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FIG. 1

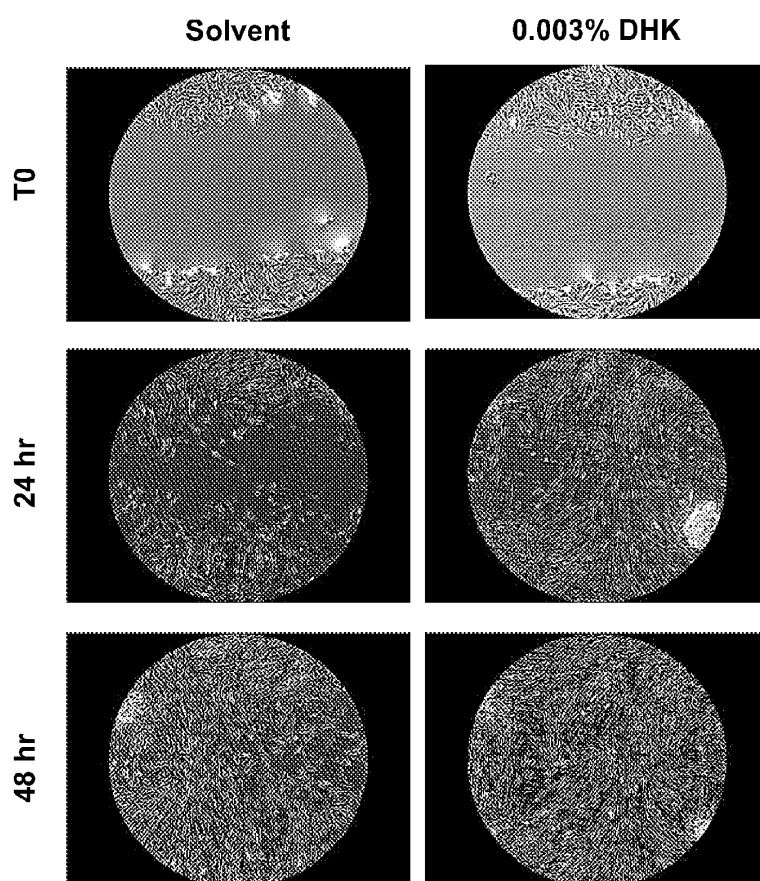
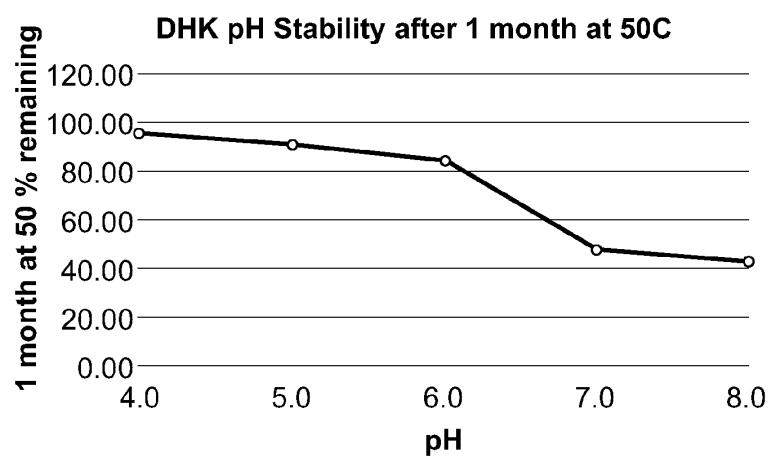
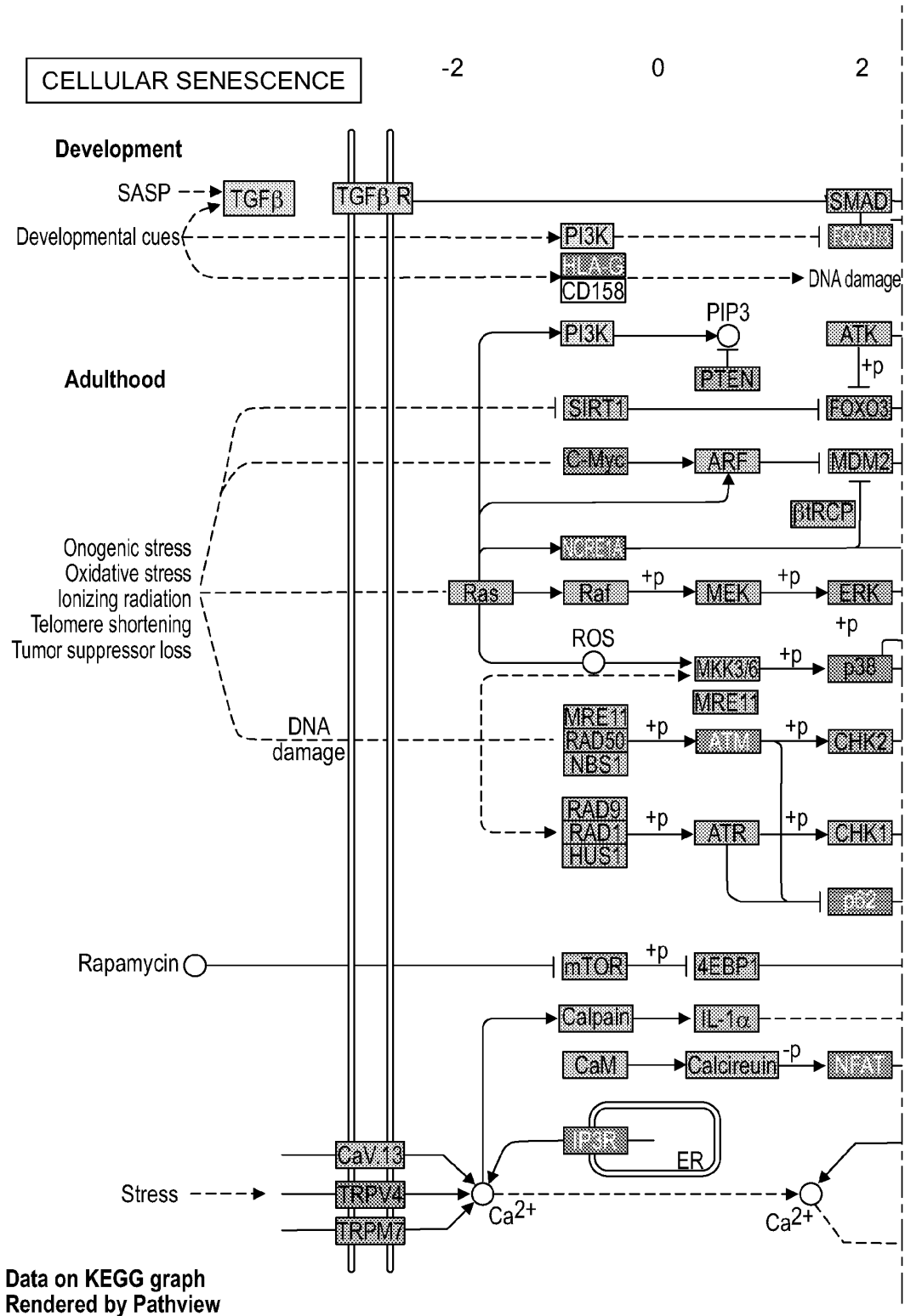


