Supplementary

Table S1 The clinical information of pMMR and dMMR CRC patients in TCGA database

Clinical information	pMMR CRC (n=398)	dMMR CRC (n=65)
Gender		
Female	177 (44.5%)	44 (67.7%)
Male	221 (55.5%)	21 (32.3%)
Age (years)	68.0 (11.9)	55.9 (13.8)
Status		
Alive	332 (83.4%)	63 (96.9%)
Dead	66 (16.6%)	2 (3.08%)
Time (days)	699 ± 580	869 ± 732
Pathologic M		
M0	319 (80.2%)	40 (61.5%)
M1	58 (14.6%)	8 (12.3%)
MX	21 (5.28%)	17 (26.2%)
Pathologic N		
N0	229 (57.5%)	32 (49.2%)
N1	91 (22.9%)	23 (35.4%)
N2	78 (19.6%)	10 (15.4%)
Pathologic T		
T1	14 (3.52%)	2 (3.08%)
T2	70 (17.6%)	12 (18.5%)
T3	265 (66.6%)	45 (69.2%)
T4	48 (12.1%)	6 (9.23%)
Tis	1 (0.25%)	0 (0%)
TNM stage		
Stage 1	75 (18.8%)	10 (15.4%)
Stage 2	149 (37.4%)	19 (29.2%)
Stage 3	114 (28.6%)	28 (43.1%)
Stage 4	60 (15.1%)	8 (12.3%)

Data are presented using the mean ± standard deviation. CRCs, colorectal cancers; TCGA, The Cancer Genome Atlas.

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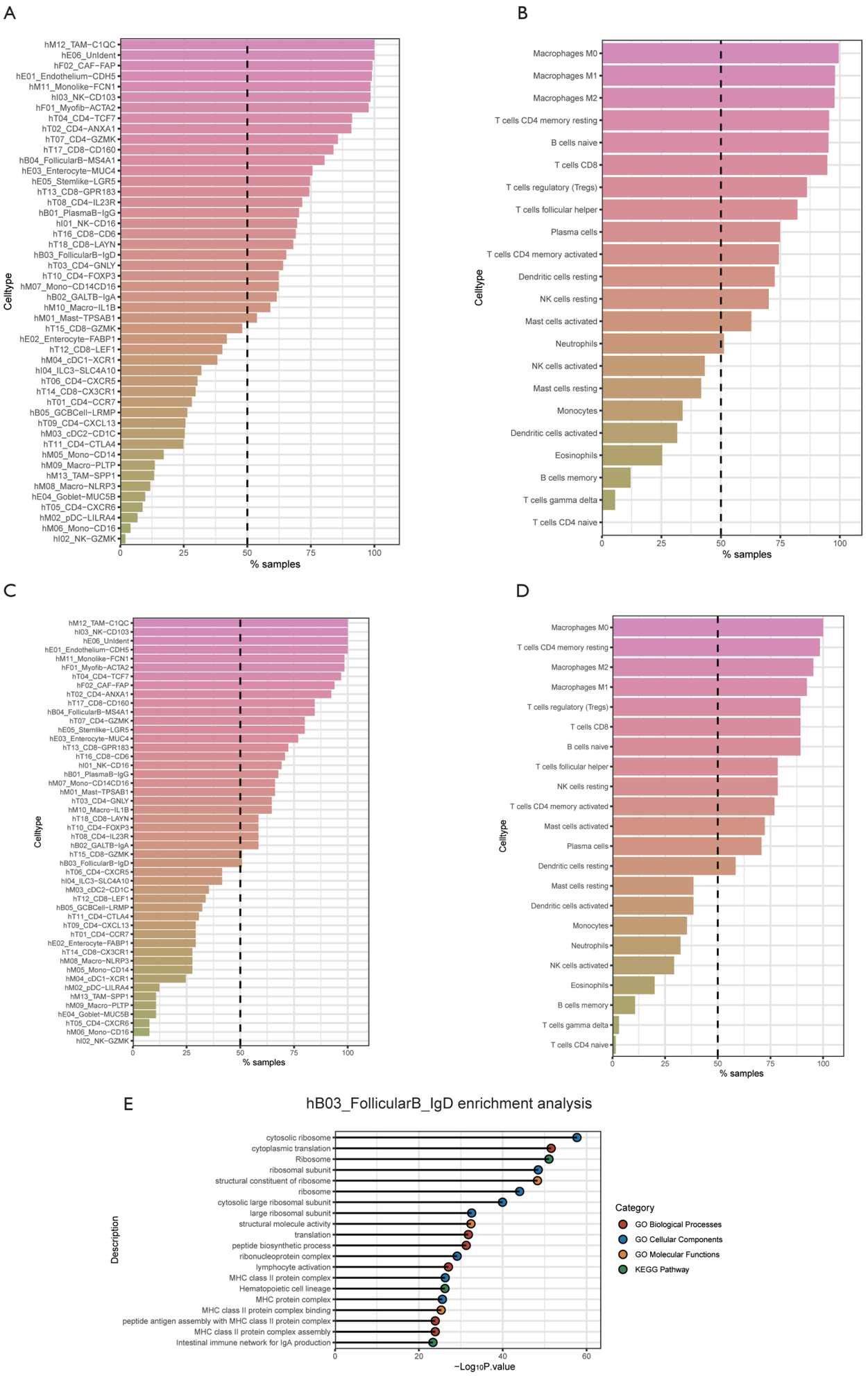

Figure S1 (A) We prefiltered and preserved those cell types with estimated proportions greater than 0 in at least 50% of the pMMR CRC samples [27 out of 48 total cell types; Zhang *et al.* (19)] to gain confidence in subsequent analyses. (B) The same prefiltered methods were use in pMMR CRC samples by another cell types reference set [LM22; Newman *et al.* (29)]. (C) We prefiltered and preserved those cell types with estimated proportions greater than 0 in at least 50% of the dMMR CRC samples [28 out of 48 total cell types; Zhang *et al.* (19)] to gain confidence in subsequent analyses. (D) The same prefiltered methods were used in dMMR CRC samples by another cell type reference set [LM22; Newman *et al.* (29)]. (E) Functional enrichments of marker genes in the hB03_FollicularB_IgD cell population identified from dMMR CRCs.

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