

SUPPLEMENTARY FIGURES

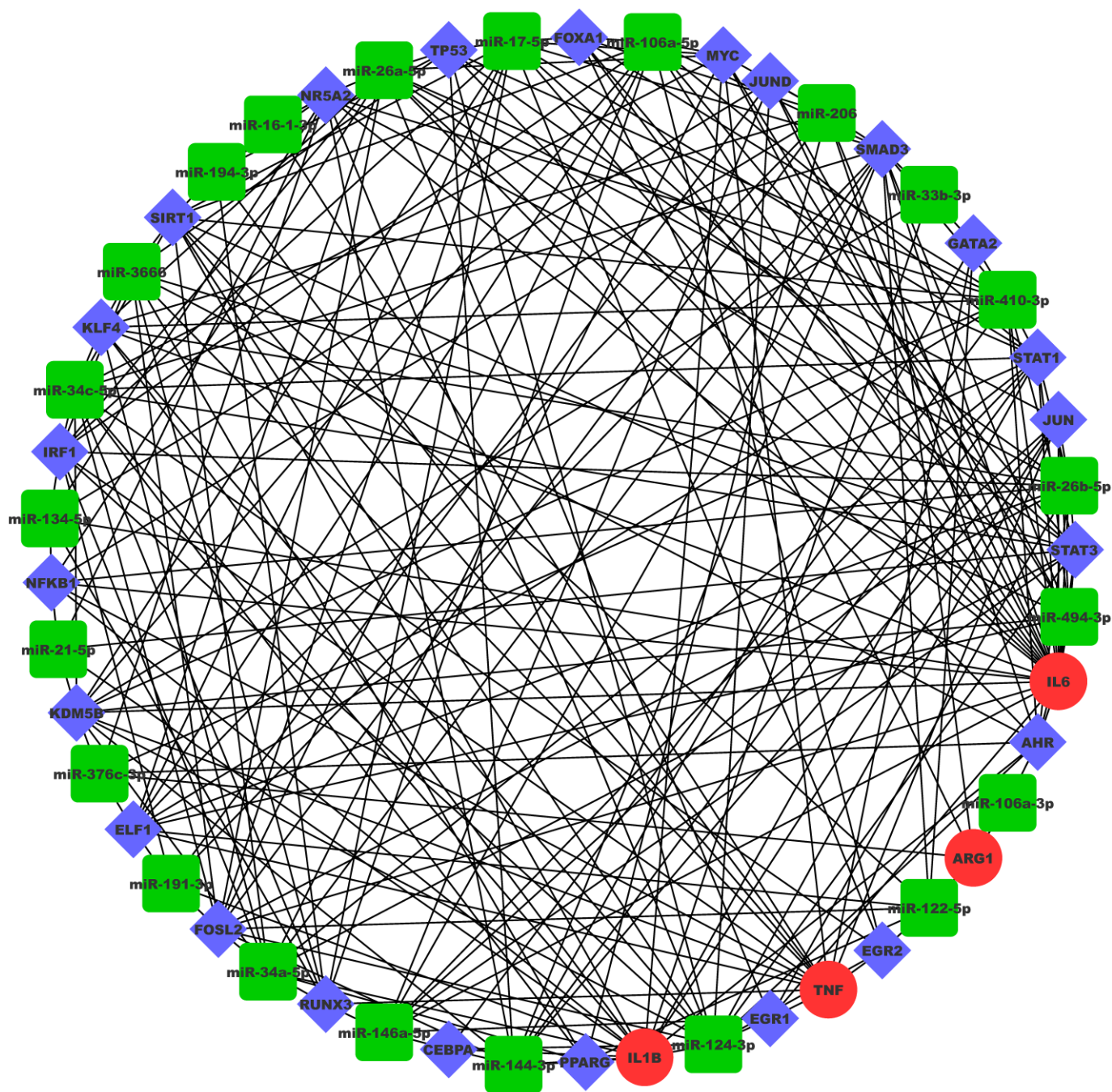


Fig.S1 NSCLC-specific 3-node miRNA–FFL regulatory network comprising 49 nodes and 242 edges. The green rectangular nodes represent NSCLC-specific miRNAs, red circular nodes represent NSCLC-specific DEGs, and blue diamond nodes represent NSCLC-specific TFs.

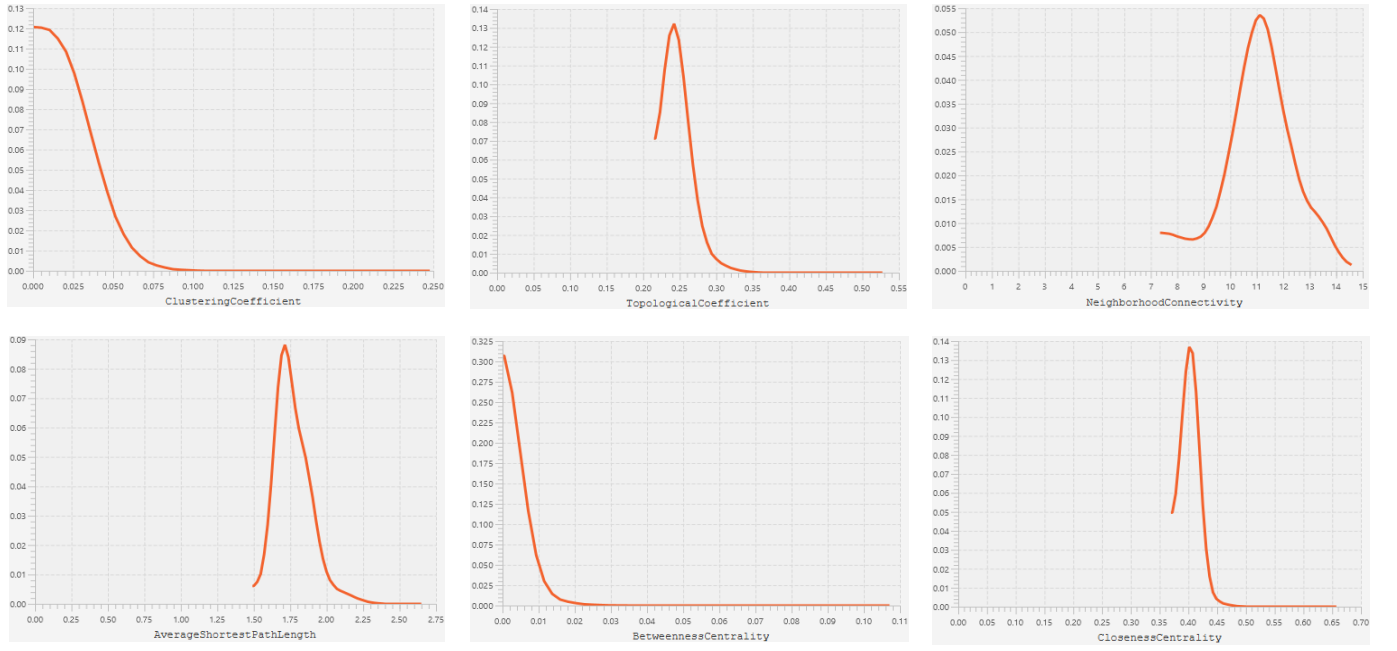


Fig.S2 Topological Graphs. Topological property / centrality plots of the NSCLC-specific 3-node miRNA FFL representing (A) Clustering coefficient, (B) Topological coefficient, (C) Neighborhood connectivity, (D) Average shortest path length, (E) Betweenness centrality, and (F) Closeness centrality as a function of degree. The lines are fitted with power laws.

