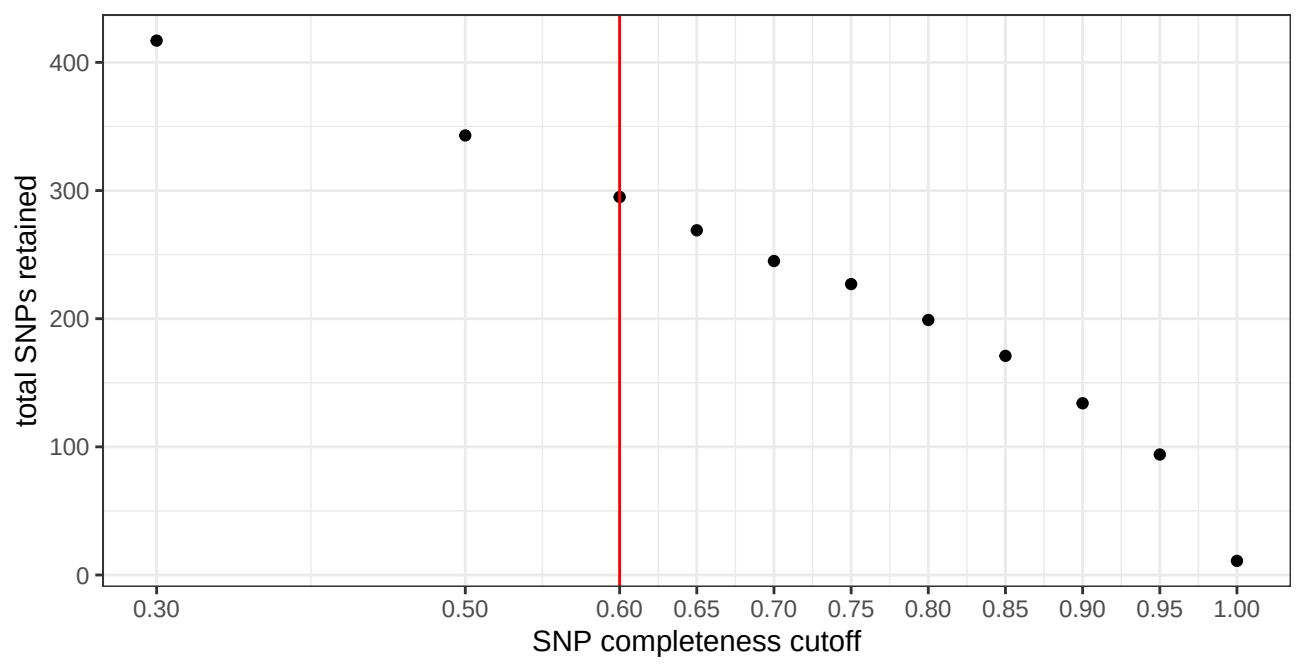
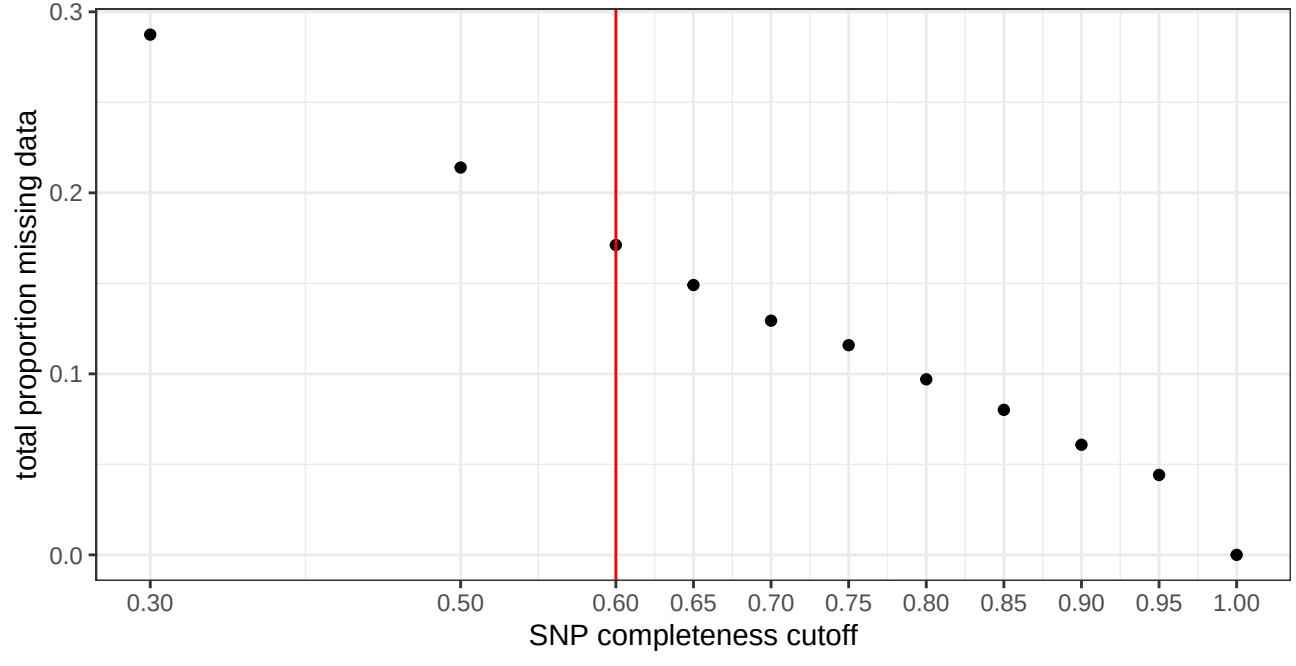
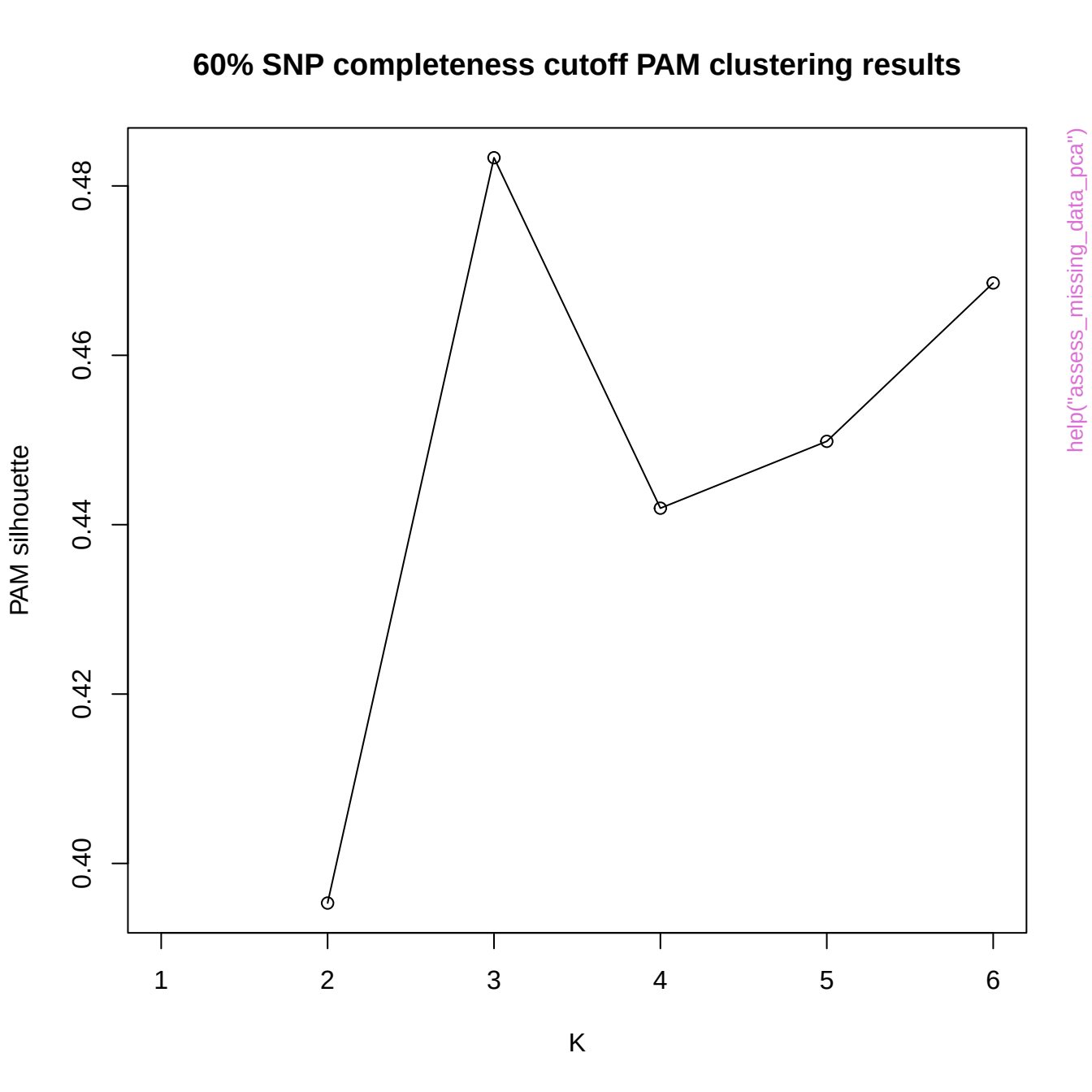
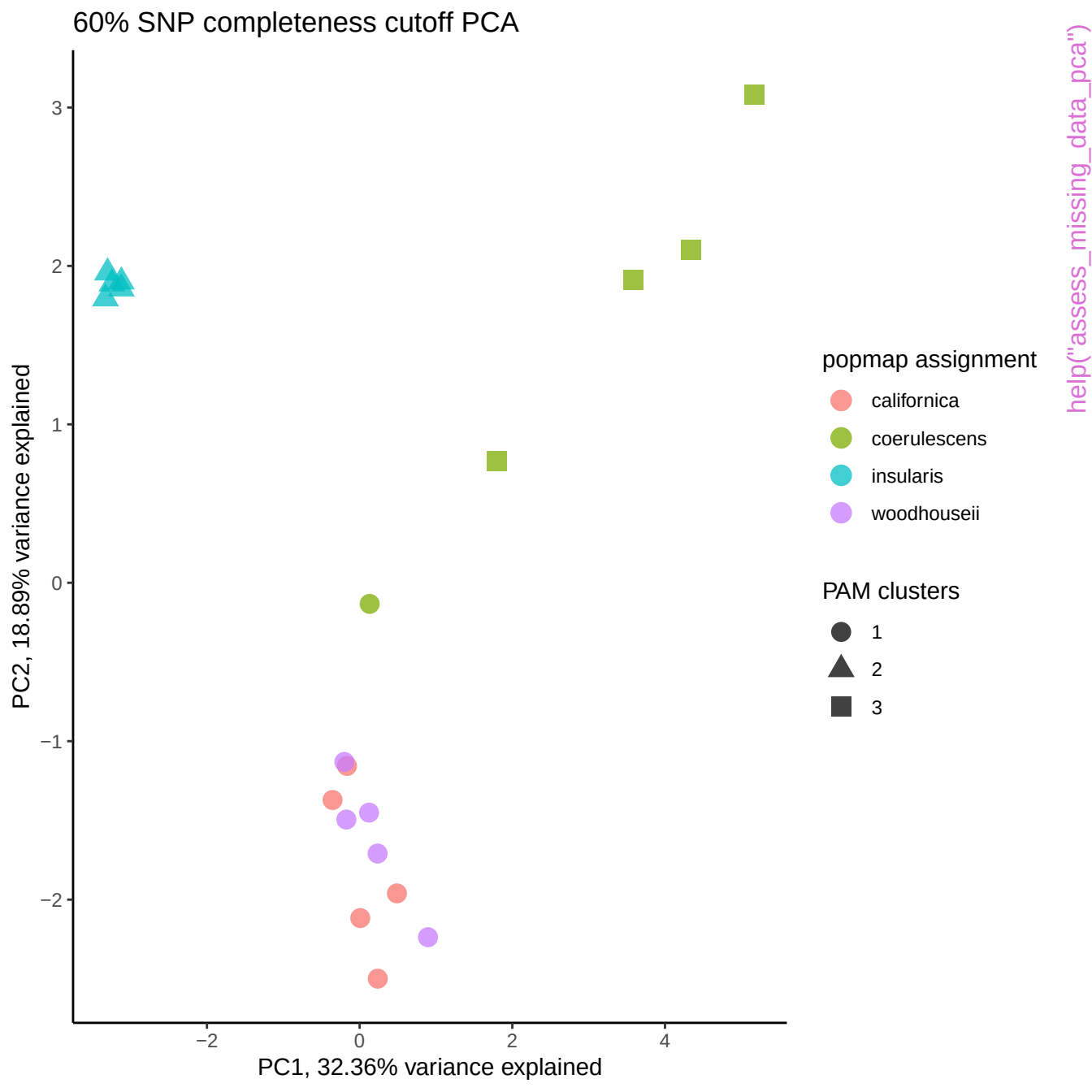
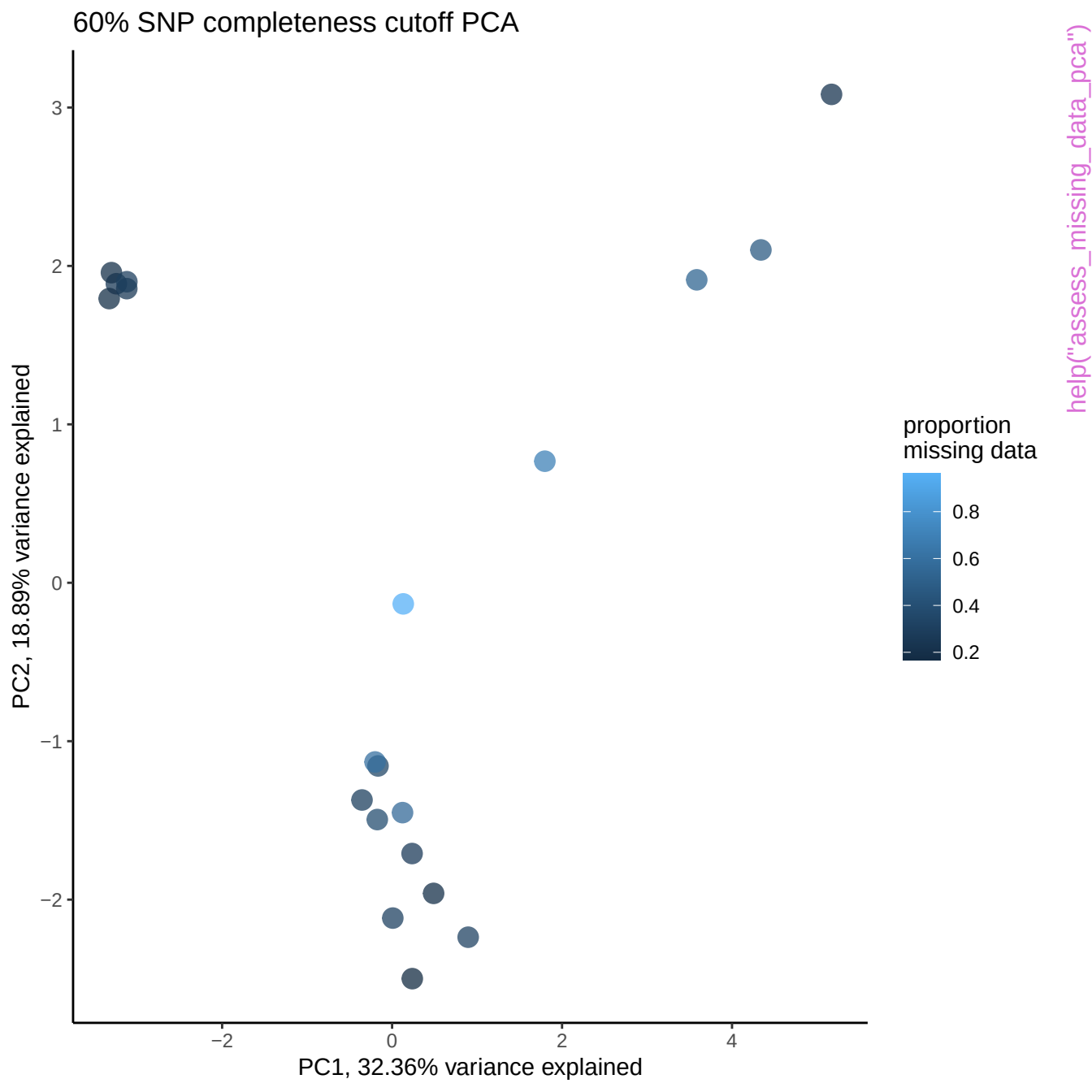


