Heterozygous missense variant of the proteasome subunit β-type 9 causes neonatal-onset autoinflammation and immunodeficiency

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Impaired proteasome activity due to genetic variants of certain subunits might lead to proteasome-associated autoinflammatory syndromes (PRAAS). Here we report a de novo heterozygous missense variant of the PSMB9 proteasome subunit gene in two unrelated Japanese infants resulting in amino acid substitution of the glycine (G) by aspartic acid (D) at position 156 of the encoded protein β1i. In addition to PRAAS-like manifestations, these individuals suffer from pulmonary hypertension and immunodeficiency, which are distinct from typical PRAAS symptoms. The missense variant results in impaired immunoproteasome maturation and activity, yet ubiquitin accumulation is hardly detectable in the patients. A mouse model of the heterozygous human genetic variant (Psmb9G156D/+) recapitulates the proteasome defects and the immunodeficiency phenotype of patients. Structurally, PSMB9 G156D interferes with the β-ring-β-ring interaction of the wild type protein that is necessary for 20S proteasome formation. We propose the term, proteasome-associated autoinflammatory syndrome with immunodeficiency (PRAAS-ID), to indicate a separate category of autoinflammatory diseases, similar to, but distinct from PRAAS, that describes the patients in this study.
Variants of proteasome subunit β-type 8 (PSMB8) were detected in autoinflammatory diseases characterized by systemic relapsing inflammations and progressive wasting, such as Nakajo-Nishimura syndrome and chronic atypical neutrophilic dermatosis with elevated temperature (CANDLE) 

Subsequently, identification of mostly biallelic variants of other proteasome subunit and chaperone genes, leading to loss-of-function of the proteasome, has defined a disease entity as proteasome-associated autoimmune/syndrome (PRAAS) 

The proteasome is a protein complex involved in intracellular protein homeostasis by degrading unnecessary or useless proteins tagged with polyubiquitin 

All eukaryotic cells have the constitutive 26S proteasome which consists of a 20S core particle and two 19S regulatory particles. The 20S core complex is composed of α1-α7 and β1-β7 subunits, among which β1, β2, and β5 mediate the protease activity. In hematopoietic cells or fibroblasts stimulated with cytokines, inducible subunits, βi1 (coded by PSMB9), β2i (coded by PSMB10), and β5i (coded by PSMB8), are substituted for β1, β2, and β5, respectively, to form the immunoproteasome. Especially in thymic cortical epithelial cells, β5t (coded by PSMB11), instead of β5i, as well as β1i and β2i are expressed to form the thymoproteasome. Immunoproteasome and thymoproteasome are involved not only in protein degradation but also in generation of antigen peptides presented with major histocompatibility complex (MHC) class I molecules and CD8 T cell repertoire, population, and responses.

In this work, we identify a de novo PSMB9 heterozygous missense variant, G156D, in two unrelated Japanese patients with manifestations, including autoinflammation and immunodeficiency, which are similar to, but distinct from those of PRAAS patients. The proteasome defect and immunodeficiency phenotypes are recapitulated in Psmb9G156D/+ mice.

Results

Clinical phenotype. Two patients from nonconsanguineous families were enrolled in this study (Supplementary Note 1). These patients showed similar features, such as neonatal-onset fever, increased inflammatory reactants, skin rash (Fig. 1a, b, and Supplementary Figs. 1a and 2a, b), myositis (Fig. 1c, and Supplementary Fig. 1b), liver dysfunction, pulmonary arterial hypertension (Fig. 1d and Supplementary Fig. 2e, f) and basal ganglia calcification (Fig. 1e and Supplementary Fig. 2c). Autoantibodies associated with dermatomyositis were not detected in either patient. The serum inflammatory cytokine levels, such as IL-6, IL-18, and IP-10, were increased in both patients. Concerning immunological functions, patient 1 showed decrease of serum IgG level and B cell numbers (Supplementary Table 1), and required IgG supplementation to control manifestations. Patient 1 also exhibited low levels of both T-cell receptor recombination excision circles (TREC) and immunoglobulin (Ig) κ-deleting recombination excision circles (KREC), indicating T as well as B cell defects. In patient 1, during immunosuppressive treatments, interferon (IFN) score was not elevated, and signal transducers and activators of transcription 1 (STAT1) phosphorylation were scarce (Supplementary Fig. 1e, f). Meanwhile, patient 2 showed decrease of monocytes, CD8 T, and γδ T cells and almost absence and decreased activity of natural killer (NK) cells (Supplementary Table 1). In patient 2, interferon (IFN) -α was not only increased in the serum but also detected in cerebrospinal fluid. Furthermore, despite the usage of prednisolone the IFN score was elevated in the whole blood, and STAT1 phosphorylation was enhanced in the skin lesion collected. This was also shown in the experiments with dermal fibroblasts (Fig. 1f–h). Patient 2 also showed manifestations compatible with hemophagocytic lymphohistiocytosis. Interestingly, polyoma (BK/JC) viruses were detected in both patient’s peripheral blood samples (Table 1). In patient 1, the viruses were detected at 4 and 10-year-old, when the effects of immunosuppressants could not be excluded, while in patient 2 they were detected at 3 days of age, at the time without any therapy.

