SUPPLEMENTAL MATERIAL

Morrison et al., http://www.jem.org/cgi/content/full/jem.20132130/DC1

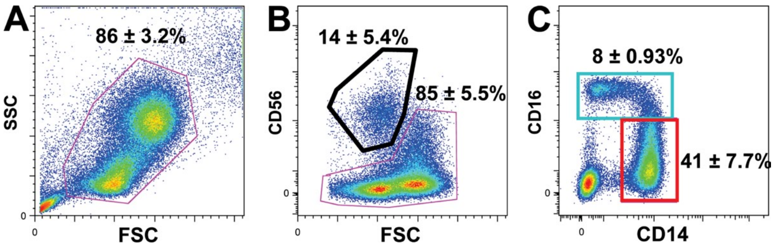

Figure S1. Flow cytometric serial selection, identification, and subsequent separation (sorting) of human peripheral blood inflammatory versus patrolling monocytes. (A) Side and forward scatter gating/selection of viable cells. (B) Identification (and exclusion) of CD56^{hi} NK cells (black). (C) Identification (and selection/sorting) of CD56^{-} CD16^{lo} CD14^{hi} inflammatory monocytes (red), and CD56^{-} CD16^{hi} CD14^{var} atypical/patrolling monocytes (cyan). All quantitative data are displayed as mean ± SEM (*n* = 4). Data are from two independent experiments, each with two mice per treatment group.