FIG. 2

FIG. 3



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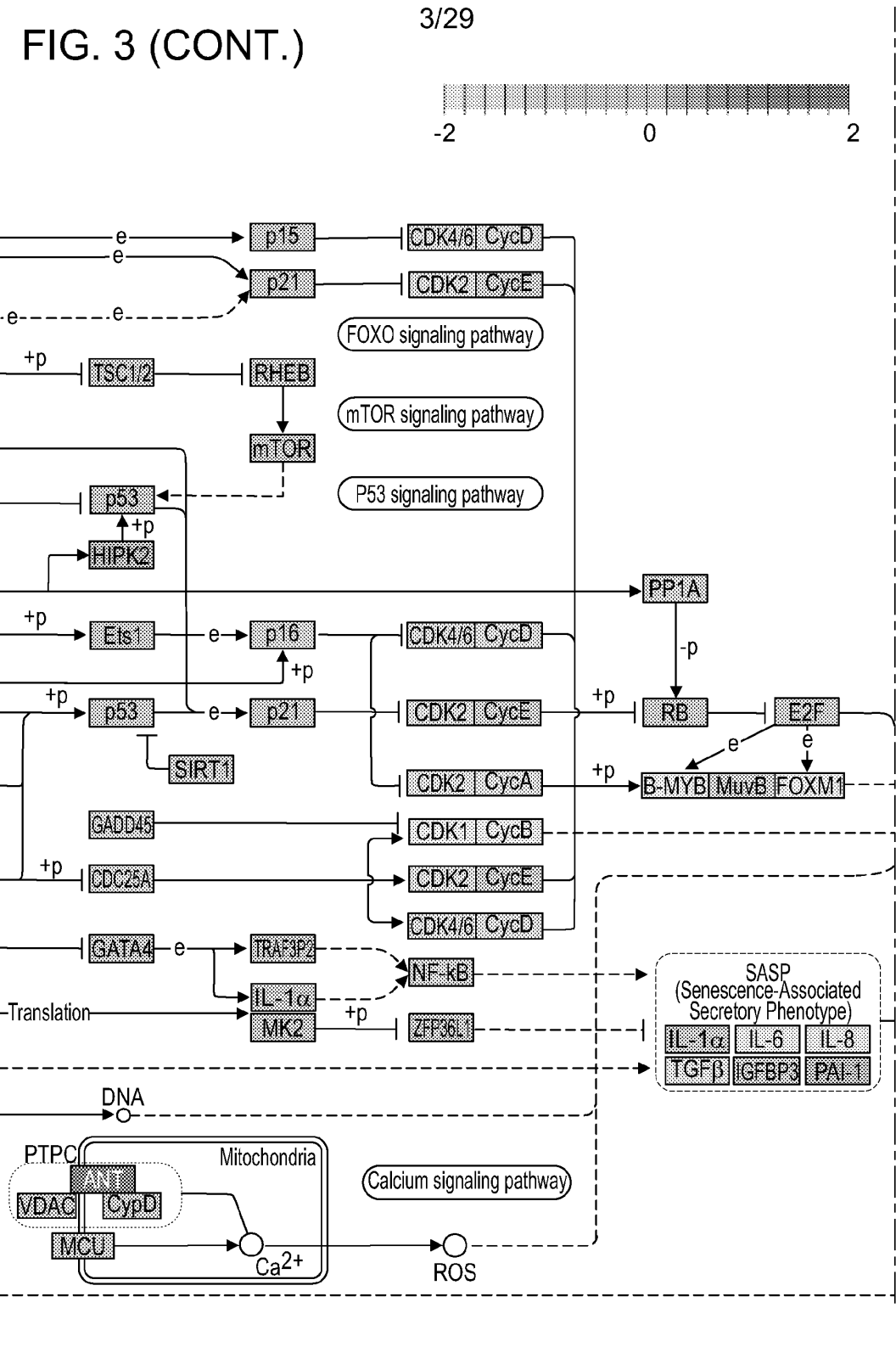
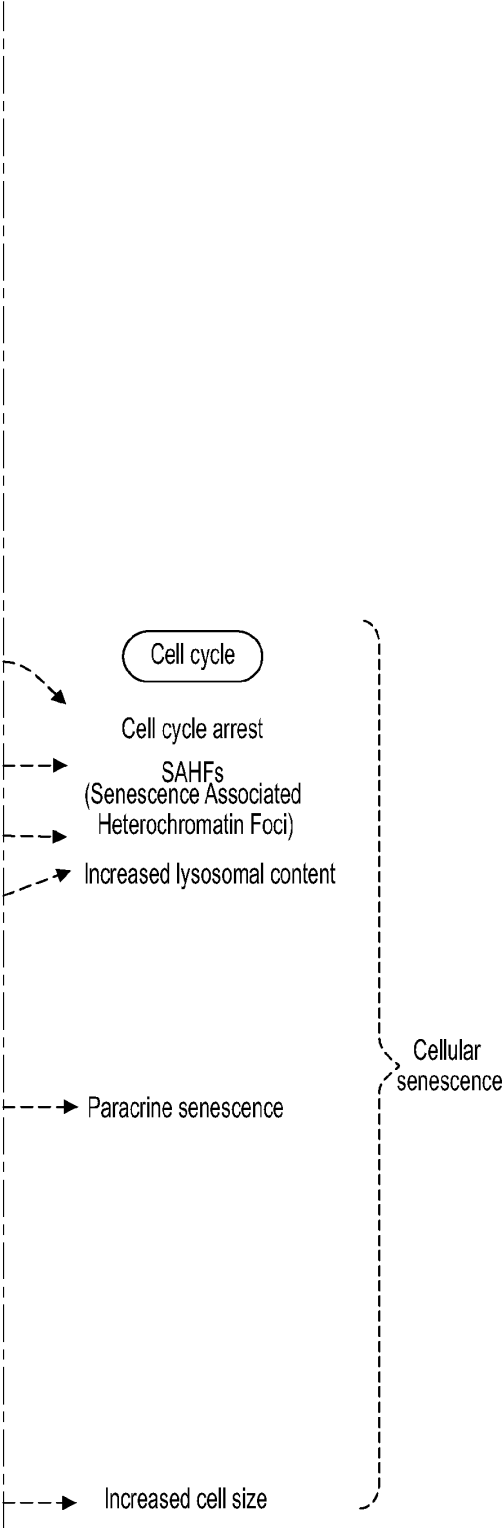


FIG. 3 (CONT.)