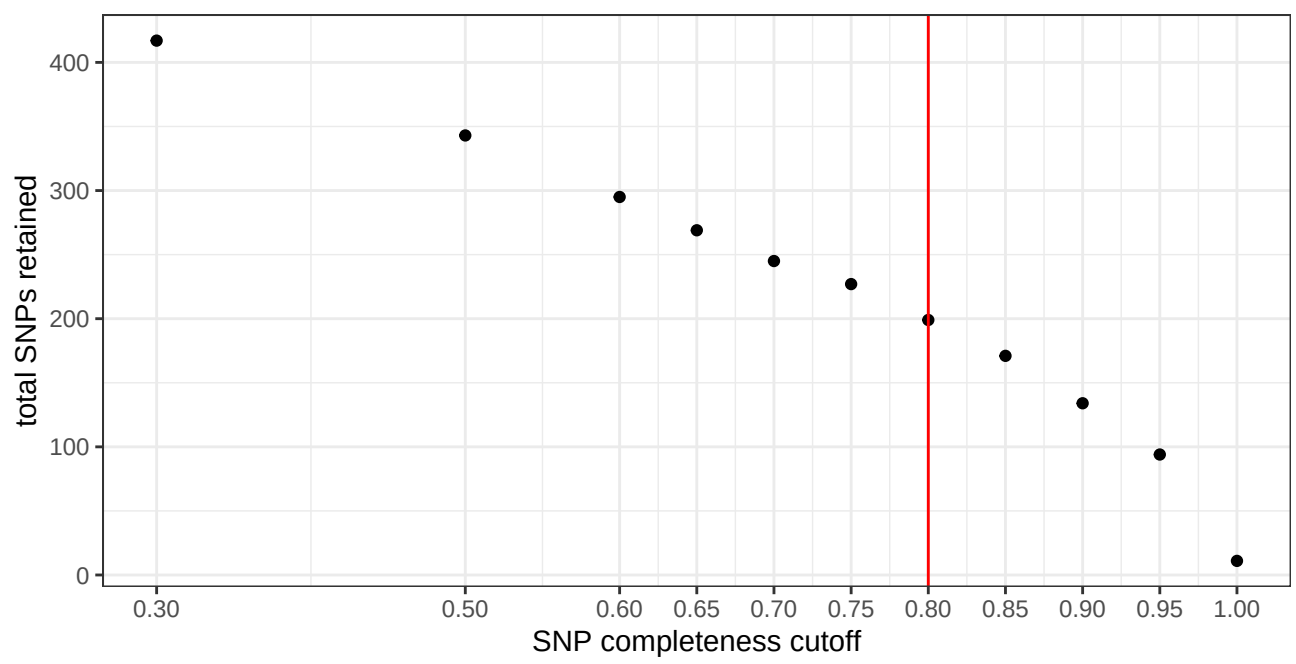
help("assess_missing_data_pca")



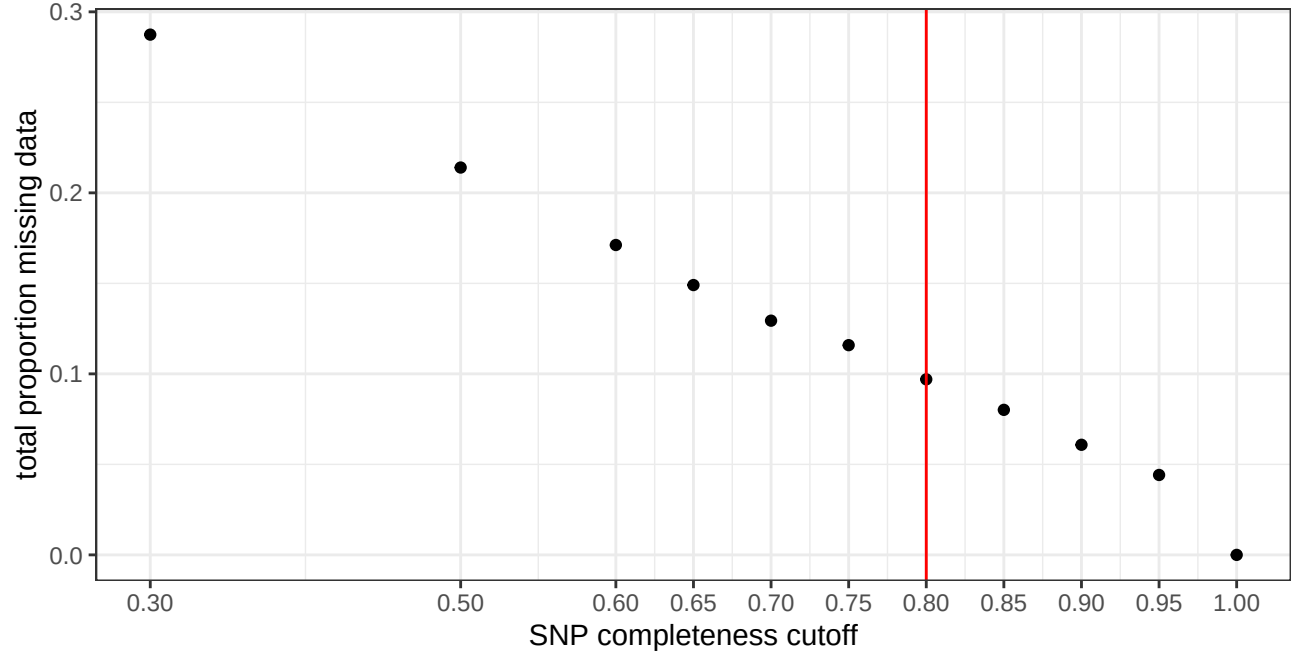

60% SNP completeness cutoff PAM clustering results
PAM silhouette
0.40
0.42
0.44
0.46
0.48
1
2
3
4
5
6
K
help("assess_missing_data_pca")

