Supplemental Data

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Kufs Disease, the Major Adult Form of Neuronal Ceroid Lipofuscinosis, Caused by Mutations in *CLN6*

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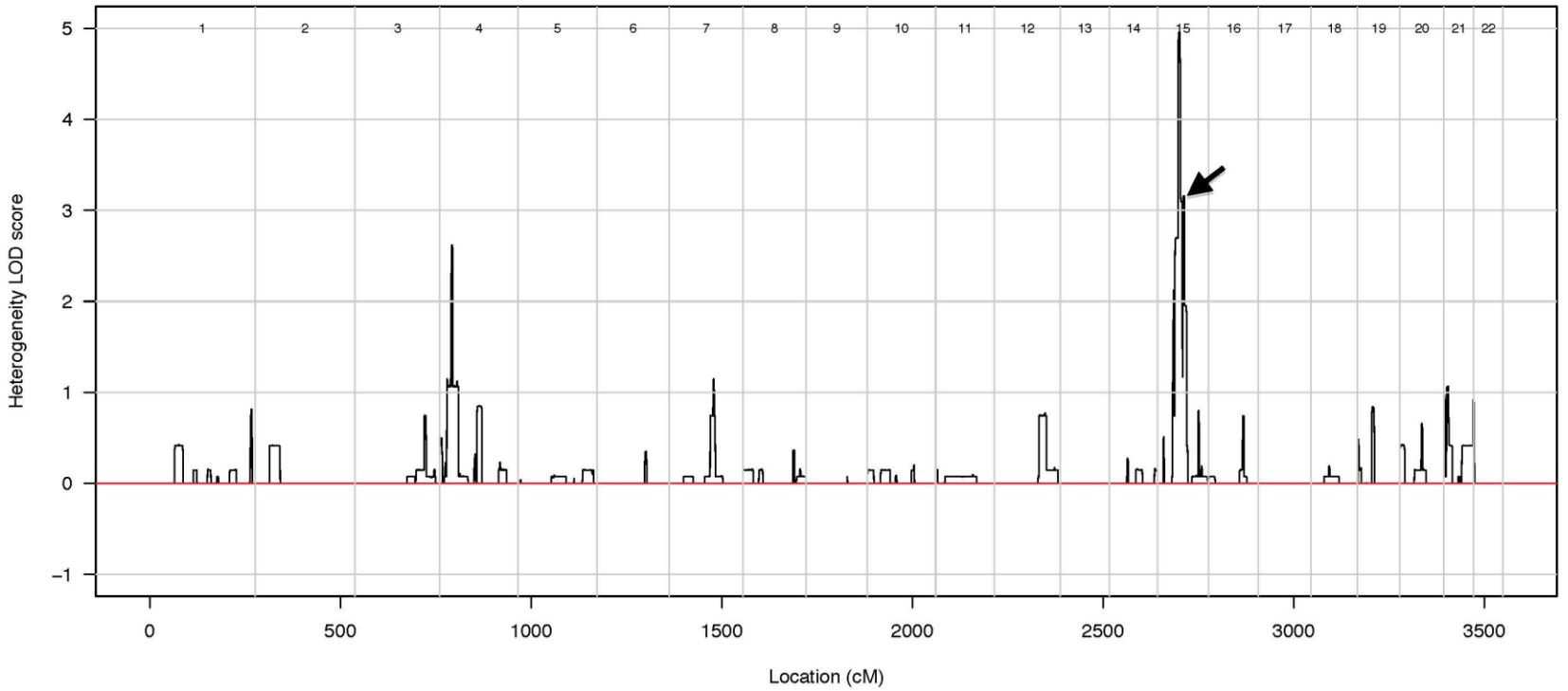

Figure S1. Results of Genome-Wide Linkage Mapping Using Ku1, Ku2, Ku3 and Ku4

Genome wide heterogeneity LOD score for the families used in the linkage analysis. Grey vertical lines delineate chromosomes. The x axis is in cM. The arrow indicates the shoulder peak on chromosome 15 that contains *CLN6*.

