Supplementary Material

Supplementary Table 1. MSI status in CRC.

| MSI state | n | Bat26 | Bat25 | D5S346 | D2S123 | D17S250 |
|-----------|---|-------|-------|--------|--------|---------|
| MSI-H     | 11| +     | +     | -      | -      | -       |
| 2         | + | +     | +     | -      | -      | -       |
| 3         | + | +     | -     | +      | -      | -       |
| 5         | + | +     | -     | +      | +      | +       |
| 2         | + | +     | -     | -      | +      | -       |
| 3         | + | +     | -     | -      | +      | -       |
| MSI-L     | 1 | -     | +     | -      | -      | -       |
| MSS       | 173| -    | -     | -      | -      | -       |
**Supplementary Table 2.** *KRAS* mutations in CRC.

| Detected region | Mutation | Base change | Mutation cases | Mutation rate (%) |
|-----------------|----------|-------------|----------------|-------------------|
| Codon 12        | G12D     | 35G > A     | 33             | 41.25             |
|                 | G12V     | 35G > T     | 18             | 22.50             |
|                 | G12A     | 35G > C     | 7              | 8.75              |
|                 | G12C     | 34G > T     | 4              | 5.00              |
|                 | G12S     | 34G > A     | 3              | 3.75              |
| Codon 13        | G13D     | 38G > A     | 15             | 18.75             |

CRC, colorectal cancer
Supplement figure 1. The gold standard for MSI testing recommended by the National Cancer Institute is using polymerase chain reaction to detect MSI markers (BAT25, BAT26, D2S123, D5S346, and D17S250). High-frequency microsatellite instability (MSI-H) with two or more genes showing instability; low-frequency microsatellite instability (MSI-L) with only one locus showing genetic deletion; microsatellite stable (MSS) CRC with no gene loss. (A–F) MSI-H; (G) MSI-L; (H) MSS.
Supplement figure 2. (A) KRAS mutation type; (B) KRAS wild type. The blue line represents GAPDH as a reference gene, whereas the red line representing the *KRAS* mutation curve.