

Figure S1

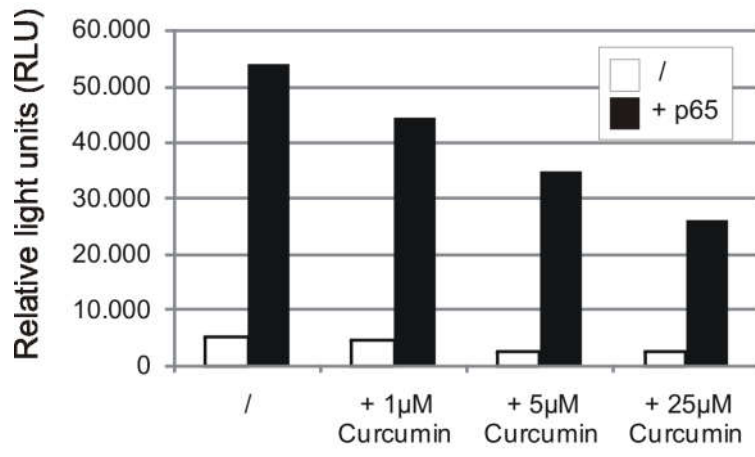


Figure S2

Transcription factor	Sequence	Start	Score
Elk-1	CTTCAGATTC	9	7.052
SPI-1	CTTCAG	9	5.359
Irf-1	AGATTCTCTT TC	13	8.520
GATA-3	TTCTCT	16	4.087
Dof2	CTCTTT	18	5.916
Dof3	CTCTTT	18	5.352
Gklf	CTCTTTCTTT	18	7.620
Gklf	TCTTTCTTTC	19	5.297
MNB1A	TCTTT	19	6.786
PBF	TCTTT	19	5.740
Gklf	CTTTCTTTCC	20	5.621
SPI-1	CTTTCT	20	4.721
Dof2	TTCTTT	22	6.891
Dof3	TTCTTT	22	4.846
Gklf	TCTTTCCCCA	23	5.420
MNB1A	TCTTT	23	6.786
PBF	TCTTT	23	5.740
Gklf	CTTTCCCCAG	24	5.389
SPI-1	CTTTCC	24	5.116
SPI-1	TTTCCC	25	5.702
MZF_5-13	TTCCCCAGA G	26	7.301
SPI-B	TTCCCCA	26	8.183
MZF_1-4	TCCCCA	27	9.085
Nkx	CAATAT	41	4.868
GATA-1	ATATCC	44	5.111
GATA-3	ATATCC	44	4.250
GATA-2	TATCC	45	6.651
SPI-B	ATCCTCT	46	6.769
MZF_1-4	TCCTCT	47	5.322
GATA-3	CTCTCA	49	4.990
c-FOS	TCACTCAC	52	8.072
Ahr-ARNT	CACTCA	53	5.297
GATA-3	CACTCA	53	4.024
SOX17	CAGAATGGT	59	5.720
Yin-Yang	AATGGT	62	7.027
deltaEF1	ATGGTG	63	4.388
SP1	TGCCTGCCT C	73	6.965
AP2alpha	GCCTCGGGT	78	4.313
TBP	CCCTGTGATT TATTT	90	6.088
Gklf	CCTGTGATTT	91	4.986
Gfi	CTGTGATTTA	92	12.073
Pax-2	CTGTGATT	92	5.062
EN-1	GTGATTTATT T	94	4.504
SRY	TTTATTTTA	98	6.434
FREAC-7	TATTTTAG	100	4.332
SPI-1	GTTCTT	107	4.249
Dof2	TTCTTT	108	6.891
Dof3	TTCTTT	108	4.846
MNB1A	TCTTT	109	6.786
PBF	TCTTT	109	5.740
Gklf	CTTTTCCCTT	110	8.951
Gklf	TTTTCCCTTG	111	5.512
SPI-1	TTTCCC	112	5.702
SPI-B	TTTCCCT	112	4.764
SPI-B	TTCCCTT	113	6.493

