**Table S6**. **Analysis of the effect ofrs66998222 *LOC102723323* on the binding of DNA to transcription factors**

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| № | Ref/  SNP allele1 | TF2 | GAIN  /LOSS3 | Motif4 | *p*-Value SNP impact5 | *p*-Value Ref6 | *p*-Value SNP7 |
| 1 | G/A | TFCP2 | Gain | TFCP2\_2 | 0.001 | 0.070 | 0.003 |
| 2 | G/A | TATA | Gain | TATA\_disc5 | 0.001 | 0.069 | 0.002 |
| 3 | G/A | RXRA | Gain | RXRA\_disc4 | 0.001 | 0.161 | 0.013 |
| 4 | G/A | RXRA | Gain | RXRA\_3 | 0.002 | 0.091 | 0.011 |
| 5 | G/A | NRF1 | Gain | NRF1\_disc2 | 0.002 | 0.058 | 0.002 |
| 6 | G/A | SPI1 | Gain | SPI1\_disc1 | 0.005 | 0.077 | 0.005 |
| 7 | G/A | PAX5 | Gain | PAX5\_disc3 | 0.006 | 0.102 | 0.007 |
| 8 | G/A | NHLH1 | Gain | NHLH1\_3 | 0.007 | 0.456 | 0.022 |
| 9 | G/A | IRF6 | Gain | IRF6\_1 | 0.009 | 0.204 | 0.012 |
| 10 | G/A | TCF7 | Gain | TCF7\_2 | 0.010 | 0.560 | 0.038 |
| 11 | G/A | SPIC | Gain | SPIC\_1 | 0.010 | 0.753 | 0.043 |
| 12 | G/A | MEIS1::HOXA9 | Gain | MEIS1::HOXA9\_1 | 0.011 | 0.234 | 0.038 |
| 13 | G/A | ZBTB16 | Gain | ZBTB16\_1 | 0.013 | 0.250 | 0.031 |
| 14 | G/A | IRF5 | Gain | IRF5\_2 | 0.014 | 0.174 | 0.020 |
| 15 | G/A | IRF8 | Gain | IRF8\_1 | 0.016 | 0.187 | 0.024 |
| 16 | G/A | SOX9 | Gain | SOX9\_7 | 0.019 | 0.272 | 0.033 |
| 17 | G/A | Myog | Gain | MA0500.1 | 0.022 | 0.306 | 0.045 |
| 18 | G/A | NHLH1 | Gain | MA0048.1 | 0.023 | 0.251 | 0.033 |
| 19 | G/A | IRF5 | Gain | IRF5\_1 | 0.024 | 0.338 | 0.048 |
| 20 | G/A | SPI1 | Gain | SPI1\_4 | 0.028 | 0.090 | 0.014 |
| 21 | G/A | NR2E3 | Gain | NR2E3\_1 | 0.028 | 0.262 | 0.038 |
| 22 | G/A | NHLH1 | Gain | NHLH1\_5 | 0.029 | 0.223 | 0.028 |
| 23 | G/A | BCL | Gain | BCL\_disc7 | 0.037 | 0.201 | 0.028 |
| 24 | G/A | SPIB | Gain | SPIB\_2 | 0.037 | 0.139 | 0.032 |
| 25 | G/A | HNF4A | Gain | HNF4A\_1 | 0.037 | 0.061 | 0.014 |
| 26 | G/A | TCF12 | Gain | TCF12\_disc4 | 0.038 | 0.368 | 0.047 |
| 27 | G/A | Nr2e3 | Gain | MA0164.1 | 0.039 | 0.256 | 0.037 |
| 28 | G/A | NR5A1 | Gain | TFCP2\_2 | 0.001 | 0.070 | 0.003 |
| 29 | G/A | AIRE | Loss | AIRE\_1 | 0.001 | 0.016 | 0.474 |
| 30 | G/A | STAT | Loss | STAT\_disc7 | 0.001 | 0.023 | 0.301 |
| 31 | G/A | RAD21 | Loss | RAD21\_disc7 | 0.001 | 0.010 | 0.221 |
| 32 | G/A | TCF12 | Loss | TCF12\_disc5 | 0.003 | 0.022 | 0.311 |
| 33 | G/A | BCL | Loss | BCL\_disc9 | 0.004 | 0.033 | 0.386 |
| 34 | G/A | CTCF | Loss | CTCF\_disc8 | 0.004 | 0.020 | 0.274 |
| 35 | G/A | MZF1 | Loss | MZF1\_4 | 0.005 | 0.014 | 0.441 |
| 36 | G/A | TFAP2C | Loss | TFAP2C\_1 | 0.008 | 0.033 | 0.459 |
| 37 | G/A | TFAP2A | Loss | TFAP2A\_4 | 0.008 | 0.030 | 0.439 |
| 38 | G/A | TFAP2A | Loss | TFAP2A\_1 | 0.008 | 0.030 | 0.439 |
| 39 | G/A | TEAD2 | Loss | TEAD2\_1 | 0.008 | 0.042 | 0.361 |
| 40 | G/A | ZBTB33 | Loss | ZBTB33\_disc4 | 0.010 | 0.020 | 0.209 |
| 41 | G/A | EGR1 | Loss | EGR1\_disc6 | 0.014 | 0.035 | 0.322 |
| 42 | G/A | GTF2I | Loss | GTF2I\_1 | 0.015 | 0.035 | 0.333 |
| 43 | G/A | ZFX | Loss | ZFX\_1 | 0.015 | 0.021 | 0.201 |
| 44 | G/A | ZNF524 | Loss | ZNF524\_1 | 0.016 | 0.025 | 0.198 |
| 45 | G/A | SMAD3 | Loss | SMAD3\_3 | 0.024 | 0.021 | 0.168 |
| 46 | G/A | TFAP2C | Loss | TFAP2C\_8 | 0.030 | 0.024 | 0.150 |
| 47 | G/A | NR4A2 | Loss | NR4A2\_2 | 0.033 | 0.043 | 0.233 |
| 48 | G/A | HNF4A | Loss | HNF4A\_10 | 0.037 | 0.012 | 0.066 |
| 49 | G/A | TFAP2A | Loss | TFAP2A\_10 | 0.038 | 0.019 | 0.066 |
| 50 | G/A | MZF1 | Loss | MZF1\_2 | 0.042 | 0.010 | 0.053 |
| 51 | G/A | ZBED1 | Loss | ZBED1\_1 | 0.043 | 0.049 | 0.282 |
| 52 | G/A | NR1H4 | Loss | AIRE\_1 | 0.001 | 0.016 | 0.474 |
| Gain | A8 | negative regulation of cell population proliferation (GO:0008285; FDR = 0.0099),  cellular response to cytokine stimulus (GO:0071345; FDR = 0.0107) | | | | | |
| Loss | G9 | regulation of interleukin-1 beta production (GO:0032651; FDR = 0.0229),  response to hypoxia (GO:0001666; FDR = 0.0302),  positive regulation of cytokine production (GO:0001819; FDR = 0.019) | | | | | |

1reference (Ref) / alternative (SNP) allele; 2TF - transcription factor; 3binding of TF to the reference (LOSS) / alternative (GAIN) allele; 4binding sites with high affinity for TF; 5*p*-value statistically confirming the potential gain or loss of function of the genomic region with SNP in terms of transcription factor binding; 6*p*-value for assessing the binding of TF to the Ref allele; 7*p*-value for assessing the binding of TF to the SNP allele; 8biological processes pathogenetically significant for UFs, in which TFs that bind to the alternative allele are jointly involved (data from the Gene Ontology resource; http://geneontology.org/); 9biological processes pathogenetically significant for UFs, in which TFs that bind to a reference allele are jointly involved (data from the Gene Ontology resource; http://geneontology.org/). SNP, single nucleotide polymorphism; TF, transcription factors; UF, uterine fibroid.