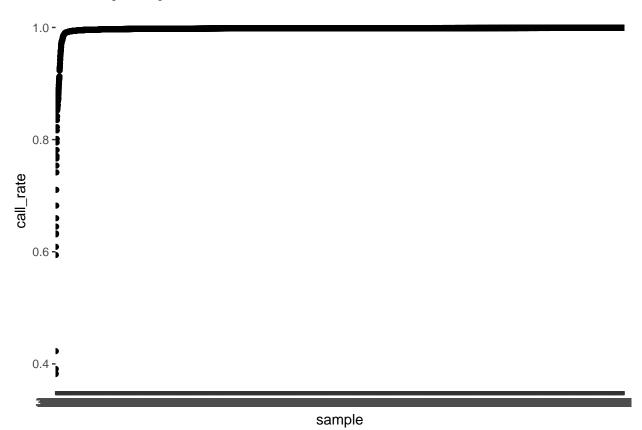
R Notebook

Rotterdam2 pre-QC

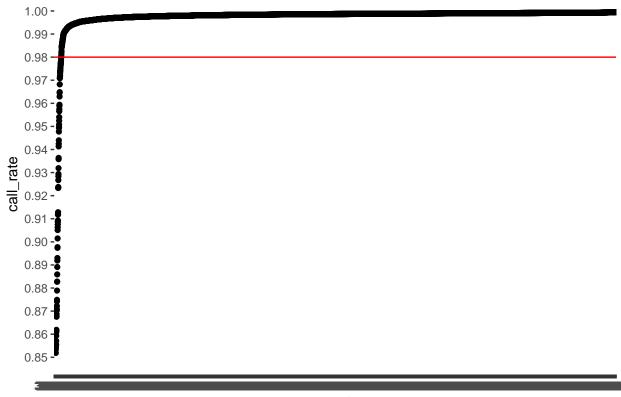
Initial quality assessment of dataset clustered by $\ensuremath{\mathsf{HUGE}\text{-}\mathsf{F}}$ in Rotterdam.

Call rate

Overall call rate per sample.



Warning: Removed 24 rows containing missing values (geom_point).

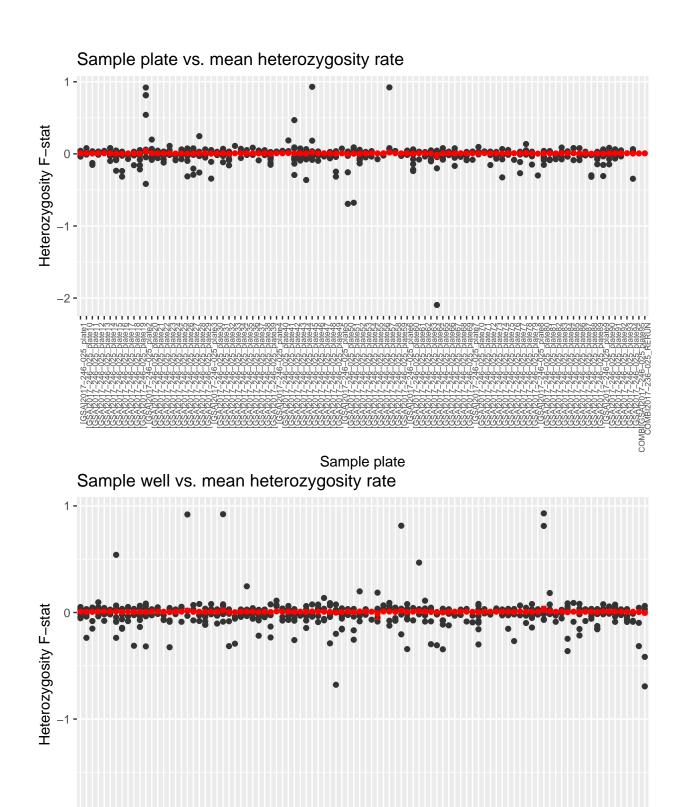


Call rate	N
(0,0.8]	18
(0.8, 0.9]	35
(0.9, 0.95]	24
(0.95, 0.96]	8
(0.96, 0.97]	4
(0.97, 0.98]	23
(0.98, 0.99]	39
(0.99, 0.995]	232
(0.995,1]	8658

Heterozygosity

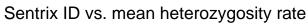
Mean heterozygosity per:

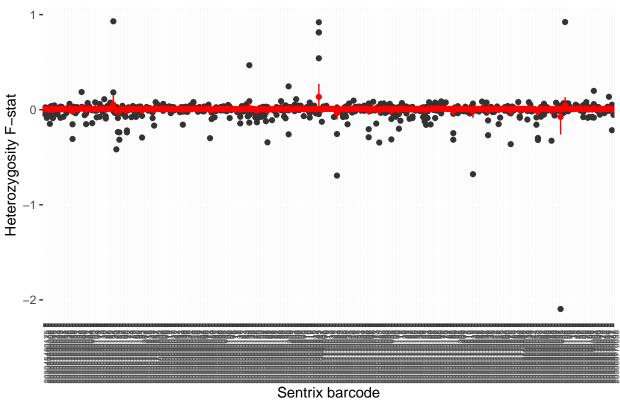
- Sample plate
- Sample well
- Sentrix Barcode/ID
- Sentrix position



