## SUPPLEMENTARY FIGURES AND TABLES

Tongwu Zhang et al.

SDHD promoter mutations ablate GABP transcription factor binding in melanoma

**Supplementary Figure 1. Confirmation of the recurrent C524, C541 and C544 SDHD promoter mutations in melanoma cell lines.** Sanger sequencing traces for both forward and reverse reads verify all three recurrent *SDHD* promoter mutation in melanoma cell lines UACC952, C021 and C077.



**Supplementary Figure 2.** *SDHD* expression difference in melanomas harboring promoter mutations compared to *SDHD* wild-type samples. *SDHD* promoter-mutant samples are grouped according to mutation. *SDHD* expression was significantly decreased in the set of tumors harboring the *SDHD* C523T promoter mutation (one-tailed student's t-test, P = 0.0135) compared to wild-type samples. "Other Hotspot Mutation" includes the *SDHD* promoter mutations C532A, C541T, C544T and C548T, while "Non-Hotspot Mutation" includes *SDHD* promoter mutations C515T, A530G, C531T, C547T and C549T. Copy number for each sample as predicted by GISTIC is denoted with different coloring (Purple/-2: homozygous deletion; Red/-1: shallow deletion; Green/0: copy-neutral; Blue/1: copy gain; Black/NA: not assessable).



SDHD Putative copy-number alterations from GISTIC • -2 • -1 • 0 • 1 • NA

Supplementary Figure 3. *SDHD* promoter activity is significantly decreased by the C541T and C544T *SDHD* hotspot mutations in multiple melanoma cell lines. A 163 bp fragment from the wild-type *SDHD* promoter sequence surrounding hotspot mutations significantly enhance luciferase reporter expression relative to vector control, whereas the same fragment containing hotspot mutations decrease enhancer activity relative to the wild-type sequence. Luciferase activity was measured 24hr after transfection and normalized to Renilla luciferase readings. Fold change over minimal promoter control (vector only) is plotted as relative luciferase activity. The experiment was performed four times with triplicates for each. Stars denote significant differences in luciferase activity by two-tailed student's t-test (\*: *P*-value <0.05; \*\*: *P*-value <0.01; \*\*\*: *P*-value <0.001).

Fig S<sub>3</sub>



**Supplementary Figure 4. Predicting** *SDHD* **promoter mutation effects on transcription factor binding sites.** Data are shown for **(A)** C541T and **(B)** C544T. Genomic sequence and coordinates are at the bottom of the display; the positions of the matches represented (light blue boxes). The position of the mutations within the motif is indicated by a red-bounded box, with the alternate allele below in red font as on the motif logo position bar above. The motif logos generated from *motfstack* are shown above using the color conventions of the genomic sequence below. Predicted transcription factor name and change score (Alterscore-Refscore) are shown to the right of each motif, and the transcription factor with the strongest score is highlighted in red. Mutations leading to disruption of transcription factor binding sites have negative change scores, while those creating new transcription factor binding sites have positive change scores.

## Fig S4



Supplementary Figure 5. mRNA expression correlation between *SDHD* and multiple ETS transcription factors in TCGA SKCM samples harboring the *SDHD* C523T promoter mutation. Pearson correlation of mRNA expression between *SDHD* and 16 transcription factors with consensus motifs altered by the C523T mutation as predicted by *motifbreakR*. Significant Pearson correlations are highlighted with one or more star (\*: *P*-value <0.05; \*\*: *P*-value <0.01; \*\*\*: *P*-value <0.001).

## Fig S5



ETS mRNA expression (RNA Seq V2 RSEM) (log2)

Supplementary Figure 6. Band-shift experiments indicate wild-type specific binding of ELF1 to the *SDHD* promoter. (A) Band-shift analysis with the C523T *SDHD* promoter mutation oligo and recombinant human ELF1 protein. (B) Band-shift analysis with the C524T *SDHD* promoter mutation oligo and recombinant human ELF1 protein. (C) Band-shift analysis with the C541T *SDHD* promoter mutation oligo and recombinant human ELF1 protein oligo and recombinant human ELF1 protein. (D) Band-shift analysis with the C544T *SDHD* promoter mutation oligo and recombinant human ELF1 protein. (D) Band-shift analysis with the C544T *SDHD* promoter mutation oligo and recombinant human ELF1 protein.

## Fig S6





D





**Supplementary Figure 7. siRNA-mediated knockdown of** *ELF1* **does not lead to decreased** *SDHD* **expression in melanoma cells.** Control siRNA or siRNAs targeting *ELF1* were transfected into cells, and expression of *ELF1* and *SDHD* were assayed by Taqman assays at day 5 following transfection. Data are shown for two melanoma cell lines, (A) UACC903 and (B) UACC1113.

Fig S7

Α

UACC903



UACC1113



В

Supplementary Figure 8. Effects of siRNA-mediated knockdown of PRDM1 or IRF4 on SDHD expression and SDHD promoter activity in melanoma cells. (A) Depletion of *PRDM1* or *IRF4* resulted in varied levels of reduction in *SDHD* expression across melanoma cell lines (UACC903, UACC1113, and C021). Control siRNA or siRNAs targeting *PRDM1* or *IRF4* were transfected into cells, and expression of *PRDM1*, *IRF4* and SDHD were assayed by Taqman assays at day five following transfection. (B) siRNA-mediated depletion of PRDM1 or IRF4 do not dramatically alter wild-type or mutant SDHD promoter activity in an allele-specific manner. A 163-bp fragment from the wild-type SDHD promoter sequence surrounding hotspot mutations significantly enhances luciferase reporter expression relative to vector control. The same fragment containing hotspot mutations results in decreased promoter activity relative to the wildtype sequence. While depletion of *PRDM1* or *IRF4* do broadly result in small alterations in reporter activity, neither alters reporter expression of these constructs in an allelespecific manner. Fold change over minimal promoter control (vector only) is plotted as relative luciferase activity. The experiment was performed four times with triplicates for each.

Α









В





Supplementary Table 1. *SDHD* promoter mutations identified in melanoma tumors datasets (TCGA, Broad and Yale) and melanoma cell lines.

Chromosome	Location	Ref	Alt	Sample	Source	Ref_bases_num	Alt_bases_num			
11	111957518	G	А	Ma-Mel-114	Broad	16				
11	111957527	Т	С	Ma-Mel-35	Broad	3				
11	111957529	С	Т	JWCI-WGS-21	7					
11	111957547	С	Т	ME014	Broad	20	13			
11	111957515	С	Т	UACC257	Cell lines	257	12			
11	111957517	С	Т	C021	Cell lines	59	53			
11	111957524	С	Т	UACC1451	Cell lines	181	5			
11	111957524	С	Т	UACC2528	Cell lines	138	5			
11	111957524	С	Т	UACC952	Cell lines	78	83			
11	111957541	С	Т	C021	Cell lines	54	50			
11	111957541	С	Т	C077	Cell lines	35	11			
11	111957544	С	Т	C077	Cell lines	20	12			
11	111957549	С	Т	C025	Cell lines	8	19			
11	111957556	С	Т	C088	Cell lines	61	37			
11	111957515	С	Т	TCGA-EE-A29M	TCGA	8	10			
11	111957523	С	Т	TCGA-D3-A51G	TCGA	16	5			
11	111957523	С	Т	TCGA-D3-A8GI	TCGA	13	3			
11	111957523	С	Т	TCGA-D9-A1JW	TCGA	11	7			
11	111957523	С	Т	TCGA-DA-A1IC	TCGA	1	6			
11	111957523	С	Т	TCGA-EE-A29D	TCGA	6	3			
11	111957523	С	Т	TCGA-EE-A2GO	TCGA	13	8			
11	111957523	С	Т	TCGA-EE-A3J5	TCGA	8	3			
11	111957523	С	Т	TCGA-HR-A2OG	TCGA	5	6			
11	111957523	С	Т	TCGA-IH-A3EA	TCGA	4	4			
11	111957523	С	Т	TCGA-W3-AA1V	TCGA	7	4			
11	111957523	С	Т	TCGA-YD-A9TA	TCGA	3	6			
11	111957530	Α	G	TCGA-EB-A5UL	TCGA	18	3			
11	111957531	С	Т	TCGA-EE-A2GU	TCGA	8	5			
11	111957532	С	А	TCGA-D3-A2JC	TCGA	12	3			
11	111957532	С	А	TCGA-EE-A2A2	TCGA	165	3			
11	111957532	С	А	TCGA-ER-A19B	TCGA	8	3			
11	111957541	С	Т	TCGA-EE-A2MD	TCGA	7	6			
11	111957541	С	Т	TCGA-EE-A2MI	TCGA	11	6			
11	111957541	С	Т	TCGA-FS-A1ZK	TCGA	0	8			
11	111957544	С	Т	TCGA-EE-A185	TCGA	6	7			
11	111957544	С	Т	TCGA-GN-A26C	TCGA	7	10			
11	111957544	С	Т	TCGA-W3-AA1Q	TCGA	12	8			
11	111957547	С	Т	TCGA-GN-A266	TCGA	12	9			
11	111957548	С	Т	TCGA-D3-A2JE	TCGA	21	8			
11	111957548	С	Т	TCGA-FR-A8YC	TCGA	2	9			
11	111957549	С	Т	TCGA-GN-A26C	TCGA	8	10			
11	111957517	С	Т	YUPADI	Yale	13	18			
11	111957523	С	Т	YUGEN8	Yale	0	43			
11	111957523	С	Т	YURIF	Yale	15	18			
11	111957524	С	Т	YUROO	Yale	16	23			
11	111957535	G	Т	YUFOLD	Yale	92	4			
11	111957544	С	Т	YUKLAB	Yale	60	29			
11	111957544	С	Т	YURUS	Yale	40	6			
11	111957548	С	Т	YUZEAL	Yale	14	28			

