Missense variants in ANKRD11 cause KBG syndrome by impairment of stability or transcriptional activity of the encoded protein (vol 24, pg 2051, 2022)

Boer, E. de; Ockeloen, C.W.; Kampen, R.A.; Hampstead, J.E.; Dingemans, A.J.M.; Rots, D.; ... ; Kleefstra, T.

Genetics in Medicine (2023) 25, 100962

ELSEVIER

Genetics in Medicine
An Official Journal of the ACMG

www.journals.elsevier.com/genetics-in-medicine

CORRECTION

Missense variants in *ANKRD11* cause KBG syndrome by impairment of stability or transcriptional activity of the encoded protein

Elke de Boer[1,2], Charlotte W. Ockeloen[1], Rosalie A. Kampen[3], Juliet E. Hampstead[1,4], Alexander J.M. Dingemans[1,2], Dmitrijs Rots[1,2], Lukas Lütje[3], Tazeen Ashraf[5,6], Rachel Baker[7], Mouna Barat-Houari[8], Brad Angle[7], Nicolas Chatron[9,10], Anne-Sophie Denommé-Pichon[11,12], Orrin Devinsky[13], Christèle Dubourg[14,15], Frances Elmslie[16], Houda Zghal Elloumi[17], Laurence Faivre[11,18,19], Sarah Fitzgerald-Butt[20], David Geneviève[21], Jacqueline A.C. Goos[22,23], Benjamin M. Helm[20,24], Usha Kini[25], Amaia Lasa-Aranzasti[26], Gaetan Lesca[9,10], Sally A. Lynch[27], Irene M.J. Mathijssen[22], Ruth McGowan[28], Kristin G. Monaghan[17], Sylvie Odent[29], Rolph Pfundt[1], Audrey Putoux[30,31], Jeroen van Reeuwijk[1,2], Gijs W.E. Santen[32], Erina Sasaki[25], Arthur Sorlin[11,18], Peter J. van der Spek[23], Alexander P.A. Stegmann[1,33], Sigrid M.A. Swagemakers[23], Irene Valenzuela[26], Eléonore Viora-Dupont[18], Antonio Vitobello[11,12], Stephanie M. Ware[20,34], Mathys Wéber[18], Christian Gilissen[1,4], Karen J. Low[35], Simon E. Fisher[2,3], Lisenka E.L.M. Vissers[1,2], Maggie M.K. Wong[3], Tjitske Kleefstra[1,2,36]

[1]Department of Human Genetics, Radboudumc, Nijmegen, The Netherlands; [2]Donders Institute for Brain, Cognition and Behaviour, Radboud University, Nijmegen, The Netherlands; [3]Language and Genetics Department, Max Planck Institute for Psycholinguistics, Nijmegen, The Netherlands; [4]Radboud Institute for Molecular Life Sciences, Radboudumc, Nijmegen, The Netherlands; [5]Department of Clinical Genetics, Great Ormond Street Hospital for Children NHS Foundation Trust, London, United Kingdom; [6]Clinical Genetics, Guy's and St Thomas' NHS Foundation Trust, London, United Kingdom; [7]Advocate Children's Hospital, Park Ridge, IL; [8]Genetic Laboratory of Rare and Autoinflammatory Diseases, Department of Medical Genetics, Rare Diseases and Personalized Medicine, Centre Hospitalier Universitaire de Montpellier, Montpellier, France; [9]Service de Génétique, Hospices Civils de Lyon, Bron, France; [10]Institut NeuroMyoGene, CNRS UMR5310, INSERM U1217, Université Claude Bernard Lyon 1, Lyon, France; [11]Génétique des Anomalies du Développement, Université de Bourgogne Franche-Comté, UMR1231-Inserm, Dijon, France; [12]Laboratoire de Génétique Chromosomique et Moléculaire, UF6254 Innovation en Diagnostic Génomique des Maladies Rares, Centre Hospitalier Universitaire de Dijon, Dijon, France; [13]Department of Neurology, NYU Grossman School of Medicine, NYU Langone Health, New York, NY; [14]Service de Génétique Moléculaire et Génomique Médicale, CHU de Rennes, Rennes, France; [15]University of Rennes, CNRS, IGDR, UMR 6290, Rennes, France; [16]South West Thames Regional Clinical Genetics Service, St George's Hospital, University of London, London, United Kingdom; [17]GeneDx, Gaithersburg, MD; [18]Centre de Génétique et Centre de Référence Anomalies du Développement et Syndromes Malformatifs de l'Interrégion Est, Centre Hospitalier Universitaire Dijon, Dijon, France; [19]Fédération Hospitalo-Universitaire Médecine Translationnelle et Anomalies du Développement (TRANSLAD), Centre Hospitalier Universitaire Dijon, Dijon, France; [20]Department of Medical and Molecular Genetics, Indiana University

