No statistical evidence for an effect of CCR5-Δ32 on lifespan in the UK Biobank cohort

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Abstract

A recent study reported that a 32-base-pair deletion in the *CCR5* gene (CCR5-Δ32) is deleterious in the homozygous state in humans. Evidence for this came from a survival analysis in the UK Biobank cohort, and from deviations from Hardy-Weinberg equilibrium at a polymorphism tagging the deletion (rs62625034). Here, we carry out a joint analysis of whole-genome genotyping data and whole-exome sequencing data from the UK Biobank, which reveals that technical artifacts are a more plausible cause for deviations from Hardy-Weinberg equilibrium at this polymorphism. Specifically, we find that individuals homozygous for the deletion in the sequencing data are underrepresented in the genotyping data due to an elevated rate of missing data at rs62625034, possibly because the probe for this SNP overlaps with the Δ32 deletion. Another variant which has a higher concordance with the deletion in the sequencing data shows no associations with mortality. A phenome-wide scan for effects of variants tagging this deletion shows an overall inflation of association p-values, but identifies only one trait at $p < 5 \times 10^{-8}$, and no mediators for an effect on mortality. These analyses show that the original reports of a recessive deleterious effect of CCR5-Δ32 are affected by a technical artifact, and that a closer investigation of the same data provides no positive evidence for an effect on lifespan.

Introduction

CCR5-Δ32 is a deletion in the coding region of the *CCR5* gene which has been reported to confer resistance against HIV infections in individuals carrying two copies of the deletion (Δ32/Δ32)[1,2,3]. Some studies have suggested that the relatively high frequency of this variant in some populations points to a selective advantage conferred by this deletion[4,5], although the case for natural selection at this variant has also been challenged[6,7]. After the announcement of the birth of two babies whose genomes were edited using CRISPR in order to knock out the *CCR5* gene, additional concerns arose about potential negative effects of this mutation[1,8].

A recent study by Wei and Nielsen investigated potential deleterious effects in homozygous carriers of this mutation using the UK Biobank data[9]. The study found that a single nucleotide polymorphism (SNP) that tags the CCR5-Δ32 deletion (rs62625034) is less common in its homozygous state than expected under Hardy-Weinberg equilibrium (HWE). The study also reported a significantly increased mortality rate in homozygous carriers of this deletion, implying that deleterious effects of this variant, rather than technical artifacts, might be the reason for the deviation from HWE. These findings have been questioned in online discussions, in particular by S. Harrison who focused on whether rs62625034 is indeed a good proxy of the CCR5-Δ32 deletion[10]. The recent release of exome sequencing data on around 10% of the UK Biobank samples makes it possible to directly test how well the CCR5-Δ32 deletion is tagged by rs62625034 and by other nearby variants. By jointly analyzing the whole genome genotyping data and whole exome sequencing data we find that deviations from HWE in the genotyping data likely are due to technical artifacts. Moreover, when testing for associations of variants in the CCR5-Δ32 deletion region to other phenotypes we do not find effects of a magnitude that could explain a strongly increased mortality in Δ32/Δ32 individuals.

Methods

Markers tagging CCR5-Δ32

Genotype data in the UK Biobank is available in three different forms: (1) Allele counts as inferred from the genotyping array intensity values; (2) Imputed genotype dosages which are commonly rounded to best guess allele count integer values, which are based on the array data genotype calls but for many variants are not equal to the array data genotype calls; and (3) Whole exome sequencing data, currently for a pilot sample of around 10% of the total sample size. Two different pipelines were used to call variants from the read data. Here we only use the variant calls from the GATK pipeline.

We analyse five variants in total, two from the array data, two imputed and one sequenced (Supplementary Table 1):

rs62625034_genotyped: This is the genotyped variant which has been used as a proxy for the CCR5-Δ32 deletion in Wei and Nielsen[9].

rs113010081_genotyped: A genotyped variant in close proximity to the CCR5-Δ32 deletion.

rs113010081_imputed: The imputed data for the same variant.

3:46414943_TACAGTCAGTATCAATTCTGGAAGAATTTCCAG_T: The CCR5-Δ32 deletion as called in the imputed data. For brevity, we refer to it as **rs333_imputed**, even though this rs ID is not used in the raw data.

3:46373452:D:32: The CCR5-Δ32 deletion as called in the exome sequencing data. rs62625034 is not present among the set of imputed SNPs. We refer to it as **rs333_sequenced**, even though this rs ID is not used in the raw data.

It cannot be assumed that any of the analyzed variants perfectly tags the CCR5-Δ32 deletion. We treated the direct exome sequencing data on CCR5-Δ32 variant itself as the ground truth, and then assess the accuracy of the genotype array variants by comparing them to the exome sequencing variant. We evaluate the concordance between these variants by comparing the counts in each genotype class (0, 1, 2) and computing linkage disequilibrium (r^2). In addition, since the questions of interest relate to the effect of the Δ32/Δ32 genotype and we are uninterested for this analysis in misclassification errors between the other two genotypes, we also computed sensitivity and specificity of correctly identifying individuals with two copies of the deletion in the exome sequencing data.

As population heterogeneity can induce deviations from HWE, we limit all of our analyses to individuals classified as “white British” in the UK Biobank. In order to be consistent with Wei and Nielsen[9,11], we do not exclude related individuals for the results shown here, though our results remain qualitatively the same when excluding related individuals. We compute approximate HWE p-values using a Chi-squared test. However, different data sets have different average deviations from HWE due to the Wahlund-effect and differences in genotype calling data and algorithms. For this reason, Wei and Nielsen[9,11] used genomic control methods to compute HWE deviations. We follow this protocol[11] and report two additional sets of HWE p-values. Specifically, we compute HWE p-values by comparing to a set of frequency matched control SNPs (P1), and by using the bootstrap to test for significant deviations from the median value in the genomic control SNPs (P2)[11]. The latter test was argued to be the preferred test as it provides some protection against outliers[11], which is why it is included here. Each of these methods tests a different null hypothesis, resulting in different p-values.

Survival rate analysis

To study the effect on survival rates, we extend the phenotypic association analysis by exploring the effects of all variants tagging the CCR5-Δ32 deletion on all phenotypes available to us.

For each of the variants, we assess the impact on mortality as previously described in Wei and Nielsen[9,11]. We use five different UK Biobank variables - age at recruitment (ID 21022), Date of attending assessment centre (ID 53), year of birth (ID 34), month of birth (ID 52), and the age at death (ID 40007) - to compute the number of individuals who are ascertained from age i to age i + 1 (N_i), and the occurrence of death observed from these N_i individuals during the interval of age i to age i + 1 (O_i). The death rate per year is calculated separately for each Δ32 genotype class as $h_i = O_i/N_i$ and the probability of surviving to age i + 1, $S_i = \prod_{n=1}^{n=i} h_n$. h_{77} is grouped together with h_{76}.

