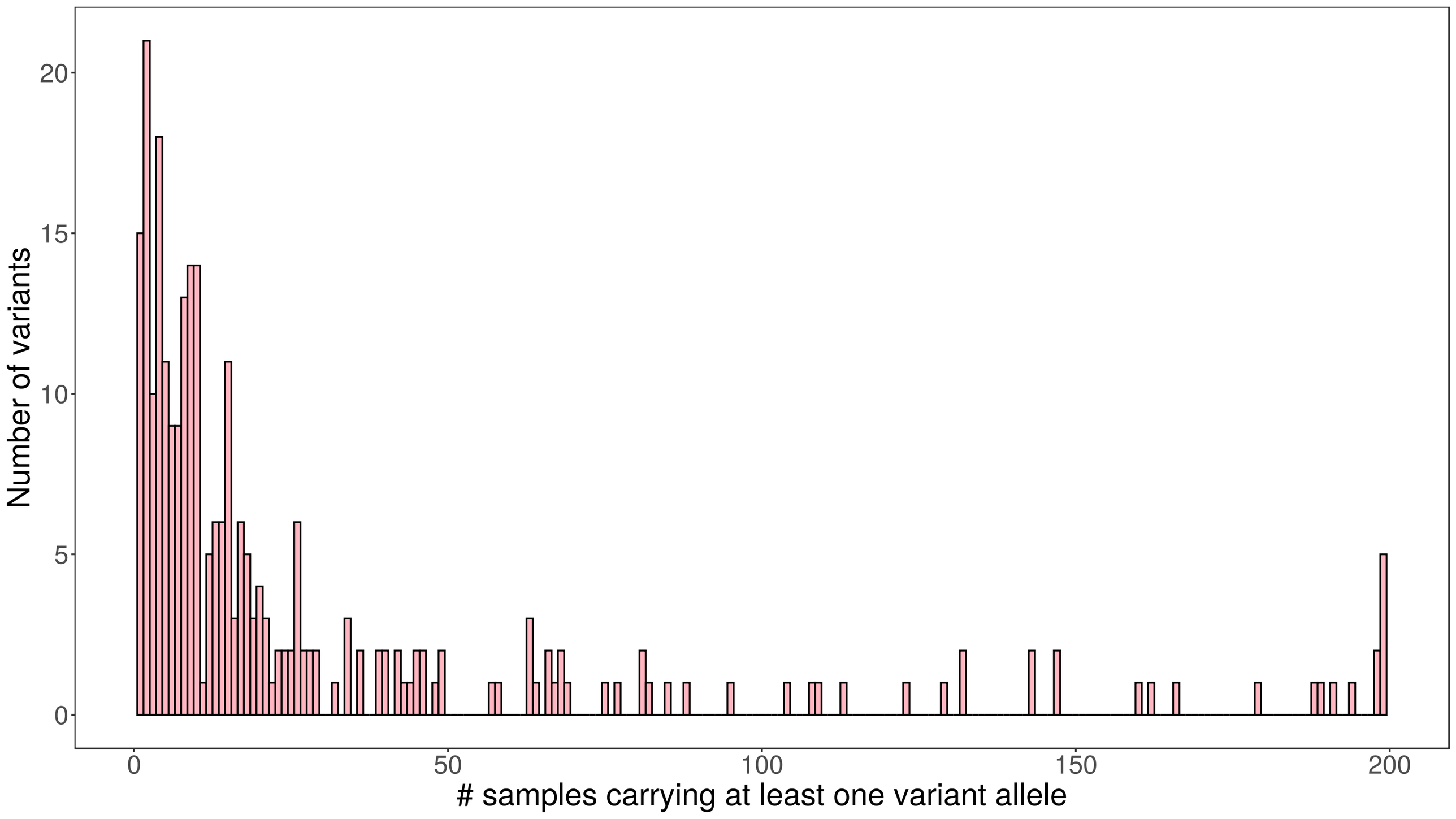
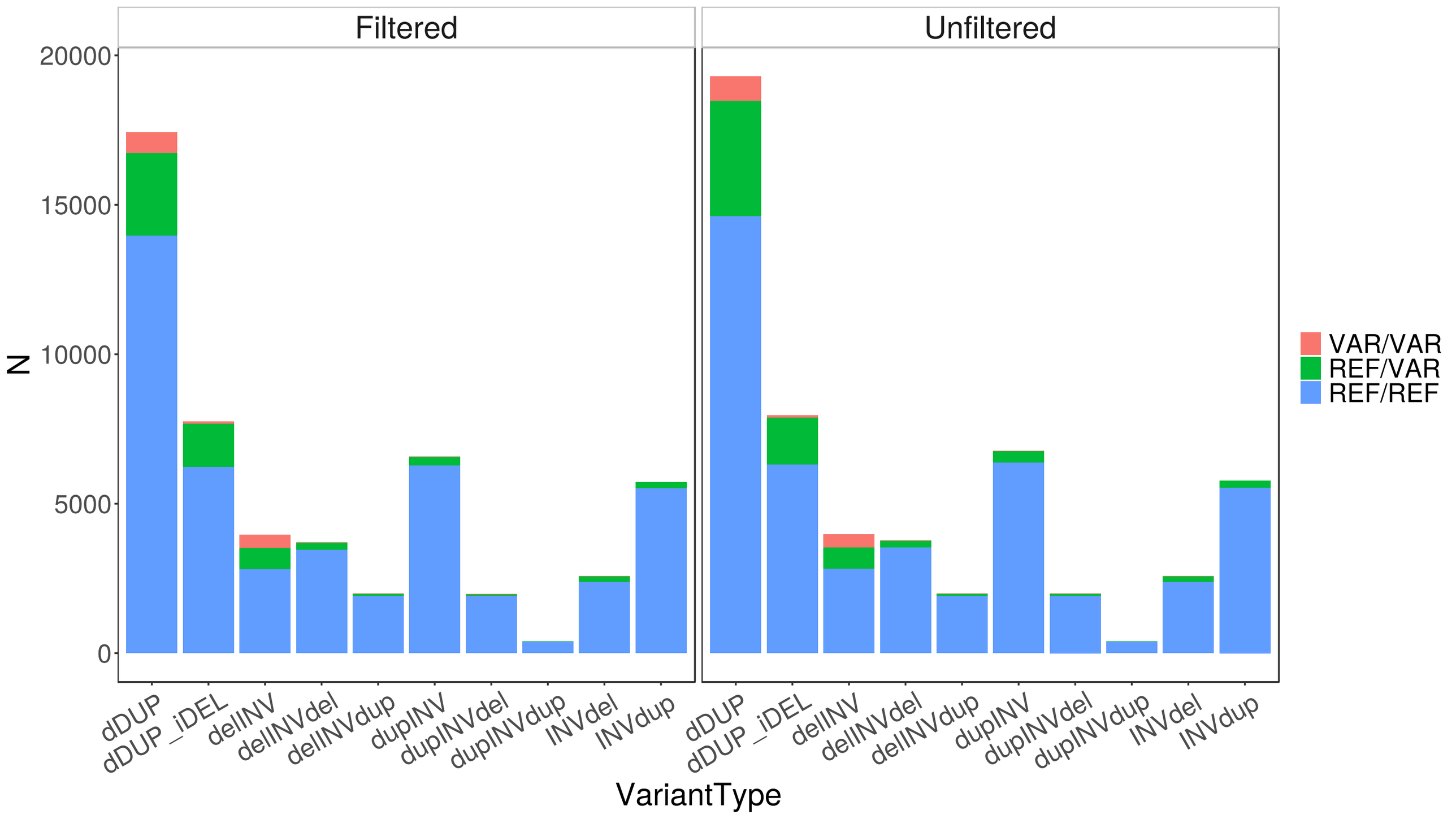