Pathway	Gene_name	log2FoldChange	padj	Description
Cell cycle	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2
Cell cycle	CDK6	-0.789007721	1.48E-14	cyclin dependent kinase 6
Cell cycle	CDKN1A	-0.541742013	1.70E-26	cyclin dependent kinase inhibitor 1A
Cell cycle	STAG1	-0.703145026	5.78E-07	stromal antigen 1
Cell cycle	CDKN1C	3.4912843	1.37E-14	cyclin dependent kinase inhibitor 1C
Cell cycle	CDKN2A	-0.952618945	6.15E-20	cyclin dependent kinase inhibitor 2A
Cell cycle	CDKN2B	-0.559997143	1.88E-06	cyclin dependent kinase inhibitor 2B
Cell cycle	CDKN2C	-1.840018466	5.96E-14	cyclin dependent kinase inhibitor 2C
Cell cycle	CDKN2D	0.720862427	9.69E-06	cyclin dependent kinase inhibitor 2D
Cell cycle	NDC80	-2.834181023	7.49E-58	NDC80 kinetochore complex component
Cell cycle	DBF4	-1.110657768	2.58E-13	DBF4 zinc finger
Cell cycle	YWHAQ	-0.517258997	2.26E-28	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta
Cell cycle	CHEK1	-0.641976893	1.58E-06	checkpoint kinase 1
Cell cycle	CDCA5	-1.738047663	9.24E-75	cell division cycle associated 5
Cell cycle	ESCO1	0.806131611	1.98E-12	establishment of sister chromatid cohesion N-acetyltransferase 1
Cell cycle	ANAPC16	0.71378337	2.61E-31	anaphase promoting complex subunit 16
Cell cycle	SGO1	-1.652484126	6.13E-14	shugoshin 1
Cell cycle	ESCO2	-1.537847781	1.09E-13	establishment of sister chromatid cohesion N-acetyltransferase 2
Cell cycle	E2F1	-0.613484701	7.13E-05	E2F transcription factor 1
Cell cycle	ORC6	-1.316761677	7.16E-20	origin recognition complex subunit 6
Cell cycle	ANAPC15	-1.337835166	9.32E-49	anaphase promoting complex subunit 15
Cell cycle	FBXO5	-1.213464515	3.91E-22	F-box protein 5
Cell cycle	MTBP	-0.605942933	0.025214701	MDM2 binding protein
Cell cycle	HDAC1	-0.514128471	1.58E-14	histone deacetylase 1
Cell cycle	MAD2L1	-1.443505246	1.61E-67	mitotic arrest deficient 2 like 1
Cell cycle	SMAD3	-0.660678576	6.52E-10	SMAD family member 3
Cell cycle	MCM2	-1.023975365	6.64E-43	minichromosome maintenance complex component 2
Cell cycle	MCM3	-0.773150347	4.62E-30	minichromosome maintenance complex component 3
Cell cycle	MCM4	-1.333784723	3.43E-40	minichromosome maintenance complex component 4
Cell cycle	MCM5	-1.269809895	7.70E-57	minichromosome maintenance complex component 5
Cell cycle	MCM6	-0.763520908	1.40E-25	minichromosome maintenance complex component 6
Cell cycle	MCM7	-1.240342504	1.28E-89	minichromosome maintenance complex component 7
Cell cycle	GADD45B	-0.895079733	2.29E-14	growth arrest and DNA damage inducible beta
Cell cycle	ATM	0.812453681	0.002891499	ATM serine/threonine kinase
Cell cycle	ORC1	-1.357546324	3.38E-26	origin recognition complex subunit 1
Cell cycle	PCNA	-0.69003319	2.83E-22	proliferating cell nuclear antigen
Cell cycle	FZR1	-0.607451367	3.37E-17	fizzy and cell division cycle 20 related 1
Cell cycle	PLK1	-4.355361139	0	polo like kinase 1
Cell cycle	PPP2CA	-0.509609413	5.36E-22	protein phosphatase 2 catalytic subunit alpha
Cell cycle	PPP2R1A	-0.693427968	1.09E-30	protein phosphatase 2 scaffold subunit Aalpha
Cell cycle	PPP2R1B	-0.594751747	6.34E-05	protein phosphatase 2 scaffold subunit Abeta

FIG. 4

Cell cycle	PPP2R5B	0.64992865	1.11E-10	protein phosphatase 2 regulatory subunit B'beta
Cell cycle	PPP2R5E	-0.566584163	3.03E-08	protein phosphatase 2 regulatory subunit B'epsilon
Cell cycle	PRKDC	-0.598853625	3.16E-12	protein kinase, DNA-activated, catalytic subunit
Cell cycle	KNL1	-2.374782096	3.55E-22	kinetochore scaffold 1
Cell cycle	RAD21	-0.603855089	2.37E-29	RAD21 cohesin complex component
Cell cycle	SKP2	-1.106810951	5.00E-30	S-phase kinase associated protein 2
Cell cycle	BUB1	-2.944762683	1.02E-80	BUB1 mitotic checkpoint serine/threonine kinase
Cell cycle	BUB1B	-2.345302592	6.43E-76	BUB1 mitotic checkpoint serine/threonine kinase B
Cell cycle	TGFBP1	-0.711574022	1.56E-21	transforming growth factor beta 1
Cell cycle	TGFB2	-1.129068552	5.00E-33	transforming growth factor beta 2
Cell cycle	TGFB3	-0.876774301	0.032751479	transforming growth factor beta 3
Cell cycle	TP53	-0.654172318	7.66E-13	tumor protein p53
Cell cycle	TTK	-2.323581955	3.02E-39	TTK protein kinase
Cell cycle	YWHAH	-0.844196884	4.98E-62	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta
Cell cycle	YWHAH	-0.677792624	1.88E-35	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
Cell cycle	YWHAH	-0.75539509	1.19E-42	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta
Cell cycle	YWHAZ	-0.655944784	3.03E-35	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta
Cell cycle	DBF4B	-1.279258812	4.10E-06	DBF4 zinc finger B
Cell cycle	SMC1A	-0.977896739	1.71E-11	structural maintenance of chromosomes 1A
Cell cycle	CDC45	-1.886043519	1.06E-30	cell division cycle 45
Cell cycle	CCNB3	2.841383388	0.003556627	cyclin B3
Cell cycle	CCNA2	-3.101014872	9.01E-232	cyclin A2
Cell cycle	CCNA1	2.773918343	1.19E-125	cyclin A1
Cell cycle	CCNB1	-2.783469794	1.66E-219	cyclin B1
Cell cycle	PKMYT1	-1.642594089	3.57E-44	protein kinase, membrane associated tyrosine/threonine 1
Cell cycle	CCNB2	-2.4290457	4.53E-69	cyclin B2
Cell cycle	BUB3	-0.639577715	2.28E-15	BUB3 mitotic checkpoint protein
Cell cycle	AURKB	-3.043479515	3.52E-134	aurora kinase B
Cell cycle	PTTG1	-1.07983346	2.37E-35	PTTG1 regulator of sister chromatid separation, securin
Cell cycle	TRIP13	-1.872439119	8.78E-78	thyroid hormone receptor interactor 13
Cell cycle	ESPL1	-1.589348595	8.57E-07	extra spindle pole bodies like 1, separase
Cell cycle	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1
Cell cycle	CDC6	-0.613174373	0	cell division cycle 6
Cell cycle	CDC20	-3.041016191	4.57E-08	cell division cycle 20
Cell cycle	CDC25A	-1.016446988	3.02E-19	cell division cycle 25A
Cell cycle	CDC25C	-1.368875355	1.44E-04	cell division cycle 25C
Cell cycle	CDC27	-0.590657313	6.85E-05	cell division cycle 27
Cell cycle	ALYREF	-1.032955903	1.08E-14	Ally/REF export factor
Spliceosome	SF3A1	-0.552254366	6.21E-05	splicing factor 3a subunit 1
Spliceosome	PIPH	-0.945937155	2.14E-17	peptidylprolyl isomerase H
Spliceosome	SRSF10	-0.702395831	6.86E-17	serine and arginine rich splicing factor 10
Spliceosome	TCERG1	-0.541066399	9.92E-08	transcription elongation regulator 1

