SUPPLEMENTARY INFORMATION

Table S1: List of Genes Commonly Regulated by S176 and S165 of YBX1

Number	Symbol	Accession number	Description	Ctrl, IL-1β/Ctrl	WT/Ctrl	S176A/WT	S165A/WT
1	A4GNT	NM_016161.1	alpha-1,4-N-acetylglucosaminyltransferase	2.0	4.8	0.1	0.2
2	APOL2	NM_145637.1	apolipoprotein L, 2	6.9	17.8	0.4	0.3
3	ASGR2	NM_080912.1	asialoglycoprotein receptor 2	4.7	34.7	0.3	0.3
4	BTBD9	NM_152733.1	BTB (POZ) domain containing 9	2.3	7.9	0.3	0.0
5	CCDC60	NM_178499.2	coiled-coil domain containing 60	16.0	31.8	0.5	0.4
6	CCDC61	NM_001080402.1	coiled-coil domain containing 61	2.1	4.7	0.5	0.4
7	CLSTN1	XM_937951.1	calsyntenin 1	8.0	36.0	0.5	0.4
8	COL12A1	NM_004370.4	collagen, type XII, alpha 1	4.1	7.3	0.1	0.1
9	CR1	XM_936516.1	complement component (3b/4b) receptor 1	4.5	4.7	0.4	0.1
10	CRYBA2	NM_057093.1	crystallin, beta A2	6.3	59.0	0.4	0.5
11	DEAF1	XM_938667.1	deformed epidermal autoregulatory factor 1	3.2	5.4	0.1	0.1
12	DPP6	NM_001936.2	dipeptidyl-peptidase 6	2.9	4.7	0.1	0.2
13	E2F8	NM_024680.2	E2F transcription factor 8	7.9	4.2	0.2	0.4
14	FAM150B	NM_001002919.2	family with sequence similarity 150, member B	7.7	17.8	0.4	0.4
15	FER1L4	NR_001442.2	fer-1-like 4 (C. elegans)	4.8	16.5	0.4	0.4
16	FLJ42258	NM_001004327.1	FLJ42258 protein	2.4	2.1	0.5	0.2
17	GABRB2	NM_021911.1	gamma-aminobutyric acid (GABA) A receptor, beta 2	5.2	5.3	0.3	0.5
18	GOLGA7	NM_001002296.1	golgi autoantigen, golgin subfamily a, 7	2.9	9.4	0.1	0.1
19	HLA-DOB	NM_002120.2	major histocompatibility complex, class II, DO beta	5.0	10.7	0.1	0.3
20		Hs.110524	cDNA clone UI-CF-EN1-aeg-h-11-0-UI 3	2.0	6.3	0.3	0.3
21		Hs.34747	cDNA clone GEN-056E10 5	3.3	11.4	0.3	0.0
22		Hs.382131	hypothetical protein LOC286083	5.6	12.5	0.2	0.5
23		Hs.528168	cDNA clone UI-E-EJ1-ajw-i-09-0-UI 5	2.9	2.7	0.3	0.0

24		Hs.537890	cDNA clone IMAGE:1635833 3	2.6	2.1	0.2	0.3
25		Hs.538491	cDNA clone UI-H-FE0-bbv-o-01-0-UI 3	6.2	11.1	0.4	0.1
26		Hs.540037	cDNA clone IMAGE:434374 3	4.1	3.7	0.3	0.3
27		Hs.541226	cDNA clone IMAGE:839579 3 similar to contains Alu repetitive element	7.3	3.0	0.0	0.2
28		Hs.544388	cDNA clone IMAGE:2584822 3	6.9	10.8	0.3	0.5
29		Hs.544491	cDNA clone IMAGE:1934100 3	3.0	2.6	0.1	0.0
30		Hs.549460	RST25702 Athersys RAGE Library Homo sapiens cDNA	3.7	10.4	0.0	0.1
31		Hs.560266	cDNA clone IMAGE:2283714 3	3.0	4.2	0.1	0.2
32		Hs.562058	cDNA clone UI-E-EJ1-ajl-b-21-0-UI 5	11.7	9.1	0.2	0.1
33		Hs.563710	cDNA clone IMAGE:3088470 3	34.4	33.4	0.3	0.3
34		Hs.564111	cDNA clone UI-CF-EC1-acc-m-06-0-UI 3	6.3	5.7	0.2	0.1
35		Hs.578836	cDNA clone TESTI2046701 3	2.8	3.2	0.4	0.5
36		Hs.580251	cDNA clone IMAGE:3904209 5	3.2	4.7	0.0	0.3
37		Hs.581788	cDNA clone IMAGE:1640337 3 similar to contains L1.t1 L1 repetitive element	2.3	3.5	0.4	0.5
38		Hs.584286	cDNA clone IMAGE:1030854 3	2.9	13.7	0.1	0.0
39	HSPCAL3	XM_084514.10	heat shock 90kDa protein 1, alpha-like 3	2.8	6.0	0.2	0.4
40	IGF1	NM_000618.2	insulin-like growth factor 1 (somatomedin C)	2.9	2.6	0.5	0.2
41	IL17C	NM_013278.3	interleukin 17C	5.0	118.0	0.1	0.2
42	IMAA	XR_000959.1	SLC7A5 pseudogene	9.4	20.6	0.1	0.1
43	IRF5	NM_002200.3	interferon regulatory factor 5	16.5	19.1	0.4	0.5
44	KCNH6	NM_030779.2	potassium voltage-gated channel, subfamily H (eag-related), member 6	14.0	34.0	0.2	0.3
45	KIAA0226	XM_936700.1	KIAA0226, transcript variant 2	3.6	10.8	0.3	0.3
46	KIAA1967	NM_021174.4	KIAA1967, transcript variant 1	2.3	2.8	0.4	0.0
47	KRTAP4-7	XM_926574.1	keratin associated protein 4-7	2.1	2.1	0.2	0.5
48	LMOD2	XM_499467.2	leiomodin 2 (cardiac)	3.0	3.3	0.2	0.3
49	LOC100128202	XM_001723719.1	hypothetical protein LOC100128202	2.0	20.8	0.1	0.3
50	LOC100130190	XR_042393.1	misc_RNA (LOC100130190)	2.3	4.7	0.1	0.1
51	LOC100130935	XM_001727014.1	similar to CSAG family, member 2	36.0	70.5	0.4	0.2
52	LOC100131733	XM_001726102.1	hypothetical LOC100131733	7.8	16.4	0.4	0.0
53	LOC100132428	XM_001720134.1	hypothetical LOC100132428	5.1	4.1	0.1	0.4
54	LOC100133401	XM_001723221.1	hypothetical protein LOC100133401	3.8	14.4	0.2	0.1
55	LOC100134041	XM_001720931.1	hypothetical protein LOC100134041 (LOC100134041)	4.6	11.9	0.5	0.1
56	LOC100134228	XR_037407.1	misc_RNA (LOC100134228)	8.6	12.1	0.2	0.1

