Figure S1. TRG repertoire of non-productive sequences determined by NGS.

**A.** Treemaps representation of T cell receptor Gamma (TRG) repertoire of non-productive sequences in peripheral blood mononuclear cells (PBMCs) samples from patients with RMRP deficiency and one representative healthy control. Each square represents a unique V to J joining and the size of the square represents relative frequency within that sample. **B and C.** Quantification of the unevenness and the diversity the TRG repertoire of non-productive sequences using the Simpson-D index of unevenness (B) and the Shannon’s H index of diversity (C) in four healthy controls and in patients with RMRP deficiency. Controls are the same that were used in previous studies [30].

![Fig. S1](image-url)