Boros et al.: Supplementary Information

Supplementary figure and table legends

Figure legends:

Supplementary Fig 1. Elk-1 expression at the RNA and protein levels in Hela and EcR-293 (Elk-En) cell lines. Where indicated cells are treated with ponasterone A (PA) for 3 hours prior to harvesting. (A) Quantitative RT-PCR analysis of *ELK1* expression. Error bars represent standard deviation calculated from 5 biologically independent replicates and average of 2 samples. (B, C) Western blot (WB) analyses of Elk-1 expression in 10 μg total cell lysate. The identities of bands corresponding to Elk-1 and Elk-En are indicated. By comparing (B) and (C), it can be seen that Elk-En levels are similar to the levels of endogenous Elk-1 found in HeLa cells.

Supplementary Fig 2. Summary of the profiles represented by target genes in clusters 1- 8. The data are presented as the average expression value of genes in each cluster under each of the six experimental conditions. For each gene, the mean of the probesets across all six conditions was set as zero, and expression levels (log2) presented relative to this value. Red arrows highlight conditions under which the expression of Elk-En (+PonA) causes a major reduction in gene expression. Motif logos of the top three sequence motifs discovered by Weeder in the promoters of each cluster are shown to the right of the graphs. The closest matching TRANSFAC matrix for known transcription factor binding sites is shown to the right of the discovered motifs.

Supplementary Fig 3. Elk-1 fusion proteins function in a promoter-specific manner. Reporter gene assays in HEK293T cells with the indicated promoter-reporter constructs and either increasing concentrations of Elk-En (0, 0.5, 5 ng) (A) or Elk-VP16 (0, 5, 10, 50 ng) (B). The results were normalized to the expression of each construct in the absence of Elk-En (taken as 1)(A) or first normalized to renilla luciferase activity, and the activity in the absence of Elk-VP16 given the value of one (B). Error bars represent standard deviation calculated from triplicate samples. While *FOS*- and *SRE*-driven reporters are efficiently down and upregulated by Elk-En and Elk-VP16 as expected, none of the other promoters tested showed significant dose-dependent changes in activity.

Supplementary Fig 4. Cluster 3 genes show minimal inducibility by PMA. (A) Schematic illustration of activation of Elk-1 through phosphorylation by ERK MAP kinases following PMA treatment. (B) Western analysis of Elk-1 activation phosphorylation at Ser383 in serum starved, or at the indicated times following PMA treatment, HeLa (top panel) or SH-Sy5y cells (bottom panel). Total Elk-1 (bottom panel only) and phospho-ERK levels were also detected. (C) The levels of mRNA expression of the indicated genes in HeLa (black bars) or SH-Sy5y (grey bars) cells was analysed by qRT-PCR. Cells were serum starved for 24 h and then treated with PMA for indicated times (hrs). Error bars represent standard deviations calculated from two biologically independent replicates which are the average of 2 samples.
Transient and robust Elk-1 activation is seen in both cell types and is accompanied by transient high level activation of *c-FOS*. However, none of the cluster 3 genes examined show high levels of induction following PMA stimulation.

Supplementary Fig 5. Depletion of SAP-1 promotes enhanced promoter occupancy by Elk-1. qPCR-ChIP analysis of Elk-1 binding to the indicated promoters in HeLa cells. Where indicated, cells were transfected with siRNA against *SAP-1* or *GAPDH*. Samples from serum starved HeLa cells taken 48 hrs after transfection with the indicated siRNAs. ChIP was performed using antibodies against Elk-1. This data is equivalent to that in Fig. 4C, except that the fold increase in Elk-1 binding was calculated from individual experiments and then the average fold increase caused by SAP-1 depletion shown (relative to binding in the presence of control GAPDH duplexes, taken as 1). Error bars represent standard deviations calculated from two biologically independent replicates each being the average of duplicate samples.

Table legends:

Supplementary table 1. Details of all genes consistently downregulated by Elk-En in at least one of three experimental conditions (serum starved, 15 mins EGF and 30 mins EGF). The gene symbol, Refseq transcript and Entrez gene identifiers (columns A, B and D respectively) correspond to the Affymetrix probe set on the microarrays (column C). Columns E, F and G indicate genes that have also been associated with transcription factor binding events for Elk-1, SRF and GABPα respectively. The remaining columns show the expression value of each gene. Columns H to M show the relative expression of the groups of probesets representing each gene. Columns N to P represent the same data but show fold change in response due to PonA treatment. The list is divided into 8 groups according to the hierarchical clustering performed on columns H to M.

Supplementary table 2. Enrichment of functionally linked gene categories in combined clusters 3, 4, 5 and 8. Gene ontology analysis of cluster genes. Gene ontology terms ("molecular function" levels 3 and 5, plus "biological function" level 5) were analysed to identify categories containing a significant proportion of gene symbols associated with the combined genes from clusters 3, 4, 5 and 8. Categories are shown that contain at least 5 genes from a gene cluster and exceed the uncorrected significance threshold of P=0.001.

