

Supplementary

Table S1 Clinical characteristics of the STAD patients from TCGA database

Characteristics	Values (N=443)
Gender	
Female	158 (35.7%)
Male	285 (64.3%)
Age (n=438)	65.7 (10.8)
Race	
Asian	89 (20.1%)
Black or African American	13 (2.93%)
Native Hawaiian or other pacific islander	1 (0.23%)
Not reported	62 (14.0%)
White	278 (62.8%)
Vital status	
Alive	267 (60.3%)
Dead	175 (39.5%)
Not reported	1 (0.23%)
Pathologic stage	
Stage I	59 (13.3%)
Stage II	130 (29.3%)
Stage III	183 (41.3%)
Stage IV	44 (9.93%)
Not reported	27 (6.09%)
Pathologic T	
T1	23 (5.19%)
T2	93 (21.0%)
T3	198 (44.7%)
T4	119 (26.9%)
TX	10 (2.26%)
Pathologic N	
N0	132 (29.8%)
N1	119 (26.9%)
N2	85 (19.2%)
N3	32 (7.22%)
N3a	49 (11.1%)
N3b	7 (1.58%)
NX	17 (3.84%)
Not reported	2 (0.45%)
Pathologic M	
M0	391 (88.3%)
M1	30 (6.77%)
MX	22 (4.97%)

Table S2 Correlation of A2M mRNA expression and EMT markers

Gene	Correlation	P value
VIM	0.4908496	1.53E-28
CDH2	0.0677188	0.1524371
CDH1	-0.147076	0.0018005
EPCAM	-0.173105	0.0002318

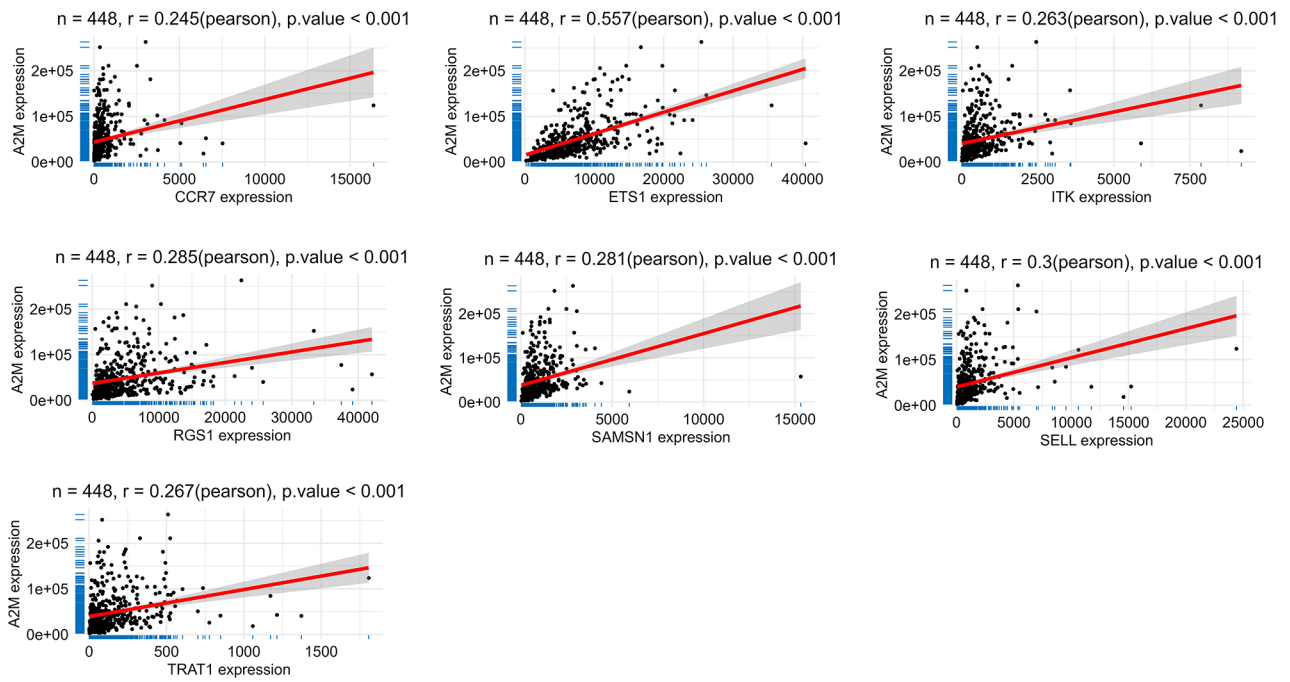


Figure S1 Correlation of A2M mRNA expression and CD4⁺ T cell related genes.