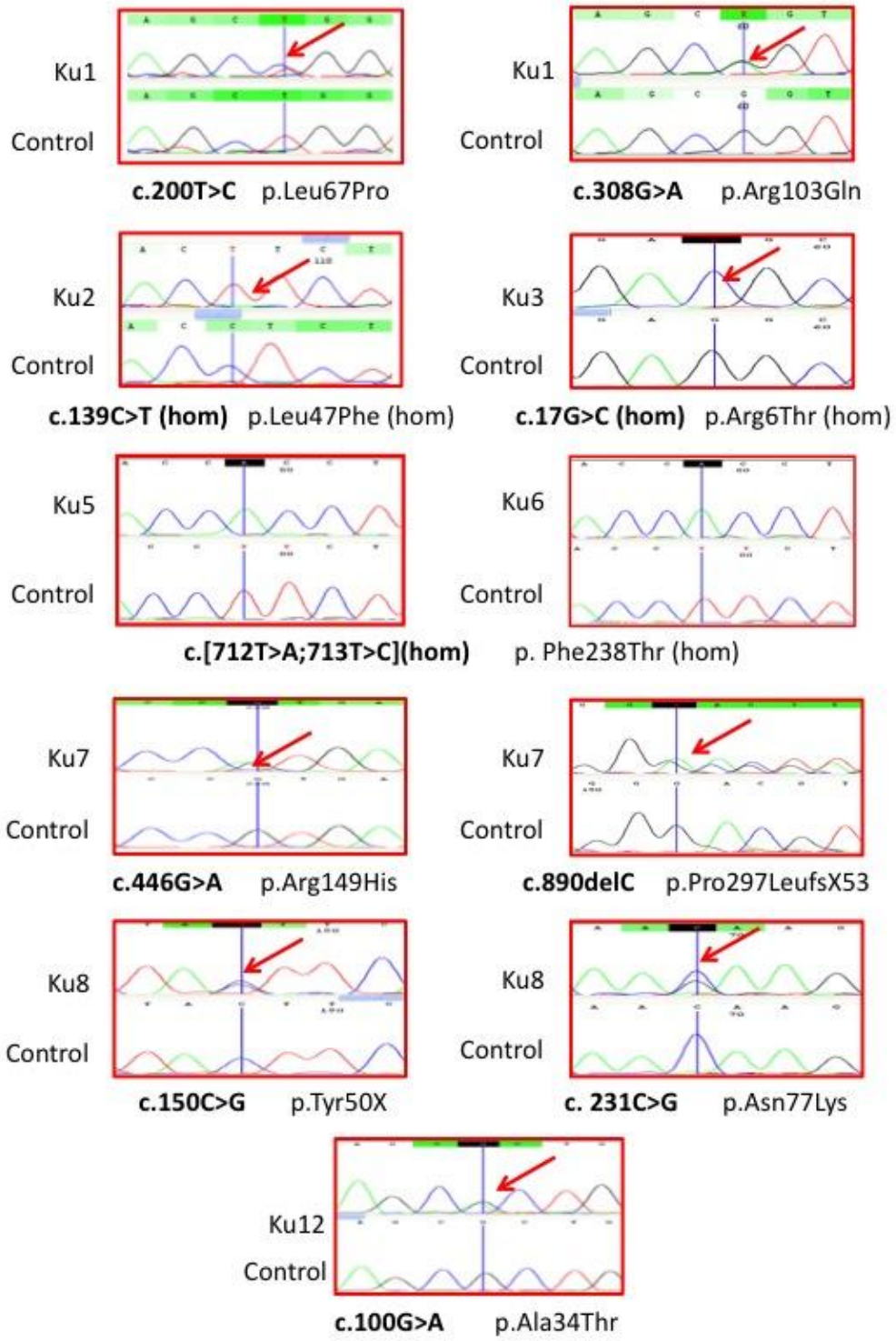

Figure S2. Sequence Traces of Nine Mutations in *CLN6* Detected in Seven Families
Note that Ku5 and Ku6 share a common homozygous mutation, p.Phe238Thr. Additionally a variant in Ku12; likely a non-pathogenic rare variant is shown.

Table S1. Evolutionary Conservation of 9 Mutated Amino Acids in CLN6 in 7 Families and One Probable Nonpathogenic Variant (Ku12)

Family[a]	**Ku1**		**Ku2**	**Ku3**	**Ku5 Ku6**	**Ku7**		**Ku8**		**Ku12**
Mutation	Leu67 Pro	Arg103Glu	Leu47 Phe	Arg6 Thr	Phe238 Thr	Arg149 His	Pro297LeufsX	Tyr50X	Asn77Lys	Ala34Thr[b]
Human	Leu	Arg	Leu	Arg	Phe	Arg	Pro	Tyr	Asn	Ala
Rhesus	Leu	Arg	Leu	-	Phe	Arg	Pro	Tyr	Asn	Ala
Mouse	Leu	Arg	Leu	Arg	Phe	Arg	Pro	Tyr	Asn	Ala
Dog	Leu	Arg	Leu	Arg	Phe	Arg	Pro	Tyr	Asn	Ala
Elephant	-	-	Leu	Arg	Phe	Arg	Pro	Tyr	Asn	Ala
Opossum	Ile	Arg	Leu	-	Tyr	Arg	Pro	Tyr	Asn	Ala
Chicken	Ile	Arg	Leu	-	Phe	Arg	Pro	Tyr	Asn	Asp
Xenopus	Ile	Arg	Leu	-	Phe	Arg	Pro	Tyr	Asn	Pro
Stickleback	Ile	Arg	Leu	-	Phe	Arg	Pro	Cys	Asn	Pro
PolyPhen-2 probability[c]	0.82	0.63	0.95	0.83	0.014	0.81	Frameshift	Truncation	0.89	0.75

[a] Sanger sequencing of *CLN6* did not detect any mutations for families Ku4, Ku9, Ku10 and Ku11.
[b] Evolutionary conservation of exon 1 was assessed on the nucleotide level.
[c] PolyPhen-2 classifier probability of the variation being damaging; benign - probability ≤ 0.18, possibly damaging - probability between 0.63 and 0.83 and probably damaging- probability ≥ 0.89 (Ref 29).