Clinical and Experimental Rheumatology 2022

Supplementary file to:

Identification of RRM2 in peripheral blood mononuclear cells as a novel biomarker for the diagnosis of rheumatoid arthritis

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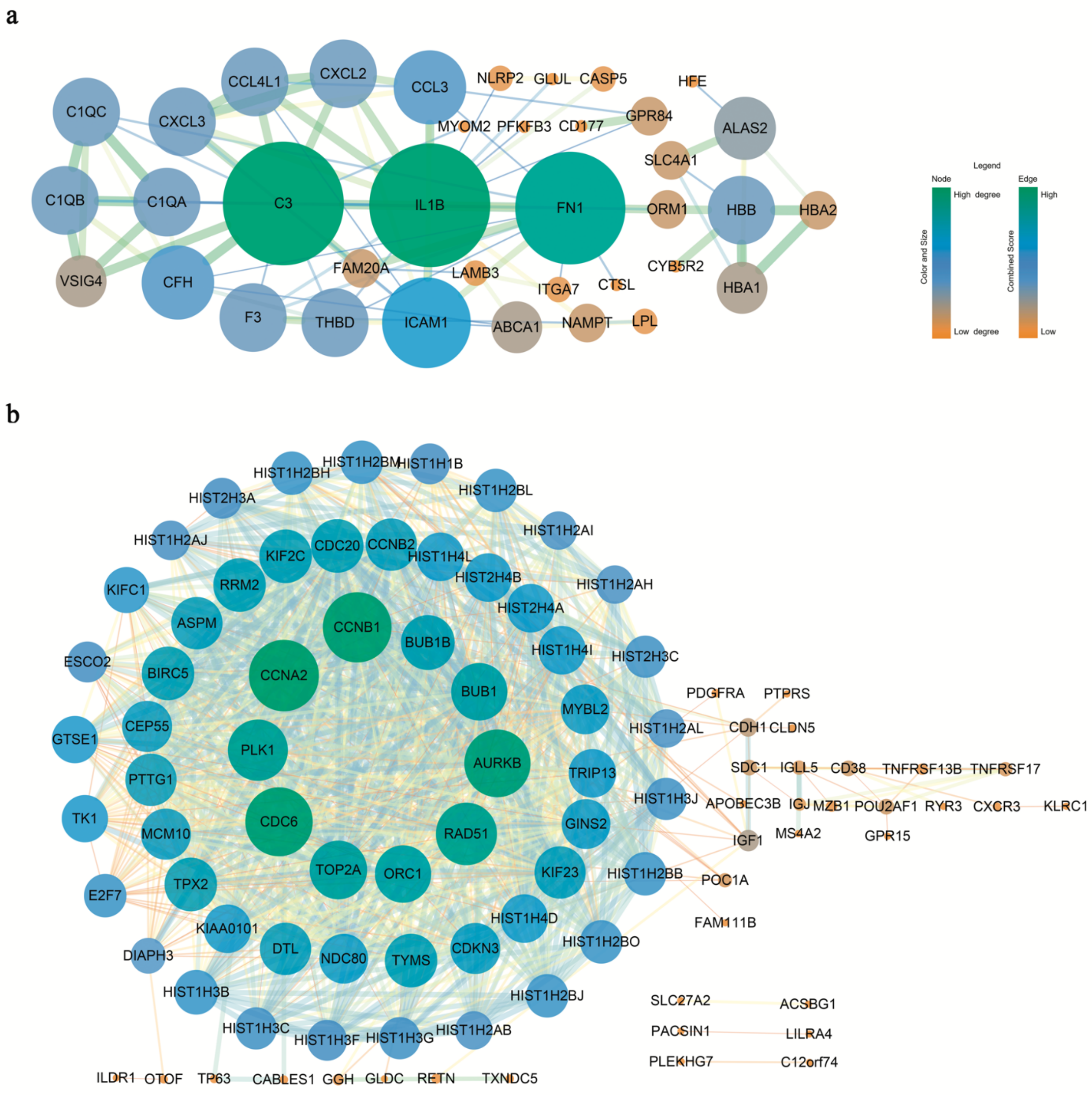
Supplementary Fig. S1. PPI network analysis.



Supplementary Table S1

							healthy controls	**healthy controls**	**healthy controls**	**healthy controls**	**RA patients**	**RA patients**	**RA patients**	**RA patients**
Gene symbol	**Gene name**	**Fold change**	**difference**	**logFC**	***p*-value**	**FDR**	Huang SC	Wang J	Lu JG	Huang JQ	An N	Cai CH	Qu WB	Wang GZ
ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	2.007838	up	-1.00564	0.032323	0.999715	40.46512	16.69448	32.67573	44.61113	21.89572	48.12466	160.0993	39.92342
ACSBG1	acyl-CoA synthetase bubblegum family member 1	-2.00858	down	1.006178	0.047823	0.999715	1.175123	1.333719	1.452255	0.763735	1.024076	0.524234	0.543119	0.238491
ADAM12	ADAM metallopeptidase domain 12	-3.22631	down	1.689885	8.83E-05	0.17575	2.554616	1.931593	2.178382	2.381057	0.731483	0.786351	0.543119	0.715474
ADAM19	ADAM metallopeptidase domain 19	-1.51246	down	0.596896	0.012538	0.999715	205.1868	176.1429	149.7033	248.9328	109.0885	144.2167	136.8055	125.6371
AHNAK2	AHNAK nucleoprotein 2	-2.06638	down	1.047108	0.031642	0.999715	8.58351	11.03767	11.01293	2.111504	4.681489	5.923841	2.051781	3.148083
AKAP2	A kinase (PRKA) anchor protein 2	-1.69827	down	0.764067	0.008994	0.999715	163.5976	182.8575	126.5882	120.2658	78.70754	141.2286	75.2521	54.18519
ALAS2	5'-aminolevulinate synthase 2	8.993923	up	-3.16895	4.77E-05	0.164723	0.970754	2.207535	2.904509	3.054941	0.585186	50.32644	8.327818	23.13364
ALOX15	arachidonate 15-lipoxygenase	-8.91989	down	3.157026	0.000146	0.20368	29.22481	1.47169	1.93634	1.392694	0.97531	0.681504	1.086237	1.049361
APOBEC3B	apolipoprotein B mRNA editing enzyme; catalytic polypeptide-like 3B	-3.66723	down	1.874689	0.038451	0.999715	2.503524	0.229952	0.665617	21.11504	0.585186	2.254205	1.20693	2.623403
AQP3	aquaporin 3 (Gill blood group)	-1.66685	down	0.737128	0.03968	0.999715	46.90275	32.88307	36.54841	92.54675	43.20625	40.99508	17.68153	23.41983
ARMC3	armadillo repeat containing 3	-2.13741	down	1.095866	0.034232	0.999715	2.758985	3.173331	4.296254	0.898512	2.096917	1.363008	0.844851	0.858568
ASPM	abnormal spindle	-2.62045	down	1.389	0.021	0.999	7.663848	4.920963	7.079742	38.63602	3.51111	1.83481	9.47440	7.44092

	microtubule assembly			814	439	715					7	8	2	5
ATHL1	ATH1; acid trehalase-like 1 (yeast)	1.694514	up	-0.76087	0.038709	0.999715	50.07048	54.72847	78.84533	24.30475	126.8391	122.3037	58.05334	45.07483
AURKB	aurora kinase B	-2.73419	down	1.451114	0.045555	0.999715	1.226216	0.551884	1.210212	6.783767	0.243828	0.419387	1.629356	1.287852
B3GNT5	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 5	2.239041	up	-1.16288	0.040058	0.999715	31.47287	24.88076	18.09267	33.78406	11.4599	27.05046	172.4703	31.48083
BCL7A	B-cell CLL/lymphoma 7A	-1.88661	down	0.915796	0.014934	0.999715	68.77027	47.14007	41.6313	18.46442	30.28338	33.184	14.6642	15.12034
BEGAIN	brain-enriched guanylate kinase-associated	-3.16751	down	1.66335	0.003972	0.999715	2.248062	3.173331	1.512765	0.988363	0.585186	0.262117	1.38797	0.286189
BIRC5	baculoviral IAP repeat containing 5	-3.69954	down	1.887347	0.019813	0.999715	2.963355	1.4257	3.025531	22.73236	0.926545	0.209694	4.344949	2.671101
BLNK	B-cell linker	-1.8585	down	0.894139	0.008202	0.999715	31.62615	31.13544	31.46552	21.83384	17.84818	25.7923	8.508858	10.25512
BMS1P20	BMS1 ribosome biogenesis factor pseudogene 20	-3.1239	down	1.64335	0.000432	0.380989	28.71389	18.67207	24.32527	119.7267	13.89817	17.45698	16.05217	13.88019
BTBD19	BTB (POZ) domain containing 19	1.924619	up	-0.94457	0.03602	0.999715	1.839324	1.47169	2.480935	2.156429	3.316055	2.516322	6.879502	2.623403
BUB1	BUB1 mitotic checkpoint serine/threonine kinase	-2.72976	down	1.448775	0.032683	0.999715	5.517971	2.897389	4.235743	40.20842	2.730869	2.306628	8.327818	6.009978
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	-2.51593	down	1.331093	0.043791	0.999715	2.707893	1.379709	2.238893	13.34291	0.633952	1.310584	2.534553	3.338876

