

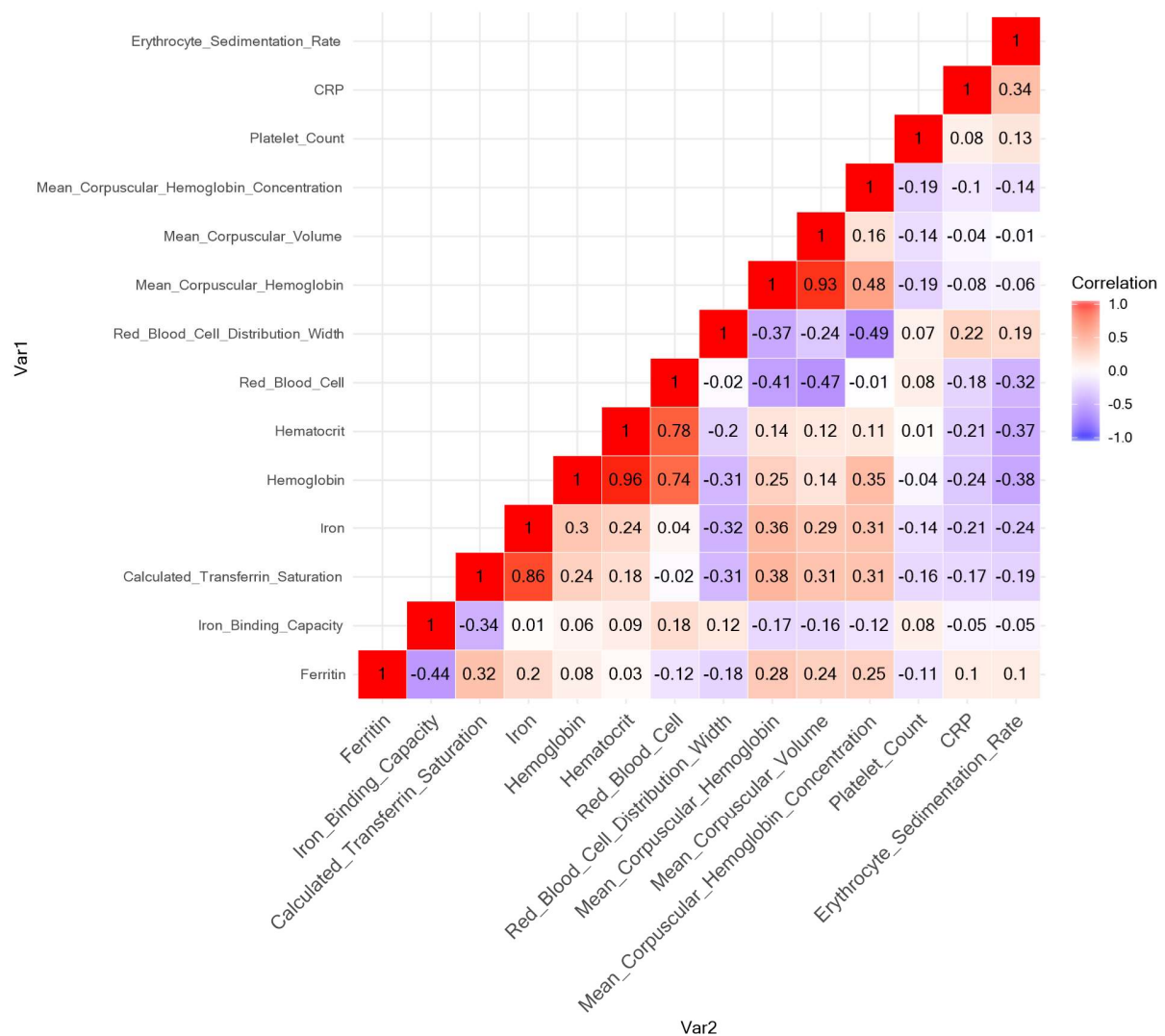
A genome-wide association meta-analysis yields 46 novel loci associated with iron homeostasis biomarkers

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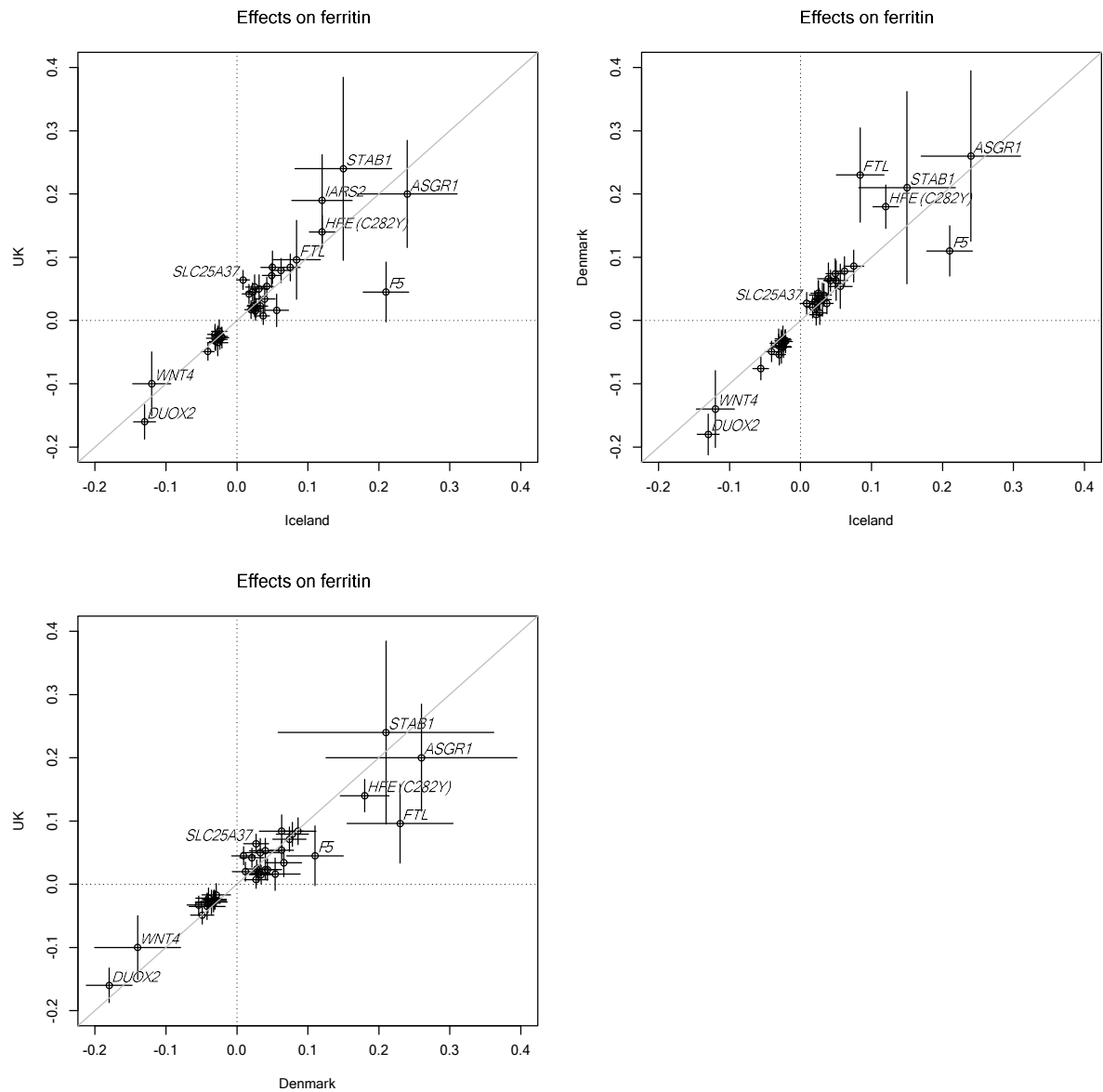
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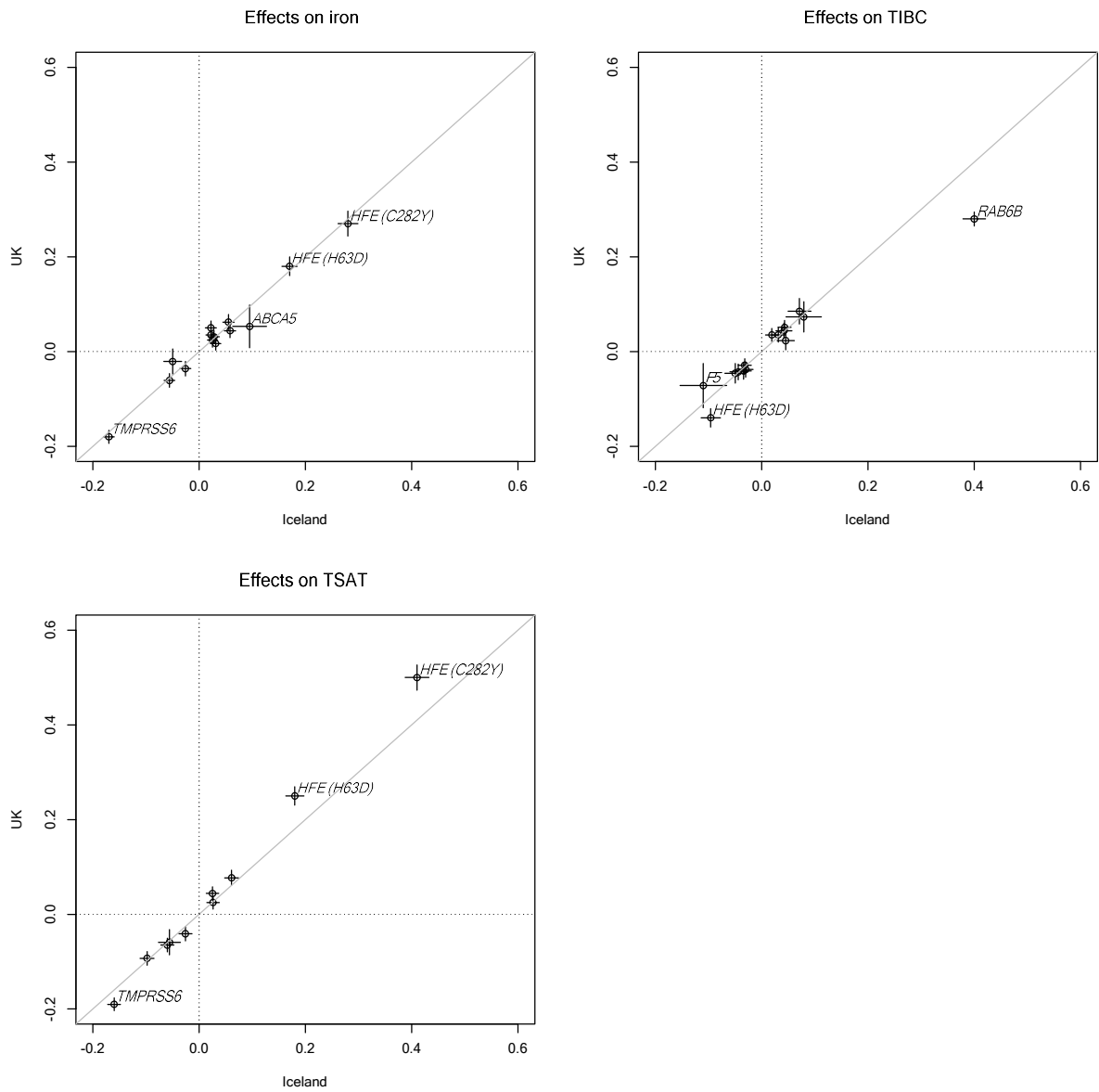
For affiliations see cover page.



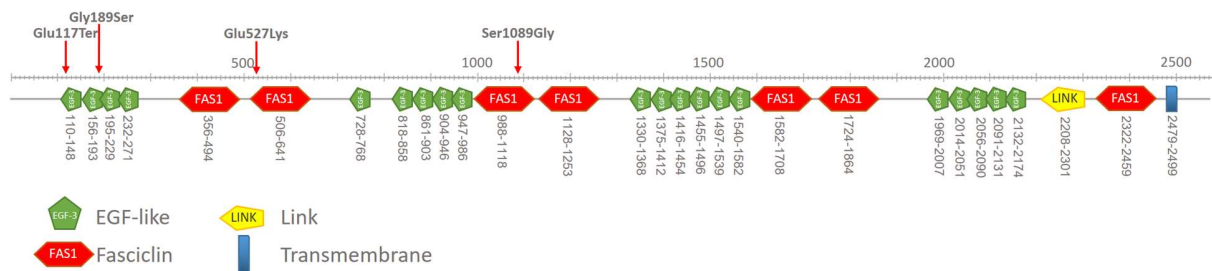
Supplementary Figure 1: Correlation between the iron biomarkers and selected other biomarkers (red blood cell indices, platelet count, erythrocyte sedimentation rate and C-reactive protein). The correlation between measured markers are shown and also indicated using a heatmap (color scheme shown to the right).



