



gQTL v1.0

A web application to run QTL analysis on Collaborative Cross Mice.

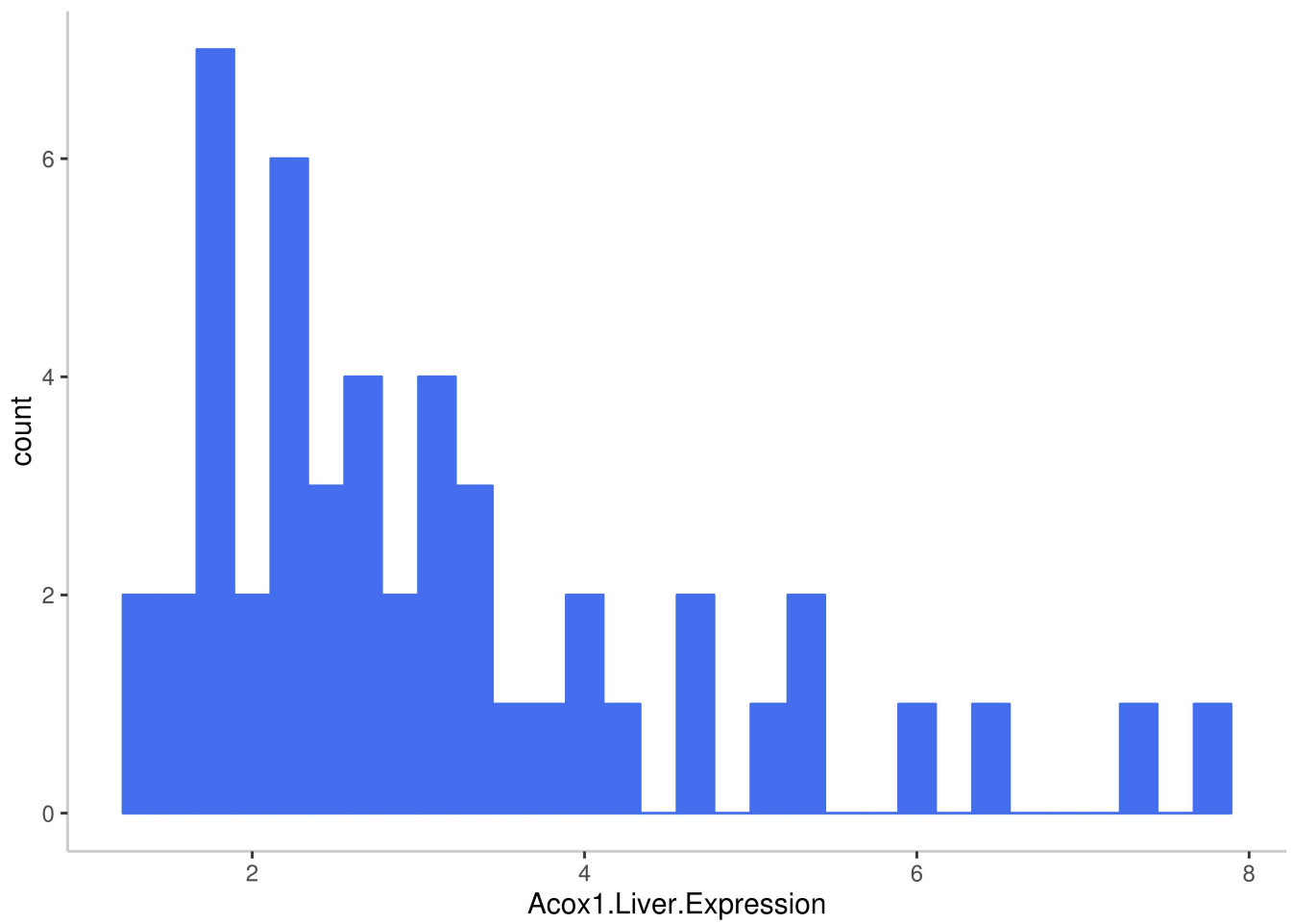
- **1. Outlier Strains**
- **2. Basic Plots**
 - 2.1 Histogram Plot(s)
 - 2.2 QQ Plot(s)
 - 2.3 Histogram Plot(s) (Normalized, Data Transformation: AUTO)
 - 2.4 QQ Plot(s) (Normalized, Data Transformation: AUTO)
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 - 3.1 Significant Thresholds
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Outlier Strains

