**Table S9.** **Analysis of the effect of rs1986649 *FOXO1* 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 | C/T | AP1 | Gain | AP1\_8 | 0.000 | 0.826 | 0.000 |
| 2 | C/T | GATA | Gain | GATA\_disc2 | 0.000 | 0.289 | 0.027 |
| 3 | C/T | HDX | Gain | HDX\_1 | 0.001 | 0.166 | 0.006 |
| 4 | C/T | GFI1 | Gain | GFI1\_3 | 0.001 | 0.450 | 0.002 |
| 5 | C/T | Gfi1 | Gain | MA0038.1 | 0.001 | 0.188 | 0.003 |
| 6 | C/T | GFI1B | Gain | GFI1B\_1 | 0.002 | 0.095 | 0.002 |
| 7 | C/T | GFI1 | Gain | GFI1\_1 | 0.002 | 0.334 | 0.013 |
| 8 | C/T | SREBF1 | Gain | MA0595.1 | 0.002 | 0.123 | 0.009 |
| 9 | C/T | PLAG1 | Gain | PLAG1\_1 | 0.003 | 0.128 | 0.023 |
| 10 | C/T | SREBF2 | Gain | MA0596.1 | 0.003 | 0.177 | 0.012 |
| 11 | C/T | OTX | Gain | OTX\_1 | 0.004 | 0.346 | 0.022 |
| 12 | C/T | SMAD3 | Gain | SMAD3\_1 | 0.005 | 0.115 | 0.010 |
| 13 | C/T | HDAC2 | Gain | HDAC2\_disc1 | 0.006 | 0.606 | 0.033 |
| 14 | C/T | GFI1 | Gain | GFI1\_2 | 0.006 | 0.536 | 0.023 |
| 15 | C/T | SPDEF | Gain | SPDEF\_3 | 0.006 | 0.443 | 0.027 |
| 16 | C/T | AP1 | Gain | AP1\_2 | 0.009 | 0.432 | 0.023 |
| 17 | C/T | MZF1 | Gain | AP1\_8 | 0.000 | 0.826 | 0.000 |
| 18 | C/T | NR3C1 | Gain | GATA\_disc2 | 0.000 | 0.289 | 0.027 |
| 19 | C/T | HMBOX1 | Gain | HDX\_1 | 0.001 | 0.166 | 0.006 |
| 20 | C/T | HMGN3 | Gain | GFI1\_3 | 0.001 | 0.450 | 0.002 |
| 21 | C/T | SMAD3 | Gain | MA0038.1 | 0.001 | 0.188 | 0.003 |
| 22 | C/T | INSM1 | Gain | GFI1B\_1 | 0.002 | 0.095 | 0.002 |
| 23 | C/T | AP1 | Gain | GFI1\_1 | 0.002 | 0.334 | 0.013 |
| 24 | C/T | RHOXF1 | Gain | MA0595.1 | 0.002 | 0.123 | 0.009 |
| 25 | C/T | IRF5 | Gain | PLAG1\_1 | 0.003 | 0.128 | 0.023 |
| 26 | C/T | VDR | Gain | MA0596.1 | 0.003 | 0.177 | 0.012 |
| 27 | C/T | HNF4A | Gain | OTX\_1 | 0.004 | 0.346 | 0.022 |
| 28 | C/T | FOXP3 | Gain | SMAD3\_1 | 0.005 | 0.115 | 0.010 |
| 29 | C/T | RARA | Gain | HDAC2\_disc1 | 0.006 | 0.606 | 0.033 |
| 30 | C/T | EP300 | Gain | GFI1\_2 | 0.006 | 0.536 | 0.023 |
| 31 | C/T | HAND1 | Loss | HAND1\_2 | 0.000 | 0.000 | 0.221 |
| 32 | C/T | HAND1 | Loss | HAND1\_1 | 0.000 | 0.000 | 0.468 |
| 33 | C/T | PAX1 | Loss | PAX1\_1 | 0.000 | 0.015 | 0.119 |
| 34 | C/T | TFCP2 | Loss | TFCP2\_3 | 0.000 | 0.002 | 0.113 |
