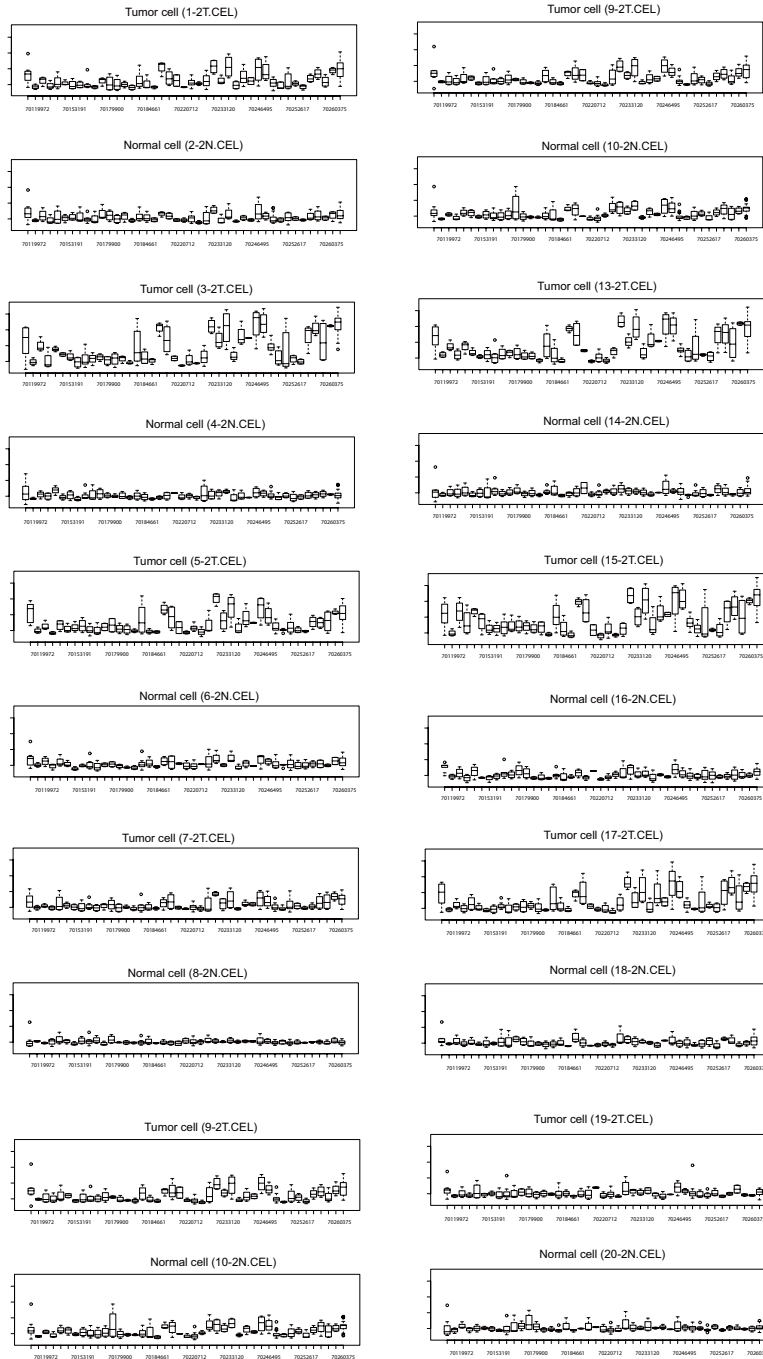


# Supplementary Figure S3:

Yoshida et al. A Statistical Framework for Genome-Wide Discovery of Biomarker Splice Variations with GeneChip Human Exon 1.0 ST Arrays



Exon expression patterns of LGR5 between normal and tumor cells across the 20 individuals. In each panel, the CEL file ID are indexed at the head. For the corresponding patient ID, refer Supplementary Table S1. The vertical axis shows the log-scaled probe intensities and the horizontal corresponds to the exonic regions which are pre-designed by the exon array system.