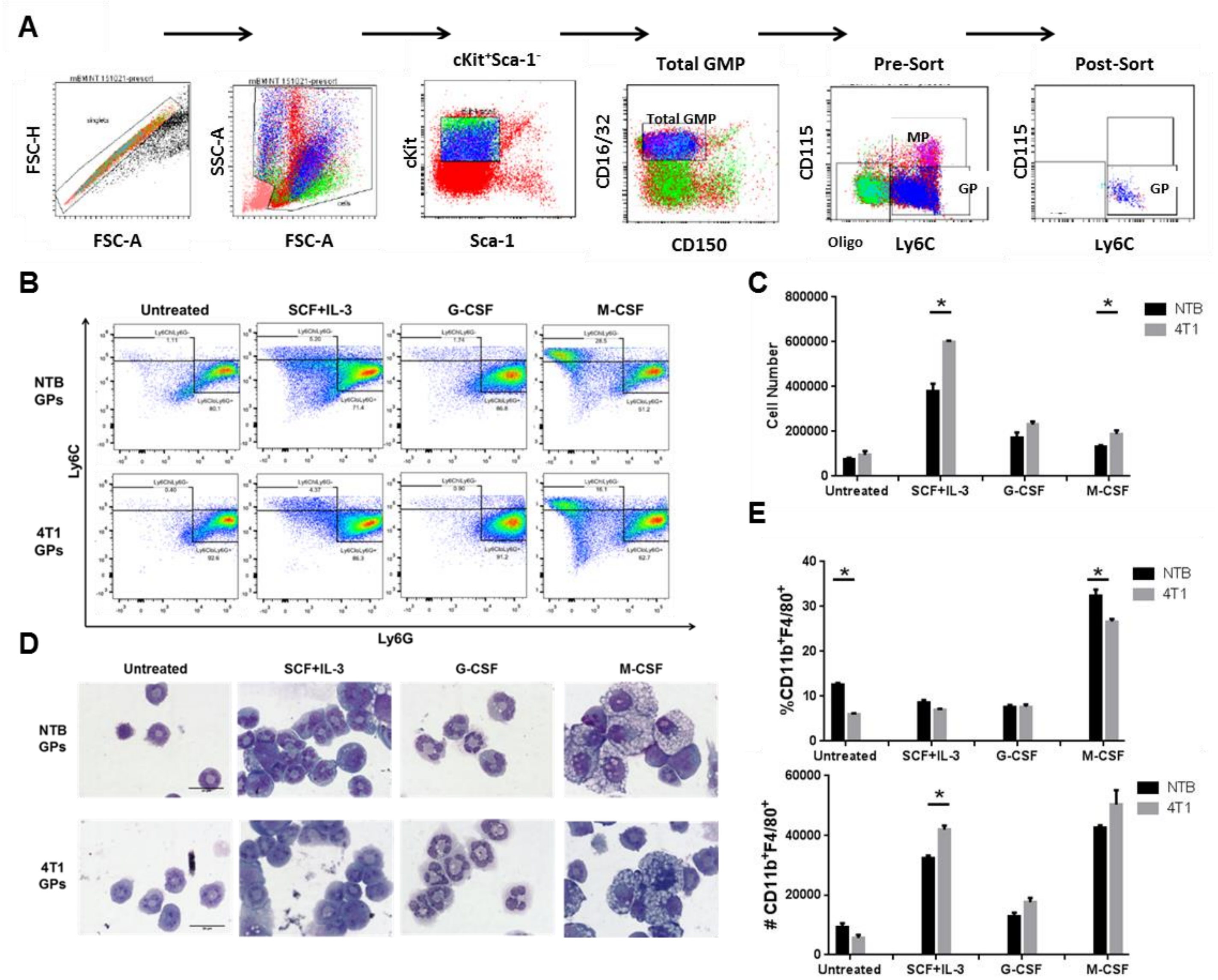
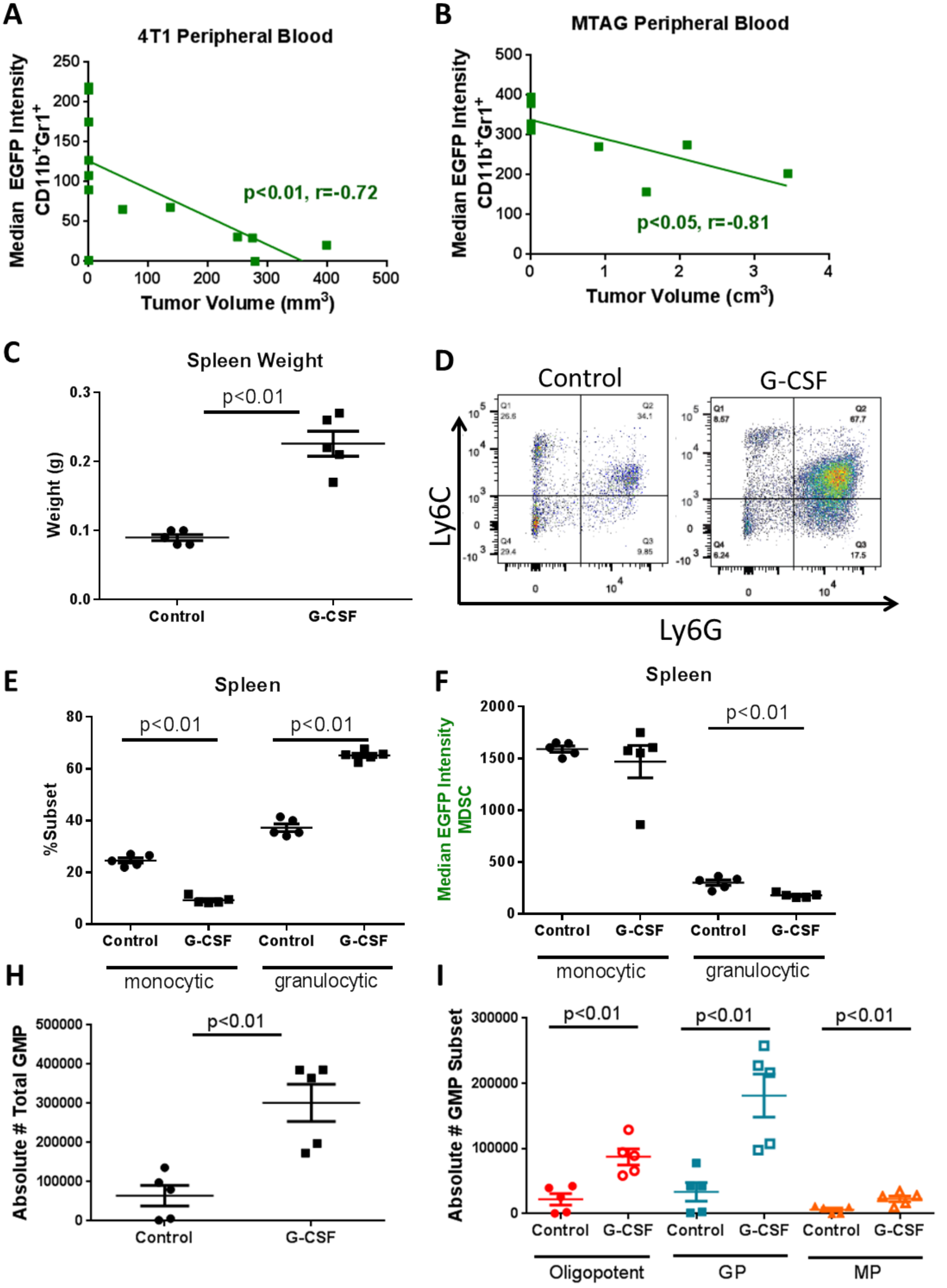


