

Table S1: Clinical baseline characteristics of patients included in the study

	Characteristic	Standard treatment n=13	TAA-DC n=5
Lung cancer	Median age, years (range)	55.8(44-62)	53.4(45-68)
	Sex, n(%)		
	Men	10(76.9)	3(60)
	Women	3(23.1)	2(40)
	Lung cancer statue, n(%)		
	NSCLC	12(92.3)	5(100)
	SCLC	1(7.7)	0
	Organ metastasis, n(%)		
	Brain	13(100)	5(100)
	Bone	4(30.8)	2(40)
	Lymph node	3(23.1)	1(20)
Others	2(15.4)	3(60)	
PD-1 treatment, n(%)	0	4(80)	
	Characteristic	Standard treatment n=28	TAA-DC n=5
GBM	Median age, years (range)	48.9(22-67)	36.6(18-55)
	Sex, n(%)		
	Men	21(75)	4(80)
	Women	7(25)	1(20)
	WHO, n(%)		
	III	1(4)	0(0)
	IV	27(96)	5(100)
Treatment, n(%)			
Systemic therapy	28(100)	5(100)	

Table S2: Primer sequences for tested genes

NO.	Ag	Forward Primer	Reverse Primer
1	AIM2	GCCTCACGTGTGTTAGATGC	ATCTTCGGGGTTTCACCAGC
2	AKAP4	ATTCCATCAGCAAGGGGCTC	CTCCTTGGTGTGCCTTAGCA
3	Art4	GGAGGTGGTCACTGAGATTC	GCACGTATTCCGGTAAGG
4	BAGE	TGGCTCGTCTCACTCTGG	TCCTGTTGAGCTGCCGTCT
5	BCAN	GGAGGAGGCGACAACTTC	GAGCTGTCTCCTTCCAGAACA
6	BSG	CCCTTCCTGGGCATCGT	CGGCGTCGTCATCATCC
7	CAIX	GGACATATCTGCACTCCTGC	TGCTTAGCACTCAGCATCAC
8	CCND1	CCTCGGTGTCCTACTTCAAAT	CTCTTTTTACGGGCTCCAG
9	CD133	AGTGGCATCGTGCAAACCTG	CTCCGAATCCATTTCGACGATAGTA
10	CDC45L	GCAGGTGAAGCAGAAGTTCC	GCATGTCCTTCATCCCAAAT
11	CDCA1	GAGAACTGAAGTCCCAGGAAAT	CTGATACTTCCATTTCGCTTCAAC
12	CEA	TGTCGGCATCATGATTGG	GCAAATGCTTTAAGGAAGAAGC
13	CSPG4	CCTTTTGGGAGGCCCATGAT	GCAGCCTCAAAGACACAGC
14	EPCAM	ACTACAAGCTGGCCGTAAAC	AGCCCATCATTGTTCTGGAG
15	EphA2	TCCCTGCTGTGCCATGCT	CCCTCAGCGGAAGTTGCA
16	EZH2	GGCCAGACTGGGAAGAAATC	ACCTCTTGAGCTGTCTCAGT
17	FABP7	AGCCTGGATGGAGACAACT	TGCCTTCTCATAGTGGCGAA
18	Fos1	CTGCCGCCCTGTACCTT	TGCTGCTACTCTTGCGATGA
19	GAGE	TATGCGGCCCGAGCAGTT	CCTGCCCATCAGGACCATC
20	gBK	GACATCACAGATCCCAAAG	GTGTTGACGGCTGCTCATC
21	glast	CATCATTGCAGTGGACTGGTTTC	CCCATTTCAACATCTCGGTTCTTC
22	gp100	ACAGGCCAACTGCAGAGG	CAGTTGGCGCCTGACCAG
23	GNTV	TCAAAGGCAGAACCCAGTCC	GTGCTGGAGCCATAAACAGT
24	HER2	ATACCCTCTCAGCGTACCCTTGT	TCCGGAGAGACCTGCAAAGA
25	HBEGF	TTCTGGCTGCAGTTCTCTCG	AAGTCACGGACTTTCCGGTC
26	HNRPL	TGGAGCAGAGGCAGCAG	TTTTGTGCGGGTCATCGTAG
27	HO1	AGTCTTCGCCCTGTCTACT	CTTCACATAGCGCTGCATGG
28	hTRET	CGTACAGGTTTCACGCATGTG	ATGACGCGCAGGAAAAATG
29	IGF2BP3	AGTTGTTGTCCCTCGTGACC	AGCCTTCTGTTGTTGGTGCT
30	IL13Ra2	GCAATGCACAAATGGATCAGAAG	TGCCAGGTTTCCAAGAACAGAGTA
31	IQGAP1	TGCTGAAGGACTCGTTGCAT	AGATTTTCGGCGTTGGTCTGT
32	ITGAV	CGCTTCTTCTCTCGGGACTC	TCACATTTGAGGACCTGCCC
33	KIF1C	ACCGCACCAAGCAAATC	CTCCCTTCTTCCGTCTTCA
34	KIF21B	GTGAACCAGGACAAGACCAG	TGTAGCATGGCATTCTCTCG
35	KIFC3	CTGCGTAAGAAGTGCCACAA	AGGTGGATGATGGAGTCGTC
36	LAGE1/CTAG2	GTGTCCGGCAACCTACTGTT	CACATCAACAGGGAAAGCTG
37	Lck	AGTCAGATGTGTGGTCTTTTGG	CCTCCGGGTTGGTCATC
38	LRR8A	AGGGAAAGGTGGGCTGCCTTT	ATACTGAAGAGGCAAGCTCCAG
39	MAGE1	ACTGCAAGCCTGAGGAAGCC	TGGGTTGCCTCTGTGAGTG
40	MAGE10	TACTGCACCCCTGAGGAGGTC	TGTGGTGGCAATTCTGTCCTG

