

## Correction

---

Sharma M, Ioannidis JP, Aasly JO, Annesi G, Brice A, Bertram L, Bozi M, Barcikowska M, Crosiers D, Clarke CE, Facheris MF, Farrer M, Garraux G, Gispert S, Auburger G, Vilarinho-Güell C, Hadjigeorgiou GM, Hicks AA, Hattori N, Jeon BS, Jamrozik Z, Krygowska-Wajs A, Lesage S, Lill CM, Lin JJ, Lynch T, Lichtner P, Lang AE, Libioulle C, Murata M, Mok V, Jasinska-Myga B, Mellick GD, Morrison KE, Meitnger T, Zimprich A, Opala G, Pramstaller PP, Pichler I, Park SS, Quattrone A, Rogaeva E, Ross OA, Stefanis L, Stockton JD, Satake W, Silburn PA, Strom TM, Theuns J, Tan EK, Toda T, Tomiyama H, Uitti RJ, Van Broeckhoven C, Wirdefeldt K, Wszolek Z, Xiromerisiou G, Yomono HS, Yueh KC, Zhao Y, Gasser T, Maraganore D, Krüger R; on behalf of GEOPD consortium. A multi-centre clinico-genetic analysis of the VPS35 gene in Parkinson disease indicates reduced penetrance for disease-associated variants. *J Med Genet.* 2012 Nov;49(11):721-726. In this paper J Theuns and C Van Broeckhoven were affiliated with institutions 14 and 15. This is an error and both authors are affiliated with institutions 13 and 14.

*J Med Genet* 2013;50:202. doi:10.1136/jmedgenet-2012-101155corr1