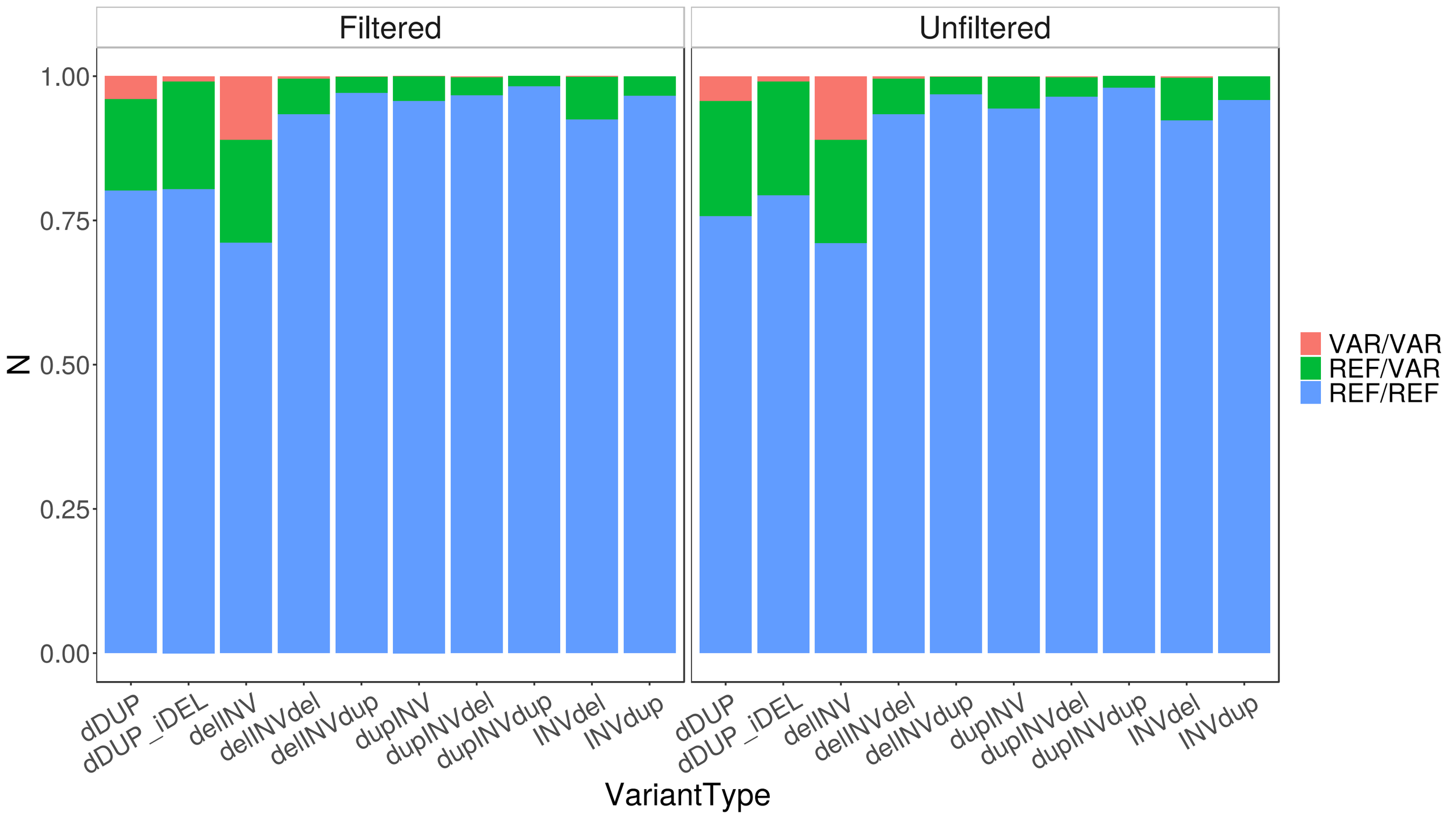
