**ASSOCIATION STUDIES ARTICLE**

**Homozygous loss-of-function variants in European cosmopolitan and isolate populations**

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**Abstract**

Homozygous loss of function (HLOF) variants provide a valuable window on gene function in humans, as well as an inventory of the human genes that are not essential for survival and reproduction. All humans carry at least a few HLOF variants, but the exact number of inactivated genes that can be tolerated is currently unknown—as are the phenotypic effects of losing function for most human genes. Here, we make use of 1432 whole exome sequences from five European populations to expand the catalogue of known human HLOF mutations; after stringent filtering of variants in our dataset, we identify a total of 173 HLOF mutations, 76 (44%) of which have not been observed previously. We find that population isolates are particularly well suited to surveys of novel HLOF genes because individuals in such populations carry extensive runs of homozygosity, which we show are enriched for novel, rare HLOF variants. Further, we make use of extensive phenotypic data to show that most HLOFs, ascertained

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in population-based samples, appear to have little detectable effect on the phenotype. On the contrary, we document several genes directly implicated in disease that seem to tolerate HLOF variants. Overall HLOF genes are enriched for olfactory receptor function and are expressed in testes more often than expected, consistent with reduced purifying selection and incipient pseudogenisation.

**Introduction**

The human genome contains more than 20 000 protein-coding genes, but it is currently unknown how many of these genes are essential for development, survival and reproduction, and how many genes are, to some degree, ‘dispensable’. All humans carry genetic variants predicted to cause loss of function (LOF) for a variety of protein-coding genes, i.e. they carry frameshift or premature stop codon mutations in the coding regions of genes, whole gene deletions, or splice site disruptions (1). In addition it has been estimated that each human genome carries around 20 of these LOF variants in the homozygous state (HLOF), resulting in a naturally occurring ‘knockout’ of the gene concerned (2).

**Results**

Across the 1432 exomes, 1 465 905 indels and single nucleotide polymorphisms (SNPs) passed the GATK default filters. These included predicted 1084 stop-gain and 1185 frameshift variants that were homozygous in at least one individual. However, the majority of these apparent HLOF variants were likely to be second-generation sequencing errors, rare errors in the reference genome or variants that do not disrupt gene function. Conservative filtering and additional conventional Sanger sequencing of variants led to the exclusion of most SNPs and indels from our analysis, reducing the number of homozygous stop-gains to 94 and the number of frameshifts to 79. In particular, Sanger sequencing revealed the importance of sequence coverage in variant calling accuracy (Supplementary Material, Fig. S1), and we conservatively set the minimum coverage for novel variants, all other sites were non-reference, assuming that these HLOFs are population-specific and that a wider variety may be discovered across diverse populations.

Population isolates provide natural laboratories for studying the roles of rare variants in complex phenotypes because the population’s evolutionary history may often lead to relatively high frequencies of rare homozygous variants. On the one hand, population isolation leads to increased levels of background relatedness and inbreeding, which increases levels of homozygosity; in addition, genetic drift is stronger in small populations, which can lead to a higher frequency of mildly deleterious variants, such as LOF mutations, in small or bottlenecked populations (11). Indeed, a recent study found a significant enrichment of low frequency LOF variants in the Finnish population relative to other Europeans, and, by making use of phenotype data in 36 262 individuals, they could identify variants affecting quantitative traits (12).

In this study, we used exome sequencing in four European isolate populations spanning the continent and a collection of more cosmopolitan Scottish samples from the Generation Scotland: Scottish Family Health Study (GS:SFHS) (13). For the first time we are able to examine the frequencies of HLOF variants across isolate populations sampled from diverse sites across Europe and compare them to a national collection. Using exome data for a total of 1432 individuals, we identify 94 validated premature stop-gain and 79 frameshift variants; a total of 76 of which had not been observed in previous surveys (2,7), including the published variants of a study of Finnish and non-Finnish Europeans (12). We find a higher prevalence of HLOF variants in the isolates, and find that novel HLOFs are significantly enriched in these populations. We also exploit phenotypic data, to explore the effects of HLOF variants on hundreds of clinically relevant quantitative traits across many physiological areas. We find that HLOFs in our dataset generally have little effect on phenotype and appear to constitute largely neutral variation.
population, whereas 9 were found exclusively in the isolates (CROATIA-Vis, CROATIA-Korcüla, NSPHS, ORCADES), at very low frequencies (Table 2). This is despite a lower number of individuals that were sequenced in isolate populations—588 in isolates versus 844 individuals in GS:SFHS—suggesting an enrichment of rare, novel HLOFs in isolate populations (Fisher’s exact test, \( P < 0.01 \)). Note that the variant at chr6:31106500 had a dbsNP validation record but was included in the Sanger-sequencing as a control; this variant was observed in four populations. Given that the Sanger sequenced variants were a priori expected to be enriched for false positives, their low validation rate is not too surprising.

