Supplementary Table 1:

Gene name	OMIM	Phenotype
ATL1	606439	SPG3A
BSCL2	606158	Silver syndrome, Neuropathy, Lipodystrophy
CYP7B1	603711	SPG5, Bile acid synthesis defect
GJC2	608803	SPG44, Hypomyelinating
HSPD1	118190	SPG13, hypomelinating leukodystrophy
KIAA0196	610657	SPG8
KIAA1840	610844	SPG11
KIF5A	602821	SPG10
L1CAM	308840	MASA syndrome
NIPA1	608145	SPG6
SPG7	602783	SPG7
PLP1	300401	SPG2, Pelizaeus-Merzbacher disease
PNPLA6	603197	SPG39
REEP1	609139	SPG31
SLC16A2	300095	Allan-Herndon-Dudley syndrome
SLC33A1	603690	SPG42
SPAST	604277	SPG4
SPG20	607111	Troyer syndrome
SPG21	608181	Mast syndrome
ZFYVE26	610243	SPG33

Supp. Table 1: List of genes that are associated with Hereditary Spastic Paraparesis.

Supp Table 2:

	Exclusion Method	Genes	Positions
	Known HSP genes in shared autosomal regions	4	6981
Homo.	… AND homozygous variations that are not homozygous in the parents	1	1
	… AND not in dbSNP/1000 Genomes	**0**	**0**
Compound Heterozygous	… AND heterozygous variations	4	23
	… AND not in dbSNP/1000 Genomes	4	20
	… AND not synonymous changes	4	14
	… AND at least one parent is heterozygous	2	2
	… AND two heterozygous hits in the same gene	**0**	**0**

Supp. Table 2: Rejection of variations in known HSP genes. The top part of the table describes a rejection process assuming a homozygous variation. The bottom part describes a rejection process assuming a compound heterozygous. The exclusion process gave an empty set for both assumptions.

Supp Table 3:

Exclusion Method	Genes	Positions
Variations that are present in the patient and not reference in the mother	38	58
… AND not in dbSNP/1000 Genomes	7	10
… AND not synonymous changes	4	5
… AND father has the same variation	3	4
… AND are supported by more than one read	**0**	**0**
… OR conserved (GERP score>2)	1	1
… AND predicted to be damaging by MutationTaster	**0**	**0**

Supp. Table 3: Rejection of variations in the shared region of chromosome X.