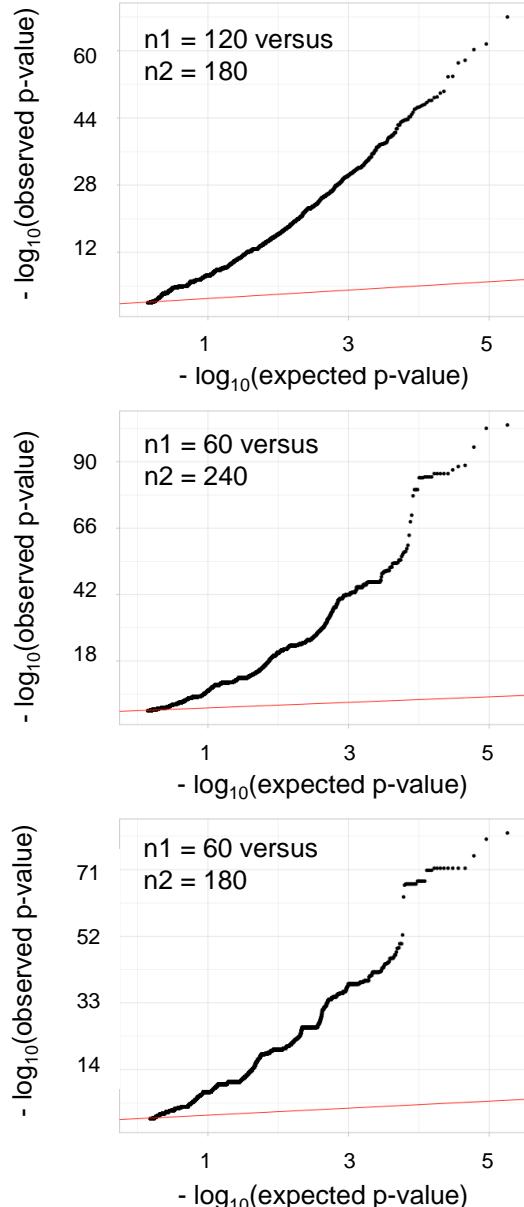


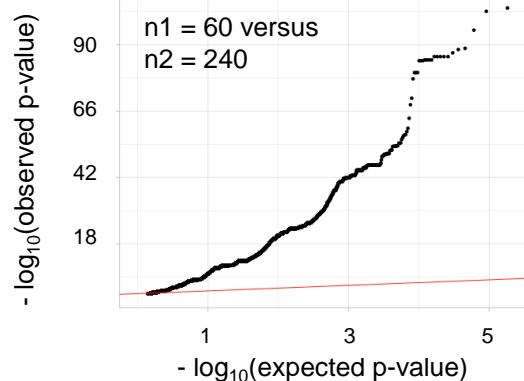
Genomes with the phenotype of interest (i.e. effective n1)

