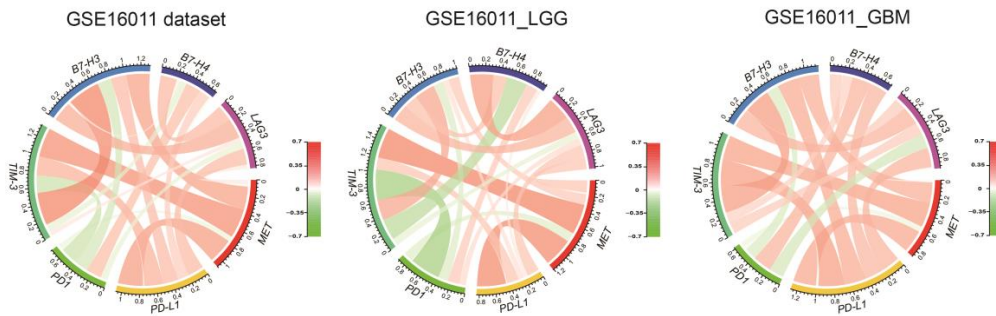
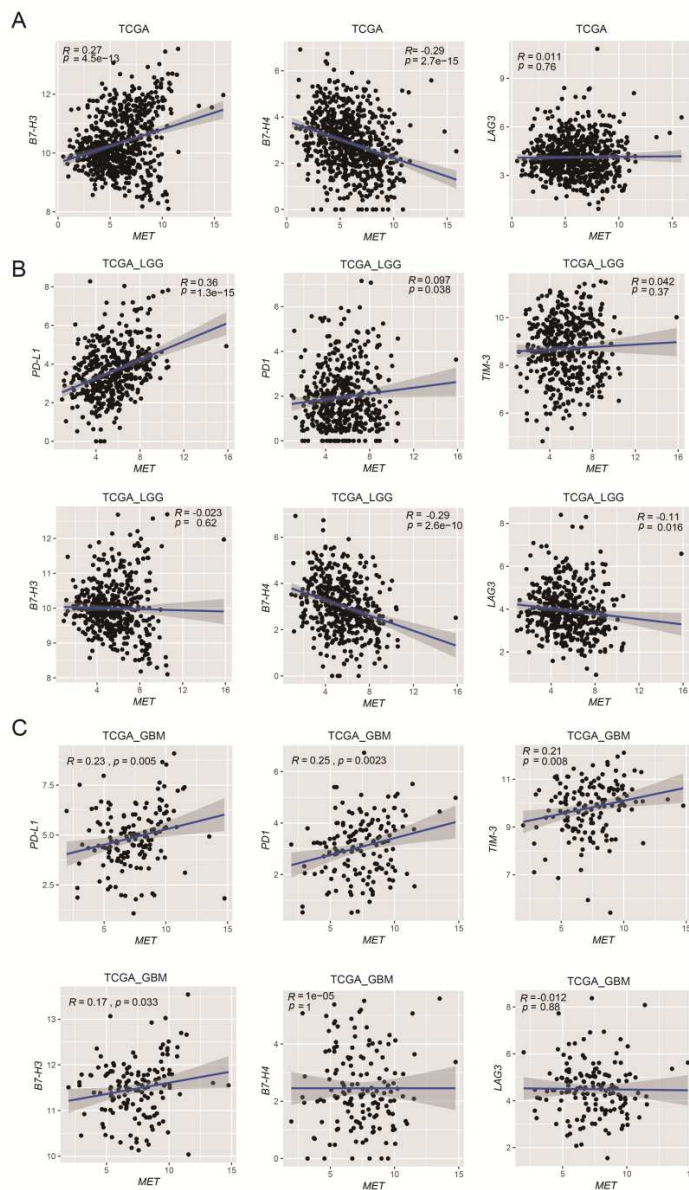


