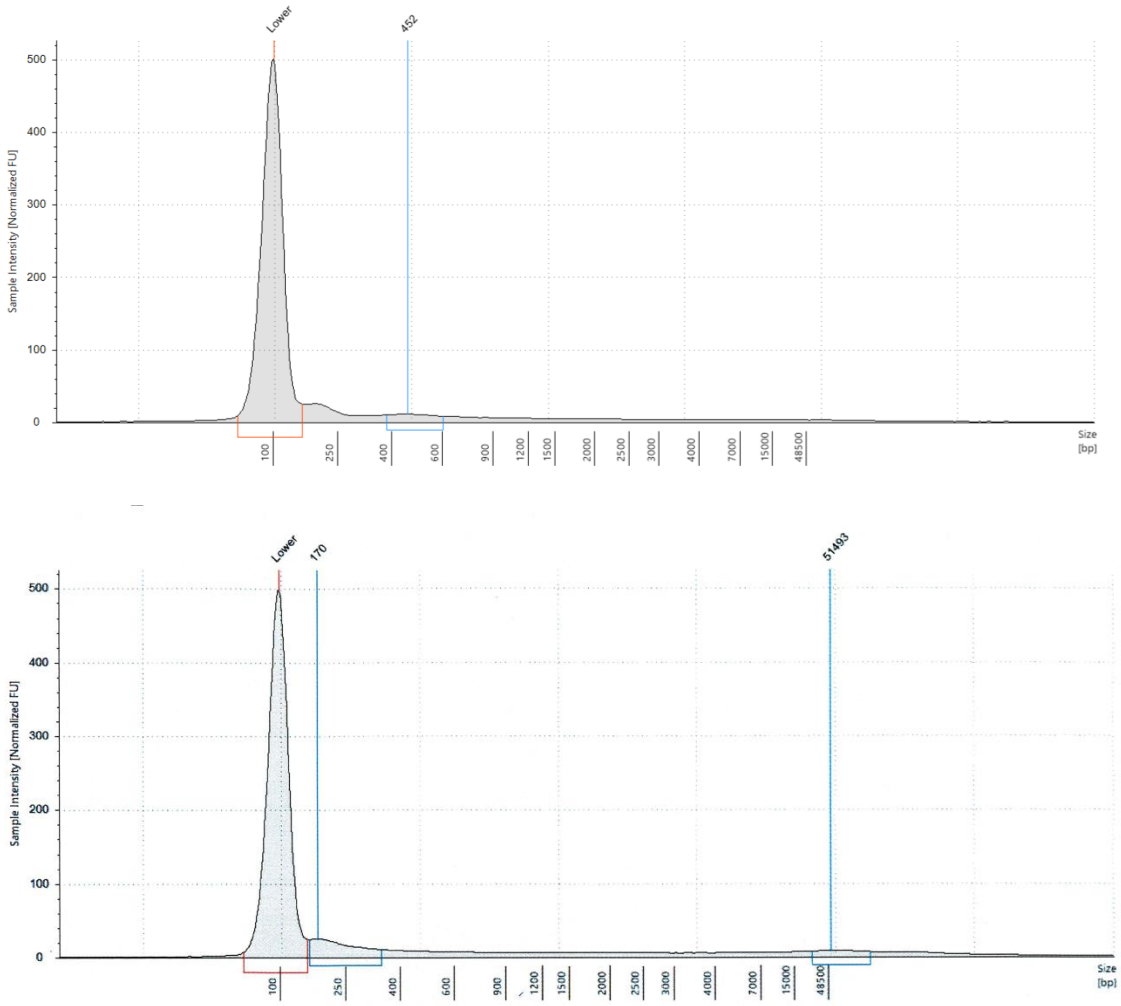
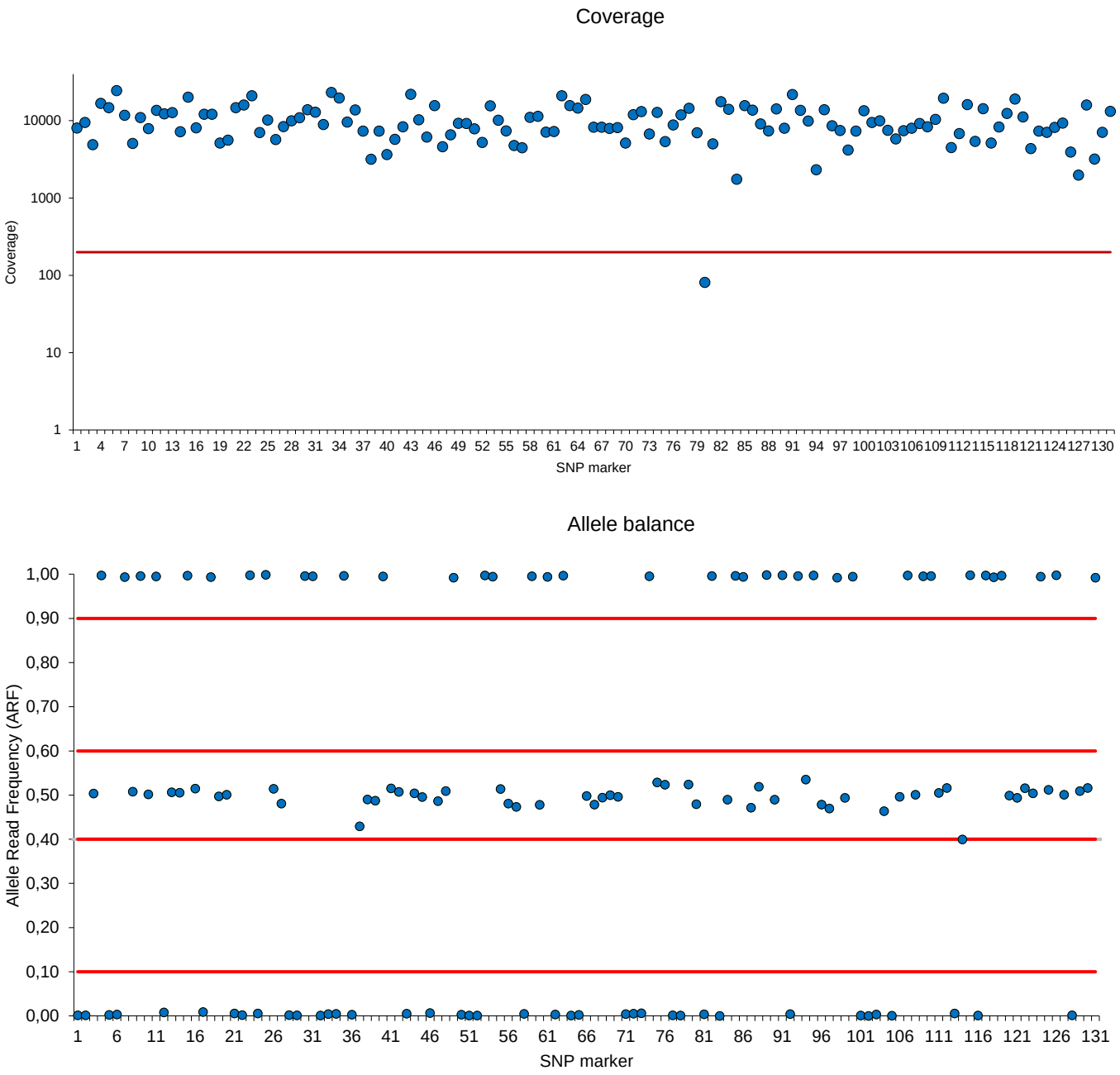
Supplementary Data to Tillmar et al., 2021 "Getting the conclusive lead with investigative genetic genealogy – A successful case study of a 16 year old double murder in Sweden"



