

Monthly Report

Haonan Tong
2017-11

Hao Chen's Data

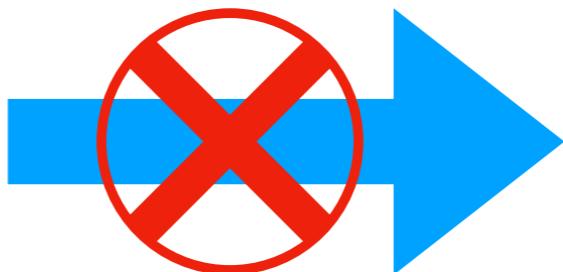
Transcription factor	Promoter	GENE NAME
AT5G61590	AT1G09610	GXM3
AT5G13910	AT1G09610	GXM3
AT3G06590	AT1G15950	ATCCR1,CCR1,IRX4
AT5G47220	AT1G15950	ATCCR1,CCR1,IRX4
AT4G37260	AT1G27440	ATGUT1,GUT2,IRX10
AT1G21910	AT1G27440	ATGUT1,GUT2,IRX10
AT1G06180	AT1G51680	4CL1
AT4G37260	AT1G51680	4CL1
AT1G21910	AT1G51680	4CL1
AT5G60850	AT1G51680	4CL1
AT1G77450	AT1G51680	4CL1
AT5G53950	AT1G51680	4CL1
AT3G02940	AT1G51680	4CL1
AT4G28110	AT1G51680	4CL1
AT3G15210	AT1G61820	BGLU46

Hao Chen Data Set And Preprocessing

- **122** validation downstream causal relationship corresponding to cell wall organization (should be associated with GO:0071555 not verified);
- Associated both the regulators and targets with our **2421 (196 TFs)** DEGs (triggered by ethylene), **57** causalities remain and validation set;
- Among the validation set, **8** unique targets and **30** unique regulators;
- All the targets are nTFs (not Transcription Factors);

TPA For Targets Of Interest (ToI)

Target	ATP
AT2G22420	4
AT2G28110	6
AT2G37090	5
AT3G18660	6
AT4G18780	6
AT5G15630	3
AT5G17420	6
AT5G44030	6



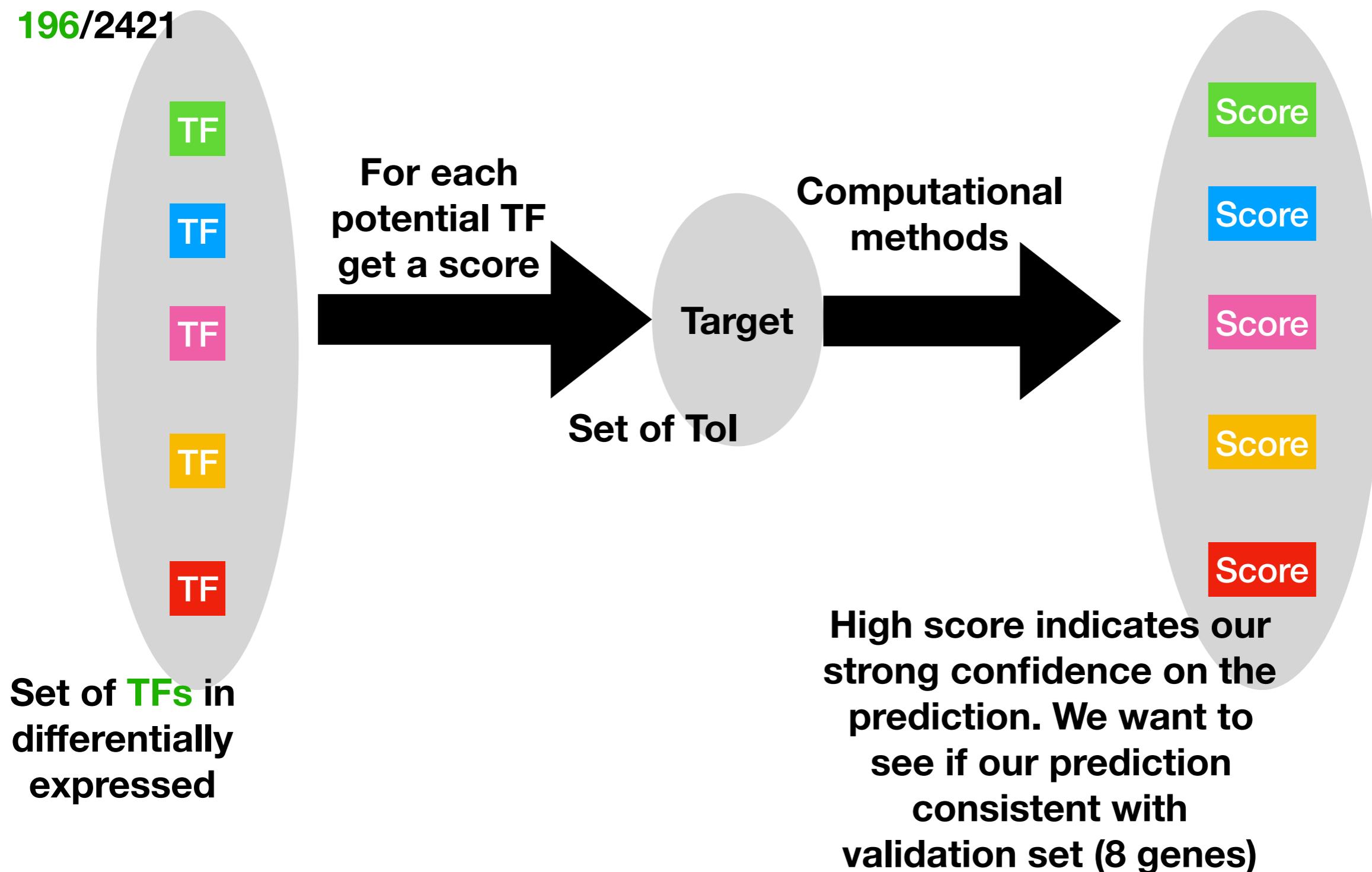
Most of them activated at 24 hours, or to say, at a pretty late time point

All the targets are **nTFs**, no need to constrain the flow of information

Relative small set of gene (8 targets), no need to consider computational cost

Computation

196/2421



Computational Methods

- **Pearson Correlation**, 7 time points;
- **BN**, 21 samples (7 time points, 3 replicates);
 - Binary discretization (`n_levels = 2`);
 - Three Level discretization (`n_levels = 3`);
- **BN**, 7 samples (7 time points);
- ***BN**, 97 samples (Interpolation)

Target	Lower bound	Upper bound			
Transcription factor	Promoter	Gene Name	Reg_ATP	Tar_ATP	Score
AT5G53950	AT5G44030	CESA4,IRX5,NWS2	6.0	6.0	-170.500842535
AT5G47220	AT5G44030	CESA4,IRX5,NWS2	3.0	6.0	
AT5G39610	AT5G44030	CESA4,IRX5,NWS2	3.0	6.0	
AT5G12870	AT5G44030	CESA4,IRX5,NWS2	5.0	6.0	-116.365812066
AT4G37260	AT5G44030	CESA4,IRX5,NWS2	6.0	6.0	-143.891472666
AT1G75490	AT5G44030	CESA4,IRX5,NWS2	6.0	6.0	-119.767009448
AT1G56650	AT5G44030	CESA4,IRX5,NWS2	5.0	6.0	-167.610470777

