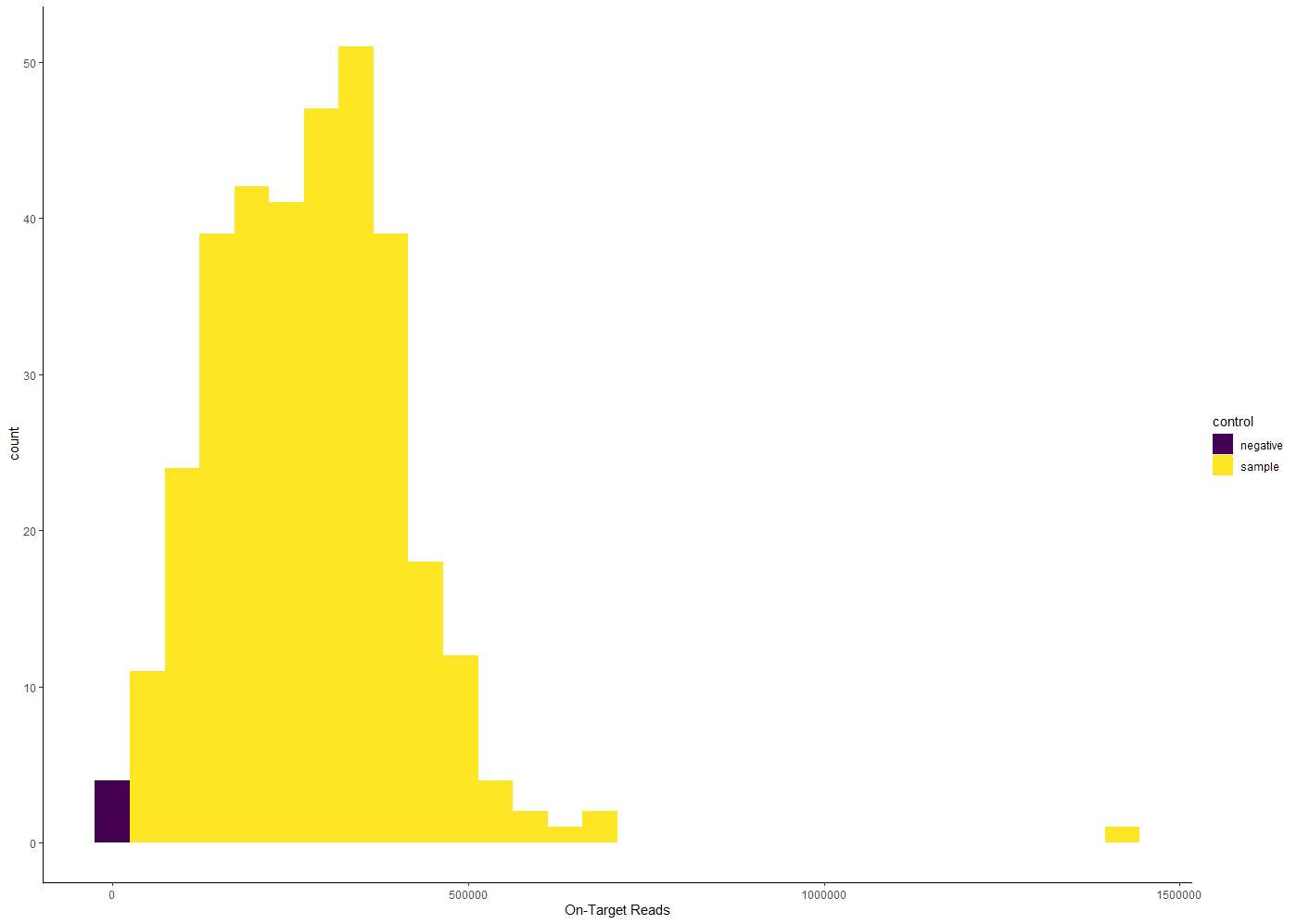
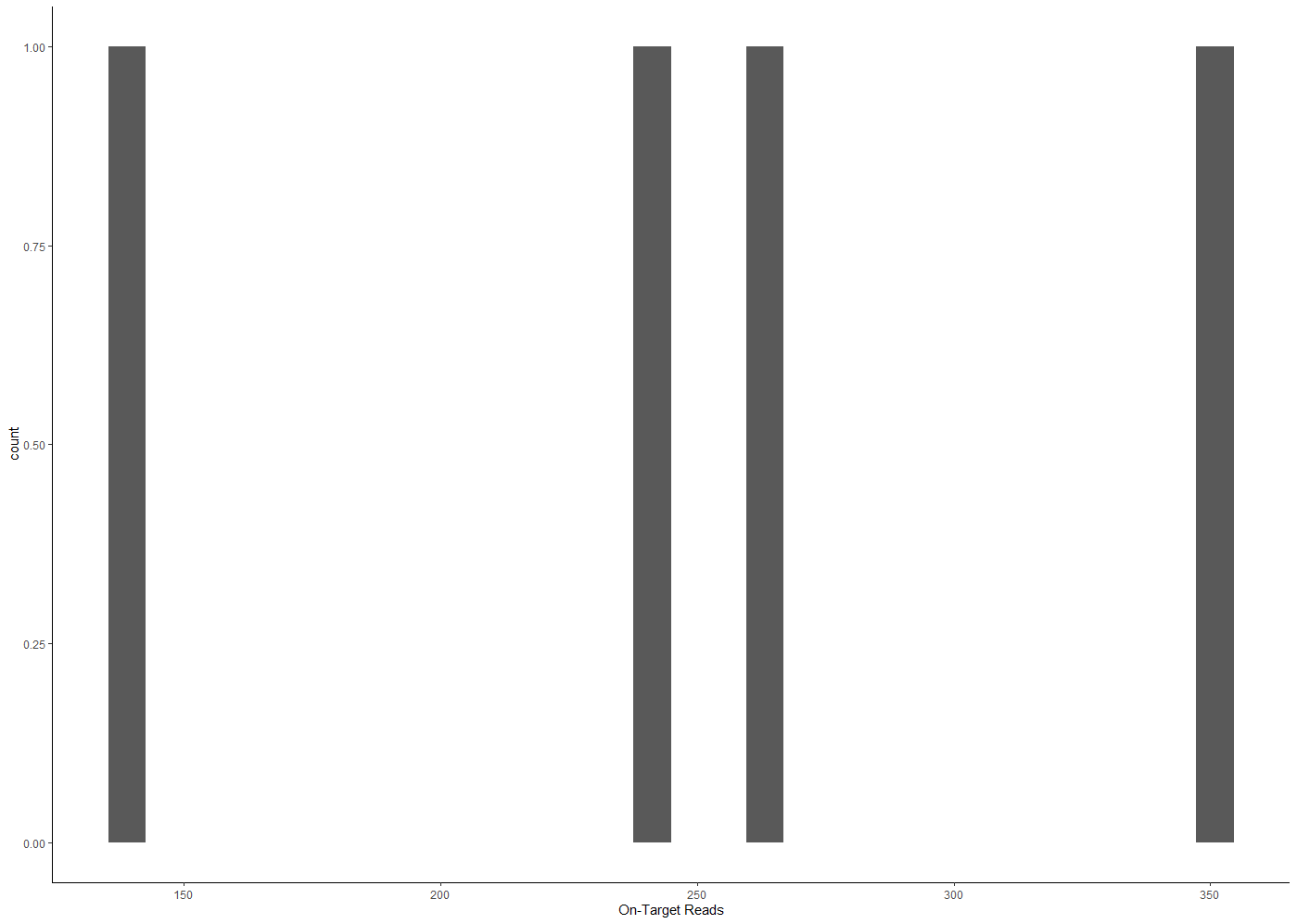
O.mykiss Siletz 2023 genotyping summary

