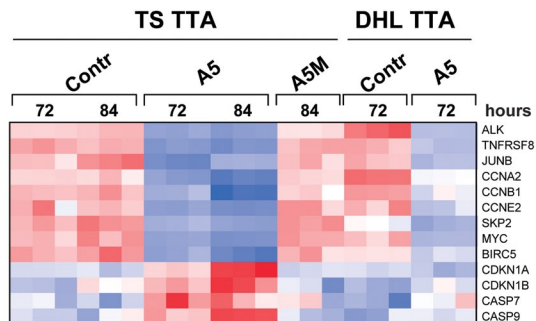
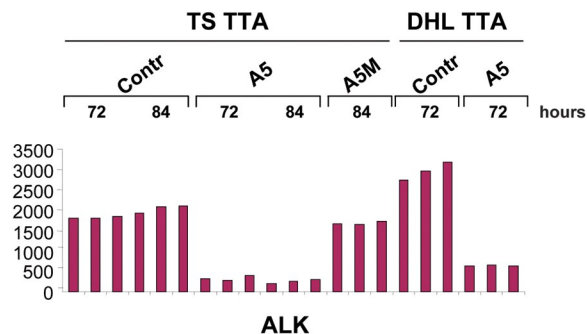
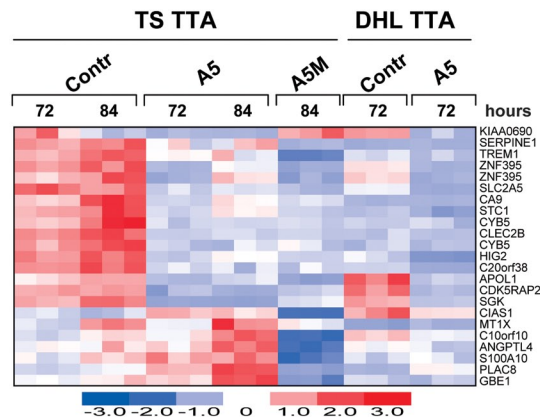
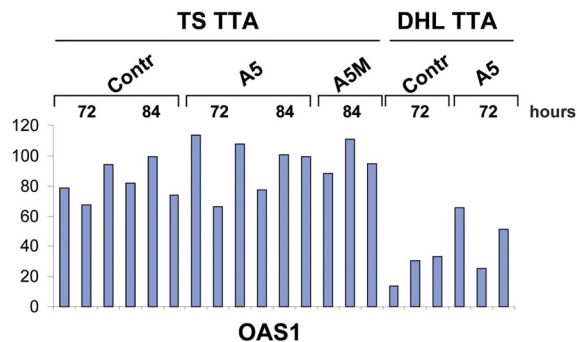


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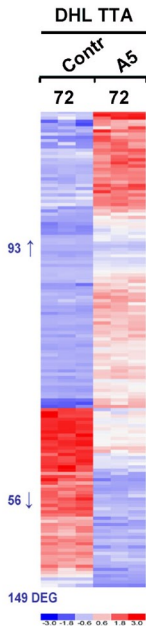


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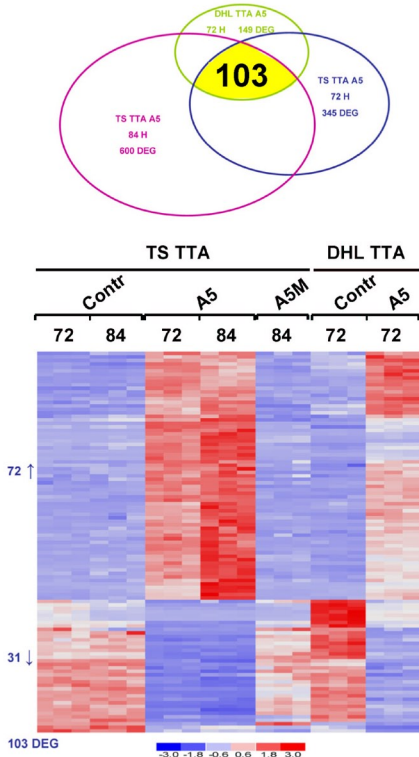


Suppl. 2

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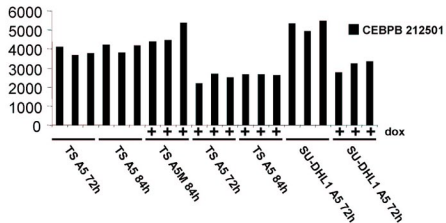


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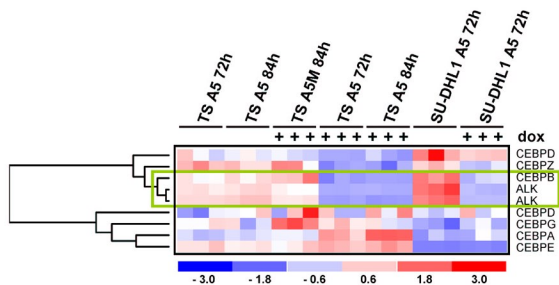