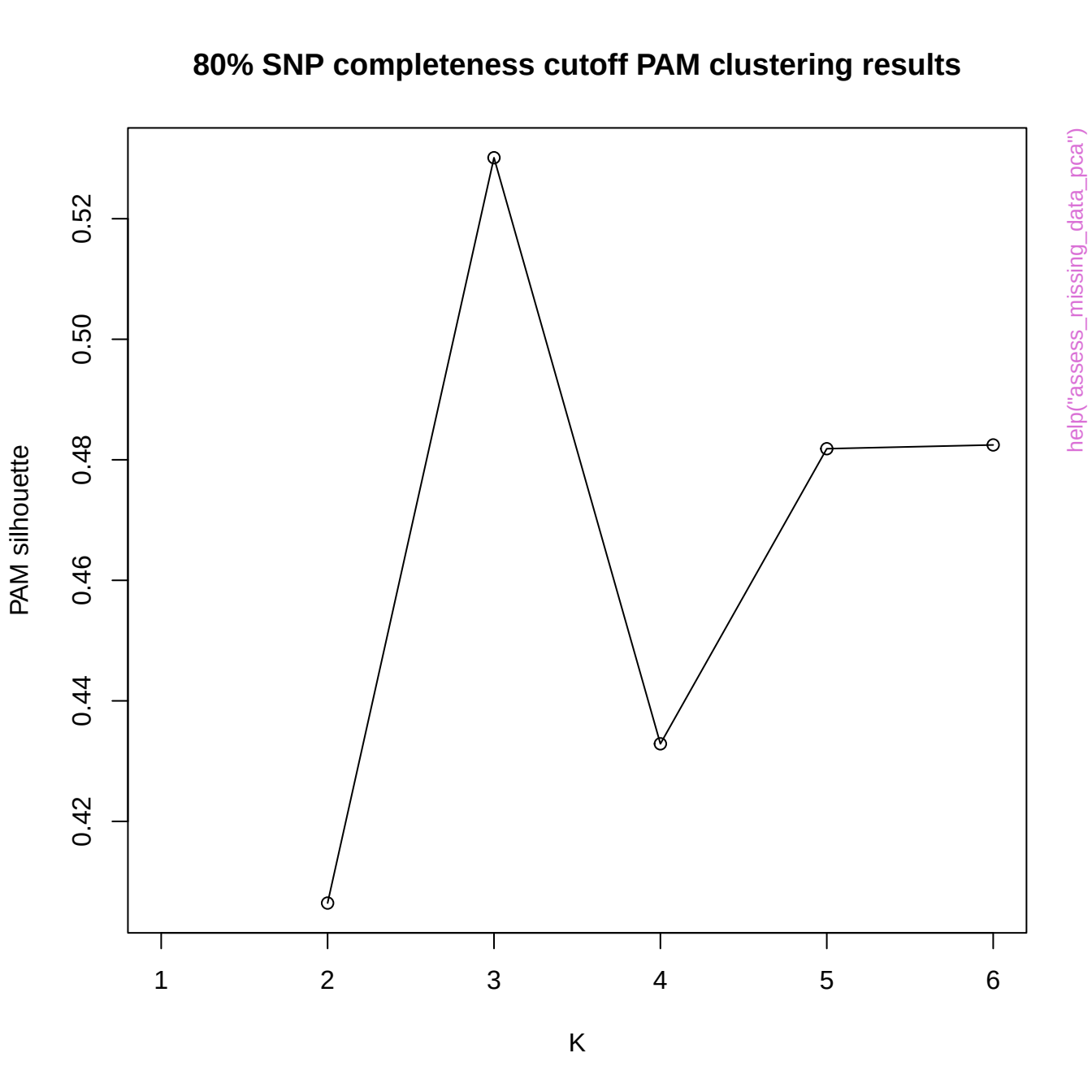

60% SNP completeness cutoff PCA
PC2, 18.89% variance explained
PC1, 32.36% variance explained
3
2
1
0
−1
−2
−2
0
2
4
popmap assignment
californica
coerulescens
insularis
woodhouseii
PAM clusters
1
2
3
help("assess_missing_data_pca")

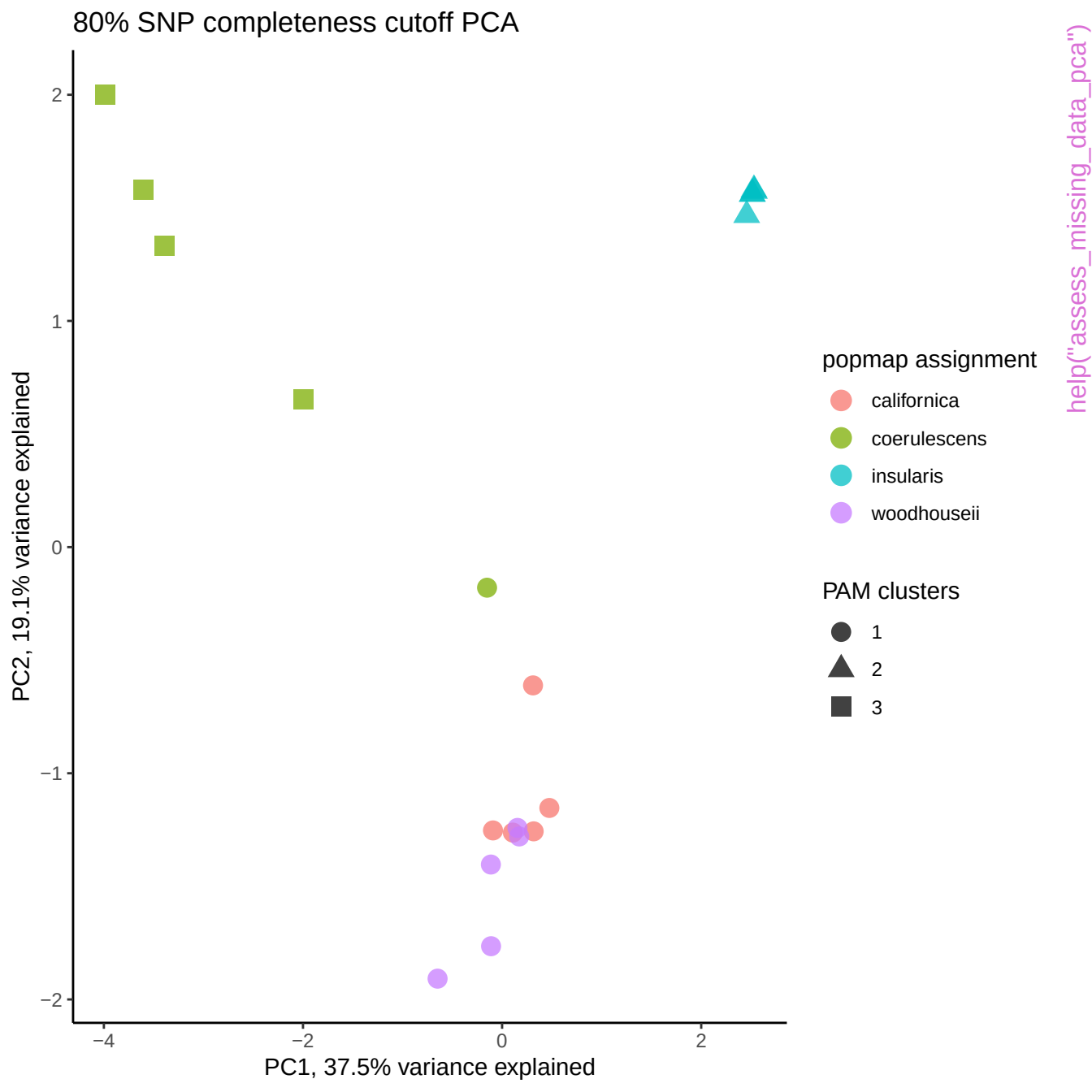

60% SNP completeness cutoff PCA
PC2, 18.89% variance explained
PC1, 32.36% variance explained
3
2
1
0
−1
−2
−2
0
2
4
proportion
missing data
0.8
0.6
0.4
0.2
help("assess_missing_data_pca")

