**Table S2. The most significant gene-gene combinations associated with the risk of UFs**

|  |  |  |  |
| --- | --- | --- | --- |
| Combinations of genotypes  (1) | Beta  (2) | *p*  (3) | Risk  (4) |
| **rs9419958×rs10929757** |  |  |  |
| rs9419958 T/C×rs10929757 A/A | 0.146 | 0.057 | H |
| rs9419958 C/C×rs10929757 C/A | -0.080 | 0.013 | L |
| rs9419958 T/C×rs10929757 C/C | 0.130 | 0.014 | H |
| **rs641760×rs9419958** |  |  |  |
| rs641760 C/C×rs9419958 T/C | 0.073 | 0.078 | H |
| rs641760 T/T×rs9419958 C/C | -0.170 | 0.066 | L |
| rs641760 C/T×rs9419958 C/C | -0.090 | 0.010 | L |
| **rs2553772×rs9419958** |  |  |  |
| rs2553772 T/T×rs9419958 T/C | 0.186 | 0.006 | H |
| rs2553772 T/G×rs9419958 T/C | 0.096 | 0.095 | H |
| rs2553772 T/T×rs9419958 C/C | -0.123 | 0.004 | L |
| **rs9419958×rs66998222** |  |  |  |
| rs9419958 T/C×rs66998222 A/G | 0.116 | 0.032 | H |
| rs9419958 C/C×rs66998222 A/G | -0.111 | 0.002 | L |
| **rs2553772×rs2235529×rs9419958** |  |  |  |
| rs2553772 T/T×rs2235529 T/T×rs9419958 T/T | -0.884 | 0.056 | L |
| rs2553772 T/G×rs2235529 T/C×rs9419958 T/T | -0.584 | 0.074 | L |
| rs2553772 T/T×rs2235529 C/C×rs9419958 T/T | 0.464 | 0.083 | H |
| rs2553772 T/T×rs2235529 C/C×rs9419958 T/C | 0.290 | 0.001 | H |
| rs2553772 T/G×rs2235529 C/C×rs9419958 T/C | 0.122 | 0.052 | H |
| rs2553772 T/T×rs2235529 T/T×rs9419958 C/C | -0.382 | 0.099 | L |
| rs2553772 G/G×rs2235529 T/T×rs9419958 C/C | 0.363 | 0.027 | H |
| rs2553772 T/T×rs2235529 C/C×rs9419958 C/C | -0.109 | 0.027 | L |
| **rs9419958×rs59760198×rs66998222** |  |  |  |
| rs9419958 C/C× rs59760198 T/C×rs66998222 A/A | -0.205 | 0.040 | L |
| rs9419958 T/T× rs59760198 T/T×rs66998222 A/G | -0.276 | 0.075 | L |
| rs9419958 C/C× rs59760198 T/C×rs66998222 A/G | -0.081 | 0.072 | L |
| rs9419958 C/C× rs59760198 C/C×rs66998222 A/G | -0.198 | 0.001 | L |
| **rs11031731×rs9419958×rs10929757×rs66998222** |  |  |  |
| rs11031731 G/G×rs9419958 C/C×rs10929757 C/A×rs66998222 A/A | -0.450 | 0.0001 | L |
| rs11031731 A/G×rs9419958 T/T×rs10929757 A/A×rs66998222 A/G | -0.565 | 0.086 | L |
| rs11031731 G/G×rs9419958 C/C×rs10929757 A/A×rs66998222 A/G | -0.234 | 0.026 | L |
| rs11031731 G/G×rs9419958 T/T×rs10929757 C/A×rs66998222 A/G | -0.427 | 0.015 | L |
| rs11031731 G/G×rs9419958 T/C×rs10929757 C/A×rs66998222 A/G | 0.152 | 0.078 | H |
| rs11031731 A/G×rs9419958 C/C×rs10929757 C/A×rs66998222 A/G | -0.205 | 0.029 | L |
| rs11031731 G/G×rs9419958 C/C×rs10929757 C/C×rs66998222 A/G | -0.170 | 0.002 | L |
| rs11031731 A/G×rs9419958 T/C×rs10929757 A/A×rs66998222 G/G | 0.400 | 0.035 | H |
| **rs2553772×rs2235529×rs10929757×rs66998222** |  |  |  |
| rs2553772 T/T×rs2235529 T/C×rs10929757 C/A×rs66998222 A/A | -0.562 | 0.086 | L |
| rs2553772 T/G×rs2235529 T/C×rs10929757 C/A×rs66998222 A/A | -0.506 | 0.029 | L |
| rs2553772 T/G×rs2235529 C/C×rs10929757 C/A×rs66998222 A/A | -0.303 | 0.039 | L |
| rs2553772 T/T×rs2235529 C/C×rs10929757 C/C×rs66998222 A/A | -0.427 | 0.040 | L |
| rs2553772 T/G×rs2235529 C/C×rs10929757 C/C×rs66998222 A/A | 0.427 | 0.065 | H |
| rs2553772 T/G×rs2235529 T/C×rs10929757 C/C×rs66998222 A/G | -0.558 | 0.003 | L |
| rs2553772 T/T×rs2235529 T/T×rs10929757 A/A×rs66998222 G/G | -0.707 | 0.031 | L |
| rs2553772 T/G×rs2235529 C/C×rs10929757 A/A×rs66998222 G/G | 0.205 | 0.023 | H |
| rs2553772 T/G×rs2235529 T/T×rs10929757 C/A×rs66998222 G/G | -0.902 | 0.051 | L |
| rs2553772 T/T×rs2235529 T/C×rs10929757 C/A×rs66998222 G/G | -0.339 | 0.006 | L |
| rs2553772 G/G×rs2235529 T/C×rs10929757 C/C×rs66998222 G/G | 0.211 | 0.024 | H |
| rs2553772 T/G×rs2235529 C/C×rs10929757 C/C×rs66998222 G/G | 0.122 | 0.043 | H |

Obtained by the MB-MDR method, taking into account correction for covariates (age, UF family history). (1) combination of genotypes; (2) beta – logistic regression coefficients for combinations of genotypes; (3) *p* – level of significance; (4) Risk: H – high; L – low. MB, model-based; MDR, multifactor dimensionality reduction; UF, uterine fibroid.