Table S1 - Details of molecular genetic findings in patients 1 and 2

	Tissue	Mutation and allele load
Patient ~~2~~ 1	Keratinocytic epidermal naevus	*HRAS* c.34G>T (p.Gly12Cys) heterozygous missense mutation (Sanger sequencing approximately 37% allele load)
	Hair root from woolly hair naevus	*HRAS* c.34G>T (p.Gly12Cys) heterozygous missense mutation (Sanger sequencing approximately 50% allele load)
	Hair root normal hair	No intact hair roots available for DNA extraction
	Blood	Wild type *HRAS*
	Buccal mucosa	Wild type *HRAS*
	Tonsils (right and left)	Wild type *HRAS*
	Urine sediment	Wild type *HRAS*
	4 fragments of fibrous dysplasia	*HRAS* c.34G>T (p.Gly12Cys) at 0% of reads (4 of 24594 next generation sequencing read depth), at 0% of reads (67 of 37547 next generation sequencing read depth), at 5% of reads (1738 of 35134 next generation read depth), at 17% of reads (757 of 4561 next generation sequencing read depth)
Patient ~~1~~ 2	Keratinocytic epidermal naevus	*HRAS* c.182A>T, p.(Gln61Leu) at 36% of reads (695 of 1905 next generation sequencing read depth)
	Blood	Wild type *HRAS*
	Archival FFPE bone biopsy tissue	No PCR product obtained for sequencing despite multiple attempts