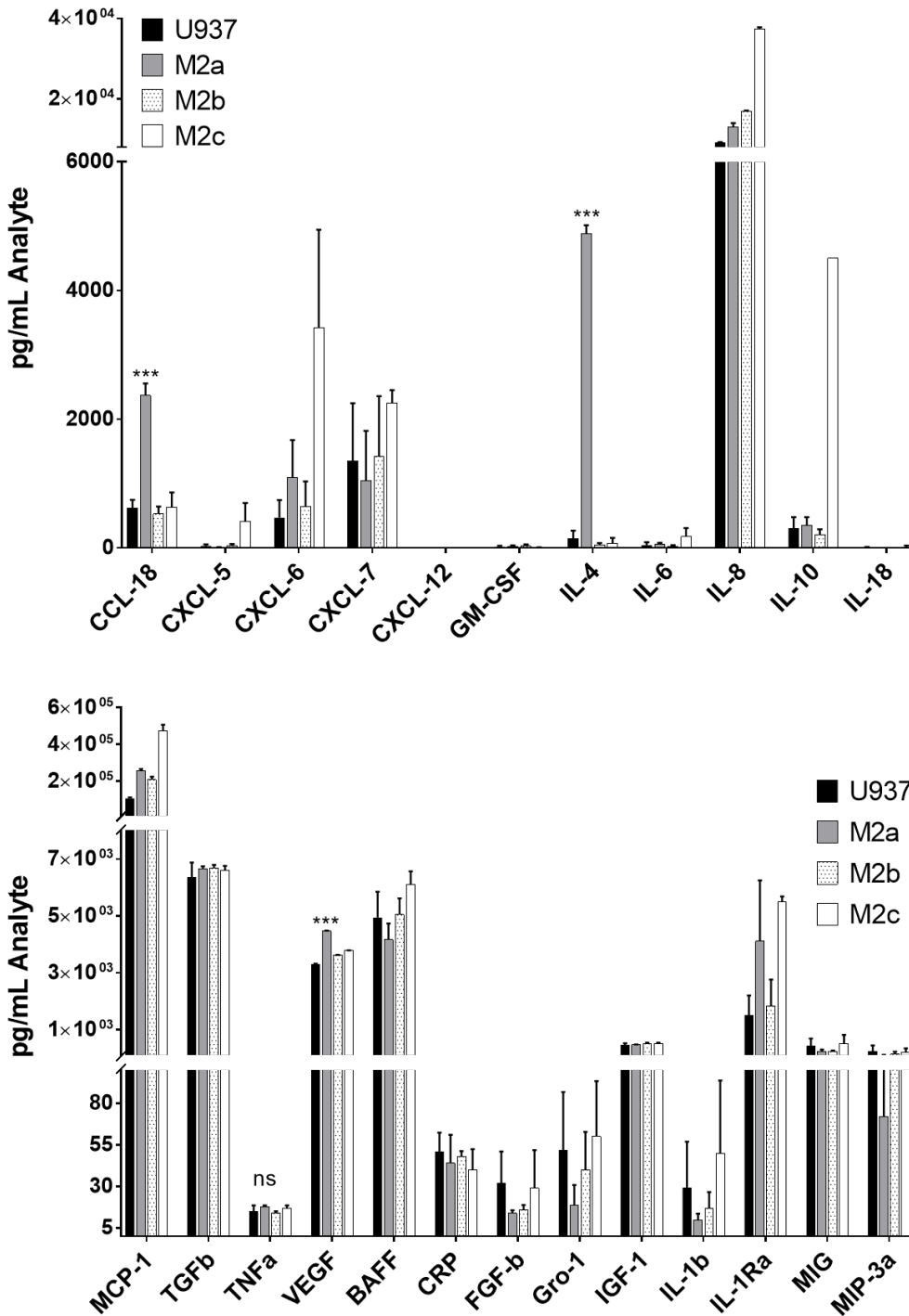
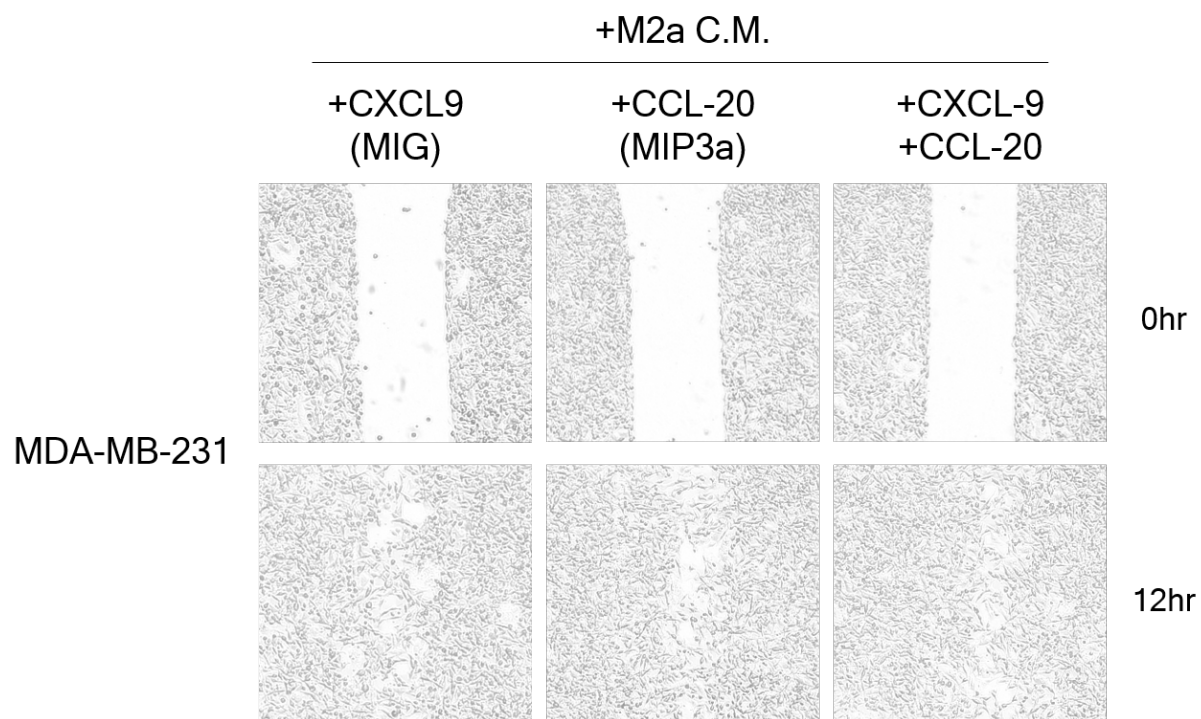


