Expanded View Figures

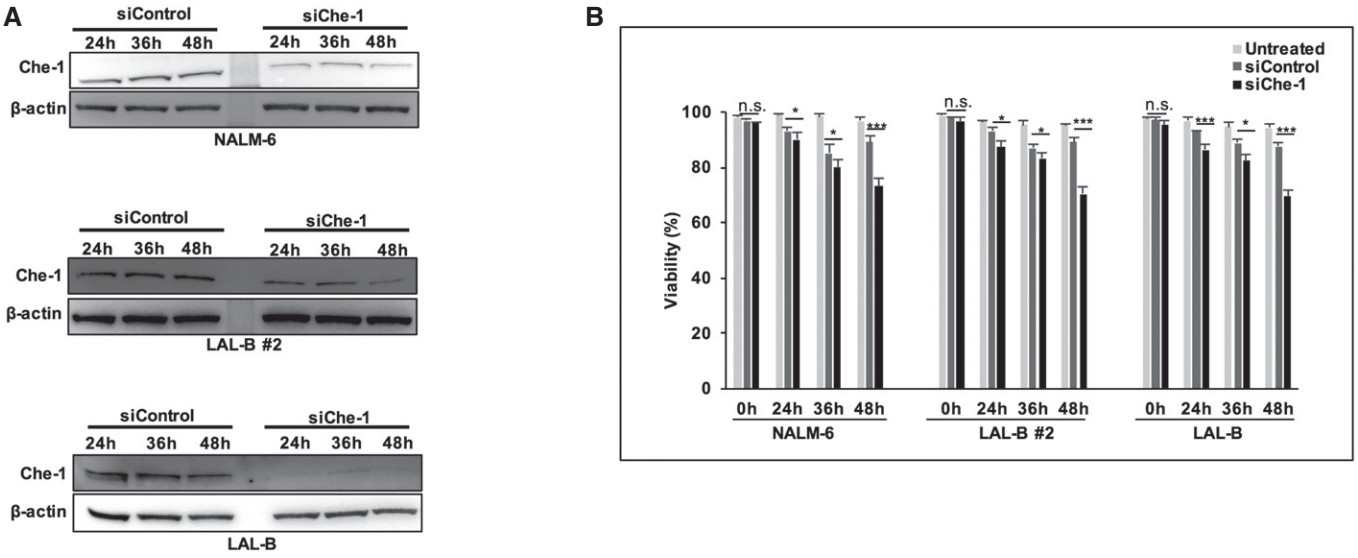


Figure EV1. Che-1 silencing slightly affects cell viability.
Related to Fig 1.

A WB analysis of Che-1 silencing performed 24, 36, and 48 h postnucleoporation in NALM-6, LAL-B, and LAL-B #2 cell lines.

B Viability assay performed in NALM-6, LAL-B, and LAL-B #2 cell lines treated as in (A). Data are presented as the means and standard deviation (SD) from three independent experiments. *$P \leq 0.05$; ***$P \leq 0.001$ by Student's *t*-test.

Source data are available online for this figure.

