Supplementary information

Table S1. Characteristics of patients with NSCLC.

Variable	Number of patients		*p*
	High (n=67)	Low（n=15）	
Gender			
Male	51	14	0.137
Female	16	1	
Age			
60≤	38	9	0.816
<60	29	6	
Smoking			
no	20	5	0.975
yes	47	10	
Histology			
Adenocarcinoma	33	7	0.933
Squamous cell carcinoma	31	7	
Other	3	1	

p value was calculated by chi-square test.

Table S2. The sequences of primers or probes used in this study

Gene	Sequences
EMSA probe (WT)	TTCCTGGCCACCCACCTGGGCACT
	AAGGACCGGTGGGTGGACCCGTGA
EMSA probe (MT)	TTCCTGGCCACCTATCTAGGCACT
	AAGGACCGGTGGATAGATCCGTGA
miR-23a (ISH)	TAGTGTAACGGTCCCTAAAGG-DIG
miR-27a (ISH)	AAGTGTCACCGATTCAAGGCG-DIG
miR-24-2 (ISH)	ACCGAGTCAAGTCGTCCTTGTC-DIG
MITF	CGAAAGTTGCAACGRGAACAGCA
	GAGCCTGCATTTCAAGTTCCTGTA
CBLB	CACCCTTCTCCCAAGCATAA
	AGACCGAACAGGAGCTTTGA
Actin	AAACTGGAACGGTGAAGGTG
	GTGGCTTTTAGGATGGCAAG

Supplementary Figure legends

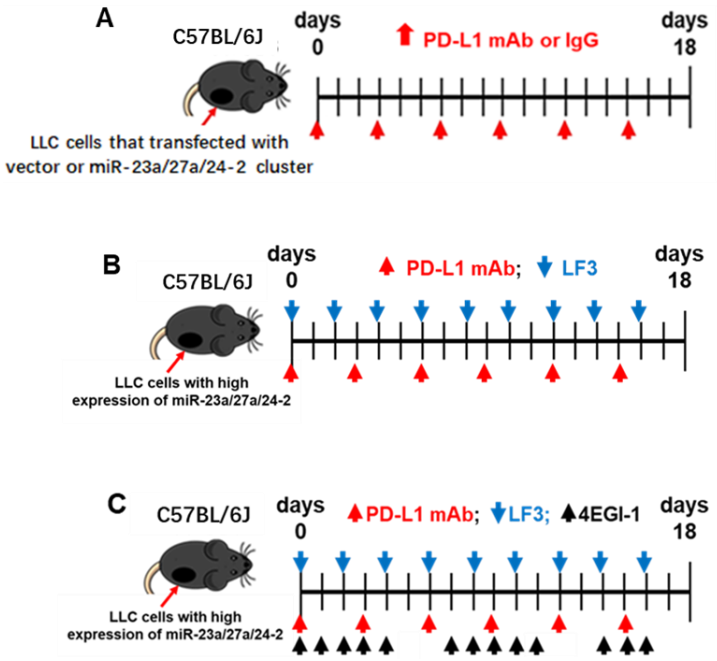

Fig S1. Drug treatment schedule. (**A**) PD-L1 mAb treatment schedule. (**B**) Drug treatment schedule for combination of LF3 and PD-L1 mAb. (**C**) Drug treatment schedule for compare the enhancing effects of LF3 and 4EGI-1 on the PD-L1 mAb therapeutic efficacy. Xenograft models were generated using C57BL/6J mice by subcutaneously injection Lewis lung cancer cells that transfected with vector or high expressing miR-23a/27a/24-2 cluster. Drug treatment was started when tumor volumes were reached about 100mm^3.