S1 Table. *SDHD* promoter mutations identified in melanoma tumors datasets (TCGA, Broad and Yale) and melanoma cell lines.

Supplementary Table 2. MotifBreakR results predicting the effects of recurrent *SDHD* promoter mutations (C523T, C524T, C541T, C544T, and C548T) on transcription factor binding sites.

S2 Table, MotifBreakR results predicting the effects of recurrent SDHD promoter mutations (C5251, C5241, C5411, C5441 and C5481) on transcript	ription factor binding site
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RFF ALT   support   monthly approximate and the support of the provider Altery and the left of alles Alter fleet. More altery approximate altery appre	S2 Ta	ble. N	lotifBreakR	results pi	redicting the effects	of recurrent SDF	<i>HD</i> promoter mutat	ions (C523T, C524T, C541T	, C544T and C548T) or	n transcriptio	n factor	binding si	tes.						
C   T   H1197544   IO   BR1   HOCOMOCO   BR14   IIII MAN   Interactince/Circle   0.390   0.311   0.11   0.21   0.331   0.311   0.11   0.331   0.311   0.331   0.311	REF	ALT	snpPos	motifPos	geneSymbol	dataSource	providerName	providerId	seqMatch	pctRe	pctAlt	scoreRef	scoreAlt	Refpvalue Altpvalue	alleleRef	alleleAlt	effect	dscore	dpct
C   T   11197544   4   BF1   HOCOMOCO   IRF1_RIMAN   entrectCreic   0.890   0.811   0.121   0.237   8.881-04   22:11-6-5   0.000   0.994   store   1.197     C   T   111957544   5   BR1   HOCOMOCO   RR1_R   INIAN   sentification   0.790   0.891   0.016   1.181   1.875   0.870   0.870   0.871   0.880   0.811   1.21   1.471-03   0.000   0.894   store   1.747     C   T   111957541   9   BR1   HOCOMOCO   IRT2_I   INIAN   caracticity   0.720   0.737   0.878   8.681   1.042   1.217.05   4.001   0.892   store   1.743   0.872   0.010   0.892   store   1.743   0.872   0.010   0.892   store   1.743   0.81   0.313   0.32   0.331   0.321   0.331   0.321   0.331   0.321   0.331   0.331   0.331   0.331   0.331	С	Т	111957544	10	IRF4	носомосо	IRF4 si	IRF4 HUMAN	ttteetCtteeetgtt	0.749	0.931	8.314	10.276	2.406E-03 4.231E-06	0.001	0.998	strong	1.961	0.182
C T 111975741 8 PRDM1 PRDM1<	С	Т	111957544	4	IRF1	HOCOMOCO	IRF1 si	IRF1 HUMAN	cattteetCtte	0.809	0.961	10.412	12.337	8.883E-04 2.271E-05	0.000	1.000	strong	1.925	0.152
C T 111957544 5 IRF1 HOCOMOCO IRF2_ID IRF2_ID IRF3 HOCOMOCO IRF3_ID IRF3 HOCOMOCO IRF8_ID IRF3 HOCOMOCO IRF8_ID IRF3 HOCOMOCO IRF8_ID REF3_ID Regattor Cagattor Ref3 REF3 HUMAN cagattor Cagattor Ref3 REF3 HUMAN Cagattor Ref3 Ref3 HUMAN Cagattor Ref3 Ref3 HUMAN Cagattor Ref3 Ref3 HUMAN Cagattor Ref3 HUMAN Cagattor Ref3 Ref3 HUMAN Cagattor Ref3 HUMAN Cagattor Ref3 HUMAN	С	Т	111957541	8	PRDM1	HOCOMOCO	PRDM1_f1	PRDM1_HUMAN	gcatttCctcttcc	0.734	0.859	11.437	13.354	1.073E-03 4.125E-05	0.001	0.994	strong	1.917	0.125
C   T   111957341   8   IRF1   HOCOMOCO   IRF2_1   IRF2_HIMAN   autcleattee   0.72   0.73   0.87   0.83   0.73   0.73   0.73   0.73   0.73   0.73   0.73   0.73   0.73   0.73   0.73   0.73   0.75   8.83   11.412   1.1452-33   6.460-65   0.10   0.78   8.83   1.0474   1.852-03   6.460-65   0.10   0.88   stores   1.55     C   T   11195753   10   IRF8   HOCOMOCO   IRF8_3   IRF8_HIMAN   agenttec/tice   0.78   8.85   7.62   8.977   2.254-31   6.566-41   0.00   0.89   5.89   1.89   1.757   1.757   1.7577	С	Т	111957544	5	IRF2	носомосо	IRF2 f1	IRF2 HUMAN	geattteetCttee	0.790	0.934	10.294	12.135	8.060E-04 1.904E-05	0.000	0.995	strong	1.841	0.144
C   T   111957341   9   IRF2   HOCOMOCO   IRF3-IT   IRF2_HUMAN   cangattCentecce   0.72   0.878   0.642   0.16   0.988   10.42   0.14110-03   7.000E-05   0.016   0.988   10.42   0.141   0.142   0.141   0.142   0.141   0.142   0.141   0.142   0.141   0.142   0.141   0.142   0.141   0.14	С	Т	111957541	8	IRF1	носомосо	IRF1 si	IRF1 HUMAN	atttCctcttcc	0.782	0.919	10.065	11.812	1.455E-03 6.670E-05	0.017	0.983	strong	1.747	0.138
C T 111957541 9 IRF3 HOCOMOCO IRF3_1 IUMAN exattlectifice 0.707 0.879 8.811 0.474 8.825-03 6.460E-05 0.018 0.928 strong 1.388 0   C T 111957543 10 IRF8 HOCOMOCO IRF8_8 IRF8, HIMAN eastteeCtice 0.80 0.885 6.61 9.651-04 0.805 0.905 0.945 strong 1.348 0   C T 111957544 6 IRF8 HOCOMOCO IRF3_8 IRF3 <himan< td=""> ecatocaticaticaticaticaticaticaticaticaticati</himan<>	С	Т	111957541	9	IRF2	HOCOMOCO	IRF2_f1	IRF2 HUMAN	catttCctcttccc	0.742	0.878	9.683	11.412	1.741E-03 7.600E-05	0.016	0.984	strong	1.730	0.135
C T 11197544 5 STAT2 HOCOMOCO STAT2_R NATA space(cg) transmitted) 0.753 8.616 19.636-03 4.806-05 0.031 0.28 store 1.38 0   C T 11197541 10 IRR8 HOCOMOCO IRR8 IRR8 HUMAN epate(cg) transmitted) 0.885 7.62 3.947 5.5276-41 0.855 0.955 0.945 store 1.348 0   C T 11197544 5 IRR8 HUMAN egattec/Circle 0.810 0.934 5.252-444 1.954-66 0.041 0.935 store 1.130 0 0.025 1.974 5.252-444 3.932-66 0.090 0.997 store 1.246-65 0.010 0.987 store 1.130 0 0.025 1.246-65 0.010 0.087 store 1.138 0 1.138 0.135 9.33 1.246-65 0.010 0.087 store 1.138 0 1.138 0 0.037 store 1.246-55 0.046 0.036 0.0626-35 0.036 0.036-36-36	С	Т	111957541	9	IRF3	HOCOMOCO	IRF3 f1	IRF3 HUMAN	cagcatttCctcttccc	0.737	0.879	8.831	10.474	1.852E-03 6.460E-05	0.018	0.982	strong	1.642	0.142
C T 111957521 10 IR78 HOCOMOCO IRF8 is IRF8 HUMAN cantCestneet 0.94 0.945 0.955	С	Т	111957544	5	STAT2	носомосо	STAT2 fl	STAT2 HUMAN	agcattteetCttee	0.760	0.907	7.258	8.616	1.963E-03 4.840E-05	0.031	0.928	strong	1.358	0.147
C T 11937544 10 RF8 HOCMOCCO IRF8 isi RIR8 HUMAN centractiticec 0.80 0.913 8:22 6:15E-04 1.06E-00 0.00 <td>С</td> <td>Т</td> <td>111957523</td> <td>10</td> <td>IRF8</td> <td>HOCOMOCO</td> <td>IRF8 si</td> <td>IRF8 HUMAN</td> <td>gacttCcggttcacc</td> <td>0.748</td> <td>0.885</td> <td>7.629</td> <td>8.977</td> <td>2.225E-03 8.056E-05</td> <td>0.055</td> <td>0.945</td> <td>strong</td> <td>1.348</td> <td>0.137</td>	С	Т	111957523	10	IRF8	HOCOMOCO	IRF8 si	IRF8 HUMAN	gacttCcggttcacc	0.748	0.885	7.629	8.977	2.225E-03 8.056E-05	0.055	0.945	strong	1.348	0.137
C T 111957544 6 IRF8 HOCOMOCO IRF8 IIIMAN cegatiteChcc 0.800 0.933 8.232 9.447 5.572E-04 1700-05 0.30 0.922 strong 11.19   C T 111957544 4 IRF7 HOCOMOCO IRF3_FILMAN recatecta 0.811 0.933 10.28 11.28 16.71E-04 51.41E-0 0.000 0.879 strong 11.30   C T 111957544 4 IRF9 HOCOMOCO IRF3_FI IRF4 HUMAN cattecctagt 0.811 0.931 7.908 12.88E-04 33.98E-04 33.98 0.00 0.82 strong 14.40 0.937 17.97 8.17 10.160-0.85 0.900 0.856 strong 0.440 0.773 8.737 4.706E-04 2.59E-05 0.000 0.856 strong 0.340 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.924 0.9	С	Т	111957541	10	IRF8	HOCOMOCO	IRF8_si	IRF8_HUMAN	catttCctcttccct	0.805	0.943	8.194	9.542	6.155E-04 1.085E-05	0.055	0.945	strong	1.348	0.137
