

Overexpression of *LINC00152* correlates with poor patient survival and knockdown impairs cell proliferation in lung cancer

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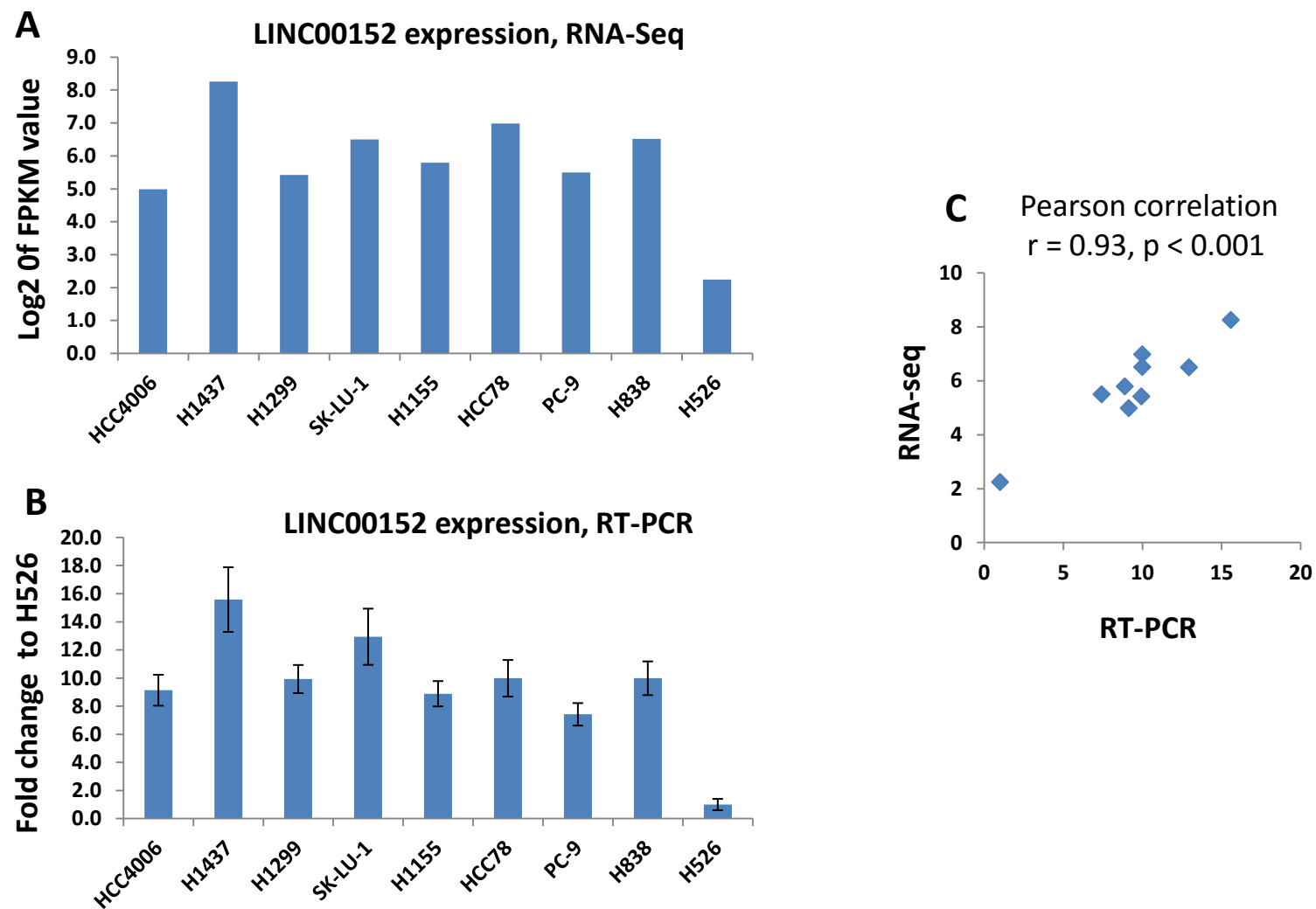
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Supplementary data

