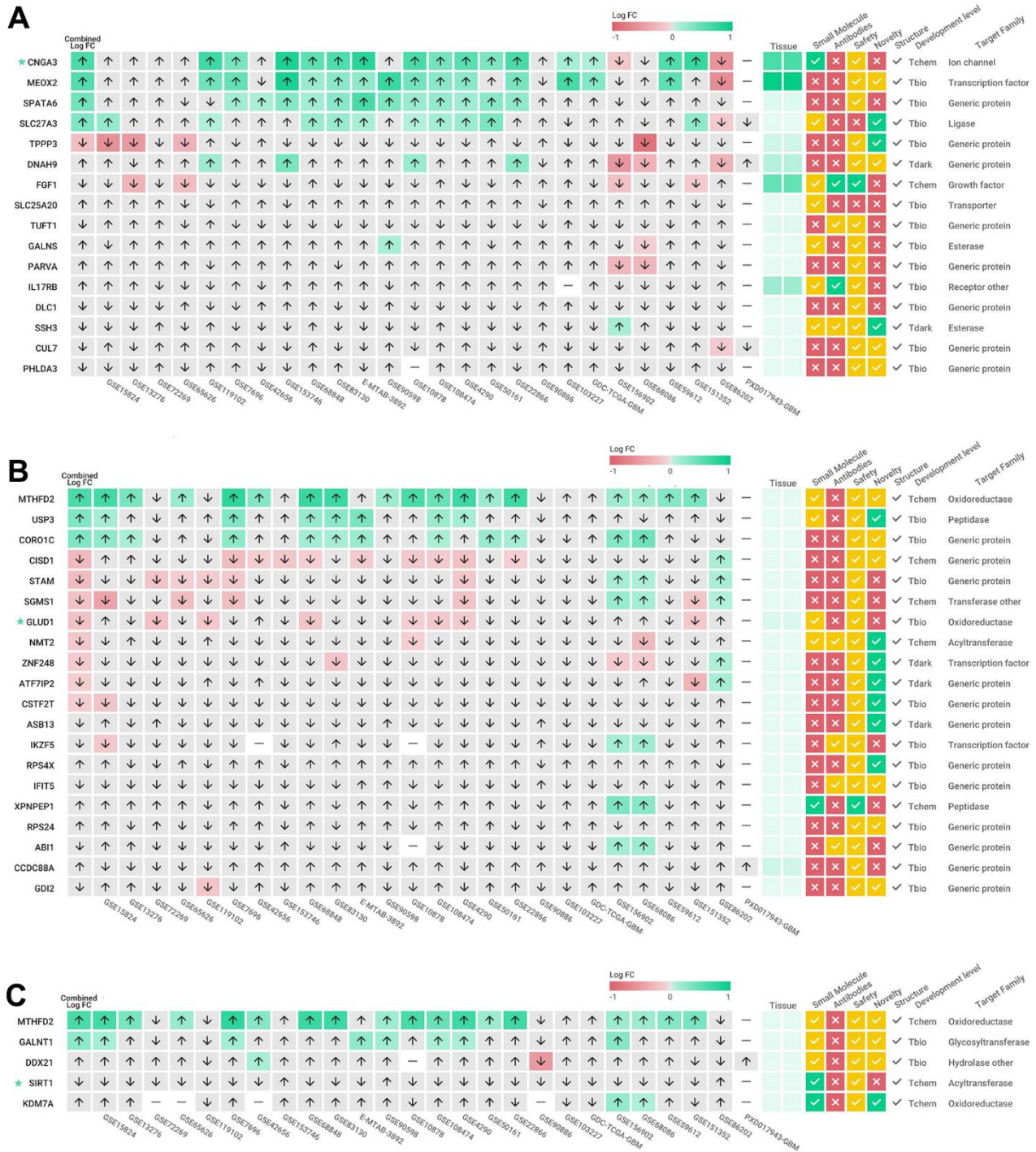


SUPPLEMENTARY FIGURE



**Supplementary Figure 1.** Combined expression analysis for the genes obtained according to strategy 1 (A), strategy 2 (B) and strategy 3 (C). Combined logarithmic fold-changes (Log FC) and Q-values across all gene expression datasets are obtained using minmax normalization for Log FC values and Stouffer's method combining p-values with further FDR correction. Significant combined Log FC values represent both magnitude and direction of gene expression changes between disease and control across multiple datasets.