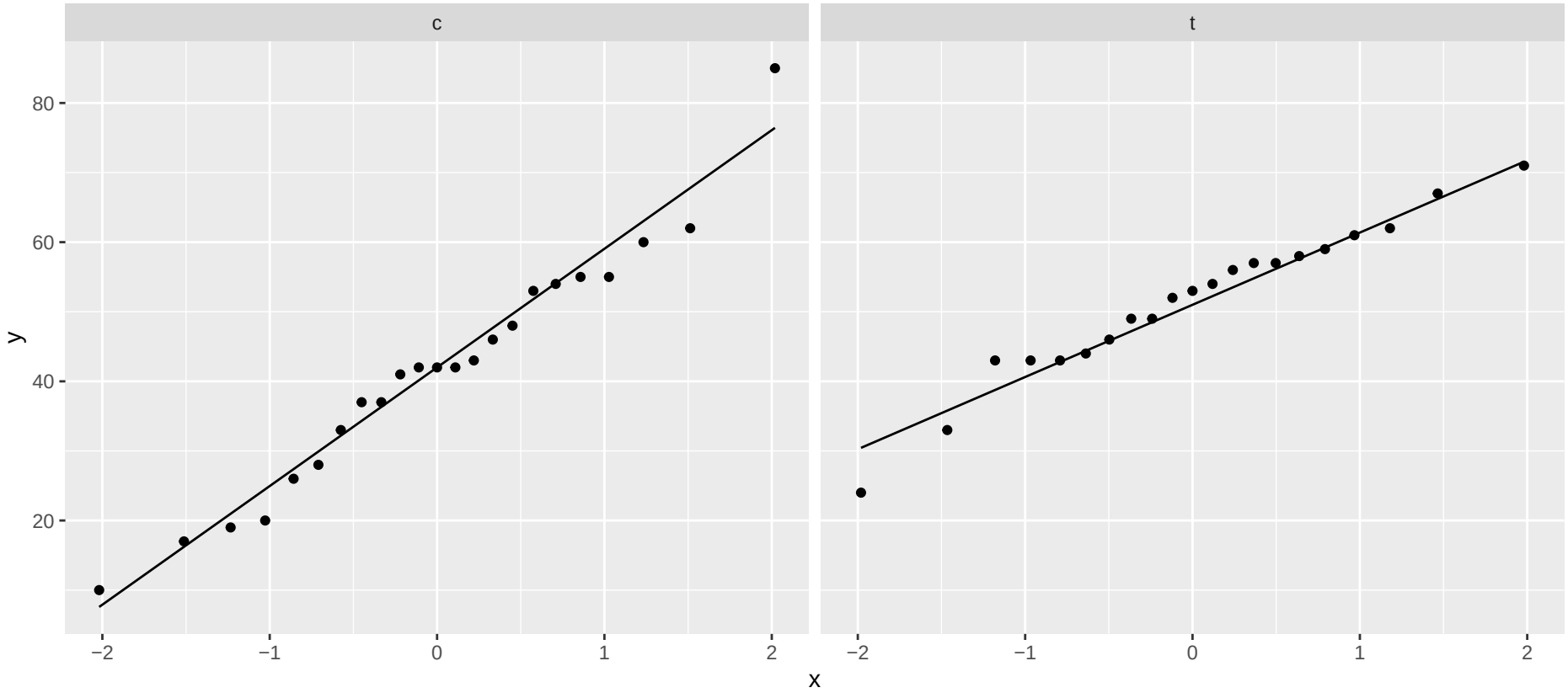



This time, highest value a little too high, but again, no real problem with normality.

# Facetting more than one sample

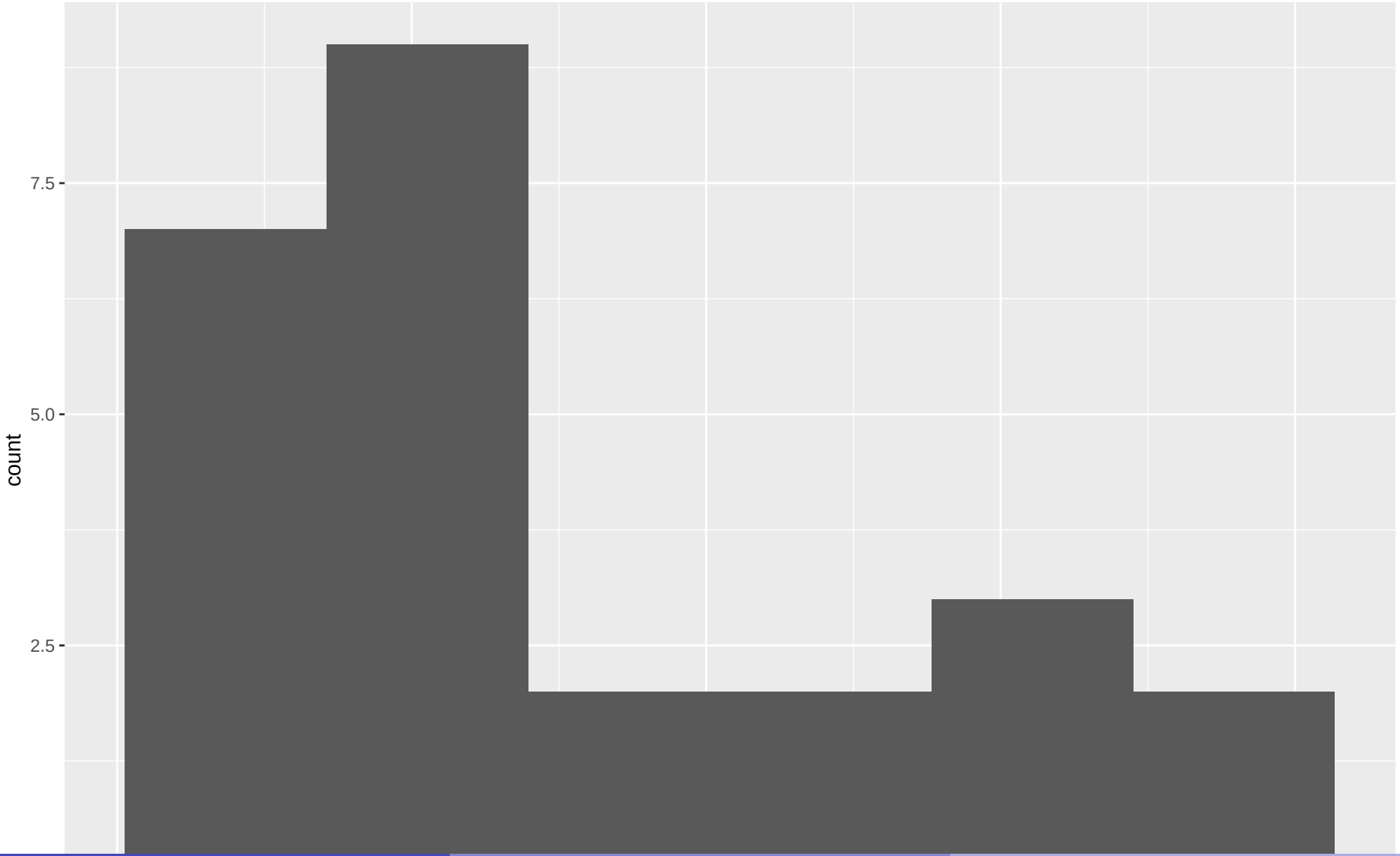
Use the whole data set and facet by groups

```
ggplot(kids, aes(sample = score)) +
  stat_qq() + stat_qq_line() + facet_wrap(~group)
```



