

1 Whole exome sequencing and characterization of coding variation in 2 49,960 individuals in the UK Biobank 3

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9 SUMMARY

10 **The UK Biobank is a prospective study of 502,543 individuals, combining extensive**
11 **phenotypic and genotypic data with streamlined access for researchers around the world. Here we**
12 **describe the first tranche of large-scale exome sequence data for 49,960 study participants, revealing**
13 **approximately 4 million coding variants (of which ~98.4% have frequency < 1%). The data includes**
14 **231,631 predicted loss of function variants, a >10-fold increase compared to imputed sequence for**
15 **the same participants. Nearly all genes (>97%) had ≥ 1 predicted loss of function carrier, and most**
16 **genes (>69%) had ≥ 10 loss of function carriers. We illustrate the power of characterizing loss of**
17 **function variation in this large population through association analyses across 1,741 phenotypes. In**
18 **addition to replicating a range of established associations, we discover novel loss of function variants**
19 **with large effects on disease traits, including *PIEZO1* on varicose veins, *COL6A1* on corneal**
20 **resistance, *MEPE* on bone density, and *IQGAP2* and *GMPR* on blood cell traits. We further**
21 **demonstrate the value of exome sequencing by surveying the prevalence of pathogenic variants of**
22 **clinical significance in this population, finding that 2% of the population has a medically actionable**
23 **variant. Additionally, we leverage the phenotypic data to characterize the relationship between rare**
24 ***BRCA1* and *BRCA2* pathogenic variants and cancer risk. Exomes from the first 49,960 participants**
25 **are now made accessible to the scientific community and highlight the promise offered by genomic**
26 **sequencing in large-scale population-based studies.**

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28

29 INTRODUCTION

30 The UK Biobank (UKB) is a prospective population-based study of over 500,000 individuals with
31 extensive and readily accessible phenotypic and genetic data¹. The release of genome-wide genotyping
32 array data² for study participants has accelerated genomic discovery through association studies, and
33 enabled advances in population genetic analyses, the exploration of genetic overlap between traits, and
34 Mendelian randomization studies^{3,4}. While array data in combination with genotype imputation capture the
35 spectrum of common genetic variants, rare variation that is more likely to modify protein sequences and
36 have large phenotypic consequences is less well captured through these approaches.

37 Here, we extend the UKB resource with the first tranche of whole exome sequencing (WES) for
38 49,960 UK Biobank participants, generated by the Regeneron Genetics Center, as part of a collaboration
39 with GlaxoSmithKline. These data are available to approved researchers through the UKB Data Showcase
40 (see **URLs**). Exome sequencing allows direct assessment of protein-altering variants, whose functional
41 consequences are more readily interpretable than non-coding variants, providing a clearer path towards
42 mechanistic and therapeutic insights, as well as potential utility in therapeutic target discovery and
43 validation⁵⁻⁸ and in precision medicine^{9,10}. Here, we provide an overview of sequence variation in UKB
44 exomes, review predicted damaging variants and their consequences in the general population and perform
45 comprehensive loss of function (LOF) burden testing with 1,741 phenotypes, illustrating its utility in studies
46 of common and rare phenotypes with a focus on deleterious coding variation.

47

48 RESULTS

49 Demographics and Clinical Characteristics of Sequenced Participants

50 A total of 50,000 participants were selected, prioritizing individuals with more complete phenotype
51 data: those with whole body MRI imaging data from the UK Biobank Imaging Study, enhanced baseline
52 measurements, hospital episode statistics (HES), and/or linked primary care records. Additionally, we
53 selected one disease area for enrichment, including individuals with admission to hospital with a primary

54 diagnosis of asthma (ICD10 codes J45 or J46). This resulted in 8,250 participants with asthma, or ~16%
 55 among sequenced participants, compared to ~13% among all 502,543 UKB participants (Table 1 and Ext.
 56 Data HESinWESvs500k_V1.xlsx). During data generation, samples from 40 participants were excluded
 57 due to failed quality control measures or participant withdrawal (Supplemental Methods), resulting in a
 58 final set of 49,960 individuals. The sequenced participants are representative of the overall 502,543 UKB
 59 participants (Table 1) for age, sex and ancestry. Due to the ascertainment strategy, sequenced participants
 60 were more likely to have HES diagnosis codes (84.2% among WES vs. 78.0% overall), were enriched for
 61 asthmatics, and many enhanced physical measures (eye measures, hearing test, electrocardiogram, Table
 62 1). The exome sequenced participants did not differ from all participants in the median number of primary
 63 and secondary ICD10 codes. The sequenced subset includes 194 parent-offspring pairs, including 26
 64 mother-father-child trios, 613 full-sibling pairs, 1 monozygotic twin pair and 195 second-degree genetically
 65 determined relationships¹¹ based on identity-by-descent (IBD) estimates between pairs of individuals in
 66 UKB WES is included in Sup. Figure 1.
 67

Demographic and Clinical Characteristics	UKB 50k WES Participants	UKB 500k Participants
N	49,960	502,543
Female, n(%)	27,243 (54.5)	273,460 (54.4)
Age at assessment, years (1st-3rd Quartiles)	58 (45-71)	58 (45-71)
Body mass index, kg/m ² (1st-3rd Quartiles)	26 (21-31)	26 (21-31)
Number of imaged participants (%)	12,075 (24.1) ^a	21,407 (4.3) ^{ab}
Number of current/past smokers, n(%)	17,515 (35.0)	216,482 (43.1)
Townsend Deprivation Index (1st-3rd Quartiles)	-2.0 (-6.1, -2.1)	-2.13 (-6.2, -1.9)
Inpatient ICD10 codes per patient	5	5
Patients with >=1 ICD10 diagnoses, n(%)	42,066 (84.2)	391,983 (78.0)
Genetic Ancestry Assignment^c		
African (%)	1.49	1.24
East Asian (%)	0.54	0.51
European (%)	93.6	94.5
Cardiometabolic phenotypes		
Coronary Disease, n(%)	3,340 (6.7)	35,879 (7.1)
Heart Failure, n(%)	300 (0.6)	4,399 (0.8)
Type 2 Diabetes, n(%)	1,541 (3.0)	17,261 (3.4)

Respiratory and immunological phenotypes		
Asthma, n(%)	8,250 (16.5)	68,149 (13.5)
COPD, n(%)	741 (1.4)	7,438 (1.4)
Rheumatoid Arthritis, n(%)	710 (1.4)	7,337 (1.4)
Inflammatory Bowel Disease n(%)	543 (1.0)	5,783 (1.1)
Neurodegenerative phenotypes		
Alzheimer's Disease, n(%)	13 (0.05)	320 (0.06)
Parkinson's Disease, n(%)	65 (0.13)	1,043 (0.21)
Multiple Sclerosis, n(%)	126 (0.25)	1,352 (0.26)
Myasthenia Gravis, n(%)	14 (0.02)	217 (0.04)
Oncology phenotypes		
Breast Cancer, n(%)	1,667 (3.3)	16,887 (3.3)
Ovarian Cancer, n(%)	162 (0.3)	1,777 (0.3)
Pancreatic Cancer, n(%)	602 (1.2)	4,611 (0.9)
Prostate Cancer, n(%)	848 (1.6)	8,855 (1.7)
Melanoma, n(%)	598 (1.1)	5,715 (1.1)
Lung Cancer, n(%)	172 (0.3)	2,581 (0.5)
Colorectal Cancer, n(%)	368 (0.7)	3,971 (0.8)
Cutaneous squamous cell carcinoma, n(%)	1,316 (2.6)	12,969 (2.6)
Enhanced measures		
Hearing test, n(%)	40,546 (81.1)	167,011 (33.2)
Pulse Rate, n(%)	40,548 (34.2)	170,761 (33.9)
Visual Acuity Measured, n(%)	39,461 (78.9)	117,092 (23.2)
IOP measured (left), n(%)	37,940 (75.9)	111,942 (22.2)
Autorefracton, n(%)	36,067 (72.1)	105,989 (21.0)
Retinal OCT, n(%)	32,748 (65.5)	67,708 (13.4)
ECG at rest, n(%)	10,829 (27.1)	13,572 (2.1)
Cognitive Function, n(%)	9,511 (19.0)	96,362 (19.1)
Digestive Health, n(%)	13,553 (28.1)	142,310 (28.3)
Physical Activity Measurement, n(%)	10,684 (21.3)	101,117 (20.1)

68
69 **Table 1 | Clinical characteristics in whole exome sequenced and all UK Biobank participants**

70 Demographics and clinical characteristics of UKB 50K sequenced participants and overall 500K
71 participants. See Supplemental Methods for definition of UKB clinical phenotype definitions. Unless
72 otherwise noted, values are expressed as median (1st and 3rd quartile). ^aThe number of samples with exome
73 sequencing data and at least one non-missing image derived phenotype value from data downloaded from
74 UK Biobank in November 2018. ^bThe number of samples with at least one non-missing image derived
75 phenotype value from data downloaded from UK Biobank in November 2018. ^cNumber of samples in 3

76 pre-defined regions of a plot of the first two genetic principal component scores, where the regions are
77 selected to represent African, East Asian, and European ancestry (Sup. Figure 2).