Among the 20 variants that failed validation by Sanger sequencing, 12 were completely absent (9 erroneously called stop-gains and 3 frameshifts); a further 3 frameshift variants were in fact heterozygous, and 2 deletions turned out to remove a multiple of 3 base pairs; 3 sequences were not clean or gave ambiguous sequencing results and were conservatively excluded. Other than low sequence coverage of these 20 variants, however, there were no indications as to why high throughput sequencing had given erroneous results.

Individuals from population isolates tend to carry longer runs of homozygosity (ROHs) compared with more cosmopolitan individuals (14). Rare HLOFs are expected to be enriched within ROHs because they represent regions that are identical-by-descent, that is, inherited from the same common ancestor (7); thus, rare variants, which would otherwise not be found in the homozygous state, are brought together (15).

To test this, we assessed, for each HLOF and carrier, whether a variant was found within or outwith a run of homozygosity (ROH). We then calculated the overall frequency of HLOFs which fell within ROHs; this value differed among populations (3% of HLOFs in GS:SFHS were found within ROHs, whereas it was 10% in CROATIA-Korcüla; 8% in NSPHS; 7% in CROATIA-Vis; 6% in ORCADES), reflecting the different overall proportions of the genome that are found within ROHs in isolate versus our cosmopolitan sample (14) (Fisher’s exact test comparing the number of HLOFs inside and outside ROHs in GS:SFHS versus each isolate population: \( P < 0.01 \) in each comparison). Singleton HLOFs that were observed only once across all populations were found more often within ROHs (15 out of 48 HLOFs = 31%)—and all seven novel singletons identified in this study fell within ROHs. Importantly, HLOF variants that were biased towards being inside ROHs had lower allele frequencies compared with variants that were mostly found outside ROHs (Fig. 1), suggesting that rare HLOFs can be found more easily in individuals with increased homozygosity.

Table 1. Filtering putative HLOF variants

<table>
<thead>
<tr>
<th>Filter</th>
<th>Stop gain mutations</th>
<th>Frameshift mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total number of variants before filtering</td>
<td>1084</td>
<td>1185</td>
</tr>
<tr>
<td>Relative position &lt; 0.9</td>
<td>883</td>
<td>973</td>
</tr>
<tr>
<td>Duke (mapability)</td>
<td>960</td>
<td>1027</td>
</tr>
<tr>
<td>DAC excluded regions (mapability)</td>
<td>1083</td>
<td>1175</td>
</tr>
<tr>
<td>CRg (mapability)</td>
<td>893</td>
<td>917</td>
</tr>
<tr>
<td>Min. 200</td>
<td>945</td>
<td>942</td>
</tr>
<tr>
<td>SureSelect &amp; TrueSeq</td>
<td>794</td>
<td>829</td>
</tr>
<tr>
<td>Ancestral allele</td>
<td>1032</td>
<td>NA</td>
</tr>
<tr>
<td>MNP/frameshift nearby</td>
<td>982</td>
<td>817</td>
</tr>
<tr>
<td>Hardy-Weinberg</td>
<td>323</td>
<td>373</td>
</tr>
<tr>
<td>All filters applied, Sanger Sequencing</td>
<td>94</td>
<td>79</td>
</tr>
</tbody>
</table>

The number of putative HLOF variants remaining after each mutational filter had been applied individually. Filters have the following meaning: ‘Relative_position < 0.9’ indicates that variants are limited to the first 90% of all splice variants of a gene. ‘Duke’, ‘DAC’ and ‘CRg’ are mapability scores of UCSC. ‘Min.200’ indicates that at least 200 individuals were sampled for each variant. ‘SureSelect & TrueSeq’ is the intersection of the two exome sequencing kits. ‘Ancestral allele’ indicates whether the LOF variant is found in other primates. The ancestral allele filter was applied to frameshift mutations only after all other filters had been applied, leading to the exclusion of seven variants. ‘MNP/frameshift nearby’ indicates whether a restoring variant was found in proximity of the focal variant. ‘Hardy-Weinberg’ indicates whether the variant passed our Hardy-Weinberg filter.

