SUPPLEMENTARY MATERIALS: Titles of Tables and Figures

Performance characteristics of next generation sequencing in clinical mutation detection of colorectal cancers

Haley et al.

Supplementary Tables S1-S4

Supplementary Figures S1-S8

Supplementary Table S1. 310 specimens from 305 tumors of 301 patients with colorectal cancers

Supplementary Table S2. 310 specimens with colorectal cancers.

Supplementary Table S3. Mutant allele frequency of positive control specimens (mean + SD).

Supplementary Table S4. Reportable ranges and reference ranges of colorectal cancer panel.

Supplementary Figure S1. Distribution of *KRAS* mutations, including 3 uncommon mutations (p.G15S [c.43G>A], p.Q22K [c.64C>A] and p.K147N [c.441G>C]).

Supplementary Figure S2. Distribution of *PIK3CA* mutations.

Supplementary Figure S3. Specimens with less than 20% tumor cellularity: challenges posted to molecular diagnosis

Supplementary Figure S4. Intra-tumor heterogeneity of *KRAS* mutation.

Supplementary Figure S5. Presence of concomitant *NRAS* and *PIK3CA* mutations in different tumor subpopulations.

Supplementary Figure S6. Concomitant mutations of different genes.

Supplementary Figure S7. Correlation of mutant allele frequencies in tumors with two mutations within the same gene.

Supplementary Figure S8. SNP array analysis of case 54.