doi: https://doi.org/10.1016/j.gim.2023.100962

School of Medicine, Indiana University, Indianapolis, IN; [21]Medical Genetic Department, Rare Diseases and Personalized Medicine, Montpellier University, Inserm U1183, CHU Montpellier, Montpellier, France; [22]Department of Plastic and Reconstructive Surgery and Hand Surgery, Dutch Craniofacial Center, Erasmus MC, University Medical Center Rotterdam, Rotterdam, The Netherlands; [23]Department of Bioinformatics, Erasmus MC, University Medical Center Rotterdam, Rotterdam, The Netherlands; [24]Department of Epidemiology, Richard M. Fairbanks School of Public Health, Indiana University, Indianapolis, IN; [25]Oxford Centre for Genomic Medicine, Oxford University Hospitals NHS Foundation Trust, Oxford, United Kingdom; [26]Department of Clinical and Molecular Genetics, Vall d'Hebron University Hospital and Medicine Genetics Group, Vall d'Hebron Research Institute, Barcelona, Spain; [27]Department of Clinical Genetics, Children's Health Ireland at Crumlin and Temple Street, Dublin, Ireland; [28]West of Scotland Centre for Genomic Medicine, Queen Elizabeth University Hospital, Scottish Genomes Partnership, Glasgow, United Kingdom; [29]CHU Rennes, Service de Génétique Clinique, Centre de Référence Maladies Rares CLAD-Ouest, ERN ITHACA, Hôpital Sud, Rennes, France; [30]Service de Génétique - Centre de Référence Anomalies du Développement, Hospices Civils de Lyon, Bron, France; [31]Équipe GENDEV, Centre de Recherche en Neurosciences de Lyon, INSERM U1028 CNRS UMR5292, Université Claude Bernard Lyon 1, Lyon, France; [32]Department of Clinical Genetics, Leiden University Medical Center, Leiden, The Netherlands; [33]Department of Clinical Genetics, Maastricht University Medical Center+, Maastricht University, Maastricht, The Netherlands; [34]Department of Pediatrics, Indiana University School of Medicine, Indianapolis, IN; [35]Department of Clinical Genetics, University Hospital Bristol and Weston NHS Foundation Trust, Bristol, United Kingdom; [36]Center of Excellence for Neuropsychiatry, Vincent van Gogh Institute for Psychiatry, Venray, The Netherlands

Correction to: *Genetics in Medicine* 2022; https://doi.org/10.1016/j.gim.2022.06.007, published online 14 July 2022.

In the article "Missense variants in *ANKRD11* cause KBG syndrome by impairment of stability or transcriptional activity of the encoded protein" (*Genet Med* 2022;24:2051–2064), the following update was made. On page 2060, Figure 3 had an error in the artwork (the EGFP and Merged fluorescence imaging of ANKRD11 p.Leu509Pro and p.Arg2512Gln are identical). The revised Figure 3 is shown below. The authors would like to apologize for any inconvenience this may have caused. The article has been corrected online and can be accessed at https://doi.org/10.1016/j.gim.2022.06.007.