Spliceosome	SF3A3	-0.510540174	5.69E-08	splicing factor 3a subunit 3
Spliceosome	LSM6	-0.588213964	8.11E-07	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated
Spliceosome	U2AF2	-0.909453055	7.89E-42	U2 small nuclear RNA auxiliary factor 2
Spliceosome	DHX15	-0.555945373	1.36E-18	DEAH-box helicase 15
Spliceosome	HNRNP A3	-0.979688152	2.12E-69	heterogeneous nuclear ribonucleoprotein A3
Spliceosome	PUF60	-0.510810731	2.23E-13	poly(U) binding splicing factor 60
Spliceosome	SF3B3	-0.544869004	1.58E-16	splicing factor 3b subunit 3
Spliceosome	FUS	-1.084454939	2.95E-63	FUS RNA binding protein
Spliceosome	PRPF31	-0.692952357	1.29E-46	pre-mRNA processing factor 31
Spliceosome	LSM3	-0.698486489	1.99E-13	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated
Spliceosome	RBMX	-0.712234185	1.59E-56	RNA binding motif protein X-linked
Spliceosome	TRA2A	-1.554295417	9.27E-64	transformer 2 alpha homolog
Spliceosome	HNRNPK	-0.500929117	1.09E-39	heterogeneous nuclear ribonucleoprotein K
Spliceosome	HSPA1B	0.607894202	5.86E-29	heat shock protein family A (Hsp70) member 1B
Spliceosome	HSPA8	-1.166589659	4.67E-91	heat shock protein family A (Hsp70) member 8
Spliceosome	HNRNPM	-0.83076516	3.46E-73	heterogeneous nuclear ribonucleoprotein M
Spliceosome	WBP11	-1.009889649	1.80E-14	WW domain binding protein 11
Spliceosome	RBM25	-1.272906175	6.65E-41	RNA binding motif protein 25
Spliceosome	SRSF1	-1.126003515	3.07E-99	serine and arginine rich splicing factor 1
Spliceosome	SRSF2	-1.666031021	2.79E-109	serine and arginine rich splicing factor 2
Spliceosome	SRSF3	-0.788055365	1.40E-21	serine and arginine rich splicing factor 3
Spliceosome	SRSF6	-1.478858925	4.95E-113	serine and arginine rich splicing factor 6
Spliceosome	SRSF7	-1.015100616	5.96E-57	serine and arginine rich splicing factor 7
Spliceosome	TRA2B	-0.771635382	3.84E-29	transformer 2 beta homolog
Spliceosome	SNRNP70	-1.041433176	6.20E-31	small nuclear ribonucleoprotein U1 subunit 70
Spliceosome	SNRPA	-0.804689785	3.83E-19	small nuclear ribonucleoprotein polypeptide A'
Spliceosome	SNRPA1	-0.999571902	1.02E-34	small nuclear ribonucleoprotein polypeptide A'
Spliceosome	SNRPB	-0.813236412	8.43E-35	small nuclear ribonucleoprotein polypeptides B and B1
Spliceosome	SNRPC	-0.521526841	2.98E-07	small nuclear ribonucleoprotein polypeptide C
Spliceosome	SNRPD1	-0.700115383	1.23E-05	small nuclear ribonucleoprotein D1 polypeptide
Spliceosome	SNRPD3	-0.658014683	0.027008148	small nuclear ribonucleoprotein D3 polypeptide
Spliceosome	SNRPE	-0.565077028	1.91E-06	small nuclear ribonucleoprotein D3 polypeptide E
Spliceosome	SNRPF	-0.655492984	1.83E-20	small nuclear ribonucleoprotein polypeptide F
Spliceosome	SNRPG	-0.727684732	3.93E-12	small nuclear ribonucleoprotein polypeptide F
Spliceosome	DDX39B	-0.847530697	4.42E-39	small nuclear ribonucleoprotein polypeptide G
Spliceosome	THOC3	-0.602534537	4.94E-17	DEXD-box helicase 39B
Spliceosome	PHF5A	-0.527216416	1.57E-08	THO complex subunit 3
Spliceosome	RBM17	-0.54471857	2.95E-08	PHD finger protein 5A
Spliceosome	PRPF4	-0.562853151	8.10E-28	RNA binding motif protein 17
Spliceosome	EFTUD2	-0.889874677	1.50E-50	pre-mRNA processing factor 4
Spliceosome	SNRNP40	-0.570078885	7.50E-16	elongation factor Tu GTP binding domain containing 2
Spliceosome	DDX23	-0.510112742	5.00E-07	small nuclear ribonucleoprotein U5 subunit 40
				DEAD-box helicase 23

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FIG. 4 (CONT.)