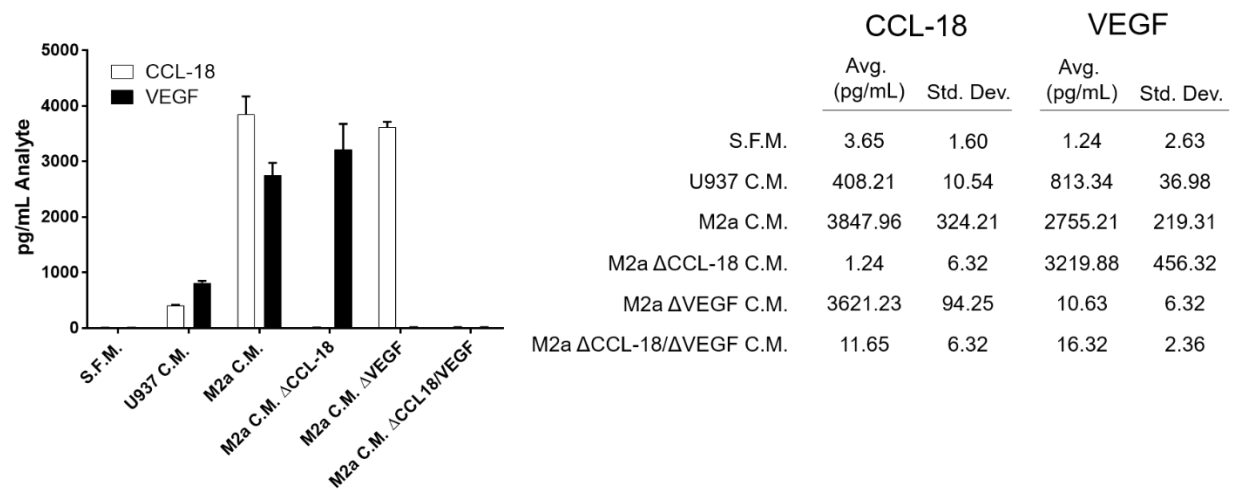
**Supplemental Figure S2.** Results from spheroid invasion assays display conditioned media from M2 macrophages has a minimal effect on human mammary epithelial cells (hME). Images are representative images selected from a single experiment (left). Averaged data is compiled from two independent experiments. Error bars represent standard deviation.



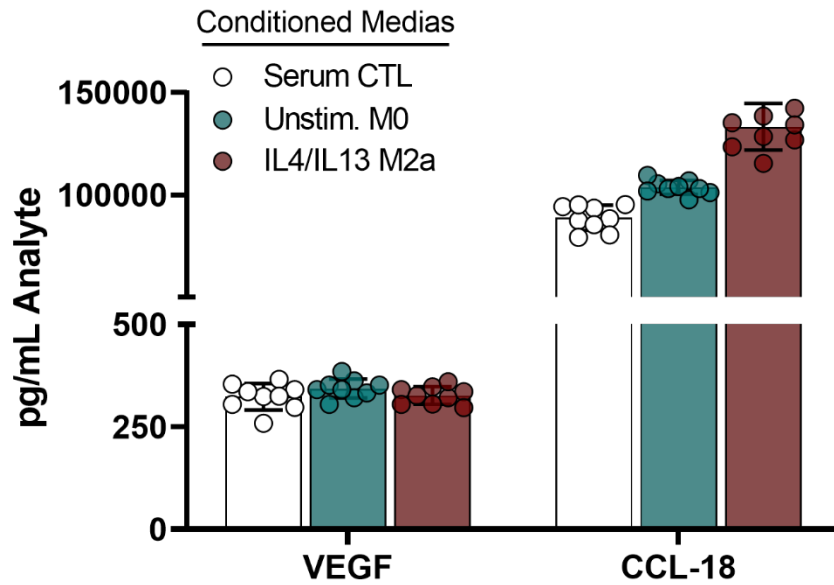
**Supplemental Figure S3.** ELISA results of various secreted components in the conditioned media isolated from either U937 monocyte or M2-macrophage cell populations. Averaged data is compiled from three independent experiments. Statistical significance was determined by one-way ANOVA; \*\*\*p<0.001. Error bars represent standard deviation.