57	LOC132203	XM_935351.1	similar to S-100 protein, alpha chain	4.7	10.8	0.1	0.1
58	LOC143188	NM_001025447.1	hypothetical protein LOC143188	3.6	17.7	0.4	0.1
59	LOC341112	XM_937671.1	similar to Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase)	3.0	11.1	0.0	0.1
60	LOC388327	XM_941035.1	hypothetical LOC388327	4.5	6.8	0.1	0.3
61	LOC389142	XM_943809.1	hypothetical LOC389142	2.2	4.8	0.2	0.4
62	LOC399965	XR_036921.1	misc_RNA (LOC399965)	2.4	2.9	0.3	0.5
63	LOC441416	XR_036927.1	misc_RNA (LOC441416)	2.2	4.5	0.1	0.4
64	LOC642398	XM_930893.1	hypothetical protein LOC642398	20.5	51.0	0.1	0.1
65	LOC643980	XM_928714.1	similar to FRG1 protein (FSHD region gene 1 protein)	5.8	16.1	0.0	0.4
66	LOC644899	XM_927985.1	similar to Telomeric repeat binding factor 2 interacting protein 1 (TRF2-interacting telomeric protein Rap1)	3.6	12.4	0.0	0.1
67	LOC645212	XM_939117.1	hypothetical LOC645212	2.3	3.4	0.4	0.4
68	LOC645485	XM_944437.1	hypothetical LOC645485	2.6	10.5	0.1	0.1
69	LOC646895	XM_929858.1	similar to zinc finger protein 539	2.4	4.0	0.2	0.3
70	LOC646999	XM_935740.1	hypothetical LOC646999	9.5	10.7	0.1	0.3
71	LOC647654	XM_936707.1	similar to Cell division cycle protein 27 homolog (CDC27Hs)	2.8	3.1	0.4	0.2
72	LOC647661	XM_936718.1	hypothetical protein LOC647661	2.2	15.8	0.1	0.1
73	LOC647806	XM_943033.1	hypothetical LOC647806	2.1	5.5	0.5	0.2
74	LOC647987	XM_937044.1	similar to Ribosome biogenesis protein BMS1 homolog	45.7	48.3	0.2	0.1
75	LOC648222	XM_937269.1	similar to Down syndrome critical region protein 3	2.9	10.6	0.1	0.1
76	LOC649848	XM_933872.1	similar to Alu subfamily SX sequence contamination warning entry	4.9	11.3	0.3	0.1
77	LOC650557	XM_942240.1	similar to HLA class II histocompatibility antigen, DQ(W1.1) beta chain precursor	26.5	53.5	0.1	0.1
78	LOC650853	XM_939941.1	hypothetical protein LOC650853	18.2	13.0	0.4	0.4
79	LOC650914	XM_940003.1	similar to golgi autoantigen, golgin subfamily a-like	8.9	10.9	0.5	0.1
80	LOC652721	XM_942346.1	similar to LIM homeobox protein 1	2.5	2.4	0.4	0.4
81	LOC652849	XM_942549.1	similar to lethal (1) G0196 CG14616-PD, isoform D	5.9	7.1	0.3	0.2
82	LOC727977	XM_001717764.1	hypothetical LOC727977	2.5	27.5	0.1	0.2
83	LOC728264	XR_041007.1	misc_RNA (LOC728264)	3.1	15.5	0.1	0.1
84	LOC729198	XR_016035.1	misc_RNA (LOC729198)	4.0	34.3	0.2	0.5

85	LOC729438	XM_001717397.1	similar to opposite strand transcription unit to Stag3	3.3	2.4	0.5	0.3
86	LOC730015	XM_927530.1	similar to LOC441178 protein	2.2	3.1	0.3	0.3
87	LOC730134	XM_001719031.1	similar to hCG1815165	4.7	5.7	0.1	0.4
88	LOC730240	Hs.516108	hypothetical protein LOC730240	2.0	3.5	0.1	0.2
89	MIB2	XM_936397.1	mindbomb homolog 2	6.5	14.6	0.2	0.4
90	MIR376C	NR_029861.1	microRNA 376c	5.8	10.0	0.1	0.5
91	NCRNA00173	NR_027346.1	non-protein coding RNA 173	11.9	13.1	0.1	0.3
92	NES	NM_006617.1	Nestin	4.9	3.5	0.3	0.4
93	NEUROG3	NM_020999.2	neurogenin 3	4.3	14.6	0.1	0.1
94	OR52A5	NM_001005160.1	olfactory receptor, family 52, subfamily A, member 5	6.2	12.2	0.1	0.1
95	OR5A1	NM_001004728.1	olfactory receptor, family 5, subfamily A, member 1	2.1	11.3	0.3	0.0
96	OR7G1	NM_001005192.1	olfactory receptor, family 7, subfamily G, member 1	2.3	7.4	0.1	0.0
97	OXER1	NM_148962.3	oxoeicosanoid (OXE) receptor 1	7.8	10.1	0.3	0.1
98	PFKL	NM_001002021.1	phosphofructokinase, liver	5.3	6.5	0.1	0.1
99	PTK2B	NM_004103.3	PTK2B protein tyrosine kinase 2 beta	3.4	24.4	0.2	0.1
100	RGR	NM_001012722.1	retinal G protein coupled receptor	2.2	2.2	0.2	0.1
101	RNU12	NR_000041.1	RNA, U12 small nuclear (RNU12) on chromosome X	5.6	15.0	0.1	0.1
102	RUFY1	NM_025158.3	RUN and FYVE domain containing 1	2.0	23.2	0.0	0.1
103	S100A13	NM_001024212.1	S100 calcium binding protein A13	5.1	11.1	0.5	0.1
104	SCARNA27	NR_003703.1	small Cajal body-specific RNA 27	4.2	6.7	0.1	0.1
105	SF4	NM_182812.1	splicing factor 4	3.9	3.3	0.3	0.4
106	SH3BP2	NM_003023.2	SH3-domain binding protein 2	2.7	8.7	0.5	0.5
107	SNAPC1	NM_003082.2	small nuclear RNA activating complex, polypeptide 1, 43kDa	2.1	3.2	0.4	0.5
108	SNORA74B	NR_002988.1	small nucleolar RNA, H/ACA box 74B	2.7	38.7	0.1	0.4
109	TGIF1	NM_173209.1	TGFB-induced factor homeobox 1	2.7	5.7	0.5	0.4
110	THAP2	NM_031435.1	THAP domain containing, apoptosis associated protein 2	3.2	4.4	0.1	0.4
111	TRIM14	NM_033220.1	tripartite motif-containing 14	2.6	10.4	0.1	0.5
112	USP2	NM_171997.1	ubiquitin specific peptidase 2	13.3	17.9	0.2	0.1
113	VENTXP1	NR_001559.2	VENT homeobox (Xenopus laevis) pseudogene 1	3.6	3.2	0.3	0.4
114	ZNF157	NM_003446.2	zinc finger protein 157	2.8	3.3	0.3	0.2
115	ZNF846	XM_091914.4	zinc finger protein 846	2.0	9.9	0.0	0.3