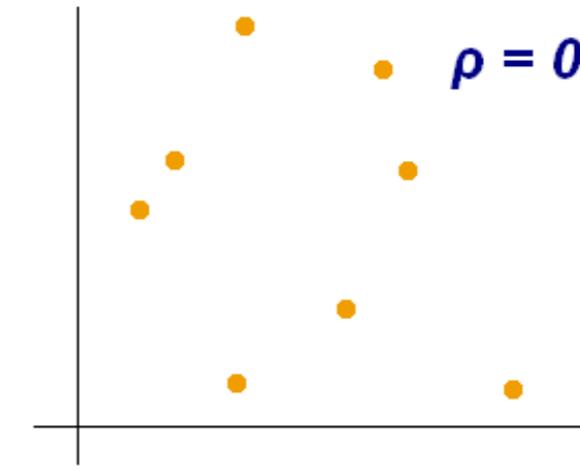
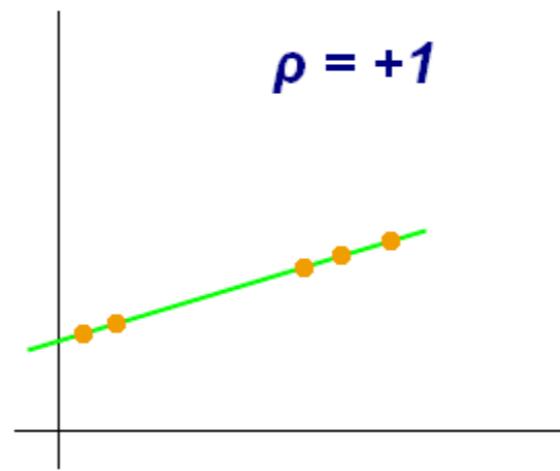
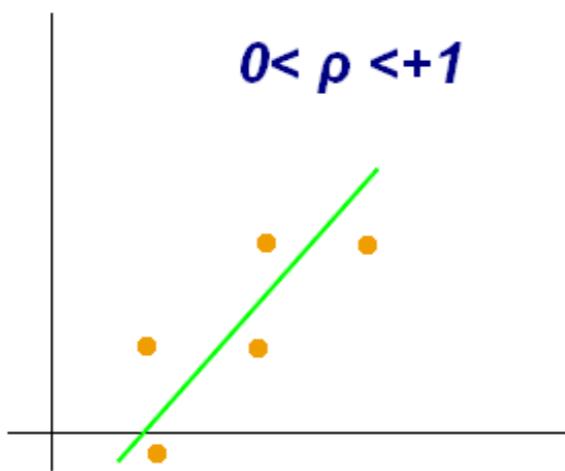
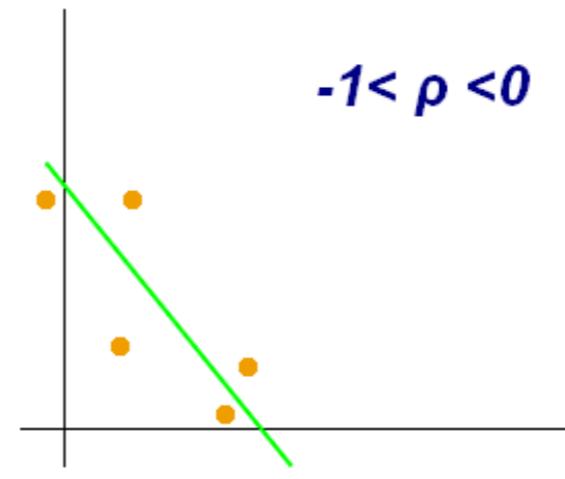
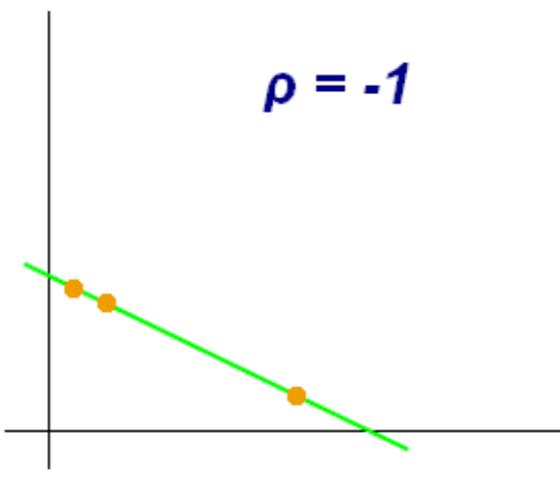
Ground Truth Table

Prediction

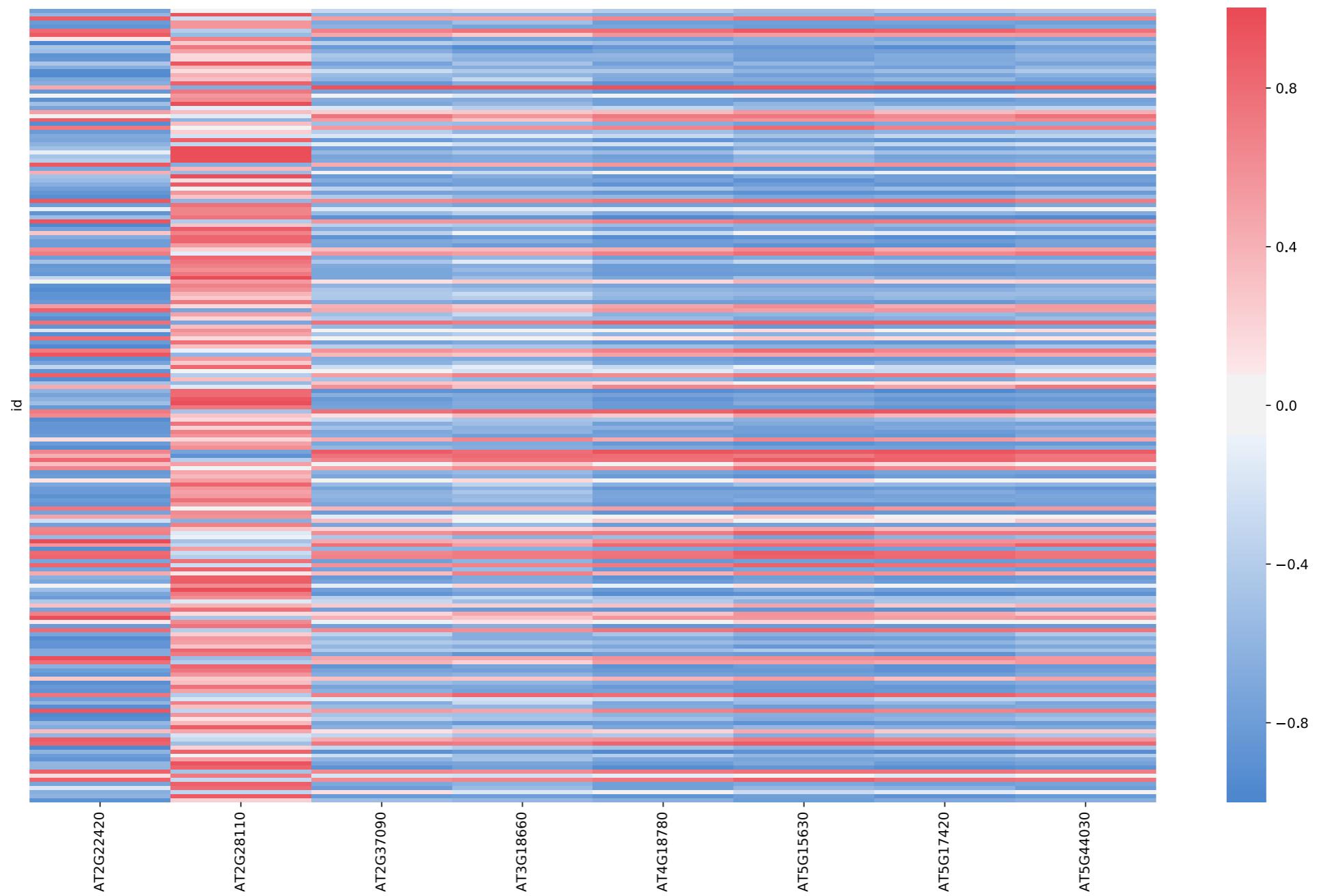
Target	Source	BDeu
AT5G44030	AT5G46690	-66.3251261597309
AT5G44030	AT2G14210	-114.979517705112
AT5G44030	AT3G56970	-116.365812066207
AT5G44030	AT4G00150	-116.365812066207
AT5G44030	AT4G01250	-116.365812066207
AT5G44030	AT5G12870	-116.365812066207
AT5G44030	AT2G34140	-116.365812066207
AT5G44030	AT5G60890	-116.365812066207
AT5G44030	AT2G25820	-117.058959246758
AT5G44030	AT2G44940	-117.058959246758
AT5G44030	AT2G22430	-117.464424354861
AT5G44030	AT4G29080	-117.464424354861
AT5G44030	AT4G18890	-117.464424354861
AT5G44030	AT4G28140	-118.668397159166
AT5G44030	AT1G52830	-119.07386226726
AT5G44030	AT2G22770	-119.07386226726
AT5G44030	AT3G60630	-119.07386226726
AT5G44030	AT1G49130	-119.767009447812
AT5G44030	AT1G74500	-119.767009447812
AT5G44030	AT1G75490	-119.767009447812
AT5G44030	AT4G00050	-119.767009447812
AT5G44030	AT5G25190	-119.767009447812
AT5G44030	AT5G59820	-119.767009447812
AT5G44030	AT3G02940	-142.099713197256
AT5G44030	AT2G40970	-143.891472666453
AT5G44030	AT5G19790	-143.891472666453
AT5G44030	AT1G34670	-143.891472666453
AT5G44030	AT1G65620	-143.891472666453
AT5G44030	AT3G24120	-143.891472666453
AT5G44030	AT4G37260	-143.891472666453
AT5G44030	AT5G47390	-143.891472666453
AT5G44030	AT1G29160	-143.891472666453
AT5G44030	AT3G27650	-143.891472666453
AT5G44030	AT4G06746	-143.891472666453
AT5G44030	AT4G39780	-143.891472666453
AT5G44030	AT1G10480	-143.891472666453
AT5G44030	AT1G12890	-143.891472666453
AT5G44030	AT2G40220	-143.891472666453
AT5G44030	AT3G18400	-143.891472666453
AT5G44030	AT3G56980	-143.891472666453
AT5G44030	AT5G14370	-143.891472666453
AT5G44030	AT5G46710	-143.891472666453
AT5G44030	AT3G03450	-144.584619847005
AT5G44030	AT5G58010	-144.584619847005
AT5G44030	AT1G65300	-144.584619847005
AT5G44030	AT1G77640	-144.584619847005
AT5G44030	AT3G14230	-144.584619847005
AT5G44030	AT5G06250	-144.584619847005
AT5G44030	AT5G13330	-144.584619847005
AT5G44030	AT1G15050	-145.277762027548

