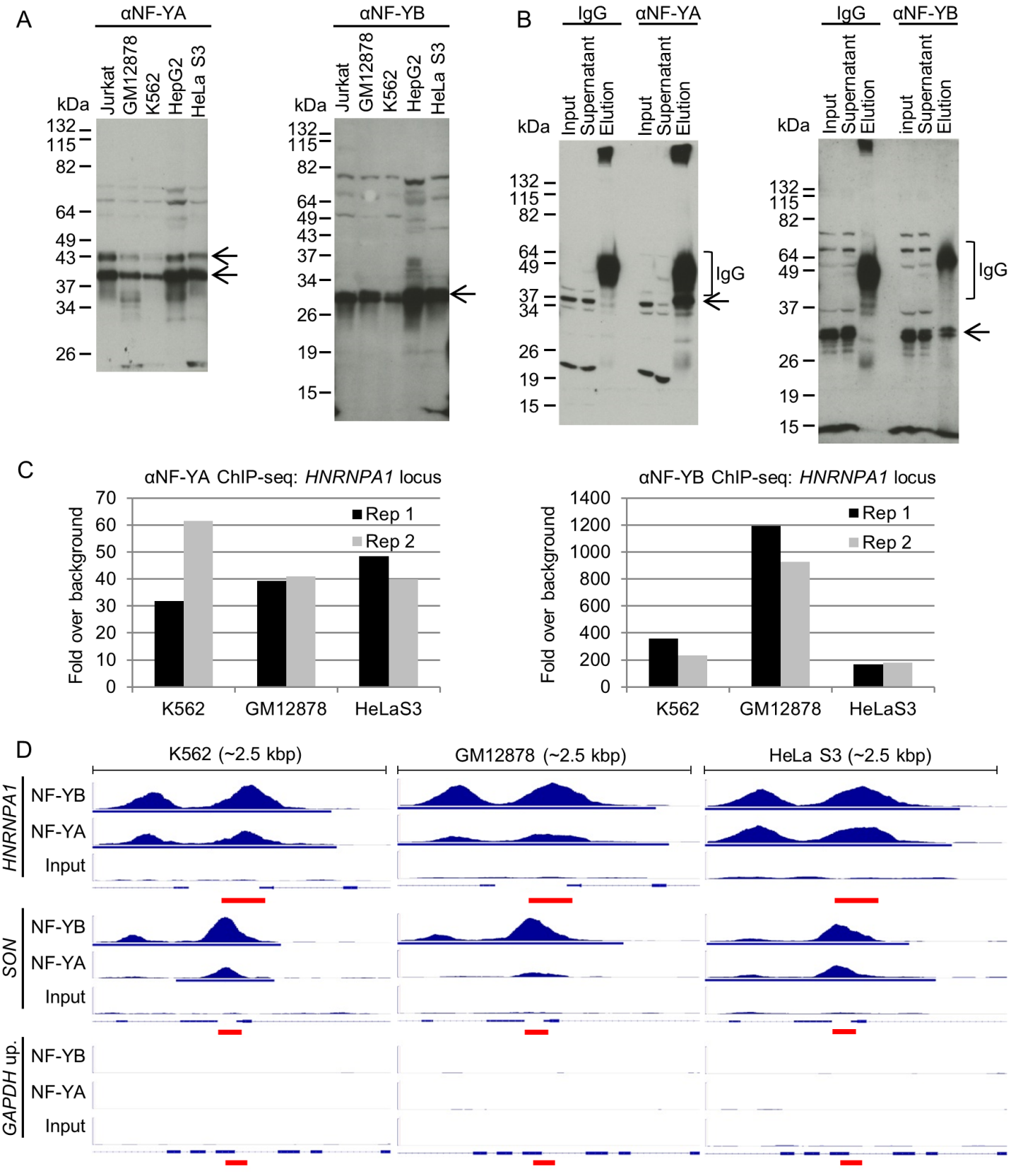
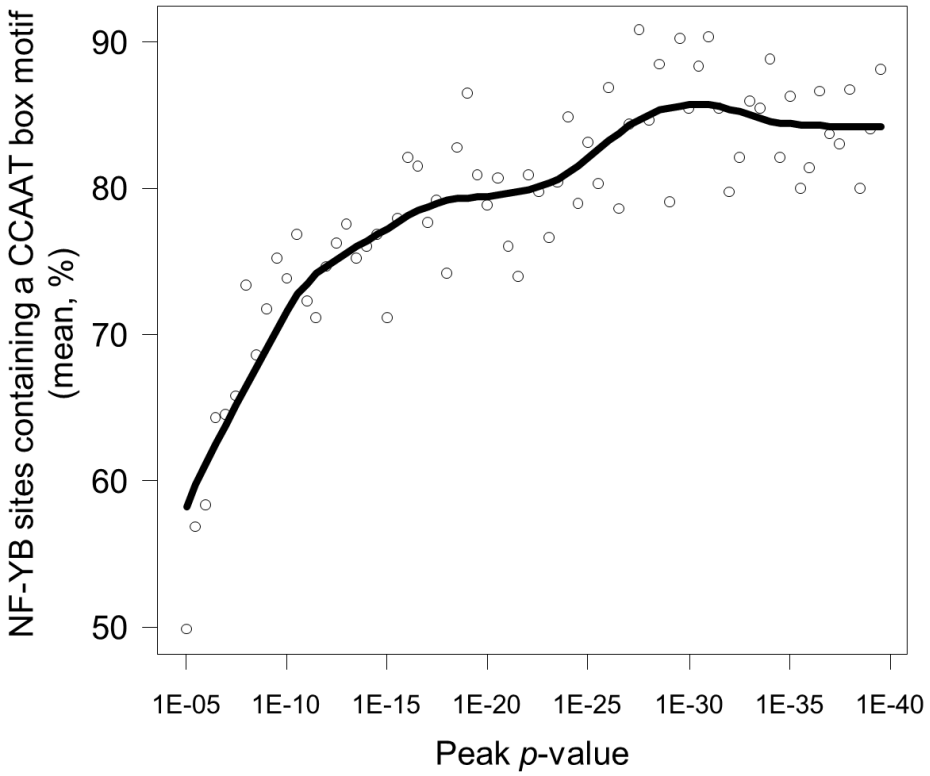


Fleming, et al. Supplemental Fig. 1

A



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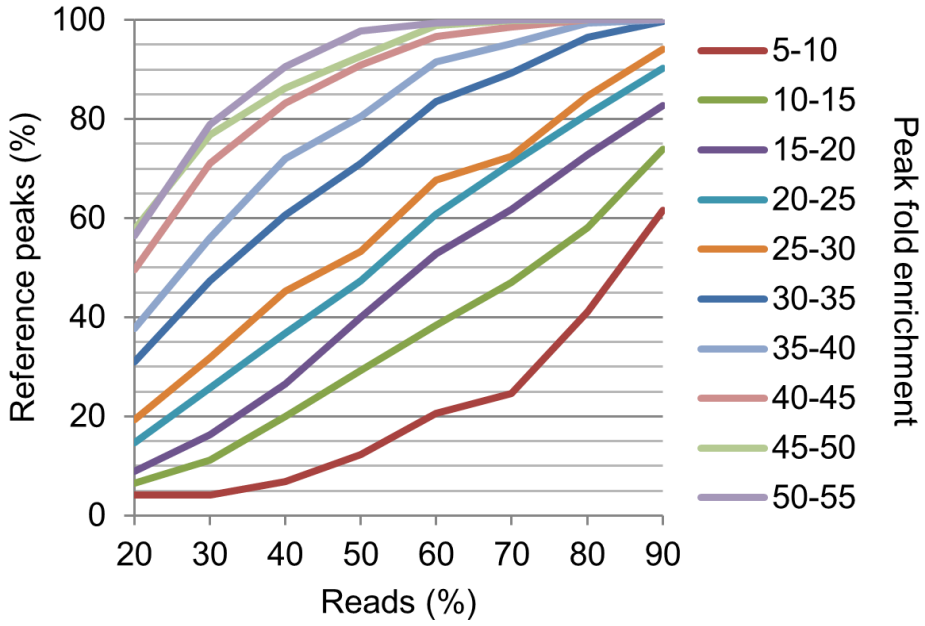
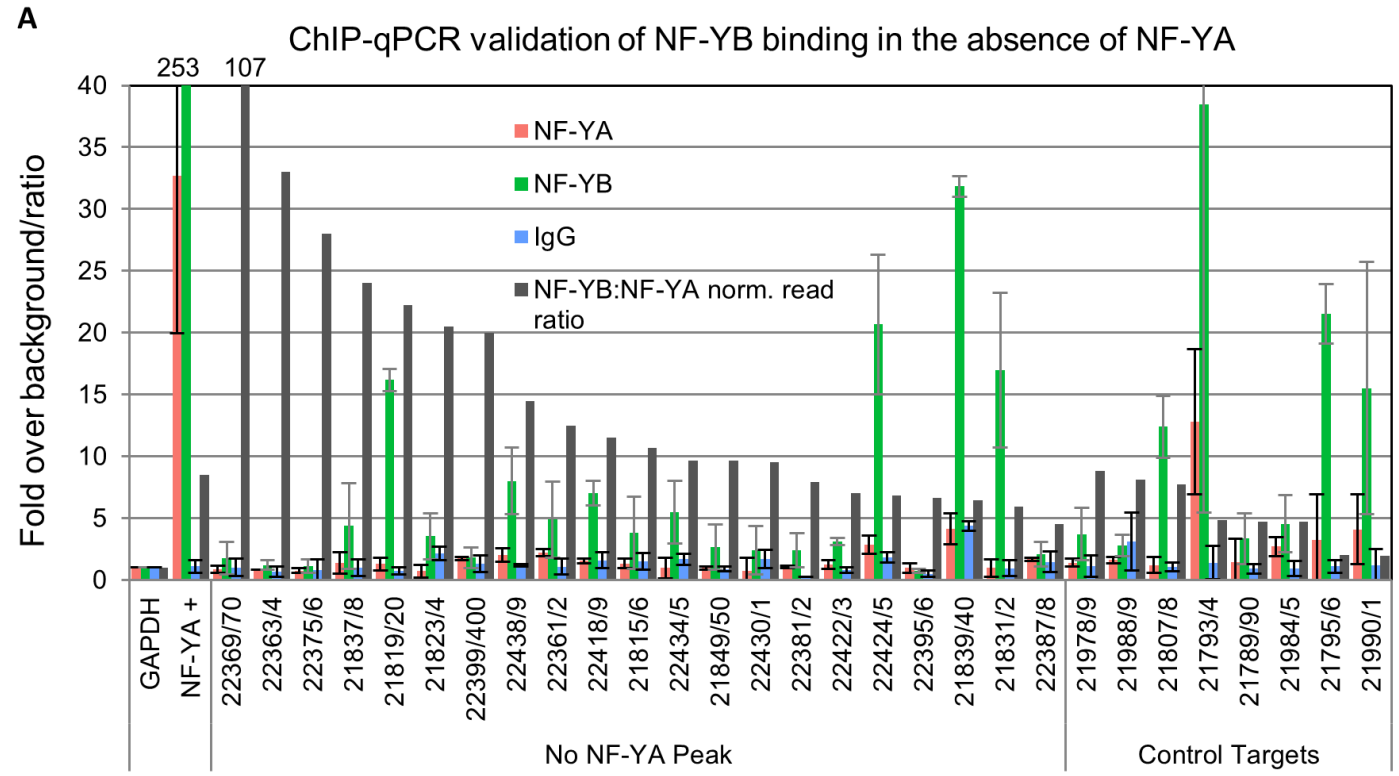
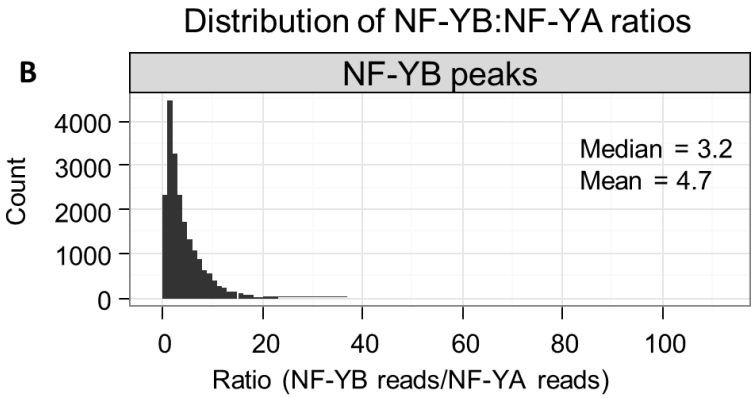


