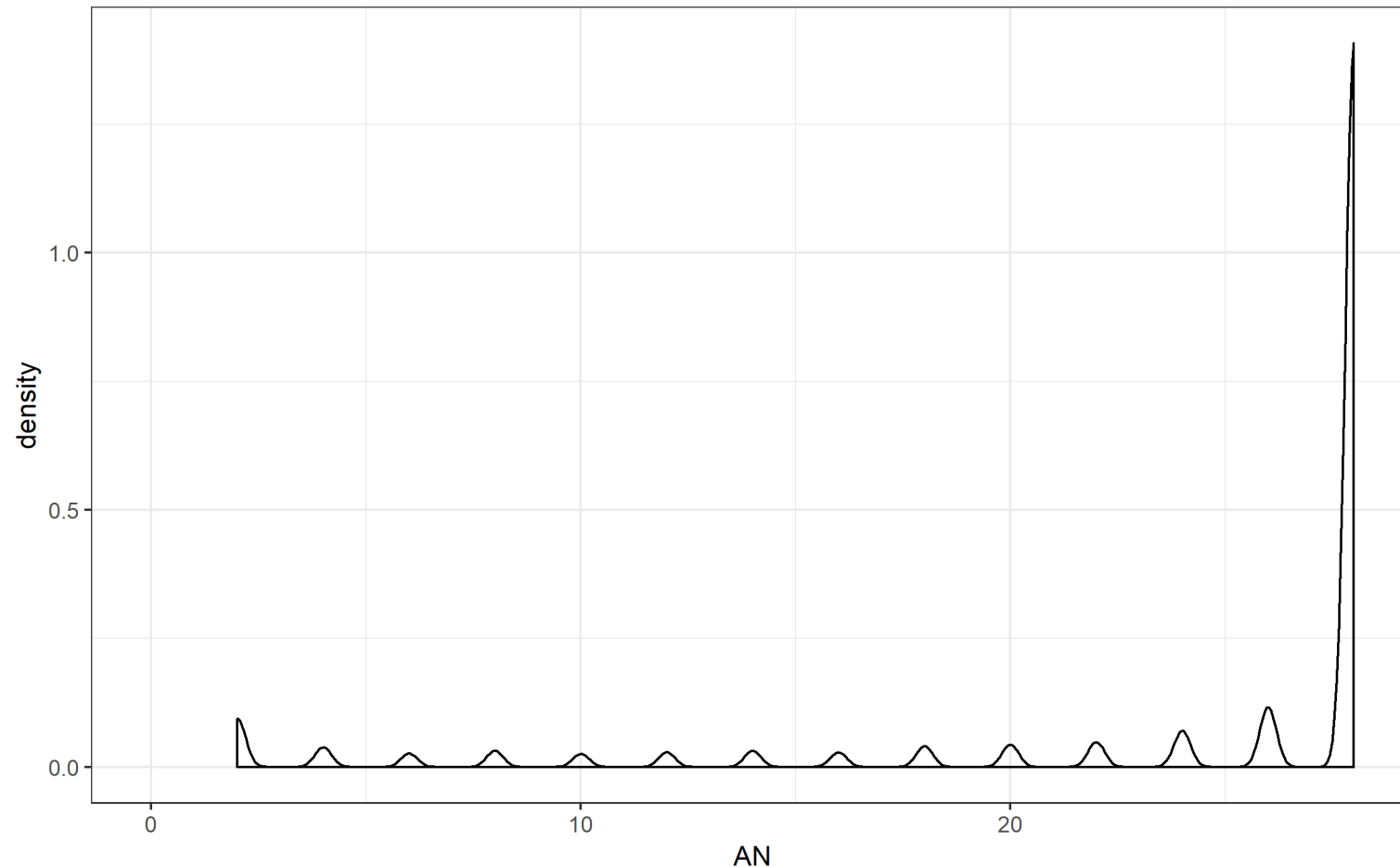


Hard-filter of Cayo exome data on chrX

Number of alleles that are genotyped AN

- There are 14 exomes → the maximum AN is 28, which means that a variant is genotyped across all 14 exomes

