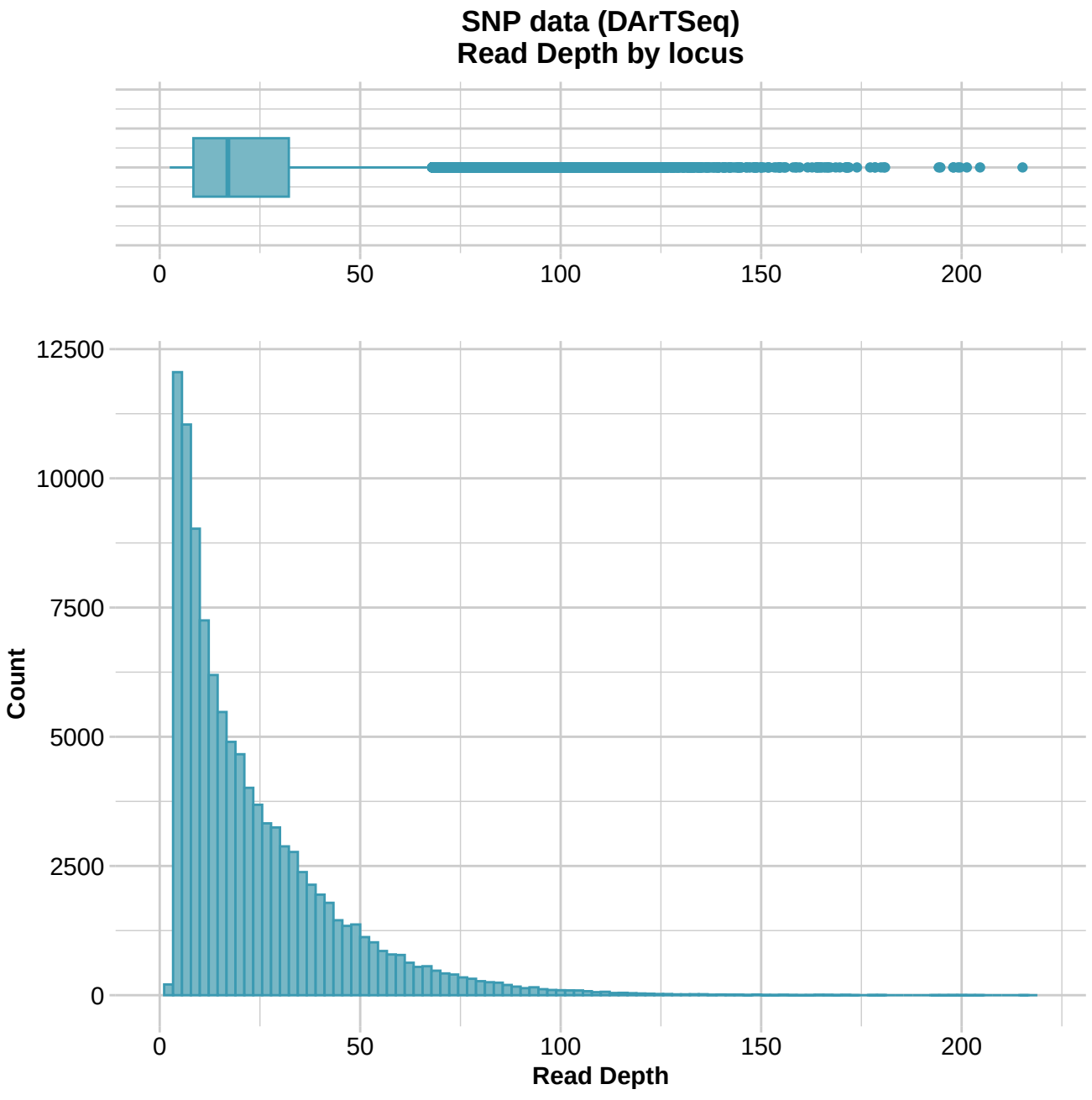
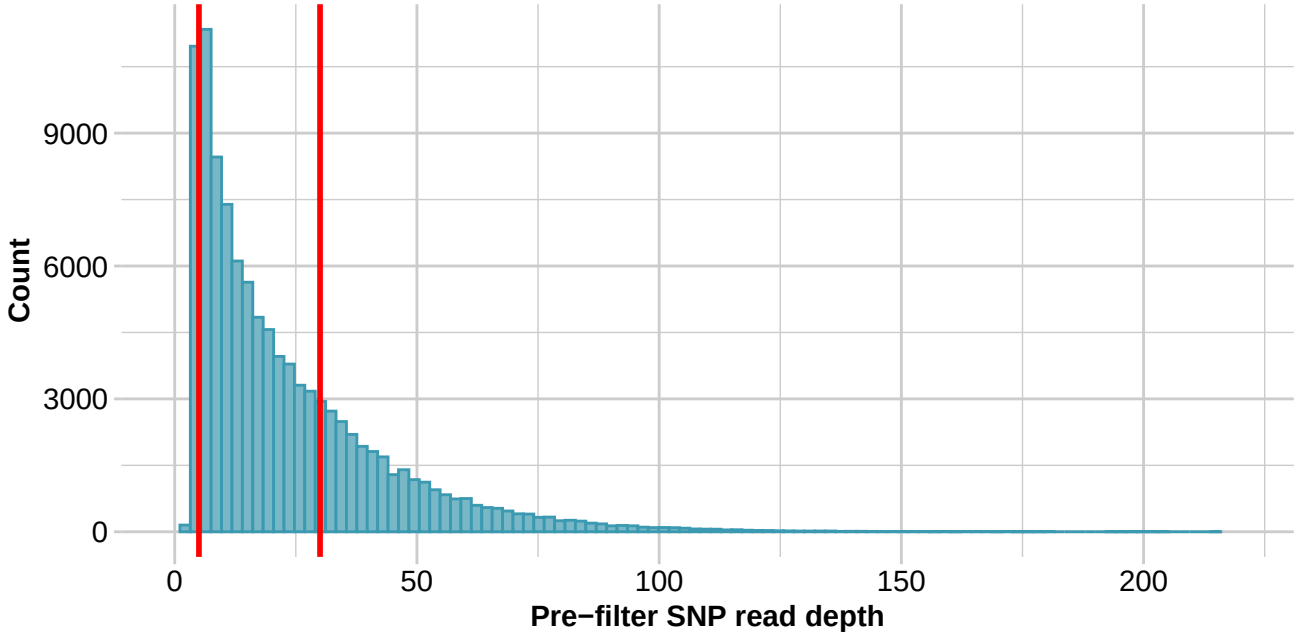
