

Table S1 Validation of polarized macrophages

Gene Name	Accession	Peptide Sequence	Precursor <i>m/z</i>	Abundance (DDA)						Abundance (PRM)					
				M0	M1	M2a	M2b	M2c	M2d	M0	M1	M2a	M2b	M2c	M2d
STAT1	P42224	YLYPNIDKDHAFGK	560.9509+++	5E+09	1.39E+10	5.18E+09	2.62E+09	1.23E+09	1.6E+09	5036393	20728490	3170040	2496375	2018556	1716847
TGM2	P21980	TVEIPDPVEAGEEVK	806.4092++	4.34E+08	3.3E+09	2.4E+10	5.03E+09	2.01E+09	3.27E+09	10062839	74437376	4.26E+08	1.17E+08	44018208	66079664
SPHK1	Q9NYA1	LFLAMEK	426.2384++	19131144	24425278	20780537	34209485	5399048	25104537	866057	1362635	1121418	2949772	700567	1251384
CXCL1	P09341	NIQSVNVK	451.2587++	23301806	60802638	39602199	2.71E+08	30829461	1.56E+08	2715829	653391	1368839	9560191	1644570	3703480
MERTK	Q12866	TDPLDRPTFSVLR	506.2755+++	NA	NA	7650404	NA	28223154	NA	409933	225259	59321	575705	2444123	22076
VEGFA	P15692	FMDVYQR	479.72683++	NA	3955721	6516734	13667979	NA	20473452	244785	384688	286471	508652	367824	1621817

Table S2 DEPs in four M2 macrophage subtypes compared with M0 macrophages

DEPs in M2a macrophages compared with M0 macrophages								DEPs in M2b macrophages compared with M0 macrophages							
Up-regulted DEPs				Down-regulated DEPs				Up-regulted DEPs				Down-regulated DEPs			
Gene Name	Accession	PSMs	M2a/M0	Gene Name	Accession	PSMs	M2a/M0	Gene Name	Accession	PSMs	M2b/M0	Gene Name	Accession	PSMs	M2b/M0
ACTG1	P63261	12773	24.1	HSP90AA2P	Q14568	1498	0.01	ACTG1	P63261	12773	13.871	TUBB8	Q3ZCM7	1161	0.01
ACTA1	P68133	5304	100	TUBB8	Q3ZCM7	1161	0.01	ACTA1	P68133	5304	100	HSP90AB4P	Q58FF6	470	0.01
FABP4	P15090	2459	9.367	TUBA8	Q9NY65	1008	0.01	POTEKP	Q9BYX7	1947	17.079	MCM5	P33992	154	0.116
POTEKP	Q9BYX7	1947	8.773	SNRPN	P63162	248	0.01	EHD1	Q9H4M9	816	9.56	ACTR3B	Q9P1U1	152	0.01
TGM2	P21980	529	27.503	ACTR3B	Q9P1U1	152	0.01	SOD2	P04179	694	16.97	KIF5C	O60282	147	0.01
ITGAM	P11215	387	13.647	GFPT2	O94808	116	0.01	NAMPT	P43490	575	9.73	GFPT2	O94808	116	0.01
HIST2H3A	Q71DI3	384	100	PABPC1L	Q4VXU2	105	0.01	IL1B	P01584	465	37.205	NRGN	Q92686	63	0.055
H3F3A	P84243	259	100	FAM49A	Q9H0Q0	80	0.01	AMPD3	Q01432	442	12.964	PZP	P20742	60	0.041
ALDH1A2	O94788	255	10.496	CD38	P28907	77	0.062	HIST2H3A	Q71DI3	384	100	PRKAR2B	P31323	51	0.01
ACOT2	P49753	252	100	PZP	P20742	60	0.026	NCF1	P14598	327	9.229	MT1X	P80297	49	0.01
PRPH	P41219	182	100	PRKAR2B	P31323	51	0.01	PLIN2	Q99541	318	8.991	KCNAB1	Q14722	49	0.01
DES	P17661	152	100	MT1X	P80297	49	0.01	H3F3A	P84243	259	100	POU2F1	P14859	45	0.01
GBP5	Q96PP8	133	8.952	KCNAB1	Q14722	49	0.01	ACOT2	P49753	252	100	SLC1A4	P43007	43	0.01
FABP5P3	A8MUU1	106	100	POU2F1	P14859	45	0.01	SRC	P12931	225	8.552	STK39	Q9UEW8	42	0.01
CCT6B	Q92526	101	100	RSRC2	Q7L4I2	41	0.01	TFPI2	P48307	200	47.044	CRABP2	P29373	40	0.01
MYL6B	P14649	96	100	RHOQ	P17081	41	0.01	WASHC2C	Q9Y4E1	198	100	TACC2	O95359	36	0.01
ITPR2	Q14571	94	100	PRTN3	P24158	32	0.058	DNM3	Q9UQ16	184	10.871	CDK12	Q9NYV4	35	0.01
LPL	P06858	94	8.915	IQGAP3	Q86VI3	31	0.01	PRPH	P41219	182	100	NBEAL2	Q6ZNJ1	32	0.01
TPT1	P13693	90	100	CHURC1	Q8WUH1	30	0.01	LPXN	O60711	177	8.027	PRTN3	P24158	32	0.065
RHOB	P62745	84	100	CTNNA2	P26232	28	0.01	PTGS2	P35354	164	8.397	ATP6V1C2	Q8NEY4	32	0.01
CALML3	P27482	84	19.113	STAG1	Q8WVM7	27	0.01	DES	P17661	152	100	IQGAP3	Q86VI3	31	0.01
EIF1B	O60739	80	100	RRAD	P55042	27	0.01	CD14	P08571	146	36.49	SPRY2	O43597	29	0.01
LGALS9C	Q6DKI2	79	100	SLFN11	Q7Z7L1	25	0.092	MYL6B	P14649	96	100	STAG1	Q8WVM7	27	0.01
ATP12A	P54707	79	100	PLG	P00747	25	0.01	LACC1	Q8IV20	95	11.457	RFX5	P48382	26	0.053
RAP2A	P10114	61	100	SBNO1	A3KN83	22	0.01	ITPR2	Q14571	94	100	CHD6	Q8TD26	25	0.01
MEF2C	Q06413	53	100	TLE4	Q04727	22	0.01	TPT1L	#N/A	90	100	PPP1R21	Q6ZMI0	20	0.01
MTX2	O75431	50	10.125	CREBBP	Q92793	22	0.01	RHOB	P62745	84	100	SCARB1	Q8WTV0	20	0.01
PKLR	P30613	50	100	GCH1	P30793	21	0.01	GRK3	P35626	81	100	RBCK1	Q9BYM8	19	0.01
PPP3CC	P48454	46	100	RNF14	Q9UBS8	21	0.01	EIF1B	O60739	80	100	USP13	Q92995	19	0.01
TMSB10	P63313	42	100	PPP1R21	Q6ZMI0	20	0.01	LGALS9C	Q6DKI2	79	100	TMOD1	P28289	18	0.01
VAT1L	Q9HCJ6	41	13.119	FOSL2	P15408	19	0.01	ATP12A	P54707	79	100	ZNRF2	Q8NHG8	17	0.01
CRABP2	P29373	40	22.347	CLK3	P49761	18	0.01	TTC39B	Q5VTQ0	69	9.124	CCND1	P24385	17	0.089
CCL5	P13501	39	25.255	CDC42SE1	Q9NRR8	18	0.01	CCL20	P78556	61	88.516	CYP51A1	Q16850	17	0.01
S100A10	P60903	39	8.733	TMOD1	P28289	18	0.01	MEF2C	Q06413	53	100	MRPL52	Q86TS9	17	0.01
CDK4	P11802	38	100	DOCK6	Q96HP0	18	0.01	MTX2	O75431	50	10.776	SLC38A1	Q9H2H9	17	0.01
XPNPEP3	Q9NQH7	29	100	CCND1	P24385	17	0.053	PKLR	P30613	50	100	PUS7	Q96PZ0	16	0.01
TIGAR	Q9NQ88	29	100	MRPL52	Q86TS9	17	0.01	PPP3CC	P48454	46	100	RBM33	Q96EV2	16	0.01
ELF1	P32519	28	9.816	PUS7	Q96PZ0	16	0.01	TMSB10	P63313	42	100	RNF113A	O15541	16	0.01
DNAJC17	Q9NVM6	27	11.678	ZMYM3	Q14202	16	0.01	ATP6V0C	P27449	40	8.407	P4HA2	O15460	15	0.01
DST	Q03001	27	15.84	EIF4EBP2	Q13542	16	0.01	CDK4	P11802	38	100	SENP8	Q96LD8	15	0.099
NINJ1	Q92982	26	100	PLD4	Q96BZ4	16	0.01	P2RX7	Q99572	32	8.683	CHD1L	Q86WJ1	14	0.01
TTN	Q8WZ42	24	100	CCL3	P10147	16	0.01	SLC7A7	Q9UM01	30	100	COG7	P83436	14	0.01
AHR	P35869	22	100	IFI44	Q8TCB0	15	0.01	XPNPEP3	Q9NQH7	29	100	INTS5	Q6P9B9	14	0.01
KIF1B	O60333	22	100	P4HA2	O15460	15	0.064	TIGAR	Q9NQ88	29	100	SPINT1	O43278	14	0.01
GPR84	Q9NQS5	21	100	COG7	P83436	14	0.01	CHST11	Q9NPF2	28	12.205	ZFAND1	Q8TCF1	14	0.01
SIK3	Q9Y2K2	20	12.198	ABTB1	Q969K4	14	0.01	DNAJC17	Q9NVM6	27	10.691	CD3EAP	O15446	14	0.01
HMGA2	P52926	20	100	ZFAND1	Q8TCF1	14	0.01	DST	Q03001	27	24.615	IPO11	Q9UI26	13	0.01
SLC7A11	Q9UPY5	19	100	NXN	Q6DKJ4	14	0.01	NINJ1	Q92982	26	100	TMEM59	Q9BXS4	13	0.01
APOBEC3F	Q8IUX4	18	100	CD3EAP	O15446	14	0.01	KCTD8	Q6ZWB6	26	100	UBP1	Q9NZI7	13	0.073
RPP30	P78346	18	25.82	TMEM199	Q8N511	14	0.01	CXCL8	P10145	25	15.846	JUN	P05412	13	0.01
CXCL10	P02778	17	100	RETREG2	Q8NC44	14	0.01	FCAR	P24071	22	14.451	MOB2	Q70IA6	13	0.01
NAF1	Q96HR8	17	16.62	CNIH1	O95406	14	0.01	AHR	P35869	22	100	BRDT	Q58F21	13	0.01
TMEM14C	Q9P0S9	16	100	UBP1	Q9NZI7	13	0.01	KIF1B	O60333	22	100	HAVCR2	Q8TDQ0	12	0.01
PIP4P2	Q8N4L2	16	100	FUCA2	Q9BTY2	12	0.01	GPR84	Q9NQS5	21	100	KIAA0391	O15091	12	0.01
EIF1AD	Q8N9N8	15	100	PPCDC	Q96CD2	12	0.01	EBI3	Q14213	21	20.016	SH2B2	O14492	12	0.01
MOCS3	O95396	15	100	SLC15A4	Q8N697	12	0.01	HMGA2	P52926	20	100	PPCDC	Q96CD2	12	0.01
INTS14	Q96SY0	15	100	FLT3	P36888	12	0.01	SLC7A11	Q9UPY5	19	100	RHBDD2	Q6NTF9	12	0.01
PAK1IP1	Q9NWT1	14	8.11	ZMYM4	Q5VZL5	11	0.01	APOBEC3F	Q8IUX4	18	100	FLT3	P36888	12	0.01
DDA1	Q9BW61	14	12.308	UBASH3B	Q8TF42	11	0.01	C4orf3	Q8WVX3	17	8.659	UBASH3B	Q8TF42	11	0.01
CHST9	Q7L1S5	14	100	KAT7	O95251	11	0.01	IL36G	Q9NZH8	16	100	KAT7	O95251	11	0.01
TOMM7	Q9P0U1	14	42.214	SLC43A2	Q8N370	11	0.01	TMEM14C	Q9P0S9	16	100	MPHOSPH8	Q99549	11	0.01

