**Table S8.** **Analysis of the effect ofrs2553772 *LOC105376626* 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 | T/G | AP1 | Gain | AP1\_disc7 | 0.000 | 0.055 | 0.000 |
| 2 | T/G | REST | Gain | REST\_disc5 | 0.000 | 0.291 | 0.000 |
| 3 | T/G | Nkx2-5 (var.2) | Gain | MA0503.1 | 0.002 | 0.270 | 0.011 |
| 4 | T/G | ZBTB33 | Gain | ZBTB33\_disc3 | 0.002 | 0.202 | 0.017 |
| 5 | T/G | CHD2 | Gain | CHD2\_disc3 | 0.004 | 0.373 | 0.032 |
| 6 | T/G | ZBTB6 | Gain | ZBTB6\_1 | 0.005 | 0.402 | 0.019 |
| 7 | T/G | NR3C1 | Gain | NR3C1\_2 | 0.006 | 0.180 | 0.016 |
| 8 | T/G | TFAP4 | Gain | TFAP4\_6 | 0.008 | 0.329 | 0.017 |
| 9 | T/G | TFAP4 | Gain | TFAP4\_4 | 0.008 | 0.112 | 0.011 |
| 10 | T/G | AR | Gain | AR\_6 | 0.012 | 0.479 | 0.048 |
| 11 | T/G | MYF6 | Gain | MYF6\_2 | 0.015 | 0.427 | 0.047 |
| 12 | T/G | SREBF2 | Gain | MA0596.1 | 0.016 | 0.243 | 0.028 |
| 13 | T/G | HDAC2 | Gain | HDAC2\_disc3 | 0.016 | 0.163 | 0.017 |
| 14 | T/G | TFAP4 | Gain | TFAP4\_3 | 0.017 | 0.054 | 0.005 |
| 15 | T/G | GATA1 | Gain | GATA1\_3 | 0.025 | 0.273 | 0.022 |
| 16 | T/G | SREBF1 | Gain | MA0595.1 | 0.028 | 0.141 | 0.024 |
| 17 | T/G | GATA3 | Gain | AP1\_disc7 | 0.000 | 0.055 | 0.000 |
| 18 | T/G | TFAP2 | Gain | REST\_disc5 | 0.000 | 0.291 | 0.000 |
| 19 | T/G | GSC | Gain | MA0503.1 | 0.002 | 0.270 | 0.011 |
| 20 | T/G | GATA1 | Gain | ZBTB33\_disc3 | 0.002 | 0.202 | 0.017 |
| 21 | T/G | GATA1 | Loss | GATA1\_1 | 0.000 | 0.000 | 0.215 |
| 22 | T/G | GATA2 | Loss | GATA2\_1 | 0.000 | 0.001 | 0.927 |
| 23 | T/G | PAX2 | Loss | PAX2\_4 | 0.000 | 0.010 | 0.706 |
| 24 | T/G | LMO2 | Loss | LMO2\_2 | 0.001 | 0.005 | 0.198 |
| 25 | T/G | PAX5 | Loss | PAX5\_4 | 0.001 | 0.017 | 0.453 |
| 26 | T/G | GATA | Loss | GATA\_1 | 0.001 | 0.018 | 0.457 |
| 27 | T/G | GATA | Loss | GATA\_2 | 0.002 | 0.005 | 0.778 |
| 28 | T/G | GBX2 | Loss | GBX2\_3 | 0.002 | 0.025 | 0.346 |
| 29 | T/G | GATA1 | Loss | GATA1\_4 | 0.003 | 0.014 | 0.398 |
| 30 | T/G | Gata1 | Loss | MA0035.3 | 0.003 | 0.014 | 0.288 |
| 31 | T/G | GATA6 | Loss | GATA6\_1 | 0.004 | 0.019 | 0.512 |
| 32 | T/G | PAX5 | Loss | MA0014.2 | 0.005 | 0.008 | 0.113 |
| 33 | T/G | GATA2 | Loss | GATA2\_2 | 0.005 | 0.009 | 0.502 |
| 34 | T/G | GATA1 | Loss | GATA1\_2 | 0.006 | 0.010 | 0.326 |
| 35 | T/G | HAND1 | Loss | HAND1\_2 | 0.006 | 0.016 | 0.377 |
| 36 | T/G | HNF1A | Loss | HNF1A\_3 | 0.006 | 0.036 | 0.552 |
| 37 | T/G | HAND1 | Loss | HAND1\_1 | 0.006 | 0.038 | 0.727 |