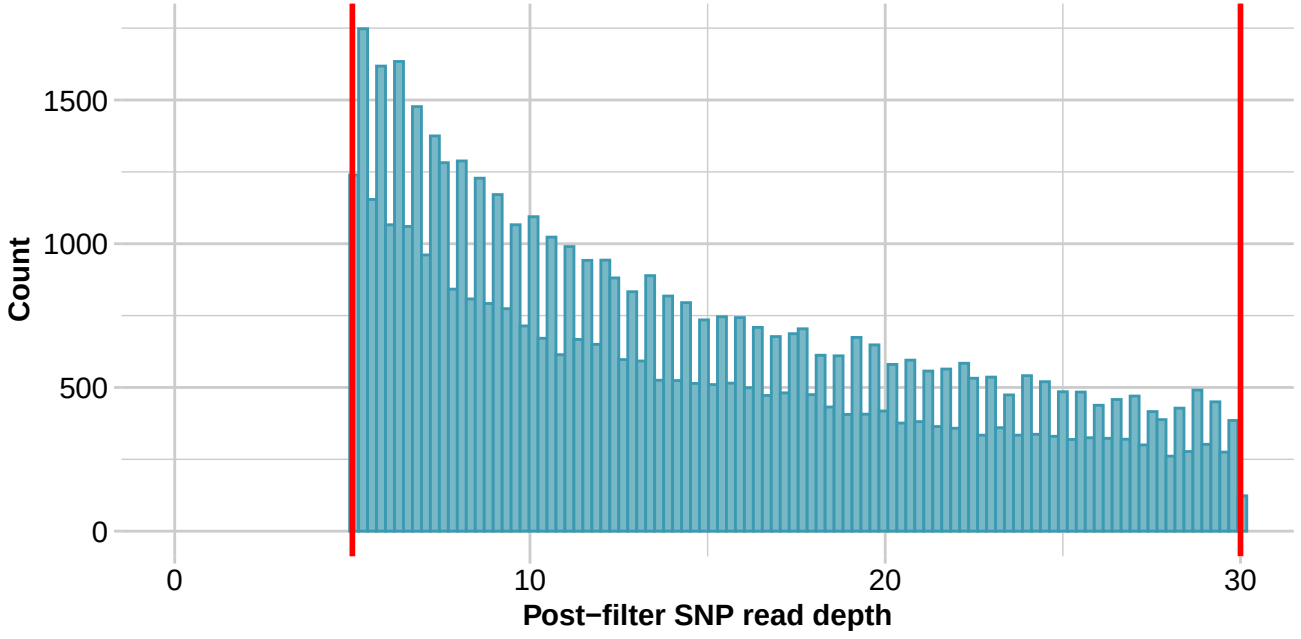
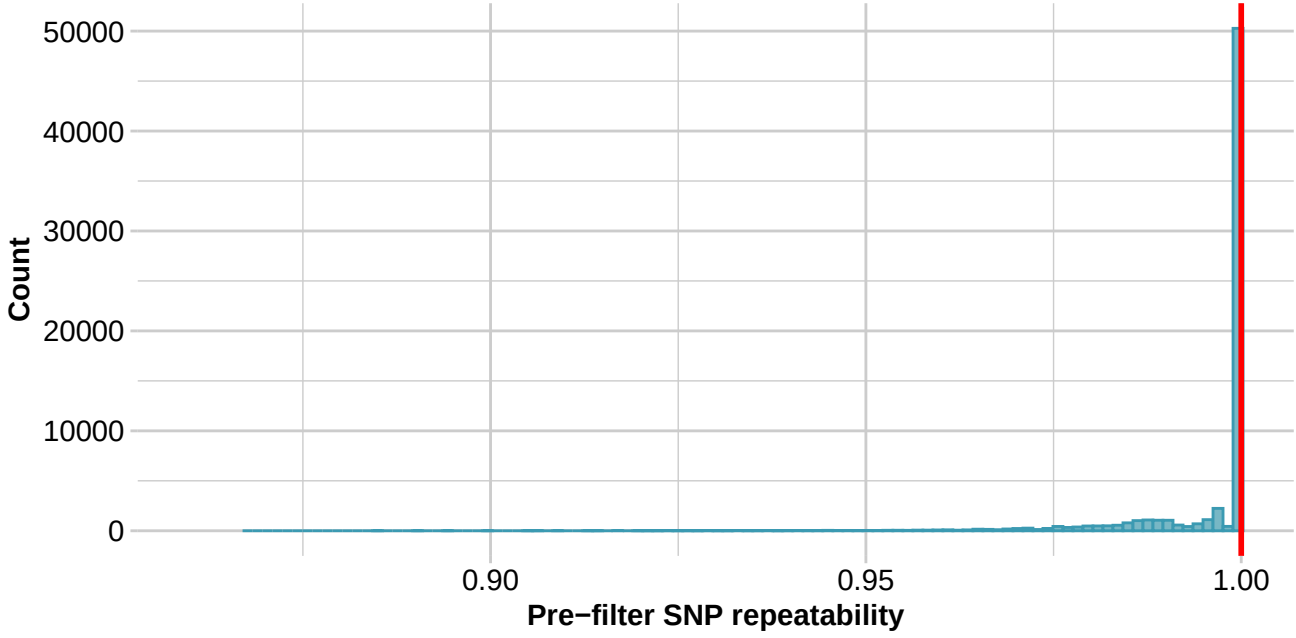
