ARTICLE
Loss-of-function and missense variants in NSD2 cause decreased methylation activity and are associated with a distinct developmental phenotype
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PURPOSE: Despite a few recent reports of patients harboring truncating variants in NSD2, a gene considered critical for the Wolf–Hirschhorn syndrome (WHS) phenotype, the clinical spectrum associated with NSD2 pathogenic variants remains poorly understood.

METHODS: We collected a comprehensive series of 18 unpublished patients carrying heterozygous missense, elongating, or truncating NSD2 variants; compared their clinical data to the typical WHS phenotype after pooling them with ten previously described patients; and assessed the underlying molecular mechanism by structural modeling and measuring methylation activity in vitro.

RESULTS: The core NSD2-associated phenotype includes mostly mild developmental delay, prenatal-onset growth retardation, low body mass index, and characteristic facial features distinct from WHS. Patients carrying missense variants were significantly taller and had more frequent behavioral/psychological issues compared with those harboring truncating variants. Structural in silico modeling suggested interference with NSD2's folding and function for all missense variants in known structures. In vitro testing showed reduced methylation activity and failure to reconstitute H3K36me2 in NSD2 knockout cells for most missense variants.

CONCLUSION: NSD2 loss-of-function variants lead to a distinct, rather mild phenotype partially overlapping with WHS. To avoid confusion for patients, NSD2 deficiency may be named Rauch–Steindl syndrome after the delineators of this phenotype.

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INTRODUCTION
Wolf–Hirschhorn syndrome (WHS, also known as 4p-syndrome, OMIM 194190) is caused by partial deletions of the short arm of chromosome 4 is one of the first microscopically recognized structural chromosomal disorders, and was named after Ulrich Wolf (Freiburg, Germany) and Kurt Hirschhorn (New York, NY, USA), who first described it in 1965.1,2 Hallmarks of the syndrome are prenatal-onset growth deficiency, microcephaly, intellectual disability (ID), epilepsy, muscular hypotonia and hypotrophy, facial clefts, congenital heart defects and other malformations, as well as a very characteristic craniofacial gestalt, often described as resembling a Greek helmet.3 With the advent of molecular cytogenetics a
A total of eight truncating, two splicing, and six missense variants were listed among many others in sequencing studies of patient cohorts with neurodevelopmental disorders, missense variants were among the reported in this study were identified by research or diagnostic exome or Mendelrome sequencing in various laboratories and collected via GeneMatcher (see Web Resources). When no developmental testing was performed, the degree of ID was estimated using the Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition (DSM-5) severity levels for ID (see Web Resources). Standard deviation scores for growth parameters were calculated based on the data sets provided by the Swiss Society of Pediatrics, which combine World Health Organization, Swiss, and German population data (see Web Resources). The facial overlay Fig. 4b was obtained using the Face2Gene RESEARCH application (FDNA Inc., Boston, MA, USA) taking one frontal photo for each patient at the youngest available age.

**Materials and Methods**

The 18 previously undescribed patients with pathogenic NSD2 variants reported in this study were identified by research or diagnostic exome or Mendelrome sequencing in various laboratories and collected via GeneMatcher (see Web Resources). When no developmental testing was performed, the degree of ID was estimated using the Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition (DSM-5) severity levels for ID (see Web Resources). Standard deviation scores for growth parameters were calculated based on the data sets provided by the Swiss Society of Pediatrics, which combine World Health Organization, Swiss, and German population data (see Web Resources). The facial overlay Fig. 4b was obtained using the Face2Gene RESEARCH application (FDNA Inc., Boston, MA, USA) taking one frontal photo for each patient at the youngest available age.

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**NSD2 variant nomenclature** refers to the NM_133330.2 transcript and pathogenicity classification is based on the American College of Medical Genetics and Genomics/Association for Molecular Pathology (ACMG/AMP) guidelines. Structural analysis of NSD2 variants was performed using SwissModel, RasMol, and Smart (see Web Resources). While the experimental crystal structure of the NSD2 N-methyltransferase domain was available (Protein Data Bank, PDB: 5LSU), the PHD and PWWP domains were modeled using the homologous domains from TRIM24 (PDB: 4ZQL) and NSD3 (PDB code: 2DAQ), respectively.