C T 111957544 4 IRF3 HOCOMOCO IRF3_fI IRF3_fILMAN tecageatteeCftce 0.81 0.93 0.028 128.16 1240e-05 0.00 0.87 strong 1178 0   C T 111957541 14 IRF4 HOCOMOCO IRF4_si IRF4_HUMAN tecctected 0.81 0.93 0.918 10.01 2.983E-04 3.393E-06 0.069 0.89 strong 1.113 0   C T 111957541 4 IRF4 HOCOMOCO STAT2_I STAT2_HUMAN catticatCitec 0.793 8.714 1.016-0.85 strong 0.944 0   C T 111957544 5 FOXMI HOCOMOCO FXAT2_HUMAN catticatCettec 0.88 0.90 7.21 8.456 0.116-08 8.516-05 0.716 0.73 8.716 0.737 8.716 0.718 0.80 0.72 0.806-05 0.166 0.85 strong 0.94 0 0.15 vact 0.94 0.228 0.306 0.306 0.660 0.806 0.806 0.806	С	Т	111957544	6	IRF8	HOCOMOCO	IRF8_si	IRF8_HUMAN	gcattteetCtteec	0.809	0.933	8.232	9.447	5.572E-04 1.760E-05	0.030	0.922	strong	1.214	0.124
C T 111957541 4 IRF7 IRF7_II IRF7_III IRF7_III IRF7_IIII IRF7_IIIIIII IRF7_IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	С	Т	111957544	5	IRF3	HOCOMOCO	IRF3_f1	IRF3_HUMAN	ccagcatttcctCttcc	0.840	0.943	10.028	11.218	1.671E-04 7.514E-06	0.041	0.913	strong	1.190	0.103
C T 111957541 14 IRF4 HOCOMOCO IRF4_si IRF4_PIUMAN entCenteceptin 0.310 9.98 0.010 2.983E-04 3.091-0 0.090 8.090 from p.1.04   C T 111957541 9 STAT2 HOCOMOCO RFAT2_fI STAT2_HUMAN geattCcgttec 0.88 0.90 7.03 8.737 4.709E-04 2.864E-05 0.116 0.856 strong 0.944 0   C T 111957544 5 FOXMI HOCOMOCO FSAT2_HUMAN egattCcgtttec 0.880 0.712 8.456 1.041E-03 8.519E-0 0.16 0.856 strong 0.944 0   C T 111957544 8 EFS2 HOCOMOCO FSAT2_HUMAN eccltetcet 0.890 0.836 6.1037 2.861E-05 8.788E-04 8.080 0.025 strong 0.430 0.030 6.55 2.851E-05 8.787E-05 2.81E-05 8.781E-05 8.72E-05 0.787 0.085 strong 0.930 0.060 5.055 5.828E-05 3.72E-05 0.787 0.08 5.	С	Т	111957544	4	IRF7	HOCOMOCO	IRF7_f1	IRF7_HUMAN	tttcctCttc	0.831	0.979	6.730	7.908	1.288E-03 1.240E-05	0.000	0.897	strong	1.178	0.149
C T 111957544 4 IRF9 HUMAN cattleCten 0.71 0.893 7.091 8.130 6.152-64 2.295-65 0.000 1.000 strong 10.49 0   C T 111957541 9 STAT2 HOCOMOCO STAT2_R STAT2_HUMAN geattCcegtttee 0.788 0.890 7.512 8.456 1.041E-03 8.519-06 0.116 0.856 strong 0.944 0   C T 111957548 S FOXMI HOCOMOCO FTAT2_R FTAT2_HUMAN cetCttcetgttut 0.828 6.307 2.861E-08 7.88E-04 0.670 0.656 strong 0.936 strong 0.947 0.056 strong 0.937 0.056 strong 0.937 0.056 strong 0.850 1.011 10.975 strong 0.947 0.056 strong 0.937 0.05 strong 0.937 0.05 strong 0.937 0.05 s	С	Т	111957541	14	IRF4	HOCOMOCO	IRF4 si	IRF4 HUMAN	ttCctcttccctgttt	0.831	0.934	9.198	10.310	2.983E-04 3.393E-06	0.069	0.890	strong	1.113	0.103
C T 111957541 9 STAT2 HOCOMOCO STAT2_Π STAT2_Π STAT2_HUMAN geattCcggttcc 0.818 0.200 7.573 8.737 4.709E-04 2.864E-05 0.116 0.856 strong 0.944 0   C T 111957548 5 FOXM1 HOCOMOCO FOXM1_FILMAN cettCcgtttt 0.832 0.920 4.940 5.312 4.527E-04 3.016-05 2.051E-04 0.760 0.252 weak 0.324 0.025 weak 0.324 0.025 weak 0.324 0.02 0.750 0.02 weak 0.635 0.025 weak 0.635 0.025 weak 0.635 0.26 weak 0.635 0.025 weak 0.635 0.65 3.036E-05 3.036E-05 3.036E-05 3.036E-05 3.036E-05 9.085E-04 0.780 8.037E-05 3.725E-05 1.000 0.000 strong -0.22 weak -0.635 0.65 5.287E-05 3.725E-05 1.000 0.000 strong -0.22 1.037 5.825E-05 3.725E-05 3.000 0.000 strong <td>С</td> <td>Т</td> <td>111957544</td> <td>4</td> <td>IRF9</td> <td>носомосо</td> <td>IRF9_f1</td> <td>IRF9 HUMAN</td> <td>cattteetCtte</td> <td>0.771</td> <td>0.893</td> <td>7.091</td> <td>8.140</td> <td>6.152E-04 2.259E-05</td> <td>0.000</td> <td>1.000</td> <td>strong</td> <td>1.049</td> <td>0.122</td>	С	Т	111957544	4	IRF9	носомосо	IRF9_f1	IRF9 HUMAN	cattteetCtte	0.771	0.893	7.091	8.140	6.152E-04 2.259E-05	0.000	1.000	strong	1.049	0.122
C T 111957523 9 STAT2 HOCOMOCO STAT2_TI STAT2_HIUMAN centCeggttue 0.788 0.890 7.512 8.456 1.011-03 8.519E-05 0.116 0.856 strong 0.944 0   C T 111957548 5 FOXMI HOCOMOCO FOXMI_HUMAN cettCtectg 0.890 0.226 4.940 5.312 4.527E-04 3.818-05 0.00 6.0 2.2 weak 0.327 0   C T 111957544 8 ETS2 HOCOMOCO PPARD_I PPARD_HUMAN tecttectect 0.879 0.813 7.460 6.301 0.357.587E-05 0.572E-05 0.577 0.58 strong 0.920 -0.57 1.11957544 5 ELK3 HOCOMOCO PEAD_I PPARD_I PPARD_I PPARD_I PPARD_I NTMC cegatttecCtggtt 0.879 0.575 5.287E-05 3.72E-03 1.000 0.000 strong -0.227 0.00 strong -0.227 0.00 strong -0.227 0.00 strong -0.237 0.000 strong -1.237	С	Т	111957541	9	STAT2	HOCOMOCO	STAT <sub>2</sub> f1	STAT2 HUMAN	gcatttCctcttccc	0.818	0.920	7.793	8.737	4.709E-04 2.864E-05	0.116	0.856	strong	0.944	0.102
C T 111957548 5 FOXM1 HOCOMOCO FOXM1_f1 FOXM1_f1 FOXM1_f1 Current Cargination   C T 111957548 8 ETS2 HOCOMOCO FTS2_f1 ETS2_f1 ETS2_f1 ETS2_f1 ETS2_f1 ETS2_f1 ETS2_f1 ETS2_f1 ETS2_HUMAN cettCreet(crest) 0.980 0.928 6.361 6.037 2.861E-05 8.788E-04 0.670 0.252 weak 0.324 0   C T 111957548 4 PPARD HOCOMOCO FPARD_HUMAN cettact(Creet) 0.889 0.836 11.611 10.375 5.878E-05 0.787 0.108 weak 0.673 0.700 0.555 0.878E-05 0.878 0.080 0.988E-04 0.865 0.889 0.755 6.882 5.655 5.287E-05 0.787 0.108 weak 0.727 0.00 0.000 strong 1.237 0.000 0.000 strong 1.237 0.000 0.000 strong 1.237 0.000 strong 1.237 0.000 strong 1.237 0.000  C T </td <td>С</td> <td>Т</td> <td>111957523</td> <td>9</td> <td>STAT2</td> <td>HOCOMOCO</td> <td>STAT2 f1</td> <td>STAT2 HUMAN</td> <td>cgacttCcggttcac</td> <td>0.788</td> <td>0.890</td> <td>7.512</td> <td>8.456</td> <td>1.041E-03 8.519E-05</td> <td>0.116</td> <td>0.856</td> <td>strong</td> <td>0.944</td> <td>0.102</td>	С	Т	111957523	9	STAT2	HOCOMOCO	STAT2 f1	STAT2 HUMAN	cgacttCcggttcac	0.788	0.890	7.512	8.456	1.041E-03 8.519E-05	0.116	0.856	strong	0.944	0.102
C T 111957544 8 ETS2 HOCOMOCO ETS2_TI ETS2_HUMAN cctCtrectg 0.980 0.928 6.361 6.037 2.861E-05 8.788E-04 0.676 0.252 weak -0.324 -0.24   C T 111957544 6 SPII HOCOMOCO PPARD_FI PPARD_FI PPARD Control 0.876 0.818 0.836 1.611 10.37 5.97E-06 5.72E-06 0.787 0.086 weak -0.632 -0.227 0.757 0.787 0.88 0.836 1.611 0.937 5.97E-06 3.72E-03 0.000 strong -1.227 0.00 0.00 strong -1.223 0.00 0.000 strong -1.233 0.01 0.010 strong -1.233 0.01	С	Т	111957548	5	FOXM1	носомосо	FOXM1 f1	FOXM1 HUMAN	cttcCctgttttc	0.852	0.920	4.940	5.312	4.527E-04 3.801E-05	0.000	0.514	weak	0.372	0.068
