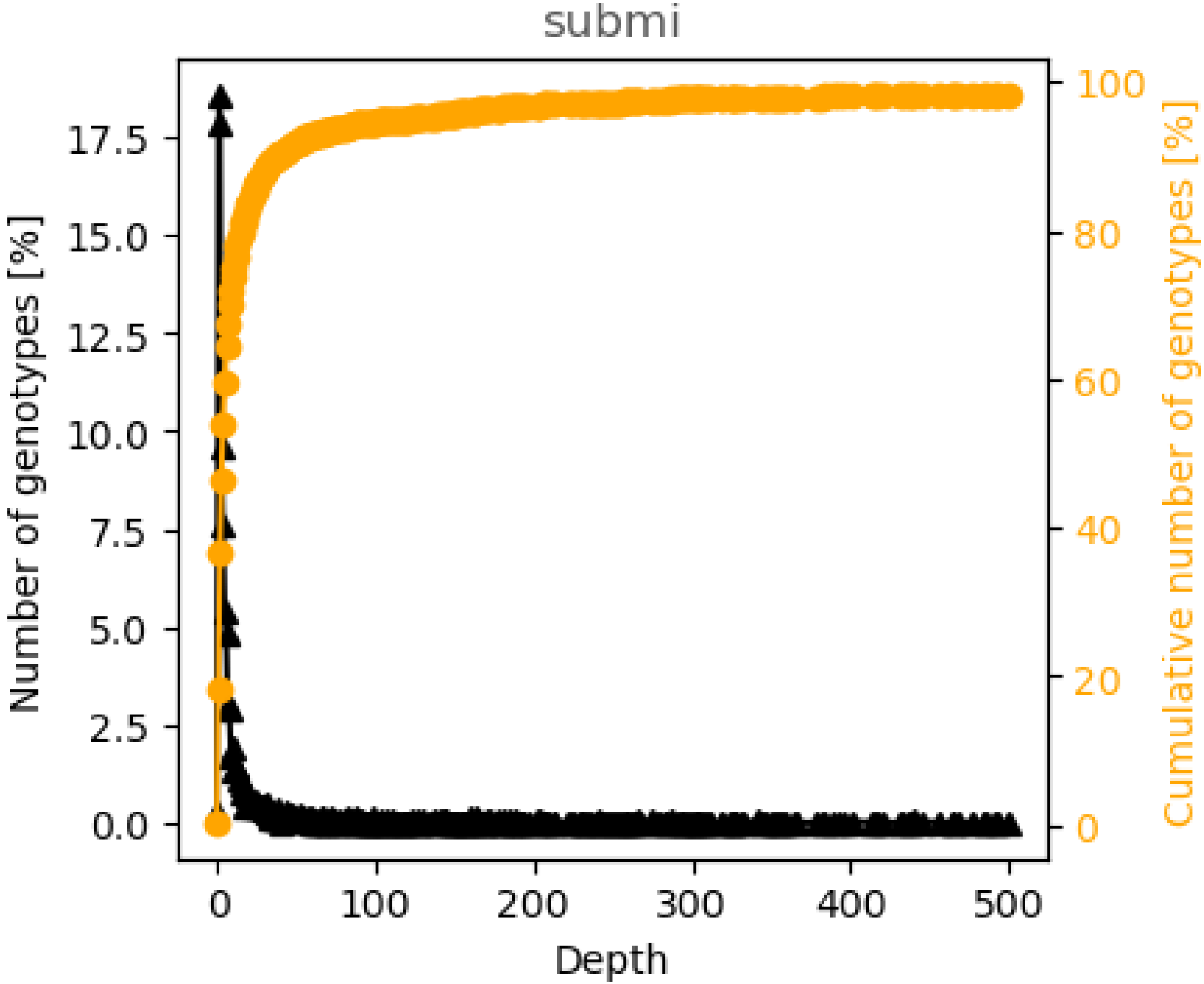
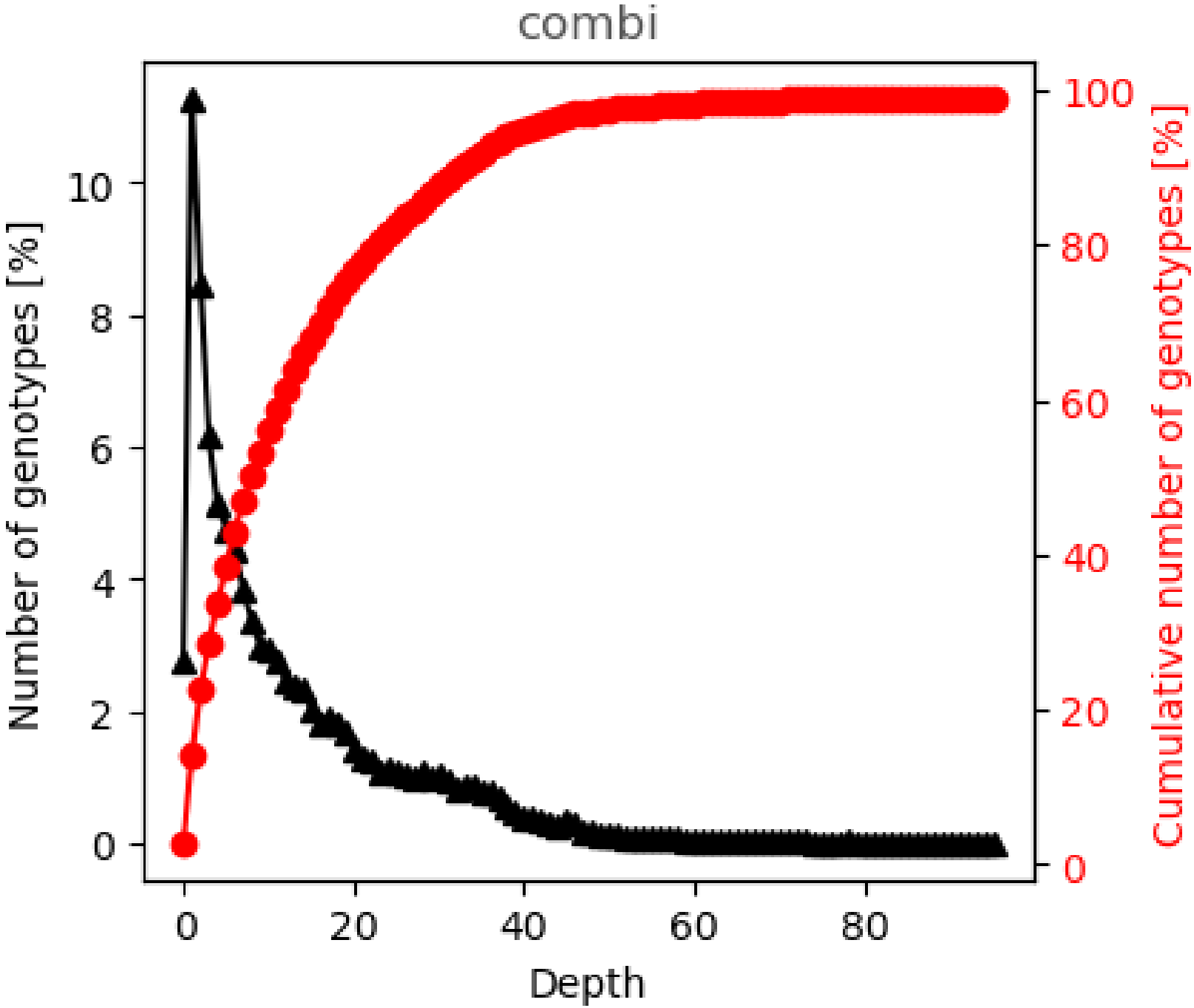
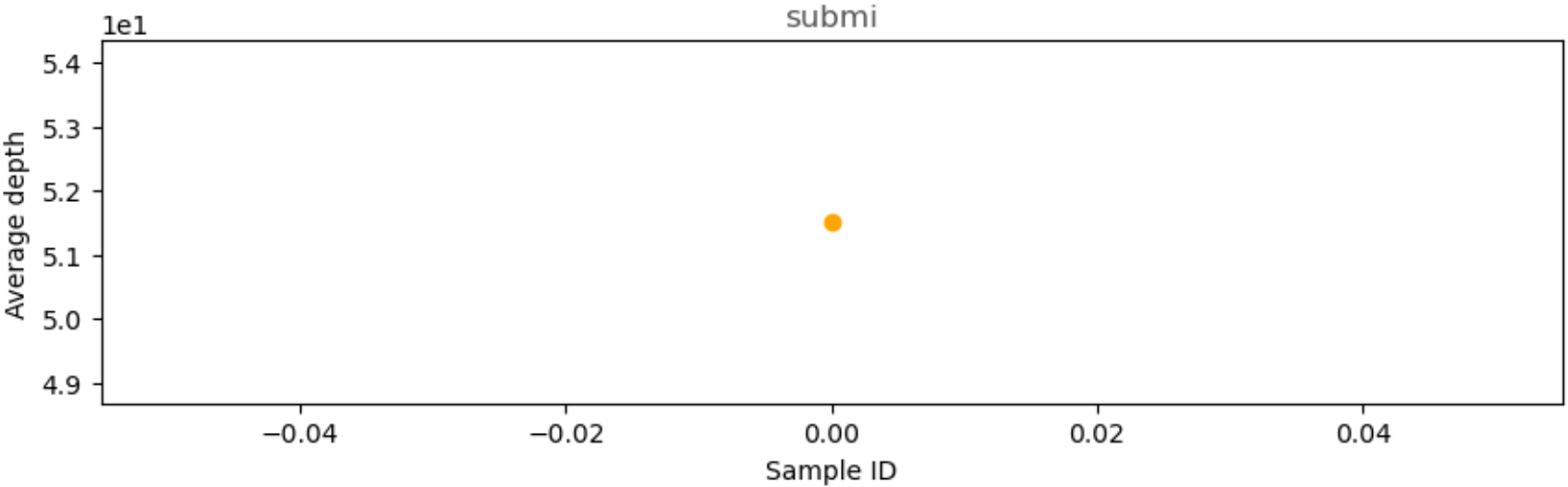
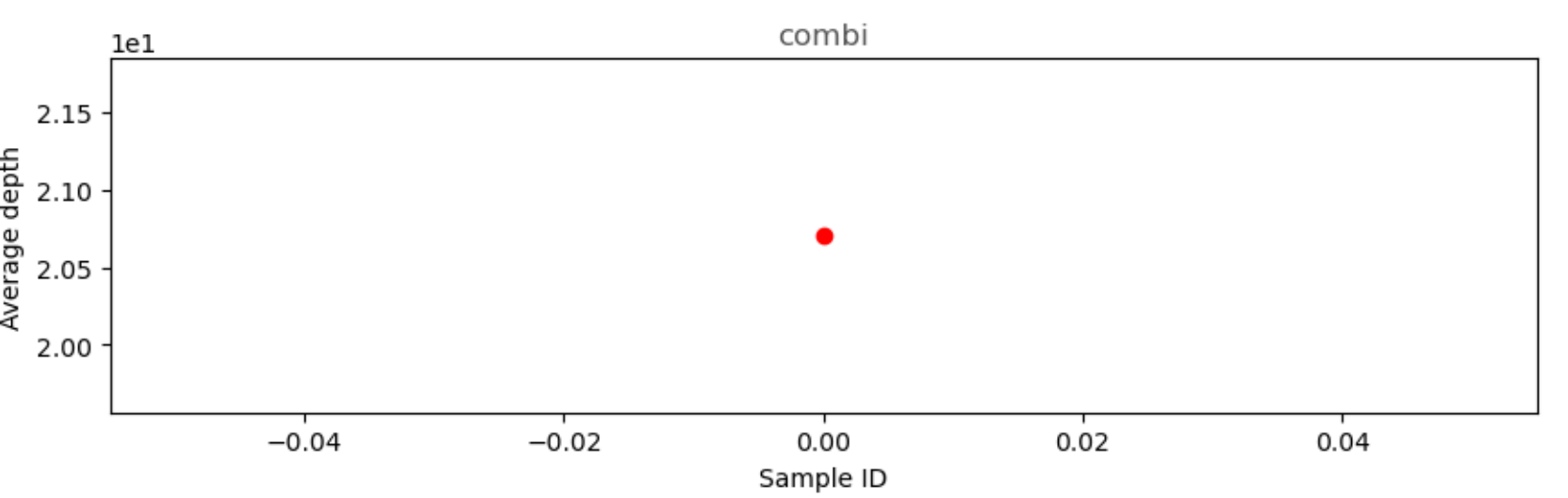
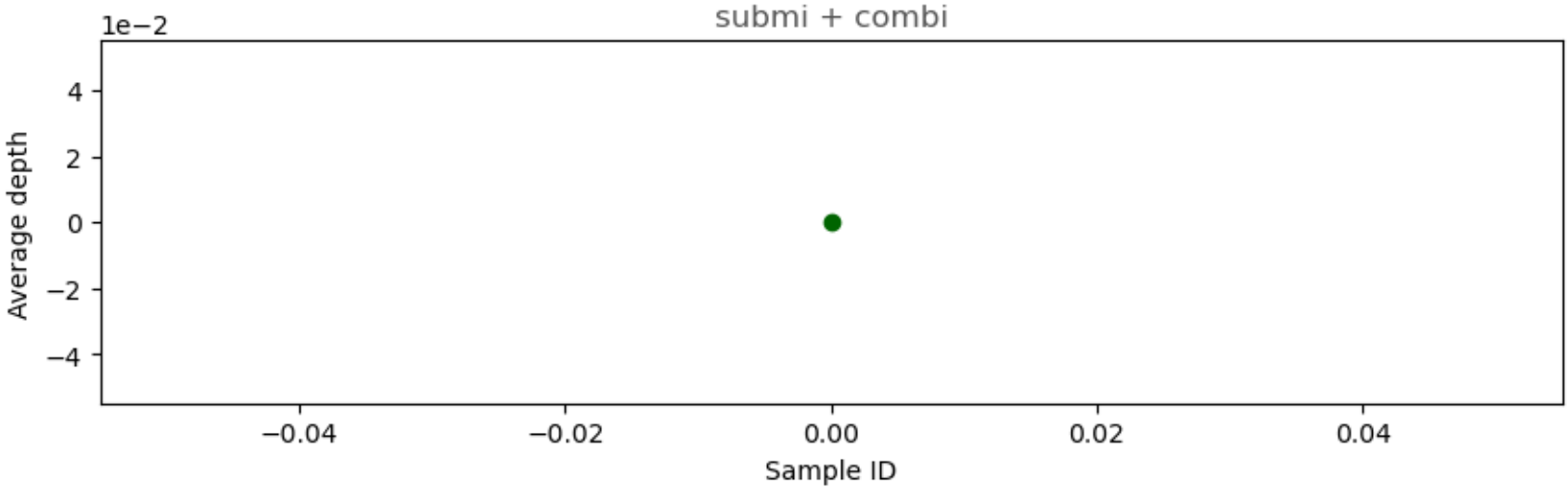
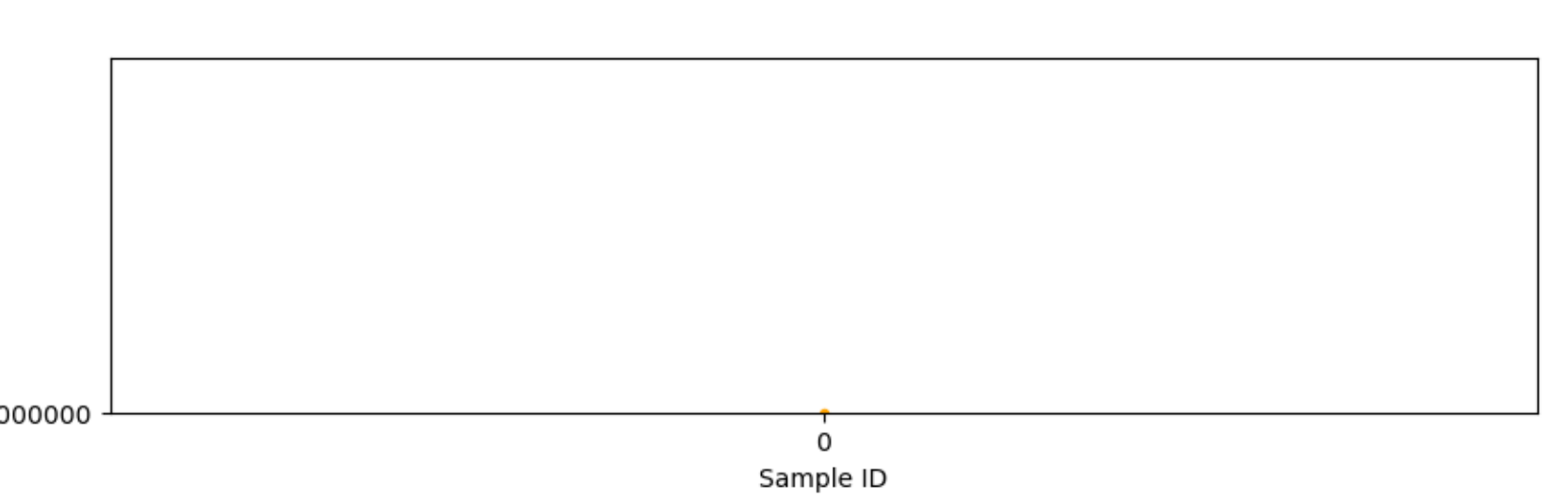