GST fusion proteins were obtained as described in the Supplementary methods. In vitro methylation assays were performed as described in Mazar et al. and the Supplemental methods using reagents listed in Table S2.

The data in Fig. 2n, p, r, s, t are represented as mean ± SD of two independent biological replicates; statistical significance was tested by one-way analysis of variance (ANOVA) followed by two-tailed Dunnett’s test without adjusting for multiple testing. The data in Fig. 3c–e are represented as mean ± SD. Groups in Fig. 3e were compared by homoscedastic two-tailed Student’s t-test after testing for equal variance by F-test.

The graphs in Figs. 3n, p, r, t and 3a–f were generated using GraphPad Prism version 5.00 for Windows, (GraphPad Software, La Jolla, CA, USA).
All statistical analyses were performed with GraphPad Prism, except for F- and t-tests, which were performed using Microsoft© Excel.

RESULTS

We describe 18 patients, 16 of whom unrelated, carrying ultrarare (absent in gnomAD) pathogenic or likely pathogenic NSD2 variants (Table S3). Of these, 6 carried 5 different missense variants while 12 carried 10 different truncating variants. Nine of the truncating and four of the missense variants were not reported previously (Fig. 1).

Variant inheritance could not be determined in 4/18 cases, and was confirmed parental in 3/18 cases and de novo in 11/18 cases.

NSD2 is the principal enzyme that dimethylates histone H3 at lysine 36 (H3K36me2) in most cell types and tissues. H3K36me2 is an evolutionarily conserved histone modification linked to transcriptional activation. The (likely) pathogenic missense variants we found map to three distinct domains of NSD2. The Cys869Tyr (patient 1-I) substitution disrupts zinc binding within a PHD finger domain (residues 831-875) and hence induces improper folding and loss of function for this domain. Although the function of the NSD2 PHD domain is unknown, these domains are virtually always found on chromatin-associated proteins and may function as epigenetic reader domains (Fig. 2a, b). The Pro895Leu variant (patients 7-I and 7-II) is located in the core of one of NSD2’s PWWP domains (Fig. 2c), another motif that generally functions as an epigenetic reader. The leucine substitution at Pro895 is predicted to destabilize the domain through steric clashes with the adjacent Trp885 (Fig. 2d).