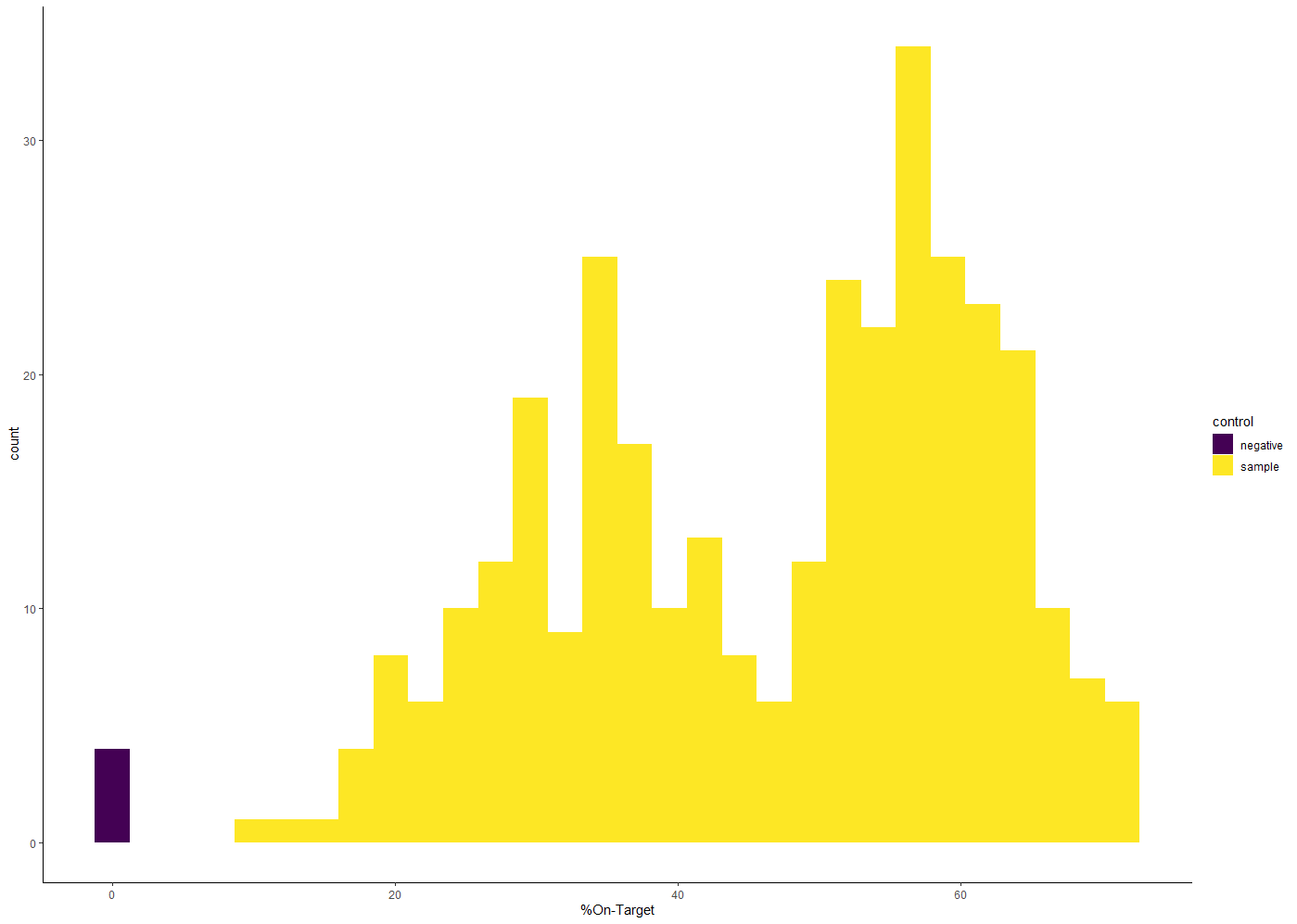
**QC**



4 negative controls. They have very few “On-Target” reads which is good.

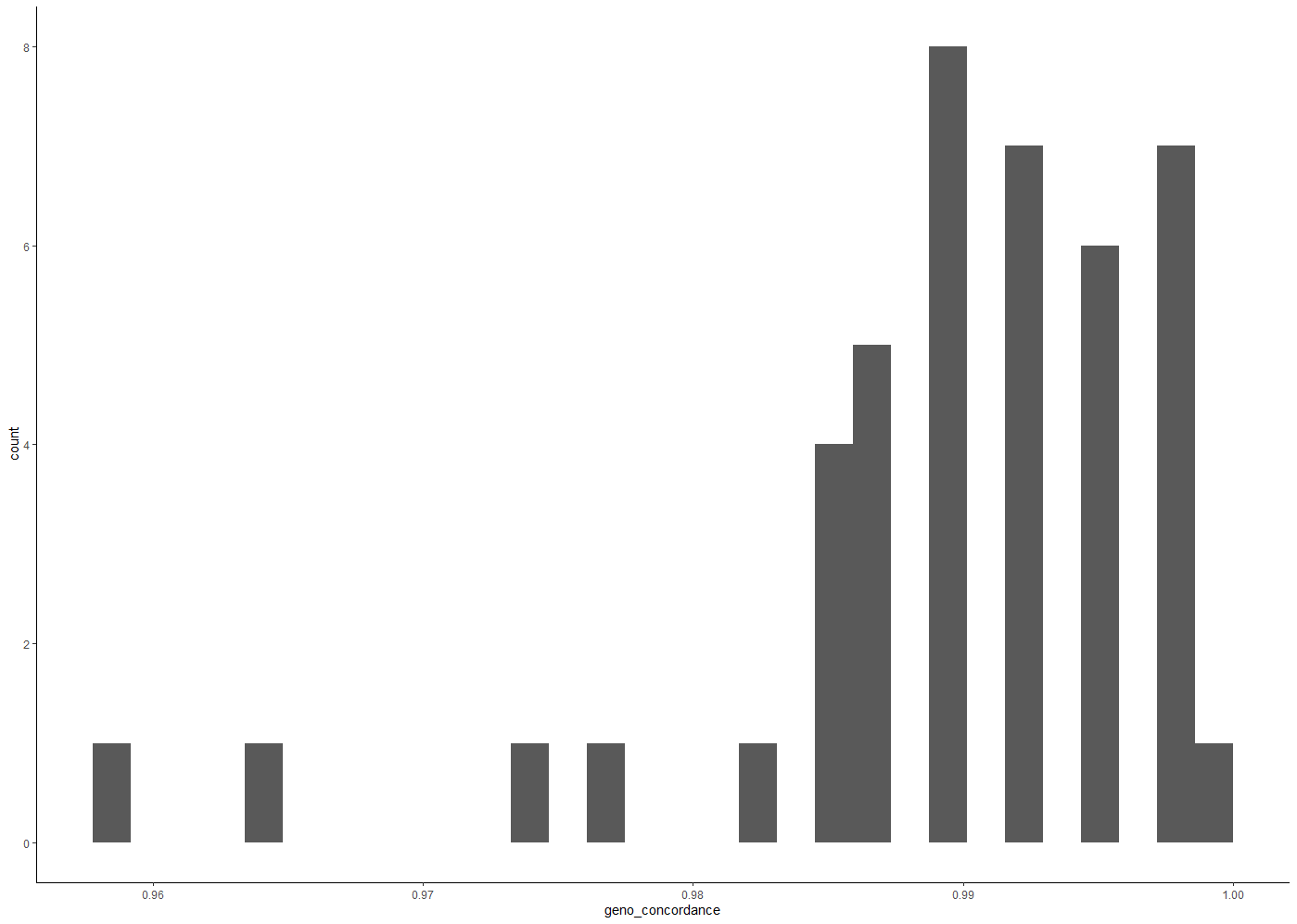


On-Target reads range 139-351 in 4 negative controls.



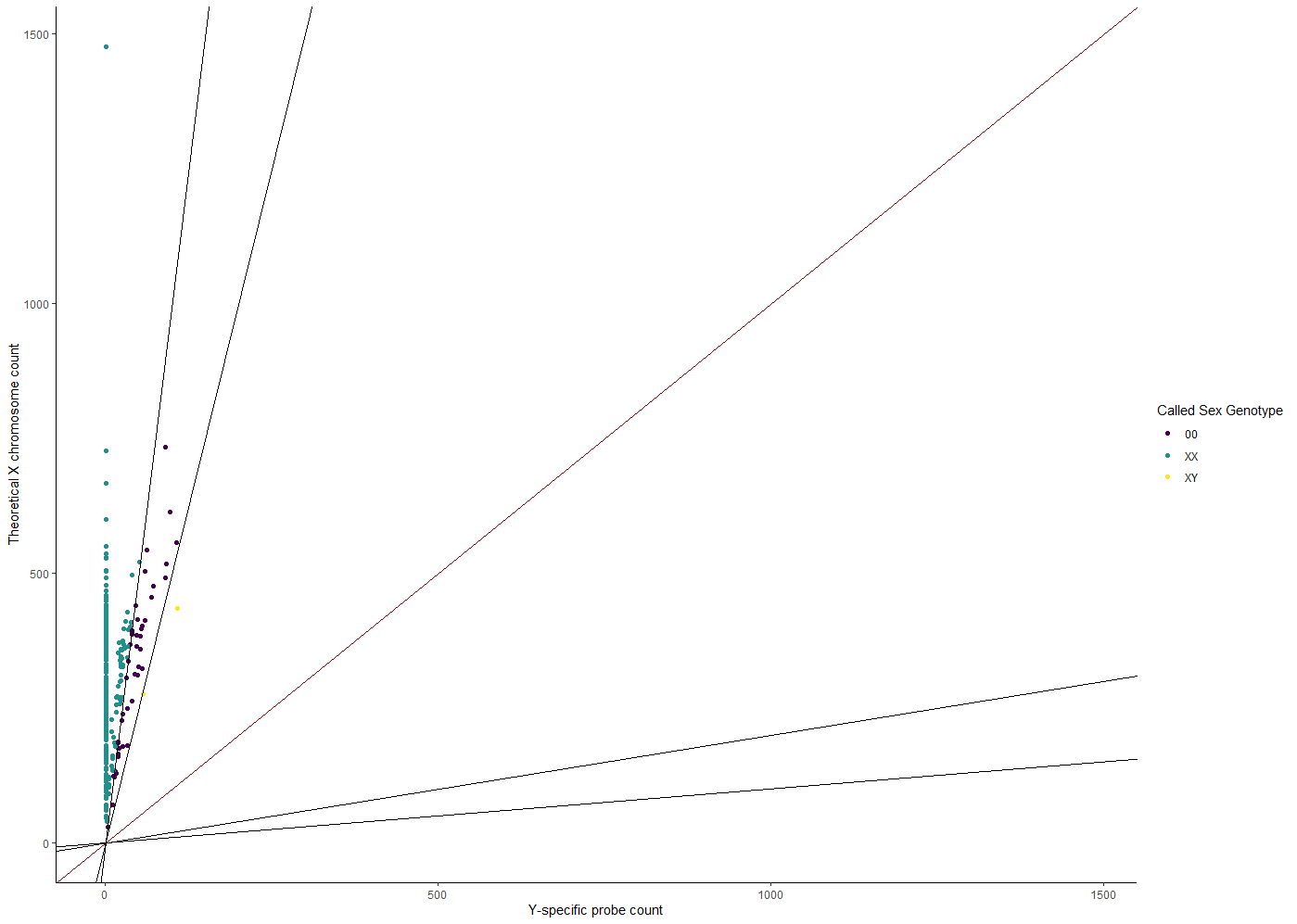
% On-Target ranges 0.03-0.16% for 4 negative controls.