submi
Number of genotypes [%]
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
Cumulative number of genotypes [%]
100
80
60
40
20
0
0
100
200
300
400
500
Depth

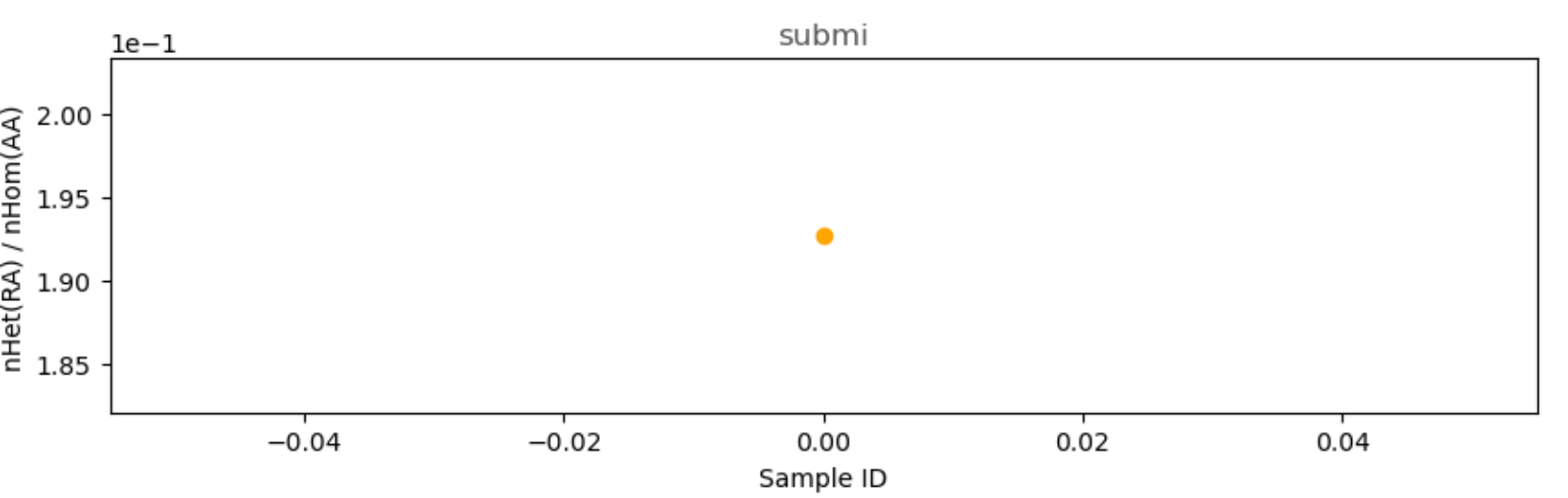

combi
Number of genotypes [%]
Cumulative number of genotypes [%]
Depth
0
2
4
6
8
10
0
20
40
60
80
100
0
20
40
60
80

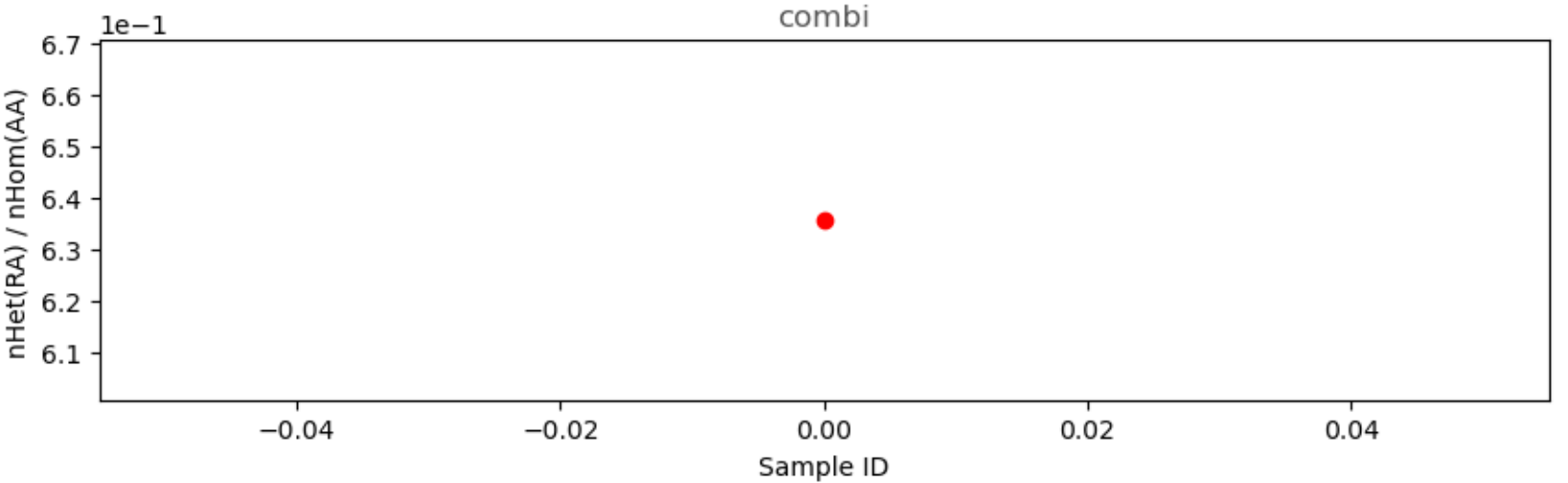

submi
1e1
5.4
5.3
5.2
5.1
5.0
4.9
Average depth
−0.04
−0.02
0.00
0.02
0.04
Sample ID

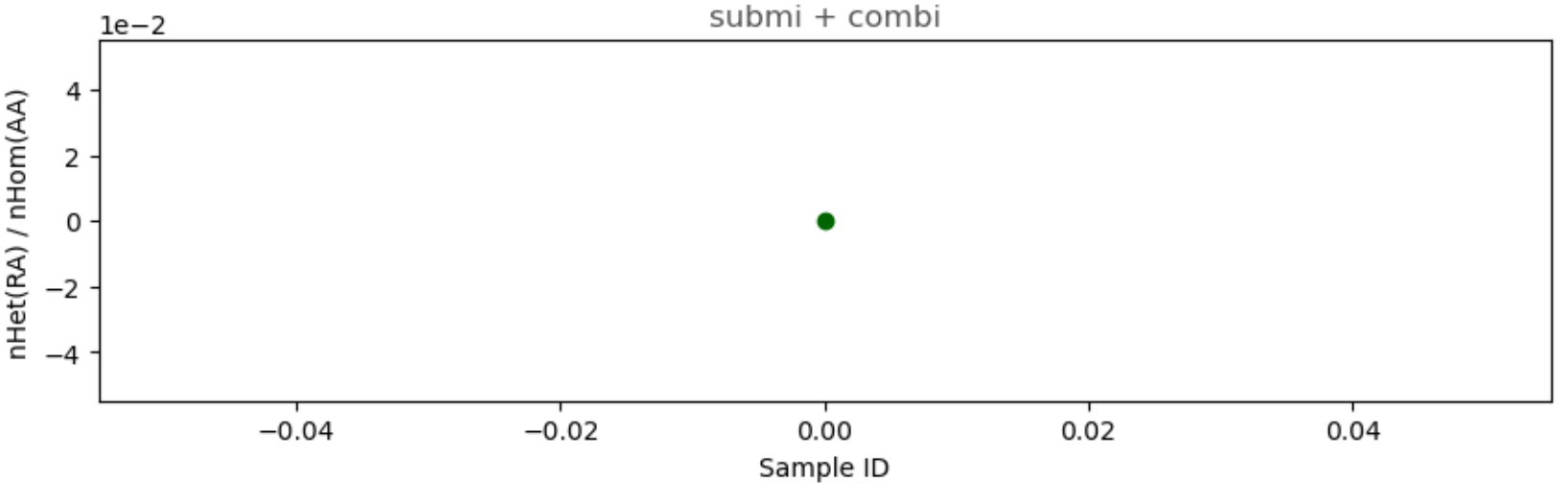

combi
1e1
2.15
2.10
2.05
2.00
Average depth
−0.04
−0.02
0.00
0.02
0.04
Sample ID

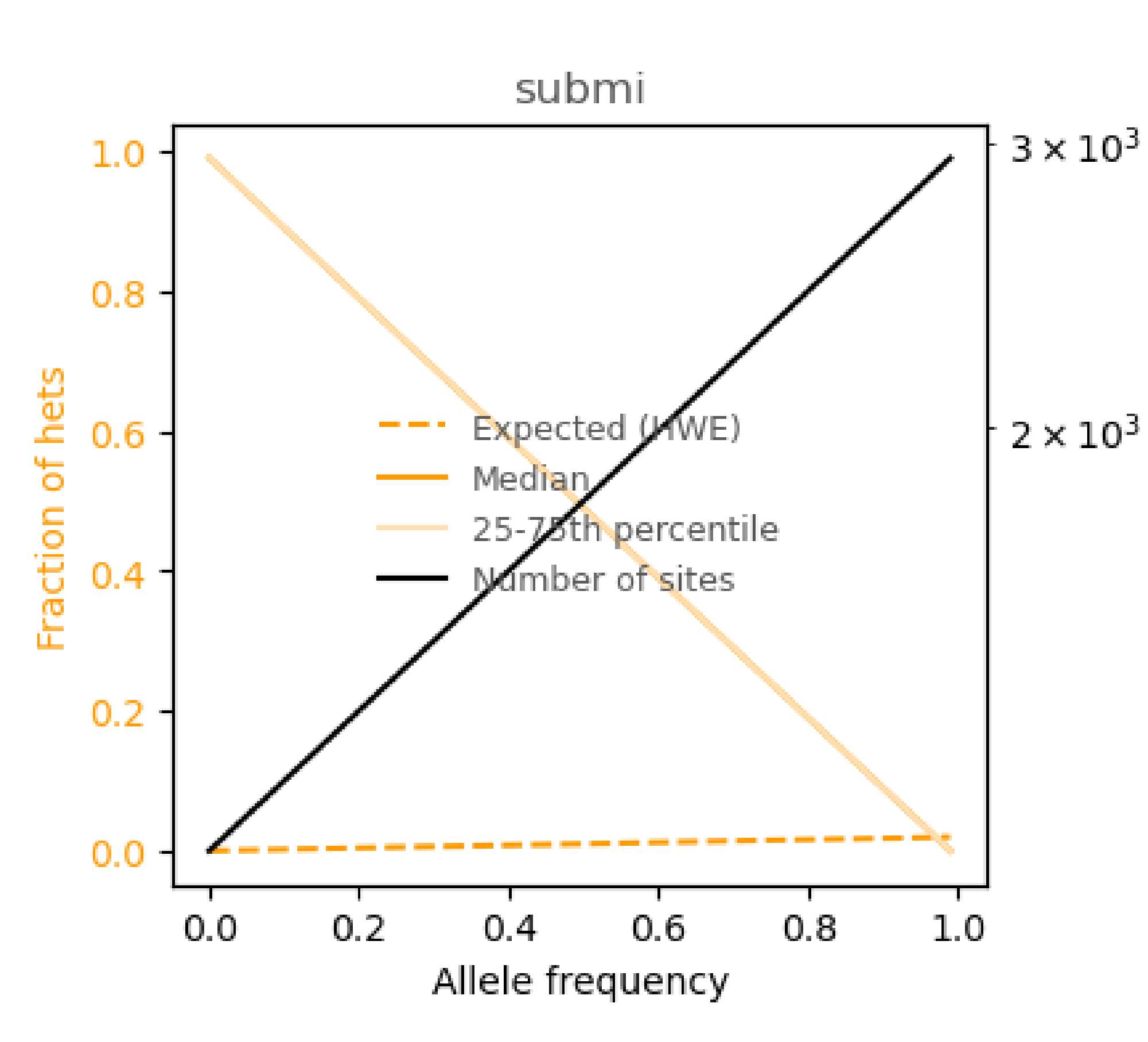

submi + combi
1e−2
4
2
0
−2
−4
Average depth
−0.04
−0.02
0.00
0.02
0.04
Sample ID