41	MAGE2	ATGCCTCTTGAGCAGAGGAG	GAGCCCTCATCGGATTGTC
42	MAGE3	GTCGTCCGAAATTGGCAGTAT	GCAGGTGGCAAAGATGTACAA
43	MAGE4	CCACTACCATCAGCTTCACTTGC	CTTCTCGGAACAAGGACTCTGC
44	MAGE6	GTCGTCCGAAATTGGCAGT	GCAGGTGGCAAAGATGTACAC
45	Mart1	GCTCATCGGCTGTTGGTATT	CTGTCCCGATGATCAAACCC
46	MELK	GCCTGCCATATCCTTACTGG	AATCTCCGTTTTGATCCGGG
47	MET	CCATCCAGTGTCTCCAGAAGTG	TTCCAGTGATAACCAGTGTGTAG
48	MUC1	AATGAATGGCTCAAACTTGG	CACTAGGTTCTCACTCGCTCAG
49	NLGN4X	AGAATGCCTGCGGAACAAGA	TCCACGAACTTCAGGCCTTC
50	NrCAM	TTGTGCAAAGAGGGAGCATG	GGGCAGTTCCTGTTGTCT
51	NY-BR-1	ATCCTAGACTGGCTTCTGCT	ACAAGCATCTCCTGCAATGT
52	NY-ESO-1	TGTCCGGCAACATACTGACT	ACTGCGTGATCCACATCAAC
53	OFA/iLRP	CTGGTCTGAAGGTGTACAGGTGC	CTTAAGAGCCTATGCAAGAACAG
54	PCNA	TCTGAGGGCTTCGACACCTA	CATTGCCGGCGCATTTTAGT
55	PIK3R1	AACGAGTGGTTGGGCAATGA	CCTCGCAACAGGTTTTTCAGC
56	PRAME	TCCAGAGCCAGAAGCAG	GGAACAGGTCTACGAGCA
57	PRKDC	ACCTGTTCTGGCAGGATGTC	TCTGAGGACGAATTGCCTTT
58	PTHLH	CCATCCAAGATTTACGGCGA	GGTGGTTCTTTGTGTTGGGA
59	PTPRZ1	ACCCCATCCTCCAGACAACA	GTAGCATGCAAGGCCGAATC
60	RPL19	CTCAGGCTTCAGAAGAGGCT	ATTGGCGATTTTATTGGTCT
61	Sart1	AAGCAGCAGCAGGATTTTC	TCCAGCAGCCCTTTGTTTC
62	Sart2	CCCTCTATGAAGGAGTTGCG	GGCCAAAGTGGTTGATGTTG
63	Sart3	GAAATGTGCTGCCGTAGA	TGCTGACAAAGACGGTGA
64	SEC61G	GGACTCCATTTCGGCTGGTTA	AGCAAATCCTATTGCTGTTGCC
65	SGT1	CTGACTAAGGCTTTGGAACAGAA	CTGTAAAAGTTTCTAGGGCAGCA
66	Sox10	ATGCCAAAGCCCAGGTGA	TGAGGGAGGTGTAGGCGATC
67	Sox11	ACGGTCAAGTGCCTGTTTCTG	TGCTGGTGCAGGTGGTTCCCTC
68	Sox2	AAATGGGAGGGGTGCAAAGAGGAG	CAGCTGTCATTTGCTGTGGGTGATG
69	Sox4	CGTCCTCAGATGACTTTCCGG	TCTGGCACTTCCTTCAAACC
70	SP17	GCTCGGAGAGAAAGGAGGTTTC	TACTCCCCATTCTGCTGGA
71	SPAG9	AGTCATCAGCCCACAAAGTAGCAG	GATTCTCCACCTTCATCACCCATT
72	SPANXB	TAGTGGTTCGCTACAGGAGGAACGTGA	TTGCCGAAGTTTGAGGGATGTAG
73	STAT3	CCAAGCGAGGACTGAGCATC	CCAGACCCAGAAGGAGAAGC
74	Survivin	ACTGAGAACGAGCCAGACTT	CGGACGAATGCTTTTTATGTTT
75	TARA	GCCATGACGCCGATCTG	AGGTGGT-GGTGAGCGAGG
76	TFT	CGCTTCAAGGAGCTCACCA	CGAAGTCCAGCAGGAAGGAG
77	TNC	TGGCATCGGAGAATGCCTTT	CAGCTTCCTCTGGGTTCCCTG
78	TPBG	GCGGACCCAGATTAACAAAC	GTGTGGGTACACTTGCTACACC
79	Trag3	AGTAGACTGTTGAGAGACGCT	TCCACTTCCTCGCCTCTTTG
80	TRP1	TGCCCCCTTTGATGATGATG	CTGATACCACCCACTGTTTCG
81	TRP2	CCTGTCTCTCCAGAAGTTTG	CAGAGTCCCATCTGCTTTATC
82	Ube2V	TCTAATGGAGTGGTGGACCC	CTGTAACACTGTCCTTCGGG
83	Whsc-2	AACGCCCTGACGACCCT	CGCTCCGCTTCAACTGC

