Mutations in signal recognition particle SRP54 cause syndromic neutropenia with Shwachman-Diamond–like features

Raphael Carapito, …, Bertrand Isidor, Seiamak Bahram


Shwachman-Diamond syndrome (SDS) (OMIM #260400) is a rare inherited bone marrow failure syndrome (IBMFS) that is primarily characterized by neutropenia and exocrine pancreatic insufficiency. Seventy-five to ninety percent of patients have compound heterozygous loss-of-function mutations in the Shwachman-Bodian-Diamond syndrome (sbds) gene. Using trio whole-exome sequencing (WES) in an sbds-negative SDS family and candidate gene sequencing in additional SBDS-negative SDS cases or molecularly undiagnosed IBMFS cases, we identified 3 independent patients, each of whom carried a de novo missense variant in srp54 (encoding signal recognition particle 54 kDa). These 3 patients shared congenital neutropenia linked with various other SDS phenotypes. 3D protein modeling revealed that the 3 variants affect highly conserved amino acids within the GTPase domain of the protein that are critical for GTP and receptor binding. Indeed, we observed that the GTPase activity of the mutated proteins was impaired. The level of SRP54 mRNA in the bone marrow was 3.6-fold lower in patients with SRP54-mutations than in healthy controls. Profound reductions in neutrophil counts and chemotaxis as well as a diminished exocrine pancreas size in a SRP54-knockdown zebrafish model faithfully recapitulated the human phenotype. In conclusion, autosomal dominant mutations in SRP54, a key member of the cotranslation protein-targeting pathway, lead to syndromic neutropenia with a Shwachman-Diamond–like phenotype.
Mutations in signal recognition particle SRP54 cause syndromic neutropenia with Shwachman-Diamond–like features

Raphael Carapito,1,2,3 Martina Konantz,4 Catherine Paillard,1,2,5 Zhichao Miao,6 Angélique Pichot,1,2 Magalie S. Leduc,7,8 Yaping Yang,7 Katie L. Bergstrom,9 Donald H. Mahoney,9 Deborah L. Shardy,9 Ghada Alsaleh,9 Lydie Naegely,1,9 Aline Kolmer,1,2 Nicodème Paul,1,2 Antoine Hanauer,1,2 Véronique Rolli,1,2,3 Joëlle S. Müller,4 Elisa Alghisi,4 Loïc Sauteur,4 Cécile Macquin,1,2 Nathalie Marle,4 Nael Osman,1,2 Olivier Lefebvre,4 Jacky G. Goetz,4 Sule Unal,15 Nurten A. Akarsu,16 Mirjana Radosavljevic,1,2,3 Marie-Pierre Chenard,17 Fanny Rialland,18 Marie-Christine Béné,19 Marion Eveillard,19 Marie Vincent,20 Julien Guy,21 Laurence Faivre,22 Christel Thauvin-Robinet,22 Julien Thevenon,22 Kasiani Myers,23 Mark D. Fleming,24 Akiko Shimamura,25 Elodie Bottollier-Lemallaz,26 Eric Westhof,26 Claudia Lengerke,27 Bertrand Isidor,20,28 and Seiamak Bahram1,2,3

1Laboratoire d'ImmunoRhumatologie Moléculaire, Plateforme GENOMAX, INSERM UMR - 5170, Faculté de Médecine, Fédération Hospitalo-Universitaire OMCARE, Fédération de Médecine Translationnelle de Strasbourg (FMTS), Université de Strasbourg, Strasbourg, France. 2LabEx TRANSPLANTEX, Faculté de Médecine, Université de Strasbourg, Strasbourg, France. 3Service d'Immunologie Biologique, Plateau Technique de Biologie, Hôpital d'enfants, CHU de Dijon, Dijon, France. 4Division of Pediatric Hematology, Hacettepe University Medical Faculty, Sihhiye, Ankara, Turkey. 5Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, Texas, USA. 6Division of Pediatric Hematology, Hacettepe University Medical Faculty, Sihhiye, Ankara, Turkey. 6Architecture et Réactivité de l’ARN, CNRS UPR 9002, LabEx NetRNA, Institut de Biologie Moléculaire et Cellulaire, Université de Strasbourg, Strasbourg, France. 7Département de Pathologie, Hôpitaux Universitaires de Strasbourg, Strasbourg, France. 8Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, Texas, USA. 9Bayor Genetics, Holcombe, Houston, Texas, USA. 10Laboratoire d'Infectiologie, Hôpital de Hautepierre, Hôpitaux Universitaires de Strasbourg, Strasbourg, France. 11Laboratoire d'Immunologie Biologique, Pôle de Biologie, Centre Hospitalier Universitaire (CHU) de Dijon, Dijon, France. 12CNRS UPR 9002, LabEx NetRNA, Institut de Biologie Moléculaire et Cellulaire, Université de Strasbourg, Strasbourg, France. 13Laboratoire de Cytogénétique, Pôle de Biologie, Centre Hospitalier Universitaire (CHU) de Dijon, Dijon, France. 14Service d'Oncologie et Hématologie Pédiatrique, Hôpital d'enfants, CHU de Dijon, Dijon, France. 15Laboratoire de Pathologie, Hôpitaux Universitaires de Strasbourg, Strasbourg, France. 16Laboratoire de Physiopathologie de la Résorption Osseuse et Thérapie des Tumeurs Osseuses Primitives, INSERM UMR – 5757, Faculté de Médecine, Nantes, France. 17Department of Medical Genetics, Hacettepe University Medical Faculty, Sihhiye, Ankara, Turkey. 18Department of Biochemistry and Genetics, Angers Hospital, Angers, France. 19Service d'Hématologie Biologique, Pôle de Biologie, Centre Hospitalier Universitaire (CHU) de Dijon, Dijon, France. 20Service de Génétique, Hôpital d'enfants, DRF, CHU de Dijon, Dijon, France. 21Service d'Hematologie Biologique, CHU de Dijon, Dijon, France. 22Department of Pathology, Hôpitaux Universitaires de Strasbourg, Strasbourg, France. 23Division of Blood and Marrow Transplantation and Immune Deficiency, The Cancer and Blood Diseases Institute, Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio, USA. 24Department of Pathology, Boston Children's Hospital, and 25Dana-Farber/Boston Children's Cancer and Blood Disorders Center, Harvard Medical School, Boston, Massachusetts, USA. 26Laboratoire d’Hématologie et Oncologie Pédiatrique, Hôpital des enfants, CHU de Dijon, Dijon, France. 27Laboratoire d’ImmunoRhumatologie Moléculaire, Plateforme GENOMAX, INSERM UMR – 5170, Faculté de Médecine, Fédération Hospitalo-Universitaire OMCARE, Fédération de Médecine Translationnelle de Strasbourg (FMTS), Université de Strasbourg, Strasbourg, France. 28Service de Radiologie Pédiatrique, Hôpital de Hautepierre, Hôpitaux Universitaires de Strasbourg, Strasbourg, France. 29Laboratoire de Physiopathologie de la Résorption Osseuse et Thérapie des Tumeurs Osseuses Primitives, INSERM UMR – 5757, Faculté de Médecine, Nantes, France.