Supplementary table 3. Enrichment of functionally linked gene categories in individual clusters 3, 4, 5 and 8. Gene ontology analysis was performed as in supplementary Table 2, except that each cluster was analysed individually rather than in combination.

Note that clusters 1, 2, 6 and 7 do not have significant GO terms (matching our criteria of at least 5 matching genes and P<0.001) despite the similar sizes of some of these clusters, although cluster 7 has a significant KEGG pathway (antigen processing and presentation; 7 genes; P=7.67E-5).

Supplementary table 4. Summary of genes identified as commonly downregulated in response to Elk-En expression and as Elk-1 targets by ChIP-chip analysis (Boros et al., unpublished). Genes are presented in groups according to the cluster assigned due to their response to Elk-En expression. The total numbers of probesets (expression values) and corresponding gene symbols within each cluster are indicated. For example, of the 87 gene symbols associated with cluster 3 genes, these represent only 77 unique events as two probe sets could not distinguish between several possible

related genes. One of the "overlapping" promoters bound by Elk-1 was assigned to one of two potential different genes associated with the same expression values. The percentage of genes in each cluster also bound by Elk-1 in ChIP-chip analysis is indicated with respect to total expression values or gene symbols. The significance of the overlap (with respect to expression values) was calculated by comparing 1000 random sets of genes (each corresponding to the number of genes found in each cluster) with the Elk-1 target list, the corresponding Z-scores are indicated. Genes highlighted in bold were not identified as also bound by GABPα in ChIP-Seq analysis (Supplementary Table 5; 30).

Supplementary table 5. Over-representation of Elk-1 binding motifs in promoters of Elk-En regulated gene clusters. The frequency of occurrence of Elk-1 motifs (represented by different sequence motifs in column 1), in repeat masked sequences in the promoters of the genes in each cluster, compared to the occurrence of the same motifs in a background data set comprised of 300 randomly selected promoters. Motifs represent parts of the 10 bp motif expected for Elk-1 from *in vitro* selection experiments (14), and discovered as the most over-represented decamer motif amongst ChIP-identified Elk-1 candidates (Boros et al., unpublished). The percentage of promoters in each cluster containing at least one of the 6 or 8 bp motifs is shown. In the case of the 8 bp motifs, the percentage of non-redundant promoters containing at least one such motif is shown. A Fisher's Exact chi-square test for 2x2 contingency tables was used to assess whether the frequency of occurrence of a particular motif found in the promoter sequences in each cluster was significantly enriched compared to the background sets of 300 sequences. All non-degenerate hexamer, and octamer motifs are enriched in the cluster 3 promoter dataset compared to the control dataset

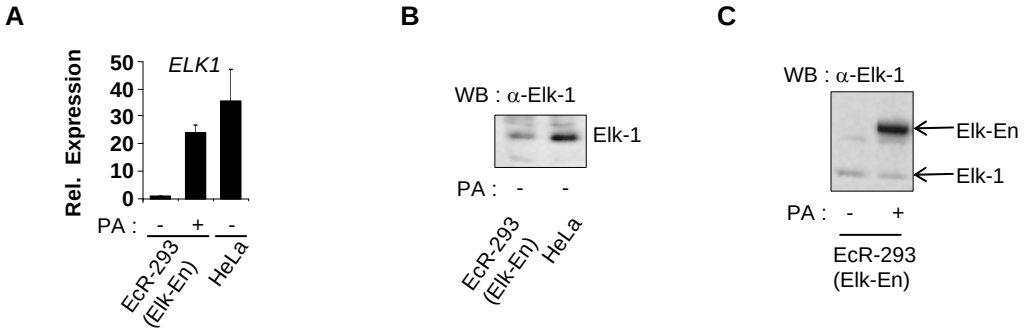
analysed, indicating that these motifs represent Elk-1-specific DNA binding. Clusters 4, 5 and 8 also show over-representation of Elk-1 binding motifs.

Supplementary table 6. Summary of genes identified as downregulated in response to Elk-En expression and as SRF targets by both ChIP-chip (Boros et al., 2009) and ChIP-Seq analysis (30). A total of 160 genes were identified as SRF targets in both studies. Genes are presented in groups according to the cluster assigned due to their response to Elk-En expression. Genes indicated in bold also are identified as direct Elk-1 targets in the Elk-1 ChIP-chip analysis (Boros et al., unpublished). The total numbers of probesets (expression values) and corresponding gene symbols within each cluster are indicated. The percentage of genes in each cluster also bound by SRF in both ChIP-chip and ChIP-Seq analysis is indicated with respect to total expression values or gene symbols. The significance of the overlap (with respect to expression values) was calculated by comparing 1000 random sets of genes (corresponding to the number of genes found in each cluster) with the SRF target list; the corresponding Z-scores are indicated.