84	WT1	GATAACCACACAACGCCCATC	CACACGTCGCACATCCTGAAT
85	XAGE-1b	TGGATTCTTTCTCCGCTACTG	AAACCAGCTTGC GTTGTTC
86	YKL39	TTGACTGTGGCGTATC	AGAGGGCTGTTGTGGC
87	YKL40	AACGATCACATCGACACCTG	TTGAGACCCAAAGTTCCATC

Tumor Microenvironment Immunosuppressive Genes

NO.	Ag	Forward Primer	Reverse Primer
1	COX1	GGAGTTTGTCAATGCCACCT	GCAACTGCTTCTTCCCTTTG
2	COX2	GGTCTGGTGCCTGGTCTGAT	TCCTGTTTAAGCACATCGCATACT
3	FOXP3	TGACCAAGGCTTCATCTGTG	AGGAACTCTGGGAATGTGCT
4	IDO1	GCCCTTCAAGTGTTCACCAA	GCCTTTCCAGCCAGACAAATAT
5	PDL1	GTGCATGATCAGCTATGGTGGTG	CAGTTCATGTTCCAGAGGTGACTGGA
6	PDL2	CTGGAATTGCAGCTTCACCAGA	GTTGCATTCCAGGGTCACATTG
7	PGE2	GTACTGGCTTCGTACGCGCG	TAGCGCTCCAGGGCCATGGC
8	TDO	GGGAACTACCTGCATTTGGA	GTGCATCCGAGAAACAACCT