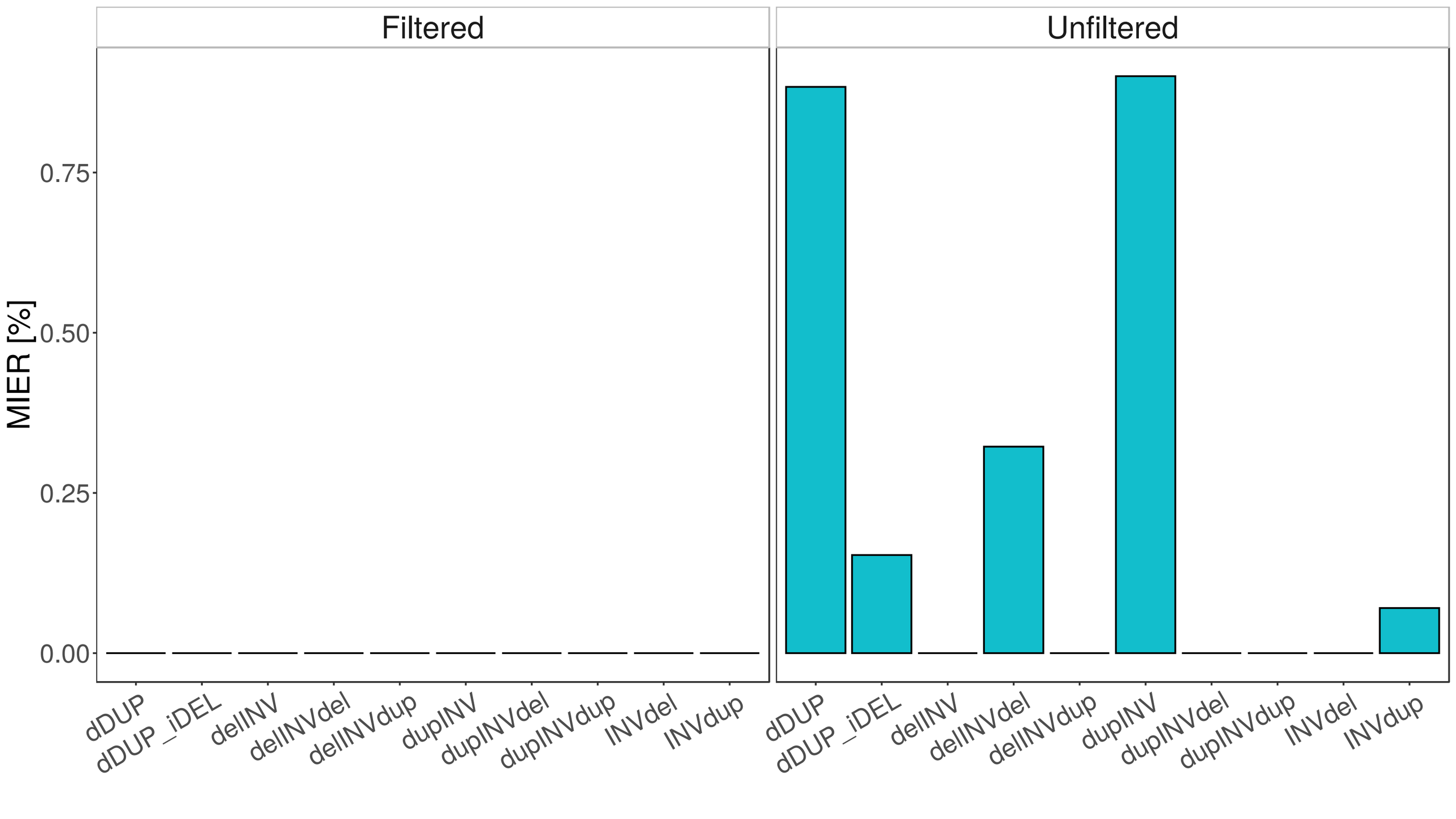
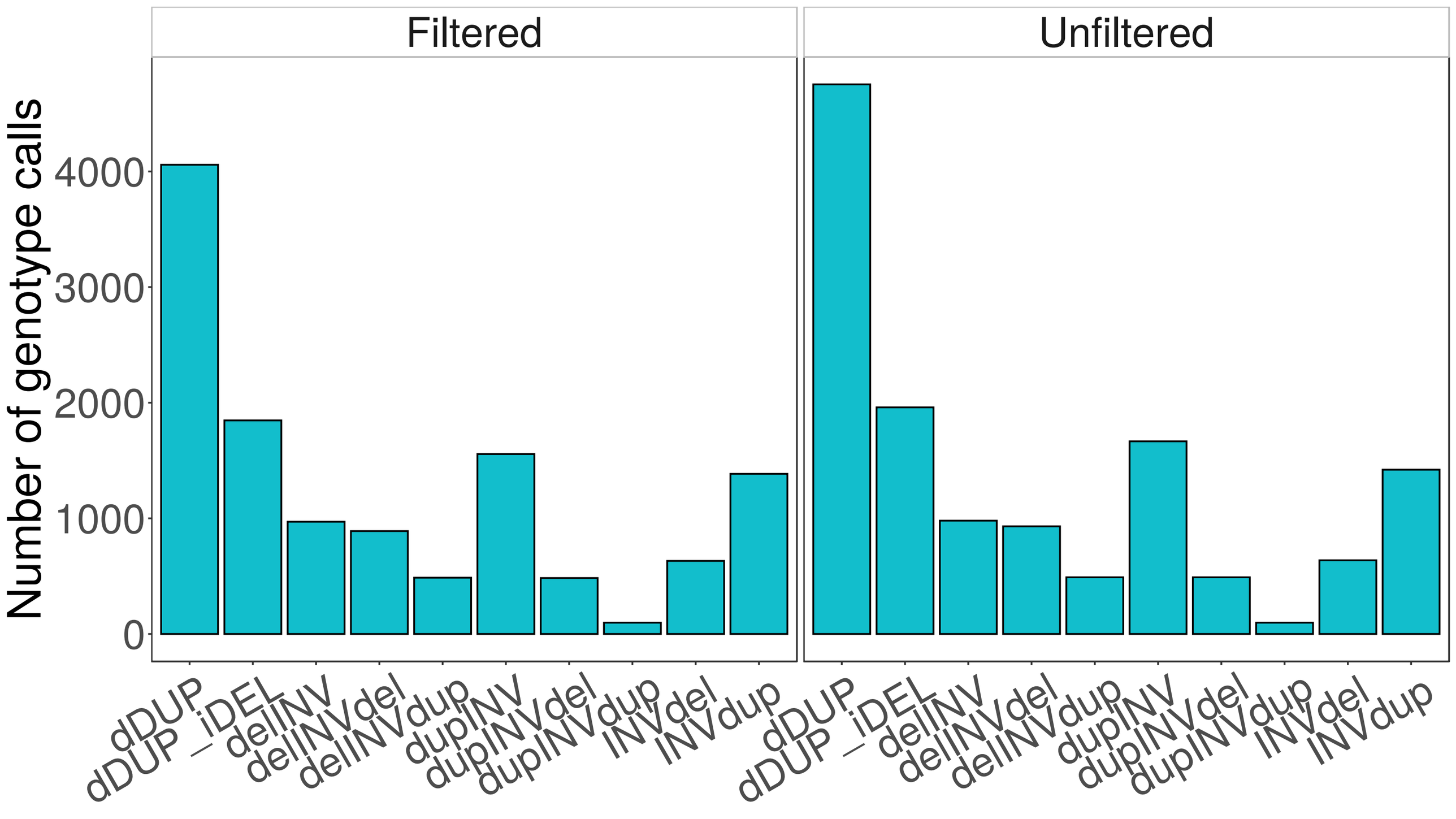