**Correlation Without
Interpolation
(7 samples over time)**

Pearson Correlation



Pearson Correlation without interpolation



	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0	0.82289	14	15

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0	-0.849502	63	64

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0	-0.713614	52	53
AT2G23340	AT2G37090	IRX9	3.0	5.0	-0.415381	150	151
AT4G37260	AT2G37090	IRX9	6.0	5.0	-0.788772	29	30
AT3G15210	AT2G37090	IRX9	1.0	5.0	0.567256	115	116
AT3G04060	AT2G37090	IRX9	6.0	5.0	-0.608617	99	100
AT3G02940	AT2G37090	IRX9	5.0	5.0	0.544554	119	120
AT3G11580	AT2G37090	IRX9	6.0	5.0	0.613418	95	96
AT1G06180	AT2G37090	IRX9	4.0	5.0	0.508846	129	130
AT1G56650	AT2G37090	IRX9	5.0	5.0	-0.732647	44	45

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0	-0.559388	107	108
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0	-0.710256	42	43
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0	-0.582122	98	99

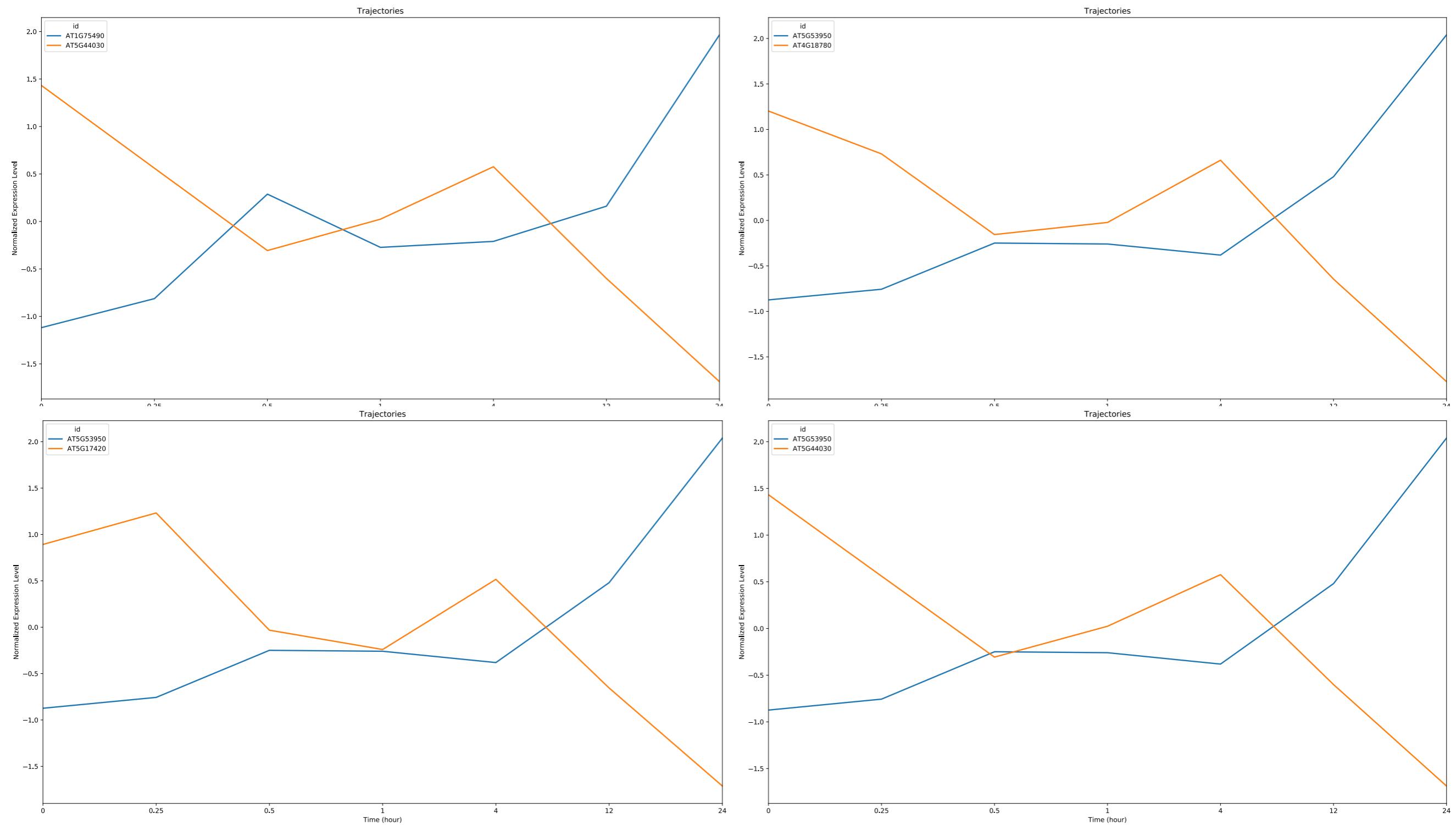
	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0	0.732988	74	75
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0	-0.839031	26	27
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0	-0.696369	88	89
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0	-0.545634	140	141
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0	-0.982011	0	1
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0	-0.326246	167	168
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0	-0.686944	96	97
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0	-0.790304	45	46
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0	-0.789646	48	49

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0	-0.646000	129	130
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0	-0.798815	59	60
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0	-0.844838	32	33
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0	0.611119	143	144
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0	-0.738345	98	99
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0	-0.711178	106	107
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0	-0.811880	50	51
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0	-0.685777	114	115
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0	0.955363	2	3
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0	-0.750520	92	93
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0	-0.950763	3	4
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0	0.874236	19	20

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-0.844319	31	32
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-0.652441	117	118
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-0.934839	7	8
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0	0.498038	154	155
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-0.874116	20	21
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-0.754840	72	73
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0	-0.629067	123	124
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-0.978797	0	1
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-0.410975	163	164
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	0.630013	122	123
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	0.886903	16	17
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-0.691028	102	103
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0	0.750170	76	77
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0	-0.774186	58	59
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0	-0.820093	43	44

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	Pearsonr	lower_index	upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-0.972014	0	1
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0	-0.539235	140	141
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0	-0.681465	95	96
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0	0.731890	67	68
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-0.800195	33	34
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-0.968382	1	2
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0	-0.745001	61	62

Trajectories With Highest Correlation

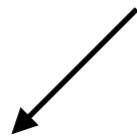


BN Without Interpolation

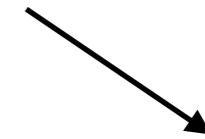
n_levels=2
21 samples

Bayesian Network

1: high expressed



0: low expressed



TF1: 0 1 0 1 0 1 0 1 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 0 1 0
TF2: 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1
Tol: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0

When TF2 low expresses, Tol high expresses definitely;

When TF2 high expresses, Tol low expresses definitely;