Table S3: Phenotypic analysis of infused DCs

Patient	Average number of DCs per infusion (10^7)	Viability (%)	CD80 (%)	CD83 (%)	CD86 (%)	CD11c (%)	CD14- (%)	HLA-ABC (%)	HLA-DR(%)	CCR7 (%)
BT001	1.8±0.8	78.6±13.0	52.2±32.3	88.7±5.4	96.3±1.9	93.5±2.9	97.3±1.8	92.2±3.2	95.8±2.2	26.3±14.1
BT045	1.8±0.9	82.6±7.2	78.3±20.2	86.8±8.6	93.4±7.2	96.4±3.3	94.8±3.2	92.2±8.6	97.9±1.9	36.5±14.3
BT051	2.4±1.2	85.9±5.3	84.1±21.4	88.2±17.2	98.0±1.3	84.3±30	95.1±5.3	92.8±9.3	95.3±10.1	36.2±12.5
BT077	2.0±0.7	89.2±2.3	84.5±9.1	89.9±4.2	98.9±3.5	98.8±1.5	92.8±5.0	96.7±4.5	98.9±3.5	46.5±20.4
BT079	1.4±0.7	91.4±3.8	87.7±7.3	73.3±16.8	96.6±2.6	89.0±18.0	74.0±23.1	92.6±6.6	96.2±3.4	32.9±20.8
BT030	1.6±0.8	85.5±7.2	75.8±0.6	78.6±14.5	95.3±5.8	94.5±4.3	90.5±10.5	95.8±4.3	98.0±2.3	46.6±26.4
BT044	1.6±0.5	84.9±7.2	74.0±17.3	78.8±14.0	91.5±13.6	92.0±10.9	96.0±2.6	96.3±2.1	98.2±1.7	31.5±11.0
BT063	1.1±0.4	90.5±3.6	88.7±8.1	84.0±9.3	94.9±3.8	94.9±2.9	80.2±11.7	97.5±2.0	98.1±1.6	39.9±11.2
BT056	2.0±1.2	85.1±2.6	53.5±27.1	85.8±8.0	95.8±3.7	90.1±10.1	97.5±6.7	95.0±1.7	98.2±1.1	17.1±12.8
BT057	1.4±1.5	84.4±6.0	78.8±24.9	93.1±6.8	97.8±0.7	98.2±0.8	83.8±16.3	97.3±1.1	98.9±0.7	46.6±21.5

Viability and phenotypes: Mean ± SEM, % positive

Table S4. Percent of immunized TAAs that induced specific T cell responses and clinical outcomes

Patients		1	2	3	4
BT001	Period	5/24/16-7/2/16	7/27/16-9/2/16		
	Percent	100%	40%		
	Outcome	PR	PR		
BT051	Period	11/2/16-12/10/16	1/3/17-2/10/17	4/7/17-5/30/17	10/3/17-10/31-17
	Percent	100%	100%	100%	100%
	Outcome	PR	PR	Lung PR, Brain PD	PD
BT077	Period	7/7/17-8/18-17	9/5/17-10/27/17		
	Percent	100%	100%		
	Outcome	PR	PR		
BT079	Period	7/11/17-8/29/17	9/19/17-11/7-17		
	Percent	50%	100%		
	Outcome	SD	PR		
BT030	Period	1/14/17-3/18-17			
	Percent	100%			
	Outcome	PD			
BT063	Period	4/14/17-6/16/17			
	Percent	33%			
	Outcome	SD			
BT057	Period	1/17/17-3/10/17			
	Percent	100%			
	Outcome	PD			

Percent of TAAs that induced specific T cell response: Percent is expressed as the number of immunized TAAs that induced a ABLR (Above Base Line Response (as calculated in Table 3)) divided by the total number of TAAs immunized to the individual patients. PR: Partial response. PD: Progressive disease. SD: Stable disease