78

79 **Summary and Characterization of Coding Variation from WES**

80 Exomes were captured using a slightly modified version of the IDT xGen Exome Research Panel
81 v1.0. The basic design targets 39 megabases of the human genome (19,396 genes among autosomes and
82 sex chromosomes) and was supplemented with additional probes to boost coverage at under-performing
83 loci. In each sample and among targeted bases, coverage exceeds 20X at 94.6% of sites on average
84 (standard deviation 2.1%). We observe 4,735,722 variants within targeted regions (Table 2). These variants
85 include 1,229,303 synonymous (97.9% with minor allele frequency, $MAF < 1\%$), 2,498,947 non-
86 synonymous (98.9% with $MAF < 1\%$), and 231,631 predicted LOF variants affecting at least one coding
87 transcript (initiation codon loss, premature stop codons, splicing, and frameshifting indel variants; 99.6%
88 with $MAF < 1\%$) (Fig. 1a). Our tally of the median number of variants per individual includes 9,619
89 synonymous (IQR 128), 8,781 missense (IQR 137) and 219 LOF variants (IQR 16) and is comparable to
90 previous exome sequencing studies^{12,13}; the increasing proportion of rare variants in the LOF and missense
91 categories is consistent with purifying selection. If we restrict analysis to LOF variants that affect all
92 ENSEMBL 85 transcripts for a gene, the number of LOF variants drops to 153,903 overall and 111 per
93 individual (a reduction of ~33.5% and ~49.3%, respectively), consistent with previous studies. In addition
94 to variants in targeted regions, we also capture exon adjacent variation. Including non-targeted regions, we
95 observe 9,693,526 indel and single nucleotide variants (SNVs) after quality control, 98.5% with $MAF < 1\%$.
96 These additional variants can be helpful aids for population genetic analyses and for applications such as
97 phasing and IBD segment detection.

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100

	Variants in WES, n=49,960 Participants		Median Per Participant (IQR)	
	# Variants	# Variants MAF<1%	# Variants	# Variants MAF<1%
Total	9,693,526	9,547,730	48,982 (627)	1,626 (133)
Targeted Regions ¹	4,735,722	4,665,684	24,332 (283)	780 (63)
Variant Type¹				
SNVs	4,520,754	4,453,941	23,529 (276)	739 (61)
Indels	214,968	211,743	803 (29)	42 (10)
Multi-Allelic	591,340	580,728	3,388 (63)	117 (18)
Functional Prediction				
Synonymous	1,229,303	1,203,043	9,619 (128)	228 (28)
Missense	2,498,947	2,472,384	8,781 (137)	380 (39)
LOF (any transcript)	231,631	230,790	219 (16)	24 (8)
LOF (all transcripts)	153,903	153,441	111 (12)	15 (6)

101

102 **Table 2 | Summary statistics for variants in sequenced exomes of 49,960 UKB participants.** Counts of

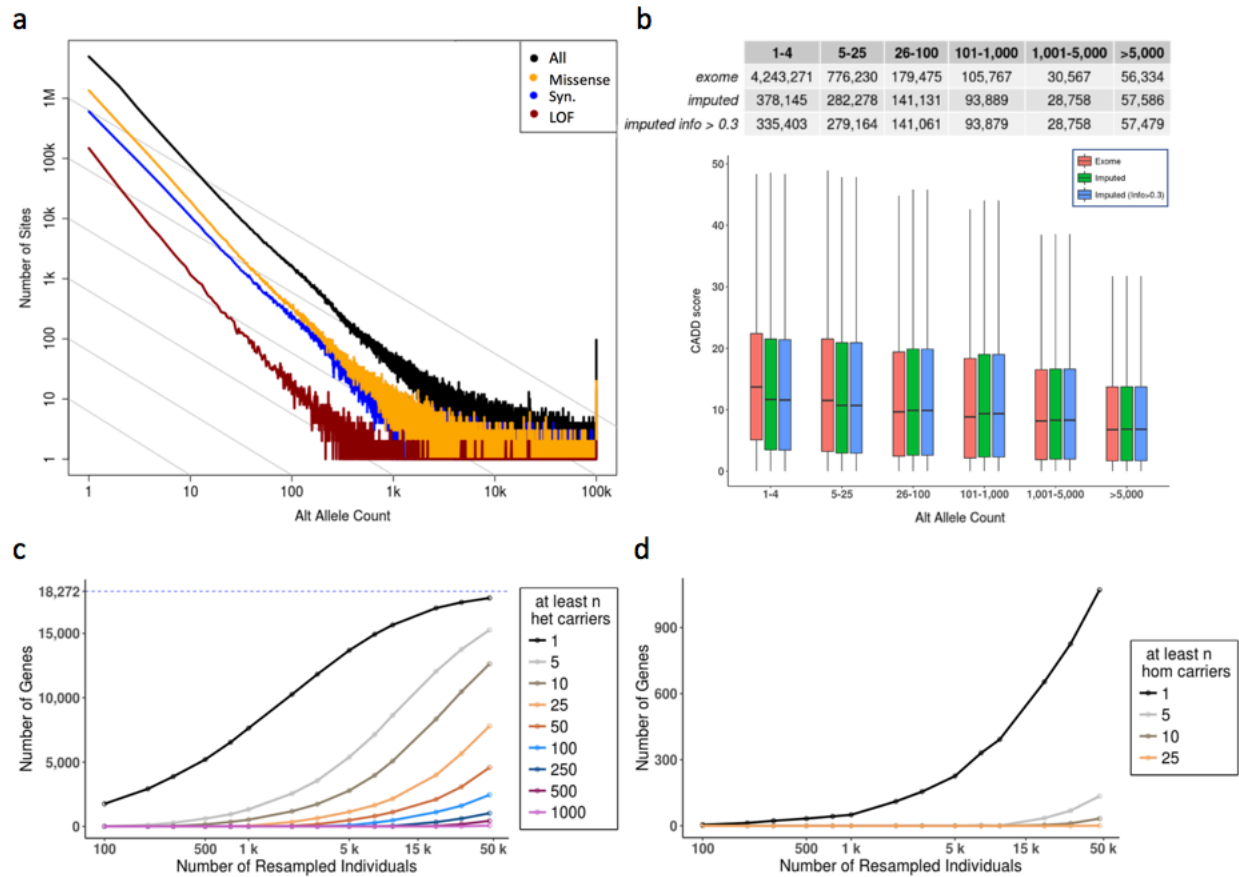
103 autosomal variants observed across all individuals by type/functional class for all and for MAF<1%

104 frequency. The number of targeted bases by the exome capture design was n=38,997,831. All variants

105 passed quality control (QC) criteria (See Supplemental Methods), individual and variant missingness <10%,

106 and Hardy Weinberg p-value>10⁻¹⁵. Median count and interquartile range (IQR) per individual for all

107 variants, and for MAF<1%.¹ Counts restricted to WES targeted regions.



