SUPPLEMENTAL MATERIAL

Afik et al., http://dx.doi.org/10.1084/jem.20151193

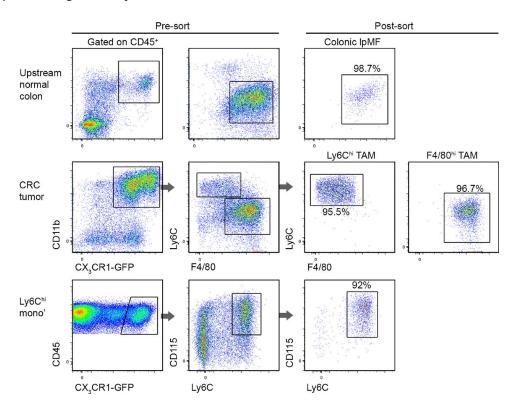


Figure S1. **Sorting strategy of Ly6C**^{hi} **monocytes, colonic lpMFs, and CRC TAMs.** Representative flow cytometry images showing the strategy that was implemented for the sorting of colonic lpMFs (top), Ly6C^{hi} and F4/80^{hi} TAM subsets from CRC tumors (middle), and of Ly6C^{hi} monocytes (mono') from the spleen (bottom). Purity degree is mentioned in percentage for each cell population.

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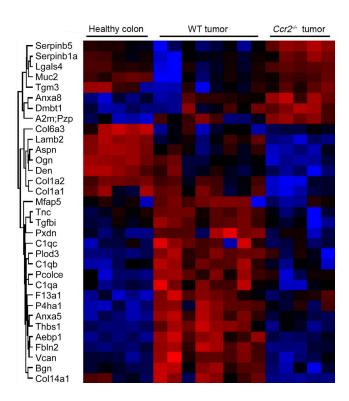


Figure S2. **CRC tumors acquire a unique ECM protein signature in comparison with healthy upstream colon that is altered in the absence of TAMs.** Color-coded heat map showing 31 ECM-related proteins that were differentially expressed between healthy upstream colon and CRC tumors, as well as between WT and $Ccr2^{-/-}$ tumors. Of note, collagens I α 1 and α 2 were not significantly changed between healthy colon and WT tumors but were added into this heat map. Data were analyzed by unpaired, two-tailed Student's t test analysis (pFDR = 0.05) and were z scored. Each column represents a biological repeat (n = 5 for normal colon, n = 8 for WT tumor, and n = 5 for $Ccr2^{-/-}$ tumors).