C12orf74	chromosome 12 open reading frame 74	-2.06376	down	1.045277	0.043039	0.999715	1.226216	1.149758	1.270723	0.763735	0.43889	1.048467	0.241386	0.381586
C1QA	complement component 1; q subcomponent; A chain	3.387368	up	-1.76016	0.001541	0.796657	4.547217	3.771205	3.691147	2.96509	3.316055	3.355096	21.60405	22.51357
C1QB	complement component 1; q subcomponent; B chain	3.522731	up	-1.81669	0.009036	0.999715	3.321001	1.103767	1.754808	2.021652	0.780248	1.625125	14.06074	12.49694
C1QC	complement component 1; q subcomponent; C chain	4.166949	up	-2.05899	0.004628	0.999715	0.459831	0.413913	0.96817	1.617322	0.390124	1.153314	5.913958	7.059339
C1QTNF3-AMACR	C1QTNF3-AMACR readthrough (NMD candidate)	4.672343	up	-2.22415	0.003058	0.960358	0	1.149758	0	0.40433	2.096917	2.096935	1.20693	2.098722
C1orf186	chromosome 1 open reading frame 186	-1.71952	down	0.782006	0.040999	0.999715	4.598309	7.634391	5.86953	4.492561	3.413586	4.089023	2.172474	3.434273
C2orf88	chromosome 2 open reading frame 88	-1.69524	down	0.761486	0.005003	0.999715	45.57435	73.03261	73.82295	56.51641	55.10503	33.44611	28.90598	29.33441
C3	complement component 3	2.366767	up	-1.24292	0.021449	0.999715	7.612756	4.41507	5.445955	3.279569	8.192606	2.201782	11.04341	27.66498
CABLES1	Cdk5 and Abl enzyme substrate 1	-2.47032	down	1.304699	0.003842	0.999715	1.634954	1.4257	1.633787	1.707173	0.877779	0.786351	0.422426	0.476982
CASP5	caspase 5; apoptosis-related cysteine peptidase	2.430426	up	-1.28121	0.016448	0.999715	3.372093	2.805409	1.99685	3.6839	2.779634	2.568745	16.53494	7.059339
CCDC180	coiled-coil domain containing 180	-1.92708	down	0.946414	0.017525	0.999715	4.496124	6.622604	5.990551	4.80704	3.462351	2.306628	1.689702	3.863557
CCL3	chemokine (C-C motif) ligand 3	2.012553	up	-1.00903	0.008531	0.999715	10.88266	8.370236	7.019231	14.9153	9.606806	19.44907	36.87172	17.12367
CCL4L2	chemokine (C-C	2.02023	up	-	0.027	0.999	5.466879	2.391496	1.93634	2.650611	2.63333	8.85955	7.60366	6.10537

	motif) ligand 4-like 2			1.01452	534	715					8			4
CCNA2	cyclin A2	-2.33647	down	1.224334	0.042417	0.999715	4.036293	3.127341	3.691147	24.57431	2.487041	2.044512	5.491532	5.151409
CCNB1	cyclin B1	-2.09595	down	1.067601	0.046415	0.999715	4.036293	2.713428	3.267573	16.35292	2.633338	2.306628	4.465642	3.195782
CCNB2	cyclin B2	-2.67208	down	1.417964	0.045943	0.999715	2.707893	1.241738	2.359914	16.6674	1.365434	0.576657	3.80183	2.861894
CD177	CD177 molecule	6.490924	up	-2.69842	0.002898	0.960358	0.204369	0.413913	1.210212	3.010016	0.243828	2.201782	18.10395	11.06599
CD38	CD38 molecule	-2.09909	down	1.069765	0.014276	0.999715	14.35694	12.8313	18.75829	61.86256	10.24076	10.79922	18.28499	12.06765
CD79A	CD79a molecule; immunoglobulin-associated alpha	-1.79459	down	0.843654	0.029786	0.999715	204.5737	193.4352	168.5826	106.7882	102.0175	182.014	40.55285	50.60783
CDC20	cell division cycle 20	-4.10285	down	2.036628	0.010801	0.999715	2.503524	1.379709	1.573276	21.51937	0.97531	0.47181	3.80183	1.335551
CDC6	cell division cycle 6	-2.84073	down	1.506261	0.040355	0.999715	1.992601	1.103767	1.815318	13.56753	0.877779	0.47181	3.500098	1.669438
CDH1	cadherin 1; type 1	-2.9475	down	1.559491	0.003359	0.995749	2.86117	3.265312	3.751658	1.078215	1.219138	1.415431	0.724158	0.333888
CDKN3	cyclin-dependent kinase inhibitor 3	-2.55058	down	1.350824	0.041307	0.999715	1.3284	0.781835	1.210212	7.412725	1.024076	0.419387	1.086237	1.669438
CELSR1	cadherin; EGF LAG seven-pass G-type receptor 1	-1.95598	down	0.967891	0.020382	0.999715	15.2766	16.41854	15.30919	5.391073	8.533965	10.11771	3.80183	4.292841
CEP55	centrosomal protein 55kDa	-3.3802	down	1.757108	0.029499	0.999715	2.299155	1.287729	1.270723	15.67904	0.341359	0.419387	3.319058	2.003326
CFH	complement factor H	2.19626	up	-1.13505	0.021602	0.999715	1.992601	3.541254	3.267573	4.178081	2.194448	14.15431	7.362274	4.86522
CHAC2	ChaC; cation transport regulator homolog 2 (E. coli)	-2.04088	down	1.029192	0.040054	0.999715	1.481677	1.011787	1.512765	3.908528	0.780248	0.996044	0.905198	1.192456

CHAD	chondroadherin	-2.0558	down	1.039702	0.034429	0.999715	3.780832	1.333719	1.754808	2.785388	1.267903	1.834818	0.965544	0.620077
CHPF	chondroitin polymerizing factor	-2.00573	down	1.004128	0.033046	0.999715	5.466879	2.483477	4.840849	12.53424	2.779634	2.778439	4.465642	2.623403
CLC	Charcot-Leyden crystal galectin	-2.37466	down	1.247718	0.000629	0.434291	117.4613	36.74626	39.02935	37.82736	19.01855	20.07815	29.87152	28.33275
CLDN5	claudin 5	-2.44737	down	1.291231	0.005057	0.999715	2.758985	4.50705	3.630637	2.56076	2.096917	0.786351	1.750049	0.858568
CLDN7	claudin 7	1.972286	up	-0.97987	0.033478	0.999715	0.715293	0.689855	0.544596	1.168066	1.706793	1.939665	1.629356	0.953965
CLEC10A	C-type lectin domain family 10; member A	1.71892	up	-0.7815	0.01518	0.999715	28.35624	17.84424	12.64672	20.66578	42.03587	18.6103	44.35468	31.76702
CLEC12A	C-type lectin domain family 12; member A	1.849213	up	-0.88691	0.00183	0.878231	93.44786	105.6397	75.63827	96.23065	164.7787	93.78542	175.2463	252.2283
CLEC12B	C-type lectin domain family 12; member B	1.786135	up	-0.83684	0.027912	0.999715	3.014447	4.093137	4.598807	3.279569	6.973468	3.72206	7.422621	8.63338
CMTM8	CKLF-like MARVEL transmembrane domain containing 8	-1.98833	down	0.99156	0.049664	0.999715	3.934109	3.633234	1.391744	1.257917	1.316669	1.887241	0.724158	1.192456
CNTNAP3	contactin associated protein-like 3	3.464383	up	-1.7926	0.004667	0.999715	1.175123	0.873816	1.512765	3.459272	0.926545	13.21069	6.155344	4.149746
COBLL1	cordon-bleu WH2 repeat protein-like 1	-1.88972	down	0.91817	0.005512	0.999715	56.71248	50.86528	52.40219	36.25496	27.60128	44.76956	14.78489	16.64668
COL4A4	collagen; type IV; alpha 4	-1.79987	down	0.847895	0.023639	0.999715	11.59796	10.39381	11.19446	10.46767	6.241986	10.37983	3.017325	4.57903
CPA3	carboxypeptidase A3 (mast cell)	-1.76428	down	0.819076	0.026435	0.999715	18.44433	13.52115	19.60544	13.61246	3.462351	10.48467	9.957174	13.02162
CPNE5	copine V	-2.11303	down	1.079316	0.000675	0.434291	39.9031	33.94085	40.78415	56.20193	22.33461	32.18795	14.00039	12.30614

