Figure S1. Overview of 29 genes and the percentage of targeted amplicons covered by at least 20 reads. For each of the 29 genes the percentage of amplicons covered by 20 or more reads is shown for the 43 samples. The green colored box indicates the first and third quantiles and the black horizontal bar within the box illustrates the median (or second quantile). Measurements are considered outliers (black dots in plot) when they are i) less than the first quantile -1.5xIQR or ii) greater than the third quantile+1.5xIQR, where the IQR is the 'interquartile range' (third quantile-first quantile).

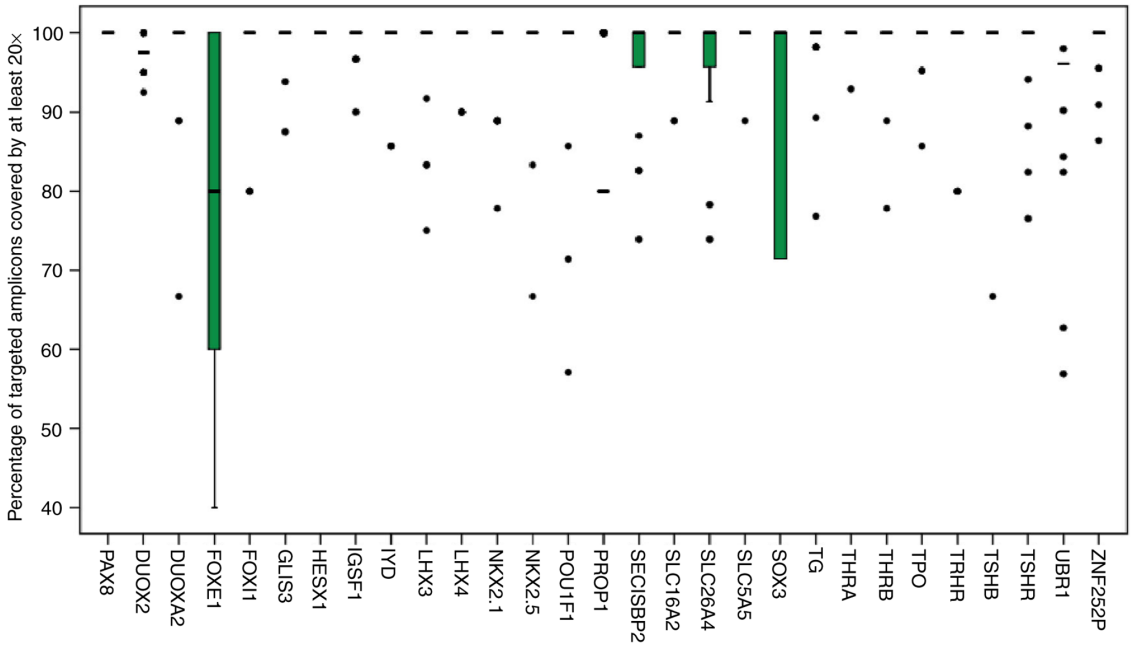

Figure S2. Sequencing chromatograms of 8 novel variants detected in this study. A. c.526T>C in *TSHR*; B. c.1852A>T in *TSHR*; C. c.1165G>A in *DUOX2*; D. c.411C>A in *DUOX2*; E. c.925T>C in *TPO*; F. c.1713C>G in *TPO*; G. c.1915C>T in *SLC5A5*; H. c.2406_2407insCCTG in *DUOX2*.

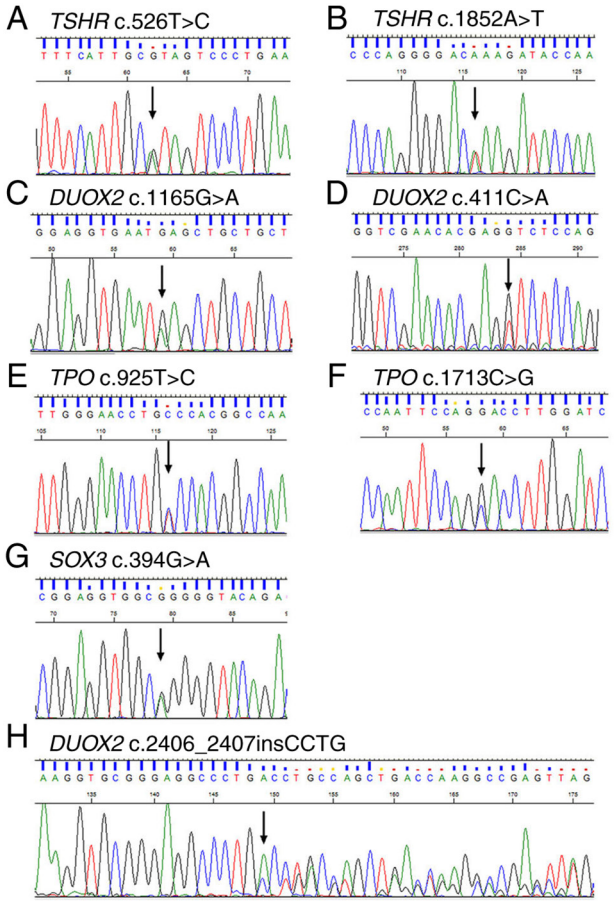

Figure S3. Location of detected missense or indel variants in (A) *DUOX2*, (B) *TPO* and (C) *TSHR* proteins. Different protein domains are represented by boxes. Labeled variants (top) represent previously reported variants. Variants previously reported in the literature are shown in black and those reported only in public population databases are shown in gray. Labeled variants (bottom) are novel variants identified in the present study. FAD, flavine adenine dinucleotide; NADPH, reduced nicotinamide adenine dinucleotide phosphate; MPO, myeloperoxidase; CCP, complement control protein; EFG, epidermal growth factor.