All remaining missense variants are located within the methyltransferase domain of NSD2. Lys1019Arg (patient 12-I) is
located in a loop of the methyltransferase domain that exhibits high local mobility or is entirely missing in the isolated NSD2 crystal structure. This hampers reliable modeling but suggests that this region is flexible and might become stabilized upon protein–protein interactions, such as binding to the nucleosome substrate. Ser1137 is located in the domain's core (Fig. 2e) and substitution to phenylalanine (p.Ser1137Phe, patient 10-I) is predicted to result in steric clashes with the adjacent Leu1163 residue (Fig. 2f), leading to domain destabilization. Glu1091 forms a salt bridge to Arg1160, which is expected to result in a drastic loss of enzymatic activity. (m) Western analysis with the indicated antibodies of whole-cell extracts (WCEs) from 293 T cells overexpressing vector control, full-length WT NSD2, or NSD2 mutants as indicated. Histone H3 is shown as a loading control. (n) Quantification of western blot data in (m), (o) in vitro methylation assay with recombinant WT NSD2 or mutants NSD2 derivatives as indicated on recombinant nucleosomes (rNuC) as substrates. Top panel, [3H]-SAM is the methyl donor and methylation is visualized by autoradiography and indicated as [3H]-H3. Bottom panel, Coomassie stain of proteins in the reaction. (p) Quantification of all detectable bands in the autoradiography in (o). (q) Western analysis with the indicated antibodies of in vitro methylation assay with nonradiolabeled SAM. (r) Quantification of all detectable bands in the western blot data in (q). (s) Western analysis with the indicated antibodies of WCEs from WT or NSD2 deficient HT1080 cells complemented with CRISPR-resistant NSD2 (WT or mutants), or control as indicated. Histone H3 and tubulin are shown as loading controls. (t) Quantification of western blots in (s). The data in (n, p, r, t) are represented as mean ± SD of two independent experiments. *p < 0.05 based on a one-way analysis of variance (ANOVA) followed by two-tailed Dunnett's test.
Patients with (likely) pathogenic NSD2 variants shared a similar facial gestalt characterized by a triangular face, broad forehead, high anterior hairline, deeply set eyes, large palpebral fissures, broad arched and laterally sparse eyebrows, periorbital hyperpigmentation, full cheeks, a thin and elevated nasal bridge, smooth short philtrum, prominent cupid bow, thick everted lower lip vermilion, and/or protruding ears (Fig. 4a, b). Noticeably, the facial appearance evolved over time, with older patients developing deeper infraorbital creases. Family 6 comprised a total of 7 clinically similarly affected individuals, with molecular confirmation available for four of them, and represents to date the largest known family affected by this disorder (Fig. 4c). The core
Fig. 3 Phenotypic features and growth parameters of the individuals carrying NSD2 pathogenic variants and comparison with Wolf–Hirschhorn syndrome (WHS). The diagram in (a) summarizes the phenotypic features of the individuals described in this study (18 additional patients together with 10 previously reported individuals) based on the type of NSD2 variant carried. In (b) all individuals are compared with WHS patients, subdivided according to the size of the 4p deletion carried, as reported in Zollino et al. Data in (a) and (b) are expressed as percentages. Growth parameters at birth (c) included the parameters at termination of pregnancy for individual 16-I and at last visit (d) are reported. The average measures for all combined individuals standard deviation score (SDS (SD)) were length (L): -2.3 (1.5); weight (W): -2.0(1.0); occipitofrontal circumference (OFC): -1.1(1.7); gestational weeks (GW): 38.5(3.8) at birth and height (H): -1.7(1.3); W: -1.7(1.5); OFC: -2.4(1.8); body mass index (BMI): -1.1(5) at last visit. (e) Comparison of the growth parameters at last visit for patients carrying missense variants (black) compared with patients carrying other variants as well as deletions encompassing NSD2 (red). *p value < 0.05 as tested by two-tailed Student’s t-test. The data in (c–e) are expressed as SDS based on the respective growth charts. Lines and whiskers represent mean ± SD. (f) Linear correlation analysis between age and BMI and last visit. ASD DD/DD developmental delay/intellectual disability, IUGR intrauterine growth restriction, SC spinal cord, SGA small for gestational age.

The phenotype of the NSD2 cohort (>50% of patients) is characterized by DD, intraterine growth retardation and low birth weight, feeding difficulties, failure to thrive, height and head circumference below the 5th centile (<-1.65 SDS), speech delay, and muscular hypotonia. Although these manifestations are present in WHS as well, the majority of the individuals in the NSD2 cohort lack many of the most common manifestations of WHS such as seizures, orofacial clefts, and coloboma, as well as genital, cardiac, and renal malformations and display a distinct facial phenotype that lacks the classical “Greek helmet” aspect. Furthermore, the severity of the ID in the NSD2 cohort was milder compared with patients carrying the most common 4p deletions (between 5 and 18 Mb), who are severely affected in 76% of the cases.1 While individuals 1-I, 13-I, and 14-I harboring the NSD2 Cys869Tyr, p.Cys1183Valfs*146, and p.Arg600* variants respectively, either had an IQ in the lower-normal range (78–81 and 89, respectively) or presented with learning difficulties, individuals old enough for evaluation commonly showed mild ID, with only three individuals presenting with severe ID. The latter carried truncating variants (3-I c.3223_3226dup p.Gly1076Valfs*16; 4-I c.1588_1589dupAA p.Ile532Glyfs*67; Bernardini et al., patient 3, exon 1–20 deletion), which may not be held responsible for the severe ID. Both siblings described as patients 2 and 3 in Bernardini et al. carry in fact the same exon 1–20 deletion, with one sibling showing mild ID, while the other had autism and severe ID.10

Behavioral and psychological issues as well as autistic features were observed in 44% and 33%, respectively, with the most frequently reported manifestations being anxiety (15%), hyperactivity (22%), and aggressiveness (11%). Individual 1-I had suicidal ideations related to his poor academic performance at the age of 11 years. Of note, all the individuals carrying missense variants presented with behavioral and psychological issues (Fig. 3a), compared to 29% of patients with truncating variants or deletions (p value = 0.0031 by two-tailed Fisher’s exact test).