CTSL	cathepsin L	2.394219	up	-1.25956	0.035132	0.999715	10.06519	13.7511	9.137103	24.12505	10.87471	6.133535	93.17501	26.61561
CUX2	cut-like homeobox 2	-1.89339	down	0.920971	0.031504	0.999715	3.014447	2.713428	2.601956	2.291206	1.024076	1.048467	1.267277	2.241817
CXCL16	chemokine (C-X-C motif) ligand 16	1.871546	up	-0.90423	0.018642	0.999715	63.71213	55.41832	45.08041	62.31182	40.96303	58.66176	210.0662	114.3804
CXCL2	chemokine (C-X-C motif) ligand 2	2.314523	up	-1.21071	0.042064	0.999715	10.37174	3.173331	3.93319	10.82707	5.949393	6.867462	45.13919	7.679416
CXCL3	chemokine (C-X-C motif) ligand 3	3.938409	up	-1.97761	0.019233	0.999715	1.481677	0.505893	0.121021	2.111504	0.780248	0.943621	13.21589	1.860231
CXCR3	chemokine (C-X-C motif) receptor 3	-2.3808	down	1.251448	0.003171	0.960358	12.82417	6.760575	9.681698	29.6509	6.095689	8.178046	4.405295	6.057676
CYB5R2	cytochrome b5 reductase 2	2.836164	up	-1.50394	0.0172	0.999715	1.072939	0.505893	0.363064	1.347768	0.682717	0.891197	5.069107	2.814196
DAB2	Dab; mitogen-responsive phosphoprotein; homolog 2 (Drosophila)	-1.65541	down	0.72719	0.002492	0.960358	46.80057	54.45252	70.37384	67.65796	45.74205	33.44611	33.06989	32.24401
DENND5B	DENN/MADD domain containing 5B	-2.12598	down	1.088125	0.000689	0.434291	41.2826	32.7451	32.67573	54.22521	19.11608	31.08706	13.27623	12.21075
DERL3	derlin 3	-1.74488	down	0.803127	0.024945	0.999715	13.43728	9.244052	12.04161	22.19325	7.558655	10.5371	9.836481	4.722125
DIAPH3	diaphanous-related formin 3	-2.87492	down	1.523523	0.027513	0.999715	1.737139	0.735845	1.149702	6.514213	0.390124	0.262117	1.689702	1.192456
DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	-2.9702	down	1.570562	0.028713	0.999715	3.014447	2.161544	2.178382	22.4628	1.950621	0.576657	4.224256	3.291178

E2F7	E2F transcription factor 7	-2.82551	down	1.498511	0.026476	0.999715	1.634954	0.505893	1.02868	4.672263	0.390124	0.262117	1.569009	0.572379
EEF1E1-BLOC1S5	EEF1E1-BLOC1S5 readthrough (NMD candidate)	-3.79538	down	1.924245	0.034472	0.999715	6.846371	4.001157	11.49702	0.898512	3.559882	0	2.353514	0.190793
EGR3	early growth response 3	2.294842	up	-1.19844	0.023815	0.999715	35.86681	30.21563	35.39871	44.97053	19.21361	42.72505	232.0927	42.16524
ELK2AP	ELK2A; member of ETS oncogene family; pseudogene	-8.62479	down	3.10849	0.000105	0.183196	117.6145	24.28288	60.4501	1019.452	25.94325	23.27598	67.82948	24.61229
EMBP1	embigin pseudogene 1	-2.54456	down	1.347417	0.001601	0.796657	19.67054	21.29351	19.90799	14.10664	2.438276	4.141447	12.79346	10.11203
ENKUR	enkurin; TRPC channel interacting protein	-1.92115	down	0.941968	0.031517	0.999715	11.3425	11.68154	10.2868	6.109882	10.43582	3.931753	2.474207	3.625066
EREG	epiregulin	2.531398	up	-1.33993	0.017226	0.999715	13.38619	10.8997	8.350465	15.18485	10.82594	6.762615	83.51957	20.08096
ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	-3.86527	down	1.950571	0.00775	0.999715	1.379493	0.551884	1.149702	7.502576	0.341359	0.262117	1.327623	0.81087
ETS2	v-ets avian erythroblastosis virus E26 oncogene homolog 2	1.800344	up	-0.84827	0.012103	0.999715	107.4982	115.4817	115.8173	99.645	97.77485	116.642	347.0528	227.9499
F3	coagulation factor III (thromboplastin; tissue factor)	3.014822	up	-1.59207	0.008585	0.999715	1.021846	0.965796	1.089191	1.572396	1.267903	1.153314	8.99163	2.718799
FAM111B		-2.53198	down	1.340265	8.13E-05	0.17575	17.47357	12.96927	12.64672	15.18485	6.534579	8.125623	5.00876	3.338876
FAM20A	family with sequence similarity 20; member A	7.234367	up	-2.85487	0.000717	0.434291	1.175123	2.851399	2.480935	2.336132	1.609262	2.044512	56.24295	4.292841

FAM231D	family with sequence similarity 231; member D	-5.21832	down	2.383584	0.005515	0.999715	3.218816	3.725215	3.570126	3.36942	0.487655	2.149358	0	0
FBXO10	F-box protein 10	-1.78339	down	0.834621	0.025261	0.999715	16.80937	10.48579	12.70723	8.356163	7.461124	10.69437	4.344949	4.57903
FCER1A	Fc fragment of IgE; high affinity I; receptor for; alpha polypeptide	-1.7062	down	0.77079	0.002232	0.960358	89.36047	68.15764	53.06781	54.80924	38.67105	37.32544	31.1388	48.36601
FEN1	flap structure-specific endonuclease 1	-1.64786	down	0.720596	0.047546	0.999715	10.6272	10.20985	13.00978	29.74075	8.387668	9.226514	11.22445	9.778138
FHIT	fragile histidine triad	2.50404	up	-1.32426	0.007113	0.999715	1.3284	1.149758	3.267573	1.617322	7.363593	5.556878	2.232821	3.195782
FKBP11	FK506 binding protein 11; 19 kDa	-1.72199	down	0.784078	0.027164	0.999715	17.9845	13.19922	19.30289	38.50124	12.24014	16.8279	14.72455	7.917907
FN1	fibronectin 1	2.635278	up	-1.39796	0.037486	0.999715	5.517971	4.645021	3.025531	12.04006	6.485813	51.11279	5.551879	3.434273
FZD6	frizzled class receptor 6	-1.89738	down	0.924007	0.045761	0.999715	2.656801	3.03536	1.815318	4.851966	1.267903	1.677548	1.025891	2.528006
GATA2	GATA binding protein 2	-1.67808	down	0.746813	0.002727	0.960358	72.34673	46.91011	53.06781	39.44468	29.60067	28.09893	33.79405	34.67662
GGH	gamma-glutamyl hydrolase (conjugase; folylpolygammaglutamyl hydrolase)	-2.57817	down	1.36635	0.026823	0.999715	2.350247	1.655651	2.299403	13.52261	1.267903	1.258161	2.836286	2.337213
GINS2	GINS complex subunit 2 (Psf2 homolog)	-3.36484	down	1.75054	0.01052	0.999715	2.094785	1.195748	1.573276	9.659005	0.780248	0.262117	1.991435	1.287852
GLDC	glycine dehydrogenase (decarboxylating)	-3.69781	down	1.886672	0.012288	0.999715	4.036293	0.735845	4.054211	22.14832	1.560496	0.62908	4.525988	1.669438