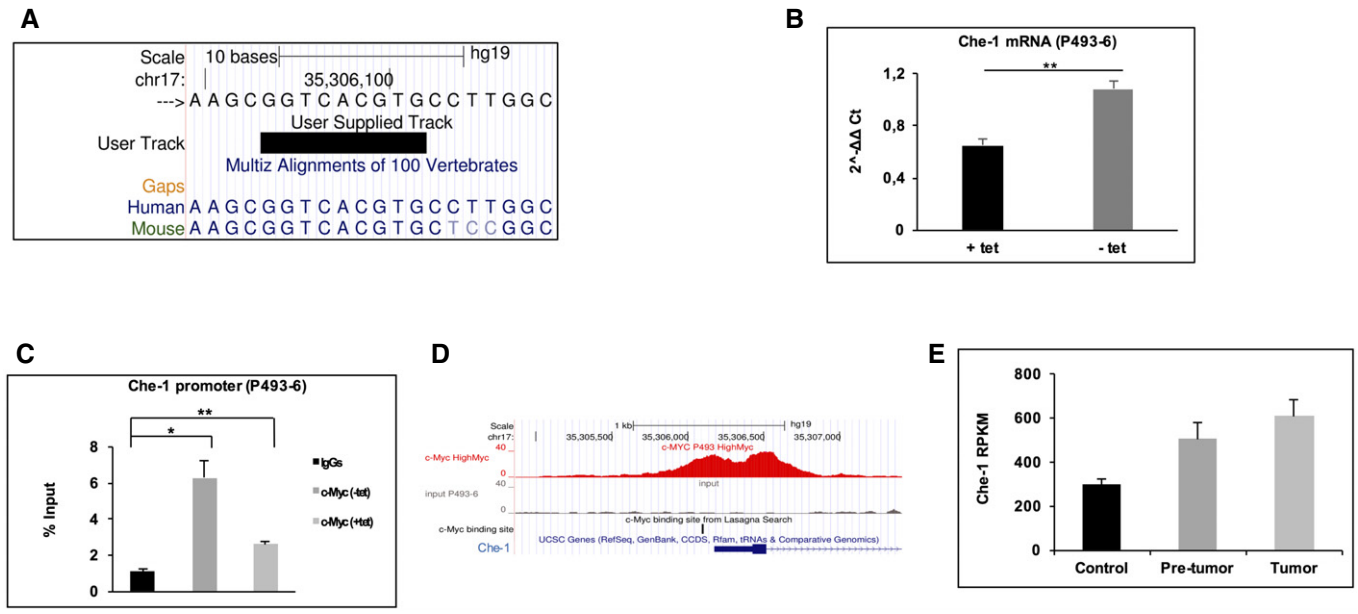


Figure EV2.

Figure EV2. Che-1 binds c-Myc promoter and is involved in c-Myc-dependent tumorigenesis.
Related to Fig 4.

A Genome Browser Screenshot of Che-1 promoter, showing E-box conservation among human and mouse.
B qRT–PCR experiment performed in P493-6 cell line untreated (−tet) or treated with 0.1 μg/ml tetracycline for 72 h (+tet). Values were normalized with actin mRNA levels using the $\Delta\Delta C_t$ method. Error bars represent the standard error of three different experiments.
C Cross-linked chromatin derived from P493-6 cells untreated or treated with 0.1 μg/ml tetracycline for 72 h was immunoprecipitated with c-Myc antibody or in the absence of antibody and analyzed by qRT–PCR (ChIP–qPCR). Data are expressed as a percentage of input. Error bars represent the standard error of three different experiments.
D c-Myc binds Che-1 promoter in P493-6 cell line. Data from Amati's group deposited at GSE51011, UCSC Genome Browser Screenshot showing only portion of MACS2-generated bigWig.
E Che-1 expression (RPKM) increasing along with tumorigenesis. RNA-seq processed data from Sabo *et al* [20] Data are presented as the means and SD from three independent experiments (GSE51011).

Data information: $*P \leq 0.05$; $**P \leq 0.01$ by Student's *t*-test.
Source data are available online for this figure.