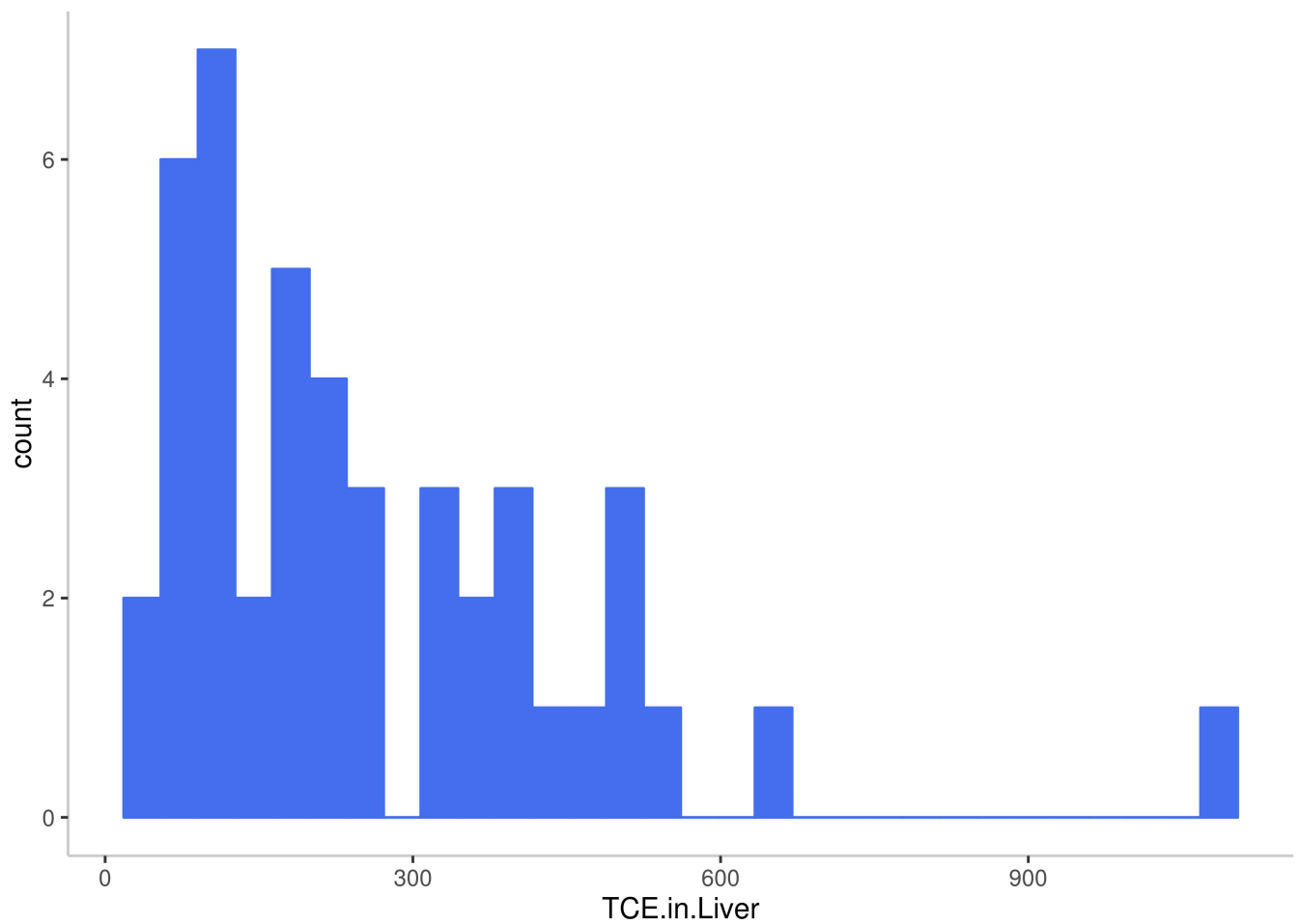
Acox1.Liver.Expression	CC010, CC016, CC004
TCE.in.Liver	CC016