Shwachman-Diamond syndrome (SDS) (OMIM #260400) is a rare inherited bone marrow failure syndrome (IBMFS) that is primarily characterized by neutropenia and exocrine pancreatic insufficiency. Seventy-five to ninety percent of patients have compound heterozygous loss-of-function mutations in the Shwachman-Bodian-Diamond syndrome (SBDS) gene. Using trio whole-exome sequencing (WES) in an SBDS-negative SDS family and candidate gene sequencing in additional SBDS-negative SDS cases or molecularly undiagnosed IBMFS cases, we identified 3 independent patients, each of whom carried a de novo missense variant in SRP54 (encoding signal recognition particle 54 kDa). These 3 patients shared congenital neutropenia linked with various other SDS phenotypes. 3D protein modeling revealed that the 3 variants affect highly conserved amino acids within the GTPase domain of the protein that are critical for GTP and receptor binding. Indeed, we observed that the GTPase activity of the mutated proteins was impaired. The level of SRP54 mRNA in the bone marrow was 3.6-fold lower in patients with SRP54-mutations than in healthy controls. Profound reductions in neutrophil counts and chemotaxis as well as a diminished exocrine pancreas size in a SRP54-knockdown zebrafish model faithfully recapitulated the human phenotype. In conclusion, autosomal dominant mutations in SRP54, a key member of the cotranslation protein-targeting pathway, lead to syndromic neutropenia with a Shwachman-Diamond–like phenotype.

Authorship note: R. Carapito, M. Konantz, and C. Paillard contributed equally to this work. C. Lengerke, B. Isidor, and S. Bahram contributed equally to this work.

Conflict of interest: The authors have declared that no conflict of interest exists.

Submitted: January 23, 2017; Accepted: August 10, 2017.


Introduction

Shwachman-Diamond syndrome (SDS) (OMIM #260400), an inherited bone marrow failure syndrome (IBMFS), is a rare multisystem disorder that was first recognized more than 50 years ago (1–4). Its cardinal features include exocrine pancreatic insufficiency and hematological abnormalities in which neutropenia is para-
mount and can be life threatening. Skeletal abnormalities, neurocognitive deficits, and a variety of other diverse symptoms are also associated with the disease (5). Like many other IBMFSs, patients with SDS have an increased risk of myelodysplasia and malignant transformation, especially acute myeloid leukemia (6). Approximately 75% to 90% of SDS patients have compound heterozygous loss-of-function mutations in the Shwachman-Bodian-Diamond syndrome (SBDS) gene (7–9). Since the identification of SBDS in 2003, only 2 other causal SDS genes, DNAJC21 (10, 11) and EFL1 (12), have been reported, in contrast to other IBMFSs, for which the situation is the opposite (e.g., >20 loci in Fanconi anemia, >10 loci in Diamond-Blackfan anemia, and several loci in severe congenital neutropenia) (13).

The SBDS protein plays a central role in ribosome biogenesis, as it is involved in the maturation of the 60S subunit (as are DNAJC21 and EFL1) prior to the assembly of the actively translating 80S ribosome (14, 15). During the biogenesis and initiation of protein translation, the ribosome associates with many partner molecules, and of these, the signal recognition particle (SRP) is a major one. SRP is a ribonucleoprotein (RNP) complex that mediates the targeting of nascent signal sequence–carrying polypeptides (including both membrane and secretory proteins) to the translocon at the surface of the ER (16). The mammalian SRP is composed of a single RNA molecule (the ∼300-nucleotide-long 7SL RNA) and the following 6 polypeptides: SRP9, SRP14, SRP19, SRP54, SRP68, and SRP72 (17). SRP54 plays a central role in this RNP complex. With its M domain, SRP54 binds to the SRP19-bound 7SL RNA and associates with the signal peptide of the nascent polypeptide chain. Then, via its N and G domains, SRP54 binds to the SRP receptor (SR) on the ER membrane (18, 19). Ultimately, SRP54 forms a link between the SRP and the ER membrane and allows insertion of the signal peptide–carrying polypeptide into the translocation channel. In addition to the SRP RNA, SRP54 is the only other universally conserved SRP component. Here, we demonstrate that mutations in SRP54 can lead to syndromic neutropenia with SDS-like features.

Results

Clinical characteristics of patients. The clinical features of the 3 patients are summarized in Supplemental Table 1 (supplemental material available online with this article; https://doi.org/10.1172/JCI92876DS1). Patient AII.1 was a white male and the second child of healthy nonconsanguineous parents (Figure 1A). The patient was born after a full-term, uneventful pregnancy and presented with neonatal transitory respiratory distress, hypotonia, and central apneas. Morphological examination of the newborn revealed small size (−1.5 SD), low weight (−1.5 SD), an occipito-frontal circumference (OFC) of +1.5 SD, low-set, asymmetric ears, thinning hair, frontal angiomia, mandibular micromegathatism, a high-arched palate, small teeth, and a pectus carinatum — a series of symptoms that are all uncommon in typical SDS patients. Complete blood counts in the first week of life showed severe neutropenia (0.28 × 10³/μl and then 0 × 10³/μl). Hemoglobin (15.8 g/dl) and platelet (265 × 10³/μl) counts were normal. He received granulocyte-CSF (G-CSF) injections, with no effect on neutrophil counts. A bone marrow smear was hypocellular and showed hypoplasia in the neutrophil lineage with retarded granulocyte maturation. Moreover, numerous cytoplasmic vacuoles were observed in myeloblasts, promyelocytes, and apoptotic cells of the granulocyte lineage (Supplemental Figure 1A). Of note, none of the erythroblasts contained vacuoles, and Perls’ staining revealed no ring sideroblasts, thus excluding Pearson syndrome. Furthermore, iron was detected in macrophages using the Prussian blue reaction. To definitively exclude a mitochondrial DNA disorder (i.e., Pearson syndrome), whole mitochondrial DNA analysis was performed using next-generation sequencing, which revealed no pathogenic mutations or rearrangements (Supplemental Figure 2).

The patient’s lymphocyte immunophenotype results and serum Ig levels were normal. There were no alloimmunizations against neutrophils or granulocyte-specific antigens. Cardiac ultrasound showed large interauricular and interventricular septal defects. The cerebral MRI was normal. At 6 months of age, the patient had feeding difficulties and diarrhea. His weight, height, and OFC were 6.5 kg (−1.5 SD), 63 cm (−1.5 SD), and 45 cm (+1.5 SD), respectively. Stool analysis revealed very low elastase levels (<15 μg/g of stool; reference value: >200 μg/g of stool). Fatty infiltration of the pancreas was documented by CT (Supplemental Figure 3A). Blood levels of the fat-soluble vitamins A, D, E, and K were very low. At 11 months of age, the patient’s ventricular and atrial septal defects required surgery. Severe neutropenia led to infections including acute ethmoiditis and perianal abscesses. At 4 years of age, the patient underwent genodentical allogeneic hematopoietic cell transplantation (HCT) without major complications. His hematologic reconstitution was uneventful. The patient showed psychomotor developmental delay and autistic behavior. At 6 years of age, he continues to receive lipase substitution (see Supplemental Table 1). Direct sequencing of the SBDS gene was performed using genomic DNA isolated from pretransplantation peripheral blood cells and failed to identify any mutations, as did panel sequencing of all known IBMFS genes. Comparative genome hybridization (CGH) also excluded pathogenic structural variants and copy number variations (CNVs) throughout the genome, including inside and in the vicinity of SBDS.