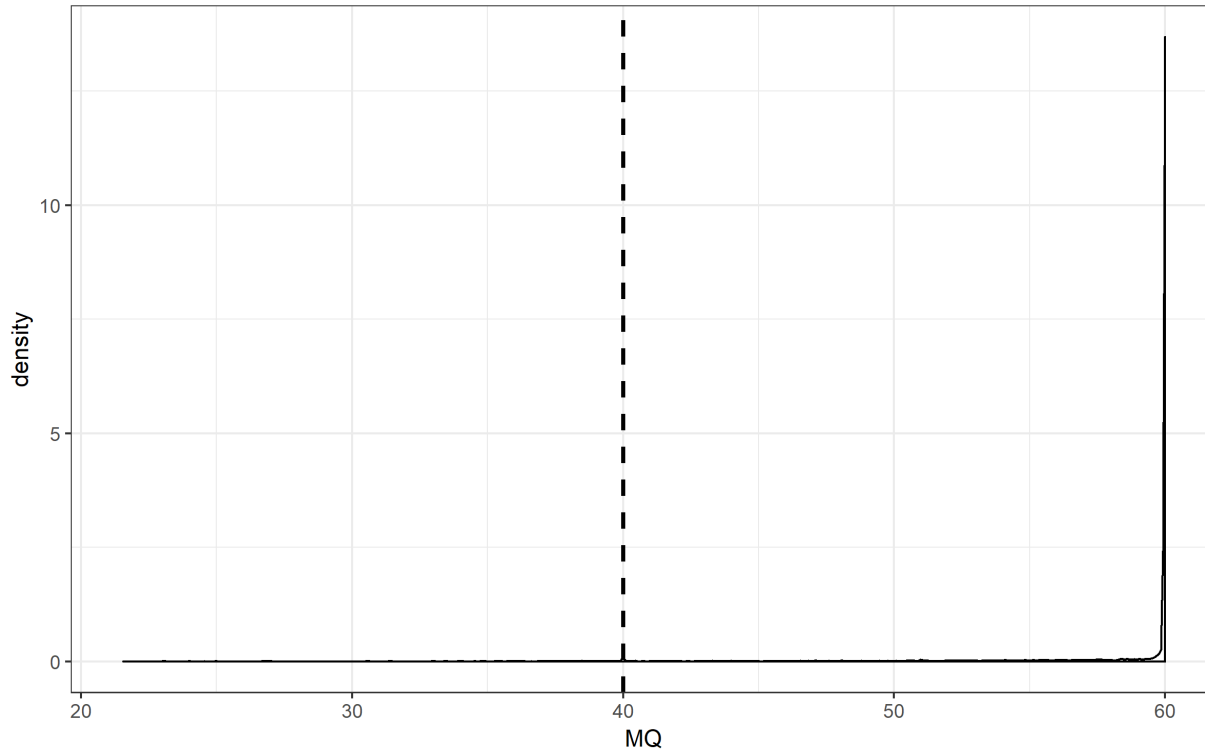


Investigating AN

		Number of variants (total = 16,299)
AN \geq 2	Called in 1 (out of 14) exomes or more	16,299
AN \geq 4	Called in 2 (out of 14) exomes or more	15,540
AN \geq 6	Called in 3 (out of 14) exomes or more	15,232
AN \geq 8	Called in 4 (out of 14) exomes or more	15,023
AN \geq 10	Called in 5 (out of 14) exomes or more	14,769
AN \geq 12	Called in 6 (out of 14) exomes or more	14,563
AN \geq 14	Called in 7 (out of 14) exomes or more	14,336
AN \geq 16	Called in 8 (out of 14) exomes or more	14,085
AN \geq 18	Called in 9 (out of 14) exomes or more	13,859
AN \geq 20	Called in 10 (out of 14) exomes or more	13,535
AN \geq 22	Called in 11 (out of 14) exomes or more	13,184
AN \geq 24	Called in 12 (out of 14) exomes or more	12,795
AN \geq 26	Called in 13 (out of 14) exomes or more	12,232
AN = 28	Called in 14 (out of 14) exomes	11,298