Supplemental Figure 1: (*A*) GPs were sorted from NTB- or 4T1 tumor-bearing lineage-depleted bone marrow cells (as described in the Methods). The scheme represents the flow sorting gating strategy shown in sequence using arrows moving left to right. The various cell populations within the bone marrow are depicted using different colors. The cell populations of interest at each step of the flow sort are specifically highlighted within the gated, boxed regions. GPs were then treated with the indicated hematopoietic cytokine (50 ng/ml) *in vitro* for 4 days. (*B*) Representative flow plots post-differentiation. (*C*) Total cell numbers post *in vitro* differentiation. (*D*) Morphologic analysis of resulting cells after differentiation, as determined by cytospin. (*E*) Frequency (upper panel) and absolute number (lower panel) of resulting CD11b$^+$F4/80$^+$ macrophages in each culture condition. Data recorded as mean ± SEM of at least triplicate determinations.



Supplemental Figure 2: (A) Peripheral blood myeloid populations were assessed for IRF8 expression over the course of 4T1 (left) and MTAG (right) tumor growth. Data compiled from multiple experiments (NTB, n=8; 4T1, n=17; WT, n=7; MTAG, n=12). Treatment with G-CSF induced splenomegaly, as determined by spleen weight (*C*). (*D*) Cells were gated, based on Ly6G and Ly6C expression. Left flow plot, Control; right flow plot, G-CSF-treated. (*E*) The percentage of each of these cell populations was calculated for the spleen, as well as their expression IRF8 levels. (*F*) Absolute numbers of total GMPs (*H*) and GMP (*I*) subsets in control and G-CSF-treated mice.

	Antigen (anti-mouse)	Clone	Company	Ref/Catalog #
Bone Marrow	CD16/32	93	eBioscience	45-0161-80
	Ly6A/E(Sca-1)	D7	eBioscience	25-5981-81
	Ly-6G/Ly-6C(Gr-1)	RB6-8C5	BioLengend	108409
	CD135(Flt3)	A2F10	eBioscience	12-1351-82
	CD117(c-kit)	2B8	eBioscience	47-1171-82
	CD135(c-fms)	AFS98	eBioscience	17-1152-82
	Ly-6C	HK1.4	BioLegend	128024
	CD11b	M1/70	BD Biosciences	563168
	CD11c	N418	BioLegend	117336
	CD8a	53-6.7	BioLegend	100742
	CD45R/B220*	RA3-6B2	BioLegend	103247
	CD150	TC15-12F12.2	BioLegend	115927
	CD105	MJ7/18	eBioscience	48-1051-82
	DAPI		ThermoFisher Scientific	D1306

Peripheral Blood/Spleen	CD11b	M1/70	BD Biosciences	563168
	Gr-1	RB6-8C5	BioLegend	108409
	CD115	AFS98	eBioscience	117-1152-82
	Ly-6C	HK1.4	BioLegend	128024
	Ly-6G	1A8	BD Biosciences	551461

*cross-reacts with human

Supplemental Table 1: Antibodies used for bone marrow and peripheral blood/spleen analyses.

