

Supporting Information

Figure S1

The analysis workflow for microarray datasets and CMap compounds screen. Details for microarray analysis with dChip were listed in methods section. The lung AC signatures drawn from differential expression analysis were used to query CMap for screening candidates, only compounds with negative scores and p -values less than 0.05 were retained as potential therapeutic agents for lung AC.

Table S1

Summary of microarray dataset GSE7670.

Figure S1

Gene Expression Omnibus(GEO)

GSE 7670

**Differential genes detection
dChip analysis**

Import expression file, gene
information and CDF file



Normalize and compute
signal values for expression level



Differential genes



Compare between two groups
 $E/B > 2$ or $B/E < 2$

**Lung adenocarcinoma gene signatures
(Probes for up- and down-regulated genes)**

**Screening candidate drugs
CMap analysis**

Candidate compounds ranked by enrichment score and p -value

Table S1

GEO datasets	GSE7670	
Organism	Homo sapiens	
Source	Taipei Veterans General Hospital, china	
Platforms	Affymetrix HG-U133A	
Characteristics	Adjacent normal-tumor matched lung cancer samples were selected at early and late stages. Totally, 66 samples including patient samples, other lung or lung AC tissue or cell lines were involved in this data set.	
Detail samples information	54 paired samples were selected in our study	
	Normal lung	Lung adenocarcinoma
	GSM185811	GSM185812
	GSM185813	GSM185814
	GSM185815	GSM185816
	GSM185817	GSM185818
	GSM185819	GSM185820
	GSM185821	GSM185822
	GSM185823	GSM185824
	GSM185825	GSM185826
	GSM185827	GSM185828
	GSM185829	GSM185830
	GSM185831	GSM185832
	GSM185833	GSM185834
	GSM185835	GSM185836
	GSM185837	GSM185838
	GSM185839	GSM185840
	GSM185841	GSM185842
	GSM185843	GSM185844
	GSM185845	GSM185846
	GSM185847	GSM185848
	GSM185849	GSM185850
	GSM185851	GSM185852
	GSM185853	GSM185854
	GSM185855	GSM185856
	GSM185857	GSM185858
GSM185859	GSM185860	
GSM185861	GSM185862	
GSM185863	GSM185864	