Patient BII.1 was a 1-year-old white girl who was the only child of healthy nonconsanguineous parents (Figure 1A). At birth, her weight, height, and OFC were 3.26 kg (0 SD), 45.5 cm (−2 SD), and 32.5 cm (+1 SD), respectively. She had no dysmorphic features. Repeated blood counts revealed severe neutropenia (e.g., 0.02 × 10³/μl), while her other blood parameters were normal, including fetal hemoglobin, cupremia, lymphocyte immunophenotyping, and Ig levels. No alloimmunization against granulocytes was found. Cerebral MRI as well as abdominal and cardiac ultrasound imaging results were normal. Her fetal elastase level was very low (<15 μg/g of stool; reference value: >200 μg/g of stool). Abdominal CT showed a fatty infiltration of the pancreas (Supplemental Figure 3B). At 6 months of age, the patient presented with facial cellulitis and ethmoiditis. She was given G-CSF without success. At 1 year of age, she underwent unrelated cord blood transplantation. Pretransplantation clinical examination revealed small stature (69 cm; −2 SD), low weight (8.5 kg; −0.5 SD), and an OFC of 48 cm (+1 SD) (Supplemental Table 1). No overt developmental delay or psychomotor retardation was observed before she passed away at 16 months of age (see below). A blood cell count revealed a total absence of neutrophils. Her other blood count parameters

The Journal of Clinical Investigation
were normal. Anomalies similar to those in patient AII.1 were observed in the bone marrow smear of this patient, who also had no ring sideroblasts and no mitochondrial DNA anomalies (Supplemental Figure 1B and Supplemental Figure 2). Her ferritin level was normal (37 μg/l). Other cell lineages were normal. HCT and hematopoietic reconstitution were uneventful. Two months after transplantation, the patient developed multiorgan failure, which rapidly led to death. Postmortem pathology showed severe veno-occlusive disease. Direct sequencing of the SBDS gene (and panel sequencing of all other IBMFS genes) using genomic DNA isolated from pretransplantation peripheral blood cells failed to identify any mutations. No pathogenic structural variants were detected via CGH array, as was the case with the previous patient.

Patient CII.1 was a Hispanic boy and the second child of healthy nonconsanguineous parents (Figure 1A), who was born after a full-term, uneventful pregnancy. His birth weight was 3.24 kg (25th percentile), and no dysmorphic features or bony abnormalities were visible. He did not have any feeding or gastrointestinal problems. At 2 years of age, he was diagnosed with language delay and autism spectrum disorder. At the same time, he was noted as having anemia (hemoglobin 10.5 g/dl) with normal iron stores and neutropenia (0.76 × 10⁹/l). At 4 years of age, the patient was referred to the hematology clinic for evaluation of mild anemia (hemoglobin 9.4–10.5 g/dl), intermittent neutropenia (0.13 × 10⁹/l to 1.88 × 10⁹/l), fevers, and recurrent episodes of mucositis, otitis media, and cellulitis (Supplemental Table 1). Serial complete blood
Table 1. Details of SRP54 sequence alterations in the 3 patients

<table>
<thead>
<tr>
<th>Nucleotide alteration</th>
<th>Patient AII.1</th>
<th>Patient BII.1</th>
<th>Patient CII.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exon</td>
<td>Chr14:35482592G&gt;A</td>
<td>Chr14:35476576A&gt;G</td>
<td>Chr14:35476582, 3547584del</td>
</tr>
<tr>
<td>cDNA alteration</td>
<td>cDNA.1074G&gt;A</td>
<td>cDNA.740A&gt;G</td>
<td>cDNA.746_748delACA</td>
</tr>
<tr>
<td>Coding sequence alteration</td>
<td>c.677G&gt;A</td>
<td>c.343A&gt;G</td>
<td>c.349_351del</td>
</tr>
<tr>
<td>Predicted causal effect</td>
<td>Disease causing</td>
<td>Disease causing</td>
<td>Disease causing</td>
</tr>
<tr>
<td>phastCon</td>
<td>8</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>physL</td>
<td>5.729</td>
<td>5.981</td>
<td>4.938</td>
</tr>
<tr>
<td>PolyPhen (HumDiv)</td>
<td>0.793</td>
<td>0.999</td>
<td>NA</td>
</tr>
<tr>
<td>Mutation Assessor</td>
<td>3.89</td>
<td>4.66</td>
<td>NA</td>
</tr>
<tr>
<td>SIFT score</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>LRT score</td>
<td>0</td>
<td>0</td>
<td>NA</td>
</tr>
<tr>
<td>GERP++_NR</td>
<td>5.11</td>
<td>5.5</td>
<td>NA</td>
</tr>
</tbody>
</table>

Predictive analyses were performed using MutationTaster (57), Polyphen-2 v2.2.2r398 (58), and the GATK analysis toolkit (59). Positions refer to GenBank transcript NM_003136.3. The closer the phastCon value is to 1, the more probable the nucleotide is conserved. Values varied between -1.4 and +6. Sites predicted to be fast evolving are assigned negative scores, while sites predicted to be slow evolving are assigned positive scores. Scores not available for deletions (indels are not supported). Function prediction tool. Variants with scores between 0.85 and 1.0 are highly confidently predicted to be damaging. Function prediction tool. Deleterious threshold: >0.65. Function prediction tool based on protein sequence conservation among homologs. Variants with scores between 0 and 0.05 are considered deleterious. DNA sequence evolutionary model expressed as a P value. DNA conservation score. Deleterious threshold: >4.4.

counts showed a cyclical pattern of neutropenia (0 \times 10^9/l to 2.92 \times 10^9/l) lasting 13–15 days. He tested negative for anti-neutrophil antibodies as well as for mutations in an IBMFS gene panel that included SBDS (the analysis was performed using genomic DNA extracted from peripheral blood) (Supplemental Table 1). His initial bone marrow evaluation at 4 years of age showed 80% cellularity with a maturation arrest at the myelocyte stage, while other cell lineages were normal (as reported in the patient’s medical records; images not available). At 8 years of age, he was started on G-CSF at 5 mcg/kg every other day, with improvement in anemia, neutrophil counts, mucositis, and infections. His early growth parameters showed height and weight in the 13th percentile, and these improved, reaching the 30th percentile with G-CSF therapy. He continues to do well on G-CSF therapy and is now 18 years of age.

In summary, all 3 patients presented with neutropenia associated with a host of various other symptoms, including exocrine pancreatic deficiency (2 of 3 patients) and/or autistic behavior (documented in 2 of 3 patients; not assessable in the third, patient BII.1, due to early death), along with a host of other morphological abnormalities and/or bone marrow morphology that are not typically observed in classical SDS (Supplemental Table 1). All 3 patients were negative for any mutations in all known IBMFS genes, including SBDS.