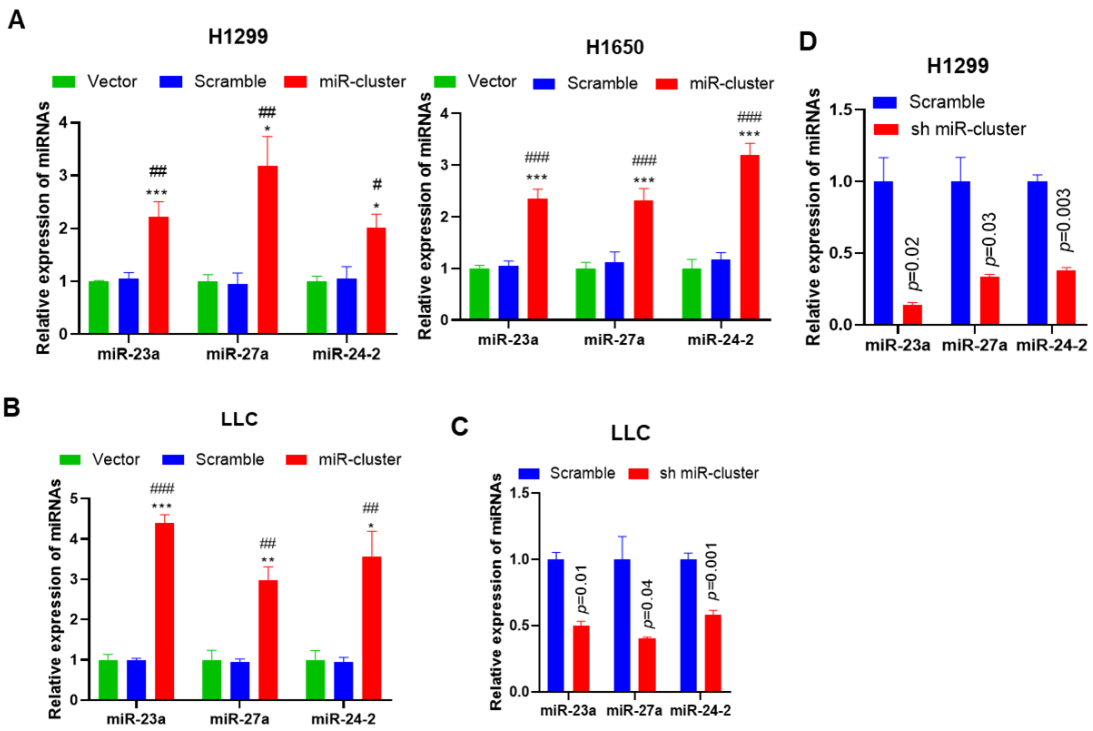

Fig S2. The expression level of miR-23a/27a/24-2 cluster was measured by qRT-PCR in NSCLC cells. Indicated cells were transfected with indicated constructs. After 72 hours of transfection, cells were subjected to qRT-PCR analysis. *p* value was calculated by one-way ANOVA test and Duncan's multiple range test (A and B) and t test (C and D). miR-cluster, miR-23a/27a/24-2 cluster expressing constructs; sh miR-cluster, miR-23a/27a/24-2 cluster shRNA expressing construct. $^{*}p<0.05$ compared to vector control; $^{**}p<0.01$ compared to vector control; $^{***}p<0.001$ compared to vector control; $^{\#}p<0.05$ compared to scramble control; $^{\#\#}p<0.01$ compared to scramble control; $^{\#\#\#}p<0.001$ compared to scramble control.

