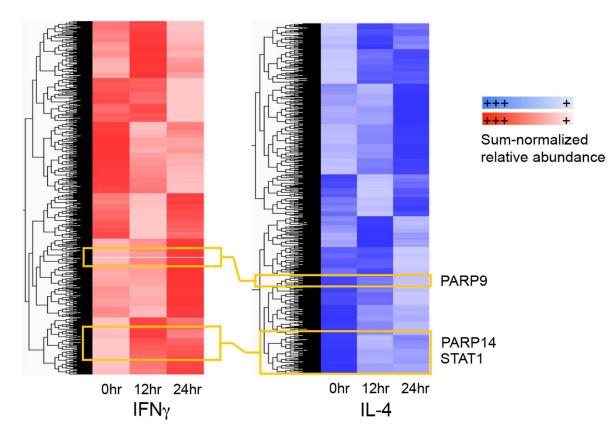


Supplementary Figure 1: Tandem mass tagging (TMT)-6plex global proteomics dataset

analyses. (a) Overview of the TMT strategy that labels six time points, for example, in the IL-4 stimulation experiment for mass spectrometric analysis. Whole cell lysate proteomes were insolution proteolyzed with Lys-C endopeptidase and labeled with one of six TMT-6plex reporter tags (colored circles). The labeled peptides were then pooled for isoelectric focusing into 24 fractions (b) subsequent mass spectrometric analysis of each fraction. (c) Each fraction was then analyzed by LC-MS/MS for simultaneous identification and quantification of the peptides. (d) A summary of the TMT-6plex experimental designs presented in this study.

Pilot study RAW264.7 cells (n = 3017 proteins)

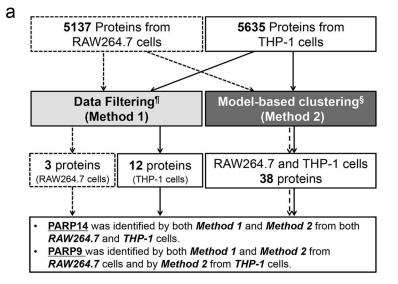


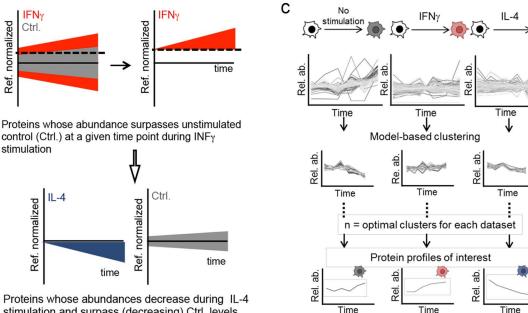
Supplementary Figure 2: Hierarchical analysis performed on the sum-normalized protein abundances from the pilot study outlined in Supplementary Fig. 1d. STAT1 was contained within clusters whose abundances increased (IFN γ) and decreased (IL-4) over the stimulation periods. PARP14 clustered with STAT1 in each experiment. PARP9 was located in clusters with similar trends as PARP14 and STAT1. Hierarchical clustering was performed using Qlucore Software (www.Qlucore.com)

b

normalized

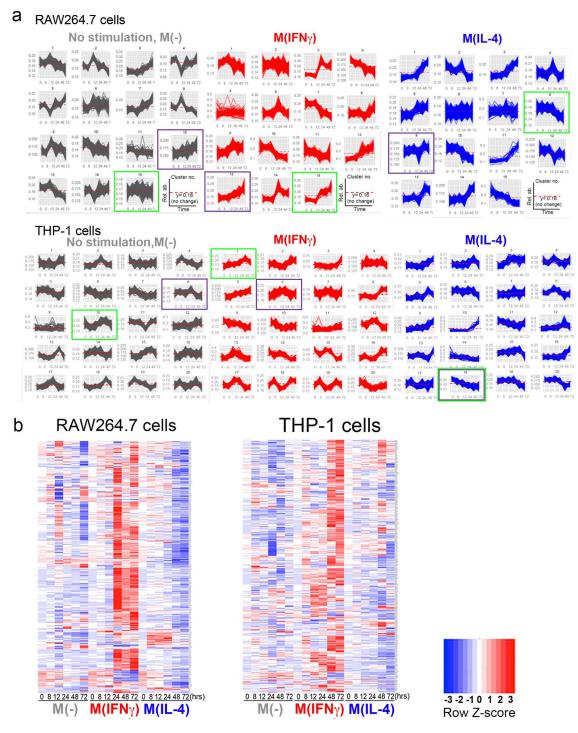
Ref.



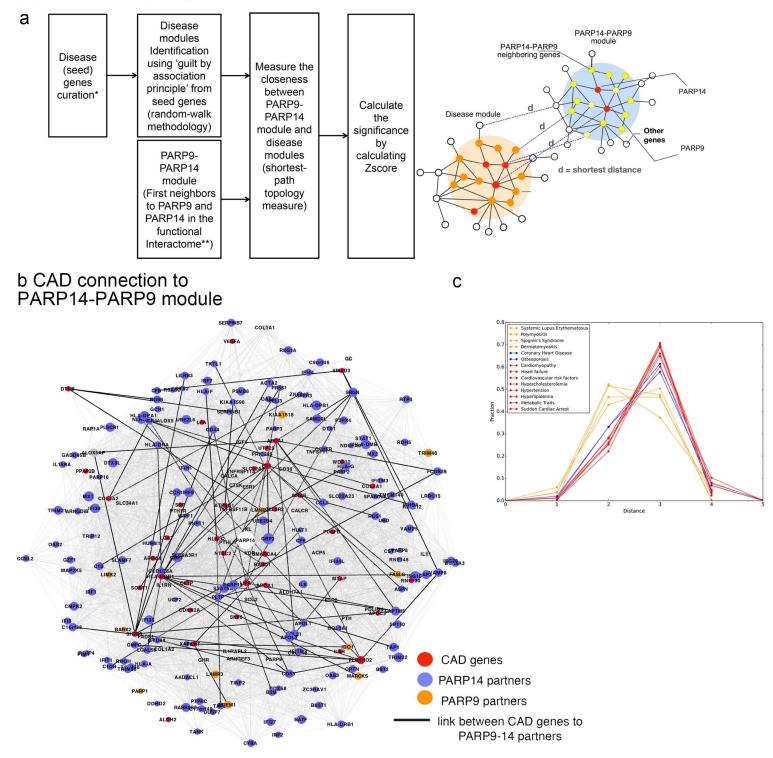


stimulation and surpass (decreasing) Ctrl. levels from 12 hours to 72 hours

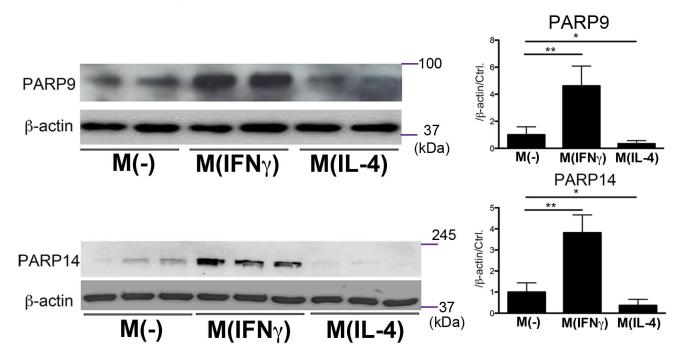
Supplementary Figure 3: A scheme for two bioinformatics methods to identify regulator protein(s) of macrophage activation. (a) Summary of the input and outputs of the data filtering and model-based clustering bioinformatics strategies. (b) Outline of the data filtering strategy that used the unstimulated control M(-) to find proteins increasing in M(IFNy) and decreasing in M(IL-4). The maximum magnitude in fold-change (positive or negative direction) of the M(-) (indicated by gray area) represents the magnitude of fluctuation in signal. First, using the dataset in IFNy stimulation (indicated by red area) against the M(-) for RAW264.7 cells, we chose a 1.34-fold cut-off since the magnitude in M(-) was maximal at this value at 8 hours. In addition, IFNy had clearly induced signal beyond the cut-off. Second, we extracted all proteins that met this criterion (n = 37). We then cross referenced the proteins in M(IL-4) (indicated by blue area) and filtered out proteins whose profiles decreased overtime. We then limited the proteins to those whose profiles were also accounted for in unstimulated control. Only three proteins, including PARP14, met these criteria. We used the same cut-off for the THP-1 cells, although THP-1 cells had a larger magnitude in M(-) fluctuation; however, the same filtering procedure only produced 12 proteins, including STAT1, PARP14 and PARP9, as final candidates. (c) Modelbased clustering of proteins accounts for the variance within each dataset, and then assumes that each protein abundance profile is derived from a mixture of underlying populations, each corresponding to a group or cluster We examined the clusters in each dataset and searched for clusters whose abundances increased over time in M(IFN_Y) and decreased over time in M(IL-4), but whose abundances did not change over time in M(-).