Identification of a candidate gene. Prior to exome sequencing, SBDS single point mutations were excluded in all 3 cases using Sanger sequencing of all coding exons. SBDS CNVs/structural variants were also excluded using CGH microarray analysis, as were mutations in other IBMFS genes using panel sequencing. were included from the Hacettepe Bone Marrow Failure Center (Ankara, Turkey). Of these, 10 had neutropenia and/or bone marrow failure, while 8 had no cytopenias. Steatosis or abnormal exocrine pancreatic function was noted in 18 of these patients, and failure to thrive was noted in 16 of them. (b) Twenty SBDS-negative patients

In the index family (family A) (Figure 1A), exome sequencing was performed in patient AII.1 and his healthy parents. Variants of the index case were ranked on the basis of coding region sequence effect, frequency in public databases, and absence in healthy parents (other modes of transmission were excluded beforehand). A single de novo c.677G>A (p.G226E) missense mutation in the SRP54 (signal recognition particle 54 kDa) gene remained after these filtering steps (Table 1 and Figure 1B). A total of 84 additional SBDS-negative potential SDS patients were screened for mutations in SRP54 using Sanger sequencing and/or WES. The inclusion criteria included SBDS-negative SDS patients and other patients with molecularly undiagnosed severe congenital neutropenia as well as other IBMFSs. This exploratory cohort was composed of the following data sets: (a) Thirty-four patients from the North American Shwachman-Diamond Syndrome Registry and local US Bone Marrow Failure Registries, including thirty-three with neutropenia and/or bone marrow failure and one with no cytopenias. Steatosis or abnormal exocrine pancreatic function was noted in 18 of these patients, and failure to thrive was noted in 16 of them. (b) Twenty SBDS-negative patients

of the latter cohort, the only available information was the presence of severe congenital neutropenia and/or a clinical SDS phenotype. During the course of this screening, we identified a second family (family B) that harbored a second de novo c.343A>G (p.T115A) missense mutation in SRP54 (Figure 1B and Table 1). To exclude additional candidate genes, we also performed WES of the proband and her parents. Finally, a third family was independently identified at Baylor College of Medicine using trio WES (family C). In this family, we identified a c.349_351del (p.T117del) de novo missense mutation in the SRP54 gene. The variant filtering strategy and the identified variants are summarized in Supplemental Figure 4 and Supplemental Table 2, respectively. All 3 mutations affected highly conserved amino acids located in the GTPase domain of the protein (Figure 1, C and D). The mutations have deleterious predictive values, as indicated by various bioinformatics analyses (Table 1). In addition, none of the 3 variants was found in the 1000 Genomes database (http://www.internationalgenome.org/1000-genomes-browsers/), the Exome Aggregation Consortium (ExAC) Browser (http://exac.broadinstitute.org/), our internal exome database, or various other databases that altogether contain more than 100,000 exomes. All 3 mutations and their de novo nature were validated using Sanger sequencing in all probands and their parents. Finally, the mutations
The Journal of Clinical Investigation

RESEARCH ARTICLE

The Journal of Clinical Investigation

RESEARCH ARTICLE

The Journal of Clinical Investigation

in SRP54 and G233, T232, and D43 in the receptor, without major rearrangements of the local protein fold (Figure 2B). This was confirmed by the modification of the electrostatic surface induced by this mutation (Supplemental Figure 5). The mutation p.T115A in family B most likely directly affects GTP binding, because T115 forms an important hydrogen bond with GTP that is lost when the residue is mutated to alanine (Figure 2C). The mutation p.T117del in family C might also impact GTP binding. Residues 115–117 correspond to a threonine triplet. When 1 of these threonines is deleted, the helix structure at Gly113 starts earlier than expected, while the 112–115 region forms extensive H-bonds with GTP. The deletion of T117 may affect GTP binding through rearrangements of residues 113–116, but this is difficult to predict.

In vivo and in vitro functional impact of the mutations. The level of SRP54 mRNA in (pretransplantation) bone marrow mononucle-ear cells from patients AII.1 and kidney (patient BII.1), thereby confirming the germline nature of these mutations.

3D modeling of srp54 mutations. We analyzed the spatial location and predicted functional impact of the 3 identified mutations (p.T115A, p.T117del and p.G226E) using 3D modeling. Figure 2A shows the locations of the 3 affected residues on the structure of SRP54 associated with the SR. The mutated residues are all located around the GTP-binding domain in highly conserved regions (G domain) (20–22). The amino acid change p.G226E, which we observed in family A, is predicted to affect receptor binding, because it would lead to extremely short contacts between E226 and G226 (Figure 2B).

We assessed the in vitro GTPase activity of recombinant WT and mutant SRP54 using a malachite green assay. The p.G226E mutation reduced the activity by a factor of 3.5. In the p.T115A mutant, phosphate release was nearly completely abolished, whereas the p.T117del (third patient) mutant showed a clear (although not attaining statistical significance; \( P = 0.0579 \)) yet moderate, 1.6-fold decrease in enzymatic activity (Figure 3B). This result is consistent with the above-mentioned structural modeling, which also predicted a milder functional impact for this mutation. Finally, when SRP54 was silenced were also validated using Sanger sequencing on genomic DNA extracted from nonhematopoietic cells, i.e., buccal swabs (patient AII.1) and kidney (patient BII.1), thereby confirming the germline nature of these mutations.

In vivo and in vitro functional impact of the mutations. The level of SRP54 mRNA in (pretransplantation) bone marrow mononucle-ear cells from patients AII.1 and BII.1 was 3.6-fold lower than those in healthy bone marrow donors (Figure 3A). We assessed the in vitro GTPase activity of recombinant WT and mutant SRP54 using a malachite green assay. The p.G226E mutation reduced the activity by a factor of 3.5. In the p.T115A mutant, phosphate release was nearly completely abolished, whereas the p.T117del (third patient) mutant showed a clear (although not attaining statistical significance; \( P = 0.0579 \)) yet moderate, 1.6-fold decrease in enzymatic activity (Figure 3B). This result is consistent with the above-mentioned structural modeling, which also predicted a milder functional impact for this mutation. Finally, when SRP54 was silenced were also validated using Sanger sequencing on genomic DNA extracted from nonhematopoietic cells, i.e., buccal swabs (patient AII.1) and kidney (patient BII.1), thereby confirming the germline nature of these mutations.

3D modeling of srp54 mutations. We analyzed the spatial location and predicted functional impact of the 3 identified mutations (p.T115A, p.T117del and p.G226E) using 3D modeling. Figure 2A shows the locations of the 3 affected residues on the structure of SRP54 associated with the SR. The mutated residues are all located around the GTP-binding domain in highly conserved regions (G domain) (20–22). The amino acid change p.G226E, which we observed in family A, is predicted to affect receptor binding, because it would lead to extremely short contacts between E226 and G226 (Figure 2B).
in 2 cell lines (HeLa and HL60), it had no impact on the expression of 2 other proteins known to be mutated in SDS (i.e., SBDS and DNAJC21) (Supplemental Figure 6) or on the mTOR pathway, which was previously linked to SDS pathophysiology (23, 24).