**Fig. S1**

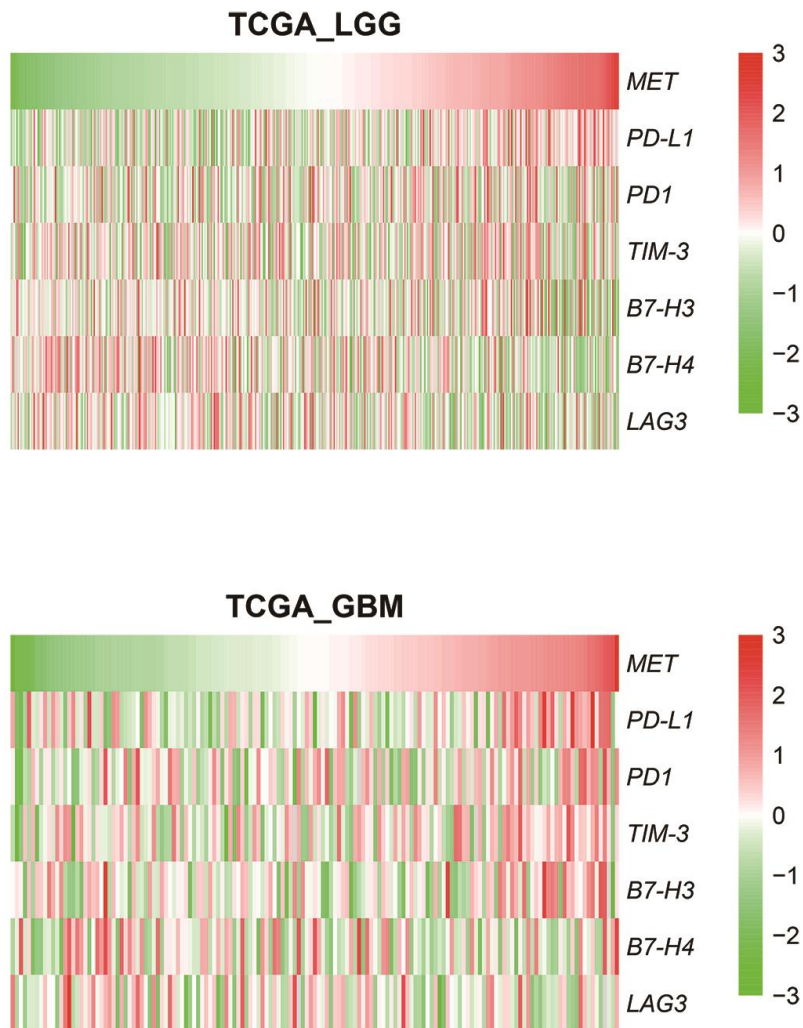
**Fig. S1** *MET* expression shows positive association with expression of *PD-L1* in GSE16011 dataset.

Fig. S2

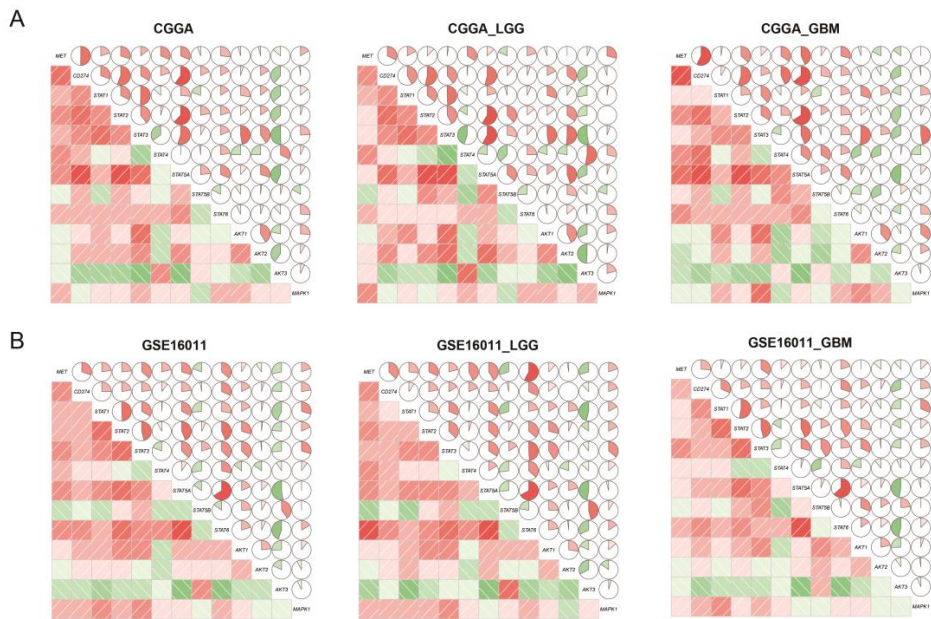


**Fig. S2** The scatter diagrams visualize the co-expression patterns of *MET* and checkpoint genes in all grade gliomas (A), LGG (B) and GBM (C).