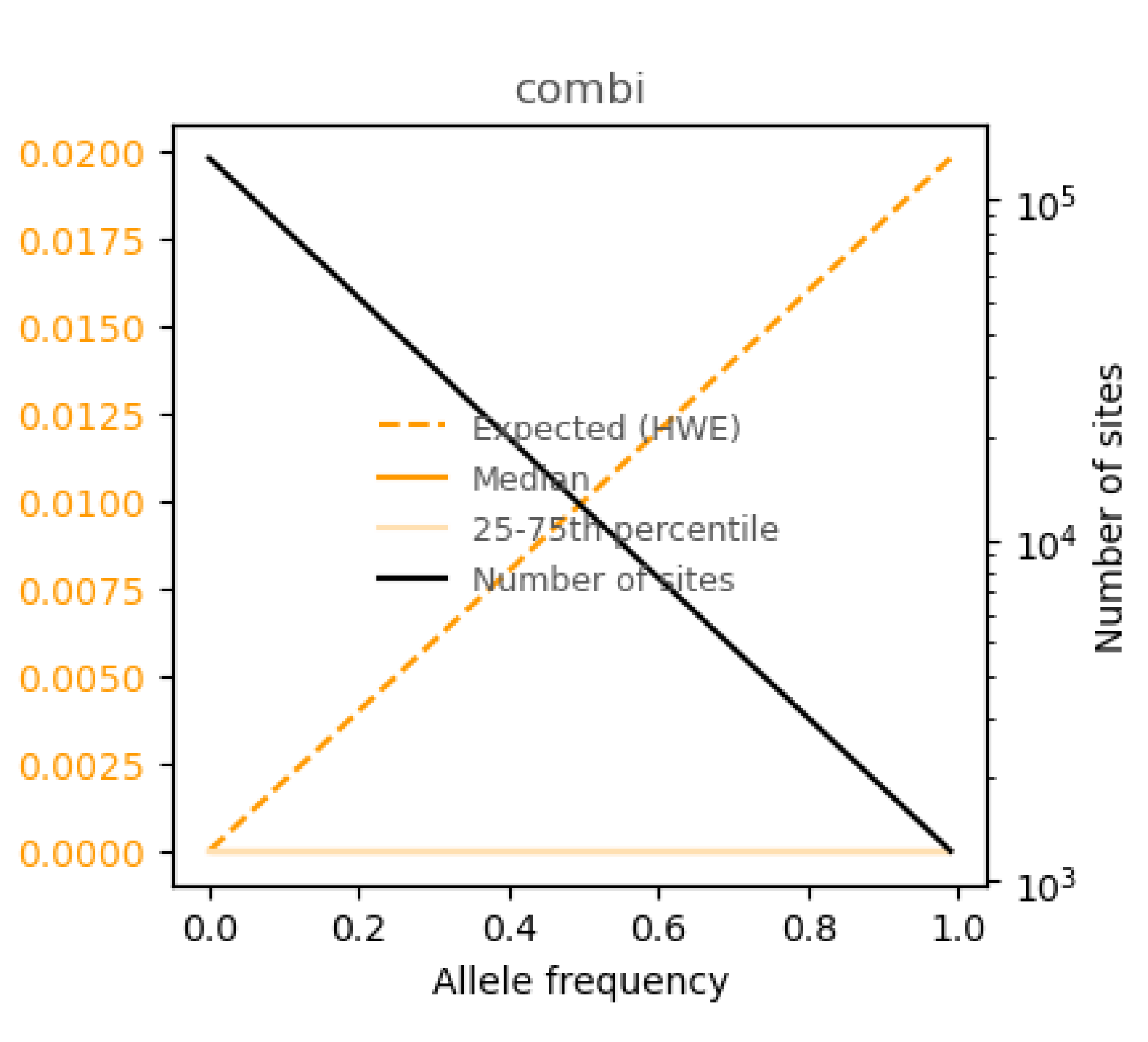

000000
0
Sample ID

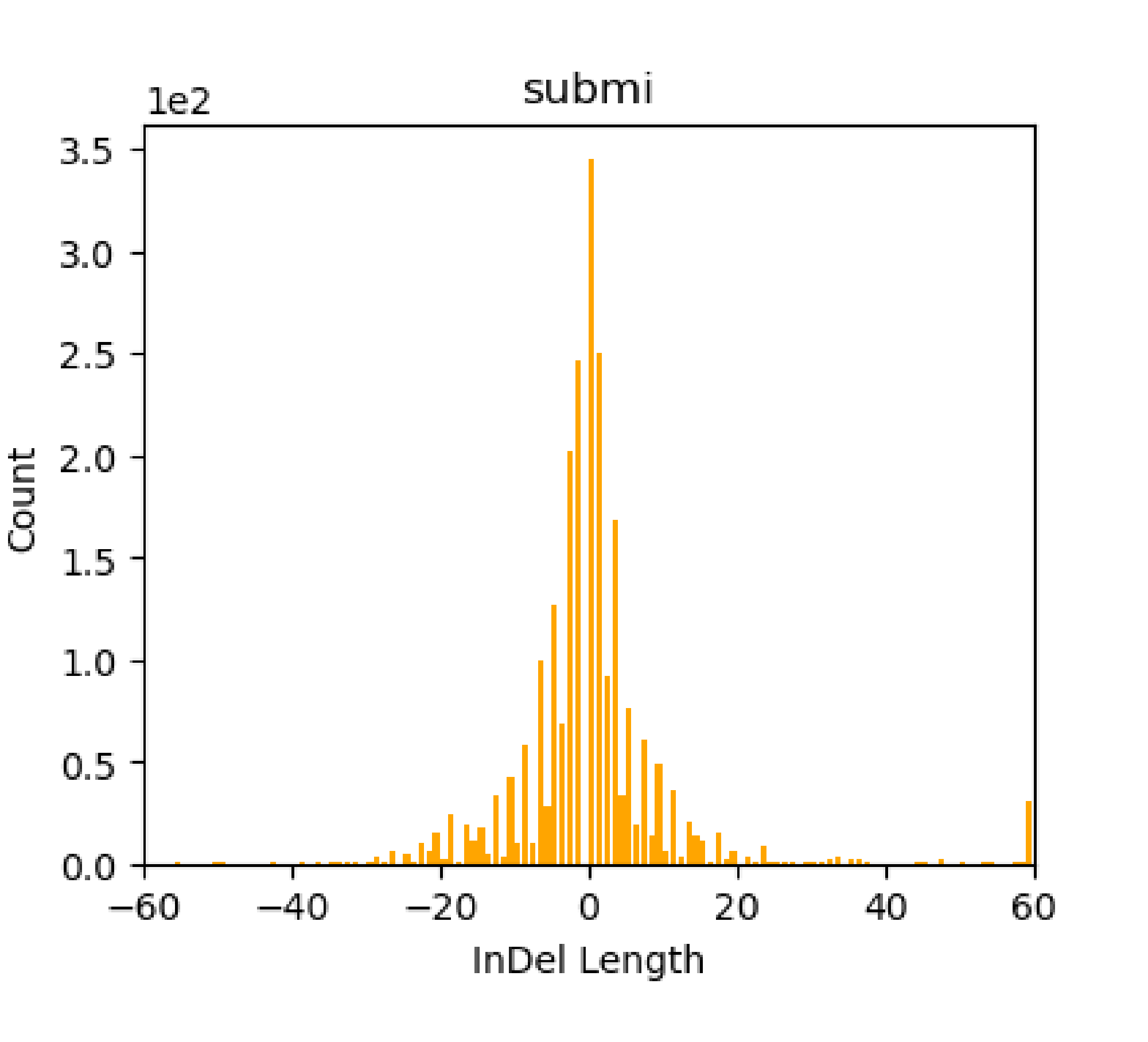

submi
1e−1
2.00
1.95
1.90
1.85
nHet(RA) / nHom(AA)
−0.04
−0.02
0.00
0.02
0.04
Sample ID

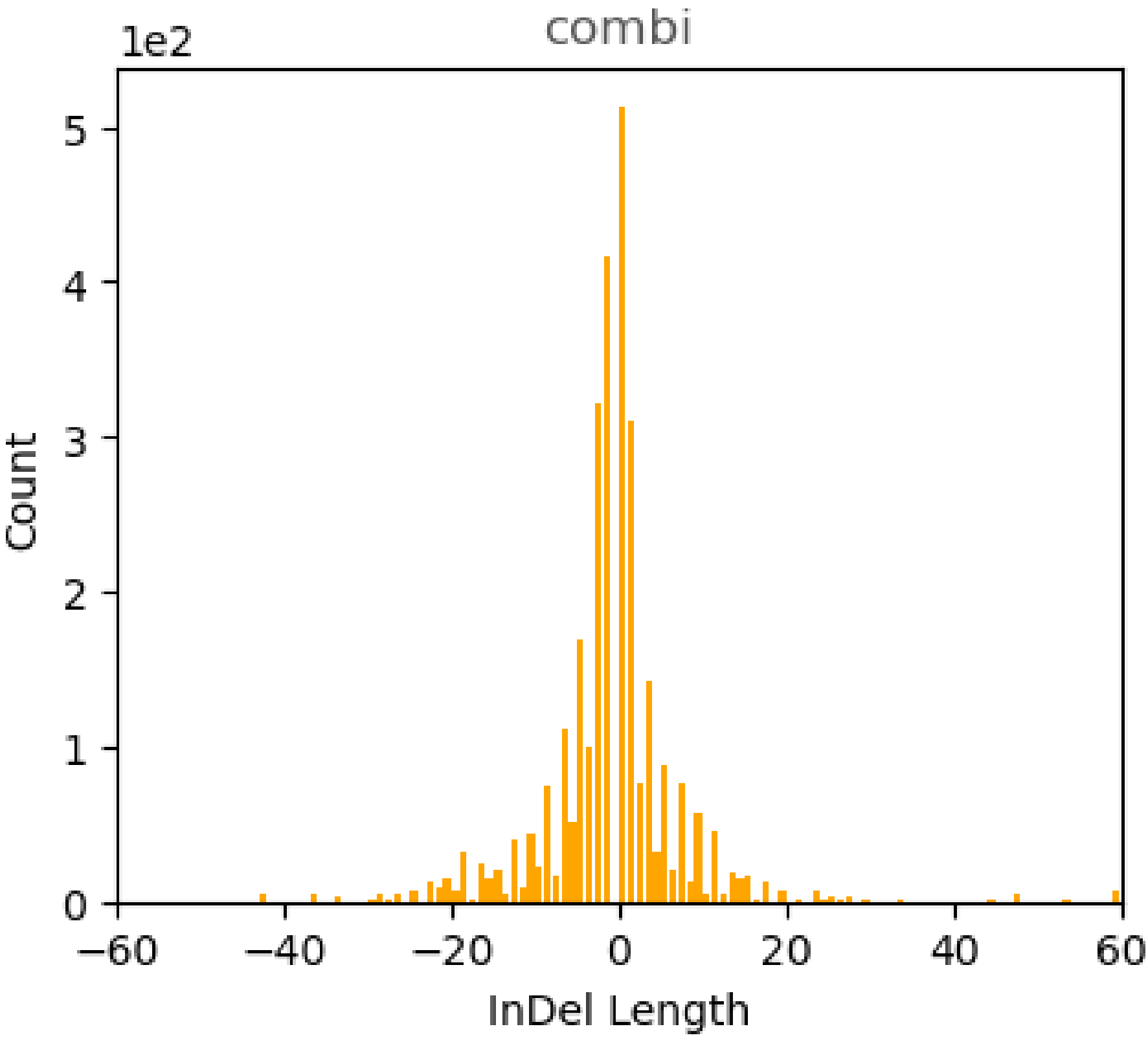

combi
1e−1
6.7
6.6
6.5
6.4
6.3
6.2
6.1
nHet(RA) / nHom(AA)
−0.04
−0.02
0.00
0.02
0.04
Sample ID