**Zebrafish model.** The zebrafish is an established model for studying hematopoiesis and development (25, 26). At 26 hours post fertilization (hpf), expression data indicated ubiquitous staining for the zebrafish homolog srp54 (bottom image, Supplemental Figure 7A). Later in development, srp54 expression was more pronounced in the anterior part of the zebrafish (top image, Supplemental Figure 7A). A similar expression pattern has been shown for the zebrafish homolog of the SBDS gene at these developmental time points (27).

To investigate the role of srp54 in zebrafish embryonic development, we performed in vivo loss-of-function experiments by treating zebrafish embryos with 2 different antisense morpholino oligonucleotides (MOs), to inhibit srp54 pre-mRNA splicing. We found that transcripts in morphants were indeed misspliced (Supplemental Figure 7B). To analyze the neutrophil numbers in developing zebrafish embryos, control and srp54 MO–injected transgenic Tg(mpex:eGFP) and Tg(lyz:DsRed) fish were first analyzed using flow cytometry, which revealed respectively fewer mpex+ and lyz+ neutrophils in dissociated srp54 morphants than in the control-injected fish, which could be partially rescued by coinjection of human SRP54 mRNA (Figure 4) (28). This suggests a conserved functional identity between the 2 orthologs, which is consistent with their high evolutionary conservation (96% sequence identity between zebrafish and human proteins) (Supplemental Figure 8). Following tail fin injury, we further observed fewer numbers of neutrophils migrating to the site of injury in srp54 morphants than in the embryos injected with the control MOs designed to induce intron retention. We found that transcripts in morphants were indeed spliced (Supplemental Figure 7B). To analyze the neutrophil numbers in developing zebrafish embryos, control and srp54 MO–injected transgenic Tg(mpex:eGFP) and Tg(lyz:DsRed) fish were first analyzed using flow cytometry, which revealed respectively fewer mpex+ and lyz+ neutrophils in dissociated srp54 morphants than in the control-injected fish, which could be partially rescued by coinjection of human SRP54 mRNA (Figure 4) (28). This suggests a conserved functional identity between the 2 orthologs, which is consistent with their high evolutionary conservation (96% sequence identity between zebrafish and human proteins) (Supplemental Figure 8). Following tail fin injury, we further observed fewer numbers of neutrophils migrating to the site of injury in srp54 morphants than in the embryos injected with the control MOs designed to induce intron retention. We found that transcripts in morphants were indeed spliced (Supplemental Figure 7B). To analyze the neutrophil numbers in developing zebrafish embryos, control and srp54 MO–injected transgenic Tg(mpex:eGFP) and Tg(lyz:DsRed) fish were first analyzed using flow cytometry, which revealed respectively fewer mpex+ and lyz+ neutrophils in dissociated srp54 morphants than in the control-injected fish, which could be partially rescued by coinjection of human SRP54 mRNA (Figure 4) (28). This suggests a conserved functional identity between the 2 orthologs, which is consistent with their high evolutionary conservation (96% sequence identity between zebrafish and human proteins) (Supplemental Figure 8). Following tail fin injury, we further observed fewer numbers of neutrophils migrating to the site of injury in srp54 morphants than in the embryos injected with the control MOs designed to induce intron retention. We found that transcripts in morphants were indeed spliced (Supplemental Figure 7B). To analyze the neutrophil numbers in developing zebrafish embryos, control and srp54 MO–injected transgenic Tg(mpex:eGFP) and Tg(lyz:DsRed) fish were first analyzed using flow cytometry, which revealed respectively fewer mpex+ and lyz+ neutrophils in dissociated srp54 morphants than in the control-injected fish, which could be partially rescued by coinjection of human SRP54 mRNA (Figure 4) (28). This suggests a conserved functional identity between the 2 orthologs, which is consistent with their high evolutionary conservation (96% sequence identity between zebrafish and human proteins) (Supplemental Figure 8). Following tail fin injury, we further observed fewer numbers of neutrophils migrating to the site of injury in srp54 morphants than in the embryos injected with the control.
MO (Figure 5, A and B), which again could be rescued by coinjection of human SRP54 mRNA. Time-lapse imaging in double-transgenic embryos further documented both the quantitative reduction in neutrophils — visualized as migrating lyz:DsRed/mpx:eGFP cells — and the chemotaxis defect in response to injury (Figure SC and Supplemental Videos 1 and 2). Pancreas development was also impaired upon srp54 knockdown, as shown by altered ptf1a expression at 72 hpf, indicating exocrine pancreatic defects (Figure 6A), while the endocrine pancreas appeared unaltered as monitored by whole-mount ISH (WISH) of insulin-a (insa) (Figure 6B). Both the neutrophil and the pancreas phenotypes were confirmed by mpx and trypsin WISH, which showed reduced numbers of neutrophils (Figure 7A and Supplemental Figure 9A) and incompletely surrounded islets (Figure 7B) in srp54 morphants versus control MO-injected embryos.
Discussion

IBMFSs are a heterogeneous group of disorders that share complex overlapping phenotypes, including dysmorphogenesis, a partial or total lack of mono- or multilineage blood cell production, and an increased risk of malignant transformation. Although traditionally classified according to characteristic clinical symptoms, a new disease nosology based on molecular etiology and pathway biology is emerging. Surprisingly, however, most, if not all, underlying mutations associated with IBMFS affect genes that are not specifically expressed in hematopoietic cells but that are instead engaged in fundamental and ubiquitous cellular processes, such as ribosome biogenesis, DNA repair, or telomere maintenance. Here, we add a key cellular entity to the genes known as mutated in IBMFS. We show that de novo mutations in SRP54 cause syndromic congenital neutropenia with a Shwachman-Diamond–like phenotype, a phenotype that was completely reproduced by knocking down the zebrafish homolog of this gene. In the cases presented here, several clinical and biological characteristics differ from those typically observed in classical SDS (summarized in Supplemental Table 1). Among them is the cell morphology of myeloid precursors that contain cytoplasmic vacuoles. This unusual feature indicates that the mechanism leading to neutropenia may be different in patients with SRP54 mutations compared with that in typical SDS patients.

Several other IBMFSs are also caused by an abnormal translational machinery. These include Diamond-Blackfan anemia and the canonical SDS (29). While all these disorders (and others) are associated with mutations that affect 40S or 60S ribosomal subunits and/or their assembly (with the exception of 2 sporadic cases of aplastic anemia that were mutated in another SRP subunit [SRP72] [ref. 30]), the SRP complex has thus far remained unaffected by any disease-causing mutations. SRP54 is therefore the second SRP component to be associated with a monogenic disease. Although several potentially pathogenic CNVs encompassing SRP54 have been reported in studies referring to unrelated phenotypes (Supplemental Table 3), to our knowledge, no pathogenic single nucleotide variant or indel has previously been reported in this gene. Several heterozygous variants predicted by bioinformatics tools to be damaging have been reported in public databases (Supplemental Table 4) (as is the case for many genes), but in contrast to the 3 de novo mutations reported here, none of them affects the conserved domains of the protein. Of note, with

