

**Table S1. Mean coverage (read depth) of genes by various NGS methods**

<b>Mean coverage (read depth) of NGS methods</b>				
<b>Gene</b>	<b>Panel: Raindance (multiplex PCR)</b>	<b>Panel: Capture</b>	<b>WES V1 (SS V4)</b>	<b>WES V2 (CRE)</b>
<i>CDKL5</i>	640	1,070	131	166
<i>PCDH19</i>	1,020	930	176	153
<i>SCN2A</i>	1,140	1,170	102	215
<i>SCN1A</i>	1,280	1,200	99	208
<i>GABRA1</i>	670	1,430	109	190
<i>GRIN2B</i>	N/A	1,350	160	163
<i>GABRG2</i>	630	1,460	114	248
<i>MECP2</i>	2,020	880	182	154
<i>KCNQ2</i>	1,090	1,150	91	81

*CRE, Clinical Research Exome; SS V4, SureSelect Human All Exon V4.*