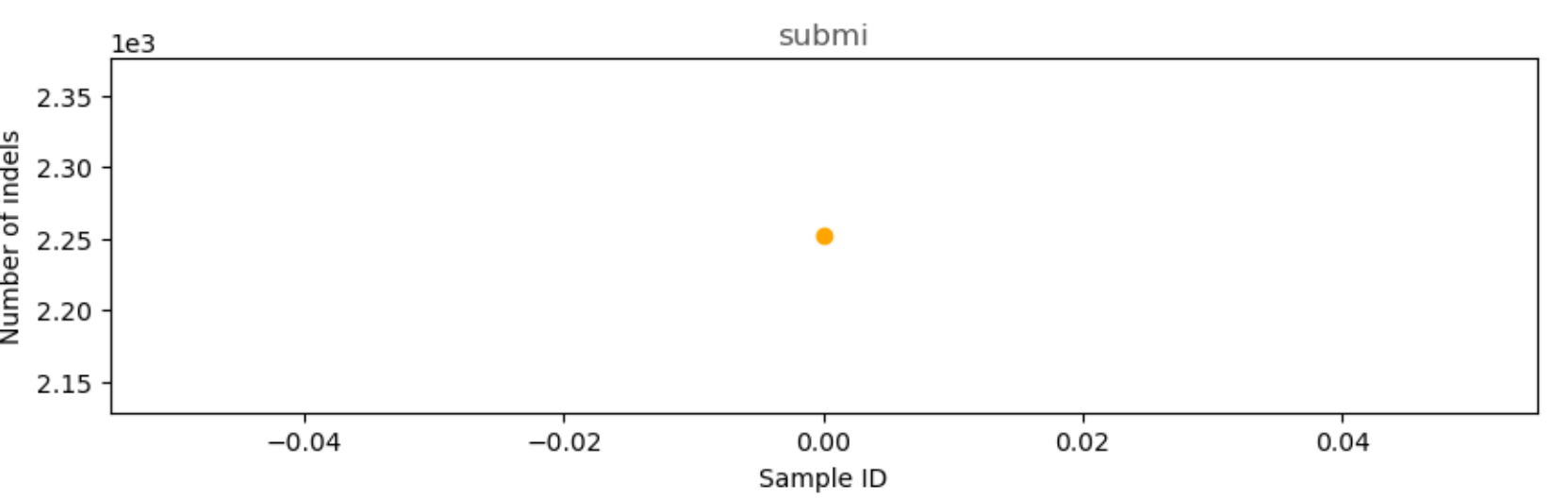

submi + combi
1e−2
4
2
0
−2
−4
nHet(RA) / nHom(AA)
−0.04
−0.02
0.00
0.02
0.04
Sample ID

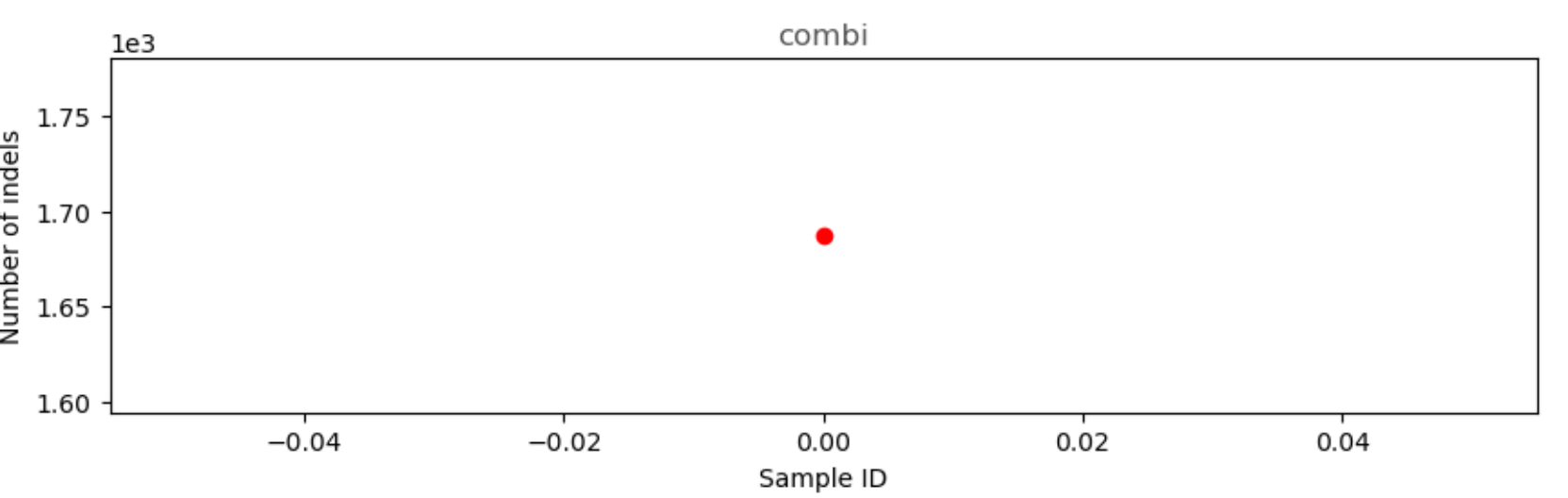

submi
Fraction of hets
1.0
0.8
0.6
0.4
0.2
0.0
3 x 10^3
2 x 10^3
Expected (HWE)
Median
25-75th percentile
Number of sites
0.0
0.2
0.4
0.6
0.8
1.0
Allele frequency

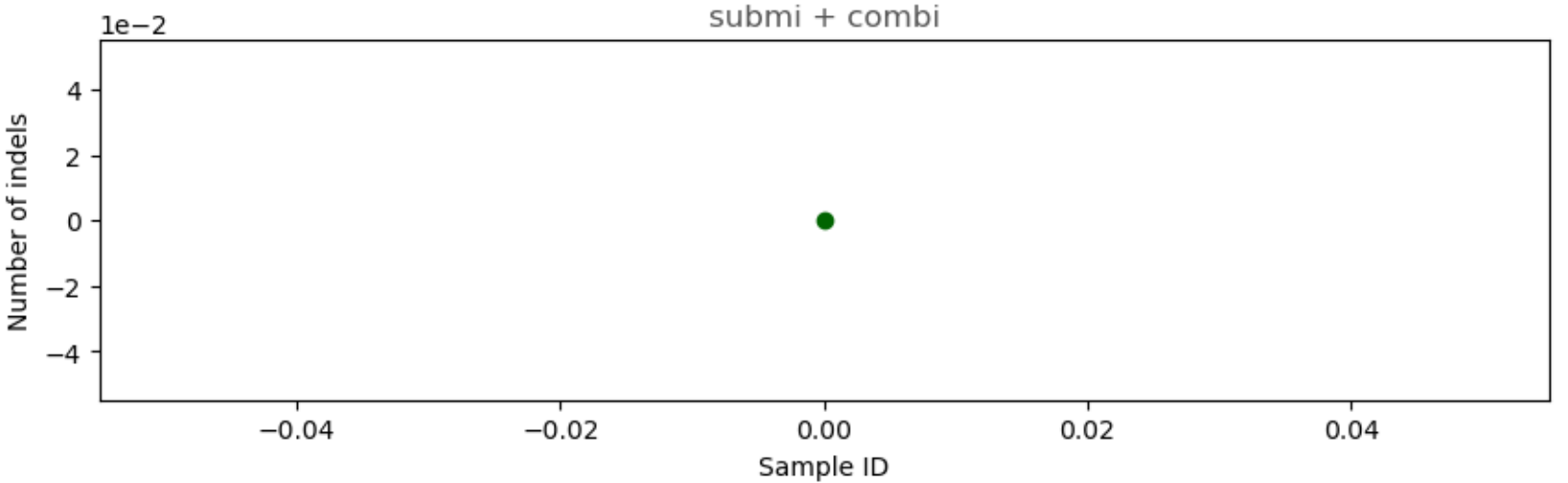

combi
0.0200
0.0175
0.0150
0.0125
0.0100
0.0075
0.0050
0.0025
0.0000
Expected (HWE)
Median
25-75th percentile
Number of sites
10^5
10^4
10^3
Number of sites
0.0
0.2
0.4
0.6
0.8
1.0
Allele frequency

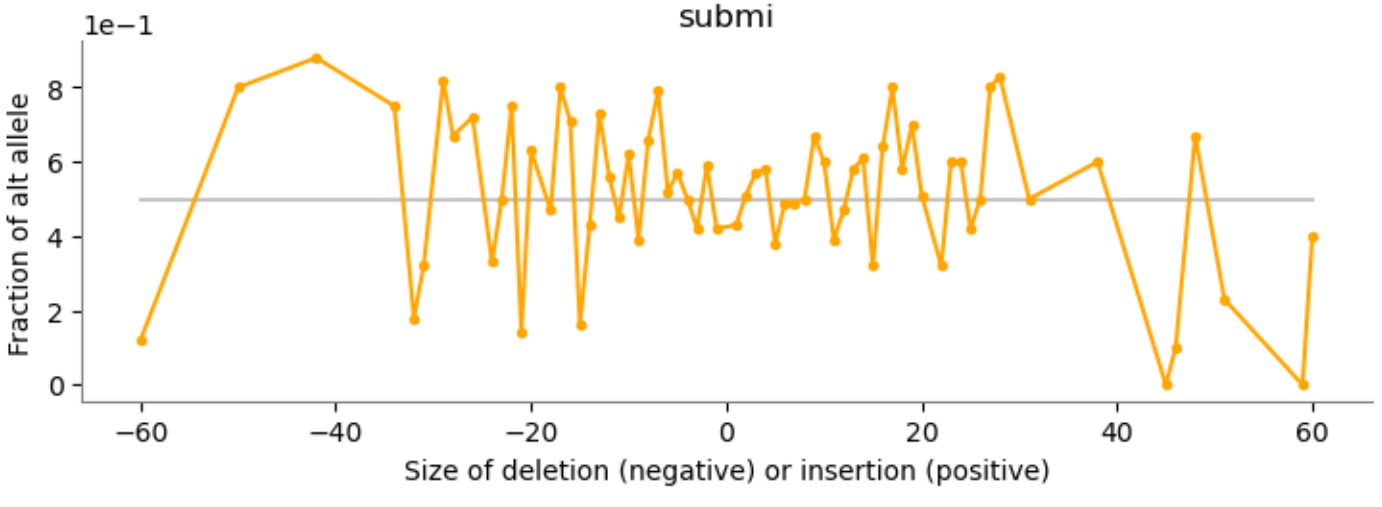

submi
1e2
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Count
−60
−40
−20
0
20
40
60
InDel Length

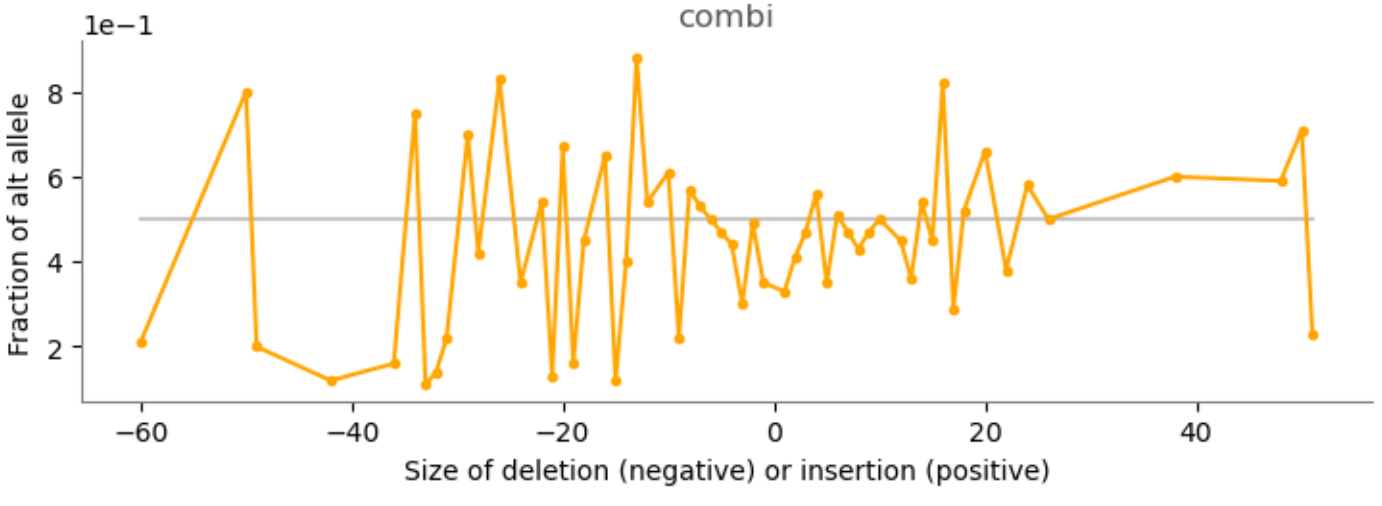

combi
1e2
5
4
3
2
1
0
Count
−60
−40
−20
0
20
40
60
InDel Length

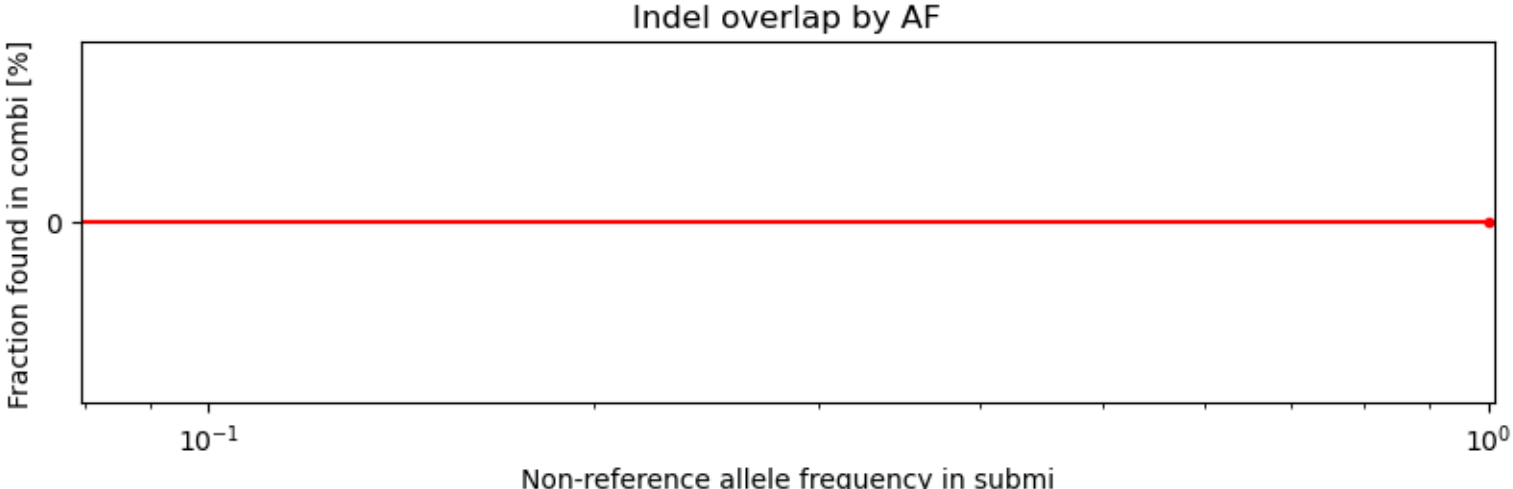

submi
1e3
2.35
2.30
2.25
2.20
2.15
Number of indels
−0.04
−0.02
0.00
0.02
0.04
Sample ID