**Figure 6. Effects of srp54 gene knockdown on pancreas development in zebrafish embryos.** (A) Confocal images of control-injected, MO-injected, and MO plus 100 pg hSRP54 mRNA-injected transgenic Tg(ptf1a:Gal4 UAS:Kaede) embryos at 72 hpf. Lateral views are shown, with anterior to the left, dorsal up. Arrows indicate downregulation ($) or rescued expression (↑) for each gene. The red boxed area corresponds to 300 µm (confocal images were taken with a ×10 objective). Original magnification, ×3, for the images below, which show enlarged views of the red boxed area. (B) WISH of insa at 72 hpf in control-injected, MO-injected and MO plus 100 pg hSRP54 mRNA-injected embryos. Dorsal views are shown, with anterior to the left. Shown are representative images from 3 biological replicate experiments with 4 or more embryos per group for each individual biological replicate experiment. Embryo size depicted: 1.75 mm (whole embryo size is 3.5 mm); original magnification of insets, ×2 (images were taken with a ×5 objective on a Leica DM 2000 LED microscope). The graphs below each panel in A and B display the percentages of embryos with normal versus decreased expression in all embryos analyzed across the biological replicates. Numbers indicate the amount of embryos with the respective phenotype/total number of embryos analyzed. ***P < 0.001, by Fisher’s exact test.
Interestingly, SRP54 function, as suggested by 3D modeling and enzymatic activity assessments and confirmed in zebrafish rescue experiments, impairs protein translocation in at least a quantitative manner. It is therefore highly probable that modification of the signal sequence of the nascent ribosome-bound polypeptide chain, to the SR on the ER membrane in a GTP-regulated manner defines the business end of the signal recognition particle, because over one-third of the human proteome (see below). Indeed, SRP54 mutations lead to repeated infections, as was also observed in all 3 patients reported here. In accordance with the results of these studies, we observed a decrease in the capacity of neutrophils to migrate toward the injury site in the zebrafish model (Figure 5).

Given our results, the underlying disease mechanism could be, at this point, either haploinsufficiency or a dominant negative effect. Haploinsufficiency is supported by: (a) decreased expression of SRP54 in the bone marrow of patients A11 and B12 as compared with that seen in healthy controls (Figure 3A); (b) the phenotype of the SRP54 knockdown zebrafish (Figures 4–6); and (c) the intolerance of the SRP54 gene to loss-of-function mutations, according to public databases (pLI score = 1.0 in the ExAC database). A dominant negative mechanism is supported by: (a) the presence of CNVs in the general population and in patients with unrelated diseases (Supplemental Table 3); (b) the presence of 1 loss-of-function variant in ExAC; and (c) the lower GTPase activity of the mutated proteins compared with that of the WT protein and the differences among mutated proteins observed in the zebrafish rescue experiments. How do SRP54 mutations lead to syndromic neutropenia with SDS-like features? SBDS is specifically required for the translation of C/EBP α and β mRNAs, both of which are key regulators of granulocytic differentiation (36). A similar mechanism may explain the selective effect of SRP54 mutations on neutrophils, because SRP54 expression levels influence TRAIL (37), which is itself involved in neutrophil apoptosis (38). However, these data do not explain the phenotype observed in the pancreas or, indeed, the potential involvement of many other organs (e.g., the skeleton and the brain). An alternative, more global explanation that is in line with the near-pleiotropic phenotype observed in SDS might be the following: nearly 40% of the almost 20,000 human protein-coding genes are predicted to be secreted or membrane bound (39). These proteins have a de facto need for SRP54 for their synthesis. Although homozygous muta-
respect to the age of first clinical manifestations) harbored an equally less severe mutation — on the basis of structural and functional analyses (including a lower impact on GTPase activity and an observed milder phenotype in zebrafish rescue experiments as compared with the other 2 mutations) — hints that SRP54 mutations could lead to diverse clinical phenotypes that may be based on the status of each patient’s specific mutation.

In conclusion, we report that heterozygous mutations in SRP54, a key component of the cotranslational protein machinery, lead to syndromic neutropenia with SDS-like features. This is directly relevant not only to patients with molecularly undiagnosed IBMFS, including SBDS-negative SDS patients, but also to the molecular nosology of IBMFS. These findings also open a window into the pathophysiology of the SRP.

**Methods**

**Subjects and exome sequencing**

The subjects reported in this study were members of 2 unrelated families of European descent (families A and B; Figure 1A) and 1 North American family of Hispanic (Mexican) origin (family C; Figure 1A). In all 3 families, the parents were nonconsanguineous and healthy, as were other siblings. Exome sequencing was performed for the parents and probands of all 3 families. Genomic DNA was extracted and purified from peripheral blood using standard protocols. For WES of family A, sequencing libraries were prepared using the Ion AmpliSeq Exome Kit (Thermo Fisher Scientific) according to the manufacturer’s recommendations and sequenced on an Ion Proton Sequencer (Thermo Fisher Scientific). Sequencing libraries for families B and C were prepared using the TruSeq Exome Kit (Illumina) and NimbleGen SeqCap EZ probes (VCRome; Roche Sequencing), respectively, and WES was performed on Illumina NextSeq 500 and HiSeq 2500 platforms, respectively. A minimum of 6.5 Gb of sequence data per individual were obtained and mapped to the hg19 reference genome using the Ion Torrent Server (Thermo Fisher Scientific) for family A and the Isaac Genome Alignment Software 2.1.0 (Illumina) for family B. The mean coverage was at least 60-fold, and more than 95 % of target sequences were covered a minimum of 10 times. CNVs were identified using Conifer software (41). Other variants were called using the Torrent Variant Caller 5.0 with low-stringency calling settings (family A) or the Isaac Variant Caller 2.1.0 (family B). Only variants covered by more than 5 variant reads were considered. Annotation was performed using the KGGSeq software package (42). Bioinformatics analysis of family C was performed as previously described (43). We focused only on protein-altering variants (i.e., missense, nonsense, and splice-site variants and coding indels) with fewer than 0.01 alternative allele
frequencies in dbSNP (build 135), 1000 Genomes Project, ExAC, an in-house database, and databases at Institut Imagine (Necker Hospital, Paris, France), Baylor College of Medicine, and Radboud University Medical Center (Nijmegen, Netherlands). To identify potential causal mutations, we focused on de novo mutations in the index cases of each family. Other modes of transmission — recessive and X-linked — were considered and excluded for all 3 families. The complete variant filtering strategy is presented in Supplemental Figure 4. Sequence variants reported here were deposited in the ClinVar (www.ncbi.nlm.nih.gov/clinvar/) public database under accession numbers SCV000583969, SCV000583970, and SCV000583971.

Targeted sequencing of SRP54

The candidate SRP54 variant identified by WES was validated using conventional capillary Sanger sequencing in the same families including the proband and his or her parents. Additional patients were screened using Sanger sequencing of all 15 exons of SRP54. Primers used for PCR amplification and sequencing are presented in Supplemental Table 5. Briefly, SRP54 exons were amplified using the Expand Long Template PCR System (Roche Diagnostics) according to the manufacturer’s recommendations. After purification with the Exostar Kit (GE Healthcare Life Sciences), PCR products were bidirectionally sequenced using the same amplification primers — except for exon 14 (Supplemental Table 5) — using the Big Dye Terminator Kit v3.1 (Thermo Fisher Scientific). Sequencing reactions were run on an ABI PRISM 3730xl sequencer (Thermo Fisher Scientific). Sanger sequencing for patient CII.1 was performed at Baylor Genetics clinical laboratories, and the primer sequences are listed in Supplemental Table 5.