Table 2. Sanger-sequencing confirmed HLOFs

<table>
<thead>
<tr>
<th>Position</th>
<th>Gene</th>
<th>Number of homozygotes</th>
<th>Population</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1:55076137</td>
<td>FAM151A</td>
<td>1</td>
<td>NSPHS</td>
</tr>
<tr>
<td>chr4:113539281</td>
<td>C4orf21</td>
<td>1</td>
<td>CROATIA-Korcüla</td>
</tr>
<tr>
<td>chr5:96222446</td>
<td>EARP2</td>
<td>1</td>
<td>CROATIA-Vis</td>
</tr>
<tr>
<td>chr6:28355864</td>
<td>ZSCAN12</td>
<td>1</td>
<td>CROATIA-Vis</td>
</tr>
<tr>
<td>chr6:31106500</td>
<td>PSORS1C1</td>
<td>26</td>
<td>ORCADES, GS:SFHS, NSPHS</td>
</tr>
<tr>
<td>chr12:70088219</td>
<td>BEST3</td>
<td>2</td>
<td>CROATIA-Vis, ORCADES</td>
</tr>
<tr>
<td>chr14:57672624</td>
<td>AL391152.1</td>
<td>2</td>
<td>NSPHS, GS:SFHS</td>
</tr>
<tr>
<td>chr15:44091290</td>
<td>SERINC4</td>
<td>1</td>
<td>CROATIA-Vis</td>
</tr>
<tr>
<td>chr17:46882286</td>
<td>TTL6</td>
<td>2</td>
<td>CROATIA-Vis, GS:SFHS</td>
</tr>
<tr>
<td>chr17:47921435</td>
<td>TAC4</td>
<td>1</td>
<td>CROATIA-Vis</td>
</tr>
<tr>
<td>chr19:36230499</td>
<td>IGFLR1</td>
<td>1</td>
<td>ORCADES</td>
</tr>
<tr>
<td>chr19:51729103</td>
<td>CD33</td>
<td>3</td>
<td>NSPHS, GS:SFHS</td>
</tr>
<tr>
<td>chrX:50659021</td>
<td>BMP15</td>
<td>1</td>
<td>ORCADES</td>
</tr>
</tbody>
</table>

The number of individuals which were homozygous for a novel, Sanger-sequencing confirmed variant, and the population where the variant was found.

Downloaded from http://hmg.oxfordjournals.org at Edinburgh University on July 23, 2015
The median C-score of our novel, Sanger sequencing-conﬁrmed, variants was 20.0; this is not signiﬁcantly different from that of the remaining, previously known, variants, which had a median score of 18.0 (Wilcoxon test: W = 1041.5; N.S.). However, there was a negative correlation between the C-score and the number of individuals carrying a HLOF variant (Spearman’s rho = −0.30; P < 0.05), consistent with the extent of purifying selection on a variant being reﬂected, to some extent, by the number of times an HLOF is observed.

Figure 1. Rare HLOFs are found within ROHs. Allele frequencies of HLOFs that are biased towards being inside or outside runs of homozygosity (ROHs) in the ﬁve populations studied (using a binomial test with P < 0.1). For GS:SFHS, CROATIA-Vis, ORCADES and NSPHS, the allele frequencies of variants that were enriched in ROHs were signiﬁcantly lower compared with variants that were found in the autozygome (Wilcoxon test; P < 0.05). In CROATIA-Korčula, only two variants were underrepresented in ROHs, and the Wilcoxon test was not signiﬁcant.