Fleming, et al. Supplemental Fig. 2





Fleming, et al. Supplemental Fig. 3

A

	GO term	*P*-value	FDR q-value	Fold enrichment	Observed hits
GM12878	G2/M DNA damage checkpoint	7.7E-11	1.1E-08	2.1	91
	M/G1 Transition	1.1E-09	8.5E-08	2.0	91
	Homologous recombination repair	1.8E-09	1.0E-07	2.0	89
	Polo-like kinase mediated events	4.5E-07	9.7E-06	2.0	62
	APC/C:Cdc20 mediated degradation of Securin	8.8E-07	1.7E-05	2.1	54
	Ubiquitin-dependent degradation of Cyclin D	1.7E-06	2.9E-05	2.4	39
	Superpathw ay of cholesterol biosynthesis	2.3E-06	3.7E-05	2.4	36
	Signaling mediated by p38-gamma and p38-delta	1.4E-05	1.7E-04	2.8	23
	Activation of ATR in response to replication stress	1.6E-05	1.8E-04	2.1	39
	Integrin alphallbbeta3 signaling	1.9E-05	2.1E-04	2.0	44
HeLaS3	G2/M checkpoints	2.3E-09	6.6E-07	2.1	79
	Homologous recombination repair	2.9E-07	1.7E-05	2.0	62
	RNA polymerase I chain elongation	4.6E-06	1.2E-04	3.2	21
	Retrograde neurotrophin signalling	5.5E-06	1.3E-04	3.6	18
	Regulation of DNA replication	6.8E-08	7.9E-06	2.6	43
	Integrin alphallbbeta3 signaling	1.7E-07	1.2E-05	2.6	39
	Alpha6Beta4Integrin	7.5E-07	2.9E-05	2.3	44
	Synthesis of DNA	2.8E-06	9.0E-05	2.0	52
	Cyclin E associated events during G1/S transition	3.1E-06	9.9E-05	2.0	52
K562	Regulation of DNA replication	2.9E-09	9.5E-08	2.1	81
	Unw inding of DNA	6.0E-09	1.9E-07	4.7	22
	Nucleosome assembly	1.6E-07	3.4E-06	2.4	46
	Ubiquitin-dependent degradation of Cyclin D	7.0E-07	1.2E-05	2.1	55
	Signaling events mediated by PRL	1.3E-06	2.0E-05	2.3	41
	RNA polymerase I transcription	2.0E-06	2.7E-05	2.1	49
	Response to elevated platelet cytosolic Ca2+	2.1E-06	2.7E-05	2.8	28
	Signaling by Rho GTPases	5.7E-06	5.8E-05	4.8	13
	Base excision repair	9.5E-06	9.1E-05	3.1	21
	Metabolism of polyamines	2.1E-05	1.9E-04	3.1	19

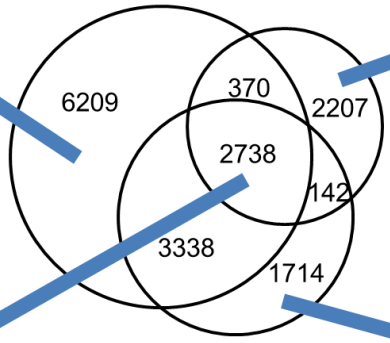
B

K562 unique

Cell line	GO biological process name	P-value	FDR q-value	Fold enrichment	Observed region hits
K562	response to cold	1.8E-06	3.8E-04	2.6	32
	negative regulation of Schwann cell proliferation	3.2E-06	6.0E-04	9.4	8
	tRNA processing	1.4E-05	2.1E-03	2.0	44
	negative regulation of activin receptor signaling pathway	1.9E-05	2.5E-03	5.0	11
	ganglioside metabolic process	2.1E-05	2.8E-03	5.0	11
	regulation of histone methylation	3.1E-05	3.8E-03	2.9	20
	rRNA transcription	3.5E-05	4.2E-03	3.8	14
	tRNA splicing, via endonucleolytic cleavage and ligation	8.0E-05	8.3E-03	11.8	5
	cellular response to hypoxia	8.9E-05	8.7E-03	5.1	9
	anterior/posterior axis specification	9.7E-05	9.0E-03	2.2	31

HeLa S3 unique

Cell line	GO biological process name	P-value	FDR q-value	Fold enrichment	Observed region hits
HeLaS3	epidermis morphogenesis	1.2E-10	2.1E-07	4.2	30
	ectoderm and mesoderm interaction	7.7E-10	1.1E-06	9.4	14
	urinary bladder development	1.3E-09	1.2E-06	8.1	15
	establishment of tissue polarity	5.4E-09	3.5E-06	7.3	15
	replicative cell aging	1.3E-08	7.2E-06	7.5	14
	tail morphogenesis	2.1E-08	1.0E-05	7.2	14
	negative regulation of growth	3.2E-08	1.3E-05	2.2	60
	positive regulation of fatty acid metabolic process	3.4E-08	1.4E-05	3.9	24
	hair follicle development	3.6E-08	1.4E-05	2.9	36
	female genitalia development	6.4E-08	1.8E-05	6.5	14



Common

Cell line	GO biological process name	P-value	FDR q-value	Fold enrichment	Observed region hits
Common	cell cycle checkpoint	8.8E-16	6.4E-13	2.4	110
	S phase	9.5E-15	6.0E-12	3.3	60
	nucleosome assembly	1.9E-13	8.3E-11	3.0	62
	chromatin assembly	2.4E-12	9.0E-10	2.8	63
	mitotic cell cycle checkpoint	2.4E-11	7.2E-09	2.5	67
	DNA integrity checkpoint	2.7E-11	8.0E-09	2.6	63
	proteasomal protein catabolic process	6.8E-10	1.4E-07	2.2	75
	regulation of gene silencing	7.0E-10	1.4E-07	7.2	17
	protein folding	5.6E-09	9.6E-07	2.1	77
	mammary gland epithelial cell proliferation	3.1E-08	4.7E-06	3.9	24

GM12878 unique

Cell line	GO biological process name	P-value	FDR q-value	Fold enrichment	Observed region hits
GM12878	I-kappaB kinase/NF-kappaB cascade	2.1E-06	2.5E-03	3.2	23
	response to metal ion	2.2E-06	2.2E-03	2.0	53
	regulation of interleukin-12 production	4.3E-06	2.6E-03	4.3	15
	toll-like receptor signaling pathway	1.7E-05	6.0E-03	4.6	12
	positive regulation of cytokine production	2.8E-05	8.4E-03	2.3	32
	positive regulation of leukocyte migration	3.3E-05	9.0E-03	3.4	16
	vasodilation	6.4E-05	1.4E-02	3.8	13
	positive regulation of macrophage chemotaxis	8.5E-05	1.5E-02	8.7	6
	regulation of tumor necrosis factor biosynthetic process	8.6E-05	1.5E-02	5.2	9
	immune response-regulating signaling pathway	1.2E-04	1.8E-02	2.4	23

