Table. S1 Clinical manifestations of the patient

Clinical Features
33, African American male
Immune Thrombocytopenic Purpura
Splenomegaly
Lymphadenopathy
Necrotizing Granulomas/ Granulocytosis
Hypogammaglobulinemia, Hyper IgM
Epstein-Barr virus, Cytomegalovirus negative

a

Chr	Start	End	Ref	Alt	Func.refGene	Gene.refGene	exonicFunc.refGene	AAChange.refGene	LJB23_LRT_pred	LJB23_MutationTaster_score
chr17	40371794	40371794	T	C	exonic	STAT5B	nonsynonymous_SNV	STAT5B:NM 012448:exon6:c.671A>G:p.Q206R	D	0.998
chr17	2417912	2417912	G	A	exonic	CD81	nonsynonymous_SNV	CD81:NM 004356:exon7:c.616G>A:p.G206S	D	1

b

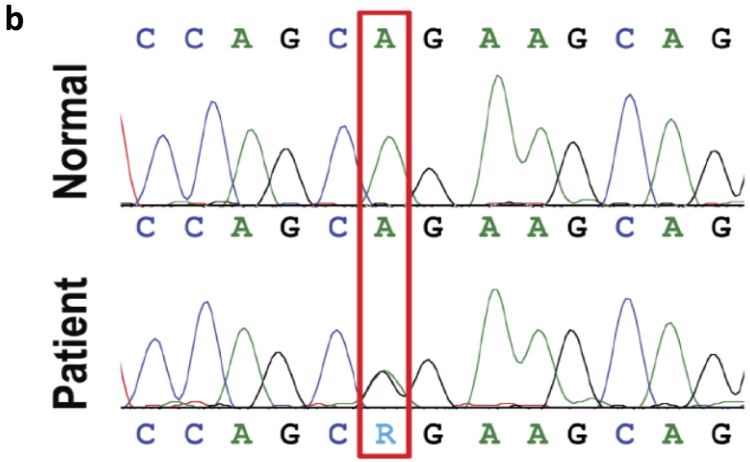

Figure S1. Novel unreported variants found in patient's Whole Exome Sequencing. (a) Table representing *STAT5B* and *CD81* variants in patient. (b) DNA sequencing of the heterozygous A>G missense mutation in *STAT5B* gene. Chromatograms shown for a healthy donor and patient with a red box indicating the mutated residue that now reads as an R for purine (A+G) at that position.

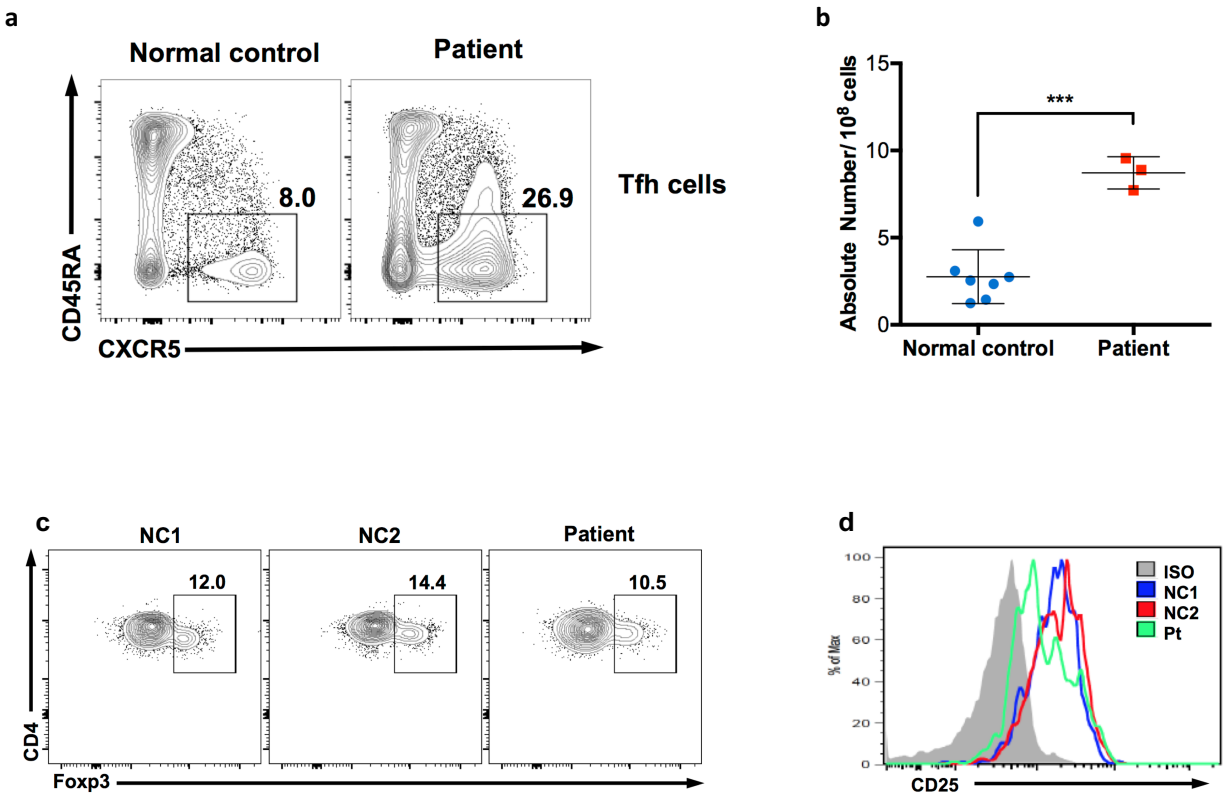

Figure S2. CD4^{+}CD45RA^{-}CXCR5^{+} follicular helper T (Tfh) cells frequency (a) and absolute number (b) in patient and normal controls' blood. Flow analysis of CD4+Foxp3+ regulatory T (Treg) cells frequency in patient's blood (c). CD25 expression on Treg cells in patient (Pt) and normal controls (NC) (d). Data are representative of at least three (a-b) and two (c-d) independent experiments