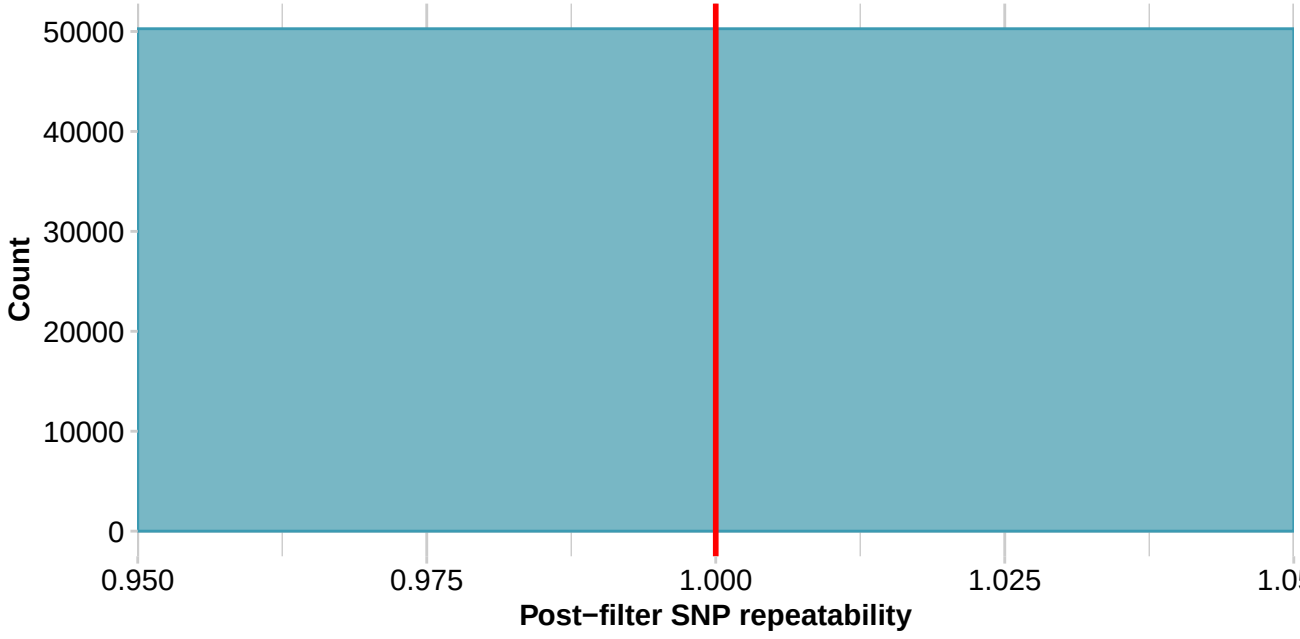
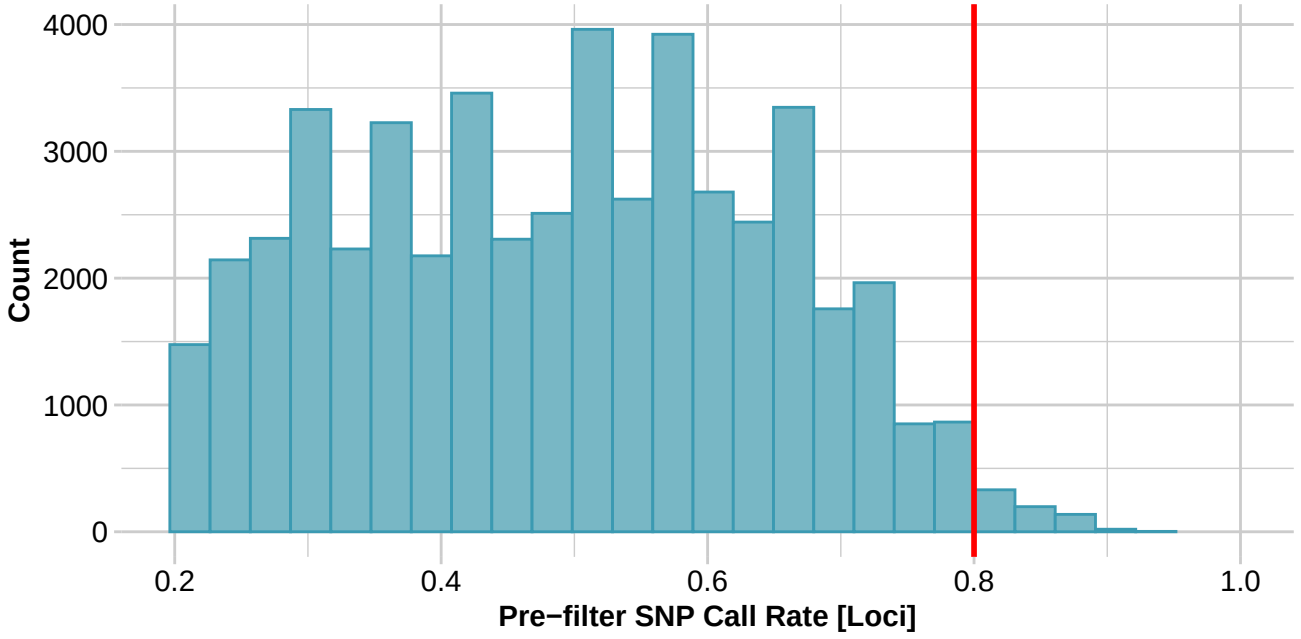