C T 111957548 4 PPARD HOCOMOCO PPARD HUMAN titecteteCcg 0.879 0.813 7.460 6.930 3.036E-05 2.651E-04 0.70 0.056 strong -0.500 -   C T 111957541 11 PPARD HOCOMOCO SP11_JILMAN cagaattecdCteccc 0.879 0.813 7.460 6.540 3.036E-05 2.651E-04 0.828 0.623 total 0.626 strong -0.520 0.62 strong -0.220 0 0.000 strong -1.227 0 0.754 6.882 5.655 5.287E-05 3.725E-03 1.000 0.000 strong -1.227 0 0.00 strong -1.227 0 0.754 6.882 5.655 5.287E-05 3.725E-03 1.000 0.000 strong -1.233 0 0.000 strong -1.237 0 7.88 8/74E-05 1.963E-03 1.000 0.000 strong -1.237 0 7.88 8/74E-05 1.963E-03 1.000 0.000 strong -1.237 0 7.850 3.7	С	Т	111957544	8	ETS2	носомосо	ETS2 f1	ETS2 HUMAN	cctCttccctg	0.980	0.928	6.361	6.037	2.861E-05 8.788E-04	0.676	0.252	weak	-0.324	-0.052
C T 111957544 6 SPI1 HOCOMOCO SPI1_si SPI1_HUMAN cagcattlcc(Tucc 0.889 0.836 11.611 10.937 5.897E-06 5.725E-05 0.082 0.028 0.000 strong -0.920 -0.920 -0.920 -0.920 -0.920 -0.920 -0.727 -0.727 -0.725 -0.727 -0.727 -0.727 -0.727 -0.725 <td>С</td> <td>Т</td> <td>111957548</td> <td>4</td> <td>PPARD</td> <td>носомосо</td> <td>PPARD fl</td> <td>PPARD HUMAN</td> <td>ttteetetteCetg</td> <td>0.879</td> <td>0.813</td> <td>7.460</td> <td>6.930</td> <td>3.036E-05 2.651E-04</td> <td>0.770</td> <td>0.056</td> <td>strong</td> <td>-0.530</td> <td>-0.065</td>	С	Т	111957548	4	PPARD	носомосо	PPARD fl	PPARD HUMAN	ttteetetteCetg	0.879	0.813	7.460	6.930	3.036E-05 2.651E-04	0.770	0.056	strong	-0.530	-0.065
C T 111957541 11 PPARD HOCOMOCO PPARD_fI PPARD_HUMAN tttCctettecetg 0.879 0.765 7.460 6.540 3.036E-05 9.085E-04 0.882 0.662 strong -0.920 -0   C T 111957523 6 ELK3 HOCOMOCO ELK3_fI ELK3_HUMAN cgaattcCggtt 0.928 0.754 6.882 5.655 5.287E-05 3.725E-03 1.000 0.000 strong -1.227 -0   C T 111957523 8 FL11 HOCOMOCO FL11_fI FL11_HUMAN tctgaattCcggttca 0.840 0.722 9.100 7.808 8.974E-05 1.963E-03 1.000 0.000 strong -1.233 -0   C T 111957523 8 ETV7 HOCOMOCO ETV7_si ETV7_HUMAN tctggaattcCggtt 0.849 0.722 9.100 7.88 8.974E-05 1.36E-02 0.900 strong -1.293 -0 C T 11195754 4 ETS2 HOCOMOCO ETS2_fI ETS2_HUMAN cctecttCtg 0.980 0.764	C	Т	111957544	6	SPI1	носомосо	SPI1 si	SPI1 HUMAN	cagcatttcctCttccc	0.889	0.836	11.611	10.937	5.897E-06 5.725E-05	0.787	0.108	weak	-0.673	-0.053
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	C	Т	111957541	11	PPARD	носомосо	PPARD fl	PPARD HUMAN	tttCctcttccctg	0.879	0.765	7.460	6.540	3.036E-05 9.085E-04	0.882	0.062	strong	-0.920	-0.113
C T 111957524 5 ELK3 HOCOMOCO ELK3_RI ELK3_HUMAN cgacttcCggtt 0.928 0.754 6.882 5.655 5.287E-05 3.725E-03 1.000 0.000 strong -1.227 -0.000   C T 111957523 8 FLI1 HOCOMOCO FLI1_FI FLI1_HUMAN tctegacttCcggttca 0.968 0.755 6.753 5.208 1.795E-05 4.244E-03 0.900 strong -1.233 -0.000 strong -1.234 -0.0000 strong	С	Т	111957523	6	ELK3	носомосо	ELK3 fl	ELK3 HUMAN	cgacttCcggtt	0.928	0.754	6.882	5.655	5.287E-05 3.725E-03	1.000	0.000	strong	-1.227	-0.174
C T 111957523 8 FLI1 HOCOMOCO FLI1_fI FLI1_HUMAN tdcgacttCggttca 0.968 0.785 6.753 5.520 1.795E-05 4.244E-03 0.924 0.000 strong -1.233 0.00   C T 111957523 8 ETV7 HOCOMOCO ETV7_si ETV7_HUMAN tctcgacttCggttca 0.849 0.722 9.100 7.808 8.974E-05 1.963E-03 1.000 0.000 strong -1.293 0.000 ctrong -1.293 0.000 strong -1.293 0.000 strong -1.294 0.000 strong <td>Ċ</td> <td>Т</td> <td>111957524</td> <td>5</td> <td>ELK3</td> <td>носомосо</td> <td>ELK3 fl</td> <td>ELK3 HUMAN</td> <td>cgacttcCggtt</td> <td>0.928</td> <td>0.754</td> <td>6.882</td> <td>5.655</td> <td>5.287E-05 3.725E-03</td> <td>1.000</td> <td>0.000</td> <td>strong</td> <td>-1.227</td> <td>-0.174</td>	Ċ	Т	111957524	5	ELK3	носомосо	ELK3 fl	ELK3 HUMAN	cgacttcCggtt	0.928	0.754	6.882	5.655	5.287E-05 3.725E-03	1.000	0.000	strong	-1.227	-0.174
C T 111957523 8 ETV7 HOCOMOCO ETV7_si ETV7_HUMAN tregacttCggttca 0.849 0.722 9.100 7.808 8.974E-05 1.963E-03 1.000 0.000 strong -1.293 -0   C T 111957524 7 ETV7 HOCOMOCO ETV7_si ETV7_HUMAN tregacttCggttca 0.849 0.722 9.100 7.808 8.974E-05 1.963E-03 1.000 0.000 strong -1.293 -0   C T 111957524 7 ETV7 HOCOMOCO ETS2_fI ETS2_HUMAN cgacttCggt 0.970 0.764 6.301 5.034 2.861E-05 1.374E-02 0.936 0.015 strong -1.327 -0   C T 111957524 4 ELK1 HOCOMOCO ETS2_fI ETS2_HUMAN cgacttcCggt 0.970 0.759 6.011 4.94 8.345E-05 1.510E-02 0.936 0.015 strong -1.327 -0   C T 111957524 4 ELK1 HOCOMOCO ELK1_fI ELK4_HUMAN gacttCggtt 0.	Ċ	Т	111957523	8	FLI1	носомосо	FLI1 fl	FLI1 HUMAN	tctcgacttCcggttca	0.968	0.785	6.753	5.520	1.795E-05 4.244E-03	0.924	0.000	strong	-1.233	-0.184
C T 111957524 7 ETV7 HOCOMOCO ETV7_si ETV7_HUMAN tetegaetteCggttea 0.849 0.722 9.100 7.808 8.974E-05 1.963E-03 1.000 0.000 strong -1.293 -0   C T 111957523 5 ETS2 HOCOMOCO ETS2_f1 ETS2_HUMAN cgattCcggt 0.970 0.764 6.301 5.007 8.345E-05 1.346E-02 0.933 0.067 strong<-1.294	Ċ	Т	111957523	8	ETV7	носомосо	ETV7 si	ETV7 HUMAN	tctcgacttCcggttca	0.849	0.722	9.100	7.808	8.974E-05 1.963E-03	1.000	0.000	strong	-1.293	-0.127
C T 111957523 5 ETS2 HOCOMOCO ETS2_fI ETS2_HUMAN cgattCcggt 0.970 0.764 6.301 5.007 8.345E-05 1.436E-02 0.933 0.067 strong -1.294 -0   C T 111957523 4 ETS2 HOCOMOCO ETS2_fI ETS2_HUMAN ccattCcggt 0.970 0.759 6.301 4.974 8.345E-05 1.510E-02 0.936 0.015 strong -1.327 -0   C T 111957524 4 ELK1 HOCOMOCO ELK1_fI ELK1_HUMAN cgattCcggt 0.970 0.759 6.301 4.974 8.345E-05 1.510E-02 0.936 0.015 strong -1.327 -0   C T 111957524 4 ELK1 HOCOMOCO ELK1_fI ELK1_HUMAN cgattCcggtt 0.990 0.868 10.675 5.333 1.95E-06 6.113E-03 0.942 0.495 0.495 0.495 0.495 0.495 0.496 0.406 0.496 0.600 strong -1.327 0 0 0.00 strong <td< td=""><td>C</td><td>Т</td><td>111957524</td><td>7</td><td>ETV7</td><td>носомосо</td><td>ETV7 si</td><td>ETV7 HUMAN</td><td>tctcgacttcCggttca</td><td>0.849</td><td>0.722</td><td>9.100</td><td>7.808</td><td>8.974E-05 1.963E-03</td><td>1.000</td><td>0.000</td><td>strong</td><td>-1.293</td><td>-0.127</td></td<>	C	Т	111957524	7	ETV7	носомосо	ETV7 si	ETV7 HUMAN	tctcgacttcCggttca	0.849	0.722	9.100	7.808	8.974E-05 1.963E-03	1.000	0.000	strong	-1.293	-0.127
