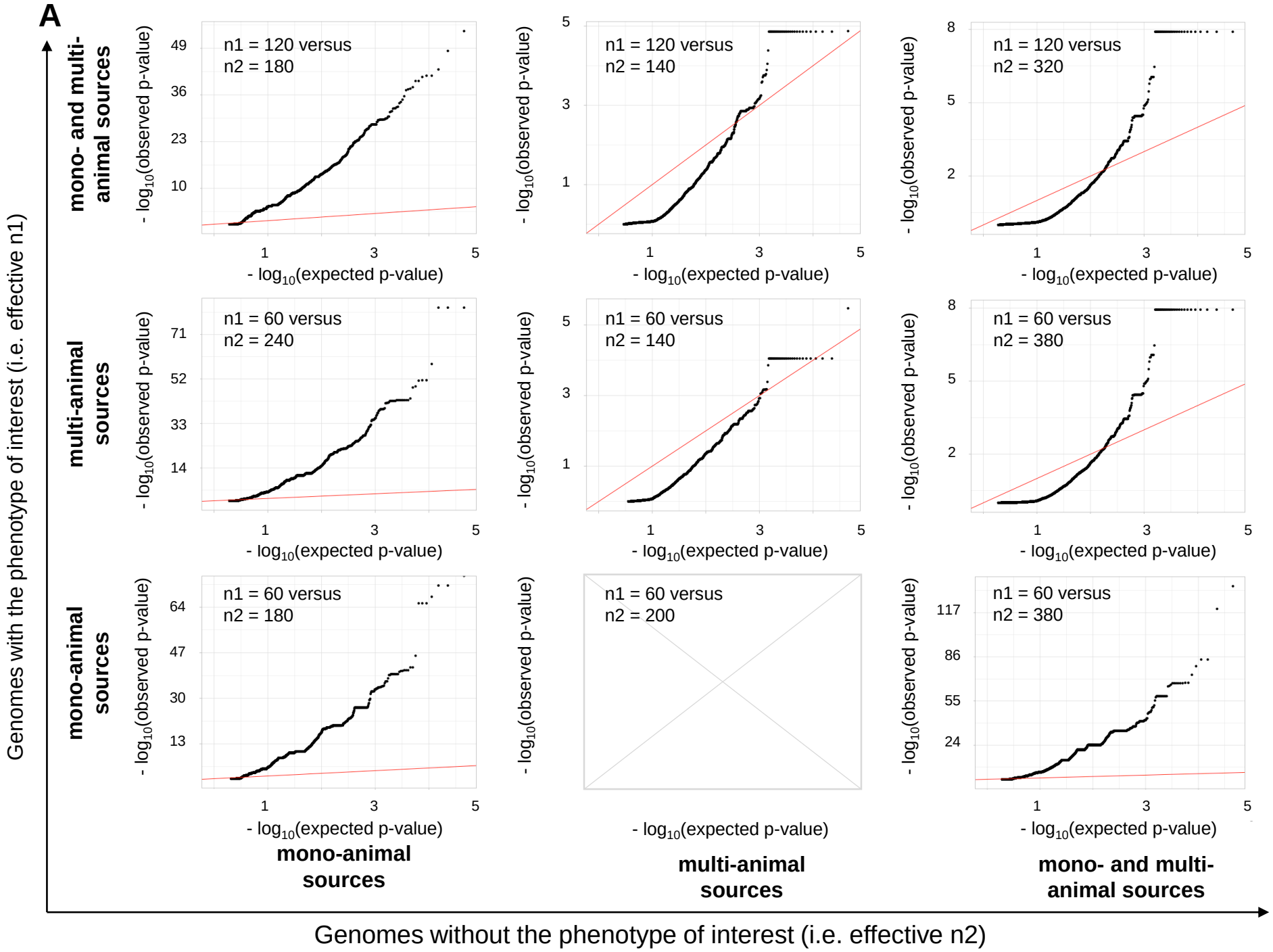
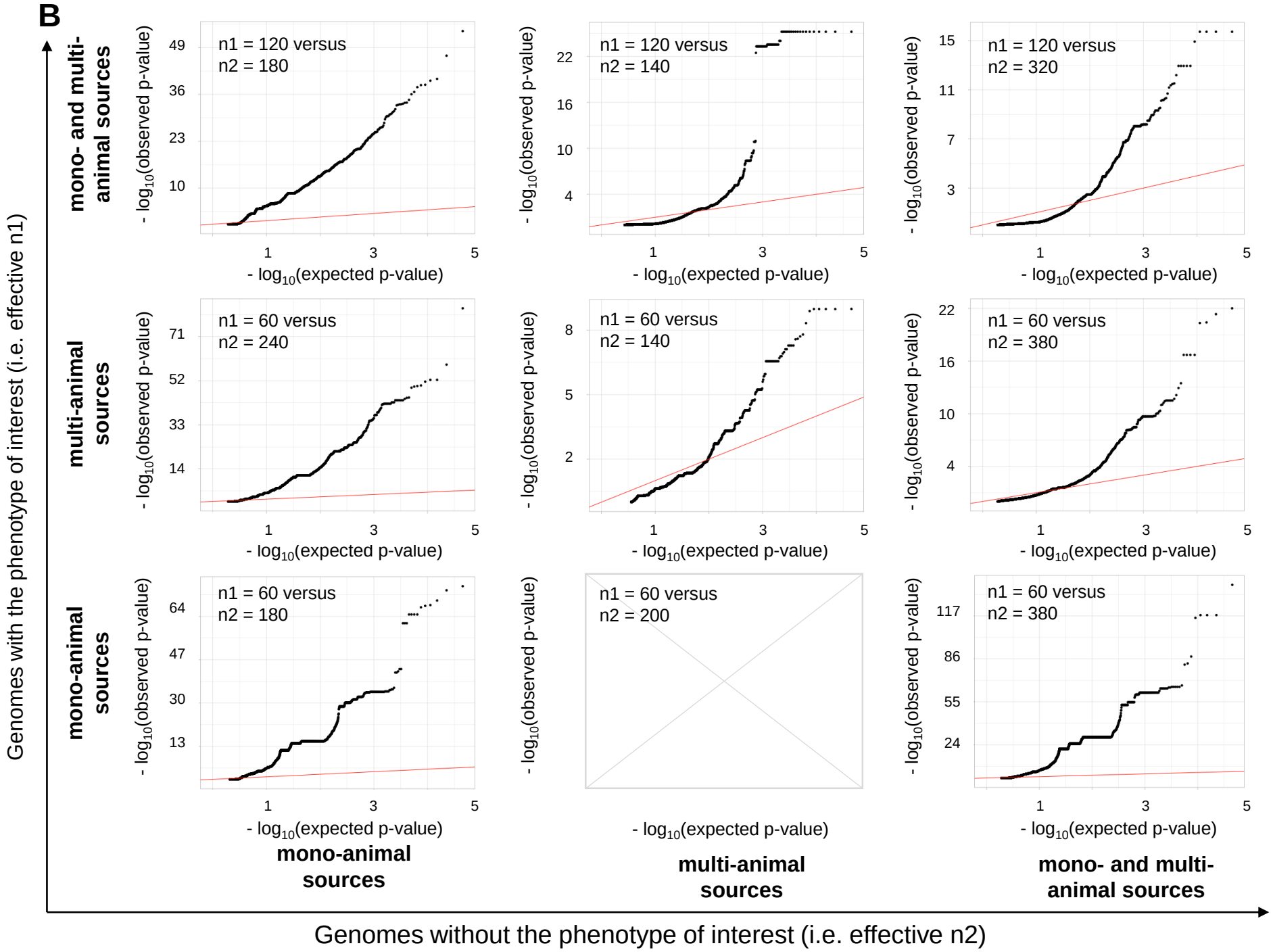
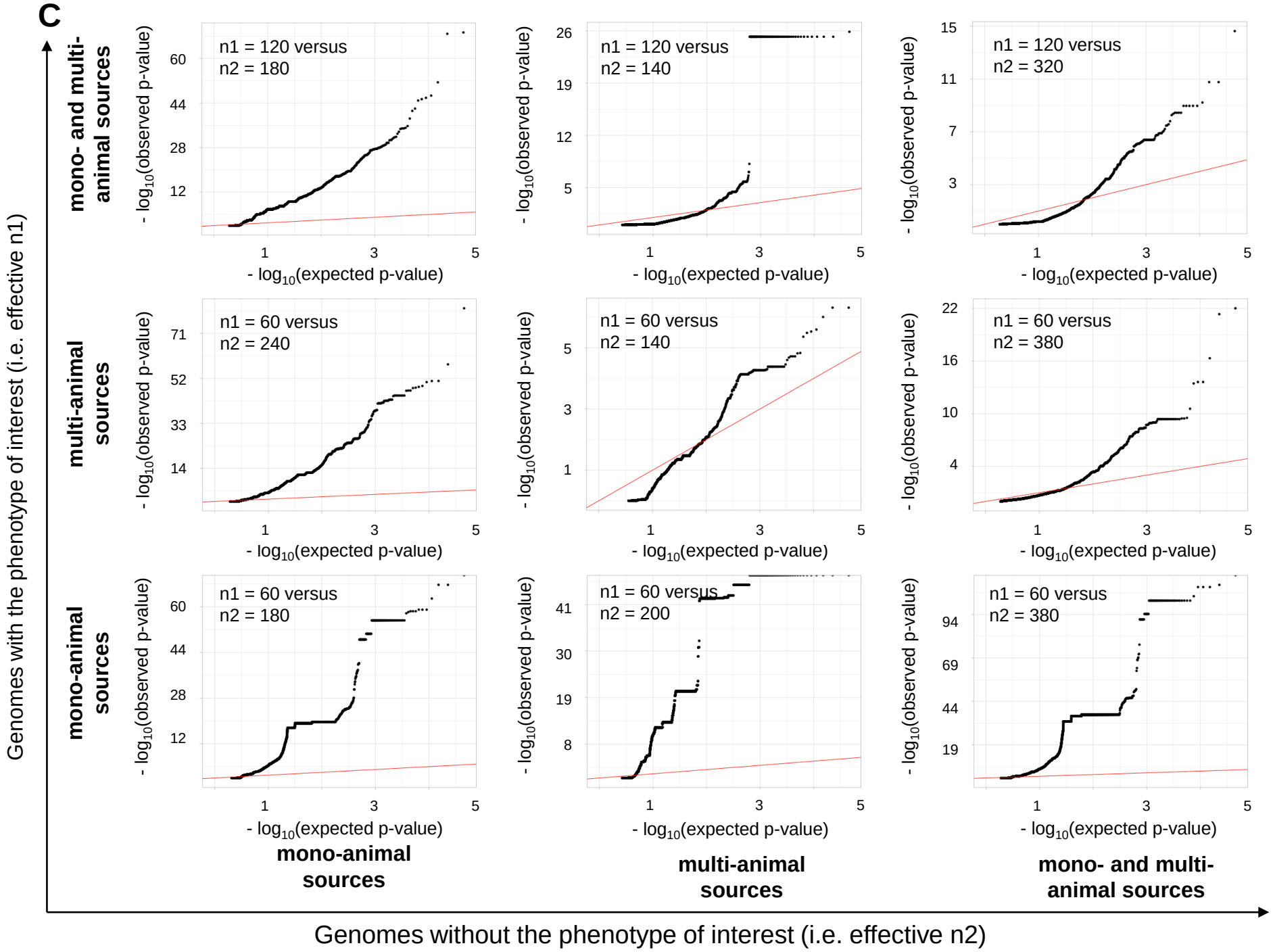
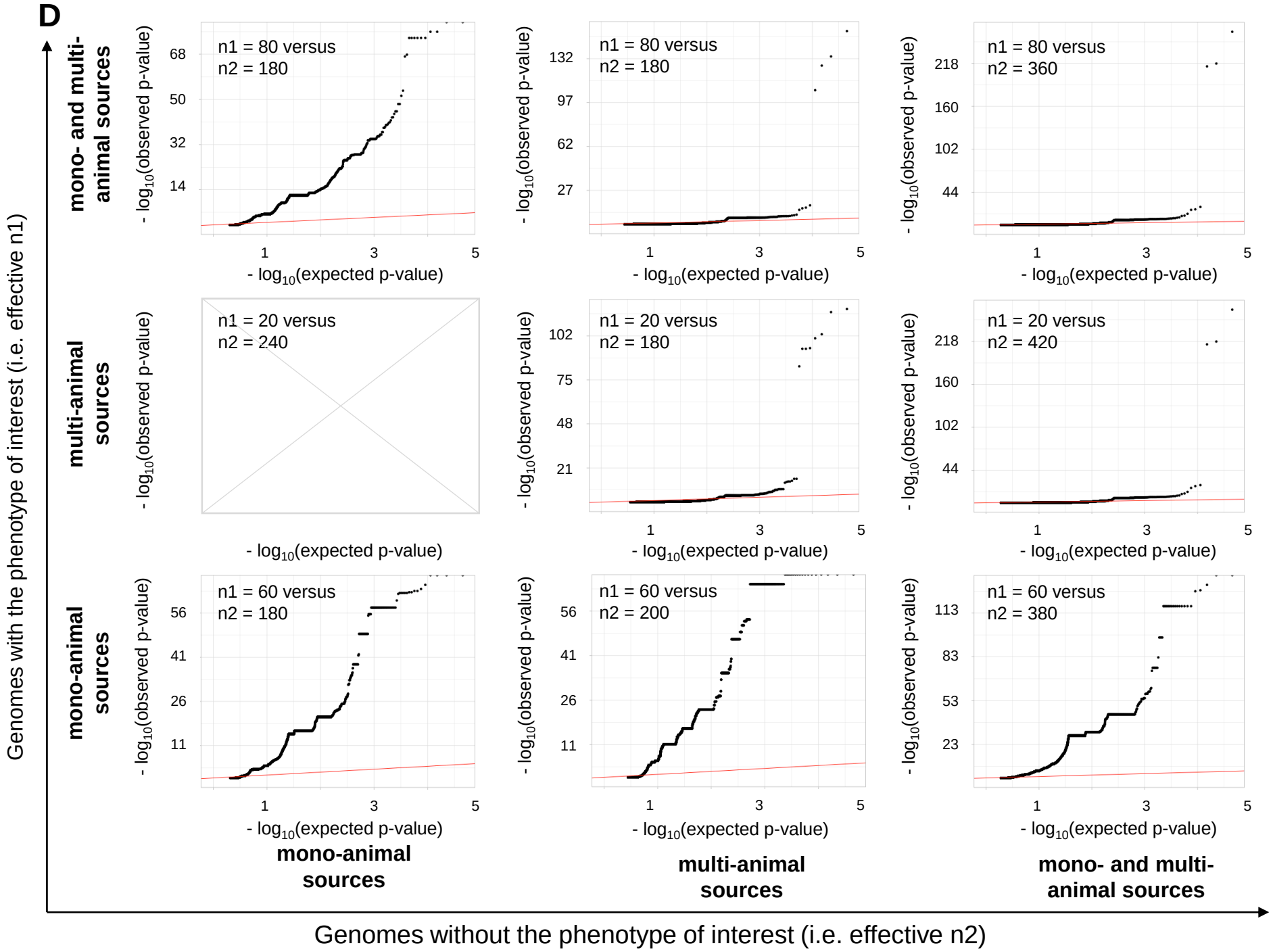

A
Genomes with the phenotype of interest (i.e. effective n1)
Genomes without the phenotype of interest (i.e. effective n2)
mono- and multi-animal sources
multi-animal sources
mono-animal sources
n1 = 120 versus n2 = 180
n1 = 120 versus n2 = 140
n1 = 120 versus n2 = 320
n1 = 60 versus n2 = 240
n1 = 60 versus n2 = 140
n1 = 60 versus n2 = 380
n1 = 60 versus n2 = 180
n1 = 60 versus n2 = 200
n1 = 60 versus n2 = 380
