Supplementary Tables

Characteristics	No. (%)		
Gender			
Male	48 (37.5)		
Female	80 (62.5)		
Age(years)			
<60	65 (50.78)		
>=60	63 (49.22)		
Smoke			
Yes	52 (40.63)		
NO	76 (59.38)		
T classification			
T1	75 (58.59)		
T2	49 (38.28)		
T3	2 (1.56)		
T4	2 (1.56)		
N classification			
N0	80 (62.50)		
N1	7 (5.47)		
N2	41 (32.03)		
M classification			
M0	127 (99.22)		
M1	1 (0.78)		
Clinical stage			
I	75 (58.59)		
	11 (8.59)		
III	41 (32.03)		
IV	1 (0.78)		
Patient survival			
Alive	99 (77.34)		
Deceased	29 (22.66)		
Expression of			
miR-135b	(1) (17) (17)		
Low expression	01 (4/.00)		
rign expression	67 (52.34)		

Table S1. Clinicopathological characteristics of patients

Primer name	Sequence
GAPDH_Fwd	GAAGGTGAAGGTCGGAGTCA
GAPDH_Rev	TTGAGGTCAATGAAGGGGTC
Bcl-2_Fwd	GACTGAGTACCTGAACCGGC
Bcl-2_Rev	CAGCCAGGAGAAATCAAACAG
Bcl-xL_Fwd	GTATTGGTGAGTCGGATCGC
Bcl-xL-Rev	TGCTGCATTGTTCCCATAGA
MMP9_Fwd	GGGACGCAGACATCGTCATC
MMP9_Rev	TCGTCATCGTCGAAATGGGC
A20_Fwd	GCGTTCAGGACACAGACTTG
A20_Rev	TTCATCATTCCAGTTCCGAGTATC
NFKBIA_Fwd	GTCAAGGAGCTGCAGGAGAT
NFKBIA_Rev	TCATGGATGATGGCCAAGT
VEGFC_Fwd	GTGTCCAGTGTAGATGAACTC
VEGFC_Rev	ATCTGTAGACGGACACACATG
IL-1β_Fwd	AGCTGATGGCCCTAAACAGA
IL-1β_Rev	CCTGAAGCCCTTGCTGTAGT
IL-6_Fwd	AGTGAGGAACAAGCCAGAGC
IL-6_Rev	CATTTGTGGTTGGGTCAGG
IL-8_Fwd	CGGAAGGAACCATCTCACTG
IL-8_Rev	AGCACTCCTTGGCAAAACTG

Table S2. DNA sequences of qRT-PCR primers

Table S3. Correlation between the clinicopathological

Characteristics	miR-135bexpression		χ^2 Test	Fisher Exact
	Low	High	<i>P</i> -Value	Test <i>P</i> -Value
Gender				
Male	24	24	0.717	-
Female	37	43		
Age(years)				
<60	26	39	0 111	
>=60	35	28	0.111	-
Smoke				
Yes	28	24	0.041	
NO	33	43	0.041	
T classification				
T1	40	35		
T2	19	30		0.429
T3	1	1	-	0.438
T4	1	1		
N classification				
NO	34	46		
N1	5	2	-	0.244
N2	22	19		
M classification				
M0	61	66		1 000
M1	0	1	-	1.000
Clinical stage				
I	32	43		
11	8	3		
III	21	20	-	0.165
IV	0	1		

features and expression of miR-135b

Supplementary Figure Legends

Figure S1 Verification of miR-135b stably up- or downregulated NSCLC cell

lines. (A) Real-time PCR measuring miR-135b level in miR-135 overexpressing cells. (B) Real-time PCR measuring miR-135b level in miR-135 inhibiting cells. Error bars represent the mean \pm SD. **, p<0.01; ***, p<0.001, two-tailed, unpaired t-test.

Figure S2 miR-135b promotes cell migration, invasion, anti-apoptosis and

angiogenesis in NSCLC *in vitro*. (A, B) Quantification of migrated (A) and invaded (B) cells in the indicated cell lines, related to Figure 3A-B. (C) Quantification of TUNEL positive cells in the indicated cell lines, related to Figure 3C. (D) Representative images of cells treated with cisplatin (DDP) taken under a bright field microscope. Scale bars, 50µm. (E) Western blotting analysis of the protein levels of PARP and cleaved-PARP in the indicated cells. β -Tubulin served as a loading control. (F) Quantification of migrated HUVECs, related to Figure 3D. Error bars represent the mean ± SD. *, *p*<0.05; **, *p*<0.01; ***, *p*<0.001, two-tailed, unpaired t-test.

Figure S3 miR-135b promotes nuclear translocation of NF-кB/p65.

Representative images (A) and quantification (B) of p65 nuclear positive cells in indicated cells, related to Figure 4G. Scale bars, 20 μ m. Error bars represent the mean \pm SD. *, *p*<0.05; **, *p*<0.01; ***, *p*<0.001, two-tailed, unpaired t-test.

Figure S4 Rescuing the expression of CYLD reversed the effects of miR-135b on cellular behaviors. (A) Quantification of EdU positive cells in indicated cell lines, related to Figure 6B. (**B**, **C**) Quantification of migrated (**B**) and invaded (**C**) cells in indicated cell lines, related to Figure 6C-D. (**D**) Quantification of TUNEL positive cells in indicated cell lines, related Figure 6E. Error bars represent the mean \pm SD. *, p<0.05; **, p<0.01; ***, p<0.001, two-tailed, unpaired t-test.