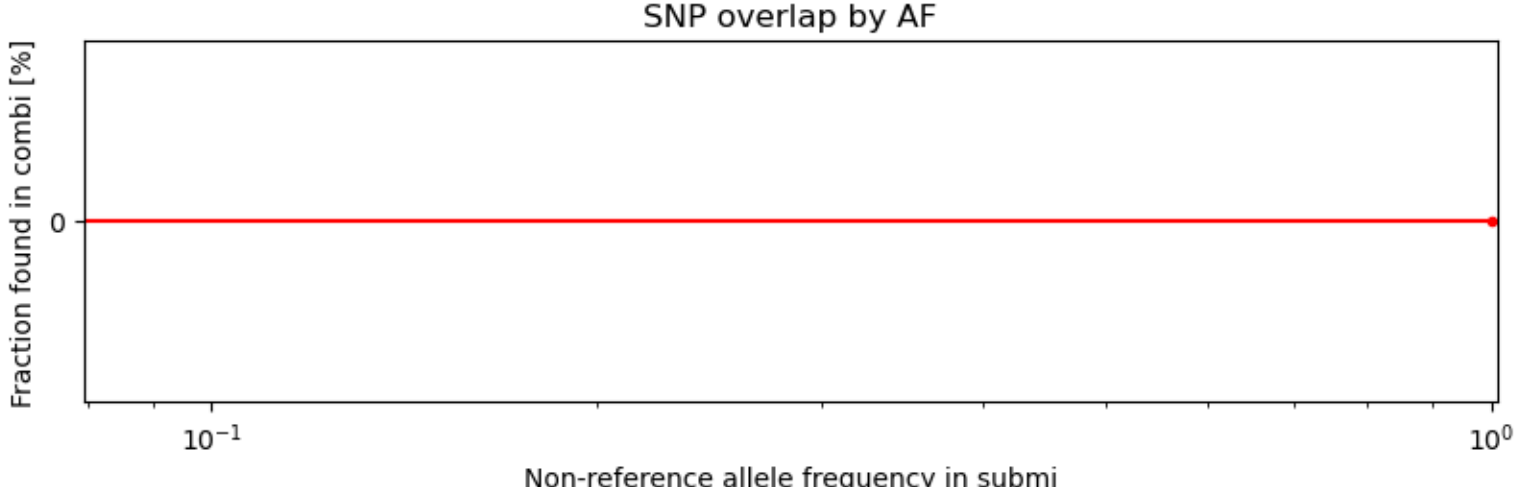

combi
1e3
1.75
1.70
1.65
1.60
Number of indels
−0.04
−0.02
0.00
0.02
0.04
Sample ID

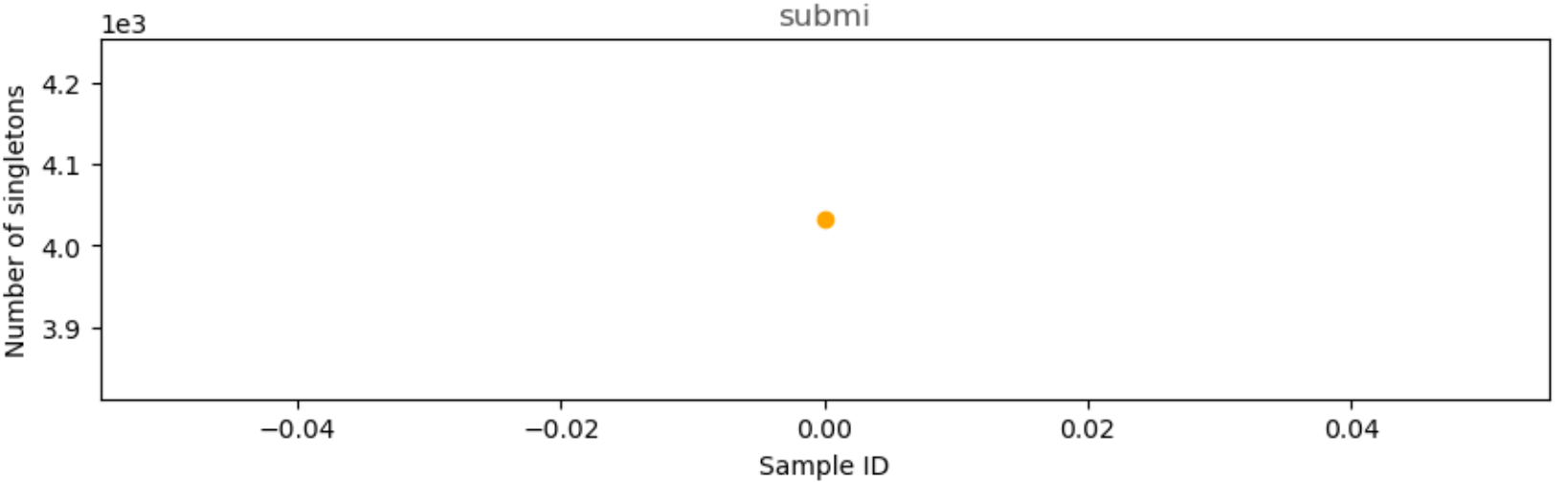

submi + combi
1e−2
4
2
0
−2
−4
Number of indels
−0.04
−0.02
0.00
0.02
0.04
Sample ID

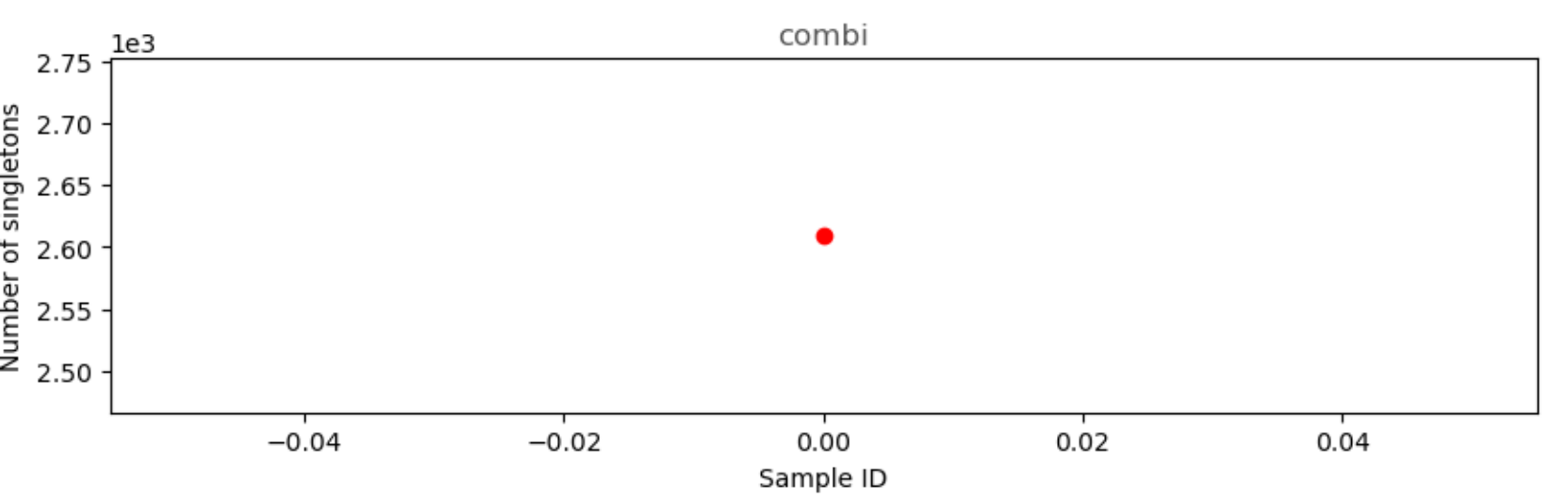

submi
1e−1
Fraction of alt allele
0
2
4
6
8
−60
−40
−20
0
20
40
60
Size of deletion (negative) or insertion (positive)

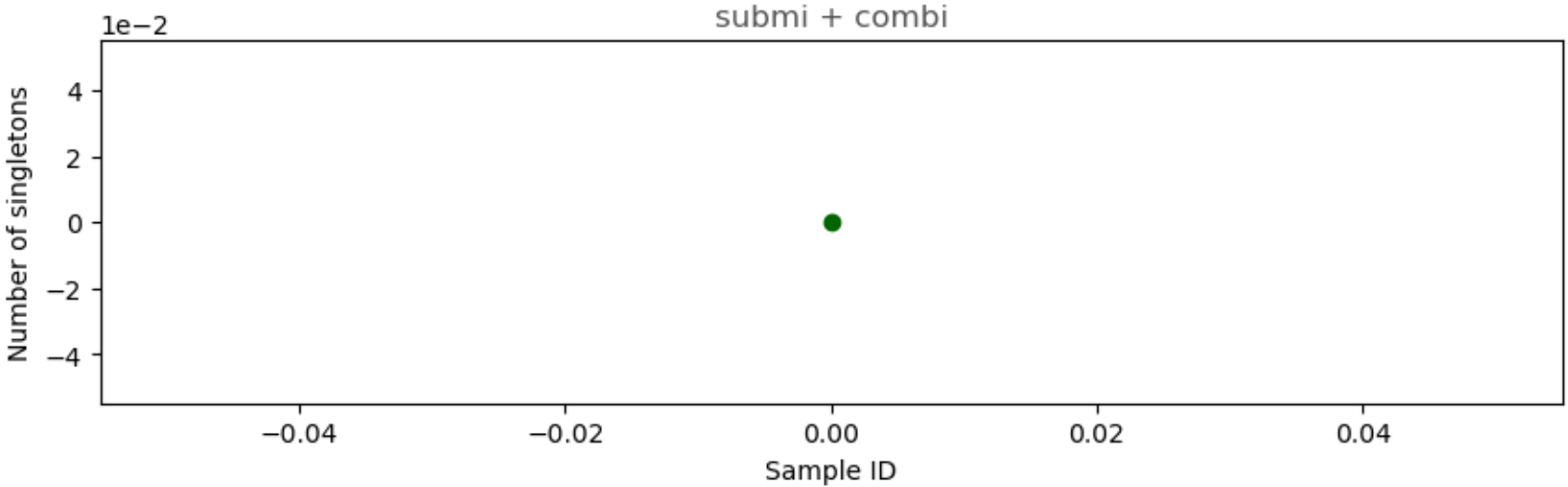

combi
1e−1
8
6
4
2
Fraction of alt allele
−60
−40
−20
0
20
40
Size of deletion (negative) or insertion (positive)

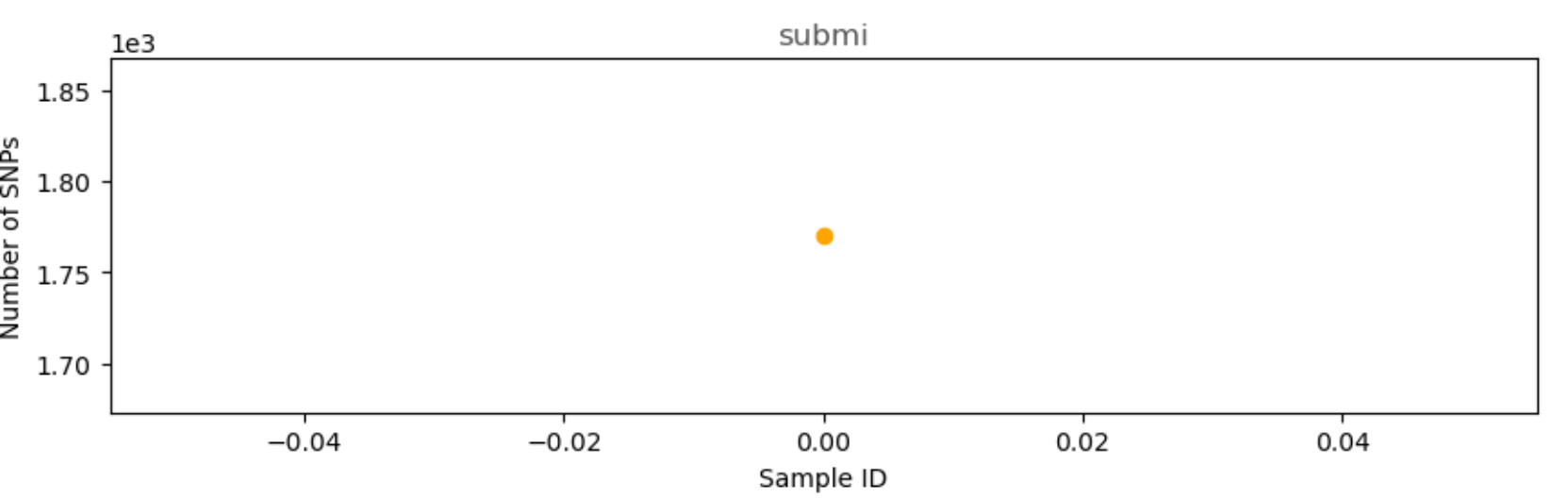

Indel overlap by AF
Fraction found in combi [%]
0
10^{-1}
10^{0}
Non-reference allele frequency in submi