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Spliceosome	DDX46	-0.796005857	3.50E-28	DEAD-box helicase 46
Motor proteins	KIF20A	-4.765267317	2.70E-210	kinesin family member 20A
Motor proteins	ACTR1A	-0.590456765	1.28E-19	actin related protein 1A
Motor proteins	DNAL4	0.84381736	1.61E-11	dynein axonemal light chain 4
Motor proteins	TUBB3	-1.926895987	1.16E-237	tubulin alpha 1b
Motor proteins	TUBB4B	-2.381235436	2.90E-104	tubulin beta 3 class III
Motor proteins	MYL9	-1.427919234	6.63E-140	tubulin beta 4B class IVb
Motor proteins	CENPE	-1.56453086	7.61E-54	myosin light chain 9
Motor proteins	KIF2C	-2.965952451	1.79E-62	centromere protein E
Motor proteins	DNAL3	-2.856788353	7.83E-84	kinesin family member 2C
Motor proteins	MYO3B	-0.881669217	0.00502175	dynein axonemal intermediate chain 3
Motor proteins	BICDL2	-1.403079429	1.18E-06	myosin IIIB
Motor proteins	KIF18B	3.733257512	2.87E-24	BICD family like cargo adaptor 2
Motor proteins	DCTN1	-2.301891471	5.67E-40	kinesin family member 18B
Motor proteins	DNAH5	-0.667158928	1.12E-67	dynactin subunit 1
Motor proteins	DYNC111	-2.443965873	8.12E-15	dynein axonemal heavy chain 5
Motor proteins	TUBB	-1.924829127	0.00157	dynein cytoplasmic 1 intermediate chain 1
Motor proteins	MYH15	-1.396875055	3.13E-188	tubulin beta class I
Motor proteins	KIF21B	-3.083965984	2.11E-14	myosin heavy chain 15
Motor proteins	KIF13B	1.871908543	4.30E-13	kinesin family member 21B
Motor proteins	KIF4A	1.282965457	6.82E-25	kinesin family member 13B
Motor proteins	KIF26A	-3.257303235	3.51E-120	kinesin family member 4A
Motor proteins	KIF24	0.858502197	2.55E-08	kinesin family member 26A
Motor proteins	TUBB2B	-1.048694943	1.30E-04	kinesin family member 24
Motor proteins	KIFC3	-1.169029115	1.17E-12	tubulin beta 2B class IIb
Motor proteins	KIF11	-0.629107836	1.36E-14	kinesin family member C3
Motor proteins	KIFC1	-2.169619609	6.72E-88	kinesin family member 11
Motor proteins	KIF22	-2.419813316	4.81E-89	kinesin family member C1
Motor proteins	MYH3	-1.340921927	1.57E-34	kinesin family member 22
Motor proteins	MYH9	0.730750266	0.037944845	myosin heavy chain 3
Motor proteins	MYL6	-0.92217839	1.74E-34	myosin heavy chain 9
Motor proteins	MYO1E	-0.896524836	8.51E-55	myosin light chain 6
Motor proteins	MYO7A	-0.575937375	6.98E-13	myosin IE
Motor proteins	MYO10	0.741546305	0.026188684	myosin VIIA
Motor proteins	DYNC2LI1	-0.511002197	1.51E-04	myosin X
Motor proteins	KIF27	0.907853565	3.15E-08	dynein cytoplasmic 2 light intermediate chain 1
Motor proteins	KIF15	1.047568021	0.005408298	kinesin family member 27
Motor proteins	ACTA2	-2.354742372	1.80E-20	kinesin family member 15
Motor proteins	ACTB	0.989373472	6.59E-06	actin alpha 2, smooth muscle
Motor proteins	ACTG1	-1.032025958	1.16E-62	actin beta
Motor proteins	TNNI3	-0.767030671	1.31E-37	actin gamma 1
		1.811419586	6.12E-04	troponin I3, cardiac type

FIG. 4 (CONT.)

Motor proteins	TNNT1	1.246894849	2.69E-32	tropomyosin T1, slow skeletal type
Motor proteins	TPM1	-1.681503954	4.61E-227	tropomyosin 1
Motor proteins	TPM2	-0.69081164	6.53E-08	tropomyosin 2
Motor proteins	TPM3	-0.794361054	8.07E-49	tropomyosin 3
Motor proteins	TUBA4A	-1.308260378	3.73E-99	tubulin alpha 4a
Motor proteins	TUBB2A	-1.509554161	5.05E-68	tubulin beta 2A class IIa
Motor proteins	TUBG1	-0.565333866	8.68E-20	tubulin gamma 1
Motor proteins	TUBA1A	-1.856669238	2.57E-113	tubulin alpha 1a
Motor proteins	MYPH14	1.014921129	6.85E-09	myosin heavy chain 14
Motor proteins	DNAI4	1.383592047	4.46E-04	dynein axonemal intermediate chain 4
Motor proteins	TUBAL3	1.133510584	0.003064433	tubulin alpha like 3
Motor proteins	KIF18A	-1.712017862	4.94E-07	kinesin family member 18A
Motor proteins	CAPZA1	-0.532722495	2.00E-21	capping actin protein of muscle Z-line subunit alpha 1
Motor proteins	CAPZB	-0.612559282	4.66E-30	capping actin protein of muscle Z-line subunit beta
Motor proteins	DCTN5	-0.626319731	1.09E-10	dynactin subunit 5
Motor proteins	TUBB6	-0.998113882	7.61E-37	tubulin beta 6 class V
Motor proteins	TUBA1C	-1.708411923	2.97E-143	tubulin alpha 1c
Motor proteins	DYNLL1	-0.610838457	1.22E-20	dynein light chain LC8-type 1
Motor proteins	KIFC2	0.802097502	1.53E-06	kinesin family member C2
Motor proteins	BICDL1	1.313197293	9.30E-13	BICD family like cargo adaptor 1
Motor proteins	KIF23	-2.150957684	7.86E-125	kinesin family member 23
Motor proteins	KIF20B	-1.583390527	1.97E-38	kinesin family member 20B
Motor proteins	KIF14	-2.572707218	9.68E-73	kinesin family member 14
Viral protein interaction with cytokine and cytokine receptor	ILF4	-2.011689984	4.41E-04	interleukin 24
Viral protein interaction with cytokine and cytokine receptor	CCR3	-2.318016754	0.021309065	C-C motif chemokine receptor 3
Viral protein interaction with cytokine and cytokine receptor	CSFIR	-1.366468847	0.02162761	colony stimulating factor 1 receptor
Viral protein interaction with cytokine and cytokine receptor	CXCL1	-1.914811968	1.10E-11	C-X-C motif chemokine ligand 1
Viral protein interaction with cytokine and cytokine receptor	CXCL2	-4.187327651	8.18E-19	C-X-C motif chemokine ligand 2
Viral protein interaction with cytokine and cytokine receptor	CXCL3	-1.537615318	5.82E-05	C-X-C motif chemokine ligand 3
Viral protein interaction with cytokine and cytokine receptor	IL6	-5.538099239	2.74E-23	interleukin 6
Viral protein interaction with cytokine and cytokine receptor	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8
Viral protein interaction with cytokine and cytokine receptor	CXCR1	-1.228667714	3.30E-07	C-X-C motif chemokine receptor 1
Viral protein interaction with cytokine and cytokine receptor	IL20	-2.314080668	2.03E-06	interleukin 20
Viral protein interaction with cytokine and cytokine receptor	IL20RB	1.273322458	1.49E-52	receptor subunit beta
Viral protein interaction with cytokine and cytokine receptor	CCL20	-1.505504073	0.009726667	C-C motif chemokine ligand 20
Viral protein interaction with cytokine and cytokine receptor	CXCL6	-1.961199152	0.031375007	C-X-C motif chemokine ligand 6
Viral protein interaction with cytokine and cytokine receptor	CXCL5	-0.683160477	0.009101564	C-X-C motif chemokine ligand 5
Viral protein interaction with cytokine and cytokine receptor	CX3CL1	1.139812406	0.001260018	C-X3-C motif chemokine ligand 1
Viral protein interaction with cytokine and cytokine receptor	TNF	-3.3890783	4.61E-31	tumor necrosis factor
Viral protein interaction with cytokine and cytokine receptor	TNFSF10	-0.924805759	1.72E-04	TNF superfamily member 10
Viral protein interaction with cytokine and cytokine receptor	TNFRSF14	0.679088167	0.001316633	TNF receptor superfamily member 14
Viral protein interaction with cytokine and cytokine receptor	TNFRSF10D	1.536127723	1.46E-33	TNF receptor superfamily member 10d