To compute p-values for the survival rate analysis, we run Cox proportional hazard models using the 'coxph' function in the R-package 'survival'. We do not use binning into age groups, as described in the previous paragraph, for this analysis. Instead we use only age at recruitment and reported age at death or, if no age at death is reported, the inferred age at time t, where t is the date of the last reported age at death in the entire cohort (16 February 2016).

We estimate power to detect effects on mortality rate in the following way. First, we extract for each sample age at death, or, if age at death has not been reported, the inferred age at time t, where t is the date of the last reported death in the entire cohort (16 February 2016). Next, we randomly draw a genotype (0 or 1) for each person from a Bernoulli distribution with a probability that depends on whether or not this person has died, in proportion to a given relative risk (RR). For individuals who have died, this probability is P(G=1|D) = P(D|G=1) * P(G=1) / P(D), where P(G=1) is the frequency of Δ32/Δ32 (0.012), P(D) is the fraction of samples with a reported age at death (0.029), and P(D|G=1) = RR * P(D|G=0) = RR * P(D) / (P(G=1)*RR + (1-P(G=1))). Similarly, for individuals who are still alive, this probability is P(G=1|A) = P(A|G=1) * P(G=1) / P(A), where P(A) = 1 - P(D) and P(A|G=1) = 1 - P(D|G=1). We then obtain a p-value from a Cox proportional hazard model for each random draw, repeat this 100 times for 11 different RR values, and compute the fraction of random draws with p-value smaller than 0.05 at each value of RR.

Associations with other phenotypes in the UK Biobank

If a genetic variant has a substantial effect on early mortality then that effect is likely to act through specific phenotypes. We therefore tested whether Δ32/Δ32 individuals were at higher risk for 3,331 diseases or disorders than Δ32/+ and +/+ individuals. We tested each of the five variants for associations with 3,911 phenotypes in the UK Biobank. We used the following logistic regression model: $y \sim x_{01,2} + c$. Here, y is a vector of phenotypes; $x_{01,2}$ is the vector of

genotypes, recoded so that each sample with zero or one copy of the deletion is 0 and each sample with two copies of the deletion is 1; and c is a set of covariates, including age, sex, genotyping array, and PC 1 to PC 20, calculated on a set of European individuals[12]. We similarly tested an additional 580 continuous phenotypes using a linear regression model.

We further conducted Poisson tests to check whether any ICD10 diagnosis codes were overrepresented as the reported cause of death in Δ32/Δ32 compared to all other individuals.

Results

Concordance rates across variants

Figure 1, Supplementary Figures 1 and 2, and Supplementary Tables 2, 3, and 4 show concordance rates, r^2, and sensitivity and specificity of the genotyped variants and the exome sequencing variant. These analyses suggest that rs113010081_genotyped is a better proxy for the CCR5-Δ32 deletion than rs62625034_genotyped.

While rs113010081_genotyped has a higher r^2 with rs333_sequenced than rs62625034_genotyped (0.977 compared to 0.968, Supplementary Table 3), these r^2 values are mostly influenced by the concordance of the more common genotypes Δ32/+ and +/+. As we are specifically interested in Δ32/Δ32 individuals and for the purpose of the present analysis are not concerned by misclassification of the two other much more common genotypes, we also computed sensitivity and specificity based on a comparison of Δ32/Δ32 individuals to the union of Δ32/+ and +/+ individuals. The sensitivity and specificity to correctly identify individuals with Δ32/Δ32 in the WES data is 0.934 and 0.998 for rs62625034_genotyped, and 0.998 and 1 for rs113010081_genotyped, suggesting that rs113010081_genotyped more accurately tags Δ32/Δ32 individuals (Supplementary Table 4). As an example of the substantially better performance, out of all individuals identified as Δ32/Δ32 by the WES data, 11.4% are classified as Δ32/+ at rs62625034_genotyped, compared to 3.3% at rs113010081_genotyped (Figure 1).

rs113010081_genotyped was not used by Wei and Nielsen[9,11] due to its relatively high rate of missing data in the overall dataset. However, detailed examination reveals that the high missingness rate (10.3%) is due to the absence of this variant from the UK BiLEVE Axiom array. This array was used to genotype the first ~ 50,000 genotyped samples in the UK Biobank. On the UK Biobank Axiom array, which was used for the remaining ~450,000 samples, this variant has a missingess rate of 0.08%, while rs62625034_genotyped has a missingness rate of 3.6%, and hence for the individuals for whom we have a genotype at this variant, there are likely to be fewer technical artifacts due to miscalling bias, and indeed, when we examined the scatterplots used for genotype calling at the two variants we confirm crisper separation of the genotype classes for rs113010081_genotyped than for rs62625034_genotyped (Figure 1). Supplementary Table 2 shows conditional genotype counts for all individuals, as well as for only those individuals genotyped on the UK Biobank Axiom array. We observed differences in missingness

between the two array types, but no differences in genotype counts. Other Supplementary Tables only show results from both arrays, as these numbers change very little when restricting to samples genotyped on the UK Biobank Axiom array.

In this work, we do not focus on the imputed variants, as they do not tag the Δ32 deletion as well as the genotyped variants. In addition, Supplementary Table 10 shows that imputation quality differs by genotype at rs11301008_imputed.

Hardy-Weinberg disequilibrium

We confirm that rs62625034_genotyped shows a highly significant deviation from HWE, caused by a deficiency of individuals with two copies of the rare (deletion tagging) allele (Supplementary Table 5). None of the other tested variants shows a significant deviation from HWE under a Chi-squared HWE test. For rs333_sequenced, the P2 p-value, which corrects for the Wahlund-effect, is 0.0276, similar to the previously reported value of 0.0272. However, the magnitude of the deviation is much smaller than for rs62625034_genotyped and the P1 value is not significant. We tested whether the reduced sample size in the exome sequencing data can explain why we do not see a similarly strong deviation from HWE at the sequenced variant. For this, we compute HWE for all variants also in the subset of samples for which we have exome sequencing data. We find that rs62625034_genotyped still has a HWE p-values of 6.1×10^{-9}, 0.0022, and < 0.0001, for Chi-squared, P1, and P2 tests, respectively. In the same subset of samples, the variants rs113010081_genotyped and rs333_sequenced show no deviations from HWE in a Chi-squared test, while P1 and P2 p-values are still nominally significant.