- log10(observed p-value)
- log10(expected p-value)
mono-animal sources
multi-animal sources
mono- and multi-animal sources


B
Genomes with the phenotype of interest (i.e. effective n1)
Genomes without the phenotype of interest (i.e. effective n2)
mono- and multi-animal sources
multi-animal sources
mono-animal sources
n1 = 120 versus n2 = 180
n1 = 120 versus n2 = 140
n1 = 120 versus n2 = 320
n1 = 60 versus n2 = 240
n1 = 60 versus n2 = 140
n1 = 60 versus n2 = 380
n1 = 60 versus n2 = 180
n1 = 60 versus n2 = 200
n1 = 60 versus n2 = 380
- log10(observed p-value)
- log10(expected p-value)
mono-animal sources
multi-animal sources
mono- and multi-animal sources


C
Genomes with the phenotype of interest (i.e. effective n1)
Genomes without the phenotype of interest (i.e. effective n2)
mono- and multi-animal sources
multi-animal sources
mono-animal sources
n1 = 120 versus n2 = 180
n1 = 120 versus n2 = 140
n1 = 120 versus n2 = 320
n1 = 60 versus n2 = 240
n1 = 60 versus n2 = 140
n1 = 60 versus n2 = 380
n1 = 60 versus n2 = 180
n1 = 60 versus n2 = 200
n1 = 60 versus n2 = 380
- log10(observed p-value)
- log10(expected p-value)
mono-animal sources
multi-animal sources
mono- and multi-animal sources


D
Genomes with the phenotype of interest (i.e. effective n1)
Genomes without the phenotype of interest (i.e. effective n2)
mono- and multi-animal sources
multi-animal sources
mono-animal sources
n1 = 80 versus n2 = 180
n1 = 80 versus n2 = 180
n1 = 80 versus n2 = 360
n1 = 20 versus n2 = 240
n1 = 20 versus n2 = 180
n1 = 20 versus n2 = 420
n1 = 60 versus n2 = 180
n1 = 60 versus n2 = 200
n1 = 60 versus n2 = 380
- log10(observed p-value)
- log10(expected p-value)
mono-animal sources
multi-animal sources
mono- and multi-animal sources