Fig. S3

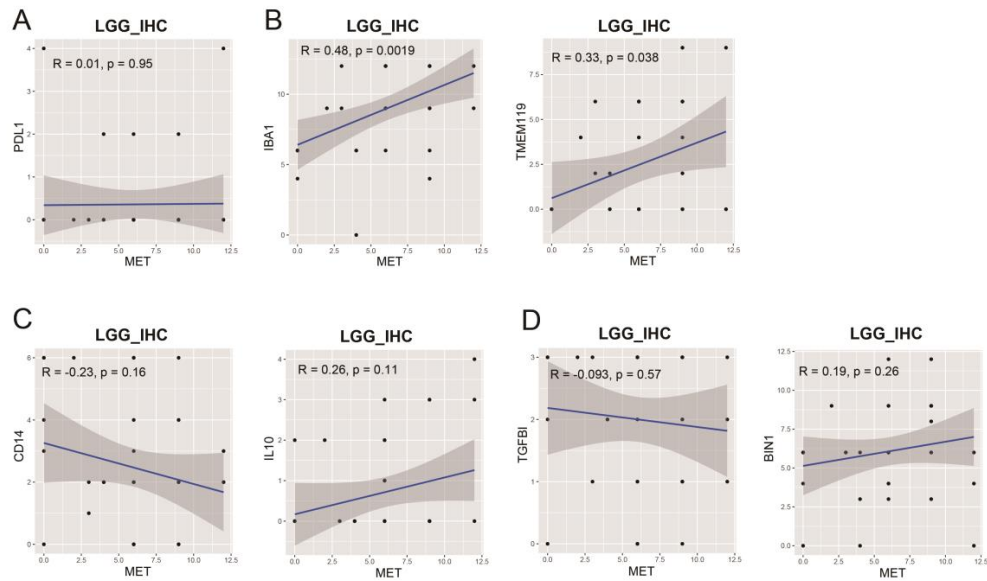


**Fig. S3** With increase of *MET* expression, the expression of *PD-L1* increases gradually in LGG and GBM.

**Fig. S4**

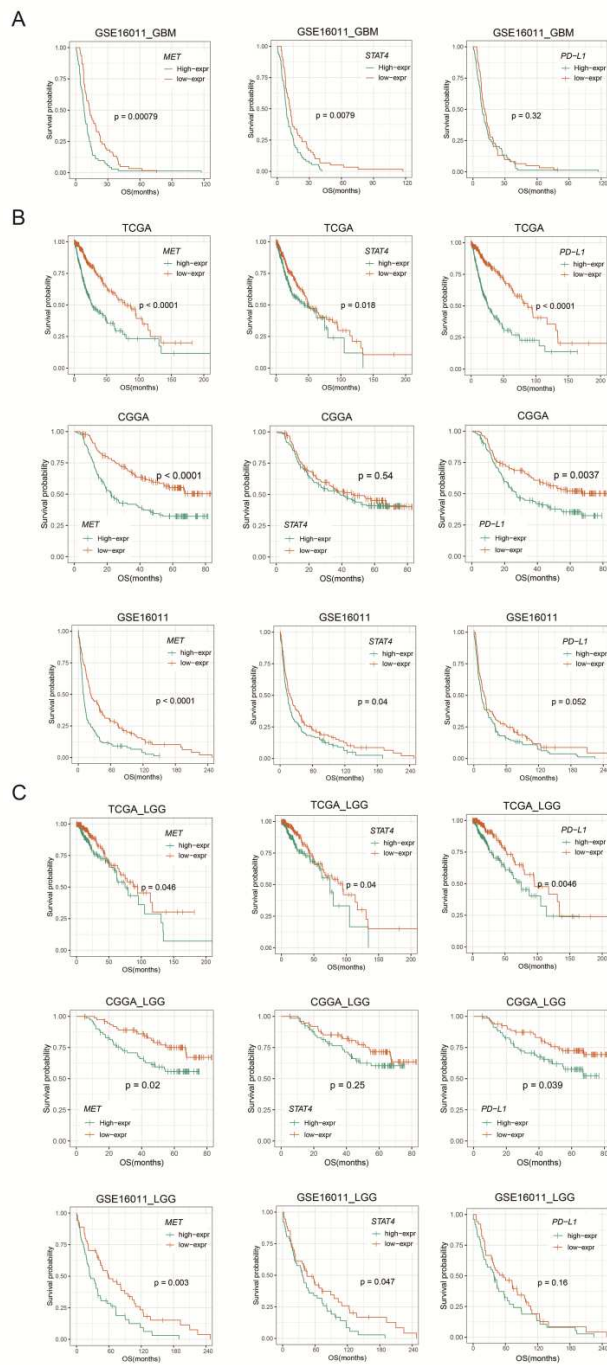
**Fig. S4** *MET/PD-L1* expression shows robust correlation with STAT pathway. **A** CGGA dataset. **B** GSE16011 dataset.