In comparing inferred genotypes from rs62625034_genotyped and rs333_sequenced, we noticed that 17.3% of individuals who were called as Δ32/Δ32 in rs333_sequenced have missing values for rs62625034_genotyped, while only 4.6% and 2.9% are missing for Δ32/+ and +/+, respectively (Figure 1). Correcting for this bias based on the empirically measured differences in missing data rate by genotype class fully explains the discrepancy between the sequencing data and the genotyping data, changing the proportion of homozygous minor alleles from 1.06% before correction to 1.38% after correction (Supplementary Tables 6). In contrast, individuals with missing data at rs113010081_genotyped are not similarly biased with respect to rs333_sequenced (Figure 1).

Figure 1 provides a plausible explanation for why rs62625034_genotyped exhibits higher missingness rates in individuals with the Δ32 deletion. The Affymetrix probe for rs62625034 is targeting a very rare G>T SNP which is located at the 3' end of the site of the Δ32 deletion. Since this variant is so rare, almost all of the called non-reference alleles indicate the presence of the Δ32 deletion, which at its 3' end closely resembles the targeted G>T SNP. Since the probe overlaps with the Δ32 deletion but matches it only imperfectly, Δ32 individuals have a higher missingess rate. In contrast, the probe for rs113010081 is 42 kb away from Δ32 and

suffers from no such problems. In conclusion, rs62625034_genotyped is a biased proxy for Δ32/Δ32, while rs113010081_genotyped shows far less evidence of bias.

We carried out a simulation study to test whether increased mortality or other negative ascertainment on Δ32/Δ32 individuals can plausibly create a highly significant HWE deviation at this deletion, but no HWE deviation at a SNP with an r^2 of 0.95 relative to the deletion. We find that ascertainment on one variant induces similarly high deviations from HWE at other variants in high LD (Supplementary Figure 3). Thus, if one variant shows a high degree of deviation from the null expectation of HWE, and another variant in high linkage disequilibrium with it shows no significant deviation from HWE, it is highly likely that a technical artifact is affecting the genotyping of at least one of the variants.

Survival rate analysis

Confirming the findings of Wei and Nielsen[9,11], we find that for rs62625034_genotyped, carriers of two copies of the rare allele tend to have a lower survival rate (Figure 1, Supplementary Figure 1, and Supplementary Table 7). We obtain a one-sided p-value from a Cox proportional hazard model of 0.009. However, none of the other tested variants shows any association with survival rate. The fact that the highly correlated rs113010081_genotyped SNP has a p-value of 0.156 when applying the same test, and the small number of deaths per year on which the signal is based (Figure 1) make this finding uncompelling. The power to detect a 20% increased mortality rate at this SNP at a 0.05 significance level is only 75% (Supplementary Figure 4), which means that we cannot rule out that the deletion does affect survival based on this analysis.

Interestingly, we find that samples with missing genotypes at rs113010081_genotyped show greatly increased mortality rates (p-value 2.7×10^{-32}). This is a genotyping batch effect: rs113010081_genotyped is absent from the UK BiLEVE Axiom array, and the individuals who were genotyped on this array were ascertained to be smokers and to be on either tail of the FEV1 distribution. This association disappears when restricting to individuals genotyped on the UK Biobank Axiom array. The same sample restriction does not explain the increased mortality rate seen for two carriers of the rare allele in rs62625034_genotyped (though the p-value increases to 0.016), but this example cautions against reporting associations between variants from the array data and mortality without controlling for possible genotyping array batch effects. We have only observed these batch effects in the array data, but not in the imputed data. Further, we only observed differences in missingness rates between the two array types, but no differences in the relative proportion of called genotypes.

Associations with other phenotypes in the UK Biobank

CCR5-Δ32 is reported to confer HIV resistance only in the presence of two copies of the deletion, and similarly, effects on mortality have also only been reported in the presence of two copies of the deletion. Despite this, for a wide range of phenotypes, only association tests of the additive effect of CCR5-Δ32 have been reported. We therefore tested whether any phenotypes are significantly different in frequency between Δ32/Δ32 individuals and all others (Δ32/+ and +/+). We tested the five variants for associations with 3,911 phenotypes and identify no traits which are significant at a p-value smaller than the classic threshold for declaring genome-wide statistical significance $5x10^{-8}$. However, it can be argued that the genome-wide significance threshold is much too stringent, since we only test the effect at one locus. When we instead apply Bonferroni multiple testing correction for 3,911 tested phenotypes, we do find phenotypes which are associated with a p-value smaller than $1.27x10^{-5}$ (< 0.05 after Bonferroni correction for 3,911 phenotypes) (Supplementary Table 8, Supplementary Figures 5 and 6). For rs113010081_genotyped, these are “Lymphocyte count” and “Mean sphered cell volume”. The association results for the other variants are similar, and since we think that rs113010081_genotyped most accurately tags Δ32, we focus on the association results for rs113010081_genotyped. The associated phenotypes are similar to the previously reported results from additive association tests and are consistent with CCR5’s role in the immune system. These results suggest that Δ32/Δ32 does have effects besides conferring resistance to HIV. We do not observe effects on any diseases which are large enough to explain a substantially increased mortality rate. However, the phenotype “Overall health rating” is associated with rs113010081_genotyped at a nominal p-value of $5.22x10^{-3}$. On average, Δ32/Δ32 individuals are 7% more likely to rate their health as “poor” or “fair” compared to other individuals (Supplementary Table 9). We also obtain p-values of $4.47x10^{-3}$ and $5.74x10^{-3}$ for two collections of diagnosis codes described as “Certain infectious and parasitic diseases”[13]. Given that Δ32/Δ32 has previously been reported to be a risk factor for symptomatic West Nile virus infection[14], this is noteworthy. We single out results for these phenotypes because they relate to previously reported effects of Δ32/Δ32, but we highlight that we tested almost 4,000 phenotypes. Many other phenotypes with more significant nominal p-values seem unrelated to any relevant health outcomes, and most of these associations are likely due to chance. Despite the large overall sample size, many phenotypes are rare, which further limits the power to detect effects of a genotype present in only 1% of the population at a reasonable significance level.

In analyzing the causes of death, we find no ICD10 codes which are overrepresented in Δ32/Δ32 individuals compared to all others, but similar power considerations apply here.

Discussion

Artificially knocking out a gene in human embryos without fully understanding its function is dangerous, especially as genes that serve no function are unlikely to survive evolutionary pressures. It seems very plausible therefore that there are negative consequences of having no

functional copy of the *CCR5* gene. However, our analysis in the UK Biobank of more markers tagging Δ32/Δ32 individuals does not provide statistical confirmation that Δ32/Δ32 individuals have shorter lifespans than other people. Additionally, in testing associations with a wide range of phenotypes we do find weak effects on a handful of traits, but none that suggest a 20% increased mortality rate.

