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CORRIGENDA

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

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Correction to: *European Journal of Human Genetics* (2016) **24,** 1460–1466; doi:10.1038/ejhg.2016.42; published online 11 May 2016

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

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

The sub-heading of Table 1 is incorrect and should read:

Previously reported patients (22)	*Patient 1*	*Patient 2*