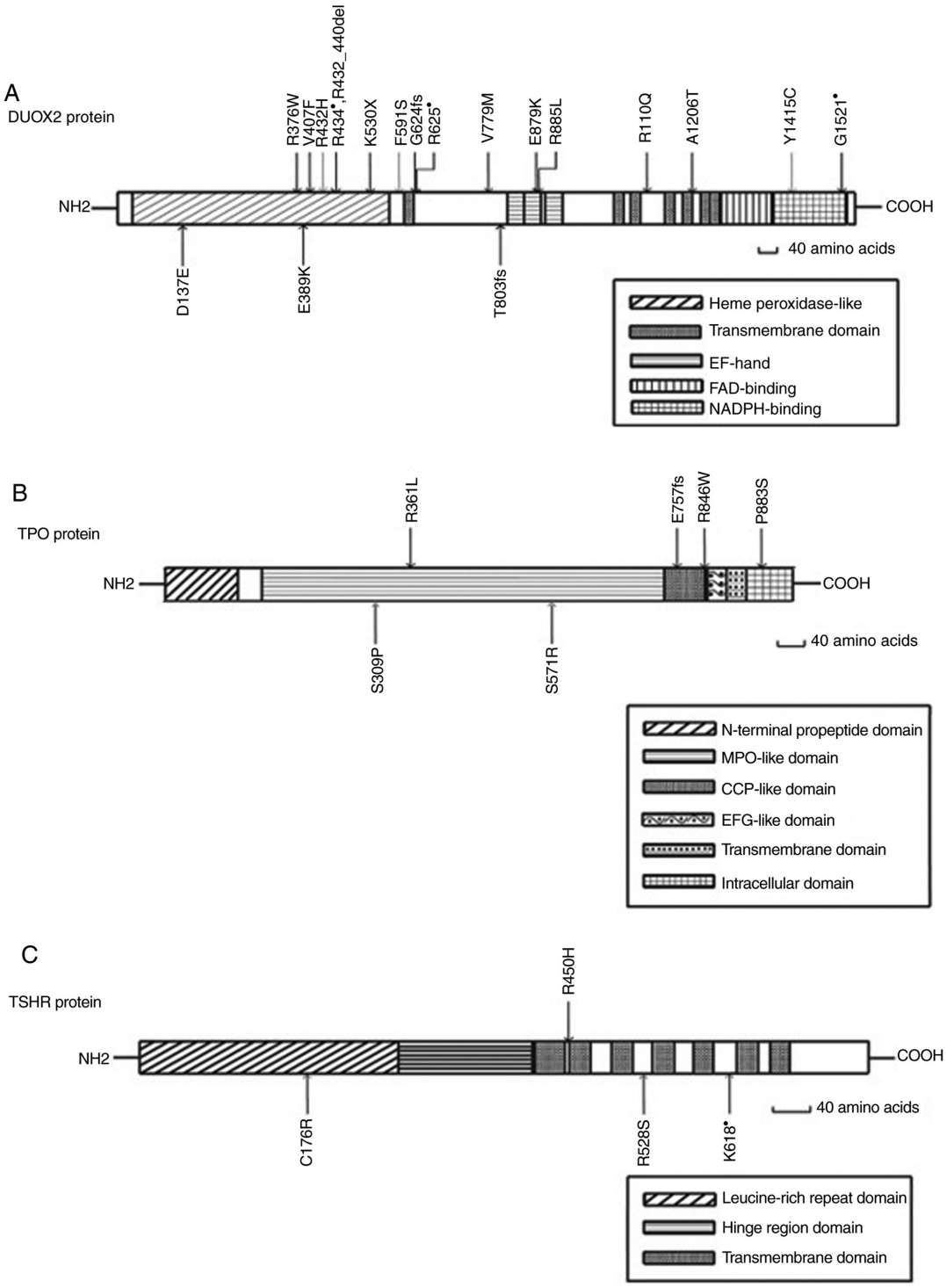

Figure S4. Comparison of serum levels of screening *TSH*, diagnostic *TSH* and *FT4* among different groups, classified according to the number of variants carried. (A) Comparison of serum levels of screening a) *TSH*, (b) diagnostic *TSH* and (c) *FT4* among patients with 0, 1 and ≧2 DUOX variants. (B) Comparison of serum levels of screening a) *TSH*, (b) diagnostic *TSH* and (c) *FT4* among patients with 0 and ≧1 TG variants. (C) Comparison of serum levels of screening a) *TSH*, (b) diagnostic *TSH* and (c) *FT4* among patients with 0 and ≧1 TPO variants. (D) Comparison of serum levels of screening a) *TSH*, (b) diagnostic *TSH* and (c) *FT4* among patients with no mutation, monogenic mutation and oligogenic mutation.