| 38 | T/G | GATA1 | Loss | GATA1\_5 | 0.006 | 0.035 | 0.337 |
| 39 | T/G | NFIC | Loss | NFIC\_1 | 0.007 | 0.039 | 0.238 |
| 40 | T/G | CDX | Loss | CDX\_1 | 0.007 | 0.021 | 0.369 |
| 41 | T/G | GATA4 | Loss | GATA4\_2 | 0.009 | 0.021 | 0.533 |
| 42 | T/G | TBX1 | Loss | TBX1\_1 | 0.011 | 0.040 | 0.282 |
| 43 | T/G | GATA3 | Loss | GATA3\_4 | 0.012 | 0.010 | 0.384 |
| 44 | T/G | Atoh1 | Loss | MA0461.1 | 0.014 | 0.010 | 0.094 |
| 45 | T/G | PAX3 | Loss | PAX3\_2 | 0.015 | 0.009 | 0.152 |
| 46 | T/G | GATA5 | Loss | GATA5\_2 | 0.017 | 0.021 | 0.579 |
| 47 | T/G | RUNX1 | Loss | RUNX1\_1 | 0.018 | 0.035 | 0.237 |
| 48 | T/G | IRF3 | Loss | IRF3\_2 | 0.018 | 0.044 | 0.221 |
| 49 | T/G | RORA\_2 | Loss | MA0072.1 | 0.018 | 0.007 | 0.061 |
| 50 | T/G | BCL | Loss | BCL\_disc3 | 0.018 | 0.011 | 0.138 |
| 51 | T/G | REST | Loss | REST\_disc2 | 0.019 | 0.032 | 0.275 |
| 52 | T/G | RORA | Loss | RORA\_2 | 0.026 | 0.007 | 0.061 |
| 53 | T/G | TAL1 | Loss | TAL1\_disc2 | 0.026 | 0.005 | 0.066 |
| 54 | T/G | ESRRA | Loss | ESRRA\_6 | 0.027 | 0.050 | 0.439 |
| 55 | T/G | YY1 | Loss | GATA1\_1 | 0.000 | 0.000 | 0.215 |
| 56 | T/G | Hand1::Tcfe2a | Loss | GATA2\_1 | 0.000 | 0.001 | 0.927 |
| 57 | T/G | HMGN3 | Loss | PAX2\_4 | 0.000 | 0.010 | 0.706 |
| 58 | T/G | GATA3 | Loss | LMO2\_2 | 0.001 | 0.005 | 0.198 |
| 59 | T/G | EBF1 | Loss | PAX5\_4 | 0.001 | 0.017 | 0.453 |
| 60 | T/G | ELF2 | Loss | GATA\_1 | 0.001 | 0.018 | 0.457 |
| 61 | T/G | MXI1 | Loss | GATA\_2 | 0.002 | 0.005 | 0.778 |
| 62 | T/G | RORA | Loss | GBX2\_3 | 0.002 | 0.025 | 0.346 |
| Gain | G8 | SREBP signaling pathway (GO:0032933; FDR = 0.00445),  cellular response to transforming growth factor beta stimulus (GO:0071560; FDR = 0.0301),  steroid metabolic process (GO:0008202; FDR = 0.00905),  negative regulation of cell population proliferation (GO:0008285; FDR = 0.00366) | | | | | |
| Loss | T9 | positive regulation of vascular endothelial growth factor production (GO:0010575; FDR = 0.0419),  positive regulation of angiogenesis (GO:0045766; FDR = 0.00625),  angiogenesis (GO:0001525; FDR = 0.000819),  muscle organ development (GO:0007515; FDR = 0.0436),  regulation of cell population proliferation (GO:0042127; FDR = 0.0175) | | | | | |

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/). FDR, false discovery rate; SNP, single nucleotide polymorphism; TF, transcription factors; UF, uterine fibroid.