Dear Editor,

The diagnosis success rates for developmental disorders have greatly improved in the last years mainly due to the widespread use of DNA next-generation sequencing. Nevertheless, several studies have stressed the importance of a critical reconsideration of genetic results and a further implementation of protocols for variant-level reevaluation and case-level reanalysis (Deignan et al., 2019). This is especially relevant in the context of syndromes, such as the chromatinopathies Cornelia de Lange syndrome (CdLS, OMIM#122470) and KBG syndrome (KBGS, OMIM #148050), with overlapping phenotypes that may evolve over time (Parenti et al., 2021). Here, we present a challenging familiar case reanalyzed in which phenotypic features of both KBGS and CdLS are observed, and where genetic variants in ANKRD11 and NIPBL were identified.

Our case is a female, first child of a non-consanguineous couple, born at 37 weeks of gestation after an uneventful pregnancy. Birth length (47.2 cm, −0.55 SD), body weight (2.680 kg, −0.52 SD), and head circumference (34 cm, 0.26 SD) were all normal. She was referred to our hospital at the age of 3 years because of facial dysmorphism, gastroesophageal reflux, and motor developmental delay. After a comprehensive physical evaluation by our clinical geneticist, she was clinically diagnosed as CdLS with a clinical score of 10, mainly due to the synophrys (HP:0000664), thick eyebrows (HP:0000574), concave nasal ridge (HP:0011120), downturned corners of mouth (HP:0002714), global developmental delay (HP:0001263), small hands (HP:0200055) and feet (HP:0001773), short fifth finger (HP:0009237), and hirsutism (HP:0001007)(Kline et al., 2018). At that time, molecular diagnosis was performed by sequencing the NIPBL gene and a potential disease-causing variant was identified [NIPBL:NM_133433.3:c.7553A>G, p.(Asp2518Gly)]. The variant, that induces changes in the surface charge of the protein (Figure 1c), was classified as likely pathogenic (PM2, PP2, and PP3) according to the ACMG/AMP 2015 guidelines (Richards et al., 2015). Segregation studies revealed that the patient's mother (II.4), one aunt (II.2), and one uncle (II.1) carried the variant. The mother (II.4) was clinically evaluated and dysmorphic facial features fully consistent with her daughter's phenotype were observed. Facial photographs of individuals II.2, II.3, and I.2 were available and checked with the Face2Gene application (Latorre-Pellicer et al., 2020). A medium-low probability of CdLS was assigned for the aunt (II.2) that was the only one with the c.7553A>G NIPBL variant (Figure 1a). Altogether, clinical and molecular findings supported the CdLS diagnosis in the patient.

However, clinical follow-up of the proband revealed an evolution from CdLS to KBGS features. At the age of six, the patient showed an evident KBGS gestalt with macrodontia (HP:0001572), triangular face (HP:0000325), or bulbous nasal tip (HP:0000414). An additional clinical analysis was carried out with Face2Gene. At 3 years old, KBGS and CdLS were the first and second syndromes suggested, respectively, whereas at 6 years old, CdLS diagnosis did not appear between the top-5 diagnosis provided by Face2Gene (Figure 1b). A molecular diagnosis reevaluation was performed by using a targeted gene panel including ANKRD11, in which a pathogenic nonsense variant was identified [ANKRD11:NM_001256183.1:c.2512C>T, p.(Arg838*)] (Figure 1d). This variant was maternally inherited, and neither the aunts (II.2 and II.3) nor the uncle (II.1) had it (Figure 1a). The variant was classified as pathogenic (PVS1, PM2, PP3, and PP5).

Considerable efforts have been made to standardize the interpretation of genetic variants in the laboratory (Latorre-Pellicer et al., 2020). However, once again, a clear example of the existing limitations is shown here, reinforcing the relevance of the implementation of protocols for periodic reevaluation of phenotypic and genetic information in clinical laboratories. Furthermore, this case highlights the clinical challenges in interpreting multiple pathogenic variants in single patients. An incorrect genetic diagnosis
can have severe consequences for prognostic and therapeutic management of the patient, and, as in this case, for the reproductive advice. Moreover, our findings seem to support recent evidences of age-dependent phenotypic evolution in individuals harboring ANKRD11 variants (Parenti et al., 2021), and demonstrate the importance of including KBGS in the differential diagnosis of young children with CdLS features. Therefore, it is crucial to include ANKRD11 in gene panels used for molecular testing of individuals presenting with clinical characteristics of CdLS.

**FUNDING INFORMATION**
European Social Fund, Grant/Award Number: B32_17R / B32_20R; Ministerio de Ciencia e Innovación; Instituto de Salud Carlos III, Grant/Award Number: PI19/01860

**ACKNOWLEDGEMENTS**
Spanish Ministry of Health (MH)-ISCIII (FIS) [Ref. PI19/01860, to F.J.R. and J.P.]; DGA- FEDER: European Social Fund [B32_17R / B32_20R, to J.P.]. MICIU-“Juan de la Cierva-Incorporación” (to A.L.P.)
CONFLICT OF INTEREST
The authors declare no competing interests.

AUTHOR CONTRIBUTIONS
A.L.-P., C.L.-C., M.G.-S., M.A., R.A., J.P., and B.P.: molecular analysis; A.A., A.A.-C., and F.J.R.: patients’ recruitment, clinical evaluation, and clinical score calculation; I.M.-A. and P.G.-P.: bioinformatics studies and variants interpretation; A.L.-P., J.P., and B.P.: manuscript writing, collection, and assembly of data; F.J.R., J.P., and B.P.: manuscript editing and approval of the manuscript. All authors have read and agreed to the submitted version of the manuscript.

ETHICS APPROVAL
The employed procedure was reviewed and approved by the Ethics Committee of Clinical Research from the Government of Aragón (CEICA; PI15/00707). All human subjects participating in the research (or their legal guardians) signed the informed consent. An additional informed consent was collected and signed for the publication of subjects’ photographs.

DATA AVAILABILITY STATEMENT
The data that support the findings of this study are available from the corresponding authors upon reasonable request.

Ana Latorre-Pellicer1
Ángela Ascaso1
Cristina Lucia-Campos1
Marta Gil-Salvador1
María Arnedo1
Rebeca Antoñanzas1
Ariadna Ayerza-Casas1,2
Iñigo Marcos-Alcalde3,4
Paulino Gómez-Puertas5
Feliciano J. Ramos5
Juan Pié5
Beatriz Puisac5

1Unit of Clinical Genetics and Functional Genomics, Department of Pharmacology-Physiology, School of Medicine, Universidad de Zaragoza, Zaragoza, Spain
2Unit of Paediatric Cardiology, Service of Paediatrics, Hospital Universitario Miguel Servet, Zaragoza, Spain
3Molecular Modeling Group, Centro de Biología Molecular Severo Ochoa, CBMSO (CSIC-UAM), Madrid, Spain
4Biosciences Research Institute, School of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain
5Unit of Clinical Genetics, Service of Paediatrics, Hospital Clínico Universitario Lozano Blesa, Department of Paediatrics, School of Medicine, Universidad de Zaragoza, Zaragoza, Spain

Correspondence
Juan Pié and Beatriz Puisac, Unit of Clinical Genetics and Functional Genomics, Department of Pharmacology-Physiology, School of Medicine, Universidad de Zaragoza, CIBERER-GCV02 and IIS-Aragon, E-50009 Zaragoza, Spain.
Email: juanpie@unizar.es (J. P.); puisac@unizar.es (B. P.)

ORCID
Beatriz Puisac https://orcid.org/0000-0003-0170-7326

REFERENCES