**Table S6.** Maximum odds ratios of the seven polymorphisms in the subgroups.

|  |  |
| --- | --- |
|  | **Odds Ratio, 95% Confidence Interval and Form of Polymorphism** |
| **Polymorphisma** | **All** | **Ever** | **Current** | **Former** | **Non** |
| *GSTM1* [2] | 1.35\* | 1.41\*  | 1.52\* | 1.35  | 1.20  |
|  | (1.17-1.56) | (1.19-1.68) | (1.13-2.04) | (1.09-1.67) | (0.92-1.56) |
|  | null | null | null | null | null |
| rs9642880 [7] | 1.34  | 1.33  | 0.87  | 1.50\*  | 1.48  |
|  | (1.14-1.58) | (1.09-1.63) | (0.62-1.21) | (1.16-1.93) | (1.10-1.99) |
|  | [T/T] | [T/T] | [G/T, T/T] | [T/T] | [T/T] |
| rs710521 [7] | 0.84  | 0.88  | 1.65  | 0.85  | 0.79  |
|  | (0.73-0.97) | (0.74-1.05) | (0.86-3.17) | (0.68-1.05) | (0.60-1.03) |
|  | [A/G, G/G] | [A/G, G/G] | [G/G] | [A/G, G/G] | [A/G, G/G] |
| rs8102137 [9] | 1.18  | 1.14  | 1.19  | 1.12  | 1.51  |
|  | (1.02-1.36) | (0.96-1.36) | (0.88-1.60) | (0.91-1.39) | (1.02-2.24) |
|  | [C/T, T/T] | [C/T, T/T] | [C/T, T/T] | [C/T, T/T] | [T/T] |
| rs11892031 [9] | 0.80  | 0.79  | 0.60  | 0.91  | 0.86  |
|  | (0.65-0.98) | (0.61-1.02) | (0.38-0.93) | (0.66-1.25) | (0.58-1.27) |
|  | [C/C] | [A/C, C/C] | [A/C, C/C] | [A/C, C/C] | [A/C, C/C] |
| rs1014971 [9] | 0.89  | 1.04  | 1.17  | 1.05  | 0.61\*  |
|  | (0.78-1.03) | (0.87-1.23) | (0.87-1.57) | (0.74-1.50) | (0.47-0.80) |
|  | [C/T, T/T] | [C/T, T/T] | [C/T, T/T] | [T/T] | [C/T, T/T] |
| rs1495741 [9,20] | 0.91  | 0.91  | 0.87  | 0.93  | 0.92  |
|  | (0.79-1.05) | (0.60-1.38) | (0.43-1.75) | (0.55-1.56) | (0.71-1.20) |
|  | [A/G, G/G] | [G/G] | [G/G] | [G/G] | [A/G, G/G] |

Considered are the six SNPs identified in previous genome-wide association studies as well as *GSTM1*. For the SNPs, the maximum odds ratios in the total study group and the different smoker subgroups are determined considering a dominant and a recessive effect of the risk allele. The polymorphism with the largest p-value in a subgroup is marked by an asterisk. Genotypes at risk are given in parenthesis.

a The numbers in the brackets refer to the (genome-wide) association study in which the respective polymorphisms were found to be associated with urinary bladder cancer and correspond to the references in the main manuscript relating to this supporting information.