GLUL	glutamate-ammonia ligase	2.06547	up	-1.04647	0.034027	0.999715	361.938	366.0829	290.3904	541.9825	233.8306	479.2545	1993.426	516.5719
GPR15	G protein-coupled receptor 15	-3.2566	down	1.703367	0.011898	0.999715	5.824525	3.173331	3.267573	30.68419	1.804324	7.444119	1.689702	2.241817
GPR84	G protein-coupled receptor 84	3.368709	up	-1.7522	0.005096	0.999715	0.715293	0.965796	1.089191	2.291206	1.072841	2.096935	10.50029	3.529669
GTSE1	G-2 and S-phase expressed 1	-2.76104	down	1.465213	0.024486	0.999715	1.686047	0.735845	1.754808	8.401088	0.487655	1.048467	1.689702	1.335551
H2AFX	H2A histone family; member X	-1.77456	down	0.827464	0.049299	0.999715	13.43728	10.80772	14.70408	47.98055	10.0457	9.174091	15.38836	14.40487
HBA1	hemoglobin; alpha 1	4.388191	up	-2.13363	0.000819	0.475313	28.04969	66.63996	125.8016	86.75135	27.89387	758.3565	167.5823	394.4167
HBA2	hemoglobin; alpha 2	4.004365	up	-2.00157	0.002818	0.960358	59.26709	127.1172	326.9388	176.2881	66.71122	1733.431	289.6029	671.6865
HBB	hemoglobin; beta	8.654476	up	-3.11345	0.000188	0.238204	70.20085	147.8588	284.6419	187.8789	63.24887	4635.537	337.4577	940.4661
HDC	histidine decarboxylase	-1.53112	down	0.614586	0.042928	0.999715	24.52431	23.08713	23.17557	12.12991	12.5815	15.09793	16.41425	10.06433
HERC2P3	hect domain and RLD 2 pseudogene 3	-2.95278	down	1.562074	9.04E-07	0.0126	20.6413	24.46684	19.9685	17.56591	7.948779	9.069244	7.060542	3.911255
HIST1H1B	histone cluster 1; H1b	-2.23641	down	1.161183	0.034351	0.999715	63.15011	38.12597	50.28432	335.6841	33.98956	30.19586	82.25229	71.45195
HIST1H2AB	histone cluster 1; H2ab	-2.65397	down	1.40815	0.009182	0.999715	6.233263	4.139128	6.595657	31.53778	4.827786	2.830862	6.094997	4.531332
HIST1H2AH	histone cluster 1; H2ah	-2.72266	down	1.445016	0.010092	0.999715	10.6783	5.334876	9.923741	56.56134	5.461738	5.714148	10.74168	8.394889
HIST1H2AI	histone cluster 1; H2ai	-2.49627	down	1.319776	0.01354	0.999715	19.3129	11.49758	16.70093	90.12077	10.97224	6.552922	19.97469	17.64835
HIST1H2AJ	histone cluster 1; H2aj	-3.2878	down	1.717124	0.013538	0.999715	8.78788	4.645021	10.52885	84.28044	4.2426	3.984176	15.93148	8.776475

HIST1H2AL	histone cluster 1; H2al	-2.24343	down	1.165704	0.028211	0.999715	12.0067	6.576614	10.40783	51.48475	6.827172	4.82295	13.94004	10.30282
HIST1H2AM	histone cluster 1; H2am	-1.74955	down	0.806983	0.025566	0.999715	35.56026	26.39844	37.6376	96.94946	26.33338	20.75966	37.95795	27.33109
HIST1H2BB	histone cluster 1; H2bb	-2.4328	down	1.282621	0.00562	0.999715	12.31325	5.426856	13.31234	39.39976	6.437048	6.133535	9.293362	7.107037
HIST1H2BE	histone cluster 1; H2be	-1.99964	down	0.999743	0.016146	0.999715	16.80937	12.92328	14.76459	57.77433	12.04508	10.27498	15.20732	13.6417
HIST1H2BF	histone cluster 1; H2bf	-1.77077	down	0.824374	0.014078	0.999715	29.73573	22.81119	38.84781	76.19383	25.26054	24.53414	25.16449	19.69937
HIST1H2BH	histone cluster 1; H2bh	-2.08125	down	1.057451	0.032954	0.999715	21.40768	14.21101	20.63412	88.54837	13.55681	8.38774	27.33697	20.31945
HIST1H2BI	histone cluster 1; H2bi	-1.71391	down	0.777292	0.026736	0.999715	29.53136	20.4197	26.14059	73.72292	21.50559	20.23542	24.37999	21.32111
HIST1H2BJ	histone cluster 1; H2bj	-2.20941	down	1.143659	0.009467	0.999715	17.67794	12.8313	20.15003	73.31859	12.48397	12.31949	17.2591	14.07098
HIST1H2BL	histone cluster 1; H2bl	-2.06175	down	1.043868	0.018663	0.999715	13.79493	7.634391	11.92059	40.20842	8.436434	5.452031	11.64688	10.15972
HIST1H2BM	histone cluster 1; H2bm	-2.61434	down	1.386447	0.008417	0.999715	13.69274	8.784149	12.58621	69.94917	9.509275	6.500498	14.06074	10.11203
HIST1H2BN	histone cluster 1; H2bn	-1.51981	down	0.60389	0.018212	0.999715	36.5821	29.80172	35.03565	50.63116	21.31053	27.62712	28.06113	23.08595
HIST1H2BO	histone cluster 1; H2bo	-2.01944	down	1.013957	0.023323	0.999715	14.40804	9.611974	13.6754	50.04713	10.24076	6.762615	14.54351	11.92456
HIST1H3B	histone cluster 1; H3b	-3.0289	down	1.598794	0.033853	0.999715	23.9623	10.71574	19.90799	189.2716	9.655572	3.197826	40.19078	27.47418
HIST1H3C	histone cluster 1; H3c	-3.33898	down	1.739407	0.027258	0.999715	6.539817	4.277099	4.659317	74.12725	3.901241	1.310584	12.61242	9.014966
HIST1H3F	histone cluster 1; H3f	-2.8279	down	1.499732	0.026451	0.999715	11.18922	5.564827	8.713528	75.29532	4.632724	2.935709	16.29356	11.78146
HIST1H3G	histone cluster 1; H3g	-4.51222	down	2.173839	0.011646	0.999715	7.766033	2.253525	4.96187	66.6696	1.999386	0.47181	8.99163	6.630055
HIST1H3H	histone cluster 1; H3h	-1.68759	down	0.754964	0.037233	0.999715	22.6339	20.51168	23.78067	69.14051	21.94448	16.04155	20.33677	22.32277
HIST1H3J	histone cluster 1; H3j	-3.05612	down	1.611	0.007	0.999	7.050741	3.863186	5.143402	40.11857	4.43766	2.88328	5.1898	5.86688

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HIST1H4B	histone cluster 1; H4b	-1.70705	down	0.771507	0.034106	0.999715	20.28365	16.83245	20.81565	51.5746	17.01916	21.38874	9.896828	15.83581
HIST1H4D	histone cluster 1; H4d	-2.25936	down	1.175915	0.010487	0.999715	22.07188	11.17564	16.21684	70.21872	9.02162	16.35609	11.04341	16.55129
HIST1H4F	histone cluster 1; H4f	-1.53301	down	0.616368	0.033239	0.999715	33.05673	30.26162	52.52321	70.21872	30.67351	25.21564	32.46642	33.00718
HIST1H4I	histone cluster 1; H4i	-2.44325	down	1.288799	0.012761	0.999715	8.123679	6.162701	8.955571	42.05037	4.730255	4.980221	8.629551	8.394889
HIST1H4L	histone cluster 1; H4l	-2.19874	down	1.136678	0.03261	0.999715	5.620156	3.265312	5.748508	26.46118	4.193834	3.984176	4.405295	6.105374
HIST2H3A	histone cluster 2; H3a	-3.62701	down	1.858782	0.014393	0.999715	7.408387	3.633234	6.535146	67.70289	2.877165	1.310584	9.112323	10.20742
HIST2H3C	histone cluster 2; H3c	-3.62701	down	1.858782	0.014394	0.999715	7.408387	3.633234	6.535146	67.70289	2.877165	1.310584	9.112323	10.20742
HIST2H4A	histone cluster 2; H4a	-2.18381	down	1.126844	0.043227	0.999715	17.06484	11.58956	17.60859	112.0894	11.94755	13.26311	25.0438	22.27508
HIST2H4B	histone cluster 2; H4b	-2.18381	down	1.126844	0.043228	0.999715	17.06484	11.58956	17.60859	112.0894	11.94755	13.26311	25.0438	22.27508
HLA-H	major histocompatibility complex; class I; H (pseudogene)	3.431068	up	-1.77866	0.004777	0.999715	4.087386	5.840769	4.598807	5.705552	51.59391	5.556878	9.233016	3.100385
HORMAD1	HORMA domain containing 1	2.006934	up	-1.00499	0.047307	0.999715	0.766385	1.4257	0.484085	1.797024	1.365434	1.467854	3.258711	3.004989
ICAM1	intercellular adhesion molecule 1	2.208397	up	-1.143	0.005154	0.999715	61.82171	70.2272	59.17938	86.21224	57.78713	88.43823	336.5525	130.0731
IFNG-AS1	IFNG antisense RNA 1	-2.23222	down	1.158477	0.005977	0.999715	4.751586	2.667438	5.203913	8.266312	2.243214	2.254205	2.172474	2.671101
IGF1	insulin-like growth factor 1 (somatomedin C)	-3.38232	down	1.758014	0.017489	0.999715	1.686047	0.735845	1.270723	9.164824	0.341359	0.576657	2.232821	0.667775
IGJ		-3.05619	down	1.611733	0.006174	0.999715	344.4133	114.2399	263.5237	1475.941	136.7873	103.0119	348.8632	130.5978