108

109 **Figure 1 | Summary statistics for variation in WES and imputed sequence** **a**, Observed site frequency

110 spectrum for all autosomal variants and by functional prediction in 49,960 UKB participants. **b**,

111 Distribution of CADD scores for variant allele counts in regions consistently covered by WES (90% of

112 individuals with >20X depth) in WES and imputed data in 49,797 UKB participants with WES and imputed

113 sequence. **c**, The number of autosomal genes with at least 1, 5, 10, etc. heterozygous and homozygous non-

114 reference genotypes **d**, LOF carriers increases with sample size. LOFs passed GL (Goldilocks) QC (see

115 Supplemental Methods for GL QC filtering definition), genotype missingness < 10%, and HWE p-value > 10⁻

116 ¹⁵. 46,808 UKB participants of European ancestry with WES were down-sampled at random to the number

117 of individuals specified on the horizontal axis. The number of genes containing at least the indicated count

118 of LOFs MAF < 1% carriers as in the legend are plotted on the vertical axis. The maximum number of

119 autosomal genes is 18,272 in this analysis (See Supplemental Methods for gene model).

120

121 **Enhancement of Coding Variation from WES Compared to Imputed Sequence**

122 To evaluate enhancements to the UKB genetic variation resource through WES, we compared the
123 number of coding variants observed in 49,797 individuals in whom both WES and imputed sequence were
124 available; this is a subset of the 49,960 individuals with WES. To capture as many variants in the overlap
125 of WES and imputed sequence as possible, only minimal filtering was applied (WES sites were filtered
126 using genotype likelihoods, with no filtering for imputed data), thus variant counts are greater than in Table
127 2 and Sup. Table 1, respectively. Among all autosomal variants, we observed increases in the total number
128 of coding variants (3,995,794 to 707,124); synonymous (1,241,804 to 267,479), missense (2,518,075 to
129 420,194), and LOF (235,915 to 19,451) in WES compared to imputed sequence, respectively (Sup. Table
130 2). This represents a >10-fold increase in the number of LOF variants identified by WES compared to those
131 in the imputed sequence.

132 Amongst nearly four million coding variants observed in the exome sequence data, only 13.7%
133 were also observed in the imputed sequence, highlighting the added value of exome sequencing for
134 ascertainment of rare coding variation. Similarly, among LOFs observed in either dataset, 92.0%
135 (n=223,427) were unique to WES and absent in the imputed sequence data. We observed 12,488 LOFs
136 present in both datasets, meaning that only 5.3% of the >235,915 LOFs identified by WES were present in
137 the imputed sequence. Since LOFs are especially informative for human genetics and medical sequencing
138 studies, this enhancement clearly emphasizes the value of exome sequencing.

139 There were 6,963 LOFs seen only in the imputed sequence. These represent both variants within
140 regions not targeted or captured in WES and errors in imputation, which are especially pronounced at low
141 allele frequencies. Amongst the 6,963 LOFs (5,939 SNVs) observed only in the imputed sequence, we
142 identified 1,730 LOF variants (24.8%, including 1,348 SNVs) in regions that were not targeted, 4,438 LOF
143 variants (63.7%, including 3,804 SNVs) that fell within consistently covered regions of WES (>20x
144 coverage in 90% of samples), and 885 LOF variants (12.7%, including 787 SNVs) in inconsistently covered
145 exome-captured target or buffer regions. Amongst the set of 4,438 LOF variants in consistently covered
146 regions seen solely in the imputed sequence, we selected 363 variant sample-sites from across the MAF
147 spectrum and manually reviewed the underlying read data in the Integrative Genomics Viewer¹⁴ (IGV) (see

148 Supplemental Methods). We observed that 76% of the selected sample sites had no sequencing evidence to
149 support the imputed LOF call. Approximately 21% had some evidence for the presence of any variation
150 (e.g. multi-nucleotide polymorphism). Only ~3% had any clear evidence of the LOF variant called in the
151 imputed data. Sites that validated were more likely to be common than rare, as expected for imputed
152 variants.

153 We also noted that amongst all the 707,124 imputed coding variants, 22.6% of them were not
154 observed in the exome sequence data; a large portion of these will similarly suffer from poor imputation
155 accuracy as observed in WES and imputed sequence concordance (Figure 2). As expected, common
156 variants across functional prediction classes were more likely to be captured by both WES and imputed
157 sequence, whereas rare variants were more likely unique to WES (Sup. Table 2). As an expected result of
158 purifying selection, we observed that lower frequency variants were predicted to be more deleterious as
159 measured by CADD¹⁵ score distributions in both datasets (Figure 1b). Interestingly, among rare variants,
160 those identified by WES were typically classified as more deleterious (Figure 1b) – likely because rare
161 variants that can be imputed may often be common in other populations even when rare in UKB.

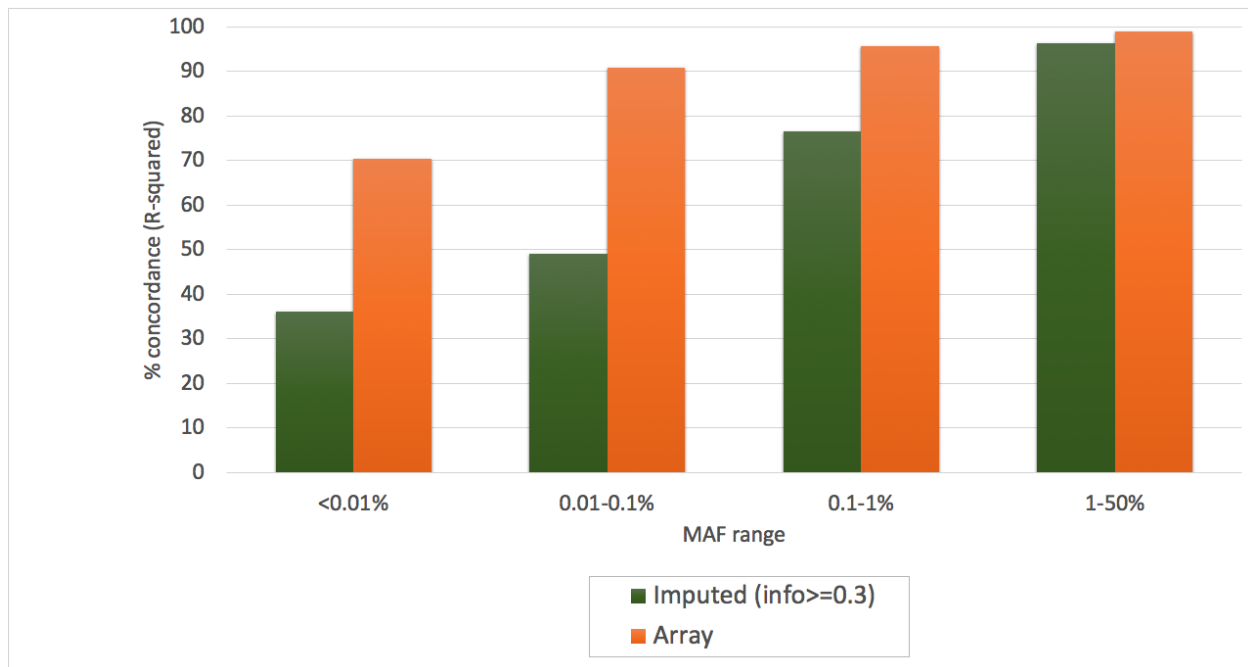
162

163 **Concordance of WES, Directly Genotyped Array, and Imputed Sequence**

164 We measured concordance between WES and array genotypes in individuals with both datasets
165 (Supplemental Methods), using the squared correlation (R^2) of allele counts in sequencing and array
166 genotyping. This measure facilitates interpretation of assessments of accuracy for both rare and common
167 variation^{16,17}. Using the same approach, we also measured concordance between WES and imputed
168 sequence. As expected, concordance between genomic measures declines with decreasing MAF (Figure 2,
169 Sup. Figures 3,4). Concordance between WES and imputed sequence ranged from 35% for MAF <0.01%
170 to 96% for allele frequencies >1%, averaging 54% across all allele frequencies. Concordance between WES
171 and array genotyped variants was substantially higher, ranging from 70% for MAF <0.01% to 99% for
172 MAF >1% (Figure 2), and averaging 99% across all allele frequencies. As expected, WES performs much

173 better in terms of concordance with array genotypes, since both directly assay the variation rather than make
174 a computational prediction. This is particularly true in the rarest allele frequencies where the accuracy of
175 imputation is limited using current imputation reference panels.