Supplementary Figure 4: Model-based clustering output for RAW264.7 and THP-1 TMT-6plex proteomics studies. M(-), grey; M(IFN γ), red; M(IL-4) blue traces. y-axis - the sum normalized relative abundance; x-axis – the time points after stimulation collected for TMT analysis. The dashed red line indicates the y = 0.16 threshold (i.e., sum-normalized no change). The location of PARP14 and PARP9 are indicated. (b) Hierarchical clustering of 490 and 414 proteins from identified in datasets of RAW264.7 cells and THP-1 cells, respectively. List of proteins are shown in the Supplementary Table 3.

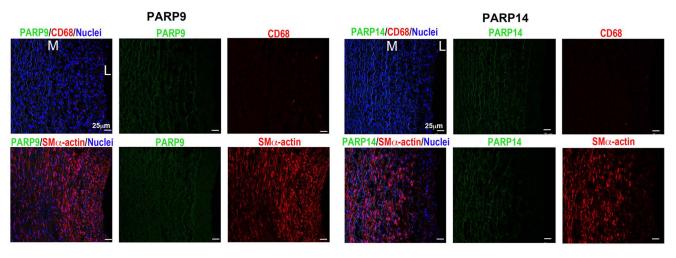


Supplementary Figure 5: Closeness between PARP9 and PARP14 module and disease modules (a) A workflow of network analysis to measure the closeness between the PARP9-PARP14 module (blue circle) and an example disease module (orange circle). **(b)** Connection of the PARP9-PARP14 module to CAD genes in the interactome. **(c)** Distribution of shortest distances between each disease module and the PARP9-PARP14 module. *: coronary artery diseases (CAD), osteoporosis, polymyositis (PM), dermatomyositis (DM), systemic lupus erythematous (SLE), metabolic traits, cardiovascular risk factor, hyperlipidemia, hyperchlestrolemia, hypertension, cardiomyopathy and sudden cardiac arrest **: GWAS, OMIM and MalaCards



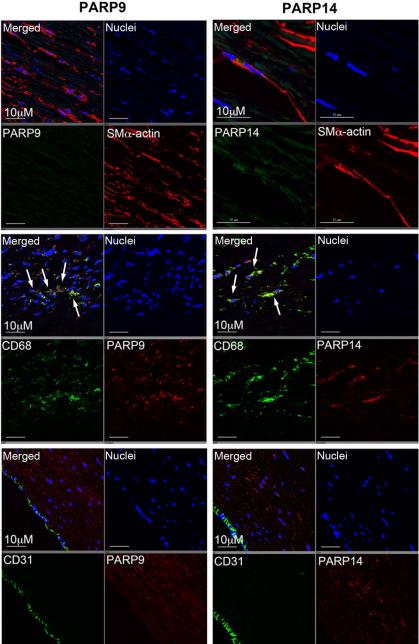
Supplementary Figure 6: PARP9 and PARP14 protein expression in M(-), M(IFN γ) **and M(IL-4).** Western blotting of PARP9 and PARP14 protein expression in THP-1 cells under stimulation for 24 hours (left panels), and their quantification (right panels) (n = 4).

Normal carotid artery, PARP9, PARP14 and CD68 а

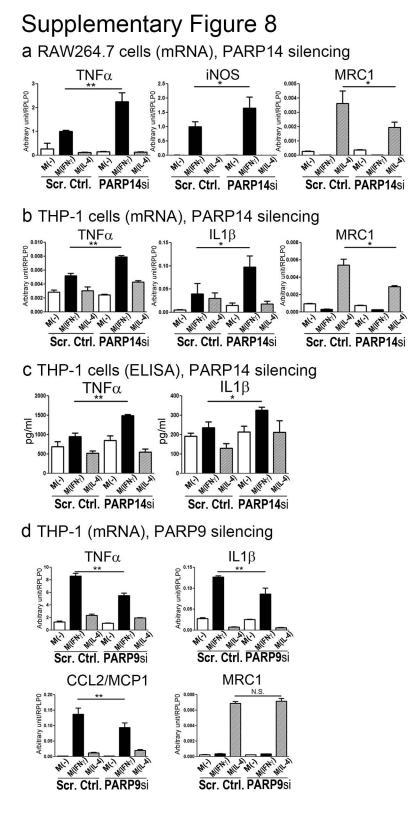


Carotid artery plaque, PARP9, PARP14 and SMa-actin/ CD68/ CD31 b

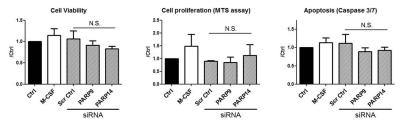
PARP9



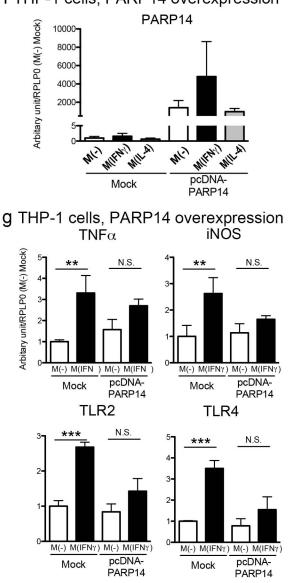
Supplementary Figure 7: PARP9 and PARP14 expression in nondiseased and diseased carotid arteries (a) PARP9 and PARP14 expression in carotid arteries without no apparent atherosclerotic changes in combination with CD68. Scale bars indicate 25µm. (b) PARP9 and PARP14 expression in atherosclerotic carotid arteries in combination with SMa-actin, CD31 and CD68. Scale bars: 10 µm. Arrows indicate co-localized signal.



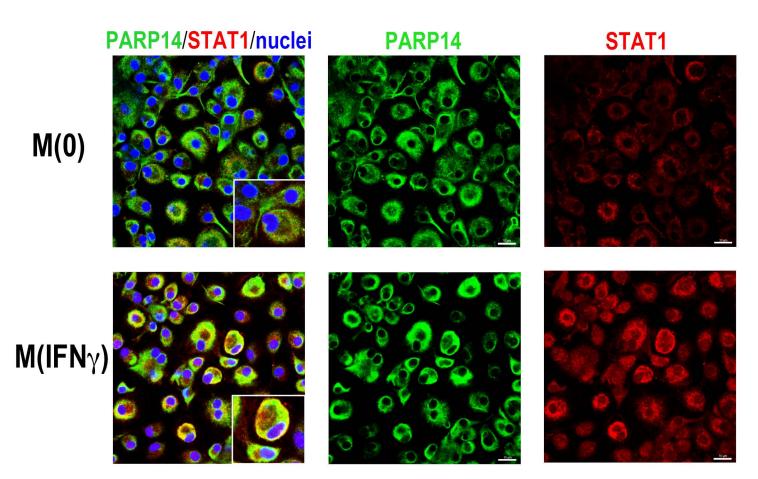
e THP1 cells (cell function), PARP9 and14 silencing



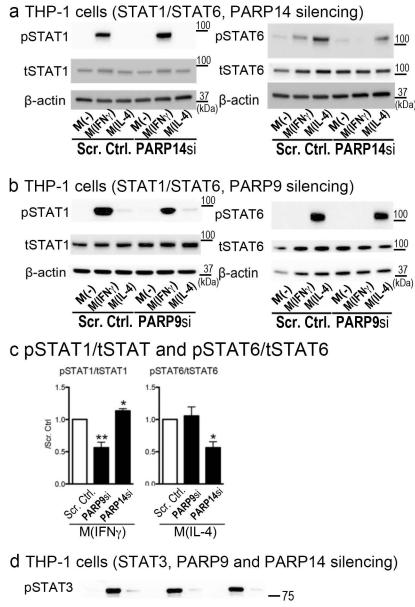
f THP-1 cells, PARP14 overexpression

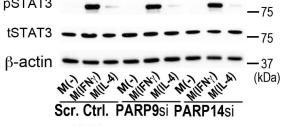


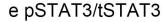
Supplementary Figure 8: The molecular functions of PARP14 and PARP9 in macrophage activation in vitro. (a, b) The consequence of PARP14 silencing on IFN γ pathway (TNF α , iNOS and IL-1 β) and IL-4 pathway (MRC1) gene expression (n = 3) in mouse RAW264.7 and human THP-1 cells. (c) PARP14 silencing increased expression levels of TNF α and IL-1 β proteins in the media of THP-1 cells (n = 3). (d) The consequence of PARP9 silencing on IFN_γ pathway (TNFα, IL-1β and CCL2/MCP1) and IL-4 pathway (MRC1) gene expression in THP-1 cells (n = 3). (e) PARP14 and PARP 9 silencing had no significant effects on viability, proliferation and apoptosis of mouse bone marrow-derived macrophages (n = 3). (f and g) Enforced expression of PARP14 in THP-1 cells increased the expression of pro-inflammatory genes TNF α , iNOS, TLR2, and TLR4 in M(IFN γ).