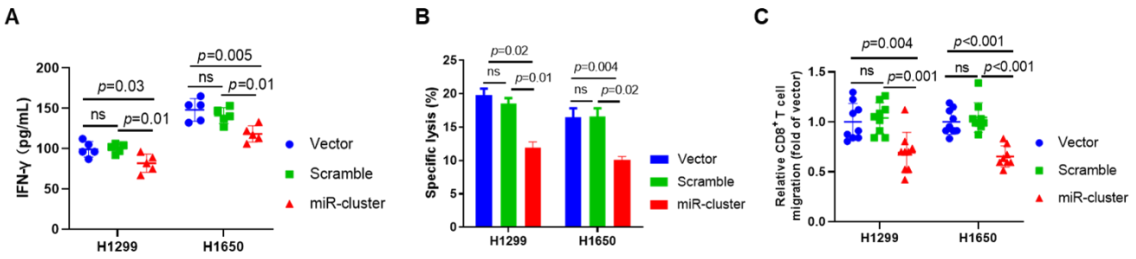

Fig. S3. Effects of miR-23a/27a/24-2 cluster high expressing NSCLC on T cell IFN-γ secretion, T cell-induced cancer cell death and T cell migration. (**A**) The concentration of IFN-γ in the culture medium after co-culturing $CD8^+$ T cells and NSCLC cells in a 10:1 ratio for 12 hours. (**B**) NSCLC cell death was measured by flow cytometry after co-culturing NSCLC cells with $CD8^+$ T cells in a 1:20 ration for 6hours. (**C**) Relative migration of human $CD8^+$ T cells incubated with culture medium supernatant from H1299 or H1650 cells. NSCLC cells were transfected with vector or scramble or miR-23a/27a/24-2 cluster expressing constructs. After 48 hours of transfection, NSCLC cells were subjected to subsequent experiments. *p* value was calculated by one-way ANOVA test and Duncan's multiple range test.

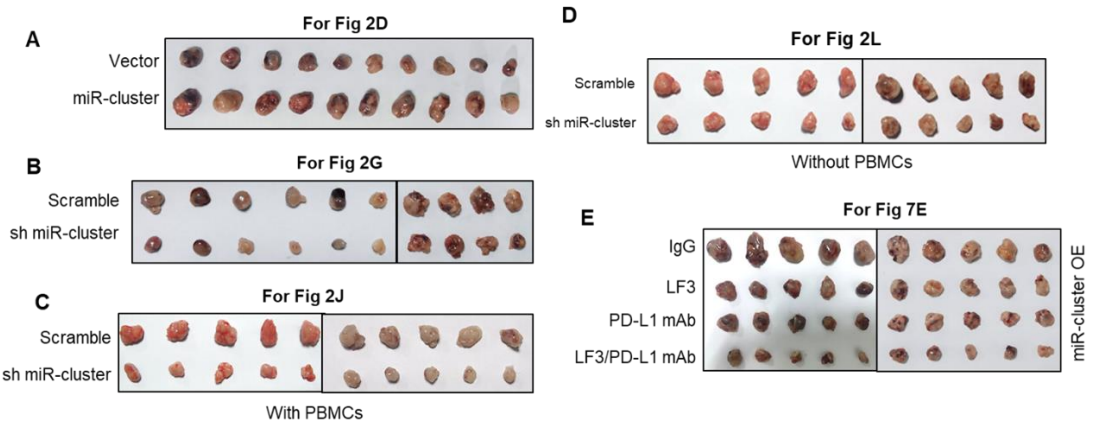

Fig. S4. Represent images of tumors from xenograft models. **(A)** Representative images of tumors for indicated groups as presented in Fig. 2D. **(B)** Representative images of tumors for indicated groups as presented in Fig. 2G. **(C)** Representative images of tumors for indicated groups as presented in Fig. 2J. **(D)** Representative images of tumors for indicated groups as presented in Fig. 2L. **(E)** Representative images of tumors for indicated groups as presented in Fig. 7E.

