

Table S4. The genotypes and the allelic frequencies of analyzed SNPs in patients homozygous for c.919-2A>G and in the control sample.

| SNPs (distance from c.919-2A>G) | Genotypes | Homozygotes for c.919- 2A>G (n=23) | Controls (n=23) | Alleles | Homozygotes for c.919-2A>G | | Controls | | <i>p</i> | δ |
|---------------------------------------|-----------|---|--------------------|---------|-------------------------------|-------------------------|----------------------|-------------------------|----------------------------------|------------|
| | | | | | Number of alleles | Frequency of alleles | Number of alleles | Frequency of alleles | | |
| rs2248464 (20276) | AA | 23 | 4 | A | 46 | 1.0 | 26 | 0.2063 | 0.1697 x 10⁻²² | 1.0 |
| | AT | 0 | 18 | | | | | | | |
| | TT | 0 | 41 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs2248465 (20270) | CC | 23 | 9 | C | 46 | 1.0 | 40 | 0.3175 | 0.3332 x 10⁻¹⁷ | 1.0 |
| | CT | 0 | 22 | | | | | | | |
| | TT | 0 | 32 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs3801943 (2232) | TT | 23 | 45 | T | 46 | 1.0 | 107 | 0.8492 | 1.0 | 1.0 |
| | TA | 0 | 17 | | | | | | | |
| | AA | 0 | 1 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs2712212 * (2183) | AA | 23 | 28 | A | 46 | 1.0 | 84 | 0.6667 | 1.0 | 1.0 |
| | AG | 0 | 28 | | | | | | | |
| | GG | 0 | 7 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| c.919-2A>G | | | | | | | | | | |
| rs2395911 * (215) | GG | 23 | 9 | G | 46 | 1.0 | 44 | 0.3492 | 0.6282x 10⁻¹⁶ | 1.0 |
| | GT | 0 | 26 | | | | | | | |
| | TT | 0 | 28 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs2712211 * (2024) | CC | 0 | 26 | C | 0 | 0.0 | 78 | 0.6190 | 0.9734 x 10⁻¹⁵ | -1.6250 |
| | CG | 0 | 26 | | | | | | | |
| | GG | 23 | 11 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs3801940 * (2318) | CC | 23 | 14 | C | 46 | 1.0 | 56 | 0.4444 | 1.0 | 1.0 |
| | CG | 0 | 28 | | | | | | | |
| | GG | 0 | 21 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs2072064 (10615) | TT | 0 | 25 | T | 0 | 0.0 | 75 | 0.5952 | 0.6892 x 10⁻¹⁴ | 1.4706 |
| | TA | 0 | 25 | | | | | | | |
| | AA | 23 | 13 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |
| rs2072065 (10763) | CC | 23 | 16 | C | 46 | 1.0 | 64 | 0.5079 | 1.0 | 1.0 |
| | CT | 0 | 32 | | | | | | | |
| | TT | 0 | 15 | | | | | | | |
| | Total | 23 | 63 | | | | | | | |

* – rs2712212, rs2395911, rs2712211, and rs3801940 were included for comparative analysis with the data from the study by Wu et al. [12]. The maximum indices of linkage disequilibrium (δ) and statistically significant ($p < 0.05$) differences in allele frequencies between the c.919-2A>G homozygotes and the control sample are in bold.