Suppl. 3

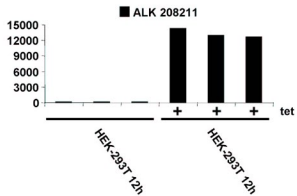
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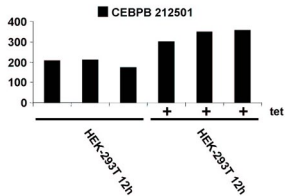
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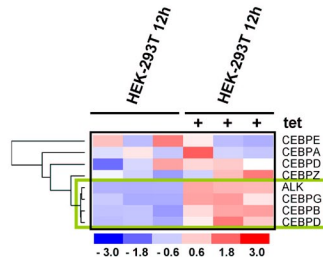
C



D



E



Probe Set ID	RefSeq Transcript ID	Gene Title	Gene Symbol	FC ALK shRNA	FC ALK inhibitors
205980_s_at	NM_001017526 /// NM_181334 /// NM_181335	Rho GTPase activating protein 8 /// PRR5- ARHGAP8 fusion	ARHGAP8 /// LOC553158	-68.5	-5.5
204456_s_at	NM_002048	growth arrest-specific 1	GAS1	-62.1	-33.6
201739_at	NM_005627	serum/glucocorticoid regulated kinase	SGK	-44.9	-4.2
214637_at	NM_020530	oncostatin M	OSM	-12.1	-29.5
204457_s_at	NM_002048	growth arrest-specific 1	GAS1	-7.6	-8.1
211269_s_at	NM_000417	interleukin 2 receptor, alpha	IL2RA	-7.5	-3.8
209325_s_at	NM_002928	regulator of G-protein signalling 16	RGS16	-7.1	-10.5
210439_at	NM_012092	inducible T-cell co-stimulator	ICOS	-6.7	-11.0
205518_s_at	NR_002174	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase)	CMAH	-5.1	-3.1
205476_at	NM_004591	chemokine (C-C motif) ligand 20	CCL20	-5.0	-159.0
220081_x_at	NM_016371	hydroxysteroid (17-beta) dehydrogenase 7	HSD17B7	-4.1	-3.6
202431_s_at	NM_002467	v-myc myelocytomatosis viral oncogene homolog (avian)	MYC	-4.1	-164.7
214794_at	NM_006191	proliferation-associated 2G4, 38kDa	PA2G4	-4.0	-3.4
208676_s_at	NM_006191	proliferation-associated 2G4, 38kDa	PA2G4	-3.9	-3.3
206729_at	NM_001243 /// NM_152942	tumor necrosis factor receptor superfamily, member 8	TNFRSF8	-3.8	-9.8
219471_at	NM_025113	chromosome 13 open reading frame 18	C13orf18	-3.6	-2.9
203498_at	NM_005822	Down syndrome critical region gene 1-like 1	DSCR1L1	-3.5	-4.6
220358_at	NM_018664	Jun dimerization protein p21SNFT	SNFT	-3.4	-5.7
218708_at	NM_013248	NTF2-like export factor 1	NXT1	-3.2	-3.2
220688_s_at	NM_016183	chromosome 1 open reading frame 33	C1orf33	-3.1	-5.7
205681_at	NM_004049	BCL2-related protein A1	BCL2A1	-3.1	-8.2
217850_at	NM_014366 /// NM_206825 /// NM_206826	guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	-3.0	-3.2
205227_at	NM_002182 /// NM_134470	interleukin 1 receptor accessory protein	IL1RAP	-3.0	-3.7
212942_s_at	NM_018689	KIAA1199	KIAA1199	-2.9	-25.9
213113_s_at	NM_014096 /// NM_017611 /// NM_199329	solute carrier family 43, member 3	SLC43A3	-2.7	-3.5
219117_s_at	NM_016594	FK506 binding protein 11, 19 kDa	FKBP11	-2.6	-2.4
205249_at	NM_000399	early growth response 2 (Krox-20 homolog, Drosophila)	EGR2	-2.6	-7.4
218336_at	NM_012394	prefoldin subunit 2	PFDN2	-2.4	-2.4
201479_at	NM_001363	dyskeratosis congenita 1, dyskerin	DKC1	-2.4	-2.6
214141_x_at	NM_001031684	splicing factor, arginine/serine-rich 7, 35kDa	SFRS7	-2.3	-2.7
201105_at	NM_002305	lectin, galactoside-binding, soluble, 1 (galectin 1)	LGALS1	2.5	1.9
214290_s_at	NM_001040874 /// NM_003516 /// XM_928387	histone 2, H2aa /// similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615) /// histone H2A/r	HIST2H2AA /// LOC653610 /// H2A/R	2.5	3.3
219014_at	NM_016619	placenta-specific 8	PLAC8	2.7	2.6
208611_s_at	NM_003127	spectrin, alpha, non-erythrocytic 1 (alpha- fodrin)	SPTAN1	3.1	3.3
201651_s_at	NM_007229	protein kinase C and casein kinase substrate in neurons 2	PACSIN2	3.4	3.1
217122_s_at	NM_182838	solute carrier family 35, member E2	SLC35E2	4.9	4.0
202039_at	NM_004740 /// NM_078471 /// NM_203318	TGFB1-induced anti-apoptotic factor 1 /// myosin XVIIIa	TIAF1 /// MYO18A	5.3	3.6
212099_at	NM_004040	ras homolog gene family, member B	RHOB	5.5	3.8
209118_s_at	NM_006009	tubulin, alpha 3	TUBA3	6.1	2.3
214925_s_at	NM_003127	spectrin, alpha, non-erythrocytic 1 (alpha- fodrin)	SPTAN1	6.4	8.5
211986_at	NM_001620 /// NM_024060	AHNAK nucleoprotein (desmoyokin)	AHNAK	6.6	3.2
201010_s_at	NM_006472	thioredoxin interacting protein	TXNIP	7.6	12.9
209684_at	NM_018993	Ras and Rab interactor 2	RIN2	7.6	4.6
205447_s_at	NM_006301	mitogen-activated protein kinase kinase kinase 12	MAP3K12	8.0	8.2
201008_s_at	NM_006472	thioredoxin interacting protein	TXNIP	8.0	23.2
201009_s_at	NM_006472	thioredoxin interacting protein	TXNIP	8.5	17.9
218537_at	NM_001002017 /// NM_001002018 /// NM_017885	host cell factor C1 regulator 1 (XPO1 dependent)	HCFC1R1	8.7	15.0