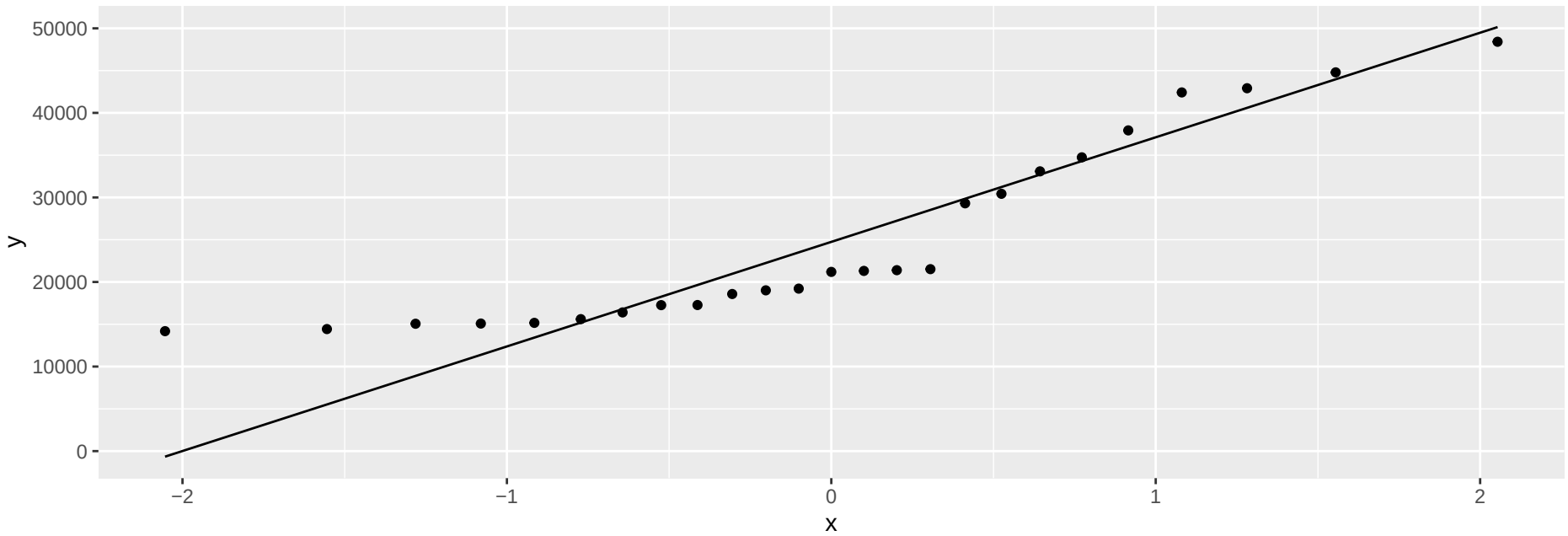
# Blue Jays attendances, skewed to right

```
ggplot(jays, aes(x = attendance)) + geom_histogram(bins = 6)
```



