

CORRIGENDA

Clinical exome sequencing for cerebellar ataxia and spastic paraplegia uncovers novel gene–disease associations and unanticipated rare disorders

Bart P van de Warrenburg, Meyke I Schouten, Susanne T de Bot, Sascha Vermeer, Rowdy Meijer, Maartje Pennings, Christian Gilissen, Michèl AAP Willemsen, Hans Scheffer and Erik-Jan Kamsteeg

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Since publication, the authors have noticed that they had reported a sibship with autosomal recessive hereditary spastic paraplegia (HSP) in whom they identified a homozygous c.772G>A (p.Glu258Lys) variant in the *TH* gene, which they classified as possibly causative. This suggested that the *TH* gene, known to be responsible for autosomal recessive dopamine-responsive dystonia,

could also be associated with HSP, as has been suggested for *GCH1*, the gene for autosomal dominant dopamine-responsive dystonia.¹ However, recently mutations in *CAPN1* were found in a new form of autosomal recessive HSP (SPG78)² and querying their exome data revealed a homozygous nonsense mutation (Chr11 (GRCh37):g.64951004C>T; NM_005186.3:c.397C>T; p.(Arg133*)) in *CAPN1* in this particular sibship. The authors believe that this is the more likely cause for the autosomal recessive HSP in this family.

Mitochondrial encephalomyopathy and retinoblastoma explained by compound heterozygosity of *SUCLA2* point mutation and 13q14 deletion

Sanna Matilainen, Pirjo Isohanni, Liliya Euro, Tuula Lönnqvist, Helena Pihko, Tero Kivelä, Sakari Knuutila and Anu Suomalainen

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Correction to: *European Journal of Human Genetics* (2015) **23**, 325–330; doi:10.1038/ejhg.2014.128

Previously reported patients (22)	Patient 1	Patient 2
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The sub-heading of Table 1 is incorrect and should read: