**Table S7. Analysis of the effect ofrs11031731 *THEM7P, WT1* 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 | GATA | Gain | GATA\_1 | 0.000 | 0.329 | 0.010 |
| 2 | G/A | IRF | Gain | IRF\_1 | 0.001 | 0.115 | 0.002 |
| 3 | G/A | RUNX1 | Gain | RUNX1\_6 | 0.001 | 0.120 | 0.003 |
| 4 | G/A | SOX5 | Gain | SOX5\_3 | 0.002 | 0.329 | 0.019 |
| 5 | G/A | IRF9 | Gain | IRF9\_3 | 0.004 | 0.507 | 0.022 |
| 6 | G/A | CEBPD | Gain | CEBPD\_1 | 0.004 | 0.492 | 0.030 |
| 7 | G/A | PAX5 | Gain | PAX5\_disc3 | 0.005 | 0.367 | 0.030 |
| 8 | G/A | HNF1A | Gain | HNF1A\_1 | 0.006 | 0.217 | 0.017 |
| 9 | G/A | SOX10 | Gain | SOX10\_2 | 0.007 | 0.623 | 0.041 |
| 10 | G/A | RUNX1 | Gain | RUNX1\_1 | 0.007 | 0.069 | 0.004 |
| 11 | G/A | STAT | Gain | STAT\_2 | 0.007 | 0.279 | 0.013 |
| 12 | G/A | SOX13 | Gain | SOX13\_1 | 0.008 | 0.363 | 0.033 |
| 13 | G/A | HNF4 | Gain | HNF4\_3 | 0.010 | 0.173 | 0.012 |
| 14 | G/A | IRF2 | Gain | MA0051.1 | 0.010 | 0.151 | 0.021 |
| 15 | G/A | IKZF2 | Gain | IKZF2\_1 | 0.010 | 0.456 | 0.017 |
| 16 | G/A | NR3C1 | Gain | NR3C1\_5 | 0.010 | 0.552 | 0.025 |
| 17 | G/A | Mecom | Gain | MA0029.1 | 0.012 | 0.225 | 0.026 |
| 18 | G/A | SPIB | Gain | SPIB\_1 | 0.012 | 0.495 | 0.027 |
| 19 | G/A | RUNX1 | Gain | RUNX1\_3 | 0.017 | 0.136 | 0.014 |
| 20 | G/A | SPI1 | Gain | SPI1\_disc2 | 0.017 | 0.298 | 0.037 |
| 21 | G/A | HNF4 | Gain | HNF4\_disc3 | 0.017 | 0.279 | 0.043 |
| 22 | G/A | HNF4A | Gain | HNF4A\_14 | 0.018 | 0.159 | 0.027 |
| 23 | G/A | REST | Gain | REST\_disc2 | 0.019 | 0.272 | 0.032 |
| 24 | G/A | IRF2 | Gain | IRF2\_2 | 0.020 | 0.193 | 0.026 |
| 25 | G/A | IRX3 | Gain | IRX3\_3 | 0.020 | 0.155 | 0.014 |
| 26 | G/A | NR4A2 | Gain | NR4A2\_1 | 0.020 | 0.420 | 0.046 |
| 27 | G/A | E2F2 | Gain | GATA\_1 | 0.000 | 0.329 | 0.010 |
| 28 | G/A | THAP1 | Gain | IRF\_1 | 0.001 | 0.115 | 0.002 |
| 29 | G/A | TFAP2C | Gain | RUNX1\_6 | 0.001 | 0.120 | 0.003 |
| 30 | G/A | E2F3 | Gain | SOX5\_3 | 0.002 | 0.329 | 0.019 |
| 31 | G/A | IKZF2 | Gain | IRF9\_3 | 0.004 | 0.507 | 0.022 |
| 32 | G/A | IRX2 | Gain | CEBPD\_1 | 0.004 | 0.492 | 0.030 |
| 33 | G/A | NR1H4 | Gain | PAX5\_disc3 | 0.005 | 0.367 | 0.030 |
| 34 | G/A | TFAP2A | Loss | TFAP2A\_4 | 0.000 | 0.000 | 0.360 |
| 35 | G/A | TFAP2A | Loss | TFAP2A\_1 | 0.000 | 0.000 | 0.360 |
| 36 | G/A | E2F1 | Loss | E2F1\_4 | 0.001 | 0.003 | 0.092 |
| 37 | G/A | E2F1 | Loss | E2F1\_5 | 0.003 | 0.004 | 0.240 |
| 38 | G/A | TFAP2C | Loss | TFAP2C\_1 | 0.003 | 0.013 | 0.357 |