A ECM Re	gulators				C Proteo	C Proteoglycans				
Gene	Ly6C(hi)	Ly6C(hi)	F4180(hi)	Resident	Gene	Ly6C(hi)	Ly6C(hi)	F4180(hi)	Resident	
Symbol	spleen	TAM	TAM	colonic	Symbol	spleen	TAM	TAM	colonic	
,	monocytes			IpMF	-,	monocytes			IpMF	
Adamdec1	6.2	6.1	7.2	10.6	Aspn	5.1	9.2	8	8.3	
LoxI2	6.3	6.6	6.4	7.1	Ogn	6.1	9.7	8.5	8.9	
Mmp15	6.6	7.2	7	9	Prelp	7.4	8.1	7.5	9.3	
Mmp13	6.9	9.2	11	12.6	Den	7.4	12	11.3	12.1	
Leprel1	7	8.4	7.5	11.1	Bgn	7.7	12.1	11.5	11.8	
Timp3	7.1	8.2	7.5	9.6	Vcan	12.3	11.9	9.5	7.7	
Mmp12	7.1	10.3	11	11.2	Srgn	13.4	13.7	13.4	13.4	
Mmp25	7.4	8.4	8.7	8.3	Oigii	15.4	10.7	15.7	10.4	
	7.4	8.1	7.7	11.5						
Tgm3 Loxl3	7.4	8.3	8.6	9.6	D ECM G	lycoproteins				
Serpinb6a	7.6	9.4	10.1	11.3	Gene	Ly6C(hi)	Ly6C(hi)	F4180(hi)	Resident	
Serpine1			9.9		Symbol	spleen	TAM	TAM	colonic	
1000000000	7.7	11.2		11.1	-,	monocytes	10.000	1,7-1,7	IpMF	
Egln3	7.7	10.5	9.6	8.9	Dpt	5.5	6.9	6.2	9.9	
Timp1	7.8	11.1	9.2	8.5	Postn	6.6	8.4	7.5	10.6	
Mmp9	8	8.6	9.2	9.1	Thbs4	7.2	8.4	8	11.3	
Adam19	8.5	8.8	8.3	11	Pxdn	7.3	8.6	7.8	8.1	
Adamtsl4	8.6	10.6	10.2	9.7		7.7	10.1	9.1	13.9	
Mmp14	8.6	11.8	11.9	12.4	Dmbt1	7.7	10.1	13	9.4	
Tgm1	9	9.7	9	8.7	Spp1	7.9	9.6	8.7	9.4	
Tgm2	9.9	13	12.2	11.8	Nid1	8	9.6	8.6	8.4	
Adam8	9.9	12.1	12.2	9.7	Aebp1	8	9.4	7.8	6.9	
Mmp19	10.2	11.3	10.3	10	Lrg1	8.2	8.5	8.1	9.5	
Ctsl	10.2	12.4	12.9	12.2	Fbln1	8.4	9.8	9.4	9.5	
Plod1	10.3	10.8	11.6	10.7	Lamc1	8.5	10.5	9.4	9.1	
Ctsev	10.3	9.1	8.6	9.7	Pcolce					
Ctso	10.5	10.3	10.9	10.2	Sparc	8.6 8.7	12 9.9	11.3 10.1	12.2 9.8	
P4ha1	10.5	11.2	11	10.5	Ltbp3	8.9	10.7	10.1	8.9	
Timp2	10.6	11.1	11.8	11.9	Spon1	8.9	9.8	10.9	9.9	
Adam9v	11.1	11.8	12	11.6	Efemp2	10.1	9.8	9.8	9.9	
Adam10	11.1	11.4	11.3	10.7	Mfap1a	10.1	12.9	12.6		
Adam17	11.2	11.2	11.3	11.1	Ecm1	11.1	10.8	10.7	12.9 10.3	
Mmp8	11.3	10.6	7.9	5.1	Mfap3	11.1	10.8	10.7		
Adam15	11.5	11.5	11.7	11.3	Vwa5a	11.3	11.7	11.6	10.9	
Ctsd	11.6	12.6	13	12.5	Fg12	11.4			11.8	
Cstb	11.6	12.4	12.1	11.8	Thbs1	12.3	13.6 11.8	13.1	13.2	
Plod3	11.8	11.2	10.8	10.2	Emilin2	13.4		11.2	9.8	
F10	11.9	11.6	9.5	7.2	Tgfbi	14.1	13.7 13.6	13.1	13.2 10.3	
Ctsh	12	12	12.2	12	Fn1	14.1	13.0	13.1	10.5	
F13a1	12.2	11.8	11.6	10.5						
Hpse	12.4	11.1	10.8	9.5	E ECM-affiliated proteins					
Ctsz	12.7	12.9	13.2	12.9	Gene	Ly6C(hi)	Ly6C(hi)	F4180(hi)	Resident	
Ctss	12.8	12.9	12.9	12.7	Symbol	spleen	TAM	TAM	colonic	
Ctsc	12.8	13.2	13.3	13.3		monocytes	.,		IpMF	
Ctsa	12.8	12.7	13	12.8	Sdc2	6.4	9	8.1	9.2	
Ctsb	12.9	12.9	13.2	13.2	Muc3	6.7	8.8	8	13.5	
Cst3	13.5	13.4	13.5	13.2	Muc13	6.9	8.4	7.8	12.1	
<u> </u>				144	Muc2	7.8	8.7	8.3	13.5	
6				14	Lgals4	8.3	10.1	9.5	13.7	
B Collage	ns				Sdc1	8.4	9.8	8.6	10	
Gene	Ly6C(hi)	Ly6C(hi)	F4180(hi)	Resident	C1qa	8.4	11.5	12.8	13.3	
Symbol	spleen	TAM	TAM	colonic	Sdc4	8.5	11.3	11.3	12.1	
	monocytes	17 (17)	17 1141	IpMF	C1qc	9.4	12.5	13.4	13.9	
Col14a1	7.4	8.7	10.8	9.7	100000000000000000000000000000000000000	10.3	12.5	13.4	15.9	
Colf4a1 Col6a2	8.2	9.3	8.8	9.7 8.7	C1qb Sdc3	11.3	11.9	12.2	11.4	
	8.2	9.3	8.8	9.4		11.3	11.9	12.2	10.6	
Col6a1	8.5 8.6	9.7	9.2	9.4	Anxa1	12.3	13.3	13.2	12.6	
Col6a1 Col1a2	8.6	9.7	9.2	9.3	Lgals1	12.6	13.3	13.2	12.8	
	9.1	10.2	9.5	9.9	Lgals3	13.1	12.9	12.7	12.8	
Col1a1	5.1	10.2	5.5	5.5	Anxa5	13.1	12.3	12.3	12.5	