Supplementary Table 1 *LINC00152* expression and clinico-pathological variables in lung cancer

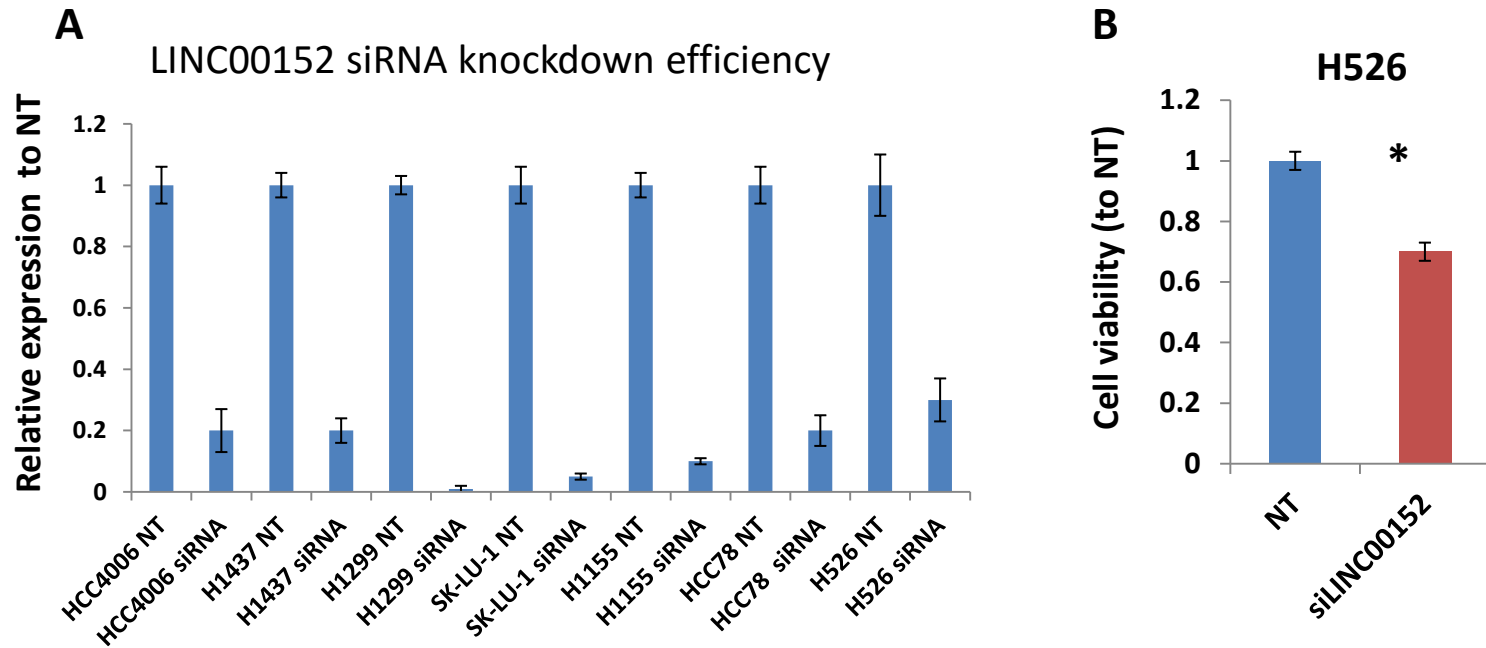
Characteristics	No. of patients	LINC00152 expression (Mean $\pm$ SD)	P Value t test
Age(years)			
≥ 60	73	2.01 $\pm$ 1.53	0.21
<60	28	1.67 $\pm$ 1.14	
Gender			
Male	48	1.73 $\pm$ 1.32	0.29
Female	53	2.02 $\pm$ 1.47	
Differentiation			
Well	28	1.52 $\pm$ 1.24	0.10
Moderate	38	2.04 $\pm$ 1.27	
Poor	34	2.0 $\pm$ 1.63	0.19
Tumor Stage:			
1	59	1.71 $\pm$ 1.56	0.39
2	16	2.05 $\pm$ 1.31	
3	26	2.18 $\pm$ 1.01	0.10
Lymph Node			
N0	70	1.79 $\pm$ 1.47	0.63
N1	12	2.02 $\pm$ 1.44	
N2	19	2.13 $\pm$ 1.11	0.28
Smoking: Pack-years			
>60	16	2.35 $\pm$ 1.48	0.18
≤ 60	85	1.79 $\pm$ 1.38	
Kras Mutation			
NO	47	1.58 $\pm$ 1.07	0.09
YES	41	2.11 $\pm$ 1.69	

