

Supplementary Figures

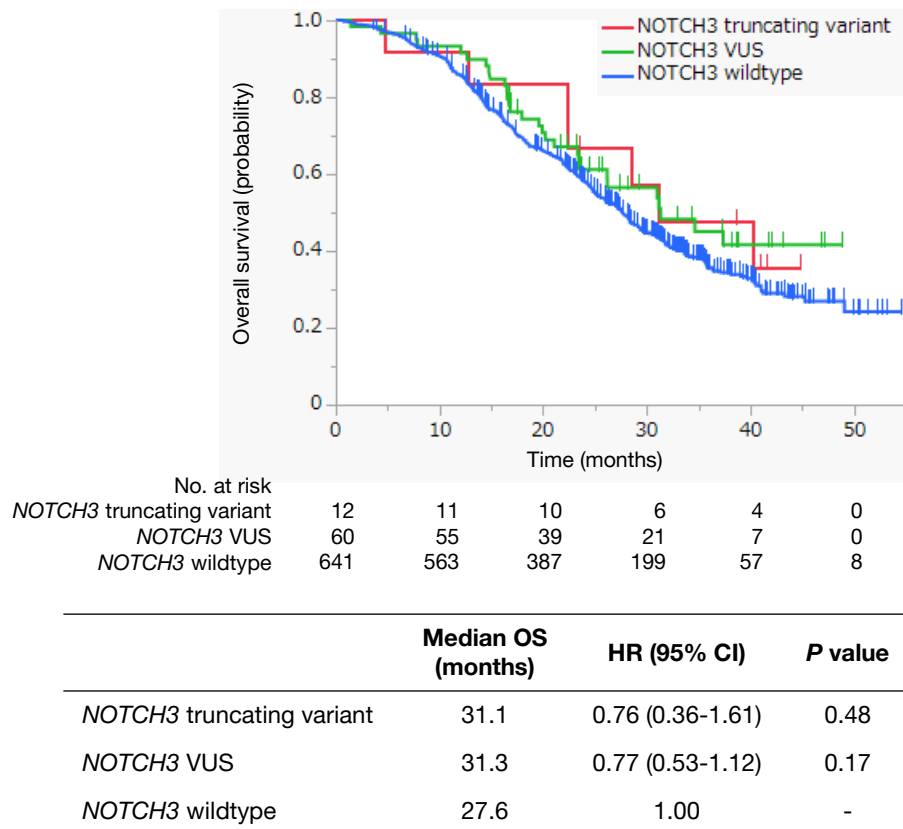
NOTCH gene alterations in metastatic colorectal cancer in the Nationwide Cancer Genome Screening Project in Japan (SCRUM-Japan GI-SCREEN)

