Supplementary Figures

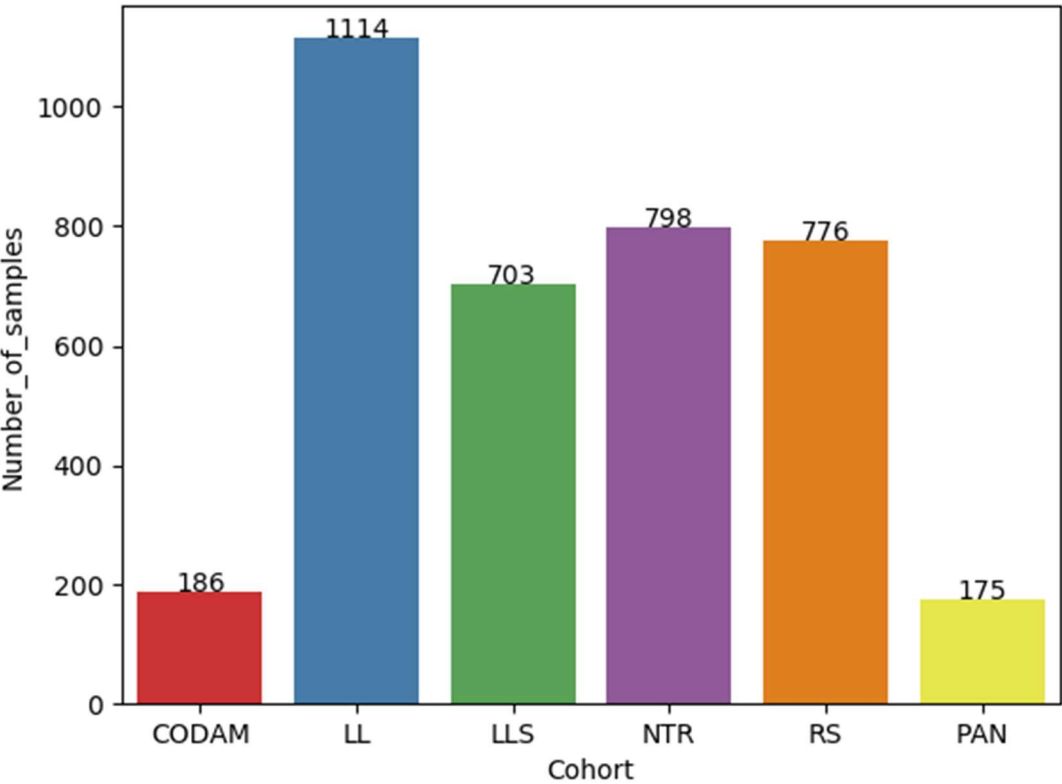**Figure S1:** The number of samples used from each cohort during calculations.

Settings eQTLgen pipeline

		run command
run type		
	Metaqtl	java -Xmx40g -Xms20g -XX:StringTableSize=10000019 -XX:MaxPermSize=512m -jar /groups/umcg-bios/tmp01/resources/genotypes-hrc-imputed-vcf/eqtl-mapping-pipeline-1.4.9-SNAPSHOT/eqtl-mapping-pipeline.jar --mode metaqtl --settings settings2.xml 2>&1 | tee cisEQtlMapping.log
	Iterative	java -Xmx40g -Xms20g -XX:StringTableSize=10000019 -XX:MaxPermSize=512m -jar /groups/umcg-bios/tmp01/resources/genotypes-hrc-imputed-vcf/eqtl-mapping-pipeline-1.4.9-SNAPSHOT/eqtl-mapping-pipeline.jar --mode conditional --iterative --settings settings2.xml 2>&1 | tee cisEQtlMapping.log
Gene to run for		settings file
	STX3	settings2.xml
	SREBF2	gene2_settings.xml