Figure S3. **TAMs express a unique signature of ECM-related genes.** (A–E) Affymetrix gene array heat map analyses showing the differential raw expression level of ECM-related genes of sorted Ly6C^{hi} and F4/80^{hi} TAMs (day-14 tumors) in comparison with their Ly6C^{hi} monocyte precursors (splenic reservoir) and colonic lpMFs sorted from upstream normal colonic mucosa. ECM genes are categorized as ECM regulators (A), collagens (B), proteoglycans (C), glycoproteins (D), and ECM-affiliated proteins (E). Values are presented as (log_2) gene expression average of two biological repeats, each performed from a pool of mice (n = 5 for splenic monocytes, and $n \ge 10$ for TAMs and colonic lpMFs).

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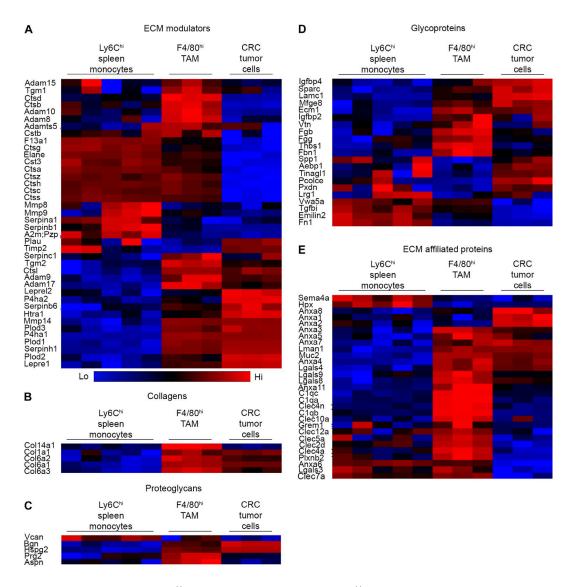


Figure S4. Proteomic profiling of sorted F4/80^{hi} TAMs in comparison with their Ly6C^{hi} monocyte precursors and colocalizing CRC tumor cells. (A–E) Color-coded heat maps presenting ECM-related proteins found by LC-MS/MS analysis to be significantly and differentially expressed in sorted F4/80^{hi} TAMs in comparison with their Ly6C^{hi} monocyte precursors and colocalizing colorectal tumor cells. For Ly6C^{hi} monocytes, five biological repeats were performed; each was extracted from a pool of three mice. For F4/80^{hi} TAMs and CRC tumor cells, three biological repeats were performed; each was extracted from a pool of five mice. Data were analyzed by unpaired, two-tailed Student's t tests (pFDR = 0.05), z scored, and divided into the following categories: ECM modulators (A), collagens (B), proteoglycans (C), glycoproteins (D), and ECM-affiliated proteins (E).

Table S1 is included as an Excel file and shows a GOEAST function enrichment analyses of the differentially expressed genes between Ly6Chi TAMs and resident colonic IpMFs and between F4/80hi TAMs and resident colonic IpMFs.

Table S2 is included as an Excel file and shows a DAVID function enrichment analyses of the differentially expressed genes between Ly6Chi TAMs and resident colonic IpMFs and between F4/80hi TAMs and resident colonic IpMFs.

Table S3 is included as an Excel file and shows an ingenuity pathway analysis of the differentially expressed genes between F4/80^{hi} TAMs and resident colonic IpMFs.