	Log$_2$			**Regulized Fold Change**	
Gene Name	NTB	GP	KO	4T1	KO
Retnlg	8.29043	10.97135	11.8355	6.4126436	11.67277215
Lars2	15.3262	17.96311	19.49702	6.2199761	18.01108052
Mmp9	8.709462	10.96415	12.71084	4.7723053	16.0153239
Mmp8	8.549451	10.79973	12.2084	4.7577624	12.63142754
Asprv1	5.900299	7.879544	7.383898	3.9428659	2.796455372
Il1r2	6.925273	8.859556	8.820317	3.8218821	3.719333651
S100a6	7.570323	9.421709	10.09404	3.6084667	5.750620152
Adam8	6.890789	8.698538	9.593756	3.5009564	6.511397948
Adam19	6.635024	8.429042	8.167524	3.4677931	2.892867296
Lilr4b	7.422225	9.132798	9.212124	3.2729078	3.457907449
Lilrb4a	8.147029	9.853144	10.12838	3.2628099	3.948630819
Cxcr2	9.153799	10.83223	11.13141	3.2007994	3.938395896
Slfn1	6.66641	8.321413	9.237446	3.1492395	5.942360984
Cd101	6.055984	7.663265	8.071147	3.04677	4.042263106
Ifitm6	7.647062	9.149564	11.46248	2.8333363	14.07850416
Tlr13	6.93427	8.432792	8.761663	2.8255311	3.548952073
Fpr2	7.039048	8.47983	10.69451	2.7146803	12.60098878
Cd300lf	7.667894	9.099444	9.79747	2.6973625	4.375886103
Lrg1	8.838277	10.25512	10.38295	2.6699992	2.917377735
Pirb	8.43428	9.831673	11.25891	2.6342507	7.084327133
Ccr1	7.652278	9.010551	9.28332	2.5637797	3.09736556
Rn45s	19.45192	20.67164	21.76547	2.3290252	4.971039894
Fpr1	6.111118	7.326751	8.473056	2.3224256	5.14060387
Rasgrp4	7.187943	8.38357	10.13587	2.2904436	7.716378772
Tgfbi	8.88655	10.05484	10.81257	2.2474542	3.800046012
Dgat2	9.793883	10.95392	11.09984	2.2346337	2.472471764
Cd33	7.942221	9.097606	10.67575	2.2274385	6.650828063
Mctp2	7.163679	8.301588	8.824375	2.2006187	3.16169116
C5ar1	7.709306	8.833099	9.945854	2.1791917	4.712681935
Bst1	5.482441	6.58988	6.533696	2.1546284	2.07233137
Grina	9.580544	10.67655	10.86787	2.1376256	2.440754478
Glipr2	9.239132	10.30204	11.35861	2.0891421	4.345371135
Rn4.5s	8.867328	9.907648	9.953512	2.056684	2.123117416
Slc2a3	8.87444	9.899414	11.55753	2.0349227	6.422289378
Cd300ld	5.46852	6.480578	6.52703	2.0167849	2.082779011
Angpt1	6.947556	5.932741	5.872452	0.4948916	0.47463671
Ly86	7.906524	6.857141	6.688623	0.4831749	0.429907643
Klf4	7.704944	6.650646	6.516185	0.4815316	0.438680303
Abcb1b	8.009921	6.943699	6.728985	0.4775679	0.41152829
Zbtb16	9.074367	8.003288	7.578669	0.4759629	0.354609228
Jun	11.17541	10.09909	10.14618	0.4742378	0.48996949
Dpp4	7.83358	6.681498	6.559544	0.4499755	0.413501278
Ly6c1	11.14542	9.93469	9.9188	0.4320503	0.427317608
Eml5	10.24874	9.02489	8.415235	0.4281395	0.280582633
Cd34	11.17917	9.953686	9.635086	0.4276555	0.342914603
Hspa1a	12.39641	11.11947	9.998023	0.412672	0.189677126
Hspa1b	12.55435	11.2336	10.13778	0.4003275	0.187301273
Irf8	11.45065	9.947257	10.37579	0.352722	0.474716134
Apba1	8.541423	6.934611	6.593027	0.328323	0.259104072
Rasa4	8.98375	7.282071	7.141088	0.307428	0.278806774
Fosb	9.139596	6.483936	7.285816	0.1586962	0.276666547

Supplemental Table 2: Differentially regulated genes detected by RNA-seq. Fold-change normalized to NTB control.