Fig. S5



**Fig. S5** Primary glioma tissue microarray verifies the association between MET and target protein in LGG. **A** PD-L1. **B** Macrophage-associated markers (IBA1 and TMEM119). **C** M2-like polarization markers (CD14 and IL-10). **D** Blood derived-like marker (TGFBI) and resident-like marker (BIN1).

Fig. S6



**Fig. S6** Kaplan–Meier survival analysis of *MET*, *STAT4* and *PD-L1* in GBM patients of GSE16011 dataset (A), all grade glioma (B) and LGG (C).

Fig. S7

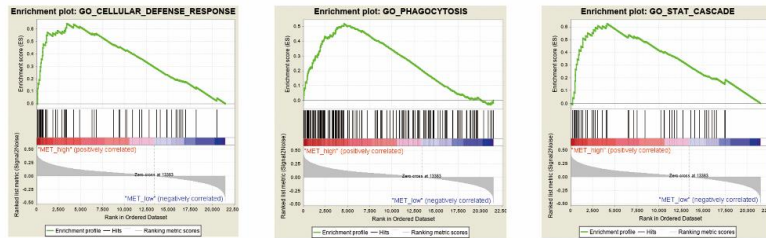
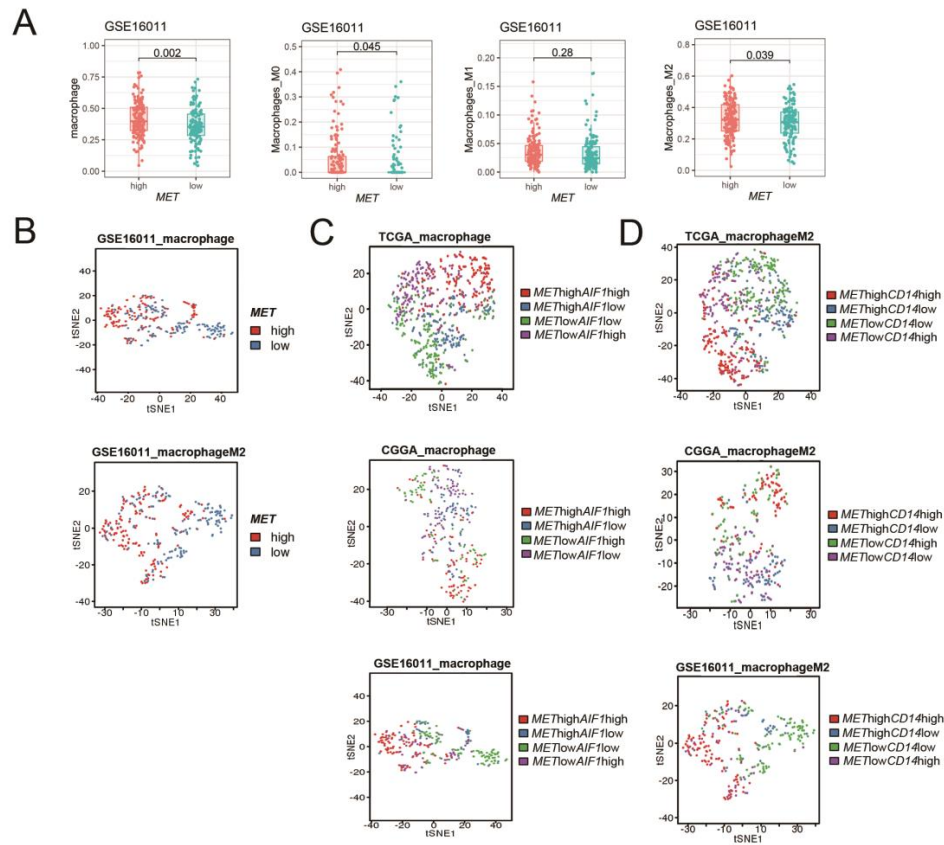


