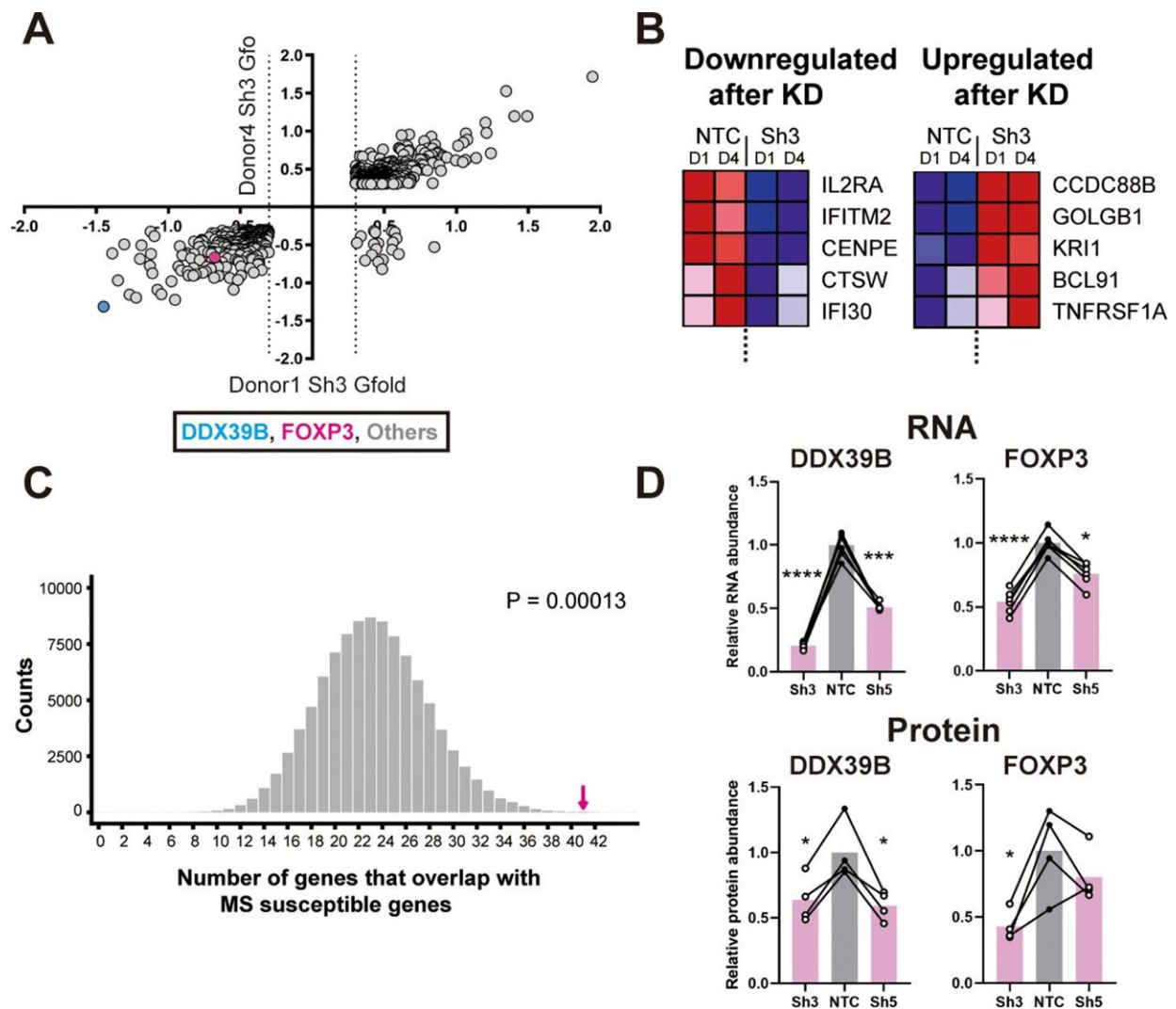


# Multiple sclerosis discovery IDs key factor that shapes your risk

June 7 2023



Loss of FOXP3 expression in DDX39B-depleted T cells. (A) RNA abundance changes between control (NTC) and DDX39B-depleted (Sh3) CD4<sup>+</sup> T cells from two healthy individuals (Donor 1 and Donor 4) identified by RNAseq. Data

points for DDX39B (cyan) and FOXP3 (magenta) are indicated. **(B)** Examples of MS susceptibility genes differentially expressed upon DDX39B knockdown. The heat map shows expression of five genes between control (NTC) and DDX39B depleted (Sh3) CD4<sup>+</sup> T cells. **(C)** Enrichment analysis of MS susceptibility genes in DEGs following DDX39B depletion. Resampling 100,000 times resulted in a distribution of the number of genes that overlap by chance, with 23 being the most common result. The observed overlap of 41 (Magenta arrow) demonstrates substantial enrichment (empirical  $p=0.00013$ ). **(D)** Levels of DDX39B RNA and FOXP3 RNA, normalized to EEF1A1 RNA levels, after DDX39B depletion in CD4<sup>+</sup> T cells and levels of DDX39B and FOXP3 protein relative to Tubulin after DDX39B depletion in CD4<sup>+</sup> T cells. Connected dots indicate samples from the same donor. In all figures the error bars indicate standard deviation. \*:  $p$

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