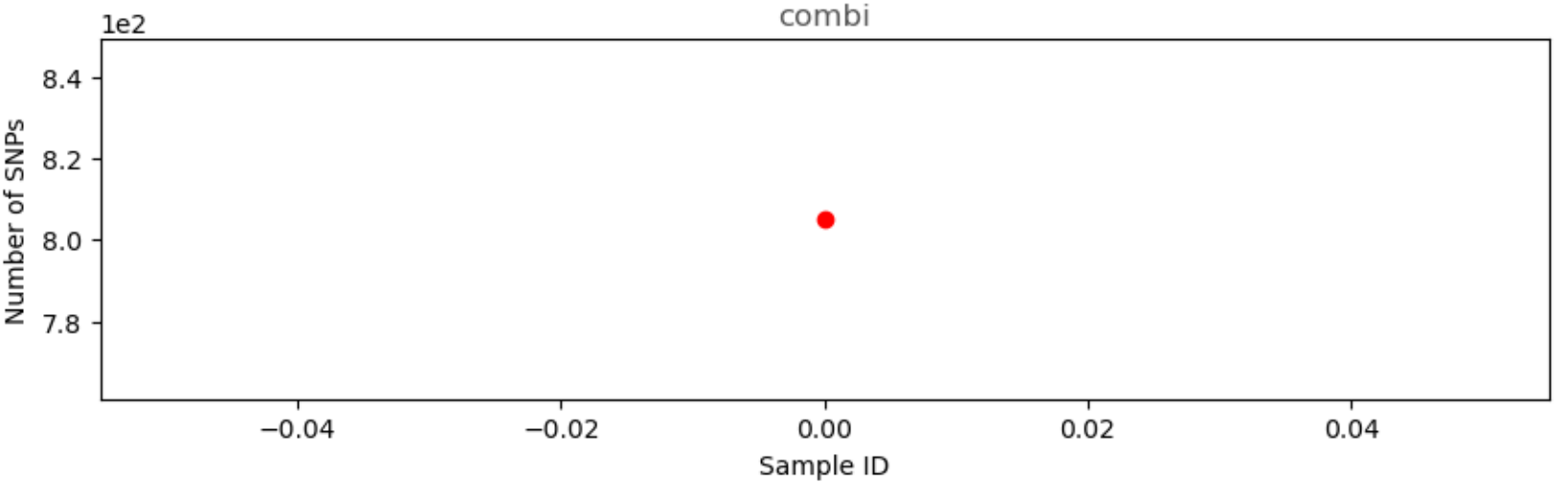

SNP overlap by AF
Fraction found in combi [%]
0
10^{-1}
10^{0}
Non-reference allele frequency in submi

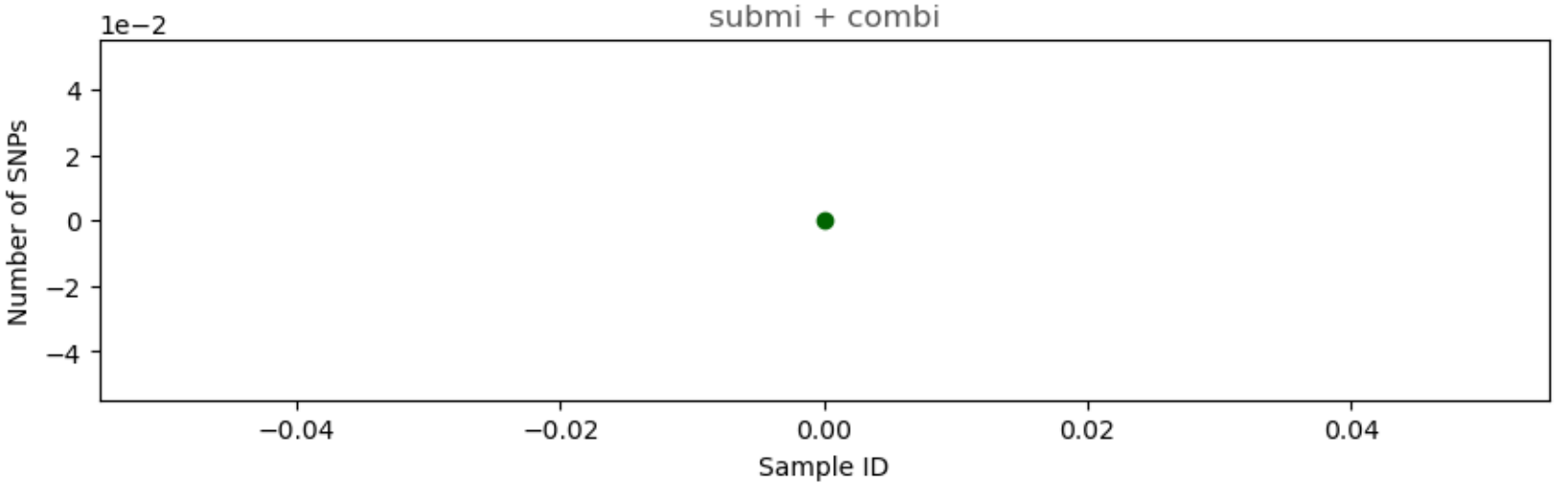

submi
1e3
4.2
4.1
4.0
3.9
Number of singletons
−0.04
−0.02
0.00
0.02
0.04
Sample ID

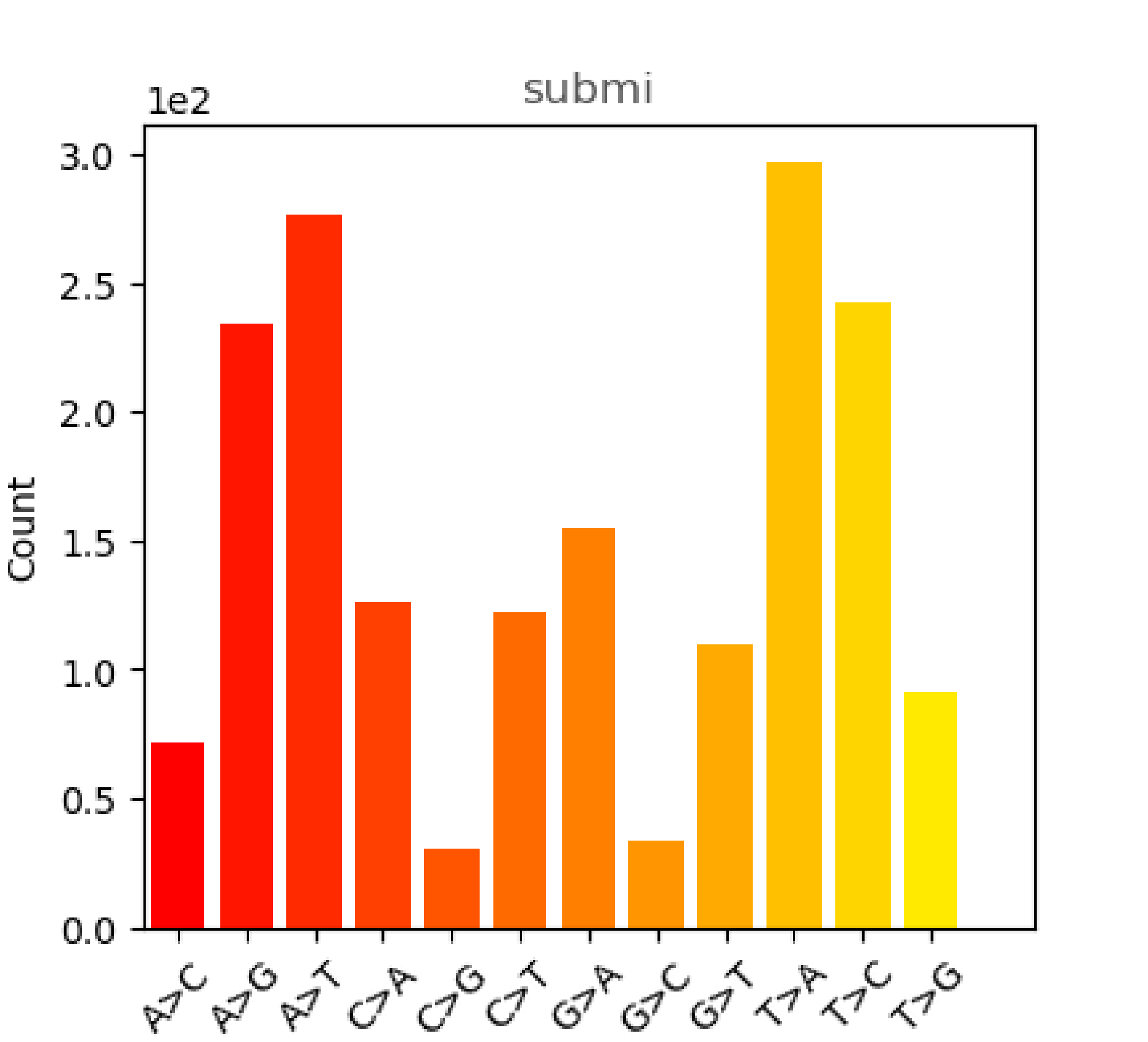

combi
1e3
2.75
2.70
2.65
2.60
2.55
2.50
Number of singletons
−0.04
−0.02
0.00
0.02
0.04
Sample ID

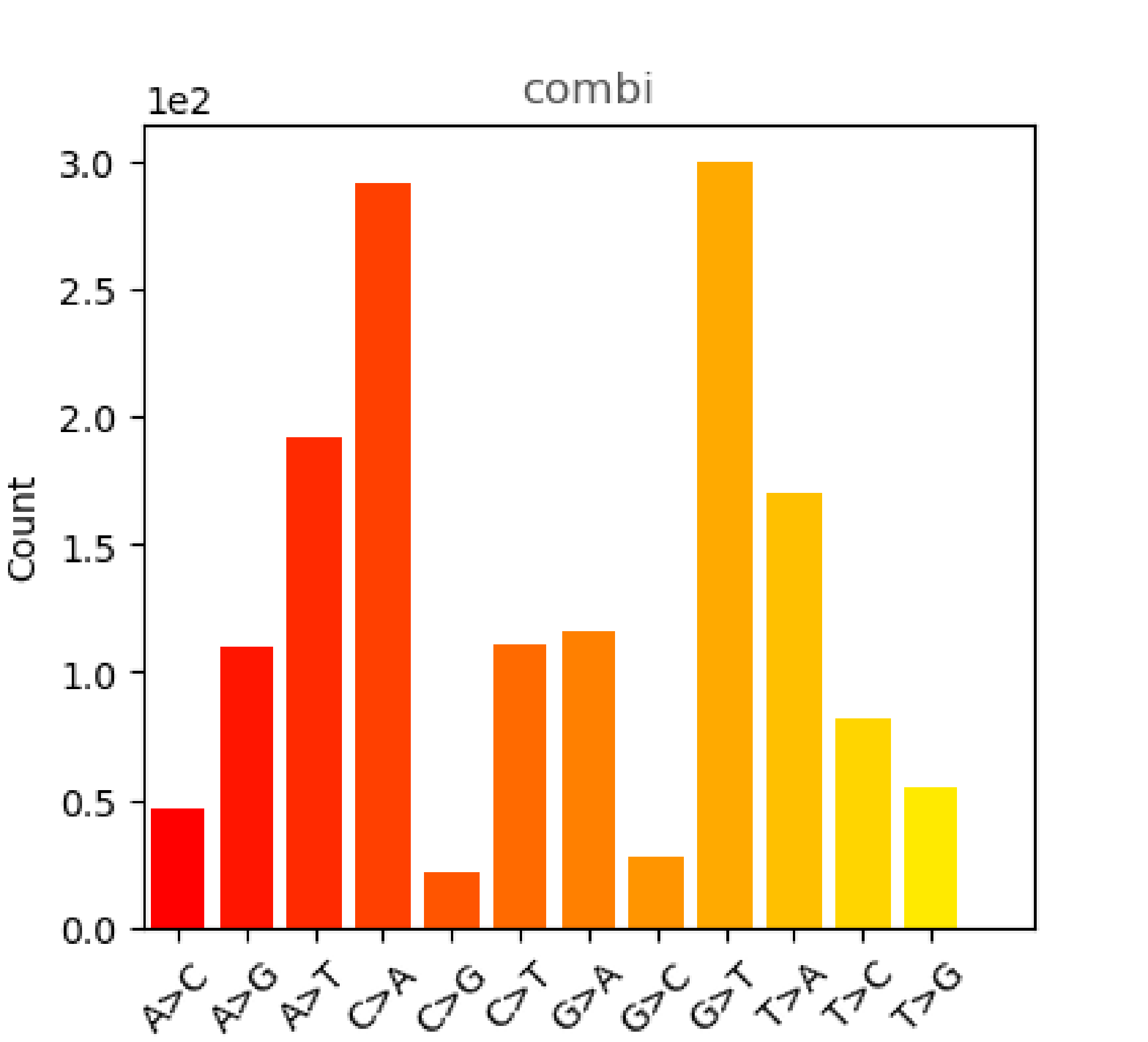

submi + combi
1e−2
4
2
0
−2
−4
Number of singletons
−0.04
−0.02
0.00
0.02
0.04
Sample ID