Basic Plots

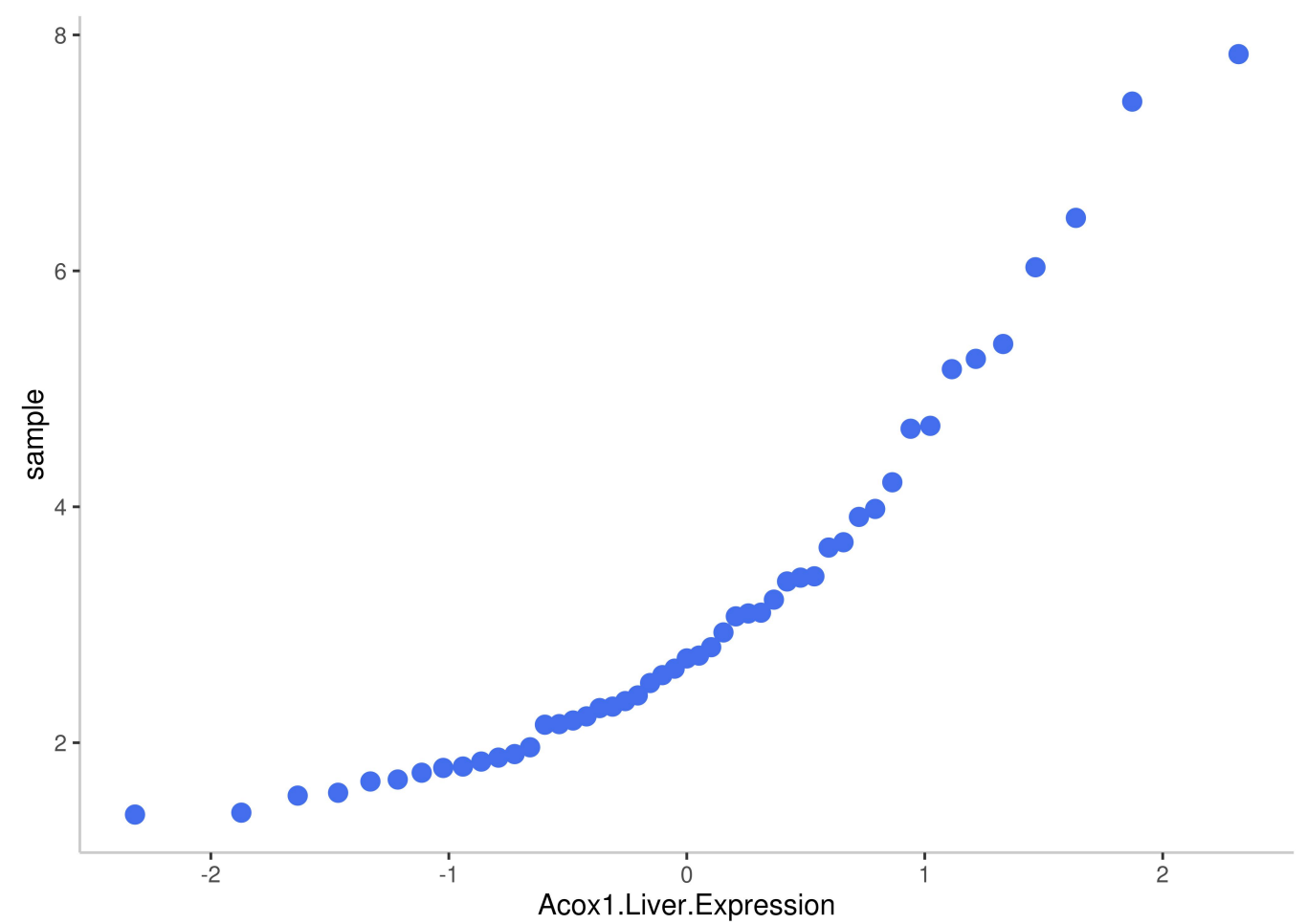
Histogram Plot



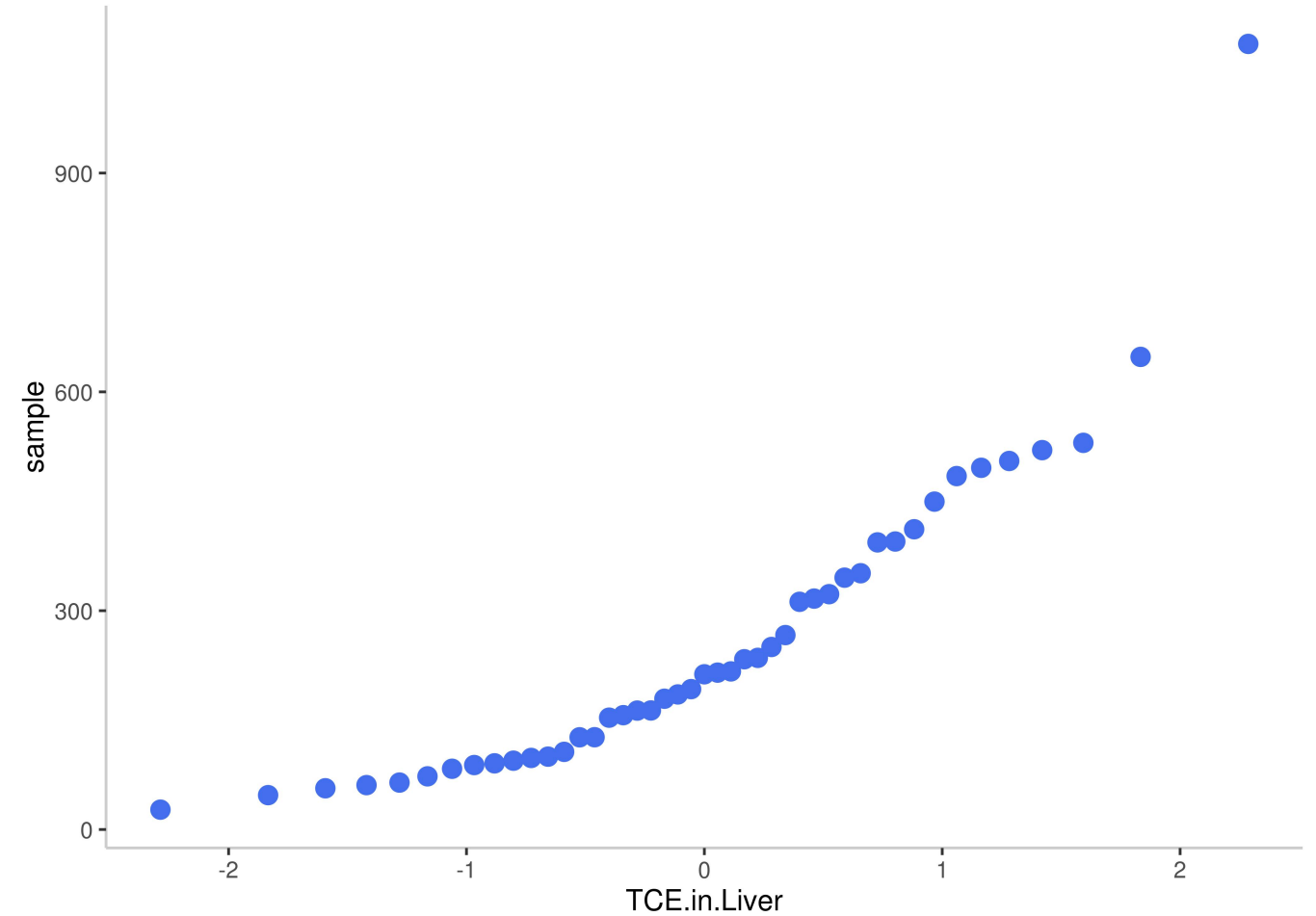
```
## Warning: Removed 4 rows containing non-finite values (stat_bin).
```