C T 111957548 4 ETS2 HOCOMOCO ETS2_fl ETS2_HUMAN cctetteCctg 0.980 0.768 6.361 5.034 2.861E-05 1.374E-02 0.936 0.015 strong -1.327 C   C T 111957524 4 ETS2 HOCOMOCO ETS2_fl ETS2_HUMAN cgattcCggt 0.970 0.759 6.301 4.974 8.345E-05 1.510E-02 0.936 0.015 strong -1.327 -0   C T 111957524 4 ELK1 HOCOMOCO ELK1_fl ELK4_HUMAN gattcCggtt 0.990 0.868 10.671 9.283 1.192E-06 2.401E-04 0.945 0.445 strong -1.340 -0   C T 111957524 7 ELI HOCOMOCO ELK4_fl HUMAN gattCctggttca 0.968 0.660 6.753 5.353 1.795E-05 6.113E-03 0.900 strong -1.400 -0   C T 111957524 5 ELK4 HOCOMOCO FEV_fl FEV_HUMAN gattCcggttacccagaca 0.903 0.662 </td <td>č</td> <td>Т</td> <td>111957523</td> <td>5</td> <td>ETS2</td> <td>носомосо</td> <td>ETS2 f1</td> <td>ETS2 HUMAN</td> <td>cgacttCcggt</td> <td>0.970</td> <td>0.764</td> <td>6.301</td> <td>5.007</td> <td>8.345E-05 1.436E-02</td> <td>0.933</td> <td>0.067</td> <td>strong</td> <td>-1.294</td> <td>-0.206</td>	č	Т	111957523	5	ETS2	носомосо	ETS2 f1	ETS2 HUMAN	cgacttCcggt	0.970	0.764	6.301	5.007	8.345E-05 1.436E-02	0.933	0.067	strong	-1.294	-0.206
C T 111957524 4 ETS2 HOCOMOCO ETS2_f1 ETS2_HUMAN cgacttcCggt 0.970 0.759 6.301 4.974 8.345E-05 1.510E-02 0.936 0.015 strong -1.327 C   C T 111957524 4 ELK1 HOCOMOCO ELK1_f1 ELK1_HUMAN acttcCggt 1.000 0.816 7.395 6.055 0.000E+00 3.193E-03 0.919 0.020 strong -1.327 C   C T 111957524 4 ELK4 HOCOMOCO ELK4, HUMAN acttCcggtt 0.999 0.868 10.671 9.283 1.192E-06 2.401E-04 0.945 0.045 strong -1.328 0.00 C 7 11957524 7 FLI1 HOCOMOCO FLV_f1 FLV_HUMAN gcattCCggttacccagca 0.968 0.706 6.753 5.353 1.795E-05 6.113E-03 0.900 0.808 strong -1.328 0.900 0.808 strong -1.328 0.900 0.915 strong -1.328 0.900 0.915 strong -1.328 0.916 <td< td=""><td>č</td><td>Т</td><td>111957548</td><td>4</td><td>ETS2</td><td>носомосо</td><td>ETS2 fl</td><td>ETS2 HUMAN</td><td>cctcttcCctg</td><td>0.980</td><td>0.768</td><td>6.361</td><td>5.034</td><td>2.861E-05 1.374E-02</td><td>0.936</td><td>0.015</td><td>strong</td><td>-1.327</td><td>-0.212</td></td<>	č	Т	111957548	4	ETS2	носомосо	ETS2 fl	ETS2 HUMAN	cctcttcCctg	0.980	0.768	6.361	5.034	2.861E-05 1.374E-02	0.936	0.015	strong	-1.327	-0.212
C T 111957524 4 ELK1 HOCOMOCO ELK1_fI ELK1_HUMAN acttC2gt 100 0.816 7.395 6.055 0.000E+00 3.193E-03 0.919 0.020 strong -1.340 0.000   C T 111957524 6 ELK4 HOCOMOCO ELK4_fI ELK4_HUMAN gacttC2ggtta 0.999 0.868 10.671 9.283 1.192E-06 2.401E-04 0.945 0.045 strong -1.348 -0   C T 111957524 7 FL11 HOCOMOCO FEV_fI FLV_HUMAN gcattC2gttcacccagca 0.968 0.760 6.753 5.353 1.795E-05 6.118E-03 0.962 0.038 strong -1.400 -0   C T 111957524 5 FEV HOCOMOCO FEV_fI FEV_HUMAN gcattC2gtt 0.957 0.779 8.291 6.792 7.153E-05 3.13E-04 0.962 0.000 strong -1.498 -0   C T 111957524 5 ELK4 HOCOMOCO FEK4_fI ELK4_HUMAN gcattC2ggtt 0.999<	Ċ	Т	111957524	4	ETS2	носомосо	ETS2_f1	ETS2 HUMAN	cgacttcCggt	0 970	0 759	6 301	4 974	8 345E-05 1 510E-02	0.936	0.015	strong	-1 327	-0.212
C T 111957523 6 ELK4 HOCOMOCO ELK4_II ELK4_HUMAN gacttCcggtt 0.999 0.868 10.671 9.283 1.192E-06 2.401E-04 0.945 0.045 strong -1.388 0.000   C T 111957524 7 FLI1 HOCOMOCO FLI1_f1 FLI1_HUMAN tettagacttCcggttca 0.968 0.606 6.753 5.353 1.795E-05 6.113E-03 0.962 0.038 strong -1.408 -0   C T 111957524 7 FLI1 HOCOMOCO FEV_f1 FEV_HUMAN gcatttCcgtt 0.957 0.779 8.291 6.792 7.153E-05 3.216E-03 1.000 0.000 strong -1.498 -0   C T 111957524 5 TFCP2 HOCOMOCO FEV_f1 ELK4_HUMAN gacttCcggtt 0.999 0.863 10.671 9.128 1.192E-06 3.138E-04 0.963 0.010 strong -1.498 -0   C T 111957524 3 GABPB1+GABPB2 HOCOMOCO ELK4_HUMAN gacttCcggtt 0.997	č	Т	111957524	4	ELK1	носомосо	ELK1_f1	ELK1 HUMAN	acttcCggt	1 000	0.816	7 395	6.055	0 000E+00 3 193E-03	0.919	0.020	strong	-1 340	-0.184
C T 111957524 7 FLI1 HOCOMOCO FLI1_fI FLI1_HUMAN tetegatteCggttca 0.968 0.760 6.753 5.353 1.795E-05 6.113E-03 0.962 0.038 strong -1.400 0.000   C T 111957524 4 FEV HOCOMOCO FEV_fI FEV_HUMAN gcatttCctc 0.957 0.779 8.291 6.792 7.153E-05 3.216E-03 1.000 0.000 strong -1.498 -0   C T 111957523 15 TFCP2 HOCOMOCO FEV_f1 FEV_HUMAN tetegatteCggtt 0.903 0.662 5.881 4.383 6.354E-05 2.268E-02 1.000 0.000 strong -1.498 -0   C T 111957524 5 ELK4 HOCOMOCO ELK4_fI ELK4_HUMAN gcattCcggt 0.999 0.853 10.671 9.128 1.192E-06 3.138E-04 0.963 0.010 strong -1.544 -0   C T 111957524 3 GABPB1+GABPB2 HOCOMOCO EHF_si EHF_HUMAN gcattCcggt	č	Т	111957523	6	ELK4	носомосо	ELK4_f1	ELK4 HUMAN	gacttCcggtt	0 999	0.868	10 671	9 283	1 192E-06 2 401E-04	0.945	0.045	strong	-1 388	-0.131
C T 111957541 4 FEV HOCOMOCO FEV_f1 FEV_HUMAN regattCctc 0.957 0.779 8.291 6.792 7.153E-05 3.216E-03 1.000 0.000 strong -1.498 -0   C T 111957523 15 TFCP2 HOCOMOCO TFCP2_f1 TFCP2_HUMAN tccggttcacccagea 0.903 0.662 5.881 4.383 6.354E-05 2.268E-02 1.000 0.000 strong -1.498 -0   C T 111957524 5 ELK4 HOCOMOCO ELK4_f1 ELK4_HUMAN gacttCcggt 0.990 0.853 10.671 9.128 1.192E-06 3.133E-04 0.963 0.010 strong -1.544 -0   C T 111957524 3 GABPB1+GABP2 HOCOMOCO GABP1+GABP2_f1 <t< td=""><td>č</td><td>Т</td><td>111957524</td><td>7</td><td>FL11</td><td>носомосо</td><td>FLI1 fl</td><td>FLI1 HUMAN</td><td>tetegaetteCggttea</td><td>0.968</td><td>0 760</td><td>6 753</td><td>5 353</td><td>1 795E-05 6 113E-03</td><td>0.962</td><td>0.038</td><td>strong</td><td>-1 400</td><td>-0.209</td></t<>	č	Т	111957524	7	FL11	носомосо	FLI1 fl	FLI1 HUMAN	tetegaetteCggttea	0.968	0 760	6 753	5 353	1 795E-05 6 113E-03	0.962	0.038	strong	-1 400	-0.209
C T 111957523 15 TFCP2 HOCOMOCO TFCP2_f1 TFCP2_HUMAN tCcggttcacccagea 0.903 0.662 5.881 4.383 6.354E-05 2.268E-05 1.000 0.000 strong -1.498 -0   C T 111957523 5 ELK4 HOCOMOCO ELK4_f1 ELK4_HUMAN gacttCcggtt 0.999 0.853 10.671 9.128 1.192E-06 3.133E-04 0.963 0.010 strong -1.544 -0   C T 111957524 3 GABPB1+GABPB2 HOCOMOCO GABP1+GABP2_f1 GABP1+GABP2_f1 GABP1+GABP2 HUMAN cgacttCcggt 0.987 0.807 8.641 7.096 1.049E-05 2.362E-03 0.973 0.027 strong -1.544 -0   C T 111957523 8 EHF HOCOMOCO EHF_si EHF_HUMAN gacttCcggttca 0.939 0.811 11.452 9.905 8.966-06 7.288E-04 0.900 strong -1.544 -0   C T 111957523 5 ELK1 HOCOMOCO GABP1+GABP2_F1 <	Č	т	111957541	4	FEV	носомосо	FEV fl	FEV HUMAN	gcatttCctc	0.957	0 779	8 291	6 792	7 153E-05 3 216E-03	1.000	0.000	strong	-1 498	-0.178
C T 111957524 5 ELK4 HOCOMOCO ELK4_f1 ELK4_HUMAN gattcCggtt 0.99 0.853 10.671 9.128 1.192F-06 3.133E-04 0.963 0.010 strong -1.544 -0   C T 111957524 3 GABPB1+GABPB2 HOCOMOCO GABP1+GABP2_f1 GABP1+GABP2_HUMAN gattCcggtt 0.987 0.807 8.641 7.096 1.049E-05 2.362E-03 0.973 0.027 strong -1.544 -0   C T 111957523 8 EHF HOCOMOCO EHF_si EHF_HUMAN gattCcggtt 0.939 0.811 11.452 9.905 8.956E-06 7.288E-04 0.940 0.000 strong -1.544 -0   C T 111957523 5 ELK1 HOCOMOCO ELK1_f1 ELK1_HUMAN acttCcggt 0.937 0.375 5.811 0.000E+00 5.070E-03 0.959 0.013 strong -1.544 -0   C T 111957523 4 GABPB1+GABPB2 HOCOMOCO GABP1+GABP2_f1 GABP1+GABP2_HUMAN gacttCcggt	č	Ť	111957523	15	TECP2	носомосо	TECP2 fl	TECP2 HUMAN	tCoottcacccaoca	0.903	0.662	5 881	4 383	6 354E-05 2 268E-02	1.000	0.000	strong	-1 498	-0.242