Supplementary Figure S1



LINC00152 expression in 9 lung cancer cell lines used in this study measured by RNA-Seq (**A**) and RT-qPCR (**B**). A significant correlation between these two methods was found using Pearson correlation analysis (**C**). Small cell lung cancer cell line H526 is the lowest expression for *LINC00152*. RNA-seq value of PC-9 was predicted value based on RT-PCR value as compared to other cells since we don't have the RNA-Seq data for PC-9 cell.

Supplementary Figure S2



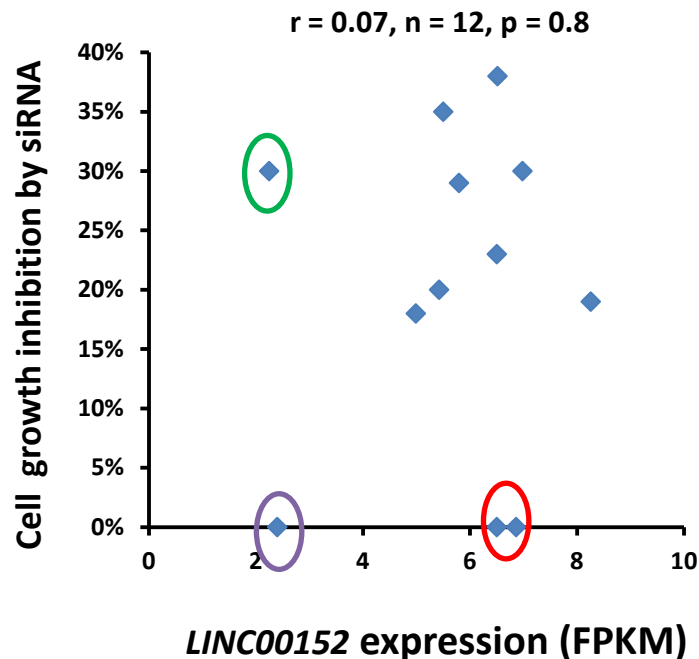
A, *LINC00152* siRNA (Dharmacon SMARTpool, 10nM) knockdown efficiency on lung cancer cell lines after siRNA treatment at 48 hours measured by RT-PCR. y-axis is relative *LINC00152* expression to NT after adjusted by GAPDH. **B**, Cell proliferation (measured by WST-1) of H526 cell line after *LINC00152* siRNA treatment at 96 hours.