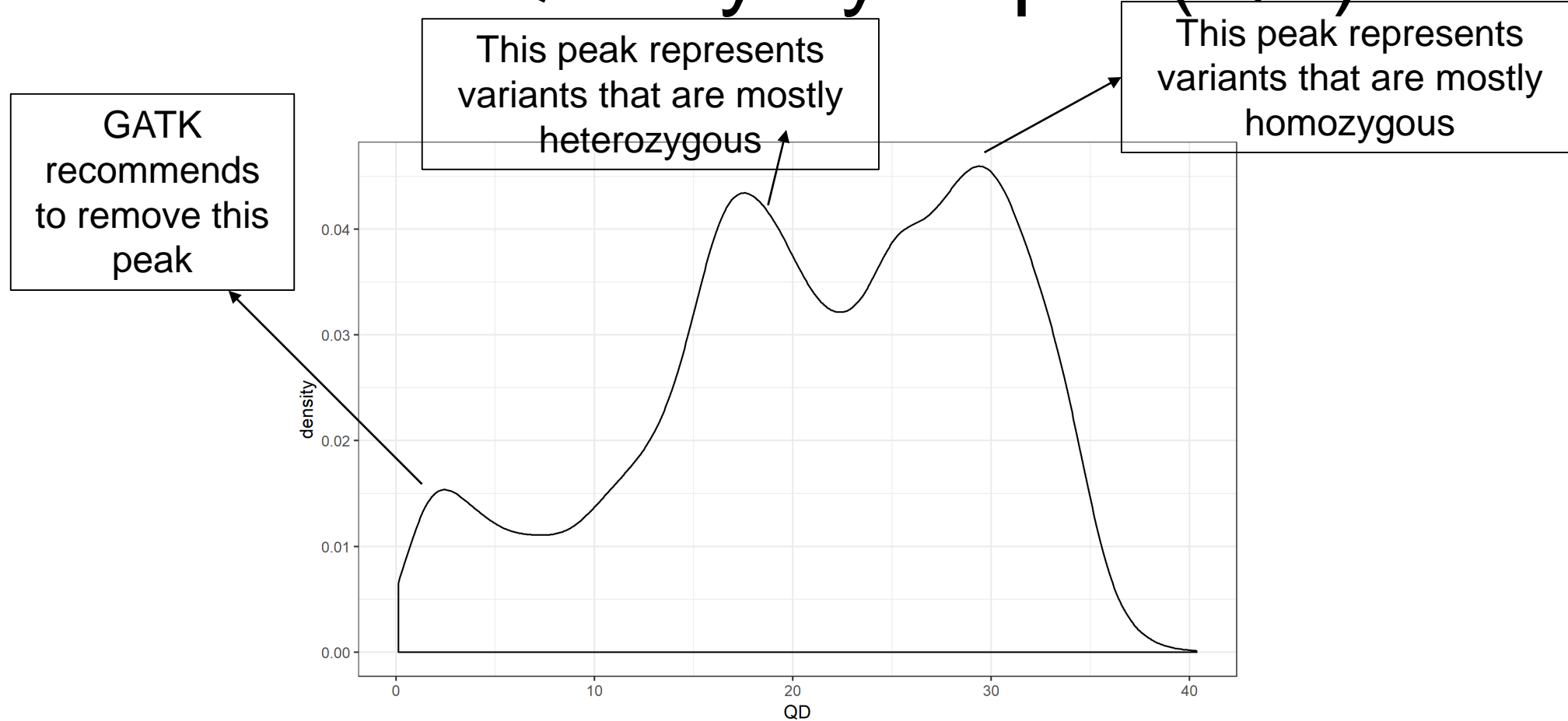
RMSMapping quality (MQ)

- From GATK: “This is the root mean square mapping quality over all the reads at the site. Instead of the average mapping quality of the site, this annotation gives the square root of the average of the squares of the mapping qualities at the site.” and “When the mapping qualities are good at a site, the MQ will be around 60.”