176



177

178 **Figure 2 | Concordance between WES, imputed sequence, and array genotypes.** R-squared correlation
179 coefficients between variants in WES and imputed sequence (green) and array genotypes and WES
180 (orange), calculated per variant and binned by minor allele frequency in WES. n=46,912 individuals and
181 n=75,334 variants were represented in the array-WES comparison (n=4,261, n=17,780, n=23,087 and
182 n=30,206 variants in <0.01%, 0.01-0.1%, 0.1-1%, and 1-50% MAF bins respectively). n=46,860
183 individuals and n=899,455 variants were represented in the imputed-WES comparison (n=346,826,
184 n=304,524, n=126,554, and n=121,551 variants in <0.01%, 0.01-0.1%, 0.1-1%, and 1-50% MAF bins
185 respectively).

186

187 **Comparison of LOF Variants Ascertained Through WES and Imputed Sequence**

188 LOF variants constitute a major class of genetic variation of great interest due to their disruption
189 of gene function, their causal role in many Mendelian disorders, and the success of leveraging protective
190 LOF variants to identify novel drug targets^{5,6,18}. Rare LOF variation is best captured by direct sequencing
191 approaches, such as WES, and we sought to quantify the improved yield of LOF variation from WES
192 compared to array genotyping and imputed sequence. We compared the number of LOF variants ascertained
193 through WES and imputed sequence among 49,797 UKB participants. Notably, not all individuals with
194 WES have imputed sequence available. We observed a larger number of LOF variants impacting any
195 transcript in WES vs imputed sequence, 235,915 and 19,451, respectively (See Sup. Table 2). Further, we
196 observed a greater number of genes with ≥ 1 heterozygous LOF variant carrier (17,751 genes from WES,
197 8,763 from imputation (info >0.3) and genes with ≥ 1 homozygous LOF variant carrier (1,071 from WES,
198 789 from imputation) (Table 3). The number of genes with LOFs at different thresholds of imputation
199 accuracy for 50k and 500k resources are included in Sup. Table 3. At equivalent sample sizes (n=46,827
200 European ancestry individuals with both WES and imputed sequence), WES data included a greater number
201 of genes with LOF variants, across all carrier count thresholds. Even more striking was that WES in 46,827
202 individuals yielded more genes (17,751) with heterozygous LOFs than imputed sequence (info>0.3) in all
203 462,427 UKB participants of European ancestry (8,724 genes). Tracking the increase in the number of
204 genes with heterozygous LOF variant carriers with the increase in the number of sequenced samples
205 suggests that we are approaching saturation for this metric, having likely observed at least one heterozygous
206 LOF variant carrier in most of the genes that tolerate these variants, and most genes overall (Figure 1c). In
207 contrast, the number of genes for which homozygous LOF variants are observed still appears to increase
208 rapidly as more samples in UKB are sequenced, suggesting that homozygous instances of LOF variants for
209 many more genes can be identified by sequencing additional individuals (Figure 1d).

210

211

212

		# Autosomal genes containing at least N LOFs, MAF < 1%					
Zygosity	Genomic resource	1	5	10	25	50	100
Het	50k exome	17,751	15,269	12,629	7,799	4,573	2,453
	50k imputed (info > 0.3)	8,763	6,999	5,933	4,297	2,965	1,911
	500k imputed (info > 0.3)	8,724	7,711	7,267	6,539	5,847	4,916
Hom	50k exome	1,071	135	33	1	0	0
	50k imputed (info > 0.3)	789	74	7	0	0	0
	500k imputed (info > 0.3)	1,752	597	351	120	21	3

213 **Table 3 | Number of autosomal genes with heterozygous, homozygous LOF variants.** Count of genes
 214 with at least the specified number of LOFs (MAF < 1%) impacting any transcript in European ancestry in
 215 approximately 50k (n=46,827 with WES and imputed sequence), and 462,427 individuals for 500k imputed
 216 sequence.

217

218 Extrapolating, we can estimate the number of genes where multiple loss of function carriers will
 219 be observed once our experiment is complete and all ~500,000 participants are sequenced. Cautiously, we
 220 currently predict that >17,000, >15,000, and >12,000 genes will have ≥ 10 , ≥ 50 , and ≥ 100 heterozygous
 221 LOF carriers in the full dataset (see Sup. Methods, Sup. Methods Fig. 1 & Table 1).

222 Our WES results are consistent with those of a recent large-scale survey¹⁹ of genetic variation in
 223 141,456 individuals from the Genome Aggregation Database (gnomAD). When we annotate both exome
 224 variant lists with the same annotation pipelines and subset results to similar numbers of individuals and
 225 ancestry, we observe 17,751 genes with LOFs in any transcript in 46,979 European individuals in UKB
 226 with WES vs 17,946 genes with LOFs in any transcript in 56,885 Non-Finnish European (NFE) individuals
 227 in gnomAD exomes. Further subsetting to high confidence LOF variants (with LOFTEE, see Sup.
 228 Methods), we obtain 17,640 genes with LOFs in UKB and 17,856 in gnomAD (Sup. Methods Table 2).

229

230 **Survey of Medically Actionable Pathogenic Variants**

231 To date, more than 5,000 genetic disorders have been described for which the molecular causes and
 232 associated genes have been defined. The American College of Medical Genetics (ACMG) has proposed 59

233 genes, ACMG SF2.0,^{20,21} which are associated with highly penetrant disease phenotypes and for which
234 available treatments and/or prevention guidelines can significantly reduce the morbidity and mortality in
235 genetically susceptible individuals. Large-scale human genomic sequencing efforts coupled with EHR data
236 provide opportunities to assess penetrance and prevalence of pathogenic (P) and likely pathogenic (LP)
237 variants in known monogenic disease genes, as well as investigate the phenotypic effects of variants of
238 unknown significance (VUS). Additionally, phenotypically agnostic population sampling provides
239 opportunities to better characterize the phenotypic spectrum of these disorders and estimate the associated
240 disease risk in the population. Furthermore, these efforts enable the implementation of precision medicine
241 by identifying individuals carrying medically actionable pathogenic variants and providing medical care
242 and surveillance preemptively.

243 We interrogated variant data for the 49,960 individuals with WES from the UKB to identify a
244 “strict” set of reported pathogenic missense and LOF variants (that is, those with ≥ 2 stars in ClinVar and
245 no conflicting interpretations) as well as a set of likely pathogenic LOF variants (that is, those in genes
246 where truncating mutations are known to cause disease) according to the current ACMG 59 gene set²¹ (see
247 Supplemental Methods). We identified a total of 555 such variants (316 in the reported pathogenic set, 239
248 in the likely pathogenic set) in 1,000 unique individuals (Table 4, Ext. Data ACMG59Variants.xlsx, 9
249 individuals carried variants in 2 genes). Of note, 47 of the likely pathogenic variants would qualify as
250 previously reported pathogenic variants using a broader definition (Sup. Table 4). Variants were observed
251 in 48 of 59 ACMG genes, with a median number of 5 variants per gene and a median 2 carriers per gene.
252 Overall, 2.0% of the sequenced individuals carry a flagged variant in one of the ACMG59 genes. Using the
253 same methodology in 91,514 participants from the Geisinger-Regeneron DiscovEHR study²² sequenced to
254 date, we observed a slightly higher percentage of individuals, 2.76%, carrying a potentially actionable rare
255 pathogenic variant in the ACMG59 genes (Sup. Table 5). This difference may reflect differences between
256 a study of individuals seeking clinical care (DiscovEHR) and a population-based study not ascertained in
257 the context of active clinical care (UKB).

258

Category	#Variants	% of Total Known ACMG59 Variants	#Carriers	% of individuals with reportable variants
Pathogenic (P)	316	4.23	694	1.39
Likely Pathogenic (LP)	239	-	315	0.63
P + LP	555	-	1,009	2.0 ¹

259

260 **Table 4 | Medically actionable variants in ACMG59 genes in UKB participants.** Of the 49,960 UKB

261 participants with WES data, 2.0% are carriers of pathogenic (P) and likely pathogenic (LP) variants in

262 ACMG59 v2.0 genes based on strict variant filtering criteria. LP variant counts include LOF variants

263 passing QC criteria in ACMG59 genes that are not reported in ClinVar (≥ 2 star). Amongst all P+LP

264 variants, 384 variants were observed in only one individual, 165 were observed in 2-10 individuals, and 6

265 were observed in >10 individuals. ¹Percent of individuals with P or LP variants is not additive, as the 2.0%

266 represents non-redundant carriers; 9 individuals were found to have 2 medically actionable variants.

