

Supplementary Table I. Probes with reduced and increased expression, in both control and LPS-treated macrophages differentiated over 9 days from the bone marrow of UV-irradiated mice. The macrophages were incubated with or without LPS for the last 24 h.

<i>Reduced Expression</i>	+LPS			-LPS		
Gene Name	Log₂Fold change	Probe Mean Expression	P.Value	Log₂Fold change	Probe Mean Expression	P.Value
RIKEN cDNA 3110099E03 gene	-0.2652	1.6075	0.0260	-0.2209	1.4986	0.0084
reticulon 1	-0.6622	3.8441	0.0095	-0.4624	4.6989	0.0154
centromere protein B	-0.2669	2.4130	0.0036	-0.2017	4.0960	0.0269
collagen, type XVIII, alpha 1	-0.3028	4.5397	0.0057	-0.2760	5.5336	0.0251
EGF-like repeats and discoidin I-like domains 3	-0.4375	2.4615	0.0007	-0.3653	3.3219	0.0073
glycoprotein galactosyl-transferase alpha 1, 3	-0.2590	8.0591	0.0291	-0.2359	6.8286	0.0282
kelch-like 36	-0.2735	3.8968	0.0326	-0.2818	4.1118	0.0456
NPC1-like 1	-0.2539	1.9919	0.0013	-0.2764	1.7859	0.0137
a disintegrin and metallopeptidase domain 6B	-0.2407	1.3791	0.0440	-0.3423	1.5897	0.0139
discs, large (Drosophila) homolog-associated protein 2	-0.2910	1.8991	0.0136	-0.2173	1.5141	0.0487
2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	-0.3534	5.9705	0.0337	-0.1527	6.8225	0.0134
thioredoxin reductase 1	-0.3438	5.9131	0.0293	-0.3469	5.8240	0.0324
cadherin-related family member 5	-0.2360	1.7370	0.0174	-0.3059	2.0282	0.0035
coactosin-like 1 (Dictyostelium)	-0.1927	8.5868	0.0186	-0.1406	9.8611	0.0072
pseudouridylate synthase 7 homolog (S. cerevisiae)	-0.3318	4.3148	0.0298	-0.2683	6.3299	0.0054
<i>Increased Expression</i>						
RIKEN cDNA 1810010D01 gene	0.2117	3.5159	0.0370	0.3277	2.9983	0.0001
predicted gene 10941	0.33797	1.8304	0.0457	0.2836	2.9432	0.0245
predicted gene 35677	0.3232	1.9031	0.0451	0.3763	2.3358	0.0010
complement component 4 binding protein, pseudogene 1	0.3730	1.8115	0.0034	0.3318	1.7738	0.0066

cell division cycle 25A	0.1743	5.1265	0.0477	0.2344	5.7825	0.0052
cystin 1	0.2055	1.8080	0.0237	0.1643	1.7696	0.0487
NFκ light polypeptide gene enhancer in B cells inhibitor 1	0.2749	4.9858	0.0213	0.2858	4.5799	0.0489
prepronociceptin	0.2350	1.8037	0.0424	0.3997	1.7500	0.0006
suppressor of cytokine signaling 7	0.1797	4.5181	0.0166	0.1400	4.8637	0.0315
predicted gene 4787	0.3188	1.4338	0.0414	0.2766	1.8809	0.0382
non-SMC condensin I complex, subunit H	0.2170	3.5045	0.0424	0.1550	6.8265	0.0254
T cell receptor gamma, variable 4	0.3393	1.3234	0.0037	0.2088	1.1654	0.0445
cytochrome P450, family 26, subfamily b, polypeptide 1	0.2793	2.2331	0.0439	0.2600	3.3314	0.0314
insulin-like 6	0.1535	8.1255	0.0432	0.1492	5.4351	0.0440
rhomoid domain containing 3	0.2549	4.4271	0.0068	0.1667	5.1889	0.0138
keratin 26	0.2043	1.3722	0.0489	0.2259	1.5326	0.0174
expressed sequence AA415398	0.6767	2.0144	0.0033	0.2399	2.1104	0.0179
RIKEN cDNA D930028M14 gene	0.2308	2.9724	0.0424	0.3599	1.9903	0.0008
proline-rich nuclear receptor coactivator 2	0.1593	9.1186	0.0346	0.1497	9.6116	0.0141
regulatory factor X, 5 (influences HLA class II)	0.1967	6.3315	0.0408	0.1680	7.0857	0.0151
ankyrin repeat domain 49	0.2340	5.1614	0.0371	0.1880	6.1490	0.0152
predicted gene 9866	0.3629	1.7717	0.0258	0.3917	2.1220	0.0215
makorin, ring finger protein 2, opposite strand	0.3376	1.7455	0.0334	0.3233	1.8538	0.0016
RIKEN cDNA 1700023E05 gene	0.2924	2.7695	0.0441	0.3674	3.0405	0.0004
tetratricopeptide repeat domain 25	0.4685	1.8064	0.0103	0.3987	1.9127	0.0078