Fig. S7 Other immune-related GO terms show enrichment in *MET* high expression group.

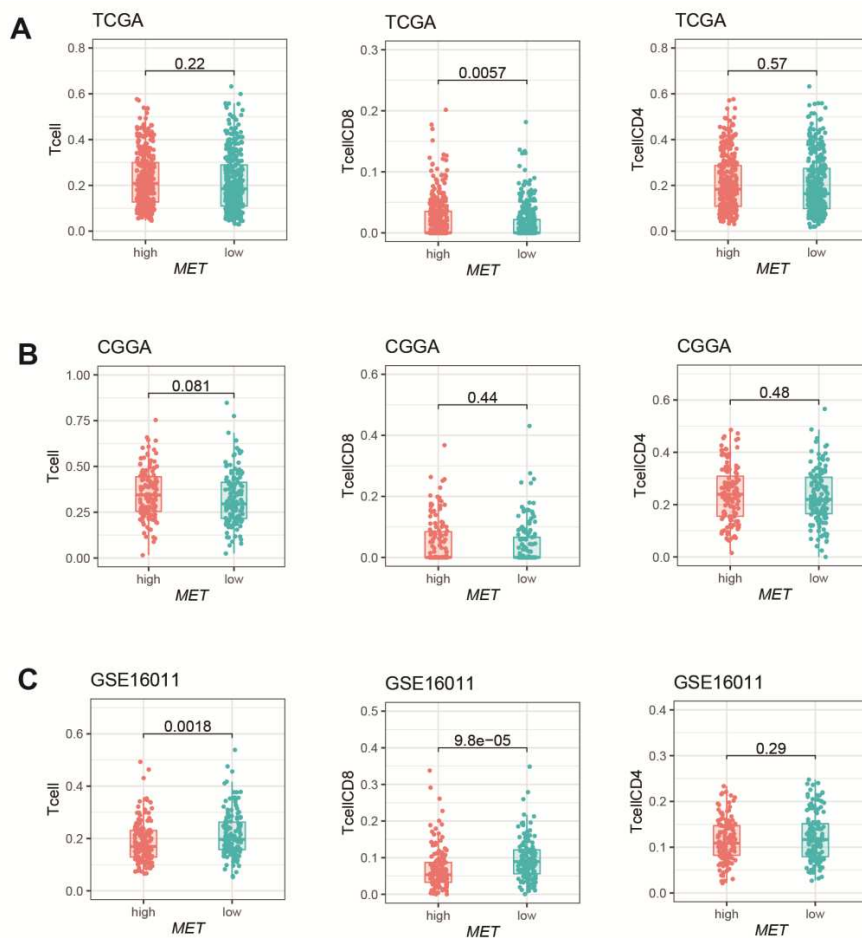
Fig. S8



**Fig. S8 A** Determining macrophage abundance with digital cytometry in CIBERSORTx. The total fraction of macrophages and subtypes (M0, M1, M2) in *MET* high and low expression groups of GSE16011 dataset. **B** TSNE plots show macrophage and M2 macrophage expression difference between *MET* high and low groups of GSE16011 dataset. **C and D** High expression of *AIF1* or *CD14* in the *MET* high group.