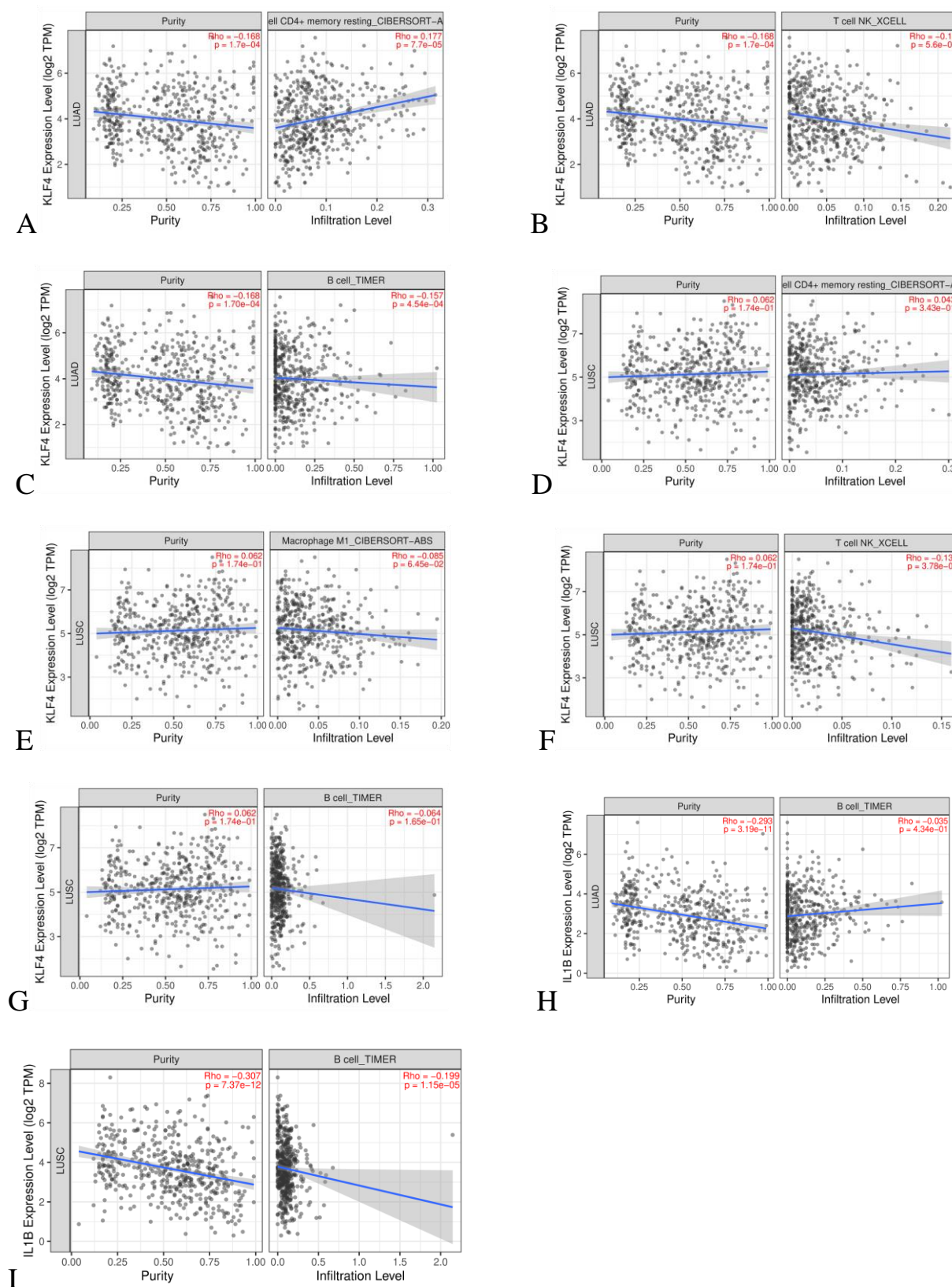


Fig.S3 Scatter plots exhibiting correlations of KLF4 with infiltrating levels of immune cells. (A) T Cell CD4+, (B) NK cell, and (C) B cell in case of LUAD and (D) T Cell CD4+, (E) M1 Macrophage, (F) NK cell and (G) B Cell in LUSC. Scatter plots showing correlations of IL-1 β with infiltrating levels of B cell in case of (H) LUAD and (I) LUSC, respectively. Left and right panel demonstrate gene expression levels against tumor purity and infiltrating levels of immune cells, respectively. In addition, Spearman's correlation value and estimated statistical significance were shown as the legends for each scatter plot.

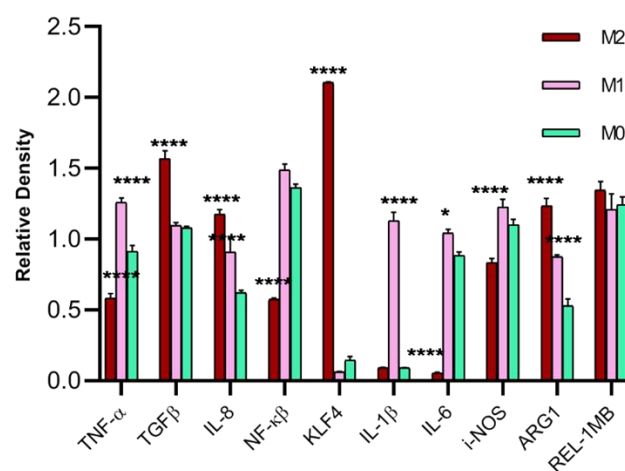
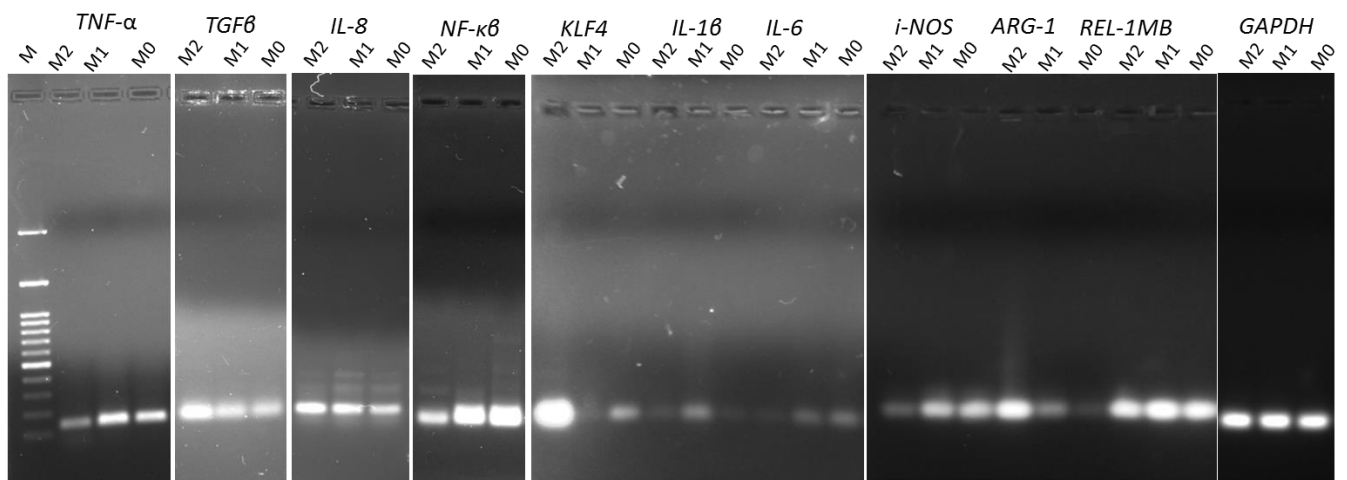


Fig.S4 Macrophage stimulation. The relative expression of M1 specific markers – TNF- α , NF- κ B, IL-1 β , IL-6, i-NOS; and M2 specific markers – TGF β , IL-8, KLF4, ARG1 and REL-1MB were checked upon stimulation of macrophages via LPS (100ng/ml, L4524, Lipopolysaccharide from *E.coli* 055:B5, sigma, Saint Louis, MO, USA) and IL-4 (10ng/ml) in M1 and M2 states via semi-quantitative RT-PCR. GAPDH was used as an endogenous control. The unstimulated state M0 was used as a control to compare the expression with M1 and M2 states. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001.