267

268 Among the 48 of the reportable ACMG59 genes, variants in cancer associated genes were the most

269 prevalent in UKB with WES; *BRCA2* (93 variants, 166 carriers), *BRCA1* (40 variants, 60 carriers), *PMS2*

270 (21 variants, 59 carriers) and *MSH6* (35 variants, 52 carriers); while variants in *LDLR*, associated with

271 familial hypercholesterolemia [MIM #143890], were the second most prevalent (35 variants, 68 carriers).

272 Cardiac dysfunction disorders were also highly represented mainly by variants in *KCNQ1* (25 variants, 55

273 carriers), *PKP2* (22 variants, 55 carriers), and *MYBPC3* (25 variants, 50 carriers) (Figure 3a). The majority

274 of variants were identified in genes responsible for dominant conditions, for which heterozygous carriers

275 are at risk (994 carriers); however, we also identified 6 individuals homozygous for pathogenic variants in

276 genes associated with autosomal recessive (familial adenomatous polyposis-2 [FAP2, MIM #608456] and

277 mismatch repair cancer syndrome [MMRCS, MIM #276300] due to biallelic pathogenic variants in

278 *MUTYH* and *PMS2*, respectively) or hemizygous for X-linked conditions (Fabry disease [MIM #301500]

279 due to pathogenic variants in *GLA*). Indeed, a male hemizygous for the c.335G>A; p.Arg112His pathogenic

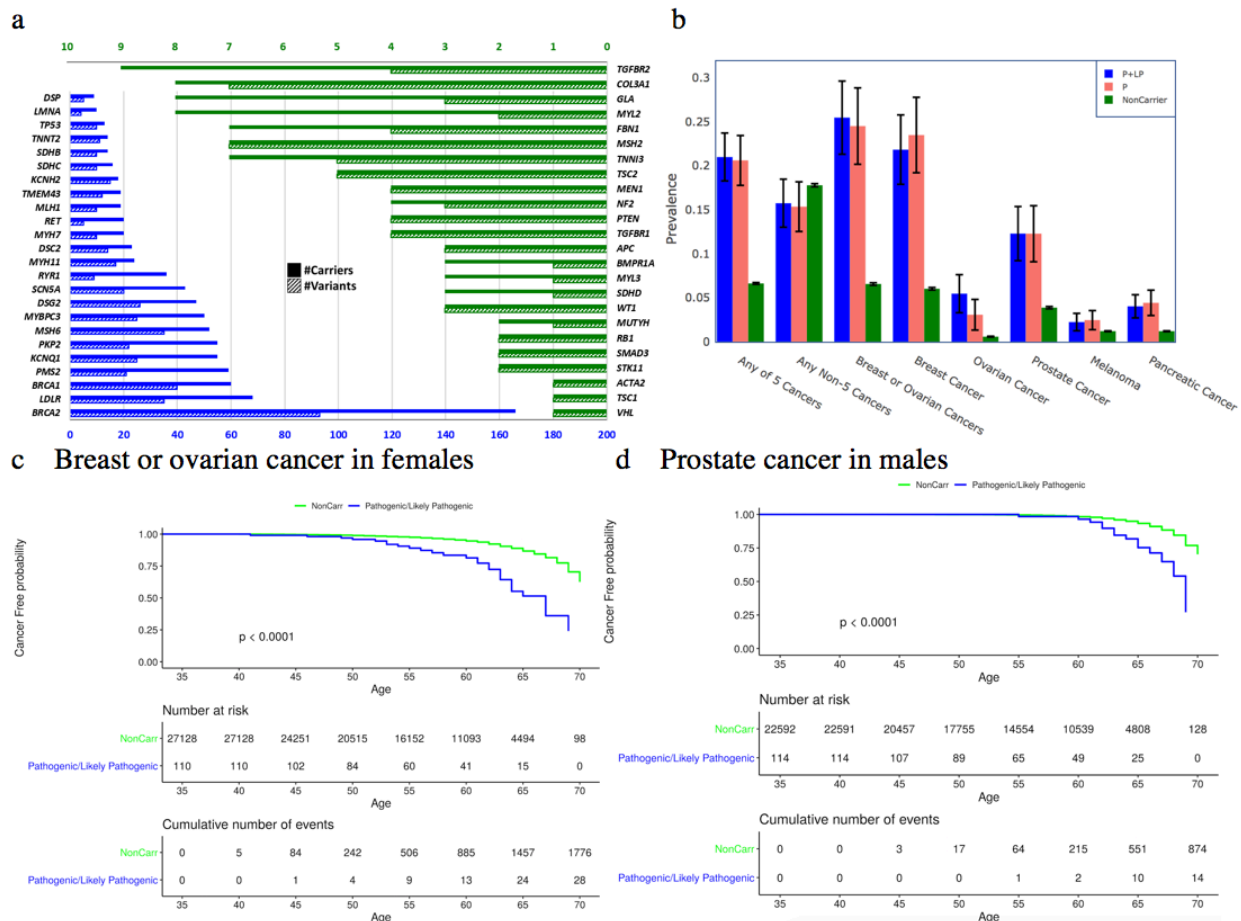
280 variant in *GLA* has diagnoses of angina pectoris, atrial fibrillation, chest pain, and chronic ischemic heart

281 disease. Similarly, one individual homozygous for a pathogenic missense variant (c.1145G>A;

282 p.Gly382Asp) in *MUTYH* has a history of benign neoplasm of colon, diverticular disease of the intestine,
283 colonic polyps, and intestinal obstruction. These examples illustrate how the extensive health data available
284 for UK Biobank participants provide a valuable resource to assess variant pathogenicity and disease risk at
285 the population level, and the potential to model outcomes for individuals harboring pathogenic variants.

286 As an example, we evaluated the risk of cancer in individuals carrying pathogenic variants in
287 *BRCA1* or *BRCA2* (Figure 3b) to compare across five previously implicated *BRCA1/2* associated cancers²³
288 as well as to explore whether risk was conferred for other cancers. While *BRCA1* and *BRCA2* have
289 differences in mechanism and risk among cancer subtypes, due to low sample sizes, we analyzed summed
290 counts in 114 males and 110 females with *BRCA1/2* reported pathogenic and likely pathogenic variants.
291 We found the prevalence of cancers to be elevated in carriers of pathogenic variants in *BRCA1/2* for the 5
292 cancers (breast in females, ovarian, prostate, melanoma, and pancreatic) previously associated with *BRCA1*
293 or *BRCA2* (cancer status was derived from self-report, HES, and cancer prevalence for any of the 5 cancers
294 was 21.0% in carriers vs 6.6% in non-carriers, OR = 3.75 (95%CI 2.71,5.18), p-value = 2×10^{-12} , (3337
295 cases, 46599 controls), and there was no significant difference between carriers and non-carriers when all
296 other cancers, excluding these 5, were combined; 15.7% in carriers vs 17.7% in non-carriers, OR = 0.86
297 (95%CI 0.58,1.29), p-value = 0.55, (8300 cases, 38424 controls). The most prevalent cancers in this group
298 were C443 and C449 unspecified malignant neoplasms of skin, and D069 carcinoma in situ of cervix.
299 Increased risk was observed in these *BRCA1/2* variant carriers for each of the five previously associated
300 cancers analyzed individually (ovarian in females OR=9.97 (95%CI 4.32,23.06), p= 5.2×10^{-5} , (162 cases,
301 27,076 controls); breast in females OR=4.37 (95%CI 2.77,6.88), p= 3.6×10^{-8} , (1,654 cases, 25,584 controls);
302 prostate in males OR=3.48 (95%CI 1.98, 6.11), p= 1.5×10^{-4} , (888 cases, 21,818 controls); melanoma
303 OR=1.9 (95%CI 0.78,4.62), p=0.20, (599 cases, 49,345 controls); and pancreatic cancer OR 3.47 (95%CI
304 1.77,6.79), p= 1.7×10^{-3} , (602 cases, 49,342) controls; (p values by Fisher's exact test). These differences in
305 overall cancer risk also manifest as clearly different disease onset and rates of cancer-free survival between
306 carriers and non-carriers (see Figure 3c for breast and ovarian cancer in females; Figure 3d for prostate

307 cancer in males). Comparing the cumulative proportion of female participants free of breast and ovarian
 308 cancer, we estimate a hazard ratio of 4.3 (95%CI 2.96,6.24, $p < 0.0001$). Comparing the cumulative
 309 proportion of male participants free of prostate cancer, the hazard ratio was 3.68 (95%CI 2.17, 6.24,
 310 $p < 0.0001$). With the UKB resource, cancer risk can be more deeply explored across broader sets of variants
 311 as well as with larger exome sequence datasets and continued accrual of incident cancers. Our results
 312 corroborate those of another recent population-based application of WES linked to health records to
 313 evaluate cancer risk in individuals with pathogenic variants in *BRCA1/2*¹⁰, demonstrating the value of WES
 314 to identify high-penetrance rare alleles associated with clinical phenotypes; such efforts can be applied
 315 across other genetic disorders, enabling the implementation of precision medicine at the population level.