Table 3. Summary of the numbers of HLOF found

<table>
<thead>
<tr>
<th>Population</th>
<th>N</th>
<th>N(HLOFs)</th>
<th>Yield</th>
<th>Private LOFs</th>
<th>Private HLOFs</th>
</tr>
</thead>
<tbody>
<tr>
<td>GS: SFHS</td>
<td>844</td>
<td>137</td>
<td>0.16</td>
<td>1</td>
<td>26</td>
</tr>
<tr>
<td>CROATIA-Vis</td>
<td>193</td>
<td>104</td>
<td>0.54</td>
<td>2</td>
<td>8</td>
</tr>
<tr>
<td>ORCADES</td>
<td>197</td>
<td>103</td>
<td>0.52</td>
<td>3</td>
<td>13</td>
</tr>
<tr>
<td>NSPHS</td>
<td>98</td>
<td>91</td>
<td>0.93</td>
<td>0</td>
<td>6</td>
</tr>
<tr>
<td>CROATIA-Korčula</td>
<td>100</td>
<td>74</td>
<td>0.74</td>
<td>1</td>
<td>4</td>
</tr>
</tbody>
</table>

The sample size, N, and the number of HLOF mutations that were found in each population, N(HLOFs); the average yield per individual (N(HLOFs)/N); the extent to which the mutations are shared across populations. Private LOFs are seen only in one population, including as heterozygotes; private HLOFs are shared as heterozygotes across populations.

Material, Table S1). The median C-score of our novel, Sanger sequencing-confirmed, variants was 20.0; this is not signiﬁcantly different from that of the remaining, previously known, variants, which had a median score of 18.0 (Wilcoxon test: W = 1041.5; N.S.). However, there was a negative correlation between the C-score and the number of individuals carrying a HLOF variant (Spearman’s rho = −0.30; P < 0.05), consistent with the extent of purifying selection on a variant being reﬂected, to some extent, by the number of times an HLOF is observed.

Gene Ontology analysis using GOrilla (http://cbl-gorilla.cs.techion.ac.il/ accessed September 2014) (18) revealed an excess of transmembrane signalling receptor genes amongst HLOF genes, including olfactory receptor genes (Table 4). Indeed, olfactory receptor genes have previously been shown to be over-represented among HLOF genes (2), and segregating polymorphisms of functional and non-functional copies of olfactory genes are common (19). Although no other GO category was over-represented among the HLOF genes discovered here, a large number of HLOF genes were expressed in testis: across 16 tissues sampled, expression was highest in testis for 28.7% of HLOF genes, i.e. for 41 out of the 143 HLOF genes that were present in the EBI
expression atlas (http://www.ebi.ac.uk/gxa/ accessed September 2014) (20,21). The proportion of testis-expressed genes amongst all genes sampled was also higher for the HLOF genes (119 out of 143 genes = 83%) compared with the overall expression profile of human protein-coding genes (77% of all human transcripts detected by (22) were found in testis, with 10% being enriched in testis). This apparent loss of function at testis-expressed genes is consistent with a recent study (23), which showed that male-specific genes in humans carried a relatively high load of deleterious polymorphisms, possibly due to reduced selection on these variants in females who do not express these genes.

Table 4. Gene Ontology

<table>
<thead>
<tr>
<th>GO term</th>
<th>Description</th>
<th>FDR adjusted q-value</th>
<th>Enrichment (N, B, n, b)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO:0004984</td>
<td>Olfactory receptor activity</td>
<td>3.35E-11</td>
<td>7.65 (17 424,362,151,24)</td>
</tr>
<tr>
<td>GO:0004930</td>
<td>G-protein coupled receptor activity</td>
<td>7.86E-06</td>
<td>3.81 (17 424,788,151,26)</td>
</tr>
<tr>
<td>GO:0004888</td>
<td>Transmembrane signalling receptor activity</td>
<td>8.29E-04</td>
<td>2.80 (17 424,1154,151,28)</td>
</tr>
<tr>
<td>GO:0004872</td>
<td>Receptor activity</td>
<td>8.60E-04</td>
<td>2.52 (17 424,1464,151,32)</td>
</tr>
<tr>
<td>GO:0038023</td>
<td>Signalling receptor activity</td>
<td>2.50E-03</td>
<td>2.58 (17 424,1253,151,28)</td>
</tr>
<tr>
<td>GO:0004871</td>
<td>Signal transducer activity</td>
<td>9.62E-02</td>
<td>2.09 (17 424,1548,151,28)</td>
</tr>
<tr>
<td>GO:0060089</td>
<td>Molecular transducer activity</td>
<td>8.25E-02</td>
<td>2.09 (17 424,1548,151,28)</td>
</tr>
</tbody>
</table>

GO analysis of genes containing HLOF variants, using, as a background set, all genes captured by the intersection of the SureSelect and TruSeq exome sequencing kits. Enrichment = (b/n)/(B/N); N = Number of genes; B = Number of genes associated with a GO term; n= number of genes in the target set; b = number of genes in the intersection.
OMIM genes in our dataset were associated with risk phenotypes, rather than Mendelian diseases: BTN2L, CARD14, TLR5 and ARM2 were associated with susceptibility to sarcoidosis, psoriasis or le- gionnaire disease and late onset macular degeneration, respect- ively; RNF212 was associated with a non-risk phenotype, variation in recombination rate (Supplementary Material, Table S1).

