



Figure S1. Whole Exome Sequencing (WES) of primary tumor tissue, standard PDOs, and PDO-derived single-cells from the same GAd patient demonstrates maintenance of genomic integrity in these in vitro models. a) Visualization of copy number variation (CNV) estimated by SNV allelic depth across the genome and depicted in denoised copy ratio plot segment. Individual targets display as points on the plot. Different copy ratio segments are indicated by alternating blue and orange color groups. The denoised median is drawn in thick black. T, primary tumor tissue; O, standard PDOs; S, PDO single-cells. b) Major tumor-related gene alterations (insertion, deletion, and SNP mutation) are similar across the three paired samples from the same patient.