Figure S1. Specificity of NPM-ALK knock-down by inducible shRNA. (A) ALK transcripts are significantly down-modulated after shRNA induction. *ALK* mRNA expression levels of TS-TTA-A5, TS-TTA-A5M, and Su-DHL1 cells (21 samples) are shown as assessed by microarray analysis. (B) Eisen plot of the expression of the selected genes as assessed by microarray analysis. (C) *OAS1* gene transcripts do not correlated with shRNA induction. Gene expression quantification of the classic interferon target gene *OAS1* as assessed by microarray analysis. (D) The genes specifically expressed in TS-TTA-A5M cells represent a minimum subset. Eisen plot of the expression of the genes uniquely modulated after DOX treatment of TTA-A5M cells (84 hours).

Figure S2. Validation of the NPM-ALK signature in Su-DHL1 cells. (A) ALK signature in SuDHL-1 cells. Identification of genes specifically expressed in Su-DHL1-TTA-A5 cells untreated *versus* treated with DOX (72 hours) by supervised analysis (3 *versus* 3). (B) Eisen plot of the expression values of the 103 common transcripts (72 increased and 31 decreased genes), which overlap after the comparison of the gene lists identified by the supervised analysis related to either to ALK silencing in Su-DHL-1-TTA-A5 or TS-TTA-A5 cells.

Figure S3. ALK signaling regulates the expression of C/EBP β in lymphoid and non-lymphoid cells. (A) C/EBP β expression is down-regulated after ALK silencing. In the histogram C/EBP β mRNA expression levels (21 samples) are represented as assessed by microarray analysis. (B) The expression of C/EBP β among the CEBP family members correlates the most with that of ALK. The expression of C/EBP family genes was evaluated in all experimental conditions (21 samples) for absolute correlation with ALK. The *CEBPB* gene clustered within the branch including the ALK probe set (green rectangle). (C) ALK expression is upregulated after tetracycline induction in HEK-293T NPM-ALK Tet-On cells. In the histogram ALK mRNA expression levels (6 samples) are represented as assessed by microarray analysis. (D) CEBPB expression is concomitantly upregulated after tetracycline

induction in HEK-293T NPM-ALK Tet-On cells. In the histogram CEBPB mRNA expression levels (6 samples) are represented as assessed by microarray analysis. (E) CEBPG//B/D expressions are most closely related to ALK expression in non-lymphoid cells. Expression of CEBP family genes evaluated in different experimental conditions (6 samples) for absolute correlation with ALK. The C/EBPG/B/G genes clustered within the branch including the ALK probe set (green rectangle).

Table S1. Common transcripts concordantly modulated across shRNA- and ALK inhibitor-treated TS-TTA-A5 cells. FC: Fold Change