AP1G2	O75843	13	100	FAM126A	Q9BYI3	11	0.01	UNC119B	A6NIH7	16	100	CDC42SE2	Q9NRR3	11	0.01
ARMH3	Q5T2E6	12	100	KIAA1143	Q96AT1	11	0.01	EIF1AD	Q8N9N8	15	100	CTDSPL2	Q05D32	10	0.01
ABCC3	O15438	12	100	RPAP1	Q9BWH6	11	0.01	MOCS3	O95396	15	100	PNKD	Q8N490	10	0.01
OXSM	Q9NWU1	12	100	CDC42SE2	Q9NRR3	11	0.01	INTS14	Q96SY0	15	100	RIOK2	Q9BVS4	10	0.01
KIAA0391	O15091	12	15.041	TTI1	O43156	10	0.01	C18orf25	Q96B23	14	8.85	COQ7	Q99807	10	0.01
MBD2	Q9UBB5	12	100	CTDSPL2	Q05D32	10	0.01	DDA1	Q9BW61	14	10.553	GPATCH8	Q9UKJ3	10	0.01
PLA2G4C	Q9UP65	11	100	PBK	Q96KB5	10	0.01	CHST9	Q7L1S5	14	100	TMEM222	Q9H0R3	10	0.01
RGL2	O15211	11	13.331	COQ7	Q99807	10	0.01	TOMM7	Q9P0U1	14	33.556	ANO10	Q9NW15	10	0.01
SPATA5L1	Q9BVQ7	11	100	HLA-DQA2	P01906	9	0.01	AP1G2	O75843	13	100	HLA-DQA2	P01906	9	0.01
NEDD4L	Q96PU5	11	100	GINS3	Q9BRX5	9	0.01	ARMH3	Q5T2E6	12	100	CEP85	Q6P2H3	9	0.01
SDAD1	Q9NVU7	11	100	GPR89B	P0CG08	9	0.01	BOD1L1	Q8NFC6	12	100	ZWILCH	Q9H900	9	0.01
FCRLA	Q7L513	10	100	SP3	Q02447	9	0.01	ABCC3	O15438	12	100	GINS3	Q9BRX5	9	0.01
GYPC	P04921	10	100	LYSMD2	Q8IV50	9	0.01	CLIP2	Q9UDT6	12	100	C7orf50	Q9BRJ6	9	0.01
TYMS	P04818	9	100	MRPS10	P82664	9	0.01	OXSM	Q9NWU1	12	100	DDX28	Q9NUL7	9	0.01
TAF6	P49848	9	100	AP5B1	Q2VPB7	9	0.01	MBD2	Q9UBB5	12	100	GPR89B	P0CG08	9	0.01
AGPAT4	Q9NRZ5	9	100	GEM	P55040	9	0.01	PLA2G4C	Q9UP65	11	100	ATP11A	P98196	9	0.01
CCM2	Q9BSQ5	9	100	LRRC25	Q8N386	9	0.01	NEDD4L	Q96PU5	11	100	CKS1B	P61024	9	0.01
AMD1	P17707	9	100	TGFBR1	P36897	8	0.01	SDAD1	Q9NVU7	11	100	GLT8D1	Q68CQ7	9	0.01
PAK4	O96013	9	100	CARD6	Q9BX69	8	0.01	DPYSL4	O14531	11	100	TGFBR1	P36897	8	0.01
GDPD1	Q8N9F7	9	100	LMBRD1	Q9NUN5	8	0.01	FCRLA	Q7L513	10	100	ITM2B	Q9Y287	8	0.01
C17orf75	Q9HAS0	9	100	ZFP36L2	P47974	8	0.01	GYPC	P04921	10	100	EEFSEC	P57772	8	0.01
EMC4	Q5J8M3	9	100	SHOX2	O60902	8	0.01	TYMS	P04818	9	100	LMBRD1	Q9NUN5	8	0.01
AFDN	P55196	8	100	MAFB	Q9Y5Q3	8	0.01	TAF6	P49848	9	100	ZFP36L2	P47974	8	0.01
TACC3	Q9Y6A5	8	100	UBE2D1	P51668	8	0.01	AGPAT4	Q9NRZ5	9	100	SHOX2	O60902	8	0.01
SCOC	Q9UIL1	8	100	RFC1	P35251	8	0.01	CCM2	Q9BSQ5	9	100	ECSIT	Q9BQ95	8	0.01
STX10	O60499	8	100	ZNF579	Q8NAF0	8	0.01	AMD1	P17707	9	100	RIN3	Q8TB24	8	0.01
DTD1	Q8TEA8	8	100	UXT	Q9UBK9	8	0.01	PAK4	O96013	9	100	RFC1	P35251	8	0.01
EBF1	Q9UH73	8	100	KRTCAP2	Q8N6L1	8	0.01	EMC4	Q5J8M3	9	100	IGF2	P01344	8	0.01
NFYB	P25208	8	100	RNF126	Q9BV68	7	0.076	AFDN	P55196	8	100	UXT	Q9UBK9	8	0.01
KIF3B	O15066	8	100	WDHD1	O75717	7	0.01	SCOC	Q9UIL1	8	100	KRTCAP2	Q8N6L1	8	0.01
NDRG2	Q9UN36	7	100	VAMP4	O75379	7	0.01	STX10	O60499	8	100	NCOR1	O75376	7	0.01
TRIM2	Q9C040	7	100	ADGRE3	Q9BY15	7	0.01	SHPK	Q9UHH6	8	12.964	WDHD1	O75717	7	0.01
PEX3	P56589	7	100	MT1F	P04733	7	0.01	EBF1	Q9UH73	8	100	MTR	Q99707	7	0.01
S100A16	Q96FQ6	7	100	DENND4A	Q7Z401	6	0.01	KIF3B	O15066	8	100	GPATCH11	Q8N954	7	0.01
OCIAD2	Q56VL3	7	100	HELZ	P42694	6	0.01	KBTBD8	Q8NFY9	8	100	ATP11C	Q8NB49	7	0.01
LAT	O43561	7	100	WDR48	Q8TAF3	6	0.01	NDRG2	Q9UN36	7	100	MRPL32	Q9BYC8	7	0.01
IGFBP5	P24593	7	100	PROCR	Q9UNN8	6	0.01	TRIM2	Q9C040	7	100	ANKMY2	Q8IV38	7	0.01
UNK	Q9C0B0	7	100	XYLB	O75191	6	0.01	S100A16	Q96FQ6	7	100	AAMDC	Q9H7C9	7	0.01
MAP1B	P46821	7	100	ZNF148	Q9UQR1	5	0.01	OCIAD2	Q56VL3	7	100	NDUFA1	O15239	7	0.01
MYH3	P11055	7	100	LYZ	P61626	5	0.01	LAT	O43561	7	100	GMEB1	Q9Y692	7	0.07
NEB	P20929	7	100	S100B	P04271	5	0.01	IGFBP5	P24593	7	100	DENND4A	Q7Z401	6	0.01
NFATC2	Q13469	6	21.495	LBH	Q53QV2	5	0.01	UNK	Q9C0B0	7	100	RCL1	Q9Y2P8	6	0.01
TAPT1	Q6NXT6	6	100	SCAMP4	Q969E2	5	0.01	MAP1B	P46821	7	100	CORO2A	Q92828	6	0.01
OCRL	Q01968	6	12.937	PHLPP1	O60346	5	0.01	MYH3	P11055	7	100	NFATC2	Q13469	6	0.01
GRK4	P32298	6	100	CCDC51	Q96ER9	5	0.01	NEB	P20929	7	100	APOC1	P02654	6	0.01
FUT4	P22083	5	20.066	PKIG	Q9Y2B9	5	0.01	ATRX	P46100	6	100	RIOX1	Q9H6W3	6	0.01
PEX13	Q92968	5	100	PHACTR4	Q8IZ21	5	0.01	TRAPPC10	P48553	6	27.62	OCRL	Q01968	6	0.01
DGUOK	Q16854	5	100	COX8A	P10176	5	0.01	MINDY3	Q9H8M7	6	100	REEP6	Q96HR9	6	0.01
SRXN1	Q9BYN0	5	100					YAP1	P46937	6	100	ALAS1	P13196	5	0.01
SEZ6L2	Q6UXD5	5	8.452					TAPT1	Q6NXT6	6	100	ZNF148	Q9UQR1	5	0.01
CCND3	P30281	5	100					GRK4	P32298	6	100	LYZ	P61626	5	0.01
LRP10	Q7Z4F1	5	100					C1R	P00736	6	100	GTPBP10	A4D1E9	5	0.01
POLB	P06746	5	100					DMAC2L	Q99766	6	100	SEZ6L2	Q6UXD5	5	0.01
TVP23C	Q96ET8	5	19.576					SRXN1	Q9BYN0	5	100	MLX	Q9UH92	5	0.01
CLYBL	Q8N0X4	5	100					CCND3	P30281	5	100	PHLPP1	O60346	5	0.01
UBE2F	Q969M7	5	100					LRP10	Q7Z4F1	5	100	METTL2B	Q6P1Q9	5	0.01
PRAMEF25	A6NGN4	5	100					POLB	P06746	5	100	CCDC51	Q96ER9	5	0.01
								CLYBL	Q8N0X4	5	100	PHACTR4	Q8IZ21	5	0.01
								PRAMEF25	A6NGN4	5	100	SRGN	P10124	5	0.01
												COX8A	P10176	5	0.01

DEPs in M2c macrophages compared with M0 macrophages								DEPs in M2d macrophages compared with M0 macrophages							
up-regulted DEPs				down-regulated DEPs				up-regulted DEPs				down-regulated DEPs			
Gene Name	Accession	PSMs	M2c/M0	Gene Name	Accession	PSMs	M2c/M0	Gene Name	Accession	PSMs	M2d/M0	Gene Name	Accession	PSMs	M2d/M0
ACTG1	P63261	12773	15.887	HSP90AA2P	Q14568	1498	0.01	ACTG1	P63261	12773	11.781	HSP90AA2P	Q14568	1498	0.01

ACTA1	P68133	5304	100	KIF5C	O60282	147	0.01	ACTA1	P68133	5304	100	TUBA8	Q9NY65	1008	0.01
POTEKP	Q9BYX7	1947	19.723	LIMS2	Q7Z4I7	103	0.01	EHD1	Q9H4M9	816	8.522	HSPA2	P54652	428	0.01
POTEJ	P0CG39	1554	8.588	CD38	P28907	77	0.072	SOD2	P04179	694	18.926	SNRPN	P63162	248	0.01
HIST2H3A	Q71DI3	384	100	PZP	P20742	60	0.01	CTSG	P08311	624	9.257	ACTR3B	Q9P1U1	152	0.01
H3F3A	P84243	259	100	AGAP3	Q96P47	57	0.058	NAMPT	P43490	575	12.645	GDF15	Q99988	148	0.082
ACOT2	P49753	252	100	MT2A	P02795	55	0.056	IL1B	P01584	465	38.786	GFPT2	O94808	116	0.01
WASHC2C	Q9Y4E1	198	100	PRKAR2B	P31323	51	0.01	AMPD3	Q01432	442	14.06	NCALD	P61601	102	0.01
PRPH	P41219	182	100	MT1X	P80297	49	0.01	HIST2H3A	Q71DI3	384	100	FAM49A	Q9H0Q0	80	0.01
DES	P17661	152	100	SMG9	Q9H0W8	49	0.01	RHOC	P08134	333	8.182	PZP	P20742	60	0.03
FABP5P3	A8MUU1	106	100	KCNAB1	Q14722	49	0.01	NCF1	P14598	327	8.637	ABI2	Q9NYB9	60	0.01
CCT6B	Q92526	101	100	ZEB2	O60315	45	0.01	H3F3A	P84243	259	100	PRKAR2B	P31323	51	0.01
MYL6B	P14649	96	100	POU2F1	P14859	45	0.01	ACOT2	P49753	252	100	KCNAB1	Q14722	49	0.01
ITPR2	Q14571	94	100	SERPINB4	P48594	44	0.01	SRC	P12931	225	8.251	SLC2A5	P22732	46	0.082
TPT1L	#N/A	90	100	RCOR3	Q9P2K3	43	0.01	TFPI2	P48307	200	45.919	POU2F1	P14859	45	0.01
RHOB	P62745	84	100	STK39	Q9UEW8	42	0.01	WASHC2C	Q9Y4E1	198	100	STK39	Q9UEW8	42	0.01
CALML3	P27482	84	30.096	RHOQ	P17081	41	0.01	PRPH	P41219	182	100	TACC2	O95359	36	0.054
GRK3	P35626	81	100	PSEN1	P49768	37	0.01	DES	P17661	152	100	CDK12	Q9NYV4	35	0.01
EIF1B	O60739	80	100	CDK12	Q9NYV4	35	0.01	CD14	P08571	146	23.084	PRTN3	P24158	32	0.071
LGALS9C	Q6DKI2	79	100	UBE2E1	P51965	34	0.01	CCT6B	Q92526	101	100	RAD21L1	Q9H4I0	31	0.01
ATP12A	P54707	79	100	PRTN3	P24158	32	0.085	MYL6B	P14649	96	100	SPRY2	O43597	29	0.01
RAP2A	P10114	61	100	MFSD2A	Q8NA29	31	0.097	ITPR2	Q14571	94	100	MKI67	P46013	27	0.01
MEF2C	Q06413	53	100	RAD21L1	Q9H4I0	31	0.01	RHOB	P62745	84	100	SLFN11	Q7Z7L1	25	0.101
PPP3CC	P48454	46	100	IQGAP3	Q86VI3	31	0.01	CALML3	P27482	84	22.844	CHD6	Q8TD26	25	0.01
TMSB10	P63313	42	100	SEMA7A	O75326	29	0.01	ITGB3	P05106	83	9.07	STAU2	Q9NUL3	21	0.01
ATP6V0C	P27449	40	13.075	MYADM	Q96S97	29	0.09	GRK3	P35626	81	100	PHRF1	Q9P1Y6	21	0.01
S100A10	P60903	39	8.829	UGGT2	Q9NYU1	29	0.01	EIF1B	O60739	80	100	PPP1R21	Q6ZMI0	20	0.01
CDK4	P11802	38	100	PARVB	Q9HBI1	28	0.01	LGALS9C	Q6DKI2	79	100	DMAP1	Q9NPF5	20	0.01
SLC7A7	Q9UM01	30	100	CTNNA2	P26232	28	0.01	TTC39B	Q5VTQ0	69	15.382	TEX10	Q9NXF1	19	0.01
XPNPEP3	Q9NQH7	29	100	RRAD	P55042	27	0.01	PLAU	P00749	63	11.351	FBP2	O00757	19	0.106
TIGAR	Q9NQ88	29	100	PLG	P00747	25	0.01	RAP2A	P10114	61	100	USP13	Q92995	19	0.01
ELF1	P32519	28	10.54	CXCL8	P10145	25	0.01	CCL20	P78556	61	100	CD84	Q9UIB8	18	0.01
CHST11	Q9NPF2	28	16.401	SLAMF7	Q9NQ25	24	0.01	IL1A	P01583	55	8.27	ACADSB	P45954	18	0.01
HMGN2	P05204	27	11.051	WIP1	Q9Y4P8	23	0.01	MEF2C	Q06413	53	100	GNL2	Q13823	18	0.01
DST	Q03001	27	21.645	GRAMD1A	Q96CP6	22	0.01	PPP3CC	P48454	46	100	MRPL52	Q86TS9	17	0.01
NINJ1	Q92982	26	100	LTF	P02788	22	0.107	AKAP2	Q9Y2D5	44	11.971	IMPA2	O14732	17	0.119
HMGN3	Q15651	26	13.258	PPP1R21	Q6ZMI0	20	0.01	TMSB10	P63313	42	100	ZMYM3	Q14202	16	0.01
TTN	Q8WZ42	24	100	MICU2	Q8IYU8	20	0.01	VAT1L	Q9HCJ6	41	8.166	CHD1L	Q86WJ1	14	0.01
AHR	P35869	22	100	PLEKHF2	Q9H8W4	19	0.01	ATP6V0C	P27449	40	10.474	COG7	P83436	14	0.01
KIF1B	O60333	22	100	SLC27A1	Q6PCB7	19	0.113	S100A10	P60903	39	9.322	ZFAND1	Q8TCF1	14	0.01
GPR84	Q9NQS5	21	100	USP13	Q92995	19	0.01	CDK4	P11802	38	100	WDR74	Q6RFH5	14	0.01
HMGA2	P52926	20	100	ACADSB	P45954	18	0.01	SLC7A7	Q9UM01	30	100	CNIH1	O95406	14	0.01
APOBEC3F	Q8IUX4	18	100	TMOD1	P28289	18	0.01	XPNPEP3	Q9NQH7	29	100	HOMER2	Q9NSB8	14	0.01
RPP30	P78346	18	9.761	CCND1	P24385	17	0.087	TIGAR	Q9NQ88	29	100	PPHLN1	Q8NEY8	13	0.01
TMEM14C	Q9P0S9	16	100	MRPL52	Q86TS9	17	0.01	CHST11	Q9NPF2	28	14.891	UBP1	Q9NZI7	13	0.059
UNC119B	A6NIH7	16	100	ASRGL1	Q7L266	16	0.01	HMGN2	P05204	27	10.111	PIK3R2	O00459	13	0.01
EIF1AD	Q8N9N8	15	100	TIFA	Q96CG3	16	0.01	DST	Q03001	27	25.651	TNFAIP8L3	Q5GJ75	13	0.101
DYSF	O75923	15	100	CCL3	P10147	16	0.01	NINJ1	Q92982	26	100	BRDT	Q58F21	13	0.01
MOCS3	O95396	15	100	AMBP	P02760	16	0.01	HMGN3	Q15651	26	9.877	DMXL2	Q8TDJ6	12	0.01
INTS14	Q96SY0	15	100	GGA3	Q9NZ52	15	0.01	KCTD8	Q6ZWB6	26	100	VLDLR	P98155	12	0.01
FDX1	P10109	14	9.517	APOO	Q9BUR5	15	0.01	CXCL8	P10145	25	10.268	HAVCR2	Q8TDQ0	12	0.01
DDA1	Q9BW61	14	8.328	P4HA2	O15460	15	0.01	FCAR	P24071	22	14.586	ELAC2	Q9BQ52	12	0.01
CHST9	Q7L1S5	14	100	COG7	P83436	14	0.01	AHR	P35869	22	100	PARP4	Q9UKK3	12	0.01
TOMM7	Q9P0U1	14	22.56	RIF1	Q5UIP0	14	0.01	KIF1B	O60333	22	100	FLT3	P36888	12	0.01
ARMH3	Q5T2E6	12	100	ZFAND1	Q8TCF1	14	0.01	GPR84	Q9NQS5	21	100	UBASH3B	Q8TF42	11	0.01
ABCC3	O15438	12	100	POLD3	Q15054	13	0.01	EBI3	Q14213	21	20.649	FBXL12	Q9NXK8	11	0.01
OXSM	Q9NWU1	12	100	PPHLN1	Q8NEY8	13	0.01	HMGA2	P52926	20	100	RPAP1	Q9BWH6	11	0.01
MBD2	Q9UBB5	12	100	VRK2	Q86Y07	13	0.01	SLC7A11	Q9UPY5	19	100	CDC42SE2	Q9NRR3	11	0.01
SDAD1	Q9NVU7	11	100	UBP1	Q9NZI7	13	0.047	AGPAT1	Q99943	19	9.487	TTI1	O43156	10	0.01
DPYSL4	O14531	11	100	JUN	P05412	13	0.01	APOBEC3F	Q8IUX4	18	100	CTDSPL2	Q05D32	10	0.01
FCRLA	Q7L513	10	100	BRDT	Q58F21	13	0.01	CXCL10	P02778	17	100	PBK	Q96KB5	10	0.01
GYPC	P04921	10	100	GGA2	Q9UJY4	12	0.01	IL36G	Q9NZH8	16	100	WIZ	O95785	10	0.01
TYMS	P04818	9	100	COA4	Q9NYJ1	12	0.01	TMEM14C	Q9P0S9	16	100	RIOK2	Q9BVS4	10	0.01
TAF6	P49848	9	100	PPCDC	Q96CD2	12	0.01	PIP4P2	Q8N4L2	16	100	PILRA	Q9UKJ1	10	0.01
EYA3	Q99504	9	100	EHHADH	Q08426	12	0.01	UNC119B	A6NIH7	16	100	TMEM222	Q9H0R3	10	0.01
CCM2	Q9BSQ5	9	100	FLT3	P36888	12	0.01	EIF1AD	Q8N9N8	15	100	BST2	Q10589	10	0.01
GDPD1	Q8N9F7	9	100	UBASH3B	Q8TF42	11	0.01	MOCS3	O95396	15	100	HLA-DQA2	P01906	9	0.01
C17orf75	Q9HAS0	9	100	KAT7	O95251	11	0.01	INTS14	Q96SY0	15	100	TPRN	Q4KMQ1	9	0.01