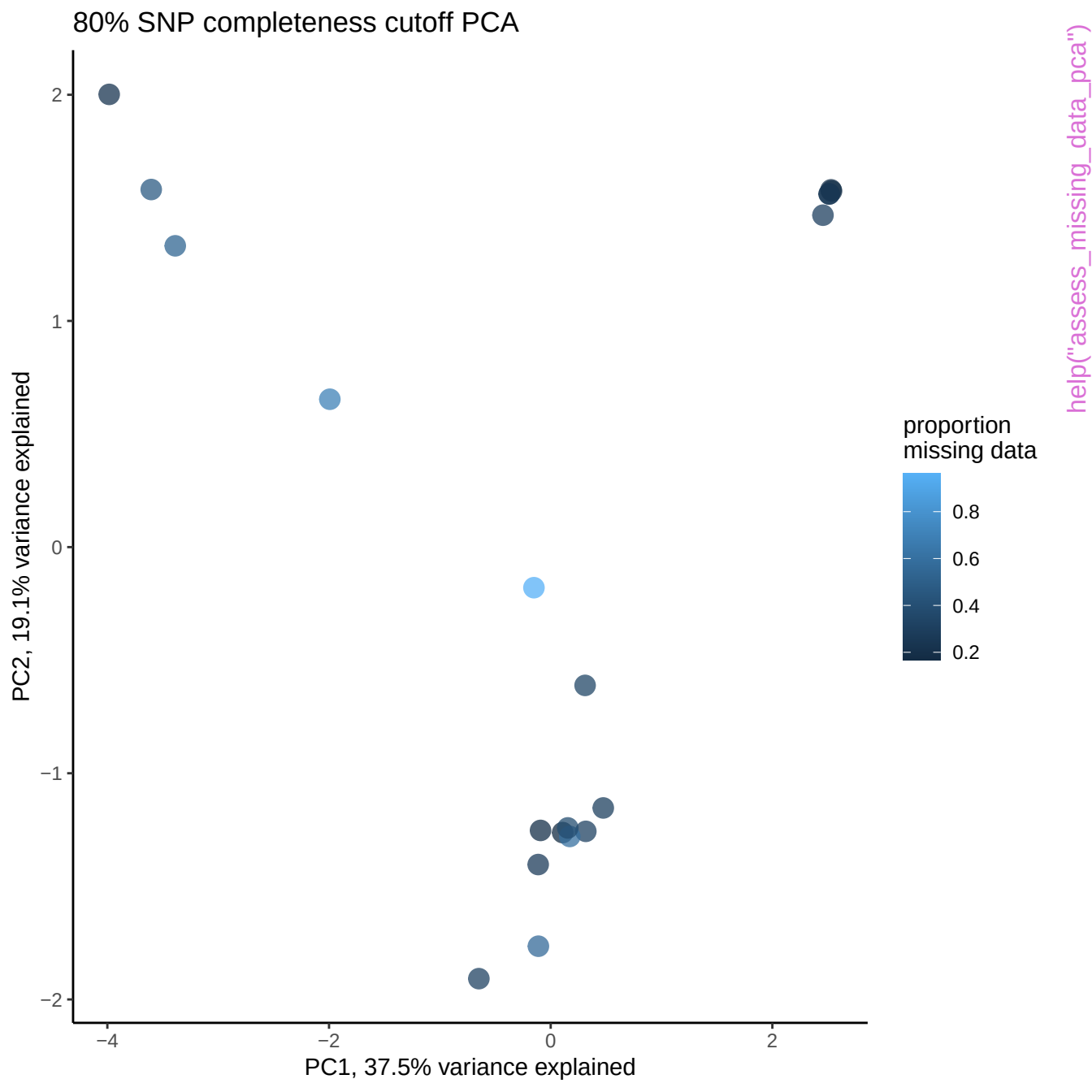


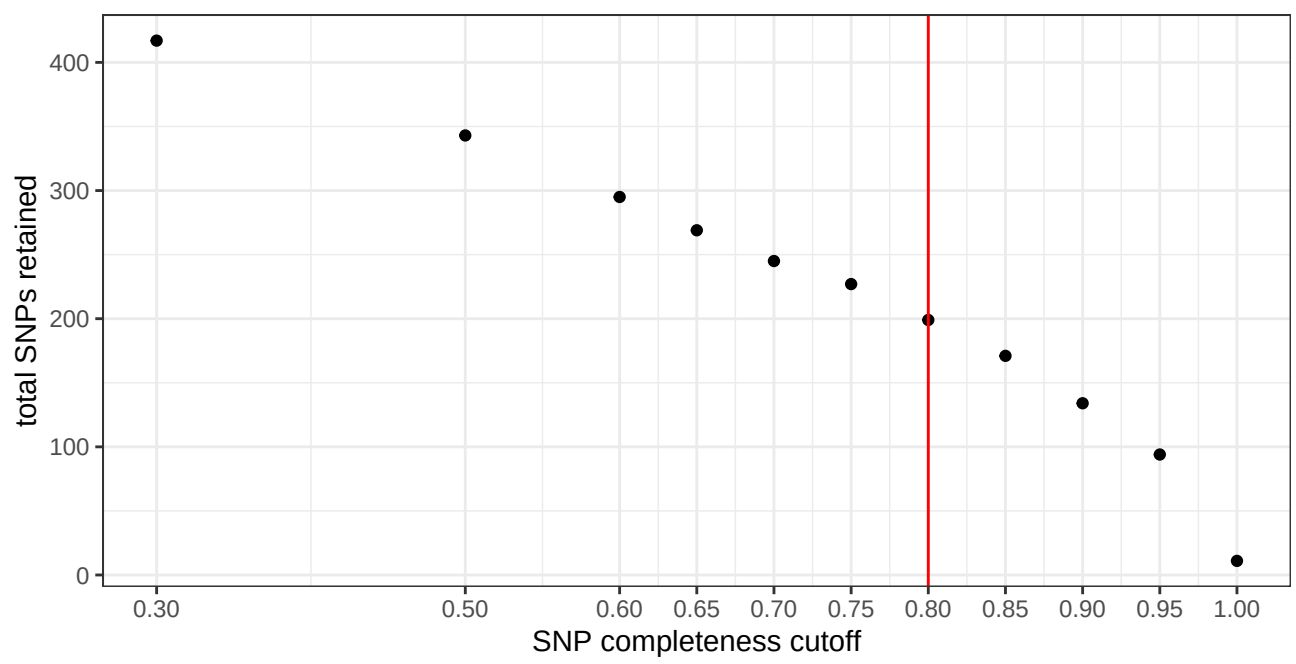
help("assess_missing_data_pca")



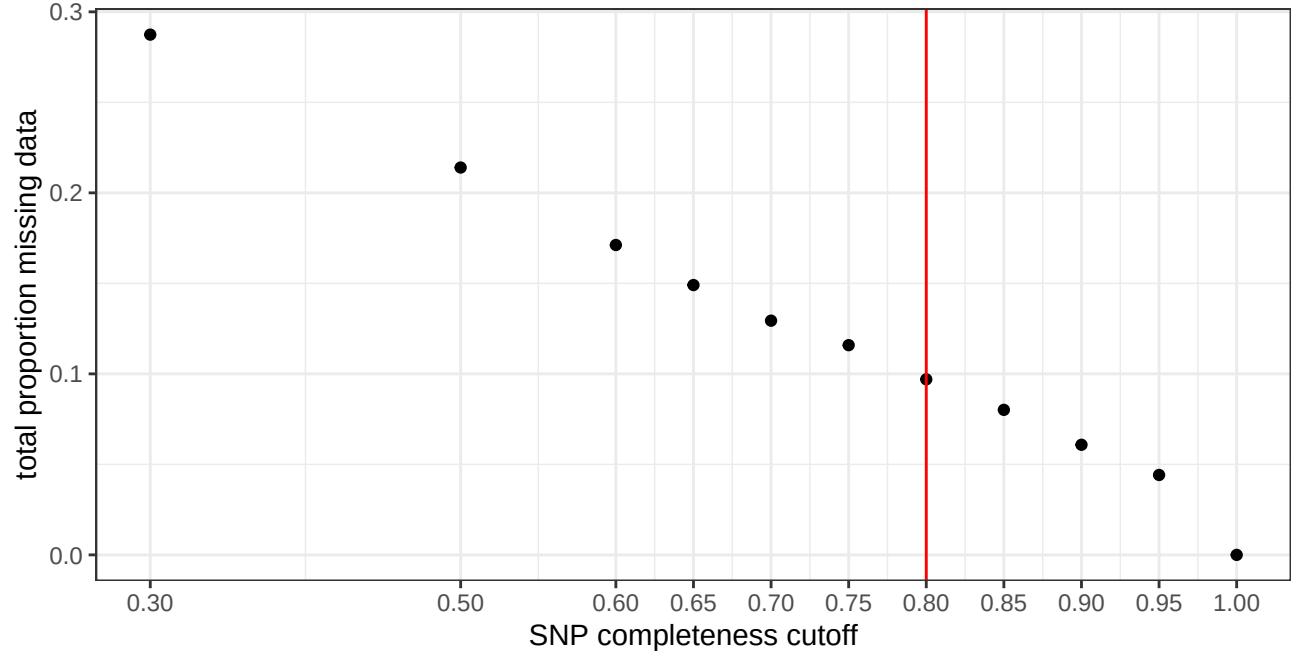

80% SNP completeness cutoff PAM clustering results
PAM silhouette
0.42
0.44
0.46
0.48
0.50
0.52
1
2
3
4
5
6
K
help("assess_missing_data_pca")

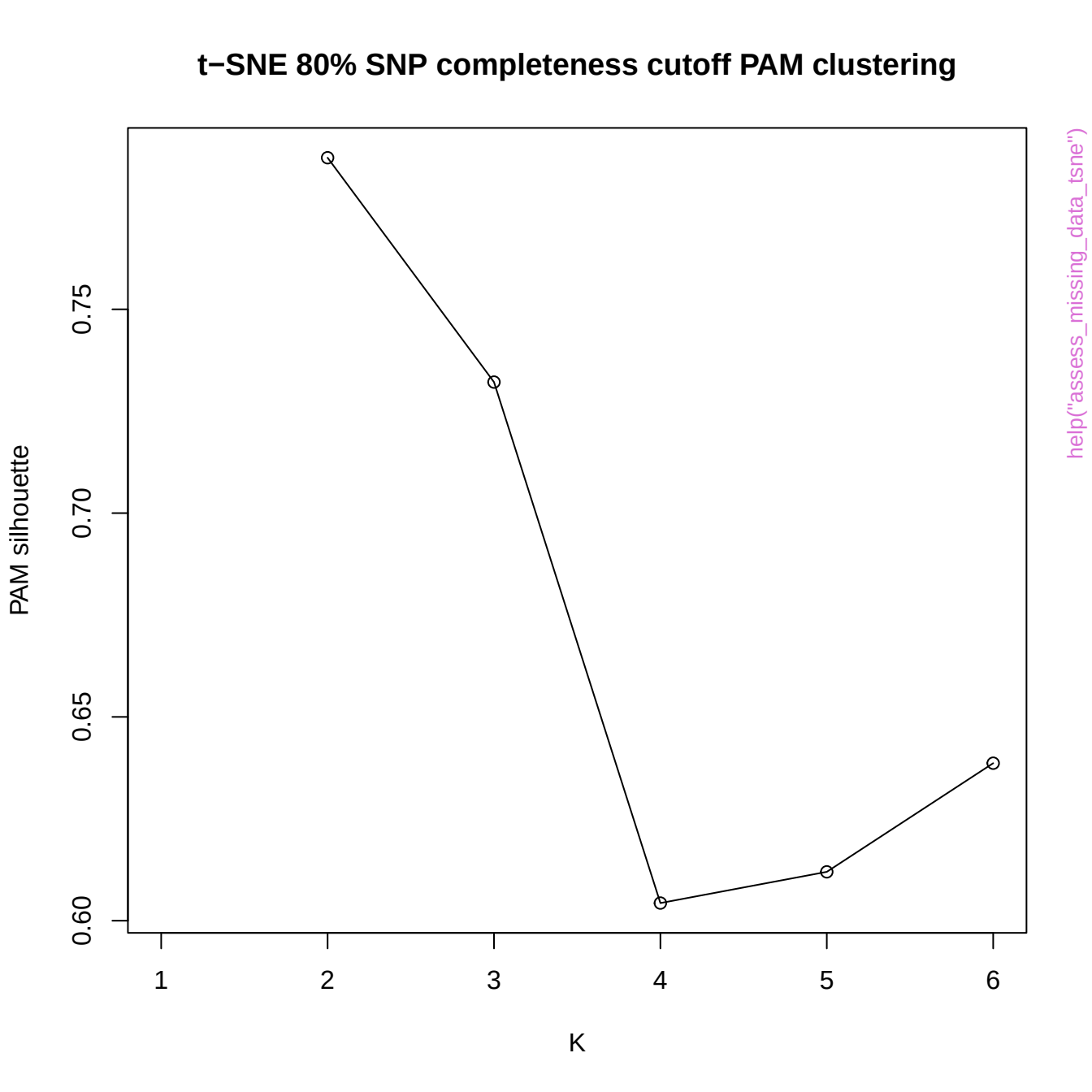

80% SNP completeness cutoff PCA
PC2, 19.1% variance explained
PC1, 37.5% variance explained
2
1
0
−1
−2
−4
−2
0
2
popmap assignment
californica
coerulescens
insularis
woodhouseii
PAM clusters
1
2
3
help("assess_missing_data_pca")

