CORRECTION

Correction: Technical standards for the interpretation and reporting of constitutional copy-number variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics (ACMG) and the Clinical Genome Resource (ClinGen)

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The original version of this article unfortunately contained a mistake. In Table 1, the default score for item 5H should be 0.15 instead of 0.30. The corrected section 5 from Table 1 is given below.

Section 5: Evaluation of inheritance pattern/family history for patient being studied			
Observed copy-number loss is de novo	5A. Use appropriate category from de novo scoring section in section 4.	Use de novo scoring categories from section 4 (4A–4D) to determine score	0.45
Observed copy-number loss is inherited	5B. Patient with specific, well-defined phenotype and no family history. CNV is inherited from an apparently unaffected parent.	–0.30 (range: 0 to –0.45)	–0.45
	5C. Patient with nonspecific phenotype and no family history. CNV is inherited from an apparently unaffected parent.	–0.15 (range: 0 to –0.30)	–0.30
	5D. CNV segregates with a consistent phenotype observed in the patient's family.	Use segregation scoring categories from section 4 (4F–4H) to determine score	0.45
Observed copy-number loss—nonsegregations	5E. Use appropriate category from nonsegregation section in section 4.	Use nonsegregation scoring categories from section 4 (4I–4K) to determine score	–0.45
Other	5F. Inheritance information is unavailable or uninformative.	0	0
	5G. Inheritance information is unavailable or uninformative. The patient phenotype is nonspecific, but is consistent with what has been described in similar cases.	0.10 (range: 0 to 0.15)	0.15
	5H. Inheritance information is unavailable or uninformative. The patient phenotype is highly specific and consistent with what has been described in similar cases.	0.15 (range: 0 to 0.30)	0.30