On the other hand, exists uncertainty for TF1

TF1->Tol: -22.6254

TF2->Tol: -4.7592

21 Samples For A Gene

id	kat_1_1	kat_2_1	kat_3_1	kat_1_2	kat_2_2	kat_3_2	kat_1_3	kat_2_3	kat_3_3	kat_1_4	kat_2_4	kat_3_4	kat_1_5	kat_2_5	kat_3_5	kat_1_6	kat_2_6	kat_3_6	kat_1_7	kat_2_7	kat_3_7
AT5G53950	0.3093	0.3111	0.4334	0.3438	0.3242	0.4734	0.2332	0.4487	0.8472	0.4928	0.4837	0.6170	0.3116	0.4554	0.6553	0.5103	0.7343	0.8223	1.1713	0.8225	1.2392
AT4G18780	6.4078	5.6188	9.1664	5.4271	5.4665	8.4650	4.4977	4.6362	6.7845	4.5259	5.5486	6.3597	6.0161	4.2699	8.8022	4.1482	4.5219	5.3482	2.8866	3.2543	3.5051



Discretization

AT5G53950	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	1	1	1	1	1
AT4G18780	1	1	1	0	0	1	0	0	1	0	1	1	1	0	0	1	0	0	0	0	0



Statistics

Score: -40.4592

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0	-38.593308	58	64
Transcription factor AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0	-34.706605	6	9
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0	-37.746011	37	40
AT2G23340	AT2G37090	IRX9	3.0	5.0	-40.053709	102	121
AT4G37260	AT2G37090	IRX9	6.0	5.0	-40.053709	102	121
AT3G15210	AT2G37090	IRX9	1.0	5.0	-40.564534	165	168
AT3G04060	AT2G37090	IRX9	6.0	5.0	-38.395482	40	52
AT3G02940	AT2G37090	IRX9	5.0	5.0	-35.622896	9	12
AT3G11580	AT2G37090	IRX9	6.0	5.0	-37.347514	17	28
AT1G06180	AT2G37090	IRX9	4.0	5.0	-38.600276	59	66
AT1G56650	AT2G37090	IRX9	5.0	5.0	-39.206412	66	74

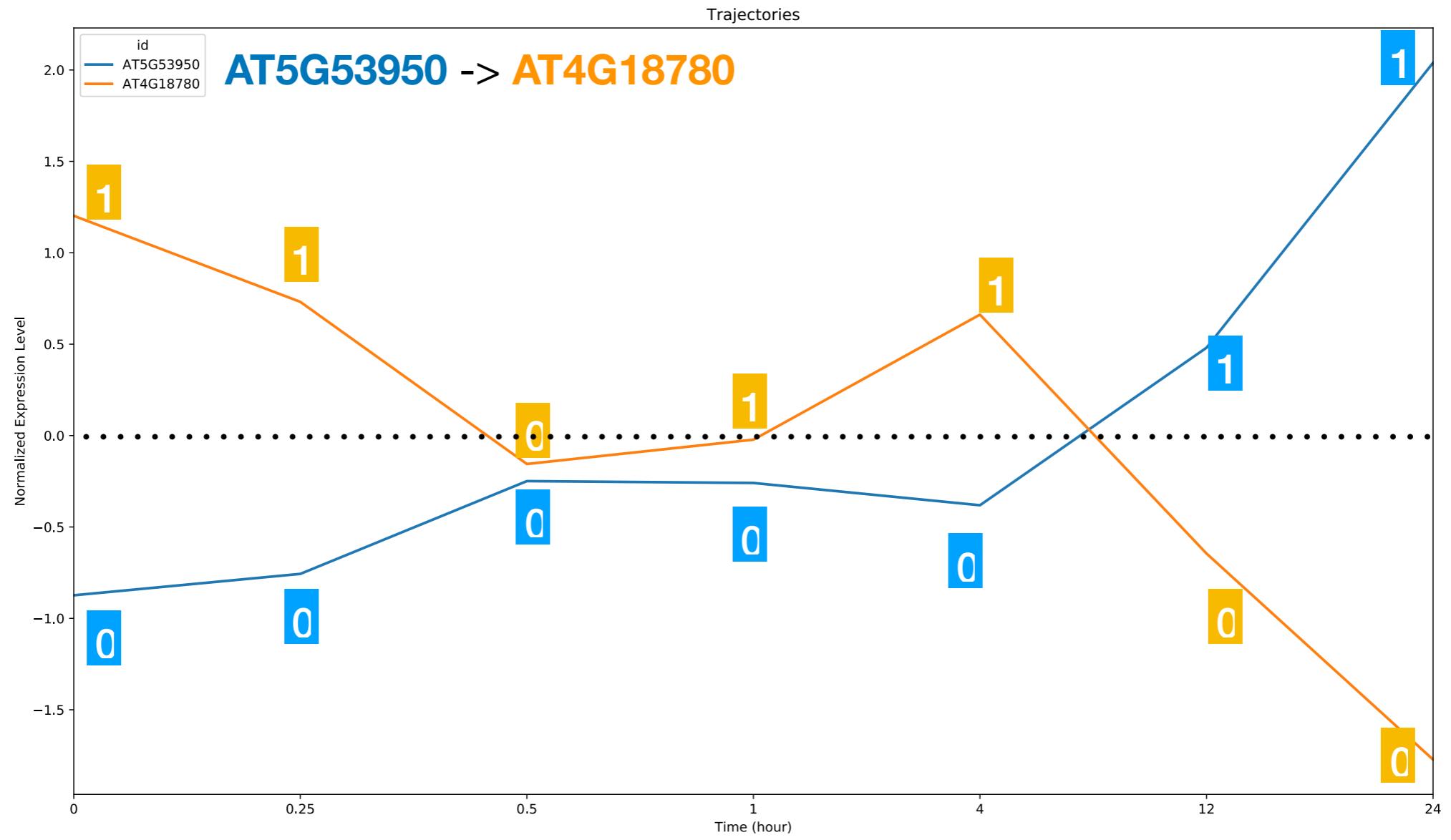
	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -40.004918		115	125
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -40.236030		126	145
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -37.414654		13	16

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -39.853038		98	115
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -38.955097		56	70
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -39.293423		70	82
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -39.293423		70	82
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -40.459174		158	162
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -37.213982		21	25
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -40.236030		128	141
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -39.542884		89	98
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -37.414654		26	30

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -39.542884		130	135
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -36.449574		40	46
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -40.236030		154	168
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -38.513264		93	101
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -40.459174		176	182
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -33.763998		17	21
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -37.213982		46	56
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -38.194811		71	88
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -37.414653		56	64
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -37.213982		46	56
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -39.293423		121	128
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -18.785336		2	5

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -37.414653		53	67
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -40.122701		136	144
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -39.447573		109	115
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0 -40.053709		133	136
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -22.580573		3	5
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -39.494093		115	131
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -33.881781		8	13
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -40.122701		136	144
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -39.494093		115	131
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -33.881781		8	13
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -31.684559		6	8
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -36.935081		41	45
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -35.961220		27	34
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -37.347514		45	53
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -35.622896		24	27

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -40.122701		180	189
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -37.907129		33	42
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -39.516566		93	103
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -36.115372		13	23
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -39.137419		82	92
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -37.907129		33	42
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -39.542884		103	110



AT5G53950	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	1	1	1
AT4G18780	1	1	1	0	0	1	0	0	1	0	1	1	1	0	0	1	0	0	0



Confusing Samples (These samples instead of providing more informations, confusing us)

BN Without Interpolation

n_levels=3
21 samples

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G13790	AT2G22420	PRX17	6.0	4.0 -71.518096		62	80

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0 -85.921395		71	82

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT1G36060	AT2G37090	IRX9	3.0	5.0 -83.436489		32	45
AT2G23340	AT2G37090	IRX9	3.0	5.0 -101.423304		156	185
AT4G37260	AT2G37090	IRX9	6.0	5.0 -99.919227		126	134
AT3G15210	AT2G37090	IRX9	1.0	5.0 -101.135622		153	156
AT3G04060	AT2G37090	IRX9	6.0	5.0 -99.919227		126	134
AT3G02940	AT2G37090	IRX9	5.0	5.0 -70.824950		20	26
AT3G11580	AT2G37090	IRX9	6.0	5.0 -85.228248		45	80
AT1G06180	AT2G37090	IRX9	4.0	5.0 -85.228248		45	80
AT1G56650	AT2G37090	IRX9	5.0	5.0 -99.343864		118	126