Viral protein interaction with cytokine and cytokine receptor	TNFRSF10C	0.73668827	0.016480141	TNF receptor superfamily member 10c
Viral protein interaction with cytokine and cytokine receptor	IL18R1	0.810301314	7.39E-07	interleukin 18 receptor 1
Viral protein interaction with cytokine and cytokine receptor	CXCL14	-1.78215239	9.24E-40	C-X-C motif chemokine ligand 14
Oocyte meiosis	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2
Oocyte meiosis	YWHAQ	-0.517258997	2.26E-28	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta
Oocyte meiosis	ADCY6	1.177667548	3.38E-18	adenylate cyclase 6
Oocyte meiosis	ADCY7	0.556298013	0.038662582	adenylate cyclase 7
Oocyte meiosis	ANAPC16	0.71378337	2.61E-31	anaphase promoting complex subunit 16
Oocyte meiosis	CPEB2	1.146051315	1.48E-04	cytoplasmic polyadenylation element binding protein 2
Oocyte meiosis	SGO1	-1.652484126	6.13E-14	shugoshin 1
Oocyte meiosis	ANAPC15	-1.337835166	9.32E-49	anaphase promoting complex subunit 15
Oocyte meiosis	FBXO5	-1.213464515	3.91E-22	F-box protein 5
Oocyte meiosis	RPS6KA6	1.107936639	1.99E-06	ribosomal protein S6 kinase A6
Oocyte meiosis	IGF1R	-0.698692669	3.97E-10	insulin like growth factor 1 receptor
Oocyte meiosis	ITPR1	0.779770267	0.023593422	inositol 1,4,5-trisphosphate receptor type 1
Oocyte meiosis	ITPR3	0.554789364	1.08E-09	inositol 1,4,5-trisphosphate receptor type 3
Oocyte meiosis	MAD2L1	-1.443505246	1.61E-67	mitotic arrest deficient 2 like 1
Oocyte meiosis	PLK1	-4.355361139	0	polo like kinase 1
Oocyte meiosis	PPP1CC	-0.565040594	7.42E-10	protein phosphatase 1 catalytic subunit gamma
Oocyte meiosis	PPP2CA	-0.509609413	5.36E-22	protein phosphatase 2 catalytic subunit alpha
Oocyte meiosis	PPP2R1A	-0.693427968	1.09E-30	protein phosphatase 2 scaffold subunit Aalpha
Oocyte meiosis	PPP2R1B	-0.594751747	6.34E-05	protein phosphatase 2 scaffold subunit Bbeta
Oocyte meiosis	PPP2R5B	0.64992865	1.11E-10	protein phosphatase 2 regulatory subunit B'beta
Oocyte meiosis	PPP2R5E	-0.566584163	3.03E-08	protein phosphatase 2 regulatory subunit B'epsilon
Oocyte meiosis	PPP3CA	-0.716280478	1.13E-26	protein phosphatase 3 catalytic subunit alpha
Oocyte meiosis	PRKACB	-0.655165045	1.50E-05	protein kinase cAMP-activated catalytic subunit beta
Oocyte meiosis	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
Oocyte meiosis	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13
Oocyte meiosis	RPS6KA2	0.5314108	3.66E-10	ribosomal protein S6 kinase A2
Oocyte meiosis	AURKA	-2.548179285	1.70E-141	aurora kinase A
Oocyte meiosis	BUB1	-2.944762683	1.02E-80	BUB1 mitotic checkpoint serine/threonine kinase
Oocyte meiosis	YWHAH	-0.844196884	4.98E-62	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta
Oocyte meiosis	YWHAE	-0.677792624	1.88E-35	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
Oocyte meiosis	YWHAH	-0.75539509	1.19E-42	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta
Oocyte meiosis	YWHAZ	-0.655944784	3.03E-35	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta
Oocyte meiosis	SMC1A	-0.977896739	1.71E-11	structural maintenance of chromosomes 1A
Oocyte meiosis	CCNB1	-2.783469794	1.66E-219	cyclin B1
Oocyte meiosis	PKMT1	-1.642594089	3.57E-44	protein kinase, membrane associated tyrosine/threonine 1
Oocyte meiosis	CCNB2	-2.4290457	4.53E-69	cyclin B2
Oocyte meiosis	PTTG1	-1.07983346	2.37E-35	PTTG1 regulator of sister chromatid separation, securin
Oocyte meiosis	ESPL1	-1.589348595	8.57E-07	extra spindle pole bodies like 1, separase
Oocyte meiosis	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1