# On a normal quantile plot

```
ggplot(jays, aes(sample = attendance)) +
  stat_qq() + stat_qq_line()
```



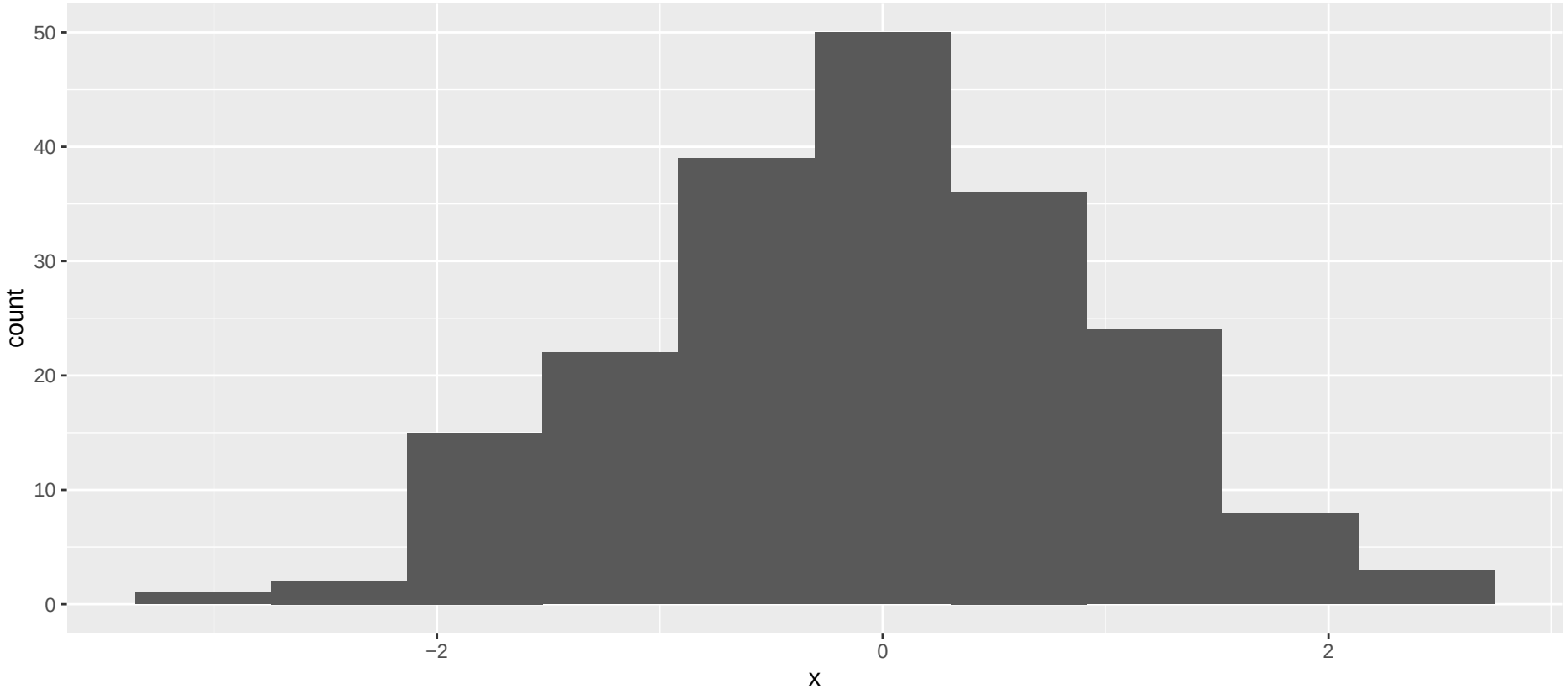

- Attendances at low end too bunched up: skewed to right.
- Right-skewness can also show up as highest values being too high, or as a curved pattern in the points.

# More normal quantile plots

- How straight does a normal quantile plot have to be?
- There is randomness in real data, so even a normal quantile plot from normal data won't look perfectly straight.
- With a small sample, can look not very straight even from normal data.
- Looking for systematic departure from a straight line; random wiggles ought not to concern us.
- Look at some examples where we know the answer, so that we can see what to expect.

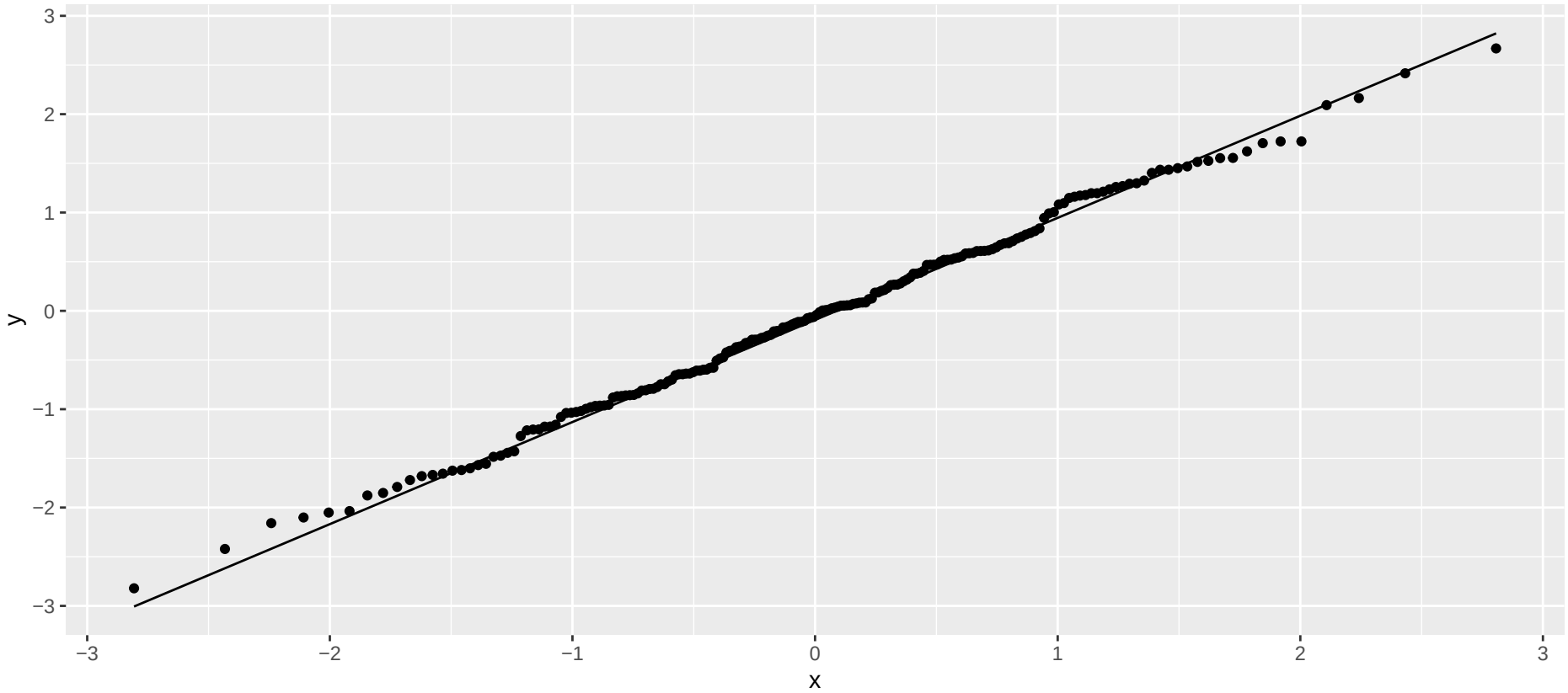
# Normal data, large sample

```
d <- tibble(x=rnorm(200))
ggplot(d, aes(x=x)) + geom_histogram(bins=10)
```