EMC4	Q5J8M3	9	100	SLC43A2	Q8N370	11	0.01	WDR92	Q96MX6	15	10.874	GIN3	Q9BRX5	9	0.01
AFDN	P55196	8	100	FBXL12	Q9NXK8	11	0.01	CCDC59	Q9P031	15	33.41	MGMT	P16455	9	0.01
TACC3	Q9Y6A5	8	100	RPAP1	Q9BWH6	11	0.01	DDA1	Q9BW61	14	12.152	FYTTD1	Q96QD9	9	0.01
SESN1	Q9Y6P5	8	100	TTI1	O43156	10	0.01	CHST9	Q7L1S5	14	100	CKS1B	P61024	9	0.01
SCOC	Q9U1L1	8	100	PBK	Q96KB5	10	0.01	TOMM7	Q9P0U1	14	22.325	AP5B1	Q2VPB7	9	0.01
STX10	O60499	8	100	WIZ	O95785	10	0.01	ARMH3	Q5T2E6	12	100	GLT8D1	Q68CQ7	9	0.01
DTD1	Q8TEA8	8	100	R1OK2	Q9BVS4	10	0.01	ABCC3	O15438	12	100	LRRC25	Q8N386	9	0.01
EBF1	Q9UH73	8	100	P1LRA	Q9UKJ1	10	0.01	GBP7	Q8N8V2	12	100	SEC11C	Q9BY50	9	0.01
KIF3B	O15066	8	100	FRY	Q5TBA9	10	0.01	CLIP2	Q9UDT6	12	100	TGFBR1	P36897	8	0.01
TRIM2	Q9C040	7	100	CXCL5	P42830	10	0.01	OXSM	Q9NWU1	12	100	ITM2B	Q9Y287	8	0.01
PEX3	P56589	7	100	COQ7	Q99807	10	0.01	MBD2	Q9UBB5	12	100	PHF3	Q92576	8	0.01
S100A16	Q96FQ6	7	100	TMEM222	Q9H0R3	10	0.01	BCAT2	O15382	12	100	LIG4	P49917	8	0.01
OCIAD2	Q56VL3	7	100	POFUT2	Q9Y2G5	10	0.01	PLA2G4C	Q9UP65	11	100	ATP9A	O75110	8	0.01
LAT	O43561	7	100	HLA-DQA2	P01906	9	0.01	NEDD4L	Q96PU5	11	100	RFC1	P35251	8	0.01
UNK	Q9C0B0	7	100	GIN3	Q9BRX5	9	0.01	SDAD1	Q9NVU7	11	100	KRTCAP2	Q8N6L1	8	0.01
MAP1B	P46821	7	100	SP3	Q02447	9	0.01	DPYSL4	O14531	11	100	NCOR1	O75376	7	0.01
MYH3	P11055	7	100	ATP11A	P98196	9	0.01	GYPC	P04921	10	100	WDHD1	O75717	7	0.01
NEB	P20929	7	100	AP5B1	Q2VPB7	9	0.01	TYMS	P04818	9	100	REEP3	Q6NUK4	7	0.01
ATRX	P46100	6	100	TGFBR1	P36897	8	0.01	TAF6	P49848	9	100	SFT2D3	Q58719	7	0.01
YAP1	P46937	6	100	LMBRD1	Q9NUN5	8	0.01	SLC8A1	P32418	9	15.964	ATP11C	Q8NB49	7	0.096
TAPT1	Q6NXT6	6	100	TWISTNB	Q3B726	8	0.01	AGPAT4	Q9NRZ5	9	100	AAMDC	Q9H7C9	7	0.01
GRK4	P32298	6	100	SHOX2	O60902	8	0.01	EYA3	Q99504	9	100	MT1F	P04733	7	0.01
DMAC2L	Q99766	6	100	IGF2	P01344	8	0.01	CCM2	Q9BSQ5	9	100	GMEB1	Q9Y692	7	0.01
SLCO2B1	O94956	5	100	PREPL	Q4J6C6	8	0.01	AMD1	P17707	9	100	DHX37	Q8IY37	6	0.01
LRP10	Q7Z4F1	5	100	NCOR1	O75376	7	0.01	PAK4	O96013	9	100	KCTD10	Q9H3F6	6	0.01
POLB	P06746	5	100	RNF126	Q9BV68	7	0.01	GDPD1	Q8N9F7	9	100	DENND4A	Q7Z401	6	0.01
CLYBL	Q8N0X4	5	100	WDHD1	O75717	7	0.01	EMC4	Q5J8M3	9	100	CORO2A	Q92828	6	0.01
				VAMP4	O75379	7	0.01	AFDN	P55196	8	100	BUD23	O43709	6	0.01
				MED20	Q9H944	7	0.01	SCOC	Q9U1L1	8	100	SYNRG	Q9UMZ2	6	0.01
				ADGRE3	Q9BY15	7	0.01	MT1A	P04731	8	100	NUS1	Q96E22	6	0.01
				IL17RA	Q96F46	7	0.01	STX10	O60499	8	100	WDR48	Q8TAF3	6	0.01
				MT1F	P04733	7	0.01	DTD1	Q8TEA8	8	100	CIB1	Q99828	6	0.01
				ACSF2	Q96CM8	6	0.01	EBF1	Q9UH73	8	100	APOC1	P02654	6	0.01
				DHX37	Q8IY37	6	0.01	KIF3B	O15066	8	100	REEP6	Q96HR9	6	0.01
				KCTD10	Q9H3F6	6	0.01	KBTBD8	Q8NFY9	8	100	QPCTL	Q9NXS2	6	0.01
				DENND4A	Q7Z401	6	0.01	PEX3	P56589	7	100	ALAS1	P13196	5	0.01
				CHCHD5	Q9BSY4	6	0.01	S100A16	Q96FQ6	7	100	LYZ	P61626	5	0.01
				CD99L2	Q8TCZ2	6	0.01	LAT	O43561	7	100	SUZ12	Q15022	5	0.01
				APOC1	P02654	6	0.01	IGFBP5	P24593	7	100	SEZ6L2	Q6UXD5	5	0.01
				OCRL	Q01968	6	0.01	UNK	Q9C0B0	7	100	MLX	Q9UH92	5	0.01
				URB1	O60287	6	0.01	MYH3	P11055	7	100	METTTL2B	Q6P1Q9	5	0.01
				REEP6	Q96HR9	6	0.01	NEB	P20929	7	100	CCDC51	Q96ER9	5	0.01
				QPCTL	Q9NXS2	6	0.01	ATRX	P46100	6	100	PHACTR4	Q8IZ21	5	0.01
				ALAS1	P13196	5	0.01	MINDY3	Q9H8M7	6	100	SRGN	P10124	5	0.01
				ZNF148	Q9UQR1	5	0.01	YAP1	P46937	6	100		P46937		
				LYZ	P61626	5	0.01	TAPT1	Q6NXT6	6	100		Q6NXT6		
				SUZ12	Q15022	5	0.01	OCRL	Q01968	6	13.22		Q01968		
				GTPBP10	A4D1E9	5	0.01	GRK4	P32298	6	100		P32298		
				MLX	Q9UH92	5	0.01	C1R	P00736	6	100		P00736		
				PHLPP1	O60346	5	0.01	DMAC2L	Q99766	6	100		Q99766		
				CCDC51	Q96ER9	5	0.01	SLCO2B1	O94956	5	100		O94956		
				PHACTR4	Q8IZ21	5	0.01	SRXN1	Q9BYN0	5	100		Q9BYN0		
				SRGN	P10124	5	0.01	LRP10	Q7Z4F1	5	100		Q7Z4F1		
				COX8A	P10176	5	0.01	POLB	P06746	5	100		P06746		
								PHLPP1	O60346	5	10.428		O60346		
								UBE2F	Q969M7	5	100		Q969M7		

Table S3 GO and KEGG analysis of DEPs in four M2 macrophage subtypes compared with M0 macrophages

Biological processes analysis of up-regulated DEPs in M2a macrophages					
Category	Term	Count	% Associated Genes	P-value	Genes
GOTERM_BP_DIRECT	GO:0030049~muscle filament sliding	6	5.263157895	0.0000036997	DES, NEB, ACTA1, MYL6B, MYH3, TTN
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	5	4.385964912	0.0019821951	TYMS, CCL5, CDK4, AHR, SLC7A11
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	4	3.50877193	0.0059920078	PAK4, CCL5, MBD2, IGFBP5
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	4	3.50877193	0.0107654446	LPL, TGM2, FABP4, CCL5
GOTERM_BP_DIRECT	GO:0045214~sarcomere organization	3	2.631578947	0.0140867709	ACTG1, MYH3, TTN
GOTERM_BP_DIRECT	GO:0010332~response to gamma radiation	3	2.631578947	0.0160038857	POLB, TIGAR, CXCL10
GOTERM_BP_DIRECT	GO:0007517~muscle organ development	4	3.50877193	0.0182998131	MEF2C, NEB, MYH3, CXCL10
GOTERM_BP_DIRECT	GO:0045859~regulation of protein kinase activity	3	2.631578947	0.0190753459	TTN, CDK4, CXCL10
GOTERM_BP_DIRECT	GO:0000183~chromatin silencing at rDNA	3	2.631578947	0.0223732276	HIST2H3A, H3F3A, MBD2
GOTERM_BP_DIRECT	GO:0001568~blood vessel development	3	2.631578947	0.0235212151	MEF2C, ALDH1A2, AHR
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	4	3.50877193	0.0241739594	LAT, CCM2, DST, ITGAM
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	4	3.50877193	0.0295232263	DES, ACTA1, MYL6B, TTN
GOTERM_BP_DIRECT	GO:0030240~skeletal muscle thin filament assembly	2	1.754385965	0.0308799602	ACTA1, TTN
GOTERM_BP_DIRECT	GO:0009157~deoxyribonucleoside monophosphate biosynthetic process	2	1.754385965	0.0308799602	TYMS, DGUOK
GOTERM_BP_DIRECT	GO:0048667~cell morphogenesis involved in neuron differentiation	2	1.754385965	0.0369416510	MEF2C, UNK
GOTERM_BP_DIRECT	GO:0061154~endothelial tube morphogenesis	2	1.754385965	0.0369416510	CCM2, RHOB
GOTERM_BP_DIRECT	GO:0045869~negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	2	1.754385965	0.0429657858	HMGA2, APOBEC3F
GOTERM_BP_DIRECT	GO:0016049~cell growth	3	2.631578947	0.0479374321	TYMS, ACTA1, PAK4
GOTERM_BP_DIRECT	GO:0050863~regulation of T cell activation	2	1.754385965	0.0489525950	LAT, CCL5
GOTERM_BP_DIRECT	GO:0047497~mitochondrion transport along microtubule	2	1.754385965	0.0549023077	KIF1B, MAP1B
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	2	1.754385965	0.0549023077	AHR, TIGAR
GOTERM_BP_DIRECT	GO:0010226~response to lithium ion	2	1.754385965	0.0549023077	ACTA1, PKLR
GOTERM_BP_DIRECT	GO:0007165~signal transduction	13	11.40350877	0.0584757692	LAT, CCND3, PAK4, CRABP2, GRK4, AFDN, NDRG2, HMGA2, OCRL, CDK4, CXCL10, ITPR2, IGFBP5
GOTERM_BP_DIRECT	GO:2000406~positive regulation of T cell migration	2	1.754385965	0.0608151515	CCL5, CXCL10
GOTERM_BP_DIRECT	GO:0001682~tRNA 5'-leader removal	2	1.754385965	0.0666913527	RPP30, KIAA0391
GOTERM_BP_DIRECT	GO:0000226~microtubule cytoskeleton organization	3	2.631578947	0.0728741835	MAP1B, TACC3, DST
GOTERM_BP_DIRECT	GO:0006629~lipid metabolic process	4	3.50877193	0.0755224036	LPL, LRP10, OCRL, GDPD1
GOTERM_BP_DIRECT	GO:0048872~homeostasis of number of cells	2	1.754385965	0.0783347257	POLB, AFDN
GOTERM_BP_DIRECT	GO:0014032~neural crest cell development	2	1.754385965	0.0783347257	TAPT1, ALDH1A2
GOTERM_BP_DIRECT	GO:0043922~negative regulation by host of viral transcription	2	1.754385965	0.0783347257	CCL5, HMGA2
GOTERM_BP_DIRECT	GO:0042573~retinoic acid metabolic process	2	1.754385965	0.0841023432	ALDH1A2, CRABP2
GOTERM_BP_DIRECT	GO:0007568~aging	4	3.50877193	0.0847399636	TYMS, POLB, MBD2, IGFBP5
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	6	5.263157895	0.0892010716	LAT, GBP5, POLB, CCL5, PLA2G4C, CXCL10
GOTERM_BP_DIRECT	GO:0090026~positive regulation of monocyte chemotaxis	2	1.754385965	0.0955305443	CCL5, CXCL10
Biological processes analysis of down-regulated DEPs in M2a macrophages					
Category	Term	Count	% Associated Genes	P-value	Genes
GOTERM_BP_DIRECT	GO:0045671~negative regulation of osteoclast differentiation	3	2.777777778	0.0080610467	CCL3, MAFB, UBASH3B
GOTERM_BP_DIRECT	GO:0008360~regulation of cell shape	5	4.62962963	0.0082067763	CCL3, S100B, CDC42SE2, RHOQ, CDC42SE1
GOTERM_BP_DIRECT	GO:0007010~cytoskeleton organization	5	4.62962963	0.0132023762	TUBA8, CCL3, ZMYM4, ZMYM3, CTNNA2
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	5	4.62962963	0.0205286057	PRKAR2B, PROCR, PRTN3, DOCK6, PLG
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	8	7.407407407	0.0267626502	CD38, CHURC1, LBH, RFC1, SP3, TGFBRI1, CREBBP, RNF14
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	11	10.18518519	0.0274823690	SHOX2, UXT, CCND1, RFC1, ZNF148, SP3, PKIG, CREBBP, TLE4, UBE2D1, COQ7
GOTERM_BP_DIRECT	GO:0006909~phagocytosis	3	2.777777778	0.0301844022	CDC42SE2, PLD4, CDC42SE1
GOTERM_BP_DIRECT	GO:0033601~positive regulation of mammary gland epithelial cell proliferation	2	1.851851852	0.0443825947	CCND1, IQGAP3
GOTERM_BP_DIRECT	GO:2000480~negative regulation of cAMP-dependent protein kinase activity	2	1.851851852	0.0443825947	PRKAR2B, PKIG
GOTERM_BP_DIRECT	GO:0070723~response to cholesterol	2	1.851851852	0.0443825947	CCL3, TGFBRI1
GOTERM_BP_DIRECT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	4	3.703703704	0.0559824250	RNF126, ABTB1, UBE2D1, RNF14
GOTERM_BP_DIRECT	GO:0045779~negative regulation of bone resorption	2	1.851851852	0.0658372566	CD38, UBASH3B
GOTERM_BP_DIRECT	GO:0010243~response to organonitrogen compound	2	1.851851852	0.0763851558	CCND1, FLT3
GOTERM_BP_DIRECT	GO:0060216~definitive hemopoiesis	2	1.851851852	0.0868151952	ZFP36L2, SP3
GOTERM_BP_DIRECT	GO:0071276~cellular response to cadmium ion	2	1.851851852	0.0919864254	MT1X, MT1F
GOTERM_BP_DIRECT	GO:0001556~oocyte maturation	2	1.851851852	0.0971286781	TUBB8, PABPC1L

