GENE	GENE NAME	OMIM	MOI	COMMENT	ENSEMBL TRANSCRIPT	CHR	POS [HG19]	VARIANT	LOCALIZATION OF THE VARIANT	COVERAGE [fold]	VARIANT FREQUENCY [%]	dbSNP	MINOR ALLELE HET *	MINOR ALLELE HOMO *	ExAC SERVER: VARIANTS
REEP1	Receptor accessory protein 1	OMIM #610250 SPASTIC PARAPLEGIA 31, AUTOSOMAL DOMINANT; SPG31	AD		ENST00000165698	2	86481810	GTAATAT>AC	intron, donor splice site	141	100	.	0	0	0
CCDC6	Coiled-coil domain containing 6	OMIM #188550 THYROID CARCINOMA, PAPILLARY		phenotype does not fit	ENST00000263102	10	61666198	G>A	5´UTR	19	100	.	0	0	0
C10orf107	Chromosome 10 open reading frame 107	No known disease associated with *C10orf107* mutations		potentially associated with hypertension	ENST00000330194	10	63440922	T>C	5´UTR	251	100	.	0	0	0

Table e-1: Homozygous variants in the autozygous region that were predicted to be disease causing by the MutationTaster2 software. **MOI**, mode of inheritance; **AD**, autosomal dominant; **UTR,** untranslated region; * Frequencies refer to the genotypes of the 1000 Genome