Figure S1 Whole genome sequencing data for samples previously reported by GeT-RM to have more than two gene copies of *GSTT1* (*GSTT1*AxN*). Panels display Stargazer's result for copy number analysis for individual samples (N=8). Genotypes from GeT-RM and Stargazer (abbreviated as "G" and "S" for brevity) are also shown, with "()" indicating non-consensus genotypes. Grey dots in each panel indicate the sample's copy number estimates computed from read depth. The navy solid line and the cyan dashed line represent copy number profiles for each haplotype. Thick colored lines represent copy number profiles for different genes for both haplotypes combined. Each panel contains gene names and scaled gene models, in which exons and introns are depicted with colored boxes and black lines, respectively. Reports in the Database of Genomic Variants supported Stargazer's gene deletion calls in NA18519, NA18861, NA19095, and NA19920.