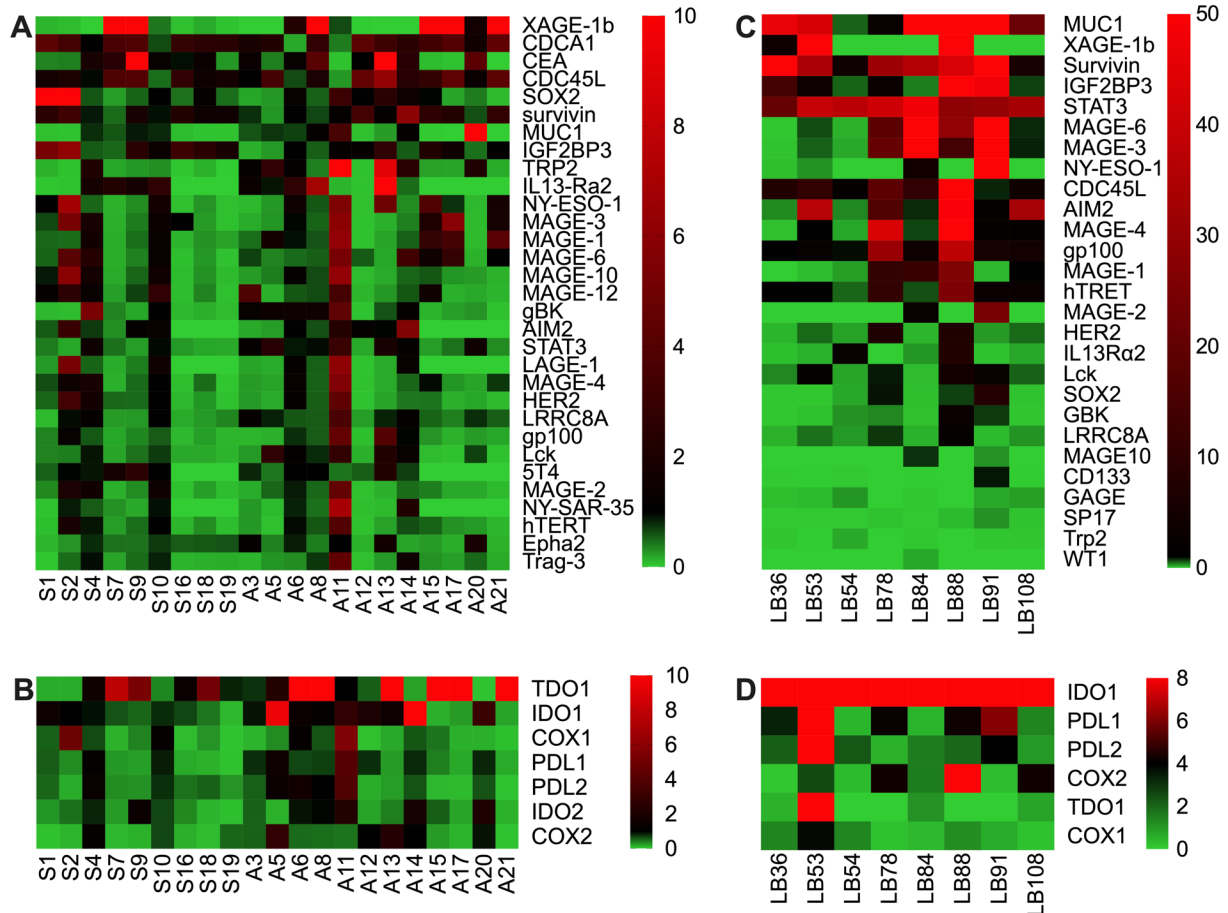


Figure S1. Heatmap of mRNA expression of TAAs and TME immunosuppressive factors in NSCLC tumor samples from lung lesion and brain metastasis. The mRNAs of the indicated TAA and TME immunosuppressive factors in tumor samples from lung and brain were assayed by qPCR in triplicates. The mRNA expression levels of the measured genes were expressed as mean fold changes calculated by $2^{-\Delta\Delta CT}$ ($\Delta\Delta CT = [(Ct \text{ TAA} - Ct \text{ GAPDH})_{\text{Sample}}] - [(Ct \text{ TAA} - Ct \text{ GAPDH})_{\text{Control}}]$). **(A)** Expression of TAAs in 21 tumor samples from lung. S1-S19, squamous cell NSCLC; A3-A21, adenocarcinoma NSCLC. **(B)** Expression of TME immunosuppressive factors in 21 tumor samples from lung as in (A). **(C)** Expression of TAAs in 8 tumor samples from NSCLC brain metastasis. **(D)** Expression of TME immunosuppressive factors in 8 tumor samples from NSCLC brain metastasis. Color bar and number represent fold changes. (A, B), lung para-tumor tissues were used as controls for comparison. (C, D), pooled samples (n=6) of normal brain tissues were used as controls for comparison.