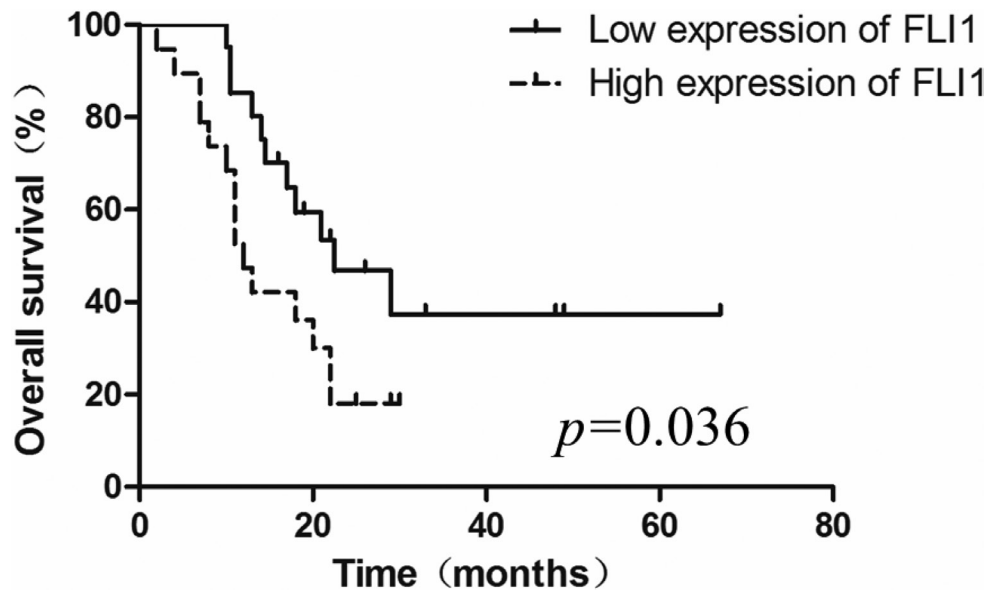


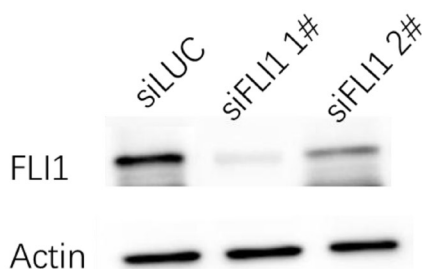
## Friend leukemia virus integration 1 promotes tumorigenesis of small cell lung cancer cells by activating the miR-17-92 pathway

### Supplementary Materials

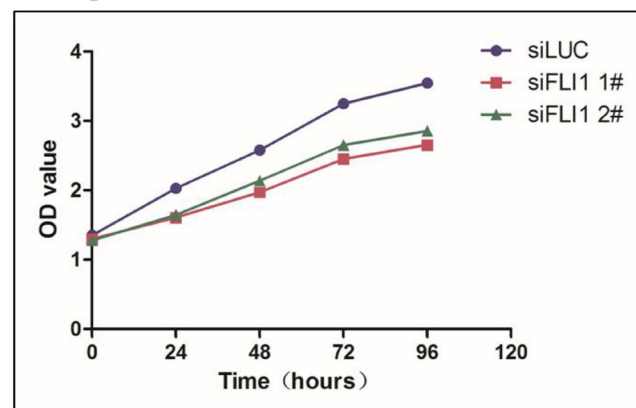


**Supplementary Figure 1: *FLI1* is a potential biomarker for the survival of SCLC.** The overall survival of SCLC was analyzed by Kaplan-Meier estimates. SCLC patients with low expression of *FLI1* had better OS than those with high expression of *FLI1* ( $p = 0.036$ ).

