

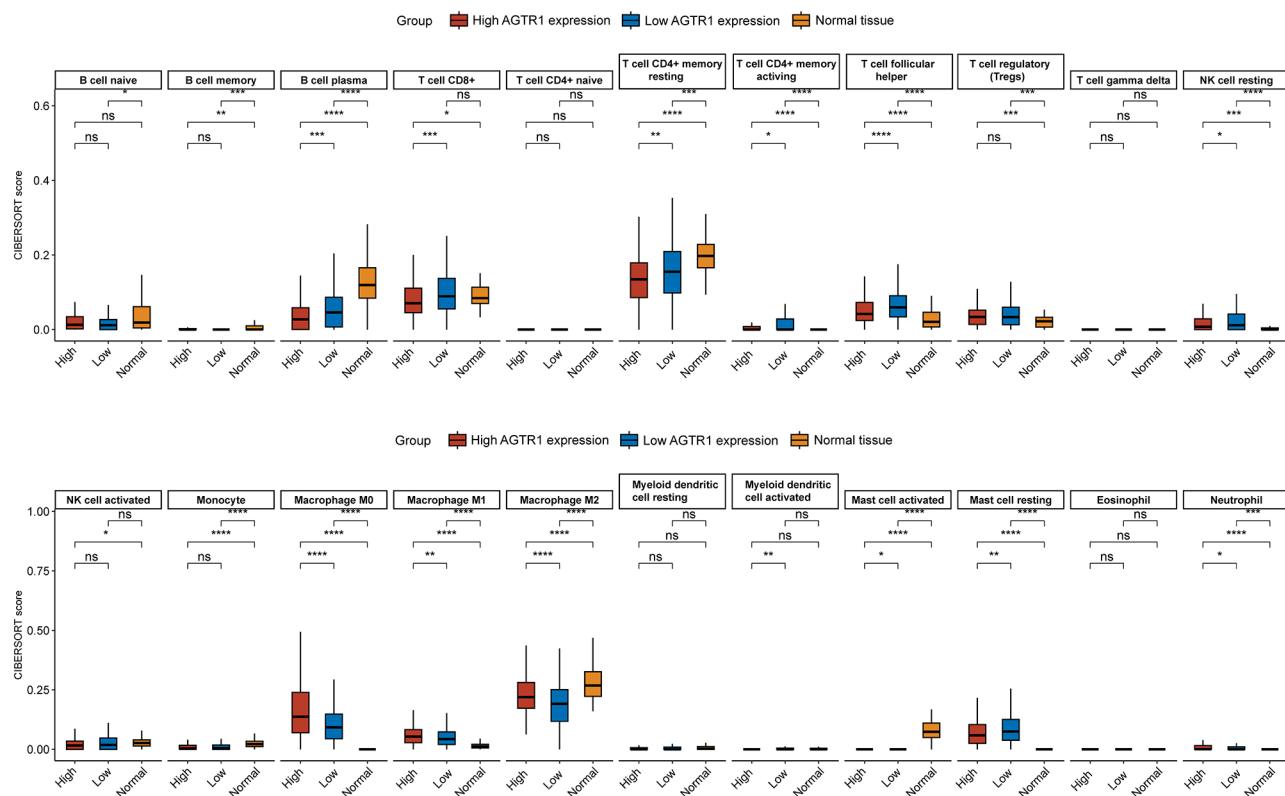


Figure S1 Comprehensive immune infiltration analysis of 22 immune cell subsets according to AGTR1 expression status in colorectal cancer. The infiltration levels of all 22 immune cell subsets estimated by the CIBERSORT algorithm were compared among AGTR1-high tumor tissues, AGTR1-low tumor tissues, and adjacent normal tissues. The x-axis represents immune cell subsets, and the y-axis represents the estimated CIBERSORT infiltration score. Statistical significance was evaluated using the Kruskal-Wallis test followed by pairwise Wilcoxon rank-sum tests with Benjamini-Hochberg correction for multiple comparisons. The FDR-adjusted P values for pairwise comparisons of all 22 immune cell subsets are provided in Table S1. *Adjusted $P < 0.05$, **adjusted $P < 0.01$, ***adjusted $P < 0.001$, ****adjusted $P < 0.0001$.

Table S1 FDR-adjusted statistical analysis of immune cell infiltration differences among AGTR1 expression groups and adjacent normal tissues in colorectal cancer

Immune cell subset	AGTR1-high vs AGTR1-low (FDR-adjusted P)	AGTR1-high vs Normal (FDR-adjusted P)	AGTR1-low vs Normal (FDR-adjusted P)
B cell naive	0.095	0.095	0.037
B cell memory	0.2	0.003	0
B cell plasma	0	0	0
T cell CD8+	0.001	0.02	0.963
T cell CD4+ naive	0.547	0.547	0.569
T cell CD4+ memory resting	0.004	0	0
T cell CD4+ memory activated	0.012	0	0
T cell follicular helper	0	0	0
T cell regulatory (Tregs)	0.451	0	0
T cell gamma delta	0.556	0.698	0.9
NK cell resting	0.012	0	0
NK cell activated	0.139	0.01	0.139
Monocyte	0.447	0	0
Macrophage M0	0	0	0
Macrophage M1	0.005	0	0
Macrophage M2	0	0	0
Myeloid dendritic cell resting	0.4	0.074	0.121
Myeloid dendritic cell activated	0.006	0.123	0.903
Mast cell activated	0.027	0	0
Mast cell resting	0.003	0	0
Eosinophil	0.757	0.37	0.37
Neutrophil	0.021	0	0

The infiltration levels of 22 immune cell subsets estimated by the CIBERSORT algorithm were compared among AGTR1-high tumor tissues, AGTR1-low tumor tissues, and adjacent normal tissues. Statistical significance was evaluated using the Kruskal-Wallis test followed by pairwise Wilcoxon rank-sum tests with Benjamini-Hochberg correction for multiple comparisons. This table presents the FDR-adjusted P values for pairwise comparisons between AGTR1-high and AGTR1-low tumor tissues, AGTR1-high tumor tissues and adjacent normal tissues, and AGTR1-low tumor tissues and adjacent normal tissues.