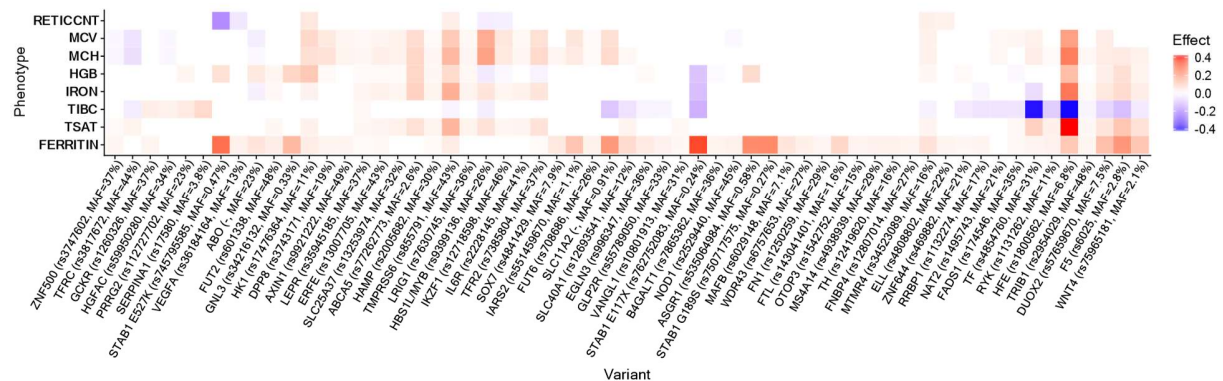
Supplementary Figure 2: Comparison of the effects on ferritin in Iceland, the UK and Denmark. Effects are shown in units of standard deviations. Crosses indicate 95% confidence intervals.



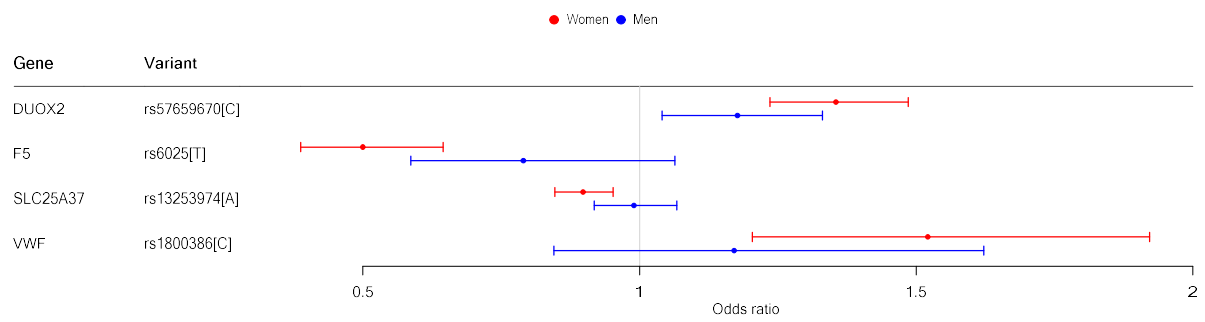
Supplementary Figure 3: Comparison of the effects on iron, TIBC and TSAT in Iceland and the UK. Effects are shown in units of standard deviations. Crosses indicate 95% confidence intervals.



