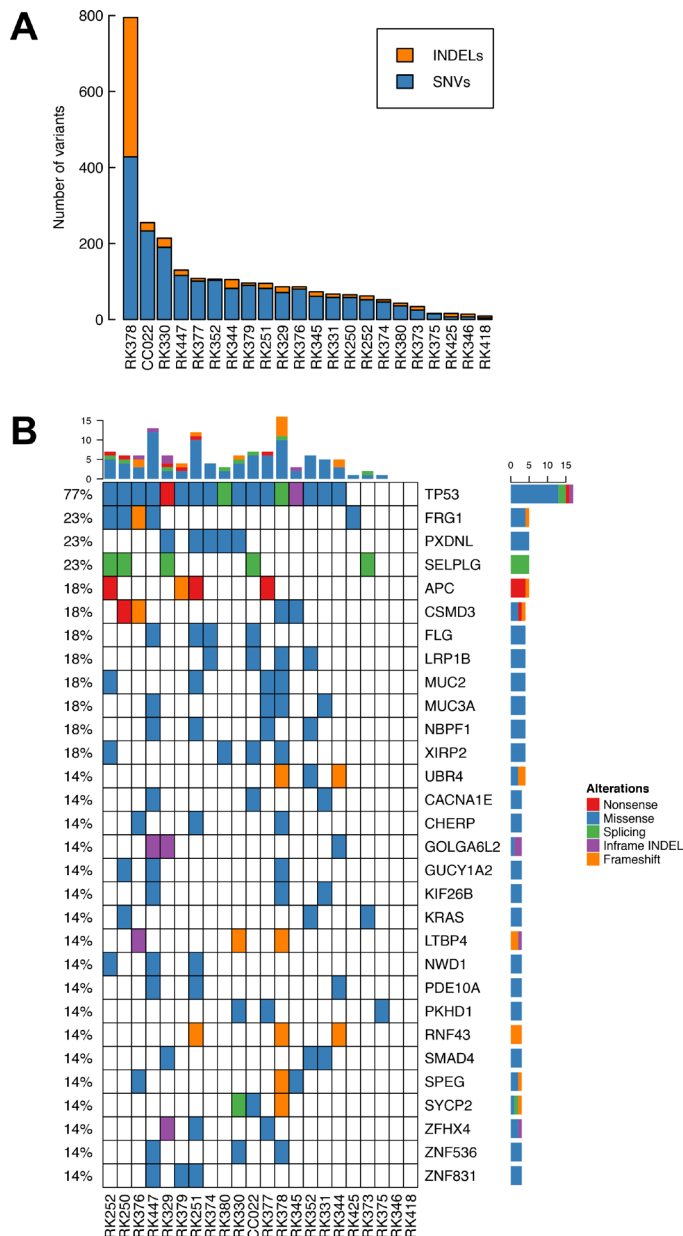
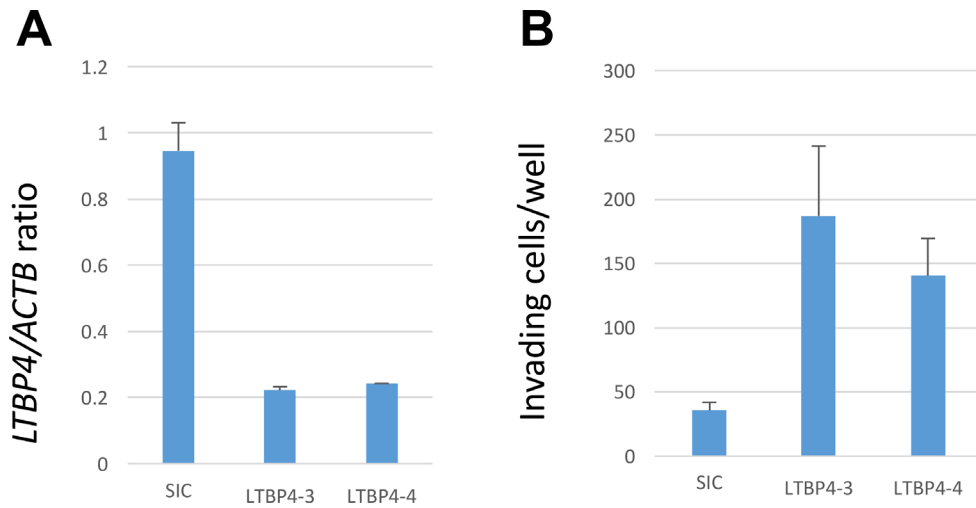


Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling

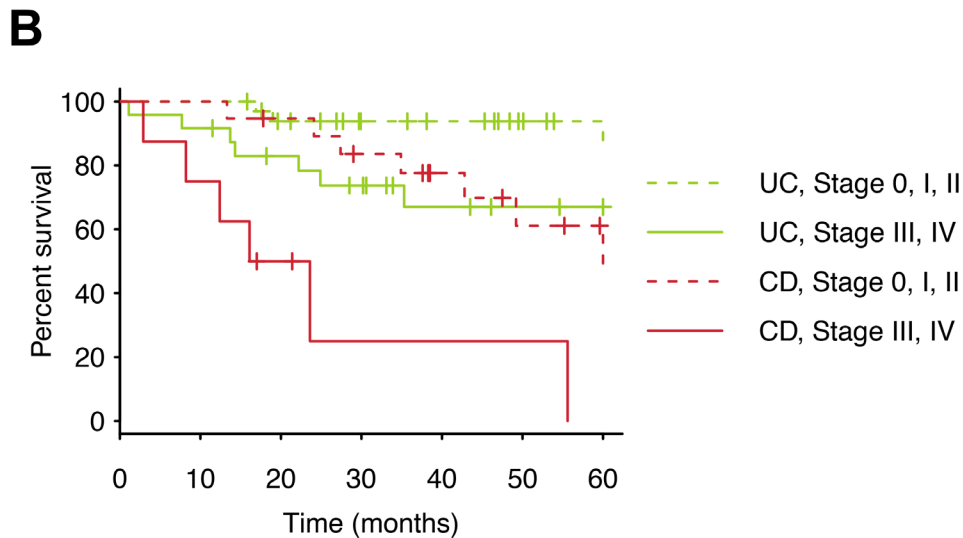
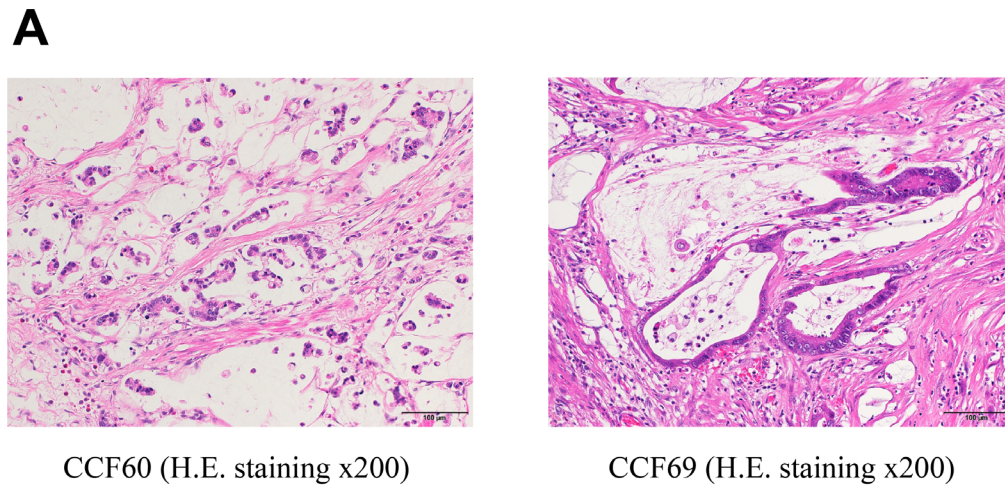
SUPPLEMENTARY MATERIALS