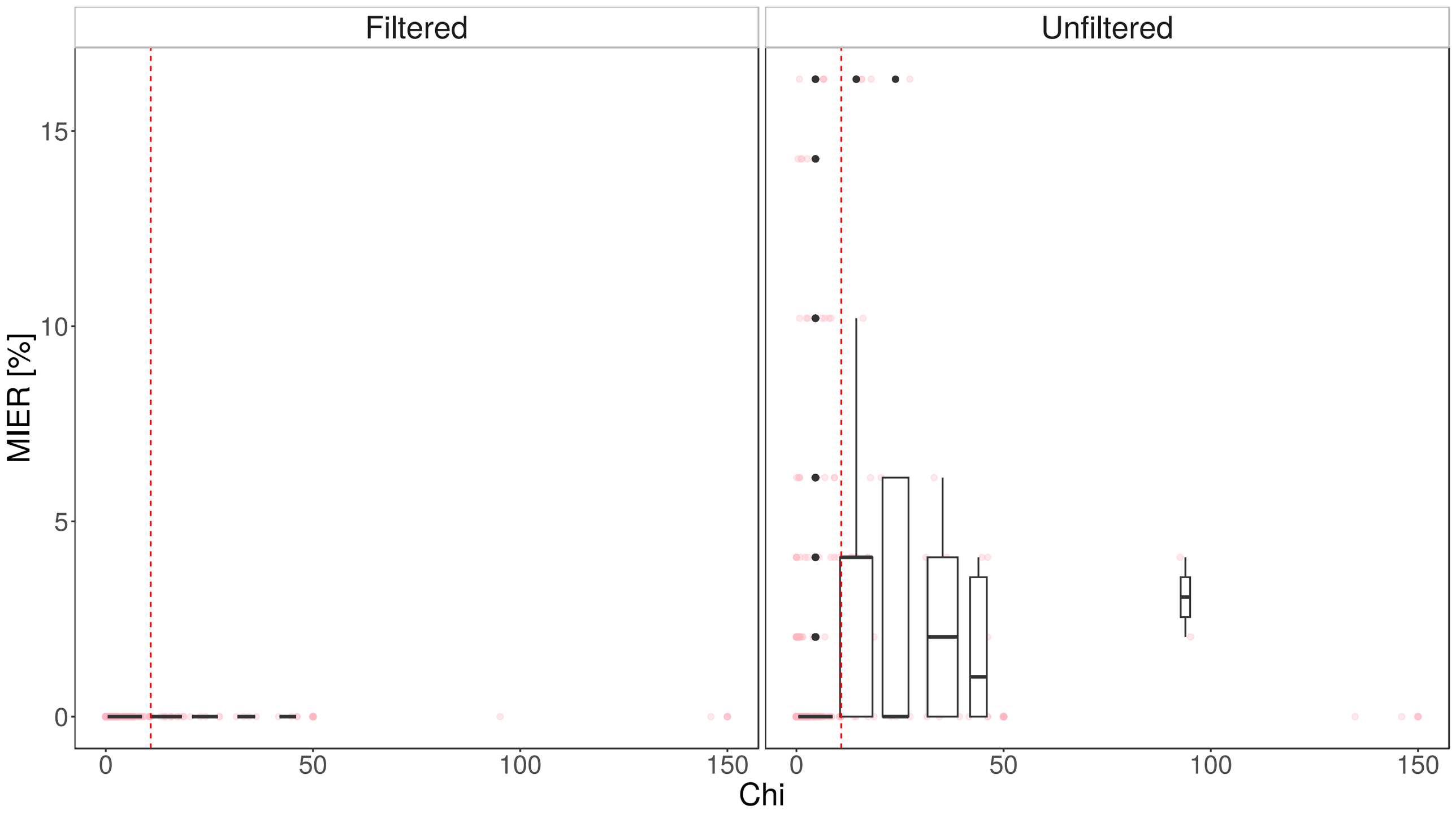