Fleming, et al. Supplemental Fig. 4

A

Description	Transcription factor complex			Chromatin remodeling complex		Histone methyltransferase complex	Hetero-chromatin	Histone deacetylase complex	Histone acetyltransferase complex	Transcriptional repressor complex
Term coverage	69%			75%		71%	64%	78%	68%	70%
Genes bound	145			64		42	36	35	34	30
	ABT1	GTF3C6	PROP1	ACTL6A	MORF4L1	ACTB	A1CF	APPL1	ACTB	APPL1
	ALX4	HAND2	PTF1A	ACTL6B	MTA2	AEBP2	BAZ1B	APPL2	ACTL6A	APPL2
	ARNT	HDAC9	PUS1	APPL1	MYSM1	C17orf49	CBX1	CBX5	ATXN7L3	ARID4A
	ARNT2	HELT	RBL1	APPL2	NCOR2	CBX5	CBX3	CHD3	BRD1	C1D
	ARNTL	HES6	RBL2	ARID1A	PHF21A	CHD8	CBX5	CHD4	BRD8	CBX5
	ASCC1	HIF1A	RBM14	ARID1B	RBBP4	E2F6	DNMT1	CIR	BRPF3	CHD3
	ATF1	HMGA1	RELA	ASF1A	RBBP7	EED	DNMT3A	CSNK2A1	C1orf149	CHD4
	ATF4	HNF1A	SATB2	BAHD1	RBM10	EZH1	DNMT3B	EVI1	C20orf20	CORO2A
	ATF7IP	HNF1B	SIX1	BAZ1B	RERE	EZH2	EED	GATAD2A	CREBBP	CSNK2A1
	BSX	HNF4A	SKI	CBX5	RSF1	HDAC9	FOXC1	HDAC1	DMAP1	CTBP2
	CCNH	HOXB13	SMAD2	CHAF1A	SALL1	INO80C	H2AFX	HDAC11	ENY2	DDX20
	CDK2	HOXD12	SMAD3	CHD3	SAP18	JARID2	H2AFY	HDAC4	EP300	ETV3
	CDK4	ING2	SMAD5	CHD4	SAP30	KIAA1076	H2AFY2	HDAC6	EP400	GATAD2A
	CEBPA	IVNS1ABP	SMAD6	CHRAC1	SATB2	KIAA1076	H3F3B	HDAC7	EPC1	HDAC1
	CLOCK	JUN	SMAD7	CIR	SIN3A	KIAA1267	H3F3B	HDAC9	ING3	HDAC4
	CREB1	KAT5	SNAI3	CSNK2A1	SIRT1	LAS1L	INCENP	ING2	KAT5	HMGB1
	CREBBP	KLF4	SOX2	DPF1	SIRT2	MAX	MAEL	MBD2	MORF4L1	JAZF1
	CREG1	LBXCOR1	STON1-GTF2A1L	DPF3	SMARCA1	MEN1	MBD2	MBD3	MYST2	MBD3
	CREM	LMO4	SUB1	ESR1	SMARCA2	MLL	MBD3	MORF4L1	MYST4	MTA2
	CRX	MAFB	SUPT3H	EVI1	SMARCA5	MLL3	MECP2	MTA2	PHF15	NCOR2
	CTNNB1	MED17	TAF1	GATAD2A	SMARCC1	MLL5	ORC2L	NCOR2	PHF17	PHF12
	DMBX1	MED27	TAF10	HDAC1	SMARCD1	MYST1	PBX4	PHF21A	RUVBL1	RBBP4
	E2F1	MED7	TAF1A	HDAC11	SMARCD2	OGT	PCGF2	RBBP4	RUVBL2	RBBP7
	E2F2	MEF2B	TAF3	HDAC4	SMARCE1	PAXIP1	RAD18	RBBP7	SAP130	RLIM
	E2F3	MEIS1	TAF4	HDAC6	SUDS3	PELP1	RNF2	RERE	SUPT3H	SALL1
	E2F5	MLXIPL	TAF4B	HDAC7	SUV39H1	PHF20	SALL1	SALL1	TADA1L	SKI
	E2F6	MMS19	TAF5L	HDAC9	TAF6L	PPP1CC	SATB1	SAP18	TAF10	SMARCE1
	E2F7	MYOD1	TAF7	ING2	TAL1	PRPF31	SIRT1	SAP30	TAF4	TBL1XR1
	E2F8	NARG1	TAF8	KIF11	TBL1XR1	RBBP4	SIRT6	SATB2	TAF5L	YWHAB
	ECSIT	NFYA	TBP	MAEL	TOP2B	RBBP7	SMARCC1	SIN3A	TAF6L	ZBTB16
	EDF1	NFYB	TBX2	MBD2	UCHL5	RNF2	SUV39H1	SUDS3	TAF7	
	EP300	NFYC	TCF12	MBD3	ZNF217	RUVBL1	SUZ12	TAF6L	TRRAP	
	EPAS1	NKX2-1	TCF3			RUVBL2	TCP1	TAL1	USP22	
	ERCC2	NKX2-5	TCF4			SETD1A	TNKS1BP1	TBL1XR1	YEATS4	
	ERCC3	NPAS2	TCF7L2			STK38	TOP2B	ZNF217		
	ETS1	NR2E3	TEAD2			SUZ12	UBE2B			
	EYA3	NR6A1	TEAD4			TAF1				
	FOS	ONECUT3	TFAP2D			TAF4				
	FOXE3	PARP1	TFDP2			TAF7				
	FOXF1	PBX1	TFDP3			TEX10				
	GATA6	PBX3	TFEB			UTX				
	GSC	PDLIM1	TP53			WDR5				
	GTF2A1	PITX2	TRRAP							
	GTF2E2	PKNOX1	USF1							
	GTF2F2	PMF1	XRCC6							
	GTF2H3	POU3F1	YY1							
	GTF3C1	POU3F2	ZEB1							
	GTF3C3	PRKDC	ZFHX3							
	GTF3C5									

Fleming, et al. Supplemental Fig. 5

B

Description	DNA-directed RNA polymerase II, holoenzyme	Mediator complex	MLL1 complex	PcG protein complex	NuA4 histone acetyl-transferase complex	SWI/SNF-type complex	RNA polymerase complex
GO ID	GO:0016591	GO:0016592	GO:0071339	GO:0031519	GO:0035267	GO:0070603	GO:0030880
Term coverage	51%	69%	74%	80%	100%	67%	46%
Genes bound	40	22	20	16	14	14	13
	C19orf2	PAF1	MED9	C17orf49	AEBP2	ACTB	ACTL6A	C19orf2
	CCNH	POLR2A	CDK8	CHD8	ASXL1	ACTL6A	ACTL6B	POLR1A
	CPSF3L	POLR2G	DKFZp434H247	E2F6	BCOR	BRD8	ARID1A	POLR1B
	CTR9	POLR2I	MED10	INO80C	CBX2	C1orf149	ARID1B	POLR1D
	EDF1	PPARGC1A	MED13	KIAA1267	CBX8	DMAP1	BAZ1B	POLR2A
	ELP2	SHFM1	MED13L	LAS1L	EED	EP400	CHAF1A	POLR2G
	ELP3	STON1-GTF2A1L	MED14	MAX	EZH1	EPC1	DPF1	POLR2I
	ELP4	SUPT3H	MED15	MLL	EZH2	ING3	DPF3	POLR3A
	ERCC2	TAF1	MED16	MYST1	JARID2	KAT5	SMARCA2	POLR3F
	ERCC3	TAF10	MED17	PELP1	PCGF2	MORF4L1	SMARCC1	POLR3H
	GTF2A1	TAF3	MED18	PHF20	PHC2	RUVBL1	SMARCD1	POLR3K
	GTF2E2	TAF4	MED19	PRPF31	RBBP4	RUVBL2	SMARCD2	PPARGC1A
	GTF2F2	TAF4B	MED21	RNF2	RBBP7	TRRAP	SMARCE1	ZNF768
	GTF2H3	TAF5L	MED24	RUVBL1	RNF2	YEATS4	TOP2B	
	INTS3	TAF7	MED26	RUVBL2	SUZ12			
	INTS4	TAF8	MED29	TAF1	YY1			
	INTS6	TBP	MED30	TAF4				
	INTS7	TP53	MED7	TAF7				
	INTS9	TRRAP	MED8	TEX10				
	MMS19	ZNF768	PPARGC1B	WDR5				
			RBM14					
			THRAP3					

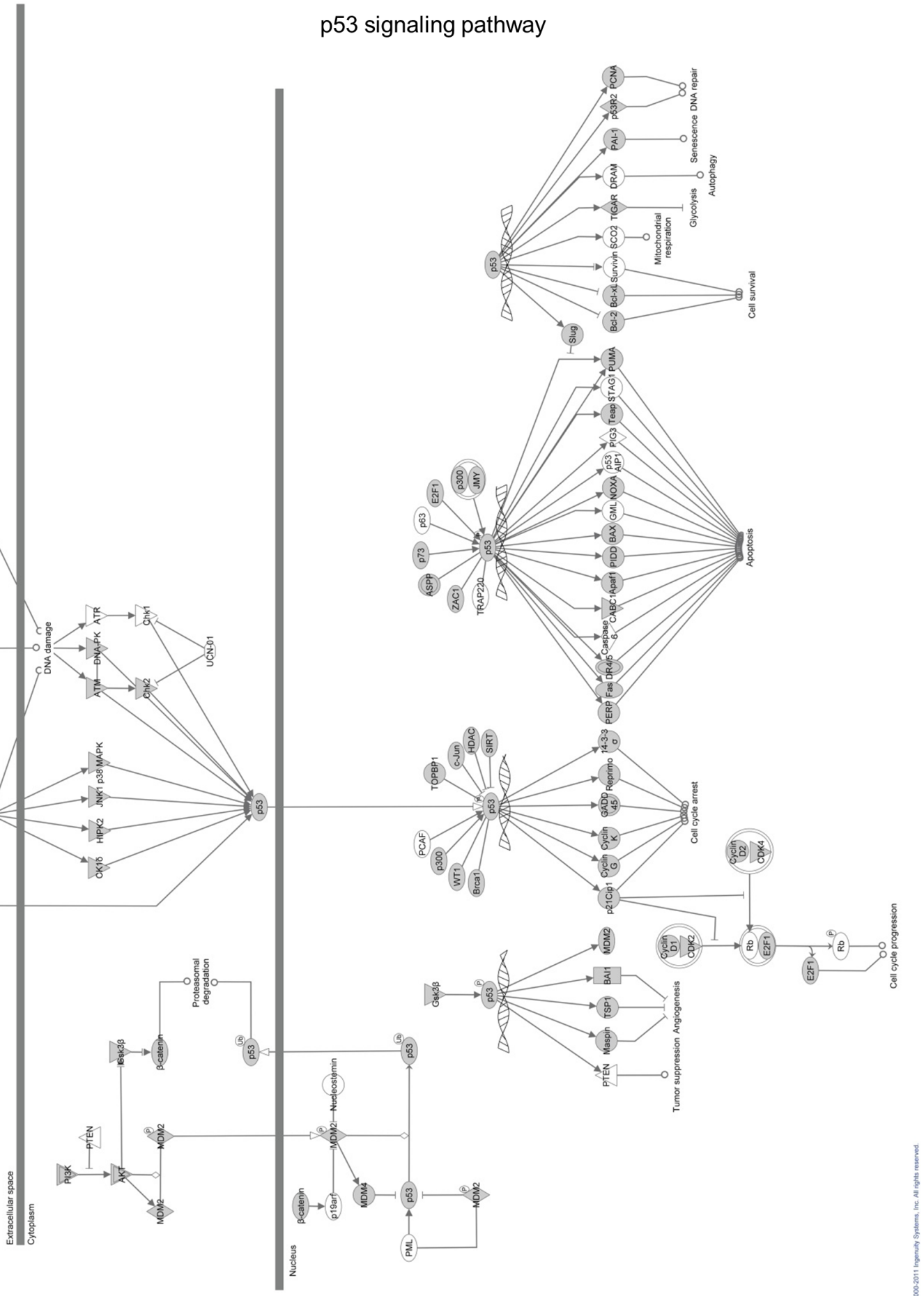
Description	NuRD complex	SAGA-type complex	Transcription elongation factor complex	Transcription factor TFIID complex	SWI/SNF complex	ESC/E(Z) complex	Nup107-160 complex	nBAF complex
GO ID	GO:0016581	GO:0070461	GO:0008023	GO:0005669	GO:0016514	GO:0035098	GO:0031080	GO:0071565
Term coverage	86%	52%	67%	50%	60%	89%	80%	67%
Genes bound	12	12	12	10	9	8	8	8
	APPL1	ATXN7L3	CTR9	EDF1	ACTL6A	AEBP2	AHCTF1	ACTL6B
	APPL2	ENY2	ELL	TAF1	ACTL6B	EED	NUP160	ARID1A
	CHD3	SAP130	ELL2	TAF10	ARID1A	EZH1	NUP37	DPF1
	CHD4	SUPT3H	ELL3	TAF3	ARID1B	EZH2	NUP43	DPF3
	CSNK2A1	TADA1L	ELP2	TAF4	SMARCA2	JARID2	NUP85	SMARCA2
	GATAD2A	TAF10	ELP3	TAF4B	SMARCC1	RBBP4	NUP98	SMARCC1
	HDAC1	TAF4	ELP4	TAF7	SMARCD1	RBBP7	SEC13	SMARCD1
	MBD3	TAF5L	NUFIP1	TAF8	SMARCD2	SUZ12	SEH1L	SMARCE1
	MTA2	TAF6L	PAF1	TBP	SMARCE1			
	RBBP4	TAF7	TAF7	TP53				
	RBBP7	TRRAP	TCEB3					
	SALL1	USP22	TTF2					

