ERRATA AND CORRIGENDA



ERRATUM: Section E6.1–6.4 of the ACMG technical standards and guidelines: chromosome studies of neoplastic blood and bone marrow–acquired chromosomal abnormalities

Fady M. Mikhail MD, PhD, Nyla A. Heerema PhD, Kathleen W. Rao PhD, Rachel D. Burnside PhD, Athena M. Cherry PhD and Linda D. Cooley MD, MBA; on behalf of the American College of Medical Genetics and Genomics (ACMG) Laboratory Quality Assurance Committee

Genet Med advance online publication, April 28, 2016; doi:10.1038/gim.2016.50

On page 5, in the left column, first paragraph under "AML," a gene name is misspelled. The correct gene name is "KMT2A (MLL)." The publisher regrets the error.

Advance online publication 19 May 2016

CORRIGENDUM: Comprehensive analysis via exome sequencing uncovers genetic etiology in autosomal recessive nonsyndromic deafness in a large multiethnic cohort

Guney Bademci MD, Joseph Foster II BSc, Nejat Mahdieh PhD, Mortaza Bonyadi PhD, Duygu Duman PhD, F.Basak Cengiz PhD, Ibis Menendez MD, Oscar Diaz-Horta PhD, Atefeh Shirkavand PhD, Sirous Zeinali PhD, Asli Subasioglu MD, Suna Tokgoz-Yilmaz PhD, Fabiola Huesca-Hernandez BSc, Maria de la Luz Arenas-Sordo MD, Juan Dominguez-Aburto BSc, Edgar Hernandez-Zamora PhD, Paola Montenegro PhD, Rosario Paredes MD, Germania Moreta MD, Rodrigo Vinueza BSc, Franklin Villegas BSc, Santiago Mendoza-Benitez MD, Shengru Guo MSc, Nazim Bozan MD, Tulay Tos MD, Armagan Incesulu MD, Gonca Sennaroglu PhD, Susan H. Blanton PhD, Hatice Ozturkmen-Akay MD, Muzeyyen Yildirim-Baylan MD and Mustafa Tekin MD

Genet Med 18: 364-371; advance online publication, July 30, 2015; doi:10.1038/gim.2015.89

In the published version of this manuscript in Table1: Family 7, pathogenic variant reported in *TPRN* as c.705_709dupCCTGC (p.R237PfsX215) is now corrected to c.701_705dupCTGCC (p.N236LfsX216); Family 52, pathogenic variant reported in *TMC1* as c.1589_1590CT is now corrected to c.1589_1590delCT; Family 123, pathogenic variant in *TMC1* reported as c.1080_1084delGATCA is now corrected to c.1083_1087delCAGAT, this variant has been previously reported by Kalay et al.; Family 1368, pathogenic variant in *TMPRSS3* reported as c.1126G>A (p.G376S) is now corrected to c.1129G>A (p.G377S); Overall identified novel variant percentage is 53% instead of 54%. In Figure 3a, typo error for "*TIME*" is now corrected to "*TMIE*". The authors regret the errors.

Kalay E, Karaguzel A, Caylan R, et al. Four novel TMC1 (DFNB7/DFNB11) mutations in Turkish patients with congenital autosomal recessive nonsyndromic hearing loss. Hum Mutat 2005;26:591.