Number of variants
0
5
10
15
20
0
50
100
150
200
# samples carrying at least one variant allele

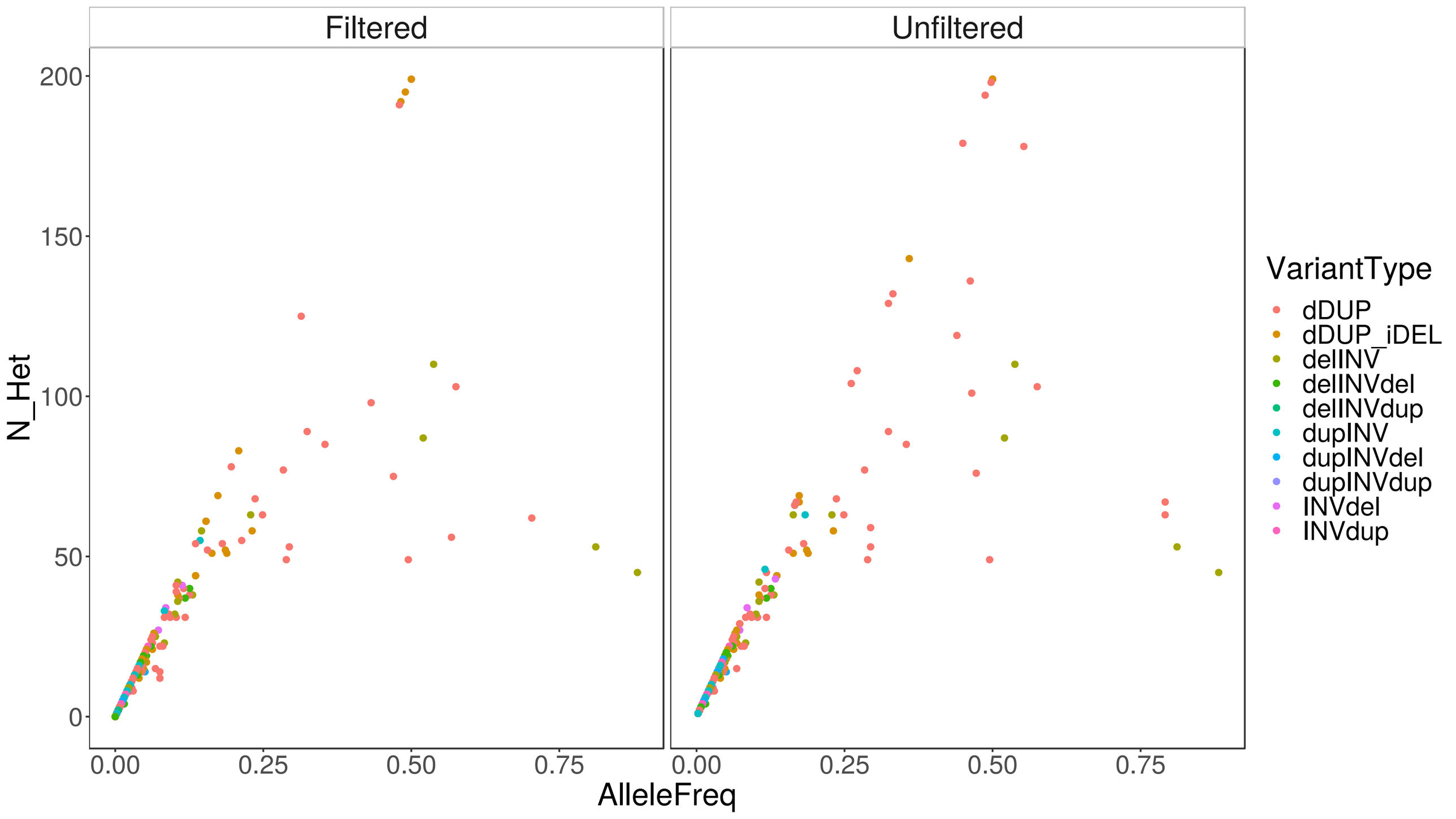

Filtered
Unfiltered
20000
15000
10000
5000
0
N
VAR/VAR
REF/VAR
REF/REF
dDUP
dDUP_iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup
VariantType

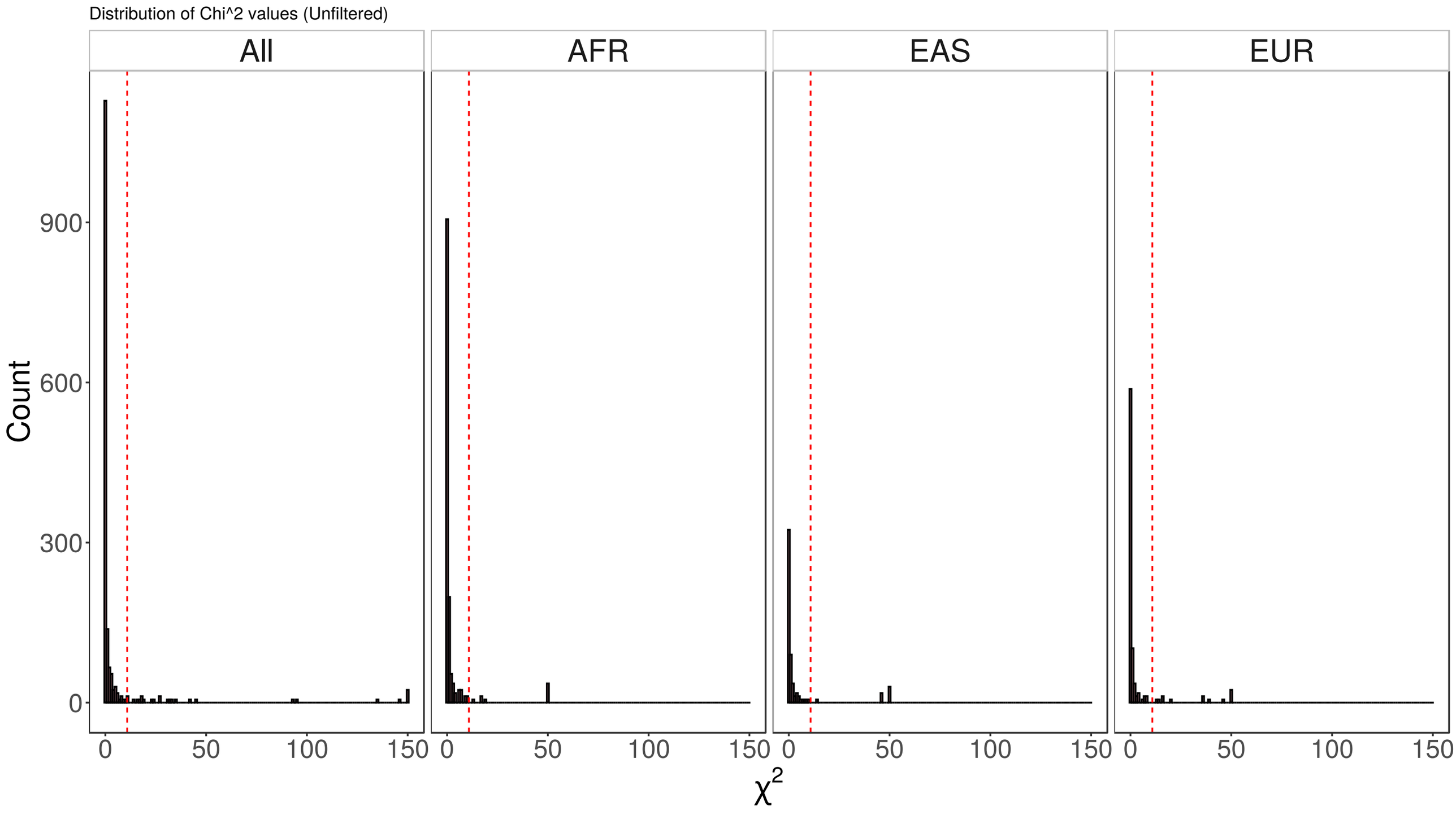

Filtered
Unfiltered
1.00
0.75
0.50
0.25
0.00
N
VAR/VAR
REF/VAR
REF/REF
dDUP
dDUP_iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup
VariantType