317

318 **Figure 3 | Summary of observed actionable ACMG59 variants, and pathogenicity of *BRCA1/2***
319 **variants. a,** Counts of variants and carriers in 48 ACMG59 genes with pathogenic (P) or likely pathogenic
320 (LP) variants. **b,** Prevalence of cancers in carriers of P, P or LP, and no P or LP variants in *BRCA1* or
321 *BRCA2*. Five major cancers related to *BRCA1/2* risk include breast in females, ovarian, prostate, melanoma,
322 and pancreatic cancers. Cases are aggregated from Cancer Registry, HES, and Self Report. **c,** Cumulative
323 proportion of female participants free of breast and ovarian cancer, and **d,** male participants free of prostate
324 cancer with P or LP variants in *BRCA1/2* compared to non-carriers by age at interview.

325

326 **Phenotypic Associations with LOF Variation**

327 The combination of WES, allowing comprehensive capture of LOF variants, with rich health information
328 allows for broad investigation of the phenotypic consequences of human genetic variation. We conducted
329 burden tests for rare (MAF < 1%) LOF variants in autosomal genes with >3 LOF variant carriers and in
330 1,741 traits (1,073 discrete traits with at least 50 cases defined by HES and self-report data, 668
331 quantitative, anthropometric, and blood traits) in 46,979 individuals of European ancestry. For each gene-
332 trait association, we also evaluated signal for the single variants included in the burden test. We identified
333 25 unique gene burden-trait associations with $p < 10^{-7}$; among these 21 were more significant than any
334 single LOF variant included in the burden test. The results include several well-established associations
335 (Table 5). For example, we observe that carriers of *MLH1* LOFs, associated with Muir-Torre and Lynch
336 syndromes²⁴ [MIM #158320, #609310], were at increased risk of malignant neoplasms of the digestive
337 organs (OR=84, $P=3.5 \times 10^{-11}$). Carriers of *PKD1* LOFs, the major cause of autosomal dominant polycystic
338 kidney disease²⁵ [MIM #173900], were at increased risk of chronic kidney disease (OR=91, $P=2.9 \times 10^{-10}$).
339 Carriers of *TTN* LOFs are at increased risk for cardiomyopathy (OR=11.9, $P=1.4 \times 10^{-8}$), consistent
340 with prior reports²⁶. In addition to Mendelian disorders, other findings with strong support in the literature
341 include *HBB* with red blood cell phenotypes²⁷, *IL33* with eosinophils (driven by rs146597587)²⁸, *KALRN*

342 with platelet volume (driven by rs56407180)²⁹, *TUBB1* with multiple platelet phenotypes³⁰, and *CALR*
 343 with hematopoietic neoplasms³¹. In some cases, we see patterns of association with traits that may be
 344 secondary to known phenotypic associations. For example, *ASXL1* and *CHEK2* are genes involved in
 345 myeloproliferative disorders³² and cancer³³, respectively, which may explain the observed associations
 346 with hematologic traits (which may be secondary to myelodysplastic disease or chemotherapy). Many
 347 other known phenotypic associations are supported by the data at more modest significance thresholds
 348 (Sup. table 6). These include, for example, associations between LOF variants in *LDLR* with coronary
 349 artery disease, *GPIBB* with platelet count, *PALB2* with cancer, and *BRCA2* with cancer risk.

350

Gene	ICD10 Code, Binary Phenotype	RRIRAIAA	OR (95% CI)	WES Burden P	N SNV	Lowest P SNV	Imputed 50k Burden P
<i>MLH1</i>	Z85.0, Personal history of malignant neoplasm of digestive organs	Ctrl:39724 910 Cases:319 610	84.4 (31.0,229.5)	3.5x10 ⁻¹¹	9	0.88	NA
<i>PKD1</i>	N18, Chronic kidney disease	Ctrl:46389 1510 Cases:210 610	91.2 (36.3,229.1)	2.9x10 ⁻¹⁰	15	NA	NA
<i>CALR</i>	D47, Other neoplasms of uncertain behavior of lymphoid, hematopoietic and related tissue	Ctrl:46552 310 Cases:52 310	866.1 (194.5,3857.1)	4.1x10 ⁻⁸	4	NA	NA
<i>TTN</i>	I42, Cardiomyopathy	Ctrl:44341 585 3 Cases:67 11 10	11.9 (6.5,21.9)	1.4x10 ⁻⁸	302	1.2x10 ⁻³	0.015

Gene	Quantitative Phenotype	RRIRAIAA	Beta (95% CI)	WES Burden P	N SNV	Lowest P SNV	Imputed 50k Burden P
<i>IL33</i>	Eosinophil percentage	44428 497 0	-0.3 (-0.4,-0.2)	5.4x10 ⁻¹²	9	5.6x10 ⁻¹²	1.4x10 ⁻¹¹
<i>IL33</i>	Eosinophil count	44423 500 0	-0.3 (-0.4,-0.2)	3.3x10 ⁻¹⁰	9	3.7x10 ⁻¹¹	7.6x10 ⁻⁹
<i>GPIBA</i>	Mean platelet thrombocyte volume	45509 98 1	0.5 (0.3,0.7)	6.4x10 ⁻⁸	12	3.0x10 ⁻⁵	0.50
<i>TUBB1</i>	Platelet distribution width	45540 28 0	1.8 (1.5,2.2)	2.5x10 ⁻²³	14	2.3x10 ⁻⁶	5.4x10 ⁻³
<i>TUBB1</i>	Mean platelet thrombocyte volume	45577 31 0	1.0 (0.6,1.3)	2.4x10 ⁻⁸	14	2.1x10 ⁻³	0.028

TUBB1	Platelet count	45422 30 0	-1.1 (-1.4,-0.7)	2.1×10^{-9}	14	1.1×10^{-7}	0.029
HBB	Red blood cell erythrocyte distribution width	45084 4 0	2.7 (1.7,3.6)	5.8×10^{-8}	2	NA	0.76
HBB	Red blood cell erythrocyte count	45609 4 0	3 (2.0,3.9)	1.7×10^{-9}	2	NA	0.23
KLF1	Red blood cell erythrocyte distribution width	45063 25 0	1.5 (1.1,1.8)	1.5×10^{-13}	6	4.4×10^{-10}	0.43
KLF1	Mean corpuscular haemoglobin	45350 27 0	-1.5 (-1.9,-1.2)	1.7×10^{-16}	6	8.8×10^{-13}	0.77
KLF1	Mean corpuscular volume	45448 27 0	-1.4 (-1.8,-1.1)	4.0×10^{-14}	6	1.1×10^{-10}	0.63
ASXLI	Platelet distribution width	45451 11 17 0	0.5 (0.34,0.7)	4.7×10^{-9}	63	4.1×10^{-5}	NA
ASXLI	Red blood cell erythrocyte distribution width	44974 11 14 0	0.6 (0.4,0.8)	2.4×10^{-11}	63	7.4×10^{-6}	NA
CHEK2	Platelet crit	45147 295 2	0.3 (0.2,0.4)	7.9×10^{-8}	21	1.2×10^{-7}	0.039
KALRN	Mean platelet thrombocyte volume	45374 233 1	-0.6 (-0.7,-0.5)	2.7×10^{-23}	22	1.1×10^{-23}	1.9×10^{-20}

351

352 **Table 5 | LOF gene burden results with previously known genetic associations.** LOF gene burden

353 association with available clinical and continuous traits in 46,979 UKB participants of European ancestry

354 with WES.

