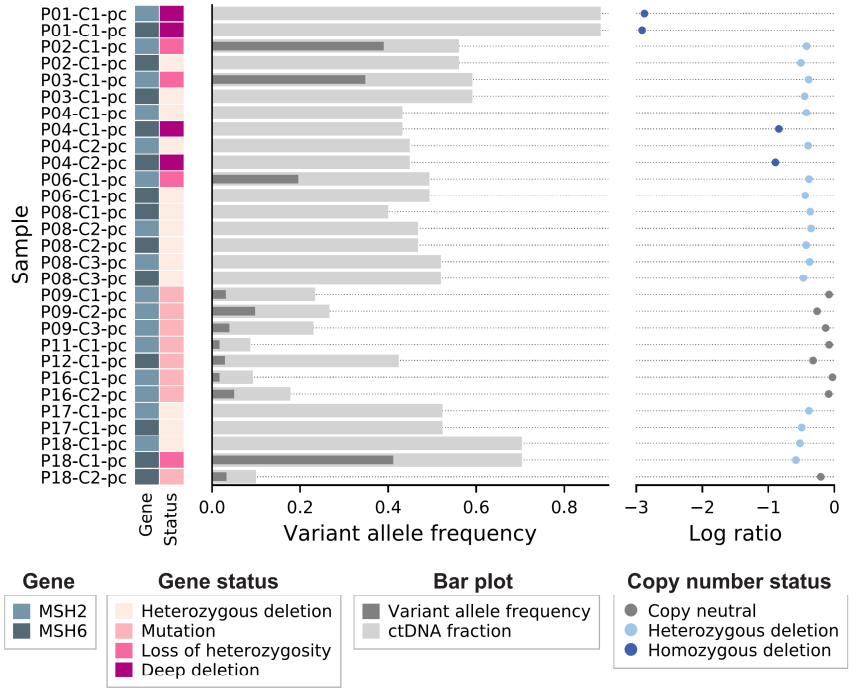

Supplementary Figure 4. Evidence for loss of heterozygosity across mismatch repair genes *MSH2* and *MSH6*. Bar plot (center) depicts both the ctDNA fraction and variant allele frequency of each identified mutation (in-set and coloured in dark gray) per patient sample. Scatter plot (right) represents the median coverage log ratio for each gene per sample, coloured according to copy-number state. Flanking matrix (left) provides gene labels and classification of gene status.