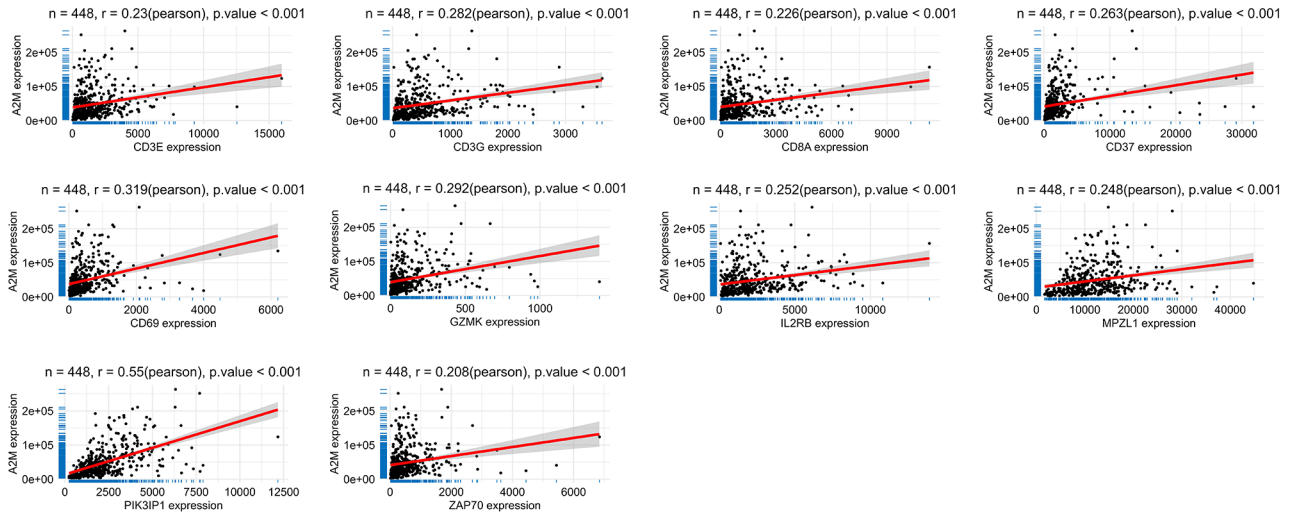


Figure S2 Correlation of A2M mRNA expression and CD8⁺ T cell related genes.

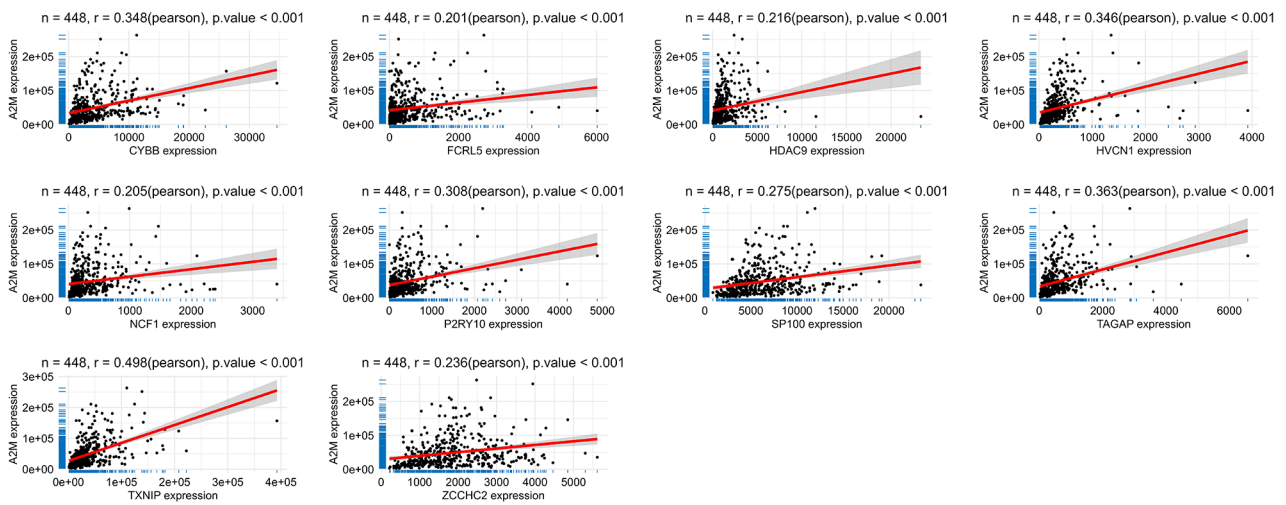


Figure S3 Correlation of A2M mRNA expression and B cell related genes.