SNP data (DArTSeq)
Read Depth by locus
0
50
100
150
200
12500
10000
7500
5000
2500
0
Count
0
50
100
150
200
Read Depth

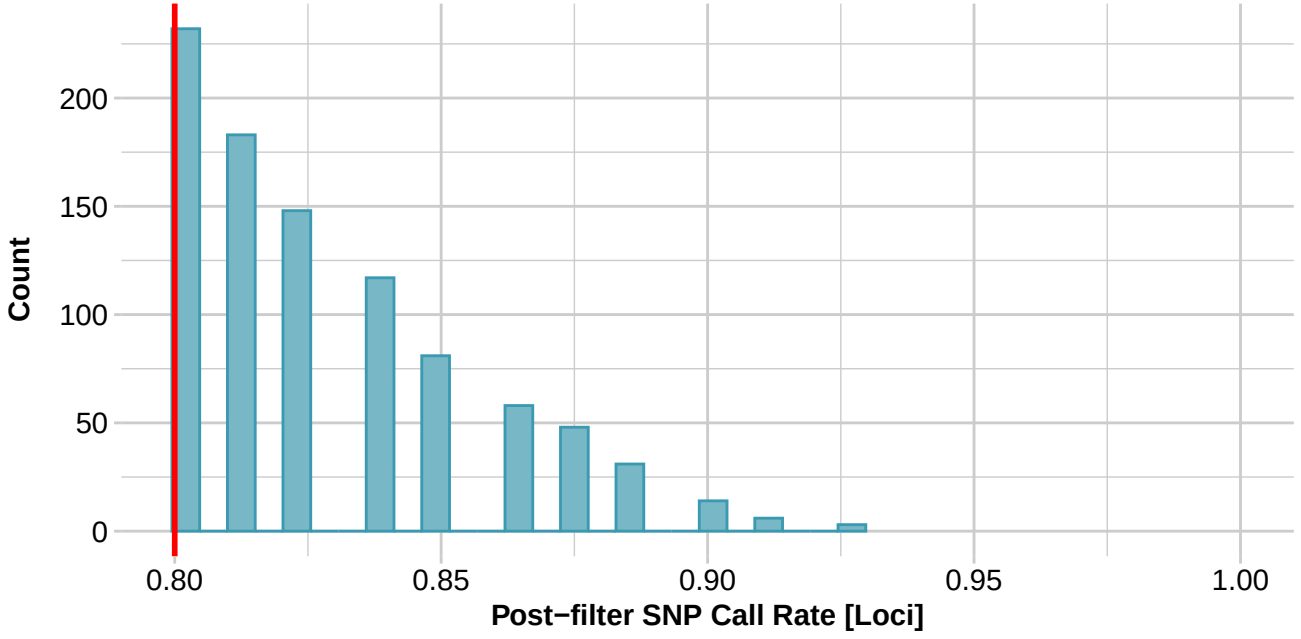

Count
9000
6000
3000
0
0
50
100
150
200
Pre−filter SNP read depth

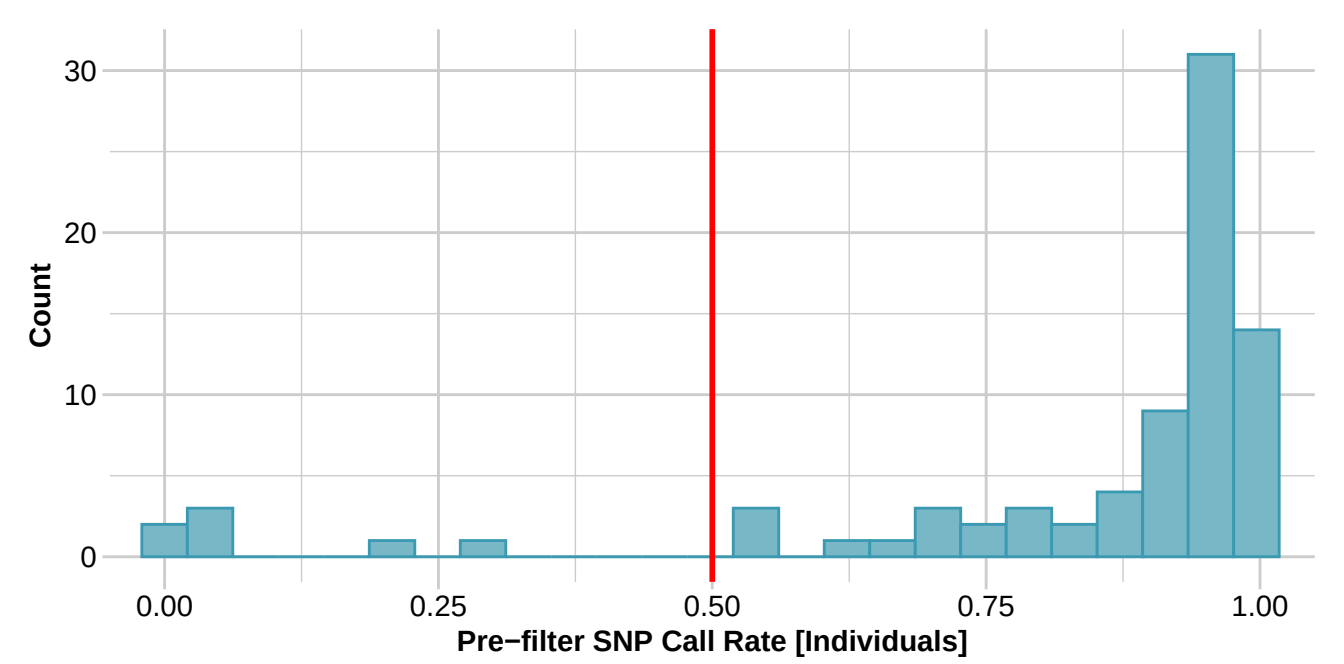

Count
1500
1000
500
0
0
10
20
30
Post−filter SNP read depth

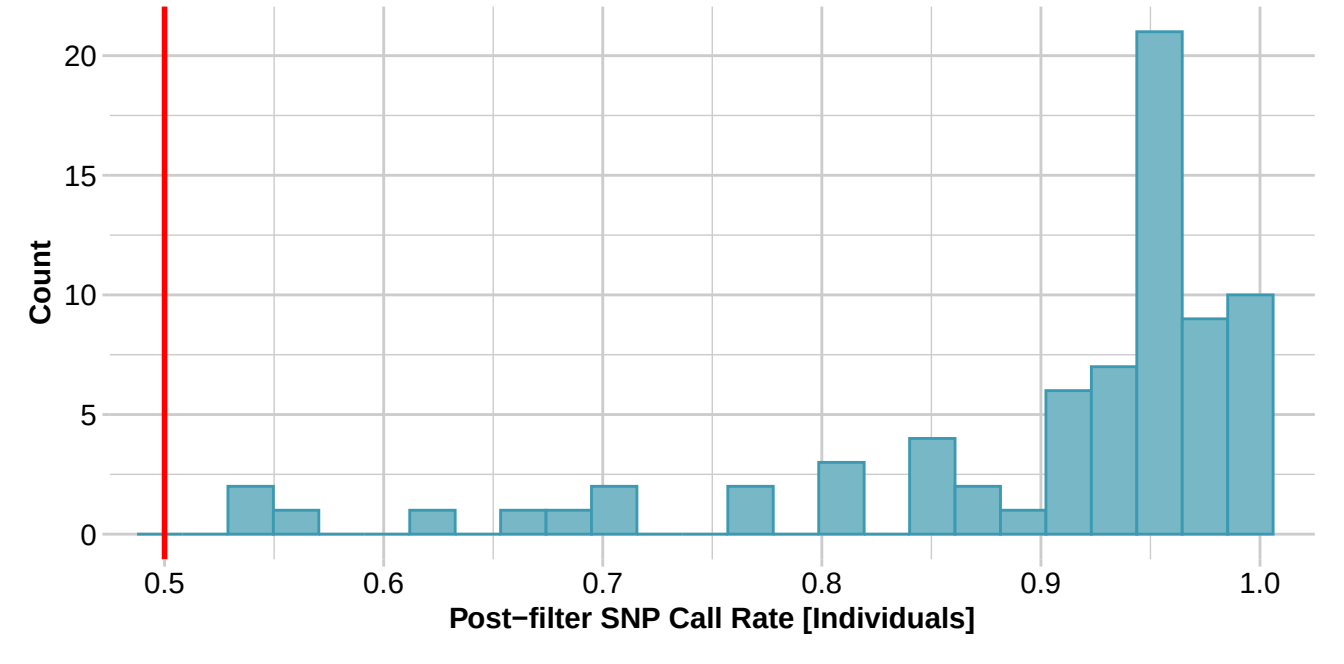

50000
40000
30000
20000
10000
0
Count
0.90
0.95
1.00
Pre−filter SNP repeatability