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0	-101.423304	130	169
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0	-101.423304	130	169
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0	-85.921395	42	65

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0	-68.810048	8	14
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0	-98.532934	80	93
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0	-102.521915	181	188
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0	-85.228248	34	58
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0	-101.017839	119	134
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0	-86.614541	67	78
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0	-101.017839	119	134
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0	-99.919227	109	119
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0	-85.228248	34	58

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0	-98.532934	89	101
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0	-85.228248	43	63
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0	-101.423304	145	172
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0	-71.518096	15	28
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0	-103.215062	183	196
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0	-71.518096	15	28
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0	-83.436489	30	43
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0	-85.228248	43	63
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0	-85.228248	43	63
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0	-101.423304	145	172
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0	-85.921395	63	77
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0	-68.116901	1	5

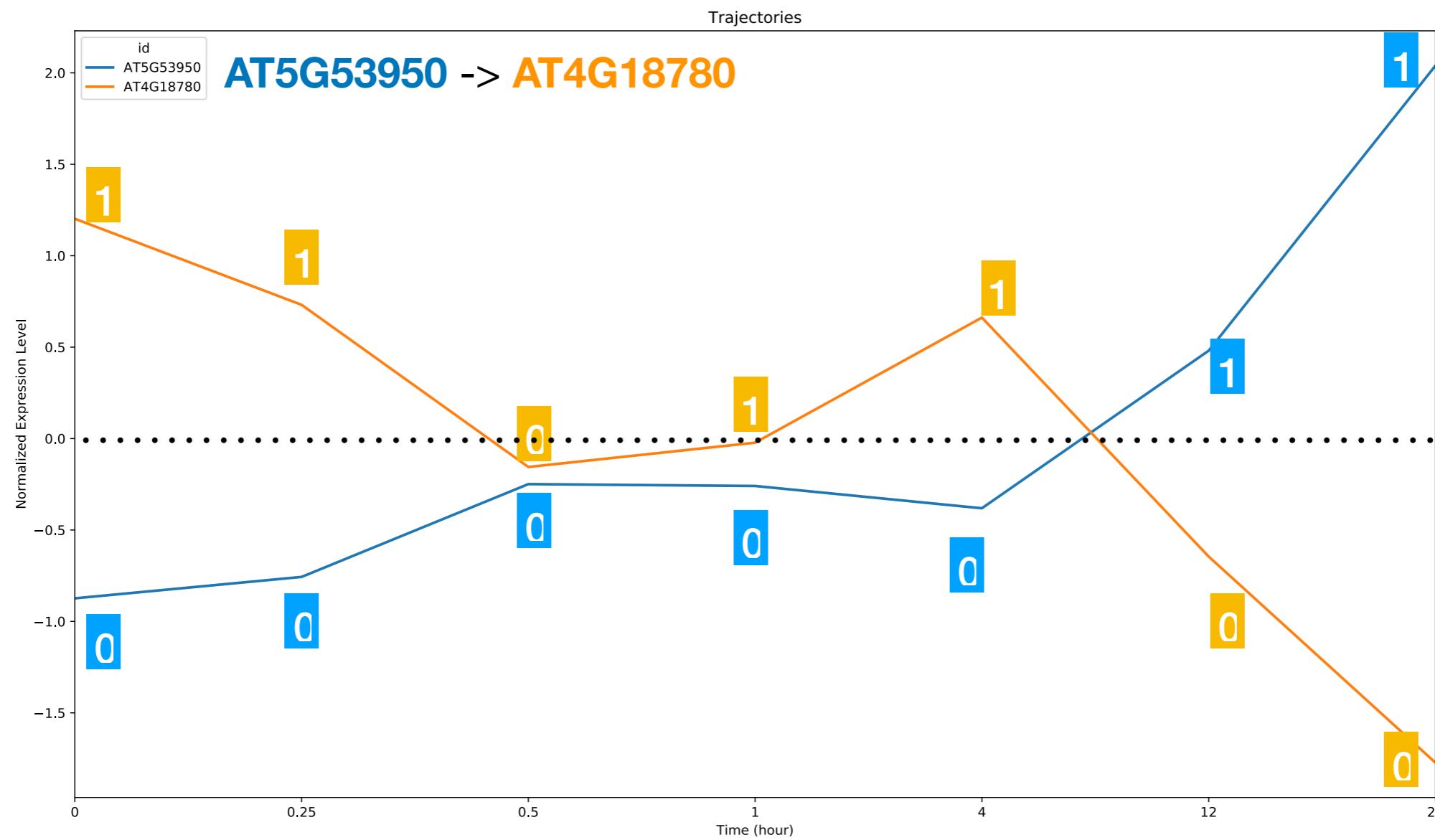
	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-85.921395	70	77
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-101.423304	145	179
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-85.921395	70	77
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0	-85.921395	70	77
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-86.614541	77	94
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-98.532934	95	109
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0	-85.228248	48	70
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-101.423304	145	179
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-99.343864	109	115
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-70.824950	29	32
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-66.730607	1	2
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-101.017839	122	140
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0	-68.116901	2	9
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0	-69.215513	19	28
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0	-101.423304	145	179

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-101.423304	145	177
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0	-71.518096	30	42
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0	-71.518096	30	42
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0	-68.116901	2	9
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-85.228248	52	87
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-71.518096	30	42
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0	-98.532934	110	118

BN Without Interpolation

**n_levels=2
7 samples**

Threshold 0



	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0 -1.386303		0	56

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0 -28.571039		39	72

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0 -29.669650		108	196
AT2G23340	AT2G37090	IRX9	3.0	5.0 -29.669650		108	196
AT4G37260	AT2G37090	IRX9	6.0	5.0 -16.770428		15	41
AT3G15210	AT2G37090	IRX9	1.0	5.0 -17.281251		41	42
AT3G04060	AT2G37090	IRX9	6.0	5.0 -29.669650		108	196
AT3G02940	AT2G37090	IRX9	5.0	5.0 -28.976504		47	108
AT3G11580	AT2G37090	IRX9	6.0	5.0 -28.976504		47	108
AT1G06180	AT2G37090	IRX9	4.0	5.0 -29.669650		108	196
AT1G56650	AT2G37090	IRX9	5.0	5.0 -16.770428		15	41

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -29.669650		108	196
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -16.770428		15	41
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -28.976504		47	108

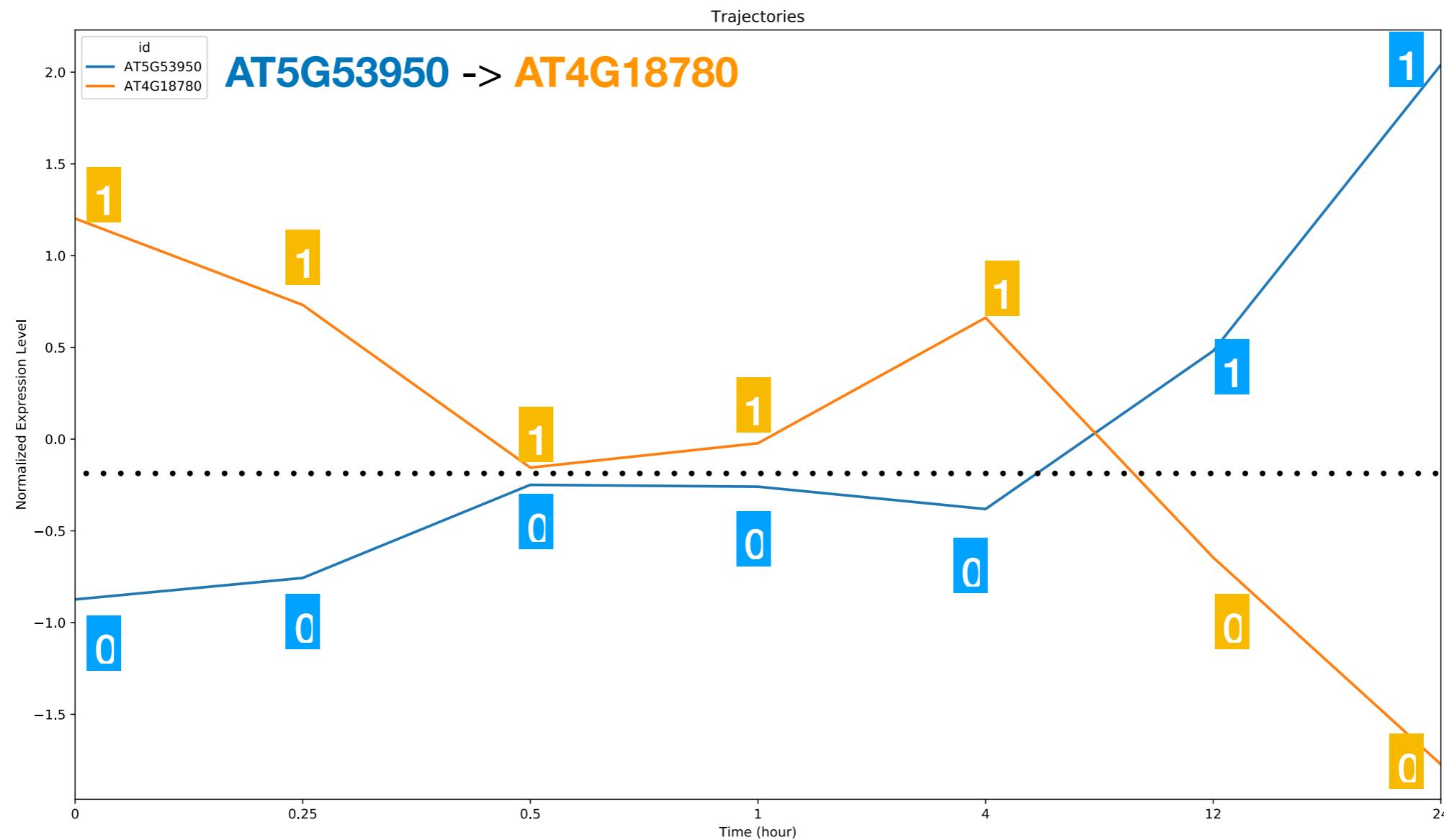
	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -29.669650		108	196
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -16.770428		15	41
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -28.976504		47	108
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -28.976504		47	108
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -16.770428		15	41
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -29.669650		108	196
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -28.976504		47	108
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -29.669650		108	196
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -16.770428		15	41