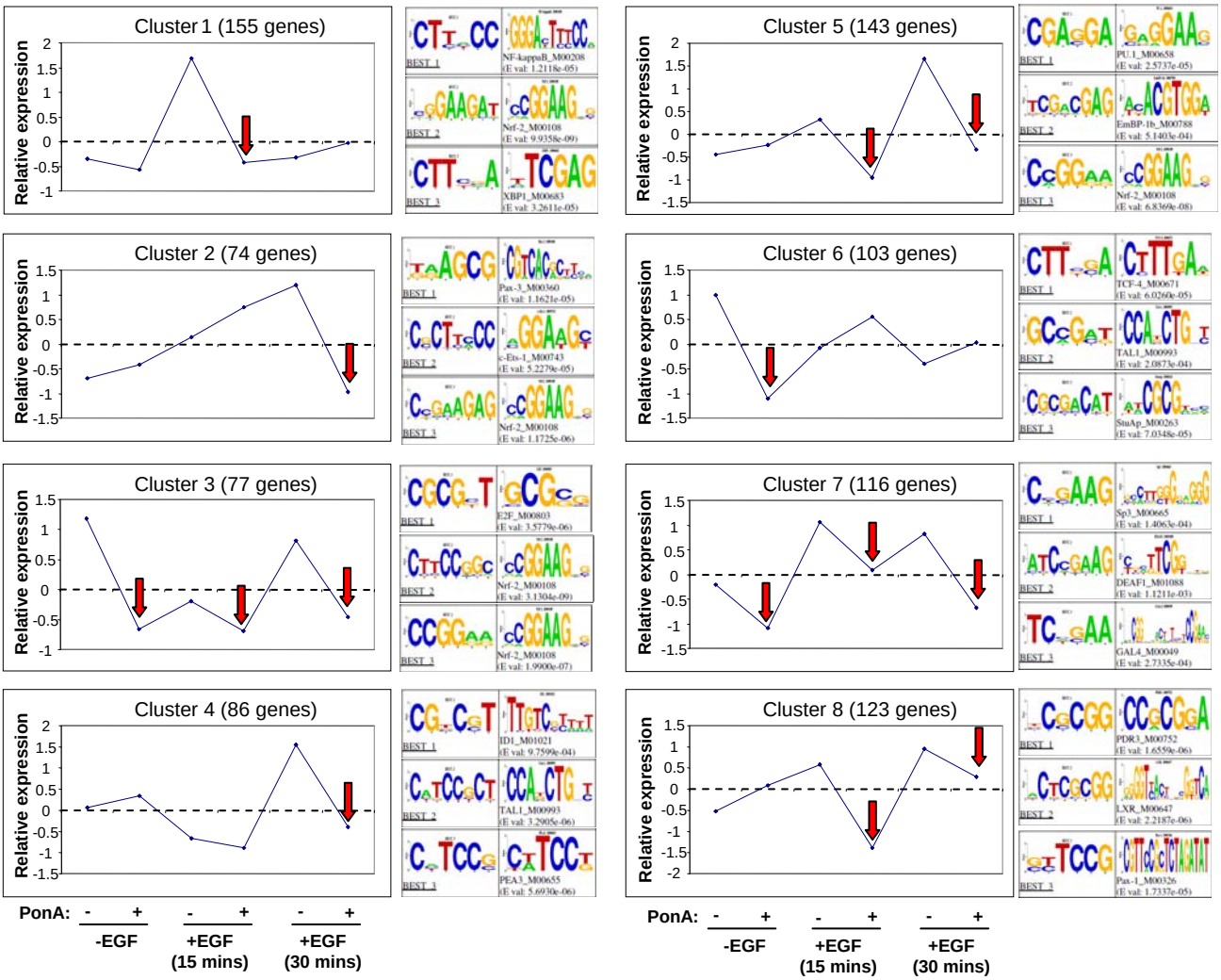
Supplementary table 7. Summary of genes identified as downregulated in response to Elk-En expression and as GABPα targets by ChIP-Seq analysis (30). Genes are presented in groups according to the cluster assigned due to their response to Elk-En expression. The total numbers of probesets (expression values) and corresponding gene symbols within each cluster are indicated. In several cases, several potential different genes from the expression analysis can be associated with the same expression values, and thus only one gene was selected for detecting overlapping binding by GABPα and Elk-1. The percentage of genes in each cluster also bound by

GABPα in ChIP-Seq analysis is indicated with respect to total expression values or gene symbols. The significance of the overlap (with respect to expression values) was calculated by comparing 1000 random sets of genes (corresponding to the number of genes found in each cluster) with the GABPα target list; the corresponding Z-scores are indicated. Genes highlighted in bold were also identified as also bound by Elk-1 in ChIP-chip analysis (Boros et al., unpublished) or by qPCR (this study).

Supplementary table 8. Primers used for ChIP q-PCR analysis. The genomic coordinates of each primer and the size of the resulting amplicon are given.

