

Table S1 Thirteen pairs of patients with lung adenocarcinoma selected for bioinformatics analysis

No.	Sample	Normal	Cell number	Tumor	Cell number	Histology	Stages	Source
1	P0006	LUNG_N06	2,839	LUNG_T06	3,426	ADC	IA	Nature Communication 2020
2	P0008	LUNG_N08	3,380	LUNG_T08	3,765	ADC	IB	
3	P0009	LUNG_N09	2,528	LUNG_T09	3,840	ADC	IIA	
4	P0018	LUNG_N18	4,628	LUNG_T18	3,705	ADC	IA	
5	P0019	LUNG_N19	3,870	LUNG_T19	4,361	ADC	IA	
6	P0020	LUNG_N20	5,798	LUNG_T20	4,021	ADC	IA	
7	P0028	LUNG_N28	3,411	LUNG_T28	4,705	ADC	IIIA	
8	P0030	LUNG_N30	3,884	LUNG_T30	4,094	ADC	IA	
9	P0031	LUNG_N31	4,241	LUNG_T31	5,578	ADC	IIIA	
10	P0034	LUNG_N34	5,222	LUNG_T34	3,280	ADC	IA3	
11	Sample3	Normal	4,235	Core	2,149	ADC	IIIB	Nature Medicine 2018
12	Sample4	Normal	2,933	Core	5,270	ADC	IIB	
13	Sample6	Normal	4,366	Core	2,098	ADC	IIIA	

ADC, adenocarcinoma.

Table S2 Clinicopathological features of five patients with lung adenocarcinoma

No.	Gender	Age (years)	Histology	Stage	Therapeutic target	Therapy history
Case 1	Female	57	ADC	IVA	EGFR 19del	None
Case 2	Male	42	ADC	IVA	–	Pemetrexed + carboplatin + cariluzumab
Case 3	Female	60	ADC	IVB	EGFR 19del	Osimertinib
Case 4	Female	58	ADC	IVA	EGFR L858R	Osimertinib
Case 5	Female	73	ADC	IVA	EGFR L858R	Osimertinib; icotinib; almonertinib

ADC, adenocarcinoma.

Table S3 Primer sequences for real-time polymerase chain reaction

Gene	Primers
<i>FABP4</i> -F	5'-GGCACCCAGCACAAATGAA-3'
<i>FABP4</i> -R	5'-CCGATCCACACGGAGTACTTG-3'
<i>EOMES</i> -F	5'-GTTAGGGGAGCAGCTCTTGG-3'
<i>EOMES</i> -R	5'-CCGGAAAACCTTCTTGACGC-3'
<i>Tbx21</i> -F	5'-GCCCACGATGAAACCTGAGA-3'
<i>Tbx21</i> -R	5'-GCTCCTTCATGCCCAAGACT-3'

FABP4, fatty acid-binding protein 4; *Tbx21*, T-box 21; *EOMES*, *eomesodermin*.

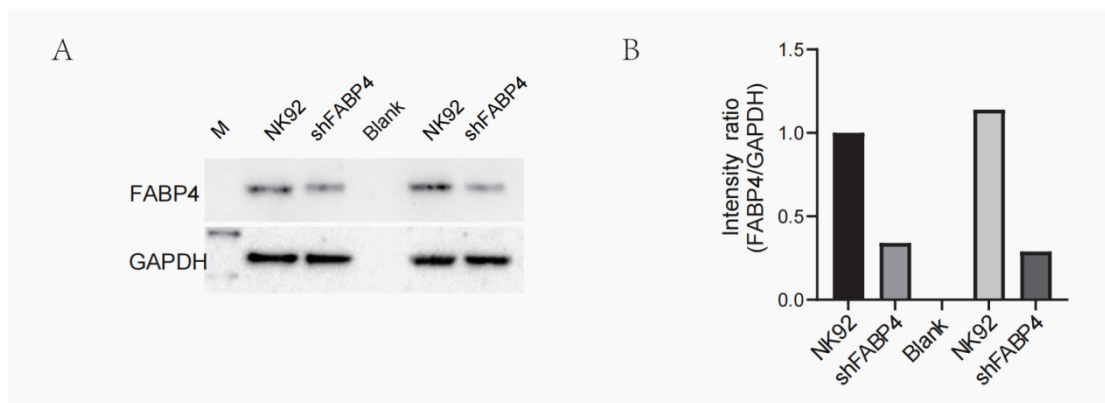


Figure S1 Validation of FABP4 knockdown in NK92 cells. (A) Western blot analysis shows FABP4 expression in shFABP4_NK92 cells. (B) Bar graph showing the quantification of FABP4 expression levels normalized to GAPDH. FABP4, fatty acid-binding protein 4; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

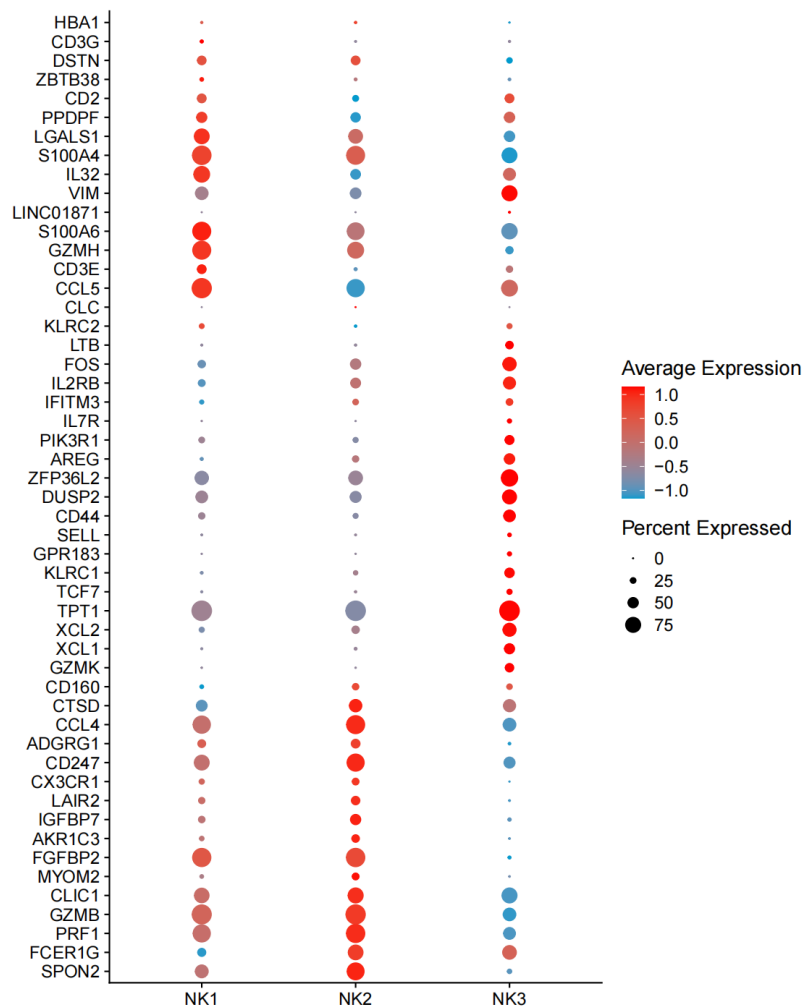


Figure S2 Dot plot illustrating the validated marker genes defining three distinct NK cell subpopulations.