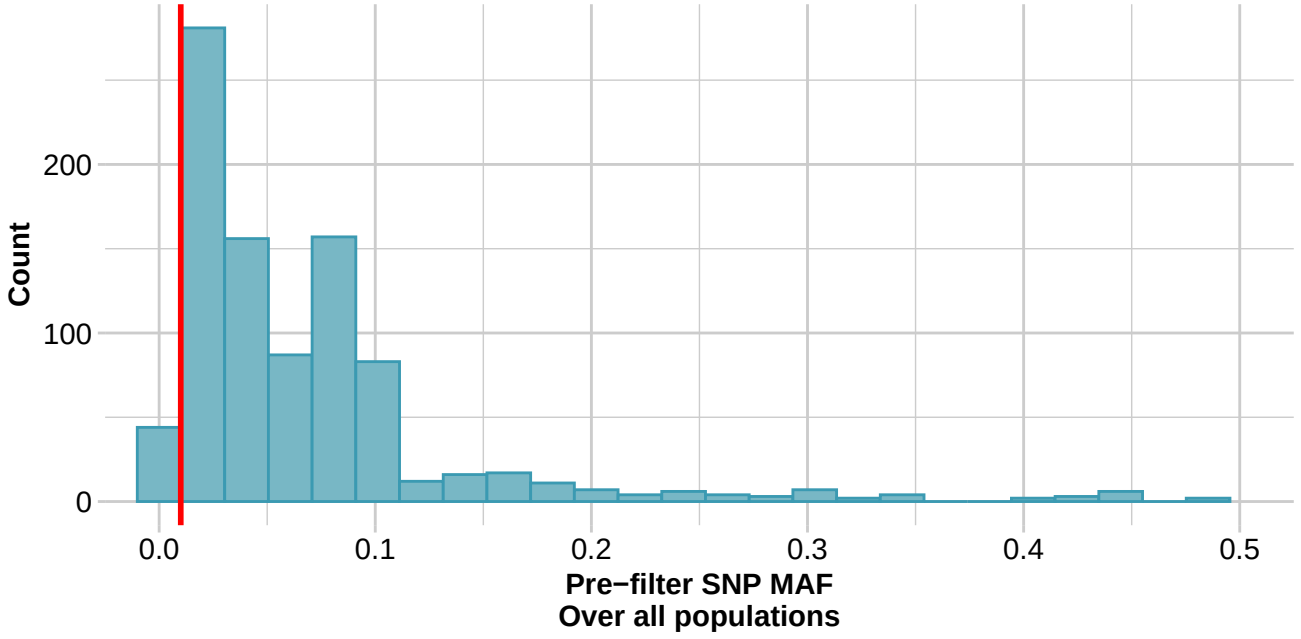

50000
40000
30000
20000
10000
0
Count
0.950
0.975
1.000
1.025
1.050
Post−filter SNP repeatability

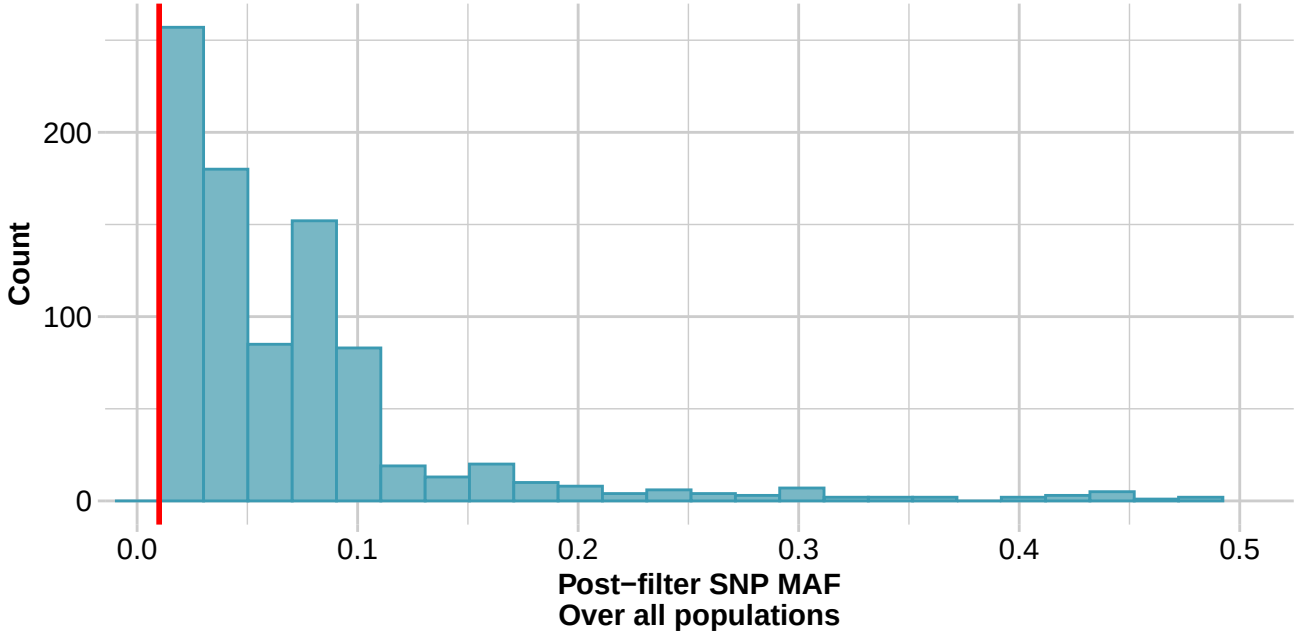

4000
3000
2000
1000
0
Count
0.2
0.4
0.6
0.8
1.0
Pre−filter SNP Call Rate [Loci]