# The normal quantile plot

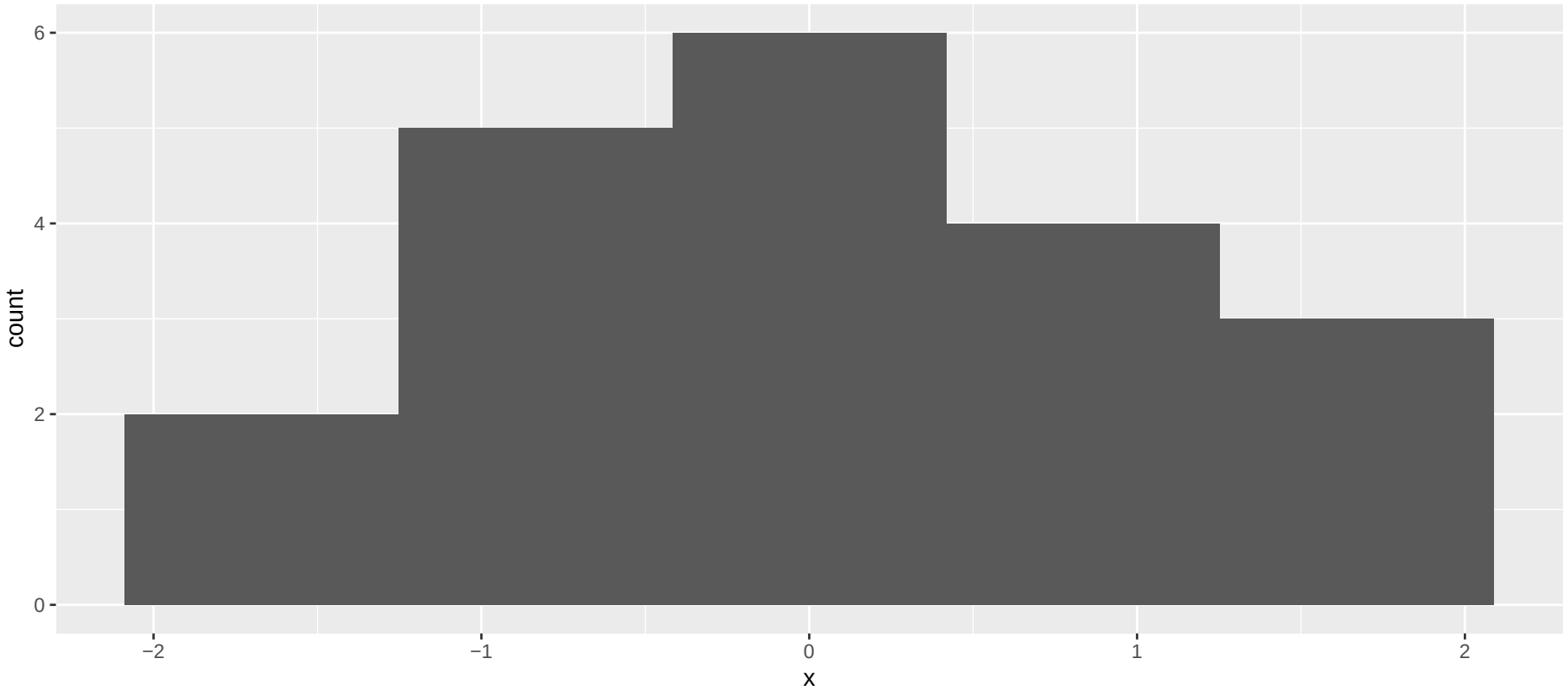
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



# Normal data, small sample

- Not so convincingly normal, but not obviously skewed:

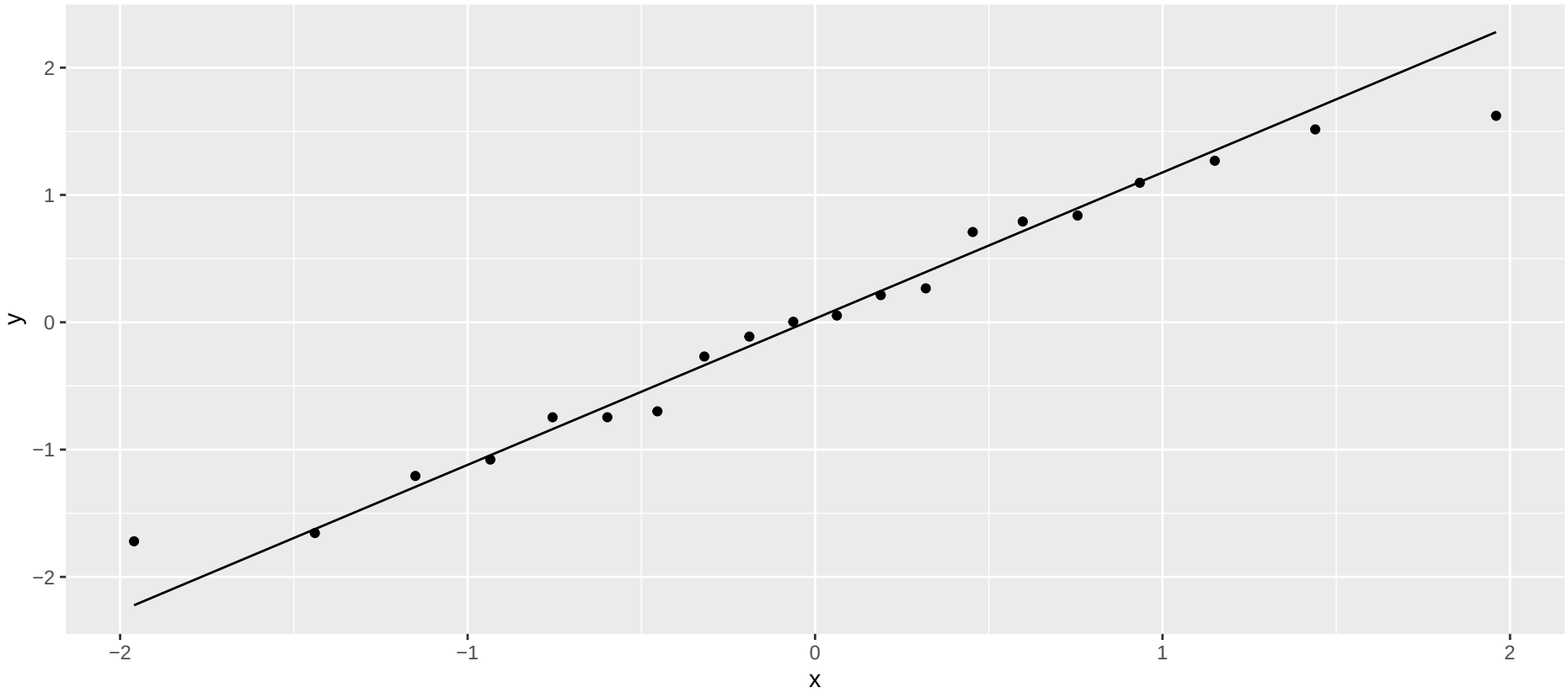
```
d <- tibble(x=rnorm(20))
ggplot(d, aes(x=x)) + geom_histogram(bins=5)
```