The detailed case reports were described in Supplementary Note 1 and summarized in Table 1. In summary, these two patients initially showed mainly severe autoinflammatory phenotypes and later manifested the immunodeficiency phenotype with periodic inflammatory exacerbation. Clinical features of both patients were partially overlapped with PRAAS. However, they apparently lacked lipoatrophy, one of the main characteristics of PRAAS, and showed pulmonary hypertension, which is rare in PRAAS. More importantly, they also manifested combined immunodeficiency (at least B and T cells in patient 1 and T and NK cells in patient 2), which is not seen in PRAAS (Table 1).

Genetic and functional analysis. In patient 1, no pathogenic variant was identified in MEFV, MVK, NLRP3, NOD2, TNFRSF1A, or PSMB8. Then, a panel of ubiquitin-proteasome system, autophagy and interferonopathy-related genes (Supplementary Table 2) were sequenced and heterozygous PSMB9 (NM_002800) c.467 G > A (p.G156D) was identified (Fig. 2a). This is a de novo variant in the immunoproteasome-specific β1i subunit gene, and 156 G is well conserved among β1 and β1i across species (Fig. 2c). Whole exome sequencing of genomic DNAs from the patient and their parents revealed two homozygous, one compound heterozygous, and 29 de novo variants in patient 1 (Supplementary Table 3). Among these genes, only PSMB9 was associated with inflammation. In patient 2, a panel of autoinflammatory disease-causing genes (Supplementary Table 2) were analyzed and de novo PSMB9 c.467 G > A (p.G156D) heterozygous variant, i.e. the same variant found in patient 1, was identified (Fig. 2b). Whole exome sequencing of genomic DNAs from the patient and their parents identified two homozygous, one compound heterozygous and 12 de novo variants in patient 2 (Supplementary Table 4). Among these genes, only PSMB9 was associated with inflammation and the PSMB9 variant was the only variant found in common between two patients. Although clinical phenotypes of the patients are similar to that of NEMO deleted exon 5-autoinflammatory syndrome (NEMO-NDAS), the possibility that they belong to NEMO-NDAS was excluded, because re-evaluation of the NEMO genes showed no variants.