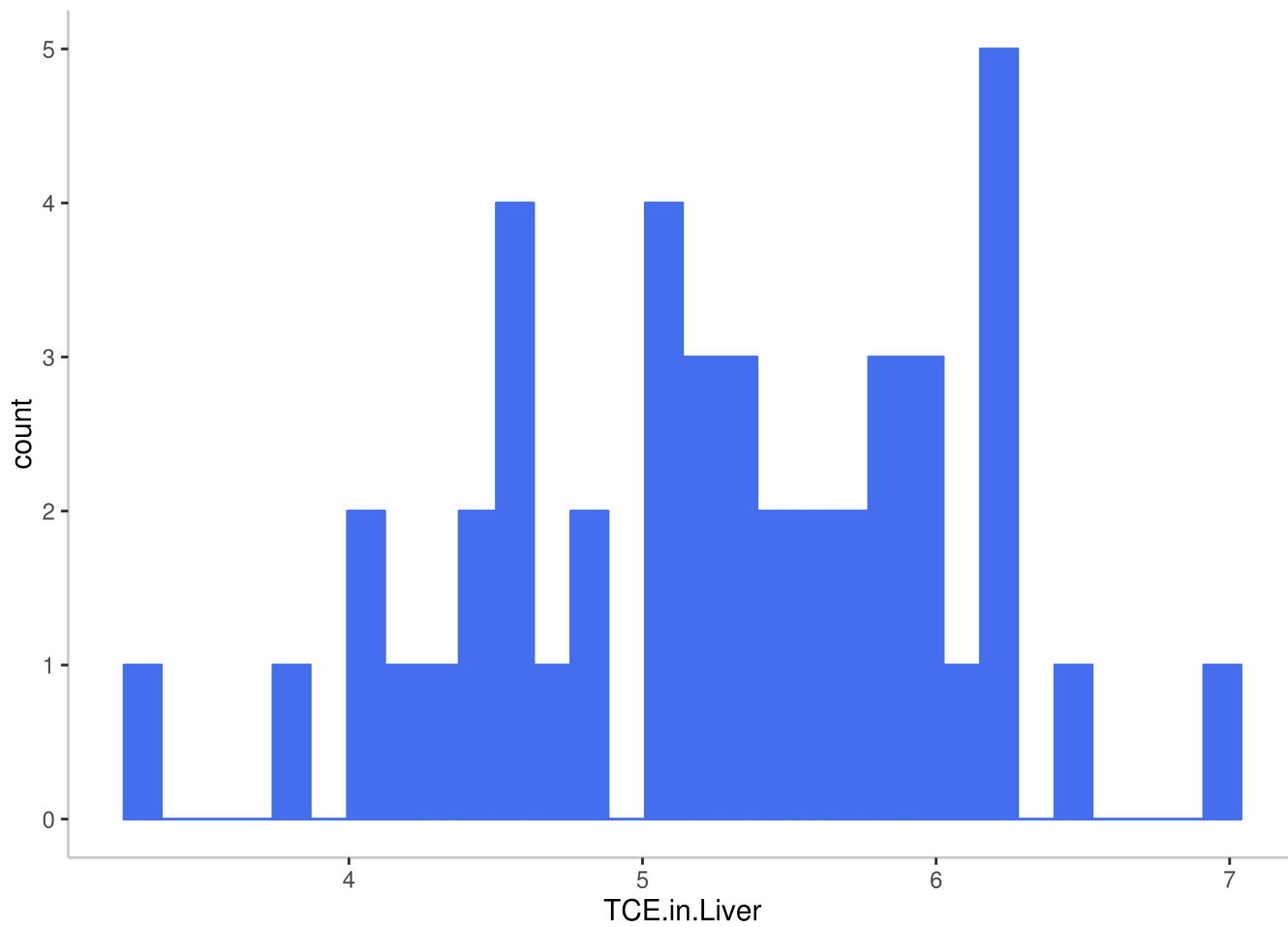
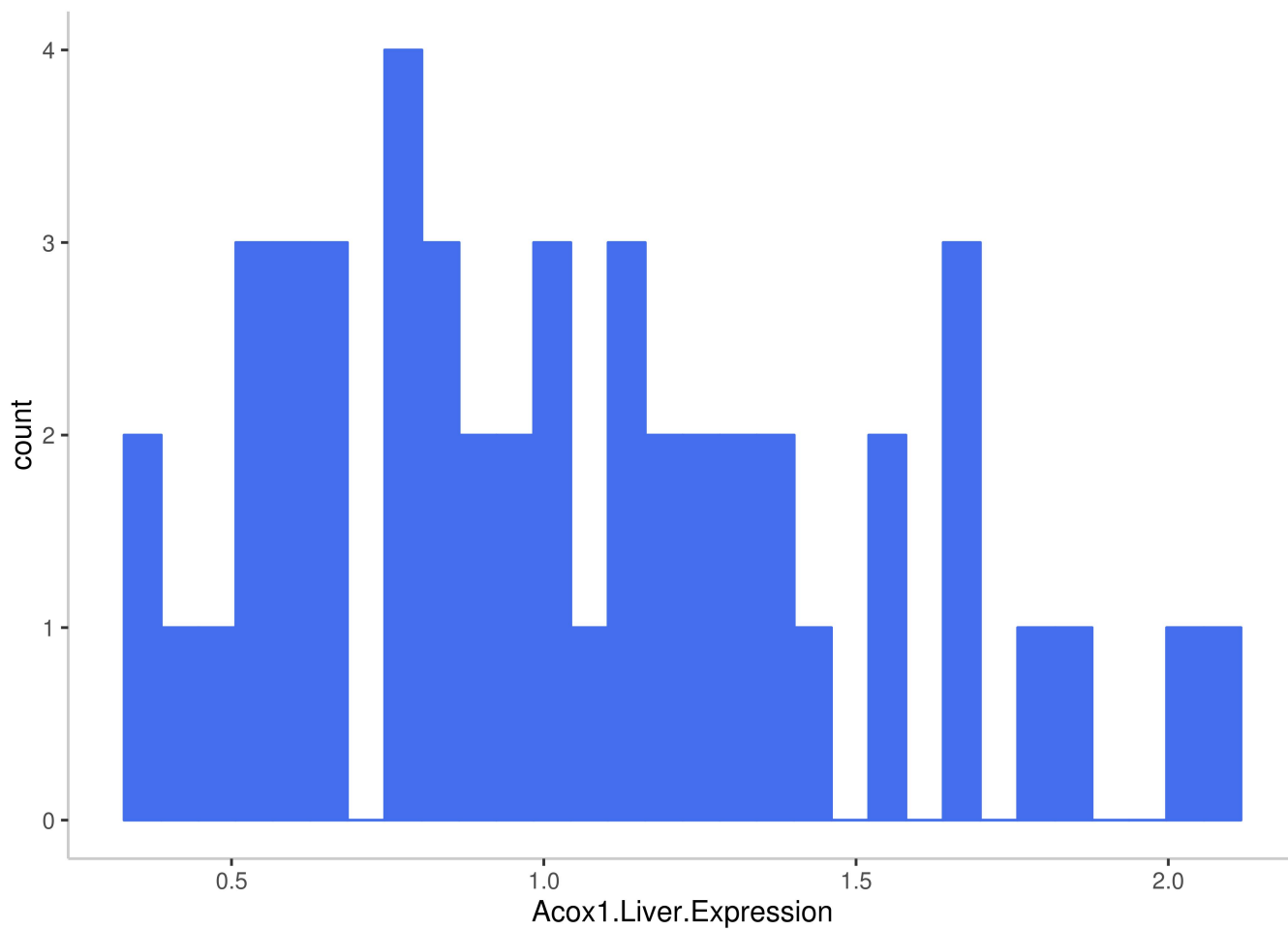
QQ Plot