# The normal quantile plot

Good, apart from the highest and lowest points being slightly off. I'd call this good:

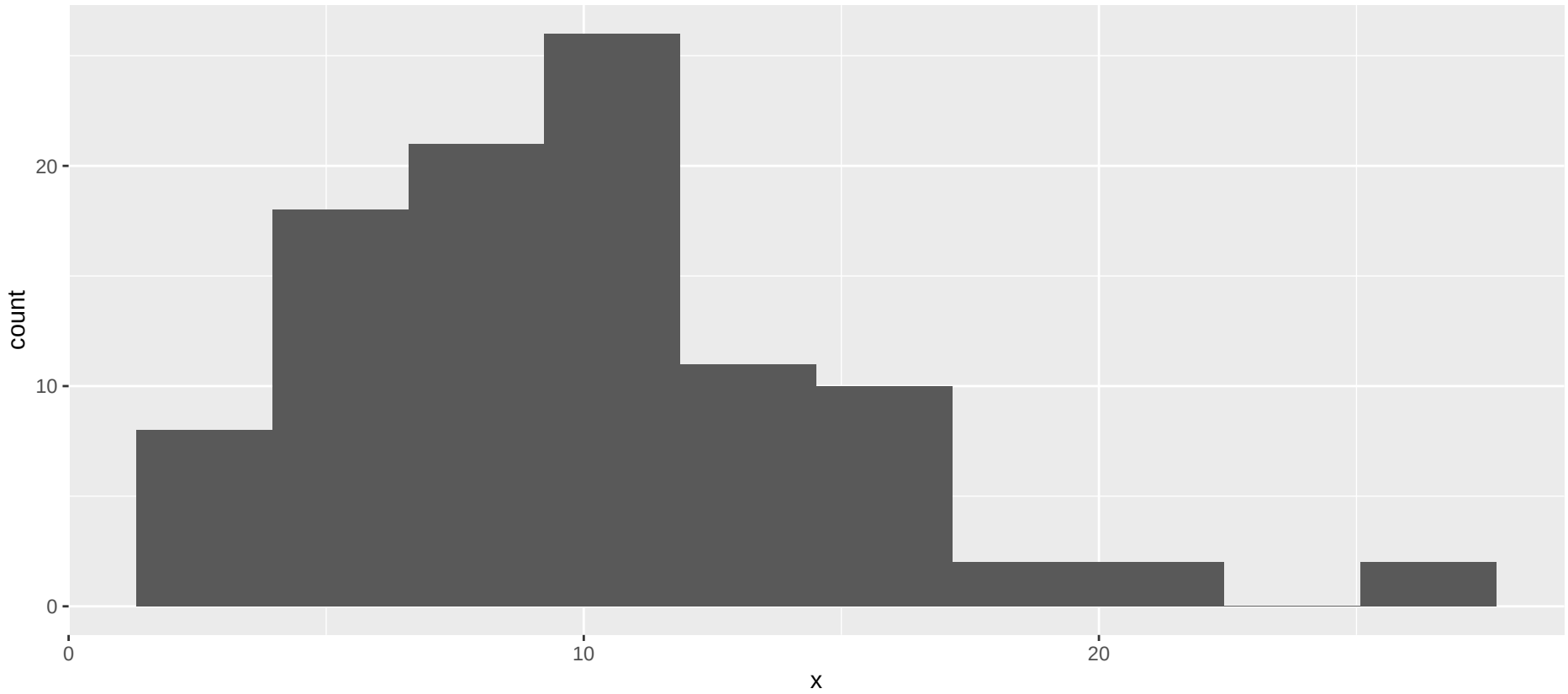
```
ggplot(d, aes(sample=x)) + stat_qq() + stat_qq_line()
```



# Chi-squared data, $df = 10$

Somewhat skewed to right:

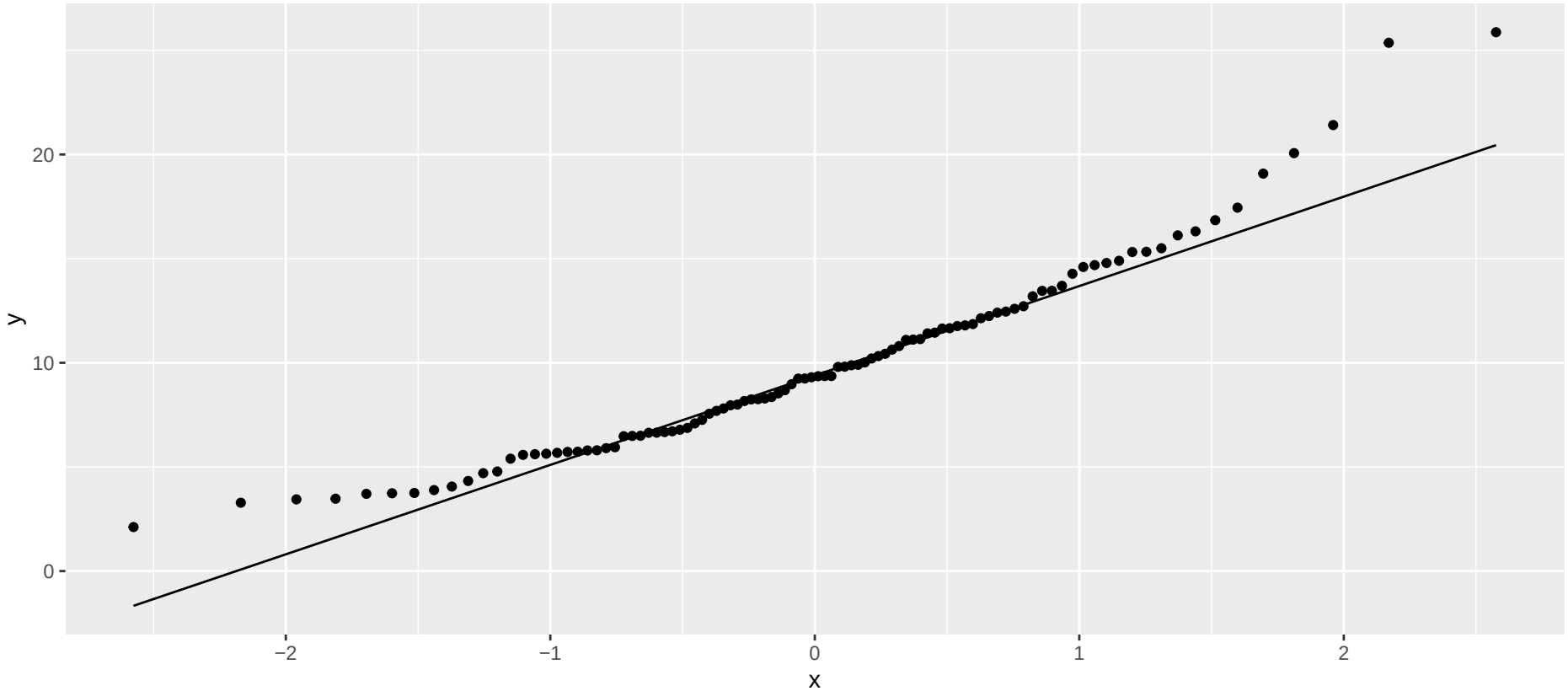
```
d <- tibble(x=rchisq(100, 10))
ggplot(d,aes(x=x)) + geom_histogram(bins=10)
```



# The normal quantile plot

Somewhat opening-up curve:

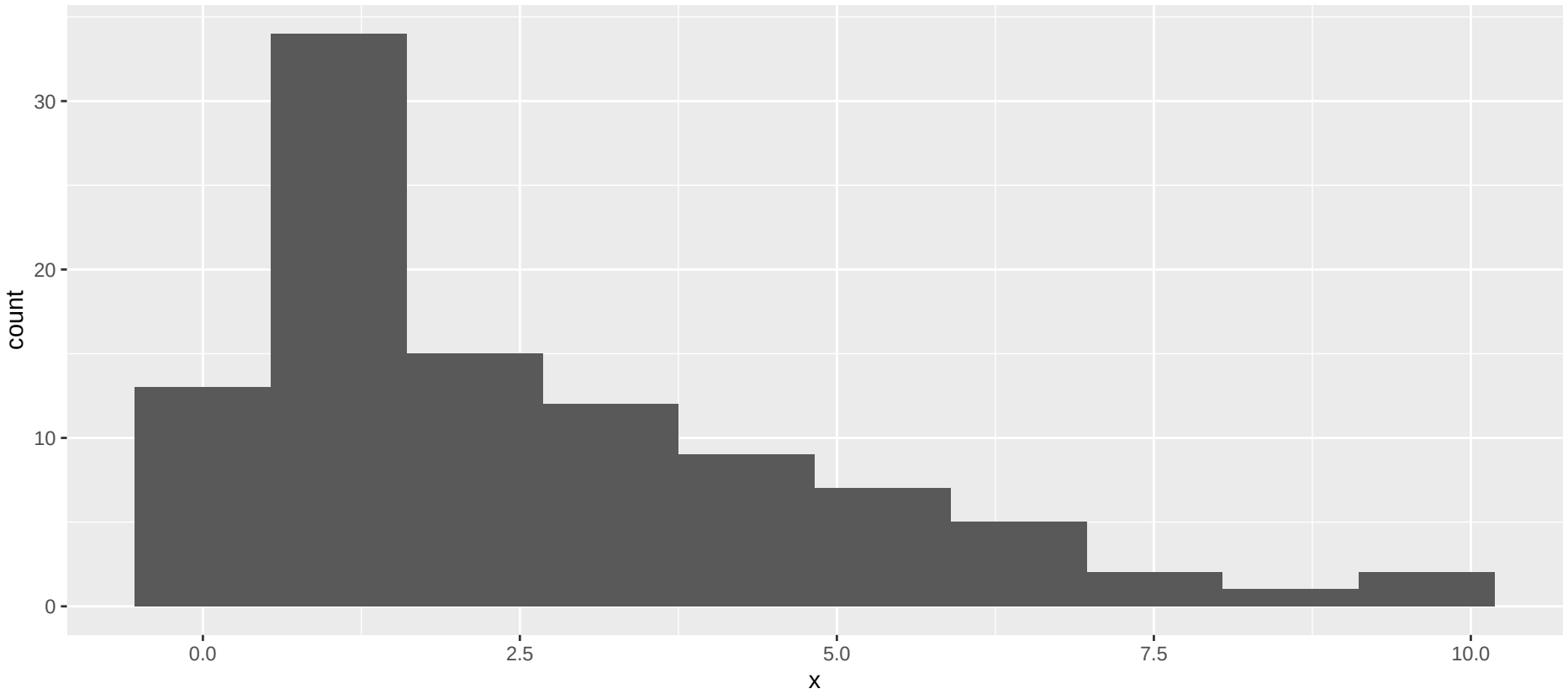
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