KEGG analysis of DEPs in M2a macrophages					
ID	Term	Term <i>P</i> -value	% Associated Genes	Nr. Genes	Associated Genes Found
KEGG:04921	Oxytocin signaling pathway	0.0000458515	6.49	10	[ACTG1, CALML3, CCND1, CD38, ITPR2, MEF2C, MYL6B, NFATC2, PLA2G4C, PPP3CC]
KEGG:04218	Cellular senescence	0.0003309456	5.63	9	[CALML3, CCND1, CCND3, CDK4, ITPR2, NFATC2, PPP3CC, TGFBR1, ZFP36L2]
KEGG:04530	Tight junction	0.0004950319	5.33	9	[ACTG1, ACTR3B, AFDN, CCND1, CDK4, MYH3, MYL6B, NEDD4L, TUBA8]
KEGG:05166	Human T-cell leukemia virus 1 infection	0.0008083799	4.57	10	[CCND1, CCND3, CDK4, CREBBP, HLA-DQA2, NFATC2, NFYB, POLB, PPP3CC, TGFBR1]
KEGG:05164	Influenza A	0.0022530998	4.71	8	[ACTG1, CCL5, CCND3, CDK4, CREBBP, CXCL10, HLA-DQA2, PLG]
KEGG:04520	Adherens junction	0.0028053101	7.04	5	[ACTG1, AFDN, CREBBP, CTNNA2, TGFBR1]
KEGG:04659	Th17 cell differentiation	0.0034104618	5.61	6	[AHR, HLA-DQA2, LAT, NFATC2, PPP3CC, TGFBR1]
KEGG:05214	Glioma	0.0834060758	4.00	3	[CALML3, CCND1, CDK4]
KEGG:04115	p53 signaling pathway	0.0758199990	4.17	3	[CCND1, CCND3, CDK4]
KEGG:04660	T cell receptor signaling pathway	0.0138971964	4.81	5	[CDK4, LAT, NFATC2, PAK4, PPP3CC]
KEGG:04720	Long-term potentiation	0.0132245151	5.97	4	[CALML3, CREBBP, ITPR2, PPP3CC]
KEGG:04924	Renin secretion	0.0685596243	4.35	3	[CALML3, ITPR2, PPP3CC]
KEGG:05416	Viral myocarditis	0.0488486625	5.00	3	[ACTG1, CCND1, HLA-DQA2]
KEGG:05221	Acute myeloid leukemia	0.0639062673	4.48	3	[CCND1, FLT3, ITGAM]
KEGG:04370	VEGF signaling pathway	0.0468586423	5.08	3	[NFATC2, PLA2G4C, PPP3CC]
KEGG:04610	Complement and coagulation cascades	0.0290050544	4.71	4	[A2M, ITGAM, PLG, PROCR]
KEGG:04658	Th1 and Th2 cell differentiation	0.0372484922	4.35	4	[HLA-DQA2, LAT, NFATC2, PPP3CC]
KEGG:04110	Cell cycle	0.0274899881	4.03	5	[CCND1, CCND3, CDK4, CREBBP, STAG1]
KEGG:00565	Ether lipid metabolism	0.0262719858	6.38	3	[GDPD1, PLA2G4C, PLD4]
KEGG:04970	Salivary secretion	0.0359964445	4.40	4	[CALML3, CD38, ITPR2, LYZ]
KEGG:04640	Hematopoietic cell lineage	0.0467109382	4.04	4	[CD38, FLT3, HLA-DQA2, ITGAM]
KEGG:04070	Phosphatidylinositol signaling system	0.0467109382	4.04	4	[CALML3, ITPR2, OCRL, PIP4P2]
Biological processes analysis of up-regulated DEPs in M2b macrophages					
Category	Term	Count	% Associated Genes	<i>P</i> -value	Genes
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	12	0.062604341	0.0000632751	LAT, P2RX7, IL36G, C5AR1, PTGS2, CCL20, CXCL8, IL1B, POLB, PLA2G4C, CD14, IL1A
GOTERM_BP_DIRECT	GO:0071498~cellular response to fluid shear stress	4	0.020868114	0.0000675299	MEF2C, PTGS2, TFP12, SRC
GOTERM_BP_DIRECT	GO:0030049~muscle filament sliding	5	0.026085142	0.0001331195	DES, NEB, ACTA1, MYL6B, MYH3
GOTERM_BP_DIRECT	GO:0007165~signal transduction	20	0.104340568	0.0003652896	NAMPT, C5AR1, CAP2, CXCL8, FADD, HMGA2, CDK4, SRC, ITPR2, LAT, LPXN, CCND3, CCL20, PAK4, IL1B, GRK4, AFDN, NDRG2, GRK3, IGFBP5
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	13	0.067821369	0.0005513908	MEF2C, C5AR1, NCF1, FADD, AHR, KIF1B, EMC4, PAK4, RHOB, IL1B, IL1A, CD14, TIGAR
GOTERM_BP_DIRECT	GO:0051602~response to electrical stimulus	4	0.020868114	0.0005848204	P2RX7, CD14, SRC, SOD2
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	6	0.03130217	0.0006154317	LAT, CCM2, ITGA1, ITGB3, DST, SRC
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	4	0.020868114	0.0008325059	C5AR1, PTGS2, IL1B, IL1A
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	6	0.03130217	0.0011189116	MEF2C, CCL20, CXCL8, SHPK, CD14, SRC
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	5	0.026085142	0.0011203438	C5AR1, CCL20, ITGA1, CXCL8, IL1B
GOTERM_BP_DIRECT	GO:0010226~response to lithium ion	3	0.015651085	0.0016500953	ACTA1, PTGS2, PKLR
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	7	0.036519199	0.0017487338	HIST2H3A, P2RX7, CD59, H3F3A, ITGB3, EHD1, TFP12
GOTERM_BP_DIRECT	GO:0031623~receptor internalization	4	0.020868114	0.0032417308	DNM3, CXCL8, GRK4, GRK3
GOTERM_BP_DIRECT	GO:0055093~response to hyperoxia	3	0.015651085	0.0060127127	POLB, CDK4, SOD2
GOTERM_BP_DIRECT	GO:0016049~cell growth	4	0.020868114	0.0068240858	TYMS, ACTA1, PAK4, ITGB3
GOTERM_BP_DIRECT	GO:0042098~T cell proliferation	3	0.015651085	0.0074923733	P2RX7, CCND3, EBI3
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	4	0.020868114	0.0078844139	P2RX7, ACTA1, MBD2, SRC
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	4	0.020868114	0.0078844139	PAK4, IL1B, MBD2, IGFBP5
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	5	0.026085142	0.0083030267	C5AR1, RHOB, CXCL8, IL1B, IL1A
GOTERM_BP_DIRECT	GO:0030168~platelet activation	5	0.026085142	0.0083030267	LAT, RHOB, ITGB3, SRC, ITPR2
GOTERM_BP_DIRECT	GO:0033198~response to ATP	3	0.015651085	0.0091188182	P2RX7, PKLR, IL1B
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	5	0.026085142	0.0101694889	C5AR1, ITGB3, SRC, SLC7A11, SLC7A7
GOTERM_BP_DIRECT	GO:0050715~positive regulation of cytokine secretion	3	0.015651085	0.0127951427	CD14, SRC, IL1A
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	4	0.020868114	0.0135604030	ACTG1, NCF1, ITGB3, SRC
GOTERM_BP_DIRECT	GO:0042493~response to drug	7	0.036519199	0.0189540793	TYMS, P2RX7, PLIN2, PTGS2, CDK4, SRC, SOD2
GOTERM_BP_DIRECT	GO:0010332~response to gamma radiation	3	0.015651085	0.0193070371	POLB, TIGAR, SOD2
GOTERM_BP_DIRECT	GO:0001660~fever generation	2	0.010434057	0.0205825378	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	4	0.020868114	0.0210595501	TYMS, CDK4, AHR, SLC7A11

GOTERM_BP_DIRECT	GO:0006928~movement of cell or subcellular component	4	0.020868114	0.0217133826	ACTG1, PTGS2, PAK4, CXCL8
GOTERM_BP_DIRECT	GO:0097192~extrinsic apoptotic signaling pathway in absence of ligand	3	0.015651085	0.0229831393	IL1B, FADD, IL1A
GOTERM_BP_DIRECT	GO:0006955~immune response	8	0.041736227	0.0268397523	LAT, C5AR1, FCAR, CCL20, CXCL8, IL1B, C1R, IL1A
GOTERM_BP_DIRECT	GO:0000183~chromatin silencing at rDNA	3	0.015651085	0.0269224251	HIST2H3A, H3F3A, MBD2
GOTERM_BP_DIRECT	GO:0045786~negative regulation of cell cycle	3	0.015651085	0.0269224251	TAF6, PTGS2, RHOB
GOTERM_BP_DIRECT	GO:0070527~platelet aggregation	3	0.015651085	0.0325631804	ACTG1, ITGB3, SLC7A11
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	3	0.015651085	0.0340398053	PTGS2, H3F3A, IL1B
GOTERM_BP_DIRECT	GO:0031622~positive regulation of fever generation	2	0.010434057	0.0340703328	PTGS2, IL1B
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	6	0.03130217	0.0353242058	MEF2C, P2RX7, ACTA1, IL1B, HMGA2, IL1A
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	3	0.015651085	0.0355421504	PTGS2, IL1B, SOD2
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	4	0.020868114	0.0379837070	DES, ACTA1, MYL6B, ITGA1
GOTERM_BP_DIRECT	GO:0000187~activation of MAPK activity	4	0.020868114	0.0379837070	P2RX7, C5AR1, ITGA1, IL1B
GOTERM_BP_DIRECT	GO:0032755~positive regulation of interleukin-6 production	3	0.015651085	0.0386223293	P2RX7, IL1B, IL1A
GOTERM_BP_DIRECT	GO:0032729~positive regulation of interferon-gamma production	3	0.015651085	0.0401993383	IL1B, FADD, CD14
GOTERM_BP_DIRECT	GO:0061154~endothelial tube morphogenesis	2	0.010434057	0.0407450121	CCM2, RHOB
GOTERM_BP_DIRECT	GO:0010042~response to manganese ion	2	0.010434057	0.0407450121	PTGS2, SOD2
GOTERM_BP_DIRECT	GO:0048667~cell morphogenesis involved in neuron differentiation	2	0.010434057	0.0407450121	MEF2C, UNK
GOTERM_BP_DIRECT	GO:0009408~response to heat	3	0.015651085	0.0434251660	HSPA2, PKLR, CD14
GOTERM_BP_DIRECT	GO:0032308~positive regulation of prostaglandin secretion	2	0.010434057	0.0473739636	P2RX7, IL1B
GOTERM_BP_DIRECT	GO:0006769~nicotinamide metabolic process	2	0.010434057	0.0473739636	NAMPT, PTGS2
GOTERM_BP_DIRECT	GO:0071639~positive regulation of monocyte chemotactic protein-1 production	2	0.010434057	0.0473739636	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0006900~membrane budding	2	0.010434057	0.0473739636	P2RX7, S100A10
GOTERM_BP_DIRECT	GO:0045869~negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	2	0.010434057	0.0473739636	HMGA2, APOBEC3F
GOTERM_BP_DIRECT	GO:0035234~ectopic germ cell programmed cell death	2	0.010434057	0.0539574977	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	7	0.036519199	0.0567560481	TAF6, PTGS2, ITGA1, CXCL8, IL1B, IL1A, SOD2
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	6	0.03130217	0.0570986321	PTGS2, RHOB, FADD, HMGA2, CDK4, SRC
GOTERM_BP_DIRECT	GO:0071223~cellular response to lipoteichoic acid	2	0.010434057	0.0604959230	CCL20, CD14
GOTERM_BP_DIRECT	GO:0045124~regulation of bone resorption	2	0.010434057	0.0604959230	ITGB3, SRC
GOTERM_BP_DIRECT	GO:0047497~mitochondrion transport along microtubule	2	0.010434057	0.0604959230	KIF1B, MAP1B
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	2	0.010434057	0.0604959230	AHR, TIGAR
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	4	0.020868114	0.0623320861	IL36G, IL1B, IL1A, EB13
GOTERM_BP_DIRECT	GO:0000902~cell morphogenesis	3	0.015651085	0.0684420833	P2RX7, CAP2, YAP1
GOTERM_BP_DIRECT	GO:0048333~mesodermal cell differentiation	2	0.010434057	0.0734386707	ITGB3, HMGA2
GOTERM_BP_DIRECT	GO:0045087~innate immune response	7	0.036519199	0.0776672002	IL36G, NCF1, FADD, C1R, APOBEC3F, CD14, SRC
GOTERM_BP_DIRECT	GO:0034498~early endosome to Golgi transport	2	0.010434057	0.0798435997	STX10, TRAPPC10
GOTERM_BP_DIRECT	GO:0045086~positive regulation of interleukin-2 biosynthetic process	2	0.010434057	0.0798435997	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0048872~homeostasis of number of cells	2	0.010434057	0.0862046333	POLB, AFDN
GOTERM_BP_DIRECT	GO:0051770~positive regulation of nitric-oxide synthase biosynthetic process	2	0.010434057	0.0862046333	NAMPT, CCL20
GOTERM_BP_DIRECT	GO:0001916~positive regulation of T cell mediated cytotoxicity	2	0.010434057	0.0862046333	P2RX7, FADD
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	3	0.015651085	0.0864655746	PTGS2, IL1B, FADD
GOTERM_BP_DIRECT	GO:0097190~apoptotic signaling pathway	3	0.015651085	0.0864655746	P2RX7, FADD, CD14
GOTERM_BP_DIRECT	GO:0042554~superoxide anion generation	2	0.010434057	0.0925220695	NCF1, SOD2
GOTERM_BP_DIRECT	GO:0071361~cellular response to ethanol	2	0.010434057	0.0925220695	ITPR2, SOD2
GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	3	0.015651085	0.0948860066	NAMPT, TYMS, CDK4
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	7	0.036519199	0.0985361441	LPXN, RHOB, NINJ1, AFDN, ITGB3, DST, PARVB
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	5	0.026085142	0.0993688264	NAMPT, IL36G, CCL20, IL1B, AFDN
Biological processes analysis of down-regulated DEPs in M2b macrophages					
Category	Term	Count	% Associated Genes	P-value	Genes
GOTERM_BP_DIRECT	GO:0006260~DNA replication	6	0.028080685	0.00548087	KAT7, MCM7, RFC1, GINS3, PCNA, MCM5
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	5	0.023400571	0.00652031	CCND1, MCM7, PCNA, IQGAP3, MCM5
GOTERM_BP_DIRECT	GO:0043085~positive regulation of catalytic activity	4	0.018720457	0.021175303	RFC1, PHACTR4, APOC1, IGF2
GOTERM_BP_DIRECT	GO:0051897~positive regulation of protein kinase B signaling	4	0.018720457	0.023282782	SPRY2, TNFAIP8L3, TGFBRI1, IGF2
GOTERM_BP_DIRECT	GO:0006296~nucleotide-excision repair, DNA incision, 5'-to lesion	3	0.014040343	0.029548563	CHD1L, RFC1, PCNA
GOTERM_BP_DIRECT	GO:0033683~nucleotide-excision repair, DNA incision	3	0.014040343	0.031044478	CHD1L, RFC1, PCNA
GOTERM_BP_DIRECT	GO:0006868~glutamine transport	2	0.009360228	0.035806991	SLC1A4, SLC38A1
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	11	0.051481256	0.036913529	SHOX2, UXT, CCND1, RFC1, ZNF148, RFX5, MLX, PKIG, NFATC2, COQ7, NCOR1
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	7	0.032760799	0.050852929	GPC4, CKS1B, ZFP36L2, MCM7, PCNA, USP13, TACC2
GOTERM_BP_DIRECT	GO:2000480~negative regulation of cAMP-dependent protein kinase activity	2	0.009360228	0.056677719	PRKAR2B, PKIG
GOTERM_BP_DIRECT	GO:0033601~positive regulation of mammary gland epithelial cell proliferation	2	0.009360228	0.056677719	CCND1, IQGAP3
GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	4	0.018720457	0.068996451	CORO2A, MOB2, PHACTR4, SH2B2
GOTERM_BP_DIRECT	GO:0051272~positive regulation of cellular component movement	2	0.009360228	0.070341977	TGFBRI1, STMN1

