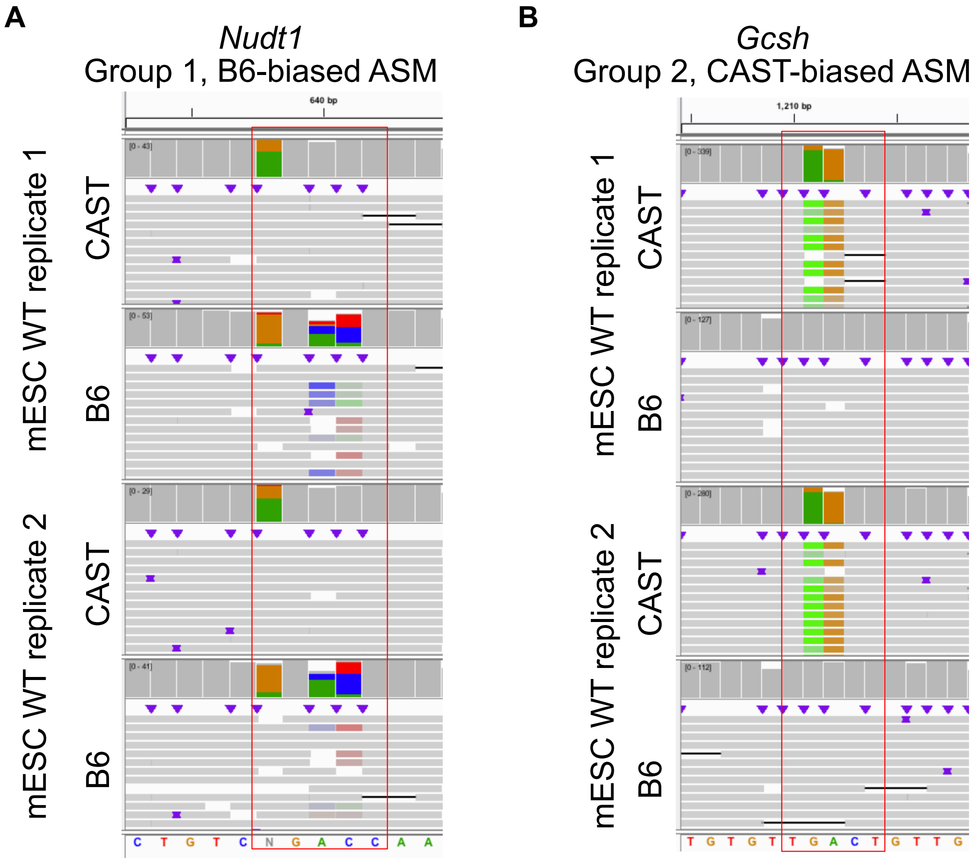

Supplemental Figure. 6 | Visual detection of ASM from long-read sequencing

Visualizing base-calling errors in the Integrated Genome Viewer browser confirm the presence of ASM sites. A) Nudt1 was identified as B6-biased ASM, showing a high-error rate in reads from B6 allele. B) Gcsh, classified under Group 2 CAST-biased ASM, demonstrates a high frequent error on reads from CAST allele. The red box represents the DRACH motif.