Figure S3. **(A** and **B)** Quantification (A) and percentages of types (B) of somatic SVs detected by long-read sequencing in each sample. Insertions were the dominated SVs in MSI-H samples. (**C** and **D**) Quantification (C) and percentages of types (D) of somatic SVs detected by long-read sequencing in each sample after the exclusion of insertions in STR regions. The X-axes in each graph represent the sample IDs.