Comments to the Authors,

This manuscript identified a novel insertional mutation in SPAST in a Chinese Han family with hereditary spastic paraplegia with genome-wide sequencing technique. The authors also demonstrated that the novel insertional mutation in SPAST (c.756insA, p.M253Nfs\*12) segregated with disease in the family and no other variant in known HSP genes or novel genes segregated with disease. It provided a novel mutation for hereditary spastic paraplegia and also demenstrated that genome-wide DNA sequencing would be great tool for the diagnosis of hereditary disease. The The study was performed rigorously and the findings are interesting. In general, I'd recommend publication if the authors can address the following concerns.

Major Compulsory Revisions

1, How many variable were found to be segregated with disease in the present family? Please provided it as the Table 2.

2, Have you check this insertional mutation (c.756insA, p.M253Nfs\*12) in the whole family? If it is not done yet, it should be done.

3, This insertional mutation should be detected in another independent hereditary spastic paraplegia samples to estimate the incidence frequency.