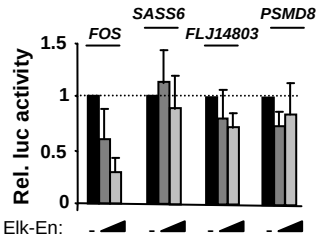


Boros et al. Supplementary Fig. 1



Boros et al. Supplementary Fig. 2

A



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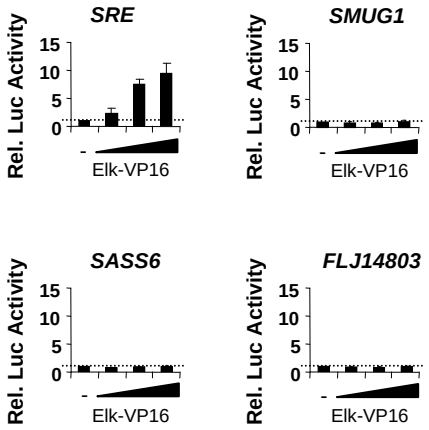
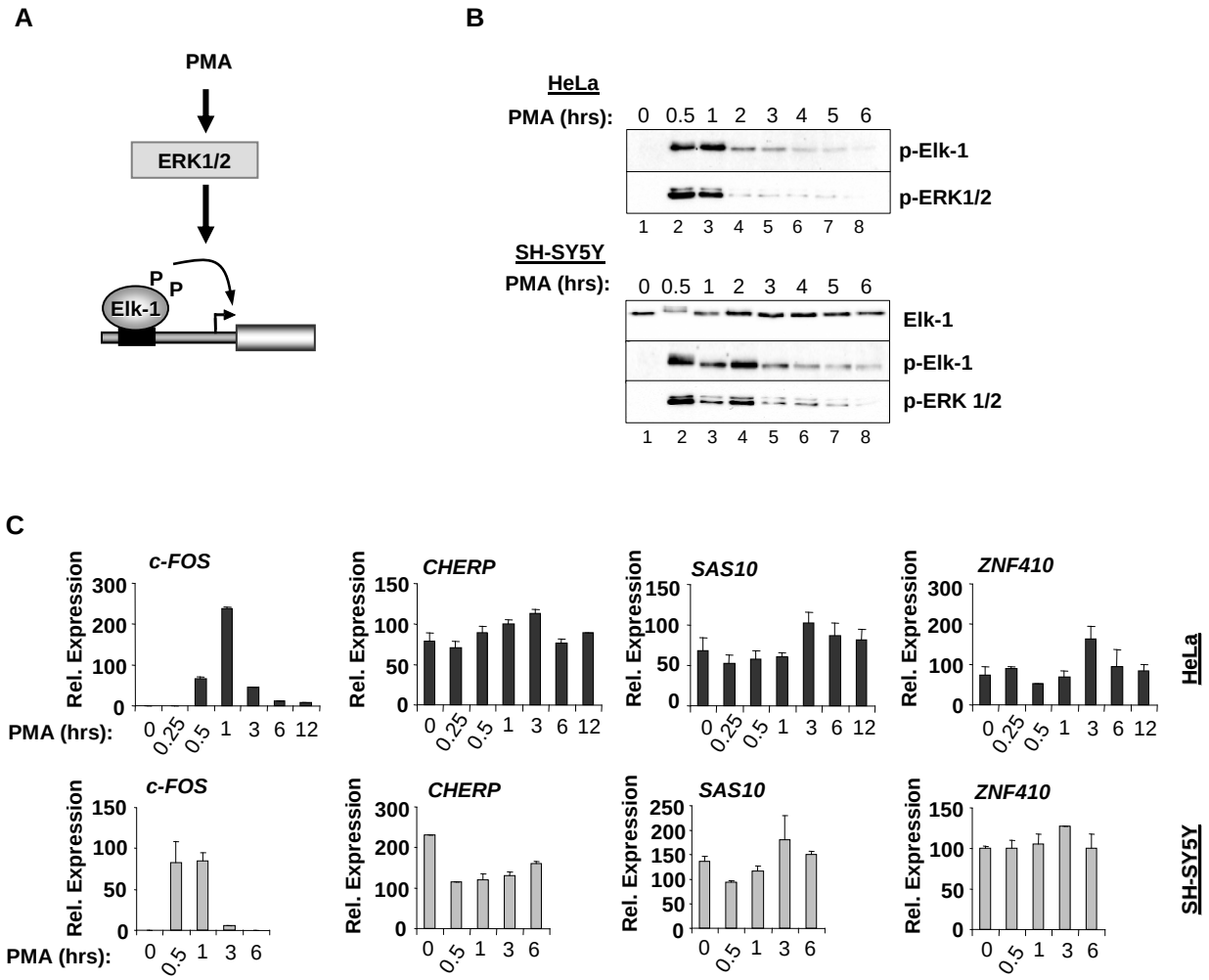
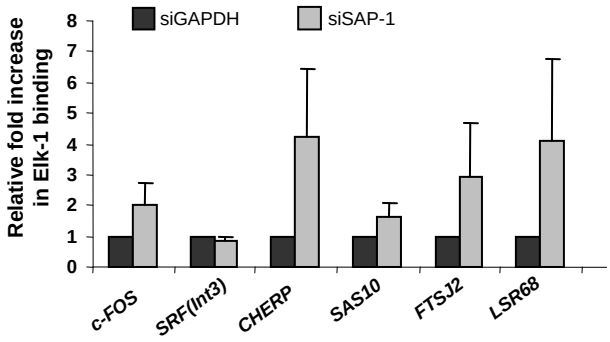


Boros et al. Supplementary Fig. 3



Boros et al. Supplementary Fig. 4



Boros et al. Supplementary Fig. 5

Supplementary Table 2: Enrichment of functionally linked gene categories in combined clusters 3, 4, 5 and 8.