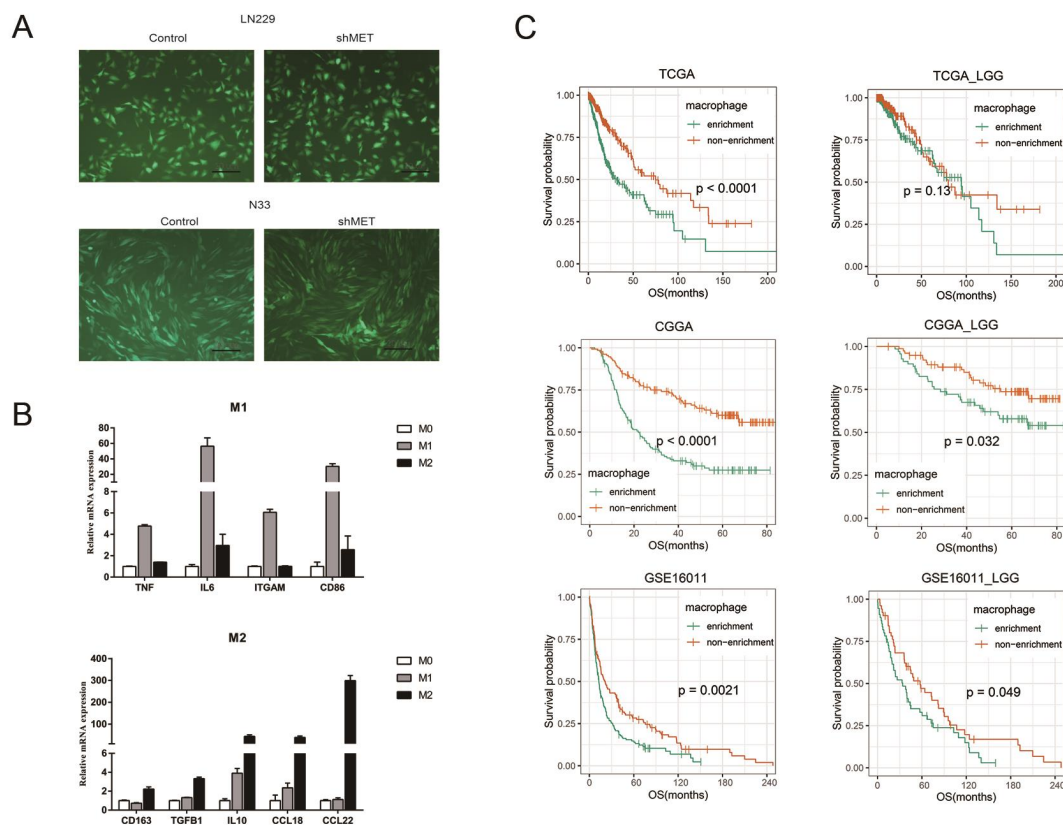


Fig. S9



**Fig. S9** Determining T cell abundance with digital cytometry in CIBERSORTx. The total fraction of T cells, CD8<sup>+</sup> T cells and CD4<sup>+</sup> T cells in *MET* high and low expression groups in TCGA (A), CGGA (B), and GSE16011 (C) dataset.

Fig. S10



**Fig. S10 A** Fluorescent images of EGFP reporter protein in stably transfected cell lines. Scale bar, 20  $\mu$ M. **B** Appearance of the **M1-** and **M2-like phenotype** demonstrated by quantitative real-time PCR. *TNF*, *IL6*, *ITGAM* and *CD86* are highly expressed in induced M1-like macrophages. *CD163*, *TGFB1*, *IL10*, *CCL18* and *CCL22* are highly expressed in induced M2-like macrophages. **C** Glioma patients of all grade or LGG with macrophage enrichment lived significantly shorter than other patients in the three datasets.