A wide range of phenotypic measurements were available for individuals from the five populations studied (Supplementary Material, Table S2). However, there was no evidence for any vari- ant possessing a measurable effect, including four variants in known disease genes:

The Macrophase Scavenger receptor 1 (MSR1, also known as SRA) is an LDL receptor, and is implicated in the pathologic de- position of cholesterol in arterial walls (24,25). A single individual (a 68 year-old female from CROATIA-Vis with a body mass index of 24.5) carried a HLOF in MSR1; this variant had not previously observed as a homozygote (2,7,12), and it was associated with a high C-score (38.0). However, the individual showed no suspi- cious phenotype, and her serum lipid levels were normal (total cholesterol 5.7 mmol/l; HDL 1.92 mmol/l; LDL 1.48 mmol/l), sug- gesting that losing function at the MSR1 gene does not have major effects on blood lipid levels.

Bone morphogenetic protein 15 (BMP15) is an X-linked gene, which is exclusively expressed in oocytes, in the oocytes of late pri- mary follicles (26), and it is associated with infertility and ovarian dysgenesis (OD), even in heterozygotes (27–29). In our dataset, we found a rare LOF variant in BMP15 in ORCADES: in the exome se- quence dataset, a single male carried a (hemizygous) LOF frame- shift variant in the mature protein-coding region of BMP15, upstream of the missense mutation described previously (29). The same variant was also found in the heterozygous state in three ORCADES females, but in no other population. We Sanger se- quenced these 4 individuals, as well as 33 additional Orcadians from the ORCADES study, all of whom were first, second or third degree relatives of the 4 known carriers. Supplementary Material, Table S3 shows their genotypes and the number of offspring: we never observed the frameshift variant in the homozygous state in females; and of the five heterozygous females, two had chil- dren. Further, the variant was present on the single X chromo- some in nine males (whose mothers must have carried the variant on at least one X), so we can conclude that the frameshift variant does not lead to OD in heterozygotes.

Among the HLOF variants in genes with OMIM entries, two variants might be rescued by alternative transcripts and reading frames. PDE6G, the first of these genes, encodes one of the three subunits of Cyclic GMP-phosphodiesterase (PDE), and incorrect splicing of the gene is reported to lead to early-onset retinitis pig- mentosa in a family-based mapping study (30). In our dataset, a HLOF was observed in six individuals, but the four carriers who were scored for eye phenotypes (from CROATIA-Vis, CROATIA- Korčula and ORCADES) did not show any abnormalities. How- ever, the frameshift variant was detected in only one of the five alternative transcripts for this gene, and function may be re- stored by the presence of alternative transcripts for which the variant is intrinsic and in the 5’ UTR respectively. Similarly, var- iants in SERAC1 are thought to cause a severe Mendelian phen- otype (MEGDEL syndrome), which includes encephalopathy, dystonia and deafness (31). We find a HLOF in a single individual from CROATIA-Vis—a healthy 33 year-old male who showed no unusual phenotype. However, SERAC1 has several transcripts in two different reading frames, and the stop-gain variant occurs a reading frame, which is expected to lead to nonsense-mediated decay (in transcripts ENST000000607071, ENST000000607742, ENST000000606965). The same variant is merely a missense vari- ant on exon 4 of the transcript (ENST00000367104), i.e. outside the lipase/esterase domain, which is implicated in causing MEG- DEL syndrome when disrupted (31).

