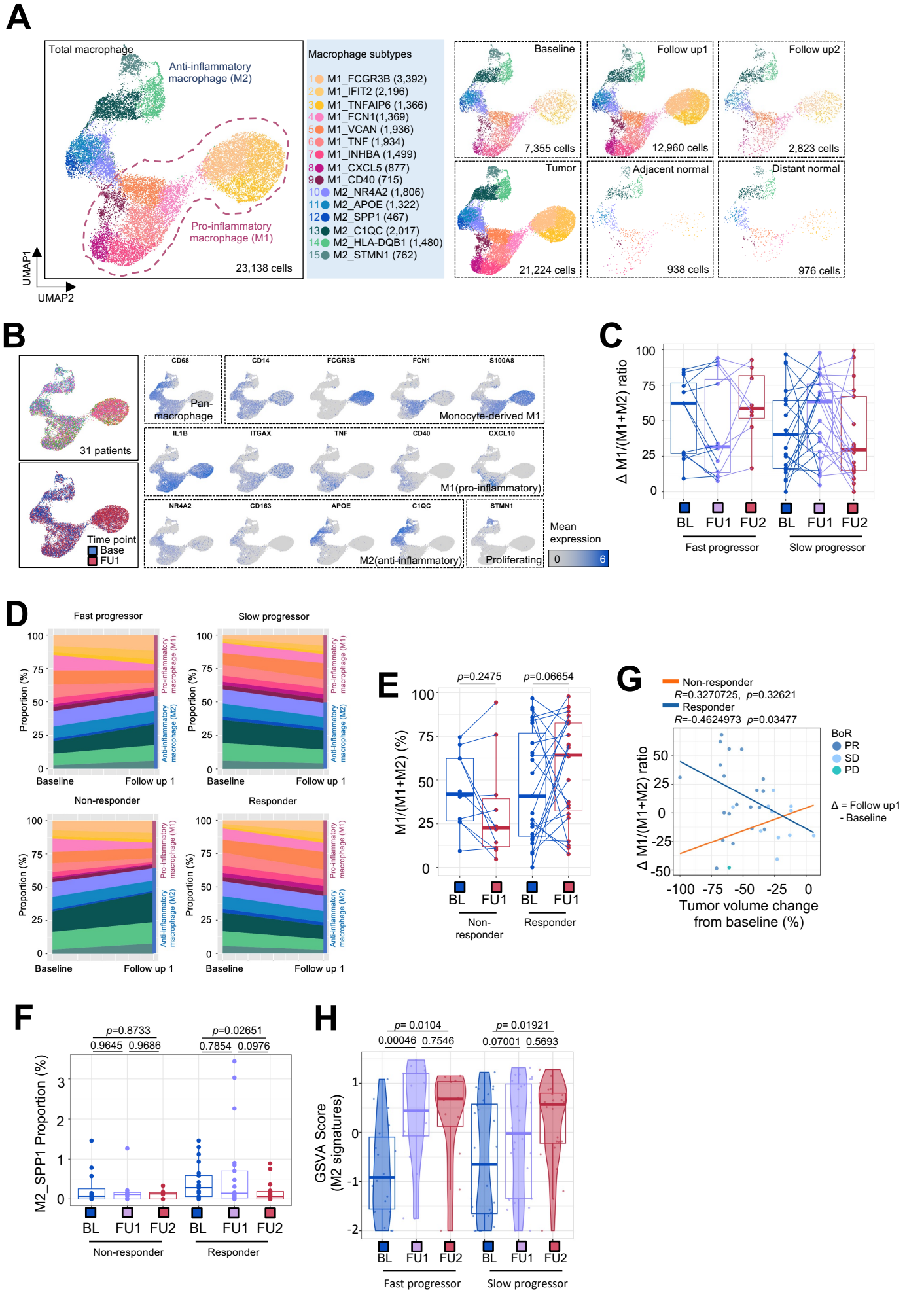
A
Total macrophage
Anti-inflammatory macrophage (M2)
Pro-inflammatory macrophage (M1)
23,138 cells
UMAP1
UMAP2
Macrophage subtypes
1 M1_FCGR3B (3,392)
2 M1_IFIT2 (2,196)
3 M1_TNFAIP6 (1,366)
4 M1_FCN1(1,369)
5 M1_VCAN (1,936)
6 M1_TNF (1,934)
7 M1_INHBA (1,499)
8 M1_CXCL5 (877)
9 M1_CD40 (715)
10 M2_NR4A2 (1,806)
11 M2_APOE (1,322)
12 M2_SPP1 (467)
13 M2_C1QC (2,017)
14 M2_HLA-DQB1 (1,480)
15 M2_STMN1 (762)
Baseline
7,355 cells
Follow up1
12,960 cells
Follow up2
2,823 cells
Tumor
21,224 cells
Adjacent normal
938 cells
Distant normal
976 cells
B
31 patients
Time point
Base
FU1
CD68
Pan-macrophage
CD14
FCGR3B
FCN1
S100A8
Monocyte-derived M1
IL1B
ITGAX
TNF
CD40
CXCL10
M1(pro-inflammatory)
NR4A2
CD163
APOE
C1QC
M2(anti-inflammatory)
STMN1
Proliferating
Mean expression
0
6
C
Δ M1/(M1+M2) ratio
BL
FU1
FU2
Fast progressor
Slow progressor
D
Fast progressor
Slow progressor
Non-responder
Responder
Proportion (%)
Pro-inflammatory macrophage (M1)
Anti-inflammatory macrophage (M2)
Baseline
Follow up 1
E
p=0.2475
p=0.06654
M1/(M1+M2) (%)
Non-responder
Responder
G
Non-responder
R=0.3270725, p=0.32621
Responder
R=-0.4624973 p=0.03477
BoR
PR
SD
PD
Δ = Follow up1 - Baseline
Δ M1/(M1+M2) ratio
Tumor volume change from baseline (%)
F
p=0.8733
0.9645 0.9686
p=0.02651
0.7854 0.0976
M2_SPP1 Proportion (%)
Non-responder
Responder
H
p= 0.0104
0.00046 0.7546
p= 0.01921
0.07001 0.5693
GSVA Score (M2 signatures)
Fast progressor
Slow progressor

**Figure S19.** (A) UMAP embedding of single cell transcriptomes of all macrophages obtained from all samples in this trial. Labeled are granular macrophage subsets separated by tumor v.s. normal tissue, and by timepoint. (B) UMAP embeddings showing marker gene expression for macrophage subsets in (A). (C) Relative M1 macrophage proportion in fast and slow progressing patients separated by timepoint. (D) Macrophage subtype proportions at baseline and FU1 in fast versus slow progressing patients, and in non-responder and responder patients. (E) Relative M1 macrophage proportion in non-responder and responder patients separated by timepoint. (F) Proportion of SPP1+ macrophages in non-responder and responder patients split by timepoint. Statistical comparisons performed using a Wilcoxon signed-rank test. (G) Change in relative M1 proportion from BL to FU1 plotted against change in tumor volume after 1 cycle of chemotherapy, segregated by non-responder and responder patients. (H) GSVA performed for M2 signatures on bulk RNA-seq samples split by timepoints and progression status.