Antoniadi and colleagues describe the implementation of a 56 gene next-generation sequencing (NGS) panel for inherited peripheral neuropathy (IPN) in 448 patients, the majority of whom met UKGTN approval criteria. This is a nicely written manuscript describing the diagnostic utility of expanded NGS-based panels for IPN, a spectrum of diseases known for their clinical and genetic heterogeneity. While this is an article of importance in its field, this manuscript would benefit from a few important revisions.

Major Compulsory Revisions
1. The authors describe an NGS-based test developed for clinical diagnostic use. As such, this manuscript should contain a brief discussion of how the test was validated and the outcomes of the validation in the methods. For example, what was the overall sensitivity and specificity and what was the specific sensitivity and specificity for SNVs vs indels? Was CNV detection validated and were CNVs confirmed by an alternate method (e.g., ddPCR or MLPA)?

2. Supplementary tables 1-3 provide a list of previously reported pathogenic variants, likely pathogenic variants, and variants of unknown clinical significance, respectively. My major concern is that these tables contain no information regarding what pieces of evidence led to each variant classification. Moreover, stating that a variant was “previously reported as pathogenic” does not constitute adequate evidence for pathogenicity. Evidence justifying each classification should be added to the tables including: allele frequency, conservation, pathogenicity predictions, splicing predictions, number of probands identified with variant in the literature and in LSDBs, co-segregation with disease if dominant, co-occurrences with another pathogenic variant if recessive, de novo occurrences, and functional studies.

Minor Essential Revisions
1. The sentence “In our experience is that NGS is more efficient and removes the need for serial gene sequencing in most cases” is grammatically incorrect.

Discretionary Revisions
1. In the end of the 4th paragraph of the background, the authors state that current testing strategies result in low diagnostic yields. Are there any data on this? If so it would be interesting to note these data and compare it to the
diagnostic yield achieved here.

2. The section regarding broadening the phenotypic spectrum associated with specific genes would benefit from some indication of which specific IPNs the genes are usually associated with. This detail would be especially useful for readers not familiar with the different forms of IPN.

**Level of interest:** An article of importance in its field

**Quality of written English:** Acceptable

**Statistical review:** No, the manuscript does not need to be seen by a statistician.

**Declaration of competing interests:**

I am an Assistant Laboratory Director at the Laboratory for Molecular Medicine, a fee-for-service clinical genetic testing laboratory.