



— Truncating variants, splice site variants and intragenic deletions predicted to cause loss of function (n=21)

- - - Missense and in-frame deletion variants (n=4)

— Large deletions spanning multiple genes, including FOXP1 (n=4)

Supplementary Figure S1: Comparison of cohort characteristics between individuals with (a) truncating variants, splice site variants and intragenic deletions predicted to cause loss of function (n=21); (b) missense variants and in-frame deletions (n=4); and (c) large deletions spanning multiple genes, including FOXP1 (n=4). Blue line: Individuals with truncating variants, splice site variants and intragenic deletions predicted to cause loss of function (n=21); Orange line: Patients with missense and in-frame deletion variants (n=6); Grey line: Patients with large deletions spanning multiple genes, including FOXP1 (n=4).