Gklf	CCCTTGTTTT	115	8.182
SOX-9	CCCTTGTTT	115	8.127
Gklf	CCTTGTTTTT	116	8.385
Gklf	CTTGTTTTT	117	6.353
SRY	CTTGTTTTT	117	7.589
Sox-5	CTTGTTT	117	6.563
HMG-IY	TTGTTTTTTTT TTTTC	118	10.515
Gklf	GTTTTTTTTT	120	4.950
Gklf	TTTTTTTTTT	121	5.398
Gklf	TTTTTTTTTT	122	5.398
Gklf	TTTTTTTTTT	123	5.398
FREAC-7	TATACACT	140	4.435
FREAC-3	TACACTTT	142	4.823
Dof2	CACTTT	144	5.518
Dof3	CACTTT	144	8.349
Nkx	CACTTTT	144	4.772
MNB1A	ACTTT	145	6.786
PBF	ACTTT	145	7.325
Gklf	CTTTTGTTTT	146	8.140
SOX-9	CTTTTGTTT	146	8.467
SRY	TTTGTTTTA	148	9.474
Sox-5	TTTGTTT	148	6.563
Gfi	CTGTGGTTTC	161	6.578
SPI-B	TTTCTCA	167	5.592
c-FOS	TTTCTCAT	167	6.556
GATA-3	TTCTCA	168	3.791
Ubx	ATGA	173	3.366
EN-1	GAGCCCTATT A	175	4.702
Nkx	CTATTAT	180	7.738
Ubx	ATTA	182	6.917
GATA-1	TTATCT	183	4.460
GATA-3	TTATCT	183	7.189
FREAC-7	TATCTCAT	184	5.530
GATA-2	TATCT	184	6.232
SOX-9	TCATTGATA	188	7.592
Pax-2	CATTGATA	189	4.238
SRY	ATTGATACC	190	7.100
Sox-5	ATTGATA	190	6.624
FREAC-3	TACCTCTC	195	4.249
SPI-B	TACCTCT	195	6.292
Gklf	CCTCTCACCT	197	5.047
GATA-3	CTCTCA	198	4.990
Snail	CACCTC	202	6.770
c-ETS	GGGAAG	217	5.777
HFH-2	AAGAAATCAT AT	220	6.922
c-ETS	AAGAAA	220	3.658
GATA-1	AAATCA	223	4.265
GATA-3	AAATCA	223	5.162
GATA-2	AATCA	224	4.000
FREAC-7	TATTTTCA	229	5.446
deltaEF1	CAGATG	235	4.562
Pax-2	AGATGACT	236	4.223
Yin-Yang	GATGAC	237	5.315
Ubx	ATGA	238	3.366
c-FOS	TGACTCGT	239	6.456
Agamous	ACTCGTAAAG G	241	5.998
HFH-2	AAAGAAAAA AC	254	8.076
RUSH1-alfa	AAGAAAAA	255	4.882

c-ETS	AAGAAA	255	3.658
Dorsal_1	AGAAAAAAC CC	256	10.026
Dorsal_1	GAAAAAAC CA	257	11.198
HMG-1	GAAAAAAC	257	7.168
HMG-1	AAAAAAC	258	4.824
cEBP	AAAATTTCAA AA	268	8.287
SAP-1	ATTTCCGTT	279	8.615
SQUA	ATTTCCGTTT AAGT	279	8.960
E74A	TTTCCGT	280	7.780
EIk-1	TTTCCGTTTA	280	8.664
SPI-1	TTTCCG	280	5.834
SPI-B	TTCCGTT	281	7.514
Ubx	ATAA	296	4.205
GATA-1	TAATCA	297	3.797
GATA-3	TAATCA	297	5.928
S8	TAATC	297	5.937
GATA-2	AATCA	298	4.000
RUSH1-alfa	AAGAAAAG	302	5.925
c-ETS	AAGAAA	302	3.658
HMG-1	GAAAAGGAG	304	6.170
deltaEF1	AAGGAG	307	5.159
c-ETS	AGGAGA	308	3.674
RUSH1-alfa	GAGAAACA	310	6.818
AML-1	AAACACAGA	313	6.667
RUSH1-alfa	GAGAGAAA	324	4.946
RUSH1-alfa	GAGAAAAA	326	7.153
HFH-2	GAAAAAAAAA AC	328	9.655
HFH-2	AAAAAAAAA CT	329	6.666
HFH-2	AAAAAAAAAC TA	330	6.540
HMG-1	AAAAAAAAAC	331	6.307
HFH-2	AAAAAACTA TG	332	9.153
HFH-1	AAAAAACTAT G	333	8.778
EN-1	AAAAAACTATG A	334	5.329
Ubx	ACTA	338	3.632
GATA-3	CTATGA	339	3.670
FREAC-7	TATGAGAA	340	4.984
Ubx	ATGA	341	3.366
Dorsal_1	TGAGAACCC CCC	342	9.040
Dorsal_2	TGAGAACCC C	342	8.283
p50	TGAGAACCC CC	342	9.779
EN-1	GAGAACCC CC	343	5.216
HMG-1	GAGAACCC	343	4.747
NF-kappaB	GAGAACCC C	343	7.172
p50	GAGAACCC CC	343	8.513
SP1	AGAACCC C	344	6.409
SP1	AACCC C	346	7.522
SP1	ACCC C	347	10.768