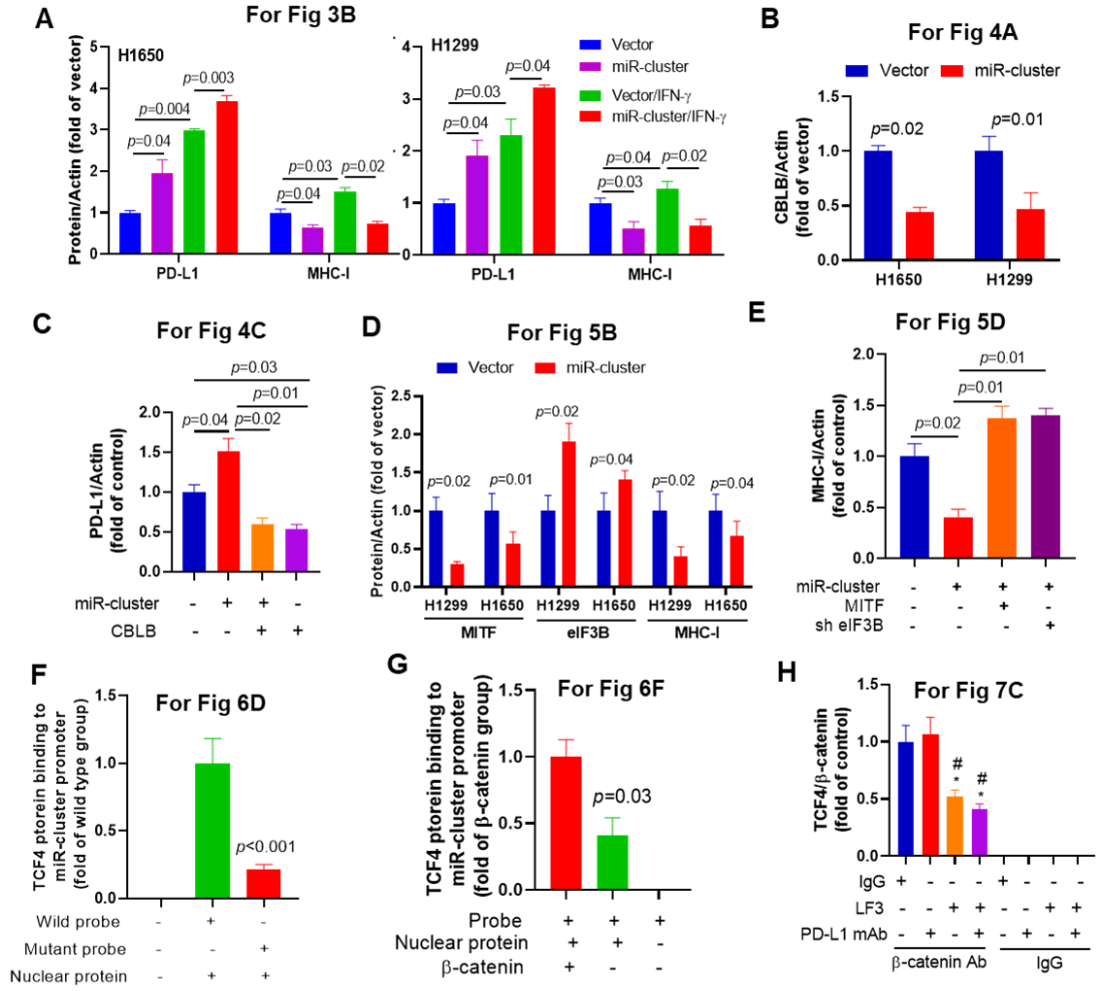

Fig. S5. Quantification of Western blot bands in **(A)** Fig. 3B**, (B)** Fig. 4A, **(C)** Fig. 4C, **(D)** Fig. 5B, **(E)** Fig. 5D, **(F)** Fig. 6D, **(G)** Fig. 6F and **(H)** Fig. 7C. Error bars indicate the mean ± SD for three independent experiments. *p* value was calculated by t test (A, B, D, F and G) and one-way ANOVA test and Duncan's multiple range test (C, E, and H). * $p<0.05$ compared to IgG control; $^{\#}$ $p<0.05$ compared to PD-L1 mAb treatment group.