Structural modeling revealed that G156 in β1i is located on the interface between two β rings and G156D substitution affects their interaction (Fig. 2d), while keeping the active site conformation (Supplementary Fig. 3a). Consistent with this modeling, immunoblotting analysis of patient 1-derived immortalized B cells showed increase of immunoproteasome intermediate containing Ump1 and immature β1i and severely diminished incorporation of all induced subunits into the 20S complex (Fig. 3a and Supplementary Fig. 3b). Meanwhile, in the 26S proteasome of patient 1-derived immortalized B cells, β2i and β5i incorporation was comparable to that of his mother-derived control cells, although β1i incorporation was impaired and immature β1i was detected. In the patient 1-derived cells, the catalytic activity of the 20S, but not the 26S proteasome, was severely impaired, whereas both the 20S and 26S proteasome showed severe defects in the activities in PRAAS patient-derived cells (Fig. 3b). Ubiquitin accumulation, which is caused by the 26S proteasome defect and is common in PRAAS, was unremarkable in the patients’ skin lesion (Fig. 3c and Supplementary Fig. 4a). Patient 2-derived fibroblasts exhibited a peptide hydrolyzing activity of the 26S proteasome comparable to that of control fibroblasts regardless...
Fig. 1 Clinical figures and IFN signature of patients. a, b Pernio-like violaceous rash in patient 1 at 7-month-old (a) and patient 2 at 1-month-old (b). c–e myositis by leg magnetic resonance imaging (c), pulmonary hypertension by echocardiogram (d), and basal ganglia calcification by head computed tomography (CT) (e) in patient 1. f IFN scores of peripheral bloods of 11 healthy participants as controls, three Aicardi–Goutières syndrome (AGS) patients with IFIH1 variant and patient 2 at 84-day old. The score was regarded as positive if it exceeded +2 SD (5.04, dotted line) of the average (solid line) IFN score from healthy controls. Statistical analysis was performed with two-sided Mann–Whitney test. g The skin biopsy samples of a healthy participant as a control and patient 2 at 52-day-old stained with anti-p-STAT1 Ab. A scale bar, 100 μm. h The STAT1 phosphorylation assay with SV40-transformed dermal fibroblasts from healthy volunteers as controls and Patient 2. The expression levels of IFN-γ-induced p-STAT1 were enhanced in patient 2 fibroblasts compared to control fibroblasts.

Table 1 Comparison of PRAAS, patients 1, patient 2, and Psmb9G156D/+ mice.

| Clinical findings                  | PRAAS | Patient 1 | Patient 2 | Psmb9G156D/+ mice |
|-----------------------------------|-------|-----------|-----------|-------------------|
| Fever                             | +     | +         | –         | –                 |
| Skin rash                         | +     | +         | +         | –                 |
| Myositis                          | +     | +         | NA        | –                 |
| Liver dysfunction                 | +     | +         | NA        | NA                |
| Pneumonia                         | +     | +         | +         | NA                |
| Splenomegaly                      | +     | +         | +         | –                 |
| Lipatrophy                        | +     | –         | –         | –                 |
| Pulmonary hypertension            | Rare  | +         | +         | NA                |
| Basal ganglia calcification       | +     | +         | +         | NA                |
| IFN score                         | Positive | Positive | Positive | –                 |
| Viremia                           | –     | Polyoma virus + | Polyoma virus + | NA                |
| Neutrophil                        | Variable | ↑        | →         | ↑                 |
| Monocyte                          | Variable | ↑        | ↓         | ↑                 |
| NK cell                           | Variable | →        | ↓         | →                 |
| Dendritic cell                    | NA    | NA        | NA        | NA                |
| T cell                            | Variable | →(CD4) ↑ (CD8) ↓ (γδ) | 1(CD8) ↓ (γδ) | ↓                 |
| B cell                            | Variable | ↓        | →         | ↓                 |
| Serum Ig                          | ↑     | ↓(IgG)    | Unevaluable | ↓                 |
| Proteasome analysis               | βII maturation | Variable | Defect | Defect |
| Proteasome activity               | 20S, 265 defect | 20S defect | 20S defect | 20S defect |
| Ubiquitin accumulation            | ++    | +/-       | +/-       | –                 |

NA not assessed.
of IFN-γ-stimulation (Supplementary Fig. 4b left), whereas the activity of 20S was decreased in IFN-γ-stimulated patient’s fibroblasts (Supplementary Fig. 4b right). Consistent with this, unstimulated fibroblasts showed no significant defects in components of the proteasomes (Supplementary Fig. 4c). However, IFN-γ-stimulated fibroblasts showed defects in the maturation of β1i and β5i and incorporation of β1i into the 20S and 26S proteasome and impaired catalytic activity of the 20S complex, with normal 26S proteasome activity (Supplementary Fig. 4c, d).