A

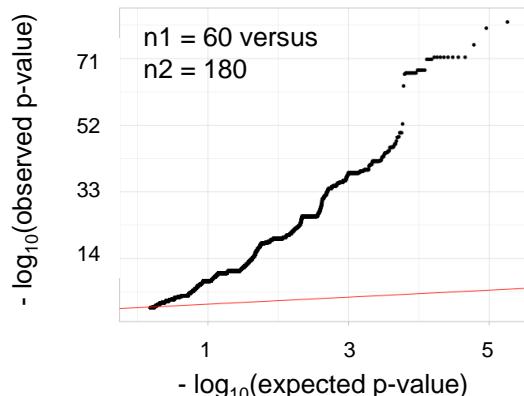
mono- and multi-animal sources



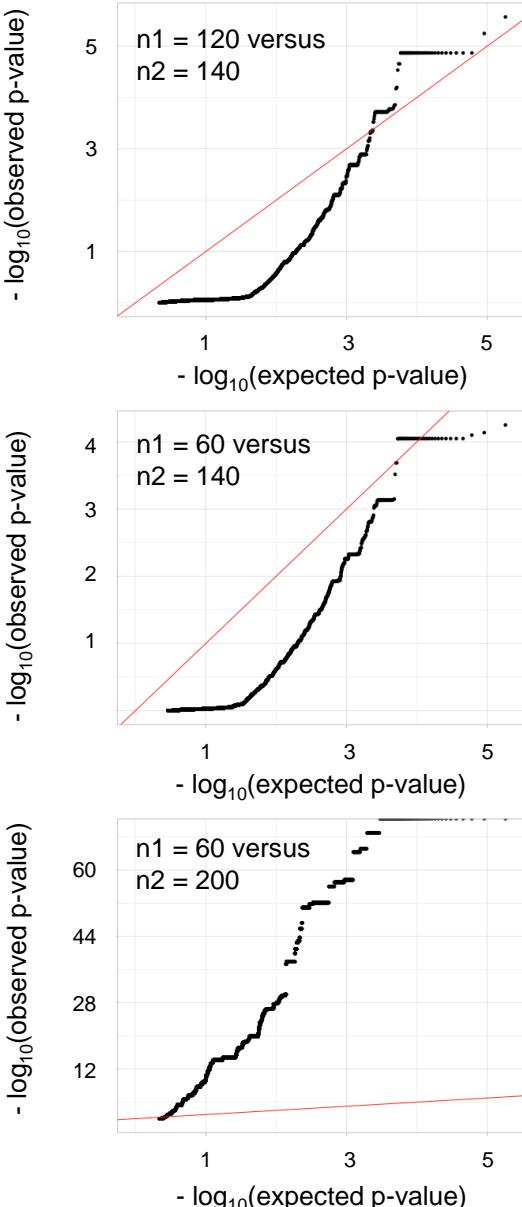
multi-animal sources



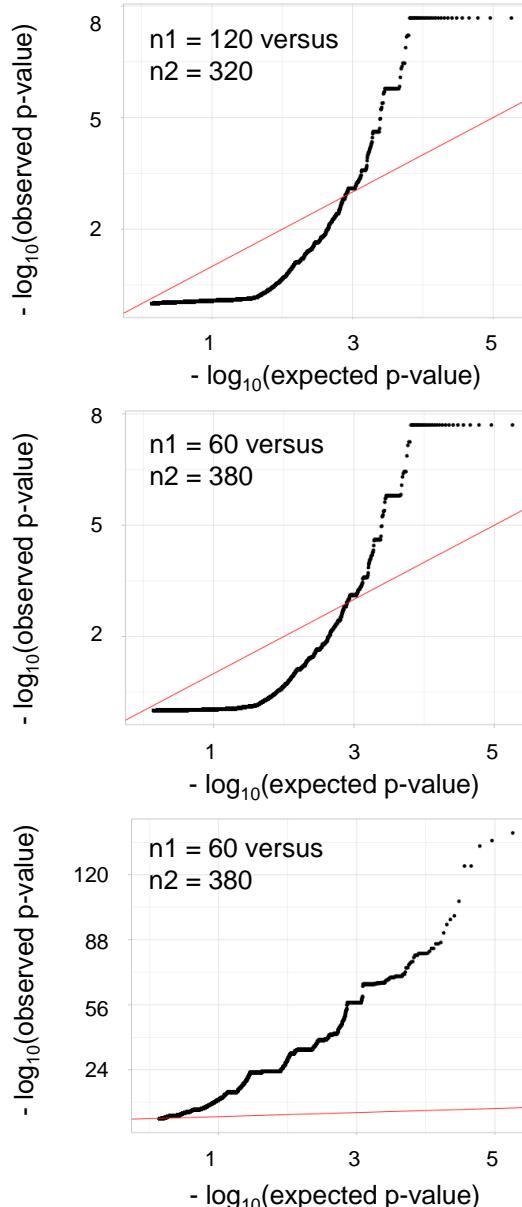
mono-animal sources



mono-animal sources



multi-animal sources



mono- and multi-animal sources

Genomes without the phenotype of interest (i.e. effective n2)