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		108	196
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -16.770428		15	41
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		47	108
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -17.281251		41	42
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		47	108
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		47	108
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -28.976504		47	108
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		47	108
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		47	108
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		47	108
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -15.384136		1	8
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		108	196

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -16.770428		15	41
AT1G21910	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -28.976504		47	108
AT1G75490	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -15.384136		1	8
AT3G15210	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	1.0	6.0 -17.281251		41	42
AT3G16770	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	4.0	6.0 -16.770428		15	41
AT5G13330	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -28.976504		47	108
AT5G47220	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	3.0	6.0 -28.976504		47	108
AT5G53950	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -16.770428		15	41
AT1G44830	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	4.0	6.0 -28.976504		47	108
AT1G06180	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	4.0	6.0 -29.669650		108	196
AT2G44940	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -29.669650		108	196
AT5G61420	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	6.0	6.0 -29.669650		108	196
AT5G12870	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	5.0	6.0 -29.669650		108	196
AT5G39610	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	3.0	6.0 -28.976504		47	108
AT1G56650	AT5G17420	ATCESA7,CESA7,IRX3,MUR10	5.0	6.0 -16.770428		15	41

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4,IRX5,NWS2	6.0	6.0 -15.671817		3	27
AT5G47220	AT5G44030	CESA4,IRX5,NWS2	3.0	6.0 -29.669650		107	196
AT5G39610	AT5G44030	CESA4,IRX5,NWS2	3.0	6.0 -29.669650		107	196
AT5G12870	AT5G44030	CESA4,IRX5,NWS2	5.0	6.0 -28.976504		40	107
AT4G37260	AT5G44030	CESA4,IRX5,NWS2	6.0	6.0 -15.671817		3	27
AT1G75490	AT5G44030	CESA4,IRX5,NWS2	6.0	6.0 -1.386303		0	2
AT1G56650	AT5G44030	CESA4,IRX5,NWS2	5.0	6.0 -15.671817		3	27

Threshold -0.24



Cheat a little bit to make
consistent with Pearsonr

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0 -1.386303		0	53
Transcription factor AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0 -29.66965		69	196
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0 -28.976504		33	100
AT2G23340	AT2G37090	IRX9	3.0	5.0 -29.669650		100	196
AT4G37260	AT2G37090	IRX9	6.0	5.0 -28.976504		33	100
AT3G15210	AT2G37090	IRX9	1.0	5.0 -15.384136		3	10
AT3G04060	AT2G37090	IRX9	6.0	5.0 -15.384136		3	10
AT3G02940	AT2G37090	IRX9	5.0	5.0 -29.669650		100	196
AT3G11580	AT2G37090	IRX9	6.0	5.0 -29.669650		100	196
AT1G06180	AT2G37090	IRX9	4.0	5.0 -28.976504		33	100
AT1G56650	AT2G37090	IRX9	5.0	5.0 -15.671817		10	22

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -29.66965		39	196
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -29.66965		39	196
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -29.66965		39	196

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -14.978671		12	80
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -14.978671		12	80
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -16.077282		82	162
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -16.077282		82	162
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -1.386302		0	12
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -16.770428		162	173
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -16.077282		82	162
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -16.077282		82	162
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -1.386302		0	12

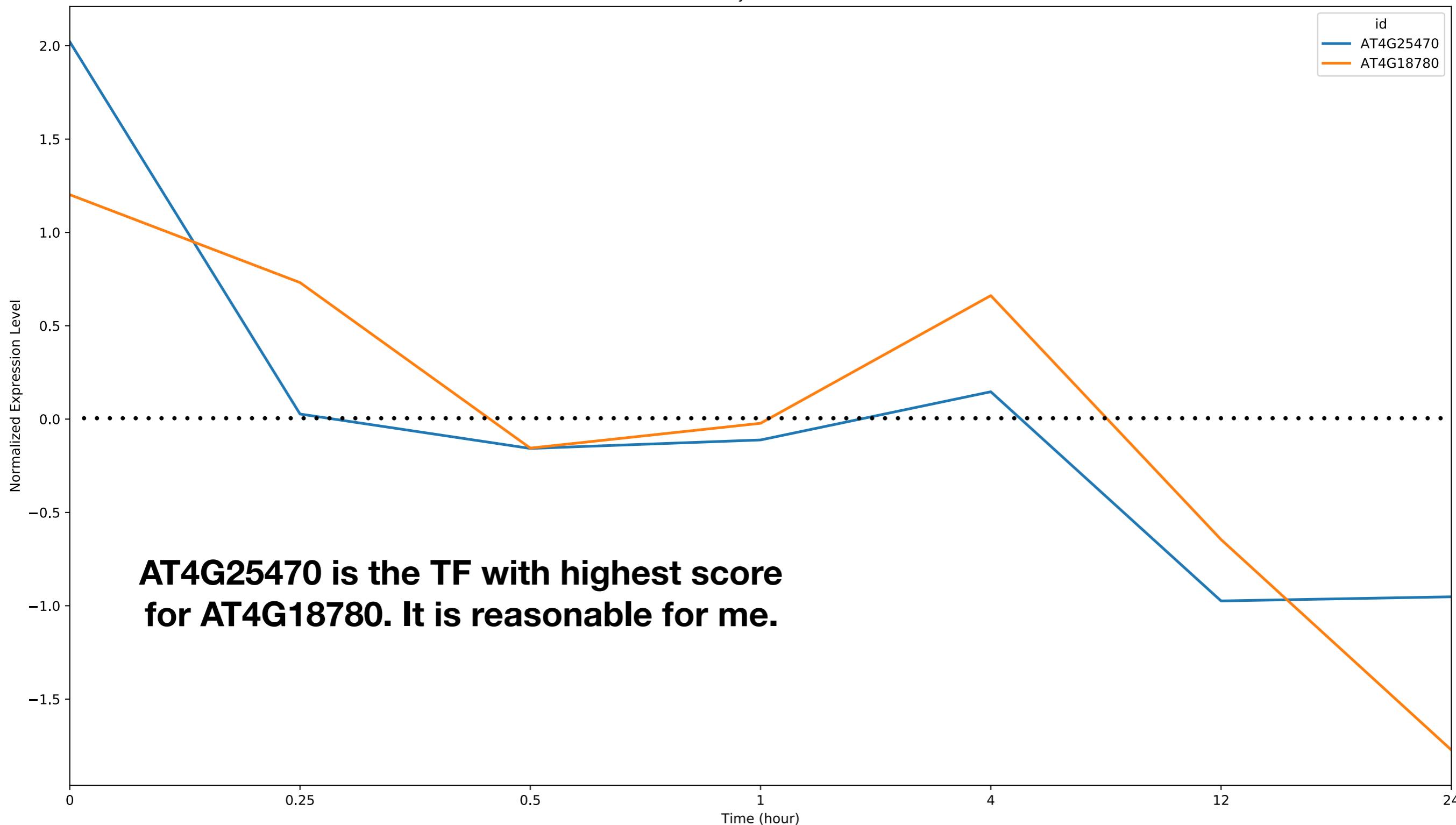
	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		157	196
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		84	157
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -16.770428		75	82
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -29.669650		157	196
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -15.384136		6	63
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -15.384136		6	63
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -15.384136		6	63
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -15.384136		6	63
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		84	157
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -15.384136		6	63
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		157	196
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		84	157

