Whole-exome sequencing identified mutational profiles of high-grade colon adenomas

SUPPLEMENTARY TABLES AND FIGURES

Supplementary Table 1: The description of whole-exome sequencing data

Samples*	Sequencing reads	Mapped reads (%)	Mapped reads in exon (%)	Coverage (mean)**	% of bases (>= 20 reads)**
HGCA 1N	71,790,807	70,664,617 (98.4%)	49,550,187 (69.0%)	85.0	94.4%
HGCA 1T	81,856,114	80,842,075 (98.8%)	60,763,865 (74.2%)	104.1	95.9%
HGCA 2N	76,800,262	75,839,271 (98.8%)	56,058,266 (73.0%)	95.6	95.0%
HGCA 2T	76,583,998	75,572,118 (98.7%)	54,199,481 (70.8%)	92.5	94.9%
HGCA 3N	78,350,099	77,375,208 (98.8%)	57,096,416 (72.9%)	97.7	94.9%
HGCA 3T	74,600,212	73,699,784 (98.8%)	53,073,976 (71.1%)	90.8	94.5%
HGCA 4N	75,254,402	74,300,376 (98.7%)	53,486,317 (71.1%)	91.0	95.0%
HGCA 4T	79,017,342	78,027,767 (98.8%)	56,450,408 (71.4%)	96.7	95.2%
HGCA 5N	77,129,411	76,205,180 (98.8%)	55,259,347 (71.6%)	94.2	95.3%
HGCA 5T	78,482,455	77,560,553 (98.8%)	56,649,509 (72.2%)	96.4	95.5%
HGCA 6N	77,334,827	76,419,755 (98.8%)	55,115,105 (71.3%)	94.3	94.7%
HGCA 6T	82,322,361	81,478,814 (99.0%)	59,839,243 (72.7%)	101.9	95.5%
HGCA 7N	91,167,035	90,417,108 (99.2%)	66,116,912 (72.5%)	112.8	96.3%
HGCA 7T	88,752,925	87,726,673 (98.8%)	60,046,191 (67.7%)	102.9	95.8%
HGCA 8N	126,637,990	125,869,988 (99.4%)	85,676,904 (72.4%)	149.7	96.9%
HGCA 8T	116,285,070	115,536,400 (99.4%)	78,530,086 (68.0%)	136.7	96.6%
HGCA 9N	130,274,028	129,023,866 (99.0%)	78,725,426 (64.8%)	136.8	96.6%
HGCA 9T	126,229,238	125,485,582 (99.4%)	86,338,226 (72.9%)	150.6	97.1%
HGCA 10N	120,764,798	120,110,578 (99.5%)	83,285,267 (73.4%)	145.8	97.2%
HGCA 10T	111,099,170	110,502,460 (99.5%)	75,574,953 (71.2%)	131.1	96.5%
HGCA 11N	106,510,816	86,796,706 (81.5%)	18,541,263 (31.0%)	30.1	57.3%
HGCA 11T	111,327,540	110,697,002 (99.4%)	78,987,996 (74.9%)	137.8	96.7%
HGCA 12N	108,292,690	91,468,110 (84.5%)	26,500,556 (28.0%)	43.1	76.4%
HGCA 12T	113,953,908	113,662,200 (99.7%)	85,745,276 (80.0%)	149.2	97.1%

*The tumor and matched normal genomes are discriminated with the use of 'T' and 'N', respectively.
**The mean coverage and the % of bases (>= 20 reads) were calculated onto the targeted regions (Agilent SureSelect 50Mb exon).

Supplementary Table 2: A list of somatic mutations identified in 12 high-grade colon adenoma samples by exome sequencing (XLS).

See Supplementary File 1

Supplementary Table 3: Non-silent somatic mutations identified in 12 high-grade colon adenoma samples (XLS).