% On-Target ranges 10.46-71.48% for samples.

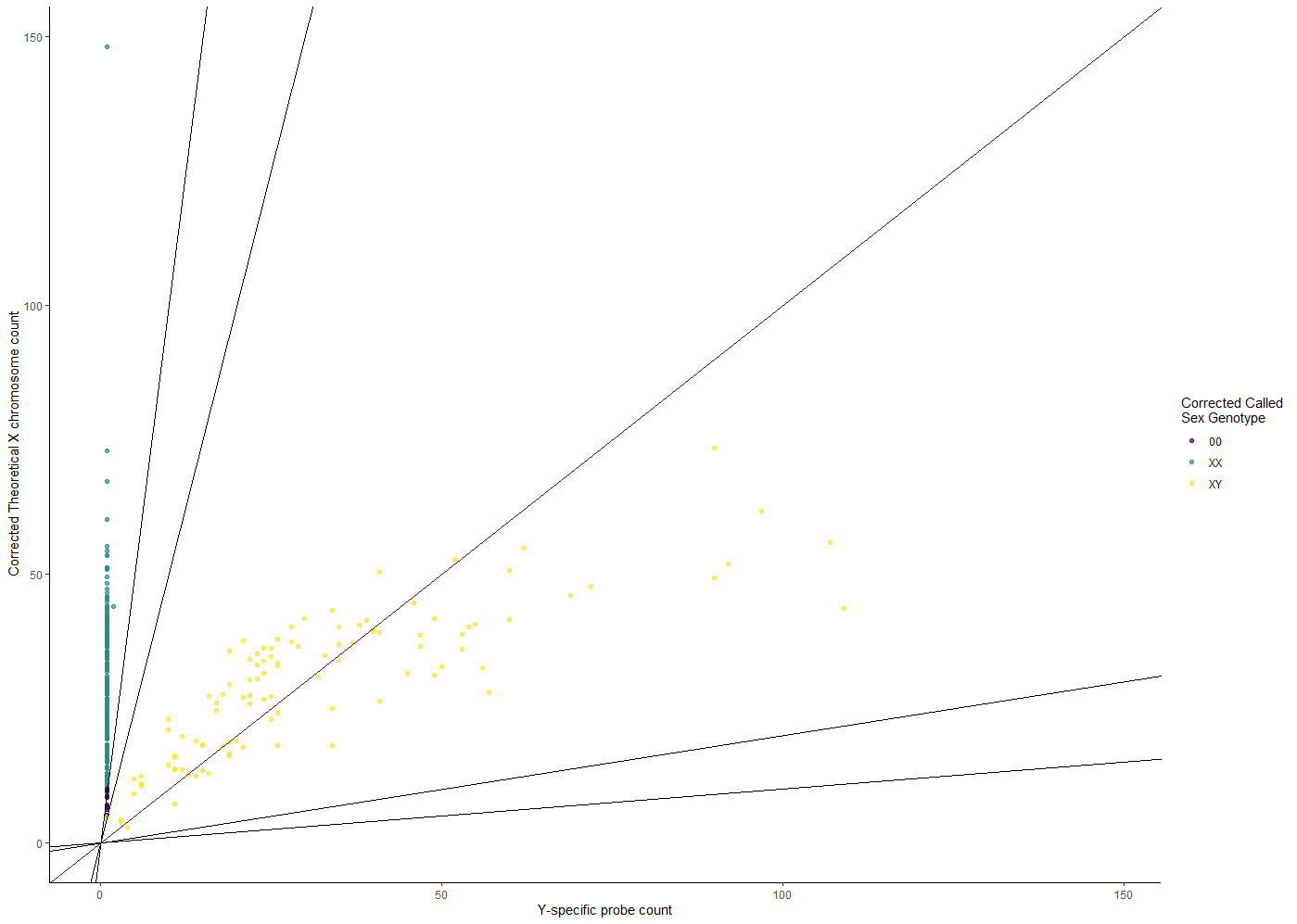


86 repeated samples. High concordance among them 0.95-1.00

291 unique sample\_simple names. Genotyped at 390 loci and a sex marker.



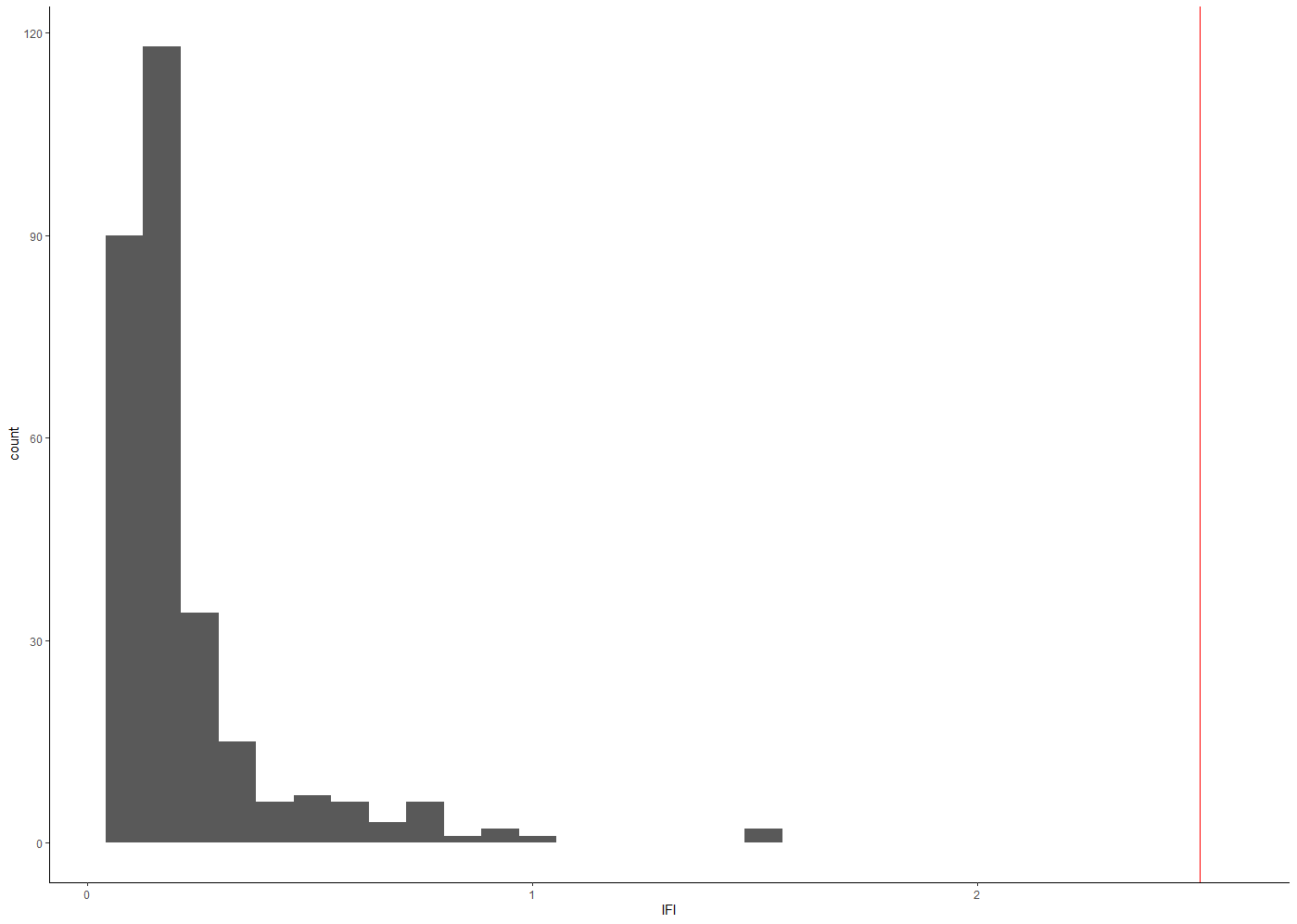
Sex genotyping needs correction. (Before correction)