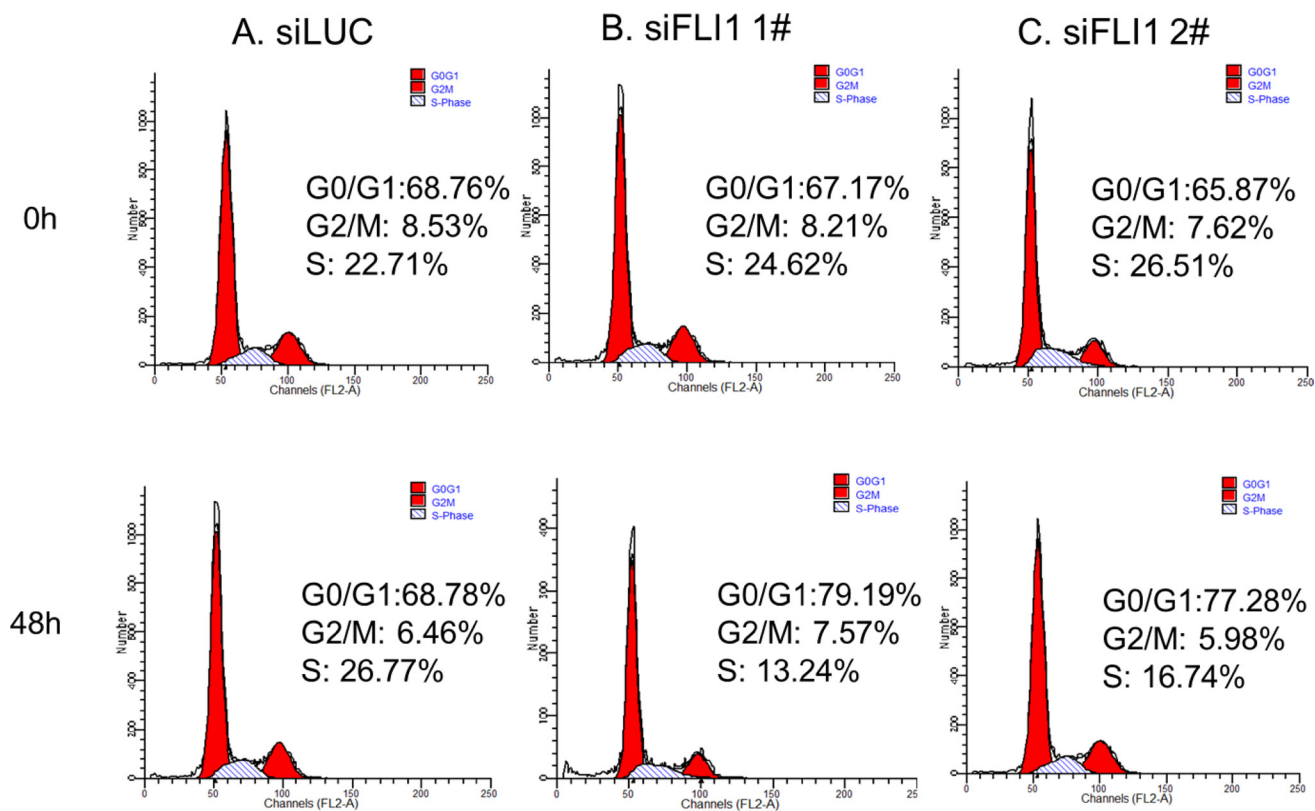
#### A. *FLI1* knockdown



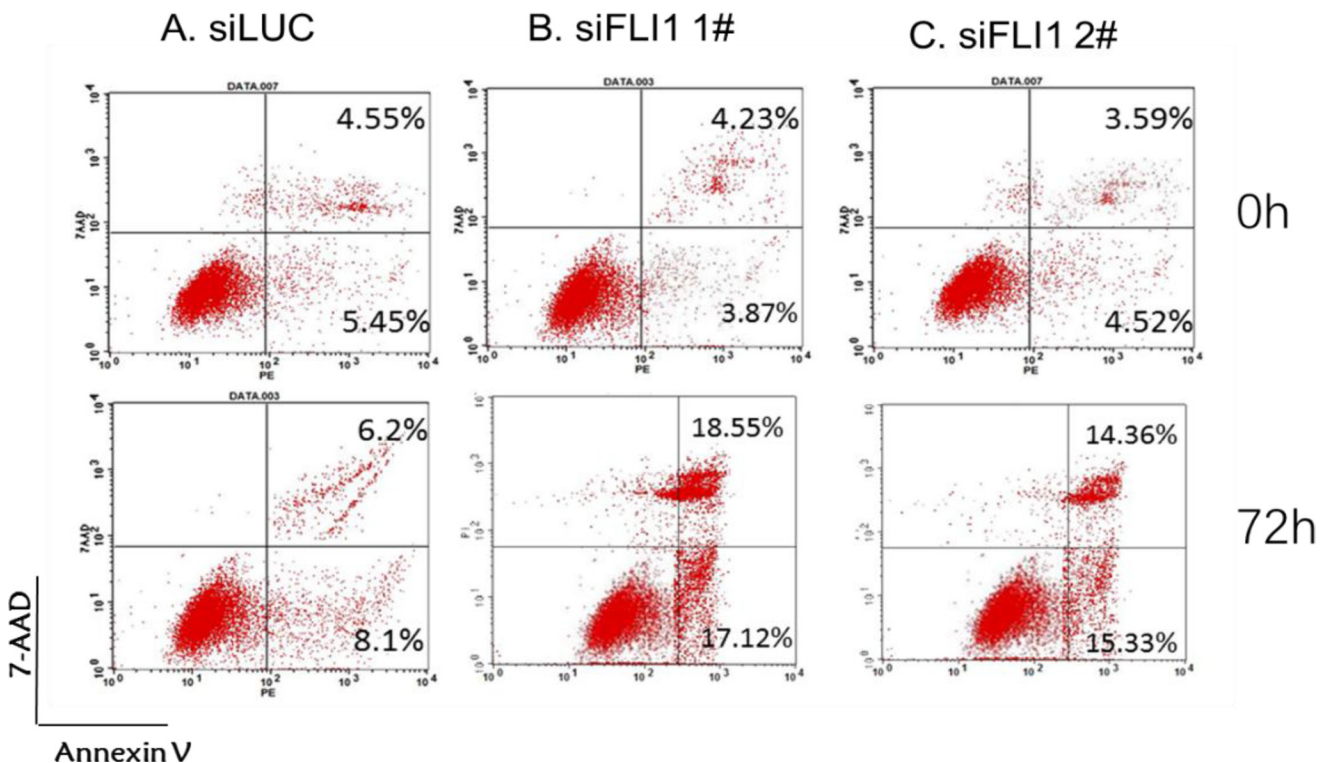
#### B. Cell proliferation



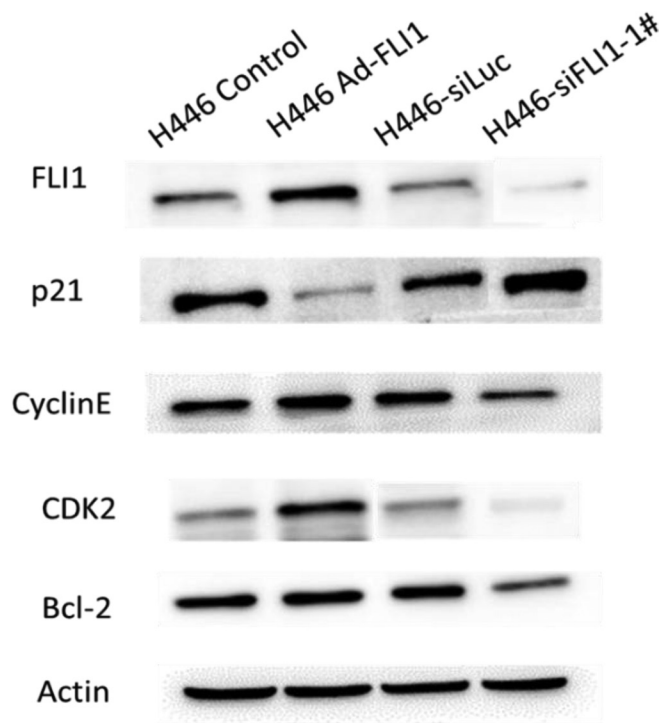
**Supplementary Figure 2: *FLI1* knockdown inhibits cell proliferation in NCI-H1688 SCLC cells.** (A) Knockdown of *FLI1* by two siRNAs (siFLI1 1#, siFLI1 2#) in NCI-H1688 cells. Expression of *FLI1* was measured by Western blot. siLUC: control siRNA that targets the photinuspyralis luciferase genes; siFLI1: siRNAs that target *FLI1*. (B) Inhibition of cell proliferation by *FLI1* siRNAs in NCI-H1688 cells. Cell proliferation is measured by the MTT assay.



