

**Table S2. The pathogenity prediction of novel variants identified in this study**

<b>Variant</b>	<b>PROVEAN</b>	<b>SIFT</b>	<b>Polyphen-2</b>	<b>MutationTaster</b>	<b>MutationAccessor</b>	<b>FATHMM</b>
<i>KCNJ11</i> : c.53C>G	N	T	D	D	L	D
<i>ABCC8</i> : c.752G>A	D	D	D	D	M	D
<i>ABCC8</i> : c.1399A>T	N	T	D	D	M	D

N, neutral; T, Tolerated; L, Low. All of them indicate that this variant might be benign.

D, damaging or deleterious; M, medium. Both of them indicate that this variant might be pathogenic.