Figure S2: The settings with which the eQTLgen pipeline was run. Both run types were used for both gene, creating four different runs. The data from the iterative runs were used for model initialization using the latest iteration where the number of identified Cis-eQTLs is above 0. The settings files are in Supplementary data 2.
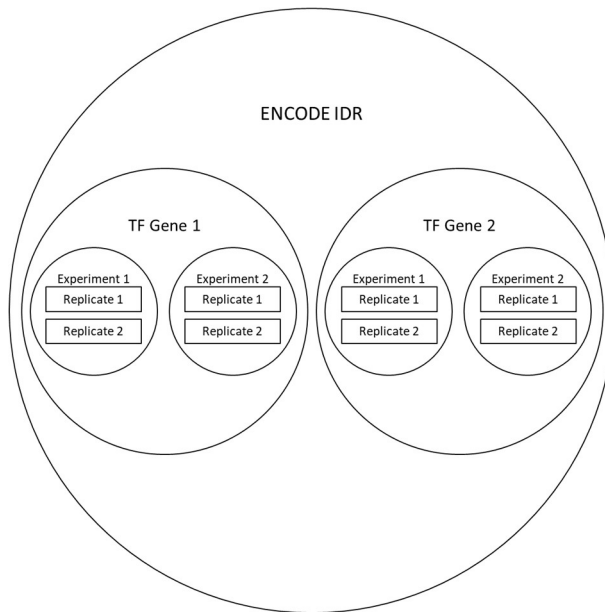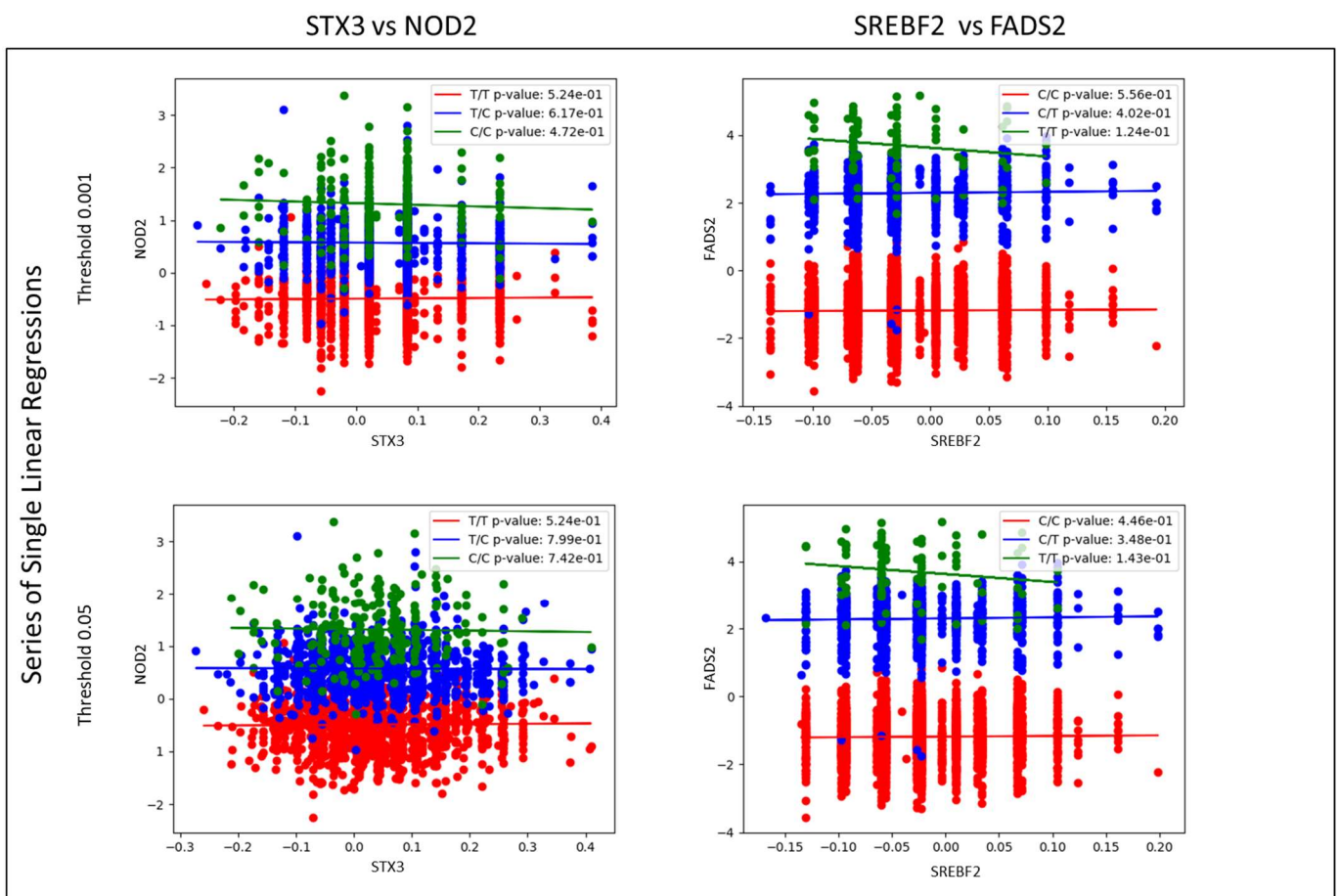
Figure S3: Structure of the ENCODE_IDR folder required for scripts to work on the folder. There is one folder for each TF gene, within those folders are folders for the CHiPs-seq experiment performed using the TF gene as the target. Within the experiment folders are .Bed, .bigBed or .bigWig files for the replicates of the experiment.
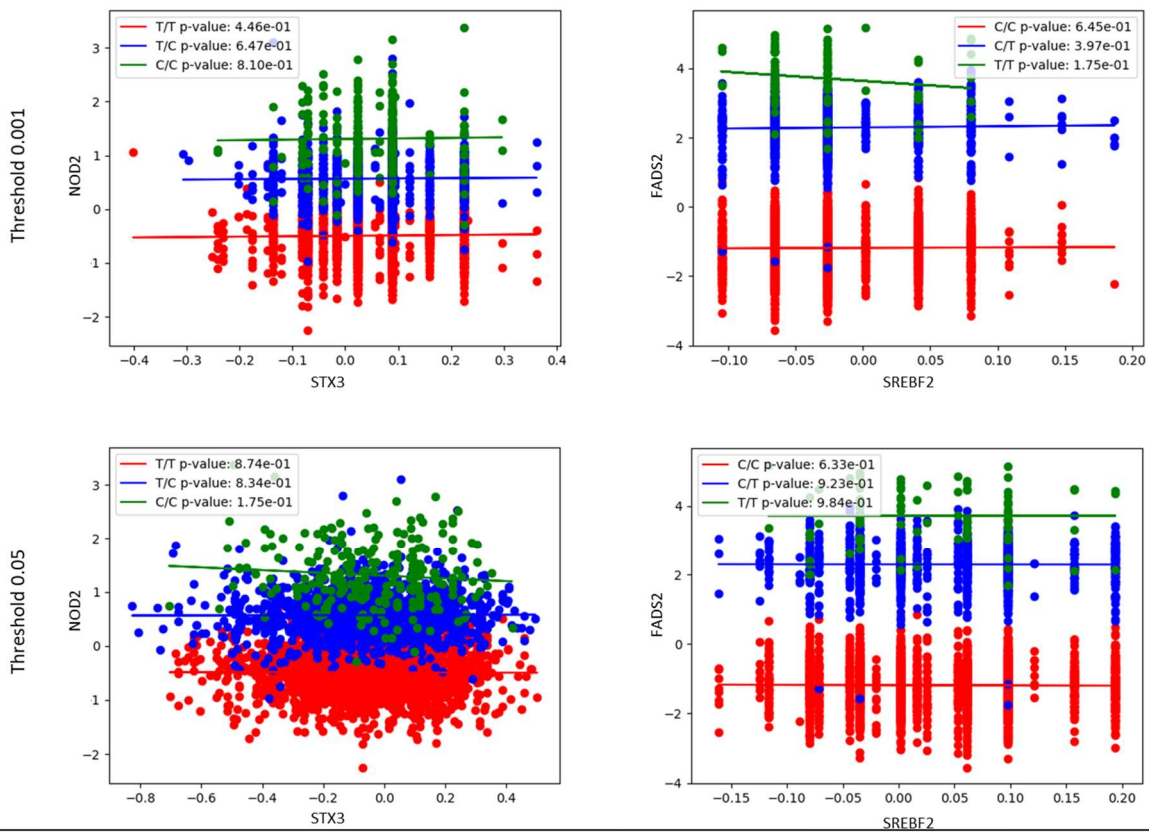
Figure S4: All interaction plots of the results of the Cis-eQTL identification algorithms. The expression of the TF gene (either STX3 or SREBF2) is on the x-axis while that of the interacting gene (either NOD2 or FADS2) is on the y-axis, red dot indicate the sample is homozygous for the major allele, blue indicates heterozygosity, and green indicates the sample is homozygous for the minor allele. In the legend of each plot are the names of the genotypes along with the p-values[1] (the probability that the association between x and y is due to chance) of the regression line for the genotype set of samples. The upper part displays the predictions made using a series of linear regressions, the lower part those made using a multivariate linear regression model. Within both parts the upper row is for the models made with the threshold value set to 0.001, and the lower row for when the threshold is set to 0.05.
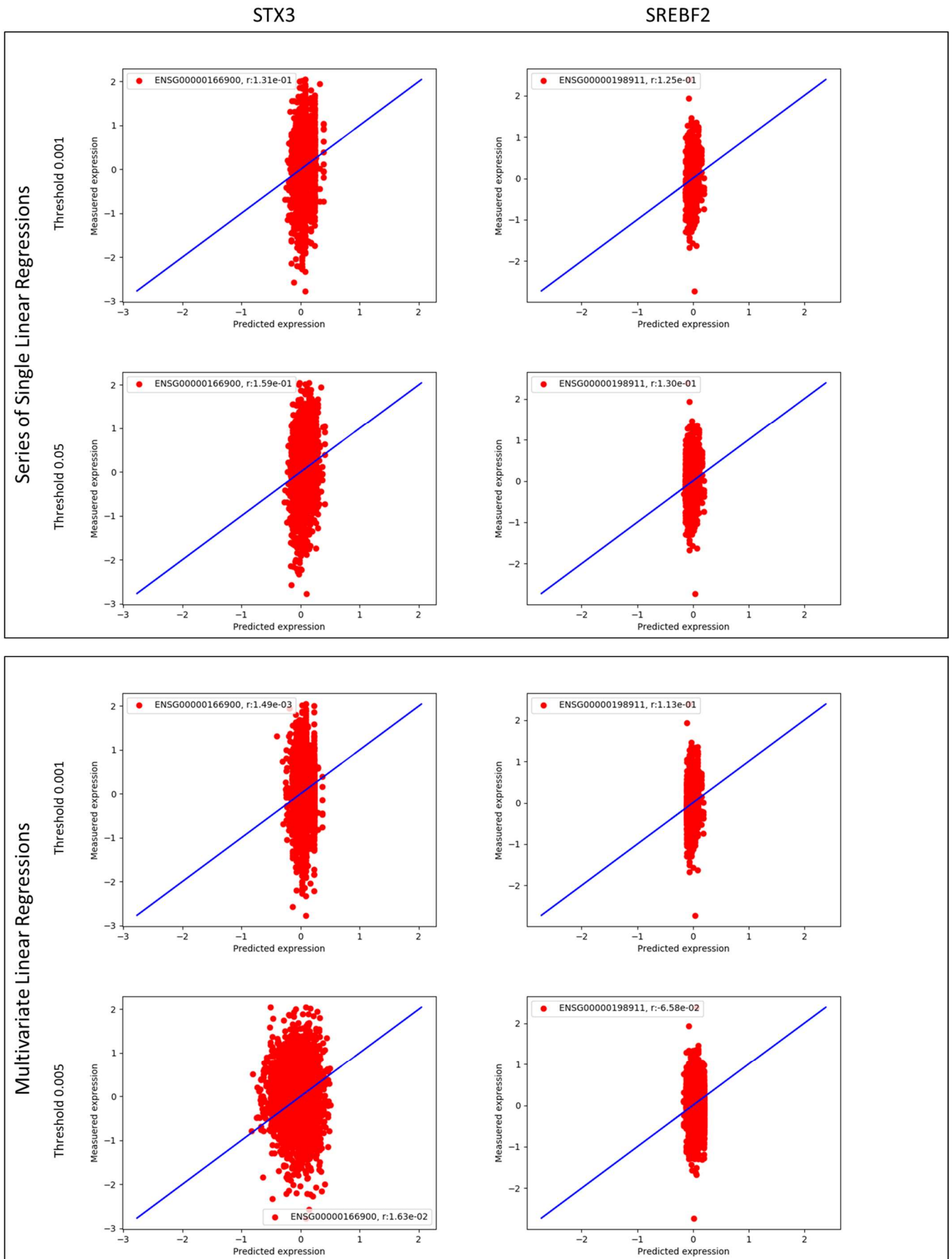
Figure S5: All predicted vs measured plots of the results of the Cis-eQTL identification algorithms. The measured expression is on the x-axis while the predicted expression is on the y-axis, the blue line use the measured expression for both coordinates and thus indicates what a perfect prediction would look like. In the legend of each plot are the ENSG code of the gene along with the Pearson r-value² between the