Table S2: List of Genes Solely Regulated by S176 of YBX1

Number	Symbol	Accession number	Description	Ctrl, IL-1β/Ctrl	WT/Ctrl	S176A/WT	S165A/WT
1	BAT1	NM_080598.4	HLA-B associated transcript 1	2.5	2.3	0.5	1.1
2	BCL2L14	NM_030766.1	BCL2-like 14	5.9	2.8	0.5	1.4
3	BRMS1L	NM_032352.3	breast cancer metastasis-suppressor 1-like	3.3	5.1	0.4	0.8
4	C1orf201	NM_178122.2	chromosome 1 open reading frame 201	6.0	11.8	0.5	1.3
5	C20orf165	NM_080608.3	chromosome 20 open reading frame 165	11.1	12.8	0.4	0.7
6	C3orf43	NM_001077657.1	chromosome 3 open reading frame 43	4.0	17.4	0.3	0.7
7	C6orf27	NM_025258.1	chromosome 6 open reading frame 27	2.8	10.7	0.1	0.8
8	C8orf31	NM_173687.1	chromosome 8 open reading frame 31	2.3	3.3	0.4	0.8
9	CILP	NM_003613.2	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	18.3	41.0	0.3	0.8
10	COLQ	NM_080539.2	collagen-like tail subunit of asymmetric acetylcholinesterase	4.9	2.8	0.5	0.8
11	CRTC1	NM_015321.1	CREB regulated transcription coactivator 1	2.6	5.7	0.3	0.7
12	EGR3	NM_004430.2	early growth response 3	3.1	2.2	0.3	0.8
13	F3	NM_001993.2	coagulation factor III	2.9	2.4	0.4	0.7
14	FBLN7	NM_153214.1	fibulin 7	3.0	10.1	0.3	0.8
15	FBXL14	NM_152441.1	F-box and leucine-rich repeat protein 14	5.0	3.6	0.4	0.7
16	FBXO43	NM_001029860.1	F-box protein 43 (FBXO43), transcript variant 2	5.4	9.2	0.3	0.8
17	FLJ40453	NM_001007542.1	FLJ40453 protein	2.3	3.4	0.4	0.8
18	FLJ46836	XR_041721.1	FLJ46836 protein	3.8	9.2	0.2	0.7
19	FPGS	NM_004957.4	folylpolyglutamate synthase	3.2	2.3	0.3	1.2
20	FSBP	NM_006550.1	fibrinogen silencer binding protein	2.0	3.7	0.5	0.8
21	GABPB2	NM_144618.1	GA binding protein transcription factor, beta subunit 2	2.6	4.6	0.3	1.1
22	GPATC4	NM_017725.1	G patch domain containing 4	2.3	3.2	0.2	0.8

23	GREM1	NM_013372.5	gremlin 1, cysteine knot superfamily, homolog	4.5	3.7	0.4	0.7
24	HBS1L	NM_006620.2	HBS1-like	3.9	2.7	0.3	0.7
25		Hs.12513	cDNA FLJ34274 fis	2.7	5.6	0.1	0.7
26		Hs.130344	cDNA clone IMAGp998G09911	2.1	4.3	0.4	1.1
27		Hs.269535	cDNA clone IMAGE:432643 3	2.4	2.8	0.1	0.8
28		Hs.444475	cDNA clone IMAGE:999931	2.3	2.7	0.0	0.8
29		Hs.444839	cDNA clone IMAGE:3271726 3	4.8	11.7	0.3	1.0
30		Hs.528210	cDNA clone UI-E-EJ1-ajv-n-10-0-UI 3	2.2	3.4	0.5	0.7
31		Hs.543865	cDNA clone UI-E-EJ1-ajq-h-17-0-UI 3	2.6	3.6	0.2	0.9
32		Hs.546062	cDNA clone IMAGE:2250546 3	5.3	15.1	0.4	0.8
33		Hs.569298	cDNA clone IMAGE:1642648 3	2.1	3.6	0.4	0.8
34		Hs.573763	cDNA clone HEMBB1001052 5	7.6	10.6	0.4	0.7
35		Hs.575024	cDNA clone MGC8.7.1.1.1.E08	5.9	4.0	0.3	0.8
36	IL32	NM_001012633.1	interleukin 32	12.2	2.2	0.3	2.2
37	KCNT2	NM_198503.2	potassium channel, subfamily T, member 2	2.3	2.3	0.3	0.8
38	LOC100127946	XM_001716544.1	hypothetical LOC100127946	2.2	3.8	0.1	1.3
39	LOC100128598	XM_001716547.1	hypothetical LOC100128598	3.9	5.9	0.3	1.1
40	LOC100129139	XR_039561.1	misc_RNA (LOC100129139)	2.6	3.4	0.4	0.7
41	LOC100132377	XM_001722278.1	hypothetical protein LOC100132377	4.8	4.7	0.1	0.9
42	LOC100133769	XM_001714042.1	similar to hCG2041993	14.8	8.3	0.4	0.7
43	LOC100133845	XR_037605.1	misc_RNA (LOC100133845)	2.1	2.1	0.3	1.0
44	LOC283157	XM_939588.1	hypothetical LOC283157	2.6	2.5	0.4	0.7
45	LOC400403	XR_018264.2	misc_RNA (LOC400403)	6.7	10.0	0.2	0.7
46	LOC440031	XR_017508.2	misc_RNA (LOC440031)	3.6	10.2	0.1	0.8
47	LOC541472	XR_039889.1	hypothetical LOC541472	2.7	4.7	0.2	0.7
48	LOC642161	XM_936316.1	similar to T-cell receptor beta chain V region CTL-L17 precursor	3.0	2.7	0.3	0.9