Analysis of mice carrying the PSMB9 G156D mutation. In order to clarify how the PSMB9 G156D variant contributes to the patients’ manifestations, we generated mice carrying the mutation by the CRISPR/Cas9 method. Psmb9G156D/G156D mice died within 6–7 months old, while the survival rate of Psmb9G156D/+ mice was similar to that of wild-type mice (Supplementary Fig. 5a). Psmb9G156D/+ mice appeared healthy at glance and lacked a sign of lipoatrophy or inflammation (Supplementary Fig. 5b and Table 1). The Psmb9G156D/+ and Psmb9G156D/G156D derived fibroblasts exhibited a peptide hydrolyzing activity of the 26S proteasome almost comparable to that of Psmb9+/+ derived fibroblasts regardless of IFN-γ-stimulation (Supplementary Fig. 5c left), whereas the activity of 20S was decreased in IFN-γ-stimulated Psmb9G156D/+ and Psmb9G156D/G156D derived fibroblasts (Supplementary Fig. 5c right). Consistent with this, the components and catalytic activities of proteasomes in unstimulated embryonic fibroblasts were comparable among Psmb9+/+, Psmb9G156D/+ and Psmb9G156D/G156D mice (Supplementary Fig. 5d, e). However, in IFN-γ-stimulated embryonic fibroblasts, immature β1i and β2i, which were undetectable in Psmb9+/+ mice, were observed and incorporation of β1i into the 20S complex was severely impaired, although incorporation of β1i into the 26S proteasome was mildly defective in Psmb9G156D/+ mice (Fig. 4a). Neither β1i nor β2i were hardly detected in 20S complex or the 26S proteasome of Psmb9G156D/G156D mice, indicating genotype-dependent defect of immunoproteasome maturation (Fig. 4a). Catalytic activity of the 20S complex was decreased in a genotype-dependent manner (Fig. 4b). Meanwhile, in Psmb9G156D/+ and Psmb9G156D/G156D mice, 26S proteasome activity was comparable to that of Psmb9+/+ mice and accumulation of ubiquitinated proteins was unremarkable (Fig. 4b, c). Thus, similar to the patients, not only Psmb9G156D/G156D mice showed severe defects mainly in 20S complex assembly and activity.

We then performed immunological analysis. In Psmb9G156D/+ mice, the thymus was small and the cortico-medullary junction was unclear (Fig. 5a). All thymocytes, including their subsets, were decreased in number (Supplementary Fig. 6a). Histological analysis of the spleen also showed defective formation of follicles and a decrease of B and T cells (Fig. 5b). Among splenocytes, B, as well as both CD4 and CD8 T cells, were decreased in number (Supplementary Fig. 6b). In remaining CD8 T cells, central and effector memory T cells were increased, while naïve T cells were prominently decreased in percentages (Supplementary Fig. 6c). Furthermore, serum levels of all Ig isotypes were severely decreased (Fig. 5c). Splenic dendritic cells (DCs) were also decreased in number and percentages (Fig. 5d and Supplementary Fig. 6b). Meanwhile, NK cells were normal, and neutrophils and monocytes were increased not only in spleen but also in BM (Fig. 5d, e and Supplementary Fig. 6b). In Psmb9G156D/+ mice, the thymus was hardly detected, and spleen lacked T, B, NK, and DCs (Fig. 5d). Thus, Psmb9G156D/+ mice showed combined immunodeficiency with increase of monocytes and neutrophils, and the homozygosity of this mutation caused severer immunodeficient phenotype.

In mutant mice lacking proteasome subunits, generation of MHC class I-restricted Ag peptides is impaired, which leads to decreased expression of MHC class I and decrease of CD8 T cells13. However, MHC class I expression was not impaired and processing and presentation of ovalbumin were also intact in splenic B cells of Psmb9G156D/+ mice, indicating that immunoproteasome of Psmb9G156D/+ mice functionally retained the MHC class I presentation activity (Supplementary Fig. 7).
Discussion

We describe a de novo heterozygous missense variant, p.G156D, in PSMB9 coding an immunoproteasome subunit, β1i, in two unrelated patients that manifest characteristic autoinflammation, similar to, but distinct from so far described PRAAS, with immunodeficiency. Although a heterozygous variant of proteasome maturation protein (POMP) leads to PRAAS, the other PRAAS-causing variants are homozygous, compound heterozygous or digenic heterozygous in proteasome subunit genes. Noteworthy, in our patients, a monogenic heterozygous variant, PSMB9 p.G156D, should be responsible for their manifestations.