Journal of Cancer Research and Clinical Oncology

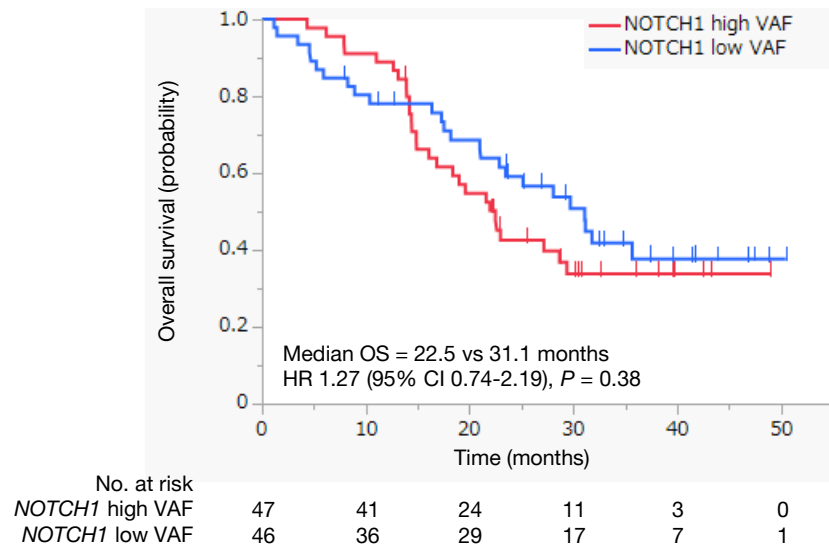
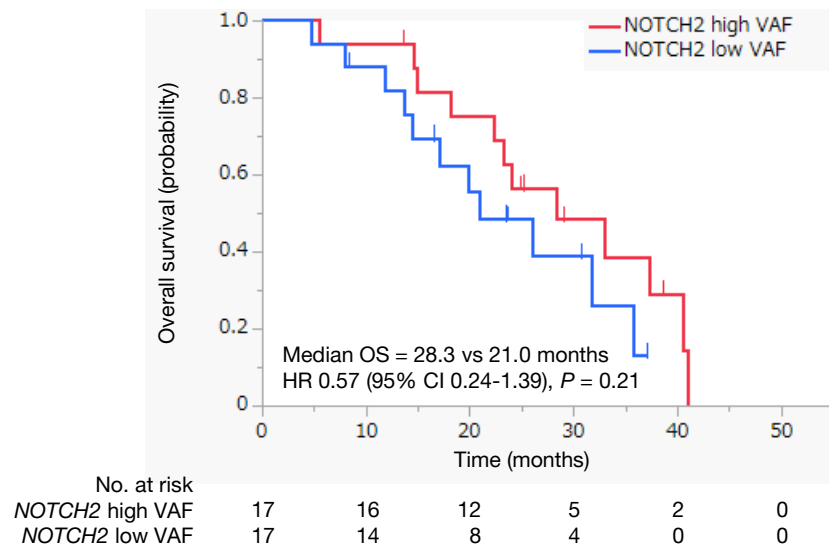
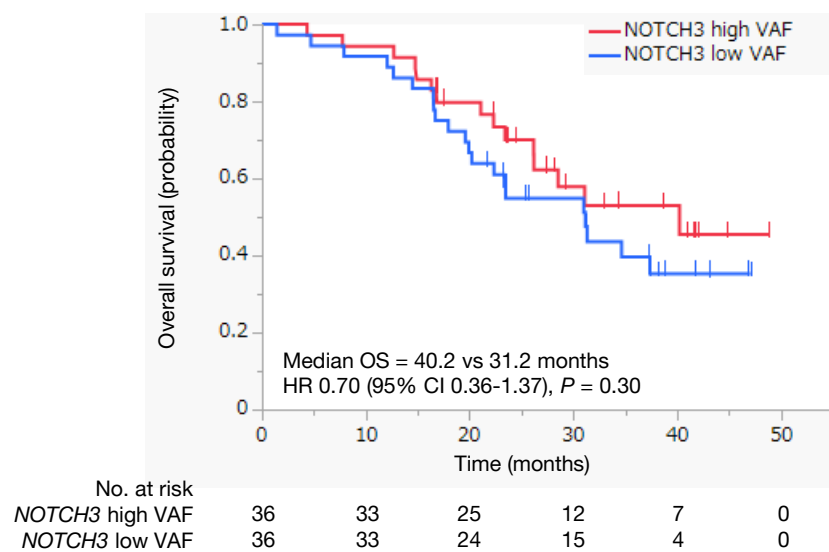
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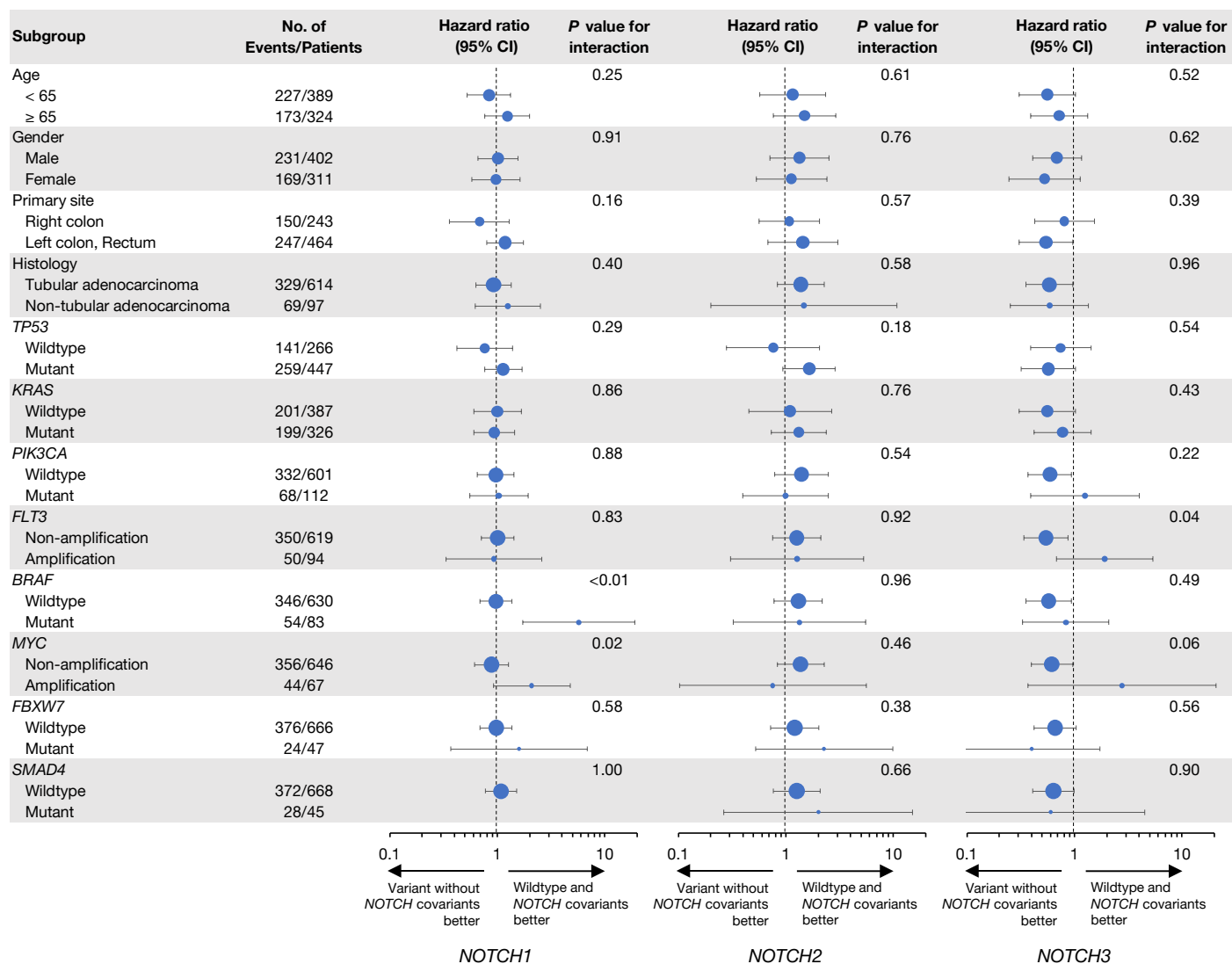


Supplementary Fig. 1 Kaplan-Meier plots of overall survival in patients with *NOTCH3* truncating variants, variants of unknown significance, and wildtype *NOTCH3*. *VUS* variant of unknown significance, *OS* overall survival, *HR* hazard ratio, *CI* confidence interval. *P* values were calculated using the Wald test

a**b****c**

Supplementary Fig. 2 Kaplan-Meier plots of overall survival in patients with high and low variant allele frequencies for **a** *NOTCH1*, **b** *NOTCH2*, and **c** *NOTCH3*. VAF variant allele frequency, OS

overall survival, *HR* hazard ratio, *CI* confidence interval. *P* values were calculated using the log-rank test



Supplementary Fig. 3 Subgroup analyses for overall survival as a function of *NOTCH1*, *NOTCH2*, and *NOTCH3* gene status. *CI* confidence interval. *P* values were calculated using the Wald test