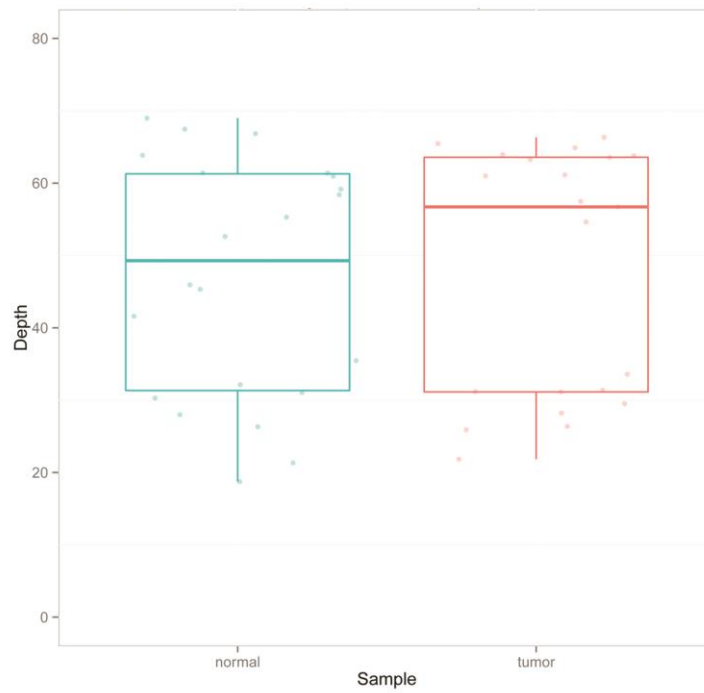


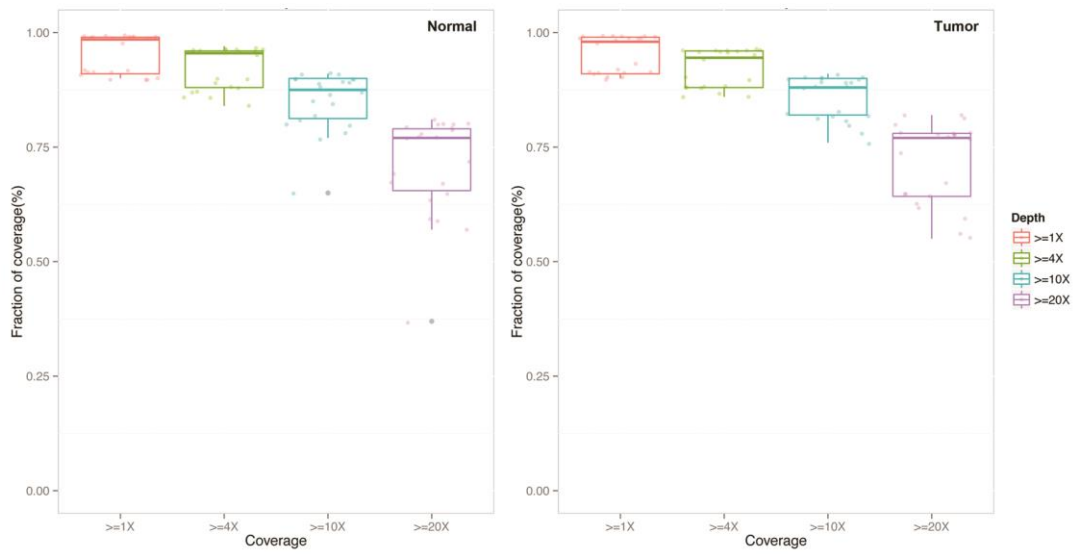
## Supplementary Figure Legends

**Fig. S1** Box-plots demonstrating the (A) depth and (B) coverage of exome sequencing of tumor and blood DNA in 22 CRC patients