49	LOC642295	XM_937245.1	hypothetical LOC642295	2.0	3.2	0.5	1.1
50	LOC642838	XM_001714030.1	similar to hCG1742442	2.9	2.3	0.5	0.9
51	LOC645320	XM_928359.1	hypothetical LOC645320	5.2	8.0	0.0	0.8
52	LOC645627	XM_928642.1	hypothetical LOC645627	10.0	12.4	0.2	0.8
53	LOC646853	XM_929811.1	similar to Nonhistone chromosomal protein HMG-17	4.1	3.4	0.2	0.7
54	LOC648041	XM_937091.1	hypothetical protein LOC648041	2.4	3.8	0.1	0.8
55	LOC648657	XM_943417.1	hypothetical LOC648657	3.3	3.0	0.1	1.0
56	LOC648684	XM_937754.1	hypothetical protein LOC648684	2.1	2.6	0.4	0.8
57	LOC728139	XR_015301.2	misc_RNA (LOC728139)	3.0	3.8	0.4	1.0
58	LOC728790	XM_001722693.1	hypothetical LOC728790	6.5	18.7	0.5	0.8
59	LOC729629	XM_001722475.1	hypothetical LOC729629	2.7	3.0	0.4	1.4
60	LOC730877	Hs.363156	hypothetical protein LOC730877	3.1	5.7	0.1	0.8
61	LOC731035	XM_942369.1	hypothetical LOC731035	2.5	5.1	0.3	0.7
62	LPA	XM_926329.1	lipoprotein, Lp(a)	2.1	2.3	0.3	0.7
63	MIR498	NR_030182.1	microRNA 498	2.2	3.7	0.5	0.8
64	MIR663B	NR_031608.1	microRNA 663b	2.0	10.8	0.4	0.8
65	MOCS1	NM_001075098.1	molybdenum cofactor synthesis 1	2.4	2.6	0.3	1.2
66	MYCL1	NM_001033082.1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived	27.0	52.5	0.4	1.0
67	NBPF10	XM_930961.1	neuroblastoma breakpoint family, member 10	2.2	2.6	0.5	0.8
68	OR2T6	NM_001005471.1	olfactory receptor, family 2, subfamily T, member 6	3.0	4.0	0.3	0.7
69	OR2W5	NM_001004698.1	olfactory receptor, family 2, subfamily W, member 5	2.0	2.3	0.4	0.9
70	PDK1	NM_002610.3	pyruvate dehydrogenase kinase, isozyme 1	2.5	38.5	0.3	1.0
71	PLEKHG7	NM_001004330.1	pleckstrin homology domain containing, family G member 7	14.6	11.0	0.4	0.9
72	PPP2R2C	NM_181876.2	protein phosphatase 2, regulatory subunit B, gamma	3.5	6.8	0.2	0.7
73	PTK6	NM_005975.2	PTK6 protein tyrosine kinase 6	2.0	11.2	0.5	0.7
74	PTP4A2	XM_944928.1	protein tyrosine phosphatase type IVA, member 2	6.7	6.7	0.4	0.7

75	RBBP6	NM_006910.4	retinoblastoma binding protein 6	4.7	4.3	0.4	0.7
76	RIN1	NM_004292.2	Ras and Rab interactor 1	2.5	3.0	0.4	0.8
77	SP3	NM_001017371.3	Sp3 transcription factor	2.4	11.2	0.2	0.8
78	ST3GAL1	NM_003033.2	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	4.0	3.4	0.4	0.7
79	STMN2	NM_007029.2	stathmin-like 2	2.3	2.5	0.4	0.8
80	TGS1	NM_024831.6	trimethylguanosine synthase homolog	3.8	5.0	0.4	0.8
81	TOMM20L	NM_207377.2	translocase of outer mitochondrial membrane 20 homolog (yeast)-like	4.5	10.9	0.5	1.4
82	UGT2B7	XM_943434.1	UDP glucuronosyltransferase 2 family, polypeptide B7	3.4	3.4	0.5	0.9

Table S3: List of Genes Solely Regulated by S165 of YBX1

Number	**Symbol**	**Accession number**	**Description**	**Ctrl, IL-1β/Ctrl**	**WT/Ctrl**	**S176A/WT**	**S165A/WT**
1	ALB	NM_000477.3	albumin	2.1	3.2	0.7	0.3
2	AMBRA1	NM_017749.2	autophagy/beclin-1 regulator 1	2.7	2.6	0.7	0.5
3	ANXA8L1	NM_001098845.1	annexin A8-like 1	5.7	3.1	1.4	0.3
4	APOBEC3D	NM_152426.3	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D	3.1	4.6	0.7	0.4
5	ARNTL2	NM_020183.3	aryl hydrocarbon receptor nuclear translocator-like 2	2.6	10.9	0.7	0.3
6	BEND3	NM_001080450.1	BEN domain containing 3	7.0	53.3	0.7	0.4
7	C19orf73	NM_018111.1	chromosome 19 open reading frame 73	3.5	3.8	1.4	0.5
8	C9orf126	NM_173690.1	chromosome 9 open reading frame 126	4.1	15.0	0.9	0.5
9	CCDC104	NM_080667.3	coiled-coil domain containing 104	2.5	3.3	1.2	0.3
10	CCL26	NM_006072.4	chemokine (C-C motif) ligand 26	10.0	14.9	0.8	0.2
11	CD59	NM_203331.1	CD59 molecule, complement regulatory protein	3.0	3.8	0.7	0.3
12	CDH20	NM_031891.2	cadherin 20, type 2	8.5	13.6	0.9	0.2

13	CDRT1	NM_006382.1	CMT1A duplicated region transcript 1	2.1	2.4	1.3	0.3
14	DAB2IP	NM_032552.1	DAB2 interacting protein	25.0	129.0	0.7	0.4
15	DCLK3	NM_033403.1	doublecortin-like kinase 3	2.6	3.9	1.2	0.2
16	DFNB59	Hs.87734	deafness, autosomal recessive 59	2.0	2.1	0.7	0.5
17	DHRS12	NM_001031719.1	dehydrogenase/reductase (SDR family) member 12	3.8	6.6	0.7	0.5
18	FAM46D	NM_152630.2	family with sequence similarity 46, member D	2.5	3.2	0.7	0.2
19	FLJ35880	NM_153264.2	hypothetical protein FLJ35880	2.0	22.2	0.7	0.4
20	FLJ38969	XM_928774.1	hypothetical protein FLJ38969	3.3	2.7	0.9	0.3
21	FLJ43950	XM_937832.1	FLJ43950 protein, transcript variant 2	2.9	5.4	0.7	0.5
22	GRAP	NM_006613.3	GRB2-related adaptor protein	17.3	32.3	0.7	0.1
23	GRIA3	NM_007325.2	glutamate receptor, ionotrophic, AMPA 3	2.4	4.4	0.7	0.4
24	GSTA3	NM_000847.3	glutathione S-transferase A3	2.6	4.5	0.7	0.3
25		Hs.130639	cDNA clone IMAGp998C184969	2.0	2.2	1.0	0.4
26		Hs.214235	cDNA clone oj15g10 5	3.0	3.7	0.7	0.2
27		Hs.452445	cDNA DKFZp762F0616	2.6	3.0	1.3	0.4
28		Hs.538833	cDNA clone IMAGE:30382396 5	3.8	6.5	0.7	0.4
29		Hs.547293	similar to contains MER22.t1 MER22 repetitive element	2.5	6.6	0.7	0.1
30		Hs.547861	Homo sapiens cDNA FLJ46067 fis, clone TESOP2002110	2.4	10.1	0.8	0.3
31		Hs.571901	cDNA clone CS0DF020YK03 of Fetal brain of Homo sapiens	7.1	11.1	0.8	0.5
32	IL17RC	NM_032732.2	interleukin 17 receptor C	4.9	13.3	0.7	0.3
33	INSL5	NM_005478.3	insulin-like 5	2.5	7.4	0.7	0.4
34	ITPKC	NM_025194.2	inositol 1,4,5-trisphosphate 3-kinase C	2.4	2.6	0.7	0.4
35	LOC100128031	XM_001721840.1	hypothetical protein LOC100128031	2.0	3.2	0.7	0.4
36	LOC100129064	XR_038994.1	misc_RNA (LOC100129064)	2.9	3.5	0.9	0.3
37	LOC100132456	XM_001714572.1	similar to SMA5 (LOC100132456)	3.7	9.1	0.7	0.4
38	LOC100133182	XM_001714164.1	hypothetical protein LOC100133182 (LOC100133182)	5.7	3.9	1.4	0.5
39	LOC100133224	XM_001717976.1	similar to hCG2041320 (LOC100133224)	6.4	13.2	0.7	0.4
40	LOC344405	NM_001080459.1	hypothetical LOC344405 (LOC344405)	10.0	124.0	0.7	0.1