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504		84	157
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.384136		6	63
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -29.669650		157	196
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0 -29.669650		157	196
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -15.671817		63	75
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.384136		6	63
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -15.384136		6	63
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.671817		63	75
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -15.384136		6	63
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -28.976504		84	157
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504		84	157
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504		84	157
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -28.976504		84	157
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -15.384136		6	63
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -15.671817		63	75

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -15.671817		10	22
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -29.669650		100	196
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -29.669650		100	196
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -28.976504		33	100
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -28.976504		33	100
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -15.384136		3	10
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -15.671817		10	22

Prediction

Trajectories



Explanation

- 21 samples BN should be better 7 samples BN; Statistics need samples;
- Try to blame the data
 - Bias to linear relationship. Strong linear relationship verified first;
 - Bias to use ethylene activated data to figure out cell wall organization relationships;
- Discretization, is limited; On the one hand it has better generalization, on the other hand it can not void lose information; MCMC BN.

THE END

BN Without Interpolation

**n_levels=3
7 samples**

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0 -1.386303		0	62
Transcription factor AT4G37260	AT2G28110	FRA8, IRX7	6.0	6.0 -28.976504		33	117
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0 -28.976504		29	106
AT2G23340	AT2G37090	IRX9	3.0	5.0 -29.669650		106	196
AT4G37260	AT2G37090	IRX9	6.0	5.0 -28.976504		29	106
AT3G15210	AT2G37090	IRX9	1.0	5.0 -17.686715		28	29
AT3G04060	AT2G37090	IRX9	6.0	5.0 -28.976504		29	106
AT3G02940	AT2G37090	IRX9	5.0	5.0 -29.669650		106	196
AT3G11580	AT2G37090	IRX9	6.0	5.0 -29.669650		106	196
AT1G06180	AT2G37090	IRX9	4.0	5.0 -28.976504		29	106
AT1G56650	AT2G37090	IRX9	5.0	5.0 -28.976504		29	106

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -29.669650		100	196
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -29.669650		100	196
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -28.976504		37	100

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -28.976504		29	106
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -28.976504		29	106
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -29.669650		106	196
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -29.669650		106	196
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -15.671817		3	20
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -29.669650		106	196
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -29.669650		106	196
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -28.976504		29	106
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -28.976504		29	106

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -15.671817		12	18
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -17.281251		35	36
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		37	100
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		37	100
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -28.976504		37	100
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		37	100
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		37	100
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -15.384136		0	12
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.384136	7		60
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0 -17.686715	84		85
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -15.671817	60		77
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.384136	7		60
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -15.384136	7		60
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.671817	60		77
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -15.384136	7		60
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -28.976504	85		167
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -28.976504	85		167
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -15.384136	7		60
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -28.976504	85		167

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -15.671817	3		20
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -29.669650	106		196
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -29.669650	106		196
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -28.976504	29		106
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -28.976504	29		106
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -1.386303	0		3
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -28.976504	29		106

BN With Interpolation

n_levels=2

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0 -21.504441		13	16
Transcription factor AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0 -27.490404		29	37
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0 -18.092199		3	7
AT2G23340	AT2G37090	IRX9	3.0	5.0 -35.752978		46	54
AT4G37260	AT2G37090	IRX9	6.0	5.0 -34.798601		41	46
AT3G15210	AT2G37090	IRX9	1.0	5.0 -35.752978		46	54
AT3G04060	AT2G37090	IRX9	6.0	5.0 -81.724045		164	165
AT3G02940	AT2G37090	IRX9	5.0	5.0 -86.714001		174	175
AT3G11580	AT2G37090	IRX9	6.0	5.0 -25.502905		14	21
AT1G06180	AT2G37090	IRX9	4.0	5.0 -86.989044		176	177
AT1G56650	AT2G37090	IRX9	5.0	5.0 -21.920838		8	9

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -87.564944		161	162
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -54.204730		46	54
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -94.046834		191	192

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -52.872835		118	120
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -32.783698		34	39
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -44.055136		91	93
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -93.024713		184	185
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -32.783698		34	39
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -51.493704		117	118
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -42.409980		77	85
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -36.967564		52	53
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -18.114178		4	5

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -61.441978		128	129
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -36.636880		53	58
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -85.772453		170	171
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -33.593494		36	44
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -72.133331		152	153
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -93.296395		185	186
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -68.102520		135	143
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -58.238737		122	123
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -21.876386		5	9
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -93.505212		189	190
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -45.118030		85	93
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -18.069726		1	4

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -32.783698		34	39
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -72.993532		156	157
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -42.409980		77	85
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0 -37.738893		53	61
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -32.783698		34	39
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -42.409980		77	85
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -93.024713		184	185
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -32.783698		34	39
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -37.738893		53	61
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -87.492949		176	177
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -18.217362		5	8
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -30.461311		24	28
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -52.872835		118	120
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -44.055136		91	93
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -18.114178		4	5

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -32.783698		34	39
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -93.024713		184	185
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -44.055136		91	93
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -52.872835		118	120
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -32.783698		34	39
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -42.409980		77	85
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -18.114178		4	5

BN With Interpolation

n_levels=3

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0	-148.523712	65	138
Transcription factor AT4G37260	AT2G28110	FRA8, IRX7	6.0	6.0	-44.451069	10	90
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0	-54.335542	8	88
AT2G23340	AT2G37090	IRX9	3.0	5.0	-54.335542	8	88
AT4G37260	AT2G37090	IRX9	6.0	5.0	-54.335542	8	88
AT3G15210	AT2G37090	IRX9	1.0	5.0	-49.833267	4	8
AT3G04060	AT2G37090	IRX9	6.0	5.0	-132.962718	163	164
AT3G02940	AT2G37090	IRX9	5.0	5.0	-136.740716	173	175
AT3G11580	AT2G37090	IRX9	6.0	5.0	-54.335542	8	88
AT1G06180	AT2G37090	IRX9	4.0	5.0	-140.247832	178	179
AT1G56650	AT2G37090	IRX9	5.0	5.0	-54.335542	8	88

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1, PGSIP1	4.0	6.0	-69.079279	13	91
AT4G37260	AT3G18660	GUX1, PGSIP1	6.0	6.0	-69.079279	13	91
AT1G21910	AT3G18660	GUX1, PGSIP1	6.0	6.0	-130.625874	165	166

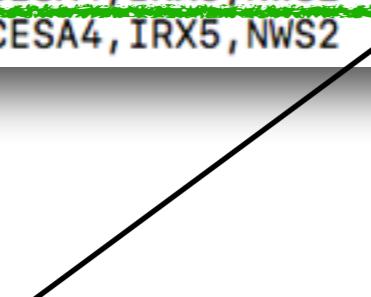
	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	5.0	6.0	-112.044351	137	139
AT4G37260	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	6.0	6.0	-44.451069	3	84
AT5G39610	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	3.0	6.0	-75.036072	102	104
AT5G47220	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	3.0	6.0	-151.424133	195	196
AT5G53950	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	6.0	6.0	-44.451069	3	84
AT1G79840	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	4.0	6.0	-84.781899	119	122
AT5G13330	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	6.0	6.0	-75.036072	102	104
AT5G25890	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	5.0	6.0	-44.451069	3	84
AT1G56650	AT4G18780	ATCESA8, CESA8, IRX1, LEW2	5.0	6.0	-44.451069	3	84