# Chi-squared data, df = 3

Definitely skewed to right:

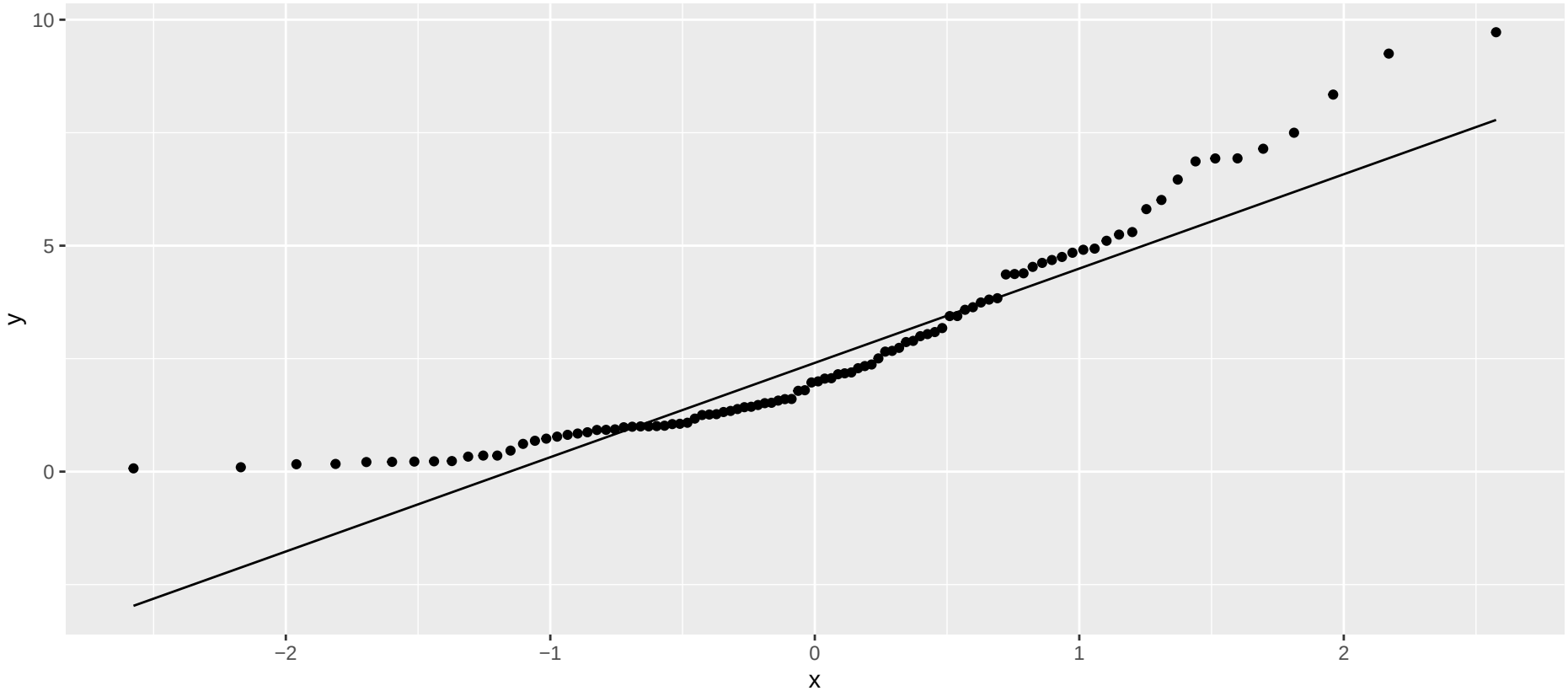
```
d <- tibble(x=rchisq(100, 3))
ggplot(d, aes(x=x)) + geom_histogram(bins=10)
```



# The normal quantile plot

Clear upward-opening curve:

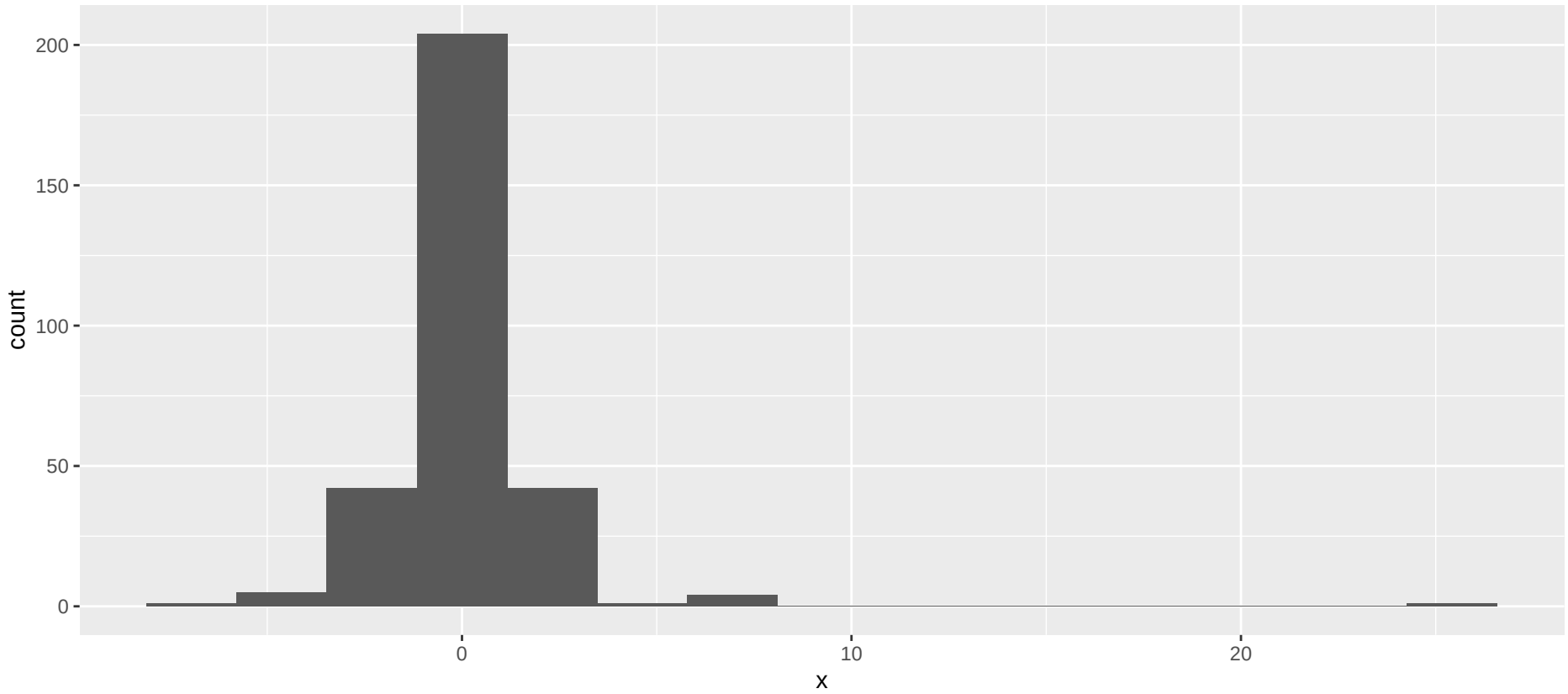
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