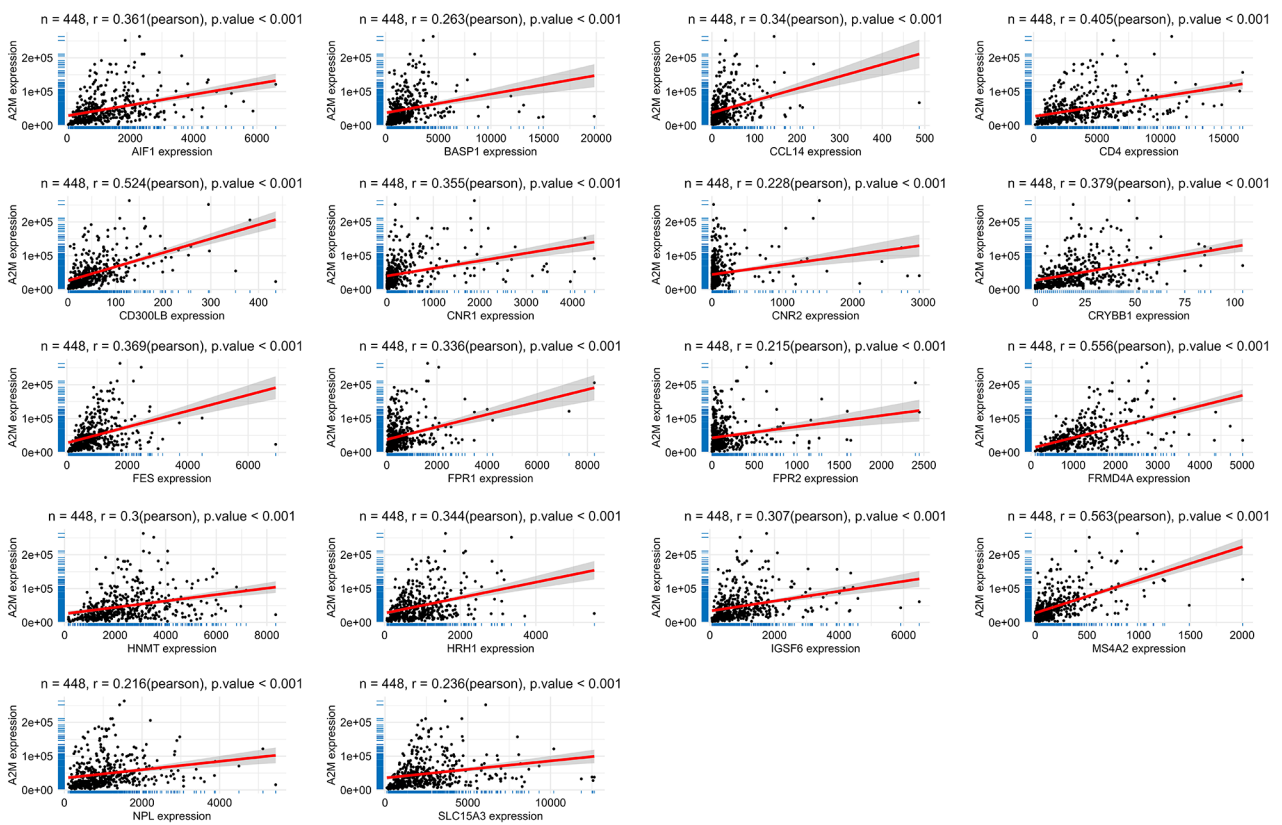


Figure S4 Correlation of A2M mRNA expression and macrophage cell related genes.