	C		
Gklf	CCCCCCCC A	348	5.599
MZF_1-4	CCCCC	348	5.636
SP1	CCCCCCCC A	348	6.724
MZF_1-4	CCCCC	349	5.636
MZF_5-13	CCCCCCCCA C	349	5.993
MZF_1-4	CCCCC	350	5.636
MZF_5-13	CCCCCCCCA C	350	5.993
MZF_1-4	CCCCC	351	5.636
MZF_1-4	CCCCCA	352	6.469
SP1	CCCCACCC C	352	6.857
Myc-Max	ACCCCGTGA TT	357	9.115
Max	CCCCGTGAT T	358	8.059
USF	CCCCGTG	358	7.859
ARNT	CCCGTG	359	6.112
n-MYC	CCCGTG	359	6.133
Gfi	CCGTGATTAT	360	6.026
Pax-2	CCGTGATT	360	7.650
Nkx	TGATTAT	363	5.018
Ubx	ATTA	365	6.917
GATA-1	TTATCA	366	4.250
GATA-3	TTATCA	366	6.894
GATA-2	TATCA	367	5.778
Ahr-ARNT	CACACA	375	6.158
Ahr-ARNT	CACTCA	379	5.297
GATA-3	CACTCA	379	4.024
Nkx	CACTCAT	379	4.410
GATA-1	TCATCG	382	5.410
GATA-3	TCATCG	382	3.658
GATA-2	CATCG	383	5.559
Agamous	AAAAAATTTG G	389	6.385
Athb-1	AAAAATTT	390	6.726
SQUA	ATTTGGATTA TTAG	394	7.425
c-ETS	TGGATT	397	4.241
Nkx	GGATTAT	398	4.441
SRY	ATTATTAGA	400	6.086
Sox-5	ATTATTA	400	7.499
Ubx	ATTA	400	6.917
Ubx	ATTA	403	6.917
RUSH1-alfa	GAGAGAGG	410	4.588
AP2alpha	GTCTGCGGC	417	6.773
EN-1	GGCTTCCAC AC	423	4.750
SPI-1	CTTCCA	425	6.483
Thing1-E47	CTTCCACACC	425	6.063
SPI-B	TTCCACA	426	6.960
MZF_1-4	TCCACA	427	4.989
FREAC-3	TACAGCGT	436	5.238
Myc-Max	ACAGCGTGG TT	437	7.989
Pax-2	GCGTGGTT	440	4.636
Gklf	TTTTTCTTCT	446	5.221
SPI-B	TTCTTCT	449	6.769
SPI-1	CTTCTC	451	5.496
Ubx	ATAA	460	4.205

c-ETS	AGCAAA	465	3.658
MYB.ph3	AAGTTGTTT	469	5.473
deltaEF1	AAGTTG	469	4.388
TBP	AGTTGTTTT GATAC	470	5.709
SRY	GTTGTTTT	471	6.260
Sox-5	GTTGTTT	471	6.563
USF	ATACGTG	481	5.702
ARNT	TACGTG	482	6.112
FREAC-3	TACGTGAC	482	5.401
deltaEF1	TACGTG	482	5.555
n-MYC	TACGTG	482	5.992
Pax-2	ACGTGACA	483	8.533
bZIP910	ACGTGAC	483	5.723
MYB.ph3	TGACAGTTT	486	8.722
SU_h	TGACAGTTTC CCACAA	486	14.526
GAMYB	GACAGTTTCC	487	6.422

Dof3	CAGTTT	489	4.076
SPI-1	GTTTCC	491	4.264
SPI-1	TTTCCC	492	5.702
MZF_1-4	TTCCCA	493	4.846
AML-1	TCCCACAAG	494	6.247
MZF_1-4	TCCCAC	494	5.004
Thing1-E47	AAGCCAGGC T	500	8.157
GATA-1	TGATCC	509	3.720
GATA-2	GATCC	510	5.047
Dof2	TCCTTT	512	6.493
Dof3	TCCTTT	512	6.702
Gklf	CCTTTTCTGT	513	5.738
MNB1A	CCTTT	513	4.751
PBF	CCTTT	513	5.740
Gklf	CTTTTCTGTC	514	4.990
SPI-B	TTTCTGT	516	5.356

Figure S3