Genetics and Molecular Biology, 35, 4, 898-898 (2012)

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Errata

Otto PA, Horimoto ARVR. Penetrance rate estimation in autosomal dominant conditions. Genetics and Molecular Biology 35(3), 583-588, 2012.

The following text on p. 586 [first paragraph of item 7 (ascertainment issues)], that reads:

Advanced computer programs that perform segregation analysis or estimate linkage, such as the classical S.A.G.E. (S.A.G.E., 2009) and LINKAGE (Lathrop *et al.*, 1985) programs we referred to in the introduction section, do not apply any ascertainment bias to the penetrance rate they indirectly estimate.

should be replaced by:

Advanced computer programs that perform segregation analysis or estimate linkage, such as the classical S.A.G.E. (S.A.G.E., 2009) and LINKAGE (Lathrop *et al.*, 1985) programs we referred to in the introduction section, do not apply any ascertainment bias **correction** to the penetrance rate they indirectly estimate.

Pardono E, Mazzeu JF, Lezirovitz K, Auricchio MTBM, Iughetti P, Nascimento RMP, Mingroni-Netto RC, Otto PA. Waardenburg syndrome: description of two novel mutations in the PAX3 gene, one of which incompletely penetrant. Genetics and Molecular Biology 29(4), 601-604, 2006.

On pages 602 and 603 the paper describes two PAX3 mutations. Dr. Andrew Phillips, from the Human Genome Database of the Institute of Medical Genetics, Cardiff University (UK), called our attention to an error in the description of the lesion found in family 2, that the text describes as a deletion of 13 base pairs [c.764-776del(TTACCCTGACATT)] in exon 5. The thirteen bases specified do appear within exon 5 at c.726-738 (instead of c.764-776) so the deletion is GCT TTT GAG AGA ^ACT CA|**t tac cct gac att**|TAT ACT AGG GAG GAA, where the caret marks the start of codon 241, and the deleted bases are shown in bold and lower case.