| 39 | G/A | E2F1 | Loss | E2F1\_6 | 0.003 | 0.004 | 0.210 |
| 40 | G/A | TFAP2A | Loss | MA0003.2 | 0.004 | 0.021 | 0.271 |
| 41 | G/A | CTCF | Loss | CTCF\_disc5 | 0.004 | 0.036 | 0.357 |
| 42 | G/A | E2F1 | Loss | E2F1\_8 | 0.005 | 0.006 | 0.245 |
| 43 | G/A | HIC1 | Loss | HIC1\_2 | 0.005 | 0.027 | 0.539 |
| 44 | G/A | TFAP2 | Loss | TFAP2\_disc2 | 0.005 | 0.030 | 0.524 |
| 45 | G/A | TFAP2A | Loss | TFAP2A\_6 | 0.006 | 0.036 | 0.504 |
| 46 | G/A | TFAP2B | Loss | TFAP2B\_1 | 0.006 | 0.015 | 0.148 |
| 47 | G/A | HIF1A | Loss | HIF1A\_1 | 0.006 | 0.005 | 0.160 |
| 48 | G/A | E2F4 | Loss | MA0470.1 | 0.008 | 0.028 | 0.374 |
| 49 | G/A | TFAP2A | Loss | TFAP2A\_9 | 0.009 | 0.048 | 0.476 |
| 50 | G/A | HNF4A | Loss | HNF4A\_6 | 0.011 | 0.005 | 0.097 |
| 51 | G/A | RREB1 | Loss | RREB1\_1 | 0.013 | 0.041 | 0.214 |
| 52 | G/A | NR2F1 | Loss | NR2F1\_4 | 0.014 | 0.024 | 0.598 |
| 53 | G/A | STAT | Loss | STAT\_disc6 | 0.014 | 0.017 | 0.115 |
| 54 | G/A | E2F1 | Loss | E2F1\_3 | 0.015 | 0.016 | 0.197 |
| 55 | G/A | RARB | Loss | RARB\_2 | 0.015 | 0.033 | 0.354 |
| 56 | G/A | EP300 | Loss | EP300\_disc4 | 0.016 | 0.040 | 0.441 |
| 57 | G/A | MZF1 | Loss | MZF1\_1 | 0.019 | 0.038 | 0.270 |
| 58 | G/A | REST | Loss | TFAP2A\_4 | 0.000 | 0.000 | 0.360 |
| 59 | G/A | TFAP2B | Loss | TFAP2A\_1 | 0.000 | 0.000 | 0.360 |
| 60 | G/A | IRX2 | Loss | E2F1\_4 | 0.001 | 0.003 | 0.092 |
| 61 | G/A | RUNX1 | Loss | E2F1\_5 | 0.003 | 0.004 | 0.240 |
| 62 | G/A | EGR | Loss | TFAP2C\_1 | 0.003 | 0.013 | 0.357 |
| 63 | G/A | SIN3A | Loss | E2F1\_6 | 0.003 | 0.004 | 0.210 |
| 64 | G/A | FOXG1 | Loss | MA0003.2 | 0.004 | 0.021 | 0.271 |
| 65 | G/A | Sox17 | Loss | CTCF\_disc5 | 0.004 | 0.036 | 0.357 |
| 66 | G/A | FOXK1 | Loss | E2F1\_8 | 0.005 | 0.006 | 0.245 |
| 67 | G/A | IRX5 | Loss | HIC1\_2 | 0.005 | 0.027 | 0.539 |
| 68 | G/A | TBX1 | Loss | TFAP2\_disc2 | 0.005 | 0.030 | 0.524 |
| Gain | A8 | regulation of adipose tissue development (GO:1904177; FDR = 0.0318),cell population proliferation (GO:0008283; FDR = 0.0478) |
| Loss | G9 | regulation of cellular response to growth factor stimulus (GO:0090287; FDR = 0.0457), negative regulation of cell population proliferation (GO:008285; FDR = 0.0023),positive regulation of apoptotic process (GO:0043065; FDR = 0.0311),negative regulation of cell differentiation (GO:0045596; FDR = 0.0130),regulation of growth (GO:0040008; FDR = 0.0495) |

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.