GOTERM_BP_DIRECT	GO:0032981~mitochondrial respiratory chain complex I assembly	3	0.014040343	0.076788766	NDUFS4, ECSIT, NDUFA1
GOTERM_BP_DIRECT	GO:0031103~axon regeneration	2	0.009360228	0.097084298	JUN, MTR
GOTERM_BP_DIRECT	GO:0010243~response to organonitrogen compound	2	0.009360228	0.097084298	CCND1, FLT3
KEGG analysis of DEPs in M2b macrophages					
ID	Term	Term <i>P</i> -value	% Associated Genes	Nr. Genes	Associated Genes Found
KEGG:04921	Oxytocin signaling pathway	0.0000090276	7.14	11	[ACTG1, CCND1, ITPR2, JUN, MEF2C, MYL6B, NFATC2, PLA2G4C, PPP3CC, PTGS2, SRC]
KEGG:04145	Phagosome	0.0000478994	6.58	10	[ACTG1, ATP6V0C, ATP6V1C2, C1R, CD14, FCAR, HLA-DQA2, NCF1, SCARB1, TUBB8]
KEGG:04530	Tight junction	0.0001170318	5.92	10	[ACTG1, ACTR3B, AFDN, CCND1, CDK4, JUN, MYH3, MYL6B, NEDD4L, SRC]
KEGG:04659	Th17 cell differentiation	0.0001160359	7.48	8	[AHR, HLA-DQA2, IL1B, JUN, LAT, NFATC2, PPP3CC, TGFB1]
KEGG:05135	Yersinia infection	0.0002574740	6.67	8	[ACTG1, ACTR3B, CXCL8, IL1B, JUN, LAT, NFATC2, SRC]
KEGG:05323	Rheumatoid arthritis	0.0003016403	7.53	7	[ATP6V0C, ATP6V1C2, CCL20, CXCL8, HLA-DQA2, IL1B, JUN]
KEGG:04218	Cellular senescence	0.0003785687	5.63	9	[CCND1, CCND3, CDK4, CXCL8, ITPR2, NFATC2, PPP3CC, TGFB1, ZFP36L2]
KEGG:04625	C-type lectin receptor signaling pathway	0.0005965039	6.73	7	[IL1B, ITPR2, JUN, NFATC2, PPP3CC, PTGS2, SRC]
KEGG:05202	Transcriptional misregulation in cancer	0.0011222058	4.84	9	[CD14, CXCL8, FLT3, H3-3A, H3C15, HMGA2, MEF2C, NCOR1, SPINT1]
KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	0.0012557879	4.76	9	[CCND1, CDK4, CXCL8, ITPR2, JUN, NFATC2, PPP3CC, PTGS2, SRC]
KEGG:04370	VEGF signaling pathway	0.0013312883	8.47	5	[NFATC2, PLA2G4C, PPP3CC, PTGS2, SRC]
KEGG:05131	Shigellosis	0.0017989186	4.18	10	[ACTG1, CD14, CXCL8, H3-3A, H3C15, IL1B, ITPR2, JUN, RBCK1, SRC]
KEGG:05219	Bladder cancer	0.0024473839	9.76	4	[CCND1, CDK4, CXCL8, SRC]
KEGG:05100	Bacterial invasion of epithelial cells	0.0816692263	4.11	3	[ACTG1, DNM3, SRC]
KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	0.002604442	6.00	6	[CCND1, CDK4, CXCL8, IL1B, JUN, TGFB1]
KEGG:05132	Salmonella infection	0.0029440655	4.21	9	[ACTG1, CD14, CXCL8, IL1B, JUN, MYH3, MYL6B, RHOB, STX10]
KEGG:05120	Epithelial cell signaling in Helicobacter pylori infection	0.0028509428	7.14	5	[ATP6V0C, ATP6V1C2, CXCL8, JUN, SRC]
KEGG:04660	T cell receptor signaling pathway	0.0032379015	5.77	6	[CDK4, JUN, LAT, NFATC2, PAK4, PPP3CC]
KEGG:05166	Human T-cell leukemia virus 1 infection	0.0034345032	4.11	9	[CCND1, CCND3, CDK4, HLA-DQA2, JUN, NFATC2, POLB, PPP3CC, TGFB1]
KEGG:05163	Human cytomegalovirus infection	0.0041057500	4.00	9	[CCND1, CDK4, CXCL8, IL1B, ITPR2, NFATC2, PPP3CC, PTGS2, SRC]
KEGG:05140	Leishmaniasis	0.0043093502	6.49	5	[HLA-DQA2, IL1B, JUN, NCF1, PTGS2]
KEGG:05133	Pertussis	0.0040740282	6.58	5	[C1R, CD14, CXCL8, IL1B, JUN]
KEGG:04932	Non-alcoholic fatty liver disease (NAFLD)	0.0047170548	4.70	7	[COX8A, CXCL8, IL1B, JUN, MLX, NDUFA1, PKLR]
KEGG:04913	Ovarian steroidogenesis	0.0054285815	7.84	4	[ACOT2, PLA2G4C, PTGS2, SCARB1]
KEGG:04115	p53 signaling pathway	0.0790827051	4.17	3	[CCND1, CCND3, CDK4]
KEGG:04658	Th1 and Th2 cell differentiation	0.0091001168	5.43	5	[HLA-DQA2, JUN, LAT, NFATC2, PPP3CC]
KEGG:04380	Osteoclast differentiation	0.0088482490	4.69	6	[IL1B, JUN, NCF1, NFATC2, PPP3CC, TGFB1]
KEGG:04657	IL-17 signaling pathway	0.0099378144	5.32	5	[CCL20, CXCL8, IL1B, JUN, PTGS2]
KEGG:04137	Mitophagy	0.0691104829	4.41	3	[JUN, SRC, TOMM7]
KEGG:05418	Fluid shear stress and atherosclerosis	0.0129595986	4.32	6	[ACTG1, IL1B, JUN, MEF2C, NCF1, SRC]
KEGG:04064	NF-kappa B signaling pathway	0.0149285728	4.81	5	[CD14, CXCL8, IL1B, LAT, PTGS2]
KEGG:05221	Acute myeloid leukemia	0.0667132661	4.48	3	[CCND1, CD14, FLT3]
KEGG:04520	Adherens junction	0.0170769785	5.63	4	[ACTG1, AFDN, SRC, TGFB1]
KEGG:05416	Viral myocarditis	0.0510559604	5.00	3	[ACTG1, CCND1, HLA-DQA2]
KEGG:05321	Inflammatory bowel disease (IBD)	0.0620370582	4.62	3	[HLA-DQA2, IL1B, JUN]
KEGG:04724	Glutamatergic synapse	0.0213753264	4.39	5	[GRK3, ITPR2, PLA2G4C, PPP3CC, SLC38A1]
KEGG:04750	Inflammatory mediator regulation of TRP channels	0.0508631207	4.00	4	[IL1B, ITPR2, PLA2G4C, SRC]
KEGG:04640	Hematopoietic cell lineage	0.0493392497	4.04	4	[CD14, FLT3, HLA-DQA2, IL1B]
KEGG:05134	Legionellosis	0.0449693725	5.26	3	[CD14, CXCL8, IL1B]
KEGG:04912	GnRH signaling pathway	0.0407380387	4.30	4	[ITPR2, JUN, PLA2G4C, SRC]
KEGG:04110	Cell cycle	0.0294154659	4.03	5	[CCND1, CCND3, CDK4, MCM5, STAG1]
KEGG:05110	Vibrio cholerae infection	0.0322886556	6.00	3	[ACTG1, ATP6V0C, ATP6V1C2]
KEGG:05144	Malaria	0.0322886556	6.00	3	[CXCL8, GYPC, IL1B]
KEGG:05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	0.0355210081	4.49	4	[JUN, LAT, NFATC2, PPP3CC]
KEGG:05222	Small cell lung cancer	0.0393950120	4.35	4	[CCND1, CDK4, CKS1B, PTGS2]
Biological processes analysis of up-regulated DEPs in M2c macrophages					
Category	Term	Count	% Associated Genes	<i>P</i> -value	Genes
GOTERM_BP_DIRECT	GO:0030049~muscle filament sliding	6	6.060606061	0.0000018232	DES, NEB, ACTA1, MYL6B, MYH3, TTN
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	5	5.050505051	0.0027227338	DES, DYSF, ACTA1, MYL6B, TTN
GOTERM_BP_DIRECT	GO:0045214~sarcomere organization	3	3.03030303	0.0107235149	ACTG1, MYH3, TTN
GOTERM_BP_DIRECT	GO:0000183~chromatin silencing at rDNA	3	3.03030303	0.0171055808	HIST2H3A, H3F3A, MBD2

GOTERM_BP_DIRECT	GO:0030240~skeletal muscle thin filament assembly	2	2.02020202	0.0268072996	ACTA1, TTN
GOTERM_BP_DIRECT	GO:0061154~endothelial tube morphogenesis	2	2.02020202	0.0320828423	CCM2, RHOB
GOTERM_BP_DIRECT	GO:0048667~cell morphogenesis involved in neuron differentiation	2	2.02020202	0.0320828423	MEF2C, UNK
GOTERM_BP_DIRECT	GO:0045869~negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	2	2.02020202	0.0373300996	HMGA2, APOBEC3F
GOTERM_BP_DIRECT	GO:0047497~mitochondrion transport along microtubule	2	2.02020202	0.0477403572	KIF1B, MAP1B
GOTERM_BP_DIRECT	GO:0016051~carbohydrate biosynthetic process	2	2.02020202	0.0477403572	CHST9, CHST11
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	2	2.02020202	0.0477403572	AHR, TIGAR
GOTERM_BP_DIRECT	GO:0000226~microtubule cytoskeleton organization	3	3.03030303	0.0567309418	MAP1B, TACC3, DST
GOTERM_BP_DIRECT	GO:0048703~embryonic viscerocranium morphogenesis	2	2.02020202	0.0580392626	MEF2C, CHST11
GOTERM_BP_DIRECT	GO:0001682~tRNA 5'-leader removal	2	2.02020202	0.0580392626	RPP30, KIAA0391
GOTERM_BP_DIRECT	GO:0006366~transcription from RNA polymerase II promoter	7	7.070707071	0.0599178318	MEF2C, ELF1, TAF6, EBF1, HMGA2, NFATC2, AHR
GOTERM_BP_DIRECT	GO:0042446~hormone biosynthetic process	2	2.02020202	0.0631473269	FDX1, CHST9
GOTERM_BP_DIRECT	GO:0071498~cellular response to fluid shear stress	2	2.02020202	0.0631473269	MEF2C, TFPI2
GOTERM_BP_DIRECT	GO:0048872~homeostasis of number of cells	2	2.02020202	0.0682279940	POLB, AFDN
GOTERM_BP_DIRECT	GO:0035264~multicellular organism growth	3	3.03030303	0.0699457743	ATRX, CCM2, H3F3A
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	3	3.03030303	0.0776802446	TYMS, CDK4, AHR
GOTERM_BP_DIRECT	GO:0007517~muscle organ development	3	3.03030303	0.0840526397	MEF2C, NEB, MYH3
GOTERM_BP_DIRECT	GO:0055093~response to hyperoxia	2	2.02020202	0.0882795848	POLB, CDK4
GOTERM_BP_DIRECT	GO:0043523~regulation of neuron apoptotic process	2	2.02020202	0.0981447391	MEF2C, TRIM2
Biological processes analysis of down-regulated DEPs in M2c macrophages					
Category	Term	Count	% Associated Genes	P-value	Genes
GOTERM_BP_DIRECT	GO:0044267~cellular protein metabolic process	6	0.029653059	0.0016966441	LYZ, LTF, IGF2, GGA2, GGA3, PLG
GOTERM_BP_DIRECT	GO:0006631~fatty acid metabolic process	4	0.019768706	0.0063815350	PRKAR2B, ACADSB, EHHADH, ACSF2
GOTERM_BP_DIRECT	GO:0045926~negative regulation of growth	3	0.01482653	0.0082576740	MT2A, MT1X, MT1F
GOTERM_BP_DIRECT	GO:0071294~cellular response to zinc ion	3	0.01482653	0.0082576740	MT2A, MT1X, MT1F
GOTERM_BP_DIRECT	GO:0036018~cellular response to erythropoietin	2	0.009884353	0.0144783729	MT2A, MT1X
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	12	0.059306118	0.0157438063	SHOX2, SUZ12, CCND1, RCOR3, PSEN1, VHL, ZNF148, SP3, MLX, ZEB2, COQ7, NCOR1
GOTERM_BP_DIRECT	GO:0043085~positive regulation of catalytic activity	4	0.019768706	0.0211753029	PSEN1, PHACTR4, APOC1, IGF2
GOTERM_BP_DIRECT	GO:0071902~positive regulation of protein serine/threonine kinase activity	3	0.01482653	0.0266470348	SLC27A1, LTF, IGF2
GOTERM_BP_DIRECT	GO:0045833~negative regulation of lipid metabolic process	2	0.009884353	0.0287488161	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0010916~negative regulation of very-low-density lipoprotein particle clearance	2	0.009884353	0.0287488161	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0051005~negative regulation of lipoprotein lipase activity	2	0.009884353	0.0358069913	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0071621~granulocyte chemotaxis	2	0.009884353	0.0358069913	CCL3, IL17RA
GOTERM_BP_DIRECT	GO:0034382~chylomicron remnant clearance	2	0.009884353	0.0428142914	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0048261~negative regulation of receptor-mediated endocytosis	2	0.009884353	0.0566777187	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0070723~response to cholesterol	2	0.009884353	0.0566777187	CCL3, TGFBRI
GOTERM_BP_DIRECT	GO:0033601~positive regulation of mammary gland epithelial cell proliferation	2	0.009884353	0.0566777187	CCND1, IQGAP3
GOTERM_BP_DIRECT	GO:0034379~very-low-density lipoprotein particle assembly	2	0.009884353	0.0566777187	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0010038~response to metal ion	2	0.009884353	0.0703419769	MT2A, MT1X
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	4	0.019768706	0.0766986394	COG7, VHL, WIZ, USP13
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	4	0.019768706	0.0780178934	CCL3, ZNF148, IQGAP3, MYADM
GOTERM_BP_DIRECT	GO:0008360~regulation of cell shape	4	0.019768706	0.0820352521	CCL3, VRK2, RHOQ, CDC42SE1
GOTERM_BP_DIRECT	GO:0045717~negative regulation of fatty acid biosynthetic process	2	0.009884353	0.0838099039	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0045779~negative regulation of bone resorption	2	0.009884353	0.0838099039	CD38, UBASH3B
GOTERM_BP_DIRECT	GO:0010717~regulation of epithelial to mesenchymal transition	2	0.009884353	0.0838099039	TGFBRI, POFUT2
GOTERM_BP_DIRECT	GO:0043922~negative regulation by host of viral transcription	2	0.009884353	0.0904711191	CCL3, JUN
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	3	0.01482653	0.0941770351	CCL3, CXCL5, CXCL8
GOTERM_BP_DIRECT	GO:0016485~protein processing	3	0.01482653	0.0964246241	CPM, PSEN1, SRGN
GOTERM_BP_DIRECT	GO:0033700~phospholipid efflux	2	0.009884353	0.0970842977	APOC3, APOC1
GOTERM_BP_DIRECT	GO:0010243~response to organonitrogen compound	2	0.009884353	0.0970842977	CCND1, FLT3
KEGG analysis of DEPs in M2c macrophages					
ID	Term	Term P-value	% Associated Genes	Nr. Genes	Associated Genes Found
KEGG:04921	Oxytocin signaling pathway	0.0001878789	5.84	9	[ACTG1, CALML3, CCND1, CD38, ITPR2, JUN, MEF2C, MYL6B, PPP3CC]
KEGG:05323	Rheumatoid arthritis	0.0013870437	6.45	6	[ATP6V0C, CCL3, CXCL5, CXCL8, HLA-DQA2, JUN]
KEGG:04659	Th17 cell differentiation	0.0028349767	5.61	6	[AHR, HLA-DQA2, JUN, LAT, PPP3CC, TGFBRI]
KEGG:05214	Glioma	0.0765115693	4.00	3	[CALML3, CCND1, CDK4]
KEGG:04218	Cellular senescence	0.0051418878	4.38	7	[CALML3, CCND1, CDK4, CXCL8, ITPR2, PPP3CC, TGFBRI]
KEGG:04530	Tight junction	0.0068993121	4.14	7	[ACTG1, AFDN, CCND1, CDK4, JUN, MYH3, MYL6B]