**A**



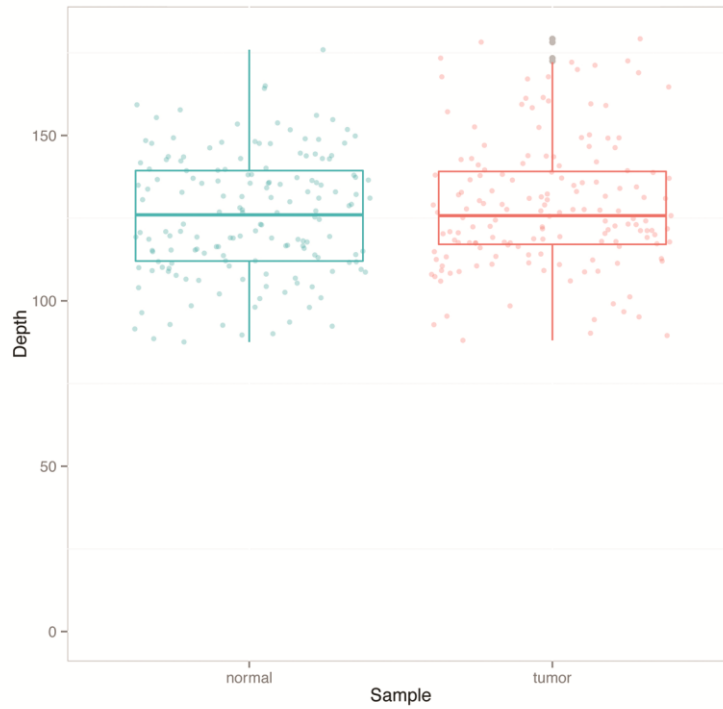
**B**



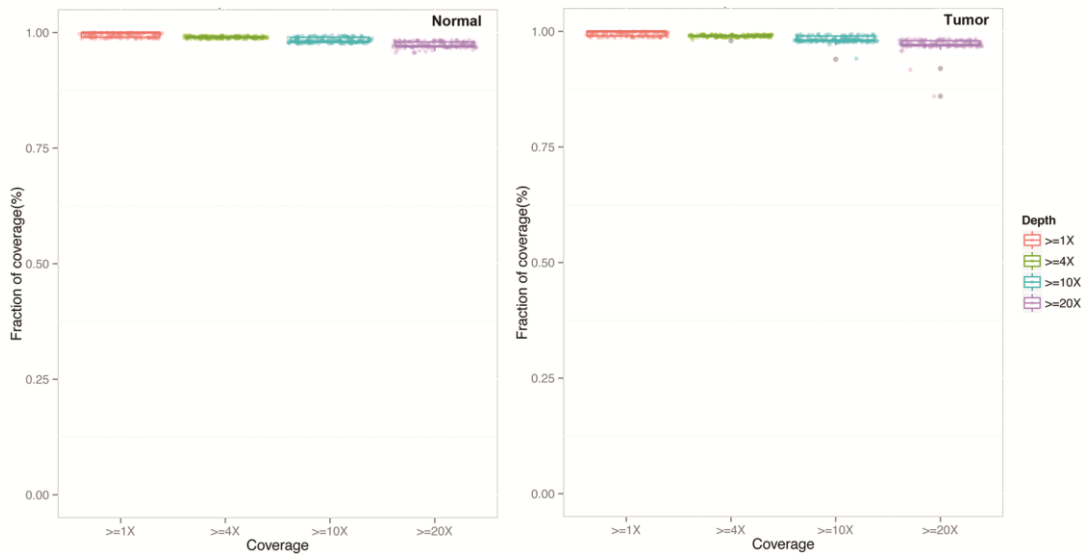
**Fig. S1**

**Fig. S2** Box-plots demonstrating the (A) depth and (B) coverage of targeted capture sequencing of 187 genes in 160 CRC patients

**A**

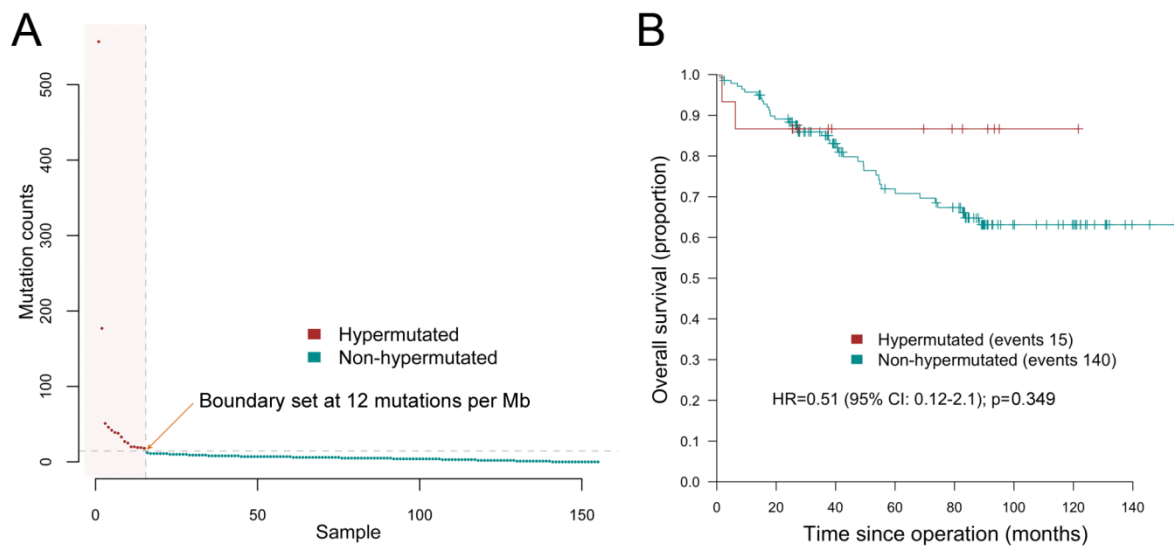


**B**



**Fig. S2**

**Fig. S3** Identification of hypermutated tumors based on somatic mutation rate in 160 capture-sequenced CRC patients. **A**, Distribution of the number of mutations identified in the target region among 160 CRC patients. **B**, Patients with hypermutated tumors showed a trend of better overall survival.