B

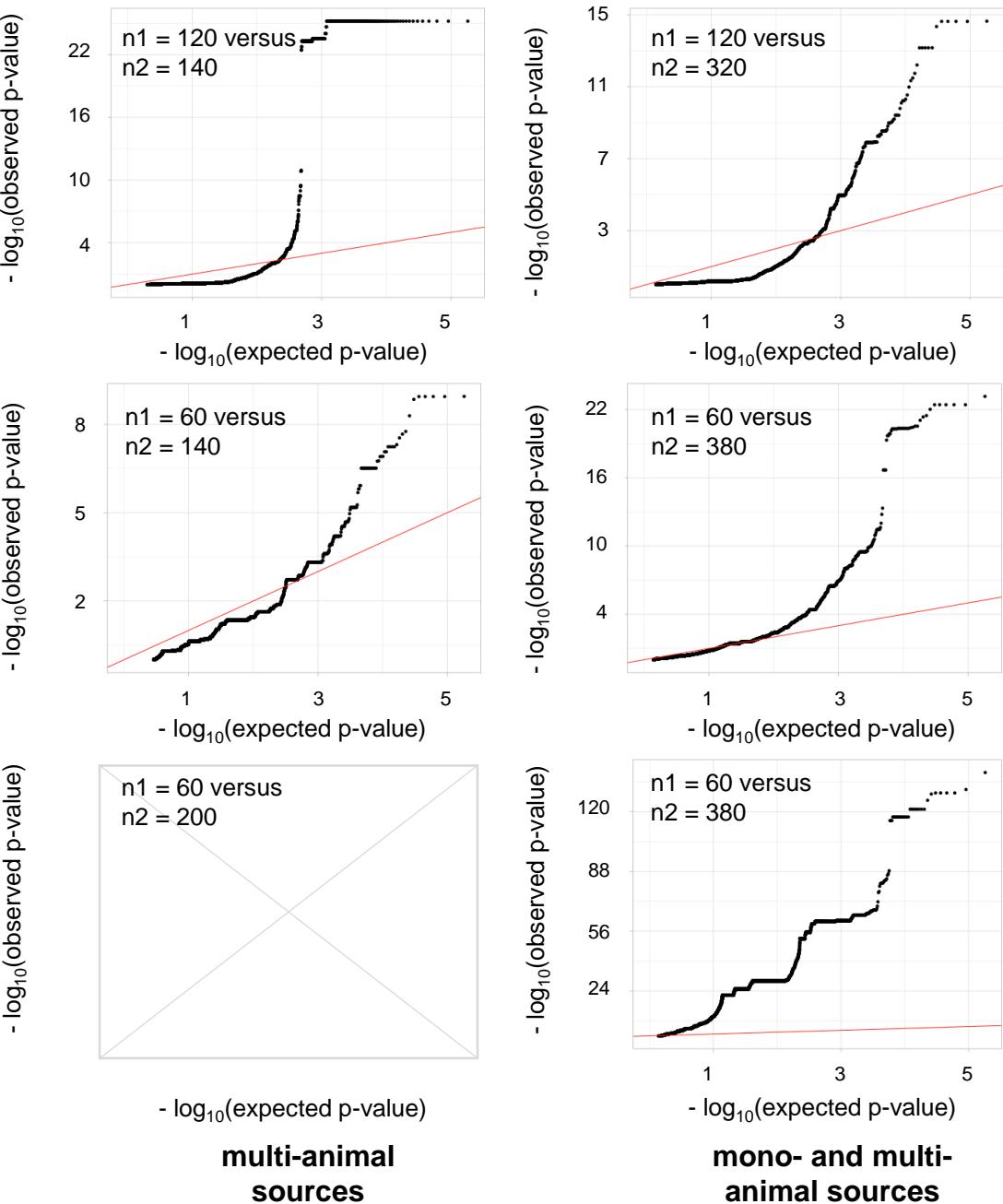
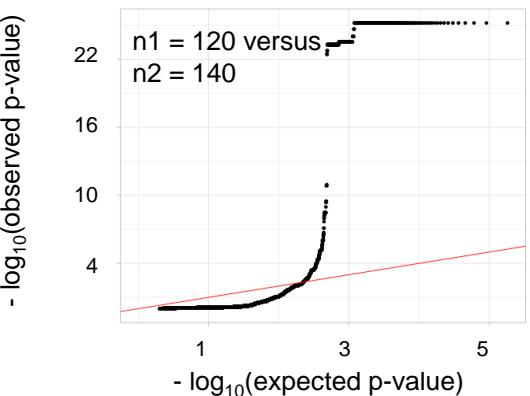
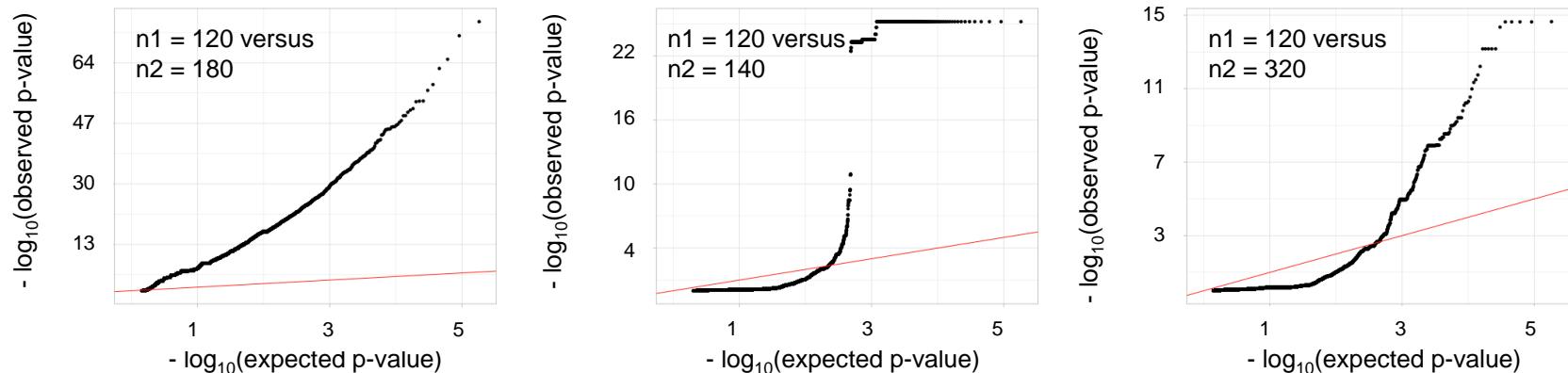