Although the variant led to defects in β1i maturation and formation and activity of immunoproteasome, it mainly caused formation and activity defects in the 20S complex, and the 26S proteasome defects were mild enough at least to avoid ubiquitin accumulation, as shown by the analysis not only of the present two patients but also of the mice carrying the heterozygous or homozygous PSMB9 G156D mutation (Supplementary Fig. 8). This is in contrast to published PRAAS cases, which mostly show impairment of both 20S and 26S formation and ubiquitin accumulation, accompanied with endoplasmic reticulum stress or type I interferonopathy. According to structural modeling analysis, PSMB9 G156 is located in the interface between two β rings and G156D variant is considered to disturb the interaction of two β rings, while keeping active site conformation. Meanwhile, most of published proteasome subunit variants, as exemplified by T75M, A92T, A94P, K105Q, or G201V in PSMB8, are found at or near the active site and should affect the active site itself or its conformation (Fig. 6a), which is necessary for both 20S complex and 26S proteasome activities. Thus, PSMB9 G156D is a variant in
proteasome subunits that causes proteasome defects by its heterozygosity and affects the interaction of two β rings.

Imunodeficiency as well as proteasome defects, observed in two patients, were recapitulated in mice carrying the heterozygous PSMB9 G156D mutation. The mutant mice showed decrease of T, B cells and DCs, decrease of serum Ig levels and increase of neutrophils and monocytes. The phenotypes significantly overlap with that of patient 1, who showed decrease of B cells and serum IgG level and increase of monocytes (Table 1). Patient 2 also showed decrease of CD8 T in addition to γδ T and NK cells, although he was too young to be evaluated for B cell generation or serum IgG level. Despite the immunodeficiency, Psmb9G156D/+ mice appeared healthy without spontaneous development of autoimmune phenotypes. Some environmental factors, although not defined yet, might be necessary for Psmb9G156D/+ mice to manifest autoimmunity. Importantly, immunodeficient phenotypes in Psmb9G156D/G156D mice were more prominent than those in Psmb9G156D/+ mice, suggesting the dosage effects of the PSMB9 G156D mutation. Although severe immunodeficiency should contribute to the early death of Psmb9G156D/G156D mice, the direct cause for the death remains unknown.

So far, mutant mice lacking either or all of β1i, β2i, β5i, and β5t and β5t have been generated to show decrease of CD8 T cell numbers and responses. However, none of them exhibited combined immunodeficient phenotypes. Furthermore, CD8 T cell decrease observed in Psmb9G156D/+ mice is not caused by defective immunoproteasome activity to generate MHC class I-restricted antigens, as observed in the induced immunoproteasome subunit(s)-deficient mice, because MHC class I expression was not impaired and class I-restricted antigen presentation was normal in Psmb9G156D/+ mice (Supplementary Fig. 7). It can be assumed that the variant does not lead to mere decrease, but alteration or modification of immunoproteasome functions, which cannot be monitored by catalytic properties of conventionally used substrate polypeptides. Thus, although it remains unclear at present why PSMB9 G156D leads to immunodeficiency, mice with PSMB9 G156D mutation are a faithful model for analyzing proteasome defects.

Imunodeficient phenotype is also observed in mice carrying a missense mutation of β2i, which is introduced by N-ethyl-N-nitrosoure (ENU) mutagenesis. The mutation is described here as PSMB10 G209W, based on the amino acid number from the first methionine. Psmb10G209W/+ mice showed defects of both CD4 and CD8 T cells, and Psmb10G209W/G209W mice lacked B as well as T cells and manifested skin disorders with hyperkeratosis and infiltration of neutrophils. G209 is highly conserved among β2 and β2i across species, which is similar to the effects of PSMB9 G156D mutation. This speculation is supported by structural modeling analysis, showing that PSMB10 G209 is located at the interface of the two β rings and faced to β6 in the other half proteasome (Fig. 6a, c). Effects of PSMB10 G209W to induce immunodeficiency seem milder than those of PSMB9 G156D. Although the detailed molecular mechanisms are still unknown, it can be assumed that PSMB9 G156D and PSMB10 G209W should lead to defective interaction of two β rings and impaired formation of the 20S complex thereby causing immunodeficiencies (Supplementary Fig. 8).
proteasome formation and activity are preserved compared with the 20S complex, although 19S regulatory subunits might help facilitate the interaction of two β rings.