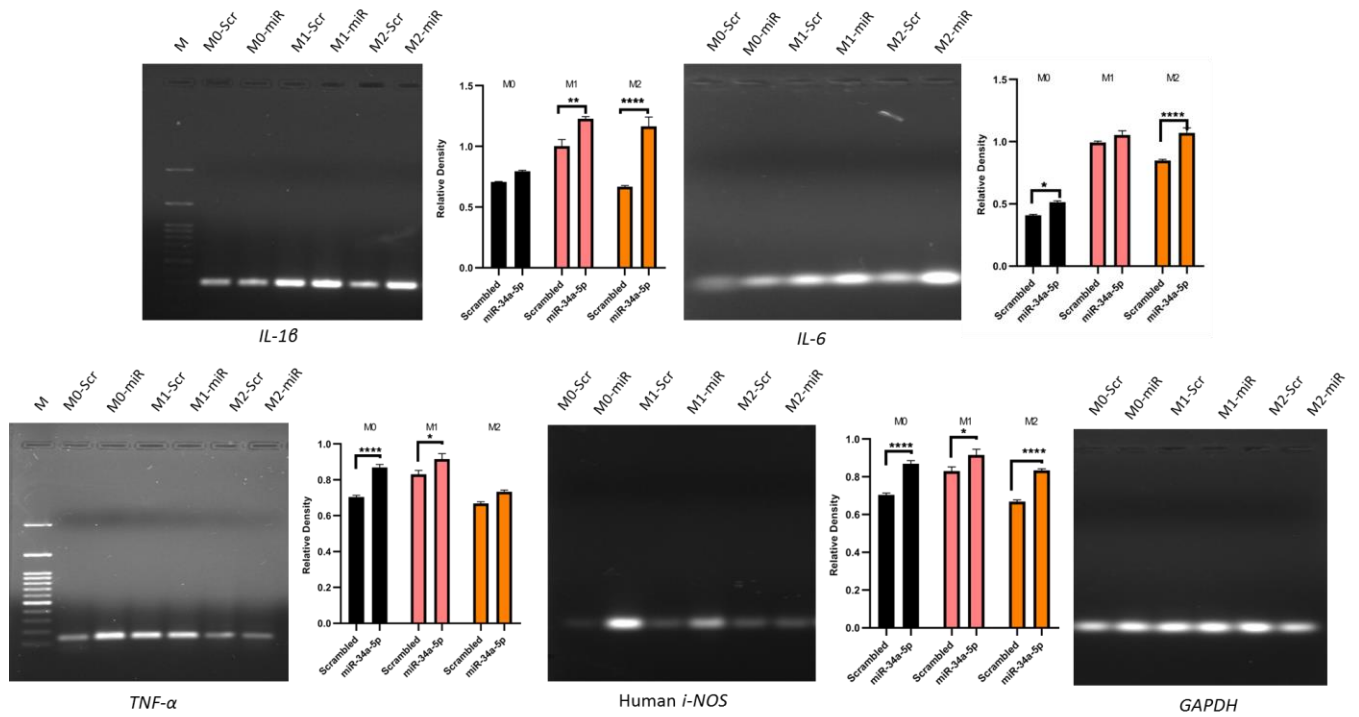


Fig.S5 Relative expression of M1 macrophage specific markers (IL-1 β , IL-6, TNF- α and Human iNOS), upon transfection of THP-1 macrophages (3 subsets- M0, M1 and M2) with Scrambled and miR-34a-5p. The expression was determined via semi-quantitative RT-PCR and relative densities of the bands are plotted. GAPDH was used as an endogenous control. (Scrambled transfection, miR-mir-34a-5p transfection). *p < 0.05, **p < 0.01, *p < 0.001, ****p < 0.0001.**

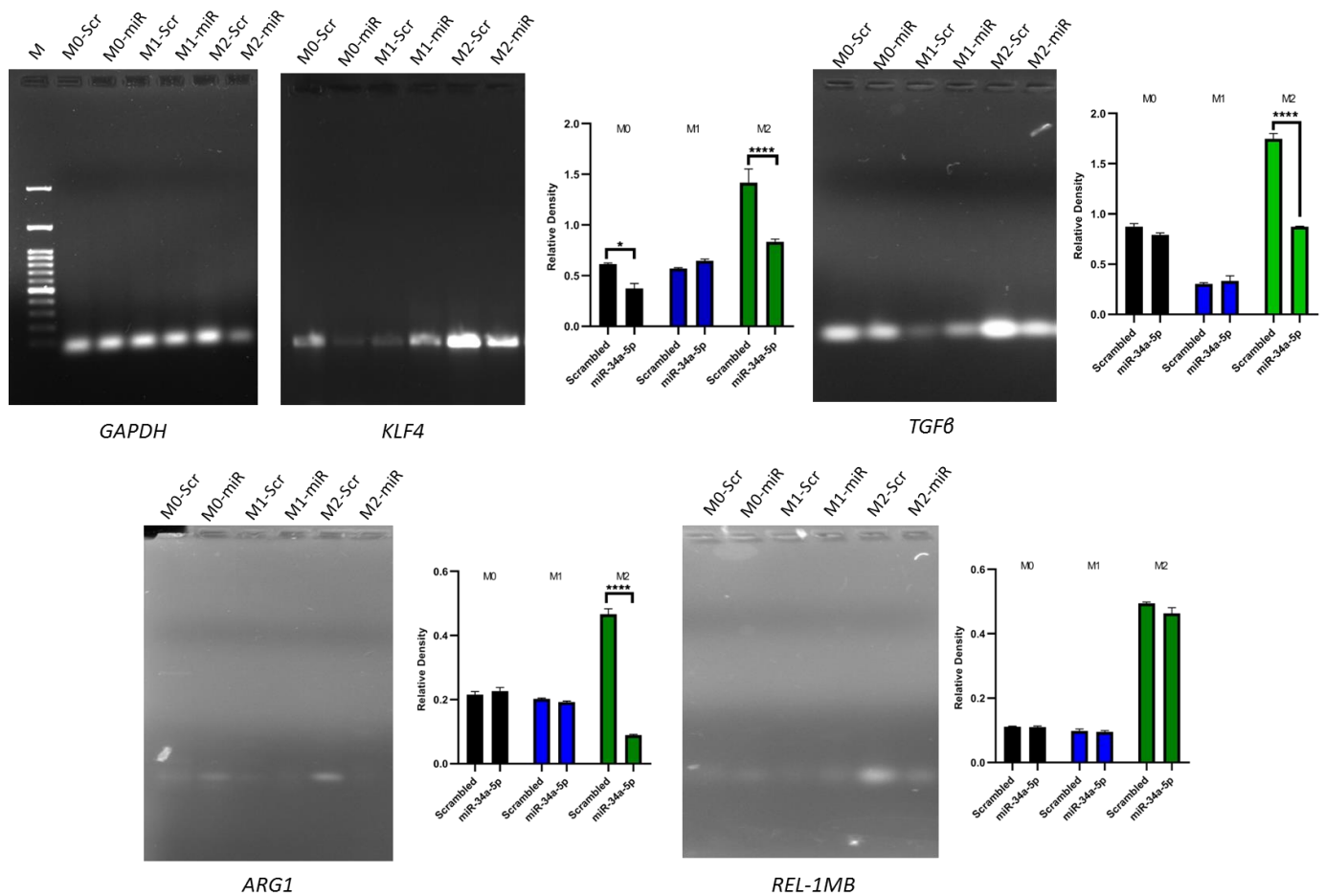


Fig.S6 Relative expression of M2 macrophage specific markers (KLF4, TGFβ, ARG1 and REL-1MB), upon transfection of THP-1 macrophages (M0, M1 and M2) with Scrambled and miR-34a-5p. The expression was determined via semi-quantitative RT-PCR and relative densities of the bands are plotted. GAPDH was used as an endogenous control. (Scr-scrambled transfection, miR-mir-34a-5p transfection). *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001.

