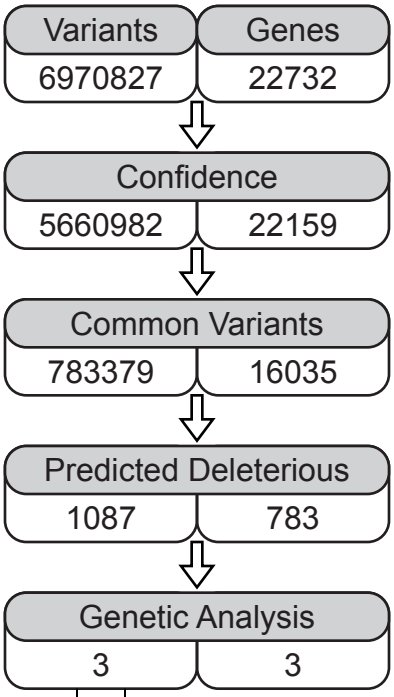
Figure S1



Chromosome	Position	Gene Region	Gene Symbol	Transcript ID	Transcript Variant	Protein Variant	Translation Impact	SIFT Function Prediction	PolyPhen-2 Function Prediction	Regulatory Site
10	104852895	Splice Site	*NT5C2*	NM_012229.4; NM_001134373.2	c.1159+1G>T					Splice Site Loss
20	25456907	Exonic	*NINL*	NM_025176.4	c.3020delC	p.P1007fs*43	frameshift			
20	36855621	Exonic	*KIAA1755*	NM_001029864.1	c.1987C>T	p.R663W	missense	Damaging	Possibly Damaging	

Chromosome	Position	Gene Region	Gene Symbol	Transcript ID	Transcript Variant	Protein Variant	Translation Impact	SIFT Function Prediction	PolyPhen-2 Function Prediction	Regulatory Site
10	104852895	Splice Site	*NT5C2*	NM_012229.4; NM_001134373.2	c.1159+1G>T					Splice Site Loss

	Allele Frequency in 108 Qatari Genomes			
Gene	Homozygous for Variant	Heterozygous	Homozygous for Reference	No Call
NT5C2	0	0	108	0
NINL	0	0	108	0
KIAA1755	0	4	104	0

Figure S1: IVA analysis of WGS data. Filters applied (see methods) revealed 3 variants in 3 genes (NT5C2, NINL and KIAA1755) at the genetic analysis filter that showed in IVA to be compatible with Mendelian recessive inheritance (upper panel). Detailed description of those 3 variants is shown in the upper table. Frequency of those 3 genetic variants in the Qatari population is shown in the bottom table with KIAA1755 variant detected as heterozygous at a frequency of 3.7% in Qatari genomes. When biological context filter is applied and hereditary spastic paraplegia is specified as the disease, the two variants, NINL and KIAA1755 ones, are filtered out leading to one single variant in *NT5C2* (middle table).