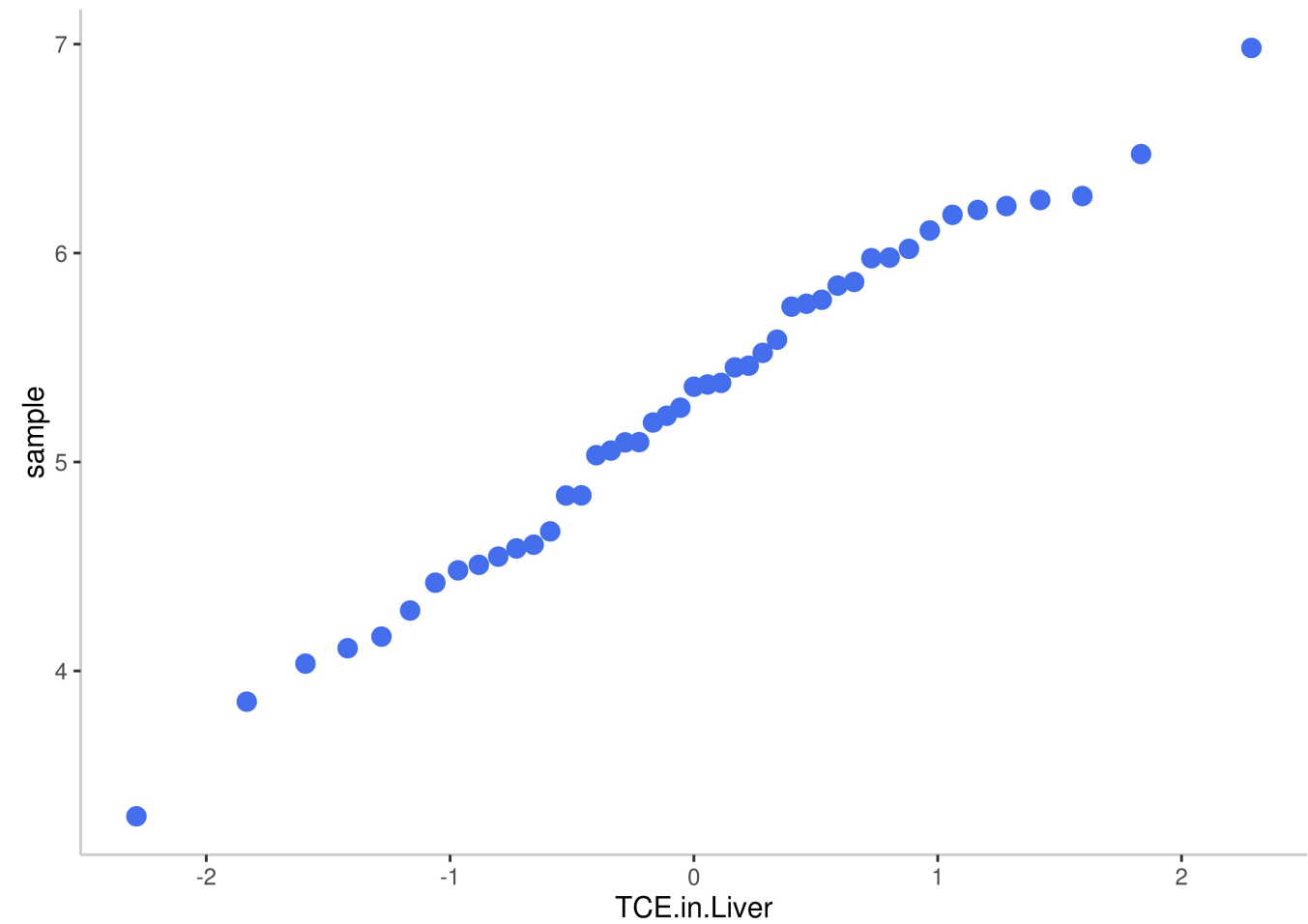
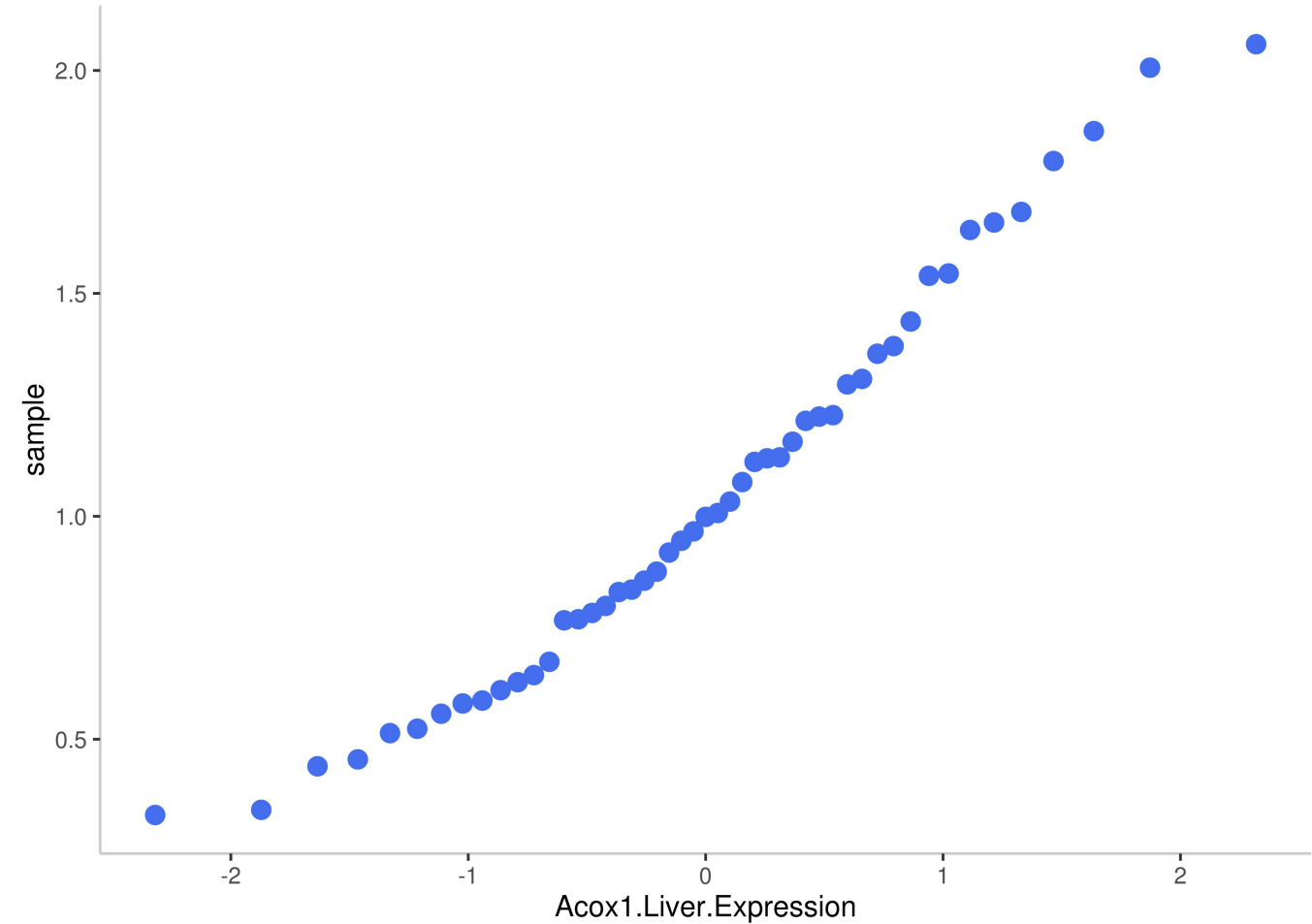
Warning: Removed 4 rows containing non-finite values (stat_qq).