Supplementary Figure 1. Analysis of the integrity of DNA extract 1 (upper) and DNA extract 2 (lower).



Supplementary Figure 2. Coverage (upper) and allele balance (allele read frequency, ARF) (bottom) for the 131 SNPs analyzed using the MPS based GeneRead™ DNAseq Targeted SNP Panel. A coverage of >200X was used as the inclusion criteria for coverage. An ARF value between 0 and 0.1 or 0.9 and 1 resulted in a homozygous call, a value between 0.4 and 0.6 resulted in a heterozygous call and a value between 0.1 and 0.4 or between 0.6 and 0.9 resulted in a no-genotype call. Coverage/ARFs are on the y-axis, and the SNPs are on the x-axis.

Supplementary Table 1

Parameters and conditions used for genotype calling of WGS data

Parameter	Description	Threshold for genotype calling
Coverage	Number of individual reads that has a certain nucleotide at a given position.	≥10 (homozygous) ≥5 per allele (heterozygous)
Allelic balance[1]	[coverage for the most common nucleotide]/ [coverage for the most common nucleotide + coverage for the second most common nucleotide].	=1 or >0.97 (homozygous)[2] 0.5≤x≤0.7 (heterozygous)
Q score	Mean quality score (nucleotide Q).	>25
Forward/Reverse read ratio	Forward and reverse read ratio for the nucleotide(s) comprising the genotype.	>0.2

[1] For markers for which a third nucleotide was detected, its coverage had to be no more than 1% of the second most common nucleotide in order to call a genotype for that marker.

[2] 1 was used for the first and second WGS analyses and 0.97 was used for the third WGS analysis.