In all of the five populations, the number of HLOFs for a given individual (which ranged from 0 to 18) was not a good predictor of the observed number of outlier traits per individual, i.e. the number of trait values in the top or bottom 1% of the population (which ranged from zero to 211); this result remained unchanged also if only strongly deleterious HLOFs (C-score >25) were included in the analysis, or if olfactory genes were excluded (Supplementary Material, Table S4). If the majority of genes con- taining HLOF variants do not have measureable phenotypic effects, this could be due to a higher than usual number of para- logues for these genes, i.e. genes belonging to the same gene fam- ily could act as a buffer on the effect. This, however, does not seem to be the explanation: when olfactory genes were excluded, the number of paralogues for HLOF-containing genes was actually lower compared with protein-coding genes in the genome as a whole (Wilcoxon test, 70% identity cut-off for paralogues: P < 0.05; Wilcoxon test, 80% identity cut-off for paralogues: P < 0.01). Fur- ther, the number of one-to-one orthologues with mouse and chimp did not differ between the set of HLOF genes and all human protein-coding genes on Ensemble (Chi-square test with Yates’s correction: N.S. for both comparisons).

### Discussion

Using exome sequences from 1432 individuals, we extend the known repertoire of human genes that are dispensable, i.e. genes that can carry homozgyous loss of function variants in healthy individuals. The vast majority of these genes do not have strong phenotypic effects, i.e. they seem to be truly dispens- able. Further, all but seven HLOF variants are shared across the five European populations as heterozygotes (Table 3), i.e. most HLOFs are relatively old and hence unlikely to be strongly dele- terious. In line with this, the predicted deleteriousness of HLOF variants is, on average, lower than that of predicted disease vari- ants. However, we do find the isolate populations to be enriched for homozgyous LOF variants of low frequency because rarer vari- ants are relatively more likely to be brought into the homozgy- gous state within the long ROHs present in these populations. Accordingly, population isolates are a good place to look for novel HLOF variants. Of course, it would be advantageous to extend the search for HLOF genes beyond those of European heri- tage populations, especially those with high levels of homoz- gosity: extended ROHs have been found in other worldwide popula- tions, such as Native American and Oceanian populations (32,33); homozgosity in these populations is presumably caused by bottlenecks and haplotypes randomly drifting to a high fre- quency. Even longer ROHs tend to be found in the Near and Mid- dle East, which has a history of recent consanguinity, and has already been used to study HLOFs (7). Intriguingly, the distribu- tion of ROHs among populations is non-uniform (32): first, this might simply be due to chance, i.e. rare recombination events can break up different associations in different populations; in addition, regions of high levels of homozgyosity often overlap with loci of recent positive selection—which are often popula- tion-specific and include loci such as the human skin pigmen- tation gene, KITLG (32). Presumably, rare HLOF variants are enriched in segments of recent positive selection, for example, due to genetic hitch-hiking (34). The best way to find these var- iants is by sequencing more individuals from a broader geo- graphical spectrum, focussing on isolated populations that are
geographically distant from Africa and/or populations that have experienced recent inbreeding.

Overall, we find a similar total number of HLOF variants as a study of consanguineous individuals (7), but many fewer than a large study of cosmopolitan individuals (2). This may be partly due to a slightly different set of filters applied; some of our filtering was very conservative, and this might have led to a relatively higher rate of exclusion of true variants. For example, neither of the two other studies removed variants that showed an excess of homozygous LOF variants in the population (the Hardy–Weinberg filter), but we show that this filter is indeed a good indicator of an erroneous SNP call. Further, we excluded all HLOF variants that occurred in the last 10% of any transcript of a gene, whereas the 1KG study (2) removed variants if they were found in the last 5% of the longest transcript for a particular gene. We also applied a mapping-based filter, i.e. the ‘uniqueness score’ of the UCSC genome browser, which had not been used before; further, the prior cosmopolitan survey also included splice sites and deletions in their set of HLOFs (2), which increases the overall number of HLOFs they report. Indeed, 29 HLOF variants of the consanguineous dataset (7) were removed by our approach, and 203 variants in the 1KG dataset (2) were removed from our homozygous set of LOFs; note that this included variants that were seen as heterozygotes in the 1KG data (2).

Despite differences in approach, it becomes clear that HLOF variants are relatively common amongst healthy individuals, with each individual carrying about 10–20 HLOFs, and many seemingly deleterious mutations can be tolerated. Even though these variants may not have any measurable effect, cataloguing them will help identifying rare mutations, which do cause severe phenotypes and diseases, by acting as negative controls. Of course, the effect of losing function at a given gene may also depend on the genomic context, and a general caveat when studying rare variants with small effects.

