

Supplementary Table 1. Linkage disequilibrium among SNPs in the same gene or region

Chromosome	gene	SNP ID	Linkage disequilibrium D' (r ²)			
1 p36	<i>MTHFR</i>	rs1801131	}	1.00 (0.86)		
		rs1801133				
1 q42	<i>mEH</i>	rs2234922	}	0.48 (0.02)		
		rs1051740				
2 p22	<i>CYP1B1</i>	rs1056836	}	1.00 (0.90)		
		rs1800440				
3 p25	<i>XPC</i>	rs2228001	}	1.00 (0.30)		
		rs2228000				
8 p22	<i>NAT2</i>	rs1801280	}	1.00 (0.85)		
		rs1799931				
		rs1799930			}	1.00 (0.71)
11 q13	<i>GSTP1</i>	rs1695	}	0.92 (0.28)		
		rs1138272				
15 q24	<i>CYP1A1</i>	rs1048943	}	1.00 (0.94)		
		rs1799814				
	<i>CYP1A2</i>	rs762551	1.00 (0.82)	}	0.49 (0.06)	
16 q22	<i>NQO1</i>	rs1800566	}			1.00 (0.62)
		rs1131341				
19 q13	<i>ERCC1</i>	rs11615	}	1.00 (0.88)		
		rs3212948				
		rs3212986			}	1.00 (0.85)

Supplementary Table 2. Regression coefficients for the effects of haplotypes on adducts and NER

Gene	Haplotype alleles	Frequency (%)	adduct model		NER model	
			Coefficient	P value	Coefficient	P value
MTHFR	CC	43	reference		reference	
	CA	39	0.06	0.4	0.41	0.02
	TA	18	0.08	0.4	0.06	0.8
CYP1B1	GA	53	reference		-	-
	GG	20	-0.09	0.3	-	-
	CA	27	-0.01	0.9	-	-
XPC	CA	50	reference		reference	
	CC	27	-0.05	0.6	-0.03	0.9
	TC	23	-0.03	0.7	-0.01	0.9
NAT2	GCG	32	reference		-	-
	ATG	30	0.03	0.7	-	-
	GTG	28	0.07	0.4	-	-
	GTA	10	0.05	0.7	-	-
GSTP1	AT	75	reference		-	-
	GT	15	-0.07	0.4	-	-
	GC	8.5	0.04	0.8	-	-
CYP1A1/A2	ACA	46	reference		-	-
	ACC	41	-0.03	0.6	-	-
	GCA	7	-0.03	0.8	-	-
	AAA	5	-0.04	0.8	-	-
NQO1	CC	69	reference		-	-
	CT	27	-0.08	0.3	-	-
	TC	4	-0.04	0.8	-	-
ERCC1	CGT	45	reference		reference	
	TCG	29	0.02	0.8	0.18	0.4
	TCT	23	0.01	0.9	-0.07	0.7
	TGT	3	0.03	0.8	-0.26	0.5

NER: Nucleotide excision repair. Only SNP's with a putative effect on DNA repair were modeled against NER capacity.