**S2 Table**: **SNP variance from Hardy-Weinberg equilibrium.** Variance is shown of each TLR polymorphism from the control group of the total study population. Statistical p values were determined by exact test.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TLR2Arg753GlnG is ancestral allele | Observed Genotype Counts, n (% of row total) |  | Observed Allele Counts, n (%) | Exact test |
| rs5743708\*MAF=0.0068\* | G/G | G/A | A/A | total | G | A | p-value |
| nonCOPD nonsmoker | 17 (89) | 2 (11) | 0 | 19 | 36 (95) | 2 (5) | 1 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TLR4Asp299GlyA is ancestral allele | Observed Genotype Counts, n (% of row total) |  | Observed Allele Counts, n (%) | Exact test |
| rs4986790\*MAF=0.0599\* | A/A | A/G | G/G | total | A | G | p-value |
| nonCOPD nonsmoker | 18 (95) | 1 (5) | 0 | 19 | 17 (97) | 1 (3) | 1 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TLR4Thr399IleC is ancestral allele | Observed Genotype Counts, n (% of row total) |  | Observed Allele Counts, n (%) | Exact test |
| rs4986791\*MAF=0.0407\* | C/C | C/T | T/T | total | C | T | p-value |
| nonCOPD nonsmoker | 18 (95) | 1 (5) | 0 | 19 | 37 (97) | 1 (3) | 1 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TLR9T1237CC is ancestral allele | Observed Genotype Counts, n (% of row total) |  | Observed Allele Counts, n (%) | Exact test |
| rs5743836\*MAF=0.1725\* | C/C | C/T | T/T | total | C | T | p-value |
| nonCOPD nonsmoker | 15 (75) | 3 (15) | 2 (10) | 20 | 33 (82) | 7 (18) | 0.07 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TLR9T1486CC is ancestral allele | Observed Genotype Counts, n (% of row total) |  | Observed Allele Counts, n (%) | Exact test |
| rs187084\*MAF=0.3776\* | C/C | C/T | T/T | total | C | T | p-value |
| nonCOPD nonsmoker | 7 (37) | 9 (47) | 3 (16) | 19 | 23 (61) | 15 (39) | 1 |

\* SNP designation and minor allele frequency (MAF) of reference genomes are from the Single Nucleotide Polymorphism Database (dbSNP).