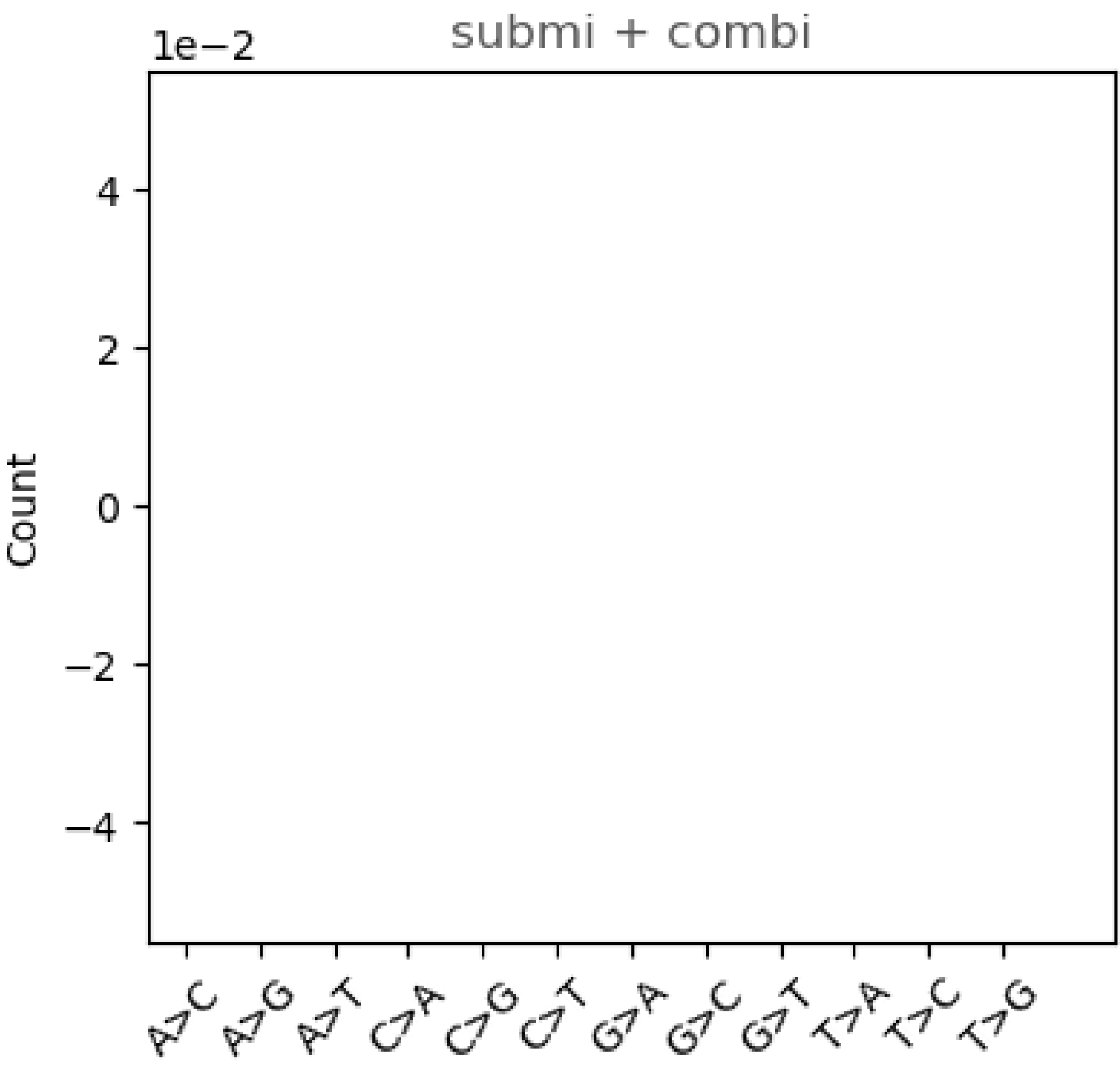

submi
1e3
1.85
1.80
1.75
1.70
Number of SNPs
−0.04
−0.02
0.00
0.02
0.04
Sample ID

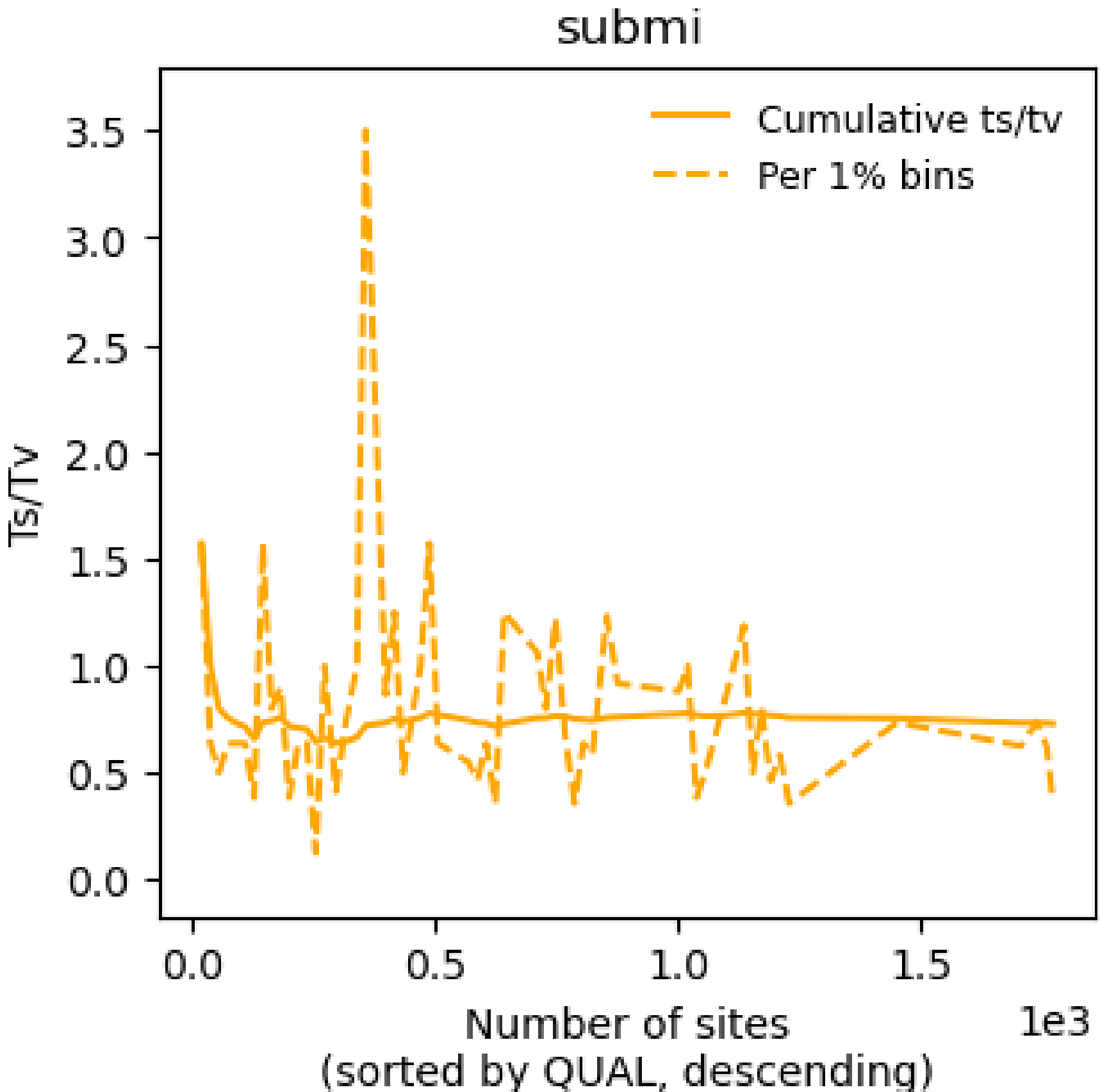

combi
1e2
8.4
8.2
8.0
7.8
Number of SNPs
−0.04
−0.02
0.00
0.02
0.04
Sample ID

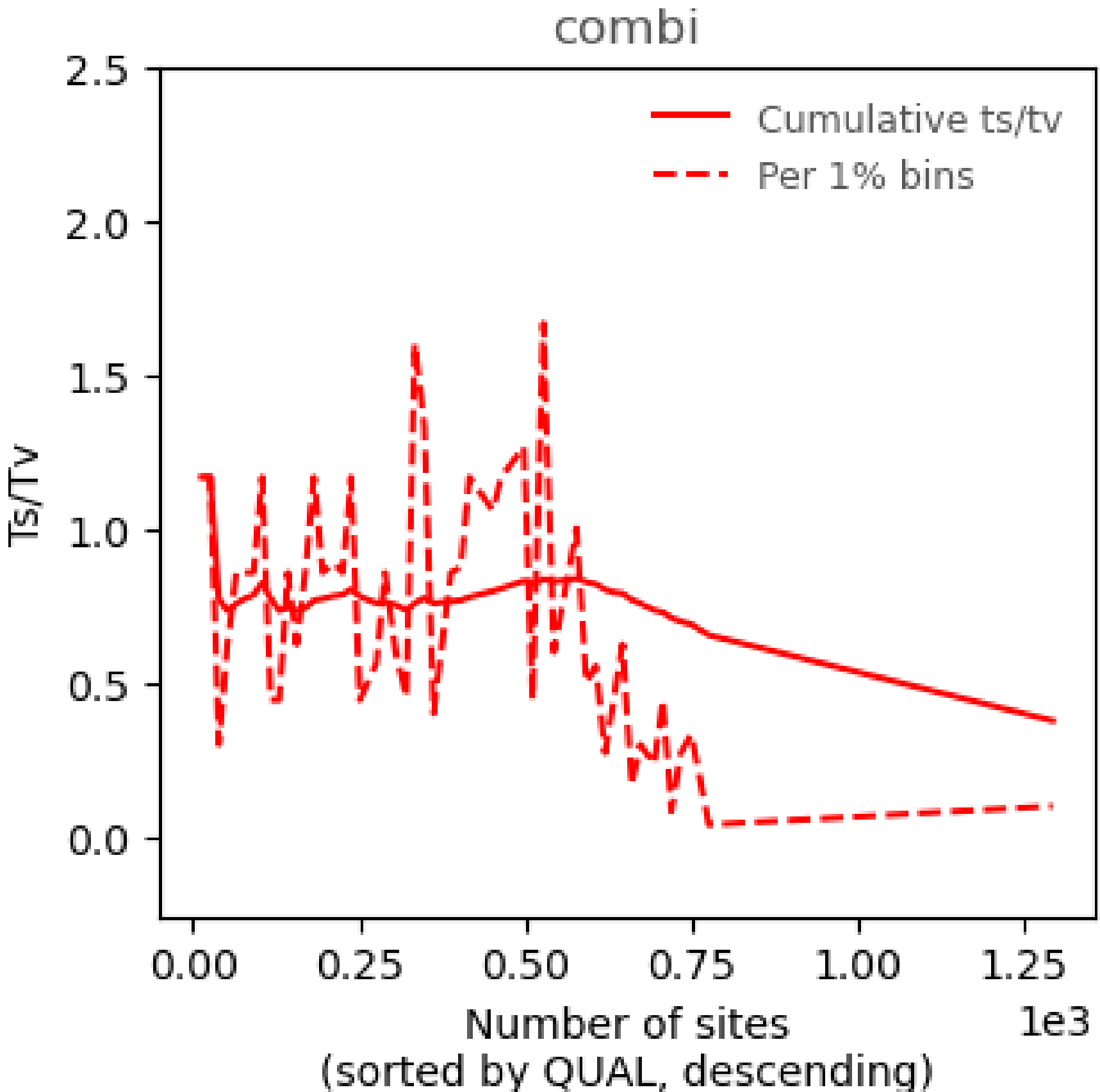

submi + combi
1e−2
4
2
0
−2
−4
Number of SNPs
−0.04
−0.02
0.00
0.02
0.04
Sample ID

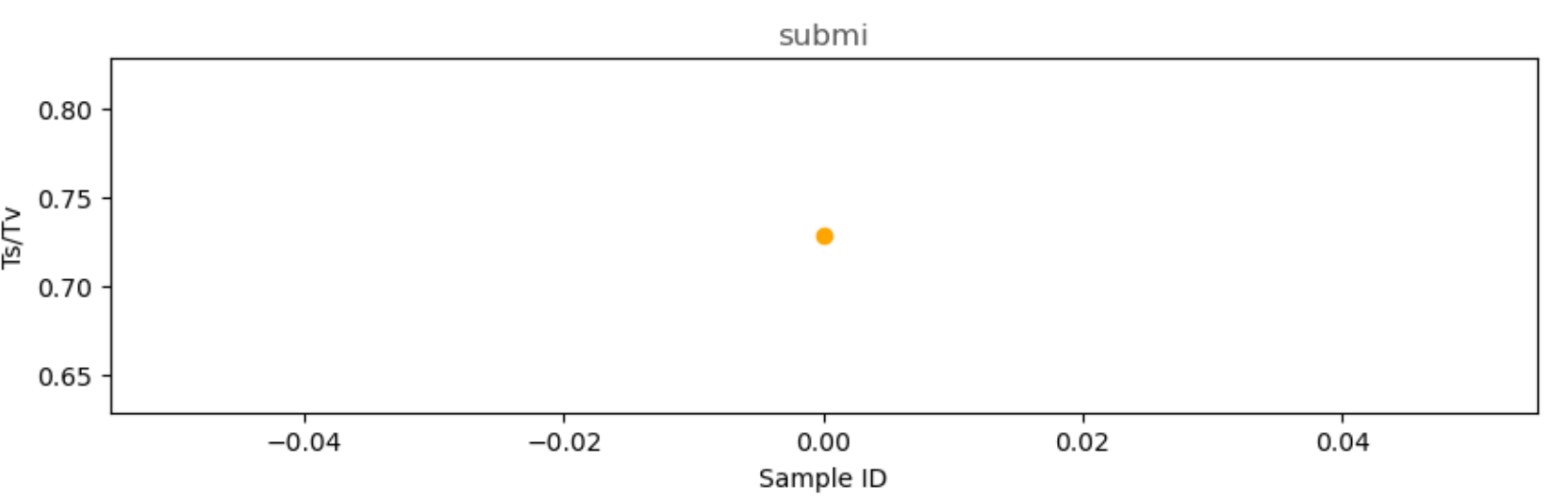

submi
1e2
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Count
A>C
A>G
A>T
C>A
C>G
C>T
G>A
G>C
G>T
T>A
T>C
T>G

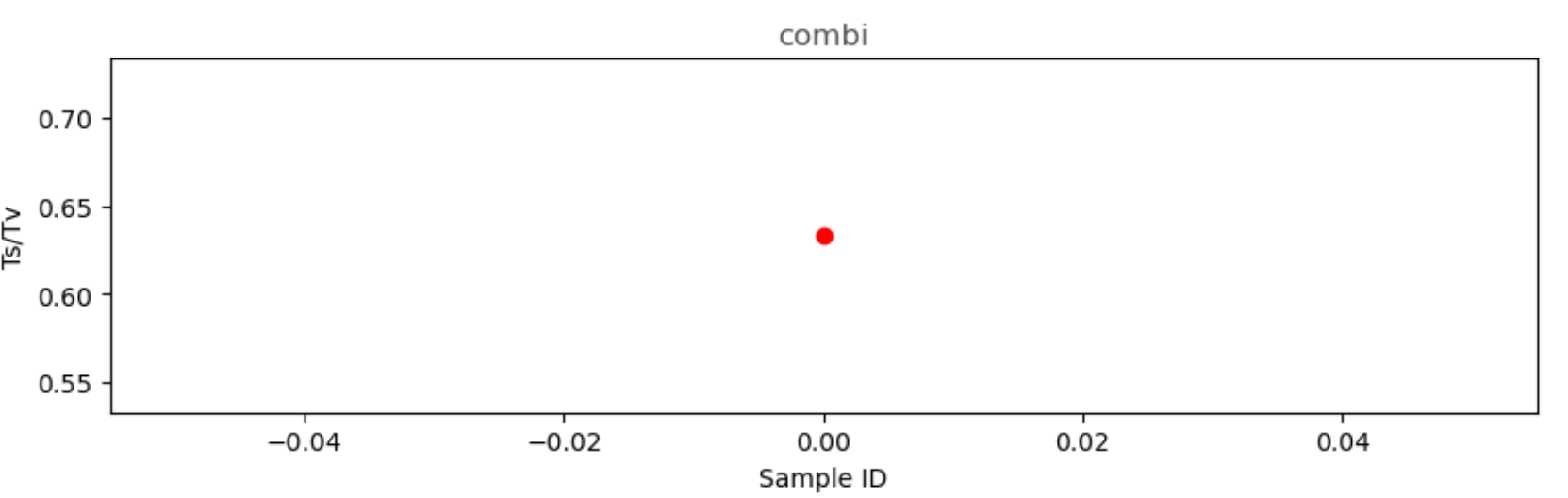

combi
1e2
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Count
A>C
A>G
A>T
C>A
C>G
C>T
G>A
G>C
G>T
T>A
T>C
T>G

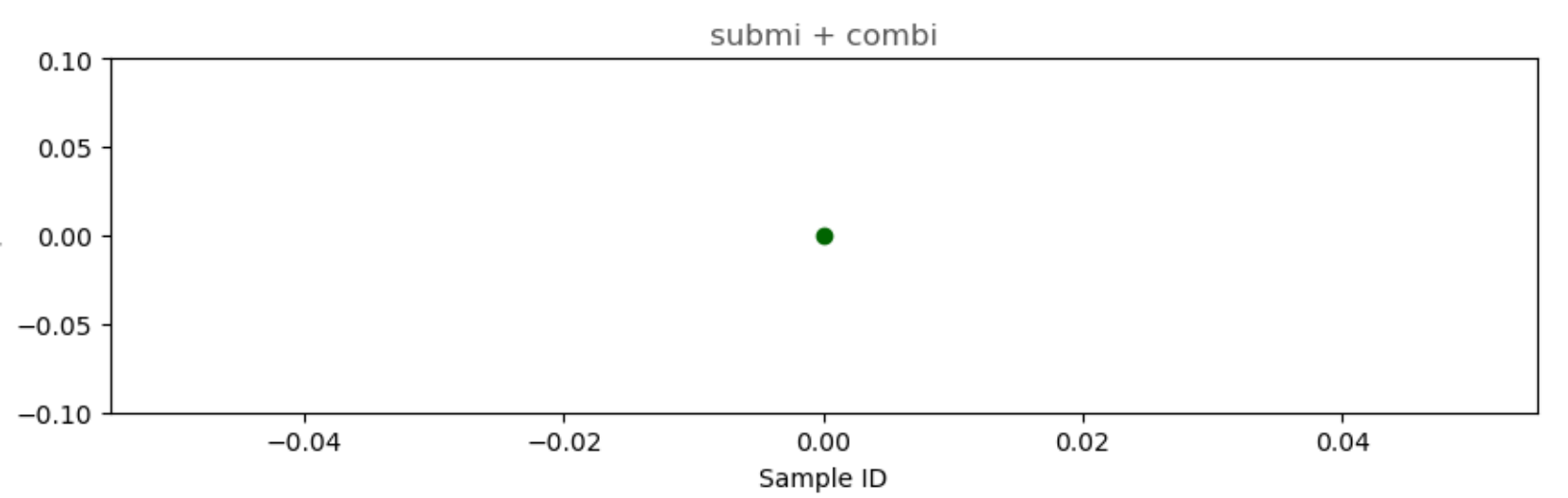

submi + combi
1e−2
Count
4
2
0
−2
−4
A>C
A>G
A>T
C>A
C>G
C>T
G>A
G>C
G>T
T>A
T>C
T>G

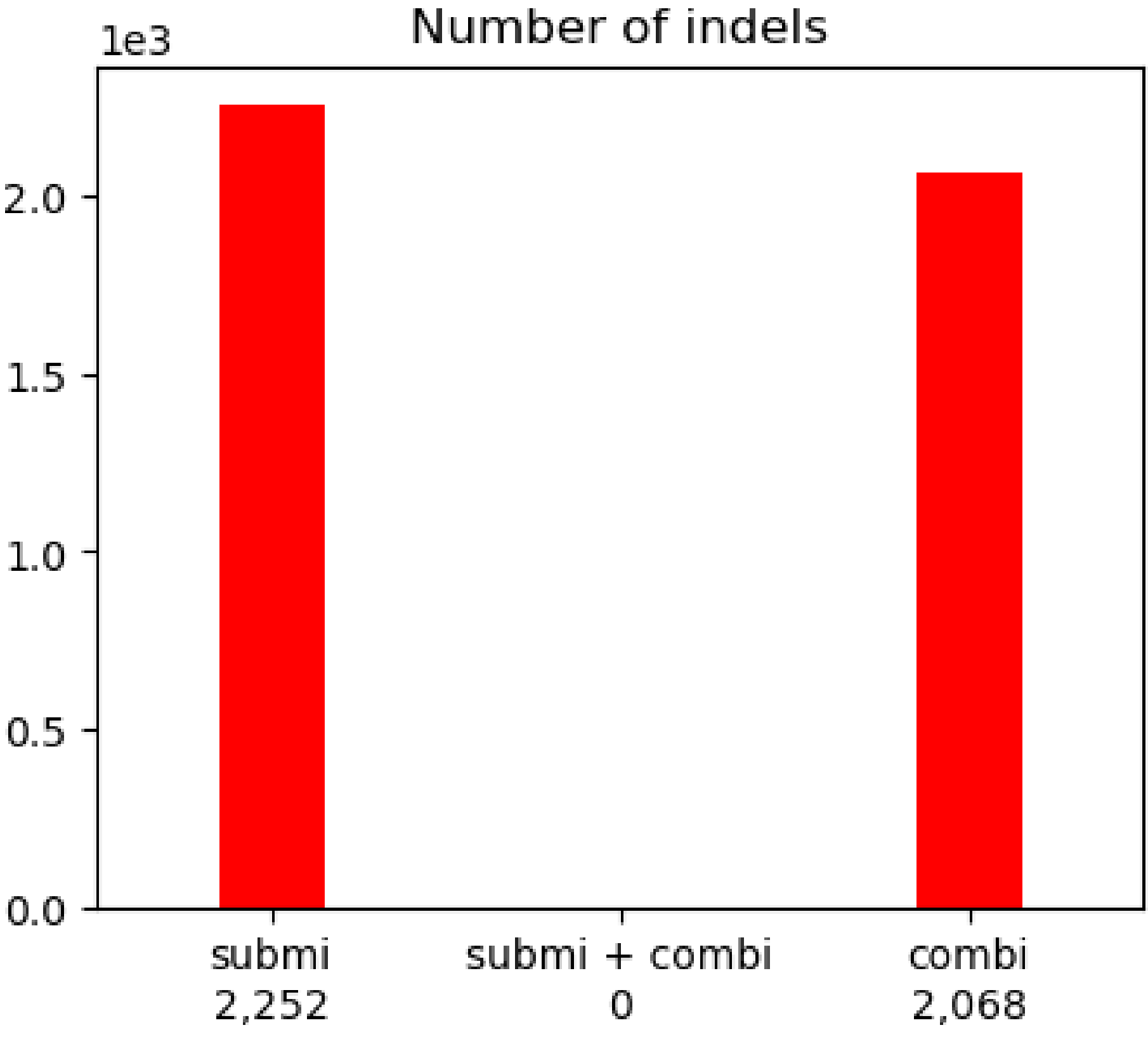

submi
Cumulative ts/tv
Per 1% bins
Ts/Tv
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.0
0.5
1.0
1.5
1e3
Number of sites
(sorted by QUAL, descending)

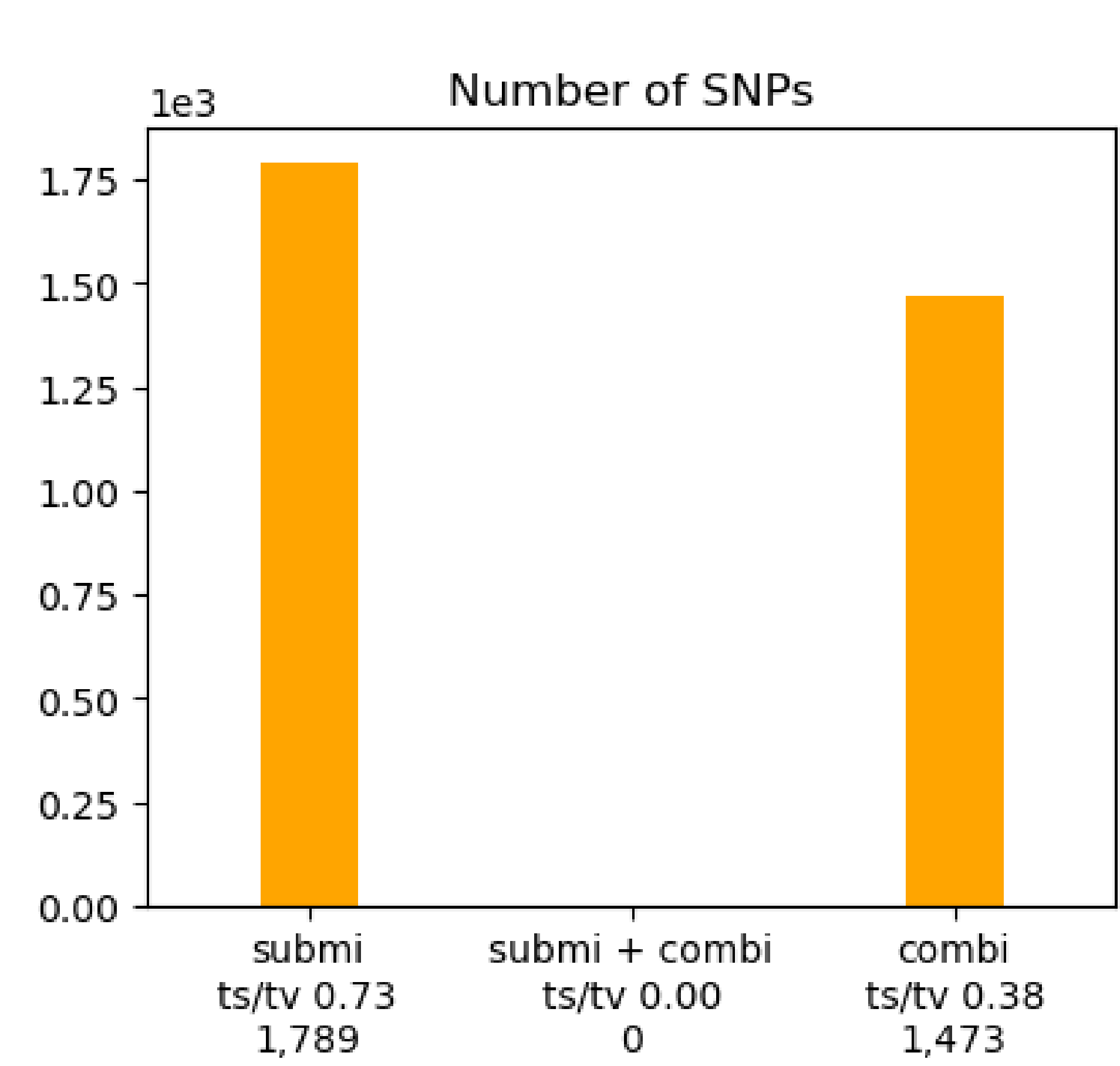

combi
Cumulative ts/tv
Per 1% bins
Ts/Tv
2.5
2.0
1.5
1.0
0.5
0.0
0.00
0.25
0.50
0.75
1.00
1.25
1e3
Number of sites
(sorted by QUAL, descending)


submi
0.80
0.75
0.70
0.65
Ts/Tv
−0.04
−0.02
0.00
0.02
0.04
Sample ID


combi
0.70
0.65
0.60
0.55
Ts/Tv
−0.04
−0.02
0.00
0.02
0.04
Sample ID


submi + combi
0.10
0.05
0.00
−0.05
−0.10
−0.04
−0.02
0.00
0.02
0.04
Sample ID


Number of indels
1e3
2.0
1.5
1.0
0.5
0.0
submi
2,252
submi + combi
0
combi
2,068


Number of SNPs
1e3
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
submi
ts/tv 0.73
1,789
submi + combi
ts/tv 0.00
0
combi
ts/tv 0.38
1,473

GCsAF

NRDs

NRDs 2 0.000000 0.000000 0.000000 0.000000

GClAF

NRDl

NRDl 2 0.000000 0.000000 0.000000 0.000000

GCsS

GCsS 2 S3_WGS-batchC_40510023O1-ST140_S9 0.000 0 0 0 0 0 0 0

GClS

GClS 2 S3_WGS-batchC_40510023O1-ST140_S9 0.000 0 0 0 0 0 0 0

GCTs

GCTs S3_WGS-batchC_40510023O1-ST140_S9 0 0 0 0 0 0 0