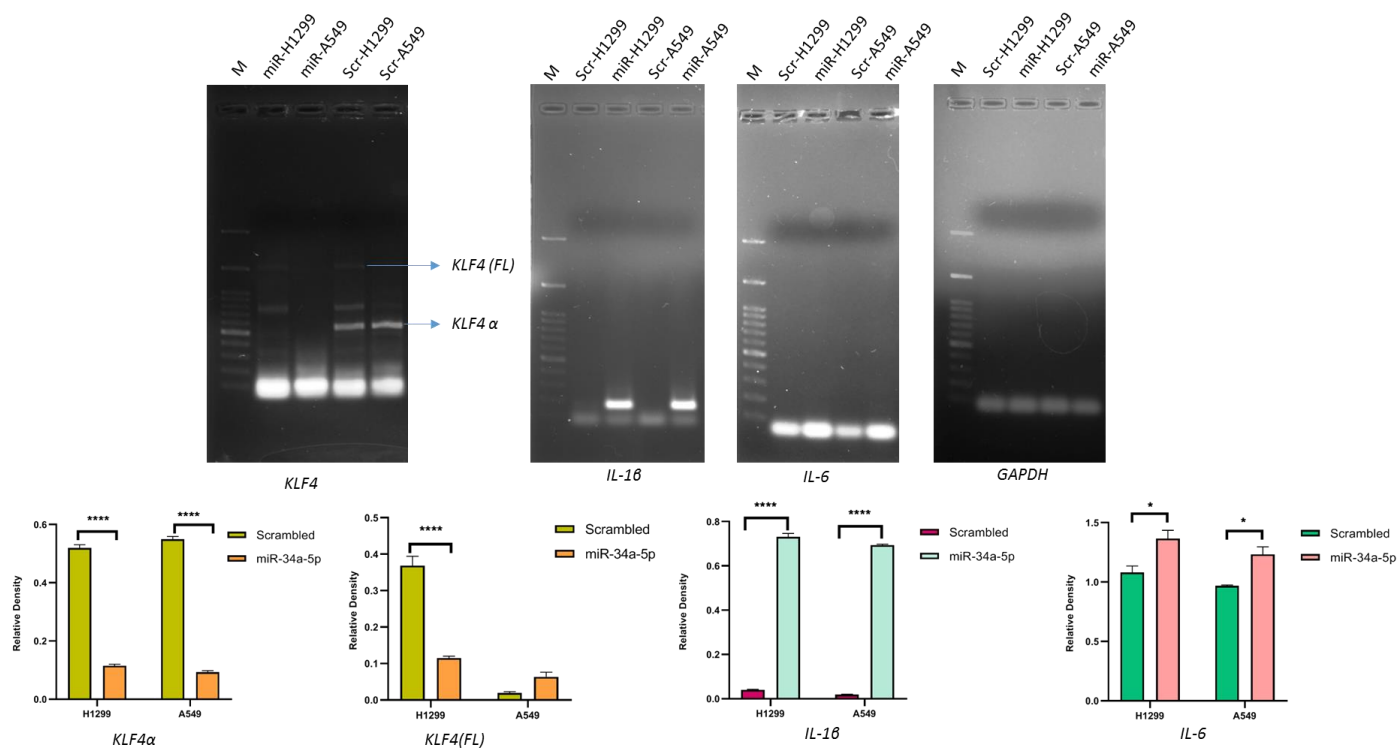


Fig.S7 Relative expression of KLF4, IL-1 β and IL-6 upon transfection of NSCLC cells with Scrambled and miR-34a-5p. The expression was determined via semi-quantitative RT-PCR and relative densities of the bands are plotted. GAPDH was used as an endogenous control. (Scr-scrambled transfection, miR-mir-34a-5p transfection). *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001.

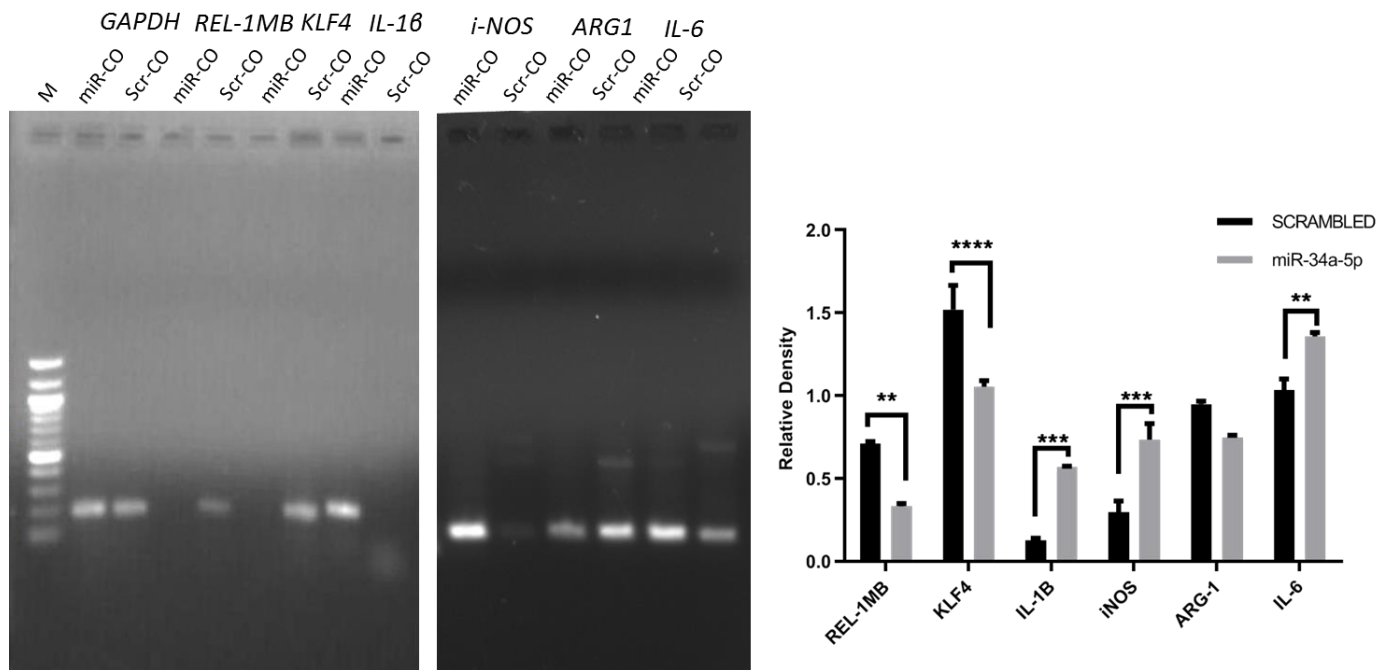
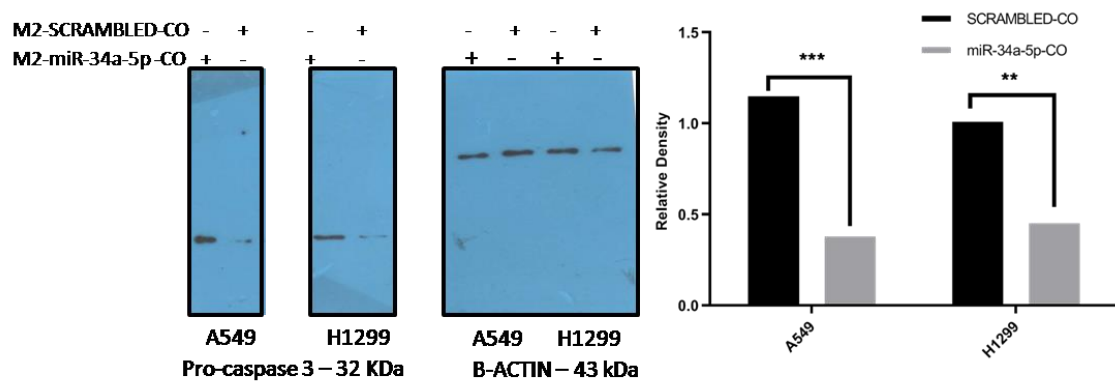
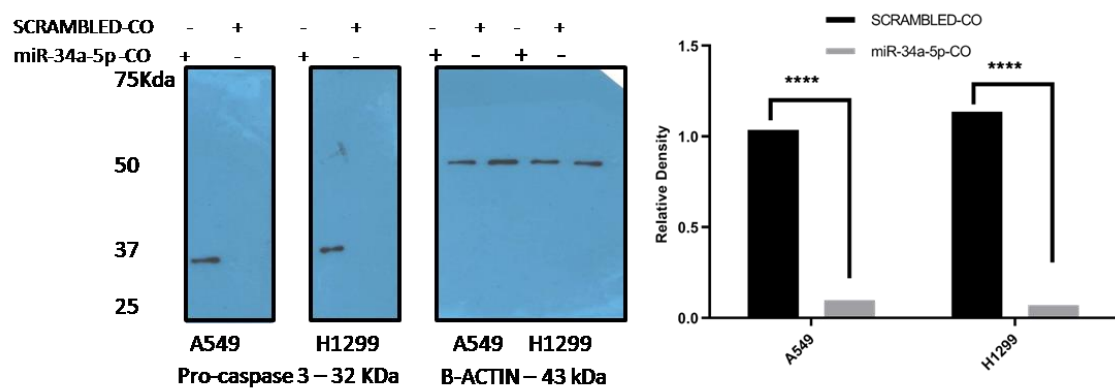


Fig.S8 Differential expression of macrophage specific markers, upon Co-culture of M2 macrophages with transfected H1299 cells. The expression was determined via semi-quantitative RT-PCR and relative densities of the bands are plotted. GAPDH was used as an endogenous control. (miR-CO -miR transfected cells co-culture, Scr-CO- scrambled transfected cells co-culture). *p < 0.05, **p < 0.01, ***p < 0.001, ****p<0.0001.