Deviations from HWE can be due to causal genetic effects on mortality or on other phenotypes which lead to survival biases. However, technical artifacts are a much more common cause for deviations from HWE. Our analysis suggests that the rs113010081_genotyped variant tags the Δ32 deletion as least as well as rs62625034_genotyped, without showing any evidence of HWE deviation. The HWE deviation observed at this SNP is, therefore, almost certainly caused by a higher missingess rate at Δ32/Δ32 individuals. Thus, deviations from HWE at rs62625034_genotyped cannot be interpreted as evidence for a deleterious effect of the Δ32/Δ32 genotype.

Beyond the specific explorations into the phenotypic effects of the CCR5-Δ32/Δ32 genotype, this study highlights the delicacy of association analysis. Specifically, it provides a case example of the subtle pitfalls - in this case related to biased missing data patterns - that can produce false-positive results, even in an extraordinarily high quality and relatively uniformly generated dataset like the UK Biobank. Our re-examination of previously published results was inspired by S. Harrison's identification of qualitatively inconsistent findings between two variants in strong linkage disequilibrium with each other[10] which we replicated and further explored here.

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Author contributions

R.M., A.A. performed analyses all except for the one presented in Supplementary Table 10, which was carried out by X.W. N.P., R.N., and D.R. supervised the study. R.M., A.A., and D.R. wrote the manuscript with critical review from all co-authors.

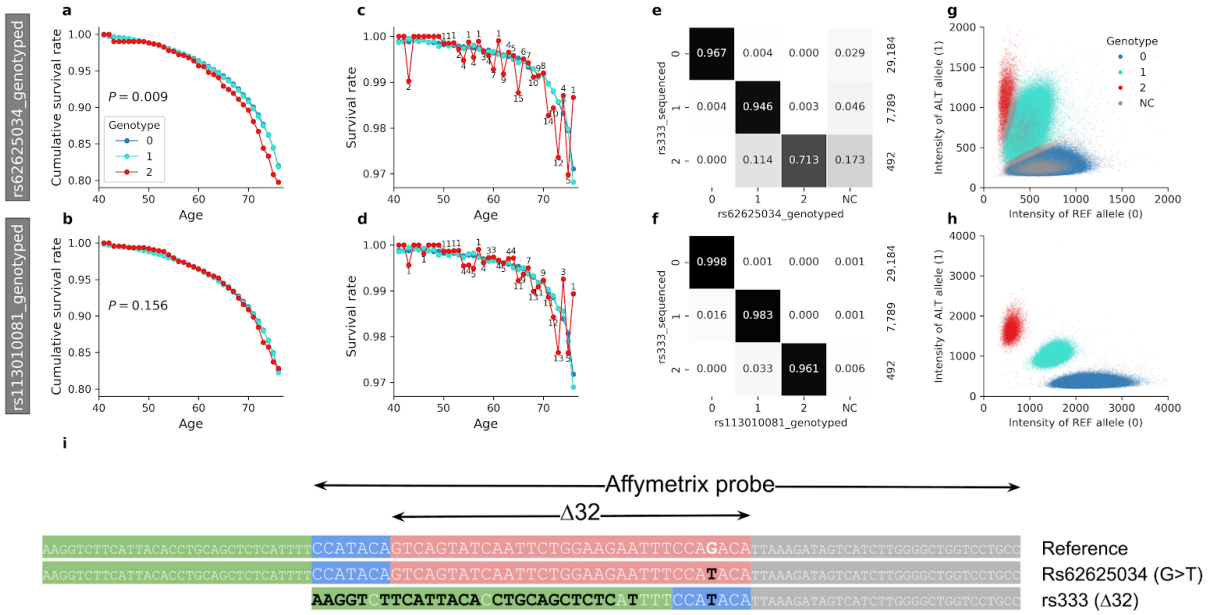

Figure 1: Survival rates for individuals with 0, 1, and 2 copies of the rare allele for two variants tagging the CCR5-Δ32 deletion, rs62625034_genotyped (first row) and rs113010081_genotyped (second row). **a, b**, Cumulative survival rates show that the evidence for increased mortality of individuals homozygous for the variant allele in rs62625034_genotyped does not replicate in rs113010081_genotyped. One-sided p-values are from a Cox proportional hazard model which compares survival rates of individuals with 0 or 1 alleles to those with 2 alleles. **c, d**, non-cumulative survival rates, which show the large year-to-year variability in the data caused by small sample counts. Numbers indicate the absolute number of Δ32/Δ32 individuals who have died in each year. **e, f**, Distribution of genotypes at the two variants (including missing genotypes) conditioned on rs333_sequenced genotypes. The total count for each row is on the right. Missing data is strongly correlated to genotype class for rs62625034_genotyped which fully explains the deviation from Hardy-Weinberg Equilibrium at this site. No such bias is present at rs113010081_genotyped. Numbers are based only on samples genotyped on the UK Biobank Axiom array, as rs113010081_genotyped data is only available for this array **g, h,** Allele intensity clusters for UK Biobank genotyping data, showing the poorer separation of genotype classes for rs62625034_genotyped compared to rs113010081_genotyped. **i**, Different haplotypes at the CCR5-Δ32 locus. Black nucleotides differ from the reference. The site of the very rare SNP rs62625034 (G>T) is located within the Δ32 deletion. Due to the sequence similarity at the 3' end, the probe tags the deletion instead. However, the rs62625034 probes match the reference genotype better than the deletion, leading to higher missingness in the presence of the deletion.

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Supplementary Tables and Figures

Variant	type	GRCh37 position	alleles	non-missing	MAF
rs62625034	genotyped	46414975	T/G	395,656	0.116
rs113010081	genotyped	46457412	C/T	364,602	0.118
rs113010081	imputed	46457412	C/T	408,911	0.119
3:46414943_TACAGTCAGTATCAATTCTGGAAGAATTTCCAG_T (rs333)	imputed	46414943	T/TACAGTCAGTATCAATTCTGGAAGAATTTCCAG	408,897	0.106
3:46373452:D:32 (rs333)	sequenced	46414943	T/TACAGTCAGTATCAATTCTGGAAGAATTTCCAG	41,059	0.117

Supplementary Table 1: Variants tagging the CCR5-Δ32 deletion.

Variant	Allele count non-sequenced	Allele count sequenced (rs333_sequenced) All samples			Allele count sequenced (rs333_sequenced) Only UK Biobank Axiom array		
		0	1	2	0	1	2
rs62625034_genotyped	0	30984	35	0	28212	33	0
rs62625034_genotyped	1	129	8094	66	120	7370	56
rs62625034_genotyped	2	0	27	380	0	25	351
rs62625034_genotyped	NA	872	381	91	852	361	85
rs113010081_genotyped	0	29127	126	0	29127	126	0
rs113010081_genotyped	1	34	7658	16	34	7658	16
rs113010081_genotyped	2	0	1	473	0	1	473
rs113010081_genotyped	NA	2824	752	48	23	4	3
rs113010081_imputed	0	31671	279	0	28901	257	0
rs113010081_imputed	1	246	8200	37	217	7480	34
rs113010081_imputed	2	NA	42	500	0	37	458
rs113010081_imputed	NA	68	16	0	66	15	0
rs333_imputed	0	31696	1150	5	28918	1032	5
rs333_imputed	1	221	7347	156	200	6720	146
rs333_imputed	2	0	24	375	0	22	340
rs333_imputed	NA	68	16	1	66	15	1

Supplementary Table 2: Cross-tabulation of allele counts for genotyped variants tagging the CCR5-Δ32 deletion against the variant in the exome sequenced data.