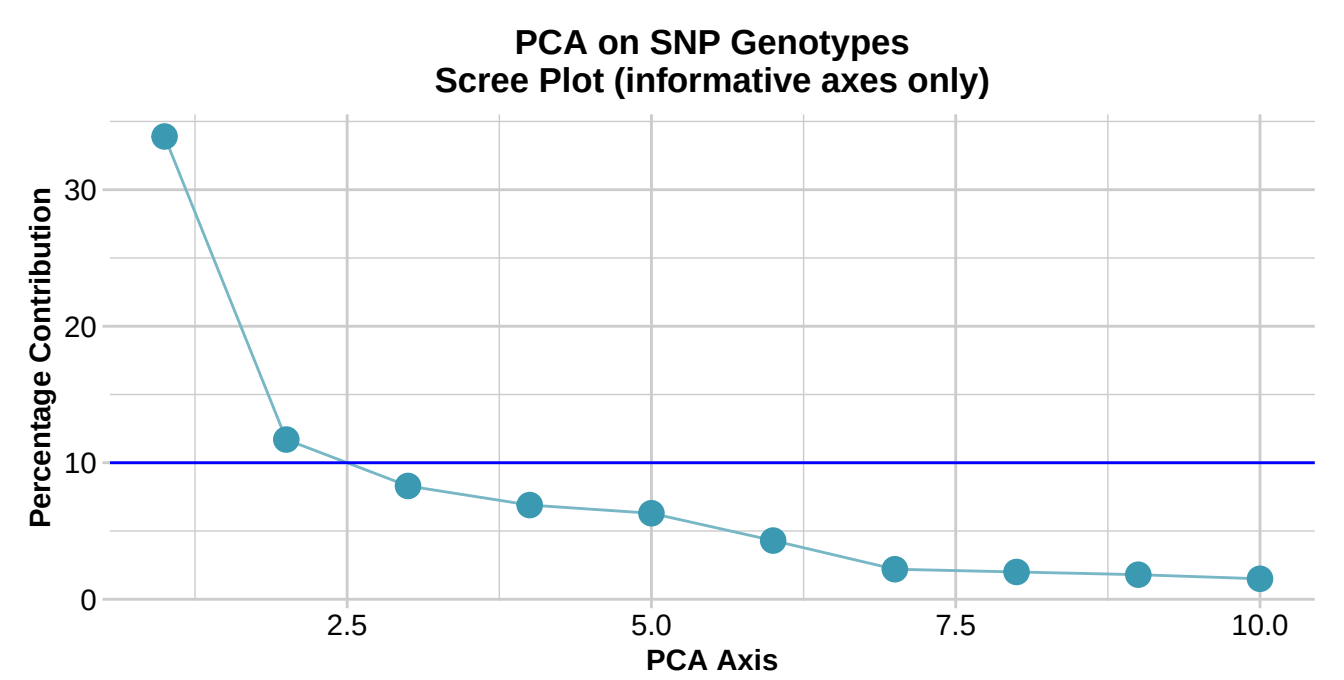

200
150
100
50
0
Count
0.80
0.85
0.90
0.95
1.00
Post−filter SNP Call Rate [Loci]

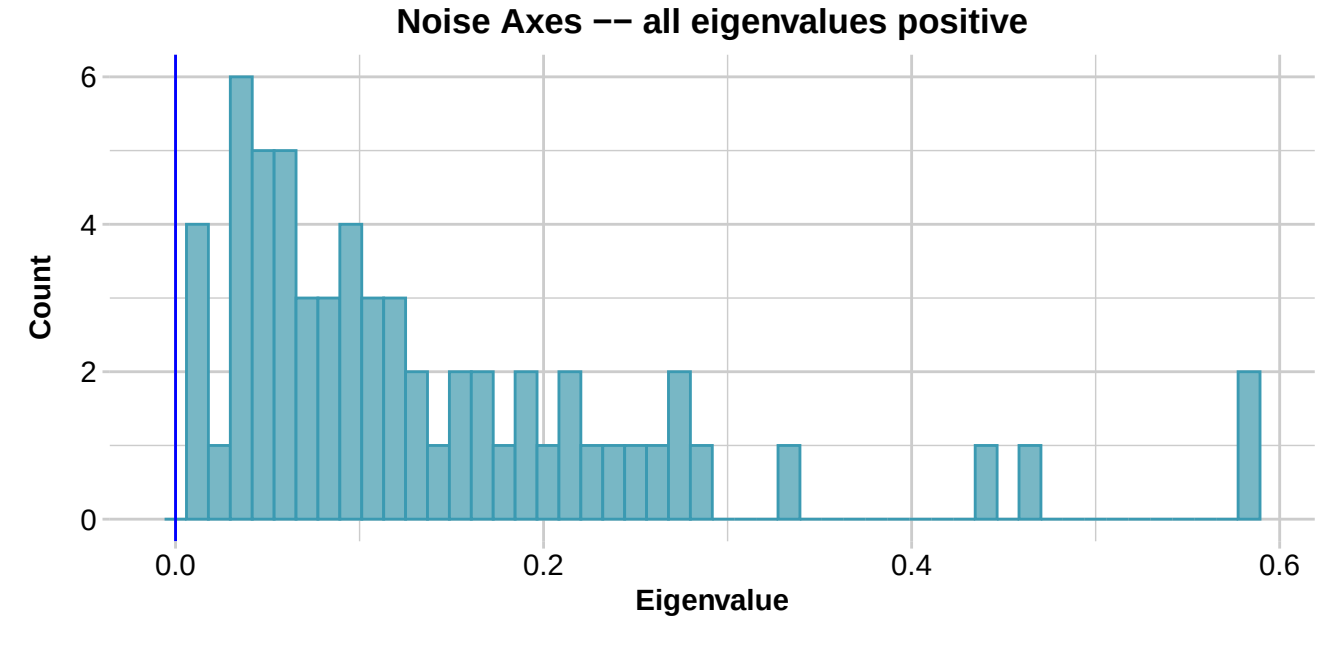

Count
30
20
10
0
0.00
0.25
0.50
0.75
1.00
Pre−filter SNP Call Rate [Individuals]