(A)



(B)



(C)

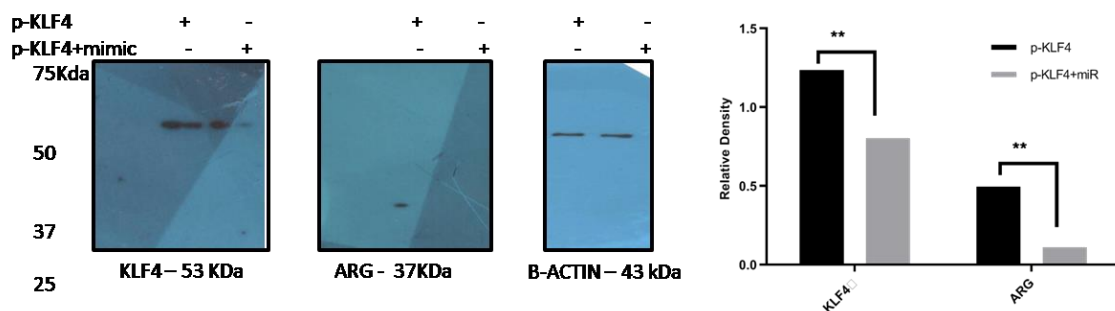
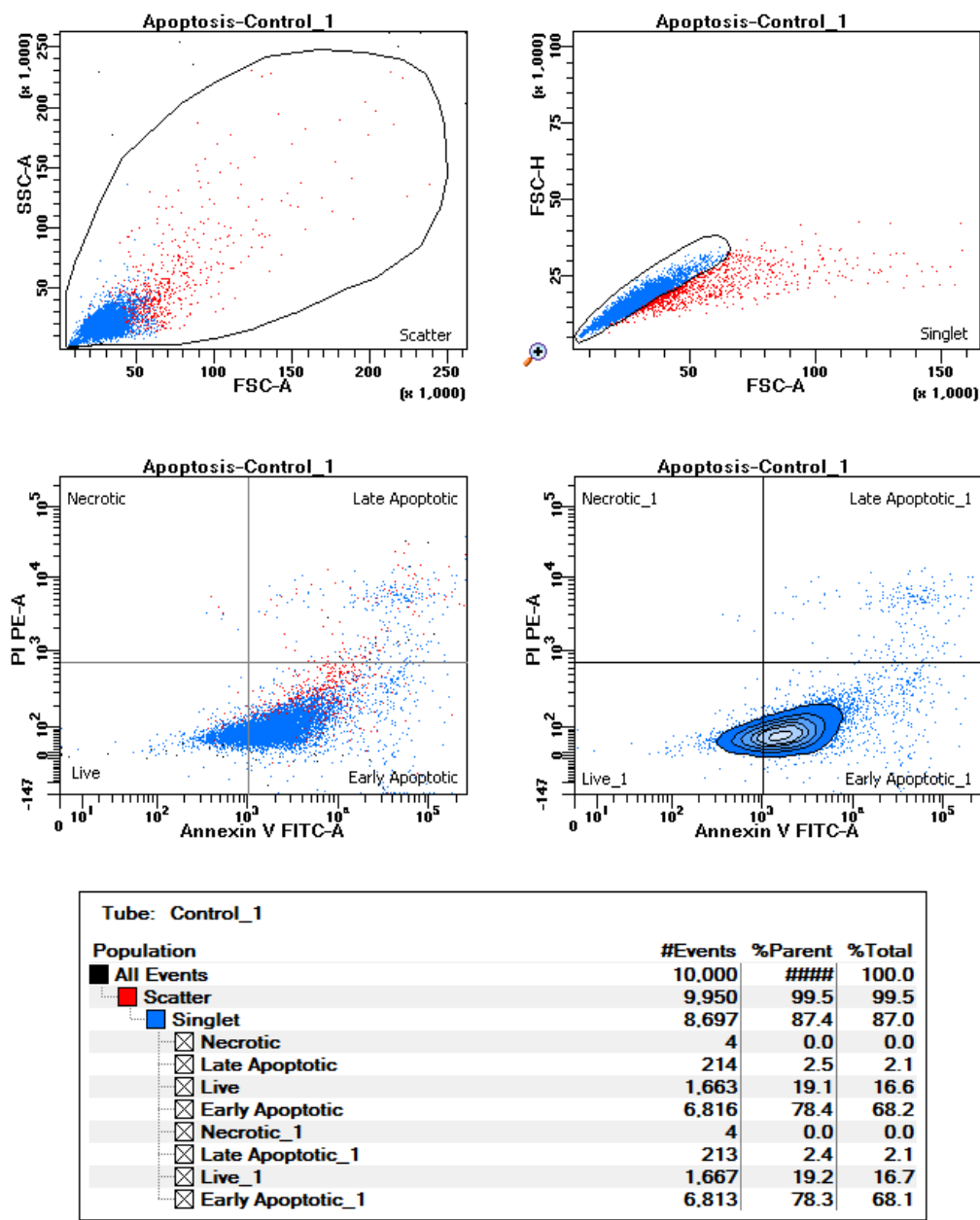


Fig.S9 Western Blotting (A) Blots and relative densitometry for Procaspase-3 and β -Actin (endogenous control) after treatment of A549 and H1299 cells with conditioned medium from co-culture of scrambled and miR-34a-5p transfected THP-1(IL-4 stimulated) and A549 cells; (B) Blots and relative densitometry for Procaspase-3 and β -Actin after treatment of A549 and H1299 cells with conditioned medium from co-culture of scrambled and miR-34a-5p transfected H1299 and THP-1 cells (IL-4

stimulated); (C) Blots and relative densitometry for KLF4, ARG1 and β -actin developed after overexpression of KLF4 and KLF4+ miR-34a-5p mimic in THP-1 cells. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001



Experiment Name:		Apoptosis_03Feb2020		
Tube Name:		Control_1		
Population	#Events	%Parent	Annexin V FIT... Median	PI PE-A Median
■ All Events	10,000	####	1,979	89
■ Scatter	9,950	99.5	1,979	89
■ Singlet	8,697	87.4	1,856	84
☒ Necrotic	4	0.0	513	2,793
☒ Late Apoptotic	214	2.5	41,156	4,734
☒ Live	1,663	19.1	717	64
☒ Early Apoptotic	6,816	78.4	2,170	90
☒ Necrotic_1	4	0.0	513	2,793
☒ Late Apoptotic_1	213	2.4	41,158	4,770
☒ Live_1	1,667	19.2	718	64
☒ Early Apoptotic_1	6,813	78.3	2,170	90

Fig.S10. (A) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells transfected with pcDNA 3.1 for 48 h (Fig.5H)