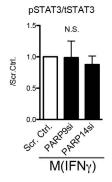


Supplementary Figure 9: Colocalization of PARP14 with STAT1 in unstimulated, M(-), and IFN γ -stimulated M(IFN γ) THP-1 cells. PARP14 (Alexa 488, green) further co-localized with STAT1 (Alexa-594, red) in the cytosol under IFN γ stimulation rather than unstimulated control. Scale bars indicate 10 μ m.





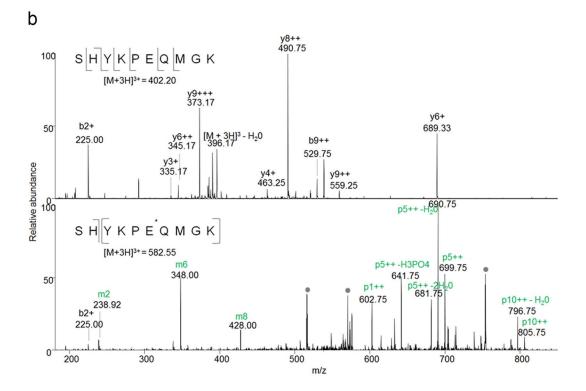




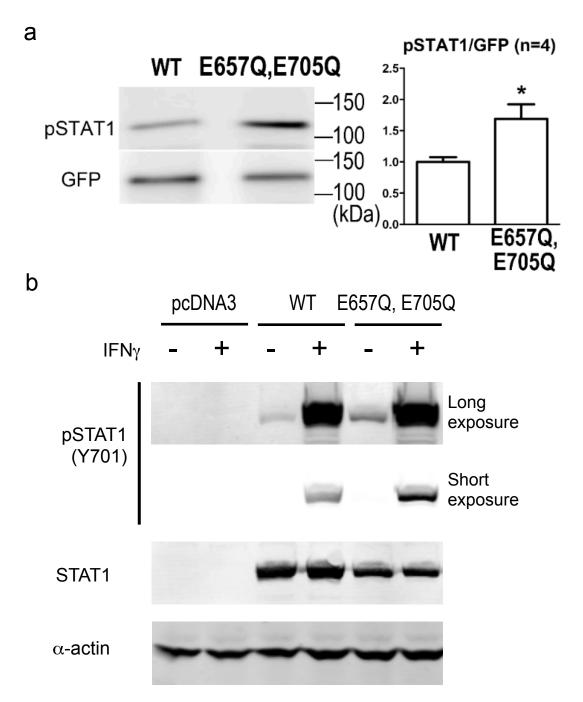
Supplementary Figure 10: The effects of PARP14 and PARP9 silencing on STAT1, 6 and 3 phosphorylation. (a) PARP14 silencing increased phosphorylation of STAT1 (pSTAT1) in IFN_γ-stimulated THP-1 cells and decreased the phosphorylation of STAT6 (pSTAT6) in IL-4stimulated THP-1 cells. (b) PARP9 silencing decreased phosphorylation of STAT1 in IFN_γ stimulated THP-1 cells, but had no effect on STAT6 in cells stimulated with IL-4 (THP-1). (c) Quantified ratios of phospho/ total STAT1 and STAT6 in PARP9 and PARP14 silencing. (n = 3) in $M(IFN\gamma)$ and M(IL-4) (d) Silencing PARP14 or PARP9 had no effect on phosphorylation of STAT3 (pSTAT3) in THP-1 cells. (e) Quantification of pSTAT3/tSTAT3 in M(-), M(IFNγ) and M(IL-4).

Supplementary Figure 11

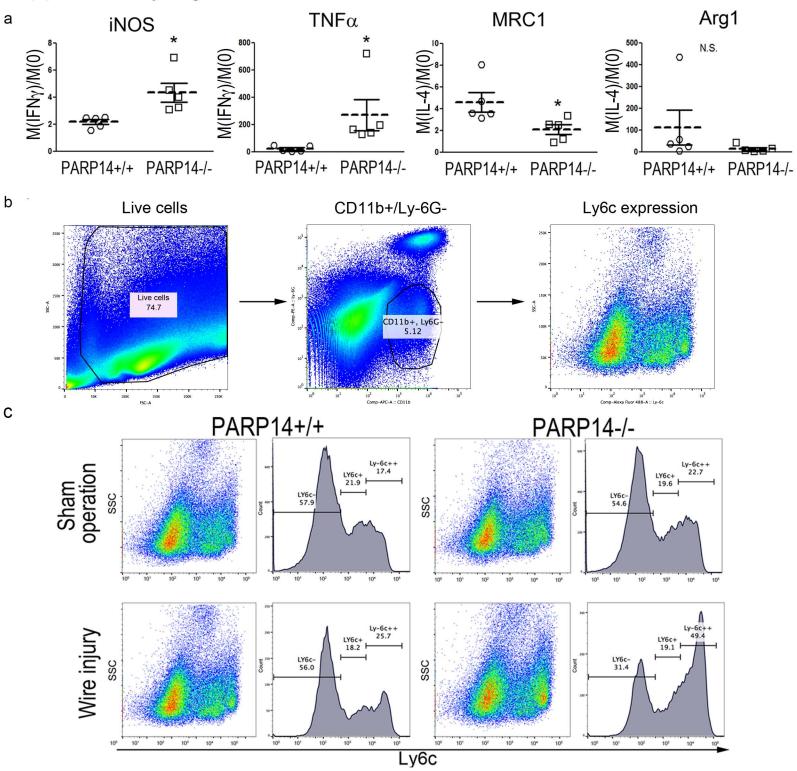




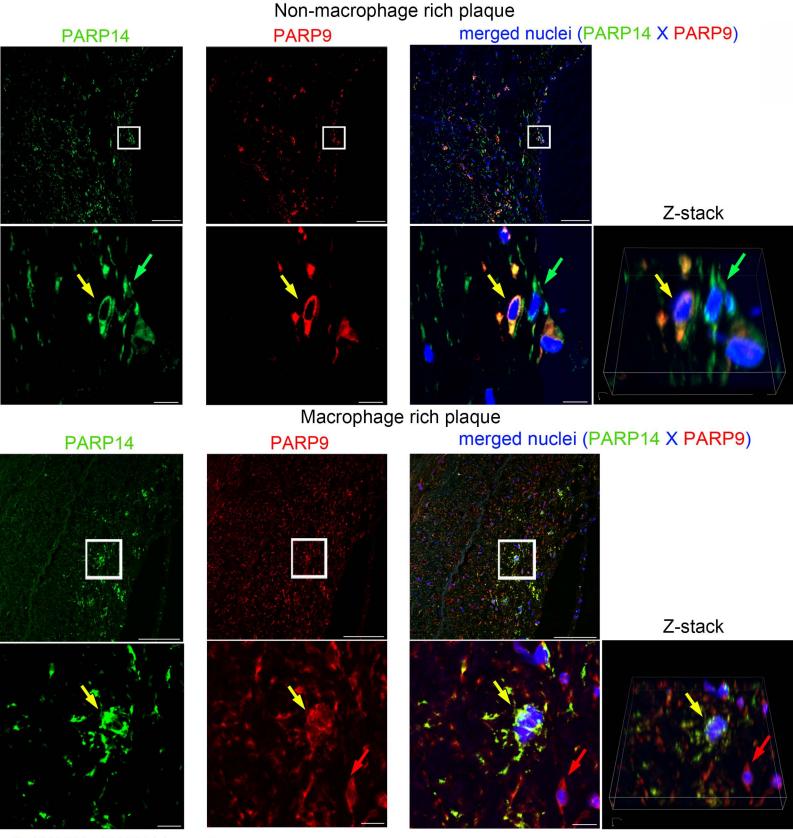
Supplementary Figure 11: Mass spectrometric-based detection of ribosylated STAT6. (a) A part of amino acid sequence of human STAT6. Green amino acids indicate the ribosylated peptide; the likely but not confirmed ribosylation site is underlined. STAT6 is known to be phosphorylated at indicated tyrosine (red). (b) MS/MS spectra for the mono-ADP-ribosylated peptide and the corresponding unmodified form. ADP-ribose fragments are annotated in green. *, likely ribosylation site; [], ribosylation moiety is contained within these amino acids, m, oxidized Met. The grey circles indicate background or undetermined ions. (c) Reference for the annotation of ADP-ribose fragment ions.



