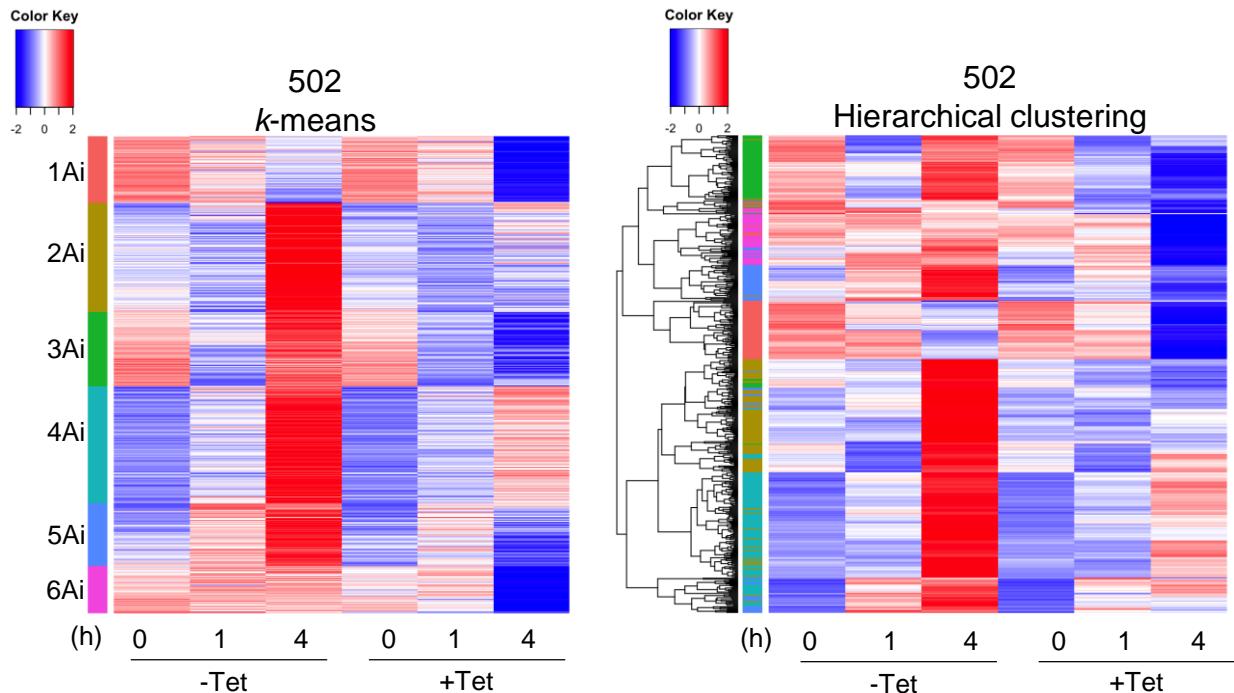


A

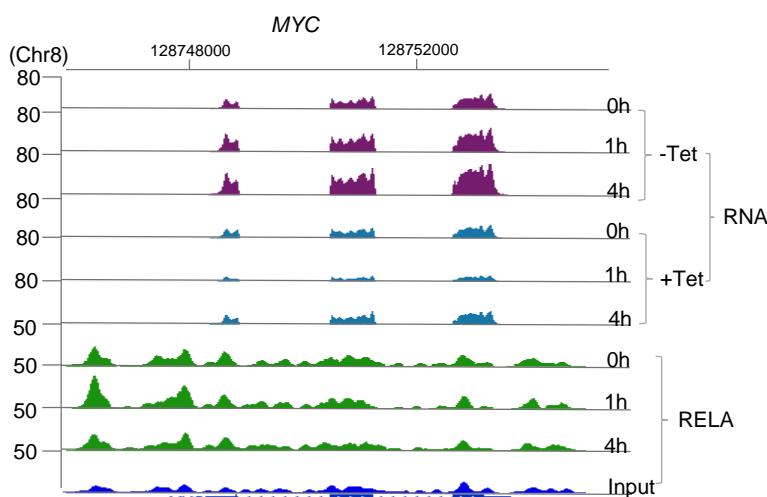


B

dnIkBa<sup>↓</sup>, no RELA binding(502)