Variant	rs333_sequenced	rs62625034_genotyped	rs113010081_genotyped	rs113010081_imputed
rs62625034_genotyped	0.968			
rs113010081_genotyped	0.977	0.946		
rs113010081_imputed	0.930	0.900	0.950	
rs333_imputed	0.818	0.789	0.808	0.803

Supplementary Table 3: r^2 between variants the CCR5-Δ32 deletion.

Variant	P	N	TP	TN	Sensitivity (TP/P)	Specificity (TN/N)
rs62625034_genotyped	407	39308	380	39242	0.934	0.998
rs113010081_genotyped	474	36961	473	36945	0.998	1.000
rs113010081_imputed	542	40433	500	40396	0.923	0.999
rs333_imputed	399	40575	375	40414	0.940	0.996

Supplementary Table 4: Sensitivity and specificity of genotyped variants to correctly identify samples with two copies of the CCR5-Δ32 deletion in the exome sequencing data.

	Chi-squared HWE p-values		P1 and P2 p-values (genomic control corrected)	
Variant	**All samples**	**Samples with WES data**	**All samples**	**Samples with WES data**
rs333_sequenced	0.22 (537, 562)	0.22 (537, 562)	N/A	0.0764, 0.0276
rs62625034_genotyped	4.8e-51 (4348, 5317)	6.1e-09 (421, 540)	0.0032, < 0.0001	0.0022, < 0.0001
rs113010081_genotyped	0.36 (4979, 5036)	0.23 (496, 520)	0.0941, 0.0023	0.0242, 0.0326
rs113010081_imputed	0.78 (5759, 5778)	0.48 (565, 580)	N/A	N/A
rs333_imputed	1.4e-05 (4301, 4563)	0.02 (416, 461)	N/A	N/A

Supplementary Table 5: HWE p-values for variants tagging the CCR5-Δ32 deletion. In brackets: observed and expected number of samples with two copies of the rare allele.

Variant	Observation from Genotyping data					Corrected Values			
	GT = 0	GT = 1	GT = 2	GT = NC	HWE *P*	GT = 0	GT = 1	GT = 2	HWE *P*
rs62625034_genotyped	308,274	83,034	4,348	13,989	4.8E-51	318,295	85,683	5,668	0.25
rs113010081_genotyped	283,877	75,746	4,979	45,043	0.36	318,088	85,835	5,722	0.43
rs113010081_imputed	317,457	85,695	5,759	734	0.78	317,764	86,194	5,687	0.07
rs333_imputed	326,808	77,788	4,301	748	1.4E-05	318,142	85,831	5,672	0.17

Supplementary Table 6: Correcting for bias can explain the extreme p-value for the violation of HWE for rs62625034_genotyped. Unbiased genotype counts is the expected number of true genotypes conditioned on observations in the genotyping array data (including missing genotypes). Conditional distribution is estimated by the joint distribution of genotyping array and UK Biobank WES data. UK Biobank WES data is considered as the ground truth. This table includes all white British samples in the UK Biobank.

Variant	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76
rs333_sequenced	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	0	1	0	0	0	0	0	0	2	0	1	2	0	0	0	1	1	0	1	0
rs62625034_genotyped	0	0	2	0	0	0	0	0	0	1	1	1	2	4	1	4	1	3	4	7	1	9	4	5	15	6	7	10	9	8	14	10	12	4	5	1
rs113010081_genotyped	0	0	1	0	0	1	0	0	0	1	1	1	1	4	4	5	1	4	3	3	4	5	4	4	11	9	7	13	11	9	11	12	13	3	5	1
rs113010081_imputed	0	0	2	0	0	1	0	0	1	1	1	1	1	4	3	6	1	4	3	7	4	6	4	5	16	9	11	14	11	16	14	13	13	4	6	1
rs333_imputed	0	0	1	0	0	0	0	0	1	1	0	1	1	3	3	5	2	2	3	7	3	3	4	4	9	9	5	10	10	10	10	10	10	5	6	1

Supplementary Table 7: Number of samples in who have died grouped by variant and age. Values correspond to the red dots in the third row of Supplementary Figure 1.

Phenotype ID	beta	SE	p-value	type	count	type	description
30120	0.087	0.015	1.27E-08	continuous	4251	continuous_irnt	Lymphocyte count
30270	-0.074	0.015	1.65E-06	continuous	4188	continuous_irnt	Mean sphered cell volume
30180	0.066	0.015	1.75E-05	continuous	4251	continuous_irnt	Lymphocyte percentage
30260	-0.066	0.015	1.88E-05	continuous	4188	continuous_irnt	Mean reticulocyte volume
670_3	1.030	0.264	9.44E-05	binary	15	binary	Type of accommodation lived in: Mobile or temporary structure (i.e. caravan)
5119	0.129	0.034	1.29E-04	continuous	881	continuous_irnt	3mm cylindrical power (left)
30050	-0.057	0.015	1.65E-04	continuous	4257	continuous_irnt	Mean corpuscular haemoglobin
L12_HIDRADENITISSUP	1.554	0.422	2.32E-04	binary	6	categorical	Hidradenitis suppurativa
30040	-0.056	0.015	2.35E-04	continuous	4257	continuous_irnt	Mean corpuscular volume