**Supplemental Figure S4.** Exogenous addition of inhibitory proteins, MIG, or MIP3a, do not affect M2a-induced migration. Results from MDA-MB-231 cells stimulated with M2a conditioned media, supplemented with recombinant CXCL-9 (MIG), CCL-20 (MIP3a), or both cytokines together, does not inhibit M2a macrophage induced migration. Images representative of 2 independent experiments.



**Supplemental Figure 5.** ELISA results from CCL-18 and/or VEGF analyte removal assay shows complete depletion of CCL-18 and/or VEGF in target concentrated medias. Raw values in pg/mL displayed right. Data is compiled from 3 independent experiments.



**Supplemental Figure 6.** ELISA results displaying levels of VEGF or CCL-18 in conditioned media from primary human macrophages. Results depict raw values of conditioned media from monocyte/macrophage serum-containing media (white), M-CSF polarized unstimulated macrophages (green), or M-CSF polarized IL-4/IL-13 stimulated M2a macrophages (red). Data is compiled from three independent experiments.

Gene	$r^2$	E %	Sequence (5'-3')
TLR4	0.981	101.832	F: TGC GTGAGACCAGAAAGC R: TTAAAGCTCAGGTCCAGGTTC
S100A9	0.999	94.193	F: TGACAGAGTGCAAGACGATG R: ACCAGCTCTTTGAATTCCCC
TLR2	0.998	94.709	F: AGACCTATAGTGACTCCCAGG R: ACCCACACCATCCACAAAG
TGF $\beta$	0.999	95.01	F: GCCTTTCCTGCTTCTCATGG R: TCCTTGCGGAAGTCAATGTAC
DCR3	0.997	93.853	F: TCAATGTGCCAGGCTCTTC R: CAGCCTCTTGATGGAGATGTC
CD86	0.985	104.115	F: TCCCTGATGTTACGAGCAATATG R: ATCCAAGGAATGTGGTCTGG
MHC2	0.993	102.598	F: CAGAATGGAGACTGGACCTTC R: TGTGCAGATTCAGACCGTG
CD68	0.981	100.29	F: CATCTCTGTACTGAACCCCAAC R: CCATGTAGCTCAGGTAGACAAC
IL1 $\alpha$	0.982	114.731	F: TGTATGTGACTGCCCAAGATG R: TTAGTGCCGTGAGTTTCCC
TGM2	0.988	123.303	F: TCAGCTACAATGGGATCTTGG R: AAGGCAGTCACGGTATTTCTC
SOCS3	0.972	98.48	F: CTATGAGAAAGTCACCCAGCTG R: CTTGTGCTTGTGCCATGTG
IL1 $\beta$	0.943	108.846	F: ATGCACCTGTACGATCACTG R: ACAAAGGACATGGAGAACACC
MGL1	0.958	107.126	F: CTTGATCCCTACAGTGACG R: CACATCACTAAGCTCCAGTACC
TNF $\alpha$	0.975	117.833	F: GAGAAGCAACTACAGACCCC R: CATGCTTTCAGTGCTCATGG
TLR1	0.99	111.135	F: TTAGAAGAAATCAGGATAACAAAG GC R: GGCAAAATGGAAGATGCTAGTC
IL10	0.99	127.98	F: ATGCCCAAGCTGAGAAC R: GCCTTGCTCTTGTTTTACAG
TLR8	0.973	125.292	F: ACAACCCGAAGGCAGAAG R: GGCGCGAAATCATGACTTAAC
CLEC7a	0.996	106.401	F: TCGACTCTCAAAGCAATACCAG R: CCACAGCTATCACCAGTATTACC
IL1R2	0.99	101.341	F: CGTGACAAAAGTACGTGAAG R: CAGGACACAGCGGTAATAGC
IL1R1	0.987	91.55	F: AGATGACAGCAAGACACCTG R: TCTGAGGCAGTAAGATGAATTTCT
CD163	0.963	77.956	F: GAGTCCCTTCACCATTACTGTG R: GACTTTCACCTCCACTCTCCC
CD80	0.952	71.178	F: AAGTGGAGTCTTACCCTGAAATC R: AAGACCCTCCAGTGATGTTTAC
MRC1	0.972	127.571	F: ACAGTTATGCCTACCATGCC R: CCCTCCAAAGCCTATACAAGC
*E % = Percent Efficiency			

**Supplemental Table 1.** RT-qPCR primer sequences and corresponding efficiency scores utilized for this study.