Reviewer #1:Specific Comments to Authors: Dear authors, Your manuscript is interesting and I can accept the publication as case report. Before we can take the final decision, could you confirm the result by using another method?

Answer：Thank you for your suggestion. We are so sorry for that we didn't describe the pathogenic gene verification process in detail in the article.

We first detected the pathogenic mutation in the proband and his parents by Whole Exome Sequencing, and then verified the mutation by Sanger Sequencing in the proband, proband's parents, great grandmother, grandmother's brother and proband's aunt.None of the normal phenotype members had this mutation (proband's father and aunt), and all of the abnormal phenotype members had this mutation , Therefore, this gene locus was identified as a pathogenic site. The CDKN1C gene c.836G>A locus sequencing map has been supplemented in the article.

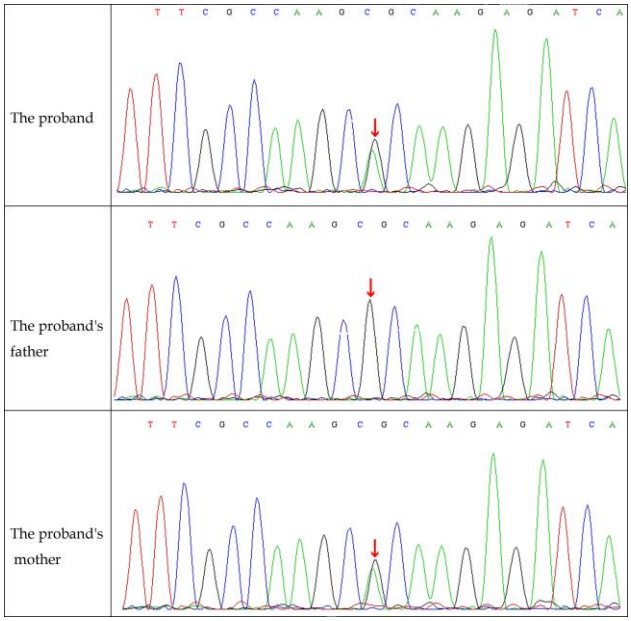

Figure 3 Sequencing map of CDKN1C gene c.836G>A locus.

Reviewer #2: Specific Comments to Authors: Generally, the findings in this case study are important to give us perspectives to explore the relationship between familial SRS and CDKN1C mutations. However, there are too many writing errrors. Overall, it seems necessary to check writing, such as spacing and using signs.

Answer： Thank you very much for your advice. As a non-native English speaker, there are indeed many problems in English writing. We have asked professionals to polish and modify it to avoid related mistakes again.