CORRECTION

# Phenotype Presentation and Molecular Diagnostic Yield in Non-5q Spinal Muscular Atrophy

*Neurol Genet* 2024;10:e200139. doi:10.1212/NXG.0000000000200139

In the Research Article "Phenotype Presentation and Molecular Diagnostic Yield in Non-5q Spinal Muscular Atrophy" by Fernández-Eulate et al.,[1] the first paragraph under the Other Non-5q SMA–Associated Genes section should read as follows to avoid any misunderstanding:

> *Other variants in genes implicated in HMNs were found. In 2 SP-SMA patients with lower-limb distal involvement,* scapula alata*, and a disease onset in adult life, heterozygous* HSPB1 *variants were found. Two patients (SP-SMA and P-SMA) carried heterozygous variants in the* VCP *and one (SP-SMA) a homozygous variant in the* VRK1 *gene, all 3 with an adult disease onset. A previously reported patient with an adult-onset PD-SMA carried a heterozygous variant in the* MORC2 *gene.*[18] *One patient with an infantile-onset PD-SMA carried a homozygous pathogenic variant in the* DNAJB2 *gene. The specific genetic variants can be seen in eTable 1 (links.lww.com/NXG/A614).*

Additionally, in eTable 1, the first variant of patient number 11 has been corrected to "(p.Arg598Cys)", and the first variant of patient number 56 has been corrected to "Homozygous c.961C>T (p.Arg321Cys)." The updated eTable 1 can be accessed at links.lww.com/NXG/A614.

The authors regret the errors.

## Reference

1. Fernández-Eulate G, Theuriet J, Record CJ, et al. Phenotype presentation and molecular diagnostic yield in non-5q spinal muscular atrophy. *Neurol Genet.* 2023;9(4):e200087. doi:10.1212/NXG.0000000000200087