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4, IRX6	6.0	3.0	-97.065552	126	127
AT4G37260	AT5G15630	COBL4, IRX6	6.0	3.0	-37.615887	2	79
AT5G47230	AT5G15630	COBL4, IRX6	3.0	3.0	-144.084139	187	188
AT3G15210	AT5G15630	COBL4, IRX6	1.0	3.0	-44.451069	79	84
AT1G21910	AT5G15630	COBL4, IRX6	6.0	3.0	-139.571510	177	178
AT5G47220	AT5G15630	COBL4, IRX6	3.0	3.0	-149.315705	194	195
AT5G13910	AT5G15630	COBL4, IRX6	2.0	3.0	-109.559004	143	144
AT1G28370	AT5G15630	COBL4, IRX6	3.0	3.0	-139.679559	178	179
AT3G18400	AT5G15630	COBL4, IRX6	6.0	3.0	-37.615887	2	79
AT3G25730	AT5G15630	COBL4, IRX6	3.0	3.0	-125.309992	155	156
AT1G75490	AT5G15630	COBL4, IRX6	6.0	3.0	-44.451069	79	84
AT2G44940	AT5G15630	COBL4, IRX6	6.0	3.0	-37.615887	2	79

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-44.451069	3	85
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-141.026797	179	180
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-44.451069	3	85
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0	-44.451069	3	85
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-44.451069	3	85
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-75.036072	101	103
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0	-151.424133	195	196
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-44.451069	3	85
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-79.788616	117	120
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0	-132.081996	164	165
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-44.451069	3	85
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0	-44.451069	3	85
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0	-112.044351	138	140
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0	-75.036072	101	103
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0	-44.451069	3	85

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-44.451069	3	84
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0	-151.424133	195	196
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0	-75.036072	102	104
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0	-112.044351	137	139
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-44.451069	3	84
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0	-3.295864	0	1
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0	-44.451069	3	84

With Interpolation, this
one shows up, again



BN Without Interpolation

Discard

n_levels=2
7 samples

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0 -1.386303		0	62
Transcription factor AT4G37260	AT2G28110	FRA8, IRX7	6.0	6.0 -28.976504		33	117
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0 -28.976504		29	106
AT2G23340	AT2G37090	IRX9	3.0	5.0 -29.669650		106	196
AT4G37260	AT2G37090	IRX9	6.0	5.0 -28.976504		29	106
AT3G15210	AT2G37090	IRX9	1.0	5.0 -17.686715		28	29
AT3G04060	AT2G37090	IRX9	6.0	5.0 -28.976504		29	106
AT3G02940	AT2G37090	IRX9	5.0	5.0 -29.669650		106	196
AT3G11580	AT2G37090	IRX9	6.0	5.0 -29.669650		106	196
AT1G06180	AT2G37090	IRX9	4.0	5.0 -28.976504		29	106
AT1G56650	AT2G37090	IRX9	5.0	5.0 -28.976504		29	106

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -29.669650		100	196
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -29.669650		100	196
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -28.976504		37	100

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -28.976504		29	106
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -28.976504		29	106
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -29.669650		106	196
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -29.669650		106	196
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -15.671817		3	20
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -29.669650		106	196
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -29.669650		106	196
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -28.976504		29	106
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -28.976504		29	106

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -15.671817		12	18
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -17.281251		35	36
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -28.976504		37	100
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		37	100
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -28.976504		37	100
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		37	100
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -28.976504		37	100
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -15.384136		0	12
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -29.669650		100	196

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.384136	7		60
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0 -17.686715	84		85
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -15.671817	60		77
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.384136	7		60
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -15.384136	7		60
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -15.671817	60		77
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -15.384136	7		60
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -28.976504	85		167
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -28.976504	85		167
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -28.976504	85		167
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -15.384136	7		60
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -28.976504	85		167

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -15.671817	3		20
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -29.669650	106		196
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -29.669650	106		196
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -28.976504	29		106
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -28.976504	29		106
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -1.386303	0		3
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -28.976504	29		106

BN Without Interpolation

Discard

n_levels=3
7 samples

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor AT5G13790	AT2G22420	PRX17	6.0	4.0	-31.409294	7	48
Transcription factor AT4G37260	AT2G28110	FRA8,IRX7	6.0	6.0	-58.829596	150	196
Transcription factor AT1G36060	AT2G37090	IRX9	3.0	5.0	-31.409294	30	111
AT2G23340	AT2G37090	IRX9	3.0	5.0	-17.699142	2	28
AT4G37260	AT2G37090	IRX9	6.0	5.0	-17.699142	2	28
AT3G15210	AT2G37090	IRX9	1.0	5.0	-3.295845	0	2
AT3G04060	AT2G37090	IRX9	6.0	5.0	-31.409294	30	111
AT3G02940	AT2G37090	IRX9	5.0	5.0	-31.409294	30	111
AT3G11580	AT2G37090	IRX9	6.0	5.0	-17.699142	2	28
AT1G06180	AT2G37090	IRX9	4.0	5.0	-45.119445	111	184
AT1G56650	AT2G37090	IRX9	5.0	5.0	-17.699142	2	28

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT3G60530	AT3G18660	GUX1,PGSIP1	4.0	6.0 -31.409294		27	108
AT4G37260	AT3G18660	GUX1,PGSIP1	6.0	6.0 -45.119445		108	157
AT1G21910	AT3G18660	GUX1,PGSIP1	6.0	6.0 -17.699142		5	27

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G12870	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -3.295845		0	43
AT4G37260	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -31.409294		70	154
AT5G39610	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -31.409294		70	154
AT5G47220	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	3.0	6.0 -31.409294		70	154
AT5G53950	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -3.295845		0	43
AT1G79840	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	4.0	6.0 -45.119445		154	172
AT5G13330	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	6.0	6.0 -58.829596		172	196
AT5G25890	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -31.409294		70	154
AT1G56650	AT4G18780	ATCESA8,CESA8,IRX1,LEW2	5.0	6.0 -31.409294		70	154

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G61590	AT5G15630	COBL4,IRX6	6.0	3.0 -45.119445		154	172
AT4G37260	AT5G15630	COBL4,IRX6	6.0	3.0 -31.409294		70	154
AT5G47230	AT5G15630	COBL4,IRX6	3.0	3.0 -31.409294		70	154
AT3G15210	AT5G15630	COBL4,IRX6	1.0	3.0 -31.409294		70	154
AT1G21910	AT5G15630	COBL4,IRX6	6.0	3.0 -31.409294		70	154
AT5G47220	AT5G15630	COBL4,IRX6	3.0	3.0 -31.409294		70	154
AT5G13910	AT5G15630	COBL4,IRX6	2.0	3.0 -31.409294		70	154
AT1G28370	AT5G15630	COBL4,IRX6	3.0	3.0 -31.409294		70	154
AT3G18400	AT5G15630	COBL4,IRX6	6.0	3.0 -3.295845		0	43
AT3G25730	AT5G15630	COBL4,IRX6	3.0	3.0 -31.409294		70	154
AT1G75490	AT5G15630	COBL4,IRX6	6.0	3.0 -31.409294		70	154
AT2G44940	AT5G15630	COBL4,IRX6	6.0	3.0 -3.295845		0	43

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT4G37260	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -31.409294		70	154
AT1G21910	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -31.409294		70	154
AT1G75490	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -31.409294		70	154
AT3G15210	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	1.0	6.0 -31.409294		70	154
AT3G16770	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -3.295845		0	43
AT5G13330	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -58.829596		172	196
AT5G47220	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -31.409294		70	154
AT5G53950	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -3.295845		0	43
AT1G44830	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -17.699142		43	70
AT1G06180	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	4.0	6.0 -31.409294		70	154
AT2G44940	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -3.295845		0	43
AT5G61420	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	6.0	6.0 -17.699142		43	70
AT5G12870	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -3.295845		0	43
AT5G39610	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	3.0	6.0 -31.409294		70	154
AT1G56650	AT5G17420	ATCESA7, CESA7, IRX3, MUR10	5.0	6.0 -31.409294		70	154

	Promoter	GENE NAME	Reg_ATP	Tar_ATP	BDeu	BDeu_lower_index	BDeu_upper_index
Transcription factor							
AT5G53950	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -31.409294		30	111
AT5G47220	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -45.119445		111	184
AT5G39610	AT5G44030	CESA4, IRX5, NWS2	3.0	6.0 -45.119445		111	184
AT5G12870	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -31.409294		30	111
AT4G37260	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -17.699142		2	28
AT1G75490	AT5G44030	CESA4, IRX5, NWS2	6.0	6.0 -58.829596		184	196
AT1G56650	AT5G44030	CESA4, IRX5, NWS2	5.0	6.0 -17.699142		2	28