Gene Pathway / Gene Ontology category	P-value
GO - Biological Process - level 3	
Cellular biosynthetic process (GO:0044249)	2.35E-06
Biopolymer metabolic process (GO:0043283)	8.55E-06
Intracellular transport (GO:0046907)	1.17E-05
Regulation of programmed cell death (GO:0043067)	2.58E-05
Organelle organization and biogenesis (GO:0006996)	2.68E-05
Nucleobase/'side/'tide and nucleic acid metabolic process (GO:0006139)	5.71E-05
Cell death (GO:0008219)	1.42E-04
Establishment of cellular localization (GO:0051649)	2.10E-04
Alcohol metabolic process (GO:0006066)	3.47E-04
Cellular localization (GO:0051641)	3.67E-04
RNA splicing (GO:0008380)	4.48E-04
GO - Biological Process - level 5	
RNA processing (GO:0006396)	2.77E-06
Intracellular transport (GO:0046907)	4.25E-05
Regulation of programmed cell death (GO:0043067)	7.88E-05
Regulation of apoptosis(GO:0042981)	1.52E-04
Apoptosis (GO:0006915)	2.85E-04
Cell death (GO:0008219)	4.72E-04
Nucleoside triphosphate biosynthetic process (GO:0009142)	6.31E-04
GO - Molecular Function - level 3	
RNA binding (GO:0003723)	3.31E-09
Ribonucleotide binding (GO:0032553)	1.60E-05
Purine nucleotide binding (GO:0017076)	3.71E-05
Hydrolase activity, acting on acid anhydrides (GO:0016817)	3.64E-04

Supplementary Table 3: Enrichment of functionally linked gene categories in individual clusters 3, 4, 5 and 8.

Gene Pathway / Gene Ontology category	P-value
GO - Biological Process - level 3	
- Cluster 3	
Biopolymer metabolic process (GO:0043283)	2.16E-05
Nucleobase/'side/'tide and nucleic acid metabolic process (GO:0006139)	2.50E-04
Transcription, DNA-dependent (GO:0006351)	9.06E-04
- Cluster 4	
Intracellular transport (GO:0046907)	8.65E-04
- Cluster 5	
Cellular biosynthetic process (GO:0044249)	2.75E-05
Macromolecule catabolic process (GO:0009057)	7.22E-04
Macromolecule biosynthetic process (GO:0009059)	7.52E-04
GO - Biological Process - level 5	
- Cluster 3	
RNA processing (GO:0006396)	3.31E-04
- Cluster 4	
Microtubule-based movement (GO:0007018)	2.78E-05
Cytoskeleton-dependent intracellular transport (GO:0030705)	6.70E-05
Protein polymerization (GO:0051258)	4.11E-04
- Cluster 5	
Hexose metabolic process (GO:0019318)	4.90E-04
Monosaccharide metabolic process (GO:0005996)	5.86E-04
Monosaccharide catabolic process (GO:0046365)	7.11E-04
Translation (GO:0006412)	8.12E-04
- Cluster 8	
Nucleoside triphosphate biosynthetic process (GO:0009142)	1.30E-05
Purine nucleotide biosynthetic process (GO:0006164)	5.09E-05
Ribonucleotide biosynthetic process (GO:0009260)	5.09E-05
GO - Molecular Function - level 3	
- Cluster 4	
Hydrolase activity, acting on acid anhydrides (GO:0016817)	4.42E-05
Purine nucleotide binding (GO:0017076)	1.70E-04
Ribonucleotide binding (GO:0032553)	2.57E-04
- Cluster 5	
RNA binding (GO:0003723)	1.81E-06

Supplementary Table 4: Overlap between Elk-1 ChIP-chip data and Elk-En regulated gene clusters

