

ASSOCIATION OF SELENOPROTEIN AND SELENIUM PATHWAY GENOTYPES WITH RISK OF COLORECTAL CANCER AND INTERACTION WITH SELENIUM STATUS

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Supplementary Figure S1: Selenium pathway genetic analysis flowchart

1040 tagging SNPs successfully analysed (of 1264) in 154 Selenium (Se) Pathway genes (< 20% missing data) in 1420 colorectal (CRC) cases and 1421 controls

Multivariable unconditional logistic regression

144 SNPs in 63 genes associated with an altered CRC risk ($P < 0.05$)*
(*note before multiple testing corrections)

21 SNPs in 12 of 24 selenoprotein genes (Pathway 1)

19 SNPs in 8 of 17 other Se transport / biosynthesis genes (Pathway 1)

104 SNPs in 43 of 113 wider Se interaction genes (Pathways 2-8)

Similar range of risk associations by sex and colon / rectum sub-site

Significant after multiple testing by Benjamini-Hochberg ($P_{BH} < 0.05$) and P-values adjusted for correlated tests ($P_{ACT} < 0.1$)

Only **TXNRD1** (rs11111979) in Selenoprotein Genes (borderline; $P_{ACT} = 0.1$)

Wider Pathway: SNPs in **SMAD3**, **SMAD7**, **C-MYC** (as found by CRC-GWAS), and also: **BAX**, **BMP2**, **FRZB**