Whole-exome sequencing analysis

The peripheral blood was sent to CIPHER GENE to perform the whole exome sequencing by Illumina HiSeq. The raw data were converted into a.fastq file through bcl2fastq and reads were aligned to the Human Reference genome (GRCh38/hg38) using the BWA ,Samtools and Picard software. The Genome Analysis Toolkit (GATK) was used to remove the repeated sequence and detected the mutation. ANNOVAR was then used for variant annotation[1,2]. The principles of screening pathogenic mutation sites: (1)Variants located in the exonic region and the non-synonymous mutation sites were screened; (2) The variant site that Normal individuals do not carriage or the carriage rate less than 5% were identifited through ExAC_EAS, ExAC_ALL, 1000Genomes and gnomAD databases; (3) The pathogenic variant sites were evaluated with reference to dbSNP, OMIM, HGMD, ClinVar and other databases; and (4) The SIFT, Polyphen2, LRT, MutationTaster, FATHMM and other protein function prediction software were used to predict protein function caused by gene variation. The pathogenic variants were screened according to the ACMG classification guidelines and the clinical phenotype of the patients. All of the potential disease-causing variants that were identified genome wide were confirmed by Sanger sequencing.

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2 **Hall G,** Gbadegesin RA, Lavin P, Wu G, Liu Y, Oh EC, Wang L, Spurney RF, Eckel J, Lindsey T, Homstad A, Malone AF, Phelan PJ, Shaw A, Howell DN, Conlon PJ, Katsanis N, Winn MP. A novel missense mutation of Wilms' Tumor 1 causes autosomal dominant FSGS. *J Am Soc Nephrol* 2015; **26:** 831-843 [PMID: 25145932 DOI: 10.1681/ASN.2013101053]