Cluster	1	2	3	4	5	6	7	8
Expression values	155	74	77	86	143	103	116	123
Gene symbols (NR)	187	89	87	96	153	113	131	129
Gene symbols present in Elk1 ChIP-chip FDR<10 set	***C21orf7***	*CHD1*	*BCL10*	*ATP6V1A*	*BAT3*	*C11orf61*	***ANKRD55***	*ANKRD40*
	CDKAL1	*FAM63A*	*C10orf97*	*BAT1*	***EGR2***	*FPGT*	*CCDC52*	***DBR1***
	CHRNA9	***LRRC50***	***C14orf43***	*CCNT1*	*HSPC152*	***NUCKS1***	*GCS1*	*ECH1*
	HIST1H2AG	*NR2C2*	*CAP1*	*CCT2*	*IER2*	*PAK1IP1*	*TAF12*	*LIG1*
	HIST1H4H	*THAP9*	*LRRC41*	*GNB2L1*	*LCMT2*	***PCDHGA1***	*ZNF557*	*NME1*
	HIST1H4I		*MCL1*	*MAP3K7*	*M6PR*	*WDR55*		*NME1-NME2*
	HIST1H4K		***MYC***	*MED6*	*MAGED2*			*PTRH2*
	OTC		***PJA1***	*YBX1*	*NCAPD2*			***RALY***
	PCDHGA1		*PRKAB1*		*PFN1*			*RPS14*
	SNAPC5		***PTER***		*PPP1R11*			*SAP30BP*
	ST7L		*PXMP3*		*PPP2R1A*			*SLC25A11*
	SYTL2		***RBL2***		*RBBP5*			*TAF1A*
	TRAPPC2		*RBM3*		*RPL29*			***WDR67***
			SEC24A		*SNRPB*			*YIPF3*
			THG1L		*TPX2*			*ZNHIT1*
					TTC31			
					YIPF5			
% of expression values	8.4	6.8	19.5	9.3	11.9	5.8	4.3	12.2
Z-score	1.0	0.1	4.9	1.1	2.8	-0.3	-0.9	2.5
% of gene symbols	7.0	5.6	17.2	8.3	11.1	5.3	3.8	11.6
Z-score	0.3	-0.3	4.2	0.8	2.3	-0.5	-1.3	2.4

Supplementary Table 5: Motifs within Elk-En regulated gene cluster promoters

	Cluster 1 (n=130)		Cluster 2 (n=69)		Cluster 3 (n=52)		Cluster 4 (n=53)		Cluster 5 (n=96)		Cluster 6 (n=88)		Cluster 7 (n=90)		Cluster 8 (n=94)		Random (n=300)
Motif	% occ.	P-value	% occ.	P-value	% occ.	P-value	% occ.	P-value	% occ.	P-value	% occ.	P-value	% occ.	P-value	% occ.	P-value	% occ.
CCGGAA	37.7	NS	40.6	NS	78.8	**<0.0001**	60.4	**0.0365**	72.9	**<0.0001**	51.1	NS	51.1	NS	68.1	**0.0013**	44.3
CGGAAG	41.5	NS	47.8	NS	84.6	**<0.0001**	69.8	**0.0027**	77.1	**<0.0001**	52.3	NS	56.7	NS	70.2	**<0.0001**	47.0
GGAAGT	65.4	NS	63.8	NS	78.8	**0.0394**	60.4	NS	69.8	NS	67.0	NS	57.8	NS	68.1	NS	64.0
CCGGAW	51.5	NS	56.5	NS	90.4	**<0.0001**	73.6	**0.023**	80.2	**<0.0001**	62.5	NS	58.9	NS	75.5	**0.001**	56.7
CGGAWG	52.3	NS	58.0	NS	88.5	**<0.0001**	86.8	**0.0002**	85.4	**<0.0001**	56.8	NS	67.8	NS	78.7	**0.0013**	60.7
GGAWGT	82.3	NS	78.3	NS	84.6	NS	84.9	NS	82.3	NS	79.5	NS	75.6	NS	80.9	NS	81.0
AACCGGAA	0.8	NS	2.9	NS	9.6	**0.0023**	5.7	**0.046**	5.2	**0.0227**	3.4	NS	3.3	NS	8.5	**0.0007**	1.0
ACCGGAAG	3.1	NS	5.8	NS	15.4	**0.0111**	11.3	NS	12.5	**0.0181**	0.0	**0.028**	7.8	NS	11.7	**0.031**	5.0
CCGGAAGT	5.4	NS	11.6	NS	25.0	**0.0036**	20.8	**0.0288**	24.0	**0.0007**	10.2	NS	10.0	NS	27.7	**<0.0001**	9.3
Total 8mers	8.5	NS	14.5	NS	34.6	**<0.0001**	32.1	**0.0002**	33.3	**<0.0001**	10.2	NS	16.7	NS	33.0	**<0.0001**	10.7
$CC(W)_6GG$	10.8	NS	8.7	NS	5.8	NS	7.5	NS	5.2	NS	11.4	NS	4.4	NS	5.3	NS	7.3
$CC[(W)_5N]GG$	36.9	NS	36.2	NS	36.5	NS	37.7	NS	35.4	NS	40.9	NS	31.1	NS	37.2	NS	36.0

Supplementary Table 6: Overlap between SRF ChIP-chip/ChIP-Seq data and Elk-En regulated gene clusters