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FIG. 4 (CONT.)				11/29	
Oocyte meiosis	CDC20	-3.041016191	0	cell division cycle 20	
Oocyte meiosis	CDC25C	-1.368875355	1.44E-04	cell division cycle 25C	
Oocyte meiosis	CDC27	-0.590657313	6.85E-05	cell division cycle 27	
p53 signaling pathway	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2	
p53 signaling pathway	CDK6	-0.789007721	1.48E-14	cyclin dependent kinase 6	
p53 signaling pathway	CDKN1A	-0.541742013	1.70E-26	cyclin dependent kinase inhibitor 1A	
p53 signaling pathway	CDKN2A	-0.952618945	6.15E-20	cyclin dependent kinase inhibitor 2A	
p53 signaling pathway	SIVA1	-0.58148449	4.02E-10	SIVA1 apoptosis inducing factor	
p53 signaling pathway	CHEK1	-0.641976893	1.58E-06	checkpoint kinase 1	
p53 signaling pathway	DDB2	-0.645131738	1.09E-09	damage specific DNA binding protein 2	
p53 signaling pathway	RCHY1	-0.594860052	6.48E-05	ring finger and CHY zinc finger domain containing 1	
p53 signaling pathway	CD82	-0.739716613	7.69E-27	CD82 molecule	
p53 signaling pathway	GADD45B	-0.895079733	2.29E-14	growth arrest and DNA damage inducible beta	
p53 signaling pathway	ATM	0.812453681	0.002891499	ATM serine/threonine kinase	
p53 signaling pathway	GTSE1	-3.37318409	5.43E-106	G2 and S-phase expressed 1	
p53 signaling pathway	PMAIP1	-1.143121196	4.45E-26	phorbol-12-myristate-13-acetate-induced protein 1	
p53 signaling pathway	CYCS	-0.68055638	9.52E-31	cytochrome c, somatic	
p53 signaling pathway	BCL2	-1.320939366	3.10E-05	BCL2 apoptosis regulator	
p53 signaling pathway	BCL2L1	0.818371467	1.34E-28	BCL2 like 1	
p53 signaling pathway	RRM2	-2.685170605	1.20E-148	ribonucleotide reductase regulatory subunit M2	
p53 signaling pathway	TP53AIP1	-0.531597438	0.025214701	tumor protein p53 regulated apoptosis inducing protein 1	
p53 signaling pathway	THBS1	-2.059142432	3.78E-180	thrombospondin 1	
p53 signaling pathway	TP53	-0.654172318	7.66E-13	tumor protein p53	
p53 signaling pathway	AIFM2	0.565766253	5.35E-07	apoptosis inducing factor mitochondria associated 2	
p53 signaling pathway	CCNB1	-2.783469794	1.66E-219	cyclin B1	
p53 signaling pathway	CCNG2	0.717631544	4.51E-26	cyclin G2	
p53 signaling pathway	CCNB2	-2.4290457	4.53E-69	cyclin B2	
p53 signaling pathway	EI24	-0.509137137	6.09E-23	EI24 autophagy associated transmembrane protein	
p53 signaling pathway	TP53I3	-1.377656486	6.39E-59	tumor protein p53 inducible protein 3	
p53 signaling pathway	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1	
DNA replication	FEN1	-1.183074852	1.50E-45	flap structure-specific endonuclease 1	
DNA replication	POLA2	-1.154846332	7.43E-22	DNA polymerase alpha 2, accessory subunit	
DNA replication	LIG1	-1.190675113	3.50E-19	DNA ligase 1	
DNA replication	MCM2	-1.023975365	6.64E-43	minichromosome maintenance complex component 2	
DNA replication	MCM3	-0.773150347	4.62E-30	minichromosome maintenance complex component 3	
DNA replication	MCM4	-1.333784723	3.43E-40	minichromosome maintenance complex component 4	
DNA replication	MCM5	-1.269809895	7.70E-57	minichromosome maintenance complex component 5	
DNA replication	MCM6	-0.763520908	1.40E-25	minichromosome maintenance complex component 6	
DNA replication	MCM7	-1.240342504	1.28E-89	minichromosome maintenance complex component 7	
DNA replication	PCNA	-0.69003319	2.83E-22	proliferating cell nuclear antigen	
DNA replication	POLE3	-0.63486216	2.63E-21	DNA polymerase epsilon 3, accessory subunit	
DNA replication	POLA1	-1.35677331	3.83E-30	DNA polymerase alpha 1, catalytic subunit	

DNA replication	POLE	-0.671784004	2.47E-07	DNA polymerase epsilon, catalytic subunit
DNA replication	POLE2	-0.837323109	0.002421891	DNA polymerase epsilon 2, accessory subunit
DNA replication	PRIM2	-0.589667352	2.71E-06	DNA primase subunit 2
DNA replication	POLE4	-0.661920468	1.57E-09	DNA polymerase epsilon 4, accessory subunit
DNA replication	POLD4	0.886968578	1.06E-23	DNA polymerase delta 4, accessory subunit
DNA replication	RFC2	-0.902016024	3.71E-24	replication factor C subunit 2
DNA replication	RFC3	-1.032946513	4.00E-27	replication factor C subunit 3
DNA replication	RFC5	-0.625725468	5.91E-08	replication factor C subunit 5
DNA replication	ALYREF	-1.032955903	1.08E-14	AlY/REF export factor
Nucleocytoplasmic transport	CSE1L	-0.779067607	5.25E-41	chromosome segregation 1 like
Nucleocytoplasmic transport	EEF1A2	1.746332823	1.58E-04	eukaryotic translation elongation factor 1 alpha 2
Nucleocytoplasmic transport	NUP188	-0.71348875	0.005210147	nucleoporin 188
Nucleocytoplasmic transport	KPNB1	-1.163141193	3.25E-46	karyopherin subunit beta 1
Nucleocytoplasmic transport	KPNA2	-1.439253612	3.36E-179	karyopherin subunit alpha 2
Nucleocytoplasmic transport	KPNA4	-0.820047781	2.85E-24	karyopherin subunit alpha 4
Nucleocytoplasmic transport	IPO5	-0.611041651	5.29E-19	importin 5
Nucleocytoplasmic transport	NUP88	-0.681636929	4.20E-20	nucleoporin 88
Nucleocytoplasmic transport	NUP98	-0.639630444	2.41E-21	nucleoporin 98 and 96 precursor
Nucleocytoplasmic transport	IPO9	-0.716442563	1.77E-09	importin 9
Nucleocytoplasmic transport	NDC1	-0.769912647	1.38E-20	NDC1 transmembrane nucleoporin
Nucleocytoplasmic transport	NUP107	-0.661453518	7.48E-07	nucleoporin 107
Nucleocytoplasmic transport	RAN	-0.791749251	7.74E-17	RAN, member RAS oncogene family
Nucleocytoplasmic transport	RANGAP1	-0.940021271	8.47E-56	Ran GTPase activating protein 1
Nucleocytoplasmic transport	UPF1	-0.53869086	7.83E-17	UPF1 RNA helicase and ATPase
Nucleocytoplasmic transport	XPO4	-0.550522705	7.71E-05	exportin 4
Nucleocytoplasmic transport	UPF3B	-0.522259955	0.009106576	UPF3B regulator of nonsense mediated mRNA decay
Nucleocytoplasmic transport	SUMO3	-0.635496321	8.81E-23	small ubiquitin like modifier 3
Nucleocytoplasmic transport	DDX39B	-0.847530697	4.42E-39	DEAD-box helicase 39B
Nucleocytoplasmic transport	THOC6	1.21081251	1.14E-43	THO complex subunit 6
Nucleocytoplasmic transport	IPO4	-0.810112189	5.39E-37	importin 4
Nucleocytoplasmic transport	THOC3	-0.602534537	4.94E-17	THO complex subunit 3
Nucleocytoplasmic transport	THOC5	-0.789783209	4.01E-14	THO complex subunit 5
Nucleocytoplasmic transport	NUP93	-0.755693249	2.79E-23	nucleoporin 93
Nucleocytoplasmic transport	NUP153	-0.500341644	4.86E-12	nucleoporin 153
TNF signaling pathway	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3
TNF signaling pathway	DNM1L	-0.508772632	1.79E-16	dynamitin 1 like
TNF signaling pathway	CEBPB	1.18648638	7.46E-26	CCAAT enhancer binding protein beta
TNF signaling pathway	CSF2	-0.794979459	0.01839132	colony stimulating factor 2
TNF signaling pathway	CREB3L4	0.873897859	2.66E-05	cAMP responsive element binding protein 3 like 4
TNF signaling pathway	JAG1	-0.989788696	4.95E-15	jagged canonical Notch ligand 1
TNF signaling pathway	EDN1	-1.247695271	6.40E-26	endothelin 1
TNF signaling pathway	MLKL	-0.627776567	0.001144238	mixed lineage kinase domain like pseudokinase