41	LOC388925	XR_016133.2	misc_RNA (LOC388925)	4.8	4.3	1.4	0.0
42	LOC401280	XM_925812.1	hypothetical gene supported by AK125637	2.2	2.9	0.7	0.1
43	LOC442329	XM_498220.2	similar to PMS1 protein homolog 2 (DNA mismatch repair protein PMS2)	2.3	16.3	0.8	0.5
44	LOC553158	NM_181334.3	PRR5-ARHGAP8 fusion	5.7	3.5	1.1	0.5
45	LOC645355	XM_932842.1	hypothetical protein LOC645355	5.3	7.4	0.8	0.3
46	LOC647042	XM_933066.1	similar to golgi autoantigen, golgin subfamily a-like	2.1	2.0	0.9	0.1
47	LOC649346	XR_018634.2	misc_RNA (LOC649346)	2.0	2.1	1.1	0.1
48	LOC653596	XM_934641.1	similar to RAN-binding protein 2-like 1 isoform 2, transcript variant 4	2.4	3.7	0.9	0.1
49	LOC728119	Hs.221513	hypothetical LOC728119	2.0	6.1	0.7	0.1
50	LOC729153	XR_015745.1	misc_RNA (LOC729153)	3.1	14.8	0.7	0.5
51	LPA	NM_005577.2	lipoprotein, Lp(a)	2.0	10.5	0.7	0.1
52	LRRN1	NM_020873.3	leucine rich repeat neuronal 1	2.2	2.7	0.7	0.2
53	NBPF8	XM_001726946.1	neuroblastoma breakpoint family, member 8	3.4	4.0	0.7	0.1
54	OSM	NM_020530.3	oncostatin M	5.1	9.4	0.8	0.3
55	PFKFB2	NM_001018053.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	8.2	17.7	0.7	0.3
56	PLXNA2	NM_025179.2	plexin A2	10.0	100.0	0.8	0.2
57	RANBP2L1	NM_005054.1	RAN binding protein 2-like 1	2.1	2.0	0.7	0.2
58	SMPD1	NM_000543.3	sphingomyelin phosphodiesterase 1, acid lysosomal	2.9	2.3	0.7	0.5
59	SNORD94	NR_004378.1	small nucleolar RNA, C/D box 94	3.1	2.8	0.9	0.3
60	SUDS3	NM_022491.2	suppressor of defective silencing 3 homolog (S. cerevisiae)	6.1	5.5	0.8	0.3
61	TMEM52	NM_178545.2	transmembrane protein 52	4.6	8.3	0.7	0.5
62	UNKL	XM_942730.1	unkempt-like (Drosophila)	16.7	15.6	0.7	0.4
63	VEZT	NM_017599.2	vezatin, adherens junctions transmembrane protein	2.9	4.0	0.7	0.1
64	VN1R4	NM_173857.2	vomeronasal 1 receptor 4	5.7	7.6	0.7	0.5
65	WFDC2	NM_006103.3	WAP four-disulfide core domain 2	5.5	12.3	1.0	0.3
66	WFDC3	NM_181522.1	WAP four-disulfide core domain 3	3.7	10.6	1.0	0.4
67	XRRA1	XM_945923.1	X-ray radiation resistance associated 1	2.1	2.4	1.1	0.3

68	ZMYM3	NM_005096.2	zinc finger, MYM-type 3	3.0	5.0	0.8	0.1
69	ZNF607	NM_032689.3	zinc finger protein 607	2.2	2.8	1.0	0.4
70	ZSCAN2	NM_001007072.1	zinc finger and SCAN domain containing 2	2.5	2.2	0.7	0.5

Table S4. IPA Summary of Genes Commonly Regulated by S176 and S165 of YBX1

Top Canonical Pathways

Name	p-value	Overlap
RhoA Signaling	3.02E-02	1.6 % 2/122
Glycolysis I	5.42E-02	4.0 % 1/25
IL-15 Production	5.84E-02	3.7 % 1/27
Hepatic Fibrosis / Hepatic Stellate Cell Activation	6.27E-02	1.1 % 2/183
B Cell Development	7.51E-02	2.9 % 1/35

Top Upstream Regulators

Upstream Regulator	p-value of overlap	Predicted Activation
JAK	1.32E-03	
CDH11	1.53E-03	
miR-4750-5p (miRNAs w/seed UCGGGCG)	1.94E-03	
SLC39A14	2.07E-03	
CYTL1	2.07E-03	

Top Diseases and Bio Functions

Diseases and Disorders

Name	p-value	#Molecules
Cancer	1.99E-02 - 4.97E-05	44
Organismal Injury and Abnormalities	2.05E-02 - 4.97E-05	45
Skeletal and Muscular Disorders	1.99E-02 - 6.46E-04	10
Gastrointestinal Disease	1.79E-02 - 7.16E-04	35
Hepatic System Disease	7.28E-03 - 1.75E-03	4

Molecular and Cellular Functions

Name	p-value	#Molecules
Cell Morphology	1.77E-02 - 2.16E-04	8
Cellular Function and Maintenance	1.97E-02 - 2.16E-04	11
Cellular Growth and Proliferation	1.99E-02 - 5.00E-04	6
Protein Degradation	7.43E-04 - 7.43E-04	4
Protein Synthesis	1.33E-02 - 7.43E-04	4

Physiological System Development and Function

Name	p-value	#Molecules
Organ Morphology	1.99E-02 - 2.16E-04	7
Skeletal and Muscular System Development and Function	1.99E-02 - 2.16E-04	4
Tissue Morphology	1.99E-02 - 2.16E-04	7
Hematological System Development and Function	2.09E-02 - 5.00E-04	7
Humoral Immune Response	1.11E-02 - 5.00E-04	3

Top Networks

ID	Associated Network Functions	Score
1	Protein Degradation, Protein Synthesis, Cellular Function and Maintenance	38
2	Cellular Development, Cellular Growth and Proliferation, Connective Tissue Development and Function	25
3	Auditory Disease, Inflammatory Disease, Organismal Injury and Abnormalities	22
4	Cell-To-Cell Signaling and Interaction, Embryonic Development, Cardiovascular System Development and Function	13
5	Inflammatory Disease, Organismal Injury and Abnormalities	2