Consensus sequence	P-value	Motif Name
	1e-11	c-Myc

C



D

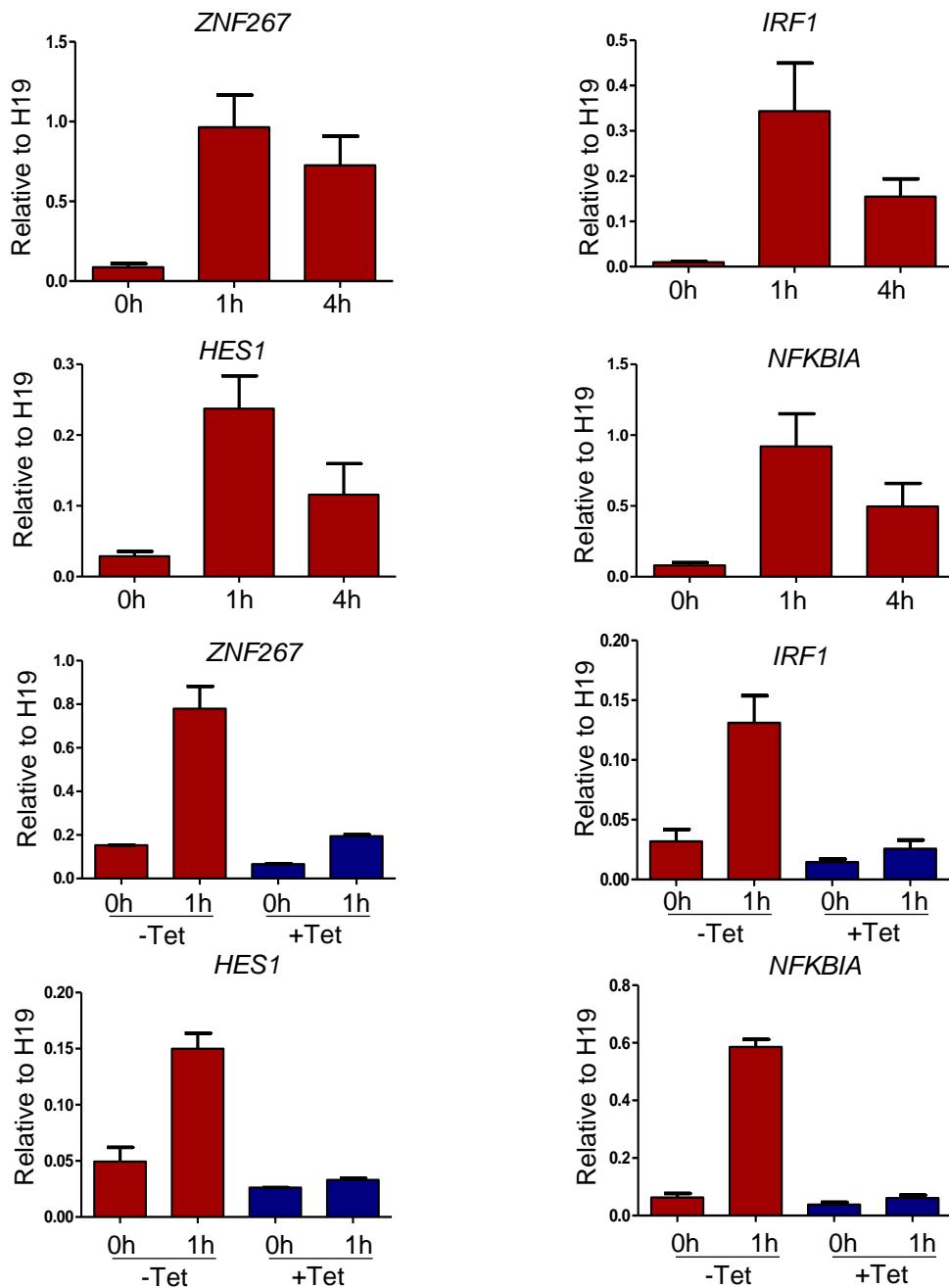
TF from 304

RUNX3	NCOA3	ELMSAN1	RELB
SPEN	SIN3A	STAT5A	BTG2
PRMT1	TP53	SNAPC4	NFKB1
STAT6	TAF4B	GPBP1	JUNB
TCF20	IRF1	GABPB1	KLF10
ZBTB2	ZBTB1	REL	HES1
DDN	POU2AF1	ZNF267	NFKBIZ
POU2F2	NR1D1	NFE2L2	
KDM2B	MYC	NFKB2	
ACTN4	UBTF	ZBTB10	

