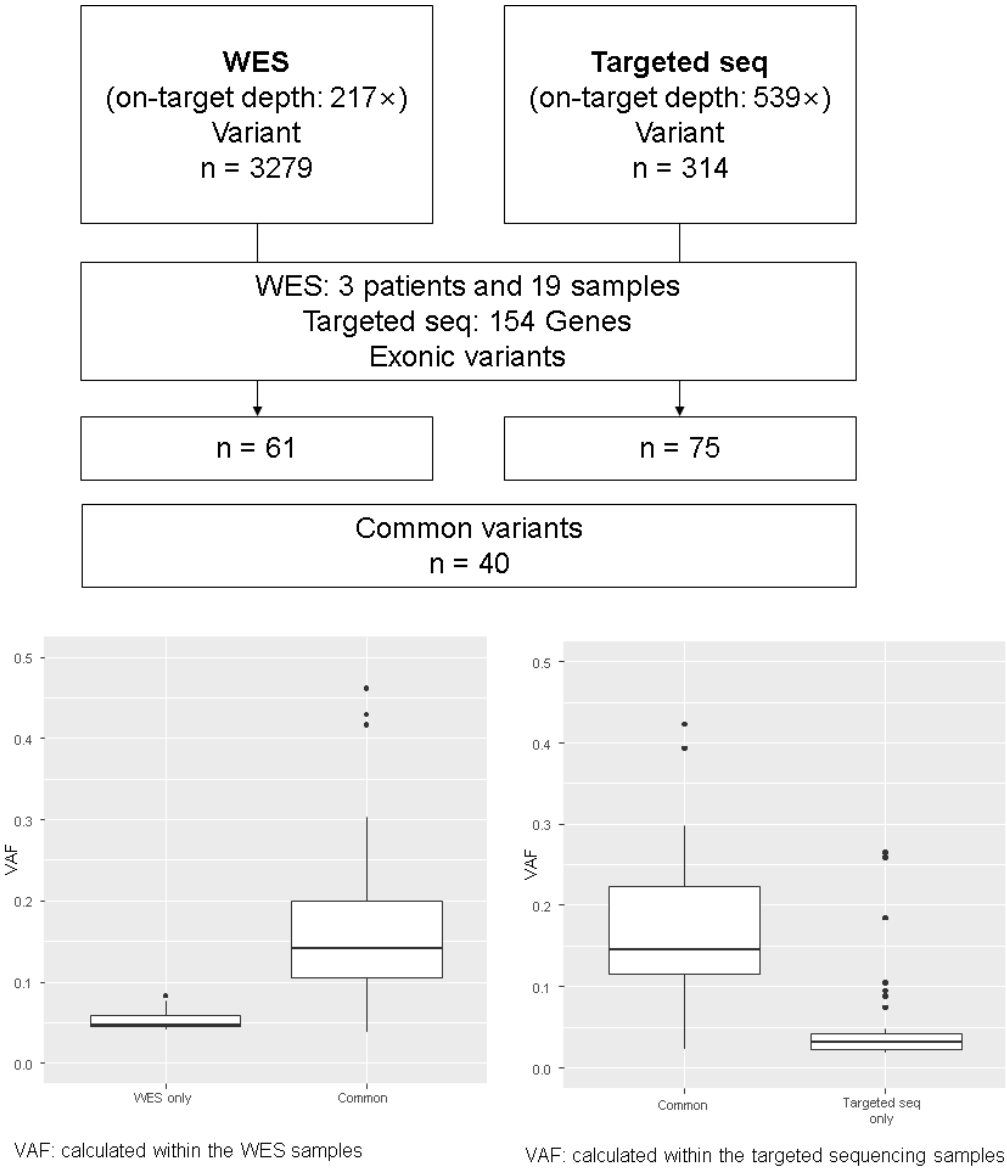

S18 Fig. Comparison of whole exome and targeted sequencing results. The boxes represent variant allele frequency (VAF), the line and whiskers represent the median and 1.5 times interquartile range, respectively. WES, whole exome sequencing. We used 75 variants identified in the targeted sequencing results (case) and 75 randomly chosen loci (control) as the gold standard. The cutoff of tumour VAF > 2% and normal VAF < 0.5% or tumour VAF > 4% and normal VAF < 1% resulted in 9,482 mutations with a sensitivity of 65% and positive predictive value of 100%. The cutoff tumour VAF > 4% and normal VAF < 1% resulted in 3,279 mutations with a sensitivity of 57% and positive predictive value of 100%.