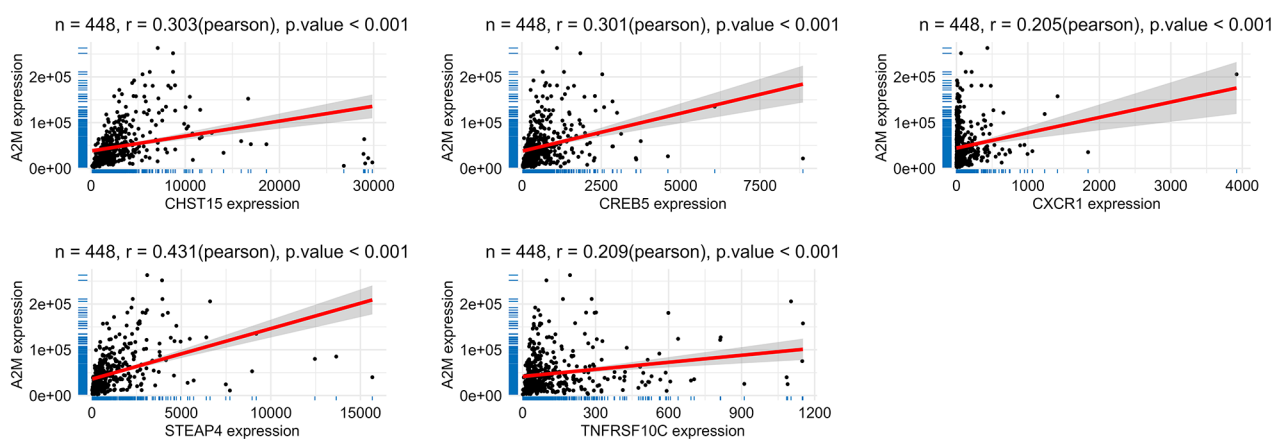


Figure S5 Correlation of A2M mRNA expression and neutrophil cell related genes.

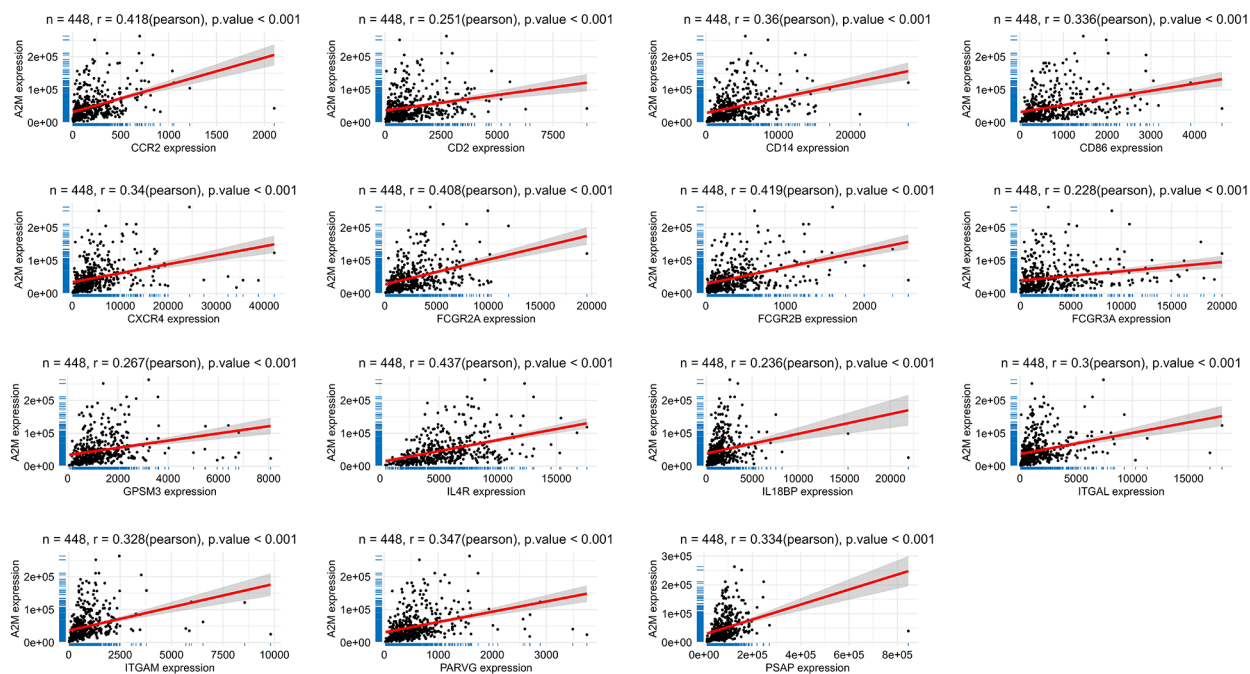


Figure S6 Correlation of A2M mRNA expression and myeloid derived suppressor cell related genes.