Description	Sin3 complex	Catenin complex	STAGA complex	Eukaryotic translation initiation factor 3 complex	npBAF complex	Transcription factor TFTC complex	Chromatin silencing complex	MLL5-L complex
GO ID	GO:0016580	GO:0016342	GO:0030914	GO:0005852	GO:0071564	GO:0033276	GO:0005677	GO:0070688
Term coverage	88%	88%	58%	47%	55%	43%	71%	63%
Genes bound	7	7	7	7	6	6	5	5
	CSNK2A1	APC2	SAP130	EIF3A	ACTL6A	SUPT3H	BAHD1	ACTB
	HDAC1	CDH1	SUPT3H	EIF3D	ARID1A	TAF10	SIRT1	MLL5
	ING2	CTNNA1	TADA1L	EIF3F	SMARCA2	TAF4	SIRT2	OGT
	MORF4L1	CTNNB1	TAF10	EIF3H	SMARCC1	TAF5L	SMARCA5	PPP1CC
	RBBP4	JUP	TAF5L	EIF3J	SMARCD1	TAF7	SUV39H1	STK38
	SIN3A	PVRL1	TAF6L	EIF3L	SMARCE1	TRRAP		
	SUDS3	SMAD7	TRRAP	EIF3M				

GO ID	GO:0016580	GO:0016342	GO:0030914	GO:0005852	GO:0071564	GO:0033276	GO:0005677	GO:0070688
Term coverage	88%	88%	58%	47%	55%	43%	71%	63%
Genes bound	7	7	7	7	6	6	5	5
	CSNK2A1	APC2	SAP130	EIF3A	ACTL6A	SUPT3H	BAHD1	ACTB
	HDAC1	CDH1	SUPT3H	EIF3D	ARID1A	TAF10	SIRT1	MLL5
	ING2	CTNNA1	TADA1L	EIF3F	SMARCA2	TAF4	SIRT2	OGT
	MORF4L1	CTNNB1	TAF10	EIF3H	SMARCC1	TAF5L	SMARCA5	PPP1CC
	RBBP4	JUP	TAF5L	EIF3J	SMARCD1	TAF7	SUV39H1	STK38
	SIN3A	PVRL1	TAF6L	EIF3L	SMARCE1	TRRAP		
	SUDS3	SMAD7	TRRAP	EIF3M				