KEGG:04115	p53 signaling pathway	0.0694815740	4.17	3	[CCND1, CDK4, SESN1]
KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	0.0102215484	5.00	5	[CCND1, CDK4, CXCL8, JUN, TGFBRI]
KEGG:04520	Adherens junction	0.0142073715	5.63	4	[ACTG1, AFDN, CTNNA2, TGFBRI]
KEGG:05120	Epithelial cell signaling in Helicobacter pylori infection	0.0649676546	4.29	3	[ATP6V0C, CXCL8, JUN]
KEGG:05133	Pertussis	0.0178477857	5.26	4	[CALML3, CXCL5, CXCL8, JUN]
KEGG:05219	Bladder cancer	0.0166055672	7.32	3	[CCND1, CDK4, CXCL8]
KEGG:05031	Amphetamine addiction	0.0627636760	4.35	3	[CALML3, JUN, PPP3CC]
KEGG:04924	Renin secretion	0.0627636760	4.35	3	[CALML3, ITPR2, PPP3CC]
KEGG:05416	Viral myocarditis	0.0445801131	5.00	3	[ACTG1, CCND1, HLA-DQA2]
KEGG:04657	IL-17 signaling pathway	0.0354862511	4.26	4	[CXCL5, CXCL8, IL17RA, JUN]
KEGG:04978	Mineral absorption	0.0409569368	5.17	3	[MT1F, MT1X, MT2A]
KEGG:04720	Long-term potentiation	0.0584635027	4.48	3	[CALML3, ITPR2, PPP3CC]
KEGG:04658	Th1 and Th2 cell differentiation	0.0331639647	4.35	4	[HLA-DQA2, JUN, LAT, PPP3CC]
KEGG:04970	Salivary secretion	0.0320373401	4.40	4	[CALML3, CD38, ITPR2, LYZ]
Biological processes analysis of up-regulated DEPs in M2d macrophages					
Category	Term	Count	% Associated Genes	P-value	Genes
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	13	0.069281603	0.0000145838	LAT, IL36G, C5AR1, PTGS2, CCL20, HCK, CXCL8, IL1B, POLB, PLA2G4C, CD14, IL1A, CXCL10
GOTERM_BP_DIRECT	GO:0071498~cellular response to fluid shear stress	4	0.021317416	0.0000710577	MEF2C, PTGS2, TFPI2, SRC
GOTERM_BP_DIRECT	GO:0030049~muscle filament sliding	5	0.02664677	0.0001422070	DES, NEB, ACTA1, MYL6B, MYH3
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	13	0.069281603	0.0006435983	MEF2C, C5AR1, NCF1, AHR, WDR92, KIF1B, EMC4, PAK4, RHOB, IL1B, IL1A, CD14, TIGAR
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	6	0.031976124	0.0006651666	LAT, CCM2, HCK, ITGB3, DST, SRC
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	4	0.021317416	0.0008748296	C5AR1, PTGS2, IL1B, IL1A
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	6	0.031976124	0.0012076963	MEF2C, CCL20, CXCL8, CD14, SRC, CXCL10
GOTERM_BP_DIRECT	GO:0010332~response to gamma radiation	4	0.021317416	0.0013171920	POLB, TIGAR, CXCL10, SOD2
GOTERM_BP_DIRECT	GO:0006955~immune response	10	0.053293541	0.0028965954	LAT, C5AR1, FCAR, CCL20, CXCL8, IL1B, C1R, IL1A, CTSG, CXCL10
GOTERM_BP_DIRECT	GO:0055093~response to hyperoxia	3	0.015988062	0.0062153681	POLB, CDK4, SOD2
GOTERM_BP_DIRECT	GO:0016049~cell growth	4	0.021317416	0.0071528341	TYMS, ACTA1, PAK4, ITGB3
GOTERM_BP_DIRECT	GO:0007165~signal transduction	17	0.090599019	0.0072220551	NAMPT, C5AR1, CXCL8, HMGA2, CDK4, OCRL, SRC, CXCL10, ITPR2, LAT, CCL20, PAK4, IL1B, GRK4, AFDN, GRK3, IGFBP5
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	4	0.021317416	0.0082620981	PAK4, IL1B, MBD2, IGFBP5
GOTERM_BP_DIRECT	GO:0030168~platelet activation	5	0.02664677	0.0088066936	LAT, RHOB, ITGB3, SRC, ITPR2
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	5	0.02664677	0.0088066936	C5AR1, RHOB, CXCL8, IL1B, IL1A
GOTERM_BP_DIRECT	GO:0044267~cellular protein metabolic process	5	0.02664677	0.0096204806	HIST2H3A, H3F3A, CCDC59, CTSG, IGFBP5
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	5	0.02664677	0.0107795205	C5AR1, ITGB3, SRC, SLC7A11, SLC7A7
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	4	0.021317416	0.0112254138	C5AR1, CCL20, CXCL8, IL1B
GOTERM_BP_DIRECT	GO:0051602~response to electrical stimulus	3	0.015988062	0.0122162804	CD14, SRC, SOD2
GOTERM_BP_DIRECT	GO:0050715~positive regulation of cytokine secretion	3	0.015988062	0.0132181331	CD14, SRC, IL1A
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	5	0.02664677	0.0137077058	IL36G, HCK, IL1B, IL1A, EBI3
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	4	0.021317416	0.0141941003	ACTG1, NCF1, ITGB3, SRC
GOTERM_BP_DIRECT	GO:0001660~fever generation	2	0.010658708	0.0209349096	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	3	0.015988062	0.0211686976	HCK, IL1B, CD14
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	4	0.021317416	0.0220193001	TYMS, CDK4, AHR, SLC7A11
GOTERM_BP_DIRECT	GO:0006928~movement of cell or subcellular component	4	0.021317416	0.0227010069	ACTG1, PTGS2, PAK4, CXCL8
GOTERM_BP_DIRECT	GO:0007517~muscle organ development	4	0.021317416	0.0248146791	MEF2C, NEB, MYH3, CXCL10
GOTERM_BP_DIRECT	GO:0045786~negative regulation of cell cycle	3	0.015988062	0.0277866903	TAF6, PTGS2, RHOB
GOTERM_BP_DIRECT	GO:2001240~negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	3	0.015988062	0.0277866903	EYA3, IL1B, IL1A
GOTERM_BP_DIRECT	GO:0000183~chromatin silencing at rDNA	3	0.015988062	0.0277866903	HIST2H3A, H3F3A, MBD2
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	5	0.02664677	0.0285438701	C5AR1, PTGS2, CTSG, CXCL10, SOD2
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	4	0.021317416	0.0301456918	SLC8A1, PTGS2, SRC, TIGAR
GOTERM_BP_DIRECT	GO:0008152~metabolic process	5	0.02664677	0.0308041614	BCAT2, NPL, AGPAT4, PLA2G4C, OXSM
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	6	0.031976124	0.0335853847	NAMPT, IL36G, CCL20, IL1B, AFDN, CXCL10
GOTERM_BP_DIRECT	GO:0070527~platelet aggregation	3	0.015988062	0.0335982481	ACTG1, ITGB3, SLC7A11
GOTERM_BP_DIRECT	GO:0071801~regulation of podosome assembly	2	0.010658708	0.0346494968	HCK, SRC
GOTERM_BP_DIRECT	GO:0031622~positive regulation of fever generation	2	0.010658708	0.0346494968	PTGS2, IL1B
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	3	0.015988062	0.0351191325	PTGS2, H3F3A, IL1B
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	3	0.015988062	0.0366663220	PTGS2, IL1B, SOD2
GOTERM_BP_DIRECT	GO:0031623~receptor internalization	3	0.015988062	0.0366663220	CXCL8, GRK4, GRK3
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	4	0.021317416	0.0396414277	SLC8A1, DES, ACTA1, MYL6B
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	5	0.02664677	0.0408793636	HIST2H3A, H3F3A, ITGB3, EHD1, TFPI2

GOTERM_BP_DIRECT	GO:0048667~cell morphogenesis involved in neuron differentiation	2	0.010658708	0.0414351857	MEF2C, UNK
GOTERM_BP_DIRECT	GO:0010042~response to manganese ion	2	0.010658708	0.0414351857	PTGS2, SOD2
GOTERM_BP_DIRECT	GO:0061154~endothelial tube morphogenesis	2	0.010658708	0.0414351857	CCM2, RHOB
GOTERM_BP_DIRECT	GO:0006769~nicotinamide metabolic process	2	0.010658708	0.0481735777	NAMPT, PTGS2
GOTERM_BP_DIRECT	GO:0071639~positive regulation of monocyte chemotactic protein-1 production	2	0.010658708	0.0481735777	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0045869~negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	2	0.010658708	0.0481735777	HMGA2, APOBEC3F
GOTERM_BP_DIRECT	GO:0042542~response to hydrogen peroxide	3	0.015988062	0.0499392597	SLC8A1, SRC, SOD2
GOTERM_BP_DIRECT	GO:0071320~cellular response to cAMP	3	0.015988062	0.0517040505	SLC8A1, ITPR2, IGFBP5
GOTERM_BP_DIRECT	GO:0006935~chemotaxis	4	0.021317416	0.0547330760	C5AR1, CCL20, CXCL8, CXCL10
GOTERM_BP_DIRECT	GO:0035234~ectopic germ cell programmed cell death	2	0.010658708	0.0548649997	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0016051~carbohydrate biosynthetic process	2	0.010658708	0.0615097762	CHST9, CHST11
GOTERM_BP_DIRECT	GO:0045124~regulation of bone resorption	2	0.010658708	0.0615097762	ITGB3, SRC
GOTERM_BP_DIRECT	GO:0010226~response to lithium ion	2	0.010658708	0.0615097762	ACTA1, PTGS2
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	2	0.010658708	0.0615097762	AHR, TIGAR
GOTERM_BP_DIRECT	GO:0071223~cellular response to lipoteichoic acid	2	0.010658708	0.0615097762	CCL20, CD14
GOTERM_BP_DIRECT	GO:0042493~response to drug	6	0.031976124	0.0633646798	TYMS, SLC8A1, PTGS2, CDK4, SRC, SOD2
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	3	0.015988062	0.0646556957	ACTA1, MBD2, SRC
GOTERM_BP_DIRECT	GO:0051216~cartilage development	3	0.015988062	0.0646556957	TAPT1, TYMS, BMP8B
GOTERM_BP_DIRECT	GO:0010038~response to metal ion	2	0.010658708	0.0681082298	MT1A, NEDD4L
GOTERM_BP_DIRECT	GO:2000406~positive regulation of T cell migration	2	0.010658708	0.0681082298	CCL20, CXCL10
GOTERM_BP_DIRECT	GO:0048333~mesodermal cell differentiation	2	0.010658708	0.0746606806	ITGB3, HMGA2
GOTERM_BP_DIRECT	GO:0048703~embryonic viscerocranium morphogenesis	2	0.010658708	0.0746606806	MEF2C, CHST11
GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis	3	0.015988062	0.0765220761	C5AR1, CCL20, CXCL10
GOTERM_BP_DIRECT	GO:0045086~positive regulation of interleukin-2 biosynthetic process	2	0.010658708	0.0811674466	IL1B, IL1A
GOTERM_BP_DIRECT	GO:0042446~hormone biosynthetic process	2	0.010658708	0.0811674466	FDX1, CHST9
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	12	0.063952249	0.0840725915	MEF2C, ATRX, NAMPT, ELF1, HMGN3, EBF1, IL1B, YAP1, HMGA2, AHR, IL1A, CXCL10
GOTERM_BP_DIRECT	GO:0035690~cellular response to drug	3	0.015988062	0.0847849617	MEF2C, RAP2A, IL1B
GOTERM_BP_DIRECT	GO:0016024~CDP-diacylglycerol biosynthetic process	2	0.010658708	0.0876288435	AGPAT4, AGPAT1
GOTERM_BP_DIRECT	GO:0048872~homeostasis of number of cells	2	0.010658708	0.0876288435	POLB, AFDN
GOTERM_BP_DIRECT	GO:0051770~positive regulation of nitric-oxide synthase biosynthetic process	2	0.010658708	0.0876288435	NAMPT, CCL20
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	3	0.015988062	0.0890139033	CCL20, CXCL8, CXCL10
GOTERM_BP_DIRECT	GO:0009791~post-embryonic development	3	0.015988062	0.0933043893	TAPT1, CHST11, SOD2
GOTERM_BP_DIRECT	GO:0044030~regulation of DNA methylation	2	0.010658708	0.0940451852	MBD2, MPHOSPH8
GOTERM_BP_DIRECT	GO:0042554~superoxide anion generation	2	0.010658708	0.0940451852	NCF1, SOD2
GOTERM_BP_DIRECT	GO:0071361~cellular response to ethanol	2	0.010658708	0.0940451852	ITPR2, SOD2
GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	3	0.015988062	0.0976539021	NAMPT, TYMS, CDK4
Biological processes analysis of down-regulated DEPs in M2d macrophages					
Category	Term	Count	% Associated Genes	P-value	Genes
GOTERM_BP_DIRECT	GO:0006260~DNA replication	7	0.034503155	0.0008265056	RFC1, GINS3, PCNA, MCM2, LIG4, MCM5, MCM6
GOTERM_BP_DIRECT	GO:0043085~positive regulation of catalytic activity	5	0.02464511	0.0026209558	SH3PXD2B, RFC1, PHACTR4, APOC1, CIB1
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	9	0.044361199	0.0045423238	GPC4, CKS1B, LIPA, MKI67, BST2, PCNA, LIG4, USP13, TACC2
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	5	0.02464511	0.0059765802	CCND1, PCNA, MCM2, MCM5, MCM6
GOTERM_BP_DIRECT	GO:0006297~nucleotide-excision repair, DNA gap filling	3	0.014787066	0.0124143361	RFC1, PCNA, LIG4
GOTERM_BP_DIRECT	GO:0045737~positive regulation of cyclin-dependent protein serine/threonine kinase activity	3	0.014787066	0.0124143361	CKS1B, CCNK, CCND1
GOTERM_BP_DIRECT	GO:0034447~very-low-density lipoprotein particle clearance	2	0.009858044	0.0211110638	APOC1, VLDLR
GOTERM_BP_DIRECT	GO:0006270~DNA replication initiation	3	0.014787066	0.0215052303	MCM2, MCM5, MCM6
GOTERM_BP_DIRECT	GO:0002328~pro-B cell differentiation	2	0.009858044	0.0280494034	FLT3, LIG4
GOTERM_BP_DIRECT	GO:0006296~nucleotide-excision repair, DNA incision, 5'-to lesion	3	0.014787066	0.0282230112	CHD1L, RFC1, PCNA
GOTERM_BP_DIRECT	GO:0033683~nucleotide-excision repair, DNA incision	3	0.014787066	0.0296552226	CHD1L, RFC1, PCNA
GOTERM_BP_DIRECT	GO:0051301~cell division	7	0.034503155	0.0384152530	CKS1B, CCNK, CCND1, LIG4, REEP3, MCM5, CIB1
GOTERM_BP_DIRECT	GO:0006266~DNA ligation	2	0.009858044	0.0417801173	MGMT, LIG4
GOTERM_BP_DIRECT	GO:0006002~fructose 6-phosphate metabolic process	2	0.009858044	0.0553184649	GFPT2, FBP1
GOTERM_BP_DIRECT	GO:0006974~cellular response to DNA damage stimulus	5	0.02464511	0.0605986997	CCNK, CCND1, CHD1L, PARP4, CIB1
GOTERM_BP_DIRECT	GO:0006268~DNA unwinding involved in DNA replication	2	0.009858044	0.0686671190	MCM2, MCM6
GOTERM_BP_DIRECT	GO:0072520~seminiferous tubule development	2	0.009858044	0.0752711359	WDR48, RAD21L1
GOTERM_BP_DIRECT	GO:0006302~double-strand break repair	3	0.014787066	0.0797092416	RAD21L1, LIG4, CIB1
GOTERM_BP_DIRECT	GO:0045779~negative regulation of bone resorption	2	0.009858044	0.0818287150	CD38, UBASH3B
GOTERM_BP_DIRECT	GO:0010243~response to organonitrogen compound	2	0.009858044	0.0948058525	CCND1, FLT3
KEGG analysis of DEPs in M2d macrophages					