30190	-0.050	0.015	7.72E-04	continuous	4251	continuous_irnt	Monocyte percentage
20003_1140868408	0.605	0.180	7.90E-04	binary	32	*NA*	*NA*
V_PREGNANCY_BIRTH	-0.364	0.111	1.01E-03	binary	111	*NA*	*NA*
30300	0.050	0.015	1.05E-03	continuous	4188	continuous_irnt	High light scatter reticulocyte count
102280	0.078	0.024	1.29E-03	continuous	618	ordinal	Milk chocolate intake
F5_SOMATOFORM	1.084	0.341	1.46E-03	binary	9	*NA*	*NA*
2744	-0.088	0.028	1.66E-03	continuous	1874	ordinal	Birth weight of first child
6149_1	0.149	0.047	1.67E-03	binary	512	binary	Mouth/teeth dental problems: Mouth ulcers
4294_9	1.309	0.420	1.85E-03	binary	6	binary	Final attempt correct: abandon
30010	0.041	0.013	1.92E-03	continuous	4257	continuous_irnt	Red blood cell (erythrocyte) count
L12_SCARCONDITIONS	0.562	0.182	2.06E-03	binary	31	categorical	Scar conditions and fibrosis of skin
20003_1140922174	-0.578	0.191	2.50E-03	binary	28	binary	Treatment/medication code: alendronate sodium
20003_1140852948	0.541	0.180	2.63E-03	binary	32	binary	Treatment/medication code: calcium+vitamin d 500units tablet
KRA_PSY_ANXIETY	0.623	0.207	2.67E-03	binary	24	categorical	Anxiety disorders
30250	0.046	0.015	2.71E-03	continuous	4188	continuous_irnt	Reticulocyte count
20003_1141169520	0.962	0.323	2.88E-03	binary	10	binary	Treatment/medication code: cosopt 2%/0.5% eye drops
30000	0.046	0.015	2.92E-03	continuous	4257	continuous_irnt	White blood cell (leukocyte) count
30200	-0.046	0.015	3.10E-03	continuous	4251	continuous_irnt	Neutrophill percentage
103990	-0.291	0.099	3.25E-03	binary	483	binary	Vegetable consumers
30220	-0.045	0.015	3.32E-03	continuous	4251	continuous_irnt	Basophill percentage
CHRONLARGE	0.946	0.322	3.32E-03	binary	10	categorical	Crohn's disease of large intestine
30290	0.045	0.016	3.62E-03	continuous	4188	continuous_irnt	High light scatter reticulocyte percentage
20003_1140865564	1.099	0.386	4.41E-03	binary	7	binary	Treatment/medication code: imodium 2mg capsule
AB1_INFECTIONS	0.269	0.095	4.47E-03	binary	117	categorical	Certain infectious and parasitic diseases
AB1_OTHER_VIRAL	0.577	0.203	4.49E-03	binary	25	categorical	Other viral diseases
2316	0.107	0.038	4.51E-03	binary	923	binary	Wheeze or whistling in the chest in last year
2030	-0.100	0.035	4.63E-03	binary	1131	binary	Guilty feelings
20002_1077	-0.892	0.317	4.97E-03	binary	10	binary	Non-cancer illness code, self-reported: heart arrhythmia
2178	0.031	0.011	5.23E-03	continuous	4365	ordinal	Overall health rating

I_INFECT_PARASIT	0.239	0.087	5.74E-03	binary	140	categorical	Certain infectious and parasitic diseases
X_EXTERNAL_MORB_MORT	0.885	0.322	5.97E-03	binary	10	*NA*	*NA*
L12_ATROPHICSKIN	0.478	0.174	6.10E-03	binary	34	categorical	Atrophic disorders of skin
20003_1140862438	1.142	0.417	6.22E-03	binary	6	binary	Treatment/medication code: uniphyllin continus 200mg m/r tablet
1628	0.031	0.012	6.53E-03	continuous	4050	ordinal	Alcohol intake versus 10 years previously
30670-0.0	0.056	0.021	7.33E-03	continuous	4175	*NA*	*NA*
41231_2	-0.313	0.119	8.53E-03	binary	93	*NA*	*NA*
22601_51112476	1.098	0.419	8.73E-03	binary	6	binary	Job coding: farmer, farming contractor, herd manager, smallholder, bailiff
20003_1140883504	0.324	0.124	9.12E-03	binary	67	binary	Treatment/medication code: cetirizine
CHRONNAS	0.640	0.246	9.31E-03	binary	17	categorical	Crohn's disease NAS
M13_SYNOTEND	0.275	0.106	9.70E-03	binary	92	categorical	Disorders of synovium and tendon
20002_1157	0.831	0.322	9.75E-03	binary	10	binary	Non-cancer illness code, self-reported: non-infective hepatitis
20003_1140916282	-0.978	0.379	9.82E-03	binary	7	binary	Treatment/medication code: venlafaxine
20002_1113	0.306	0.119	9.85E-03	binary	74	binary	Non-cancer illness code, self-reported: emphysema/chronic bronchitis

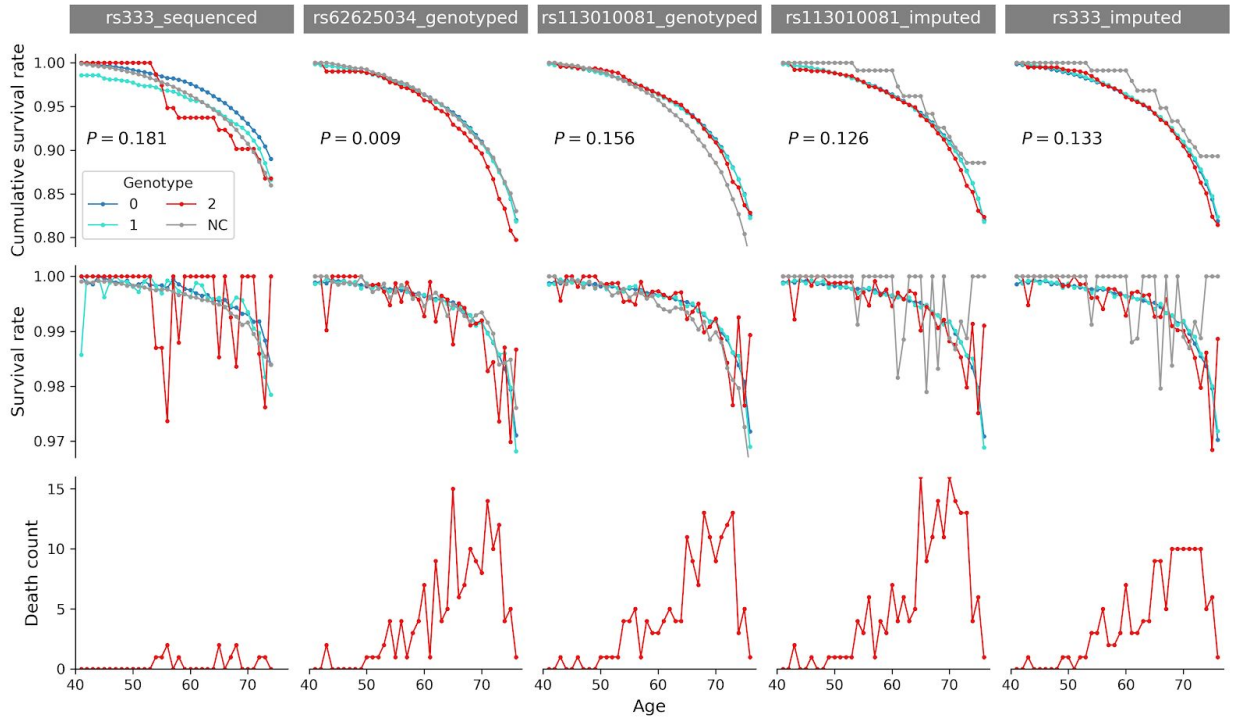
Supplementary Table 8: Association results for rs113010081_genotyped showing phenotypes with p-value < 0.01. Phenotypes with p-value < 1.27×10^{-5} are significant after Bonferroni correction for 3,911 phenotypes. The count column lists the number of Δ32/Δ32 individuals who are cases (for binary phenotypes) or who have non-missing phenotype information (for all other phenotypes).