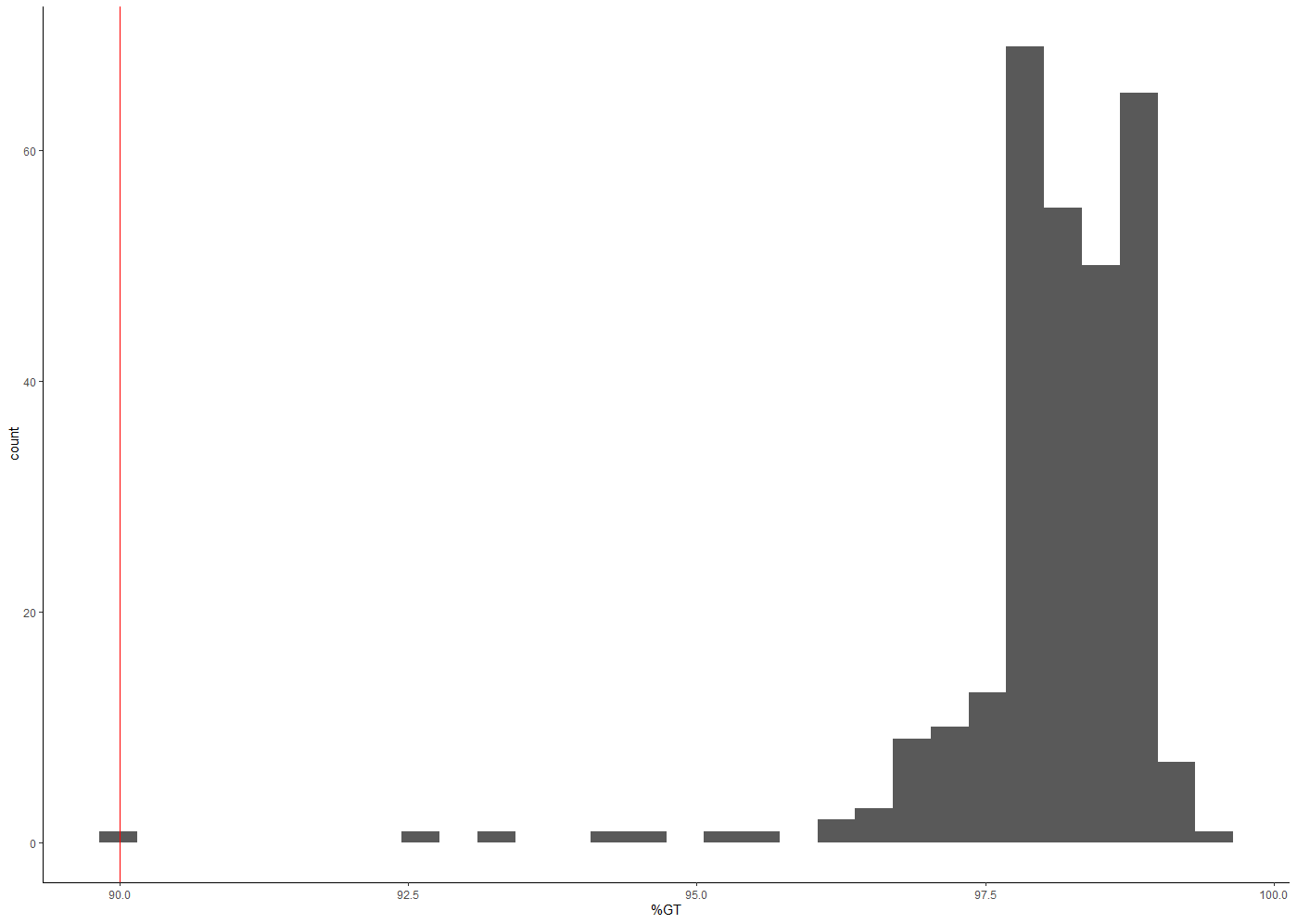
Correction appears to work. (After correction).

95 males, 187 females, 9 undetermined in 291 unique samples.

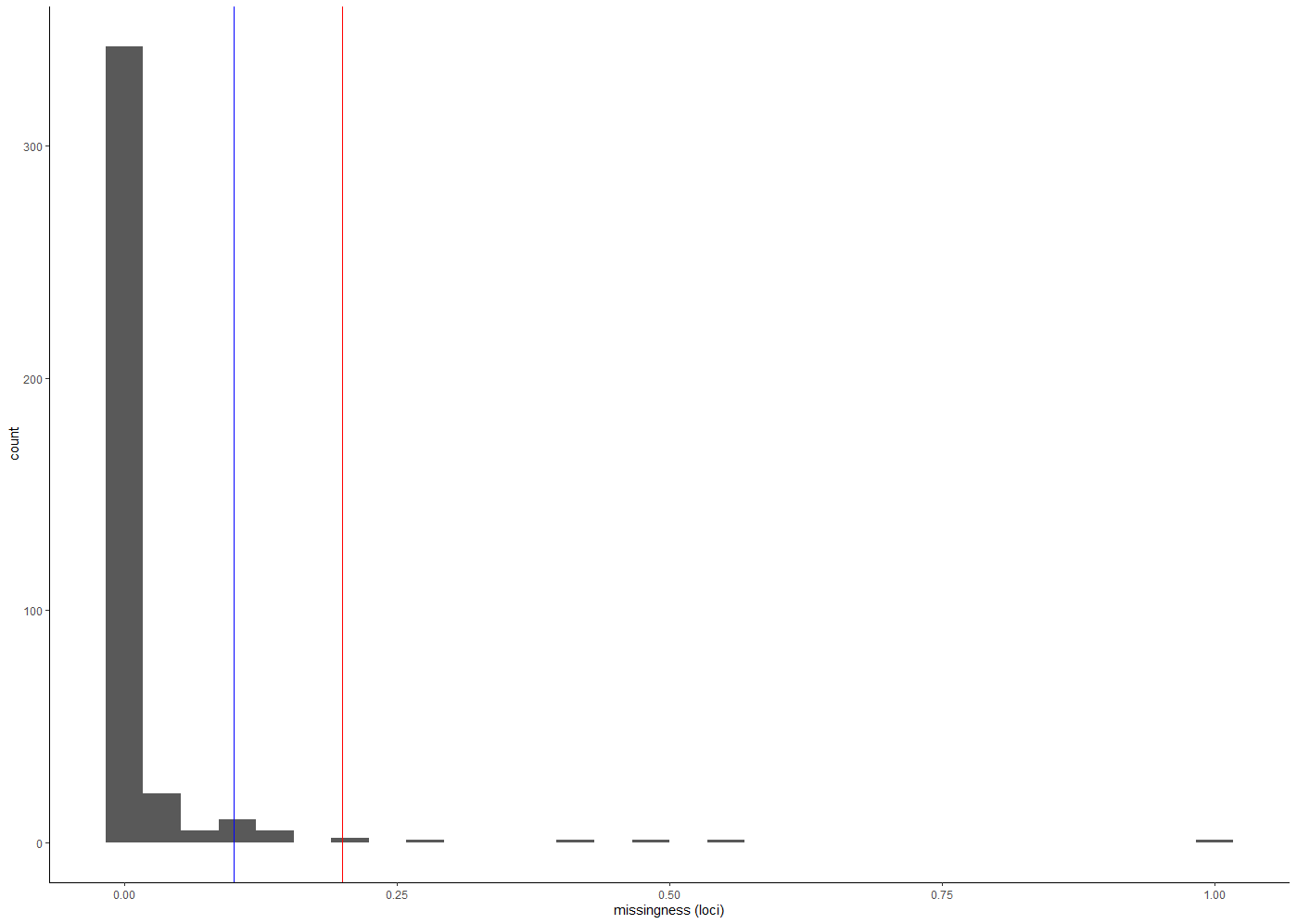
**Filtering**



Low IFI scores for 291 samples which is good.