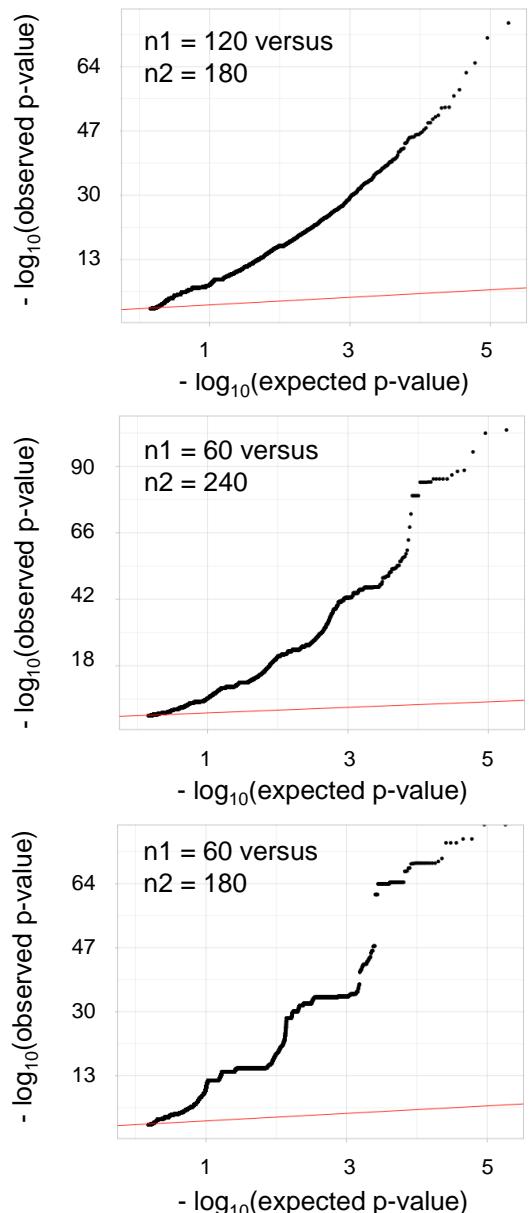
Genomes with the phenotype of interest (i.e. effective n1)