predicted and measured values[3], which is indicative of how strong the correlation is between the predicted and measured values. The upper part displays the predictions made using a series of linear regressions, the lower part for those using a multivariate linear regression model. Within both parts the upper row is for the models made with the threshold value set to 0.001, and the lower row for when the threshold is set to 0.05. All graphs on the left half are for the predictions of STX3 and those of the right for those of SREBF2.
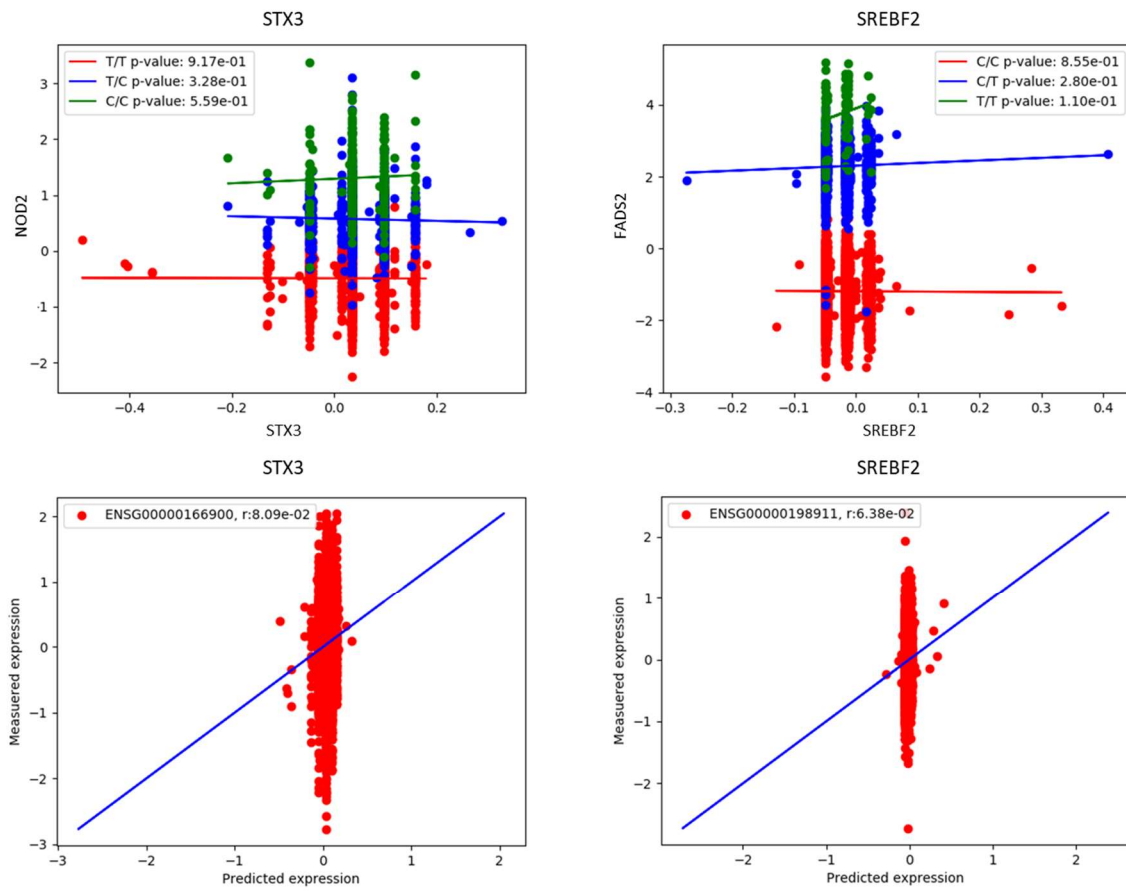

Figure S6: The interactions plots and predicted vs measured plots made using Cis-eQTL SNPs identified by the eQTLgen pipeline. The top row is for interaction plots, the bottom row for the the predicted vs measured plots. The left half is for STX3 the right for SREBF2.

Rank	interacting chrom	interacting ENSG	interacting gene	interacting snp	intercept p-value	SNP p-value	Gene p-value	interaction p-value
1	17	ENSG00000141295	SCRN2	rs62076106	8.1559E-112	0	0.115891922	0.000694171
2	10	ENSG00000107771	CCSER2	rs1343111	2.75065E-69	1.0509E-144	0.939916668	0.008714595
3	21	ENSG00000159256	MORC3	rs11909469	6.25407E-06	3.7255E-140	0.059885007	0.015490838
4	12	ENSG00000079337	RAPGEF3	rs145192203	4.6798E-101	0	0.014091076	0.01557548
5	6	ENSG00000135587	SMPD2	rs7754650	3.8611E-184	3.025E-228	0.136286435	0.019084121
6	15	ENSG00000128944	KNSTRN	rs34034104	6.42644E-81	1.4851E-196	0.046094446	0.021872941
7	11	ENSG00000236304	AP001189.1	rs11236839	1.22E-133	0	0.256015886	0.035729649
8	13	ENSG00000132932	ATP8A2	rs9578952	3.36889E-61	6.5555E-103	0.082696262	0.050837379
9	3	ENSG00000170248	PDCD6IP	rs9311031	7.12347E-66	5.6677E-228	0.385986742	0.066689171
10	7	ENSG00000188707	ZBED6CL	rs10952249	3.7878E-182	0	0.371895042	0.069064166
11	9	ENSG00000050555	LAMC3	rs10901333	3.8205E-151	2.7229E-221	0.123300274	0.069204098
12	19	ENSG00000104936	DMPK	rs1799894	7.6612E-175	1.9669E-252	0.099366261	0.072024793
13	2	ENSG00000144580	CNOT9	rs2303566	1.7493E-223	1.5098E-280	0.70449736	0.086933116
14	1	ENSG00000116213	WRAP73	rs9662052	6.4242E-149	1.0274E-221	0.086150603	0.090663654
15	22	ENSG00000183473	N.A.	rs13053175	4.0876E-166	6.6055E-191	0.078102838	0.09228508
16	20	ENSG00000130590	SAMD10	rs2427581	6.5491E-274	0	0.535399582	0.095651988
17	8	ENSG00000147439	BIN3	rs7005025	2.3719E-267	0	0.463416089	0.10430304
18	5	ENSG00000152684	PELO	rs139420269	0.003313328	2.229E-268	0.640736503	0.107721895
19	14	ENSG00000198208	RPS6KL1	rs11159109	1.9685E-116	3.2576E-217	0.056157637	0.168156993
20	18	ENSG00000166347	CYB5A	rs12458414	1.45339E-76	1.9553E-168	0.562068677	0.213250437
21	16	ENSG00000159648	TEPP	rs2241771	2.0363E-244	1.024E-265	0.223354157	0.224272242
22	4	ENSG00000151725	CENPU	rs6552800	2.9595E-139	9.2316E-183	0.086551063	0.236061223

Figure S7: Table with the top interactions with NF-κB (ENSG00000109320) identified for each chromosome using method 1. Columns are as following: *Rank* indicates the how highly the interaction was ranked out of the 22 based on the interaction p-value; *interacting chrom* indicates the chromosome on which the interacting gene is located; *interacting ENSG* gives the ENSG/Ensembl database code of the interacting gene; *interacting gene* gives the name of the interacting gene; *interacting SNP* gives the code of the Cis-eQTL SNP which modulates the interaction; the *intercept p-value*, *SNP p-value*, *Gene p-value* and *interaction p-value* columns contains the p-values of respectively the intercept, the modulating Cis-eQTL SNP, the TF gene (NF-κB) and the interaction components of the interaction model.