**Fig. S3**

**Fig. S4** Survival analysis of five-gene signature in different molecular subgroups of CRC patients, namely (A) MSS (Asian cohort), (B) MSI-low/high (Asian cohort), (C) *KRAS* wild-type (Asian cohort), (D) *KRAS* mutant (Asian cohort) and (E) MSS (TCGA cohort).

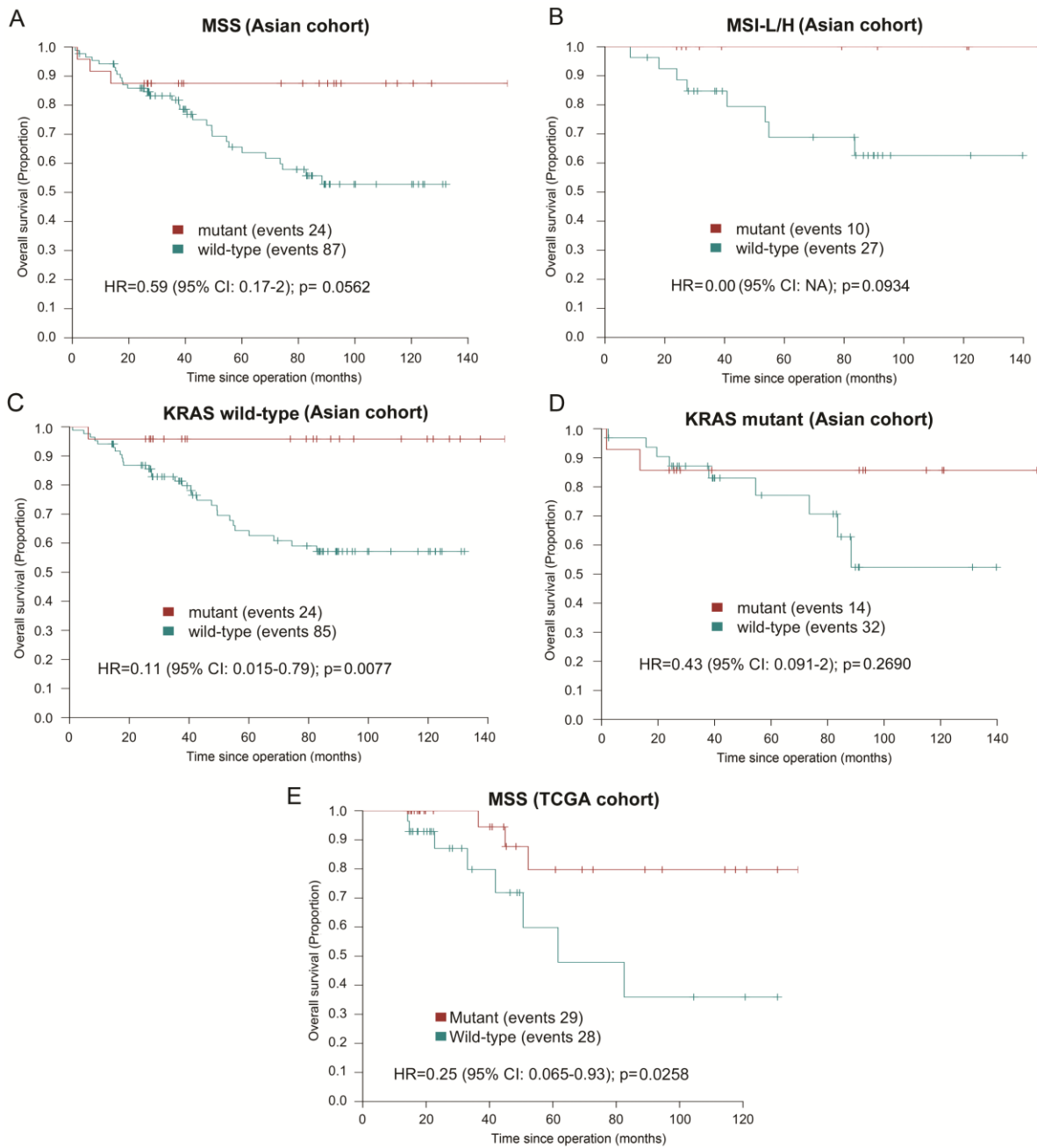


Fig. S4