	1	2	3	4	5	6	7	8
Expression values	155	74	77	86	143	103	116	123
Gene symbols (NR)	187	89	87	96	153	113	131	129
Gene symbols present in SRF ChIP-chip FDR<10 and ChIP-seq sets			***BCL10*** ***C14orf43*** ***MCL1*** ***PTER***	*TPM4*	***EGR2*** *LAG3* *MLF2* ***PFN1*** ***PPP1R11*** ***RBBP5*** ***YIPF5***		*OPA3*	***ECH1*** *RAB5B* ***SLC25A11***
% of expression values	0	0	5.2	1.2	4.9	0	0.9	2.4
Z-score	-1.1	-0.8	4.4	0.3	5.5	-0.9	0	1.9
% of gene symbols	0	0	4.6	1.0	4.6	0	0.8	2.3
Z-score	-1.3	-0.9	3.7	0.2	5.0	-1.0	-0.1	1.8

Supplementary Table7: Overlap between GABPα ChIP-Seq data and Elk-En regulated gene clusters

Cluster	1	2	3	4	5	6	7	8
Expression values	155	74	77	86	143	103	116	123
Gene symbols (NR)	187	89	87	96	153	113	131	129
Gene symbols present in GABPα ChIP-Seq dataset	*AKAP10* *APOF* *C17orf62* *CEP135* *CSAD* *DDX25* *FBXL8* ***HIST1H2AG*** ***HIST1H4H*** ***HIST1H4I*** *IFT140* *MAP2K1* *MBTD1* *MLLT1* *POLM* *POU2F1* *RQCD1* ***SNAPC5*** ***ST7L*** *TLN1* ***TRAPPC2*** *UCKL1* *VAPA* *ZNF225* *ZNF271*	*ACN9* *AHDC1* *C4orf18* *C4orf30* ***CHD1*** *CORO1A* *DFFA* *FAM108A1* ***FAM63A*** *FLJ11151* *HTF9C* *IQCE* ***NR2C2*** *PSENEN* *SLC17A5* *ST8SIA4* *STK16* ***THAP9*** *VCPIP1*	*ACBD3* *AKTIP* ***BCL10*** ***C10orf97*** *C14orf104* *C7orf49* ***CAP1*** *CBLL1* *CCDC47* *CDKN2AIP* ***CHERP*** *DAZAP1* *DNAJB1* *DPP8* *DR1* *FAM48A* *FAM8A1* ***FTSJ2*** *KBTBD2* *KCTD5* *KIAA0495* *KIN* ***LRRC41*** ***MCL1*** ***MOAP1*** *MORC3* *NIP7* *OBFC2B* *POLI* ***PRKAB1*** ***PXMP3*** *RAP2C* ***RBM3*** *RNF25* *RRS1* ***SEC24A*** *SFRS10* *SLC25A16* *SMCR7L* *STIP1* *TCEB3* *TFB2M* ***THG1L*** *TMF1* *UTP14A* *YRDC* *YWHAB* *ZNF12* *ZNF294* *ZNF417* *ZNF430* *ZNF587*	*ACOX1* ***ATP6V1A*** ***BAT1*** *C12orf10* *C20orf30* ***CCNT1*** ***CCT2*** *COG8* *CSNK2A1* *CSNK2B* *DPM2* *EIF2S3* ***GNB2L1*** *HARS* ***MAP3K7*** *MCM4* ***MED6*** *NCBP1* *PCBP2* *PDF* *PGK1* *POLE3* *PPIB* *PWP2* *RUVBL2* *SULT1A3* *SULT1A4* *TM9SF1* *TMED2* *TMEM147* *TUBB2C* *TYK2* *VCP* ***YBX1*** *ZDHHC4* *ZFYVE21* *ZNF7*	*ABCF1* *ACTB* *ALDOA* *AP2M1* *ARHGDIA* *BAP1* ***BAT3*** *BCAP31* *BCAT2* *C10orf88* *C12orf44* *CDC37* *CINP* *CLN8* *COG7* *COPE* *CSTF2* *DAXX* *DDOST* *DDX56* *DEAF1* *EEF2* *ENO1* *ERGIC3* *G6PD* *GAPDH* *GTF3C5* ***HSPC152*** ***IER2*** ***LCMT2*** *LIMK2* ***M6PR*** *MAD2L1BP* ***MAGED2*** *MAPKAP1* *MCM5* *MCM7* *MLF2* ***NCAPD2*** *NOL12* *NONO* *NSUN5* *NUDT6* *P4HB* *PCBP1* ***PFN1*** *PLD3* *PMPCA* *POLR2J* *POLR2J2* *POLR2J3* *PPP1CA* ***PPP1R11*** ***PPP2R1A*** *PRCC* *PRMT1* *PRPF8* *PSMC3* ***RBBP5*** *RFC2* *RPL18A* ***RPL29*** *RPL8* *RPS2* *RPS5* *SDF4* *SEC61A1* ***SNRPB*** *SRM* *SRPR* *TMEM115* ***TPX2*** *TRIB3* *TRIOBP* ***TTC31*** *TUFM* *UBE2G2* *UBE2M* *USP11* *XRCC3* ***YIPF5*** *ZRSR2*	*ANTXR1* *ATP11B* *BMI1* ***C11orf61*** *C16orf59* *E2F8* ***FPGT*** *GTF2H2* *KCNC4* *KCTD9* *LOC730394* *METTL2A* *METTL2B* *METTL5* *MRPS31* *NEK11* ***PAK1IP1*** *RAMP3* *RECQL* *RFX1* *SCLY* *SCNN1D* *SHQ1* *SP1* *SSB* *TRIM16* *VILL* ***WDR55***	*BFAR* ***CCDC52*** *CENPB* *DNAI1* *EDC4* *EMILIN1* *EXOSC4* ***GCS1*** *GDAP1* *GMDS* *GPAA1* *ISG20L2* *KLHL18* *MAP3K11* *MRPS18C* *NT5C* *OPA3* *PDAP1* *PSMB10* *SEC22B* *SIRT7* *SPTBN2* ***TAF12*** *YKT6* *ZNF44* ***ZNF557***	*AHSA1* ***ANKRD40*** *AP2S1* *ATP6V0B* *BUD31* *C11orf48* *C17orf81* *C1orf86* *CCDC44* *CCT7* *CIB1* *CLPP* *COMMD4* *COMT* *DHX30* *DNAJB14* *DPM3* *DTYMK* ***ECH1*** *ENO1* *EXOC3* *FAM96B* *GPX1* *GUK1* *IPO4* *ITPKB* *JOSD1* ***LIG1*** *MAD1L1* *MAGED1* *MAPBPIP* *MRPL12* *MRPL23* *NDUFA13* *NDUFS8* *NDUFV1* ***NME1*** ***NME1-NME2*** *NME3* *PFKP* *PMM2* *PPAN* *PRKCZ* *PRPF31* ***PTRH2*** *RAB5B* *RCOR1* *RPL18* ***RPS14*** *SAMSN1* ***SAP30BP*** *SCAND1* ***SLC25A11*** *SPINT2* *STUB1* ***TAF1A*** *TIMM13* *TRAPPC4* *TRIM28* *UQCR* *VGLL4* *WDR45* ***YIPF3*** ***ZNHIT1***
% of expression values	16.1	25.7	67.5	43.0	57.3	27.2	22.4	52.0
Z-score	-3.2	-0.4	7.9	3.2	7.9	0.1	-1.1	6.1
% of gene symbols	13.4	21.3	59.8	38.5	53.6	24.8	19.8	49.6
Z-score	-4.2	-1.3	7.0	2.5	7.4	-0.6	-2.0	5.5