Supplementary Figure 12: The effects of wild type and mutated STAT1 on phosphorylation of STAT1 (Tyr701) HEK293 cells were transfected with wild type (WT) or mutated STAT1 (E657Q, E705Q). Two independent experiments at the Masanori Aikawa (a) and Mark Boothby (b) laboratories demonstrated similar results. * indicates p < 0.05 by Student's t-test

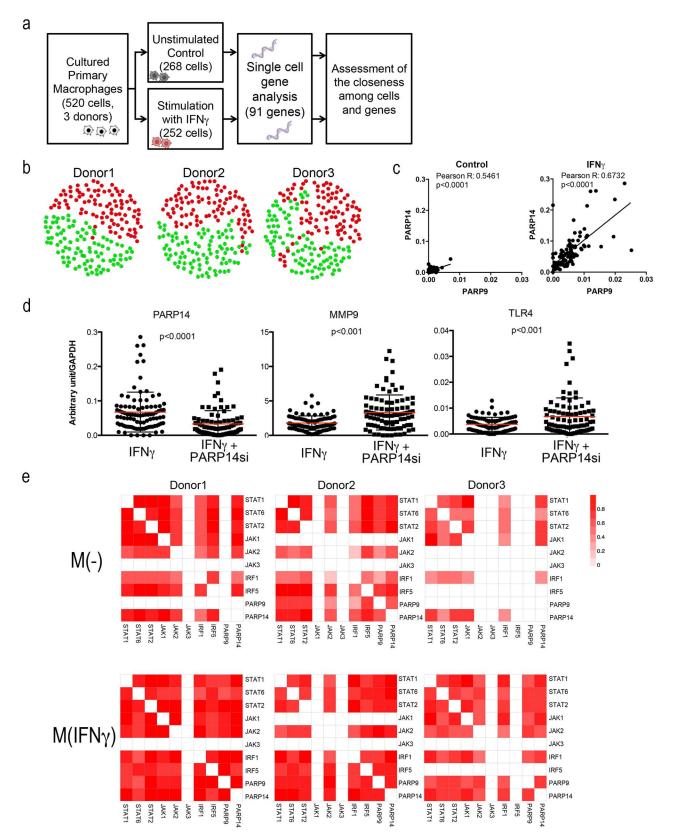


Supplementary Figure 13: Characteristics of bone marrow-derived macrophages in PARP14-/- and +/+ mice, and splenic inflammatory monocytes/macrophages (a) IFN γ - and IL-4-pathway gene expression data from bone marrow derived macrophages from PARP14^{-/-} and PARP14^{+/+} mice. Each data point is the average of quadruplicate samples per donor (n = 5). * and N.S. indicate p < 0.05 and not significant by Student's t-test. (b) Ly6c expression in splenic CD11b+/LY6g- monocytes/macrophages. (c) Ly6c expression in splenic monocytes/macrophages in sham operated and animals after wire injury in PARP14^{+/+} and PARP14^{-/-} mice.

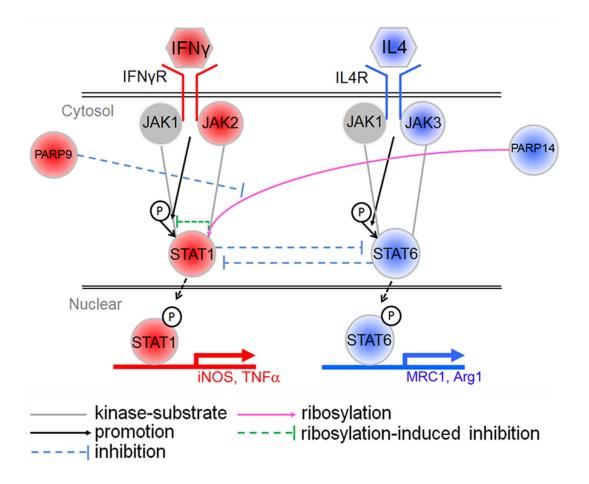


→ PARP9+/PARP14+ → PARP9-/PARP14+ → PARP9+/PARP14-

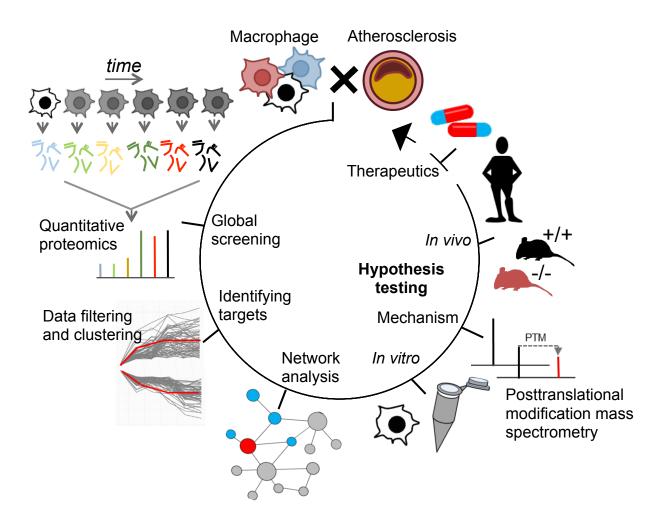
Supplementary Figure 14: Differential expression of PARP9/PARP14 in macrophage-rich and no macrophage-rich plaques. Green arrows, PARP9-/PARP14+ cells; yellow arrows, PARP9+/PARP14+ cells; red arrows: PARP9+/PARP14- cells. Scale bars indicate 10μm.



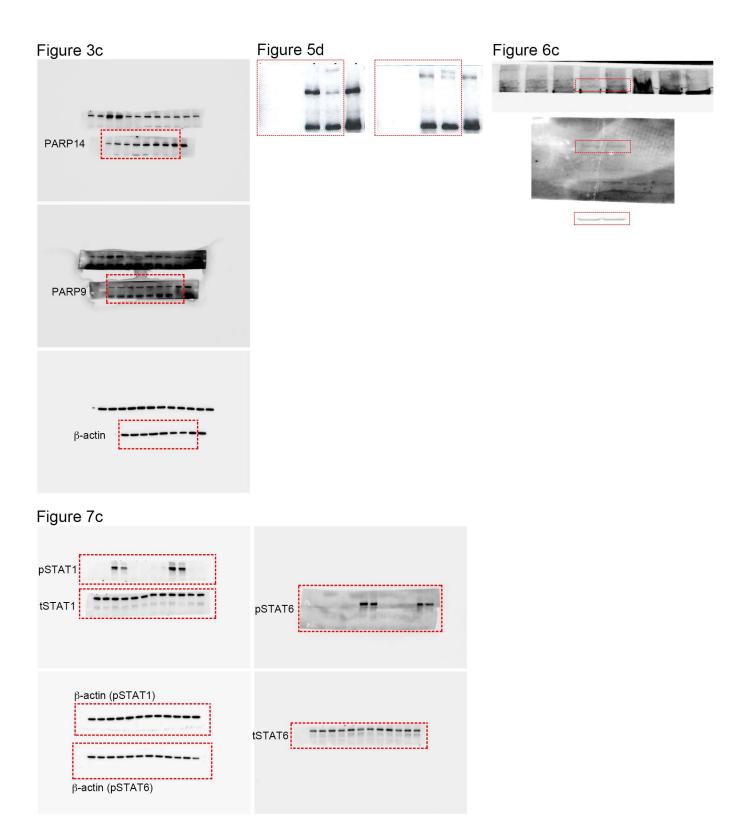
Supplementary Figure 15: Overview and additional analysis regarding heterogeneity and PARP14 function in IFN_Y-induced activation of human primary macrophages. (a) Schema of the workflow in single cell gene profiling in human primary macrophages. (b) Heterogeneity in $M(IFN_Y)$ (red) compared to M(-) (green) in individual donor samples. (c) The positive correlation of PARP9 and PARP14 gene expression at the single cell level. (d) Single cell gene analysis in $M(IFN_Y)$ with or without PARP14 silencing. (e) Similarity maps of samples from all donors (Donors 1 to 3) in both M(-) and $M(IFN_Y)$, demonstrating the closeness of genes related IFN_Y pathway in macrophages.



