MF (×10⁻⁵) deletion / insertion

```
CTAAAACCAG   GAGCTATTTA   ATGGCAACAG   TTAACCAGCT   GGTACGCAAA   CCACGTGCTC   40
                 SD
      0/0.23      0.02/0                                   4.4/0.37
GCAAAGTTGC   GAAAAGCAAC   GTGCCTGCGC   TGGAAGCATG   CCCGCAAAAA   CGTGGCGTAT   100
      0/0.21      0.11/0          16.76/1.45             11.09/0.3
GTACTCGTGT   ATATACTACC   ACTCCTAAAA   AACCGAACTC   CGCGCTGCGT   AAAGTATGCC   160
                            37.76/2.35   0.22/0
GTGTTCGTCT   GACTAACGGT   TTCGAAGTGA   CTTCCTACAT   CGGTGGTGAA   GGTCACAACC   220
                                                        0/0.09
TGCAGGAGCA   CTCCGTGATC   CTGATCCGTG   GCGGTCGTGT   TAAAGACCTC   CCGGGTGTTC   280
GTTACCACAC   CGTACGTGGT   GCGCTTGACT   GCTCCGGCGT   TAAAGACCGT   AAGCAGGCTC   340
GTTCCAAGTA   TGGCGTGAAG   CGTCCTAAGG   CTTAA                                  375
```
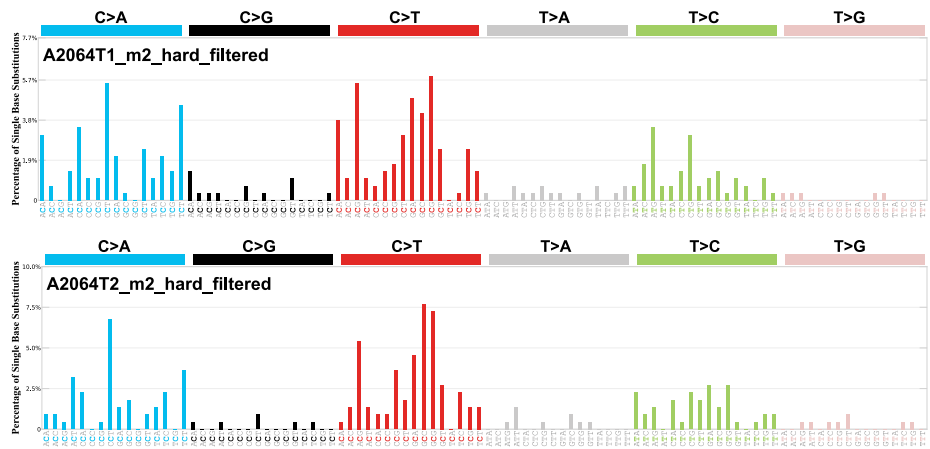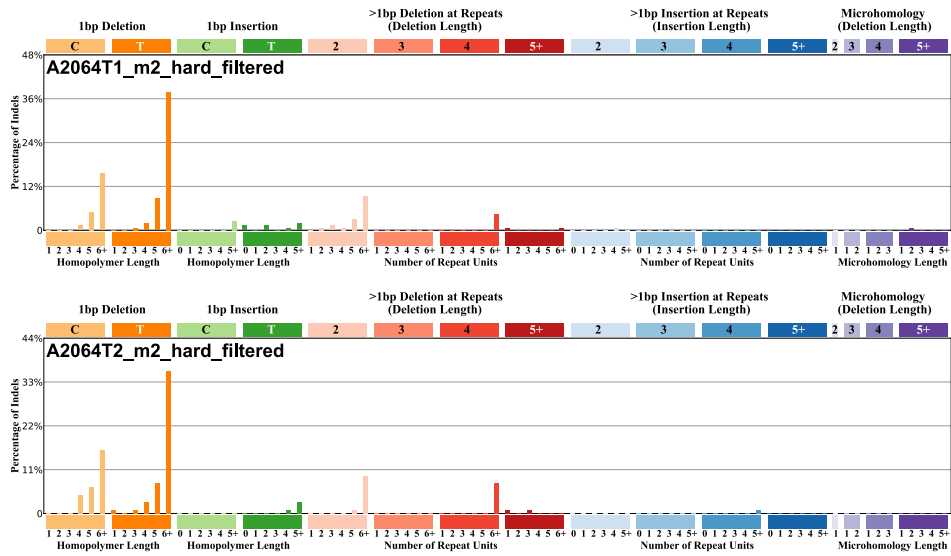
Supplemental Figure S1. Hotspots of adenine 1-indel mutations in the *rpsL* gene

The mutation frequency (MF) of adenine 1-indel was calculated and mapped onto the *rpsL* coding sequence. The MF of deletion (left) and insertion (right) at each locus is indicated as deletion/insertion within colored panels. blue: control mice, bule: KBrO₃-treated mice. SD: Shine-Dalgarno sequence. Squares indicate start and stop codons. Mononucleotide adenine repeat sequences [(A)ₙ] are highlighted in magenta. The (A)₆ site emerged as the most frequent hotspot for adenine 1-indel mutations, followed by the (A)₅ site.

Supplemental Fig S2. Mutational profiles in *Msh2*^{−/−} tumor

Mutational profiles based on tumor-specific variants identified using WES of tumors. Two tumors were isolated from a *Msh2*^{−/−} mouse treated with 0.15% KBrO₃. (A) SBS signature. (B) ID signature.