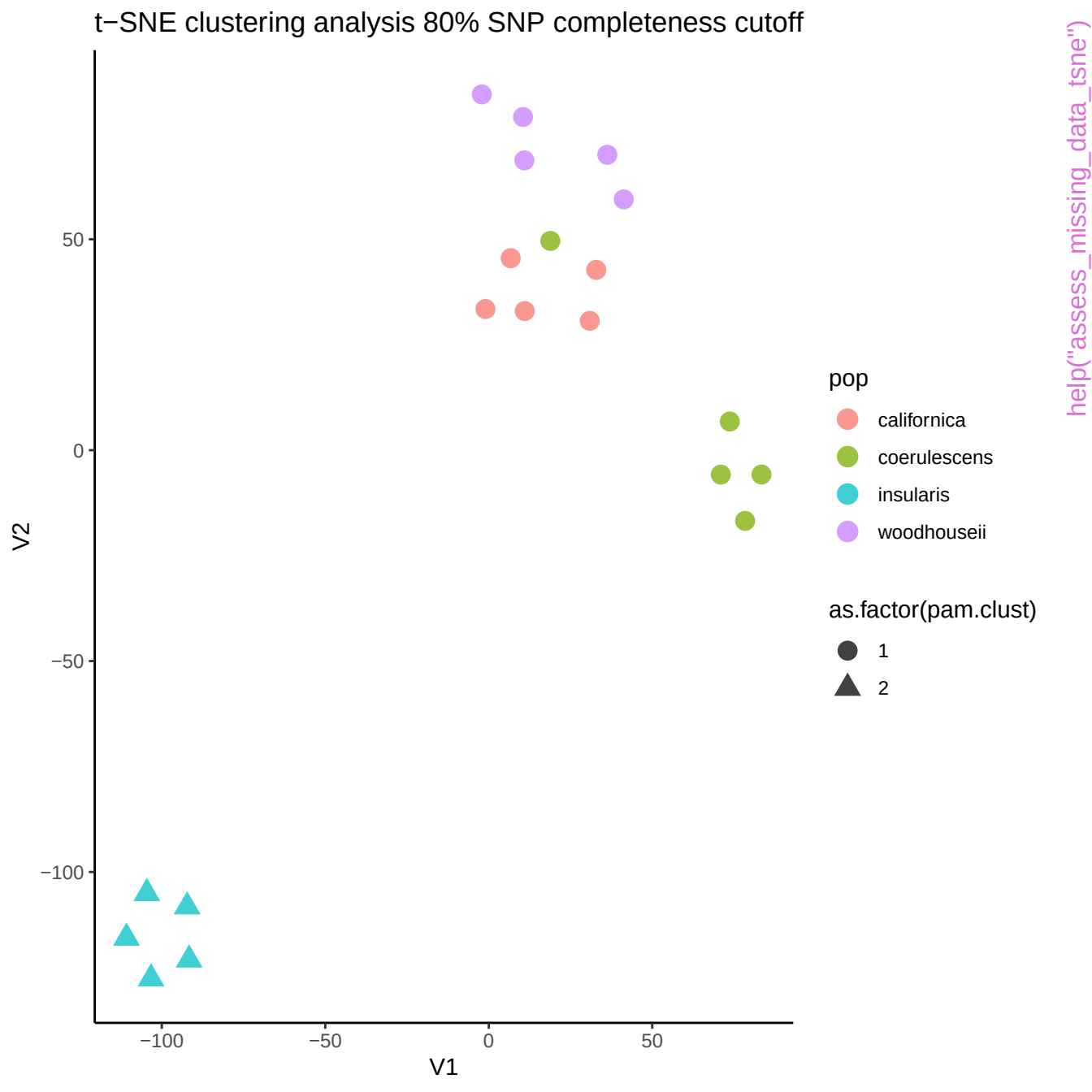

80% SNP completeness cutoff PCA
PC2, 19.1% variance explained
PC1, 37.5% variance explained
2
1
0
−1
−2
−4
−2
0
2
proportion
missing data
0.8
0.6
0.4
0.2
help("assess_missing_data_pca")

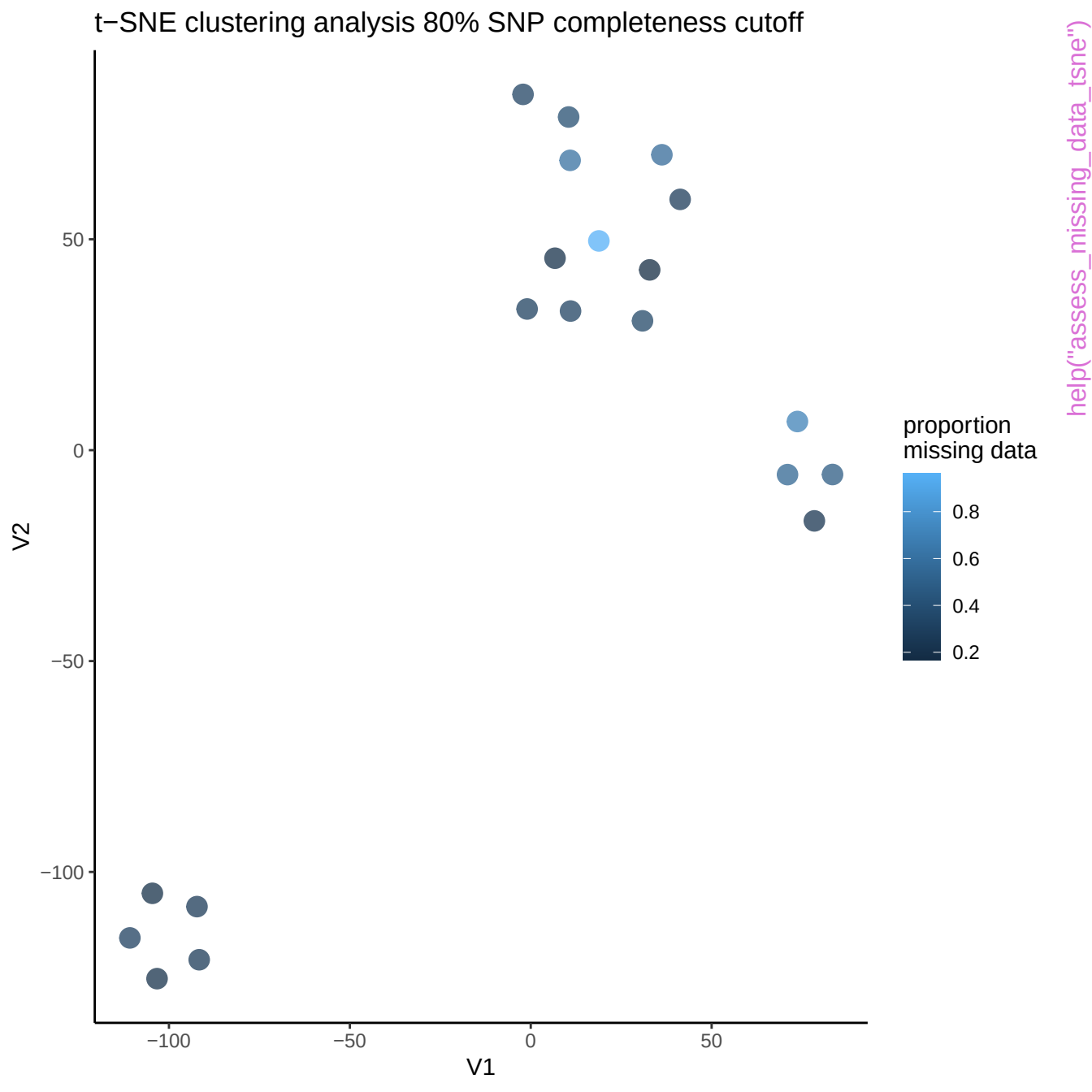


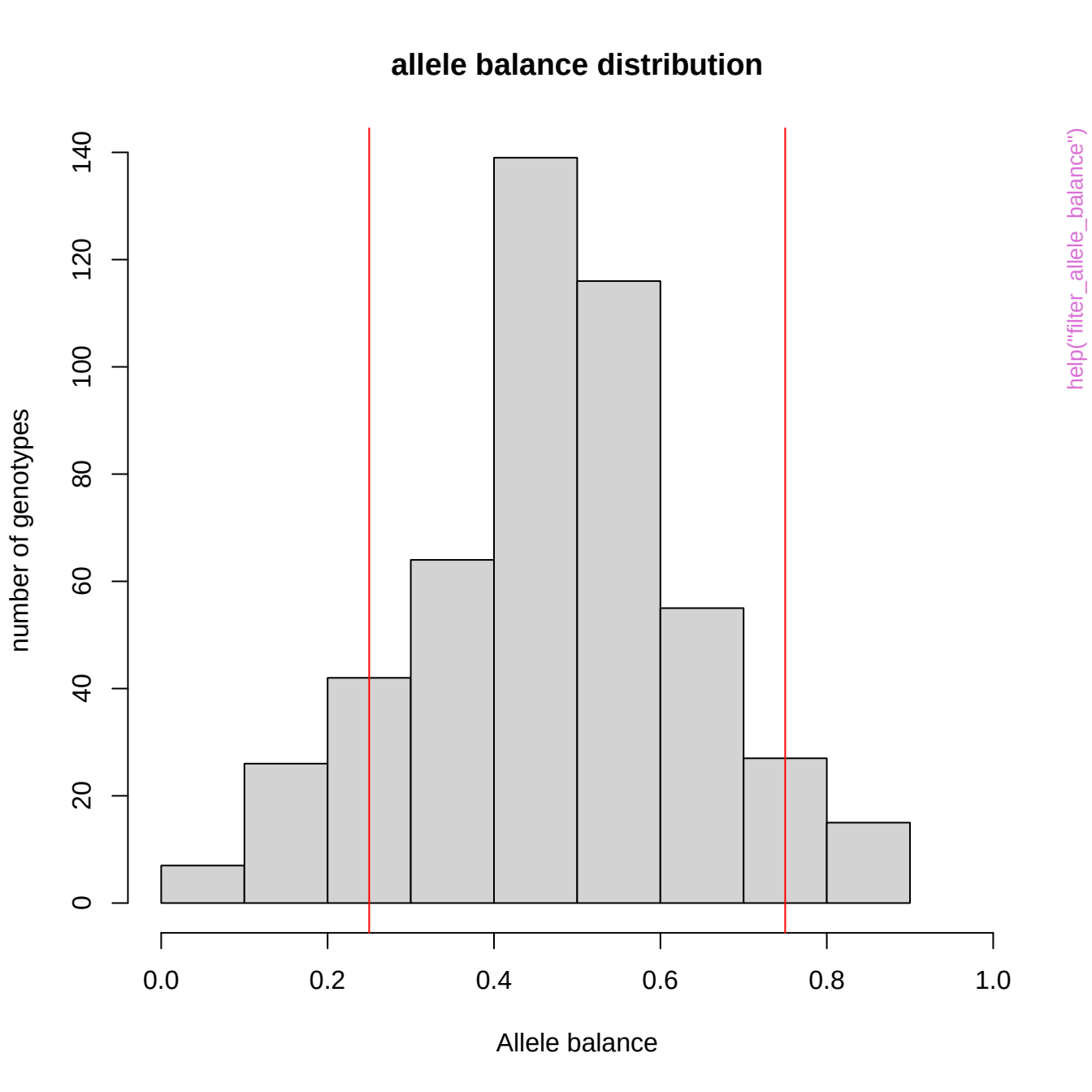
help("assess_missing_data_tsne")