Ump1 coded by POMP is a chaperone used for proteasome assembly and heterozygous truncating variants of this gene cause autoinflammatory phenotypes with type I IFN signature. The variants also result in immune dysregulation, such as lymphocyte abnormalities showing CD4 T cell increase and B cell decrease, and the authors propose a designation as POMP-related autoinflammatory disease (PRAID). The manifestations are similar, but distinct from those of our cases (Table 1) and Psmb9G156D+/ mice, because the POMP variants lead to both the 20S complex and the 26S proteasome defects with ubiquitin accumulation and hyper-γ-globulinemia with autoantibodies.

Here we would propose a designation “proteasome-associated autoinflammatory syndrome with immunodeficiency (PRAAS-ID)” to indicate a category of autoinflammatory diseases, similar to, but distinct from PRAAS, as represented by the patients in this study. Psmb9 G156D mutant mice are useful to clarify not only the pathogenesis of proteasome dysfunctions but also homeostatic roles of immunoproteasome and to develop effective therapeutic maneuvers for PRAAS and immunodeficiency. It is also noteworthy that proteasome-related genes be candidate genes for screening patients with primary immunodeficiency of unknown etiology.

**Fig. 5 Immunological phenotype of mice carrying the PSMB9 G156D mutation.** a A photograph and histological images of the thymus. Scale bars in the leftmost and the other two panels represent 5 mm and 500 μm, respectively. Representative images from three mice were shown. b Cryosections of the spleen stained with hematoxylin and eosin (HE, left panel), anti-B220 Ab (middle panel), or anti-Thy1.2 Ab (right panel). Scale bars,500 μm. Representative images from three individual mice were shown. c Serum immunoglobulin levels. n = 6 in each group. Statistical analysis was performed with two-sided Welch’s t-test. d FACS analysis of B and T cells, DCs, and NK cells, in the spleen or bone marrow. The numbers represent the percentages of the cells within the indicated gates or each quadrant among splenocytes or bone marrow cells. e FACS analysis of neutrophils and monocytes in the spleen. The left and right panels show FcεRI− DX5− Siglec-F− and FcεRI− DX5− Siglec-F− Ly6G− cells, respectively. The numbers represent the percentages of neutrophils and monocytes among splenocytes.
Fig. 6 Characterization of proteasome subunit missense variants. 

a Locational distribution of published missense variant sites on the schematic model of β rings in the immunoproteasome (https://infevers.umai-montpellier.fr/web/index.php). The mutant residues are represented by red circles. Catalytic active sites in β1i, β2i, and β5i are marked with orange circles. Notably, PSMB9 G156 and PSMB10 G209 are at the interface of two β rings, while most of mutated residues in PSMB8 are at or around active sites.

b Multiple alignments of PSMB10 (β2i) and PSMB2 (β2) in various species. Conserved amino acids among all these species are indicated by asterisks. G209 in murine PSMB10 and the corresponding amino acids are indicated in red.

c The structure model of wildtype and PSMB10 G209W mutant of the 20S complex, based on the β2i-subunit structure (Protein Data Bank (PDB) ID code 3UNH). The overall structure of the 20S complex is shown as a ribbon model. β2i and β6 subunits are shown as light blue and orange, respectively. W209 and some of the potential interacting residues of PSMB10 G209W mutant are shown in stick representation.

Methods

Patients. Written informed consent was obtained from the patients’ parents and all other study participants.

Approval for this study. Studies on human participants were approved by the Ethics Committee of the University of the Ryukyus for Medical and Health Research Involving Human Subjects, the ethics boards of Gifu University, the Ethics Committee on Human Genome/Gene Analysis Research Nagasaki University, and the Research Ethics Committee of Wakayama Medical University. All animal experiments were done at Wakayama Medical University and approved by the Animal Research Committee of Wakayama Medical University.

Genetic studies. Whole exome sequencing was performed by using genomic DNAs obtained from peripheral blood of patients and parents30. In brief, exon fragments were enriched from genomic DNA samples of a patient and his parents using the SureSelect Human All Exon Kit V5 kit (Agilent Technologies), according to the manufacturer’s instructions. The prepared libraries were sequenced by the HiSeq2500 sequencer (Illumina) to obtain 100 bp+100 bp paired-end reads. The reads were mapped by the Novoalign software (Novocraft Technologies Sdn Bhd) on the hg19 human reference genome. The Genome Analysis Toolkit was used for following local realignment and variants call to obtain SNV and small insertion/deletion (indel) calls with in-house workflow management tool21.22. Using data from the patient and his parents, called variants that can be de novo variants in the patients were selected using an in-house tool. Selected variants were annotated by using the ANNOVAR software23. Finally, the variants that meet the following criteria were selected as “deleterious” variants: (1) leads stop gain, stop loss, nonsynonymous variant, or splice site variant, (2) alternative allele frequencies in databases including Complete Genomics whole genome data, the 1000 genome project, NHLBI GO ESP, the human genome variation database of the Japanese population24 and an in-house database are all ≤0.5%, (3) not included in segmental duplication region defined in the UCSC genome browser25,26.