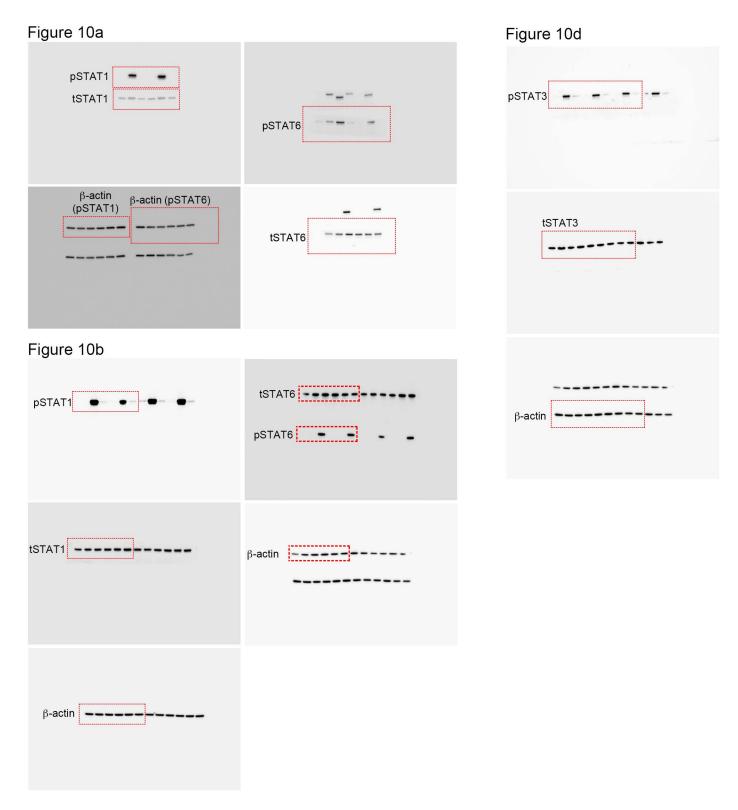
Supplementary Figure 16: A model for multidirectional macrophage activation incorporating our own novel findings on PARP14 and PARP9.



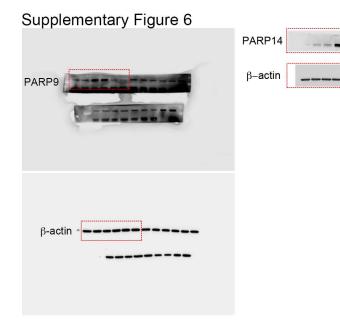
Supplementary Figure 17: Schematic workflow of integrated target discovery research from global screening to validations to drug development.



Supplementary Figure 18: Uncropped western blotting images (Figure 3c – 7c)



Supplementary Figure 19: Uncropped western blotting images (Figure 10a, b and d)



Supplementary Figure 12a

1.0.01				1 I	1221	-	1 1		1 1
GFP									
1.1	111	1111	111	-			1111	HILL.	111
-	_	1	_	4	-	-	-	-	-

Supplementary Figure 20: Uncropped western blotting images (Supplementary Figure 6 and 12a

Supplementary Table 1: Overview of quantified proteomes

R	AW264.7 cell	s		THP-1 cells				
Untimulated Control	IFNΥ	IL-4	Untimulated control	IFNΫ	IL-4			
4,234	4,234 6,393		6,338	6,817	6,772			
Filtered for the number of unique peptides >1								
2,934	4,786	3,966	4,713	4,623	5,027			

Total proteins quantified by MS/MS

Supplementary Table 2: The number of unique peptides and spectral counts for PARP9 and PARP14

RAW264.7 cells

		PARP14			PARP9	
-	Control	IFNg	IL-4	Control	IFNg	IL-4
Number of unique peptides	6	40	13	2	8	4
Spectral counts	8	68	17	3	15	7
THP-1 cells		PARP14			PARP9	
	Control	IFNg	IL-4	Control	IFNg	IL-4
Number of unique peptides	12	28	13	7	16	16
Spectral counts	22	54	20	7	30	20

