Supplemental Figure 1. Visualized NGS results using Integrative Genomics Viewer (KCNJ5 gene)

The coverage track displays the depth of reads as a gray bar chart. Integrative genomics viewer colors the bar where potential genetic alteration exists in proportion to the read count of each base (red, T; blue, C; green, A). In alignment track, read bases that match the reference are displayed in gray. Read bases that do not match are colored. B2T1, CYP11B2 positive tumor specimen 1; T1, CYP11B2 negative tumor specimen 1; Refseq, reference sequence.