Rank	interacting chrom	interacting ENSG	interacting gene	interacting snp	intercept p-value	SNP p-value	Gene p-value	interaction p-value
1	1	ENSG00000233355	CHRM3-AS2	rs12021900	9.7015E-138	0	0.000960834	6.23E-07
2	9	ENSG00000147883	CDKN2B	rs2069426	8.67872E-40	3.0223E-180	0.055994436	1.39425E-05
3	15	ENSG00000259703	N.A.	rs144197278	1.10097E-05	3.28382E-05	0.118812773	6.75427E-05
4	12	ENSG00000258546	CENPUP2	rs10842464	9.93994E-10	1.98976E-08	0.000195905	7.75708E-05
5	17	ENSG00000108309	RUNDC3A	rs2011895	5.88663E-64	1.88731E-65	0.010225063	0.000123872
6	6	ENSG00000146285	SCML4	rs6568505	1.65081E-45	8.4392E-206	0.000120806	0.000135871
7	14	ENSG00000203485	INF2	rs4072285	0.013960625	1.48858E-47	0.015906353	0.000204883
8	19	ENSG00000169136	ATF5	rs78331666	2.28702E-14	0.00051247	0.09701789	0.000297953
9	5	ENSG00000154153	RETREG1	rs35004	9.72385E-20	2.1156E-17	0.005702224	0.00067312
10	22	ENSG00000100241	SBF1	rs76275199	0.043491972	3.5003E-36	0.239983953	0.001003543
11	7	ENSG00000002726	AOC1	rs28891172	1.3541E-136	2.4761E-156	0.021330694	0.001046796
12	16	ENSG00000007520	TSR3	rs11865640	6.68646E-06	1.04223E-29	0.015213948	0.001072636
13	3	ENSG00000163376	KBTBD8	rs2364281	0.229661322	1.17266E-07	0.006693913	0.001242143
14	2	ENSG00000242766	IGKV1D-17	rs2162488	0.003317251	8.49104E-23	0.200862759	0.001617933
15	8	ENSG00000104361	NIPAL2	rs10103296	1.3061E-120	0	0.456192611	0.001899512
16	20	ENSG00000101138	CSTF1	rs6024857	0.140082167	9.83071E-59	0.560911933	0.001969193
17	4	ENSG00000179979	N.A.	rs28481697	1.34775E-37	2.3186E-219	0.736222894	0.002153895
18	11	ENSG00000254750	CASP1P2	rs1792755	4.87739E-83	2.18688E-89	0.011089217	0.002824272
19	10	ENSG00000119906	SLF2	rs10883567	3.27418E-35	1.37607E-42	0.000878645	0.003711664
20	13	ENSG00000213995	NAXD	rs61969228	1.45402E-49	4.80009E-80	0.012634866	0.005775403
21	18	ENSG00000266053	NDUFV2-AS1	rs4797359	8.75659E-06	2.4455E-06	0.017718645	0.006867808
22	21	ENSG00000228107	AP000692.1	rs28385572	0.290180824	9.92486E-09	0.16426215	0.014090076

Figure S8: Table with the top interactions with NF-κB (ENSG00000109320) identified for each chromosome using method 2. Columns are as following: Rank indicates the how highly the interaction was ranked out of the 22 based on the interaction p-value; *interacting chrom* indicates the chromosome on which the interacting gene is located; *interacting ENSG* gives the ENSG/Ensembl database code of the interacting gene; *interacting gene* gives the name of the interacting gene; *interacting SNP* gives the code of the Cis-eQTL SNP which modulates the interaction; the *intercept p-value*, *SNP p-value*, *Gene p-value* and *interaction p-value* columns contains the p-values of respectively the intercept, the modulating Cis-eQTL SNP, the TF gene (NF-κB) and the interaction components of the interaction model.

Figure S9: The predicted vs measured plots of STX3 and SREBF2 models used in conjunction with the interaction models. The measured expression is on the x-axis while the predicted expression is on the y-axis, the blue line use the measured expression for both coordinates and thus indicates what a perfect prediction would look like. In the legend of each plot are the ENSG code of the gene along with the Pearson r-value[2] between the predicted and measured values[3], which is indicative of how strong the correlation is between the predicted and measured values. The top row is the models initialized using Cis-eQTL SNPs identified by the eQTLgen pipeline, the lower row for those from toRegressOut.log.gz.

NOD2   FADS2

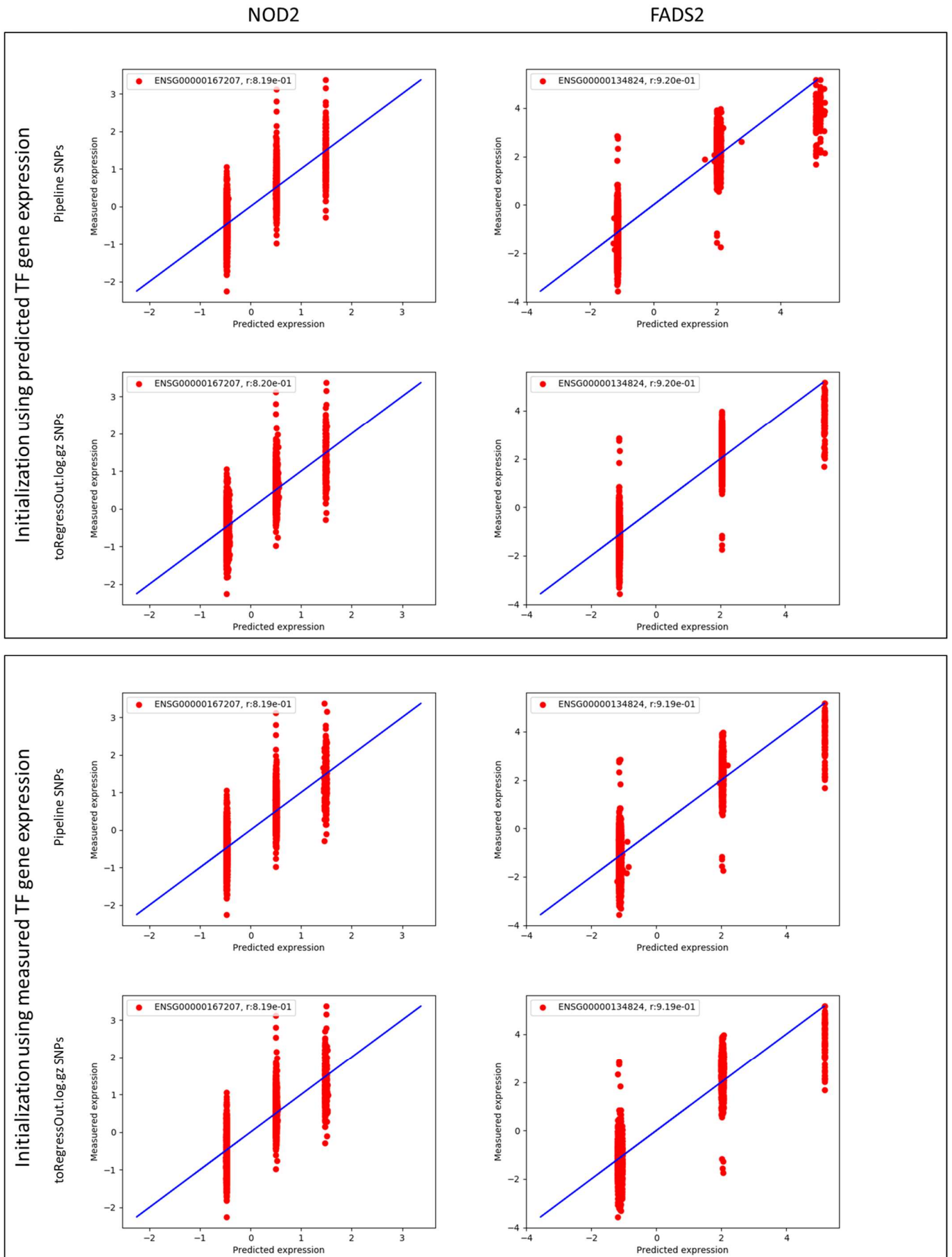**Figure S10:** All predicted vs measured plots of the STX3-NOD2 and SREBF2-FADS2 interaction models. The measured expression is on the x-axis while the predicted expression is on the y-axis, the blue line use the measured expression for both coordinates and thus indicates what a perfect prediction would look like. In the legend of each plot are the ENSG code of the gene along with the Pearson r-value^2 between the

predicted and measured values[3], which is indicative of how strong the correlation is between the predicted and measured values. The upper part displays the predictions made using models initialized with predicted values for STX3 or SREBF2, the lower part those using models initialized with measured values. Within both parts the upper row is for the models made SNPs from the eQTLgen pipeline, and the lower row for model with SNPs from toRegressOut.log.gz. All graphs on the left half are for the predictions of NOD2 and those of the right for those of FADS2.