Overall health rating	Δ32/+ and +/+	Δ32/Δ32 observed	Δ32/Δ32 expected
Excellent	54436	676	751.59
Good	185795	2592	2569.13
Fair	62757	913	868.30
Poor	12720	184	175.98

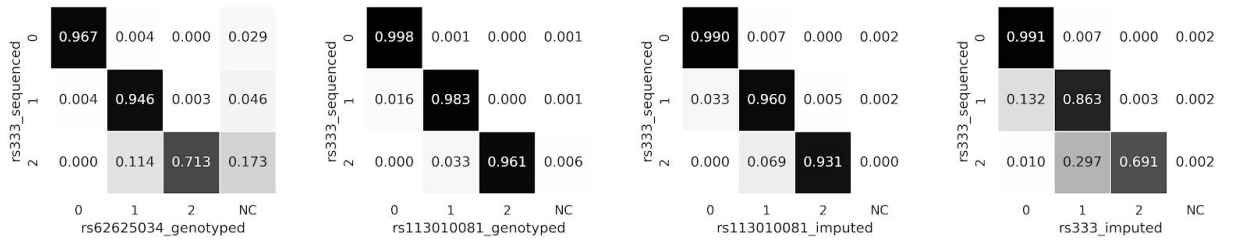
Supplementary Table 9: Contingency table of self-reported health rating and Δ32 status inferred from rs113010081_genotyped. The odds ratio of “Fair” or “Poor” health vs “Excellent” or ”Good” health is 1.068. Adjusted and unadjusted p-values are 0.0052 and 1.

Imputation/WES	Genotype	Δ32/Δ32 [3]	Δ32/+ [3]	+/+ [3]
rs113010081 decimal dosage [1]	C/C	373	36	0
	C/T	30	4024	161
	T/T	0	127	901
rs113010081 integer dosage [2]	C/C	126	5	0
	C/T	7	4178	85
	T/T	0	152	30770

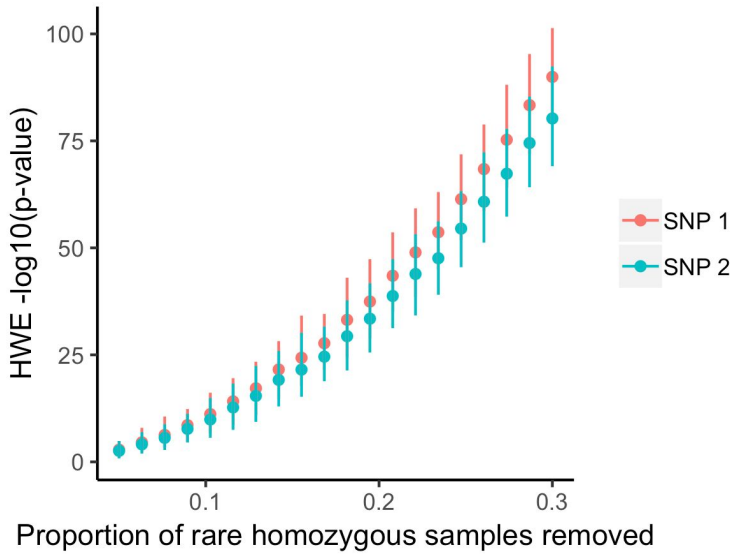
Supplementary Table 10: Genotype calls at rs11301008_imputed and rs333_sequenced in the UK Biobank White British. [1]Individuals with imputed dosage (0,0.5] as C/C, (0.5,1.5) as C/T, and [1.5,2) as T/T. [2] Individuals with imputed dosage 0 as C/C, 1 as C/T, and 2 as T/T. [3]Individuals with Δ32/Δ32, Δ32/+, and +/+ genotypes in the UK Biobank WES data. Notice the relative increase in Δ32/Δ32, Δ32/+ genotypes with decimal dosage (low confidence imputation) relative to integer dosage (high confidence imputation), and the relative large discrepancy between the exome sequencing data and imputation based genotyping data for decimal dosage genotypes. For example, within the class of genotypes with decimal dosage, 30/403 homozygous minor genotypes in the exome sequencing data are called as heterozygous in the UK Biobank decimal dosage imputation data, and 36/409 homozygous minor genotypes in the UK Biobank decimal dosage imputation data are called as heterozygous in the exome sequencing data.



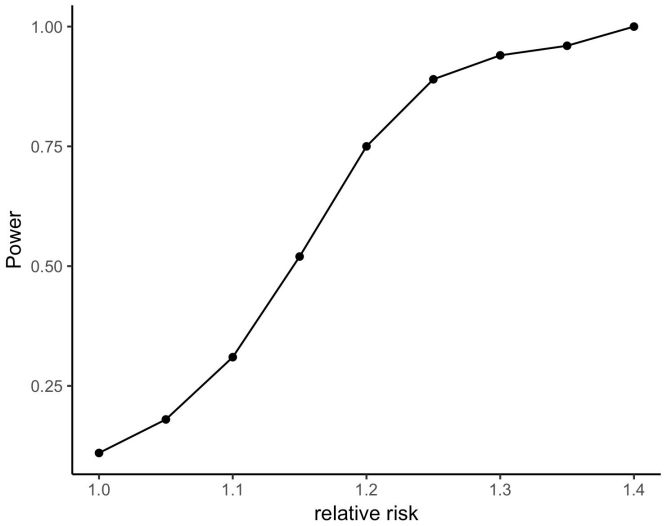
Supplementary Figure 1: Survival rates for individuals with 0, 1, or 2 copies of the rare allele or No Call (NC) for variants tagging the CCR5-Δ32 deletion. First row: Cumulative survival rates. Numbers are one-sided p-values of a Cox proportional hazard model which compares survival rates of individuals with 0 or 1 alleles to those with 2 alleles. Second row: non-cumulative survival rates. Third row: Number of individuals who have died in any given year with 2 copies of rare allele (see also Supplementary Table 7).