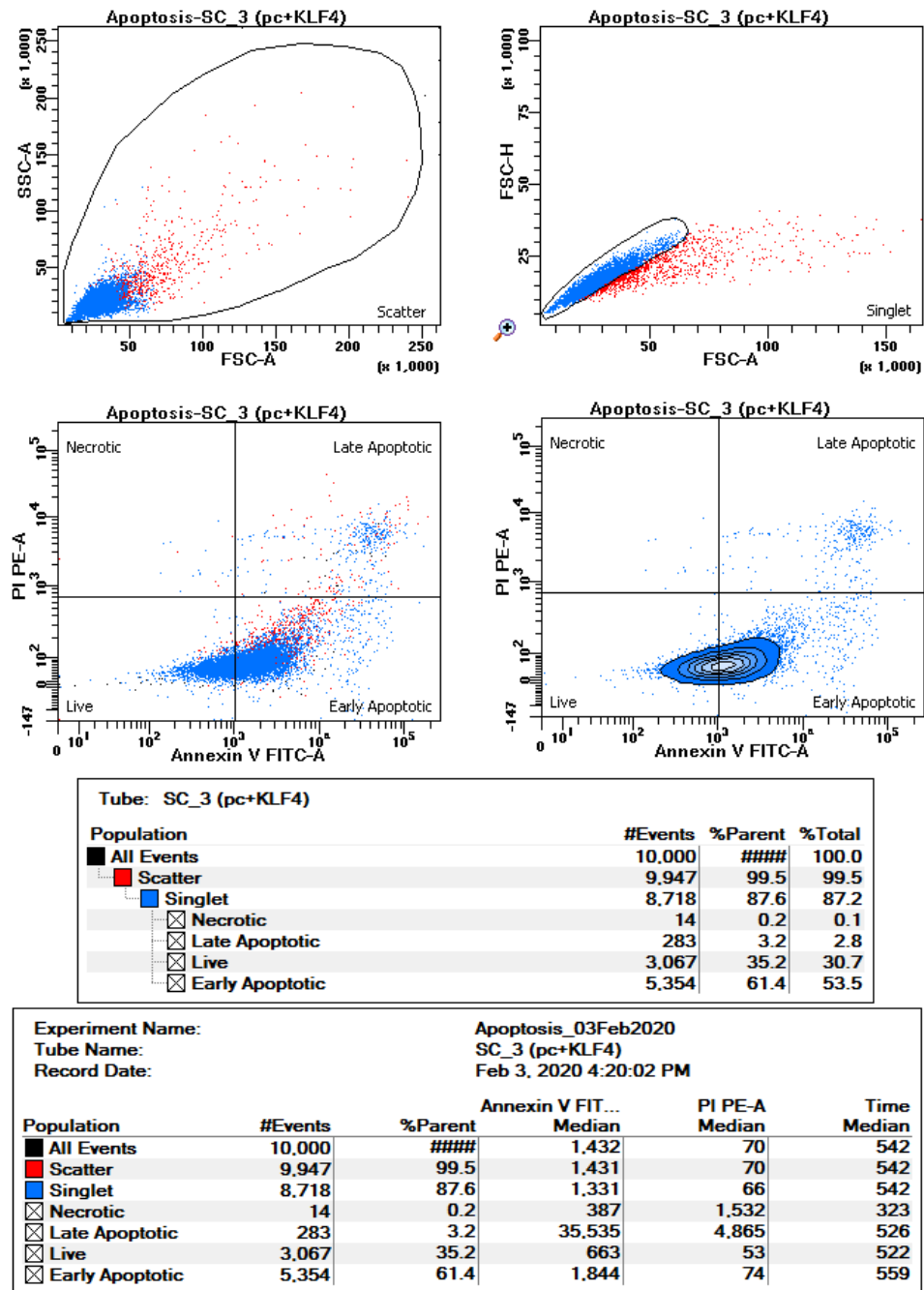


Fig.S10 (B) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells transfected with pcDNA 3.1+ KLF4 for 48 h (Fig.5H).

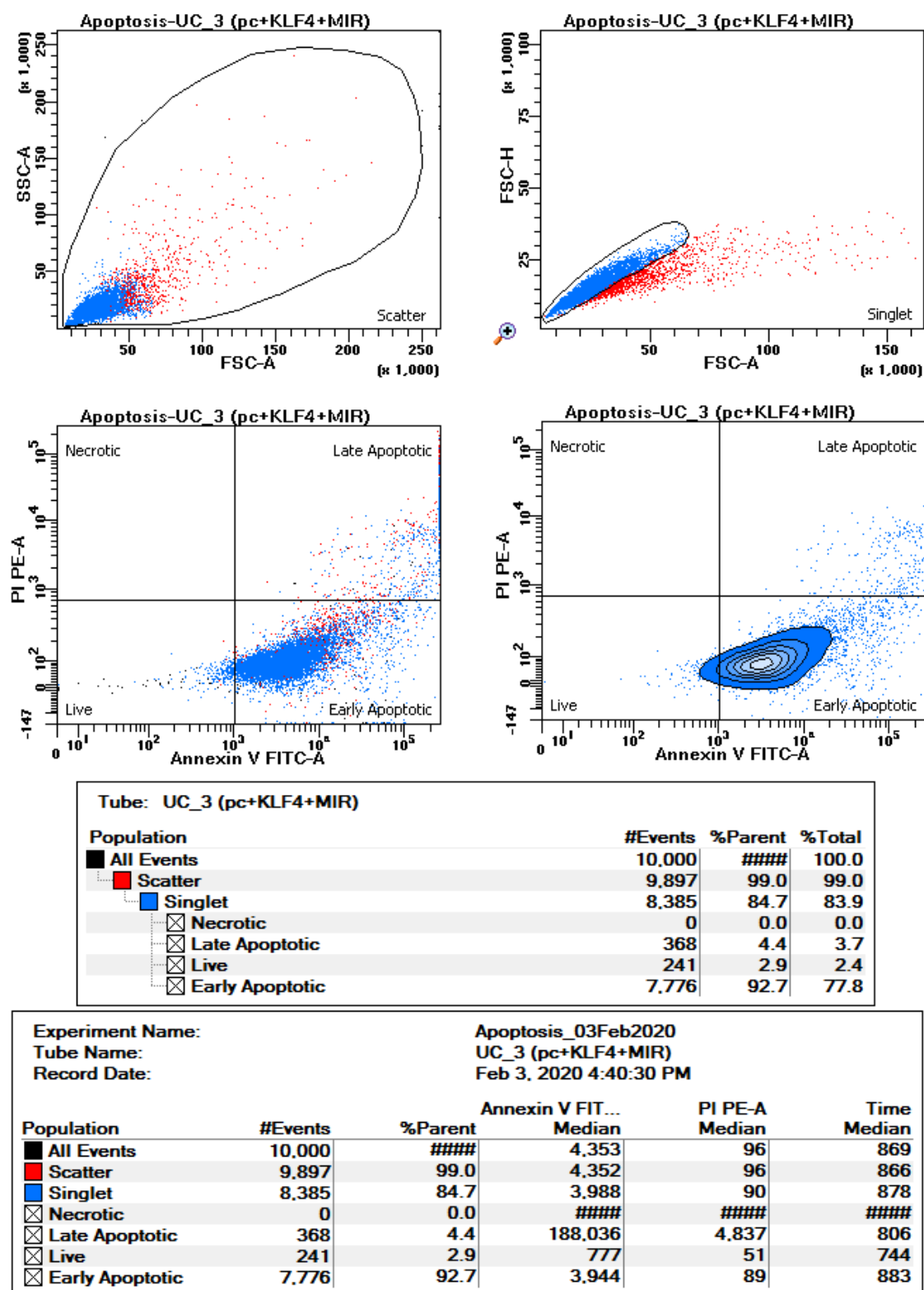


Fig.S10 (C) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells transfected with pcDNA 3.1+ KLF4+miR for 48 h (Fig.5H).

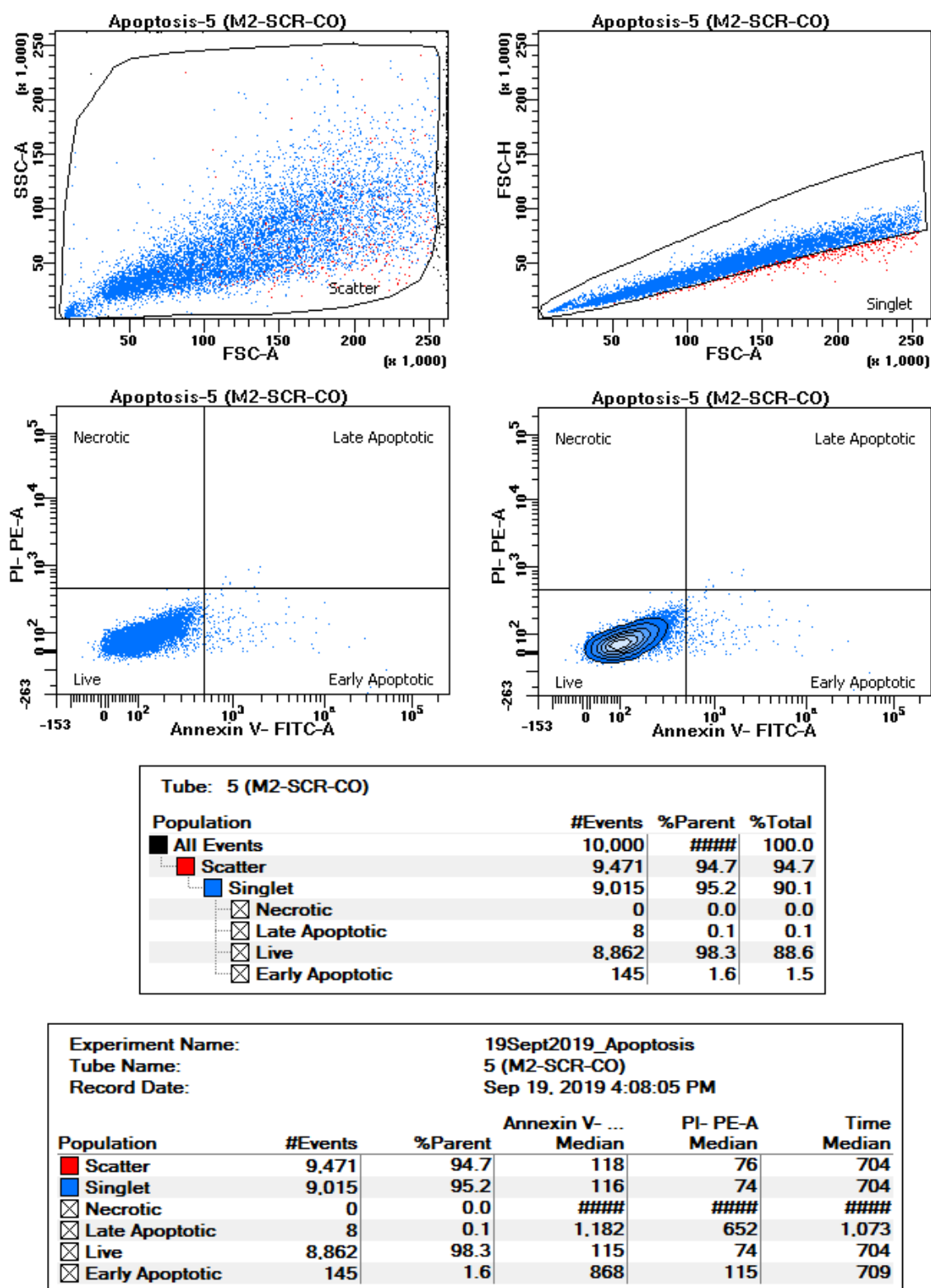


Fig.S11 (A) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells treated with Co-culture Conditioned medium of M2 macrophages (THP-1) cells transfected with Scrambled for 48 h (Fig.6P).