355

356 **LOF Associations and Novel Gene Discovery**

357 Our LOF gene burden association analysis identified five gene-trait LOF associations with $p < 10^{-7}$

358 that have not previously been reported (Table 6). We identified a novel association between *PIEZO1* LOFs

359 (cumulative allele frequency = 0.2%) and increased risk for varicose veins (OR=4.8, $P=2.7 \times 10^{-8}$). This

360 finding is driven by a burden of rare LOF variants, with the most significant *PIEZO1* single variant LOF

361 association achieving a p-value of 2.3×10^{-3} . ‘Leave-one-out’ (LOO) analyses indicated no single variant

362 accounted for the entire signal and step-wise regression analyses indicated that 11 separate variants (5 of

363 which had minor allele count (MAC)>1) were contributing to the overall burden signal (Sup. Table 8 and

364 Ext. Data SingleVariantLOFs.xlsx). We replicated this finding for varicose veins (1,572 cases, 75,704
 365 controls) in WES data from the DiscovEHR study (OR= 3.8, p= 1.5x10⁻⁶) (Sup. Table 10). This region had
 366 previously been implicated by common non-coding variants with small effects³⁴ (rs2911463 , OR = 0.996;
 367 Supplemental Table 9). *PIEZO1* encodes a 36 transmembrane domain cation channel that is highly
 368 expressed in the endothelium and plays a critical role in the development and adult physiology of the
 369 vascular system, where it translates shear stress into electrical signals³⁵. This previous report of the
 370 rs2911463 variant mapped the association to *PIEZO1* through evidence of gene function and analysis using
 371 DEPICT, but did not find strong eQTL evidence that would clarify mechanism to modulate the target
 372 therapeutically³⁴. Rare missense variants have been reported³⁴ in families segregating autosomal dominant
 373 dehydrated hereditary stomatocytosis (DHS, MIM #194380) characterized by hemolytic anemia with
 374 primary erythrocyte dehydration due to decreased osmotic fragility. Whereas biallelic loss of function
 375 variants in *PIEZO1* have been reported in families with lymphatic malformation syndrome [MIM #616843],
 376 a rare autosomal recessive disorder characterized by generalized lymphedema, intestinal and/or pulmonary
 377 lymphangiectasia and pleural and/or pericardial effusions. Interestingly, some of the reported patients
 378 presented with varicose veins and deep vein thrombosis³⁶. Our data provide compelling support for *PIEZO1*
 379 as the causal gene in this locus, but also clarifies direction of effect in that loss of gene function in
 380 heterozygous carriers leads to increased risk of developing varicose veins.
 381

Gene	ICD10 Code, Binary Phenotype	RRIRAIAA	OR (95% CI)	WES Burden P	N SNV	Lowest P SNV	Imputed 50k Burden P
<i>PIEZO1</i>	I83.9, Asymptomatic varicose veins of lower extremities	Ctrl:43285114210 Cases:126712010	4.8 (3.1,7.8)	2.7x10 ⁻⁸	65	2.3x10 ⁻³	0.083
Gene	Quantitative Phenotype	RRIRAIAA	Beta (95% CI)	WES Burden P	N SNV	Lowest P SNV	Imputed 50k Burden P
<i>MEPE</i>	Heel bone mineral density	42898115010	-0.5 (-0.6,-0.3)	1.4x10 ⁻⁸	16	6.2x10 ⁻⁵	0.033
<i>COL6A1</i>	Corneal resistance factor mean	3562111710	-1.5 (-2.0,-1.0)	3.6x10 ⁻¹⁰	11	1.5x10 ⁻⁴	NA ¹

<i>COL6A1</i>	Corneal hysteresis mean	3562011710	-1.3 (-1.8,-0.9)	2.1×10^{-8}	11	4.6×10^{-4}	NA ¹
<i>IQGAP2</i>	Mean platelet thrombocyte volume	45443116510	0.7 (0.5,0.8)	1.1×10^{-19}	53	9.3×10^{-8}	0.10
<i>GMPR</i>	Mean corpuscular haemoglobin	45195118210	0.4 (0.3,0.6)	1.1×10^{-8}	13	6.0×10^{-8}	6.2×10^{-6}

382 **Table 6 | Novel LOF gene burden associations.** LOF gene burden association with available clinical and
 383 continuous traits in 46,979 UKB participants of European ancestry with WES. ¹No *COL6A1* LOFs were
 384 observed in imputed sequence.

385

386 We also identified a novel LOF burden association with *MEPE* (cumulative MAF 0.18%) and
 387 decreased bone density (as measured by heel bone mineral density, -0.50 standard deviations (SD), p-value
 388 = 1.4×10^{-8}). LOO analyses (Sup. Table 11) suggested that the aggregate signal is driven by multiple variants,
 389 one of which could be imputed (rs753138805, encoding a frameshift predicted to result in early protein
 390 truncation). In analysis of all 500k UKB participants, rs753138805 was significantly associated with
 391 decreased BMD (-0.4 SD, $P=8.1 \times 10^{-19}$) and showed a trend for increased risk of osteoporosis (N=3,495
 392 cases, OR=1.9, $P=0.10$, Sup. Table 16). These findings are corroborated by a query of the HUNT study³⁷,
 393 where rs753138805 was associated with decreased BMD (-0.5 SD, $P=2.1 \times 10^{-18}$) and increased risk of any
 394 fracture (N=24,155 cases, $P=1.6 \times 10^{-5}$, OR=1.4) (Sup. Table 16). In DiscovEHR, we observed a
 395 directionally consistent, but nonsignificant, association for *MEPE* LOFs with femoral neck BMD T-score
 396 ($B = -0.19$, $P = 0.22$). The *MEPE* locus was previously implicated in GWAS³⁸, with six independent signals
 397 with modest effects on bone mineral density. While two of the previously reported non-coding variants are
 398 in moderate ($r^2=0.5$) or high ($r^2=0.78$) linkage disequilibrium (LD) with two variants contributing to the
 399 burden test (Sup. Table 12), the burden association is only partially attenuated in conditional analyses
 400 ($p \sim 2 \times 10^{-4}$ with all 6 variants together). *MEPE* encodes a secreted calcium-binding phosphoprotein with a
 401 key role in osteocyte differentiation and bone homeostasis^{39,40}. Studies in *Mepe*^{-/-} knockout mice
 402 (*Mepe*^{tm1Tbrw}) have yielded inconsistent results, with two groups reporting an increase in BMD^{40,41} and
 403 another reporting no change⁴².

404 In another novel signal, *COL6A1* LOFs (cumulative allele frequency = 0.03%) are associated with
405 a 2.7 mmHg decrease in corneal resistance factor (CRF) (-1.5 SD, p-value = 3.6×10^{-10}) and corneal
406 hysteresis (CH) (-1.3 SD, p-value = 2.1×10^{-8}), which are measures of corneal biomechanics⁴³. *COL6A1*
407 encodes a component of collagen type VI microfibrils, which play important roles in maintaining structure
408 and function of the extracellular matrix, and which are major components of the human cornea⁴⁴. This
409 locus has previously been implicated in ocular traits; rs73157695 and nearby common variants have been
410 associated with myopia⁴⁵ (OR = 0.94; p = $\sim 10^{-13}$) and intraocular pressure⁴⁶. LOO analyses indicate
411 multiple variants are driving the association with both corneal traits (Sup. Tables 13, 14) and that these are
412 not in strong LD with previously reported variants (Sup. Table 15). *COL6A1* protein levels were reduced
413 in eyes from patients with keratoconus⁴⁷, and individuals with keratoconus and other corneal diseases such
414 as Fuchs' corneal dystrophy have reduced CH and CRF⁴⁸. Measures of CH and CRF were not available in
415 DiscovEHR for replication analyses.