3D modeling of SRP54 mutations

The structure of the SRP54 protein was modeled using PDB 2j37 chain W as a template (44). The GTP-binding site was modeled according to the superimposition of the SRP54 model and PDB 2j7p. The position of the SR (FtsY) was determined according to the structure of PDB 1r9 (45). The mutant side-chain structures were modeled using the mutagenesis wizard of the PyMOL program (46). Electrostatic surfaces were calculated using PDB2PQR (47) and APBS (48). All figures were generated using PyMOL (46).

Quantification of SRP54 transcripts

Total RNA was extracted from mononuclear bone marrow cells (cells from 5 healthy bone marrow donors were obtained from Caltag Medsystems Ltd.) using TRizol Reagent (Invitrogen, Thermo Fisher Scientific) and reverse transcribed using the iScript cDNA Synthesis Kit (Bio-Rad) according to the manufacturer’s instructions. Real-time quantitative PCR was performed in a total volume of 20 μl using the SsoAdvanced SYBR Green Supermix Kit (Bio-Rad) and the following primers: 5′-GGTTGAAGTCAACGGA-3′ and 5′-GATTGCAAGGGAGTGGTAAAGCAACAACAT-3′. The primers used to generate the T115A mutant were 5′-TGGATGCCTCCATT-GAGCAGGCTTGGAAAGC-3′ and 5′-GCTTCACAGACGCTGCT-CAATGGAGGCATCCA-3′. The primers used to generate the T115A mutant were 5′-GATTTCGAAAGGGATGTTAAGCAGAACAT-GTTCAAGCCT-3′ and 5′-AGCTTTGAAACATGGTTGTGCTTAC-CACCCCTTGGAAATC-3′. The primers used to generate the T117del mutant were 5′-GTTGGAATGGAGGAGTGTGAAAGCAAACAT-GTTCAAGCCT-3′ and 5′-CTTGGACATGTGTGTGTTTTACCCACCCCTTGGAAATC-3′. The GTPase activity assay

GTPase activity assay

pQChIP plasmids containing the WT or the 3 mutated forms (mutations G226E, T115A, and T117del) were amplified by PCR from pCS2- plasmids with the forward 5′-GGCGGACCGGTATG-GTTCTTGACCAGCCTTGGAAGAAATAC-3′ and reverse 5′-GGCGGTTTATTATATATATATGTTGTGTTAATAT ATGATGCTATTATGAAATCCCATCATGGCT-3′ primer pairs and then cloned using restriction enzymes AgeI and PacI into the pQChIP plasmid (Clontech) with the addition of a 6-histidine tag at the C-terminus.

Zebrafish experiments

Zebrafish husbandry and genetic strains. Zebrafish were bred and maintained at 28°C as described by Nüsslein-Volhard and Dahm (49). Staging was performed in hpf as summarized by Warga and Kimmel (50) and according to Federation of European Laboratory Animal Science Associations (FELASA) and Swiss federal law guidelines. The following lines were used in this study: WT Tübingen strains, Tg(mp14:GFP) (51), Tg(lyz:DsRed) (52), and Tg(ptf1a:Gal4;UAS:Kaede) (53).
MO design and validation. Human and zebrafish SRP54 share a high (96%) degree of sequence homology (Supplemental Figure 8). Two SRP54 splice MOs to prevent pre-mRNA splicing and a standard control MO were synthesized by Gene Tools (Gene Tools LLC): MO1, GTTTTACCTGGTACTTACCTGGAC; MO2, ACTACCCAAATATGGCTACCTTGA, and the control MO, CCTCTTCTCCTCGATTACATTATA. Embryos were injected at the single-cell stage. Phenol red (0.05%) (Sigma-Aldrich) was added as an injection tracer. Embryos were raised to appropriate stages and fixed in 4% paraformaldehyde (PFA) in 1× PBS for gene expression analysis. For validation, control-injected and MO-injected embryos were collected, and mRNA was isolated using the RNeasy Mini Kit (QIAGEN). cDNA was synthesized using the Transcriptor First Strand cDNA Synthesis Kit (Roche) according to the manufacturer’s protocol. Real-time PCR (RT-PCR) was performed using the following primers to verify splice modification on agarose gels: MO1, TAGCTGATCTGGGAGGAAGAAGTCTG and GTTCTTGGAAAAAGGCATGT; MO2, CACATGTCTTGTGGTCTCGC and ACCACCTGTGCCAGGATA. For rescue experiments, human WT and mutated SRP54 cDNAs cloned into the pc2-2-expression vector (RPZD) were used (refer to the previous paragraph on cloning and site-directed mutagenesis of SRP54 cDNA). Capped RNA from each of the 4 constructs (WT, G226E, T115A, and T117del) was synthesized using the mMessage mMachine SP6 Kit (Ambion, Life Technologies, Thermo Fisher Scientific). RNA (50–100 pg) was synthesized using the mMessage mMachine SP6 Kit (Ambion, Life Technologies, Thermo Fisher Scientific), and the plasmid was then linearized using the appropriate enzyme. RT-PCR was used to generate riboprobes for further antisense probe production. The insa probe was generated by PCR using the following primers: forward, 5′-ATGGCAGTAGCTGCTTACGAGGAC-3′ and reverse, 5′-GAATTCTCTAGTATCTCTATGATTCCTGA-3′. After PCR products were purified from agarose gels using the QIAquick Gel Extraction Kit (QIAGEN), the products were subcloned using the Dual Promoter TA Cloning Kit (Invitrogen, Thermo Fisher Scientific), and the plasmid was then linearized using the appropriate enzyme. RT-PCR was used to generate riboprobes for globin, mpx, srp54, and trypsin using the following gene-specific primers: srp54 (forward, GGGAGACATTGAGGGACTGA; reverse, GGCTCACCTTAG), mpx (forward, CCAGCAGATTGTGGTT-CAAGTG; reverse, GAAAATCCGAGATGGCGATA); trypsin (forward, CAGCGGACACGATCTATTAG; reverse, GCTCTGCAA-CAGCGGCTACC); and globin (forward, CCAGCAGATTGTGGT-GATG; reverse, GCCCTCTTGTGACAGTGTG). Each antisense primer was designed with the T7-promoter sequence tagged to its 5′ end. Riboprobes were labeled with digoxigenin- or fluorescein 12–labeled (insa-labeled) UTP (Roche). Stained embryos mounted in 89% glycerol were photographed using a Leica digital microscope and SYTOX Blue (Thermo Fisher Scientific) was used to identify dead cells. For the tail fin wounding experiments, larvae were anesthetized using tricaine. The tail fins were cut at the end of the spinal cord using a sterile scalpel blade, and the embryos were then allowed to recover at 29°C in embryo medium for 6 to 8 hours. Embryos were then either fixed overnight in 4% PFA with PBS or mounted in 0.8% low-melting agarose on glass-bottomed slides for live imaging. Immunostaining was performed to detect neutrophils at the wound site according to standard protocols, using a rabbit polyclonal antibody against mpx (GTX128379; GeneTex International Corp.). Stained embryos were then mounted in 0.8% low-melting agarose. Images and videos were obtained using a Zeiss LSM 720 (Carl Zeiss) or a Leica SP5-2-II Matrix (Leica Microsystems) confocal microscope. Mpx-positive cells from both WISH and immunostaining were semiautomatically counted using Fiji software (56). Finally, confocal time-lapse live imaging was performed in Tg(mxpx:GFP lyz:DsRed) embryos for 9 hours starting 30 minutes after the tail fin was amputated at 48 hpf.