Growth parameters at birth were largely below the norm (Fig. 3c). Feeding difficulties were described in 52% of the affected individuals and may at least in part contribute to the failure to thrive. Short stature and growth retardation persisted later in life (Fig. 3d). Delayed bone age was detected in 6 individuals (22%). Length and occipitofrontal circumference (OFC) at birth as well as all growth parameters at last visit were normally distributed according to a D’Agostino–Pearson omnibus normality test, while birth weight was skewed toward lower values (p = 0.0002). Notably, heterozygotes for missense variants were significantly taller than patients carrying truncating variants as well as small deletions encompassing NSD2 (p = 0.03 by homoscedastic t-test after checking for comparable variance by F-test; Fig. 3e) and none of them fell below the 5th centile for height at last visit. Weight and OFC at last visit were also higher in patients carrying missense variants, although this difference was not statistically significant (p = 0.27 and 0.17, respectively). Finally, a linear regression analysis showed that older patients had significantly higher body mass index (BMI) values (r² = 0.1786, p = 0.0396; Fig. 3f).

Gastrointestinal abnormalities were also quite common (43%), with constipation representing the most frequent manifestation (26%). Ophthalmological abnormalities were observed in 29% of patients and mostly included mild refraction defects and strabismus, while no individual presented with coloboma, which is considered a recurrent feature in WHS (see Fig. 3b). One exception is represented by individual 3-I, who presented with bilateral keratoconus, retinitis pigmentosa, and optic atrophy and received a corneal transplant at the age of 32. Reanalysis of her exome data revealed three rare variants of unknown significance in RHO, KRT3, and UNC45B (Table S3), which were, however, maternally inherited and also present in her healthy sister. Skeletal and limb abnormalities were reported in 39% of the cases. Individual 12-I presented with a craniosynostosis that was surgically corrected at the age of 6 months, which may be explained by the patient’s additional de novo heterozygous AGO2 variant (Table S3). Also, of note, individual 7-II presented with 11 ossified ribs and 6 non-rib-bearing lumbar vertebrae. Dental abnormalities were also quite frequent (32%). Brain and spinal cord malformations were present in 5 individuals (18%) and were mostly of minor importance except for individual 16-I, who presented with vermis hypoplasia. Less frequent manifestations among patients carrying NSD2 pathogenic variants included a history of aspiration, cardiac and renal anomalies, neonatal jaundice, sleep disturbances, hearing loss, genital abnormalities, and orofacial clefts (Table S3). Immunological abnormalities as well as recurrent infections, which represent a common morbidity and mortality cause in WHS, were quite frequent in the NSD2 cohort, where patient 5-I presented with latex allergy, patient 11-I with low IgA and IgG levels, and patients 2-I, 11-I and Dear-1 with recurrent respiratory infections. Seizures, which are common in WHS (Fig. 3b), were reported only in individual 10-I, while individual 15-I presented subclinical electroencephalogram (EEG) abnormalities at the age of 4 4/12 years. Endocrinological abnormalities seem not to be part of the phenotypic spectrum, with only individual 5-I presenting limited signs of precocious puberty at 15 months of age, which were nonprogressive and were associated with a normal endocrine evaluation. Likewise, metabolic abnormalities were only observed in individual 2-I.

DISCUSSION

In this work we describe a large series of patients carrying pathogenic variants in NSD2, thus allowing delineation of the associated manifestations, which include prenatal-onset failure to thrive with all body measurements below the mean and low BMI, mild DD and muscular hypotonia, and a distinct facial gestalt. Furthermore, we provide in silico and in vitro mechanistic data showing loss of histone methylation activity as a common feature of NSD2 deficiency.