ID	Term	Term <i>P</i> -value	% Associated Genes	Nr. Genes	Associated Genes Found
KEGG:05418	Fluid shear stress and atherosclerosis	0.0001406922	6.47	9	[ACTG1, CALML3, IL1A, IL1B, ITGB3, MEF2C, NCF1, PIK3R2, SRC]
KEGG:04145	Phagosome	0.0002764745	5.92	9	[ACTG1, ATP6V0C, C1R, CD14, FCAR, HLA-DQA2, ITGB3, NCF1, TUBA8]
KEGG:04530	Tight junction	0.0006031390	5.33	9	[ACTG1, ACTR3B, AFDN, CDK4, MYH3, MYL6B, NEDD4L, SRC, TUBA8]
KEGG:05133	Pertussis	0.0006699755	7.89	6	[C1R, CALML3, CD14, CXCL8, IL1A, IL1B]
KEGG:05202	Transcriptional misregulation in cancer	0.0011954192	4.84	9	[CD14, CXCL8, FLT3, H3-3A, H3C15, HMG2A, MEF2C, NCOR1, PLAUI]
KEGG:05135	Yersinia infection	0.0014655730	5.83	7	[ACTG1, ACTR3B, CXCL8, IL1B, LAT, PIK3R2, SRC]
KEGG:04921	Oxytocin signaling pathway	0.0014308281	5.19	8	[ACTG1, CALML3, ITPR2, MEF2C, MYL6B, PLA2G4C, PPP3CC, SRC]
KEGG:04218	Cellular senescence	0.0018247946	5.00	8	[CALML3, CDK4, CXCL8, IL1A, ITPR2, PIK3R2, PPP3CC, TGFBRI]
KEGG:05323	Rheumatoid arthritis	0.0019256751	6.45	6	[ATP6V0C, CCL20, CXCL8, HLA-DQA2, IL1A, IL1B]
KEGG:04380	Osteoclast differentiation	0.0021242080	5.47	7	[IL1A, IL1B, ITGB3, NCF1, PIK3R2, PPP3CC, TGFBRI]
KEGG:05164	Influenza A	0.0026675931	4.71	8	[ACTG1, CDK4, CXCL10, CXCL8, HLA-DQA2, IL1A, IL1B, PIK3R2]
KEGG:05214	Glioma	0.0887473002	4.00	3	[CALML3, CDK4, PIK3R2]
KEGG:04750	Inflammatory mediator regulation of TRP channels	0.0027817863	6.00	6	[CALML3, IL1B, ITPR2, PIK3R2, PLA2G4C, SRC]
KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	0.0027817863	6.00	6	[CDK4, CXCL8, IL1A, IL1B, PIK3R2, TGFBRI]
KEGG:04640	Hematopoietic cell lineage	0.0026446700	6.06	6	[CD14, FLT3, HLA-DQA2, IL1A, IL1B, ITGB3]
KEGG:04070	Phosphatidylinositol signaling system	0.0026446700	6.06	6	[CALML3, IMPA2, ITPR2, OCRL, PIK3R2, PIP4P2]
KEGG:05132	Salmonella infection	0.0031265842	4.21	9	[ACTG1, CD14, CXCL8, IL1B, MYH3, MYL6B, RHOB, S100A10, STX10]
KEGG:04625	C-type lectin receptor signaling pathway	0.0033841825	5.77	6	[CALML3, IL1B, ITPR2, PIK3R2, PPP3CC, SRC]
KEGG:04659	Th17 cell differentiation	0.0038961414	5.61	6	[AHR, HLA-DQA2, IL1B, LAT, PPP3CC, TGFBRI]
KEGG:05152	Tuberculosis	0.0037889217	4.44	8	[ATP6V0C, CALML3, CD14, HLA-DQA2, IL1A, IL1B, PPP3CC, SRC]
KEGG:05163	Human cytomegalovirus infection	0.0043551000	4.00	9	[CALML3, CDK4, CXCL8, IL1B, ITGB3, ITPR2, PIK3R2, PPP3CC, SRC]
KEGG:04062	Chemokine signaling pathway	0.0050831032	4.23	8	[CCL20, CXCL10, CXCL8, GRK3, GRK4, NCF1, PIK3R2, SRC]
KEGG:05100	Bacterial invasion of epithelial cells	0.0833705515	4.11	3	[ACTG1, PIK3R2, SRC]
KEGG:04611	Platelet activation	0.0079456205	4.84	6	[ACTG1, ITGB3, ITPR2, PIK3R2, PLA2G4C, SRC]
KEGG:05134	Legionellosis	0.0083027976	7.02	4	[CD14, CXCL8, HSPA2, IL1B]
KEGG:04370	VEGF signaling pathway	0.0093637817	6.78	4	[PIK3R2, PLA2G4C, PPP3CC, SRC]
KEGG:05120	Epithelial cell signaling in Helicobacter pylori infection	0.0755821168	4.29	3	[ATP6V0C, CXCL8, SRC]
KEGG:05230	Central carbon metabolism in cancer	0.0730618015	4.35	3	[FLT3, PIK3R2, TIGAR]
KEGG:04924	Renin secretion	0.0730618015	4.35	3	[CALML3, ITPR2, PPP3CC]
KEGG:05146	Amoebiasis	0.0143164434	4.90	5	[CD14, CTSG, CXCL8, IL1B, PIK3R2]
KEGG:04620	Toll-like receptor signaling pathway	0.0154630356	4.81	5	[CD14, CXCL10, CXCL8, IL1B, PIK3R2]
KEGG:04064	NF-kappa B signaling pathway	0.0154630356	4.81	5	[CD14, CXCL8, IL1B, LAT, PLAUI]
KEGG:04660	T cell receptor signaling pathway	0.0154630356	4.81	5	[CDK4, LAT, PAK4, PIK3R2, PPP3CC]
KEGG:04520	Adherens junction	0.0175879765	5.63	4	[ACTG1, AFDN, SRC, TGFBRI]
KEGG:04664	Fc epsilon RI signaling pathway	0.0705802217	4.41	3	[LAT, PIK3R2, PLA2G4C]
KEGG:05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.0229831394	5.19	4	[ACTG1, DES, ITGB3, SLC8A1]
KEGG:05140	Leishmaniasis	0.0229831394	5.19	4	[HLA-DQA2, IL1A, IL1B, NCF1]
KEGG:05219	Bladder cancer	0.0196652692	7.32	3	[CDK4, CXCL8, SRC]
KEGG:05332	Graft-versus-host disease	0.0196652692	7.32	3	[HLA-DQA2, IL1A, IL1B]
KEGG:04940	Type I diabetes mellitus	0.0223116521	6.98	3	[HLA-DQA2, IL1A, IL1B]
KEGG:04919	Thyroid hormone signaling pathway	0.0260526538	4.20	5	[ACTG1, ITGB3, NCOR1, PIK3R2, SRC]
KEGG:04724	Glutamatergic synapse	0.0221189931	4.39	5	[GRK3, HOMER2, ITPR2, PLA2G4C, PPP3CC]
KEGG:05221	Acute myeloid leukemia	0.0681378618	4.48	3	[CD14, FLT3, PIK3R2]
KEGG:04720	Long-term potentiation	0.0681378618	4.48	3	[CALML3, ITPR2, PPP3CC]
KEGG:04978	Mineral absorption	0.0479955412	5.17	3	[MT1A, MT1F, SLC8A1]
KEGG:05321	Inflammatory bowel disease (IBD)	0.0633726716	4.62	3	[HLA-DQA2, IL1A, IL1B]
KEGG:04213	Longevity regulating pathway	0.0565304719	4.84	3	[HSPA2, PIK3R2, SOD2]
KEGG:05414	Dilated cardiomyopathy (DCM)	0.0461589955	4.17	4	[ACTG1, DES, ITGB3, SLC8A1]
KEGG:05144	Malaria	0.0330269448	6.00	3	[CXCL8, GYPC, IL1B]
KEGG:04657	IL-17 signaling pathway	0.0432740301	4.26	4	[CCL20, CXCL10, CXCL8, IL1B]
KEGG:05410	Hypertrophic cardiomyopathy (HCM)	0.0378200747	4.44	4	[ACTG1, DES, ITGB3, SLC8A1]
KEGG:04666	Fc gamma R-mediated phagocytosis	0.0418710373	4.30	4	[LAT, NCF1, PIK3R2, PLA2G4C]
KEGG:04912	GnRH signaling pathway	0.0418710373	4.30	4	[CALML3, ITPR2, PLA2G4C, SRC]

Table S4 Commonly regulated proteins in the four M2 macrophage subtypes

Abundance ratio of commonly up-regulated proteins											Abundance ratio of commonly down-regulated proteins										
Gene Name	Accession	PSMs	M2a/M0	M2b/M0	M2c/M0	M2d/M0	M2a/M1	M2b/M1	M2c/M1	M2d/M1	Gene Name	Accession	PSMs	M2a/M0	M2b/M0	M2c/M0	M2d/M0	M2a/M1	M2b/M1	M2c/M1	M2d/M1
ACTG1	P63261	12773	24.1	13.871	15.887	11.781	100	100	100	100	CD38	P28907	77	0.062	0.189	0.072	0.138	0.094	0.205	0.11	0.163
ACTA1	P68133	5304	100	100	100	100	100	100	100	100	ASNS	P08243	56	0.197	0.352	0.279	0.217	0.28	0.38	0.354	0.196
POTEKP	Q9BYX7	1947	8.773	17.079	19.723	7.076	3.693	8.464	9.868	3.452	KCNAB1	Q14722	49	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
ITGAV	P06756	282	3.999	3.432	4.498	3.725	4.97	3.797	4.19	3.58	LIMK2	P53671	35	0.48	0.2	0.441	0.324	0.309	0.143	0.318	0.251
TIMP1	P01033	97	5.15	3.274	2.736	3.925	6.139	3.956	3.294	5.033	CD70	P32970	23	0.203	0.351	0.356	0.347	0.188	0.233	0.247	0.265
IVNS1ABP	Q9Y6Y0	95	4.379	3.526	3.738	5.151	3.265	2.45	2.486	3.911	PPP1R21	Q6ZMI0	20	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
RHOB	P62745	84	100	100	100	100	100	100	100	100	CDC42SE1	Q9NRR8	18	0.01	0.254	0.207	0.239	0.01	0.24	0.166	0.191
EIF1B	O60739	80	100	100	100	100	100	100	100	100	COG7	P83436	14	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
NACA4P	Q9BZK3	72	6.425	5.279	4.601	6.957	4.471	3.427	3.058	4.422	HLA-DQA2	P01906	9	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
IL1A	P01583	55	3.724	6.176	2.408	8.27	2.735	7.204	2.458	6.856	CARD6	Q9BX69	8	0.01	0.256	0.175	0.296	0.01	0.296	0.203	0.338
CDK4	P11802	38	100	100	100	100	100	100	100	100	MT1F	P04733	7	0.01	0.49	0.01	0.01	0.01	0.383	0.01	0.01
HMGAA2	P52926	20	100	100	100	100	100	100	100	100	LYZ	P61626	5	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
NPL	Q9BXD5	16	2.756	4.714	4.542	6.063	100	100	100	100	PKIG	Q9Y2B9	5	0.01	0.173	0.156	0.163	0.01	0.154	0.139	0.145
MRPS18C	Q9Y3D5	16	6.148	2.272	3.244	2.3	3.153	2.025	2.692	2.316	PHACTR4	Q8IZ21	5	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
EIF1AD	Q8N9N8	15	100	100	100	100	100	100	100	100											
MOCS3	O95396	15	100	100	100	100	100	100	100	100											
INTS14	Q96SY0	15	100	100	100	100	100	100	100	100											
OXSM	Q9NWU1	12	100	100	100	100	100	100	100	100											
CDS2	O95674	12	3.557	2.411	3.759	5.284	100	100	100	100											
S100A16	Q96FQ6	7	100	100	100	100	100	100	100	100											
UNK	Q9C0B0	7	100	100	100	100	100	100	100	100											
GEMIN2	O14893	5	6.763	2.568	2.689	2.97	15.896	7.301	7.646	8.443											
LRP10	Q7Z4F1	5	100	100	100	100	100	100	100	100											
TVP23C	Q96ET8	5	19.576	2.569	2.437	2.022	100	100	100	100											

Table S5 Targeted Proteomics of commonly up-regulated proteins in the four subtypes of M2 macrophages

Gene Name	Accession	Peptide Sequence	Precursor <i>m/z</i>	Abundance (PRM)					
				M0	M1	M2a	M2b	M2c	M2d
ACTG1	P63261	MEEEEIALVIDNGSGMCK	1004.9549++	362744	1282108	8810688	5483603	3785535	5656159
ITGAV	P06756	IYIGDDNPLTLIVK	787.4454++	1977316	3842934	15374011	12261451	18587204	15134024
IVNS1ABP	Q9Y6Y0	MMGNMTSPR	512.7223++	1074521	1898108	4299042	4353469	4152663	5721726
IL1A	P01583	SAPFSFLSNVK	598.8191++	1311696	967674	13537409	10937382	18544132	10277334
TIMP1	P01033	GFQALGDAADIR	617.3148++	8199097	9197439	34273236	26055910	19368980	23149502

Table S6 Spescailly regulated proteins in M2a, M2d, M2c, or M2d macrophages

Abundance ratio of uniquely up-regulated proteins in M2a macropphages								Abundance ratio of uniquely down-regulated proteins in M2a macropphages							
Gene Name	Accession	PSMs	M2a/M0	M2a/M1	M2a/M2b	M2a/M2c	M2a/M2d	Gene Name	Accession	PSMs	M2a/M0	M2a/M1	M2a/M2b	M2a/M2c	M2a/M2d
FABP4	P15090	2459	9.367	15.981	18.623	2.703	20.723	CSTA	P01040	147	0.225	0.056	0.105	0.241	0.055
TGM2	P21980	529	27.503	7.17	4.661	10.687	7.542	SESN2	P58004	27	0.258	0.32	0.36	0.378	0.349
HSP90AB4P	Q58FF6	470	2.314	4.125	100	2.119	2.42	FCGR1A	P12314	40	0.278	0.325	0.492	0.443	0.417
ITGAM	P11215	387	13.647	17.699	11.094	2.228	10.694	UPF3B	Q9BZI7	34	0.327	0.495	0.461	0.234	0.334
ALDH1A2	O94788	255	10.496	29.821	8.174	21.45	14.212	IFI44	Q8TCB0	15	0.01	0.01	0.058	0.01	0.01
NES	P48681	165	2.9	2.666	5.413	2.714	4.23	ABTB1	Q969K4	14	0.01	0.01	0.01	0.01	0.01
DBN1	Q16643	138	3.007	12.353	2.691	2.26	7.257	GCH1	P30793	21	0.01	0.01	0.01	0.01	0.01
ABCB1	P08183	103	2.408	2.444	4.421	2.086	3.955	ZMYM4	Q5VZL5	11	0.01	0.01	0.01	0.01	0.01
CBR3	O75828	102	4.047	3.564	3.309	2.803	5.331	RSRC2	Q7L4I2	41	0.01	0.01	0.01	0.01	0.01
CAMK2A	Q9UQM7	85	3.669	2.672	8.616	2.991	4.357	PTPRA	P18433	38	0.151	0.233	0.268	0.088	0.385
SLC27A3	Q5K4L6	80	2.677	2.499	5.641	2.964	3.517	TLE4	Q04727	22	0.01	0.01	0.01	0.01	0.01
SLC5A3	P53794	61	2.749	10.49	2.448	4.263	4.177	NXN	Q6DKJ4	14	0.01	0.01	0.01	0.01	0.01
CTTN	Q14247	50	4.415	3.103	2.276	2.568	2.671	CLK3	P49761	18	0.01	0.01	0.01	0.01	0.01
CD209	Q9NNX6	50	2.553	3.871	5.887	5.335	6.55	CREBBP	Q92793	22	0.01	0.01	0.01	0.01	0.01
SERPINB4	P48594	44	5.278	15.503	5.222	100	2.744	UBP1	Q9NZI7	13	0.01	0.01	0.01	0.01	0.01
CRABP2	P29373	40	22.347	10.471	100	17.649	32.319	CARD6	Q9BX69	8	0.01	0.01	0.01	0.01	0.01
PKIB	Q9C010	27	3.143	5.732	2.941	2.643	2.336	CHURC1	Q8WUH1	30	0.01	0.01	0.01	0.01	0.01
RDH10	Q8IZV5	26	3.566	2.653	2.852	2.119	3.544	PLD4	Q96BZ4	16	0.01	0.01	0.01	0.01	0.01
TTN	Q8WZ42	24	100	100	100	2.135	100	FAM126A	Q9BYI3	11	0.01	0.01	0.01	0.01	0.01
SPINT1	O43278	14	3.251	3.361	100	2.196	6.447	PARL	Q9H300	13	0.354	0.028	0.395	0.498	0.437
PIK3R2	O00459	13	2.29	100	4.098	5.675	100	MAFB	Q9Y5Q3	8	0.01	0.01	0.01	0.01	0.01
AP1G2	O75843	13	100	3.587	2.705	100	100	CDC42SE1	Q9NRR8	18	0.01	0.01	0.01	0.01	0.01
SPATA5L1	Q9BVQ7	11	100	100	100	100	100	HELZ	P42694	6	0.01	0.01	0.01	0.01	0.01
FCRLA	Q7L513	10	100	100	2.175	3.594	100	WDR45	Q9Y484	5	0.183	0.5	0.146	0.268	0.233
C7orf50	Q9BRJ6	9	6.419	100	100	3.535	3.853	LYSMD2	Q8IV50	9	0.01	0.01	0.01	0.01	0.01
S100A16	Q96FQ6	7	100	100	3.799	7.033	6.308	TMEM199	Q8N511	14	0.01	0.01	0.01	0.01	0.01
REEP6	Q96HR9	6	3.621	100	100	100	100	RETREG2	Q8NC44	14	0.01	0.01	0.01	0.01	0.01
PEX13	Q92968	5	100	100	100	100	100	SLC15A4	Q8N697	12	0.01	0.01	0.01	0.01	0.01
SEZ6L2	Q6UXD5	5	8.452	100	100	6.017	100	UBE2D1	P51668	8	0.01	0.01	0.01	0.01	0.01
								MRPS10	P82664	9	0.01	0.01	0.01	0.01	0.01
								SCAMP4	Q969E2	5	0.01	0.01	0.01	0.01	0.01
								ZNF579	Q8NAF0	8	0.01	0.01	0.01	0.01	0.01
								PROCR	Q9UNN8	6	0.01	0.01	0.01	0.01	0.01
								GEM	P55040	9	0.01	0.01	0.01	0.01	0.01
								DOCK6	Q96HP0	18	0.01	0.01	0.01	0.01	0.01
								PKIG	Q9Y2B9	5	0.01	0.01	0.01	0.01	0.01