For target capture sequencing, ubiquitin-proteasome-system, autophagy and interferonopathy-related gene panel were purchased from Integrated DNA Technologies (IDT) (Coralville, IA). Gene capture and library construction were performed using Hybridization capture of DNA libraries using xGen Lockdown Technology (IDT) (Coralville, IA). Gene capture and library construction were performed using Hybridization capture of DNA libraries using xGen Lockdown Probes and Reagents (IDT) according to the manufacturer’s instructions. The libraries were sequenced by the MiSeq sequencer to obtain 300 bp+300 bp paired-end reads. For the reads, mapping, SNV/indel calling, annotation, and narrowing were performed as with the exome analysis. Identified candidate variants were confirmed with Sanger sequencing. NEMO gene was amplified with long-range PCR and then the regions of exon and exon-intron boundaries were amplified by PCR for direct sequencing27.

TREC and KREC levels in the patients’ peripheral blood mononuclear cells (PBMC) were measured by real-time polymerase chain reaction (PCR). Genomic DNA from peripheral blood was prepared, and TREC and KREC levels were measured by real-time PCR (LightCycler 96, Roche Diagnostics). Primer pairs and probes are shown in Supplementary Table 5. A range of more or <100 copies/ug DNA is defined as positive or undetectable, respectively28.

IFN score. Total RNA was extracted from human blood samples collected into Paxgene Blood RNA tubes (762165, Becton, Dickinson and Company) and was
reverse transcribed by PrimeScript II 1st strand cDNA synthesis kit (6210 A, Takara). Quantitative real-time PCR was performed with Taqman Gene Expression Master Mix (4369016, Applied Biosystems) and probes (Supplementary Table S1) on the StepOnePlus Real-Time PCR system (Applied Biosystems). The expression levels of each transcript were determined in triplicate and normalized to the level of β-actin. Results were shown relative to a single calibrator. Median fold change of the six IFN-stimulated genes was used to calculate the IFN score for each sample. The score was regarded as positive if it exceeded +2 SD of the average IFN score from healthy controls9,30.

To calculate IFN score in mice, total RNA was extracted with RNeasy micro kit (QiAGEN) from Pbm9+/− and Pbm9G156D+/− spleenocytes and reverse transcribed by PrimeScript II 1st strand cDNA synthesis kit (RR037A, Takara). Quantitative real-time PCR was performed with TB Green Premix Ex Taq II (RR820A, Takara) and specific primers for six-IFN-stimulated genes on the StepOnePlus Real-Time PCR system (Applied Biosystems). The primers are shown in Supplementary Table S5. The expression levels of each transcript were normalized to the levels of 18S ribosomal RNA, which were determined by TaqMan probes (TaqMan Gene Expression Assay, Applied Biosystems). Median fold change of the six IFN-stimulated genes was used to calculate the IFN score for Pbm9+/− and Pbm9G156D/+ mice. The score was regarded as positive if it exceeded +2 SD of the average IFN score from Pbm9+/− mice.

Predictive analysis of the protein structure. Structural models of wildtype and mutated immunoproteasomes were created based on the structure of the immunoproteasome (PDB 3E96) using the Swiss-Model server32 and CNS (Crystallographic and NMR system) program33.

Cytokine measurement by ELISA. Human serum samples were stored at −80 °C until assayed. The concentrations of TNF-α, IL-1β, IL-6, IL-18, and IFN-γ were measured with ELISA kits (Invitrogen for TNF-α, IL-1β, and IL-6, R&D for IP-10, MBL for IL-18, and PBL Assay Science for IFN-γ). The primers are shown in Supplementary Table 5. The expression levels of the six IFN-stimulated genes were normalized to the levels of 18S ribosomal RNA, which were determined by TaqMan probes (TaqMan Gene Expression Assay, Applied Biosystems). Median fold change of the six IFN-stimulated genes was used to calculate the IFN score for Pbm9+/− and Pbm9G156D/+ mice. The score was regarded as positive if it exceeded +2 SD of the average IFN score from Pbm9+/− mice.