Additional details regarding Methods can be found in the supplemental material.

Statistics
Data shown represent the mean ± SEM or the percentage of expression. P values were derived using a 1-way ANOVA for multiple comparisons, followed by a Newman-Keuls test for pairwise comparisons, a Mann-Whitney U test, a 2-tailed t test, or Fisher’s exact test for comparison of 2 groups. A P value of less than 0.05 was considered statistically significant. Statistical analyses were performed using GraphPad Prism 6.

Study approval
All participants (and their parents) gave written informed consent for genetic analyses in this study, which was approved by the IRBs of Strasbourg University Hospitals (protocol DC-2013-1911) and Baylor College of Medicine (protocol H-22769).

Author contributions
RC and SB designed the study, analyzed the data, and wrote the manuscript. MK and CL designed zebrafish experiments, performed the experiments, and analyzed the data. JSM, EA, and SU performed the experiments, and analyzed the data. JSM, EA, and SU performed sequencing experiments. AK, NP, and YY designed methods for genetic analyses in this study, which was approved by the IRBs of Baylor College of Medicine (protocol H-22769).
Acknowledgments

We thank Taco (TW) Kuijpers (Academic Medical Center, Amsterdam, Netherlands), Charlotte Niemeyer and Marcin Wlodarski (University of Freiburg, Germany), and Jameel Chelly (University of Strasbourg) for discussions and critical reading of this manuscript and/or providing us with samples. We thank Dean R. Campagna (Boston Children’s Hospital, Boston, Massachusetts, USA) and Deniz Ceylan (Hacettepe University, Sihhiye, Ankara, Turkey) for their technical assistance. We thank the following groups for sending us patients’ samples and/or for ongoing collaboration on the genetics of severe congenital neutropenia: Myungshin Kim and Sung Sup Park (Seoul National University Hospital, Seoul, South Korea); Sabine Mellor-Heinkele, Cornelia Zeidler, Karl Heinrich Welte, Saskia Biskup, and Heinz Gabriel (Center for Genomics and Transcriptomics, Tübingen, Germany); Dirk Lebrecht (University Medical Center, Freiburg, Germany); Albert Catala Temprano and Juan I. Aróstegui (Hospital Sant Joan de Deu, Barcelona, Spain); Juliá Sevilla, Eva Gálvez de la Villa, and Luis I. Gonzalez-Granado (Hospital Nino Jesus, Madrid, Spain); Marielle Alders (Academisch Medisch Centrum Universiteit, Amsterdam, Netherlands); Sofia Douzgou and Nicolau Marchant (Central Manchester University Hospitals, Manchester, United Kingdom); Edward G. Brooks (South Texas Pediatric Blood and Cancer Center, San Antonio, Texas, USA); Dean John (University of Aberdeen, School of Biological Sciences, Aberdeen, United Kingdom); and Mirella Filocamo and the “Cell Line and DNA Biobank from Patients Affected by Genetic Diseases,” member of the Telethon Network of Genetic Biobanks (project GTB12001), which is funded by Telethon Italy. We are grateful to Christine Bole-Feyssot and Alexander Hoischen for screening the databases of Institut Imagine (Necker Hospital, Paris, France) and Radboud University Medical Center (Nijmegen, Netherlands), respectively, for the presence of SRPS54 variants. We thank Chunjing Qu for providing quality control data for the exome data produced at Baylor College of Medicine. Additionally, we thank Judith Konantz (Center for Regenerative Therapies [CRT], Dresden, Germany) for her help with the zebrafish pancreas data. We would also like to thank the patients and their families for their continued engagement in this research. This work was supported by grants from the Agence Nationale de la Recherche (ANR) (ANR-11-LABX-0070 TRANSPANTLEX), INSERM UMR – S1109; and the Institut Universitaire de France (IUF) (all to SB); the University of Strasbourg (IDEX UNISTRA, to CP and SB); the INTERREG V European regional development fund (European Union) program (project 3.2 TRIDIG, to RC, SB, and CL); and the Swiss National Science Foundation (SNF) (149735, to CL).

Address correspondence to: Seiamak Bahram or Raphael Carapito, Centre de Recherche d’Immunologie et d’Hématologie, 4 rue Kirschlager, 67085 Strasbourg Cedex, France. Email: siamak@unistra.fr (S. Bahram); carapito@unistra.fr (R. Carapito). Or to: Claudia Lengerke at Department of Biomedicine, University Hospital Basel, Helbelstrasse 20, 4031 Basel, Switzerland. Email: claudia.lengerke@unibas.ch.


4. Shwachman H, Diamond LK, Oski FA, Madrid, Spain); Marielle Alders (Academisch Medisch Centrum Universiteit, Amsterdam, Netherlands); Sofia Douzgou and Nicola Marchant (Central Manchester University Hospitals, Manchester, United Kingdom); Edward G. Brooks (South Texas Pediatric Blood and Cancer Center, San Antonio, Texas, USA); Dean John (University of Aberdeen, School of Biological Sciences, Aberdeen, United Kingdom); and Mirella Filocamo and the “Cell Line and DNA Biobank from Patients Affected by Genetic Diseases,” member of the Telethon Network of Genetic Biobanks (project GTB12001), which is funded by Telethon Italy. We are grateful to Christine Bole-Feyssot and Alexander Hoischen for screening the databases of Institut Imagine (Necker Hospital, Paris, France) and Radboud University Medical Center (Nijmegen, Netherlands), respectively, for the presence of SRPS54 variants. We thank Chunjing Qu for providing quality control data for the exome data produced at Baylor College of Medicine. Additionally, we thank Judith Konantz (Center for Regenerative Therapies [CRT], Dresden, Germany) for her help with the zebrafish pancreas data. We would also like to thank the patients and their families for their continued engagement in this research. This work was supported by grants from the Agence Nationale de la Recherche (ANR) (ANR-11-LABX-0070 TRANSPANTLEX), INSERM UMR – S1109; and the Institut Universitaire de France (IUF) (all to SB); the University of Strasbourg (IDEX UNISTRA, to CP and SB); the INTERREG V European regional development fund (European Union) program (project 3.2 TRIDIG, to RC, SB, and CL); and the Swiss National Science Foundation (SNF) (149735, to CL).

Address correspondence to: Seiamak Bahram or Raphael Carapito, Centre de Recherche d’Immunologie et d’Hématologie, 4 rue Kirschlager, 67085 Strasbourg Cedex, France. Email: siamak@unistra.fr (S. Bahram); carapito@unistra.fr (R. Carapito). Or to: Claudia Lengerke at Department of Biomedicine, University Hospital Basel, Helbelstrasse 20, 4031 Basel, Switzerland. Email: claudia.lengerke@unibas.ch.