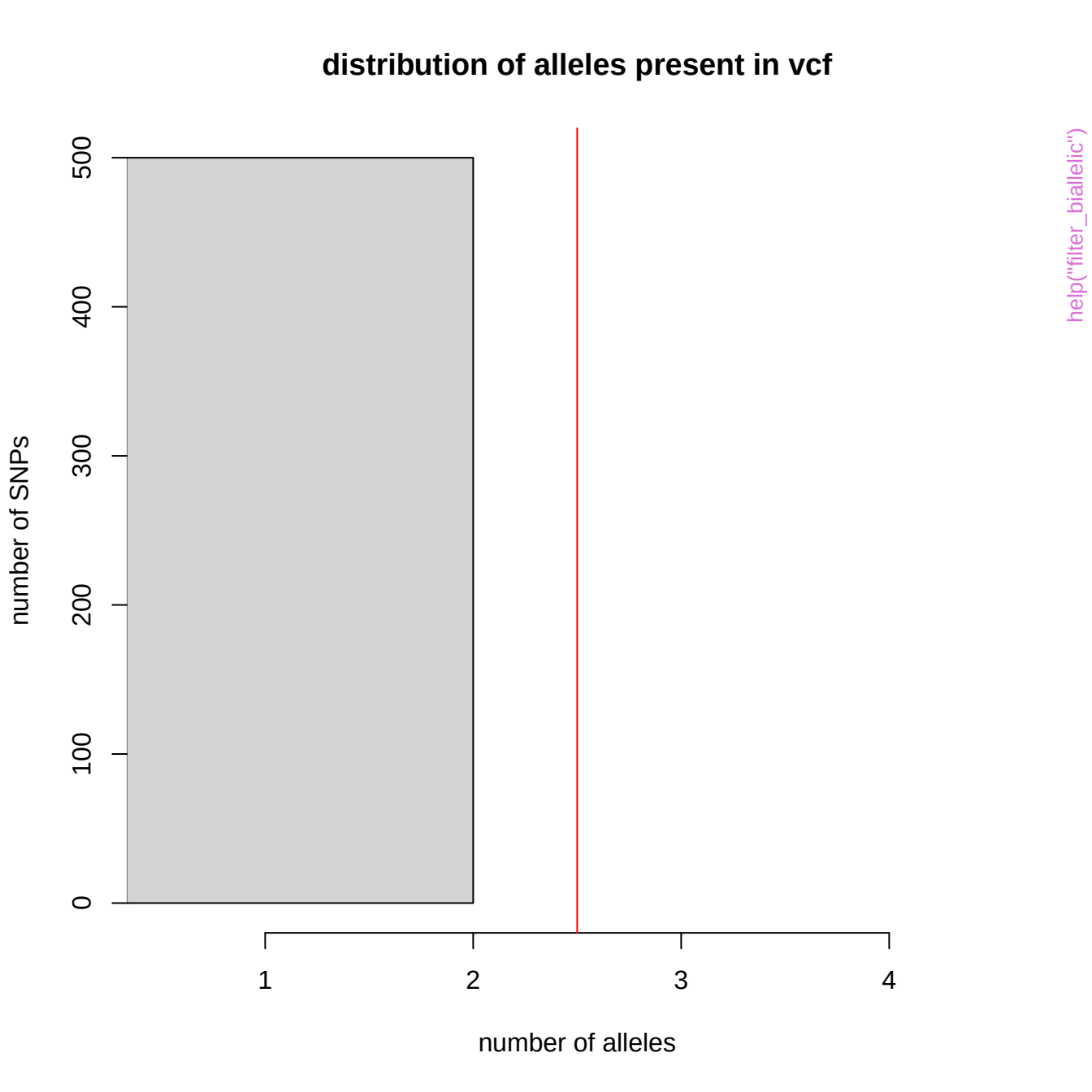


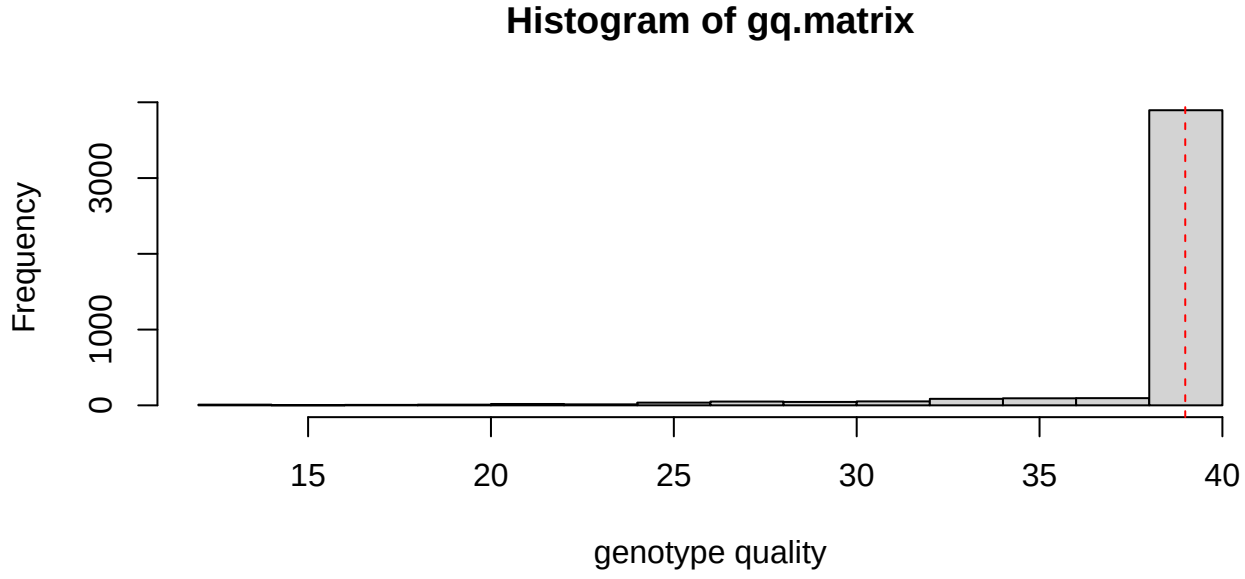

t−SNE 80% SNP completeness cutoff PAM clustering
PAM silhouette
0.60
0.65
0.70
0.75
1
2
3
4
5
6
K
help("assess_missing_data_tsne")

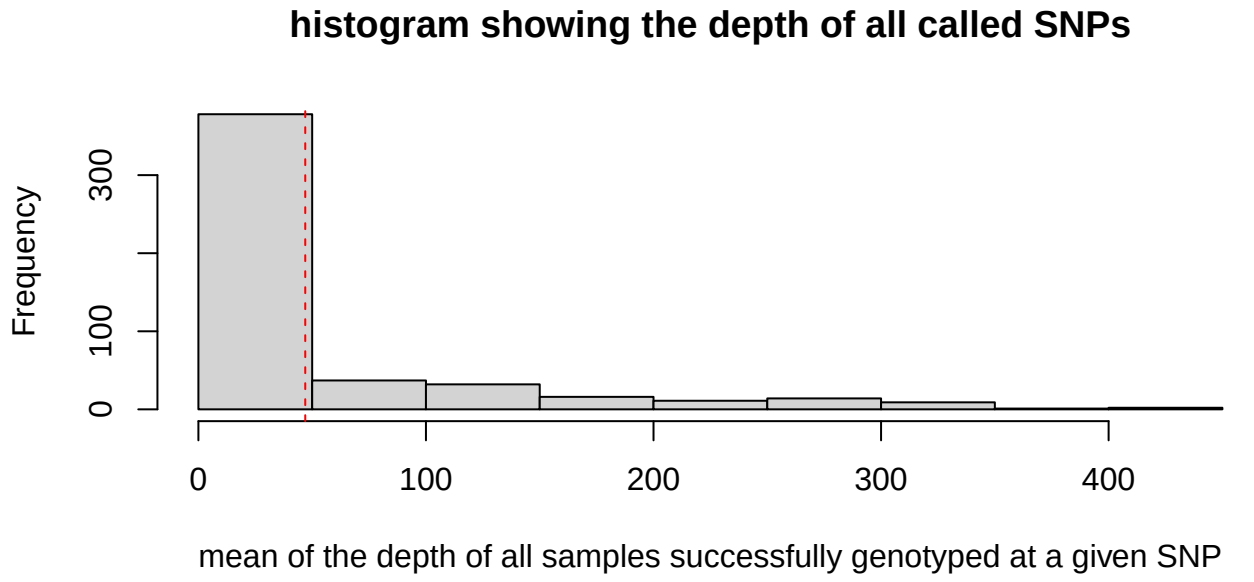

t−SNE clustering analysis 80% SNP completeness cutoff
50
0
−50
−100
V2
−100
−50
0
50
V1
pop
californica
coerulescens
insularis
woodhouseii
as.factor(pam.clust)
1
2
help("assess_missing_data_tsne")


t−SNE clustering analysis 80% SNP completeness cutoff
50
0
−50
−100
V2
−100
−50
0
50
V1
proportion
missing data
0.8
0.6
0.4
0.2
help("assess_missing_data_tsne")

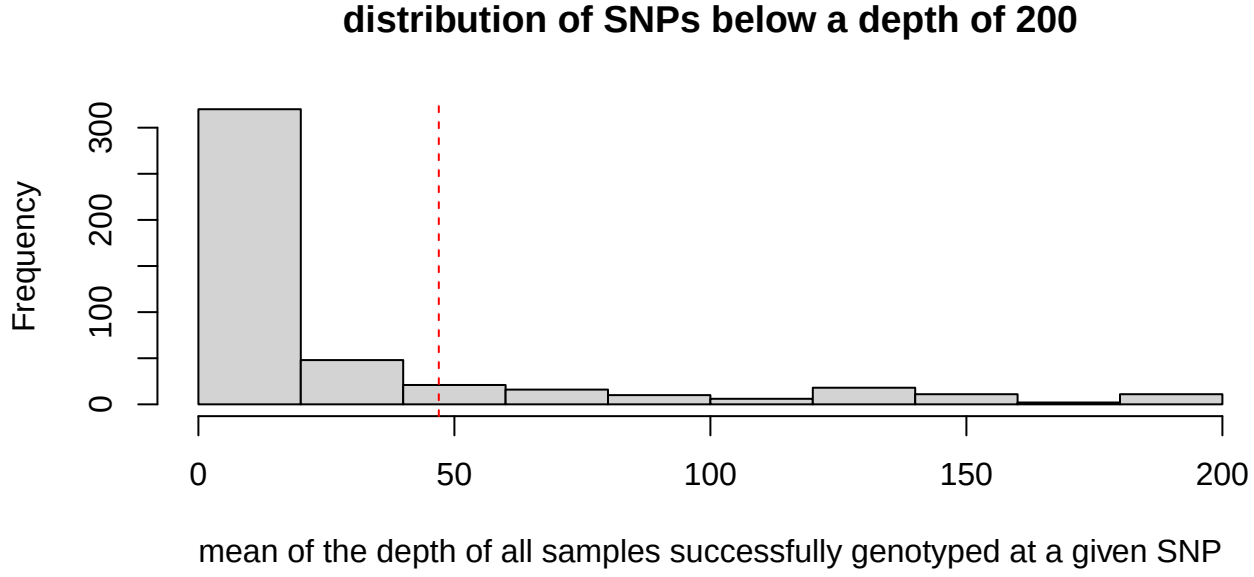

allele balance distribution
number of genotypes
0
20
40
60
80
100
120
140
0.0
0.2
0.4
0.6
0.8
1.0
Allele balance
help("filter_allele_balance")

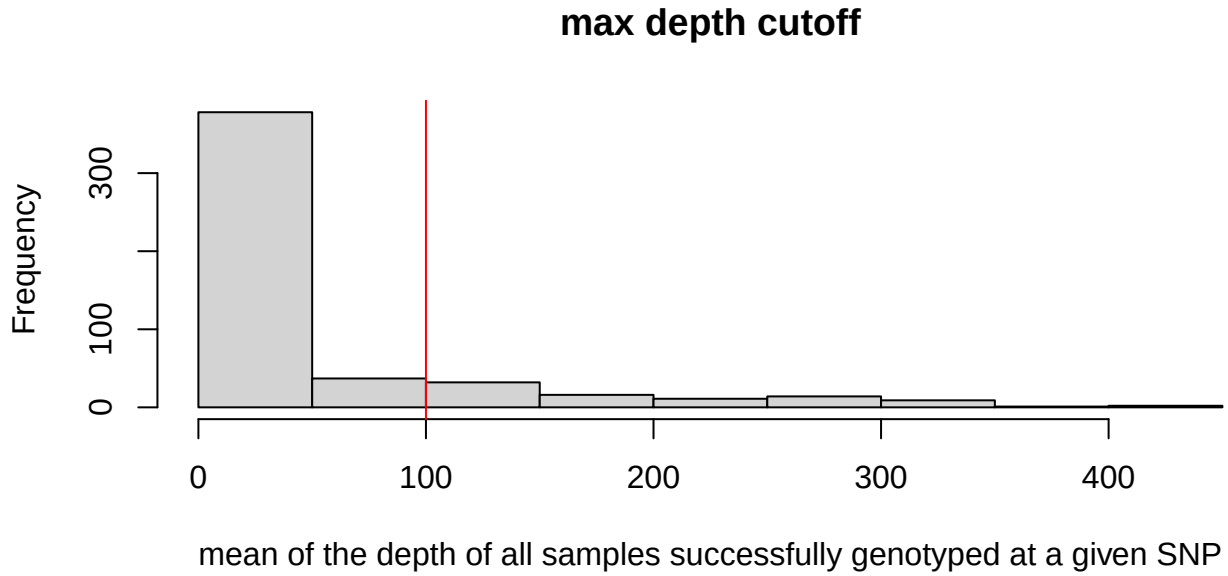

distribution of alleles present in vcf
number of SNPs
0
100
200
300
400
500
1
2
3
4
number of alleles
help("filter_biallelic")