Cell lysates, glycerol gradient analysis, measurement of proteasomal activity, and western blotting. Cells were lysed in buffer containing 25 mM Tris-HCl (pH7.5), 0.5% NP-40, 1 mM DTT, 2 mM ATP, 5 mM MgCl2, and 1 mM phenylmethylsulfonyl fluoride (PMSF) and clarified by centrifugation at 20,000 × g for 10 min at 4 °C. For glycerol gradient centrifugation analysis, clarified cell lysates were subjected to 8-32% (v/v) glycerol linear gradient centrifugation (22 h, 83,000 × g) and separated into 32 fractions, and peptidase activities of each fraction were measured using a fluorescent peptide substrate, succinyl-Leu-Leu-Val-Tyr-7-amido-4-methylcoumarin (Suc-LLVY-AMC), for chymotrypsin-like activity with ARVO MX 1420 (Perkin Elmer)34. To verify that the peptidase activity was dependent on the proteasome, cells were treated with a selective proteasome inhibitor, carfilzomib (CFZ, LC laboratories), at 100 nM for 6 h. The Abs against Ump1, β1, β2, β5, β1, β2, β5, a2, a6, and polyubiquitin were established by S. Murata35,37.

Histology in mice. Thymus and spleen were fixed with 4% paraformaldehyde and embedded in OCT compound (Sakura Finetek) or FSC22 frozen section compound (Leica Microsystems), and 5 μm cryosections were prepared. The sections were stained with hematoxylin and eosin (Muto Pure Chemicals). To detect B and T cells, sections were stained with biotinylated Abs against B220 (RA3-E82, ebioscience 13-0452-85, 1 μg mL−1) or Thy1.2 (30-H12, BD Bioscience 553311, 1 μg/mL) and streptavidin-conjugated alkaline phosphatase (Carbaprep, Biovendor). Biotinylated Abs were developed with VECTASTAIN ABC Standard kit and ImmPACT DAB (Vector Laboratories). Hematoxylin was used as counterstain.

Measurement of serum Ig levels in mice. Serum Ig levels were measured by ELISA developed in hand. In brief, serum samples were incubated with ELISA plate coated with goat anti-mouse IgM, IgG1, IgG2b, IgG2c, or IgA Abs (Southern Biotech) and detected with biotinylated goat Abs against each class (Southern Biotech) and streptavidin-conjugated alkaline phosphatase. The plate was developed by alkaline phosphatase buffer (50 mM NaHCO3, 10 mM MgCl2, pH 9.8) containing phosphatase substrate tablet (S0942, Sigma-Aldrich). Purified mouse IgM, IgG1, IgG2b, IgG2c, IgG3 (Southern Biotech) were used as standard.

Statistical analysis. Statistical significance was determined using two-sided Student’s t-test, two-sided Welch’s t-test, two-sided Mann–Whitney test, or Log-rank test as indicated in the figure legends using GraphPad Prism 7 or 9 (GraphPad Software). p < 0.05 was considered significant.

Reporting summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability
The exome sequencing datasets generated and analyzed in this study are not publicly available due to patient privacy confidentiality but are available from the corresponding author on reasonable request. The sequence data on PSM89/G.467G>A (p.G156D) variant is deposited in NCBI ClinVar under the accession number VC001299361 (https://www.ncbi.nlm.nih.gov/clinvar/variation/1299361). Source data are provided with this paper.
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20. Ichihara, S. et al. The 【Author contributions】

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N. Kanazawa, H.H., H.O., and T. Kai designed the research. N. Kanazawa, H.H., N. Kinjo, K.-i.Y., and T. Kai generated and analyzed the murine model. N. Kinjo, H.O., H.K., N. Kawamoto, S.K., and K.-i.Y. saw the patients and analyzed the patients’ materials. H.M., A.K., and K.-I.Y. performed genomics analyses. T.M. performed simulation analyses. Y. Imai, T. Kai, and H.H. wrote and edited the manuscript.

Competing interests

The authors declare no competing interests.

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