Supplementary Table 3

Mouse proteins from RAW264.7 cells

No	Gene	No	Gene	No	Cono	No	Cono	No	Gene	No	Cono	No	Cono
		No. 71	Cmpk2	No. 141		No. 211		No. 281	Nup210	No. 351	Gene Rad17		Gene
	Aacs Abcb1b		Cmpk2 Cnot10		Fdps		Kpnb1						Srpk2
		72		142	Fhod1	212	Krr1	282	Nup88	352	Rad18		Srpr
_	Abcd1	73	Cnot3		Fkbp4	213	Las1I		Nup93	353	Rad50		Ssr4
-	Abce1	74		_	Fli1	214	Lbr	284	Nup98	354	Ranbp2	424	Stat1
	Abcf2	75	Cpd	145	Fndc3b	215	Lcp2	285	Oas1a	355	Rbl1		Stim2
6	Abl2	76	Crnkl1	146	Ftsj3	216	Lonp2	286	Oas2	356	Rbm14		Stk16
7	Abt1	77	Ctbp1	147	Ftsjd2	217	Lrrc8d	287	Oas3	357	Rbm28	427	Stt3a
8	Acsl5	78	Ctbp2	148	Fxr1	218	Lsg1	288	Oasl1	358	Rbm34	428	Sun2
9	Adam10	79	Ctr9	149	Gars	219	Lsm2	289	Obfc2b	359	Rcl1	429	Supt16h
10	Afg3l1	80	Ctu2	150	Gbf1	220	Ltv1	290	Osbpl1a	360	Rfc3	430	Supt5h
_	Agpat6	81	Cul4b	151	Gbp7	221	Map3k2	291	Paf1	361	Rfc5		Suz12
	Agps	82	Cyb5b	152	Gch1	222	Map3k7	292	Pak1ip1	362	Rgs3		Sympk
_	Ahctf1	83	Cyp51a1	152	Gemin4	223	Mapk8	293	Papola	363	Riok1	_	Tbl2
_		_		_	Gfm1					_		_	
	AI607873	84		154					Parp12	364	Rnaseh2b		Tbl3
_	Aim1	85	D1Bwg0212e	155	Gfpt1	225	Mark2	295	Parp14	365	Rnaset2		Tbrg4
	Aim2	86			Glyr1	226	Mcm3ap	296	Parp9	366	Rnf2	436	Tcp1
	Aldh18a1	87	Dars2	157	Gm4294	227	Mcm5	297	Pbrm1	367	Rnf213	437	Tdrd7
18	Aldh1l2	88	Daxx	158	Gm5745	228	Mdn1	298	Pcnt	368	Rnf220	438	Tecr
19	Alox5	89	Ddx10	159	Gmds	229	Med17	299	Pcx	369	RpI10a	439	Tfip11
20	Anapc1	90	Ddx18	160	Grsf1	230	Mepce	300	Pdcd11	370	Rpl13	440	Thoc1
_	Anapc5	91	Ddx20	161		231	Mgat2	301	Pde2a	371	Rpl13a	441	Thoc2
	Anapc7	92	Ddx27	162	Gtf3c1	232	Mipep	302	Pdia5	372	RpI14	442	Thoc5
	Ankle2	93		163	Gtpbp1	233	Morf4I1	303	Pds5a		RpI18	443	Tir2
	Api5	94	Ddx41	164	Gtpbp10	234	Mov10	304	Pds5b	374	Rpl2211	444	Tmem199
		94	Ddx41 Ddx46	164	Guf1	234	Mrpl21	304	Pelo	374	Rpl2211	444	Tmpo
	Aqr											_	
	Arhgef2	96	Ddx50	166	Gvin1	236	Mrpl30	306	Pes1	376	RpI3	446	Toe1
	Arhgef6	97	Ddx51	167	Hck	237	Mrpl44	307	Pex14	377	RpI5	447	Tomm40
	Asrgl1	98	Ddx56	168	Hdac6	238	Mrpl47	308	Phax	378	Rpl8	448	Top2a
29	Atg101	99	Ddx58	169	Heatr1	239	Mrps34	309	Phb2	379	Rps11	449	Top2b
30	Atg2b	100	Dennd4a	170	Hexim1	240	Msh2	310	Phf11	380	Rps9	450	Top3b
31	Atg4b	101	Dgkz	171	Hira	241	Msh6	311	Phip	381	Rrp1	451	Trim56
32	Atp2a2	102	Dhx15	172	Hist1h1c	242	Mta1	312	Pik3ap1	382	Rrp12	452	Trip13
33	Atp6ap1	103	Dhx16	173	Hs2st1	243	Mta2	313	Pik3c2a	383	Rrp8	453	Trrap
	Atp6ap2	104	Dhx30	174	Hsd17b4	244	Mybbp1a		Pik3cd	384	Rtcd1	454	Ttc27
	Atpaf2	105	Dhx36	175	Hsp90b1	245	Myl12a		Pkp2	385	Rtn4	455	Ttc39b
	Bag6	106	Dhx37		Hspa5	246	Naa15		Pla2g4a	386	Rtn4ip1	456	Tubgcp2
37	Bago Baz1a	100	Dhx58	177	Hspd1	240	Naa25		Plekha2	387	Samd9l	457	Ube2i
38	Baz1b	108	Dhx8	178	Hyou1	248	Nars	318	Plin2	388	Sdad1	458	Ube2o
39	Baz2b	109	Dhx9	179	Ibtk	249	Nat10		Pirg1	389	Sdcbp	459	Ubtf
40	BC006779	110	Diablo	180	Icam1	250	Ncapd2	320	Pml	390	Sec24d	460	Uhrf1bp1l
41	Birc6	111	Diexf	181	ldh3a	251	Ncapg	321	Pnn	391	Senp1	461	Upf2
42	Bloc1s2	112	Dimt1	182	lfi203	252	Ndrg2	322	Pno1	392	Senp3	462	Uqcrq
43	Bms1	113	Dis3	183	lfi44	253	Ndufa12	323	Pnpt1	393	Setd1a	463	Urb1
44	Bnip1	114	Dkc1	184	lfih1	254	Ndufa6	324	Pogz	394	Sf3b3	464	Usp19
45	Bptf	115	Dnajc3	185	lgtp	255	Nedd1	325	Polr1a	395	Sin3a	465	Usp25
46	Brix1	116	Dnajc9		Ikbkap		Nemf	326	Polr1e		Skiv2l2		Usp48
47	Bst2	117	Dph5	187	Ikbkb	257	Nfx1	327	Polr2a	397	SIc16a1	467	Utp11I
47	Btaf1	118	Dtx3l	188	ll1m	257	Nipbl	328	Polr2b	398	Slc16a10	467	Utp15
40	Bud31	110	Eef1a1	189	llf2	258	Nirp3	329	Polr3a	399	SIc23a2	469	
_													Utp6
50	Bzw2	120	Eefsec	190	Impad1	260	Nmi	330	Polr3b	400	Slc30a1	470	Wapal
51	C130026I21	121	Eftud2	191	Inpp5b	261	Noc2l	331	Pom121	401	Slc38a2	471	Wdr18
	C330027C0		Eif2b1		Ints1	_			Pop1	_	Slc3a2		Wdr3
	Ca2		Eif2b3		Ints3		Noc4I		Por		Slc4a7		Wdr36
54	Cad	124	Eif3d	194	Ints4	264	Nol10	334	Ppat	404	Smarca4	474	Wdr43
55	Caprin1	125	Eif3e	195	Ipo13	265	Nom1	335	Ppp2ca	405	Smarca5	475	Wdr46
	Carm1		Eif3I		Ipo7		Nomo1		Ppwd1		Smarcad1		Wdr47
	Ccdc134		Eif4a1		Ipo9		Nop56		Prkra		Smarcal1		Wdr75
	Ccdc47	_	Eif4g2		Irf5		Npm1		Prmt1		Smc2	_	Xab2
	Ccdc50		Eml4		Irg1		Nr3c1		Prmt3		Smc4		Xpc
-	Ccdc30 Ccdc72		Endod1		Irgm2		Nsdhl		Prmt5		Smc4 Smchd1	_	Xpo5
													Yme1l1
	Ccnt1		Ensa		Isyna1		Nt5dc3		Prpf31		Smpd4		
	Cct4		Etnk1		Junb		Nudcd1		Prpf6		Smpdl3b		Ythdc2
	Cct8		Exosc2		Kat7		Nudt16I1		Prpf8		Smu1		Zc3h18
	Cdk5rap2		Fam105a		Katna1		Numa1		Ptrh2		Snd1		Zc3h7a
65	Cebpz	135	FAM120A	205	Kdm1a	275	Nup107	345	Pus1	415	Snrnp200	485	Zc3hav1
	Cep128		Far1		Kiaa0020		Nup133		Pwp2		Sp100		Zfhx4
	Chd2		Fasn		Kiaa0664		Nup155		Pycr2		Sp110	487	
	Chd8		Fastkd2		Kidins220		Nup160		Rab11fip1		Sptlc2		Zmat2
69		100											
		100	Eof1	200								400	
69	Cirh1a Ckap4		Fcf1 Fcgr1		Kif15 Kif2a		Nup188 Nup205		Rab31 Rac2		Srp14 Srpk1		Znf800 Znfx1