| 35 | C/T | TFCP2 | Loss | TFCP2\_4 | 0.000 | 0.005 | 0.334 |
| 36 | C/T | RUNX3 | Loss | RUNX3\_4 | 0.001 | 0.006 | 0.463 |
| 37 | C/T | TFCP2 | Loss | TFCP2\_5 | 0.001 | 0.002 | 0.182 |
| 38 | C/T | ETS | Loss | ETS\_disc4 | 0.002 | 0.017 | 0.250 |
| 39 | C/T | GRHL1 | Loss | GRHL1\_3 | 0.002 | 0.018 | 0.692 |
| 40 | C/T | TATA | Loss | TATA\_disc3 | 0.002 | 0.011 | 0.284 |
| 41 | C/T | TFCP2 | Loss | TFCP2\_1 | 0.002 | 0.028 | 0.266 |
| 42 | C/T | RUNX | Loss | RUNX\_1 | 0.003 | 0.035 | 0.421 |
| 43 | C/T | RUNX3 | Loss | RUNX3\_2 | 0.003 | 0.019 | 0.560 |
| 44 | C/T | GLI | Loss | GLI\_1 | 0.003 | 0.014 | 0.203 |
| 45 | C/T | RXRA::VDR | Loss | MA0074.1 | 0.004 | 0.020 | 0.212 |
| 46 | C/T | RUNX2 | Loss | MA0511.1 | 0.004 | 0.016 | 0.377 |
| 47 | C/T | RUNX2 | Loss | RUNX2\_3 | 0.004 | 0.027 | 0.360 |
| 48 | C/T | RUNX1 | Loss | MA0002.2 | 0.004 | 0.008 | 0.145 |
| 49 | C/T | RXRA | Loss | RXRA\_4 | 0.005 | 0.021 | 0.407 |
| 50 | C/T | TFCP2L1 | Loss | TFCP2L1\_1 | 0.005 | 0.009 | 0.113 |
| 51 | C/T | RAD21 | Loss | RAD21\_disc10 | 0.005 | 0.043 | 0.374 |
| 52 | C/T | IRF6 | Loss | IRF6\_1 | 0.006 | 0.042 | 0.647 |
| 53 | C/T | ATF3 | Loss | ATF3\_disc3 | 0.006 | 0.029 | 0.593 |
| 54 | C/T | GRHL1 | Loss | GRHL1\_2 | 0.007 | 0.009 | 0.188 |
| 55 | C/T | RUNX1 | Loss | RUNX1\_9 | 0.007 | 0.008 | 0.138 |
| 56 | C/T | ZNF354C | Loss | ZNF354C\_1 | 0.007 | 0.013 | 0.260 |
| 57 | C/T | Tcfcp2l1 | Loss | MA0145.2 | 0.008 | 0.009 | 0.110 |
| 58 | C/T | TP73 | Loss | TP73\_1 | 0.008 | 0.030 | 0.217 |
| 59 | C/T | IRF5 | Loss | IRF5\_1 | 0.008 | 0.020 | 0.468 |
| 60 | C/T | NRF1 | Loss | NRF1\_disc2 | 0.009 | 0.005 | 0.067 |
| 61 | C/T | IRF4 | Loss | IRF4\_1 | 0.009 | 0.031 | 0.348 |
| 62 | C/T | RUNX | Loss | RUNX\_2 | 0.011 | 0.028 | 0.309 |
| 63 | C/T | RFX5 | Loss | RFX5\_disc2 | 0.011 | 0.047 | 0.583 |
| 64 | C/T | SP2 | Loss | SP2\_disc1 | 0.012 | 0.035 | 0.389 |
| 65 | C/T | EGR1 | Loss | HAND1\_2 | 0.000 | 0.000 | 0.221 |
| 66 | C/T | RUNX2 | Loss | HAND1\_1 | 0.000 | 0.000 | 0.468 |
| 67 | C/T | NFYA | Loss | PAX1\_1 | 0.000 | 0.015 | 0.119 |
| 68 | C/T | AP1 | Loss | TFCP2\_3 | 0.000 | 0.002 | 0.113 |
| 69 | C/T | RUNX2 | Loss | TFCP2\_4 | 0.000 | 0.005 | 0.334 |
| 70 | C/T | HMBOX1 | Loss | RUNX3\_4 | 0.001 | 0.006 | 0.463 |