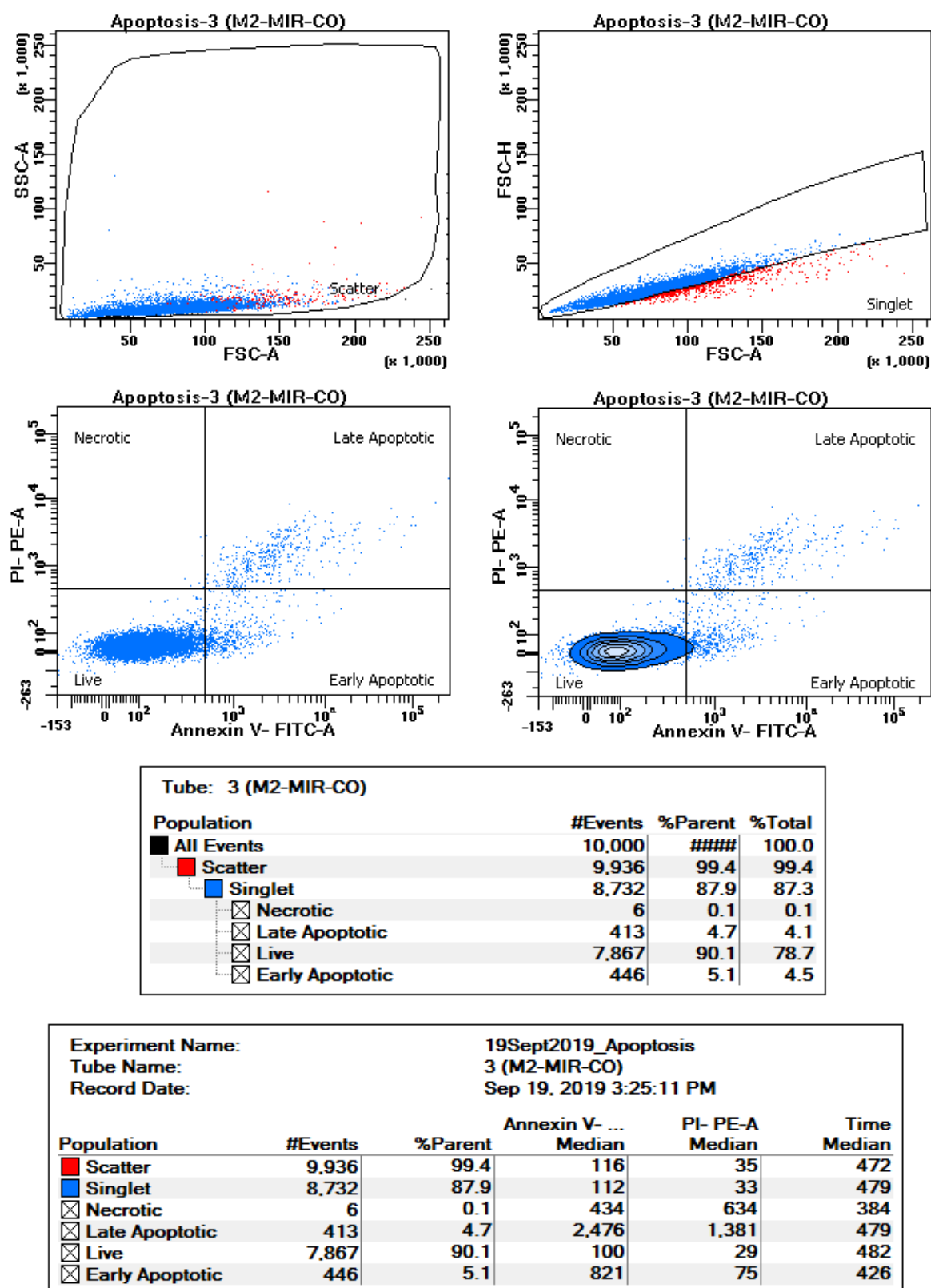


Fig.S11 (B) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells treated with Co-culture Conditioned medium of M2 macrophages (THP-1) cells transfected with miR-34a-5p mimic for 48 h (Fig.6P).

