

Supplementary Tables 1 and 2

Supplementary Table 1. Laboratory values for patients with missense mutations in *BACH2*.

All laboratory readings are reported from the date of initial presentation as adults to medical services except for immunoglobulin levels, which were measured at the ages shown. Parameters are given with respect to the normal ranges of the reporting laboratories. Note that values in **Fig. 1** are those from the research laboratory and measured at a later time from those here. L, low; Ab, antibody; N/A, not assessed; ND, not detected; * patient is on intravenous immunoglobulin so these parameters could not reliably be assessed. † A tetanus antitoxoid IgG concentration of 0.47 iU/mL would be considered in the lowest 25th centile for healthy controls (Median tetanus antibody levels aged 20-60 years = 2.7iU/mL IQR 0.6-4.0iU/mL: ⁶⁹).

Patient		N-terminus (L24P)	C-terminus (E788K)		
		A.II.1	B.II.1	B.III.2	
RBC	x 10 ¹² /L	4.7 (L)	4.8	3.9	
WBC	x 10 ⁹ /L	3.4 (L)	7.64	9.7	
Neutrophils	x 10 ⁹ /L	2.8 (L)	5.6	6.9	
Monocytes	x 10 ⁹ /L	0.3 (L)	0.6	1.1	
Eosinophils	x 10 ⁹ /L	0 (L)	0.23	0.3	
Basophils	x 10 ⁹ /L	0 (L)	0.03 (L)	0 (L)	
Lymphocytes	x 10 ⁹ /L	0.3 (L)	1.1 (L)	1.5	
CD3	cells/mL	279 (L)	844	1226	
CD4	cells/mL	183 (L)	622	643	
CD8	cells/mL	89 (L)	162 (L)	571	
CD4/CD8 ratio	ratio	2.1	3.8	1.1	
NK cells	cells/mL	24 (L)	31	56	
B cells (CD19 ⁺)	cells/mL	87 (L)	143	92	
CD27 ⁺ B cells	% of B cells	0.8 (L)	0.6 (L)	8.7 (L)	
IgG ⁺ B cells	% of B cells	0.2 (L)	0.2 (L)	3.7	
IgA ⁺ B cells	% of B cells	0.1 (L)	0 (L)	N/A	
IgM ⁺ B cells	% of B cells	4.0	12.6	4.2	
IgD ⁺ B cells	% of B cells	81.2 (H)	12.6	N/A	
Immunoglobulins					
<i>Age at examination</i>		21yrs	63yrs	19yrs	40yrs
IgG	mg/dL	400 (L)	560 (L)	2182	1946
IgM	mg/dL	24 (L)	10 (L)	292	383
IgA	mg/dL	20 (L)	ND	ND	ND
IgE	iU/mL	ND	ND	9.7	11
Tetanus antitoxoid IgG	iU/mL	0.1 (L)	*	0.47 [†]	
Diphtheria antitoxoid	iU/mL	0.05 (L)	*	0.16	

Supplementary Table 2. Bioinformatic evaluation of missense mutations in *BACH2*.

Conservation scores (GERP, PhastCons and PhyloP) were obtained from the UCSC genome browser. Global minor allele frequencies (gMAF) were derived from the 1000 genomes and ExAc databases, respectively. Multiple sources (PolyPhen2, SIFT, LRT, MutationAssesor Functional Impact, MutationTaster and Combined Annotation-Dependent Depletion (CADD)) were queried to predict the functional impact of each missense mutation using dbNSFP, as described^{56,57}. CADD scores of 17 and 19 places the mutation within the top 2% and 1.3%, respectively, of likely deleterious mutations across the genome⁷⁰. The CADD-based mutation significance cutoff (MSC) at 99% confidence interval (CI) was calculated as described⁵⁸.

Family	A	B
GRCh37/Hg19 physical position (Chr6)	90,718,493	90,642,291
PhyloP (100wayall)	8.83	5.28
PhastCons	1	0.99
GERP	5.33	5.51
cDNA change	c.T71>C	c.G2362>A
Amino acid substitution	p.Leu24Pro	p.Glu788Lys
gMAF in 1000 genomes	0	0
gMAF in ExAc	0	0.00002478
PolyPhen2	Probably damaging	Benign
SIFT	Damaging	Tolerated
LRT	Damaging	Damaging
Mutation Assesor Functional Impact	High	Low
MutationTaster	Disease causing	Disease causing
CADD scaled score	17	19
MSC-CADD score (99% CI) Impact Prediction	High	High