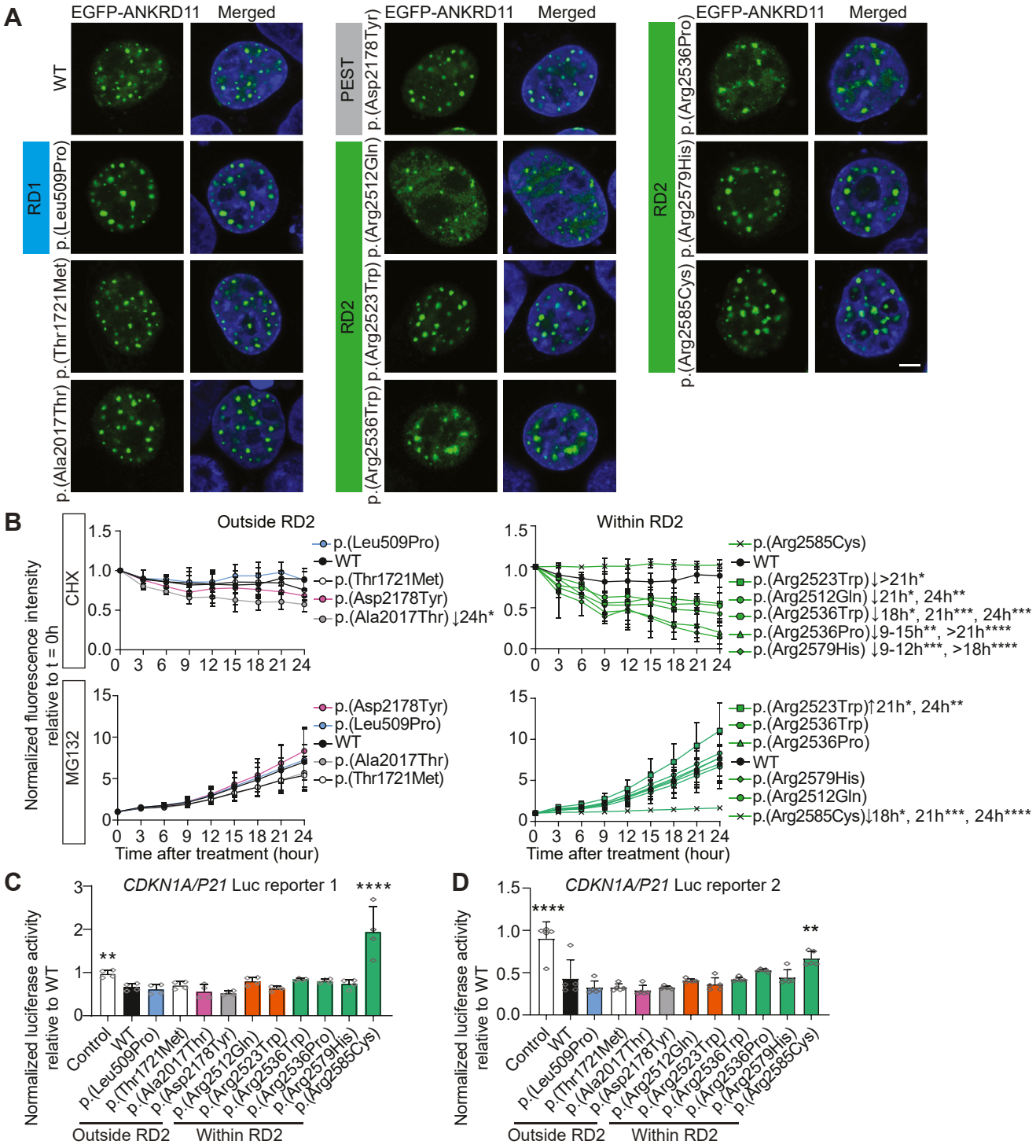

Figure 3 ***ANKRD11* variants in RD2 result in reduced protein stability and impaired proteasome degradation or loss of *CDKN1A/P21* transcriptional repression.** A. Direct fluorescence imaging of cells expressing EGFP-tagged variants of the ANKRD11 protein using confocal microscopy. Wild type and all variants showed a speckle-like pattern in the nucleus. Nuclei are stained with Hoechst 33342 (blue). Protein domains in which variants are located are indicated. Results are representative of 3 independent experiments. Scale bar = 5 μm. B. Relative fluorescence intensity of EGFP-tagged ANKRD11 variants overexpressed in HEK293T/17 cells treated with translation inhibitor cycloheximide (CHX; 50 μg/mL) shown in upper panels and with proteasome inhibitor MG132 (5 μg/mL) in the lower panels. Equal volume of dimethyl sulfoxide was used as a vehicle control. Fluorescence intensity was measured for 24 hours with 3-hour intervals. Values are expressed relative to t = 0 hour and represent the mean ± SD of 3 independent experiments, each performed in triplicate (*P < .05, **P < .01, ***P < .001, ****P < .0001; 2-way analysis of variance and a post hoc Dunnett's test). C-D. Results of luciferase assay with constructs containing WT and ANKRD11 variants and 2 firefly luciferase reporter constructs with a *CDKN1A/P21* promoter. Values are expressed relative to the control condition that used an EGFP-C2 construct without ANKRD11 and represent the mean ± SD of 4 (C) or 5 (D) independent experiments, each performed in triplicate (*P < .05, **P < .01, ****P < .0001 vs WT; 1-way analysis of variance and a post hoc Dunnett's test). RD, repressor domain; WT, wild type.