# t-distributed data, df = 3

Long tails (or a very sharp peak):

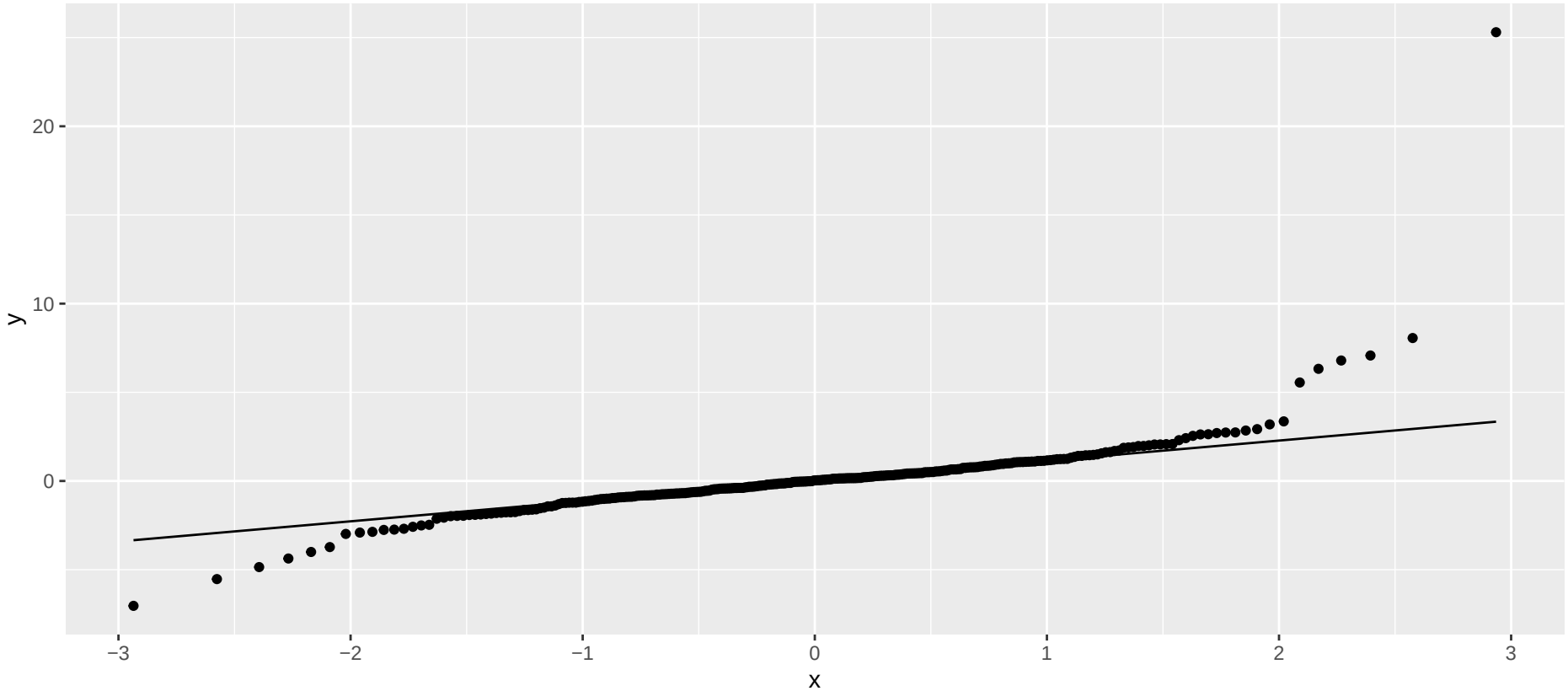
```
d <- tibble(x=rt(300, 3))
ggplot(d, aes(x=x)) + geom_histogram(bins=15)
```



# The normal quantile plot

Low values too low and high values too high for normal.

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



# Summary

On a normal quantile plot:

- points following line (with some small wiggles): normal.
- kind of deviation from a straight line indicates kind of nonnormality:
  - a few highest point(s) too high and/or lowest too low: outliers
  - else see how points at each end off the line:

| | High points | |
|---|---|---|
| **Low points** | **Too low** | **Too high** |
| **Too low** | Skewed left | Long tails |
| **Too high** | Short tails | Skewed right |

- short-tailed distribution OK for $t$ (mean still good), but others problematic (depending on sample size).