Supplementary Figure S3

A

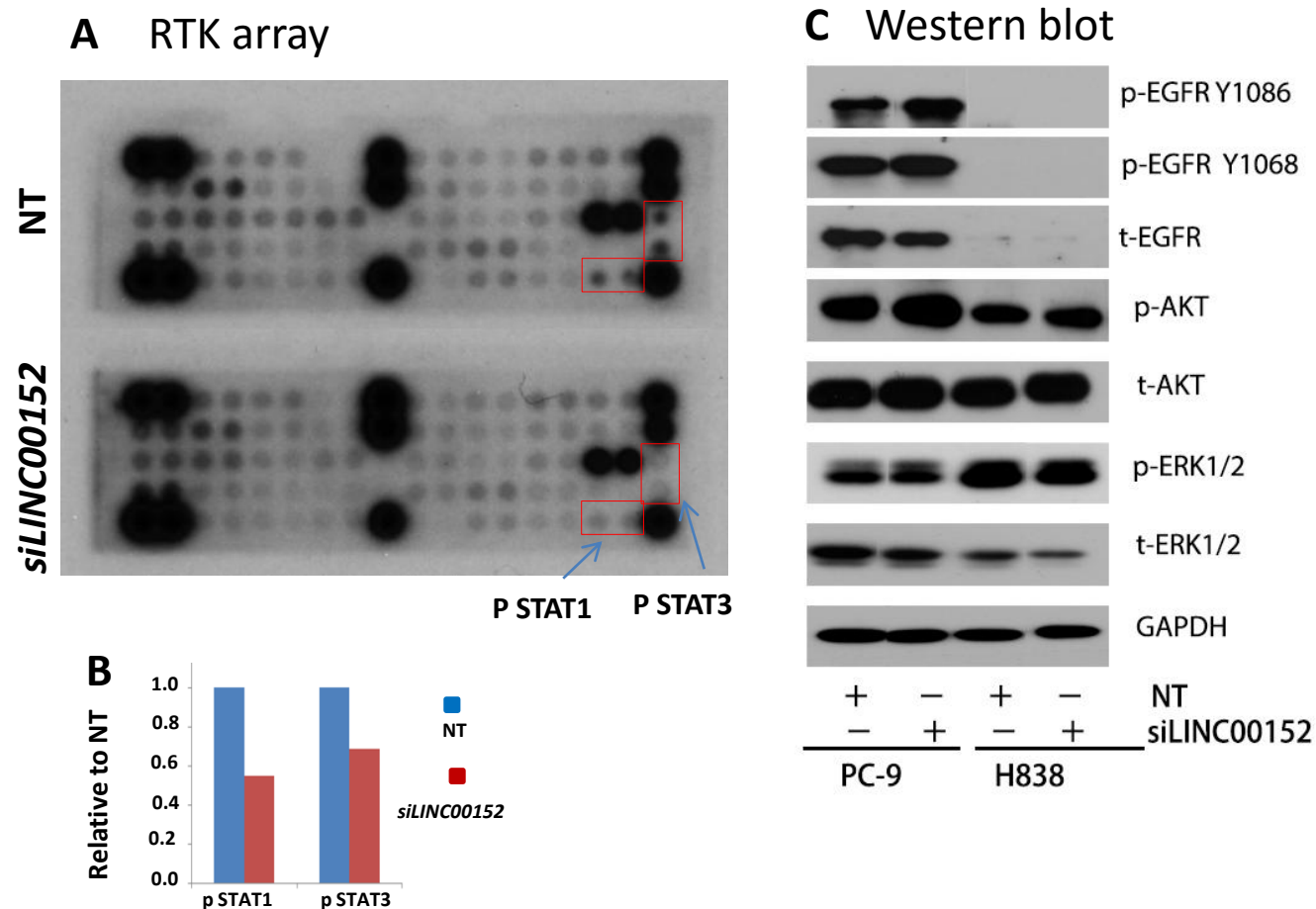
Cell	RNA-seq <i>LINC00152</i>	si <i>LINC00152</i> WST down
H838	6.5	38%
PC-9	5.5	35%
HCC78	7.0	30%
H526	2.2	30%
H1155	5.8	29%
SK-LU-1	6.5	23%
H1299	5.4	20%
H1437	8.3	19%
HCC4006	5.0	18%
H1975	6.9	0%
H1650	6.5	0%
H146	2.4	0%

