CORRIGENDA

Next-generation sequencing (NGS) as a diagnostic tool for retinal degeneration reveals a much higher detection rate in early-onset disease

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Correction to: European Journal of Human Genetics (2013) 21, 274-280; doi:10.1038/ejhg.2012.172

The authors would like to apologise for the following errors in Table 2.

Three references cited in Table 2 were absent from the final reference list:

ABCA4 N965S

Sun H, Smallwood PM, Nathans J: Biochemical defects in ABCR protein variants associated with human retinopathies. *Nat Genet* 2000; **26**: 242–246.

CRX Y258X

Chau KY, Chen S, Zack DJ, Ono SJ: Functional domains of the conerod homeobox (CRX) transcription factor. *J Biol Chem* 2000; 275: 37264–37270.

GUCY2D R838H

Wilkie SE, Newbold RJ, Deery E *et al*: Functional characterization of missense mutations at codon 838 in retinal guanylate cyclase correlates with disease severity in patients with autosomal dominant cone-rod dystrophy. *Hum Mol Genet* 2000; **9**: 3065–3073.

The dbSNP entry rs61749449 refers to N965D rather than N965S.

CRB1T, 745K should read CRB1, T745K.

Also, the following errors were found in Supplementary Table 2: ABCA4 c.322C>T should read c.3322C>T ABCA4 c.5882G>C should read c.5882G>A ABCA4 c.6379C>T should read c.6391G>A PRPF8 c.6926T>G should read c.6926A>C

Mortality in neurofibromatosis 1: in North West England: an assessment of actuarial survival in a region of the UK since 1989

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	In the first row of Table 4 the PMR (95% CI) should be 4.1 (2.4, 6.4) rather than 4.1 (2.4, 2.6).
The authors would like to apologize for the following error that has	Also, the first sentence on page 1189 should read: cardiovascular disease was reported four times more frequently in NF1 males (PMR = 4.1 ; 95% CI, 2.4–6.4) than the general population.