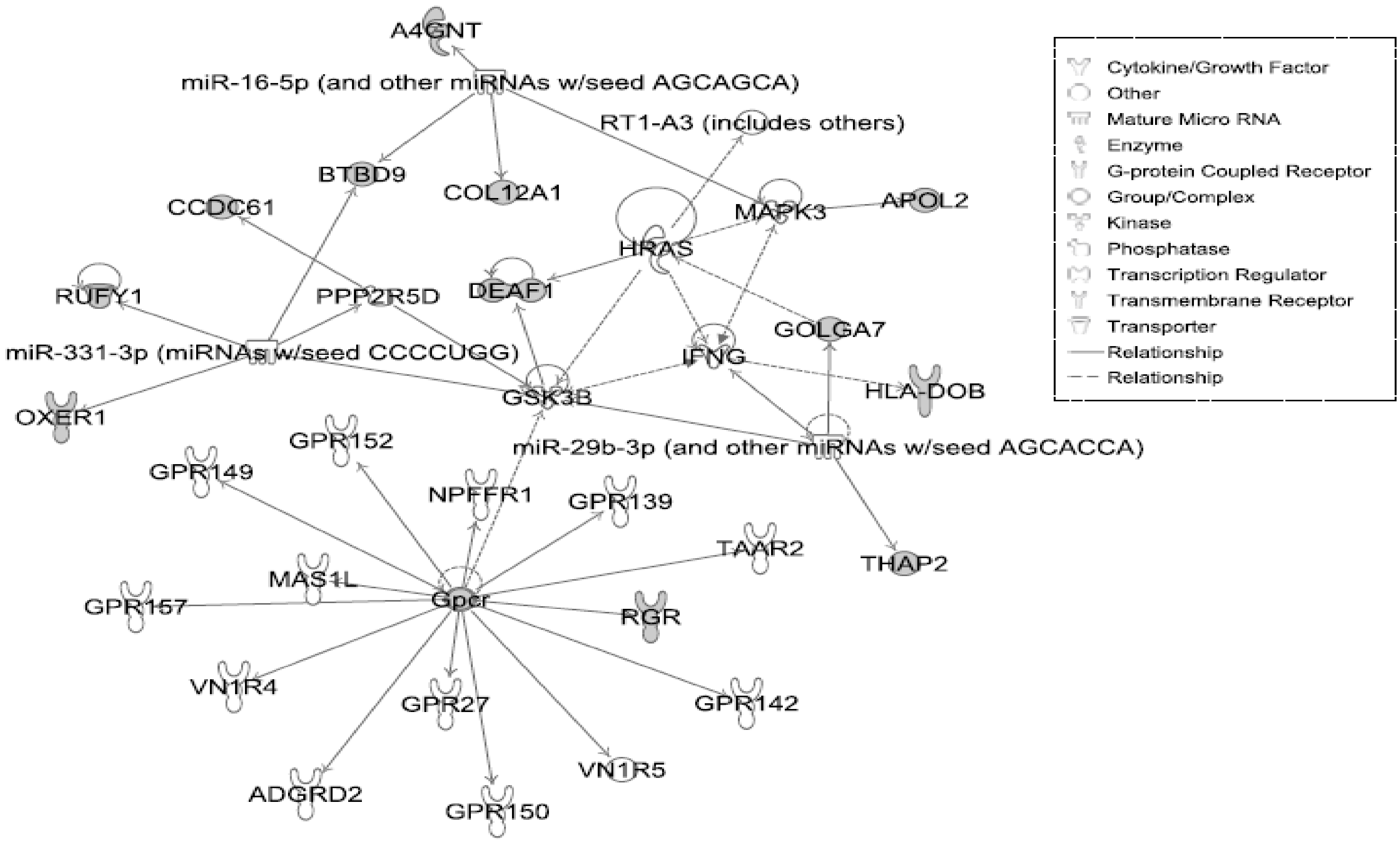
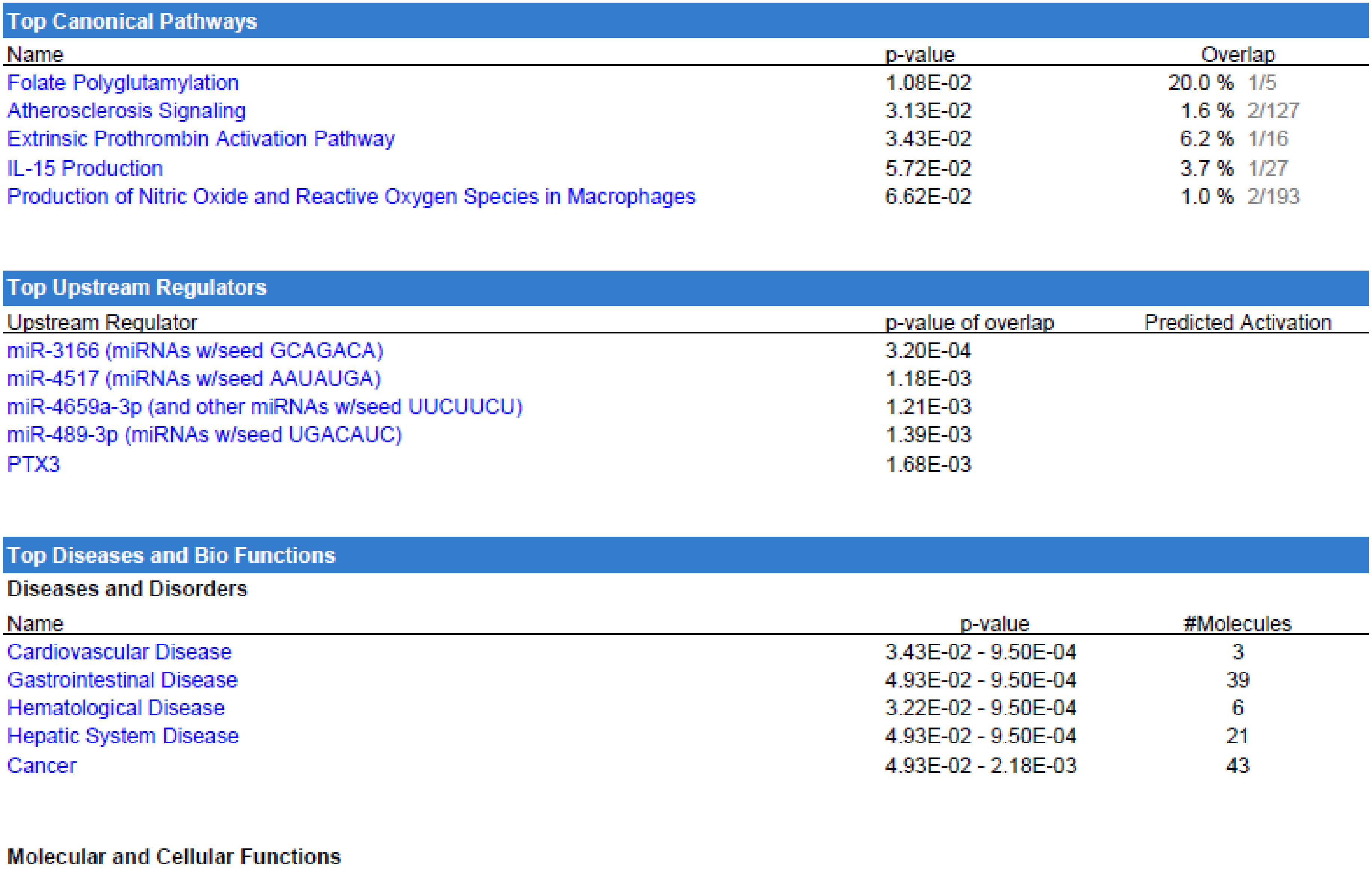


Fig. S1. S176 and S165 of YBX1 commonly regulated gene network, example #2. Genes that are involved in cellular development, cellular growth and proliferation, connective tissue development and function are indicated.