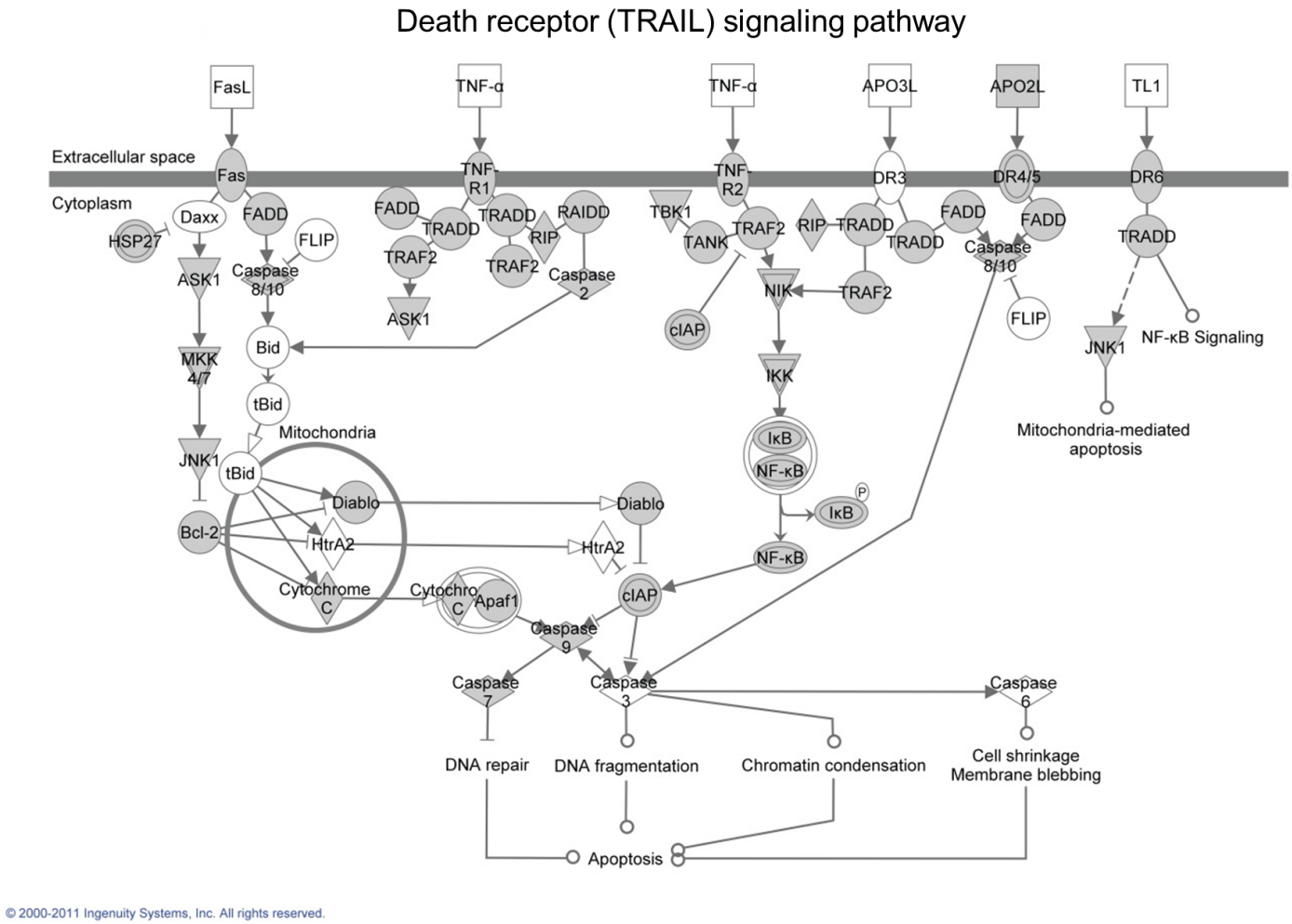
Fleming, et al. Supplemental Fig. 5

C



Fleming, et al. Supplemental Fig. 5

D



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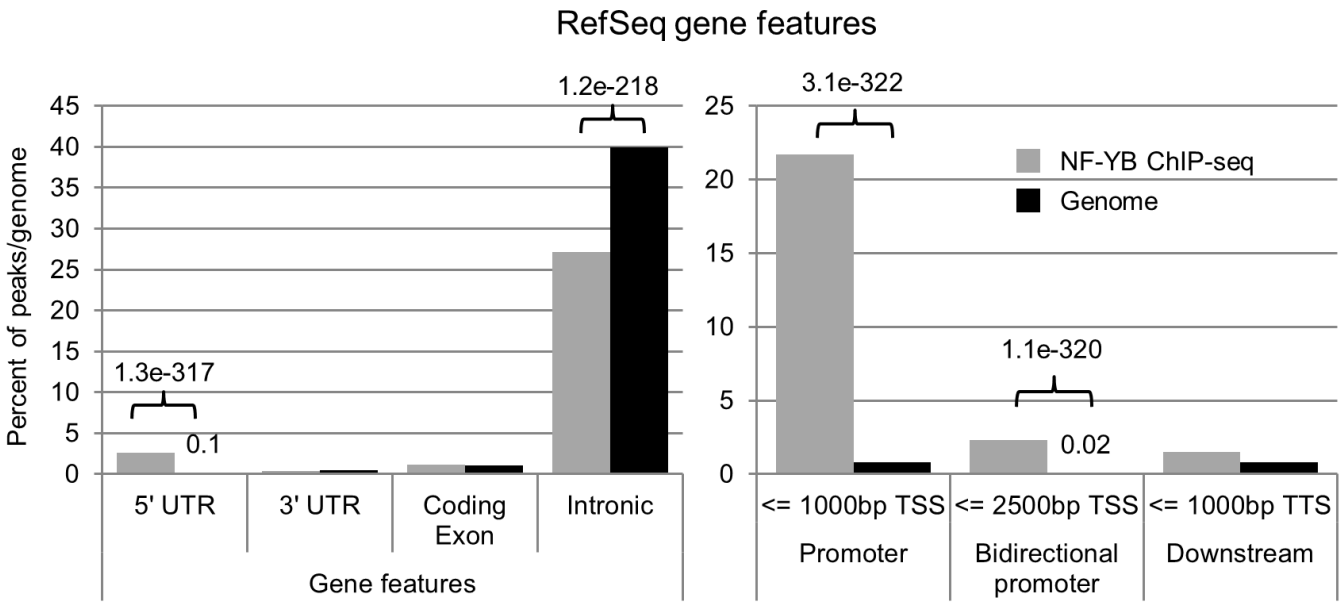
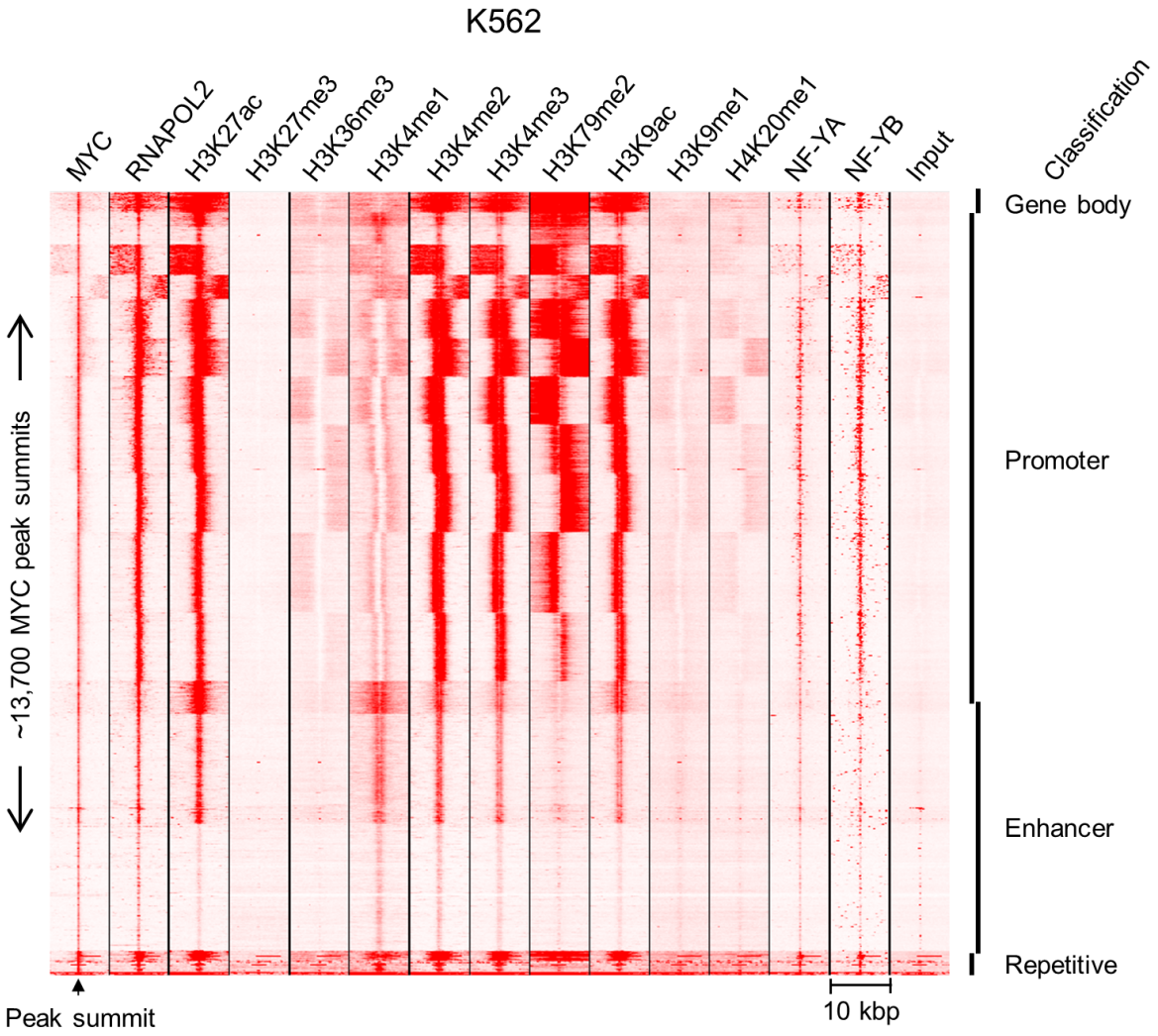
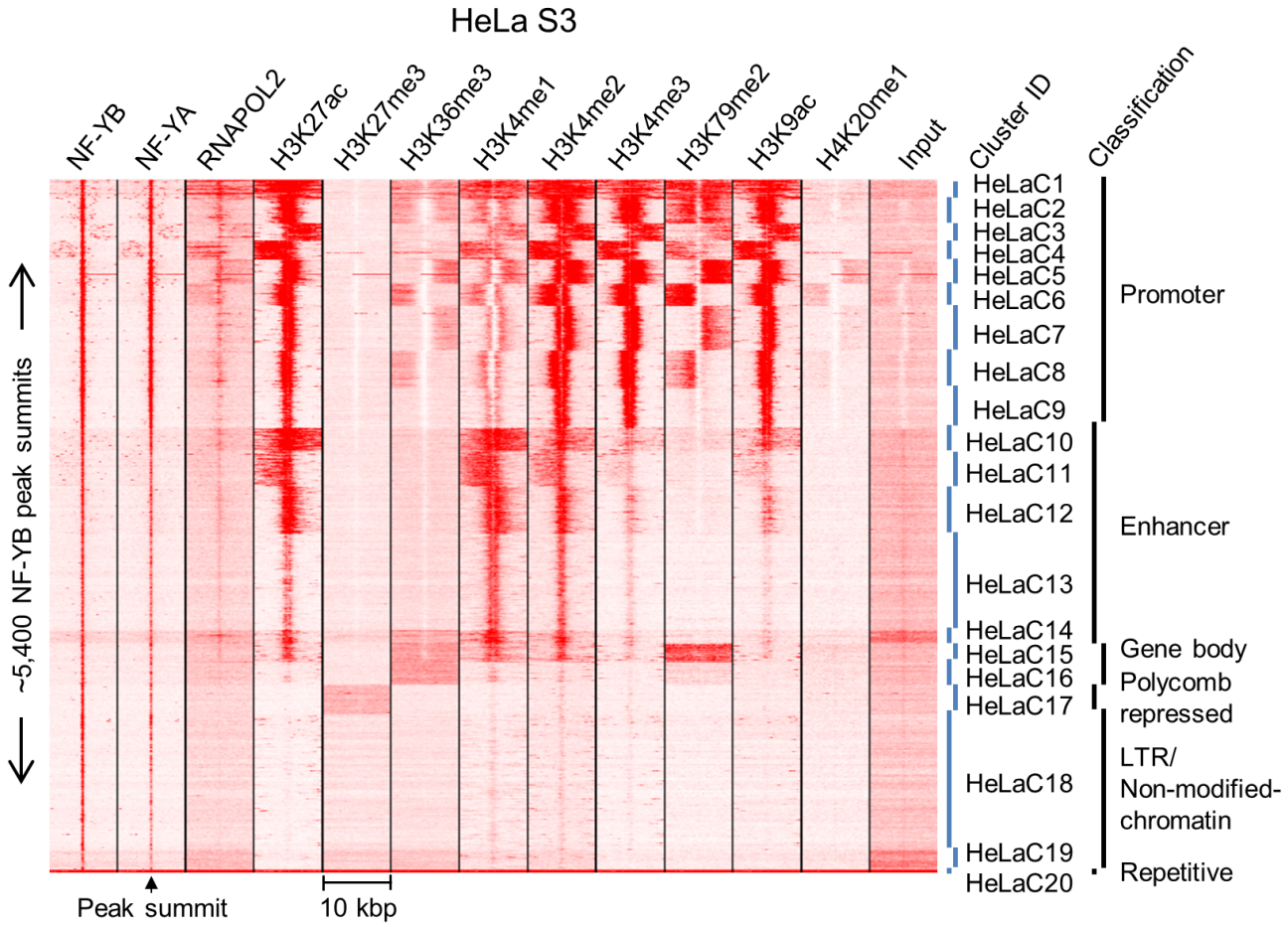
Fleming, et al. Supplemental Fig. 5



Fleming, et al. Supplemental Fig. 6

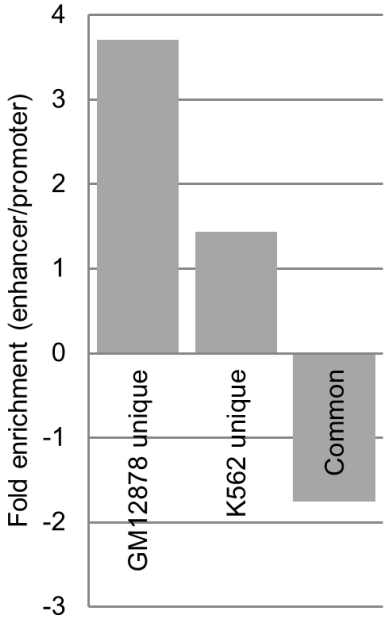


Fleming, et al. Supplemental Fig. 7



Fleming, et al. Supplemental Fig. 8

A



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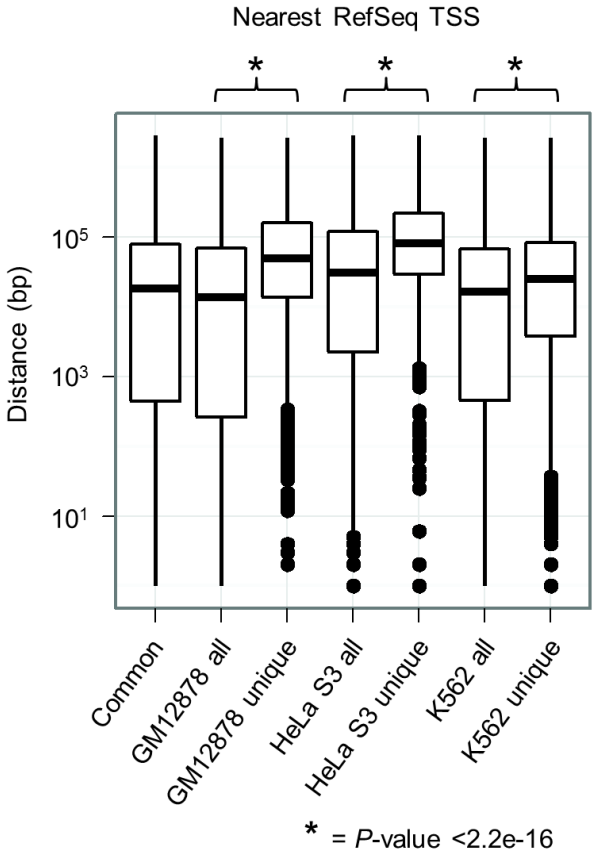
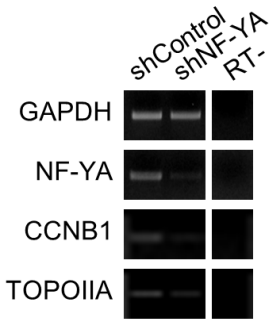
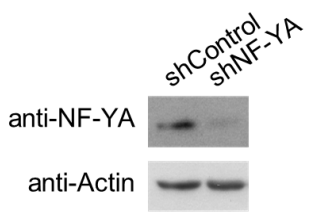