C T 111957524 3 GABPB1+GABPB2 GABP1+GABP2 fi	č	Ť	111957524	5	FLK4	носомосо	ELK4 fl	FLK4 HUMAN	gactteCoott	0.999	0.853	10 671	9 1 2 8	1 192E-06 3 133E-04	0.963	0.010	strong	-1 544	-0.146
C T 111957523 8 EHF HOCOMOCO EHF_si EHF_HUMAN gattCcggttca 0.93 0.811 11.452 9.905 8.956E-06 7.288E-04 0.940 0.000 strong -1.547 0   C T 111957523 5 ELK1 HOCOMOCO EHF_si EHF_HUMAN gattCcggttca 0.939 0.811 11.452 9.905 8.956E-06 7.288E-04 0.940 0.000 strong -1.547 0   C T 111957523 5 ELK1 HOCOMOCO ELK1_f1 ELK1_HUMAN acttCcggt 1.000 0.783 7.395 5.811 0.000E+00 5.070E-03 0.959 0.013 strong -1.547 0   C T 111957523 4 GABPB1+GABPB2 HOCOMOCO GABP1+GABP2_f1 GABP1+GABP2_HUMAN cgattCcggt 0.987 0.780 8.641 6.865 1.049E-05 4.217E-03 1.000 0.000 strong -1.776 0   C T 111957523 6 ELF5 HOCOMOCO ELF5_f11 ELF5_HUMAN gattCcggtt	č	Ť	111957524	3	GABPB1+GABPB2	HOCOMOCO	GABP1+GABP2 fl	GABP1+GABP2 HUMAN	coactteCoo	0.987	0.807	8 641	7 096	1.049E-05 2.362E-03	0.973	0.027	strong	-1 544	-0.180
C T 111957523 5 ELK1 HOCOMOCO ELK1_FI ELK1_HUMAN actCcggt 1.00 0.780 5.81 0.000E/0 5.070E/0 0.059 0.013 strong -1.584 0   C T 111957523 5 ELK1 HOCOMOCO ELK1_FI ELK1_HUMAN actCcggt 1.00 0.780 5.81 0.000E/0 5.070E/0 0.000 strong -1.584 0   C T 111957523 4 GABPB1+GABP22_FI GABP1+GABP2_HUMAN cgacttCcgg 0.987 0.780 8.641 6.865 1.049E/05 4.217E-03 1.000 0.000 strong -1.776 0   C T 111957523 6 ELF5 HOCOMOCO ELF5_FI ELF5_HUMAN gacttCcggtt 0.952 0.723 7.604 5.814 6.806E-02 1.000 0.000 strong -1.790 0   C T 111957523 6 ELF5 FI ELF5_HUMAN gacttCcggtt 0.952 0.723 7.604 5.814 6.806E-02 1.000 0.000 strong <t< td=""><td>Č</td><td>т</td><td>111957523</td><td>8</td><td>EHE</td><td>носомосо</td><td>EHE si</td><td>EHE HUMAN</td><td>gacttCcggttca</td><td>0.939</td><td>0.811</td><td>11 452</td><td>9 905</td><td>8 956E-06 7 288E-04</td><td>0.940</td><td>0.000</td><td>strong</td><td>-1 547</td><td>-0.128</td></t<>	Č	т	111957523	8	EHE	носомосо	EHE si	EHE HUMAN	gacttCcggttca	0.939	0.811	11 452	9 905	8 956E-06 7 288E-04	0.940	0.000	strong	-1 547	-0.128
C T 111957523 4 GABPB1+GABPB2 HOCOMOCO GABP1+GABP2_f1 GABP1+GABP2	č	Ť	111957523	5	ELK1	носомосо	ELK1_fl	FLK1 HUMAN	acttCcoot	1.000	0.783	7 395	5 811	0.000E+00_5.070E-03	0.959	0.013	strong	-1 584	-0.217
C   T   111957523   6   ELF5   HOCOMOCO   ELF5_f1   ELF5_HUMAN   gattCcggtt   0.952   0.723   7.604   5.814   6.890E-05   1.500E-02   1.000   0.000   strong   -1.790   -0	č	Ť	111957523	4	GABPB1+GABPB2	HOCOMOCO	GABP1+GABP2 fl	GABP1+GABP2 HUMAN	cgacttCcgg	0.987	0.780	8 641	6 865	1 049E-05 4 217E-03	1.000	0.000	strong	-1 776	-0.207
	c	т	111957523	6	FLF5	носомосо	FLE5 fl	FLF5 HUMAN	gaettCeggtt	0.952	0.723	7 604	5 814	6 890E-05 1 560E-02	1.000	0.000	strong	-1 790	-0.229
C T LL1957524 5 ELF5 HUCOMOCO ELF5 f1 ELF5 HUMAN gatteCogt 0.952 0.723 7.604 5.814 6.890E-05 1.560E-02 1.000 0.000 strong -1.790 -0	č	Ť	111957524	5	ELF5	носомосо	ELE5_f1	ELF5 HUMAN	gaetteCoott	0.952	0.723	7.604	5 814	6 890E-05 1 560E-02	1.000	0.000	strong	-1 790	-0.229
C T 111957541 6 ELES HOCOMOCO ELES 1 ELES ENMAN cattered 0.72 0.725 .044 5.054 5.0500 0.1000 0.000 stang 1.790 0	c	Ť	111957524	6	ELF5	носомосо	ELES_f1	ELF5 HUMAN	catttCctctt	0.970	0.742	7 745	5 955	2 480E-05 1 425E-02	1.000	0.000	strong	-1 790	-0.229
C T 111957513 5 ELET HOCOMOCO ELETT ELETTIONIC cancel 0.70 7.078 9.083 7.203 6.676E.06.4.254E.03 1.000 0.000 strong 1.881_C	c	Ť	111957523	5	ELF 5 FLF1	носомосо	ELFJ_fl	ELFI HUMAN	gacttCoggt	0.997	0.788	9.083	7 203	6 676E-06 4 254E-03	1.000	0.000	strong	-1 881	-0.209
C T 111957524 4 FIF1 HOCOMOCO FIF1 FI FIF1 HIMAN gatteregg, 0.977 0.788 9.083 7.203 6.676E.06.4.54E.03 1.000 0.000 strong 1.881.6	c	т	111957523	4	ELF1 ELF1	носомосо	ELF1_f1	ELF1 HUMAN	gaetteCggt	0.997	0.788	9.083	7 203	6 676E-06 4 254E-03	1.000	0.000	strong	-1 881	-0.209
C T 11195753 5 FTS1 HOCOMOCO ETS1 si FTS1 HIMAN april-Cent 0.985 0743 7521 5952 15562-05 15662-09 0.000 studig -1.061-0	č	T	111957523	5	ETS1	HOCOMOCO	ETS1_si	ETSI HUMAN	acttCeggt	0.997	0.743	7 821	5 925	1 526E-05 1 568E-02	0.996	0.000	strong	-1 806	-0.243
C T 111957541 9 SPIL HOCOMOCO SPIL si SPIL HUMAN caecute cherce 0.880.0739 11611 9.608 5.807E.06.1082E.03.004 0.005 strong -1.03.2	c	т	111957541	9	SPI1	НОСОМОСО	SPI1 ei	SPI1 HUMAN	cagcatttCetetteee	0.985	0.730	11 611	9.698	5 897E-06 1 082E-02	0.994	0.005	strong	_1 913	-0 150
C T 11957574 4 FTS1 HOCOMOCO ETS1 si ETS1 HIMAN acticCot 0.095 0.757 1301 5050 507500 1002203 0.774 0.000 studig 1.131 50	č	т	111957524	4	ETS1	НОСОМОСО	ETS1 si	ETS1 HUMAN	actteCoot	0.009	0.738	7 821	5 887	1 526E-05 1 577E-02	1 000	0.000	strong	-1 93/	-0 247
C T 11195751 7 FIE HOCOMOCO EHE si EHE HIMAN andre Contra 0.030.0756 1.1452 0.467 8.0562 0.1572.000 0.000 studig -1.539 0	č	т	111957524	7	EHE	НОСОМОСО	EHE of	EHE HUMAN	aactteCaattea	0.285	0.756	11 452	9 4 87	8 956E-06 1 537E-02	1.000	0.000	strong	-1 966	-0.162
C T 111957525 7 ERG HOCOMOCO ERG fl FRG HIMAN 20204/Contr 0.052 0.1/10 11.372 0.301 1007E.06 0166E.01 1.000 0.000 studig -1.300 -0	č	т	111057572	5	EBC	НОСОМОСО	ERG fl	FRG HUMAN	caacttCegat	0.739	0.770	11 372	9 207	1 907E-06 0 186E 04	1.000	0.000	strong	_1 080	-0 172
C T 111957525 4 ERG HOCOMOCO ERG EL ERG-HOMAN eggetteCggt 0.705 0.011 11.372 0.302 1.0012-04 1.000 0.000 studig -1.300 -0 C T 111957524 4 ERG HOCOMOCO ERG EL ERG-HUMAN eggetteCggt 0.705 0.011 11.372 0.302 1.0072-0.60 1862.04 1.000 0.000 studig -1.300 -0	č	т	111957524	Л	ERG	НОСОМОСО	ERG_f1	FRG HUMAN	cgaetteCoot	0.783	0.011	11 372	9 302	1.907E-06 0.186E 04	1.000	0.000	strong	_1 080	-0.172
C T 11195757 7 GARPA HOCOMOCO CARPA FI GARPA HIMAN coacter 0983 0820 12201 12201 10205 333E-05 7427E-04 1000 0.000 studie -1.205 -205 -205 -205 -205 -205 -205 -205 -	č	T	111957524	7	GARPA	HOCOMOCO	GABPA fl	GARPA HUMAN	cgaettCeggt	0.983	0.820	12 201	10 205	3 353E-06 7 427E-04	1.000	0.000	strong	-1 995	-0.162
C T 11195754 6 GARPA HOCOMOCO GARPA FI GARPA HUMAN construction 0.963 0.800 12.201 10.205 333E-06 7.477E-04 1.000 0.000 strong -1.995 -0	c	Ť	111957524	6	GABPA	НОСОМОСО	GABPA fl	GABPA HUMAN	coactteCootte	0.983	0.820	12.201	10 205	3 353E-06 7 427E-04	1.000	0.000	strong	-1 995	-0.162

