**Table S4.** **The most significant gene-environmental combinations associated with the risk of UFs**

|  |  |  |  |
| --- | --- | --- | --- |
| Combinations of genotypes (1) | Beta (2) | *P* (3) | Risk(4) |
| **Ind\_abort×rs2553772** |  |  |  |
| 0×rs2553772 T/T | -0.236 | 5.54×10-5 | L |
| 0×rs2553772 G/G | -0.101 | 0.014 | L |
| 1×rs2553772 G/G | 0.060 | 0.071 | H |
| **Ind\_abort×rs1986649** |  |  |  |
| 0×rs1986649 C/C | -0.167 | 4.09×10-6 | L |
| 1×rs1986649 C/C | 0.095 | 0.002 | H |
| **Ind\_abort×rs11031731×rs1986649** |  |  |  |
| 1×rs11031731 A/A×rs1986649 C/T | 0.396 | 0.088 | H |
| 1×rs11031731 A/A×rs1986649 C/C | 0.385 | 0.019 | H |
| 0×rs11031731 G/G×rs1986649 C/C | -0.222 | 4.59×10-8 | L |
| 1×rs11031731 G/G×rs1986649 C/C | 0.069 | 0.044 | H |
| **Ind\_abort×rs2553772×rs1812266** |  |  |  |
| 0×rs2553772 T/T×rs1812266 C/G | -0.345 | 3.21×10-5 | L |
| 1×rs2553772 T/G×rs1812266 C/G | 0.123 | 0.023 | H |
| 0×rs2553772 T/T×rs1812266 G/G | -0.160 | 0.094 | L |
| 0×rs2553772 G/G×rs1812266 G/G | -0.179 | 0.010 | L |
| **Ind\_abort×rs2553772×rs59760198×rs66998222** |  |  |  |
| 0×rs2553772 T/G× rs59760198 T/T×rs66998222 A/A | 0.387 | 0.094 | H |
| 1×rs2553772 T/T× rs59760198 T/C×rs66998222 A/A | -0.348 | 0.047 | L |
| 0×rs2553772 G/G× rs59760198 T/C×rs66998222 A/A | -0.396 | 0.087 | L |
| 1×rs2553772 T/G× rs59760198 T/C×rs66998222 A/A | -0.311 | 0.100 | L |
| 0×rs2553772 T/T× rs59760198 C/C×rs66998222 A/A | -0.881 | 0.057 | L |
| 1×rs2553772 G/G× rs59760198 C/C×rs66998222 A/A | 0.328 | 0.045 | H |
| 0×rs2553772 G/G× rs59760198 C/C×rs66998222 A/G | -0.251 | 0.062 | L |
| 1×rs2553772 G/G× rs59760198 C/C×rs66998222 A/G | -0.211 | 0.016 | L |
| 0×rs2553772 T/T× rs59760198 T/T×rs66998222 G/G | -0.292 | 0.096 | L |
| 0×rs2553772 G/G× rs59760198 T/T×rs66998222 G/G | -0.226 | 0.080 | L |
| 1×rs2553772 T/G× rs59760198 T/T×rs66998222 G/G | 0.192 | 0.090 | H |
| 0×rs2553772 T/T× rs59760198 T/C×rs66998222 G/G | -0.200 | 0.062 | L |
| 1×rs2553772 G/G× rs59760198 T/C×rs66998222 G/G | 0.112 | 0.035 | H |
| 1×rs2553772 T/G× rs59760198 T/C×rs66998222 G/G | 0.129 | 0.043 | H |
| 0×rs2553772 T/T× rs59760198 C/C×rs66998222 G/G | -0.276 | 0.018 | L |

Obtained by the MB-MDR method, taking into account correction for covariates (age, UF family history).(1)combination of genotypes;(2)eta – logistic regression coefficients for combinations of genotypes; (3) *p* – level of significance;(4) Risk: H – high; L – low. Environmental factors are indicated as follows: 0 = no abortions, 1 = abortions in anamnesis. MB, model-based; MDR, multifactor dimensionality reduction; UF, uterine fibroid.