Human proteins from THP-1 cells

1	Gene	No.		No.	Gene	No.		No.	Gene	No.	
	ABCB1	_	CSTF1		HEATR5B	_	METTL3	281	PSAP	351	SSBIP1
	ABL2		CTNNA1		HEBP1		MOGS	282	PSMA4	352	STAT1
_	ACBD3	_	CTSL1		HGS		MORF4L2		PSMA7	_	STIP1
	ACTN4		CUTA	_	HIRA	-	MPHOSPH10	_	PSMD13	-	
_	AHSA1		CYLD	_	HIST1H1C		MRPL30	285	PSMD8	355	STK39
_	AK2		DDX17	_	HK2		MRPL39	_	PSMF1	356	SUB1
_	AKAP13		DDX39B	-	HMBS	_	MRPL46	287	PTER	357	SUPV3L1
_	ALDOA	_	DDX58		HMGB1		MRTO4		PTK2B	358	SYAP1
9	ALKBH5	_	DDX59	_	HMGB2	_	MSI2	289	PXN	359	SYF2
_	ANKLE2	_	DECR1	150	HMGB3		MSR1	290	RAB18	360	SYNCRIF
_	ANKS1A	_	DHRS7		HMOX2		MSRA	291	RABEP2	361	SYNRG
_	ANP32A	_	DHX38		HNRNPA1		MTIF3	292	RAD23B	362	TAF4
	AP2B1	_	DLAT		HNRNPA2B1		MTMR3	293	RAP1B	363	TALDO1
_	APC		DLD	-	HNRNPA3	-	MTPN	294	RBBP5	364	TAP2
	ARFIP1	_	DLGAP4		HNRNPD	_	NAGK	295	RBM10	365	TDO2
_	ARHGAP12	_	DMAP1		HNRNPF	_	NANS		RBM12	366	TEX264
_	ARHGAP15	_	DNAJA2	_	HPCAL1	-	NAP1L1	297	RBM15	367	TFCP2
_	ARHGAP31		DNAJC16		HS2ST1	_	NCOA3	298	RBM5	368	TGFB1
_	ARL15		DNAJC9	_	HSP90AA1		NDST1	299	RBM8A	369	TIMM8A
_	ARL3	_	DRAP1	-	HSPA13		NEK6	300	RBMX	370	TLK2
	ARPC5L	_	DYNC1I2	_	HSPA8	_	NFATC2IP	301	REL	371	TMED8
	ARSB		DYNLL2		HSPA9		NFU1	302	RELB	372	TMF1
_	ASPSCR1		ECHDC1		HSPD1		NFX1	303	RGC32	373	TMOD3
	ATM		EEA1		HSPE1		NIT2	304	RNF13	374	TNS3
_	ATP2A3		EEF1B2		IFI16	_	NKTR	305	RPE	375	TOMM20
_	ATP2C1	96	EFTUD1	166	IFIH1		NME2	306	RPL12	376	TOP1
	ATP5C1	97	EHMT1	167	IFIT1		NMI	307	RPL24	377	TRIM13
28	ATP6V1B2	_	EIF2AK2	168	IFIT3	238	NR3C1	308	RPL28	378	TRIM25
29	ATRX	_	EIF2B2	169	IFIT5	239	NUCKS1	309	RPL29	379	TRIM33
30	ATXN10		EIF2S1	170	IL1B	240	NUDCD1	310	RPL37	380	TRRAP
31	BCAS2	101	EIF4H	171	IL1RN	241	NUDT5	311	RPLP1	381	TSPYL5
	BDH1	102	ENO1	172	ILKAP		NUFIP2		RPS12	382	TTC1
33	BLZF1	103	ENPP4	173	IMPA1	243	NUMB	313	RPS13	383	TTI2
34	C11orf54		ENSA	174	IMPDH2	244	NUP155		RPS19	384	TUBG1
35	C11orf58	105	EPHX1	175	IPO5	245	NUP188	315	RPS21	385	TXNL1
36	C19orf10	106	ERLEC1	176	IRF2BP2	246	NUP214	316	RPS6	386	UBE2L3
37	C1orf198	107	ERP44	177	IRF2BPL	247	NXT1	317	RPS6KA5	387	UBE3A
38	C1orf31	108	EVI2B	178	ISG20L2	248	NXT2	318	RRP9	388	UFM1
39	CACYBP	109	FAM105A	179	JUNB	249	OAS1	319	RRS1	389	UQCRC1
40	CAMSAP1	110	FAM105B	180	KIAA1468	250	OAS2	320	S100A8	390	USP11
41	CAPZA1	111	FAM136A	181	KIAA1598	251	OPTN	321	S100A9	391	USP40
42	CARD6	112	FAM82B	182	LACTB2	252	OSBPL8	322	SACM1L	392	UTP14A
43	CARHSP1	113	FBXO6	183	LAMP2	253	OSTF1	323	SARNP	393	UTP20
44	CASP4	114	FCF1	184	LASP1	254	P4HB	324	SEC22B	394	VAPA
45	CBX3	115	FNBP4	185	LCLAT1	255	PAG1	325	SEC24C	395	VPS25
46	CBX5	116	FOSL2	186	LCP2	256	PAICS	326	SEC62	396	VPS29
47	CCDC149	117	FOXK2	187	LEPRE1	257	PARK7	327	SEMA7A	397	WARS2
	CCDC50			1.0.0	104104		DADDIA	220	SEPT6		WDR11
_		118	FUBP3	188	LGALS1	258	PARP14	328		398	WDRII
_	CCDC56	118 119	FUBP3 FUS	188 189	LGALST LGALS3		PARP14 PARP9	328	SFXN1	398 399	WDR75
48 49	CCDC56 CCDC58	119		189		259				399	
48 49		119	FUS	189	LGALS3	259 260	PARP9	329	SFXN1	399	WDR75
48 49 50 51	CCDC58	119 120 121	FUS G3BP1	189 190 191	LGALS3 LIMK1	259 260 261	PARP9 PDIA3	329 330 331	SFXN1 SGK223	399 400 401	WDR75 XIAP XIRP1
48 49 50 51 52	CCDC58 CCL20	119 120 121 122	FUS G3BP1 G3BP2	189 190 191 192	LGALS3 LIMK1 LMNA	259 260 261 262	PARP9 PDIA3 PDSS2	329 330 331 332	SFXN1 SGK223 SIPA1L1	399 400 401 402	WDR75 XIAP XIRP1
48 49 50 51 52 53	CCDC58 CCL20 CCPG1	119 120 121 122 123	FUS G3BP1 G3BP2 GABPA	189 190 191 192 193	LGALS3 LIMK1 LMNA LPL	259 260 261 262 263	PARP9 PDIA3 PDSS2 PEA15	329 330 331 332 333	SFXN1 SGK223 SIPA1L1 SLAIN2	399 400 401 402 403	WDR75 XIAP XIRP1 YBX1
48 49 50 51 52 53 54	CCDC58 CCL20 CCPG1 CCT5	119 120 121 122 123 124	FUS G3BP1 G3BP2 GABPA GAPDH	189 190 191 192 193 194	LGALS3 LIMK1 LMNA LPL LRCH1	259 260 261 262 263 264	PARP9 PDIA3 PDSS2 PEA15 PELO	329 330 331 332 333 333	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1	399 400 401 402 403 404	WDR75 XIAP XIRP1 YBX1 YWHAE
48 49 50 51 52 53 54 55	CCDC58 CCL20 CCPG1 CCT5 CCZ1B	119 120 121 122 123 124 125	FUS G3BP1 G3BP2 GABPA GAPDH GBP5	189 190 191 192 193 194 195	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12	259 260 261 262 263 264 265	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5	329 330 331 332 333 334 335	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6	399 400 401 402 403 404 405	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A
48 49 50 51 52 53 54 55 56	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109	119 120 121 122 123 124 125 126	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2	189 190 191 192 193 194 195 196	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1	259 260 261 262 263 264 265 266	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1	329 330 331 332 333 334 335 336	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1	399 400 401 402 403 404 405 406	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC8
48 49 50 51 52 53 54 55 56 57	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276	119 120 121 122 123 124 125 126 127	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM	189 190 191 192 193 194 195 196 197	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1 LRRC8D	259 260 261 262 263 264 265 266 266 267	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2	329 330 331 332 333 334 335 336 337	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLTM	399 400 401 402 403 404 405 406 407	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC8
48 49 50 51 52 53 54 55 56 57 58	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD38	119 120 121 122 123 124 125 126 127 128	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCSH	189 190 191 192 193 194 195 196 197 198	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1	259 260 261 262 263 264 265 266 266 267 268	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHF6	329 330 331 332 333 334 335 336 337 338	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLTM SMYD5	399 400 401 402 403 404 405 406 407 408	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC8 ZDHHC5 ZFP106
48 49 50 51 52 53 54 55 56 57 58 59	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD38 CD40	119 120 121 122 123 124 125 126 127 128 129	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCSH GCCT	189 190 191 192 193 194 195 196 197 198 199	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1 LRRFIP2	259 260 261 262 263 264 265 266 267 268 269	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHF6 PHLDA1	329 330 331 332 333 334 335 336 337 338 339	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SLTM SMYD5 SNRPC	399 400 401 402 403 404 405 406 407 408 409	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC8 ZDHHC5 ZFP106
48 49 50 51 52 53 54 55 56 57 58 59 60	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD38 CD40 CDC37	119 120 121 122 123 124 125 126 127 128 129 130	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCCH GCSH GGCT GLIPR2	189 190 191 192 193 194 195 196 197 198 199 200	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1 LRRASD LRRFIP1 LRRFIP2 LYRM7	259 260 261 262 263 264 265 266 267 268 269 270	PARP9 PDIA3 PDS2 PEA15 PELO PFDN5 PGK1 PHC2 PHF6 PHLDA1 PIKFYVE	329 330 331 332 333 334 335 336 337 338 339 340	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLTM SMYD5 SNRPC SNX17	399 400 401 402 403 404 405 406 407 408 409 410	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC8 ZCHC8 ZDHHC5 ZFP106 ZFP36L1
48 49 50 51 52 53 54 55 56 57 58 59 60 61	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD276 CD38 CD40 CD40 CDC37 CDK12 CEBPB	119 120 121 122 123 124 125 126 127 128 129 130 131	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCCH GGCT GLIPR2 GLO1 GLOD4	189 190 191 192 193 194 195 196 197 198 199 200 201	LGALS3 LIMK1 LMNA LPL LRCH1 LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1 LRRFIP2 LYRM7 MALT1	259 260 261 263 264 265 266 267 268 269 270 271	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHFC6 PHLDA1 PIKFYVE PIKFYVE PIN1	329 330 331 332 333 334 335 336 337 338 339 340 341	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLTM SMYD5 SNRPC SNX17 SNX8 SOD2	399 400 401 402 403 404 405 406 407 408 409 410 411	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC8 ZDHHC5 ZFP106 ZFP106 ZFP36L1 ZFP91 ZFYVE16
48 49 50 51 52 53 54 55 56 57 58 59 60 61 62	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD38 CD40 CDC37 CDC37 CDK12 CCBPB CHTOP	119 120 121 122 123 124 125 126 127 128 129 130 131 132	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCSH GCSH GCSH GLIPR2 GLO1 GLOD4 GTF2F1	189 190 191 192 193 194 195 196 197 198 199 200 201 202	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRRAP1 LRRC8D LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2	259 260 261 262 263 264 265 266 267 268 269 270 271 272	PARP9 PDIA3 PDSS2 PEA15 PEL0 PFDN5 PGK1 PHC2 PHC2 PHF6 PHLDA1 PIKFYVE PIN1 PLEKHO2 PLSCR1	329 330 331 332 333 334 335 336 337 338 337 338 339 340 341 342	SFXN1 SGK223 SIPA1L1 SLA1N2 SLC12A6 SLC20A1 SLC25A1 SLTM SMYD5 SNRPC SNX17 SNX8 SOD2 SP110	399 400 401 402 403 404 405 406 407 408 407 408 409 410 411 412	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZFP10 ZFP10 ZFP10 ZFP20 L1 ZFP20
48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63	CCDC58 CCL20 CCPG1 CCZ1B CD276 CD276 CD276 CD38 CD40 CDC37 CDK12 CCBPB CHTOP CLASP2	119 120 121 122 123 124 125 126 127 128 129 130 131 132 133	FUS G3BP1 G3BP2 GAPDA GAPDH GBP5 GCC2 GCLM GCSH GCSH GCSH GLOPA GLOD4 GTF2F1 GTF2F2	189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2 MAPKAP1	259 260 261 262 263 264 265 266 267 268 269 270 271 272 273	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHF6 PHLDA1 PIKFYVE PIN1 PLEKHO2 PLSCR1 PNPO	329 330 331 332 333 334 335 336 337 338 337 338 339 340 341 342 343	SFXN1 SGK223 SIPA1L1 SLA1N2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SNXPC SNXPC SNX17 SNX8 SOD2 SP110 SPAG1	399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZFP106 ZFP36L1 ZFP91 ZFYVE11 ZFYVE11 ZFYVE11 ZFYVE12
48 49 50 51 52 53 55 56 57 58 59 60 61 62 63 64	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD38 CD40 CDC37 CDK12 CEBPB CLTOP CLASP2 CLPX	119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134	FUS G3BP1 G3BP2 GABPA GBP5 GCC2 GCLM GCSH GCSH GLOTA GLOT4 GLOT4 GTF2F1 GTF2F2 GTF3C4	189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 203 204	LGALS3 LIMK1 LMK1 LPL LRCH1 LRP12 LRPAP1 LRRFIP1 LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2 MAPKAP1 MARK2	259 260 261 262 263 264 265 266 267 268 269 270 271 272 272 273 274	PARP9 PDIA3 PDS2 PEA15 PELO PFDN5 PGK1 PHC2 PHF6 PHLDA1 PIKFYVE PIN1 PLEKHO2 PLSCR1 PNPO PNPT1	329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SLC25A1 SMYD5 SNRPC SNX17 SNX8 SOD2 SP110 SPAG1 SPAG7	399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZFP10 ZFP10 ZFP10 ZFP20 L1 ZFP20
48 49 50 51 52 53 55 56 57 58 59 60 61 62 63 64 65	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD276 CD40 CDC37 CDK12 CEBPB CHTOP CLASP2 CLASP2 CCPX CORO1A	119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135	FUS G3BP1 G3BP2 GAPDA GAPDH GBP5 GCC2 GCLM GCSH GCC4 GCSH GCC7 GLIPR2 GLO1 GLOD4 GTF2F1 GTF2F2 GTF3C4 H1F0	189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 204 205	LGALS3 LIMK1 LMK1 LPL LRCH1 LRCH1 LRCBD LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2 MAPKAP1 MARK2 MARK3	259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHFC2 PHLDA1 PHLDA1 PHLDA1 PIKFYVE PIN1 PLEKHO2 PLSCR1 PNPO PNPT1 PPIA	329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 344 345	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SLC25A1 SLC25A1 SLC25A1 SLC25A1 SLC25A1 SNX8 SON25 SNX17 SNX8 SOD2 SP110 SPAG1 SPAG7 SPI1	399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZFP106 ZFP36L1 ZFP91 ZFYVE11 ZFYVE11 ZFYVE11 ZFYVE12
48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD276 CD276 CD40 CDC37 CDK12 CEBPB CHTOP CLASP2 CLPX CORO1A CPSF2	119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCSH GGCT GLIPR2 GLO1 GLOD4 GTF2F1 GTF2F2 GTF3C4 H1F0 HAT1	189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	LGALS3 LIMK1 LMK1 LPL LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2 MAPKAP1 MARK2 MARK3 MAZ	259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHC2 PHC2 PHC4 PHC4 PHC4 PHC4 PHC4 PHC4 PHC4 PHC4	329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SLTM SMRPC SNRPC SNX8 SOD2 SPAG1 SPAG7 SPP1	399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC6 ZFP106 ZFP36L1 ZFP91 ZFYVE11 ZFYVE11 ZFYVE11 ZFYVE12
48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 66 67	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD38 CD40 CDC37 CDK12 CEBPB CHTOP CLASP2 CLPX COR01A CPSF2 CRIP1	119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GGCT GLIPR2 GLOD4 GTF2F1 GTF3C4 H1F0 HAT1 HCFC1	189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 202 203 204 205 206 207	LGALS3 LIMK1 LMNA LPL LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2 MAPKAP1 MARK2 MARK3 MAZ MCM3	259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHF6 PHKFYVE PIN1 PLEKH02 PLSCR1 PNPO PNP1 PPIG PPM1B	329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SLC25A1 SNX7 SNX7 SNX8 SOD2 SP110 SPAG1 SPAG7 SPP1 SPP1 SRRM2	399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC8 ZDHHC5 ZFP106 ZFP36L1 ZFP91 ZFYVE11 ZFYVE11 ZFYVE11 ZFYVE12
48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68	CCDC58 CCL20 CCPG1 CCT5 CCZ1B CD109 CD276 CD276 CD276 CD40 CDC37 CDK12 CEBPB CHTOP CLASP2 CLPX CORO1A CPSF2	119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138	FUS G3BP1 G3BP2 GABPA GAPDH GBP5 GCC2 GCLM GCSH GGCT GLIPR2 GLO1 GLOD4 GTF2F1 GTF2F2 GTF3C4 H1F0 HAT1	189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208	LGALS3 LIMK1 LMK1 LPL LRCH1 LRP12 LRPAP1 LRRC8D LRRFIP1 LRRFIP2 LYRM7 MALT1 MAN1A1 MAP3K2 MAPKAP1 MARK2 MARK3 MAZ	259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278	PARP9 PDIA3 PDSS2 PEA15 PELO PFDN5 PGK1 PHC2 PHC2 PHC2 PHC4 PHC4 PHC4 PHC4 PHC4 PHC4 PHC4 PHC4	329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348	SFXN1 SGK223 SIPA1L1 SLAIN2 SLC12A6 SLC20A1 SLC25A1 SLC25A1 SLTM SMRPC SNRPC SNX8 SOD2 SPAG1 SPAG7 SPP1	399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	WDR75 XIAP XIRP1 YBX1 YWHAE ZBTB7A ZCCHC6 ZCCHC6 ZCCHC6 ZCCHC8 ZDHHC5 ZFP106 ZFP36L1 ZFP91 ZFYVE11 ZFYVE11 ZFYVE11 ZFYVE12