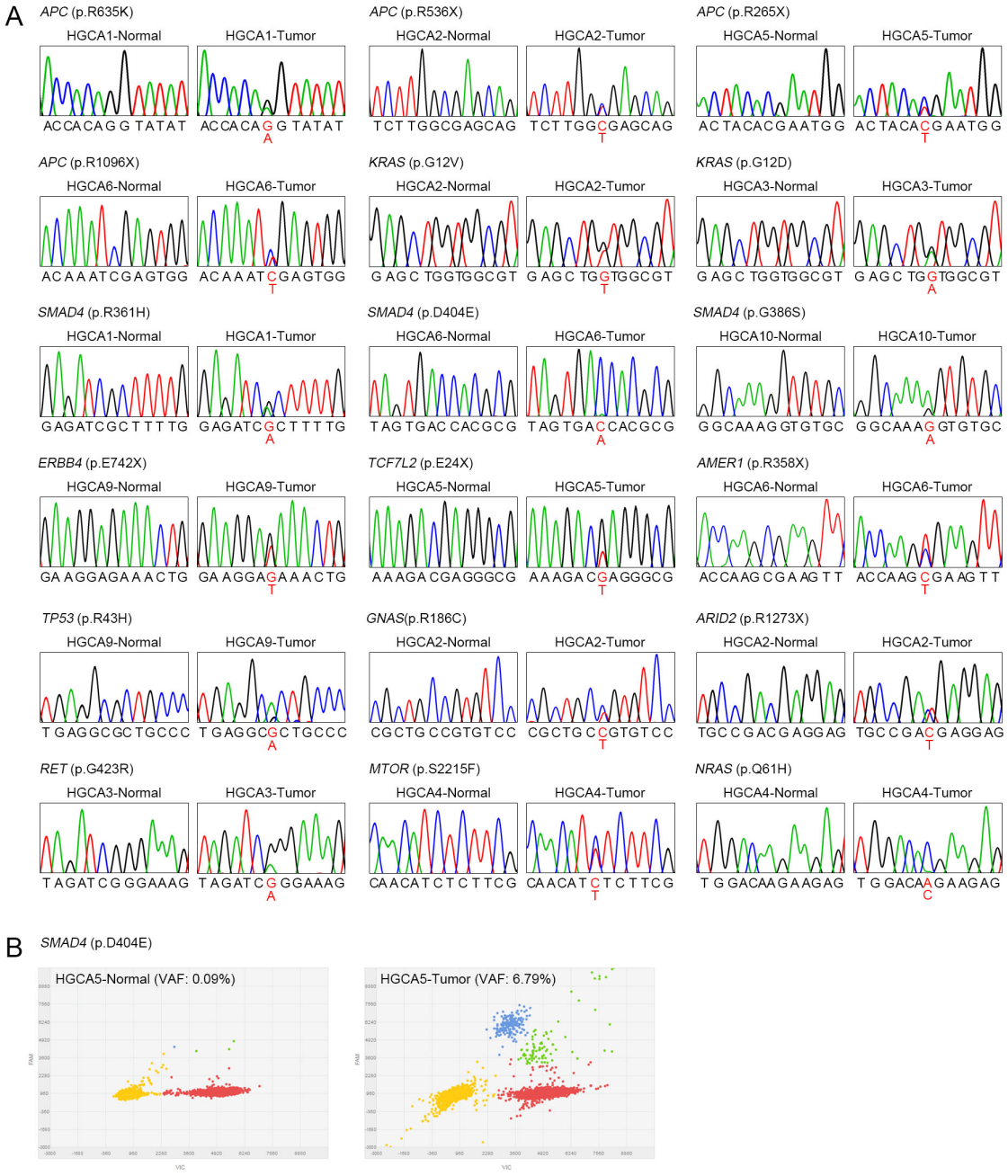
See Supplementary File 2

Supplementary Table 4: Copy number alterations identified across 12 colorectal adenoma samples (XLS).

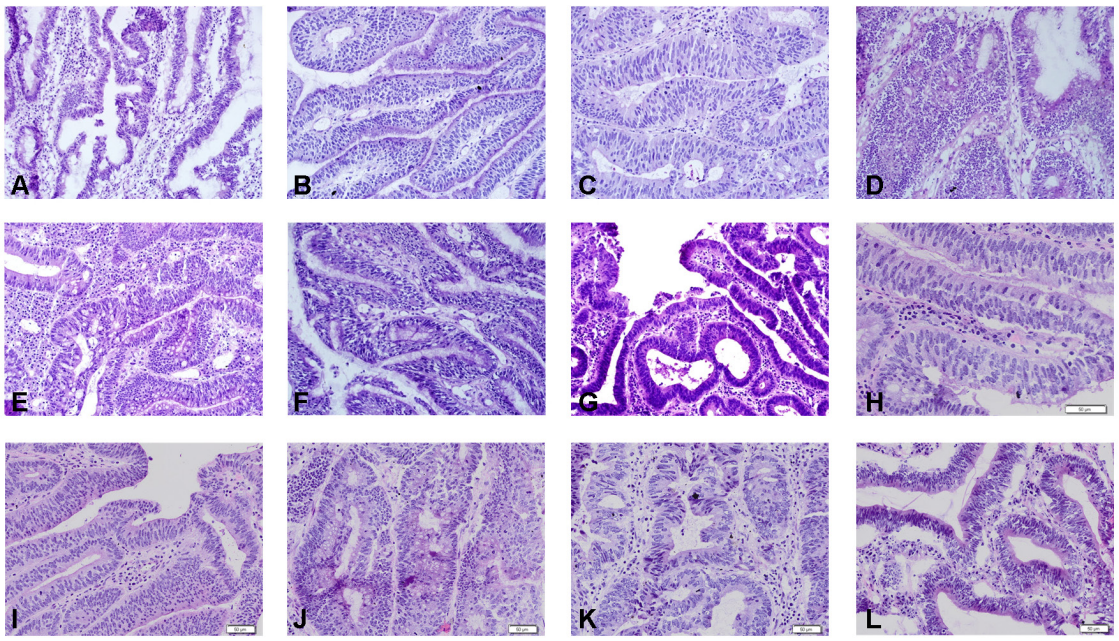
See Supplementary File 3

Supplementary Table 5: Functional annotation and Pathway analysis of somatic mutations using DAVID (XLS).

See Supplementary File 4



Supplementary Figure 1: Validation of mutations identified in the high-grade colon adenoma samples by either Sanger sequencing A. or digital PCR B.



Supplementary Figure 2: Representative figures of the high-grade colon adenoma cases (x200) A. HGCA 1T, B. HGCA 2T, C. HGCA 3T, D. HGCA 4T, E. HGCA 5T, F. HGCA 6T, G. HGCA 7T, H. HGCA 8T, I. HGCA 9T, J. HGCA 10T, K. HGCA 11T, L. HGCA 12T