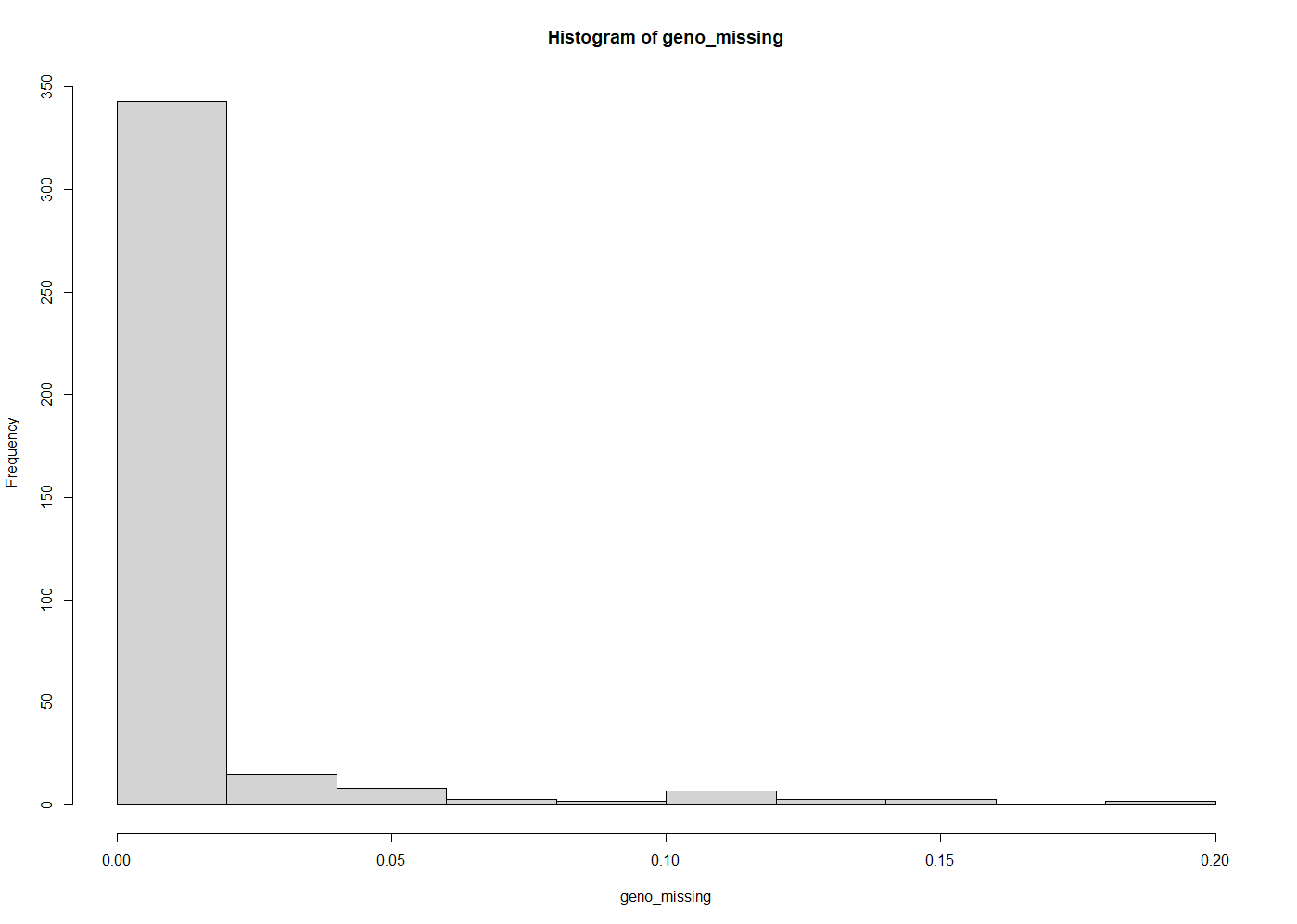
Percentage of loci genotyped in each sample range 90-99% which is good.

  
Most loci amplified in the great majority of samples. One locus (Omy\_RAD40520-48) didn’t amplify in any sample….

Removed two loci that amplified in less than half of samples (Omy\_RAD40520-48 & Omy\_RAD2277-7).

After removing these 2 loci, recalculated IFI. Range 0.05 – 1.6. Still well below final cutoff of 2.5. Good.

Removed three loci that amplified in less than 80% of samples (Omy\_104569-114, Omy\_RAD14541-72, Omy\_RAD43117-55)



Dataset now has 291 individuals genotyped at 385 loci and a sex marker. All markers are genotyped in > 80% of individuals.

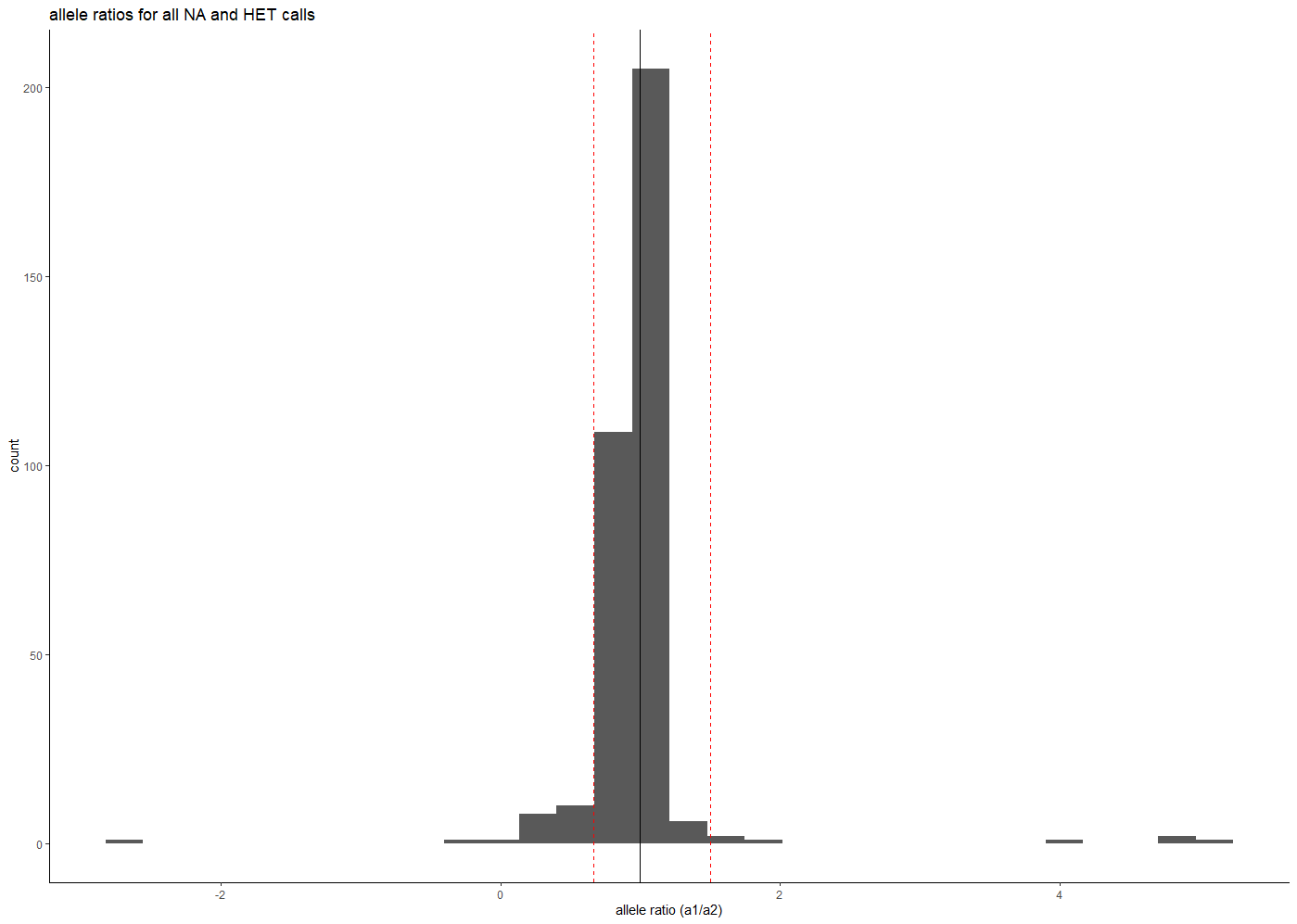
Call rates of individuals ranges 91-100%.

15 markers with ‘moderately poor’ genotyping rates (10 – 20% missing call rate):

OmyR40319Pearse, Omy\_118205-116, Omy\_CRBF1-1, Omy\_Ogo4-212,

Omy\_RAD13073-16, Omy\_RAD27740-55. Omy\_RAD2976-26, Omy\_RAD30230-25, Omy\_RAD30243-74, Omy\_RAD69583-33, Omy\_RAD74691-49, Omy\_RAD92485-64, Omy\_cd59b-112, Omy\_gsdf-291, Omy\_hus1-52

Evaluate ‘allelic balance’ in these 15 markers in heterozygote individuals. Why is heterozygote allelic balance only evaluated in loci with 10-20% missing call rates?