mono- and multi-animal sources

- $\log_{10}(\text{observed p-value})$

- $\log_{10}(\text{expected p-value})$

$n1 = 120 \text{ versus}$
 $n2 = 180$

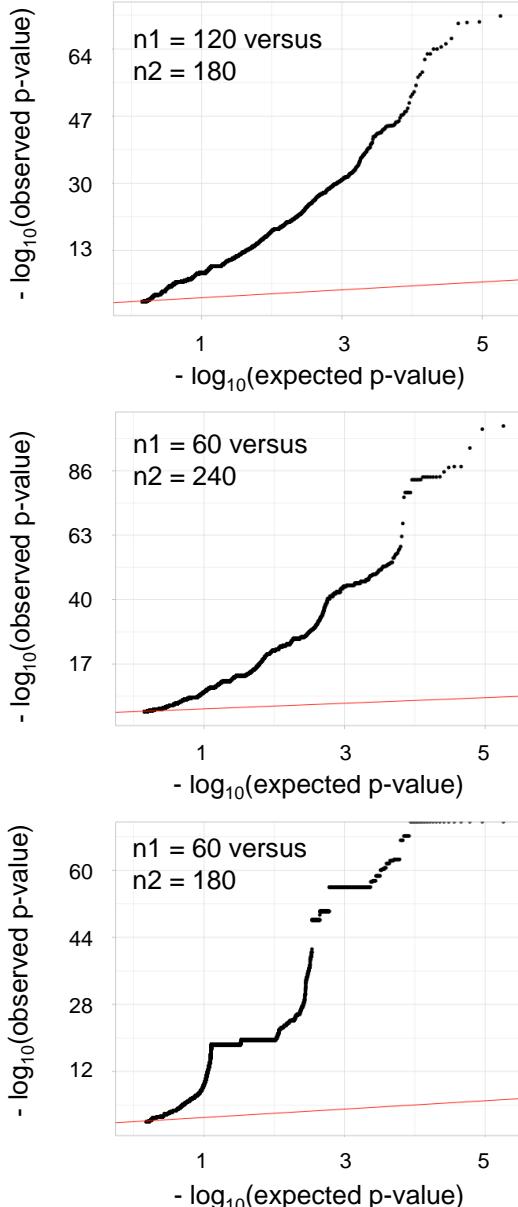


Genomes without the phenotype of interest (i.e. effective n2)

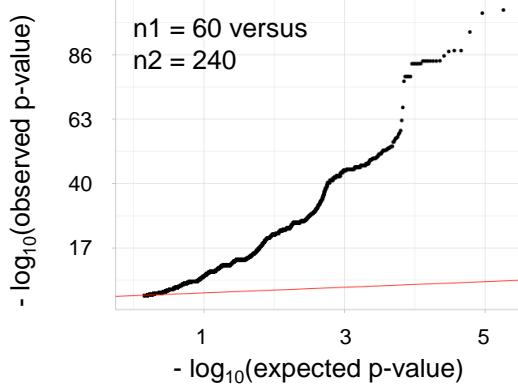
Genomes with the phenotype of interest (i.e. effective n1)