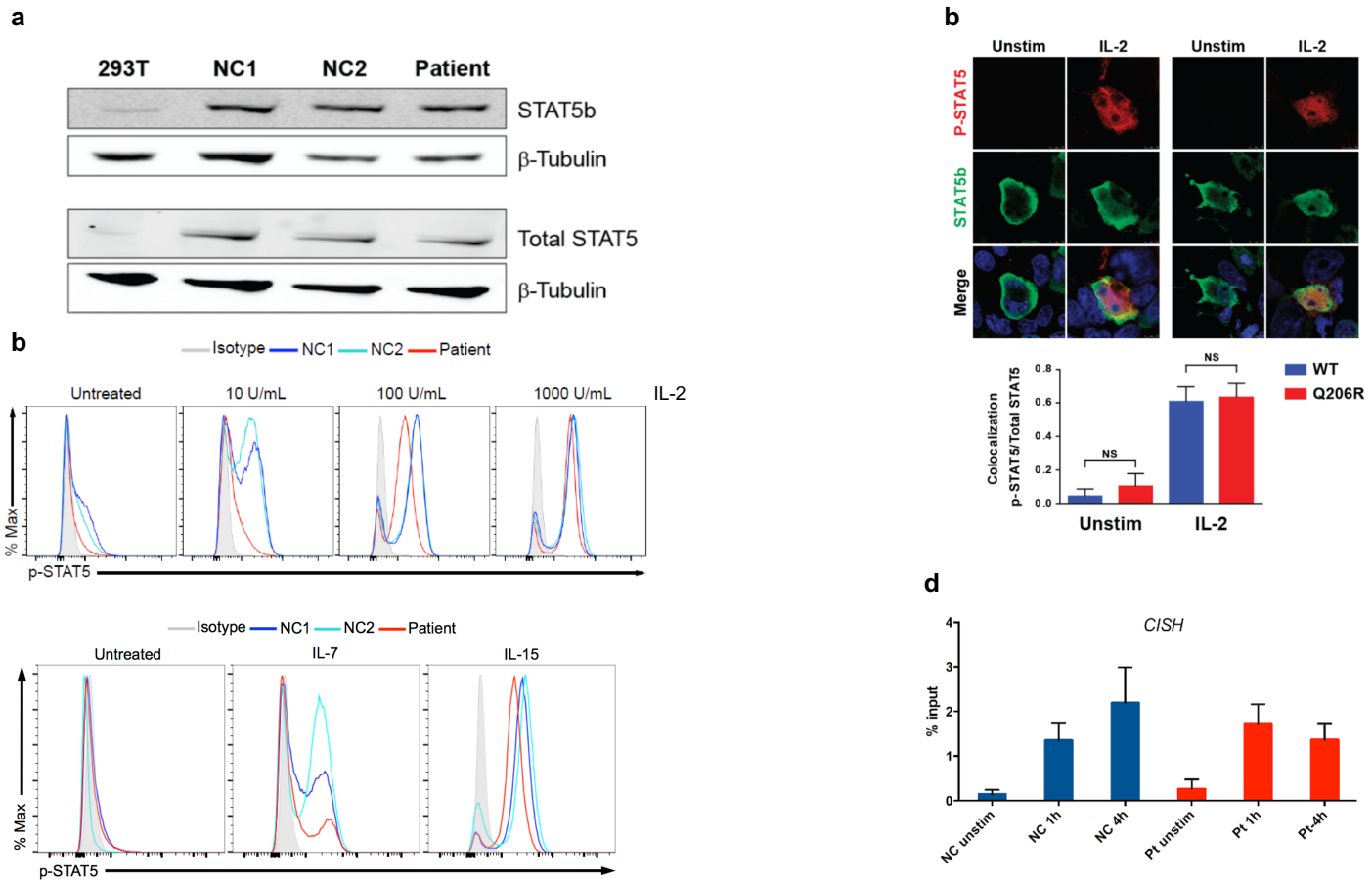

Figure S3. (a) Immunoblot analysis of STAT5B, total STAT5 and β-tubulin protein loading controls in cycling T cells from two normal controls (NC) and the patient compared to transfected 293T cells. (b) Phosphorylation of STAT5 in serum-starved T cell blasts from healthy controls (NC1 and NC2, blue lines) and patient (red line). T cell blasts left untreated or stimulated for 10 min with either 10, 100 or 1000 IU/mL of IL-2 or 10 ng/mL of IL-7 or IL-15. Gray shaded line indicates the isotype control. (b) Upper panel, confocal microscopy of the translocation of STAT5B (green) and p-STAT5 (red) into nucleus (stained blue with Hoescht) of HEK 293T cells transfected with either WT or Q206R STAT5B and unstimulated (left) or stimulated with 100 IU/mL of IL-2 for 30 min (right). Lower panel, co-localization analysis of p-STAT5 with total STAT5B in the nucleus of cells transfected with either WT STAT5B (blue bar) or Q206R STAT5B (red bar), unstimulated or in the presence of 100 IU/mL of IL-2 for 30 min. (d) Chromatin-immunoprecipitation of healthy control subject (NC, blue bar) and patient (Pt, red bar) serum-starved T cell blasts that were activated for 1h or 4h with 100 IU/mL IL-2 followed by PCR analysis of the binding of STAT5B to *CISH* locus; results are presented relative to input DNA. Data are representative of three independent experiments.