- GATK’s hard-filter suggests to remove variants with $MQ < 40$
- 15,740 out of 16,299 variants with $MQ > 40$

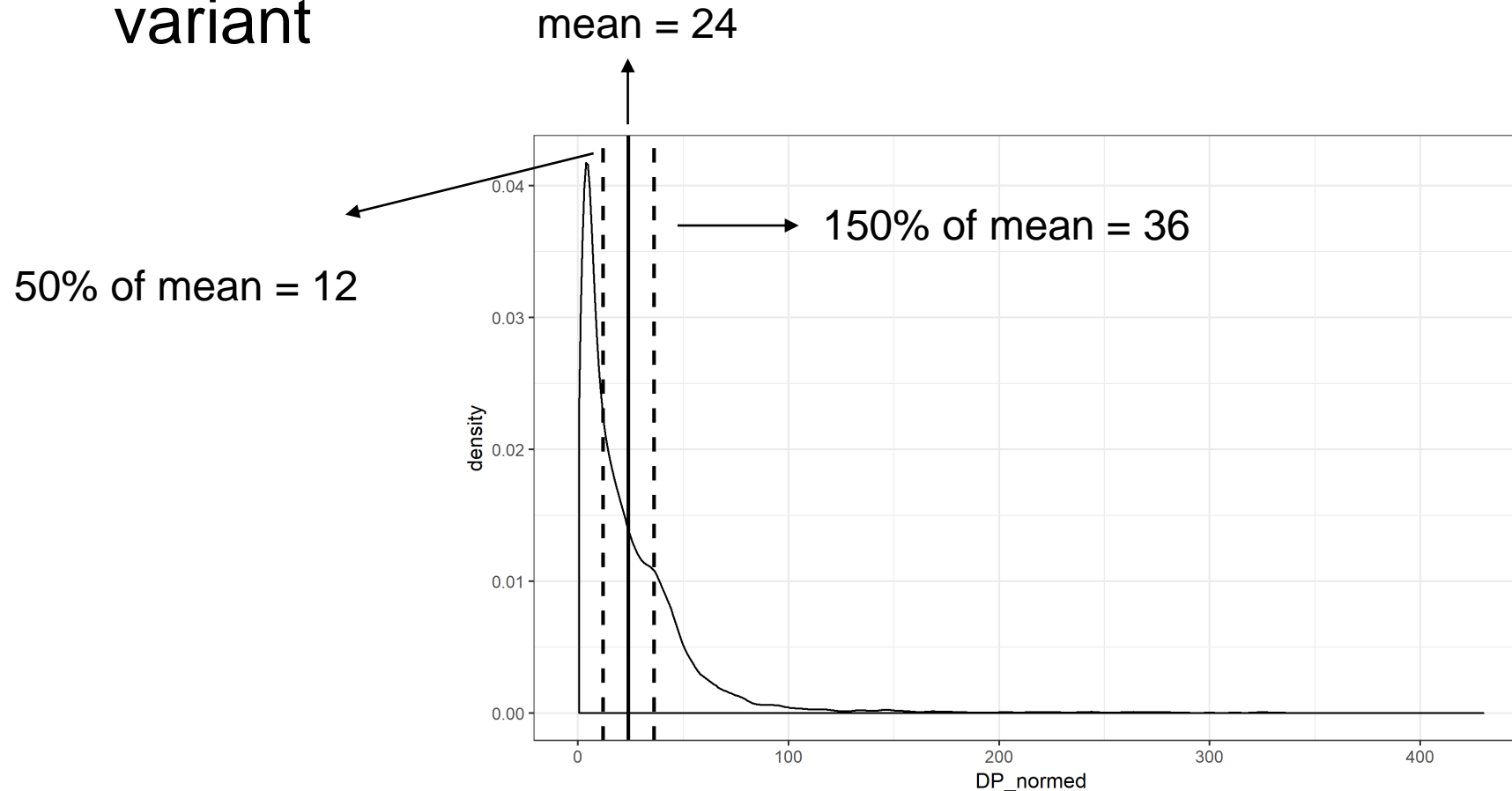
Quality by depth (QD)



- Use QD threshold of 5
- There are 15,152 out of 16,299 variants with $QD > 5$

Total depth of coverage over all sample (DP)

- DP from the INFO field from VCF file is summed across all samples. To get the mean, I divided DP by (AN/2) for that variant



Investigating DP

	Number of variants
0-25X	10,613
25-50X	3,979
50-100X	1,366
100-150X	185
150-200X	63
200-250X	43
250-300X	32
300-350X	15
350-400X	2
>400X	1