**Supplemental Table 1.** Potential function of the five selected SNPs in *XPG* gene as predicted by SNPinfo (http://snpinfo.niehs.nih.gov/snpinfo/snpfunc.htm) software

| rs | Chr | Allele | Position [a] | Location | TFBS | Splicing (ESE or ESS) | miRNA (miRanda) | miRNA (Sanger) | Reg Potential | Conservation | Nearby Gene | Distance (bp) | Allele | Asian | CHB |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2094258 | 13 | C/T | 102294760 | 5' near gene | Y | -- | -- | -- | 0 | 0.001 | BIVM\|\|ERCC5 | -2878\|\|-1415 | C | 0.627 | 0.661 |
| rs751402 | 13 | C/T | 102296199 | 5' UTR | Y | Y | -- | -- | 0.25613 | 0 | ERCC5 | 24\|\|30147 | C | 0.591 | 0.619 |
| rs2296147 | 13 | T/C | 102296376 | 5' UTR | Y | -- | -- | -- | 0.175993 | 0 | ERCC5 | 201\|\|29970 | T | 0.838 | 0.768 |
| rs1047768 | 13 | T/C | 102302518 | exon | -- | Y | -- | -- | 0.24405 | 0.914 | ERCC5 | 6343\|\|23828 | T | 0.778 | 0.720 |
| rs873601 | 13 | G/A | 102326338 | 3' UTR | -- | Y | Y | Y | 0 | 0.005 | ERCC5 | 30163\|\|8 | G | 0.517 | 0.464 |

[a] The position is based on HapMap Data Rel 27 Phase II+III, Feb09, on NCBI B36 assembly, dbSNP b126.

SNP, single nucleotide polymorphism; XPG, xeroderma pigmentosum group G; TFBS, transcription factor binding site; ESE, exon splicing enhancer; ESS, exon splicing silencer; bp, base pair; CHB, Han Chinese in Beijing, China; UTR, untranslated region; ERCC5, excision repair cross-complementation group 5.

**Supplemental Table 2.** *XPG* mRNA expression by the genotypes of SNPs, using genotype data from the HapMap and mRNA expression data were from SNPexp [a]

| Population | rs2094258 C>T | | | | | rs751402 C>T | | | | | rs873601 G>A | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | genotypes | No. | Mean ± SD | *P* [b] | $P_{trend}$ [c] | genotypes | No. | Mean ± SD | *P* [b] | $P_{trend}$ [c] | genotypes | No. | Mean ± SD | *P* [b] | $P_{trend}$ [c] |
| CHB | CC | 19 | 9.77 ± 0.21 | | **0.027** | CC | 15 | 9.90 ± 0.19 | | 0.064 | GG | 8 | 9.96 ± 0.15 | | **0.003** |
| | CT | 23 | 9.90 ± 0.21 | **0.044** | | CT | 22 | 9.86 ± 0.21 | 0.596 | | AG | 26 | 9.88 ± 0.19 | 0.314 | |
| | TT | 3 | 9.96 ± 0.16 | 0.142 | | TT | 8 | 9.71 ± 0.24 | 0.055 | | AA | 11 | 9.69 ± 0.23 | **0.011** | |
| | Dominant | 26 | 9.91 ± 0.20 | **0.027** | | Dominant | 30 | 9.82 ± 0.22 | 0.264 | | Dominant | 37 | 9.82 ± 0.22 | 0.112 | |
| | Recessive | 42 | 9.84 ± 0.21 | 0.349 | | Recessive | 37 | 9.88 ± 0.28 | **0.046** | | Recessive | 34 | 9.90 ± 0.18 | **0.003** | |
| Asian | CC | 30 | 9.72 ± 0.20 | | 0.186 | CC | 30 | 9.79 ± 0.21 | | 0.196 | GG | 20 | 9.77 ± 0.25 | | 0.106 |
| | CT | 52 | 9.77 ± 0.23 | 0.292 | | CT | 47 | 9.76 ± 0.22 | 0.537 | | AG | 49 | 9.80 ± 0.21 | 0.682 | |
| | TT | 8 | 9.82 ± 0.24 | 0.246 | | TT | 13 | 9.69 ± 0.23 | 0.188 | | AA | 21 | 9.67 ± 0.20 | 0.132 | |
| | Dominant | 60 | 9.78 ± 0.23 | 0.230 | | Dominant | 60 | 9.75 ± 0.22 | **0.046** | | Dominant | 70 | 9.76 ± 0.21 | 0.776 | |
| | Recessive | 82 | 9.76 ± 0.22 | 0.423 | | Recessive | 77 | 9.77 ± 0.22 | 0.233 | | Recessive | 69 | 9.79 ± 0.22 | **0.021** | |
| All [d] | CC | 147 | 9.74 ± 0.19 | | 0.074 | CC | 119 | 9.78 ± 0.22 | | **0.030** | GG | 83 | 9.81 ± 0.22 | | **0.001** |
| | CT | 108 | 9.78 ± 0.23 | 0.121 | | CT | 119 | 9.77 ± 0.21 | 0.693 | | AG | 114 | 9.77 ± 0.20 | 0.301 | |
| | TT | 15 | 9.81 ± 0.25 | 0.212 | | TT | 32 | 9.67 ± 0.21 | **0.010** | | AA | 64 | 9.69 ± 0.20 | **0.002** | |
| | Dominant | 123 | 9.79 ± 0.23 | 0.084 | | Dominant | 151 | 9.75 ± 0.21 | 0.220 | | Dominant | 178 | 9.74 ± 0.20 | **0.029** | |
| | Recessive | 255 | 9.76 ± 0.21 | 0.387 | | Recessive | 238 | 9.77 ± 0.21 | **0.008** | | Recessive | 197 | 9.79 ± 0.21 | **0.001** | |

[a] Genotyping data for *XPG* by genotypes were obtained from the HapMap phase II release 23 data (http://hapmap.ncbi.nlm.nih.gov/) from EBV-transformed lymphoblastoid cell lines from 270 individuals and mRNA expression data were from SNPexp (http://app3.titan.uio.no/biotools/help.php?app5snpexp) also from the 270 individuals.

[b] Calculated by two-side Student's *t* test within the stratum.

[c] Trend test of *XPG* mRNA expression among three genotypes by a general linear model.

[d] There were missing data for the genotypes were not available for nine CEU subjects.