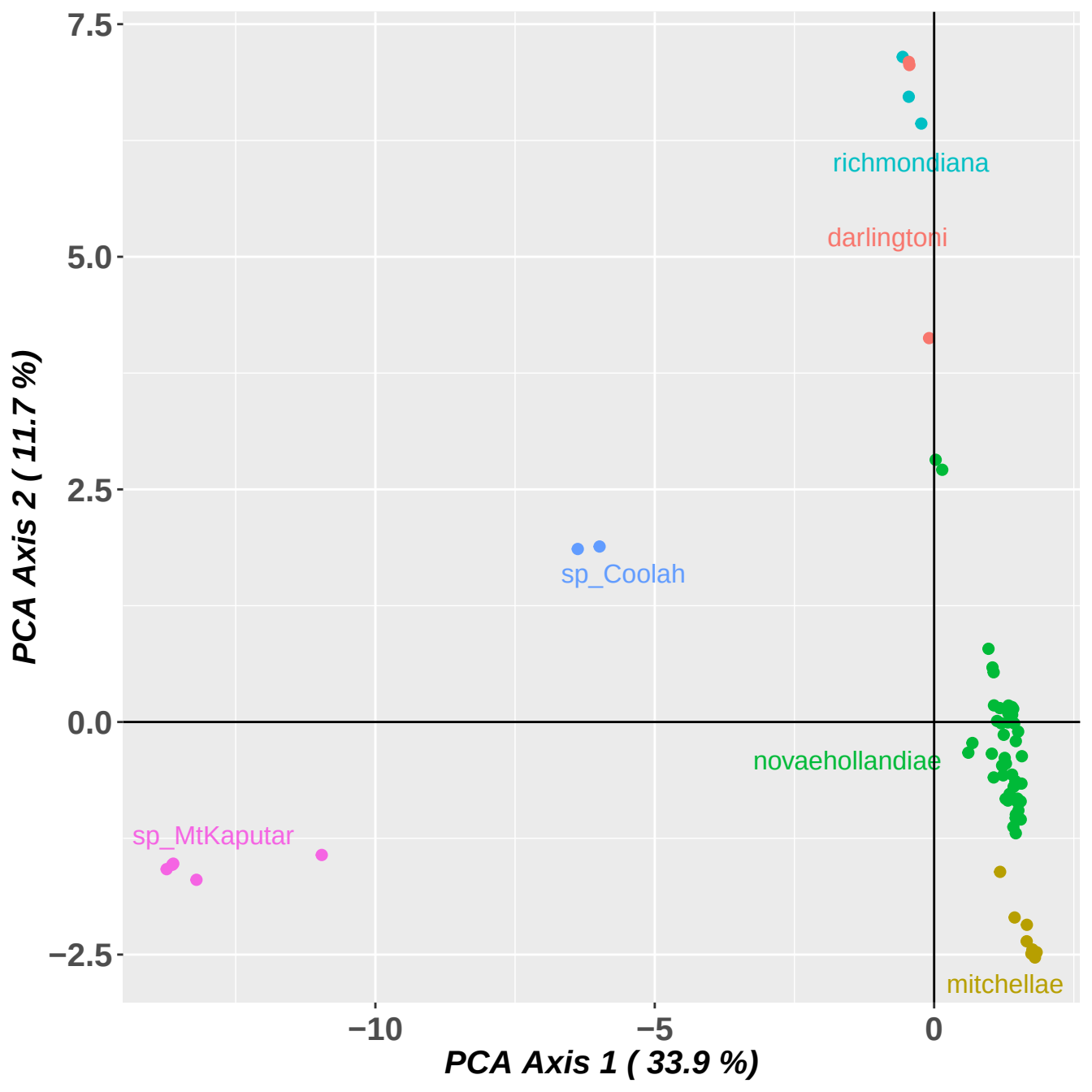

Count
20
15
10
5
0
0.5
0.6
0.7
0.8
0.9
1.0
Post−filter SNP Call Rate [Individuals]