Fleming, et al. Supplemental Fig. 9

A



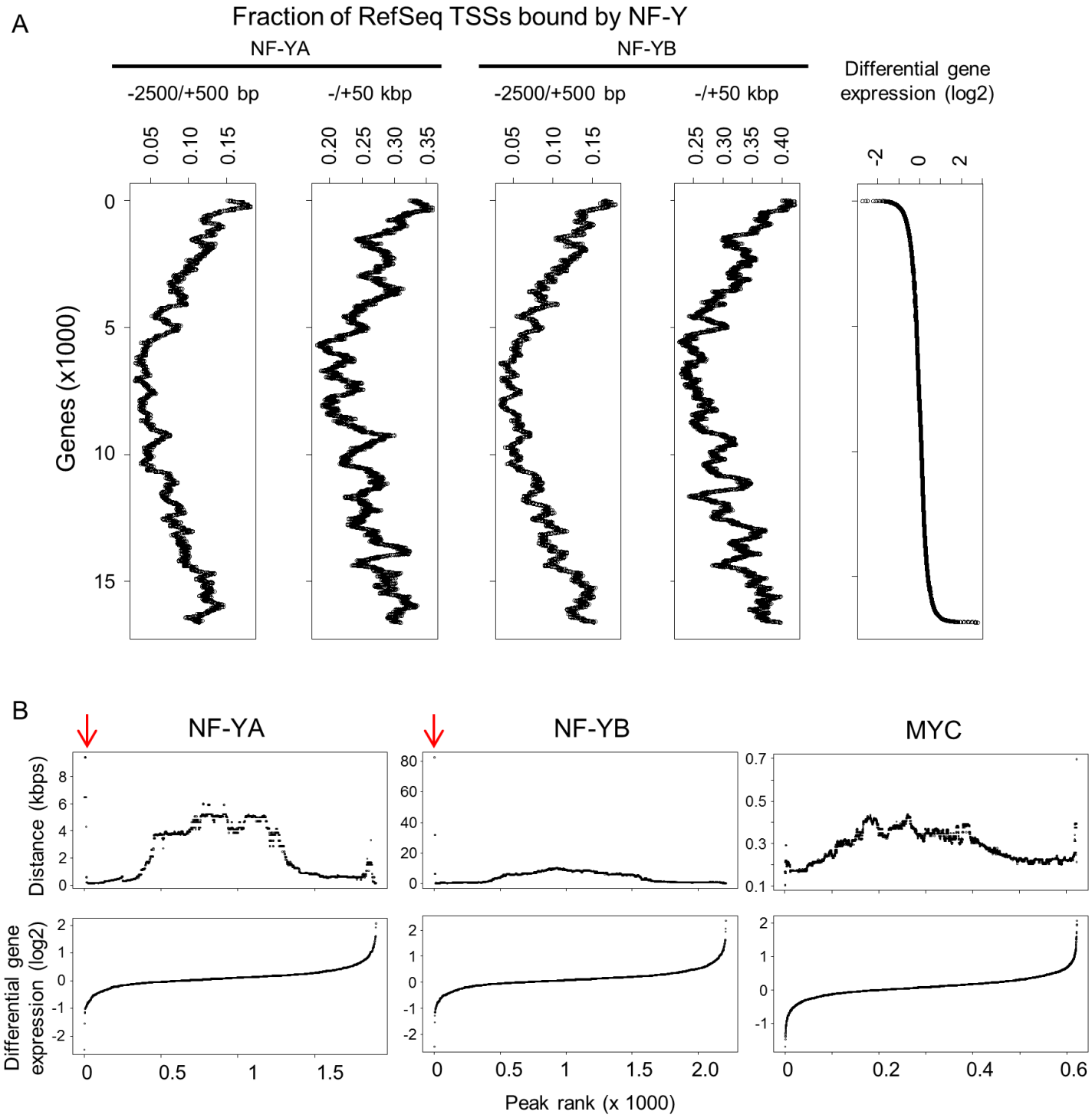
B



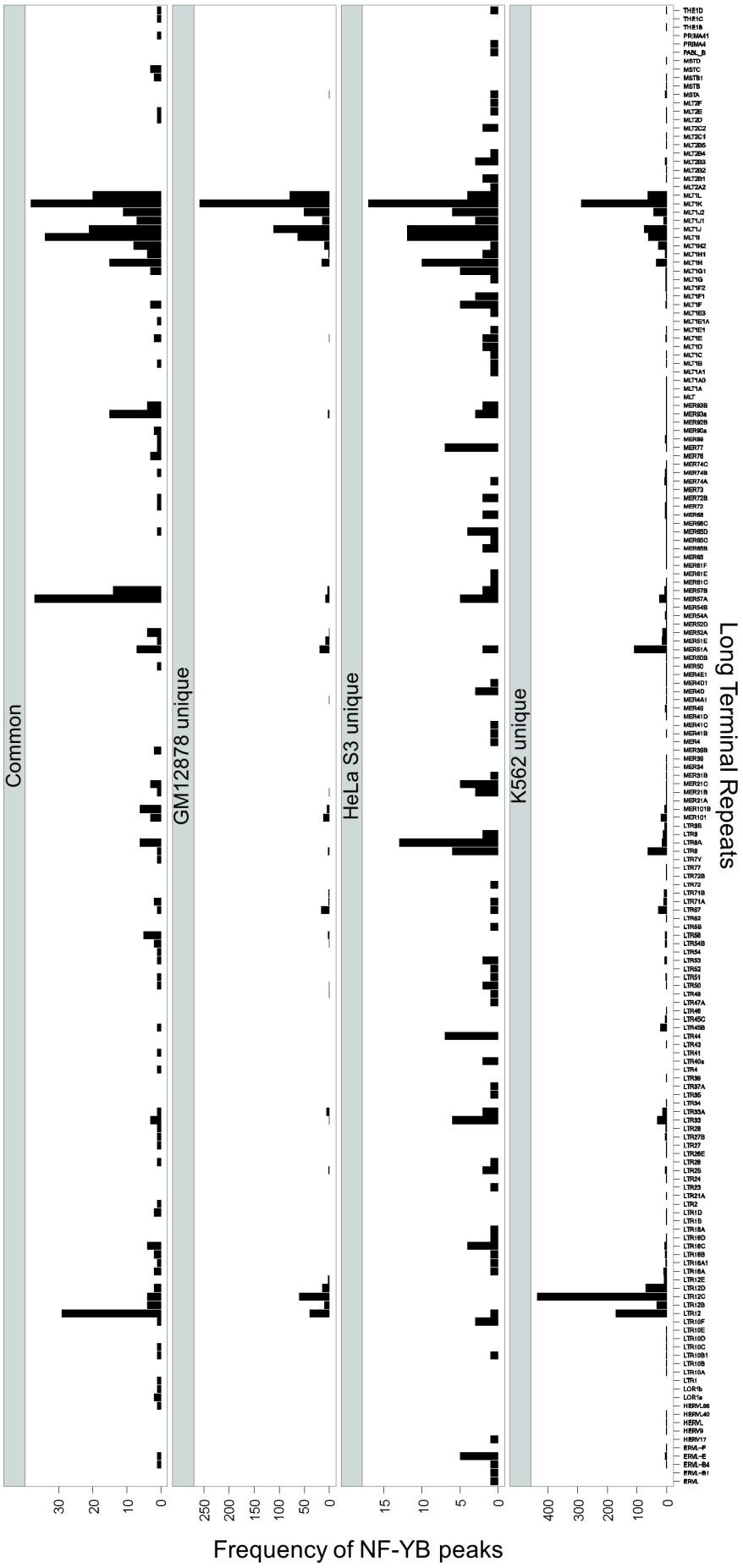
C

Cutoff *p*-value (adjusted)	Genes differentially regulated		NF-YA bound				NF-YB bound			
			-2.5kbps, +500bps		+/-50kbps		-2.5kbps, +500bps		+/-50kbps	
			#	*P*-value	#	*P*-value	#	*P*-value	#	*P*-value
1.00E-06 (7.5E-04)	Down	9	2	1.8E-01	2	2.0E-01	2	1.0E+00	2	7.3E-01
	Up	25	3	4.7E-01	3	5.0E-01	10	1.7E-01	11	1.9E-01
1.00E-05 (2.0E-03)	Down	27	2	1.0E+00	3	7.3E-01	3	8.1E-02	3	2.2E-02
	Up	91	15	1.3E-02	15	2.6E-02	45	3.3E-06	50	3.4E-06
1.00E-04 (6.7E-03)	Down	84	3	1.2E-01	4	1.9E-01	9	6.8E-04	9	1.5E-05
	Up	252	34	8.5E-03	37	4.1E-03	98	1.3E-05	110	2.6E-05
1.00E-03 (2.7E-02)	Down	220	5	2.2E-04	6	2.3E-04	19	4.3E-11	28	2.4E-10
	Up	629	101	5.9E-10	108	1.3E-10	233	1.6E-09	264	4.5E-09
1.00E-02 (1.1E-01)	Down	513	12	4.9E-09	18	7.6E-07	54	3.7E-19	79	1.8E-16
	Up	1518	223	9.8E-17	245	9.7E-20	536	4.3E-16	624	4.4E-18