| 71 | C/T | SOX2 | Loss | TFCP2\_5 | 0.001 | 0.002 | 0.182 |
| 72 | C/T | TCF12 | Loss | ETS\_disc4 | 0.002 | 0.017 | 0.250 |
| 73 | C/T | VDR | Loss | GRHL1\_3 | 0.002 | 0.018 | 0.692 |
| 74 | C/T | HNF4A | Loss | TATA\_disc3 | 0.002 | 0.011 | 0.284 |
| 75 | C/T | AP1 | Loss | TFCP2\_1 | 0.002 | 0.028 | 0.266 |
| 76 | C/T | MEF2A | Loss | RUNX\_1 | 0.003 | 0.035 | 0.421 |
| 77 | C/T | AP1 | Loss | RUNX3\_2 | 0.003 | 0.019 | 0.560 |
| 78 | C/T | EP300 | Loss | GLI\_1 | 0.003 | 0.014 | 0.203 |
| 79 | C/T | PBX | Loss | MA0074.1 | 0.004 | 0.020 | 0.212 |
| 80 | C/T | RFX5 | Loss | MA0511.1 | 0.004 | 0.016 | 0.377 |
| 81 | C/T | PBX1 | Loss | RUNX2\_3 | 0.004 | 0.027 | 0.360 |
| 82 | C/T | TCF7L2 | Loss | MA0002.2 | 0.004 | 0.008 | 0.145 |
| 83 | C/T | RUNX2 | Loss | RXRA\_4 | 0.005 | 0.021 | 0.407 |
| 84 | C/T | RUNX3 | Loss | TFCP2L1\_1 | 0.005 | 0.009 | 0.113 |
| 85 | C/T | SREBF1 | Loss | RAD21\_disc10 | 0.005 | 0.043 | 0.374 |
| 86 | C/T | FOXI1 | Loss | IRF6\_1 | 0.006 | 0.042 | 0.647 |
| 87 | C/T | TP53 | Loss | ATF3\_disc3 | 0.006 | 0.029 | 0.593 |
| Gain | T8 | SREBP signaling pathway (GO:032933; FDR = 0.00667),  positive regulation of transforming growth factor beta production (GO:0071636; FDR = 0.0206),  regulation of interleukin-5 production (GO:0032674; FDR = 0.0239),  SMAD protein signal transduction (GO:0060395; FDR = 0.034),  positive regulation of interleukin-4 production (GO:0032753; FDR = 0.038),  cellular response to transforming growth factor beta stimulus (GO:0071560; FDR = 0.00424),  regulation of transforming growth factor beta receptor signaling pathway (GO:0017015; FDR = 0.0427) | | | | | |
| Loss | C9 | positive regulation of vitamin D receptor signaling pathway (GO:0070564; FDR = 0.0069),  intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (GO:0042771; FDR = 0.00349),  negative regulation of canonical Wnt signaling pathway (GO:0090090; FDR = 0.0118),  transforming growth factor beta receptor superfamily signaling pathway (GO:0141091; FDR = 0.0216),  response to decreased oxygen levels (GO:0036293; FDR = 0.0176),  response to growth factor (GO:0070848; FDR = 0.0214) | | | | | |

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.