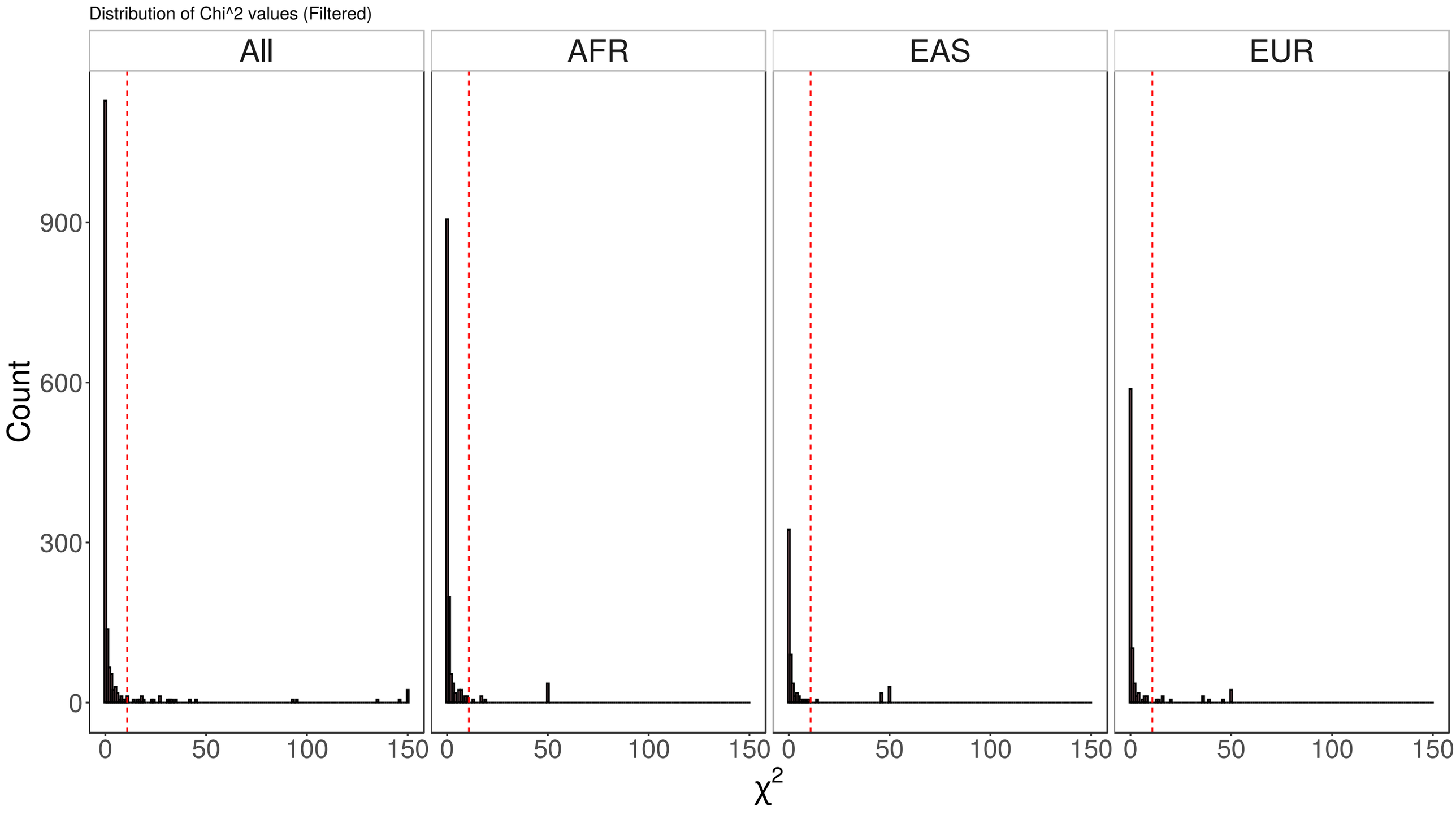

Filtered
Unfiltered
MIER [%]
0.00
0.25
0.50
0.75
dDUP
dDUP_iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup

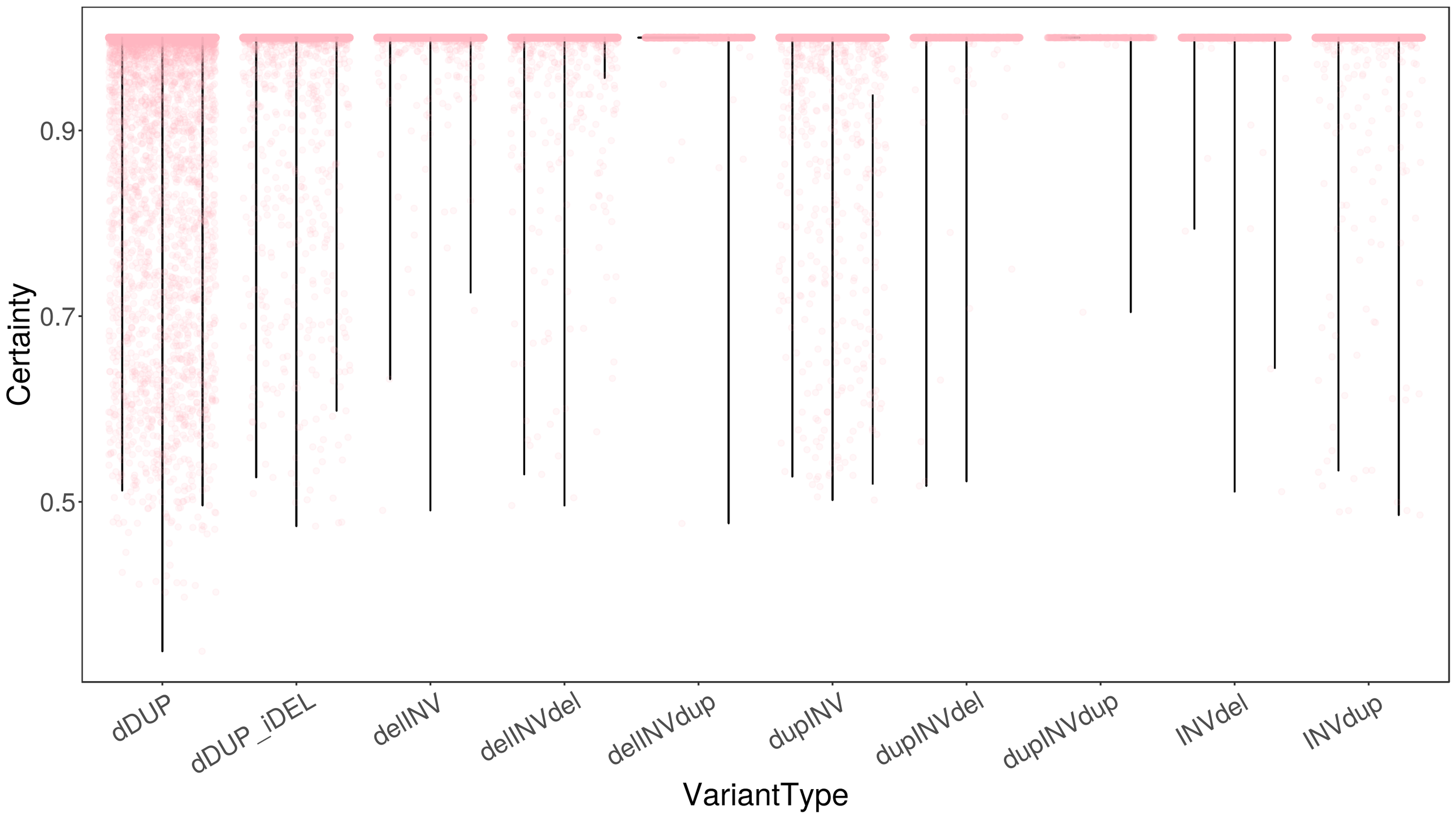

Filtered
Unfiltered
Number of genotype calls
0
1000
2000
3000
4000
dDUP
dDUP_iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup

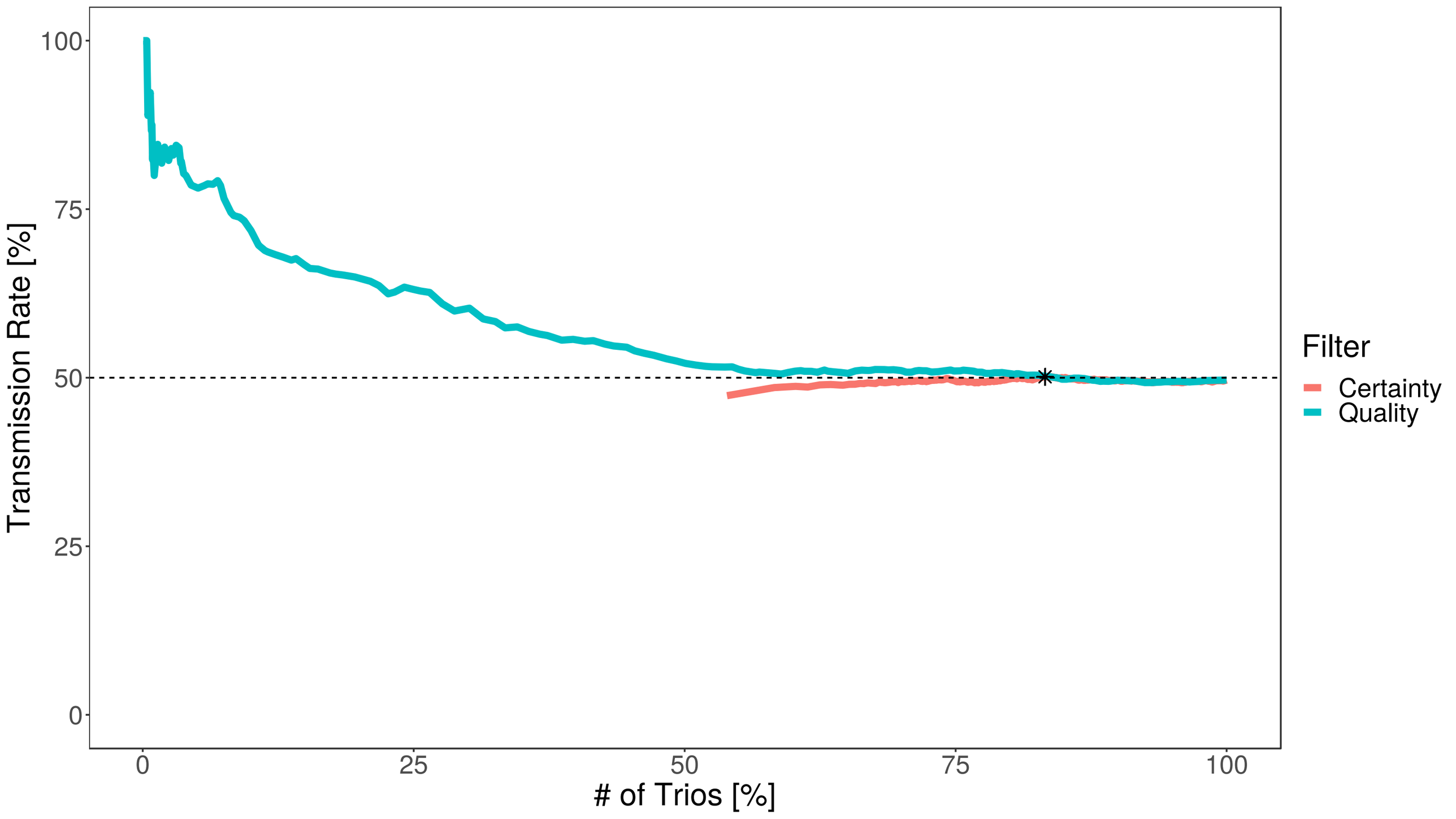

Filtered
Unfiltered
MIER [%]
15
10
5
0
0
50
100
150
Chi

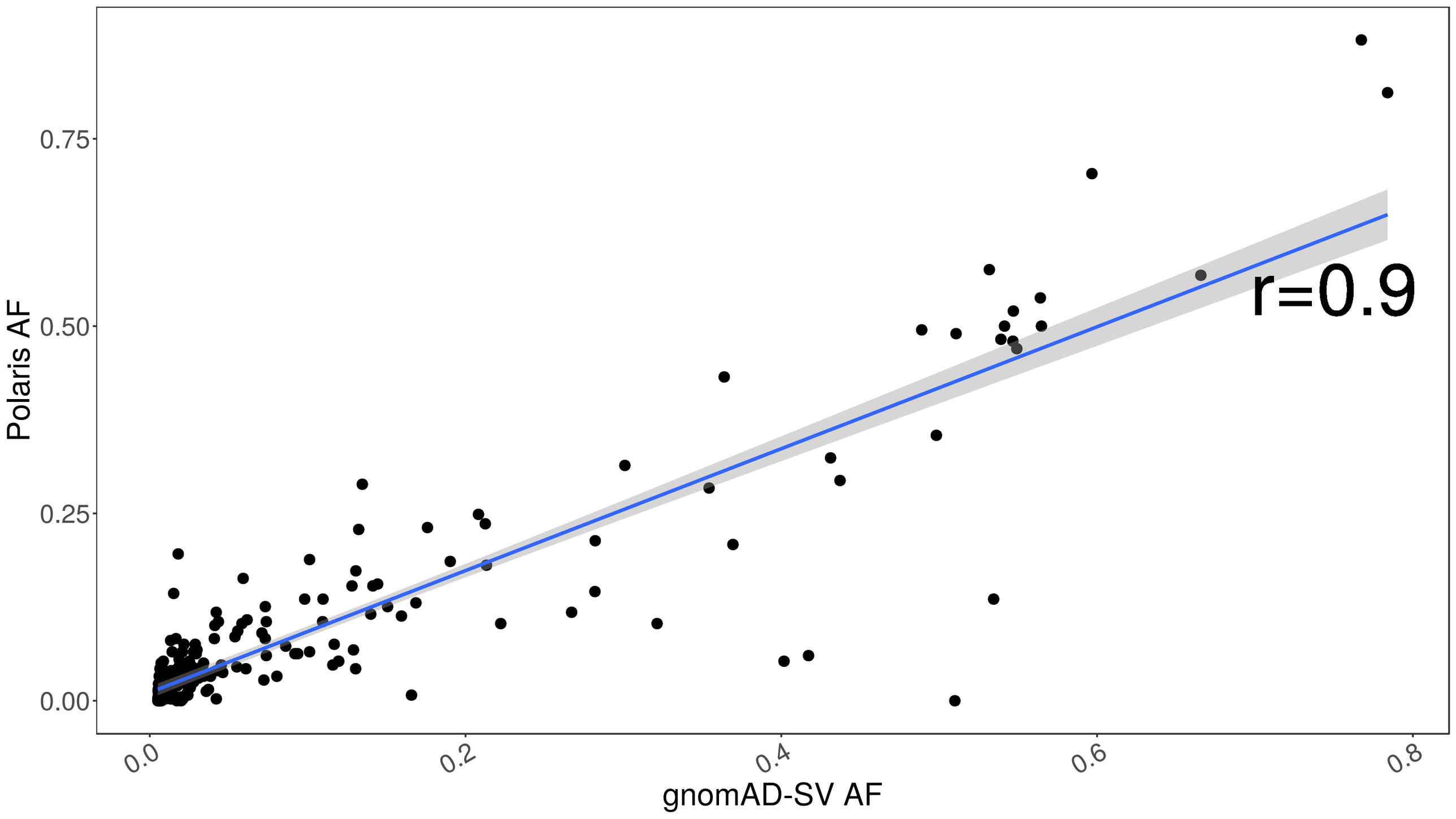

Filtered
Unfiltered
N_Het
AlleleFreq
200
150
100
50
0
0.00
0.25
0.50
0.75
VariantType
dDUP
dDUP_iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup

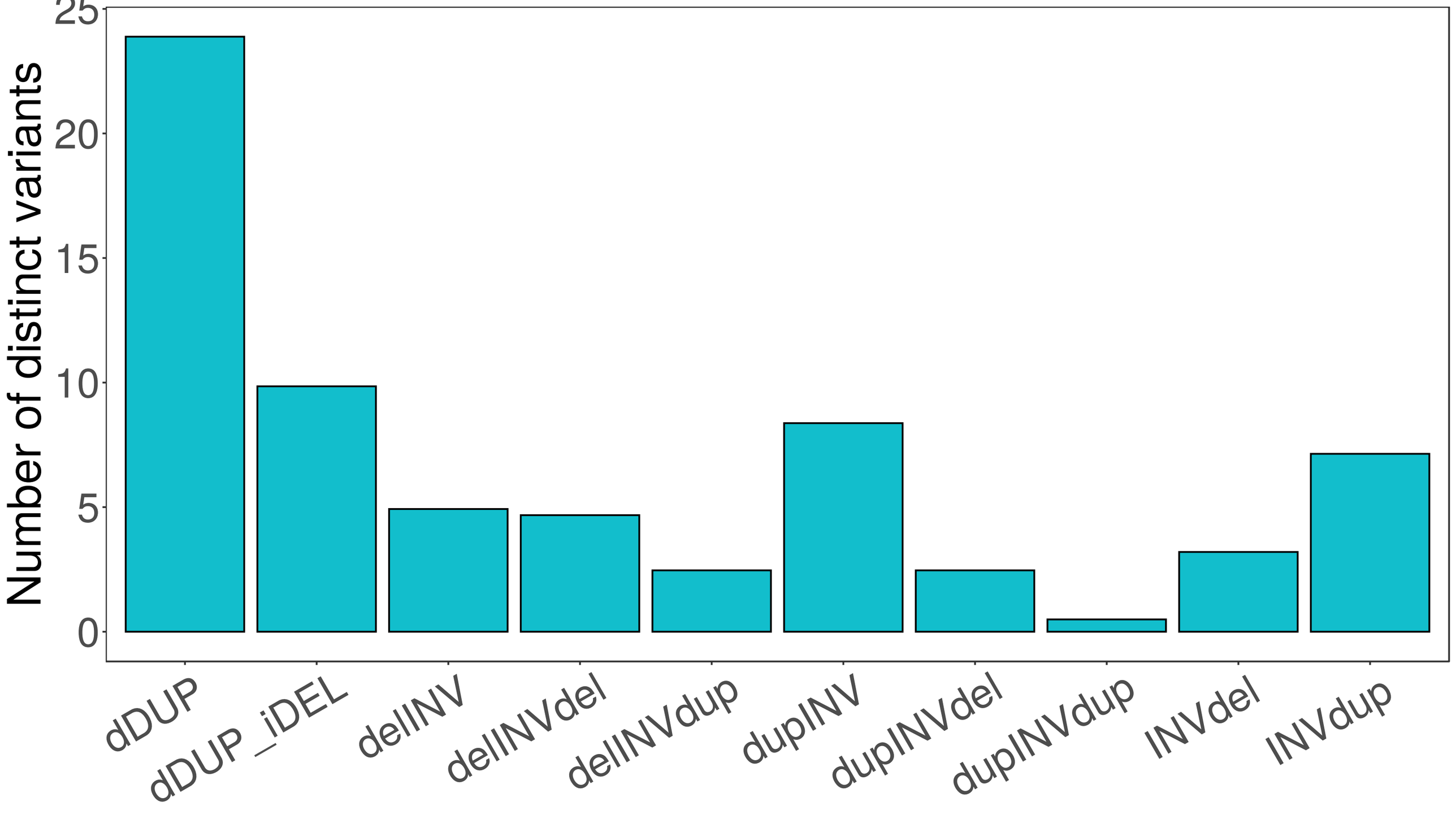

Distribution of Chi^2 values (Unfiltered)
All
AFR
EAS
EUR
Count
900
600
300
0
0
50
100
150
χ2


Distribution of Chi^2 values (Filtered)
All
AFR
EAS
EUR
Count
900
600
300
0
0
50
100
150
$\chi^2$


Certainty
0.9
0.7
0.5
dDUP
dDUP_iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup
VariantType


100
75
50
25
0
Transmission Rate [%]
0
25
50
75
100
# of Trios [%]
Filter
Certainty
Quality


r=0.9
Polaris AF
gnomAD-SV AF
0.00
0.25
0.50
0.75
0.0
0.2
0.4
0.6
0.8


Number of distinct variants
25
20
15
10
5
0
dDUP
dDUP _iDEL
delINV
delINVdel
delINVdup
dupINV
dupINVdel
dupINVdup
INVdel
INVdup