Note: REF :the reference allele for the SNP ALT :the alternate allele for the SNP snpPos :the coordinates of the SNP motifPos :the coordinates of the SNP within the TF binding motif geneSymbol :the geneSymbol corresponding to the TF of the TF binding motif dataSource :the source of the TF binding motif providerName, providerId :the name and id provided by the source seqMatch : the sequence on the 5' -> 3' direction of the "+" strand that corresponds to DNA at the position that the TF binding motif was found. pctRef :The score as determined by the scoring method, when the sequence contains the reference SNP allele, normalized to a scale from 0 - 1. If filterp = FALSE, this is the value that is thresholded. pctAlt :The score as determined by the scoring method, when the sequence contains the alternate SNP allele, normalized to a scale from 0 - 1. If filterp = FALSE, this is the value that is thresholded. scoreRef :The score as determined by the scoring method, when the sequence contains the reference SNP allele scoreAlt :The score as determined by the scoring method, when the sequence contains the alternate SNP allele Refpvalue :p-value for the match for the pctRef score, initially set to NA. see calculatePvalue for more information Altpvalue :p-value for the match for the pctAlt score, initially set to NA. see calculatePvalue for more information alleleRef : The proportional frequency of the reference allele at position motifPos in the motif alleleAlt :The proportional frequency of the alternate allele at position motifPos in the motif effect :one of weak, strong, or neutral indicating the strength of the effect. dscore: scoreAlt-ScoreRef dpct: pctAlt-pctRef