C

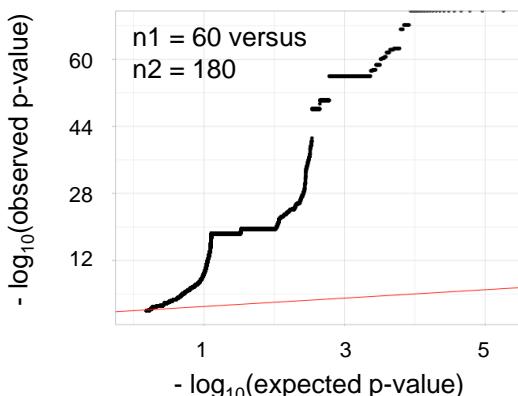
mono- and multi-animal sources



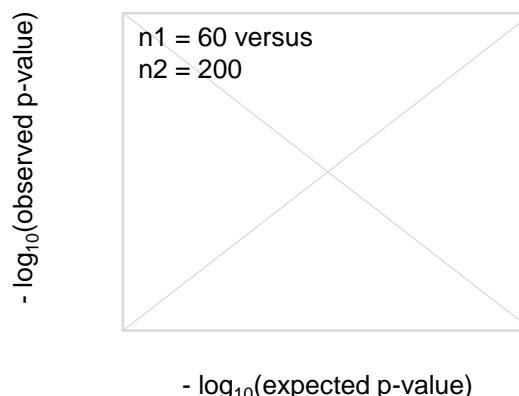
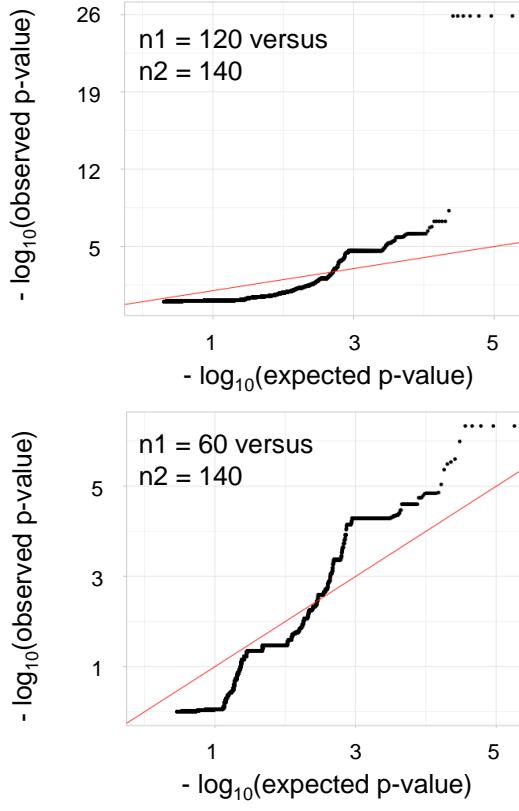
multi-animal sources



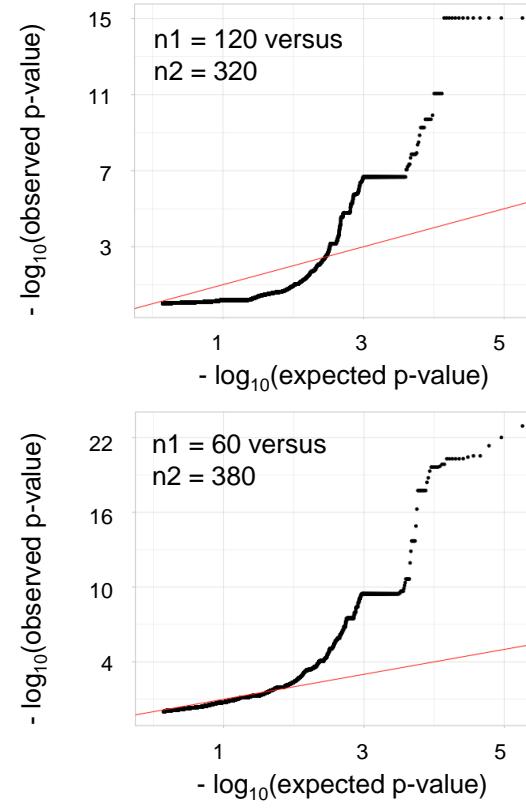
mono-animal sources



mono-animal sources



multi-animal sources



mono- and multi-animal sources

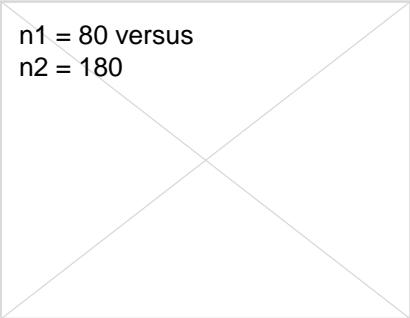
Genomes without the phenotype of interest (i.e. effective n2)

Genomes with the phenotype of interest (i.e. effective n1)