nr	ENSG	name	chrom of gene	interacting chrom	interacting ENSG	interacting gene	interacting snp	intercept p-value	SNP p-value	Gene p-value	interaction p-value
1	ENSG00000100376	FAM118A	22	1	ENSG00000233355	CHRM3-AS2	rs12021900	4.4586E-137	0	0.423595169	8.88527E-12
2	ENSG00000226752	CUTALP	9	1	ENSG00000233355	CHRM3-AS2	rs12021900	5.003E-136	0	0.470151887	2.03121E-08
3	ENSG00000164308	ERAP2	5	10	ENSG00000188690	UROS	rs10901520	1.45862E-42	1.28825E-30	0.000299166	4.44586E-05
4	ENSG00000124587	PEX6	6	5	ENSG00000248874	C5orf17	rs77824697	7.77427E-30	0	0.116353341	5.0313E-10
5	ENSG00000013573	DDX11	12	3	ENSG00000144820	ADGRG7	rs140174756	8.73775E-22	0	0.522770568	3.75024E-07
6	ENSG00000226278	PSPHP1	7	19	ENSG00000268433	MTDHP3	rs8110320	2.2768E-197	0	0.003266607	1.20396E-06
7	ENSG00000110455	ACCS	11	6	ENSG00000137312	FLOT1	rs115114376	9.08979E-19	8.31946E-26	0.13533332	5.87095E-06
8	ENSG00000197728	RPS26	12	17	ENSG00000108352	RAPGEFL1	rs117330222	6.78503E-13	0	0.16444393	3.4562E-05
9	ENSG00000258289	CHURC1	14	7	ENSG00000240859	AC093627.4	rs76029673	4.07937E-11	2.4928E-201	0.047347673	1.20962E-12
10	ENSG00000003137	CYP26B1	2	20	ENSG00000125885	MCM8	rs236106	3.074E-117	1.2627E-240	0.458490524	9.9263E-06

Rank	ENSG	name	chrom of gene	interacting chrom	interacting ENSG	interacting gene	interacting snp	intercept p-value	SNP p-value	Gene p-value	interaction p-value
1	ENSG00000174652	ZNF266	19	3	ENSG00000144820	ADGRG7	rs140174756	4.20255E-22	0	0.164284314	3.76148E-05
2	ENSG00000167034	NKX3-1	8	5	ENSG00000113119	TMCO6	rs3138076	1.00868E-39	4.57032E-43	0.156212751	3.24198E-06
3	ENSG00000170448	NFXL1	4	8	ENSG00000104361	NIPAL2	rs10103296	1.0899E-125	0	0.006864054	1.76769E-14
4	ENSG00000168874	ATOH8	2	8	ENSG00000104361	NIPAL2	rs10103296	2.4266E-127	0	0.075659901	2.23268E-19
5	ENSG00000164048	ZNF589	3	3	ENSG00000144820	ADGRG7	rs140174756	5.73202E-22	0	0.548990894	3.09512E-18
6	ENSG00000167766	ZNF83	19	1	ENSG00000171680	PLEKHG5	rs10779790	4.09E-193	0	0.562424166	1.52446E-06
7	ENSG00000125618	PAX8	2	11	ENSG00000255860	AP000812.2	rs7939676	3.0383E-151	0	0.651032188	3.81003E-05
8	ENSG00000160113	NR2F6	19	3	ENSG00000173905	GOLIM4	rs4266235	1.36238E-06	0.008620967	0.009893282	1.42068E-05
9	ENSG00000131849	ZNF132	19	19	ENSG00000204920	ZNF155	rs62116613	3.8128E-164	0	0.173518717	1.39749E-07
10	ENSG00000101057	MYBL2	20	3	ENSG00000144820	ADGRG7	rs140174756	4.59186E-21	0	0.479418989	1.97817E-08

Figure S11: Two lists containing the top interactions identified for both sets of 10 TF genes, The columns are as following: *Rank* is the rank of the TF gene based on the Pearson rank correlation between the measurements and the predictions by a multivariate linear regression model using the SNPs in toRegressOut.log.gz; *ENSG* is the ENSG/Ensembl database code of the TF gene; *name* is the name of the TF gene; *chrom of gene* is the chromosome on which the TF gene is located; *interacting chrom* is the chromosome on which the interacting gene is located; *interacting ENSG* is the ENSG/Ensembl database code of the interacting gene; *interacting gene* gives the name of the interacting gene; *interacting snp* gives the code of the cis-eQTL SNP modulating the interaction the *intercept p-value*, *SNP p-value*, *Gene p-value* and *interaction p-value* columns contains the p-values of respectively the intercept, the modulating Cis-eQTL SNP, the TF gene (NF-κB) and the interaction components of the interaction model. The top list is for the first set of TF genes, the lower one for the second set of TF genes.

	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
			Using IDR Thresholded Peaks data					
ENCSR162IEM_ENCFF299JBQ	bigBed	0	2	1245	14371	0.790621875	0.37391215	False
ENCSR162IEM_ENCFF974VPH	bigBed	0	2	893	14723	1.379572684	0.240173948	False
ENCSR162IEM_ENCFF707ZNN	bigBed	0	2	1400	14216	0.630320077	0.427237932	False
ENCSR000BRO_ENCFF773YDN	bigBed	0	2	2442	13174	0.1329683	0.71537404	False
ENCSR000BRO_ENCFF176QIX	bigBed	1	1	3216	12400	0.023698631	0.87765421	False
ENCSR000BRO_ENCFF233AOX	bigBed	0	2	1664	13952	0.432437621	0.510795262	False
ENCSR581KCO_ENCFF848JYU	bigBed	1	1	4611	11005	0.019725122	0.888307494	False
ENCSR581KCO_ENCFF576PAR	bigBed	1	1	3047	12569	0.038299236	0.844843493	False
ENCSR581KCO_ENCFF650QJC	bigBed	1	1	5338	10278	0.075002533	0.784187675	False
ENCSR162IEM_ENCFF948SLV	Bed	0	2	876	14740	1.420627629	0.233300126	False
ENCSR162IEM_ENCFF136TBA	Bed	0	2	1383	14233	0.645987192	0.421551027	False
ENCSR162IEM_ENCFF637PFI	Bed	0	2	1227	14389	0.812099114	0.367500374	False
ENCSR000BRO_ENCFF404IFN	Bed	0	2	2385	13231	0.146332343	0.702065235	False
ENCSR000BRO_ENCFF712RNF	Bed	1	1	3155	12461	0.028493414	0.86595402	False
ENCSR000BRO_ENCFF381YQV	Bed	0	2	1621	13995	0.459694882	0.497766605	False
ENCSR581KCO_ENCFF710UTD	Bed	1	1	2990	12626	0.044196321	0.833488781	False
ENCSR581KCO_ENCFF325ZNW	Bed	1	1	4529	11087	0.015580767	0.900663725	False
ENCSR581KCO_ENCFF904DOZ	Bed	1	1	5260	10356	0.067549623	0.794938517	False
			Using Conservative IDR Thresholded Peaks data					
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR162IEM_ENCFF939XYJ	bigBed	1	1	1084	14532	1.008427777	0.31527979	False
ENCSR000BRO_ENCFF516BRL	bigBed	0	2	2510	13106	0.118225864	0.730966706	False
ENCSR581KCO_ENCFF599ZNQ	bigBed	1	1	5035	10581	0.048055295	0.826482431	False
ENCSR162IEM_ENCFF410VRF	Bed	1	1	1067	14549	1.035659382	0.308833138	False
ENCSR000BRO_ENCFF408FLG	Bed	0	2	2459	13157	0.129163674	0.719300751	False
ENCSR581KCO_ENCFF182JRE	Bed	1	1	4955	10661	0.041853732	0.837898839	False