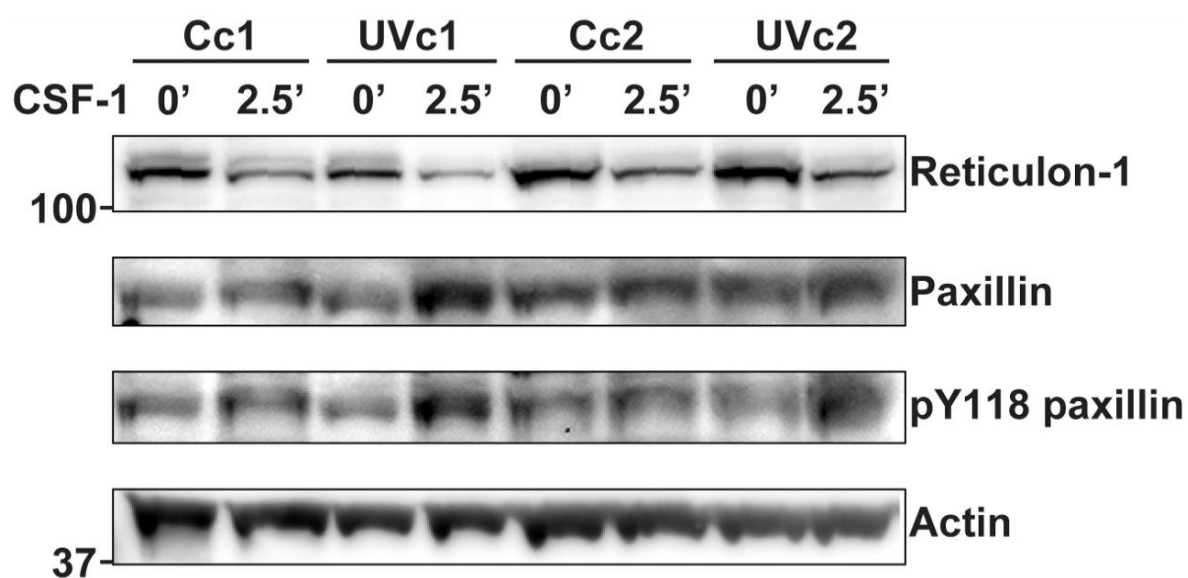
Supplementary Table II. Western blots of lysates of macrophages differentiated for 9 days from the bone marrow of control- and UV-chimeric mice. Macrophages were starved for 16 h of CSF-1, before a 2.5 minute pulse at 37°C with, or without CSF-1 (120 ng/ml). Densities for binding of antibodies to the different signalling molecules were quantified and standardized to expression of actin. Lysates were prepared from 4 pairs of macrophage cultures, with each pair prepared on separate days from a control- and matched UV-chimeric mouse. Mean \pm SEM.

	-CSF-1		+CSF-1 (2.5 min)	
	C-chim	UV-chim	C-chim	UV-chim
CSF-1R	47.0 \pm 24.3	38.5 \pm 14.4	173.1 \pm 33.5	182.6 \pm 25.3
pErk	33.5 \pm 16.2	24.9 \pm 10.9	184.8 \pm 24.6	184.8 \pm 28.4
PI3K	75.3 \pm 10.1	78.1 \pm 13.2	103.6 \pm 10.0	118.9 \pm 10.6
pY FAK	58.1 \pm 13.0	49.9 \pm 8.9	149.7 \pm 11.0	158.1 \pm 23.6
P85	143.6 \pm 37.2	127.5 \pm 27.1	43.7 \pm 12.9	67.8 \pm 12.0
pY Pyk2	84.6 \pm 24.6	96.9 \pm 17.2	129.4 \pm 21.2	154.3 \pm 26.9
P110d	79.1 \pm 11.2	73.6 \pm 9.9	105.0 \pm 8.7	120.2 \pm 9.9
paxillin	105.4 \pm 33.2	144.5 \pm 30.7	120.7 \pm 25.9	178.9 \pm 22.6*
pS Akt	69.5 \pm 16.2	66.2 \pm 18.4	149.0 \pm 48.3	146.2 \pm 26.9

* $p < 0.01$, paired t-test

1 **Supplementary Figure 1. Western blot of reticulon-1, paxillin, phosphoY118paxillin and**
2 **actin expression.** Macrophages were differentiated from the BM of 4 control- and 4 UV-
3 chimeric mouse, and exposed or not to CSF-1 for 2.5 min. The density of the bands for
4 reticulon-1, paxillin and actin were quantified and are shown in Fig 5C and D.

5



6