## **Description of Additional Supplementary Files**

File Name: Supplementary Data 1

**Description**: Sequencing error of LoopSeq and Illumina on ERCC sample. S1A: Sequencing error per site. S1B: Pearson correlation comparing LoopSeq and Illumina sequencing error.

File Name: Supplementary Data 2

**Description**: Target sequence selection.

File Name: Supplementary Data 3

**Description**: Gene short-read count.

File Name: Supplementary Data 4

**Description**: Differentially expressed genes.

File Name: Supplementary Data 5

**Description**: Differentially expressed isoforms.

File Name: Supplementary Data 6

**Description**: Differentially expressed genes and isoforms.

File Name: Supplementary Data 7

**Description**: Total SNVs identified in colon cancer samples.

File Name: Supplementary Data 8

**Description**: Unevenly distributed SNV isoforms within a gene.

File Name: Supplementary Data 9

**Description**: Differential expression of SNV isoforms compared with wild type counterparts.

File Name: Supplementary Data 10

**Description**: SNV isoform validation via targeted RNA sequencing. S10A: Gene FAM104A.

S10B: Gene PABPC1.

File Name: Supplementary Data 11

**Description**: Switching SNV isoforms between tumor and metastasis.

File Name: Supplementary Data 12

**Description**: Colon cancer related mutations/SNVs.

File Name: Supplementary Data 13

**Description**: Supporting reads for novel fusion detection. S13A: Summary table. S13B: STAMBPL1 - FAS (1M). S13C: STAMBPL1 - FAS (2M). S13D: SMYD3 - ZNF124 (3L). S13E:

ECHDC1 - PTPRK (3T). S13F: ECHDC1 - PTPRK (3L).

File Name: Supplementary Data 14

**Description**: LoopSeq targeted sequencing on-target rate.

File Name: Supplementary Data 15

**Description**: Primers and probes design.