Histogram of gq.matrix
Frequency
0
1000
3000
15
20
25
30
35
40
genotype quality
help("hard_filter")

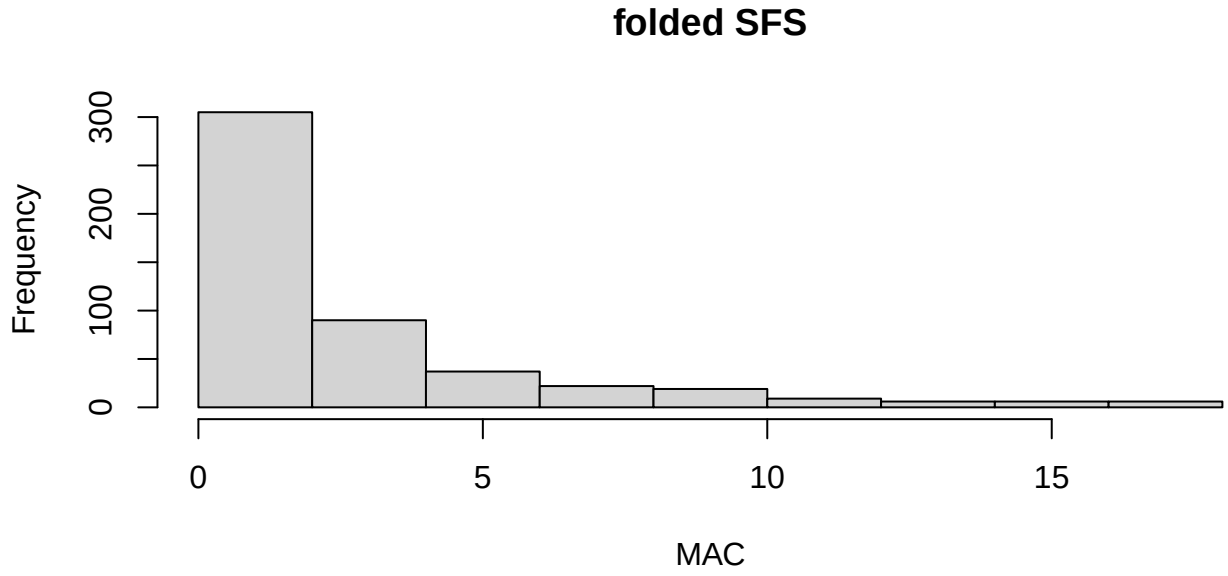


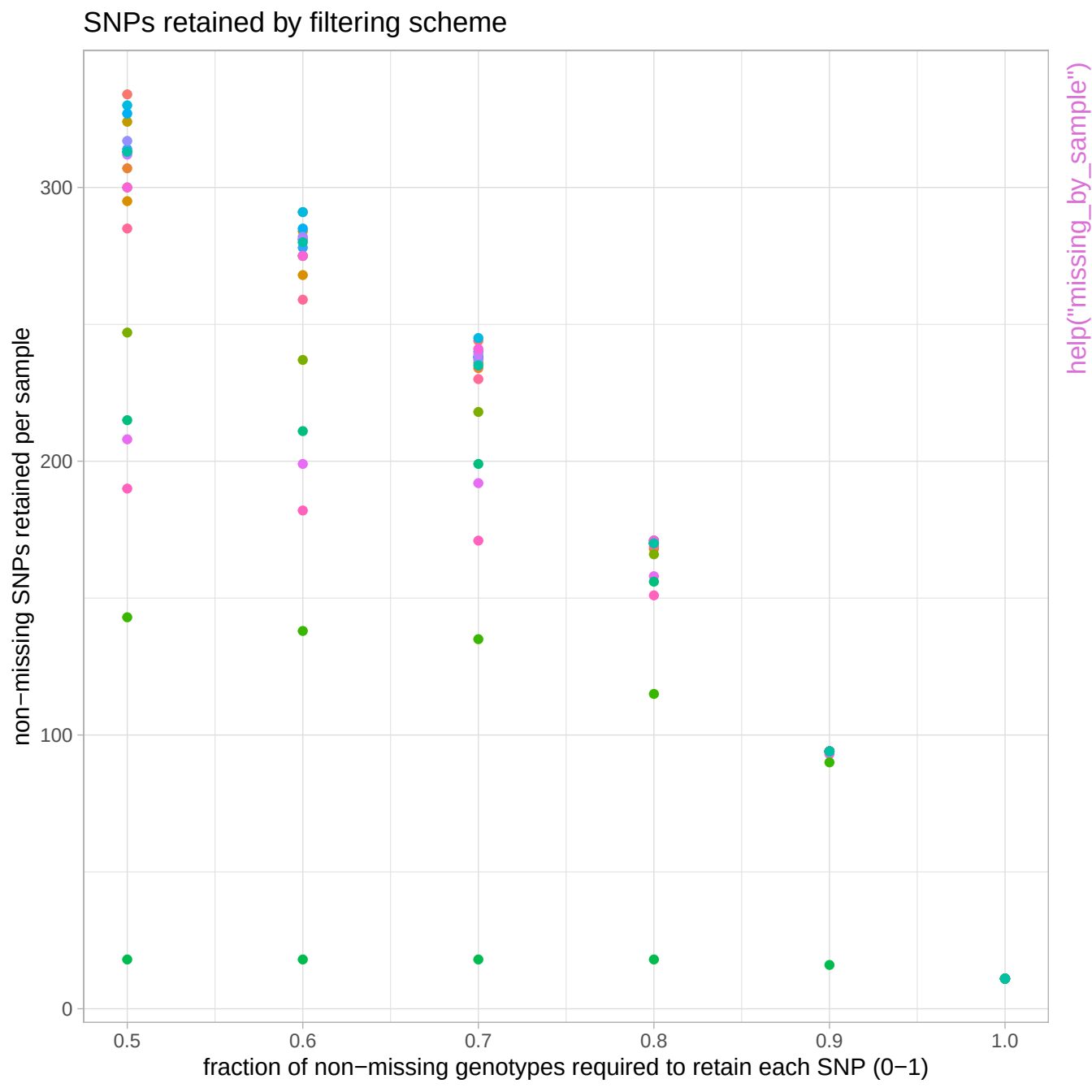
help("max_depth")



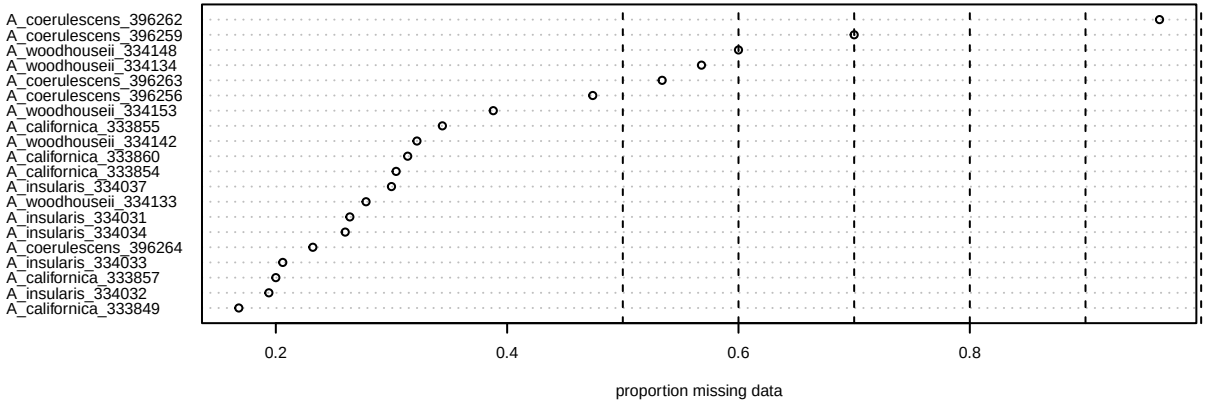


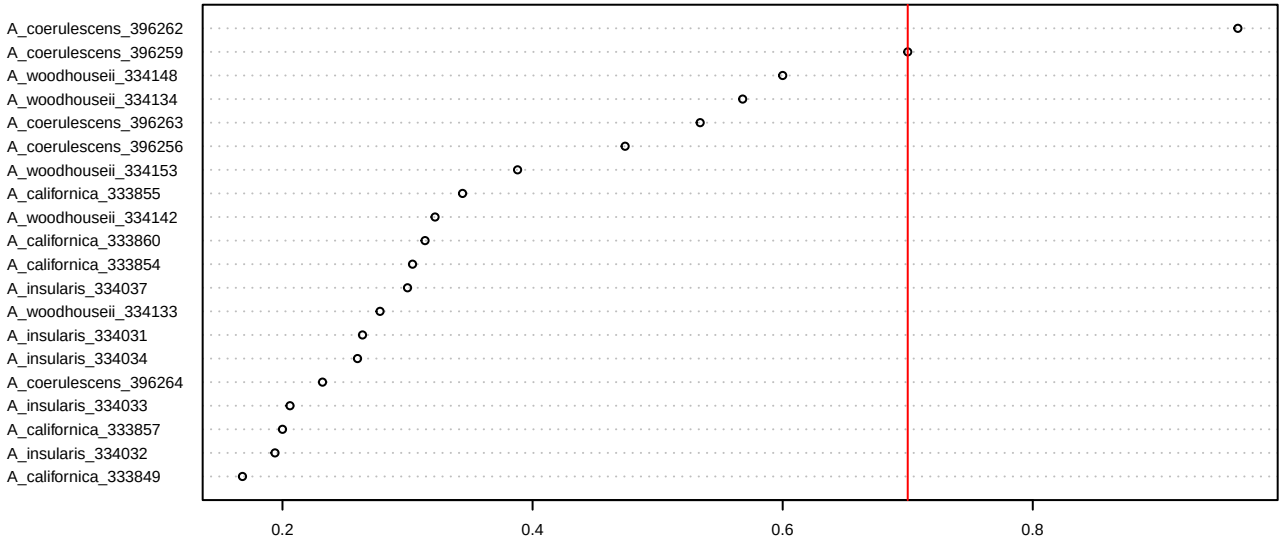
help("max_depth")

