Supplemental Table: Interactions of HMOX1 and GST polymorphisms and decline in PM10 on the change in the product of $\operatorname{FVC}$ * $\mathrm{FEF}_{25-75}$ in the whole study population

| Gene Polymorphism |  |  | Effect of a $10 \mu \mathrm{~g} / \mathrm{m}^{3}$ decrease in PM10 over 10.92 years (mean follow-up) on change in the product of FEF25-75 * FVC (L²/s) 1 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Heme Oxygenase-1 Single Nucleotide Polymorphisms |  |  |  |  |  |  |
| allele $\quad N$ |  |  |  |  |  |  |
| $\begin{aligned} & \text { HMOX } \\ & \text { rs2071746 } \end{aligned}$ | AA | 1401 | 0.8 | 0.3 | to | 1.3 |
|  | AT | 2089 | 0.9 | 0.4 | to |  |
|  | TT | 763 | 0.8 | 0.1 | to | 1.4 |
| $\begin{gathered} \text { HMOX } \\ \text { rs } 735266 \end{gathered}$ | AA | 1669 | 0.6 | 0.1 | to | 1.1 |
|  | AT | 2022 | 1.0 | 0.5 | to | 1.6 |
|  | TT | 595 | 0.7 | -0.1 | to | 1.5 |
| $\begin{aligned} & \text { HMOX } \\ & \text { rs5995098 } \end{aligned}$ | CC | 2021 | 0.6 | 0.2 | to | 1.1 |
|  | CG | 1876 | 1.1 | 0.6 | to | 1.6 |
|  | GG | 427 | 0.7 | -0.2 | to | 1.6 |
| Heme Oxygenase-1 Haplotypes ${ }^{2}$ |  |  |  |  |  |  |
| No of alleles |  | $N$ |  |  |  |  |
| Haplotype 1 (AAC) | 0 | 798 2178 | 0.8 | 0.1 | to | 1.4 |
|  |  | 2178 | 0.9 |  | to | 1.4 |
|  | 2 | 1389 | 0.7 | 0.2 | to | 1.3 |
| Haplotype 3 (ATC) | 0 | 3925 | $0.9{ }^{\text {a }}$ | 0.5 | to | 1.3 |
|  | 1 | 431 | 0.0 | -0.9 | to | 0.8 |
|  | 2 | 9 | 4.5 | -0.8 | to | 9.9 |
| Haplotype 7 <br> (TTC) | 0 | 3873 | 0.8 | 0.4 | to | 1.2 |
|  | 1 | 478 | 0.7 | -0.2 | to | 1.5 |
|  | 2 | 14 | 1.4 | -1.2 | to | 4.1 |
| Haplotype 8 (TTG) | 0 | 2057 | 0.6 | 0.2 | to | 1.1 |
|  | 1 | 1895 | 1.1 | 0.5 | to | 1.6 |
|  | 2 | 413 | 0.7 | -0.2 | to | 1.6 |
| Heme Oxygenase-1 Promoter Repeat Polymorphism |  |  |  |  |  |  |
| long allele (>=33 repeats) |  |  |  |  |  |  |
| HMOX (GT) ${ }_{\text {n }}$ | no | 3919 | $0.7{ }^{\text {b }}$ | 0.3 | to | 1.2 |
|  | yes | 446 | 1.4 | 0.6 | to | 2.2 |
| Glutathione S-Transferase Polymorphisms |  |  |  |  |  |  |
| complete deletion / allele   <br> GSTM1 $^{3}$ deletion $\boldsymbol{N}$  <br> no 2032  |  |  |  |  |  |  |
|  |  |  | 0.8 | 0.3 | to | 1.3 |
| GSTM1 deletion ${ }^{3}$ | yes | 2319 | 0.8 | 0.3 | to | 1.3 |
| GSTT1 deletion ${ }^{3}$ | no | 3554 | 0.9 | 0.5 | to | 1.3 |
|  | yes | 797 | 0.4 | -0.3 | to | 1.1 |
| GSTP1 Val/lle Polymorphism | lle / Ile | 2061 | 0.9 | 0.4 | to | 1.3 |
|  | $\mathrm{Ile/Val}$ | 1892 | 0.5 | 0.0 | to | 1.1 |
|  | Val/Val | 401 | $1.5{ }^{\text {c }}$ | 0.6 | to | 2.4 |

[^0]${ }^{1}$ Positive values represent attenuations of the decline in the product of $\mathrm{FEF}_{25-75}$ * FVC
compared to a reference group experiencing no air pollution reduction.
${ }^{2}$ Determined from rs2071746, rs735266 and rs5995098 SNPs (in this sequence) using PHASE software v2.1
${ }^{3}$ Deletion means homozygous gene deletion (null vs. non-null)


[^0]:    a $\mathbf{p}_{\text {interaction }}=0.038$ under dominant genetic mode
    b $\mathbf{p}_{\text {interaction }}=0.104$
    e $\mathbf{p}_{\text {interaction }}=0.072$ under recessive genetic model