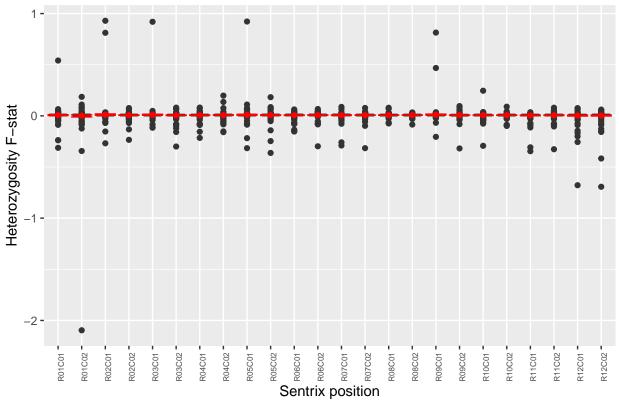
Sample well

-2 **-**





Sentrix position vs. mean heterozygosity rate

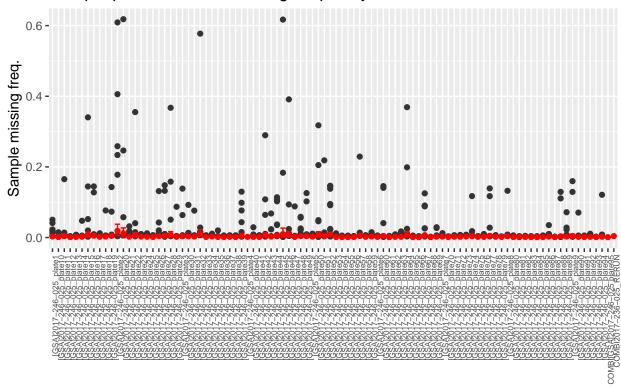


Call rate

Mean call rate per:

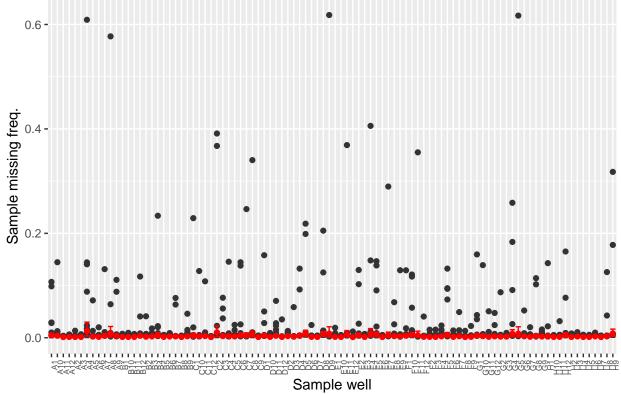
- Sample plate
- Sample well
- Sentrix Barcode/ID
- Sentrix position

Sample plate vs. mean missing frequency

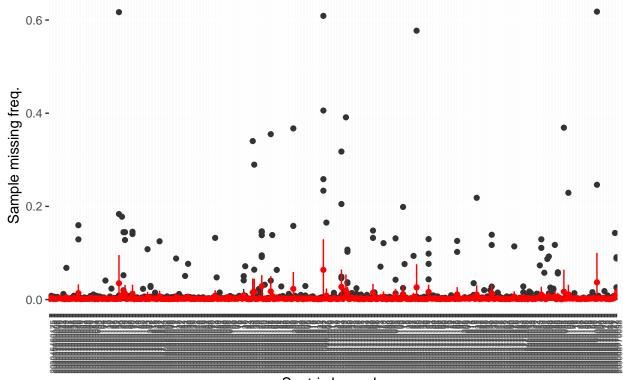


Sample plate

Sample well vs. mean missing frequency

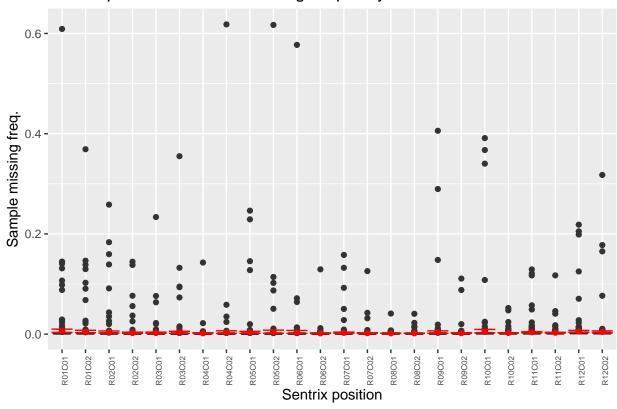


Sentrix ID vs. mean missing frequency



Sentrix barcode

Sentrix position vs. mean missing frequency



Call rate vs. heterozygosity

Plots showing relationship between call rate and heterozygosity F-stat. Higher missingness yields more heterozygous calls.