This project is part of a current effort to catalogue and understand the impact of naturally occurring loss of function mutations in humans. Another possible field of research—loss of function at regulatory elements—has so far been neglected in population surveys, even though the effects of variants at non-coding sequence may potentially be just as severe as those in translated regions. This is certainly an area that will become more accessible with whole genome sequencing becoming cheaper—though the associated computational challenges will be even greater.

Materials and Methods

We used whole exome sequences from GS:SFHS (13) and four isolate populations: two Croatian Islands (CROATIA-Vis and CROATIA-Korčula) (37,38), the Northern Swedish Population Health Study (NSPHS) recruited in the northernmost two counties of Sweden (39) and the Orkney Complex Disease Study (ORCADES), sampled in the Orkney Isles (Orcadians) (37). Originally, these individuals had been recruited for population-based studies of complex traits, i.e. a range of phenotypic data had been collected, including anthropometry, lipids, glycaemic traits, body composition, blood biochemistry, glycomics, cognitive function, etc. (Supplementary Material, Table S2). Notably, these individuals were generally healthy (from population-based sampling), except for some in the GS:SFHS cohort, which included obese individuals, as well as individuals with major depression. The Generation Scotland cohort 1 (GS:SFHS 1) contains 432 samples that were sequenced at the GenePool facility (University of Edinburgh) using the Illumina TruSeq capture kit (Illumina, CA, USA) with a mean coverage per sample of ~38×. Generation Scotland cohort 2 (GS:SFHS 2) contains 428 samples that were sequenced at the Wellcome Trust Sanger Institute, as part of the UK10K project, using the Agilent SureSelect capture kit v3 (Agilent Technologies, CA, USA), with a mean coverage of ~86×. A total of 588 individuals were sequenced from isolate populations: 193 from CROATIA-Vis, 107 from ORCADES, and 98 from NSPHS were sequenced at the Wellcome Trust Sanger Institute using the Agilent SureSelect capture kit v3 with a mean coverage of ~59×. Ninety ORCADES samples and 100 from CROATIA-Korčula were sequenced at Source Biosciences, Nottingham, using the Agilent SureSelect v2 kit with a mean coverage of 30×.
Reads were aligned to the human reference genome GRCh37 using bwa (version 0.62 for CROATIA-Korcula and version 0.59 for all other samples) (40). For each aligned sample, duplicate reads were marked with Picard (version 1.79), and Samtools 0.1.16 (41) was used at various points along the analysis pipeline, e.g. the merging or indexing of bam files. Realignment around insertions/deletions (indels), base quality score recalibration and variant discovery were performed using the Genome Analysis Tool Kit (GATK) 2.7.2, according to GATK best practice recommendations for exome sequence analysis (42,43). Variant discovery was carried out for the target intervals covered by either TruSeq or SureSelect, with an additional 50 bp of padding around the target regions. SNP and indel calling was performed with UnifiedGenotyper, using reduced alignments and downsampling (to 250) across all 1432 samples simultaneously. Variant recalibration was performed with GATK version 2.8.1 and dbSNP version 137 was used throughout this pipeline.

Bam and vcf files were submitted to the European Nucleotide Archive (ENA) at the European Bioinformatics Institute (http://www.ebi.ac.uk/), with accession numbers XXX (to be added upon publication).

We extracted all sequence variants (SNPs or indels) which passed the GATK recalibration, showed a homozygous non-reference allele in at least one individual and were predicted to introduce premature stop-gain or a frameshift into the coding region, as determined by the variant effect predictor (44), using Ensembl 75 gene models. We did not consider splice disruption mutations since they would have required validation using expression data in multiple tissues. Multi-allelic variants were separated out into their respective variants using bcftools, and the remaining homozygous stop-gain and frameshift variants constituted our pool of putative HLOF mutations.

Next, variants were subjected to a range of filters, in order to remove false positives due to sequencing and variant calling errors, annotation errors, as well as variants that are unlikely to cause a true loss of function to the protein (Table 1). In particular, because of the expected high rate of false positives in the initial dataset, we set our filters to be very conservative, and describe these in the following.

Protein sequences for transcripts affected by putative stop-gain or frameshift mutations were downloaded from Ensembl biomart (http://www.ensembl.org/biomart, accessed June 2014), and the relative position of the variants assessed. Variants often clustered near the end of the end and beginning of a transcript (Supplementary Material, Fig. S2), reflecting reduced functional consequences for variants located in the extreme and of a reading frame, alternative start codons (2), or a lower sequence coverage near the start codon. We only kept variants if they fell into the first 90% of all transcripts annotated for a particular gene; notably, the excess of variants near the start codon were removed by other filters that we applied.

