**Whole-exome sequencing and germline variant analyses**

Germline DNA exomes were captured by using the TruSeq DNA exome kit (Illumina, CA, USA). Paired-end sequencing reads were mapped to the human reference genome (GRCh38) with Parabricks software, a graphics processing unit—accelerated bwa-like mapping application. Germline single-nucleotide variations/indels were identified by following the GATK best practice for quality score calibration and indel realignment.1,2 Detected variants were annotated by using ANNOVAR.3 Mutations in *SMARCB1* were visually reviewed with IGV to ensure good support with read count and read quality. Germline copy number variants (CNVs) were detected by CNVkit and cn.MOPS.4,5 Detected CNVs were intersected with protein coding gene annotation using bedtools and visually inspected for coverage and supporting reads to ensure good quality.6

**References**

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