D

mono- and multi-animal sources

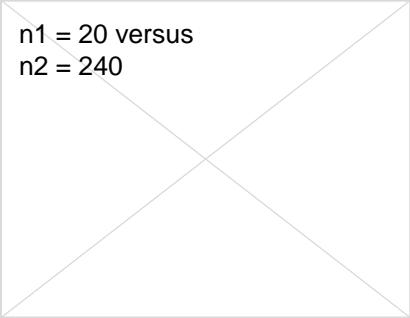
- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

multi-animal sources

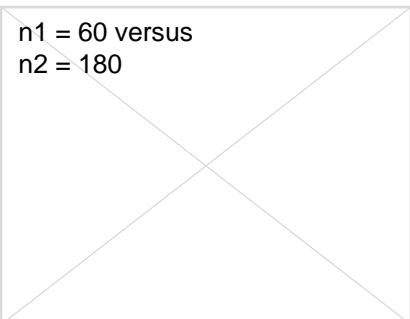
- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

mono-animal sources

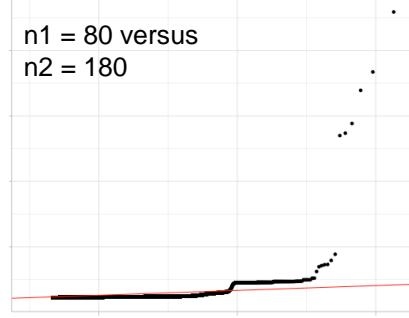
- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

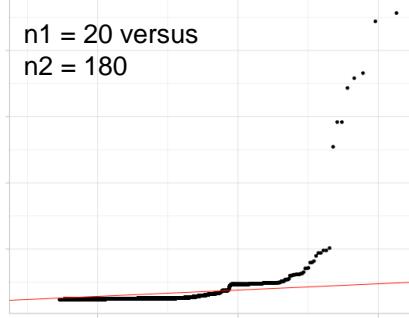
mono-animal sources

- $\log_{10}(\text{observed p-value})$



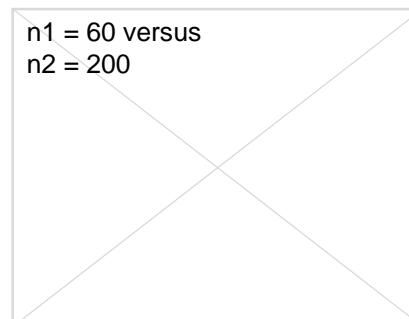
- $\log_{10}(\text{expected p-value})$

- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

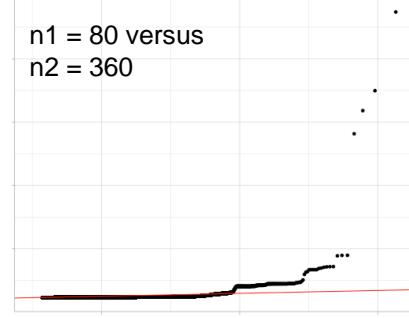
- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

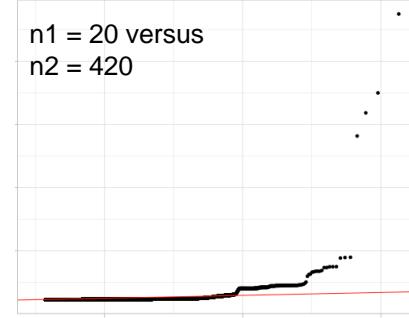
multi-animal sources

- $\log_{10}(\text{observed p-value})$



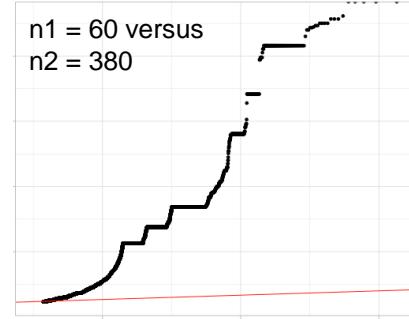
- $\log_{10}(\text{expected p-value})$

- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

- $\log_{10}(\text{observed p-value})$



- $\log_{10}(\text{expected p-value})$

mono- and multi-animal sources

Genomes without the phenotype of interest (i.e. effective n2)