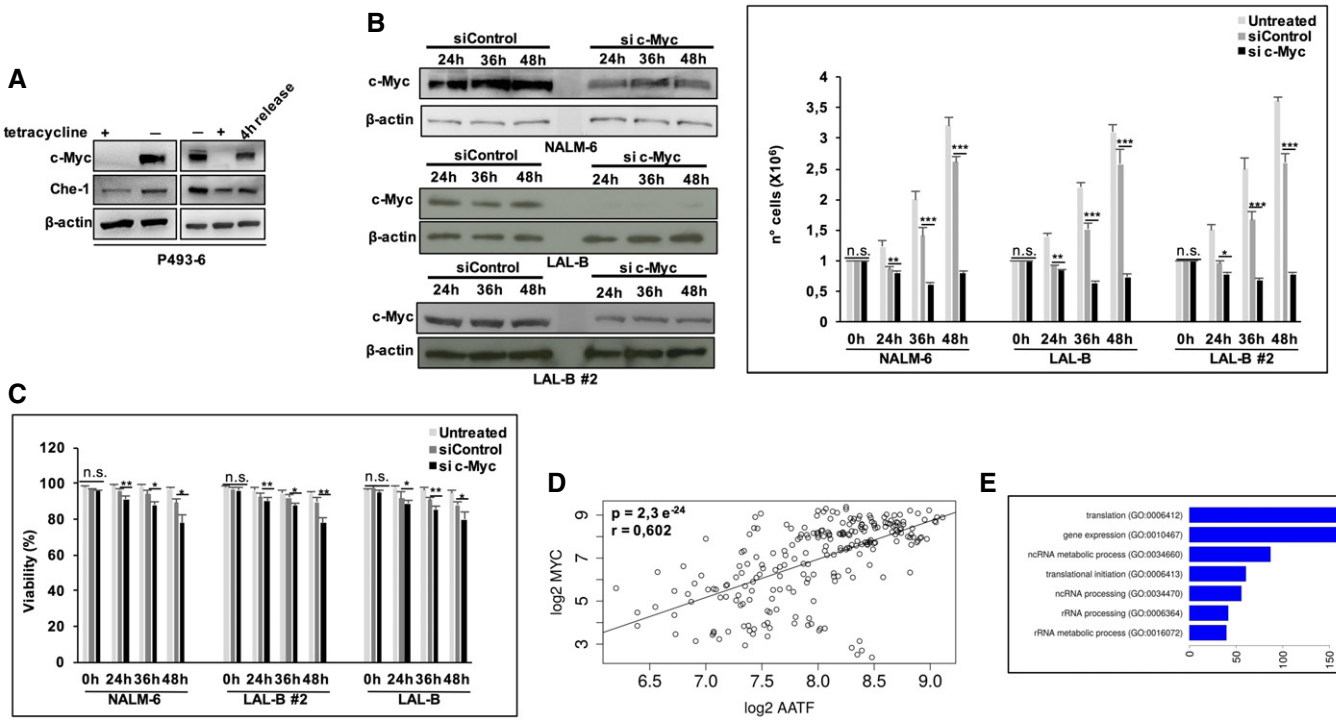


Figure EV3. c-Myc silencing affect cell viability and proliferation with a major effort.
Related to Fig 5.

A WB analysis of P493-6 cells untreated (−tet), treated with tetracycline for 72 h (+tet) and 4 h after release. β-actin was used as loading control.
B WB and proliferation assay of c-Myc silencing performed 24, 36, and 48 h postnucleoporation in NALM-6, LAL-B, and LAL-B #2 cell lines. Data are presented as the means and standard deviation (SD) from three independent experiments.
C Viability assay performed in NALM-6, LAL-B, and LAL-B #2 cell lines treated as in (B). Data are presented as the means and standard deviation (SD) from three independent experiments.
D Che-1/c-Myc transcript correlation in the "Exp B Cells" dataset comprising of several hematological samples.
E Gene Ontology enrichment for the 1,372 gene Che-1/c-Myc-r-PLUS overlap showed in Fig 5H.

Data information: $*P \leq 0.05$; $**P \leq 0.01$; $***P \leq 0.001$ by Student's *t*-test.
Source data are available online for this figure.