Table S5. IPA Summary of Genes Solely Regulated by S176 of YBX1



Top Canonical Pathways

Name	p-value	Overlap
Folate Polyglutamylation	1.08E-02	20.0 % 1/5
Atherosclerosis Signaling	3.13E-02	1.6 % 2/127
Extrinsic Prothrombin Activation Pathway	3.43E-02	6.2 % 1/16
IL-15 Production	5.72E-02	3.7 % 1/27
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	6.62E-02	1.0 % 2/193

Top Upstream Regulators

Upstream Regulator	p-value of overlap	Predicted Activation
miR-3166 (miRNAs w/seed GCAGACA)	3.20E-04	
miR-4517 (miRNAs w/seed AAUAUGA)	1.18E-03	
miR-4659a-3p (and other miRNAs w/seed UUCUUCU)	1.21E-03	
miR-489-3p (miRNAs w/seed UGACAUC)	1.39E-03	
PTX3	1.68E-03	

Top Diseases and Bio Functions

Diseases and Disorders

Name	p-value	#Molecules
Cardiovascular Disease	3.43E-02 - 9.50E-04	3
Gastrointestinal Disease	4.93E-02 - 9.50E-04	39
Hematological Disease	3.22E-02 - 9.50E-04	6
Hepatic System Disease	4.93E-02 - 9.50E-04	21
Cancer	4.93E-02 - 2.18E-03	43

Molecular and Cellular Functions

Name	p-value	#Molecules
Amino Acid Metabolism	3.43E-02 - 2.18E-03	1
Cell Death and Survival	4.90E-02 - 2.18E-03	5
Cell-To-Cell Signaling and Interaction	4.48E-02 - 2.18E-03	8
Cellular Assembly and Organization	4.90E-02 - 2.18E-03	11
Cellular Development	4.69E-02 - 2.18E-03	13

Physiological System Development and Function

Name	p-value	#Molecules
Embryonic Development	4.90E-02 - 2.18E-03	6
Hematological System Development and Function	4.69E-02 - 2.18E-03	8
Immune Cell Trafficking	2.18E-03 - 2.18E-03	1
Organ Development	3.50E-02 - 2.18E-03	3
Organismal Development	4.48E-02 - 2.18E-03	9

Top Networks

ID	Associated Network Functions	Score
1	Cancer, Dermatological Diseases and Conditions, Gastrointestinal Disease	42
2	Cancer, Hematological Disease, Hereditary Disorder	33
3	Lipid Metabolism, Small Molecule Biochemistry, Auditory Disease	20
4	Amino Acid Metabolism, Developmental Disorder, Drug Metabolism	2
5	Cancer, Organismal Injury and Abnormalities, Renal and Urological Disease	2

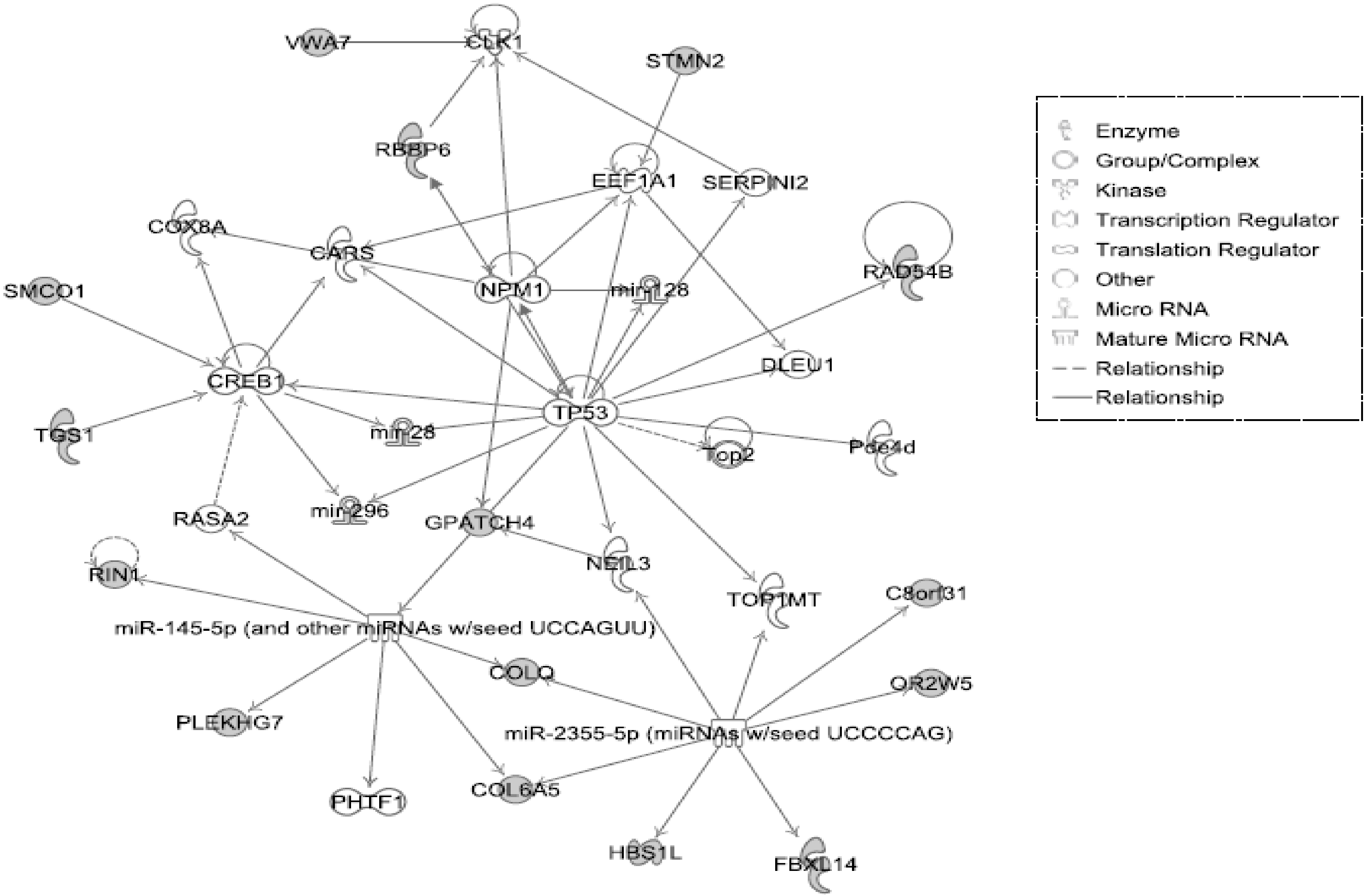


Fig. S2. S176 of YBX1 regulated gene network, example #2. Genes that are involved in cancer, hematological diseases, and hereditary disorders are indicated.