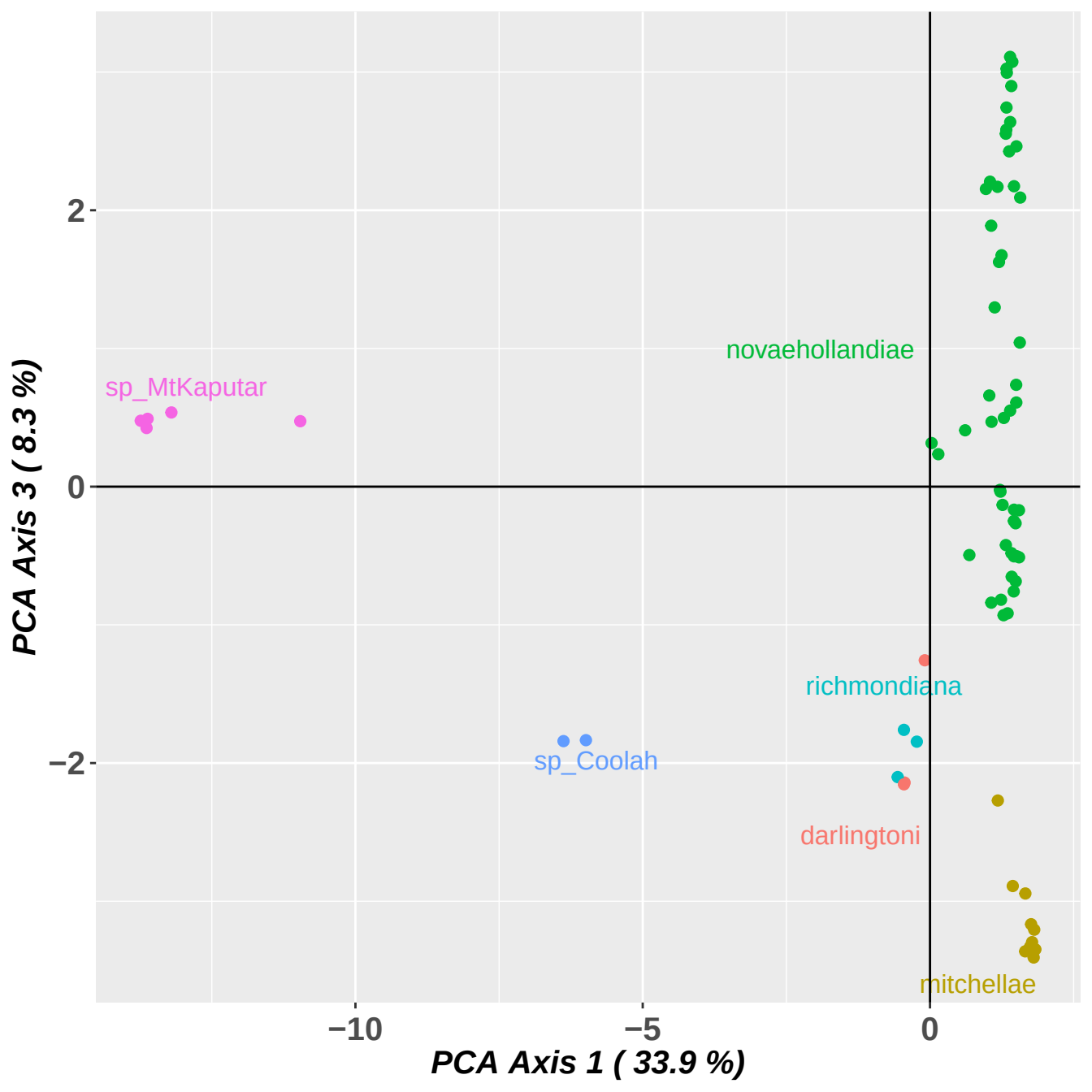

Count
200
100
0
0.0
0.1
0.2
0.3
0.4
0.5
Pre−filter SNP MAF
Over all populations

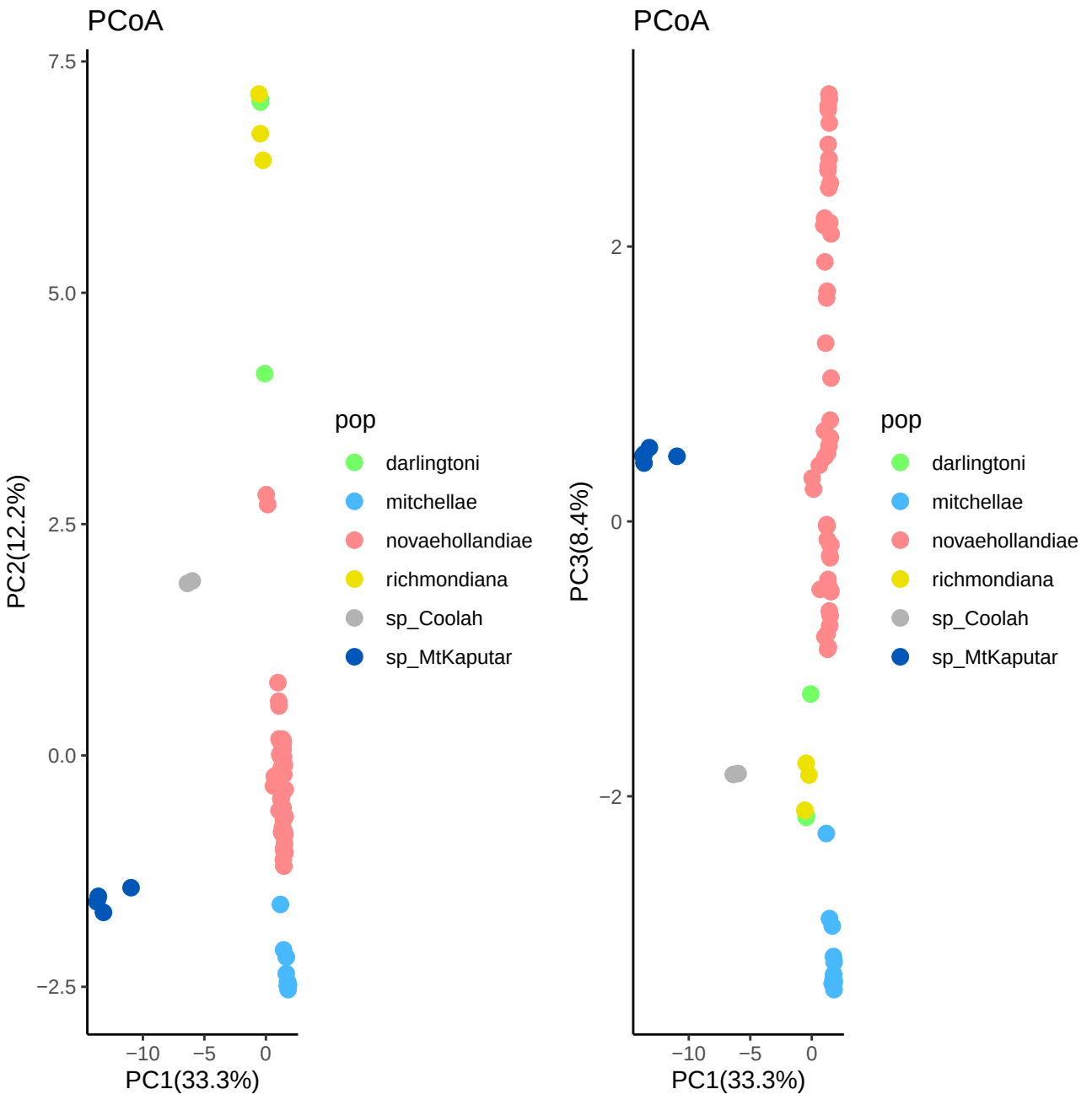

Count
200
100
0
0.0
0.1
0.2
0.3
0.4
0.5
Post−filter SNP MAF
Over all populations


PCA on SNP Genotypes
Scree Plot (informative axes only)
Percentage Contribution
30
20
10
0
2.5
5.0
7.5
10.0
PCA Axis


Noise Axes −− all eigenvalues positive
Count
6
4
2
0
0.0
0.2
0.4
0.6
Eigenvalue


7.5
5.0
2.5
0.0
−2.5
−10
−5
0
PCA Axis 2 ( 11.7 %)
PCA Axis 1 ( 33.9 %)
richmondiana
darlingtoni
sp_Coolah
novaehollandiae
sp_MtKaputar
mitchellae


sp_MtKaputar
novaehollandiae
richmondiana
sp_Coolah
darlingtoni
mitchellae
2
0
−2
−10
−5
0
PCA Axis 3 ( 8.3 %)
PCA Axis 1 ( 33.9 %)


PCoA
7.5
5.0
2.5
0.0
−2.5
PC2(12.2%)
−10
−5
0
PC1(33.3%)
pop
darlingtoni
mitchellae
novaehollandiae
richmondiana
sp_Coolah
sp_MtKaputar
PCoA
2
0
−2
PC3(8.4%)
−10
−5
0
PC1(33.3%)
pop
darlingtoni
mitchellae
novaehollandiae
richmondiana
sp_Coolah
sp_MtKaputar