Removed:

Omy\_CRBF1-1

Omy\_RAD13073-16

Omy\_RAD69583-33

Omy\_RAD74691-49

Omy\_cd59b-112

Omy\_hus1-52

Could not evaluate in, so Removed:

OmyR40319Pearse (monomorphic for “A1”)

Omy\_RAD27740-55 (low MAF in allele “A2”, very few A2 homozygotes or heterozygotes)

Omy\_RAD2976-26 (monomorphic for “A1”)

Omy\_RAD30243-74 (monomorphic for “A1”)

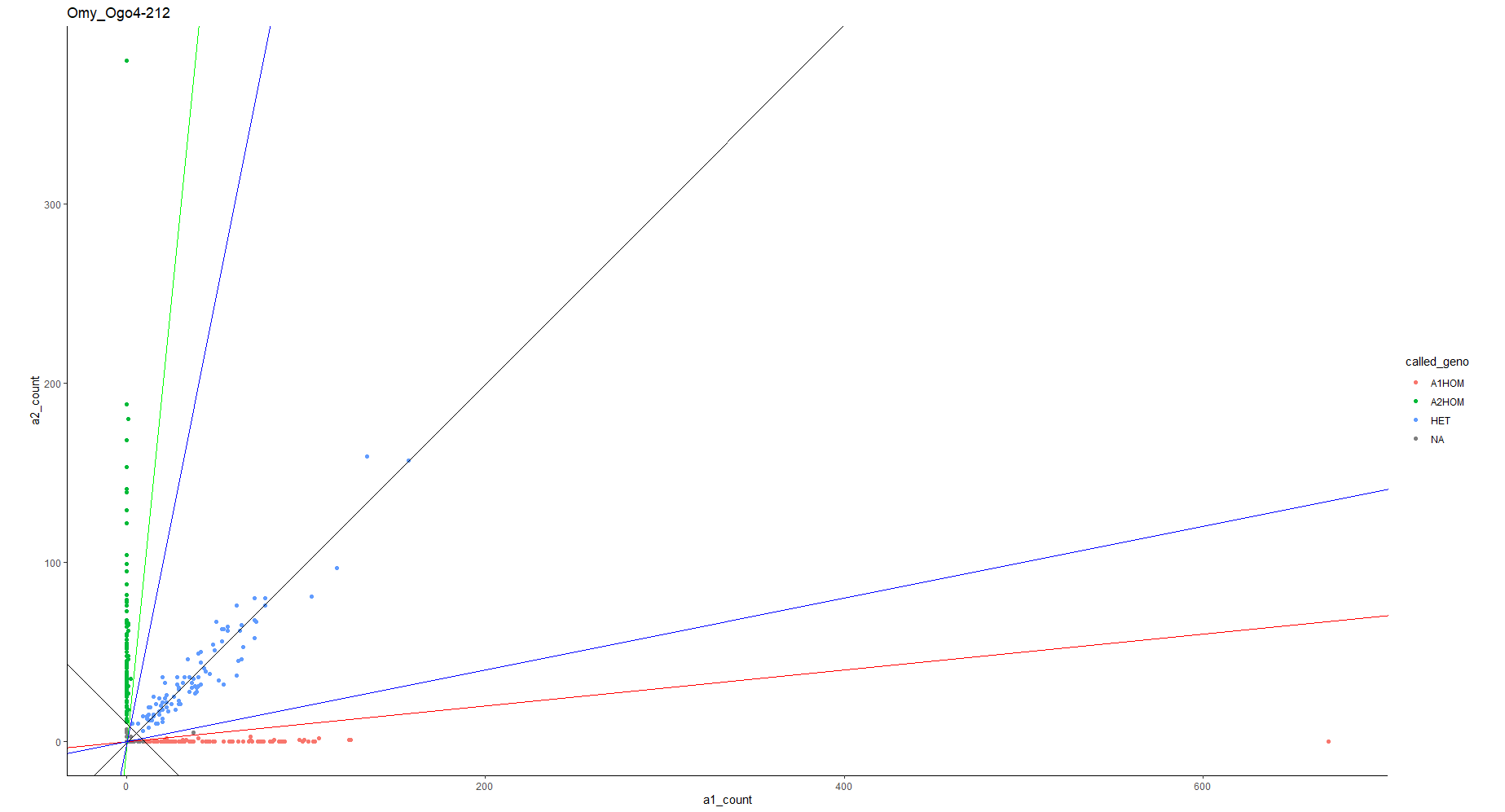
Kept:

Omy\_118205-116

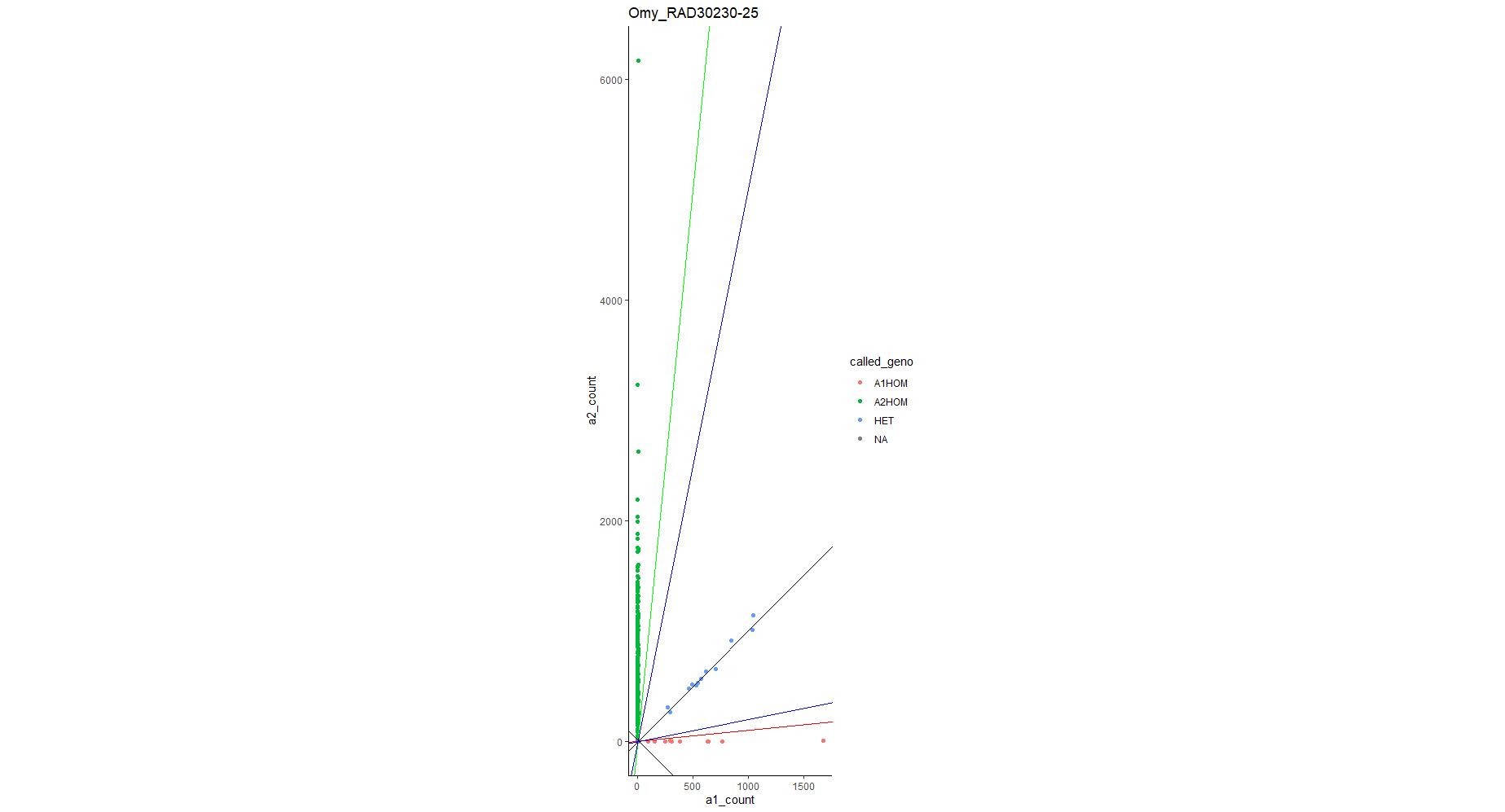
A graph of lines and numbers

Description automatically generated

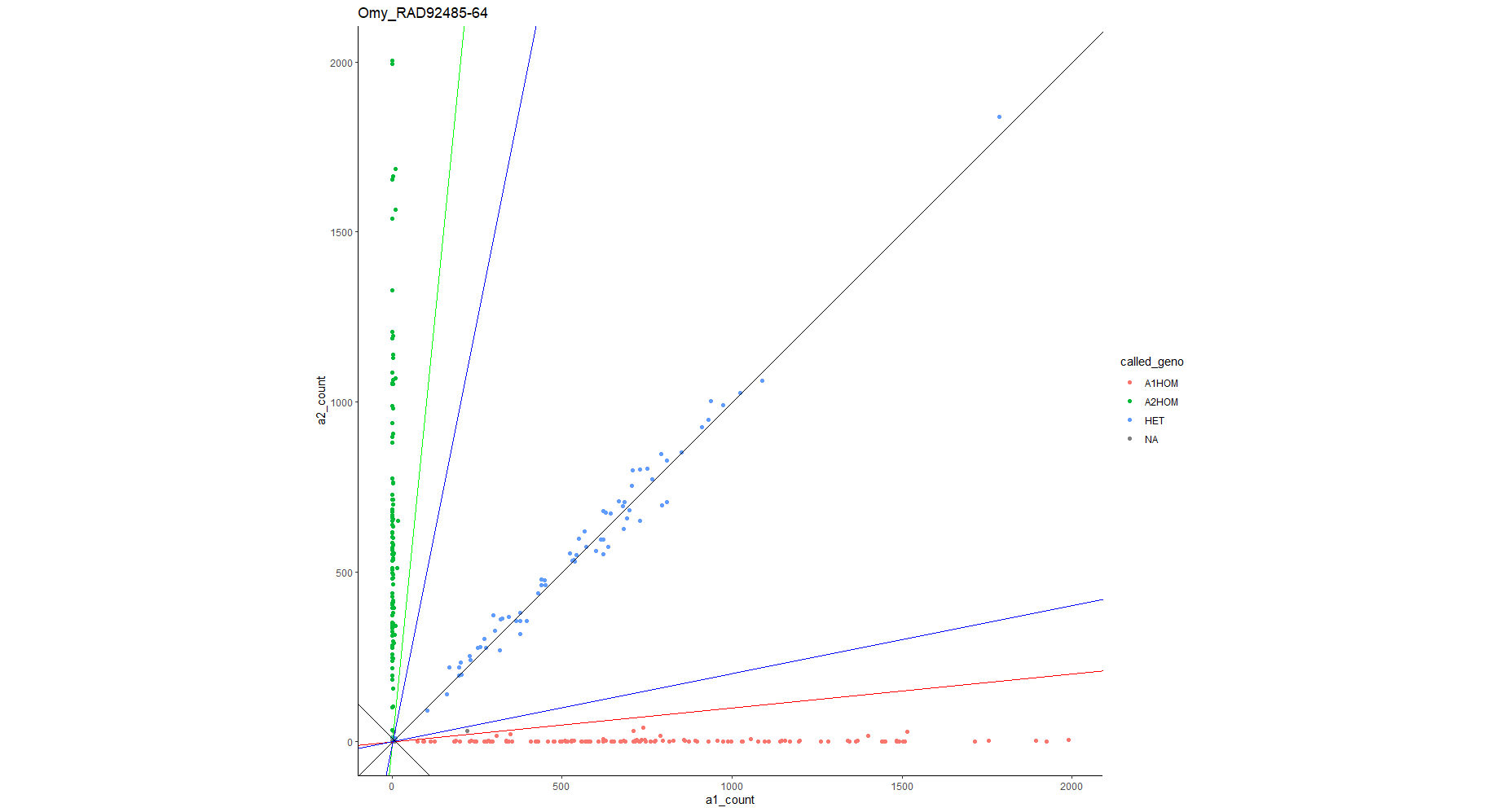
Omy\_Ogo4-212



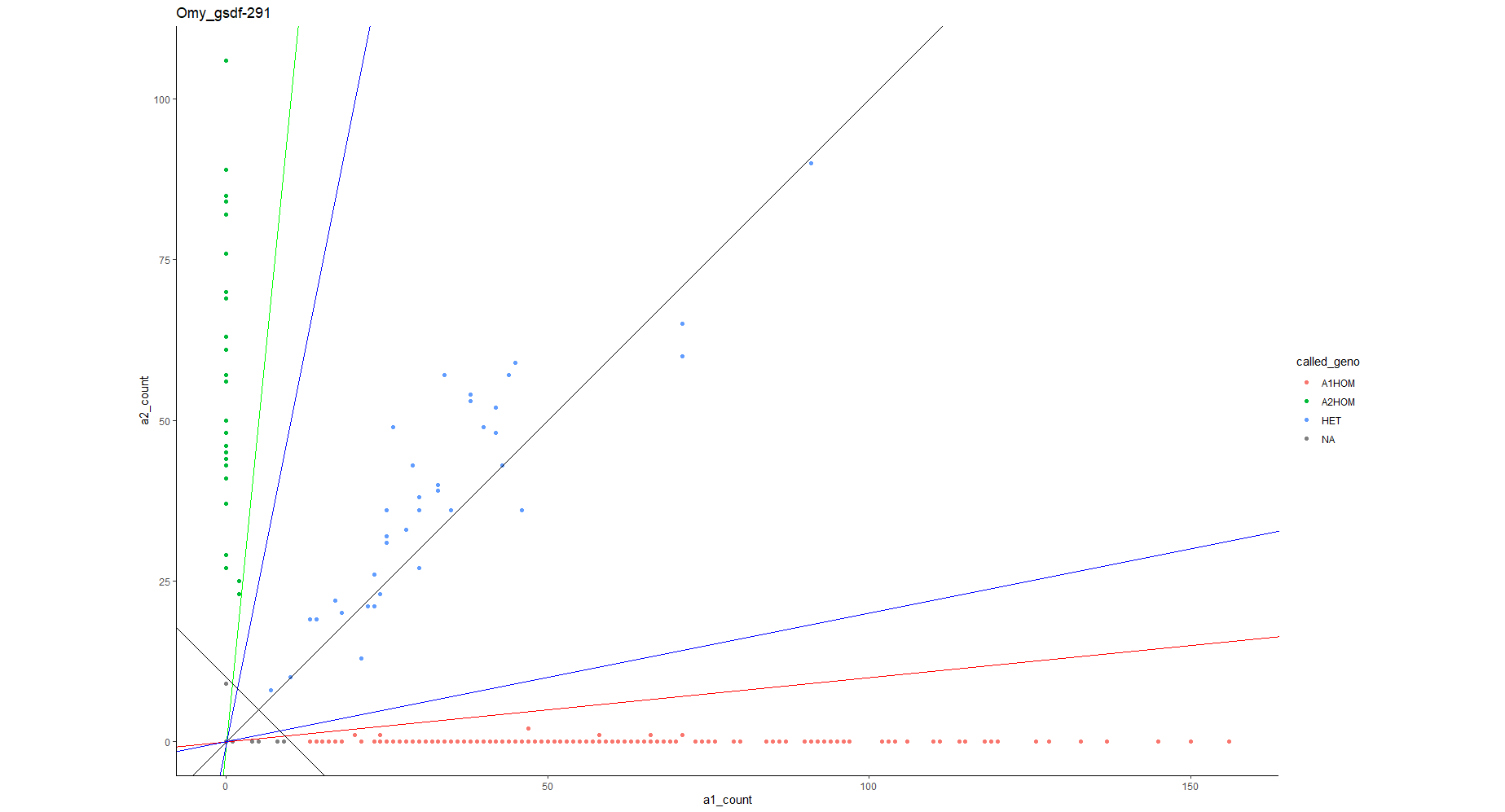
Omy\_RAD30230-25



Omy\_RAD92485-64



Omy\_gsdf-291



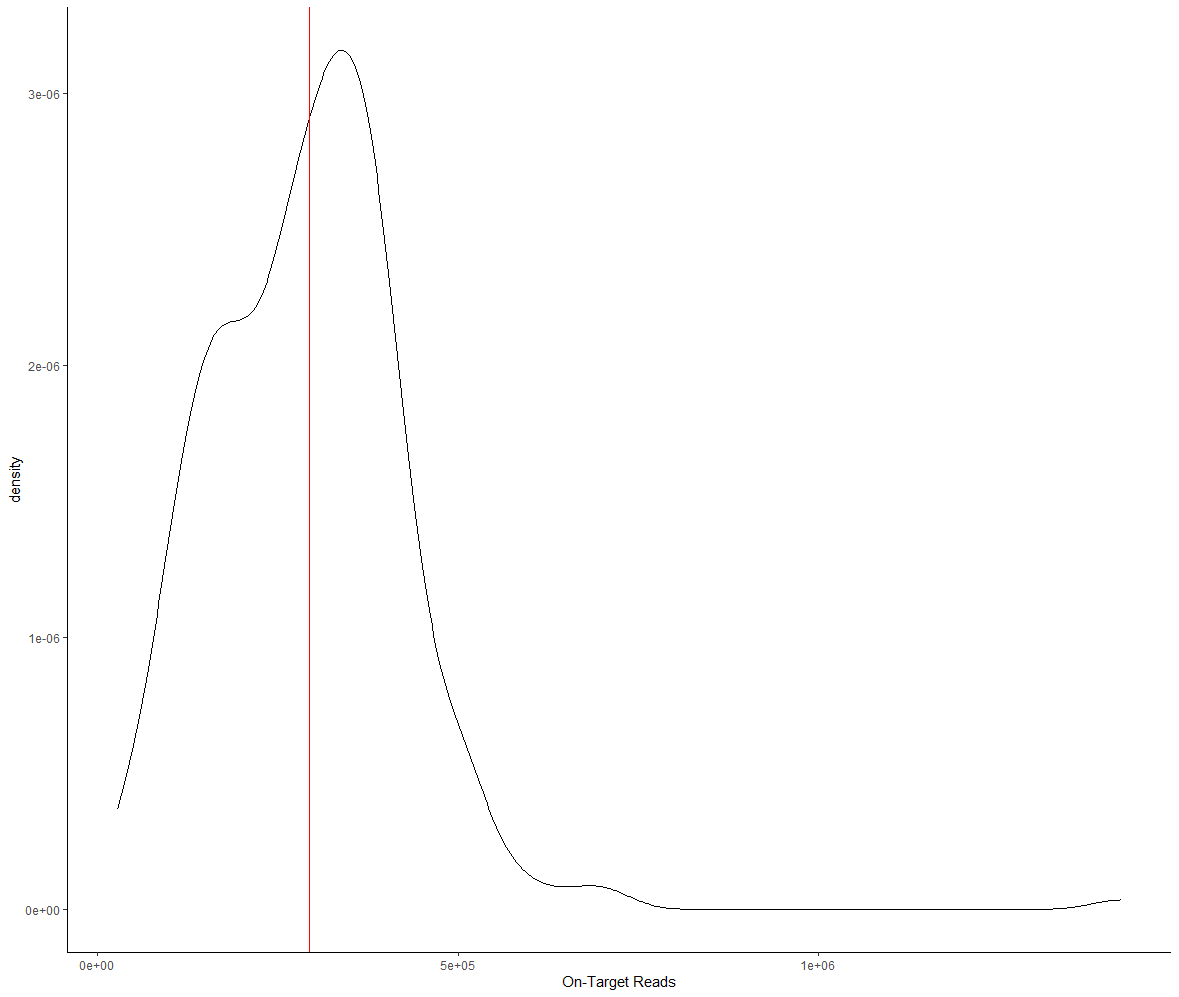
Dataset now has 291 individuals genotyped at 375 loci and a sex marker.