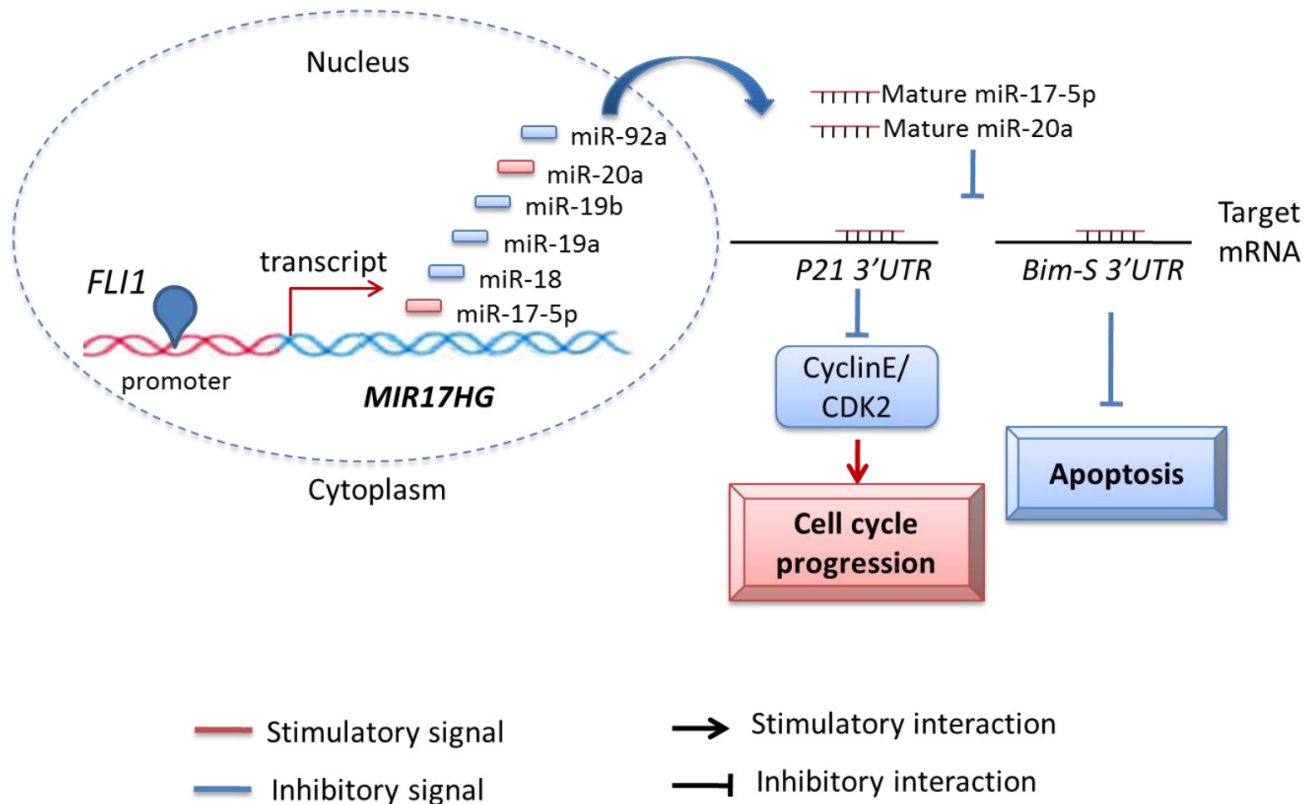
**Supplementary Figure 3: *FLII* knockdown induces G0/G1 cell cycle arrest in NCI-H1688 cells** Cell cycle was examined by flow cytometry (FACS) in NCI-H1688 cells treated with the control siRNA (siLUC) and *FLII* siRNAs (siFLI1 1# and siFLI1 2#).



**Supplementary Figure 4: *FLII* knockdown promotes apoptosis in NCI-H1688 cells** After knockdown of *FLII*, NCI-H1688 cells were subject to flow cytometry analysis for cell apoptosis.



**Supplementary Figure 5: Expression of the *FLI1*-miR-17-92 pathway target genes After *FLI1* knockdown, the downstream target genes of the miR-17-92 pathway was quantitated by Western blot.** The expression of CyclinE and CDK2 was upregulated when *FLI1* was overexpressed, but was significantly decreased when *FLI1* was knocked down.



**Supplementary Figure 6: The putative model of the *FLI1*-miR17-92 pathway in SCLC.** The overexpressed *FLI1* oncoprotein binds to a conserved ETS binding site in the miR-17-92 promoter and activates the transcription of the microRNA cluster in SCLC cells. Two major members of the cluster, miR-17-5p and miR-20a, regulate a large subset of key genes that promote proliferation and cell cycle progression in SCLC. By targeting the downstream *Bim-S* and *P21*, the oncogenic *FLI1* regulates apoptosis, cell cycle, and finally the development of SCLC.