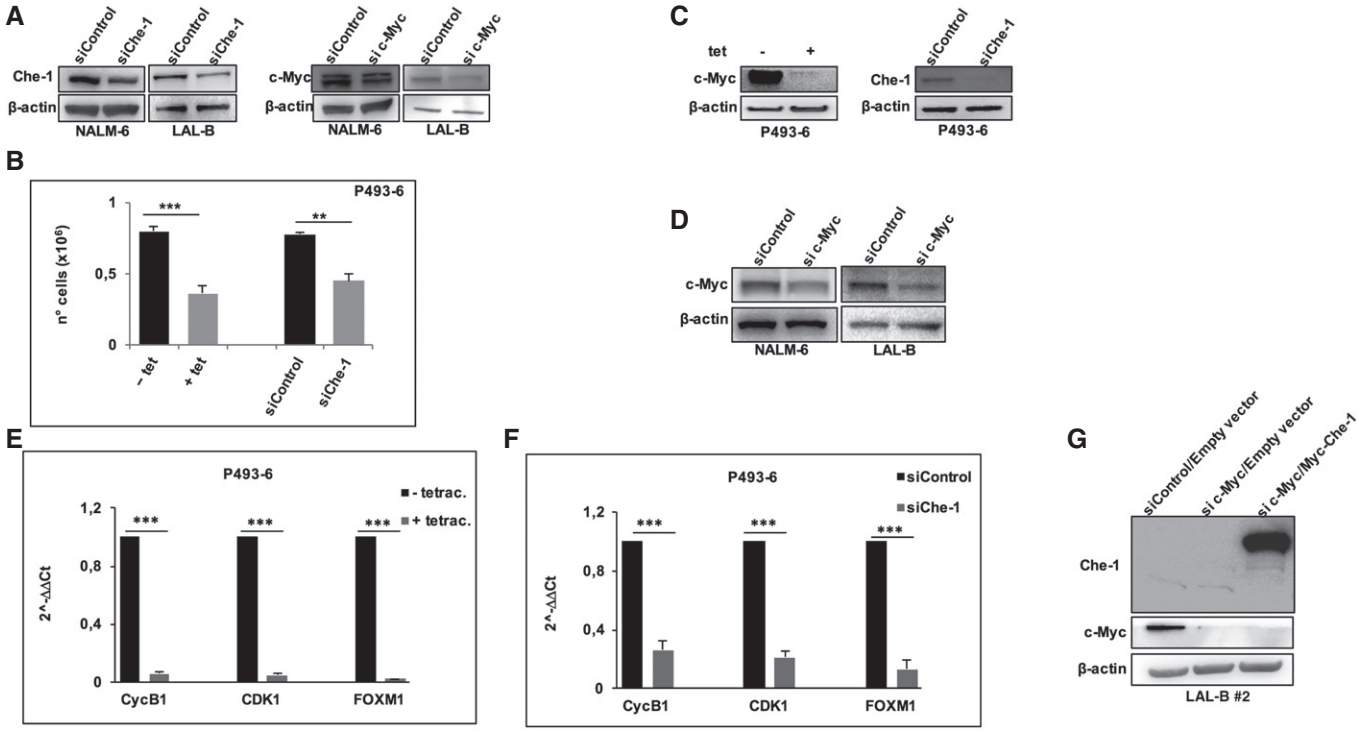


Figure EV4. Che-1 and c-Myc cooperate in controlling proliferation.
Related to Fig 6.

A WB analysis of NALM-6 and LAL-B cell lines nucleoporated with siRNA targeting Che-1 (siChe-1), c-Myc (si c-Myc), or with control siRNA (siControl), and subjected to cell number analysis (Fig 6A). β-actin was used as loading control.

B Cell number analysis performed on P493-6 cells transiently transfected either with siRNA targeting Che-1 (siChe-1) or with control siRNA (siControl), and untreated or treated with tetracycline for 72 h. Data are presented as the means ± SD from three independent experiments.

C WB analysis of P493-6 cells treated as in (B).

D WB analysis of NALM-6 and LAL-B cell lines treated as in (A), and subjected to RNA-seq experiment (Fig 6B).

E, F qRT–PCR analysis performed in P493-6 cells treated as in (B), to validate the downregulation of some genes (Cyclin B1, Cdk1, Foxm1) emerged from the RNA-seq experiment. Error bars represent the standard error of three different experiments.

G LAL-B #2 cells were nucleoporated with Control siRNA (siControl) in combination with a Myc-tagged empty vector (Empty vector) or with siRNA c-Myc (si c-Myc) in combination with empty vector, or with si c-Myc and Myc-tagged Che-1 expressing vector (Myc-Che-1), and harvested after 36 h. WB analysis of TCEs with the indicated Abs is shown. It is representative of three independent experiments.

Data information: $^{**}P \leq 0.01$; $^{***}P \leq 0.001$ by Student's *t*-test.
Source data are available online for this figure.

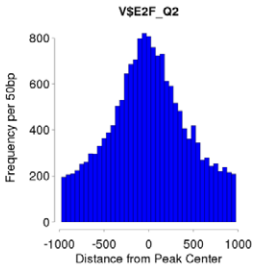
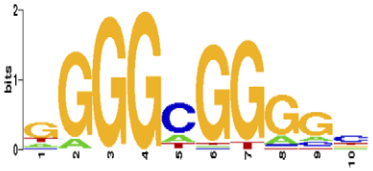
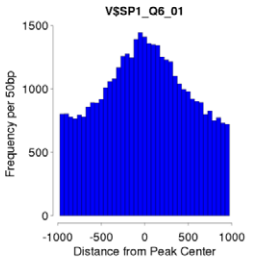
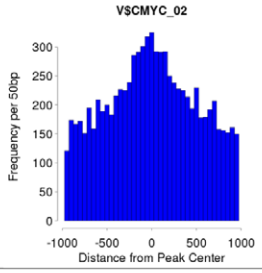
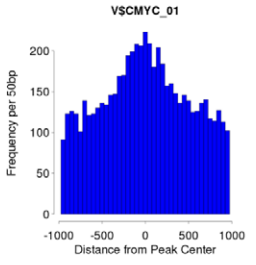
Motif	Logo	Dist.	pval
V$E2F_Q2			0
V$SP1_Q6_01			0
V$CMYC_02			6.14e-7
V$CMYC_01			1.3e-5

Figure EV5. Significant c-Myc motifs emerged from Centdist ChIP-seq MACS2 analysis.
Related to Fig 7.