TF from 85

FOSB	BACH2	STAT3	MEF2C
FOS	BTG2	ZNF395	EGR1
NR4A3	DDIT3	ARID3A	SETX
NR4A1	IER2	MEF2B	AFF1
KLF6	RCOR1	TCF4	NCOA2
ZNF165	HBP1	TSC22D1	

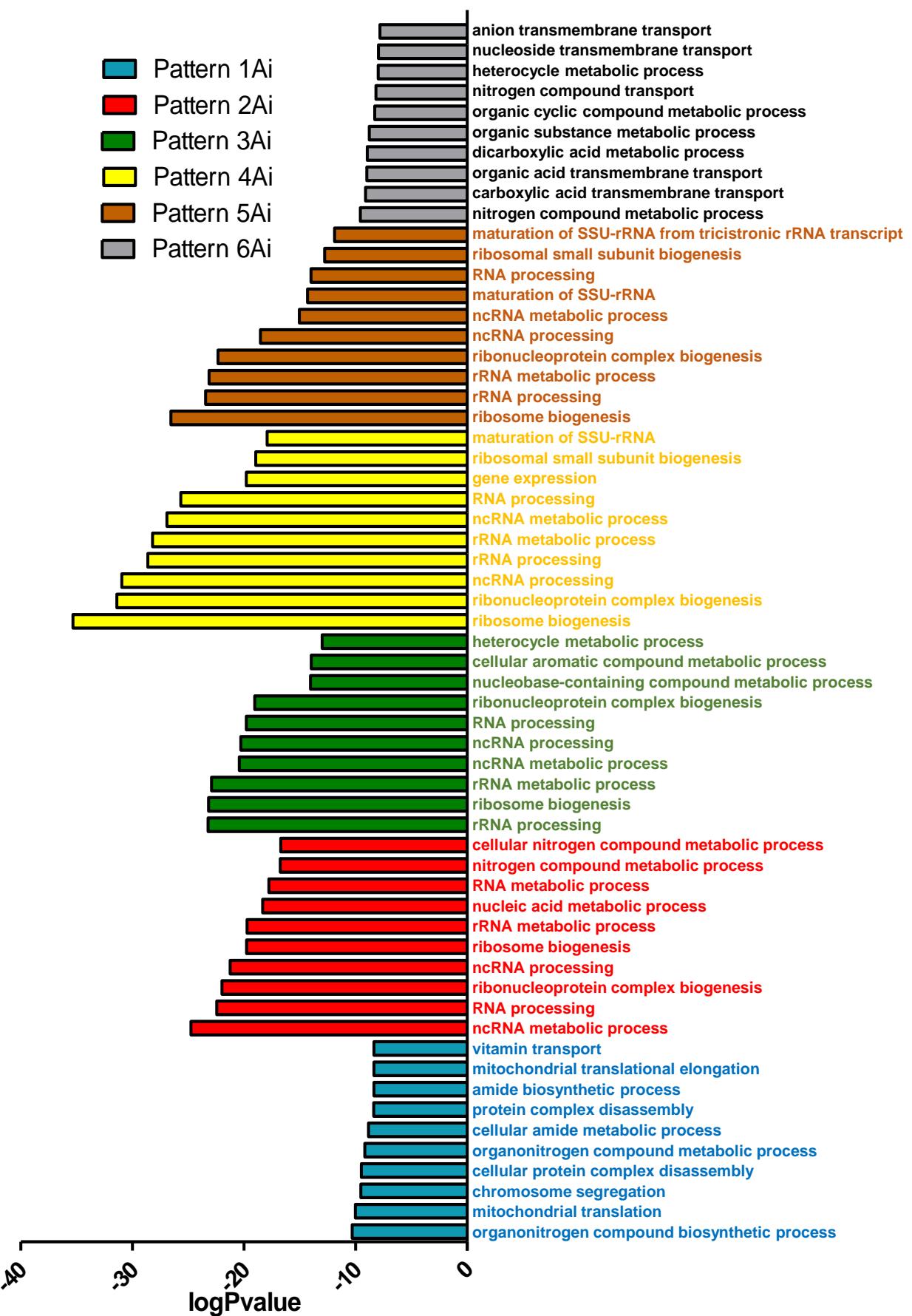
E

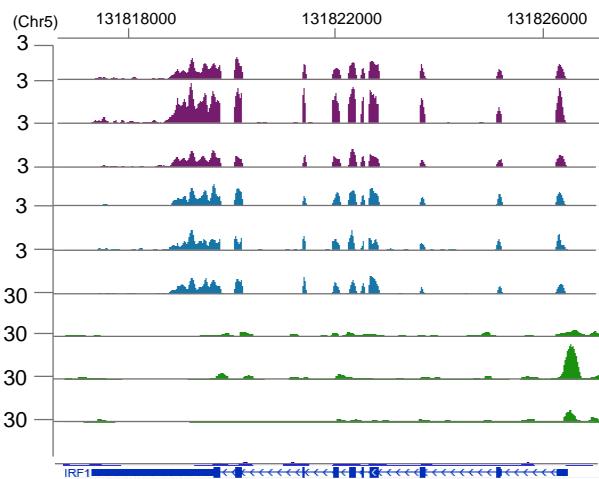
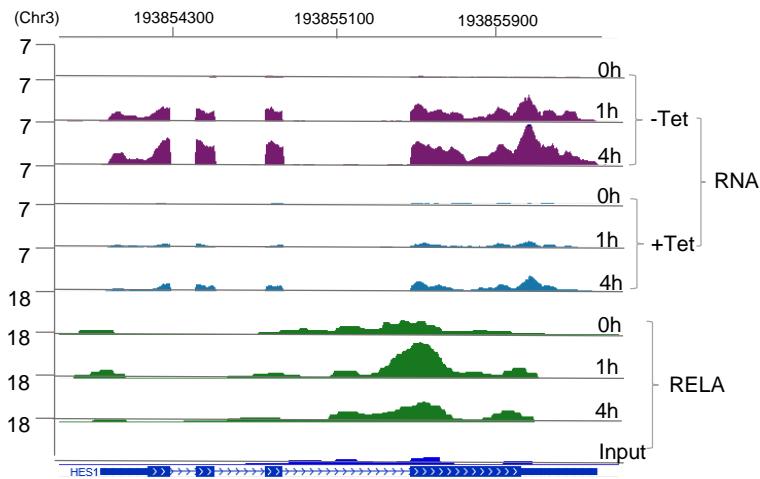
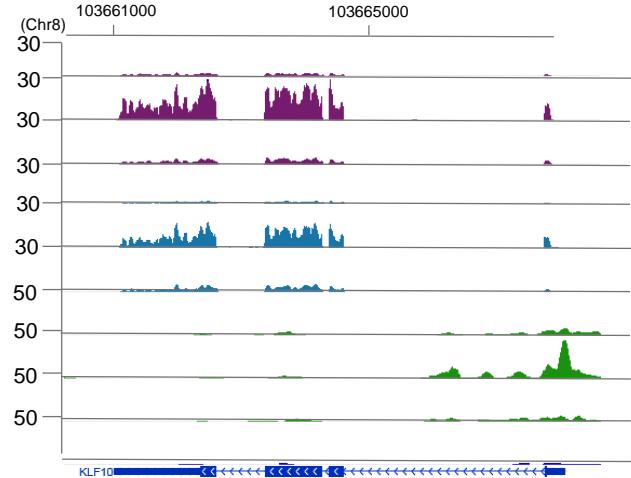


F

#### Motifs present in > 20% of promoters

Pitx1	Ptf1a	BMAL1	MITF	Isl1	n-Myc
KLF14	CRX	Nkx2.5	KLF3	Eomes	Arnt:Ahr
SCL	Erra	PU.1-IRF	Nkx3.1	c-Myc	ZFX
KLF5	Smad4	Nkx2.2	COUP-TFII	E2A	Elk4
AR-halfsite	Znf263	ETV1	Foxo1	Elk1	TATA-Box
THRb	Smad2	E2A	PR	AP-2gamma	KLF10
Smad3	NPAS	HIF-1b	ETS1	BMYB	Etv2
Maz	Egr1	E2F6	Meis1	AMYB	AP-2alpha
Nanog	Fli1	ERG	NF1-halfsite	Klf9	Ap4
Tgif2	ZNF416	Sp1	GABPA	E2F4	Rbpj1
Tbx5	Bapx1	ZNF467	Olig2	EHF	NPAS2
Tgif1	ZNF711	Ascl1	Nkx6.1	ELF1	GATA3
Nkx2.1	HEB	MYB	NFY	GSC	



**H***IRF1**HES1**KLF10**ZNF267*