IGLL5	immunoglobulin lambda-like polypeptide 5	-4.41539	down	2.14254	0.001023	0.569936	674.061	204.105	444.753	3562.78	198.6219	226.9932	486.8756	194.0364
IL1B	interleukin 1; beta	2.738205	up	-1.45323	0.000465	0.380989	38.52361	20.51168	21.6628	63.61466	47.44884	70.56186	188.4018	88.95721
ILDR1	immunoglobulin-like domain containing receptor 1	-2.17575	down	1.121511	0.015003	0.999715	1.3284	1.011787	1.815318	1.212991	0.487655	0.838774	0.543119	0.572379
ITGA7	integrin; alpha 7	4.136399	up	-2.04838	0.002095	0.941466	0.919662	0.781835	0.726127	0.943438	1.072841	0.996044	10.01752	2.003326
ITM2C	integral membrane protein 2C	-2.82879	down	1.500187	0.000503	0.38917	52.47182	30.12365	50.46585	186.2616	29.99079	23.85264	33.91474	25.13697
JUN	jun proto-oncogene	-1.59609	down	0.674545	0.045091	0.999715	234.0028	190.2619	176.3884	369.3334	122.499	215.9843	196.4279	72.8829
KCNH3	potassium channel; voltage gated eag related subfamily H; member 3	1.735586	up	-0.79542	0.033831	0.999715	2.912262	5.886759	4.296254	6.424362	7.070999	7.234426	12.43138	7.250132
KIAA0101	KIAA0101	-2.93265	down	1.552204	0.015769	0.999715	2.554616	2.069564	2.480935	14.5559	0.97531	0.838774	3.439751	2.146421
KIAA0125	KIAA0125	-1.65538	down	0.727163	0.039481	0.999715	38.42143	41.06935	50.34483	38.99543	30.23462	44.82199	12.91415	13.97558
KIF23	kinesin family member 23	-2.32813	down	1.219169	0.033544	0.999715	2.707893	2.115554	3.630637	14.5559	1.950621	1.363008	3.138018	3.434273
KIF2C	kinesin family member 2C	-2.45724	down	1.29704	0.04086	0.999715	1.839324	1.747632	1.331234	11.50096	0.97531	1.310584	2.112128	2.289515
KIFC1	kinesin family member C1	-2.6718	down	1.417813	0.040636	0.999715	2.86117	1.287729	2.359914	18.73398	1.755558	0.891197	3.80183	3.004989
KIFC2	kinesin family member C2	1.613459	up	-0.69016	0.03178	0.999715	16.40064	21.75342	17.97165	10.78215	29.79573	33.65581	30.83707	13.68939
KLRC1	killer cell lectin-like receptor subfamily	-3.02448	down	1.596686	5.23E-05	0.164723	8.685695	15.6827	15.00663	12.9835	3.852476	5.976265	1.750049	5.67609

	C; member 1													
LAMB3	laminin; beta 3	2.176249	up	-1.12184	0.044386	0.999715	2.043693	1.51768	1.210212	1.527471	1.462965	1.782395	8.508858	2.051024
LILRA4	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 4	-2.02304	down	1.016522	0.008943	0.999715	10.6272	6.530624	9.742209	14.96023	5.510503	4.089023	3.077672	7.965605
LINC00920	long intergenic non-protein coding RNA 920	2.041112	up	-1.02936	0.037535	0.999715	0.919662	1.4257	1.452255	0.314479	2.584572	2.463899	1.448316	1.860231
LOC100287072		-2.25365	down	1.172264	0.022428	0.999715	1.634954	0.965796	1.391744	1.168066	0.43889	0.996044	0.663812	0.190793
LOC100379224		2.615911	up	-1.38731	0.004168	0.999715	0.970754	0.551884	0.96817	0.40433	2.877165	1.415431	1.810395	1.430947
LOC283710		-4.2361	down	2.082736	0.000224	0.260401	1.839324	1.149758	1.694297	4.80704	0.780248	0.209694	0.663812	0.572379
LPAR1	lysophosphatidic acid receptor 1	-1.67026	down	0.740069	0.040021	0.999715	8.328049	10.80772	8.713528	17.79054	7.802482	4.298717	6.39673	8.824173
LPL	lipoprotein lipase	2.385099	up	-1.25405	0.041041	0.999715	1.3284	0.873816	2.420425	3.504197	9.509275	4.875374	0.663812	4.340539
MACROD2	MACRO domain containing 2	-3.32624	down	1.733891	0.003125	0.960358	12.36434	22.94916	12.16263	4.851966	4.486427	8.38774	2.172474	0.667775
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	-1.92396	down	0.944079	0.036297	0.999715	5.160325	3.679225	3.872679	13.38783	3.852476	2.726015	3.319058	3.672764
MCM10	minichromosome maintenance 10 replication initiation factor	-3.05721	down	1.612216	0.035127	0.999715	2.094785	1.057777	1.391744	12.39947	0.487655	0.366964	3.077672	1.62174
MCM2	minichromosome maintenance	-1.74857	down	0.806173	0.024728	0.999715	19.15962	14.257	18.87931	48.74428	13.55681	13.63008	18.28499	12.35384

	complex component 2												
MEIS1	Meis homeobox 1	-1.97774	down	0.983854	0.012023	0.999715	6.693094	12.87729	8.774039	11.50096	8.777792	4.19387	3.379405	3.768161
MGAM	maltase-glucoamylase	1.858433	up	-0.89409	0.030333	0.999715	28.91825	17.43033	30.43684	25.6076	12.09385	53.10488	85.45066	39.68493
MMD	monocyte to macrophage differentiation-associated	-1.50485	down	0.589623	0.041997	0.999715	57.01903	73.5385	95.24371	75.07069	81.43841	42.93474	33.55266	41.92675
MOB3B	MOB kinase activator 3B	-1.55531	down	0.6372	0.029301	0.999715	19.87491	20.60366	18.39523	13.1632	13.65434	12.73888	8.086432	11.78146
MS4A2	membrane-spanning 4-domains; subfamily A; member 2	-2.08909	down	1.062872	0.000126	0.195344	26.51692	19.40791	16.64042	19.54264	9.948165	9.069244	11.04341	9.253457
MS4A7	membrane-spanning 4-domains; subfamily A; member 7	1.783125	up	-0.83441	0.02668	0.999715	88.38972	80.29908	49.31615	56.11208	76.80568	50.6934	126.5466	234.7707
MTRNR2L2	MT-RNR2-like 2	3.394768	up	-1.76331	0.001592	0.796657	0.919662	0.781835	1.149702	1.078215	2.194448	1.100891	2.474207	7.584019
MTRNR2L8	MT-RNR2-like 8	2.120764	up	-1.08458	0.010027	0.999715	2.758985	2.759418	2.238893	1.707173	4.096303	3.250249	4.525988	8.204096
MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	-3.83673	down	1.939876	0.00655	0.999715	15.3277	4.828982	19.00033	80.37191	2.487041	1.625125	14.78489	12.25845
MYO15B	myosin XVB	1.752552	up	-0.80946	0.002397	0.960358	87.06132	73.35454	83.56516	46.76756	103.6267	178.554	118.7016	108.6089
MYO1D	myosin ID	-1.77758	down	0.829	0.025	0.999	20.74348	11.17564	13.73591	36.25496	9.02162	15.4124	13.3365	8.34719