No.	Gene	No.	Gene	No.	Gene	No.	Gene
1	ABCA1	31	GALANT2	61	Nfe2L2	91	VPS4
2	ABCD1	32	GJA1	62	NFKB		
3	ABCG1	33	HOMX1	63	NOS2		
4	ACTA2	34	HPRT1	64	NUDCD1		
5	ADM	35	IFNGR1	65	OAS1		
6	ARG1	36	IL10	66	OLR1		
7	ATF1	37	IL12B	67	PARP1		
8	CCL2	38	IL1b	68	PARP14		
9	CCL22	39	IL4R	69	PARP2		
10	CCL5	40	IL6	70	PARP9		
11	CCND1	41	IL8	71	PDCD4		
12	CD14	42	IRF1	72	PGC1a		
13	CD200R	43	IRF2	73	PPARa		
14	CD36	44	IRF3	74	PPARg		
15	CD80	45	IRF5	75	S100A9		
16	CD86	46	IRF8	76	SNX1		
17	COL1A1	47	IRF9	77	SNX2		
18	CPT1a	48	IRG1	78	SORT1		
19	CPT1b	49	JAK1	79	Sp110		
20	CTSK	50	JAK2	80	SRA		
21	CXCL10	51	JAK3	81	STAT1		
22	CXCL11	52	KLF4	82	STAT2		
23	CXCL6	53	LAMP2	83	STAT3		
24	CXCL6	54	LDLR	84	STAT6		
25	DTX3L	55	MMP1	85	TAGLN		
26	EGR1	56	MMP12	86	TCF4		
27	EGR2	57	MMP8	87	TLR2		
28	F3	58	MMP9	88	TLR4		
29	FCGRT	59	MRC1	89	TNF		
30	GADD45a	60	MYC	90	TRIB1		

Supplementary Table 4: List of genes evaluated in single cell analysis