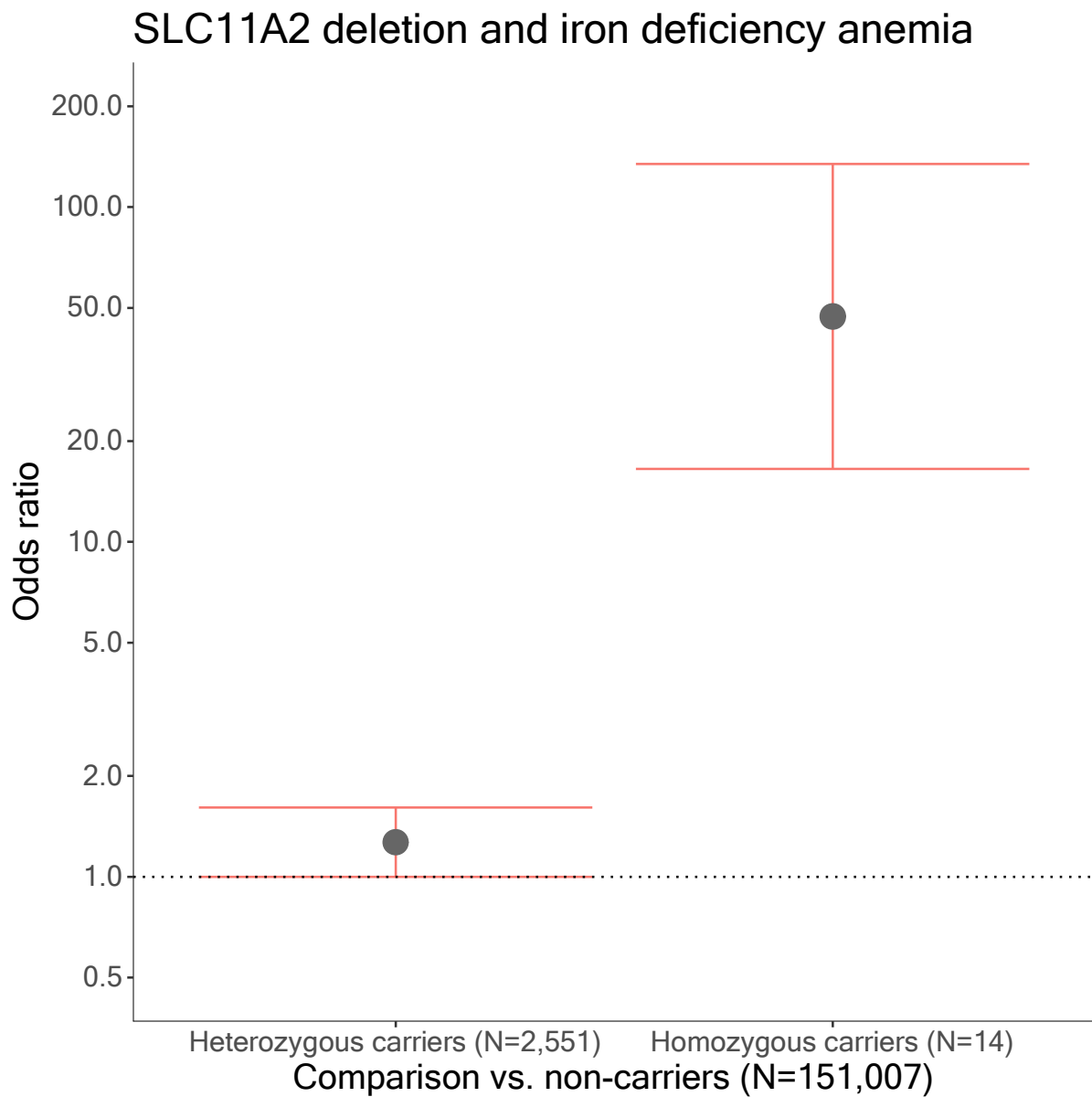
Supplementary Figure 4: ScanProsite results together with ProRule-based predicted intra-domain features of Stablin-1 (STAB1). STAB1 encodes a large, transmembrane scavenger receptor. The protein contains seven fasciclin (FAS1/BlgH3) domains, 20 epidermal growth factor (EGF)-like domains, C-type lectin-like hyaluronan-binding Link (Link) domain and a transmembrane domain. The four coding variants associating with ferritin levels are represented by red arrows.



Supplementary Figure 5: Association of iron homeostasis variants with ferritin (N=172,764), total iron binding capacity (TIBC, N=95,314), transferrin saturation (TSAT, N=91,308), serum iron (N=123,314), hemoglobin (HGB, N=286,622), mean corpuscular hemoglobin (MCH, N=286,245), mean corpuscular volume (MCV, N=286,248) and reticulocyte count (RETICCNT, N=19,031) in the Icelandic data. Effects are in units of standard deviations and are shown for the allele having a positive effect on ferritin. Variants are ordered based on a hierarchical clustering algorithm. Effects that did not reach a false discovery rate (FDR) threshold of $FDR < 0.05$ are shown as zero (white).



Supplementary Figure 6: Novel iron homeostasis variants showing sexual dimorphism for iron deficiency anemia (IDA). A forest plot showing the odds ratio for IDA (error bars showing 95% confidence intervals) for each of the genetic variants showing sexual dimorphism.



Supplementary Figure 7: The effects of SLC11A2 deletion genotype classes on iron deficiency anemia (IDA). The plot shows the odds ratio for IDA (error bars showing 95% confidence intervals) for heterozygous and homozygous SLC11A2 deletion carriers compared to wild-type.