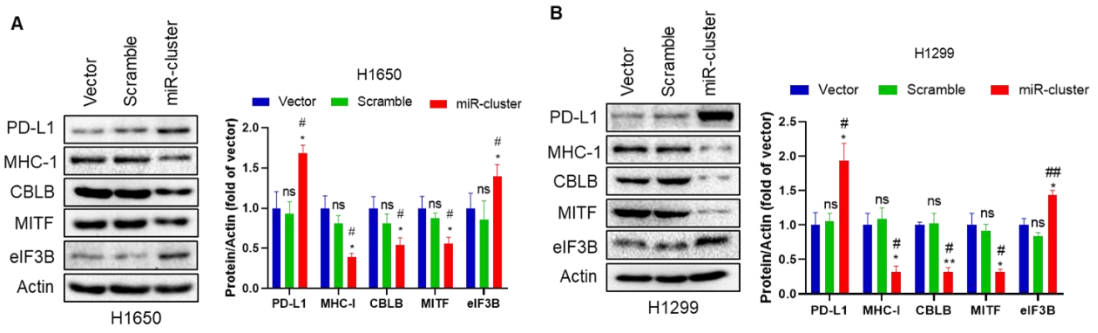

Fig. S6. Effects of the miR-23a/27a/24-2 cluster on the expression of PD-L1, MHC-I, CBLB, MITF and eIF3B in NSCLC cells were examined by Western blot analysis. The Western blot band intensities were quantified and error bars indicate the mean ± SD for three independent experiments. Indicated NSCLC cells were transfected with indicated plasmids. After 72 hours of transfection, cells were subjected to Western blot analysis. *p* value was calculated by one-way ANOVA and Duncan's multiple range test. * $p<0.05$ compared to vector control; ** $p<0.01$ compared to vector control; $^{\#}$ $p<0.05$ compared to scramble group; $^{\#\#}$ $p<0.01$ compared to scramble group. ns, no significant, miR-cluster, miR-23a/27a/24-2.

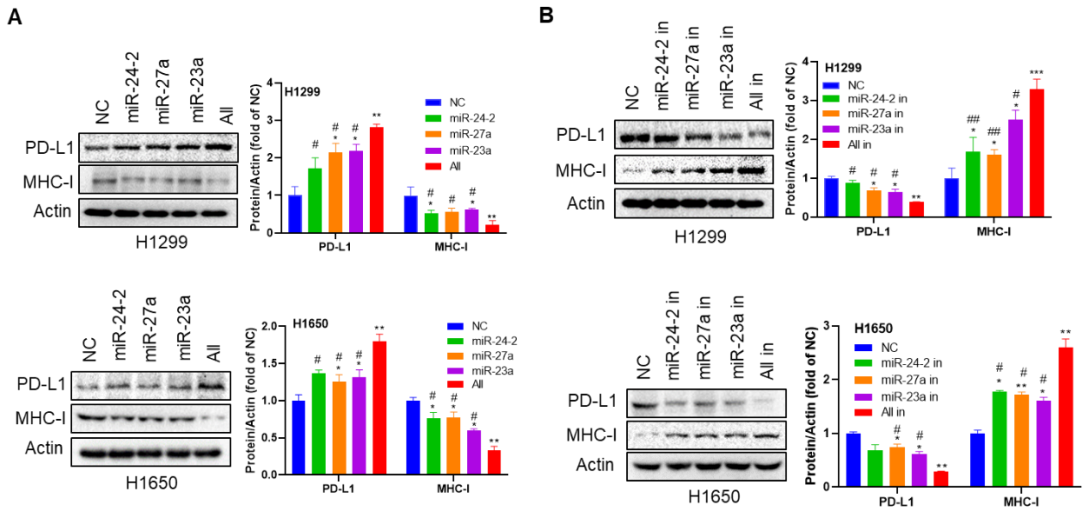

Fig. S7. Effects of miRNAs of miR-23a/27a/24-2 cluster on the expression of PD-L1 and MHC-I in NSCLC cells were examined by Western blot analysis. (A) Effects of

overexpression or (B) inhibition of miRNAs at miR-23a/27a/24-2 cluster on the expression of PD-L1 and MHC-I in NSCLC cells were examined by Western blot analysis. The Western blot band intensities were quantified and error bars indicate the mean ± SD for three independent experiments. Indicated NSCLC cells were transfected with indicated miRNAs or inhibitor of miRNAs. After 72 hours of transfection, cells were subjected to Western blot analysis. NC, non-specific control; miR-23a in, miR-23a inhibitor; miR-27a in, miR-27a inhibitor; miR-24-2 in, miR-24-2 inhibitor; All, co-transfection of all miRNAs at miR-23a/27/24-2 cluster; All in, co-transfection of all inhibitor of miRNAs at miR-23a/27/24-2 cluster. *p* value was calculated by one-way ANOVA and Duncan's multiple range test. * $p<0.05$ compared to vector control; ** $p<0.01$ compared to vector control; *** $p<0.001$ compared to vector control; $^{\#}$ $p<0.05$ compared to scramble group; $^{\#\#}$ $p<0.01$ compared to scramble group.