In order to avoid spurious calling of SNPs due to mapping of reads from paralogous genomic regions, we downloaded UCSC tracks of Crg (36mer) and Duke (35mer) Alignability scores, as well as DAC blacklisted regions; SNPs and indels that fell into non-unique regions of the genome (with Alignability scores <1.0) were excluded from further analyses, as were variants within UCSC blacklisted regions.

To remove sites that are potentially difficult to sequence and hence more prone to sequencing or alignment errors, we restricted our set of HLOF variants to sites that were called in at least 200 individuals, and, to make a comparison possible across populations, we only considered sites that were captured by both exome capture techniques (TrueSeq and SureSelect), plus 50 bp of padding around the target region.

By the intersection, the target region was reduced from a total of 51.5 MB (for SureSelect) and 62.1 MB (TrueSeq) to 33.4 MB.

We excluded variants that were also found in the genome assemblies of primate outgroup species (chimp, gorilla, orangutan). These variants are potentially mis-annotated in the human genome (e.g. due to sequencing errors), or the variant that we detect might be an ancient polymorphic stop loss mutation in the primate lineage. For the primate comparison, vertebrate multiZ alignments were downloaded from the UCSC genome browser, and the human variants were compared to those in the other three primate species. To allow for alignment ambiguity in the case of frameshift variants, 5 bp upstream and downstream of an indel were extracted and compared. A frameshift was filtered out if (1) at least two primates had aligning sequence present in the region, (2) all species, which showed an alignment, carried the non-reference variant and (3) the position, length and type (insertion or deletion) of the primate variant matched the one seen in humans (according to (2)). Stop-gain variants were filtered out whenever one or more of the primate species carried the human non-reference allele.

Multinucleotide polymorphisms (MNs), i.e. variants that consist of two or more adjacent SNPs, were filtered out if a stop-gain variant was found within the same codon as another SNP. For frameshift variants, the corresponding filter was slightly more sophisticated. In the simplest case, a transcript contained only a single frameshift variant, which was then kept. Frameshifts were also kept for further analyses if (a) a transcript contained two or more homoyzgous frameshift variants that were separated by 10 or more amino acids in the translated protein or (b) nearby frameshift variants (<10 amino-acids apart) did not result in a restoration of the reading frame, i.e. the sum of bases inserted or deleted was not a multiple of three. In contrast, frameshift variants were filtered out if (i) if two nearby variants resulted in the restoration of the reading frame or (ii) whenever three or more frameshifts occurred within close vicinity of each other because insertions or deletions resulting in triplets were possible for these variants.

The high false positive rates due to sequencing errors among LOF mutations can, at least partially, be corrected by considering the overall allele frequencies and contrast these with the frequencies of homoyzgous versus heterozygous individuals within a population, i.e. testing for Hardy–Weinberg equilibrium (HWE). Accordingly, we filtered out any putative LOF variants that were found in more homoyzgous individuals than expected under HWE in any of the five population samples considered separately with a P-value <0.01. This approach is based on the assumption that loss of function mutations are not subject to positive selection, i.e. they are either removed by selection (leading to a reduction in the number of homozygotes) or effectively neutral. An excess of homozygotes can also be observed when there is population substructure; however, as a control, we show that the variants confirmed previously (2,7) had fewer deviations from HWE than our unfiltered, raw variants (Supplementary Material, Fig. S3), which is why we conservatively applied the Hardy–Weinberg filter. For the allele frequency calculations, we included all individuals with a coverage of at least 5x; however, to be kept in the analysis, a variant had to be observed in a homoyzgous state in at least one individual with a coverage of 20x.

Last, to validate our filtered set of HLOF variants, we Sanger-sequenced any novel variants that we detected in our samples; these included 33 variants which were neither found in the set of HLOF variants of (2) nor (7), and had no validation record in
were 867, 455, 194, 444 and 82 in a total of 2426 Orcadians, 1145 Omni1 arrays. The number of traits which we used for analysis typed on Illumina HumanHap300, CNV370, OmniExpress or had been sequenced, as well as individuals who had been geno-

Since the Sanger sequencing revealed the importance of se-

Supplementary Material

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