Abundance ratio of uniquely up-regulated proteins in M2b macropphages								Abundance ratio of uniquely down-regulated proteins in M2b macropphages							
Gene Name	Accession	PSMs	M2b/M0	M2b/M1	M2b/M2a	M2b/M2c	M2b/M2d	Gene Name	Accession	PSMs	M2b/M0	M2b/M1	M2b/M2a	M2b/M2c	M2b/M2d
CTSD	P07339	428	2.698	8.32	4.867	3.492	2.391	HSP90AB4P	Q58FF6	470	0.01	0.01	0.01	0.01	0.01
PLIN2	Q99541	318	8.991	3.8	3.734	2.125	2.232	SLC1A4	P43007	43	0.01	0.01	0.01	0.01	0.01
MMP9	P14780	206	6.651	7.993	6.68	3.154	2.349	CRABP2	P29373	40	0.01	0.01	0.01	0.01	0.01
HBA1	P69905	127	2.136	3.463	4.124	7.374	2.418	TACC2	O95359	36	0.01	0.01	0.01	0.01	0.01
THBS1	P07996	81	3.878	3.511	4.216	3.779	2.341	LIMK2	P53671	35	0.2	0.143	0.099	0.481	0.5
PKLR	P30613	50	100	100	2.101	100	100	NBEAL2	Q6ZNJ1	32	0.01	0.01	0.01	0.01	0.01
HBD	P02042	49	2.941	4.837	5.823	10.997	3.946	SCARB1	Q8WTV0	20	0.01	0.01	0.01	0.01	0.01
PLG	P00747	25	2.258	5.639	100	100	2.851	RBCK1	Q9BYM8	19	0.01	0.01	0.01	0.01	0.01
SLC7A11	Q9UPY5	19	100	5.499	10.033	100	2.136	ZNRF2	Q8NHG8	17	0.01	0.01	0.01	0.01	0.01
C4orf3	Q8WVX3	17	8.659	8.073	6.902	6.7	8.069	CYP51A1	Q16850	17	0.01	0.01	0.01	0.01	0.01
BOD1L1	Q8NFC6	12	100	100	100	100	100	SLC38A1	Q9H2H9	17	0.01	0.01	0.01	0.01	0.01
DNAJC19	Q96DA6	11	3.134	100	4.251	2.817	3.204	RBM33	Q96EV2	16	0.01	0.01	0.01	0.01	0.01
								RNF113A	O15541	16	0.01	0.01	0.01	0.01	0.01
								CCR1	P32246	16	0.242	0.438	0.494	0.195	0.369
								INTS5	Q6P9B9	14	0.01	0.01	0.01	0.01	0.01
								SPINT1	O43278	14	0.01	0.01	0.01	0.01	0.01
								TMEM59	Q9BXS4	13	0.01	0.01	0.01	0.01	0.01
								MOB2	Q70IA6	13	0.01	0.01	0.01	0.01	0.01
								KIAA0391	O15091	12	0.01	0.01	0.01	0.01	0.01
								SH2B2	O14492	12	0.01	0.01	0.01	0.01	0.01
								RHBDD2	Q6NTE9	12	0.01	0.01	0.01	0.01	0.01
								MPHOSPH8	Q99549	11	0.01	0.01	0.01	0.01	0.01
								PNKD	Q8N490	10	0.01	0.01	0.01	0.01	0.01
								GPATCH8	Q9UKJ3	10	0.01	0.01	0.01	0.01	0.01

	ANO10	Q9NW15	10	0.01	0.01	0.01	0.01	0.01
	CEP85	Q6P2H3	9	0.01	0.01	0.01	0.01	0.01
	EEFSEC	P57772	8	0.01	0.01	0.01	0.01	0.01
	RIN3	Q8TB24	8	0.01	0.01	0.01	0.01	0.01
	ATP11C	Q8NB49	7	0.01	0.01	0.01	0.01	0.01
	MRPL32	Q9BYC8	7	0.01	0.01	0.01	0.01	0.01
	NDUFA1	O15239	7	0.01	0.01	0.01	0.01	0.01
	RCL1	Q9Y2P8	6	0.01	0.01	0.01	0.01	0.01
	NFATC2	Q13469	6	0.01	0.01	0.01	0.01	0.01
	RIOX1	Q9H6W3	6	0.01	0.01	0.01	0.01	0.01

Abundance ratio of uniquely up-regulated proteins in M2c macrophages								Abundance ratio of uniquely down-regulated proteins in M2c macrophages							
Gene Name	Accession	PSMs	M2c/M0	M2c/M1	M2c/M2a	M2c/M2b	M2c/M2d	Gene Name	Accession	PSMs	M2c/M0	M2c/M1	M2c/M2a	M2c/M2b	M2c/M2d
ITGB5	P18084	156	3.14	2.413	2.114	3.769	2.115	NCF2	P19878	282	0.454	0.223	0.458	0.415	0.483
PABPC1L	Q4VXU2	105	2.044	100	100	2.534	3.904	CPM	P14384	183	0.162	0.218	0.441	0.3	0.111
MSR1	P21757	71	3.581	4.164	2.351	4.902	3.265	LIMS2	Q7Z4I7	103	0.01	0.01	0.01	0.01	0.01
PYCR1	P32322	24	3.145	2.129	3.713	2.324	3.31	PZP	P20742	60	0.01	0.083	0.184	0.16	0.192
PLD4	Q96BZ4	16	2.188	4.339	100	4.204	3.797	MT2A	P02795	55	0.056	0.029	0.18	0.078	0.038
DYSF	O75923	15	100	100	100	100	100	F2	P00734	51	0.433	0.262	0.309	0.136	0.221
SESN1	Q9Y6P5	8	100	100	100	100	100	SMG9	Q9H0W8	49	0.01	0.01	0.01	0.01	0.01
								HBD	P02042	49	0.246	0.454	0.499	0.091	0.367
								ZEB2	O60315	45	0.01	0.01	0.01	0.01	0.01
								SERPINB4	P48594	44	0.01	0.01	0.01	0.01	0.01
								RCOR3	Q9P2K3	43	0.01	0.01	0.01	0.01	0.01
								PSEN1	P49768	37	0.01	0.01	0.01	0.01	0.01
								UBE2E1	P51965	34	0.01	0.01	0.01	0.01	0.01
								SEMA7A	O75326	29	0.01	0.01	0.01	0.01	0.01
								UGGT2	Q9NYU1	29	0.01	0.01	0.01	0.01	0.01
								CXCL8	P10145	25	0.01	0.01	0.01	0.01	0.01
								SLAMF7	Q9NQ25	24	0.01	0.01	0.01	0.01	0.01
								WIP12	Q9Y4P8	23	0.01	0.01	0.01	0.01	0.01
								GRAMD1A	Q96CP6	22	0.01	0.01	0.01	0.01	0.01
								MICU2	Q8IYU8	20	0.01	0.01	0.01	0.01	0.01
								PLEKHF2	Q9H8W4	19	0.01	0.01	0.01	0.01	0.01
								ASRGL1	Q7L266	16	0.01	0.01	0.01	0.01	0.01
								TIFA	Q96CG3	16	0.01	0.01	0.01	0.01	0.01
								GGA3	Q9NZ52	15	0.01	0.01	0.01	0.01	0.01
								APOO	Q9BUR5	15	0.01	0.01	0.01	0.01	0.01
								RIF1	Q5UIP0	14	0.01	0.01	0.01	0.01	0.01
								POLD3	Q15054	13	0.01	0.01	0.01	0.01	0.01
								VRK2	Q86Y07	13	0.01	0.01	0.01	0.01	0.01
								GGA2	Q9UJY4	12	0.01	0.01	0.01	0.01	0.01
								EHHADH	Q08426	12	0.01	0.01	0.01	0.01	0.01
								FRY	Q5TBA9	10	0.01	0.01	0.01	0.01	0.01
								POFUT2	Q9Y2G5	10	0.01	0.01	0.01	0.01	0.01
								TWISTNB	Q3B726	8	0.01	0.01	0.01	0.01	0.01
								RNF126	Q9BV68	7	0.01	0.01	0.01	0.01	0.01
								MED20	Q9H944	7	0.01	0.01	0.01	0.01	0.01
								IL17RA	Q96F46	7	0.01	0.01	0.01	0.01	0.01
								ACSF2	Q96CM8	6	0.01	0.01	0.01	0.01	0.01
								URB1	O60287	6	0.01	0.01	0.01	0.01	0.01

Abundance ratio of uniquely up-regulated proteins in M2d macrophages								Abundance ratio of uniquely down-regulated proteins in M2d macrophages							
Gene Name	Accession	PSMs	M2d/M0	M2d/M1	M2d/M2a	M2d/M2b	M2d/M2c	Gene Name	Accession	PSMs	M2d/M0	M2d/M1	M2d/M2a	M2d/M2b	M2d/M2c
PLAU	P00749	63	11.351	12.919	7.924	2.163	4.225	GDF15	Q99988	148	0.082	0.361	0.223	0.332	0.256
METTL1	Q9UBP6	26	5.296	3.489	4.016	3.397	2.654	NCALD	P61601	102	0.01	0.01	0.01	0.01	0.01
MMP1	P03956	19	3.229	3.877	6.665	4.211	4.447	MKI67	P46013	27	0.01	0.01	0.01	0.01	0.01
IL36G	Q9NZH8	16	100	100	100	3.764	100	ATF3	P18847	22	0.287	0.245	0.402	0.39	0.299
RIF1	Q5UIP0	14	6.865	9.452	2.241	2.723	100	PHRF1	Q9P1Y6	21	0.01	0.01	0.01	0.01	0.01
BCAT2	O15382	12	100	100	100	100	100	DMAP1	Q9NPF5	20	0.01	0.01	0.01	0.01	0.01
SSBP4	Q9BWG4	12	2.007	2.871	3.263	5.684	2.199	WDR74	Q6RFH5	14	0.01	0.01	0.01	0.01	0.01
KAT7	O95251	11	2.136	100	100	100	100	HOMER2	Q9NSB8	14	0.01	0.01	0.01	0.01	0.01
PNKD	Q8N490	10	2.021	2.579	2.896	100	2.248	DMXL2	Q8TDJ6	12	0.01	0.01	0.01	0.01	0.01
L3MBTL3	Q96JM7	6	4.349	2.525	8.056	3.948	2.343	VLDLR	P98155	12	0.01	0.01	0.01	0.01	0.01
PHLPP1	O60346	5	10.428	100	100	100	100	PARP4	Q9UKK3	12	0.01	0.01	0.01	0.01	0.01
								TIMM17A	Q99595	12	0.42	0.321	0.259	0.307	0.351

	BST2	Q10589	10	0.01	0.01	0.01	0.01	0.01
	TPRN	Q4KMQ1	9	0.01	0.01	0.01	0.01	0.01
	MGMT	P16455	9	0.01	0.01	0.01	0.01	0.01
	LIG4	P49917	8	0.01	0.01	0.01	0.01	0.01
	ATP9A	O75110	8	0.01	0.01	0.01	0.01	0.01
	REEP3	Q6NUK4	7	0.01	0.01	0.01	0.01	0.01
	SFT2D3	Q587I9	7	0.01	0.01	0.01	0.01	0.01
	SYNRG	Q9UMZ2	6	0.01	0.01	0.01	0.01	0.01

Table S7 Targeted Proteomics of specially up-regulated proteins in M2a, M2d, M2c or M2d macrophages

Subtype	Gene Name	Accession	Peptide Sequence	Precursor <i>m/z</i>	Abundance (PRM)					
					M0	M1	M2a	M2b	M2c	M2d
M2a	FABP4	P15090	NTEISFILGQEFDEVTADDRK	809.7273+++	16159521	83482168	656530752	12956103	248498448	36728816
	ITGAM	P11215	SLPISLVFLVPVR	720.4529++	943946	2928009	47275260	3265412	16111452	4681101
	ALDH1A2	O94788	IAKEEIFGPVQEILR	581.3331+++	366353	1255891	44272448	888554	2179588	995264
	NES	P48681	SLEEEGQELPQSADVQR	957.9556++	289216	285346	8496107	857652	3009295	254469
	DBN1	Q16643	SPSDSSTASTPVAEQIER	931.4423++	9443238	1876362	27935518	2794280	13103931	2468363
	ABCB1	P08183	AGAVAEEVLAAIR	635.3617++	2676726	3830552	8902299	2743171	3712716	1530318
M2b	CTSD	P07339	LSPEDYTLK	533.2768++	54119924	26205206	43154536	205927360	46921812	73517744
	PLIN2	Q99541	SVVSGSINTVLGSR	688.3806++	9077852	15202454	15386712	42542376	12161696	17683226
	MMP9	P14780	EYSTCTSEGR	595.2431++	2125408	1927419	1773403	17691928	3105160	5582624
	HBA1	P69905	VGAHAGEYGAEALER	765.3708++	41731816	53172464	53946728	125338600	18441724	42239788
	THBS1	P07996	DFTAYR	386.6849++	533320	490753	544292	3950485	1034041	1587976
	PLG	P00747	TPENFPCK	496.7289++	8489514	6751698	3994107	17086568	2313595	6092429
M2c	ITGB5	P18084	HTEHVFALRPVGFR	417.2298++++	488901	606698	4059312	1500895	9553942	1544251
	PABPC1L	Q4VXU2	ALYDTFSTFGNILSCK	918.9455++	62117	659979	661710	117522	2194506	456339
	MSR1	P21757	FQEVFMEHMSNMEK	596.2581+++	506570	189879	1260411	290142	2716296	29143
M2d	PLAU	P00749	VSHFLPWIR	385.5538+++	118928	91845	222430	1896810	194236	3223694
	METTL1	Q9UBP6	IISPTLLAEYAYVLR	574.6661+++	229019	838849	123542	782986	901911	2691831
	RIF1	Q5UIP0	ELDPSLVSANDSPSGMQTR	1002.4706++	497368	238900	457600	569794	368535	1265367
	KAT7	O95251	SQQQPTPVTPK	605.8250++	434856	346865	281474	389469	428210	1270961

Table S8 Disease correlation analysis of four M2 macrophage subtypes.

The top 5 most relevant diseases predicted by uniquely regulated proteins and associated proteins of M2a macrophages.			
Rank	Disease name	Counts	Genes
1	Ras- Associated Autoimmune Leukoproliferative Disorder	3	ALDH1A2, CRABP2, RDH10
2	Thrombocytopenia	4	ABCB1, CD209, FCGR1A, ITGAM
3	Inflammatory Bowel Disease	5	ABCB1, CD209, FCGR1A, ITGAM, PROCR
4	Systemic Lupus Erythematosus	6	ITGAM, IFI44, FCGR1A, PROCR, SLC15A4, ABCB1
5	Breast Cancer	7	ABCB1, CTTN, FABP4, PIK3R2, SESN2, TLE4, GCH1

The top 5 most relevant diseases predicted by uniquely regulated proteins and associated proteins of M2b macrophages.			
Rank	Disease name	Counts	Genes
1	Hemolytic Anemia	3	ATP11C, HBA1, PKLR
2	Congenital Hemolytic Anemia	4	ATP11C, HBA1, HBD, PKLR
3	Hepatitis C Virus	4	C4ORF3, PNKD, SCARB1, HBD
4	Multiple Sclerosis	5	BOD1L1, HBD, CCR1, MMP9, RNF113A
5	Breast Cancer	6	CTSD, MMP9, PLG, TACC2, THBS1, HBD

The top 5 most relevant diseases predicted by uniquely regulated proteins and associated proteins of M2c macrophages.			
Rank	Disease name	Counts	Genes
1	Multiple Sclerosis	3	CXCL8, HBD, RIF1
2	Breast Cancer	3	MSR1, CXCL8, HBD
3	Systemic Lupus Erythematosus	4	CXCL8, F2, SLAMF7, MT2A
4	Hepatitis C Virus	5	SLAMF7, CXCL8, HBD, MSR1, PZP
5	Dilated Cardiomyopathy	5	PSEN1, CXCL8, F2, ITGB5, LIMS2

The top 5 most relevant diseases predicted by uniquely regulated proteins and associated proteins of M2d macrophages.			
Rank	Disease name	Counts	Genes
1	Immune Deficiency Disease	2	BST2, LIG4
2	B-Cell Lymphoma	2	MGMT, MKI67
3	Dilated Cardiomyopathy	2	GDF15, MMP1
4	Multiple Sclerosis	3	REEP3, RIF1, SYNRG
5	Breast Cancer	4	GDF15, MKI67, MMP1, ATF3