**Table S1 Clinicopathological Characteristics of the patients**

Variable		TCGA dataset	CGGA dataset	GSE16011 dataset
Patient number	Total	702	265	276
Age	<45	295	145	106
	≥45	338	119	170
Gender	NA	69	1	0
	Male	366	159	184
	Female	267	106	92
Grade	NA	69	0	0
	II	222	117	24
	III	246	38	85
	IV	165	110	159
<i>IDH1/2</i> status	NA	69	0	8
	Mutation	441	115	81
	Wild type	245	147	140
1p/19q status	NA	16	3	55
	Codeleted	172	41	46
	Intact	519	224	88
Histological subtype	NA	11	0	142
	Astrocytoma (II, III)	171	71	37
	Oligoastrocytoma (II, III)	117	56	28
	Oligodendroglioma (II, III)	180	28	52
	Glioblastoma (IV)	165	110	159
	NA	69	0	0

**Table S2. List of antibodies.**

<b>Antibody</b>	<b>Dilution</b>	<b>Source</b>	<b>Identifier</b>	<b>Usage</b>
MET	1: 1000	Cell Signaling	Cat# 8198	WB
pMET (Tyr1234/1235)	1: 1000	Cell Signaling	Cat# 3077	WB
PD-L1	1: 1000	Abcam	Cat# ab213524	WB
pSTAT4 (Tyr693)	1: 1000	Cell Signaling	Cat# 5267	WB
STAT4	1: 1000	Abcam	Cat# ab68156	WB
pSTAT3 (Tyr705)	1: 2000	Cell Signaling	Cat# 9145	WB
STAT3	1: 5000	Abcam	Cat# ab119352	WB
pSTAT6 (Tyr641)	1: 1000	Cell Signaling	Cat# 56554	WB
STAT6	1: 1000	Abcam	Cat# ab32520	WB
GAPDH	1: 5000	Proteintech	Cat# 60004-1-Ig	WB
MET	1: 1000	Abcam	Cat# ab216574	IHC
PD-L1	1: 1	ZSGB Bio	Cat# za-0629	IHC
IBA1	1: 2500	Abcam	Cat# ab178846	IHC
TMEM119	1: 1000	Proteintech	Cat# 27585-1-AP	IHC
IL10	1: 200	Proteintech	Cat# 60269-1-1g	IHC
CD14	1: 200	Proteintech	Cat# 17000-1-AP	IHC
TGFBI	1: 100	Abcam	Cat# ab170874	IHC
BIN1	1: 100	Abcam	Cat# ab182562	IHC
STAT4	1: 50	Cell Signaling	Cat# 2653	CHIP

WB, western blot; IHC, immunohistochemistry; CHIP, Chromatin immunoprecipitation.

**Table S3. List of primers.**

Number	Primer Name	Sequence(5'to 3')	Base Number
1	CD86-For	TGGAAACTGACAAGACGCGG	20
2	CD86-Rev	AAACACGCTGGGCTTCATCA	20
3	CCL18-For	CTGCTGCCTCGTCTATACCTC	21
4	CCL18-Rev	GGCATAGCAGATGGGACTCT	20
5	CCL22-For	ATGGATCGCCTACAGACTGC	20
6	CCL22-Rev	CGGCACAGATCTCCTTATCCC	21
7	TGFB1-For	AGCCTGAGGCCGACTACTAC	20
8	TGFB1-Rev	GGTTGCTGAGGTATCGCCAG	20
9	ITGAM-For	ATATCAGCACATCGGCCTGG	20
10	ITGAM-Rev	CTGGGCAAGGGGCACAC	17
11	IL10-For	GCCTTCAGCAGAGTGAAGACT	21
12	IL10-Rev	CCACGGCCTTGCTCTTGTTT	20
13	TNF-For	CTGCTGCACTTTGGAGTGAT	20
14	TNF-Rev	GGGAGTAGATGAGGTACAGGC	21
15	IL6-For	GGTACATCCTCGACGGCATC	20
16	IL6-Rev	GCTCTGGCTTGTTCCCTCACT	20
17	GAPDH-For	GGTCACCAGGGCTGCTTTTA	20
18	GAPDH-Rev	TGATGACCCTTTTGGCTCCC	20
19	CD163-For	GCTGGGACAGTTACGATGCT	20
20	CD163-Rev	GGCTGCCTCCACCTCTAAGT	20