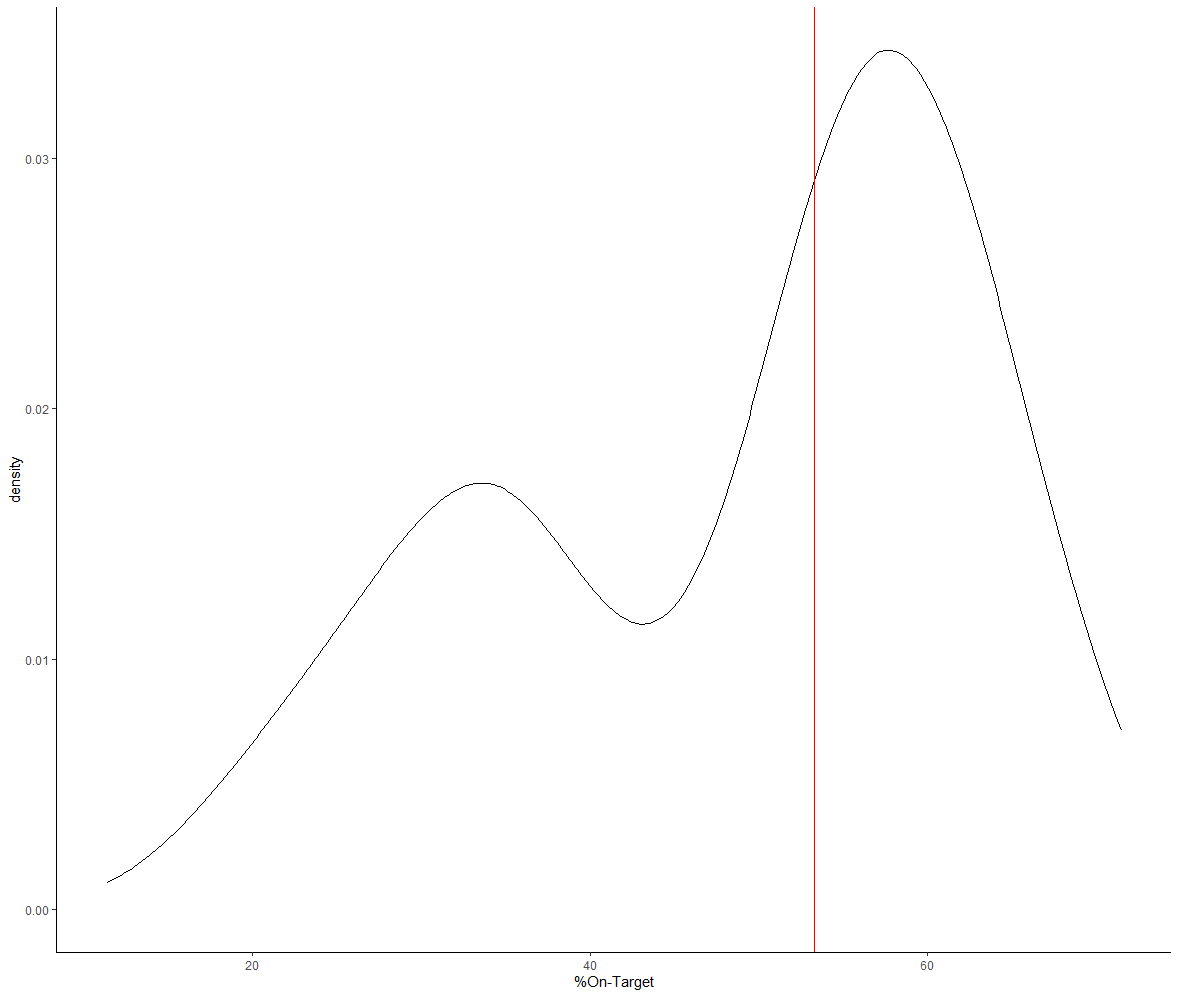
Removed remaining monomorphic markers.

Dataset now has 291 individuals genotyped at 350 loci and a sex marker.

Range in genetic distance among samples 59-219. Thus, no duplicates.

**Summary Stats**



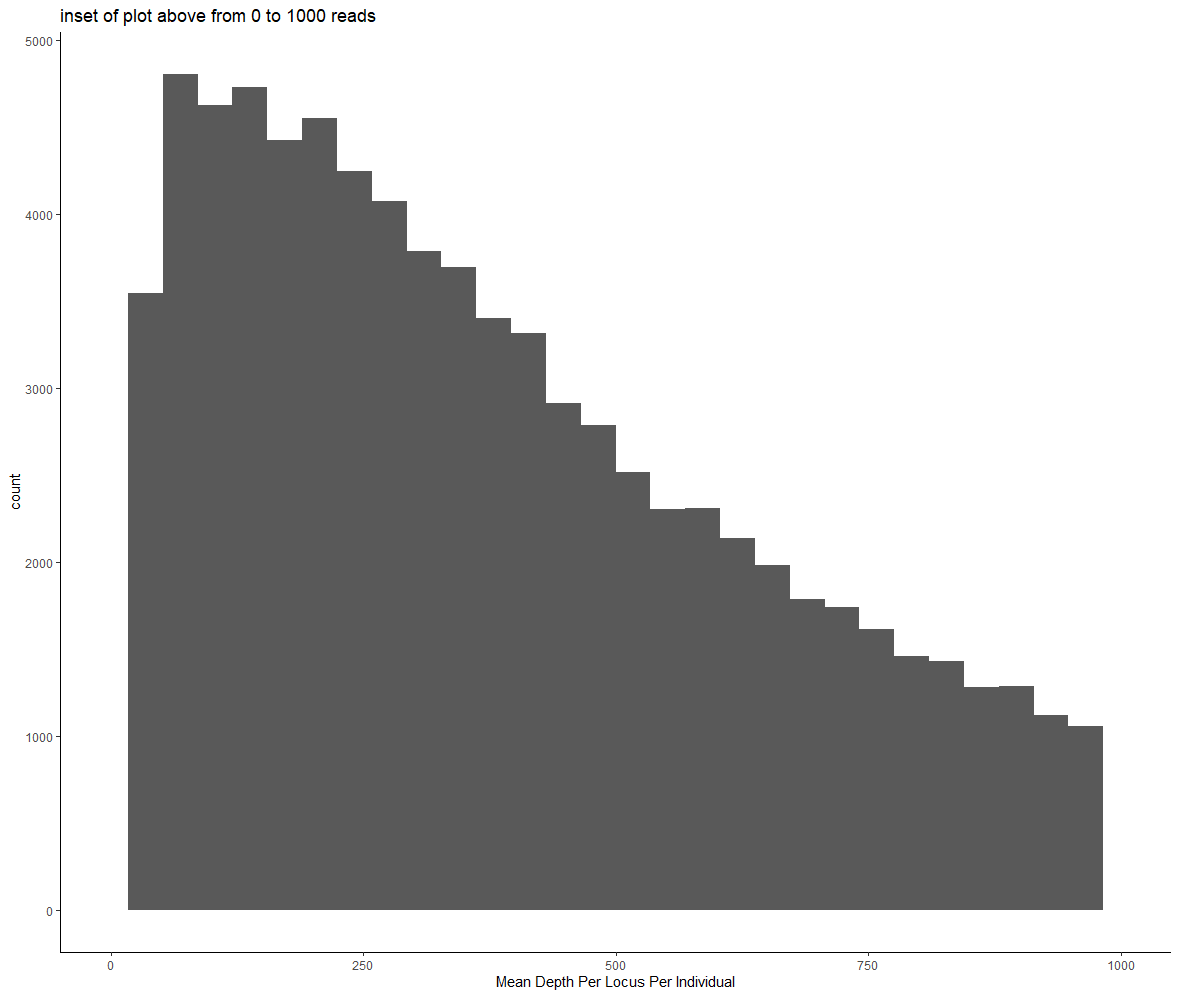


Looks good.

Sequencing depth:

Mean = 752; median = 443; sd = 1048

Good coverage, although quite variable.



Looks good.