The phenotype observed in the NSD2 cohort is consistent with many of the known functions of NSD2. First, NSD2 has long been known to regulate embryonic development and body growth,
with heterozygous Nsd2 constitutive knockout mice growing at a much slower rate compared with wild-type littermates, homozygous knockout mice dying in the first days of life, and common variants showing strong ($p = 10^{-24}$) association with height in genome-wide association study (GWAS). Recently $NSD2$ was shown to regulate adipose tissue development in mice by controlling the activity of the master adipogenic transcription factor peroxisome proliferator-activated receptor-γ (PPARγ). Interestingly, in this work mice overexpressing the mutant histone protein H3.3K36M, an NSD2 inhibitor, resisted white adipose tissue expansion in response to a high-fat diet. These findings support the idea that the low BMI observed in the NSD2 cohort may be due to the inability of body fat to expand in response to feeding rather than a consequence of the neonatal feeding difficulties that, although observed in multiple affected individuals, disappear later in life. Furthermore, $NSD2$ has been shown to play a key role in promoting adipogenesis and myogenesis in precursor cells, as well as thermogenesis in brown adipose tissue and insulin sensitivity in white adipose tissue. In pancreatic β-cell lines in vitro NSD2 has also been shown to promote proliferation and to

Fig. 4  Clinical data. (a) Facial features of the affected individuals reported in this study. The age in years (y) and months (m) is reported beside each patient ID. (b) Combined facial gestalt obtained by combining frontal photos using the Face2Gene online research tool (see Materials and Methods and Web Resources). Photos from 12 different patients, including those depicted in (a), were used for this purpose. (c) Family tree of family number 6 in this study. M+/−/? = presence (+), absence (−), or unknown status (?) for the p.Asp1158Glyfs*11 variant in each $NSD2$ allele. Clinically affected individuals are shown as full symbols.

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regulate insulin secretion. However, since diabetes has not been reported as a recurrent feature neither in our cohort nor in patients with WHS we assume that in humans, glycemic control may be maintained despite impaired NSD2 function.

Likewise, some other known or supposed functions of NSD2 did not result in a recurrent phenotype in our cohort. NSD2 has been suggested to contribute to the immune defects typical of WHS by regulating the hematopoietic process at multiple stages as well as B- and T-cell differentiation. Nevertheless, only a minority of the patients in this series presented with recurrent infections. Also, while heterozygous Nsd2 deficient mice present with heart defects and de novo variants in NSD2 were shown to associate with congenital heart malformations, cardiac anomalies were present only in a minority of the individuals in this series, and, with the exception of individual 16-I, were of minor clinical importance. The low prevalence of epilepsy in this cohort is compatible with the assumption that other genes such as LETM1 are responsible for seizures in WHS.

While heterozygotes for missense variants were on average significantly taller, the overall clinical severity correlated only loosely with the measured alteration in NSD2 enzymatic function. Furthermore, for the Cys869Tyr (patient 1-I) variant, which can be categorized as likely pathogenic based on the current ACMG/AMP recommendations, we did not detect significant loss of methylation activity in our in vitro assays. These data suggest that in addition to H3K36 dimethylation, other functions of NSD2 such as its genomic localization, and likely other potential genetic differences among the patients, contribute to the pathogenesis of the complex phenotypes described here. Moreover, as the missense variants that we tested did not display any obvious stability issue upon overexpression, dominant negative effects cannot be excluded. Finally, second hits or blending phenotypes with additional variants in other (known or unknown) genes associated with the clinical phenotypes described in this study could contribute to the observed clinical variability.

Patients 11-I and 15-I carried the same protein-elongating p.Pro1343Glnfs*49 variant. Although this variant occurs too distally in the messenger RNA (mRNA) sequence to induce nonsense-mediated decay, its pathogenicity is supported by the fact that in the mRNA sequence to induce nonsense-Pro1343Glnfs*49 variant. Although this variant occurs too distally in the observed clinical variability.

The clinical phenotypes described in this study could contribute to the observed clinical variability.

