Supplementary material to article by E. Uusitalo et al. "Neurofibromatosis Type 1 Gene Mutation Analysis Using Sequence Capture and High-throughput Sequencing"

Table SII. Overview of the sequencing results: size of reads, numbers of passed and mapped reads, mean coverage, coverage SD and number of bases $<\!20\times$

	Average size of reads (bp)	Passed reads	Mapped reads	Mean coverage	Coverage SD	Bases < 20× n (%)
Set A (10 samples)	403	115,519	109,675	41	23	19,399 (12.07)
Set B (6 samples)	408	130,293	126,401	74	59	19,014 (19.73)