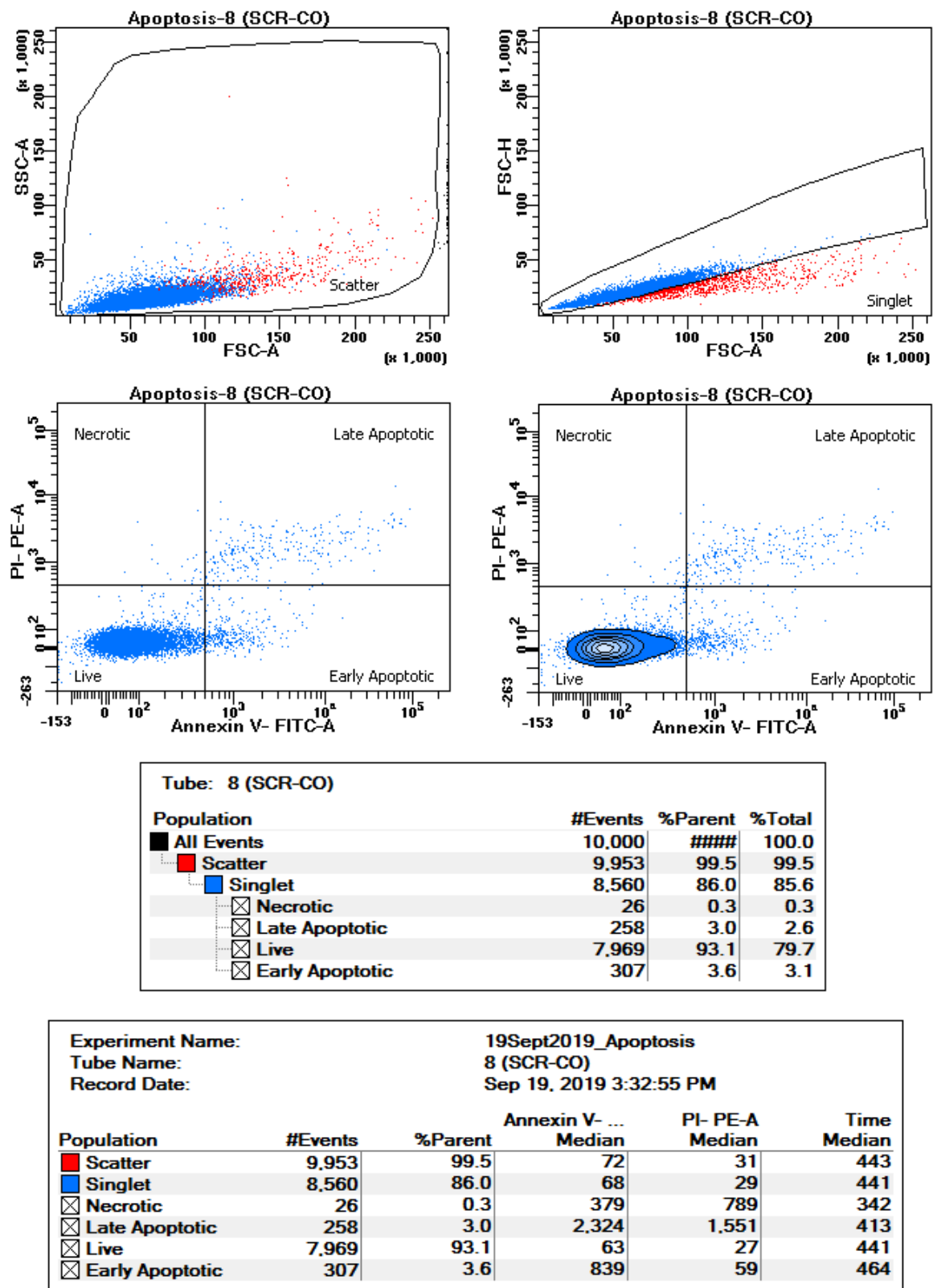
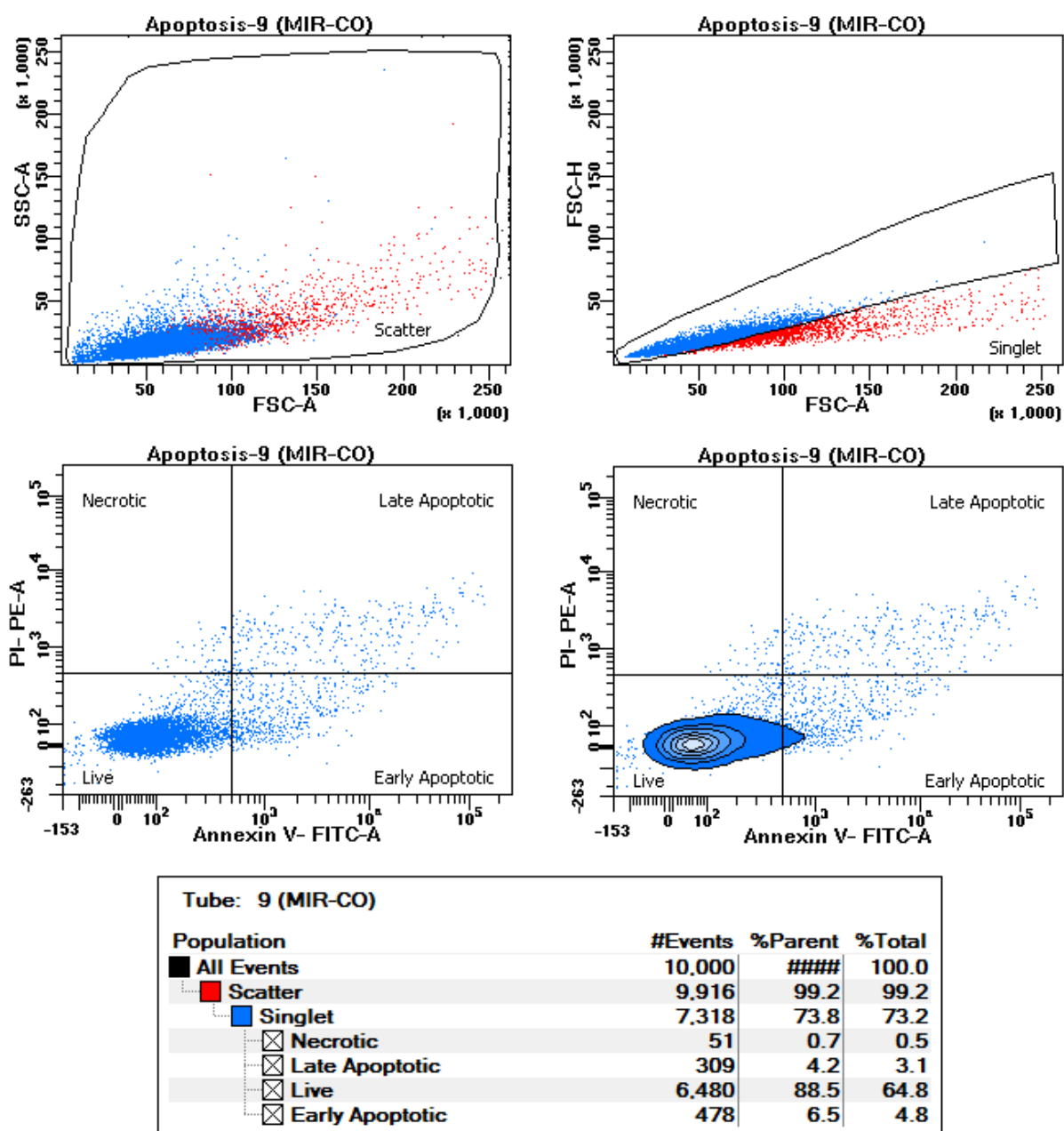


Fig.S12 (A) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells treated with Co-culture Conditioned medium of H1299 cells transfected with Scrambled for 48 h (Fig.7O).



Experiment Name:		19Sept2019_Apoptosis			
Tube Name:		9 (MIR-CO)			
Record Date:		Sep 19, 2019 3:33:56 PM			
Population	#Events	%Parent	Annexin V- ... Median	PI- PE-A Median	Time Median
Scatter	9,916	99.2	90	43	739
Singlet	7,318	73.8	84	40	730
Necrotic	51	0.7	347	721	537
Late Apoptotic	309	4.2	4,915	1,536	753
Live	6,480	88.5	73	35	728
Early Apoptotic	478	6.5	1,138	130	760

Fig.S12 (B) SSC/FSC plots of Flow cytometry based apoptotic analysis using AnnexinV /FITC – PI staining of A549 cells treated with Co-culture Conditioned medium of H1299 cells transfected with miR-34a-5p mimic for 48 h (Fig.70).

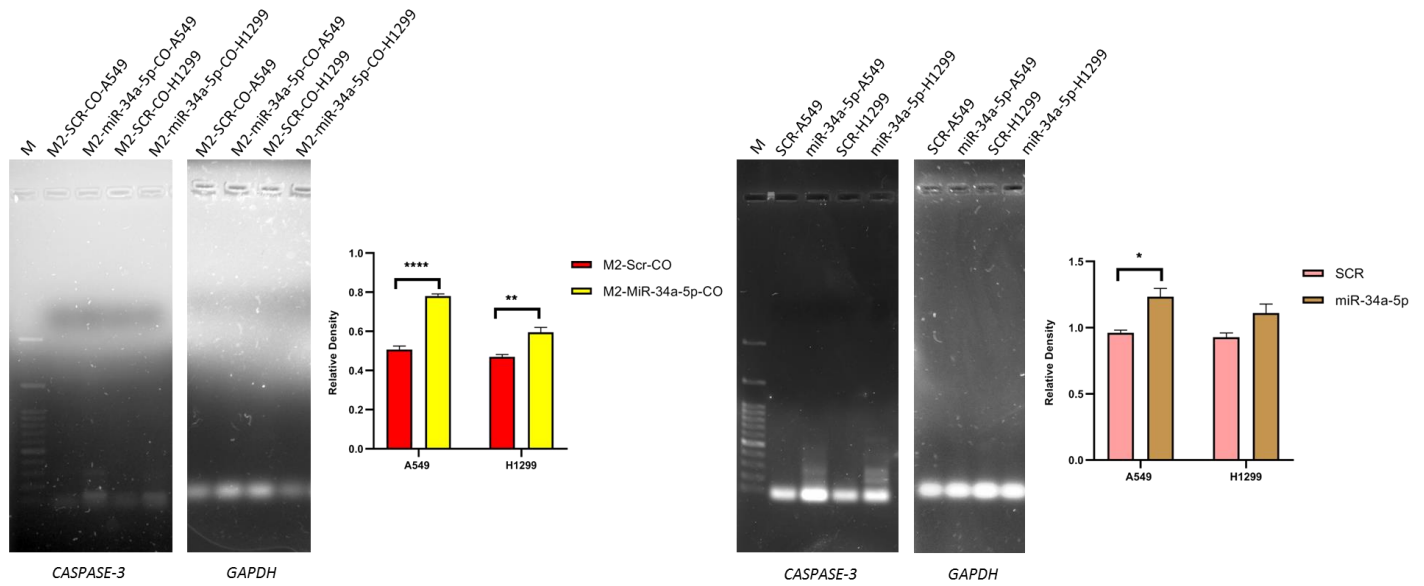


Fig.S13 Relative expression of Caspase-3 upon transfection of (A) M2-Scr-CO and M2-miR-34a-5p-CO in A549 and H1299 cells; (B) Scrambled and miR-34a-5p in A549 and H1299 cells. The expression was determined via semi-quantitative RT-PCR and relative densities of the bands are plotted. GAPDH was used as an endogenous control. (Scr-scrambled transfection, miR-mir-34a-5p transfection). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.