Supplementary Table 3. Oligonucleotide design for quantitative mass spectrometry.

S3 Table. Oligonucleotide design for quantitative mass spectrometry.

Oligo name	Forward	Reverse
WT_SDHD	5'-GTGCACCGCCTCTCGACTTCcGGTTCACCCAGCATTTcCTcTTCCCTGTTTTCTTTCGTCG-3'	5'- CGACGAAAGAAAACAGGGAAgAGgAAATGCTGGGTGAACCgGAAGTCGAGAGGCGGTGCAC-3'
C524T	5'-GTGCACCGCCTCTCGACTTCtGGTTCACCCAGCATTTCCTCTCCCTGTTTTCTTTCGTCG-3'	5'-CGACGAAAGAAAACAGGGAAGAGGAAATGCTGGGTGAACCaGAAGTCGAGAGGCGGTGCAC-3'
C541T	5'-GTGCACCGCCTCTCGACTTCCGGTTCACCCAGCATTTtCTCTTCCCTGTTTTCTTTCGTCG-3'	5'-CGACGAAAGAAAACAGGGAAGAGaAAATGCTGGGTGAACCGGAAGTCGAGAGGCGGTGCAC-3'
C544T	5'-GTGCACCGCCTCTCGACTTCCGGTTCACCCAGCATTTCCTtTTCCTGTTTTCTTTCGTCG-3'	5'- CGACGAAAGAAAACAGGGAAaAGGAAATGCTGGGTGAACCGGAAGTCGAGAGGCGGTGCAC-3'

Design Location: chr11:111,957,504-111,957,564