**Supplemental Table 2. Multivariable regression analyses on main effects and interactions of individual SNPs in the four genes that significantly interacted with regular use of NSAIDs on colorectal cancer risk in burden component test at FDR<0.2.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **SNPs** | **Main effect**a |  | **Interaction with NSAID use**a |
|  |  | **Beta** | **SE** | **p-value** |  | **Beta** | **SE** | **p-value** |
| *DPP10* | 2:114609811\_T/C | -0.004 | 0.021 | 0.834 |  | -0.023 | 0.035 | 0.500 |
|  | 2:114713366\_C/A | 0.147 | 0.076 | 0.054 |  | -0.082 | 0.128 | 0.525 |
|  | 2:115712680\_A/G | 0.064 | 0.035 | 0.067 |  | -0.075 | 0.059 | 0.205 |
|  | 2:115917198\_C/A | -0.172 | 0.192 | 0.370 |  | 0.103 | 0.318 | 0.745 |
|  | 2:115917621\_T/C | 0.248 | 0.155 | 0.109 |  | -0.140 | 0.264 | 0.596 |
|  | 2:115929277\_G/A | -0.030 | 0.030 | 0.324 |  | 0.046 | 0.051 | 0.367 |
|  | 2:115929914\_C/T | 0.147 | 0.186 | 0.430 |  | 0.073 | 0.309 | 0.813 |
|  | 2:115936103\_A/C | -0.253 | 0.145 | 0.081 |  | 0.070 | 0.249 | 0.779 |
| *KRT16* | 17:39258773\_A/G | -0.081 | 0.114 | 0.477 |  | -0.062 | 0.182 | 0.733 |
|  | 17:39268784\_G/A | -0.020 | 0.343 | 0.954 |  | 0.276 | 0.656 | 0.674 |
|  | 17:39270180\_G/A | 0.036 | 0.360 | 0.920 |  | -0.085 | 0.679 | 0.901 |
|  | 17:39980077\_T/G | -0.947 | 2.320 | 0.683 |  | 7.358 | 4.388 | 0.094 |
|  | 17:39981248\_A/G | -0.649 | 3.229 | 0.841 |  | -7.644 | 5.810 | 0.188 |
|  | 17:39987130\_T/C | 1.606 | 1.453 | 0.269 |  | 0.335 | 2.349 | 0.887 |
|  | 17:40078224\_A/G | -0.022 | 0.084 | 0.795 |  | -0.034 | 0.140 | 0.810 |
|  | 17:40145953\_C/T | -0.078 | 0.087 | 0.369 |  | -0.053 | 0.143 | 0.708 |
| *CD14* | 5:139065246\_C/T | -0.017 | 0.040 | 0.675 |  | -0.036 | 0.066 | 0.590 |
|  | 5:139066854\_C/A | -0.011 | 0.038 | 0.774 |  | 0.008 | 0.063 | 0.905 |
|  | 5:139145084\_C/T | 0.052 | 0.039 | 0.184 |  | -0.146 | 0.065 | 0.025 |
|  | 5:139422232\_G/A | 0.044 | 0.092 | 0.632 |  | -0.173 | 0.155 | 0.263 |
|  | 5:139466410\_T/G | 0.007 | 0.104 | 0.945 |  | -0.021 | 0.173 | 0.902 |
|  | 5:139514964\_T/C | -0.007 | 0.026 | 0.791 |  | -0.022 | 0.043 | 0.612 |
|  | 5:139621887\_C/T | 0.010 | 0.055 | 0.864 |  | -0.002 | 0.093 | 0.985 |
|  | 5:139932417\_T/G | 0.018 | 0.513 | 0.972 |  | 0.752 | 0.879 | 0.392 |
|  | 5:139950138\_C/T | -0.019 | 0.514 | 0.971 |  | -0.734 | 0.880 | 0.404 |
|  | 5:140086704\_C/T | 0.049 | 0.066 | 0.458 |  | -0.032 | 0.115 | 0.780 |
|  | 5:140750597\_C/T | -0.960 | 1.805 | 0.595 |  | 2.772 | 2.444 | 0.257 |
|  | 5:140757906\_A/G | 0.947 | 1.803 | 0.599 |  | -2.741 | 2.442 | 0.262 |
| *CYP27A1* | 2:219595001\_C/T | 0.075 | 0.055 | 0.173 |  | -0.134 | 0.092 | 0.142 |
|  | 2:219631297\_G/A | -2.088 | 3.359 | 0.534 |  | -2.632 | 7.917 | 0.740 |
|  | 2:219631960\_G/A | 2.071 | 3.367 | 0.538 |  | 2.532 | 7.933 | 0.750 |
|  | 2:219647487\_G/A | -0.087 | 0.186 | 0.640 |  | 0.199 | 0.303 | 0.513 |
|  | 2:219656190\_G/A | 0.040 | 0.143 | 0.781 |  | 0.039 | 0.233 | 0.868 |
|  | 2:219671910\_T/C | -0.070 | 0.044 | 0.111 |  | 0.134 | 0.074 | 0.070 |

\* Beta: Coefficient estimates (log-transformed odds ratios); SE: standard error

a Both coefficients and standard errors were estimated using multivariable generalized linear regression models by including main effects and interaction effects of all available SNPs within each gene set, adjusting for age, sex, study and principle components.