B



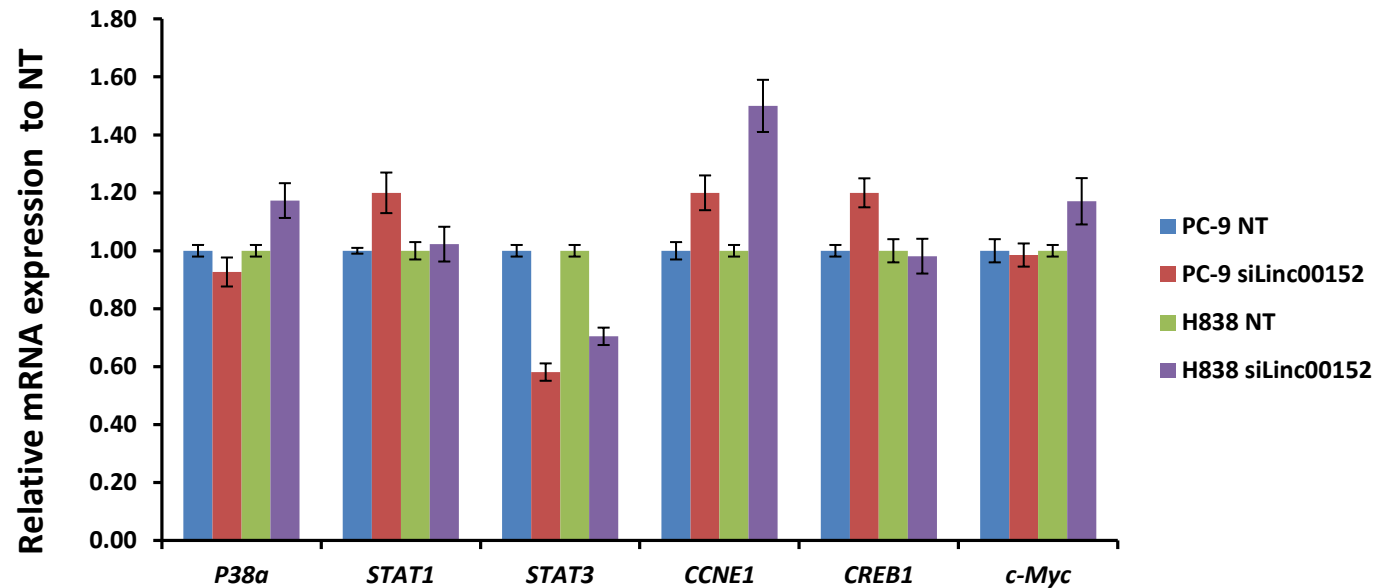
The correlation between *LINC00152* expression and rate of cell growth inhibition by *LINC00152* knockdown with siRNA. The cell growth in H1975 and H1650 cells (indicated by red cycle) were not affected by *LINC00152* siRNA knockdown although these cells have relative higher level of *LINC00152* expression. Whereas, cell growth in H526 (indicated by green cycle) was affected by *LINC00152* knockdown although this cell has relative low level of *LINC00152* expression. The cell growth in H146, another low level of *LINC00152* expression cell line, was not affected(indicated by purple cycle).