Score	Peptide Sequence	m/z	Ion Mass	Ion Mass(calc)	Delta	Charge
144.12	K.MQQNIQELEEQLEEEESAR.Q + Oxidation (M)	1175.0284	2348.0422	2348.0437	-0.0015	2
136.03	K.LQVELDNVTGLLSQSDSK.S	973.5078	1945.001	1945.0004	0.0006	2
132.99	K.TQLEELEDELQATEDAK.L	981.4631	1960.9116	1960.9113	0.0003	2
118.38	R.IAEFTTNLTEEEEK.S	827.3971	1652.7797	1652.7781	0.0017	2
117.65	K.SMEAEMIQLQEELAAAER.A + 2 Oxidation (M)	1040.9784	2079.9422	2079.9452	-0.003	2
117.42	K.MQQNIQELEEQLEEEESAR.Q	1167.0299	2332.0452	2332.0488	-0.0036	2
116.88	R.IAQLEEELEEEQGNTELINDR.L	1236.5882	2471.1618	2471.1663	-0.0044	2
111.74	K.TELEDTLDSTAAQQELR.S	960.4645	1918.9145	1918.912	0.0025	2
110.91	K.KLEEEQIILEDQNCK.L + Propionamide (C)	951.9761	1901.9376	1901.9404	-0.0028	2
108.36	R.KKVEAQLQELQVK.F	770.9566	1539.8987	1539.8984	0.0003	2
102.99	R.KLEGDSTDLSDQIAELQAQIAELK.M	1308.172	2614.3294	2614.3337	-0.0043	2
102.82	K.SMEAEMIQLQEELAAAER.A + Oxidation (M)	1032.9812	2063.9478	2063.9503	-0.0024	2
101.68	R.NTDQASMPDNTAAQK.V	796.3549	1590.6953	1590.6944	0.0009	2
100.5	R.IAQLEEELEEEQGNTELINDR.L	824.7298	2471.1676	2471.1663	0.0013	3
98.78	R.QLLQANPILEAFGNAK.T	863.9787	1725.9429	1725.9413	0.0015	2
97.24	K.KVEAQLQELQVK.F	706.9091	1411.8037	1411.8035	0.0003	2
95.76	K.DFSALESQLQDTQELLQEENR.Q	1247.088	2492.1614	2492.1667	-0.0052	2
94.44	K.EQADFAIEALAK.A	653.3375	1304.6604	1304.6612	-0.0008	2
92.2	R.LTEMETLQSQLMAEK.L + Oxidation (M)	884.4287	1766.8429	1766.843	-0.0001	2
91.95	R.LTEMETLQSQLMAEK.L + 2 Oxidation (M)	892.4258	1782.837	1782.8379	-0.0009	2
91.62	R.DELADEIANSSGK.G	674.815	1347.6154	1347.6154	0.0001	2
91.55	K.NLPIYSEEIVEMYK.G + Oxidation (M)	872.4291	1742.8437	1742.8436	0	2
91.03	R.ELEDATETADAMNR.E	783.341	1564.6674	1564.6675	-0.0001	2
90.67	K.HSQAVEELAEQLEQTK.R	920.4575	1838.9005	1838.901	-0.0005	2
90.4	K.NMDPLNDNIATLLHQSSDK.F + Oxidation (M)	1071.5089	2141.0032	2141.0059	-0.0026	2
89.2	R.IMGIPEEEQMGLLR.V	808.4124	1614.8102	1614.8109	-0.0007	2
88.48	K.RQLEEAEEEAQR.A	744.3575	1486.7004	1486.7011	-0.0007	2
88.35	K.ASITALEAK.I	452.2613	902.5081	902.5073	0.0008	2
88.14	K.DFSALESQLQDTQELLQEENR.Q	831.7289	2492.165	2492.1667	-0.0017	3
86.99	K.LEEEQIILEDQNCK.L + Propionamide (C)	887.9299	1773.8453	1773.8454	-0.0001	2
86.57	K.EEVGEEAIVELVENGK.K	872.4357	1742.8569	1742.8574	-0.0005	2
86.22	K.KANLQIDQINTDLNLER.S	999.5342	1997.0539	1997.0541	-0.0003	2
85.52	R.NTDQASMPDNTAAQK.V + Oxidation (M)	804.3493	1606.6841	1606.6893	-0.0052	2
82.6	K.ANLQIDQINTDLNLER.S	935.4889	1868.9633	1868.9592	0.0042	2
82.52	K.NLPIYSEEIVEMYK.G	864.4315	1726.8484	1726.8487	-0.0003	2
82.3	R.HEMPPHIYAITDTAYR.S + Oxidation (M)	965.9584	1929.9022	1929.9043	-0.0021	2
81.89	R.IAEFTTNLTEEEEK.S	1653.7838	1652.7765	1652.7781	-0.0016	1
81.18	R.VISGVLQLGNIVFK.K	743.954	1485.8935	1485.8919	0.0016	2
78.77	R.LQQELDDLLVDLDHQR.Q	975.4994	1948.9842	1948.9854	-0.0012	2
78.03	R.IAEFTTNLTEEEEKSK.S	934.9582	1867.9019	1867.9051	-0.0032	2
76.91	K.VIQYLAYVASSHK.S	739.9041	1477.7937	1477.7929	0.0008	2
76.86	R.DELADEIANSSGK.G	1348.6236	1347.6163	1347.6154	0.001	1
76.55	K.SGFEPASLKEEVGEEAIVELVENGK.K	1330.6655	2659.3164	2659.3228	-0.0064	2
76.55	R.ELEDATETADAMNR.E + Oxidation (M)	791.3387	1580.6628	1580.6624	0.0004	2
76.51	K.VSHLLGINVTDFTR.G	1571.8515	1570.8442	1570.8468	-0.0025	1
76.42	R.QLLQANPILEAFGNAK.T	576.3211	1725.9416	1725.9413	0.0003	3
75.61	R.RGDLPFVVPR.R	578.3361	1154.6576	1154.656	0.0016	2
74.65	R.EMEAELEDER.K + Oxidation (M)	1266.5139	1265.5066	1265.5081	-0.0015	1
74.11	R.ALEQQVEEMKTQLEELEDELQATEDAK.L + Oxidation (M)	1055.1643	3162.4711	3162.4761	-0.0051	3
73.54	K.DMFQETMEAMR.I + 2 Oxidation (M)	710.7807	1419.5468	1419.5469	0	2

Figure S2. MH^+ ions detected in trypsin digests by LCMS. THP-1 cells were stimulated with 50 ng/ml CCL2 for 10 min at 37°C, followed by lysis, GTP loading with 100 µM GTPγS for 10 min, affinity precipitation by PBD pulldown, and using Coomassie staining to identify Rac-associated bands. A 226 kD protein was in-gel trypsin-digested, and eluted peptides were run on LCMS by the Yale Keck Proteomic Core Facility. The table displays the peptide sequence, m/z, ion mass, and charge of top 50 (by score) Myh9 peptide species identified by mass spectrometry. Data are from two independent experiments, each with two treatment groups.

S2 VEGF-driven arteriogenesis requires Mϕ Myosin IIA | Morrison et al.