AUTHOR CORRECTION OPEN



Author Correction: Accurate long-read sequencing identified *GBA1* as major risk factor in the Luxembourgish Parkinson's study

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Correction to: *npj Parkinson's Disease* https://doi.org/10.1038/s41531-023-00595-w, published online 23 November 2023

In this article the wrong Table appeared as Table 3.; the Table should have appeared as shown below. The original article has been corrected.

The following text that describes data from the previous version of Table 3 has also been removed: "Compared to severe (6.4 \pm 4.7) and risk (4.4 \pm 4.9) variant carriers, the mild (1.7 \pm 1.4) variant carriers show a significantly shorter disease duration (Table 3)."

Features	All pathogenic variants $(n = 67)$		Mild (n = 7)	Risk (n = 39)	Non carriers (n = 554)
AAA, mean (SD)	[OR = 0.31;	65.1 (±10.2) [OR = 0.08; p = 0.292]	[OR = 0.59;	67.1 (±9.2) [OR = 0.57; p = 0.7512]	
Sex, Male n (%)	[OR = 0.71;	13 (61.9%) [OR = 0.78; p = 0.5795]	[OR = 1.19;	22 (56.4%) [OR = 0.62; p = 0.151]	
AAO, mean (SD)	[OR = 0.35;	58.6 (±13.1) [OR = 0.02; $p = 0.1158$]		62.5 (±9.3) [OR = 0.9; p = 0.9548]	

Features		Severe (<i>n</i> = 21)	Mild (n = 7)	Risk (n = 39)	Non carriers (<i>n</i> = 554)
AAO < 45, N (%)	8 (11.9%) [OR = 1.74; p = 0.1767]	5 (23.8%) [OR = 4.02; p = 0.0098*]	2 (28.6%) [OR = 5.14; p = 0.0549]	1 (2.6%) [OR = 0.34; p = 0.2907]	40 (7.2%)
Disease Duration, mean (SD)	4.7 (±4.8) [OR = 0.79; p = 0.7303]	6.4 (\pm 4.7) [OR = 4.07; p = 0.2238]	1.7 (\pm 1.4) [OR = 0.04; p =0.0981]	4.4 (±4.9) [OR = 0.57; p = 0.5103]	5.0 (±5.2)
Family History, N (%)	25 (37.3%) [OR = 1.74; p = 0.0401*]	8 (38.1%) [OR = 1.8; p = 0.2001]	2 (28.6% [OR = 1.17; p = 0.8508]	15 (38.5%) [OR = 1.83; p = 0.0782]	141 (25.5%)

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