Figure S12: The results of the χ2 contingency tests for MYBL2 from the output of interaction identification with initialization using predicted values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the

models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
				Using IDR Thresholded Peaks data				
ENCSR085DDI_ENCFF874VFC	bigBed	0	2	676	14945	2.065012474	0.150713695	False
ENCSR085DDI_ENCFF263GHD	bigBed	0	2	975	14646	1.202984956	0.272725897	False
ENCSR085DDI_ENCFF619QDE	bigBed	0	2	1378	14243	0.651091706	0.419722636	False
ENCSR417DKD_ENCFF906UKQ	bigBed	0	2	218	15403	8.100099303	0.004426283	True
ENCSR417DKD_ENCFF505SHB	bigBed	0	2	276	15345	6.2216625	0.012619656	True
ENCSR417DKD_ENCFF662JTI	bigBed	defect	defect	defect	defect	defect	defect	defect
ENCSR746XEG_ENCFF560YQY	bigBed	0	2	451	15170	3.488987963	0.061778341	False
ENCSR746XEG_ENCFF513WDR	bigBed	1	1	852	14769	1.479580331	0.223840195	False
ENCSR746XEG_ENCFF153GOU	bigBed	0	2	490	15131	3.147289102	0.076053216	False
ENCSR085DDI_ENCFF341CNM	Bed	0	2	1349	14272	0.679054268	0.409912574	False
ENCSR085DDI_ENCFF032WGR	Bed	0	2	960	14661	1.233057421	0.266813266	False
ENCSR085DDI_ENCFF421BCS	Bed	0	2	666	14955	2.107608155	0.146568248	False
ENCSR417DKD_ENCFF142NAV	Bed	0	2	269	15352	6.405288194	0.011378096	True
ENCSR417DKD_ENCFF666XIB	Bed	defect	defect	defect	defect	defect	defect	defect
ENCSR417DKD_ENCFF757WEB	Bed	0	2	212	15409	8.353219836	0.003850045	True
ENCSR746XEG_ENCFF378CEO	Bed	0	2	482	15139	3.212832533	0.073062897	False
ENCSR746XEG_ENCFF057NHJ	Bed	1	1	846	14775	1.49531699	0.221393328	False
ENCSR746XEG_ENCFF862IMV	Bed	0	2	446	15175	3.537156205	0.060008263	False
				Using Conservative IDR Thresholded Peaks data				
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR085DDI_ENCFF327CKW	bigBed	0	2	1223	14398	0.8174422	0.365929069	False
ENCSR417DKD_ENCFF616EIN	bigBed	0	2	207	15414	8.575382592	0.003407384	True
ENCSR746XEG_ENCFF540XZV	bigBed	1	1	744	14877	1.802872699	0.179365587	False
ENCSR085DDI_ENCFF929ILB	Bed	0	2	1203	14418	0.84229934	0.358739985	False
ENCSR417DKD_ENCFF615ZOP	Bed	0	2	204	15417	8.713916424	0.003157901	True
ENCSR746XEG_ENCFF347YUY	Bed	1	1	737	14884	1.827183625	0.176460564	False

Figure S13: The results of the χ2 contingency tests for NFXL1 from the output of interaction identification with initialization using predicted values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted

but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
				Using IDR Thresholded Peaks data				
ENCSR138RCE_ENCFF059PLV	bigBed	defect	defect	defect	defect	defect	defect	defect
ENCSR138RCE_ENCFF698IXC	bigBed	0	1	40	15534	96.60059599	8.48E-23	True
ENCSR138RCE_ENCFF462JMU	bigBed	defect	defect	defect	defect	defect	defect	defect
ENCSR138RCE_ENCFF806BPT	Bed	defect	defect	defect	defect	defect	defect	defect
ENCSR138RCE_ENCFF293RLS	Bed	0	1	40	15534	96.60059599	8.48E-23	True
ENCSR138RCE_ENCFF526IGV	Bed	defect	defect	defect	defect	defect	defect	defect
				Using Conservative IDR Thresholded Peaks data				
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR138RCE_ENCFF416WCZ	bigBed	0	1	39	15535	99.09673372	2.40E-23	False
ENCSR138RCE_ENCFF296JEF	Bed	0	1	39	15535	99.09673372	2.40E-23	False

Figure S14: The results of the χ2 contingency tests for ZNF132 from the output of interaction identification with initialization using predicted values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

		Using IDR Thresholded Peaks data						
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR603XLW_ENCFF320PEM	bigBed	0	2	2152	13441	0.210964186	0.646012732	False
ENCSR603XLW_ENCFF770FHN	bigBed	0	2	3621	11972	0.003558984	0.952428643	False
ENCSR603XLW_ENCFF263ZYJ	bigBed	0	2	2413	13180	0.138815686	0.70946123	False
ENCSR603XLW_ENCFF345IHK	Bed	0	2	3538	12055	0.006102409	0.937734257	False
ENCSR603XLW_ENCFF583FMH	Bed	0	2	2355	13238	0.152883544	0.695794832	False
ENCSR603XLW_ENCFF186VTU	Bed	0	2	2098	13495	0.229060293	0.632221484	False
		Using Conservative IDR Thresholded Peaks data						
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR603XLW_ENCFF650JKE	bigBed	0	2	3591	12002	0.004394813	0.947144247	False
ENCSR603XLW_ENCFF704LLO	Bed	0	2	3496	12097	0.007670716	0.930208414	False

Figure S15: The results of the χ2 contingency tests for ZNF589 from the output of interaction identification with initialization using predicted values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

Rank	ENSG	name	chrom of gene	interacting chrom	interacting ENSG	interacting gene	interacting snp	intercept p-value	SNP p-value	Gene p-value	interaction p-value
1	ENSG00000100376	FAM118A	22	1	ENSG00000233355	CHRM3-AS2	rs12021900	5.6695E-137	0	0.630961921	1.63685E-10
2	ENSG00000226752	CUTALP	9	1	ENSG00000233355	CHRM3-AS2	rs12021900	6.4874E-136	0	0.070890512	6.69869E-11
3	ENSG00000164308	ERAP2	5	8	ENSG00000104361	NIPAL2	rs10103296	1.8012E-128	0	0.320963258	5.02292E-09
4	ENSG00000124587	PEX6	6	3	ENSG00000144820	ADGRG7	rs140174756	9.84383E-22	0	0.903966048	7.89475E-07
5	ENSG00000013573	DDX11	12	3	ENSG00000144820	ADGRG7	rs140174756	7.09329E-22	0	0.460335318	6.56893E-12
6	ENSG00000226278	PSPHP1	7	14	ENSG00000140090	SLC24A4	rs61977316	1.50338E-08	6.22563E-53	0.81814787	1.16253E-06
7	ENSG00000110455	ACCS	11	17	ENSG00000166579	NDEL1	rs2133336	5.26052E-28	4.24981E-36	2.22607E-09	1.33899E-05
8	ENSG00000197728	RPS26	12	5	ENSG00000248874	C5orf17	rs77824697	4.61204E-30	0	0.769651658	1.02029E-05
9	ENSG00000258289	CHURC1	14	1	ENSG00000162437	RAVER2	rs114269697	0.000512004	1.15591E-39	0.230002115	4.38628E-11
10	ENSG00000003137	CYP26B1	2	20	ENSG00000125885	MCM8	rs236106	2.8796E-117	2.7016E-240	0.333325814	8.94661E-07

Rank	ENSG	name	chrom of gene	interacting chrom	interacting ENSG	interacting gene	interacting snp	intercept p-value	SNP p-value	Gene p-value	interaction p-value
1	ENSG00000174652	ZNF266	19	1	ENSG00000233355	CHRM3-AS2	rs12021900	1.3366E-137	0	0.006102456	1.3037E-07
2	ENSG00000167034	NKX3-1	8	1	ENSG00000233355	CHRM3-AS2	rs12021900	1.3916E-136	0	0.901618131	1.62535E-08
3	ENSG00000170448	NFXL1	4	8	ENSG00000104361	NIPAL2	rs10103296	6.2115E-128	0	0.210322639	2.63775E-20
4	ENSG00000168874	ATOH8	2	8	ENSG00000104361	NIPAL2	rs10103296	1.4976E-127	0	0.561421543	3.10788E-13
5	ENSG00000164048	ZNF589	3	3	ENSG00000144820	ADGRG7	rs140174756	2.6207E-22	0	0.217487219	1.95697E-29
6	ENSG00000167766	ZNF83	19	15	ENSG00000215252	GOLGA8B	rs144215799	1.26893E-35	1.4354E-160	1.17412E-05	1.5396E-07
7	ENSG00000125618	PAX8	2	3	ENSG00000144820	ADGRG7	rs140174756	1.02163E-21	0	0.708754713	3.00323E-06
8	ENSG00000160113	NR2F6	19	5	ENSG00000205571	SMN2	rs474776	3.85669E-11	8.48167E-69	0.405577693	5.91616E-06
9	ENSG00000131849	ZNF132	19	3	ENSG00000144820	ADGRG7	rs140174756	9.78537E-22	0	0.594866309	1.01572E-09
10	ENSG00000101057	MYBL2	20	3	ENSG00000144820	ADGRG7	rs140174756	1.03784E-21	0	0.236059487	3.20809E-29

Figure S16: The top interactions for both sets of 10 TF genes identified by initializing models using measured expression of the TF genes, The columns are as following: *Rank* is the rank of the TF gene based on the Pearson rank correlation between the measurements and the predictions by a multivariate linear regression model using the SNPs in toRegressOut.log.gz; *ENSG* is the ENSG/Ensembl database code of the TF gene; *name* is the name of the TF gene; *chrom of gene* is the chromosome on which the TF gene is located; *interacting chrom* is the chromosome on which the interacting gene is located; *interacting ENSG* is the ENSG/Ensembl database code of the interacting gene; *interacting gene* gives the name of the interacting gene; *interacting snp* gives the code of the cis-eQTL SNP modulating the interaction; the intercept, SNP, gene and interaction p-value columns contains the p-values of respectively the intercept, the modulating Cis-eQTL SNP, the TF gene (NF-κB) and the interaction components of the interaction model. The top list is for the first set of TF genes, the lower one for the second set of TF genes.

Using IDR Thresholded Peaks data							
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR161CZA_ENCFF772HNB	bigBed	0	2	1557	14044	0.502420048	0.4784387	False
ENCSR161CZA_ENCFF650DTU	bigBed	0	2	1067	14534	1.035617546	0.30884291	False
ENCSR161CZA_ENCFF951PHQ	bigBed	0	2	593	15008	2.458757162	0.116871223	False
ENCSR161CZA_ENCFF723JPN	Bed	0	2	1058	14543	1.05042152	0.305410027	False
ENCSR161CZA_ENCFF846XXK	Bed	0	2	584	15017	2.508749382	0.113215747	False
ENCSR161CZA_ENCFF520POQ	Bed	0	2	1536	14065	0.517682438	0.471831966	False
Using Conservative IDR Thresholded Peaks data							
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR161CZA_ENCFF337ZRI	bigBed	0	2	1419	14182	0.612097507	0.433999153	False
ENCSR161CZA_ENCFF096THK	Bed	0	2	1406	14195	0.623674269	0.429685173	False

Figure S17: The results of the χ2 contingency tests for ATOH8 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their

modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

			Using IDR Thresholded Peaks data					
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR162IEM_ENCFF299JBQ	bigBed	2	4	1243	14369	2.372473327	0.123491259	False
ENCSR162IEM_ENCFF974VPH	bigBed	1	5	892	14720	0.076172022	0.782553601	False
ENCSR162IEM_ENCFF707ZNN	bigBed	1	5	1399	14213	0.002925661	0.956863952	False
ENCSR000BRO_ENCFF773YDN	bigBed	1	5	2441	13171	0.242649533	0.622298998	False
ENCSR000BRO_ENCFF176QIX	bigBed	1	5	3216	12396	0.071114107	0.789721495	False
ENCSR000BRO_ENCFF233AOX	bigBed	0	6	1664	13948	0.033968949	0.853772881	False
ENCSR581KCO_ENCFF848JYU	bigBed	1	5	4611	11001	0.059190527	0.80777995	False
ENCSR581KCO_ENCFF576PAR	bigBed	0	6	3048	12564	0.477864827	0.489391057	False
ENCSR581KCO_ENCFF650QJC	bigBed	1	5	5338	10274	0.22506525	0.635207262	False
ENCSR162IEM_ENCFF948SLV	Bed	1	5	875	14737	0.084150508	0.771749628	False
ENCSR162IEM_ENCFF136TBA	Bed	1	5	1382	14230	0.002025134	0.964106125	False
ENCSR162IEM_ENCFF637PFI	Bed	2	4	1225	14387	2.436921555	0.118508595	False
ENCSR000BRO_ENCFF404IFN	Bed	1	5	2384	13228	0.223269429	0.63655999	False
ENCSR000BRO_ENCFF712RNF	Bed	1	5	3155	12457	0.085502142	0.76997508	False
ENCSR000BRO_ENCFF381YQV	Bed	0	6	1621	13991	0.027004856	0.86947015	False
ENCSR581KCO_ENCFF710UTD	Bed	0	6	2991	12621	0.453646877	0.500608179	False
ENCSR581KCO_ENCFF325ZNW	Bed	1	5	4529	11083	0.046754276	0.828810519	False
ENCSR581KCO_ENCFF904DOZ	Bed	1	5	5260	10352	0.202700791	0.65254962	False
			Using Conservative IDR Thresholded Peaks data					
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR162IEM_ENCFF939XYJ	bigBed	1	5	1084	14528	0.017842221	0.89373883	False
ENCSR000BRO_ENCFF516BRL	bigBed	1	5	2509	13103	0.266441139	0.60572914	False
ENCSR581KCO_ENCFF599ZNQ	bigBed	1	5	5035	10577	0.144202824	0.704138077	False
ENCSR162IEM_ENCFF410VRF	Bed	1	5	1067	14545	0.021059965	0.884615717	False
ENCSR000BRO_ENCFF408FLG	Bed	1	5	2458	13154	0.248529937	0.618112101	False
ENCSR581KCO_ENCFF182JRE	Bed	1	5	4955	10657	0.125593367	0.72304547	False

Figure S18: The results of the χ2 contingency tests for MYBL2 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an

interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

Using IDR Thresholded Peaks data								
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR085DDI_ENCFF874VFC	bigBed	0	2	676	14945	2.0650124738351394	0.150713695492147	False
ENCSR085DDI_ENCFF263GHD	bigBed	0	2	975	14646	1.2029849562181385	0.2727258969237438	False
ENCSR085DDI_ENCFF619QDE	bigBed	0	2	1378	14243	0.6510917058966946	0.419722636460353	False
ENCSR417DKD_ENCFF906UKQ	bigBed	0	2	218	15403	8.100099303068244	.00442628335026075	True
ENCSR417DKD_ENCFF505SHB	bigBed	0	2	276	15345	6.221662499879473	0.0126196560203445	True
ENCSR417DKD_ENCFF662JTI	bigBed	defect	defect	defect	defect	defect	defect	defect
ENCSR746XEG_ENCFF560YQY	bigBed	0	2	451	15170	3.488987962942583	0.06177834134671319	False
ENCSR746XEG_ENCFF513WDR	bigBed	1	1	852	14769	1.4795803311773807	0.22384019492423904	False
ENCSR746XEG_ENCFF153GOU	bigBed	0	2	490	15131	3.1472891020611966	0.07605321606861308	False
ENCSR085DDI_ENCFF341CNM	Bed	0	2	1349	14272	0.6790542679828014	0.4099125738438323	False
ENCSR085DDI_ENCFF032WGR	Bed	0	2	960	14661	1.2330574205521927	0.2668132655311633	False
ENCSR085DDI_ENCFF421BCS	Bed	0	2	666	14955	2.107608154782116	0.14656824832572107	False
ENCSR417DKD_ENCFF142NAV	Bed	0	2	269	15352	6.405288193755464	.01137809563724212	True
ENCSR417DKD_ENCFF666XIB	Bed	defect	defect	defect	defect	defect	defect	defect
ENCSR417DKD_ENCFF757WEB	Bed	0	2	212	15409	8.353219836048352	.00385004473253950	True
ENCSR746XEG_ENCFF378CEO	Bed	0	2	482	15139	3.212832533495503	0.07306289708869754	False
ENCSR746XEG_ENCFF057NHJ	Bed	1	1	846	14775	1.4953169904664196	0.22139332778568907	False
ENCSR746XEG_ENCFF862IMV	Bed	0	2	446	15175	3.5371562049718075	0.06000826318255517	False
Using Conservative IDR Thresholded Peaks data								
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR085DDI_ENCFF327CKW	bigBed	0	2	1223	14398	0.8174422	0.365929069	False
ENCSR417DKD_ENCFF616EIN	bigBed	0	2	207	15414	8.575382592	0.003407384	True
ENCSR746XEG_ENCFF540XZV	bigBed	1	1	744	14877	1.802872699	0.179365587	False
ENCSR085DDI_ENCFF929ILB	Bed	0	2	1203	14418	0.84229934	0.358739985	False
ENCSR417DKD_ENCFF615ZOP	Bed	0	2	204	15417	8.713916424	0.003157901	True
ENCSR746XEG_ENCFF347YUY	Bed	1	1	737	14884	1.827183625	0.176460564	False

