**Table S2:** Association of sIL-6R with the *IL6R* region, in 3,605 samples.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| SNP | Genotype | N (frequency) | b (se) | % change (se) | R2(diff) | *P* |
| rs2228145 | A/A | 1,309 (0.36) | 0 (reference) | Reference | 29.3% | <10-300 |
|  | A/C | 1,709 (0.47) | 0.129 (0.003) | +34.6 (0.7) |  |  |
|  | C/C | 587 (0.16) | 0.239 (0.004) | +73.4 (0.9) |  |  |
| rs4329505 | T/T | 2,517 (0.70) | 0 (reference) | Reference | 1.1% | 7.43x10-29 |
|  | T/C | 1,008 (0.28) | 0.031 (0.003) | +7.4 (0.7) |  |  |
|  | C/C | 80 (0.02) | 0.066 (0.009) | +16.4 (2.1) |  |  |
| rs1386821 | T/T | 2,340 (0.65) | 0 (reference) | Reference | 0.4% | 5.07x10-11 |
|  | T/G | 1,139 (0.32) | -0.016 (0.003) | -3.8 (0.7) |  |  |
|  | G/G | 126 (0.03) | -0.031 (0.007) | -7.4 (1.6) |  |  |

b = regression coefficient for a model containing all three SNPs. se=standard error of b. R2 (diff) = the difference in the square of the correlation coefficient for a model with and without the listed SNP. *P* is for the addition of the listed SNP to a model containing the other two SNPs.