In conclusion, our data support the concept that NSD2 loss of function is associated with a distinct phenotype that only partially overlaps with WHS and constitutes a differential diagnosis to Silver–Russell and similar syndromes. This phenotype is in line with the distinct features described in the first patient with a small deletion encompassing NSD2 by Rauch et al. This patient now at age 26 years is 172 cm tall (-0.55 SDS), weighs 45–50 kg (ca. -2.5 SDS), and has a “small head.” Despite his normal eating behavior, all attempts to gain weight have been unsuccessful. He has an IQ in the lower-normal range, a calm and content personality, and lives with his parents. As a reflection of the distinct facial gestalt and the greatly different disease severity, especially concerning ID, of NSD2 deficiency and contiguous gene deletions leading to WHS, which may also be important for families’ and physicians’ perception of the patients’ prognosis, the NSD2-related disorder may be named Rauch–Steindl syndrome after the delineators of this phenotype.

WEB RESOURCES

DECIPHER: https://decipher.sanger.ac.uk

DSM-5 severity levels for intellectual disability: https://dsm.psychiatryonline.org/doi/full/10.1176/appi.books.9780890425596.dsm01

Face2Gene: https://www.face2gene.com/

GeneMatcher: https://genematcher.org

gnomAD: https://gnomad.broadinstitute.org/

Growth curves of the Swiss society of pediatrics: https://www.kispi.uzh.ch/de/zuweiser/broschueren/Seiten/document.axd?id=56c0bb56-1793-48f3-968e-238915f47bbd9

HGMD Professional: http://www.hgmd.cf.ac.uk/ac/index.php

HPO: https://hpo.jax.org/app/

OMIM: http://www.omim.org/

PDB: https://www.wwpdb.org

RasMol: http://www.rasmol.org/

Smart: http://smart.embl-heidelberg.de/

SwissModel: https://swissmodel.expasy.org/

Uniprot databank entry for NSD2: https://www.uniprot.org/

Entry O96028

DATA AVAILABILITY

All materials, data sets, and protocols presented in this work are available upon request to the corresponding authors. NSD2 variants have been deposited in the DECIPHER database (see Web Resources) under the following IDs: 422873, 422875, 422876, 422877, 422878, 422879, 422880, 422881, 422882, 422883, 422885, 422886, 422887, 422888, 422889, 422890, 422891, 422892.

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AUTHOR CONTRIBUTIONS

Conceptualization: K.S., O.G., A.R. Formal analysis: P.Z., D.S., H.S. Funding acquisition: A.R., H.S., O.G., B.B.A.d.V. Investigation: P.Z., K.S., D.S., H.S., P.J., A.B., M.L.M., C.M.A.R.-A., M.S., M.A., A.T.-B., I.M., N.B., V.B., G.D., B.B.A.d.V., G.S., D.L., A.L., J.M., K.O., G.P., R.P., K.R., L.S.B., V.T., A.F., L.F., P.G.W., M.R.W., M.W., M.Z. Project administration: P.Z., A.R., O.G. Supervision: A.R., O.G. Visualization: P.Z., D.S., H.S. Writing—original draft: P.Z. Writing—review & editing: K.S., D.S., A.R., H.S., O.G.

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COMPETING INTERESTS

O.G. is a co-founder and member of the Board of Directors of Epicypher, Inc. The other authors declare no competing interests.
ETHICS DECLARATION
This study was performed as part of a research study approved by the ethics commission of the Canton of Zurich (PB_2016-02520). Written informed consent for genetic testing and publication of genetic and clinical data, and photos was obtained from each individual, their parents, or their legal guardian. Genetic testing in collaborating centers was performed either in the setting of routine diagnostic without the requirement for institutional review board (IRB) approval or within research settings, under the following approvals: p.3-I: Comité de Protection des Personnes (Dijon), #DC2011-1332; p.4-I: Colorado Multiple Institutional Review Board, #19-0751; p.5-I: Western Institutional Review Board, #20120789; p.15-I: #287/M-15, The Ethics Committee of University of Tartu.

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