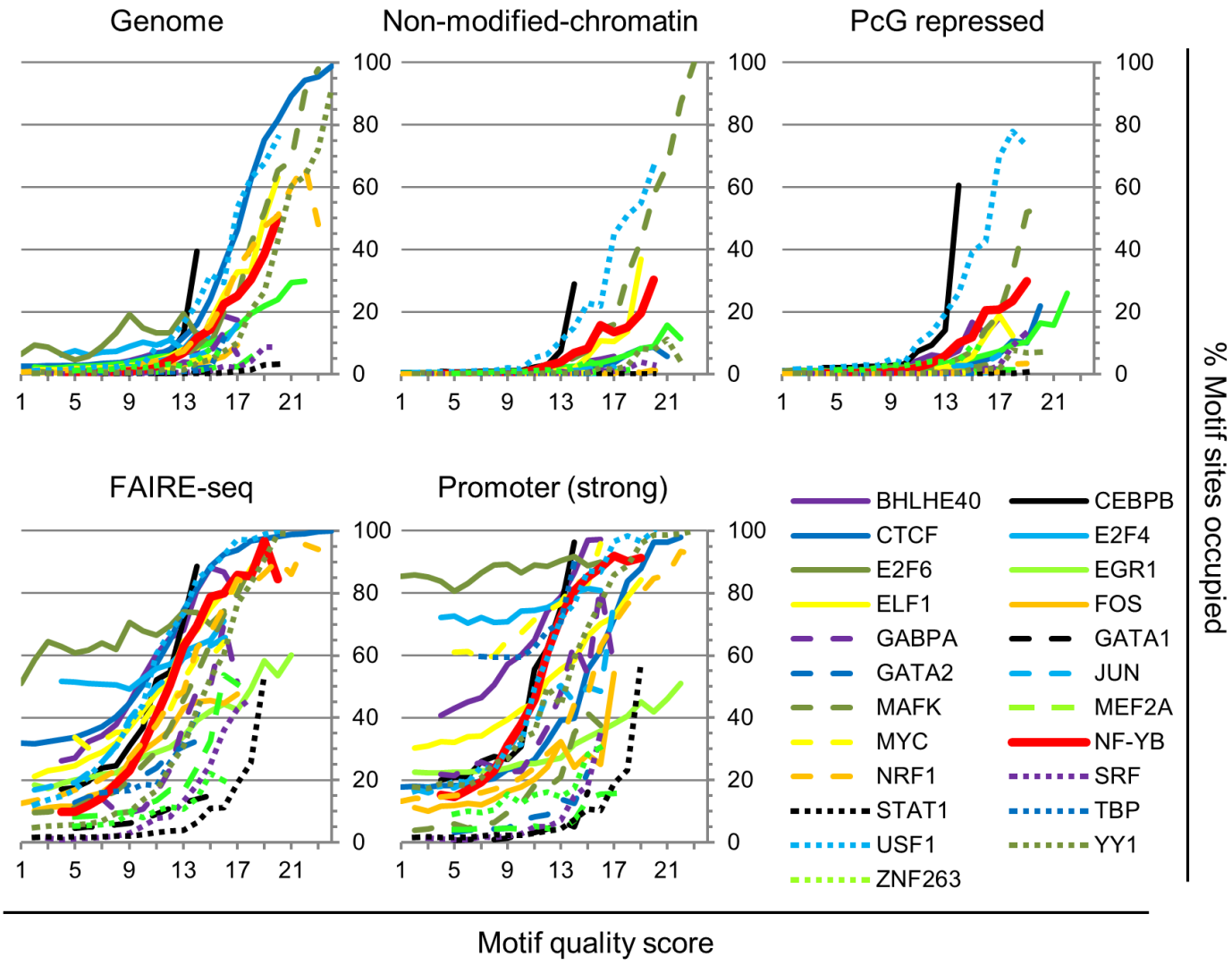
Fleming, et al. Supplemental Fig. 10



Fleming, et al. Supplemental Fig. 11



Fleming, et al. Supplemental Fig. 12



Fleming, et al. Supplemental Fig. 13

A

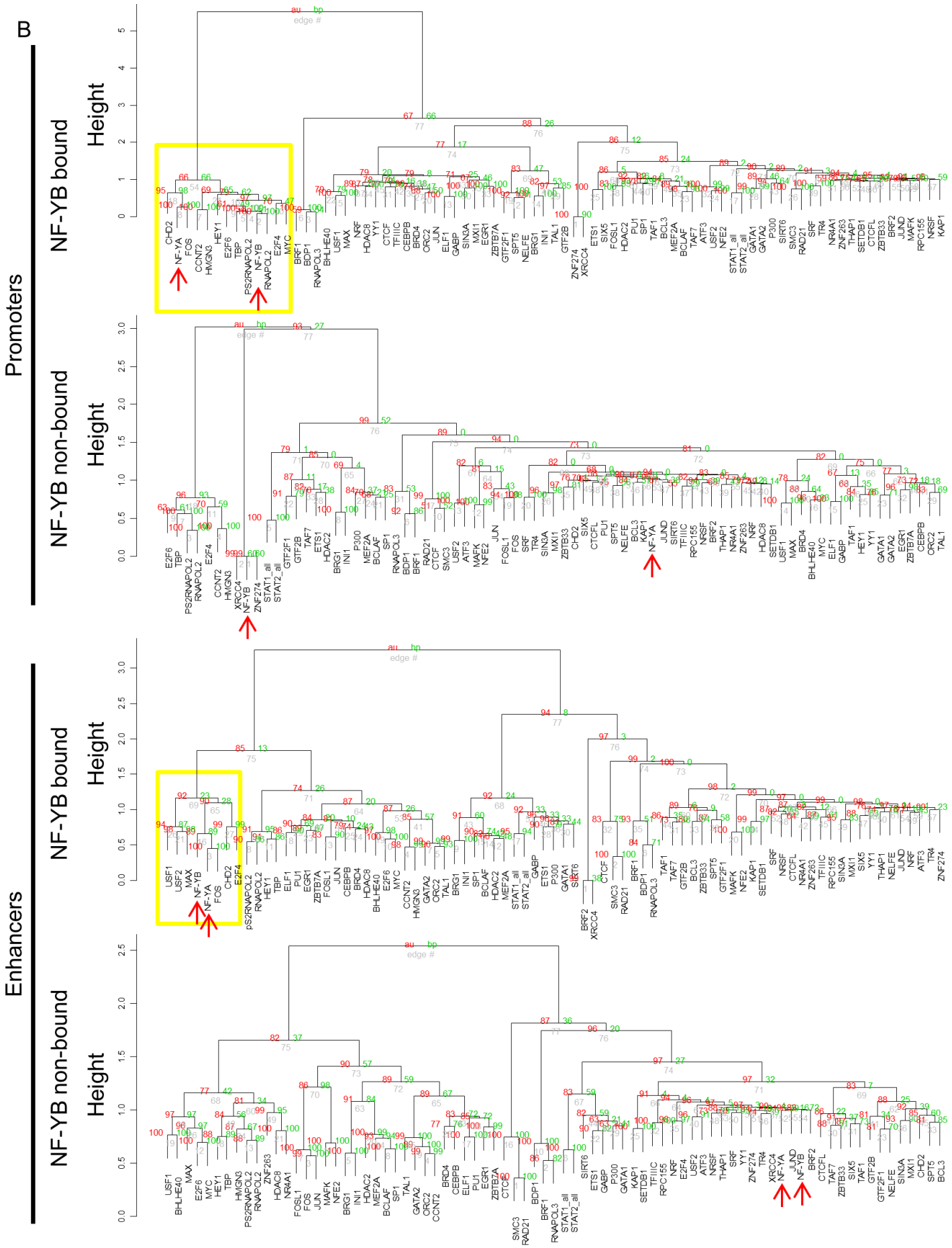
Promoters (strong)

Overlapping factor	Genomic peaks	Regions with factor	Expected overlap	Actual overlap	*P*-value
RNAPOL2	23,586	9,809	1,697	2,485	<1.0E-300
FOS	14,404	1,995	345	1,552	<1.0E-300
TBP	14,496	8,225	1,423	2,324	<1.0E-300
CHD2	6,932	2,752	476	1,181	8.7E-280
E2F4	9,862	6,058	1,048	1,875	4.0E-276
pS2RNAPOL2	29,410	8,782	1,520	2,304	1.1E-271
MYC	13,693	6,228	1,078	1,809	3.3E-215
E2F6	20,609	8,036	1,391	2,107	1.6E-212
HEY1	9,229	5,051	874	1,507	8.6E-170
HMGN3	18,815	7,180	1,242	1,810	6.2E-129
ORC2	15,401	3,231	559	1,037	2.0E-122
CCNT2	20,895	6,742	1,167	1,708	2.3E-117
ELF1	17,951	3,519	609	1,038	3.6E-95
GTF2B	2,475	1,501	260	569	1.8E-90
JUN	18,480	2,664	461	831	3.2E-85
MAX	6,402	2,160	374	709	2.2E-81
GABPA	5,025	2,450	424	750	4.3E-71
BHLHE40	16,358	3,568	617	986	6.6E-71
HDAC8	9,860	1,986	344	632	3.4E-65
USF1	21,313	1,631	282	546	1.1E-63
CEBPB	44,168	1,881	325	589	1.9E-57
YY1	5,250	2,658	460	722	6.6E-45
SIN3A	2,701	1,041	180	361	8.2E-45
NRF1	3,328	1,823	315	540	7.5E-44
MXI1	3,020	1,358	235	417	4.0E-37
USF2	1,623	455	79	184	2.7E-32
TFIIIC	10,004	1,964	340	504	1.3E-23
GTF2F1	885	385	67	147	8.5E-23
SP1	5,576	302	52	124	9.5E-23
TFIIF	10,662	4,857	840	1,056	3.4E-22
EGR1	19,094	1,914	331	478	1.1E-19
TAL1	24,841	1,194	207	323	2.2E-18
BRD4	10,746	3,318	574	747	3.0E-18
NELFE	1,136	322	56	120	7.0E-18
JUND	945	262	45	101	2.2E-16
CTCF	46,476	2,860	495	640	1.1E-14
ATF3	939	436	75	141	1.2E-14
SPT5	1,839	248	43	93	2.7E-14
THAP1	1,606	419	73	135	5.1E-14
SIX5	3,397	309	53	99	2.3E-10

Enhancers (all)

Overlapping factor	Genomic peaks	Regions with factor	Expected overlap	Actual overlap	*P*-value
FOS	14,404	5,969	76	1,246	<1.0E-300
E2F4	9,862	1,587	20	384	<1.0E-300
E2F6	20,609	6,617	85	619	<1.0E-300
RNAPOL2	23,586	5,706	73	587	<1.0E-300
TBP	14,496	3,494	45	471	<1.0E-300
USF1	21,313	6,384	82	869	<1.0E-300
USF2	1,623	517	7	242	<1.0E-300
HMGN3	18,815	4,655	59	503	2.5E-300
CCNT2	20,895	8,639	110	649	1.9E-297
CHD2	6,932	1,205	15	302	1.9E-290
MYC	13,693	4,985	64	478	2.5E-261
MAX	6,402	2,002	26	321	4.7E-243
ELF1	17,951	7,866	100	539	5.4E-225
pS2RNAPOL2	29,410	4,819	62	431	1.4E-222
ORC2	15,401	8,890	114	562	4.0E-218
HEY1	9,229	2,340	30	296	1.9E-193
BHLHE40	16,358	7,291	93	468	2.2E-182
JUN	18,480	10,399	133	526	6.6E-161
HDAC8	9,860	5,473	70	335	4.4E-123
SP1	5,576	2,228	28	204	9.0E-106
EGR1	19,094	8,427	108	386	3.4E-103
GATA2	9,025	5,876	75	314	6.2E-100
TAL1	24,841	15,864	203	545	2.2E-98
ZBTB7A	8,031	3,773	48	235	2.5E-87
SIX5	3,397	330	4	81	2.5E-77
GTF2B	2,475	452	6	88	2.1E-74
GABPA	5,025	1,212	15	128	6.3E-74
TFIIF	10,662	3,308	42	197	5.6E-70
BRD4	10,746	5,039	64	240	1.2E-66
CEBPB	44,168	11,470	146	387	2.0E-66
STAT2_30m	2,514	1,580	20	128	2.0E-60
HDAC2	8,831	4,700	60	219	3.4E-59
PU1	25,479	8,424	108	302	7.6E-57
NRF1	3,328	478	6	74	3.1E-55
GATA1	3,182	1,665	21	120	2.3E-51
FOSL1	11,393	6,742	86	246	1.7E-47
ATF3	939	78	1	35	4.6E-45
CTCF	46,476	6,031	77	224	1.8E-44
BRG1	11,209	5,363	68	196	5.0E-38
NFE2	3,477	2,213	28	118	1.1E-37
MEF2A	10,209	4,337	55	170	1.1E-36
ETS1	2,607	1,153	15	82	4.1E-35
BCLAF1	6,616	2,712	35	127	7.1E-35
MAFK	17,914	6,532	83	212	1.2E-33
MXI1	3,020	517	7	55	1.0E-32
YY1	5,250	791	10	66	1.4E-32
STAT2_6h	2,174	1,149	15	78	4.1E-32
TFIIIC	10,004	3,164	40	127	1.3E-28
NR4A1	5,514	1,685	22	85	6.6E-26
P300	2,969	1,038	13	63	1.2E-23
TAF7	4,536	1,237	16	65	4.5E-21
SIN3A	2,701	318	4	34	6.8E-21
JUND	945	256	3	31	8.8E-21
SIRT6	1,794	1,227	16	64	1.3E-20
GTF2F1	885	90	1	20	2.7E-19
SRF	2,005	666	9	39	9.9E-15
TAF1	4,126	573	7	36	1.3E-14
BCL3	3,924	492	6	32	1.4E-13