Figure S19: The results of the χ2 contingency tests for NFXL1 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
Using IDR Thresholded Peaks data								
ENCSR647CXR_ENCFF282DTV	bigBed	0	1	2203	13410	1.063037069	0.302523521	False
ENCSR647CXR_ENCFF367FTG	bigBed	0	1	2164	13449	1.094128612	0.295558249	False
ENCSR647CXR_ENCFF031ZWH	bigBed	0	1	3463	12150	0.448479851	0.503057734	False
ENCSR647CXR_ENCFF750IYO	Bed	0	1	2124	13489	1.127240711	0.288364666	False
ENCSR647CXR_ENCFF446KWJ	Bed	0	1	2177	13436	1.083637084	0.297885338	False
ENCSR647CXR_ENCFF435AEQ	Bed	0	1	3415	12198	0.463060289	0.496197205	False
Using Conservative IDR Thresholded Peaks data								
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR647CXR_ENCFF337JRD	bigBed	0	1	3354	12259	0.482258263	0.487401193	False
ENCSR647CXR_ENCFF838IXI	Bed	0	1	3304	12309	0.498578582	0.480125348	False

Figure S20: The results of the χ2 contingency tests for NKX3-1 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

		Using IDR Thresholded Peaks data						
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR138RCE_ENCFF059PLV	bigBed	defect	defect	defect	defect	defect	defect	defect
ENCSR138RCE_ENCFF698IXC	bigBed	0	1	40	15534	96.60059599	8.48E-23	True
ENCSR138RCE_ENCFF462JMU	bigBed	defect	defect	defect	defect	defect	defect	defect
ENCSR138RCE_ENCFF806BPT	Bed	defect	defect	defect	defect	defect	defect	defect
ENCSR138RCE_ENCFF293RLS	Bed	0	1	40	15534	96.60059599	8.48E-23	True
ENCSR138RCE_ENCFF526IGV	Bed	defect	defect	defect	defect	defect	defect	defect
		Using Conservative IDR Thresholded Peaks data						
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR138RCE_ENCFF416WCZ	bigBed	0	1	39	15535	99.09673372	2.40464E-23	True
ENCSR138RCE_ENCFF296JEF	Bed	0	1	39	15535	99.09673372	2.40464E-23	True

Figure S21: The results of the χ2 contingency tests for ZNF132 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

		Using IDR Thresholded Peaks data						
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR603XLW_ENCFF320PEM	bigBed	0	2	2152	13441	0.210964186	0.646012732	False
ENCSR603XLW_ENCFF770FHN	bigBed	0	2	3621	11972	0.003558984	0.952428643	False
ENCSR603XLW_ENCFF263ZYJ	bigBed	0	2	2413	13180	0.138815686	0.70946123	False
ENCSR603XLW_ENCFF345IHK	Bed	0	2	3538	12055	0.006102409	0.937734257	False
ENCSR603XLW_ENCFF583FMH	Bed	0	2	2355	13238	0.152883544	0.695794832	False
ENCSR603XLW_ENCFF186VTU	Bed	0	2	2098	13495	0.229060293	0.632221484	False
		Using Conservative IDR Thresholded Peaks data						
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR603XLW_ENCFF650JKE	bigBed	0	2	3591	12002	0.004394813	0.947144247	False
ENCSR603XLW_ENCFF704LLO	Bed	0	2	3496	12097	0.007670716	0.930208414	False

Figure S22: The results of the χ2 contingency tests for ZNF589 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was

predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. *defect* value for columns indicate that that replicate, lacked information for one or more chromosomes and were thus considered defective. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

Using IDR Thresholded Peaks data								
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR257XVY_ENCFF253QVA	bigBed	0	2	936	14642	1.277732998	0.258320972	False
ENCSR257XVY_ENCFF827JCQ	bigBed	0	2	2100	13478	0.227669822	0.633257029	False
ENCSR257XVY_ENCFF340RTV	bigBed	0	2	2474	13104	0.124567299	0.724132727	False
ENCSR263XFO_ENCFF063ZOT	bigBed	0	2	630	14948	2.263968493	0.132414352	False
ENCSR263XFO_ENCFF585ZKF	bigBed	0	2	1833	13745	0.337514685	0.561267318	False
ENCSR263XFO_ENCFF450KKE	bigBed	0	2	2338	13240	0.156626371	0.692281722	False
ENCSR257XVY_ENCFF776CQO	Bed	0	2	2036	13542	0.250680072	0.616596625	False
ENCSR257XVY_ENCFF451LLC	Bed	0	2	2406	13172	0.139914222	0.708366302	False
ENCSR257XVY_ENCFF424VEQ	Bed	0	2	915	14663	1.323777869	0.249915165	False
ENCSR263XFO_ENCFF621IOC	Bed	0	2	2305	13273	0.165262584	0.684356884	False
ENCSR263XFO_ENCFF561KKX	Bed	0	2	624	14954	2.293225654	0.129939627	False
ENCSR263XFO_ENCFF243OPS	Bed	0	2	1808	13770	0.349892962	0.554173728	False
Using Conservative IDR Thresholded Peaks data								
	filetype	interaction peak	interaction no peak	no interaction peak	no interaction no peak	chi^2-statistic	p-value	significant with a probability of 95.0%
ENCSR257XVY_ENCFF065PYE	bigBed	0	2	2130	13448	0.217507021	0.640946044	False
ENCSR263XFO_ENCFF706OWL	bigBed	0	2	1980	13598	0.272407592	0.601721293	False
ENCSR257XVY_ENCFF009CYN	Bed	0	2	2080	13498	0.234661534	0.628088708	False
ENCSR263XFO_ENCFF007OPT	Bed	0	2	1961	13617	0.280140485	0.596609153	False

Figure S23: The results of the χ2 contingency tests for ZNF83 from the output of interaction identification with initialization using measured values. The index is composed as {experiment}_{replicate}, the columns are as following: *filetype* indicates in what type of file the data was stored, a .Bed or .bigBed file; *interaction peak* indicates the number of interaction models for which an interaction was predicted and had a CHiP-seq binding peak near them; *interaction no peak* indicates the number of interaction models for which an interaction was predicted but had no CHiP-seq binding peak near them; *no interaction peak* indicates the number interaction model for which no interactions were predicted but had a CHiP-seq binding peak near them; *no interaction no peak* indicates the number interaction model for which no interactions were predicted and had no CHiP-seq binding peak near them; *chi^2-statistic* gives the χ2-statistic of the test; *p-value* gives the p-value of the test; *significant with a probability of 95.0%* indicates whether or not there is a significant difference between the models of with predicted interactions and those without, in regard to how often they have a CHiP-seq binding peak near their modulating SNP. **A,** the results for the data of the IDR thresholded Peaks. **B,** the results for the data of the Conservative IDR thresholded peaks.

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