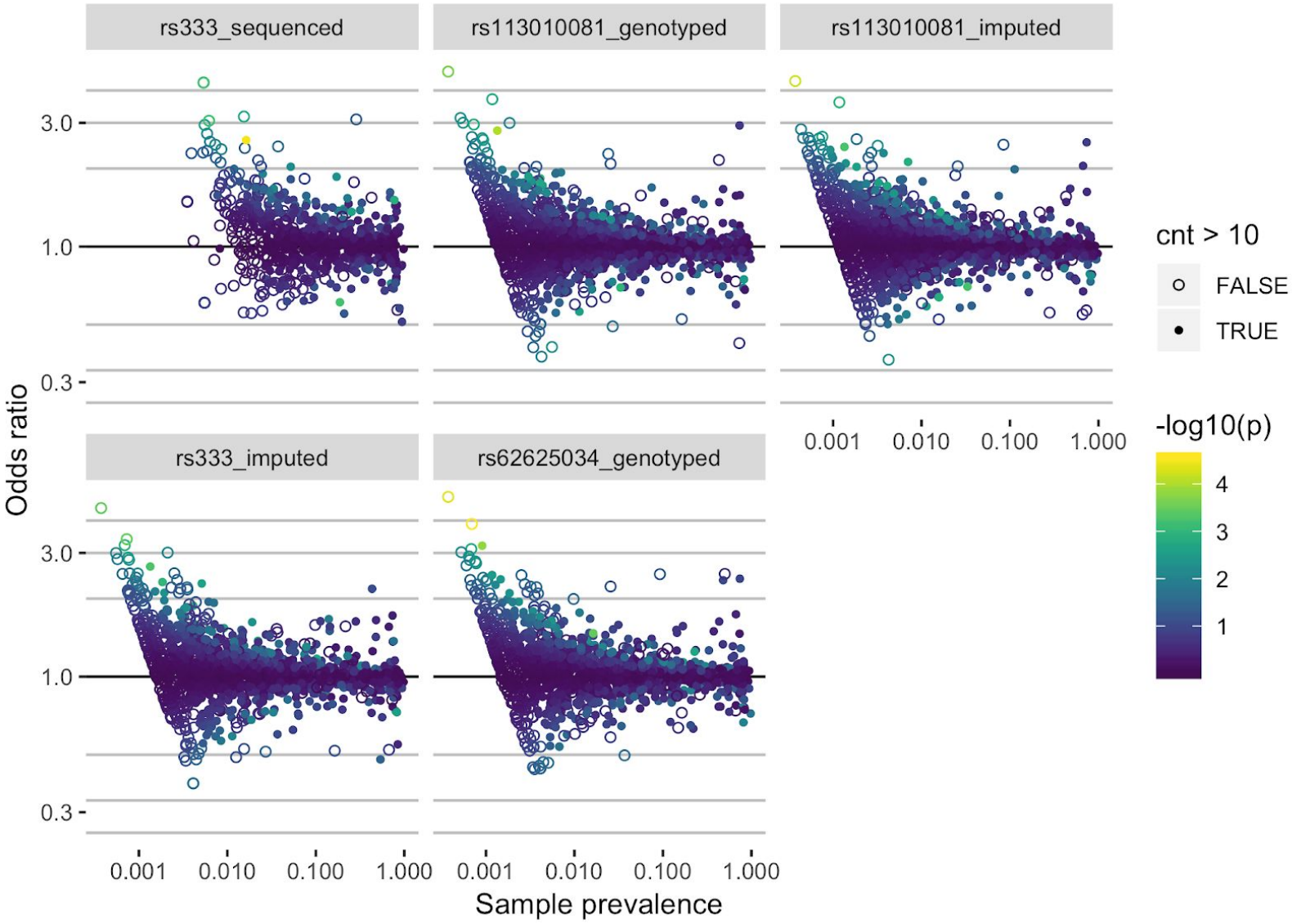
Supplementary Figure 2: Confusion matrix for different markers with missing data. The last column of the first panel shows that individuals with missing genotype at rs62625034_genotyped are enriched for Δ32/Δ32 according to rs333_sequenced. This can lead to a violation of HWE at rs62625034_genotyped. All white British samples of UK Biobank WES data shared with UK Biobank Axiom array data are used in this figure.



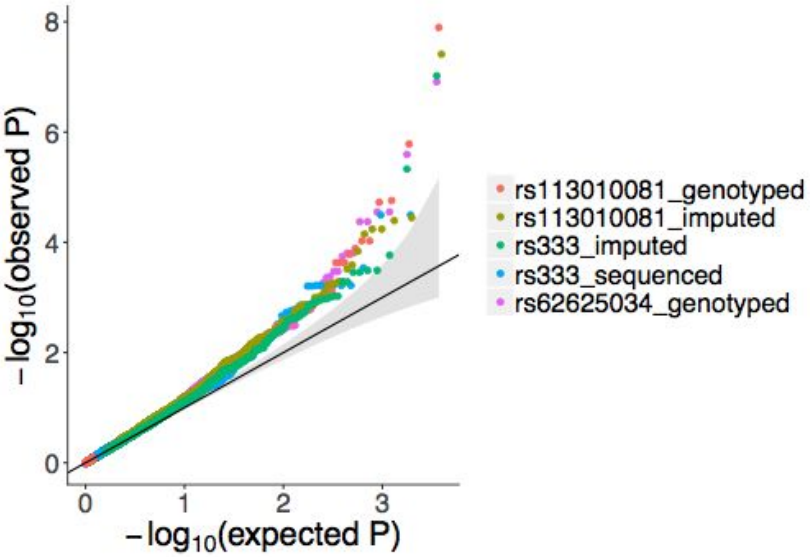
Supplementary Figure 3: Simulated HWE Chi-squared p-values at two variants with minor allele frequency of 11% with r^2 of 0.95, in a sample of 400,000 individuals. Both variants are initially in HWE. We then remove a subset of samples which are homozygous for the rare allele at SNP 1. This leads to a deviation from HWE at SNP 1, but it also leads to a similar deviation from HWE at SNP 2. Only simultaneous selection acting in the opposing direction on SNP 2, or technical artifacts which create a dependence of missingness in one SNP on genotype in the other SNP explain a situation where HWE p-values are very different at both SNPs. Error bars denote the 5th and 95th percentile out of 100 replicates in each bin.



Supplementary Figure 4: Power to detect effects on mortality of a genotype with the frequency of Δ32/Δ32 in a sample of the same total size and mortality rate as the cohort studied here, as a function of relative risk. The power to detect a 20% increase in mortality rate is 75%.



Supplementary Figure 5: Odds ratios (exp(beta)) for all case-control phenotypes in five variants as a function of sample prevalence. Colors represent uncorrected p-values. Open circles represent case-control phenotypes with 10 or fewer cases in Δ32/Δ32 individuals. Only phenotypes with more than five cases in Δ32/Δ32 individuals are shown.



Supplementary Figure 6: QQ-plot of the associations across all phenotypes. Each variant is plotted in a different color. Only phenotypes with more than five cases in Δ32/Δ32 individuals are shown.