Histogram Plot (Normalized, Data Transformation: Auto)



QQ Plot (Normalized, Data Transformation: Auto)

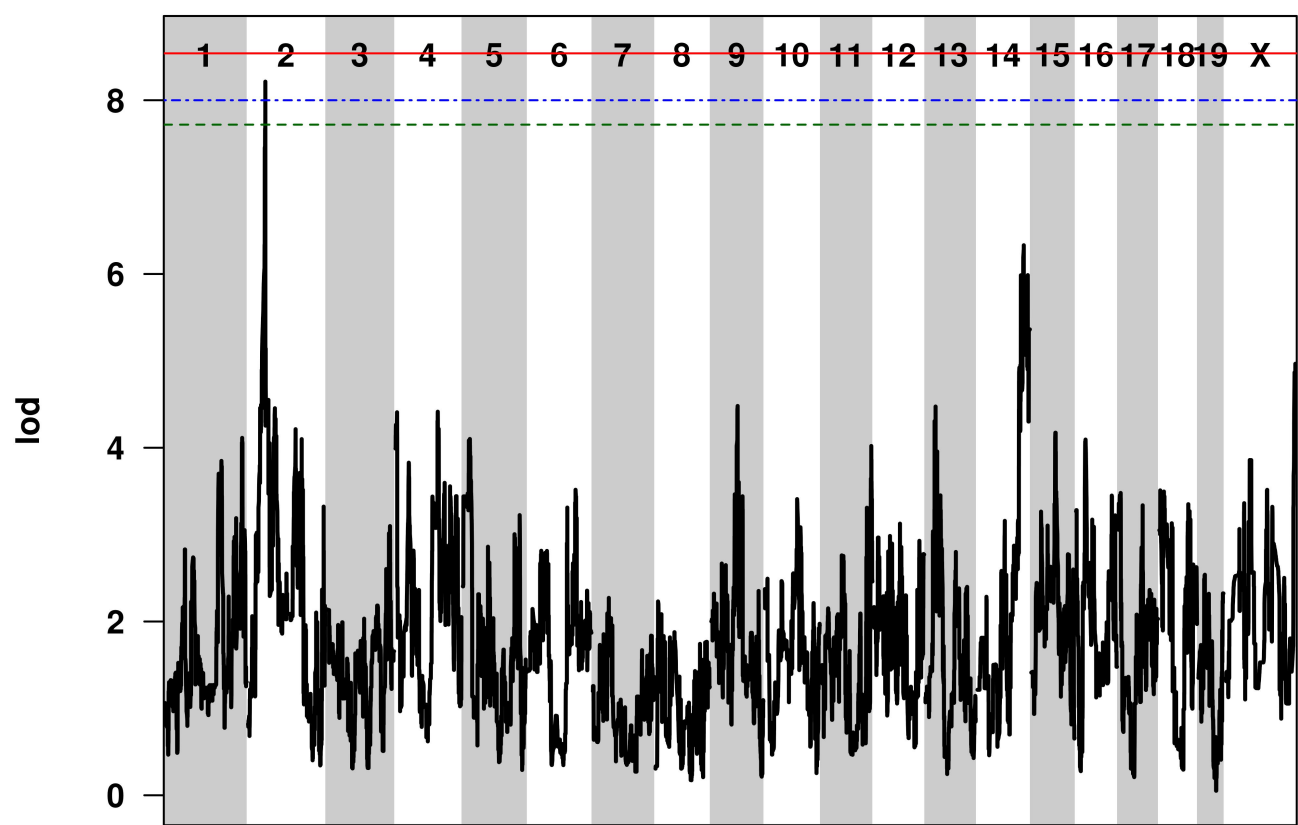


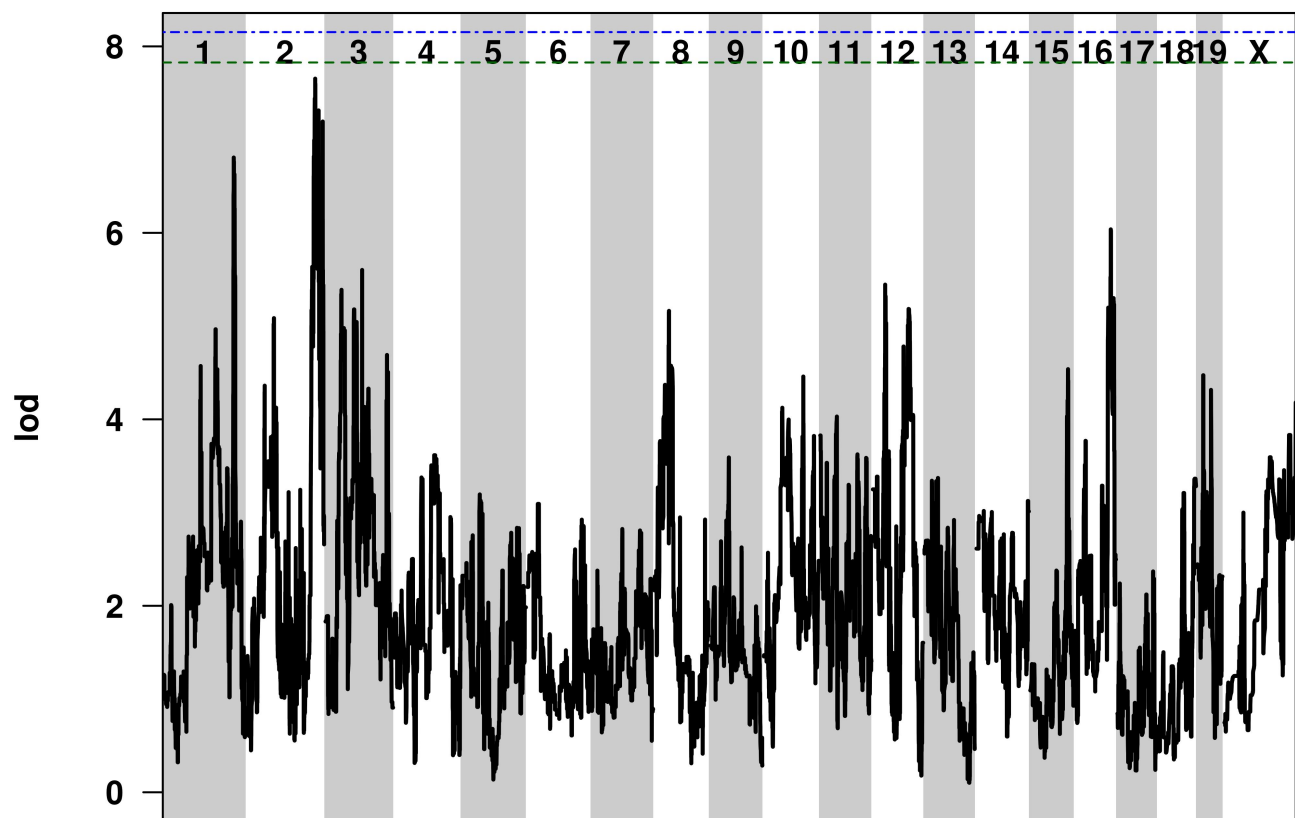
QTL Analysis

Significant Thresholds

	85%	90%	95%
Acox1.Liver.Expression	7.718916	7.999829	8.539686
TCE.in.Liver	7.827359	8.153166	8.578304

Manhattan Plots





Significant QTL

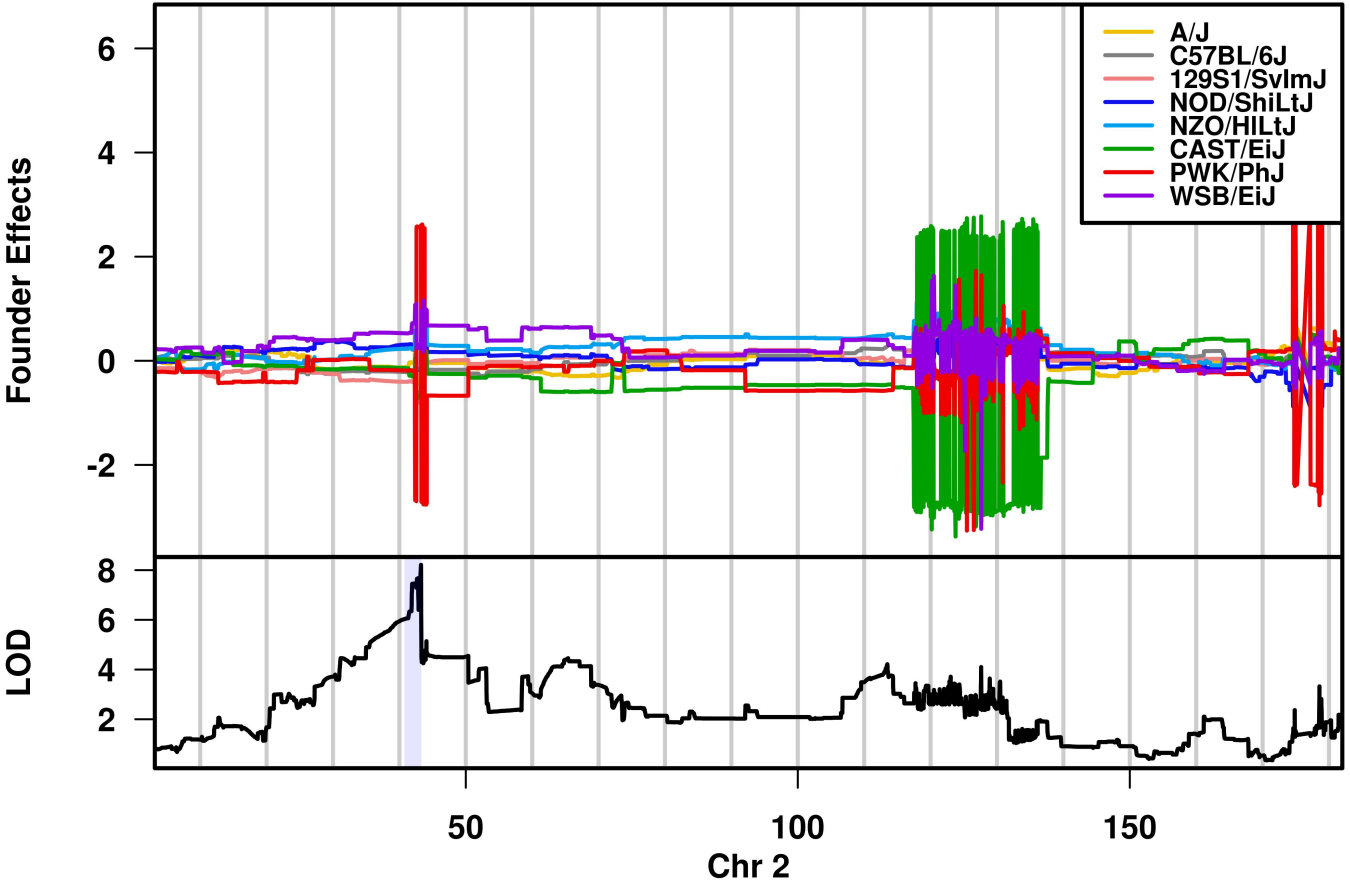
All **NA** values for a phenotype means that, significant QTL has not been detected or QTL analysis has not been run.

Phenotype	SNP	Chr	Pos (Mb)	Pos (cM)	LOD	P-Value	% Var	Proximal (Mb)	Distal (Mb)
Acox1.Liver.Expression	UNC2949898	2	43.255497	25.522	8.21381342152747	0	53.789325	40.747796	43.316497
TCE.in.Liver	NA	NA	NA	NA	NA	NA	NA	NA	NA

Allele Effects Plots

The plots may have also been rendered for any additional selected chromosomes.

Acox1.Liver.Expression



UNC2949898
Chr 2 : 43255497 Mb