Supplementary Figure S4



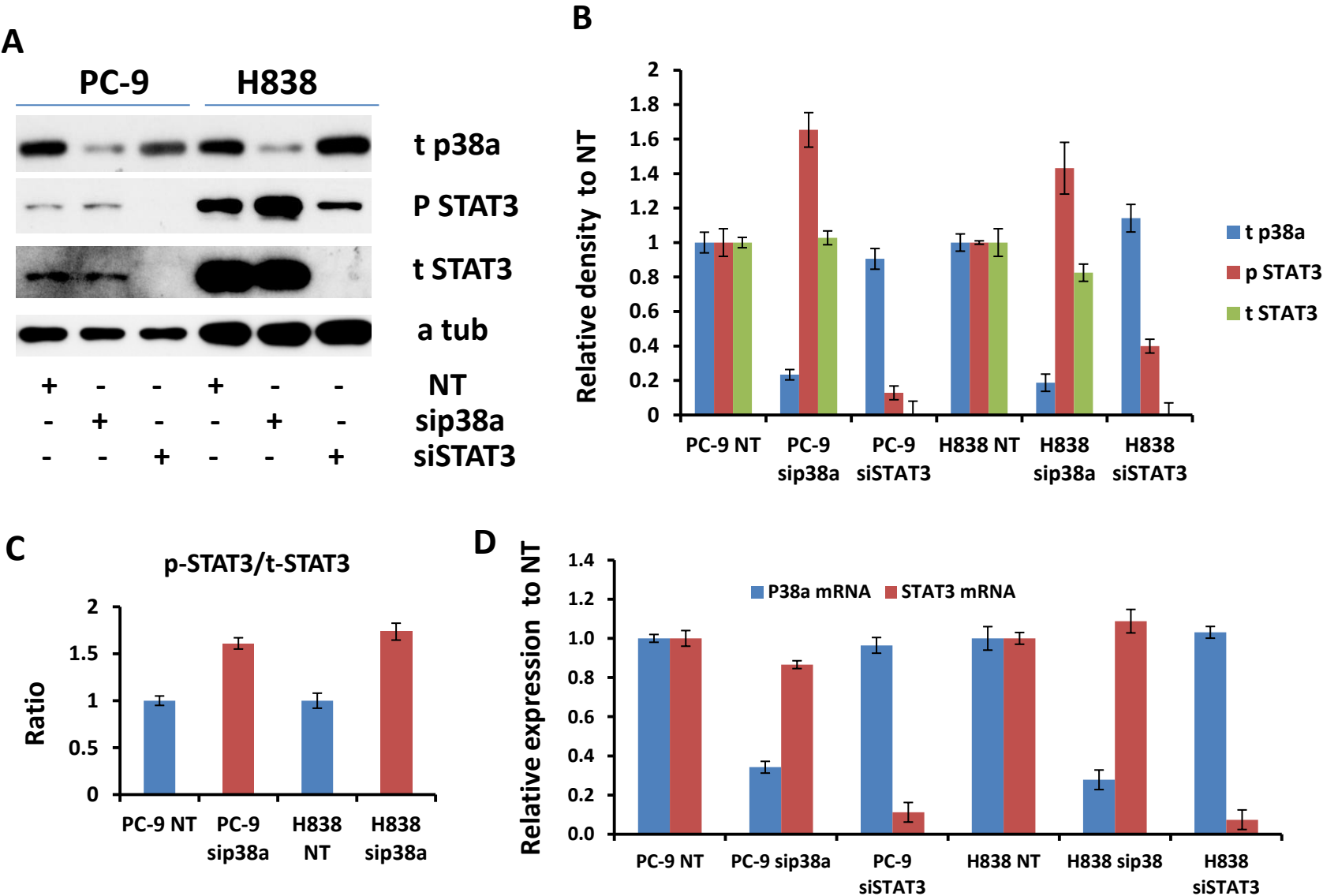
A, The whole blot of Receptor tyrosine kinases (RTK) array. Red box indicated that p-STAT1 and p-STAT3 expression were decreased. **B**, Quantitative analysis of p-STAT1 and p-STAT3 expression by Image J, relative to NT (NT=1). **C**, Western blot showing EGFR, AKT and ERK1/2 proteins were not changed after *LINC00152* siRNA treatment at 72 hours.

Supplementary Figure S5



The mRNA expressions of genes in Figure 5B after *LINC00152* siRNA treatment at 48 hours measured by RT-PCR, y-axis is relative mRNA value to NT after adjusted by *GAPDH*. *STAT3* mRNA is decreased by 30-40%, whereas *CCNE1* mRNA in H838 is increased by 1.5 fold. Other genes are not changed.

Supplementary Figure S6



Protein (A-C) and mRNA (D) expression after p38a or STAT3 siRNAs treatment at 48 hours on PC-9 and H838 cell lines. The ratios of p-STAT3/t-STAT3P were increased by 1.6 -1.7 fold (vs. NT) after p38a knockdown (C), but the mRNA levels of 38a and STAT3 are not affected each others.