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MYO7B	myosin VIIB	-1.95099	down	0.964203	0.031903	0.999715	11.3425	11.54357	9.500166	5.705552	6.290751	1.677548	8.327818	3.24348
MYOM2	myomesin 2	9.93152	up	-3.31201	1.51E-05	0.104907	2.299155	2.437486	3.025531	5.93018	43.01118	1.729971	7.482967	84.04429
MZB1	marginal zone B and B1 cell-specific protein	-3.79798	down	1.925232	0.002812	0.960358	18.75088	5.97874	15.24867	100.0044	6.339517	5.661724	19.00915	5.866883
NABP1	nucleic acid binding protein 1	1.882447	up	-0.91261	0.024162	0.999715	38.37033	41.11534	35.27769	48.11532	30.47845	65.42437	168.9702	41.87905
NAMPT	nicotinamide phosphoribosyltransferase	3.163894	up	-1.6617	0.00674	0.999715	416.5046	305.2377	237.1411	469.5175	145.2725	564.5997	3101.267	708.3188
NDC80	NDC80 kinetochore complex component	-2.07283	down	1.051602	0.021802	0.999715	5.517971	4.001157	3.812169	14.78052	2.8284	3.407519	4.103563	3.24348
NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	1.837209	up	-0.87752	0.032018	0.999715	546.8922	632.8266	580.2363	244.6199	524.083	815.2359	1760.73	582.8247
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; zeta	1.609396	up	-0.68652	0.019043	0.999715	293.4232	308.595	275.0207	302.0798	335.6043	349.9785	753.9089	458.2846
NINL	ninein-like	1.843927	up	-0.88278	0.036096	0.999715	2.554616	2.069564	2.541446	1.437619	3.511117	3.459943	6.094997	2.814196
NLRP2	NLR family; pyrin domain containing 2	2.741853	up	-1.45515	0.001891	0.878231	1.021846	3.173331	3.025531	1.572396	5.851862	7.653813	7.724353	2.909592
NLRP3	NLR family; pyrin domain containing 3	1.833234	up	-0.87439	0.02949	0.999715	96.46231	104.168	85.86456	99.42037	83.43779	74.33635	380.4847	169.3287
NUAK1	NUAK family;	3.554842	up	-	0.005	0.999	1.124031	0.643864	1.573276	1.12314	0.92654	3.30267	10.5606	1.14475

	SNF1-like kinase; 1			1.82979	668	715					5	3	4	8
NUGGC	nuclear GTPase; germinal center associated	-1.65614	down	0.727824	0.027859	0.999715	15.22551	11.17564	11.376	23.94535	6.973468	11.27103	10.3796	8.681079
NXPH4	neurexophilin 4	-2.73928	down	1.453794	0.029099	0.999715	1.226216	2.621448	2.722978	0.763735	0.877779	1.467854	0.060347	0.238491
ORC1	origin recognition complex; subunit 1	-2.29987	down	1.201552	0.042209	0.999715	3.321001	1.47169	2.843999	12.6241	2.048152	0.996044	3.439751	2.337213
ORM1	orosomucoid 1	2.189152	up	-1.13037	0.027621	0.999715	0.613108	1.51768	1.512765	1.797024	1.267903	1.939665	3.741484	5.008315
OSBPL10	oxysterol binding protein-like 10	-2.10063	down	1.070825	0.009068	0.999715	53.95349	49.16364	36.36688	26.55103	25.99202	35.07124	7.301928	10.63671
OTOF	otoferlin	-4.31533	down	2.109472	0.047938	0.999715	0.357646	1.333719	0.907659	40.47797	0.43889	1.258161	7.241581	1.049361
PACSIN1	protein kinase C and casein kinase substrate in neurons 1	-2.42763	down	1.279546	0.000388	0.380989	7.408387	5.794779	8.047912	10.46767	2.974696	2.935709	3.077672	4.05435
PCDHGC3	protocadherin gamma subfamily C; 3	-2.00005	down	1.000034	0.02301	0.999715	2.554616	1.609661	2.904509	1.797024	1.560496	0.943621	0.784505	1.097059
PDGFRA	platelet-derived growth factor receptor; alpha polypeptide	-2.06867	down	1.048701	0.041075	0.999715	1.021846	1.103767	2.541446	1.392694	1.024076	0.943621	0.241386	0.667775
PDLIM1	PDZ and LIM domain 1	-1.57722	down	0.657384	0.008563	0.999715	55.28189	58.3617	56.63793	51.934	35.15994	47.28588	35.18201	23.27674
PFKFB3	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 3	3.048141	up	-1.60793	0.002536	0.960358	77.14941	111.2965	73.21784	126.0613	61.10319	134.4135	771.9525	214.5467
PHLDA1	pleckstrin homology-like domain; family A; member 1	2.774144	up	-1.47204	0.014542	0.999715	10.26956	9.703955	7.140252	10.37782	5.754331	11.4283	78.08838	8.871872

PKIG	protein kinase (cAMP-dependent; catalytic) inhibitor gamma	-1.73742	down	0.796946	0.044605	0.999715	14.76568	20.46569	15.49072	6.783767	11.55743	11.4283	5.069107	5.008315
PLA2G4C	phospholipase A2; group IVC (cytosolic; calcium-independent)	2.088724	up	-1.06262	0.048248	0.999715	2.554616	0.689855	3.207063	2.470908	2.438276	2.044512	6.21569	7.917907
PLAC4	placenta-specific 4	-2.28963	down	1.195114	0.020363	0.999715	4.087386	3.219322	2.601956	0.673884	1.4142	1.048467	1.086237	1.049361
PLD4	phospholipase D family; member 4	-1.58131	down	0.66112	0.038888	0.999715	28.96935	24.88076	32.13114	10.91692	16.92163	13.78735	13.759	16.74208
PLEKHG7	pleckstrin homology domain containing; family G (with RhoGef domain) member 7	-2.25902	down	1.175698	0.025548	0.999715	2.707893	2.023574	1.815318	1.347768	0.877779	1.782395	0.482772	0.333888
PLK1	polo-like kinase 1	-3.31302	down	1.728147	0.015693	0.999715	3.576463	1.149758	3.086041	20.48608	1.219138	0.733927	3.922523	2.671101
PLK3	polo-like kinase 3	1.727802	up	-0.78894	0.018933	0.999715	38.5747	42.2191	30.31582	20.48608	35.98895	43.45898	102.4684	45.55181
PNOC	prepronociceptin	-1.83081	down	0.872485	0.034449	0.999715	7.561664	6.392653	6.172083	6.963469	3.608648	6.605345	2.715593	1.860231
POC1A	POC1 centriolar protein A	-2.43515	down	1.284008	0.044013	0.999715	1.226216	0.965796	1.391744	6.109882	0.877779	0.262117	1.508663	1.335551
POU2AF1	POU class 2 associating factor 1	-2.06935	down	1.049175	0.000606	0.434291	106.3231	96.25771	97.72464	194.1685	57.54331	87.96642	57.26884	36.20296
PTPRS	protein tyrosine phosphatase; receptor type; S	-2.00178	down	1.001286	0.000282	0.302015	36.53101	25.84655	39.15037	27.31477	16.43398	15.36005	11.58653	20.89183
PTTG1	pituitary tumour-transforming 1	-2.3999	down	1.262975	0.017894	0.999715	5.466879	3.219322	3.570126	18.91368	2.38951	2.463899	5.008763	3.148083
RAD51	RAD51 recombinase	-2.64744	down	1.4046	0.013871	0.999715	1.634954	1.701641	1.875829	8.17646	0.780248	1.100891	1.508663	1.669438

RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	-2.86266	down	1.517357	0.00308	0.960358	2.094785	1.51768	2.420425	1.617322	0.926545	1.048467	0.482772	0.190793
RASGEF1B	RasGEF domain family; member 1B	2.155938	up	-1.10832	0.014341	0.999715	26.36364	26.67438	20.63412	17.29636	18.3846	26.42138	119.1844	32.24401
RETN	resistin	-2.24258	down	1.165161	0.045101	0.999715	7.817125	13.98105	1.875829	5.615701	1.4142	1.258161	4.043216	6.343865
RRM2	ribonucleotide reductase M2	-2.93939	down	1.555516	0.033357	0.999715	13.89711	9.106081	12.70723	127.3641	6.924703	3.092979	29.4491	16.02661
RYR3	ryanodine receptor 3	-2.15657	down	1.108741	0.012485	0.999715	3.627555	4.599031	3.449105	1.572396	1.511731	1.415431	1.327623	1.860231
SCAMP5	secretory carrier membrane protein 5	-1.80582	down	0.85265	0.041297	0.999715	7.766033	3.357292	5.445955	9.928559	3.218524	2.306628	4.767374	4.388238
SDC1	syndecan 1	-6.28349	down	2.651566	0.003655	0.999715	1.021846	0.229952	1.02868	11.00677	0.341359	0.209694	1.327623	0.238491
SEC11C	SEC11 homolog C; signal peptidase complex subunit	-1.77299	down	0.826181	0.030601	0.999715	27.2833	16.09661	24.80935	68.51155	14.92225	16.51336	27.15593	18.55461
SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	-1.77994	down	0.831825	0.002297	0.960358	189.7569	154.2515	151.6396	206.2535	79.92668	153.3908	88.58868	72.45362
SERF1B	small EDRK-rich factor 1B (centromeric)	-2.74923	down	1.459028	0.020821	0.999715	8.78788	16.83245	1.875829	6.289585	1.316669	3.617213	6.57777	0.81087
SERPINF1	serpin peptidase inhibitor; clade F (alpha-2 antiplasmin; pigment epithelium derived factor); member 1	-1.64231	down	0.715723	0.026423	0.999715	9.094433	8.232265	9.80272	12.66902	5.803096	6.448075	5.1898	6.773149
SIGLEC12	sialic acid binding Ig-like lectin 12 (gene/pseudogene)	-2.64411	down	1.402783	0.004881	0.999715	1.175123	2.161544	1.089191	2.515834	0.877779	0.47181	0.905198	0.381586
SLA	Src-like-adaptor	1.510145	up	-	0.012	0.999	87.21459	86.69173	83.56516	76.05905	117.915	89.4867	162.814	133.507

				0.59469	951	715							9	4
SLC22A16	solute carrier family 22 (organic cation/carnitine transporter); member 16	2.706796	up	-1.43659	0.040045	0.999715	0.408739	1.057777	0.060511	3.324495	2.291979	2.306628	5.310493	3.386575
SLC25A37	solute carrier family 25 (mitochondrial iron transporter); member 37	1.974517	up	-0.9815	0.013203	0.999715	31.57506	33.38896	34.30952	43.17351	25.74819	66.31557	146.4006	42.92841
SLC27A2	solute carrier family 27 (fatty acid transporter); member 2	-2.58442	down	1.369841	0.028735	0.999715	1.634954	1.747632	1.149702	7.277948	0.292593	1.153314	1.508663	1.62174
SLC4A1	solute carrier family 4 (anion exchanger); member 1 (Diego blood group)	5.900634	up	-2.56087	5.91E-05	0.164723	1.992601	3.771205	2.601956	3.728825	1.316669	32.2928	9.414055	28.52354
SNCA	synuclein; alpha (non A4 component of amyloid precursor)	1.779387	up	-0.83138	0.030616	0.999715	8.328049	16.41854	12.16263	12.17484	13.36175	43.61625	14.6642	15.74042
SNX25	sorting nexin 25	-1.55647	down	0.638281	0.049891	0.999715	25.13742	24.42085	23.3571	20.84548	18.43336	22.80417	7.362274	11.59067
SOD2	superoxide dismutase 2; mitochondrial	1.590894	up	-0.66984	0.048628	0.999715	226.9521	227.606	220.5007	332.2249	185.9429	304.7371	658.9235	452.9901
SPATA6	spermatogenesis associated 6	1.577486	up	-0.65763	0.046713	0.999715	11.59796	8.278255	9.923741	9.928559	13.02039	8.807127	17.80222	23.03825
STMN1	stathmin 1	-1.86193	down	0.896798	0.024067	0.999715	31.42178	23.17912	25.53548	99.68992	27.45498	19.23938	24.86276	25.04157
TBC1D16	TBC1 domain family; member 16	1.76984	up	-0.823	0.041942	0.999715	5.517971	5.702798	3.328084	3.773751	8.338903	12.05738	3.560444	8.490286

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TCF4	transcription factor 4	-1.53862	down	0.621634	0.004649	0.999715	95.23609	85.03608	87.37733	87.15568	57.49454	66.89223	50.32899	55.85463
TGFB2	transforming growth factor; beta 2	-1.91314	down	0.935942	0.043397	0.999715	1.175123	1.931593	1.99685	1.347768	1.024076	1.205738	0.543119	0.572379
THBD	thrombomodulin	2.670207	up	-1.41695	0.039498	0.999715	19.3129	22.99515	10.22629	52.60789	8.875323	31.71614	215.3767	24.94618
TK1	thymidine kinase 1; soluble	-2.04935	down	1.035163	0.045653	0.999715	4.445032	4.139128	4.356764	19.90204	2.584572	3.092979	5.793265	4.57903
TMEM156	transmembrane protein 156	-1.72517	down	0.786737	0.043128	0.999715	14.30585	8.002314	9.197613	14.24142	5.754331	11.2186	3.319058	6.20077
TNF	tumour necrosis factor	1.695271	up	-0.76152	0.020077	0.999715	11.2914	13.70511	13.00978	13.79216	15.94632	12.00495	33.79405	26.13863
TNFRSF10D	tumour necrosis factor receptor superfamily; member 10d; decoy with truncated death domain	1.504296	up	-0.58909	0.038907	0.999715	17.47357	17.66028	19.66595	18.91368	27.69881	17.29971	40.6132	25.32776
TNFRSF13B	tumour necrosis factor receptor superfamily; member 13B	-2.16353	down	1.113385	0.012925	0.999715	3.934109	4.782992	7.261274	10.91692	2.925931	5.242337	1.810395	2.43261
TNFRSF17	tumour necrosis factor receptor superfamily; member 17	-3.45525	down	1.788788	0.009315	0.999715	5.517971	1.195748	4.477785	24.61923	1.511731	1.205738	5.129453	2.528006
TOP2A	topoisomerase (DNA) II alpha	-2.32283	down	1.215886	0.044546	0.999715	15.78753	9.474003	13.97795	78.44011	6.241986	3.931753	22.81098	17.69604
TP63	tumour protein p63	-2.40021	down	1.263163	0.007428	0.999715	4.802678	1.931593	2.904509	7.682279	1.901855	1.572701	2.172474	1.574042
TPD52	tumour protein D52	-1.74469	down	0.802971	0.002858	0.960358	55.63954	46.58818	44.95939	45.91397	25.4556	41.72901	20.33677	23.13364

TPX2	TPX2; microtubule-associated	-2.58915	down	1.37248	0.037359	0.999715	9.758634	3.311302	5.264423	43.98217	3.072227	2.254205	10.74168	8.013303
TREM1	triggering receptor expressed on myeloid cells 1	1.860309	up	-0.89554	0.014285	0.999715	69.63884	74.73425	58.1507	82.07908	55.20256	100.3383	267.4557	106.6056
TREML3P	triggering receptor expressed on myeloid cells-like 3; pseudogene	2.137964	up	-1.09624	0.025401	0.999715	0.6642	0.413913	0.605106	1.212991	1.4142	1.100891	2.474207	1.287852
TRIM47	tripartite motif containing 47	-2.37663	down	1.248916	0.022981	0.999715	1.583862	1.241738	1.149702	4.133156	0.633952	1.572701	0.482772	0.715474
TRIP13	thyroid hormone receptor interactor 13	-2.78516	down	1.477759	0.017239	0.999715	1.686047	1.241738	1.875829	9.030047	0.877779	0.786351	2.172474	1.144758
TSPAN13	tetraspanin 13	-1.76541	down	0.820001	0.028429	0.999715	22.17407	20.32772	17.85063	9.299601	10.33829	16.19882	7.362274	5.532995
TXNDC5	thioredoxin domain containing 5 (endoplasmic reticulum)	-3.38403	down	1.758743	0.002825	0.960358	209.1209	83.15048	146.0121	1058.447	87.63163	74.59846	195.7037	84.37818
TYMS	thymidylate synthetase	-3.45823	down	1.790034	0.018593	0.999715	6.233263	3.311302	5.506466	54.22521	1.85309	1.205738	9.776134	7.202433
VENTX	VENT homeobox	1.627513	up	-0.70267	0.026841	0.999715	9.145526	8.600188	12.58621	9.883633	13.75187	10.3274	23.05237	18.31612
VNN1	vanin 1	1.989635	up	-0.9925	0.030269	0.999715	19.05744	23.17912	7.382295	22.41788	29.99079	16.46094	79.11427	17.93454
VSIG4	V-set and immunoglobulin domain containing 4	2.573438	up	-1.3637	0.000444	0.380989	3.883017	3.173331	2.96502	3.099867	6.827172	13.94462	7.664007	5.3899
WDR34	WD repeat domain 34	-1.92122	down	0.942022	0.016773	0.999715	4.904863	5.150915	4.235743	8.580791	2.096917	3.669636	3.198365	2.957291
YBEY	ybeY metallopeptidase	-1.72643	down	0.787791	0.023307	0.999715	10.52502	10.53178	5.86953	13.07335	7.070999	5.085067	5.491532	5.532995

ZNF608	(putative) zinc finger protein 608	-1.87061	down	0.90351	0.042128	0.999715	12.05779	11.95748	7.805869	3.773751	3.608648	8.54501	3.862177	3.004989

Supplementary Table S2. Primers used in the present study.