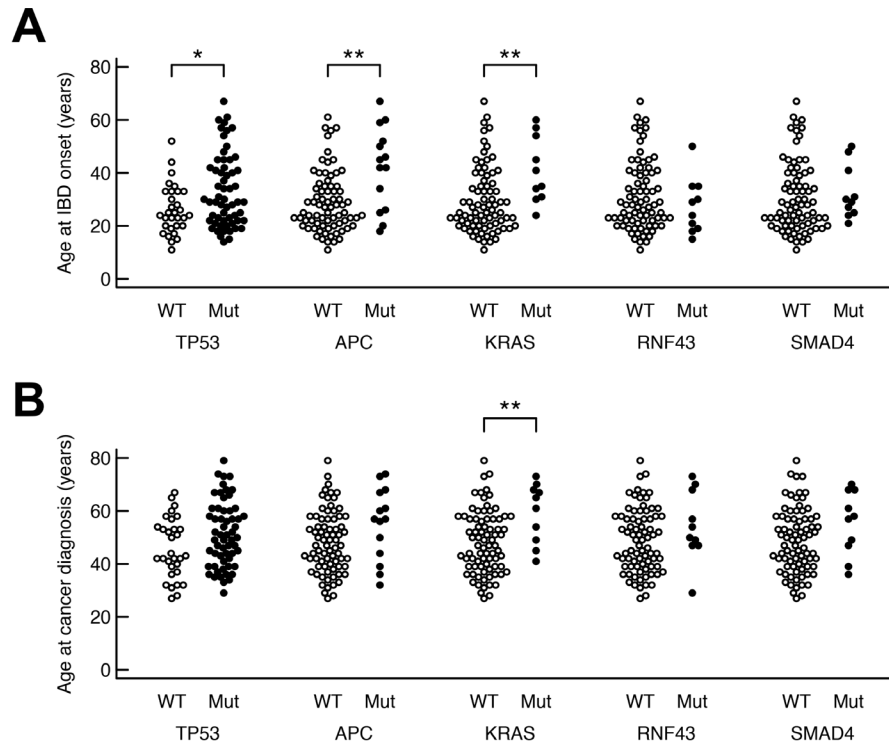
Supplementary Figure 1: Mutations in the whole-exome sequencing of 22 UC-associated cancers. (A) Number of somatic mutations. (B) Recurrently mutated genes. Genes that were mutated in more than 2 patients and had mutation rate of >10/Mbp were shown.



Supplementary Figure 2: Silencing *LTBP4* promoted invasion of SW480 colon cancer cell line. (A) Efficacy of *LTBP4* silencing as measured by quantitative RT-PCR. **(B)** Invasiveness of *LTBP4*-silenced cells.



Supplementary Figure 3: Unique features of CD-CAC. (A) Mucinous carcinoma arising in anal canal and hemorrhoid fistula in Japanese Crohn's disease. CCF60 (H.E. staining $\times 200$) and CCF69 (H.E. staining $\times 200$). **(B)** Overall survival of CAC patients. Patients were grouped as follows: UC, stage 0, I, II ($n = 34$); UC, stage III, IV ($n = 24$); CD, stage 0, I, II ($n = 19$); CD, stage III, IV ($n = 8$).



Supplementary Figure 4: Association of mutations and timeline of disease in 90 CACs. (A) Mutations and the age at IBD onset. (B) Mutations and the age at cancer diagnosis. ***p*-value < 0.01; **p*-value < 0.05 using Wilcoxon rank sum test.

Supplementary Table 1: Clinico-pathological features of the colitis-associated cancers (CACs). See Supplementary_Table_1

Supplementary Table 2: Sequence information of siRNAs

Duplex name	Sense	Antisense
LTBP4-3	5'-CUCCUUUGCCUGUACUUGUdTdT-3'	5'-ACAAGUACAGGCAAAGGAGdTdT-3'
LTBP4-4	5'-CAGACUUAGGUCCACCUUAdTdT-3'	5'-UAAGGUGGACCUAAGUCUGdTdT-3'

Supplementary Table 3: Summary of exome sequencing of 22 CACs. See Supplementary_Table_3

Supplementary Table 4: Somatic mutations in the 22 CAC exomes. See Supplementary_Table_4

Supplementary Table 5: Targeted genes for resequencing of the 90 CAC. See Supplementary_Table_5

Supplementary Table 6: Sequencing metrics in the targeted resequencing of 90 CACs. See Supplementary_Table_6

Supplementary Table 7: Mutations in the targeted resequencing of 90 CACs. See Supplementary_Table_7