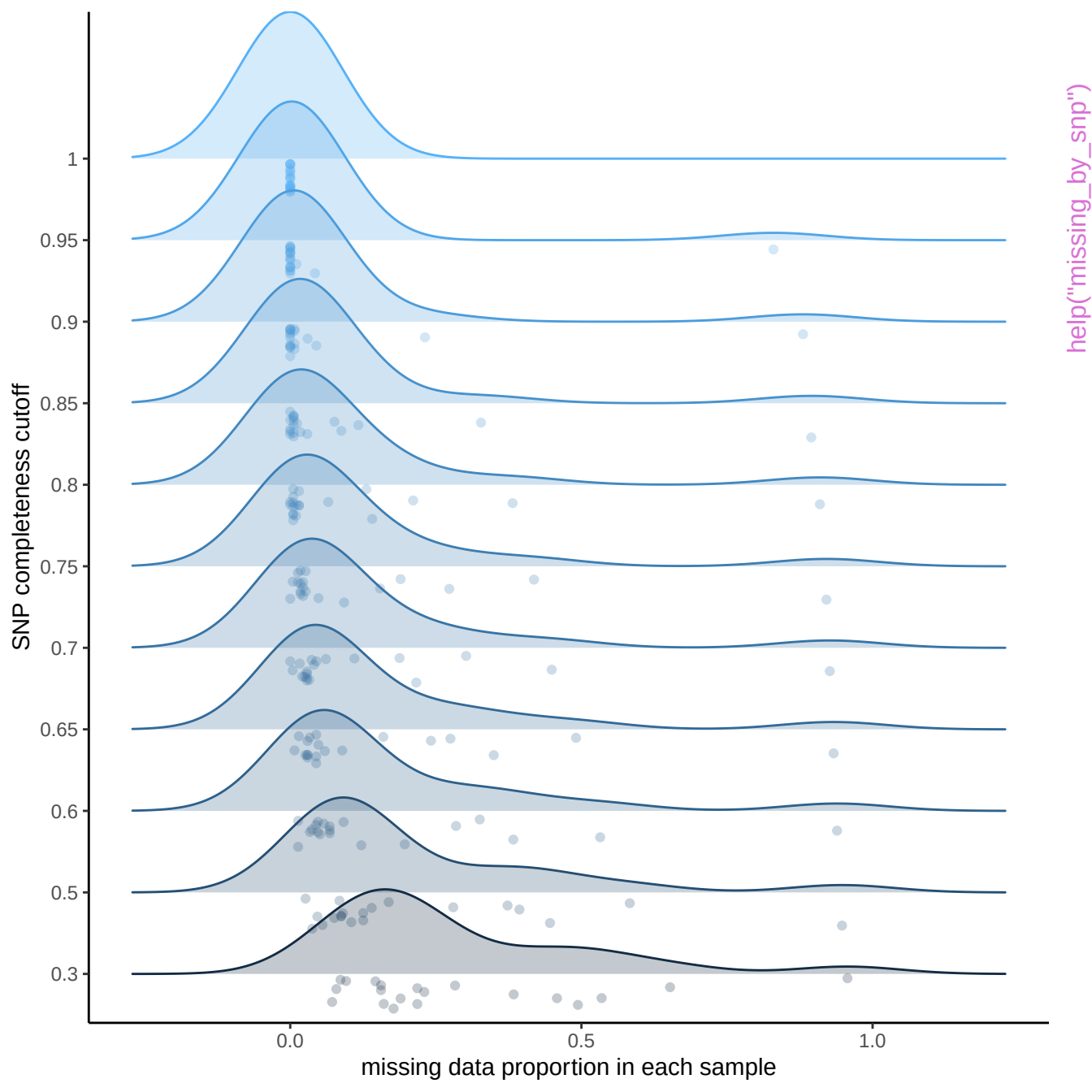


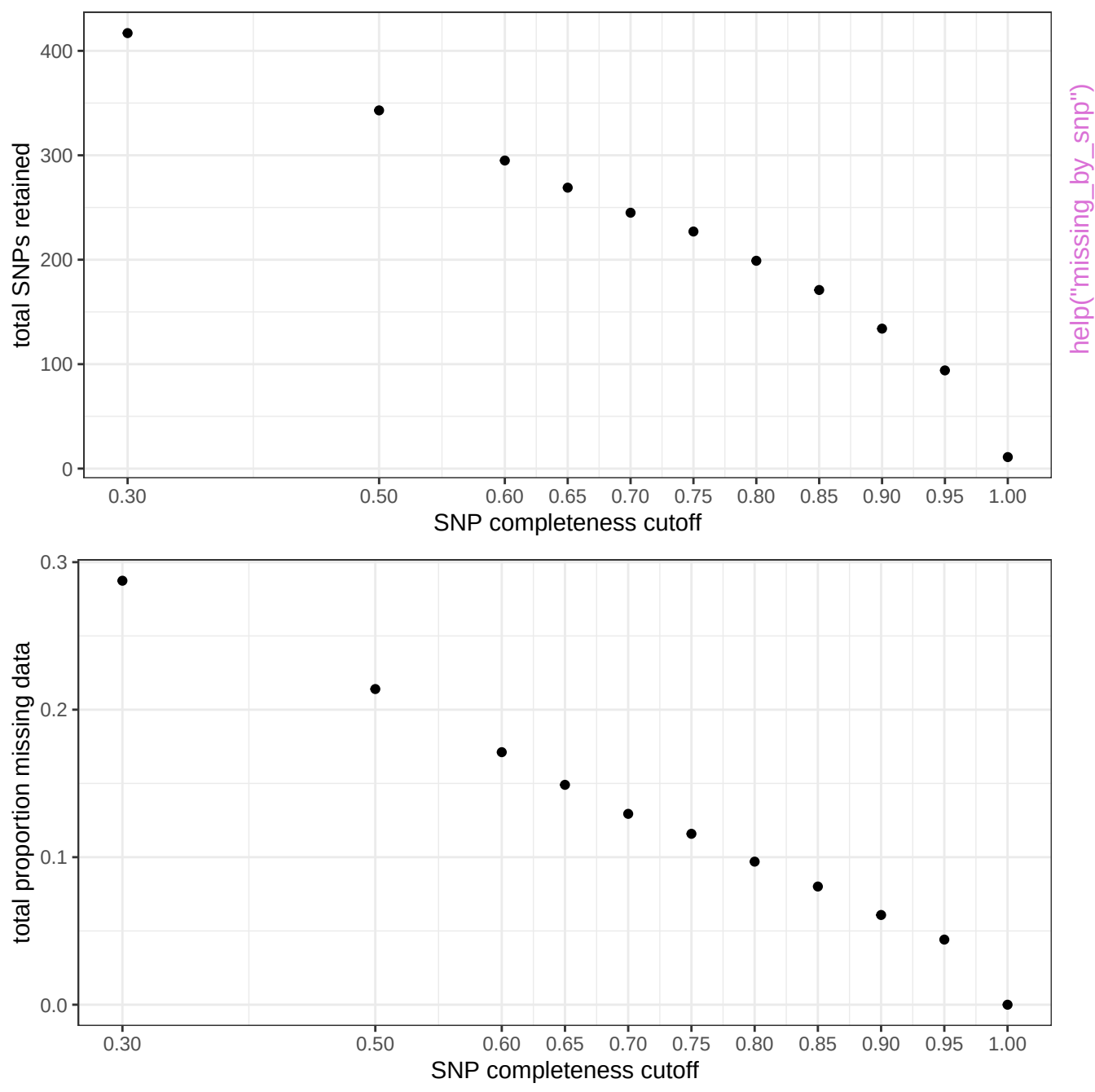

SNPs retained by filtering scheme
non−missing SNPs retained per sample
300
200
100
0
0.5
0.6
0.7
0.8
0.9
1.0
fraction of non−missing genotypes required to retain each SNP (0−1)
help("missing_by_sample")

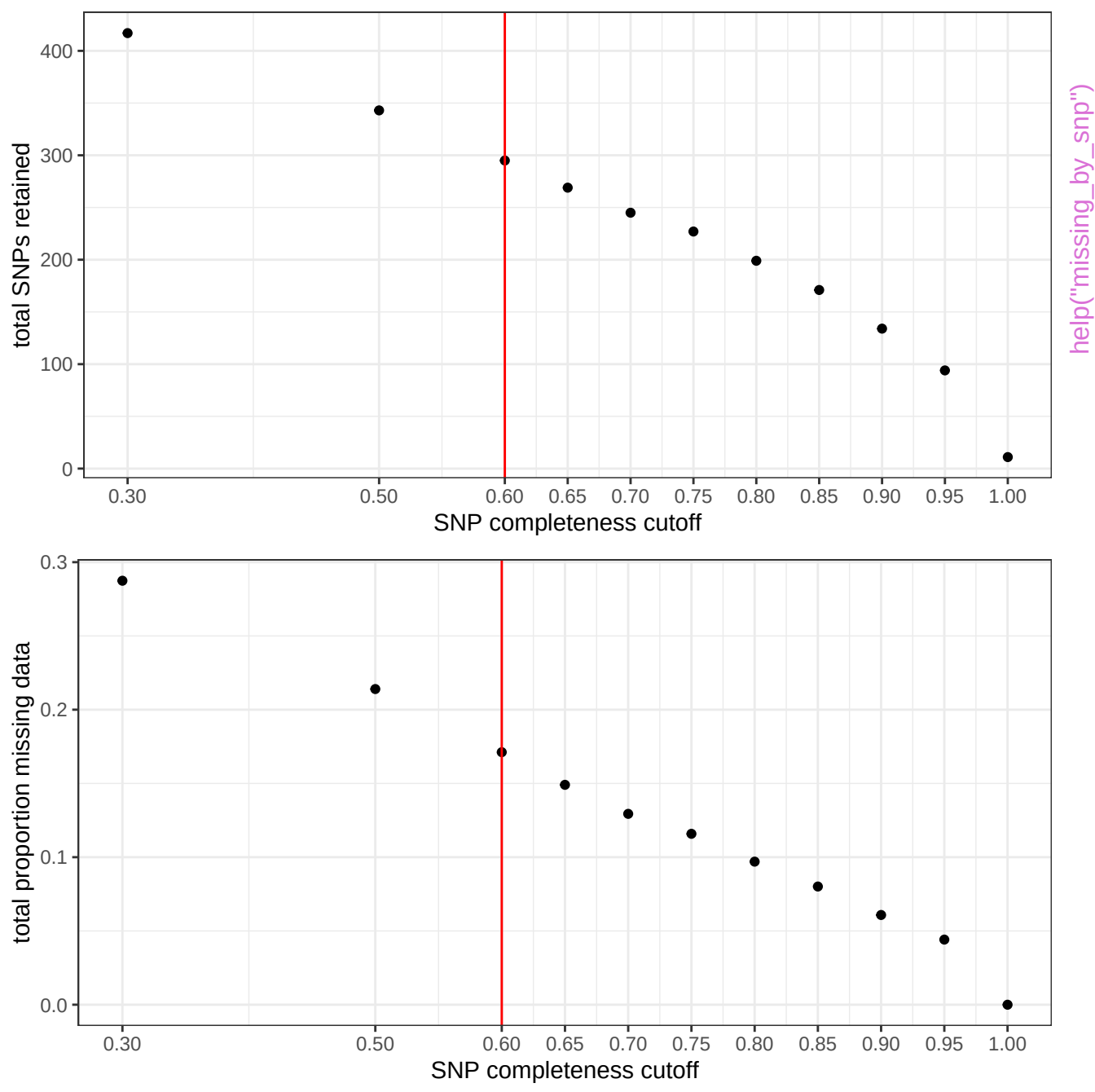
help("missing_by_sample")






SNP completeness cutoff
1
0.95
0.9
0.85
0.8
0.75
0.7
0.65
0.6
0.5
0.3
0.0
0.5
1.0
missing data proportion in each sample
help("missing_by_snp")


total SNPs retained
400
300
200
100
0
0.30
0.50
0.60
0.65
0.70
0.75
0.80
0.85
0.90
0.95
1.00
SNP completeness cutoff
help("missing_by_snp")
total proportion missing data
0.3
0.2
0.1
0.0
0.30
0.50
0.60
0.65
0.70
0.75
0.80
0.85
0.90
0.95
1.00
SNP completeness cutoff


total SNPs retained
400
300
200
100
0
0.30
0.50
0.60
0.65
0.70
0.75
0.80
0.85
0.90
0.95
1.00
SNP completeness cutoff
help("missing_by_snp")
total proportion missing data
0.3
0.2
0.1
0.0
0.30
0.50
0.60
0.65
0.70
0.75
0.80
0.85
0.90
0.95
1.00
SNP completeness cutoff