Fleming, et al. Supplemental Fig. 14

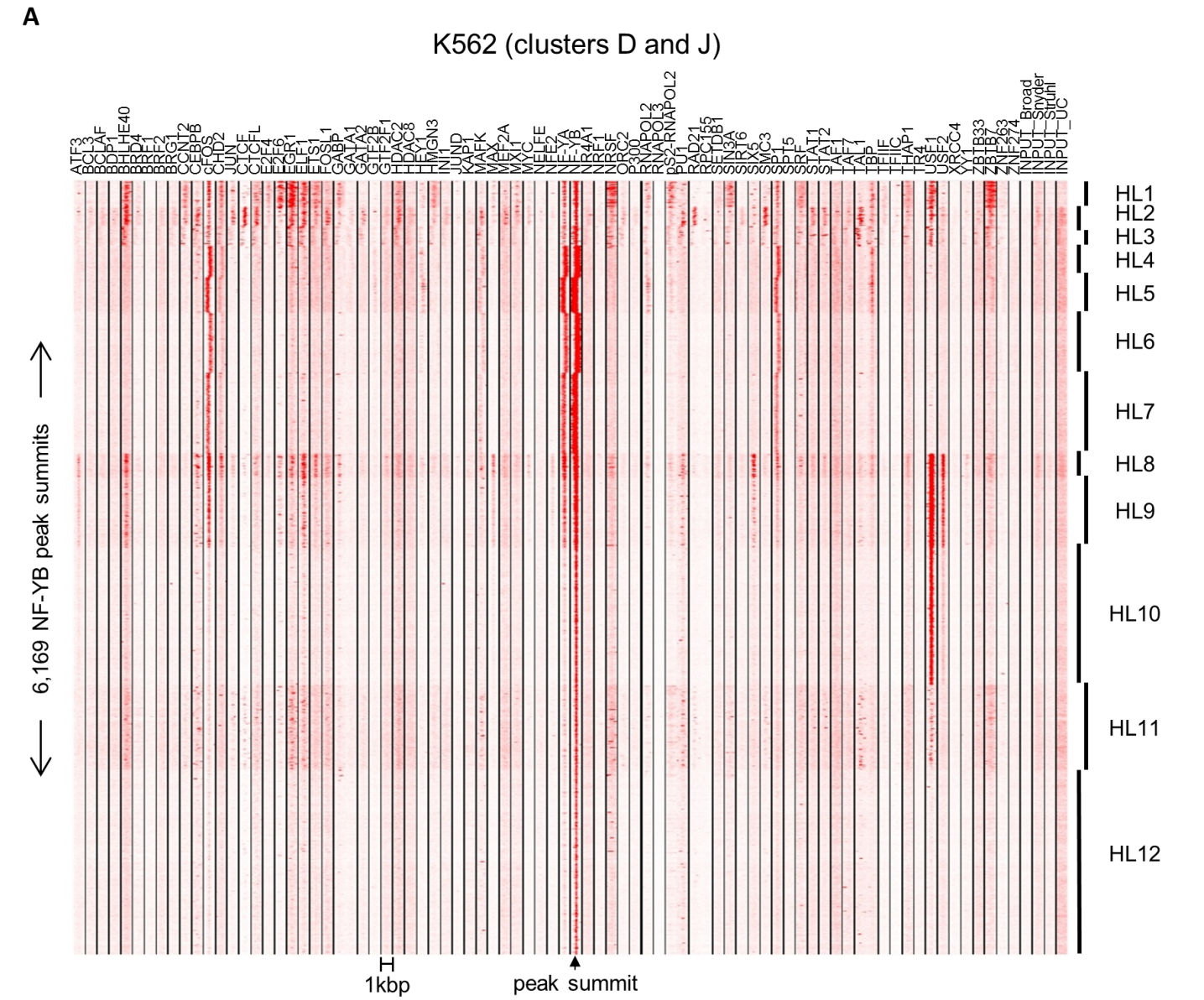


Fleming, et al. Supplemental Fig. 14

C

	NF-YB Bound Strong Promoters			NF-YB Non-Bound Strong Promoters			NF-YB Bound Enhancers			NF-YB Non-Bound Enhancers		
		#	%		#	%		#	%		#	%
1-way overlap	E2F6	2107	77.9	E2F6	1749	28.3	FOS	1246	39.0	TAL1	8379	11.7
	E2F4	1875	69.3	HMGN3	1638	26.5	USF1	869	27.2	CEBPB	6198	8.7
	HMGN3	1810	66.9	E2F4	944	15.3	E2F6	619	19.4	JUN	5639	7.9
	MYC	1809	66.9	MYC	866	14.0	ORC2	562	17.6	PU1	4654	6.5
	FOS	1552	57.4	HEY1	762	12.3	TAL1	545	17.1	EGR1	4633	6.5
	HEY1	1507	55.7	BRD4	717	11.6	ELF1	539	16.9	ORC2	4572	6.4
	CHD2	1181	43.7	BHLHE40	656	10.6	JUN	526	16.5	ELF1	4227	5.9
	ELF1	1038	38.4	CTCF	610	9.9	HMGN3	503	15.8	BHLHE40	3906	5.5
	ORC2	1037	38.4	YY1	540	8.7	MYC	478	15.0	CTCF	3844	5.4
	BHLHE40	986	36.5	ELF1	516	8.3	BHLHE40	468	14.7	FOSL1	3757	5.3
2-way overlap	E2F6-E2F4	1654	61.2	HMGN3-E2F6	1074	17.4	USF1-FOS	412	12.9	TAL1-ORC2	3166	4.4
	E2F6-MYC	1616	59.8	HMGN3-E2F4	746	12.1	TAL1-ORC2	346	10.8	FOSL1-JUN	2555	3.6
	HMGN3-E2F6	1578	58.4	E2F6-E2F4	715	11.6	JUN-FOS	339	10.6	TAL1-GATA2	2536	3.6
	HMGN3-E2F4	1489	55.1	E2F6-MYC	679	11.0	E2F6-FOS	307	9.6	JUN-FOS	2476	3.5
	E2F4-MYC	1443	53.4	HMGN3-MYC	596	9.6	ORC2-JUN	296	9.3	TAL1-CEBPB	2371	3.3
	HMGN3-MYC	1351	50.0	E2F6-BHLHE40	450	7.3	E2F6-MYC	291	9.1	ORC2-GATA2	2123	3.0
	HEY1-E2F6	1235	45.7	HMGN3-BRD4	442	7.1	HMGN3-FOS	280	8.8	ORC2-JUN	2078	2.9
	E2F6-FOS	1218	45.0	E2F4-MYC	431	7.0	TAL1-GATA2	275	8.6	TAL1-EGR1	1976	2.8
	HEY1-MYC	1144	42.3	HMGN3-BHLHE40	408	6.6	ORC2-FOS	269	8.4	TAL1-JUN	1945	2.7
	E2F4-FOS	1105	40.9	E2F6-BRD4	401	6.5	ORC2-GATA2	261	8.2	FOSL1-FOS	1824	2.6
3-way overlap	HMGN3-E2F6-E2F4	1353	50.0	HMGN3-E2F6-E2F4	590	9.5	TAL1-ORC2-GATA2	246	7.7	TAL1-ORC2-GATA2	1988	2.8
	E2F6-E2F4-MYC	1343	49.7	HMGN3-E2F6-MYC	512	8.3	ORC2-JUN-FOS	200	6.3	FOSL1-JUN-FOS	1790	2.5
	HMGN3-E2F6-MYC	1253	46.3	E2F6-E2F4-MYC	382	6.2	Usf2-USF1-FOS	189	5.9	TAL1-ORC2-JUN	1322	1.9
	HMGN3-E2F4-MYC	1193	44.1	HMGN3-E2F4-MYC	376	6.1	TAL1-ORC2-JUN	181	5.7	TAL1-ORC2-CEBPB	1255	1.8
	HEY1-E2F6-MYC	1020	37.7	HMGN3-E2F6-BHLHE40	339	5.5	TAL1-ORC2-MYC	173	5.4	TAL1-ORC2-HDAC2	1202	1.7
	HEY1-E2F6-E2F4	982	36.3	HMGN3-E2F6-BRD4	338	5.5	ORC2-MYC-JUN	169	5.3	TAL1-ORC2-BHLHE40	1173	1.6
	E2F6-E2F4-FOS	981	36.3	HMGN3-E2F4-BRD4	296	4.8	TAL1-ORC2-BHLHE40	164	5.1	TAL1-ORC2-EGR1	1168	1.6
	E2F6-MYC-FOS	941	34.8	E2F6-MYC-BHLHE40	272	4.4	ORC2-MYC-BHLHE40	159	5.0	TAL1-FOSL1-JUN	1144	1.6
	HEY1-E2F4-MYC	907	33.5	E2F6-E2F4-BRD4	261	4.2	ORC2-E2F6-MYC	159	5.0	TAL1-HDAC2-GATA2	1122	1.6
	HMGN3-E2F6-FOS	903	33.4	HMGN3-E2F4-BHLHE40	253	4.1	FOSL1-JUN-FOS	158	4.9	ORC2-JUN-FOS	1110	1.6
4-way overlap	HMGN3-E2F4-E2F6-MYC	1124	41.6	HMGN3-E2F6-E2F4-MYC	337	5.4	TAL1-ORC2-GATA2-MYC	138	4.3	TAL1-ORC2-HDAC2-GATA2	953	1.3
	HEY1-E2F4-E2F6-MYC	842	31.1	HMGN3-E2F6-E2F4-BRD4	246	4.0	TAL1-ORC2-GATA2-JUN	128	4.0	TAL1-ORC2-GATA2-CEBPB	898	1.3
	E2F6-MYC-E2F4-FOS	792	29.3	HMGN3-E2F6-E2F4-BHLHE40	224	3.6	TAL1-ORC2-GATA2-BHLHE40	124	3.9	TAL1-ORC2-GATA2-EGR1	863	1.2
	HMGN3-E2F4-E2F6-FOS	787	29.1	HMGN3-E2F6-MYC-BHLHE40	222	3.6	TAL1-ORC2-HMGN3-GATA2	122	3.8	TAL1-ORC2-GATA2-BHLHE40	840	1.2
	HMGN3-E2F6-HEY1-E2F4	769	28.4	HMGN3-E2F6-MYC-BRD4	208	3.4	TAL1-ORC2-HDAC2-GATA2	121	3.8	TAL1-ORC2-GATA2-JUN	836	1.2
	HMGN3-E2F6-HEY1-MYC	753	27.8	HMGN3-E2F4-MYC-BRD4	186	3.0	TAL1-ORC2-JUN-FOS	118	3.7	ORC2-FOSL1-JUN-FOS	826	1.2
	HMGN3-MYC-E2F6-FOS	722	26.7	E2F6-E2F4-MYC-BHLHE40	180	2.9	ORC2-MYC-JUN-FOS	117	3.7	TAL1-ORC2-GATA2-MYC	803	1.1
	HMGN3-E2F4-HEY1-MYC	721	26.7	HMGN3-E2F4-MYC-BHLHE40	176	2.8	TAL1-ORC2-GATA2-ELF1	117	3.7	TAL1-FOSL1-JUN-FOS	779	1.1
	E2F6-MYC-E2F4-CHD2	710	26.3	E2F6-MYC-E2F4-BRD4	172	2.8	Usf2-USF1-Max-FOS	116	3.6	TAL1-ORC2-FOSL1-JUN	763	1.1
	HMGN3-E2F4-E2F6-CHD2	699	25.9	HMGN3-HEY1-E2F6-MYC	138	2.2	ORC2-FOSL1-JUN-FOS	111	3.5	TAL1-ORC2-HMGN3-GATA2	761	1.1

Fleming, et al. Supplemental Fig. 14



Fleming, et al. Supplemental Fig. 15