Table S6. IPA Summary of Genes Solely Regulated by S165 of YBX1

Top Canonical Pathways

Name	p-value	Overlap
Sphingomyelin Metabolism	1.51E-02	12.5 % 1/8
LXR/RXR Activation	2.20E-02	1.7 % 2/121
Atherosclerosis Signaling	2.41E-02	1.6 % 2/127
Role of IL-17A in Psoriasis	2.44E-02	7.7 % 1/13
IL-12 Signaling and Production in Macrophages	3.12E-02	1.4 % 2/146

Top Upstream Regulators

Upstream Regulator	p-value of overlap	Predicted Activation
miR-885-3p (miRNAs w/seed GGCAGCG)	6.82E-04	
miR-766-3p (miRNAs w/seed CUCCAGC)	7.95E-04	
miR-135a-5p (and other miRNAs w/seed AUGGCUU)	8.09E-04	
miR-2114-5p (miRNAs w/seed AGUCCCU)	8.82E-04	
miR-4508 (and other miRNAs w/seed CGGGGCU)	1.20E-03	

Top Diseases and Bio Functions

Diseases and Disorders

Name	p-value	#Molecules
Cancer	4.81E-02 - 2.24E-04	39
Organismal Injury and Abnormalities	4.81E-02 - 2.24E-04	39
Reproductive System Disease	3.24E-02 - 6.03E-04	23
Hypersensitivity Response	3.91E-02 - 1.45E-03	3
Antimicrobial Response	2.44E-02 - 1.89E-03	5

Molecular and Cellular Functions

Name	p-value	#Molecules
Cell Death and Survival	4.99E-02 - 7.18E-04	6
Cell Morphology	3.72E-02 - 7.73E-04	8
Cellular Movement	4.94E-02 - 1.45E-03	12
Amino Acid Metabolism	9.44E-03 - 1.89E-03	2
Cell Cycle	3.91E-02 - 1.89E-03	4

Physiological System Development and Function

Name	p-value	#Molecules
Reproductive System Development and Function	3.24E-02 - 7.89E-04	6
Hematological System Development and Function	4.94E-02 - 1.45E-03	8
Immune Cell Trafficking	4.94E-02 - 1.45E-03	7
Connective Tissue Development and Function	2.99E-02 - 1.89E-03	3
Embryonic Development	3.54E-02 - 1.89E-03	5

Top Networks

ID	Associated Network Functions	Score
1	Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Developmental Disorder	42
2	Cell Morphology, Cell Death and Survival, Reproductive System Development and Function	34
3	Cellular Development, Cardiovascular System Development and Function, Organismal Development	18
4	Carbohydrate Metabolism, Cell Cycle, Cellular Development	2

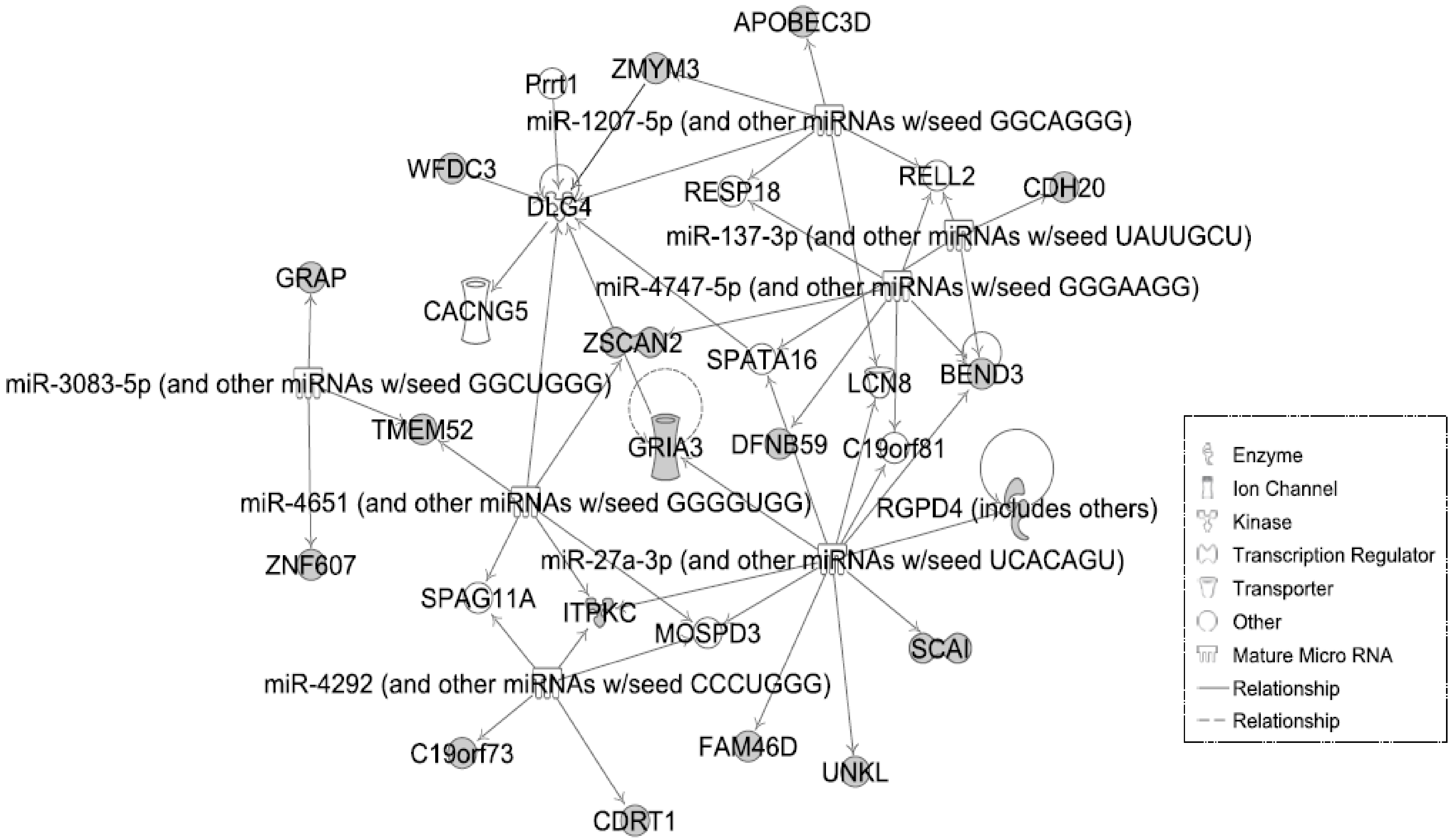


Fig. S3. S165 of YBX1 regulated gene network, example #2. Genes that are involved in cell-to-cell signaling and interaction, nervous system development and function, and developmental disorders are indicated.