416 The remaining novel LOF associations in *IQGAP2* and *GMPR* (driven by rs147049568) are for
417 hematologic traits in which variants in/near each gene have previously been implicated by GWAS^{29,49}. Our
418 results for these two genes, each of which replicated in DiscovEHR (Sup. Table 7), provide additional
419 evidence for causal roles for these genes and establishes direction of effect with respect to gene function on
420 hematologic traits. In equivalent sample sizes, LOF burden results from imputed sequence would not have
421 uncovered the novel LOF associations at $p < 10^{-7}$ as identified by WES (Table 6). Further, for 19 of 25 LOF
422 burden results described herein, gene burden results from WES in 50k were more significant than burden
423 results from imputed sequence in all 500k UKB participants (Sup. table 10), demonstrating the value of
424 rare variants captured by WES to power these associations.

425

426 DISCUSSION

427 Integration of large scale genomic and precision medicine initiatives offer the potential to
428 revolutionize medicine and healthcare. Such initiatives provide a foundation of knowledge linking genomic

429 and molecular data to health-related data at population scale, allowing for the ability to more completely
430 and systematically study genetic variation and its functional consequences on health and disease. Here, we
431 describe the initial tranche of large-scale exome sequencing of 49,960 UK Biobank participants, which to
432 our knowledge is currently the largest open access resource of exome sequence data linked to health records
433 and extensive longitudinal study measures. These data greatly extend the current genetic resource,
434 particularly in ascertainment of rare coding variation, which we demonstrate has utility in resolving variant
435 to gene links and directionality of gene to phenotype associations.

436 After quality control, we observed nearly four million single nucleotide and indel coding variants.
437 Only approximately 14% of coding variants identified by WES were observed in the imputed sequence of
438 49,797 participants with both WES and imputed sequence, highlighting the added value of exome
439 sequencing. This enrichment was even more pronounced with LOF variation where WES identified
440 >230,000 LOF variants and only approximately 5% of these were present in the imputed sequence. Further,
441 22.6% of the coding variants in the imputed sequence were not observed in the exome sequence data which
442 may represent a large proportion of rare variants that have poor imputation accuracy, as observed in our
443 concordance and visual validation analyses. A small proportion of these variants, seen only in the imputed
444 sequence, also represents variants not in the regions targeted by exome capture design and sequencing, a
445 limitation of the targeted capture approach. Increasing numbers of individuals and ancestral diversity in
446 imputation reference panels are expected to improve imputation accuracy for rare variants.

447 As with previous studies of this size²², we observed a large number of LOF variants, including at
448 least one rare heterozygous LOF variant carrier in >97% of autosomal genes (compared to >36% of
449 autosomal genes in the imputed sequence for the same participants). It is important to note that our LOF
450 annotation strategy is geared towards increasing sensitivity for identification of LOF variants and novel
451 downstream association discovery. While the number of genes with heterozygous instances of LOF variants
452 is approaching saturation at this sample size, exome sequencing of the entirety of the UKB resource will
453 dramatically increase the number of LOF carriers and the ability to detect phenotypic associations. We also

454 observe 1,071 autosomal genes with homozygous instances of rare LOF variants, and this number of genes
455 will also increase with continued sequencing of all UKB participants; however, studies in populations with
456 a high degree of parental relatedness^{50,51} will provide yet more genes with homozygous LOFs and
457 complement efforts such as UKB. LOF variation is an extremely important class of variation for identifying
458 drivers of high genetic risk, novel disease genes, and therapeutic targets. Very large samples sizes are
459 needed to detect novel LOF associations given their collective rare allele frequencies. The exome sequence
460 data provides a substantial enhancement to the number of LOF variants identified and power for detecting
461 novel associations, which will only improve with continued sequencing of all UKB participants.

462 We illustrate the unique value of this expanded exome sequence resource in the UKB to assess
463 pathogenic and likely pathogenic variants in an unascertained large-scale population-based study with
464 longitudinal follow up. We conducted a survey of pathogenic and likely pathogenic variants in the
465 medically actionable ACMG59 genes. Using stringent variant filtering criteria, we arrived at an estimated
466 prevalence of 2% of individuals in this study population having a clinically actionable finding. This
467 resource allows us to characterize disease risk profiles for individuals who carry pathogenic and likely
468 pathogenic variants in medically relevant disease genes, including cancer susceptibility genes, such as
469 *BRCA1* and *BRCA2*. We observed that pathogenic and likely pathogenic variant carriers had 3.75-fold
470 greater odds of any of the 5 cancers previously associated with *BRCA1/2*; prevalence for any of the 5 cancers
471 was 21.0% in carriers vs 6.6% in non-carriers. We further explored whether these variants conferred risk to
472 any other cancers and did not observe any such associations. This resource will be valuable for assessment
473 of variant pathogenicity, particularly for variants of unknown significance and novel variants, and in
474 exploring the full spectrum of disease risk and phenotypic expression. One limitation of the resource for
475 such purposes is limited ancestral diversity. This and other similar studies also highlight the value and
476 potential to apply large scale sequencing at the population scale to identify a meaningful proportion of
477 individuals who are at high risk of diseases where effective interventions are available that can significantly

478 reduce the morbidity and mortality of genetically susceptible individuals; such precision medicine
479 approaches could substantially reduce the burden of many diseases.

480 We conducted gene burden association testing for LOF variants across all genes and encompassing
481 greater than 1,700 binary and quantitative traits. In addition to replication of numerous positive controls,
482 we also identified a handful of significant novel LOF associations highlighting novel biology and genetics
483 of large effect on disease traits of interest; this included *PIEZO1* for varicose veins, *MEPE* for bone density,
484 and *COL6A1* for corneal thickness, amongst others. We identified a novel burden association in *PIEZO1*,
485 a mechanosensing ion channel present in endothelial cells in vascular walls, that confers a nearly five-fold
486 increased odds of varicose veins in heterozygous LOF carriers. We also identified a novel LOF burden
487 association in *MEPE* with decreased BMD and an approximately 2-fold increased odds of osteoporosis and
488 1.5-fold increased risk of fractures. Overall, through WES and gene burden tests of association for LOF
489 variants, we identified 25 unique gene-trait associations exceeding a $p < 10^{-7}$ of which 21 were substantially
490 more significant than any single LOF variant included in the burden test, highlighting the value of WES
491 and the ability to detect novel associations driven by rare coding variation. While these regions had
492 previously been identified in genome-wide association studies of $>10x$ the sample size, a key strength of
493 the current approach is compelling identification of likely causal genes and the direction of effect: two key
494 pieces of information required for translation towards novel therapeutics. This survey of rare LOF
495 associations was limited by sample size for most binary traits but was well powered for many quantitative
496 traits. While surveys of LOF variation in the entire UKB study using array and imputed sequence have
497 identified LOF associations in previous reports^{52,53}, WES identifies novel associations, unique to exome
498 sequence and detected in only approximately one tenth of the sample size; this highlights the considerable
499 power of exome sequencing for LOF and rare variant association discovery and the further promise of novel
500 biological insights through sequencing all participants in the UKB resource.

501 Efforts are underway to sequence the exomes of all 500,000 UKB participants; these efforts will
502 greatly expand the total amount of rare coding variation ascertained, including the number of heterozygous

503 LOF instances that can now be observed in nearly all genes and the number of genes for which naturally
504 occurring homozygous knockouts can be observed. Coupled with rich laboratory, biomarker, health record,
505 imaging, and other health related data continually added to the UKB resource, exome sequencing will
506 enhance the power for discovery and will continue to yield many important findings and insights. The WES
507 data is available to approved researchers through similar access protocols as existing UK Biobank data (see
508 URLs).

509

510 **ACKNOWLEDGEMENTS**

511 The authors thank the UKBiobank participants and researchers for creating an open scientific
512 resource for the research community; the MyCode Community Health Initiative participants for taking
513 part in the DiscovEHR collaboration; and the participants of the Nord-Trøndelag Health Study (HUNT), a
514 collaboration between the HUNT Research Centre (Faculty of Medicine, Norwegian University of
515 Science and Technology NTNU), the Nord-Trøndelag County Council, the Central Norway Health
516 Authority and the Norwegian Institute of Public Health. This work was referring UKB application 26041.

517

518 **URLs**

519 **UK Biobank website and data access** <http://ukbiobank.ac.uk/>

520

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662 **Competing interests**

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