Genes	Primer sequences (5’-3’)
CDC6	Forward primer: TGTTCTCCTCGTGTAAAAGCC
	Reverse primer: GGGGAGTGTTGCATAGGTTGT
CCNB1	Forward primer: TTGGGGACATTGGTAACAAAG
	Reverse primer: ATAGGCTCAGGCGAAAGTTTTT
RRM2	Forward primer: CACGGAGCCGAAAACTAAAGC
	Reverse primer: TCTGCCTTCTTATACATCTGCCA
ASPM	Forward primer: GGCCCTAGACAACCCTAACGA
	Reverse primer: AGCTTGGTGTTTCAGAACATCA
DTL	Forward primer: TCACTGGAATGCCGTCTTTGA
	Reverse primer: CTCACCAGCTTTTACGTCCC
GAPDH	Forward primer: CCTGCACCACCAACTGCTTA
	Reverse primer: GGCCATCCACAGTCTTCTGAG

Supplementary Table S3-1. GO analysis of mRNAs involved in biological processes.

Downregulated			
Term	Function	Count	*p*-value
GO:0006954	inflammatory response	9	9.11E-06
GO:0006955	immune response	8	1.57E-04
GO:0007155	cell adhesion	6	8.91E-03
GO:0006508	proteolysis	6	1.26E-02
GO:0015701	bicarbonate transport	5	6.74E-06

Supplementary Table S3-2. KEGG pathway analysis of mRNAs.

Upregulated			
Term	Function	Count	*p*-value
GO:0006334	nucleosome assembly	19	5.09E-20
GO:0007067	mitotic nuclear division	15	7.51E-10
GO:0051301	cell division	14	4.33E-07
GO:0044267	cellular protein metabolic process	13	1.45E-11
GO:0031047	gene silencing by RNA	12	1.42E-10

Supplementary Table S4. Degree, closeness and betweenness scores for the top 10 upregulated genes.

Downregulated			
Term	Function	Count	*p*-value
hsa04610	Complement and coagulation cascades	7	7.31E-07
hsa05150	Staphylococcus aureus infection	6	4.96E-06
hsa05142	Chagas disease	6	1.22E-04
hsa05143	African trypanosomiasis	5	1.63E-05
hsa05144	Rheumatoid arthritis	4	8.37E-03

Gene ID	**Gene name**	**Degree**	**Closeness**	**Betweenness**
CCNB1	cyclin B1	48	82.08333	597.6878
CDC6	cell division cycle 6	47	81.83333	582.0712
TOP2A	topoisomerase (DNA) II alpha	40	76.95	380.6416
BIRC5	baculoviral IAP repeat containing 5	36	78.58333	824.264
KIF2C	kinesin family member 2C	35	73.11667	51.22497
RRM2	ribonucleotide reductase M2	35	74.91667	152.8886
CDC20	cell division cycle 20	35	73.11667	51.22497
ASPM	abnormal spindle microtubule assembly	35	73.11667	128.5843
KIF23	kinesin family member 23	34	72.61667	12.64816
DTL	denticleless E3 ubiquitin protein ligase homolog	34	72.61667	12.64816

Upregulated			
Term	Function	Count	*p*-value
hsa05322	Systemic lupus erythematosus	23	1.05E-22
hsa05034	Alcoholism	23	5.85E-20
hsa05203	Viral carcinogenesis	13	2.49E-07
hsa04110	Cell cycle	10	1.57E-06
hsa05202	Transcriptional misregulation in cancer	8	7.72E-04

Supplementary Table S5. Three modules from the PPI network with MCODE scores ≥5 and >5 nodes.

Cluster	Score	Nodes	Edges
1	32.667	34	539
2	24.75	25	297
3	6.667	16	50

Supplementary Table S6. Laboratory indicator and clinical characteristics of RA patients investigated.

Characteristics		**ASPM**	**DTL**	**RRM2**
IL-1α (pg/ml)[b]	154.00(121.76,166.71)	r=-0.085	r=-0.141	r=-0.128
		p=0.592	*p*=0.344	*p*=0.390
IL-1β (pg/ml)[b]	48.20(45.29,52.37)	r=0.031	r=0.229	r=0.086
		p=0.846	*p*=0.122	*p*=0.563
TNF-α (pg/ml)[a]	60.65±15.03	r=-0.250	r=-0.301	r=-0.244
		p=0.110	*p*=0.040	*p*=0.098
IFN-γ (pg/ml)[a]	511.68±217.29	r=-0.010	r=0.259	r=0.116
		p=0.948	*p*=0.079	*p*=0.439
IL-6 (ng/ml)[b]	33.46(26.66,39.10)	r=-0.255	r=-0.500	r=-0.103
		p=0.103	*p*=0.738	*p*=0.493
IL-8 (pg/ml)[b]	1507.78(1239.72,1809.17)	r=-0.178	r=-0.323	r=-0.180
		p=0.259	*p*=0.027	*p*=0.225
WBC (×109/L)[b]	7.13(5.33,8.40)	r=-0.027	r=-0.235	r=-0.132
		p=0.867	*p*=0.111	*p*=0.378
Lymphocyte ($\times 10^9$/L)[b]	1.53(1.25,2.00)	r=0.034	r=-0.123	r=-0.027
		p=0.831	*p*=0.409	*p*=0.856
Monocyte ($\times 10^9$/L)[a]	0.51±0.29	r=0.082	r=-0.104	r=-0.048
		p=0.608	*p*=0.488	*p*=0.747
CRP (mg/L)[b]	25.14(5.10,73.40)	r=0.200	r=-0.036	r=0.092
		p=0.205	*p*=0.812	*p*=0.539
ESR (mm/h)[a]	61.17±34.13	r=0.036	r=0.138	r=0.216
		p=0.819	*p*=0.355	*p*=0.145
DAS28-CRP[a]	4.06±1.14	r=0.210	r=0.164	r=0.271
		p=0.182	*p*=0.271	*p*=0.066
DAS28-ESR[b]	4.90(4.10,5.70)	r=0.167	r=0.263	r=0.350
		p=0.292	*p*=0.074	*p*=0.016
SDAI[a]	21.79±11.76	r=0.190	r=0.154	r=0.263
		p=0.227	*p*=0.301	*p*=0.075
CDAI[a]	17.89±9.83	r=0.173	r=0.258	r=0.336
		p=0.273	*p*=0.080	*p*=0.021
Disease duration (month)[b]	1008.00(158.40,1872.00)	r=0.138	r=-0.009	r=0.063
		p=0.383	*p*=0.953	*p*=0.673
Swollen joints[b]	6.00(2.00,10.00)	r=0.162	r=0.217	r=0.293
		p=0.305	*p*=0.143	*p*=0.046
Tender joints[b]	6.00(3.00,10.00)	r=0.199	r=0.274	r=0.362
		p=0.207	*p*=0.062	*p*=0.012

[a]Expressed as mean±standard deviation; [b]Expressed as the median (25th to 75th percentile).

Supplementary Table S7. ROC curve validates the diagnostic value of differentially expressed genes from patients with RA.

Variables	**AUC**	***p*-value**	**95%CI**	**Sensitivity**	**Specificity**	**Cut-off value**
ASPM	0.654	0.019	0.540-0.756	0.571	0.821	0.001906858
DTL	0.995	<0.001	0.949-1.000	1.000	0.975	0.000000004
RRM2	0.990	<0.001	0.941-1.000	1.000	0.975	0.000000026