Supplementary Table 8: Primers used for ChIP q-PCR analysis

NAME	ADS#		SEQUENCE	REGION AMPLIFIED (Mar. 2006 (hg18) assembly)	PCR PRODUCT SIZE
ChIP_*MCL1*	ADS 1861 ADS 1862	FORWARD PRIMER REVERSE PRIMER	AGTCCCCAACTATGCCCTCT CTCTGTGCTTCCCTGAGACC	chr1:148819047-148819234	188bp
ChIP_*c-FOS*	ADS 4055 ADS 4056	FORWARD PRIMER REVERSE PRIMER	GAGCAGTTCCCGTCAATCC GCATTTCGCAGTTCCTGTCT	chr14:74814930-74815094	165bp
ChIP_*CHERP*	ADS 1589 ADS 1590	FORWARD PRIMER REVERSE PRIMER	CCCGGTCTCGACTAACACC GAAACTCCGGAAGTGAGAGC	chr19:16514334-16514512	179bp
ChIP_*SAS10*	ADS 1601 ADS 1602	FORWARD PRIMER REVERSE PRIMER	CGTTTCCACACGGAAAGATT GCAGACTCCTGATCGGCTAC	chr4:71772947-71773133	187bp
ChIP_*ZNF410*	ADS 1591 ADS 1592	FORWARD PRIMER REVERSE PRIMER	GAAGGCCGAGAGTGAGTGAG ACAGGAAGTTTGGCTGACCC	chr14:73423082-73423274	193bp
ChIP_*FTSJ2*	ADS 1593 ADS 1594	FORWARD PRIMER REVERSE PRIMER	CGCTCTCCTTGTCTCTCTCC ATTCCAGGAGTCGTGGTGAC	chr7:2248439-2248626	188bp
ChIP_*INT3 SRF*	ADS 1273 ADS 1274	FORWARD PRIMER REVERSE PRIMER	GCCACAGGGCAGTAGATGTT TCAGGCCCAAGTATCCACTC	chr6:43251941-43252121	181bp
ChIP_*LSR68*	ADS 1599 ADS 1600	FORWARD PRIMER REVERSE PRIMER	AACATTTCGTCACCGTCTCC GGAAGGCGTCCTTAAACCTC	chr14:73296828-73297012	185bp
ChIP_*MOAP1*	ADS 1603 ADS 1604	FORWARD PRIMER REVERSE PRIMER	CCGGATCTCACCTTCCTGT GGATTCCACCTGTTTTGGTC	chr14:92720957-92721141	185bp