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FIG. 4 (CONT.)

TNF signaling pathway	AKT1	-0.682588564	1.49E-36	AKT serine/threonine kinase 1
TNF signaling pathway	AKT2	-0.685786005	7.43E-19	AKT serine/threonine kinase 2
TNF signaling pathway	FOS	0.672332148	1.18E-05	Fos proto-oncogene, AP-1 transcription factor subunit
TNF signaling pathway	CXCL1	-1.914811968	1.10E-11	C-X-C motif chemokine ligand 1
TNF signaling pathway	CXCL2	-4.187327651	8.18E-19	C-X-C motif chemokine ligand 2
TNF signaling pathway	CXCL3	-1.537615318	5.82E-05	C-X-C motif chemokine ligand 3
TNF signaling pathway	IL6	-5.538099239	2.74E-23	interleukin 6
TNF signaling pathway	IRF1	-1.131813157	2.00E-13	interferon regulatory factor 1
TNF signaling pathway	JUN	-0.660542672	3.59E-09	Jun proto-oncogene, AP-1 transcription factor subunit
TNF signaling pathway	JUNB	0.562722829	5.47E-09	JunB proto-oncogene, AP-1 transcription factor subunit
TNF signaling pathway	MAP3K5	0.761199202	2.68E-05	mitogen-activated protein kinase kinase kinase 5
TNF signaling pathway	MIMP3	2.261554434	0.008397801	matrix metalloproteinase 3
TNF signaling pathway	MIMP9	-0.686898684	5.05E-06	matrix metalloproteinase 9
TNF signaling pathway	ATF4	0.692778056	1.09E-13	activating transcription factor 4
TNF signaling pathway	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1
TNF signaling pathway	NFKBIA	-1.603390073	5.96E-23	NFkB inhibitor alpha
TNF signaling pathway	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
TNF signaling pathway	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
TNF signaling pathway	MAPK10	0.77092048	0.019720607	mitogen-activated protein kinase 10
TNF signaling pathway	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13
TNF signaling pathway	MAP2K3	-0.703932792	8.05E-33	mitogen-activated protein kinase kinase 3
TNF signaling pathway	CCL20	-1.505504073	0.009726667	C-C motif chemokine ligand 20
TNF signaling pathway	CXCL6	-1.961199152	0.031375007	C-X-C motif chemokine ligand 6
TNF signaling pathway	CXCL5	-0.683160477	0.009101564	C-X-C motif chemokine ligand 5
TNF signaling pathway	CX3CL1	1.139812406	0.001260018	C-X3-C motif chemokine ligand 1
TNF signaling pathway	NOD2	1.79550162	1.20E-06	nucleotide binding oligomerization domain containing 2
TNF signaling pathway	TNF	-3.3890783	4.61E-31	tumor necrosis factor
TNF signaling pathway	TNFAIP3	-0.819893733	1.57E-07	TNF alpha induced protein 3
TNF signaling pathway	TRAF2	-0.51861214	5.00E-07	TNF receptor associated factor 2
TNF signaling pathway	TRAF3	-0.790267127	9.87E-06	TNF receptor associated factor 3
TNF signaling pathway	VEGFC	-0.703205693	2.86E-11	vascular endothelial growth factor C
TNF signaling pathway	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
TNF signaling pathway	TRADD	0.65210189	2.27E-09	TNFRSF1A associated via death domain
TNF signaling pathway	IL18R1	0.810301314	7.39E-07	interleukin 18 receptor 1
TNF signaling pathway	MAP3K14	-0.803587589	1.11E-21	ribosomal protein S6 kinase A4
TNF signaling pathway	RPS6KA4	-0.945716011	2.32E-06	mitogen-activated protein kinase kinase kinase 14
TNF signaling pathway	SOC3	-2.414386151	4.34E-24	suppressor of cytokine signaling 3
TNF signaling pathway	CREB3L1	0.563062213	0.009932305	cAMP responsive element binding protein 3 like 1
TNF signaling pathway	CREB5	-0.644508992	0.009403112	cAMP responsive element binding protein 5
TNF signaling pathway	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3
Focal adhesion	MYL9	-1.56453086	7.61E-54	myosin light chain 9
Focal adhesion	COL1A1	-2.891665838	1.95E-206	collagen type I alpha 1 chain

FIG. 4 (CONT.)

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Focal adhesion	COL1A2	-2.825395338	7.11E-30	collagen type I alpha 2 chain
Focal adhesion	COL4A1	-2.061513116	7.83E-168	collagen type IV alpha 1 chain
Focal adhesion	COL4A2	-1.446583367	7.61E-83	collagen type IV alpha 2 chain
Focal adhesion	COL4A4	2.249962242	0.020614975	collagen type IV alpha 4 chain
Focal adhesion	COL6A1	0.731009193	2.24E-10	collagen type VI alpha 1 chain
Focal adhesion	COL6A2	0.983041664	0.001231668	collagen type VI alpha 2 chain
Focal adhesion	COL6A3	-5.313792395	0.001799028	collagen type VI alpha 3 chain
Focal adhesion	COL9A2	-1.399832078	2.87E-15	collagen type IX alpha 2 chain
Focal adhesion	COMP	-0.85014817	0.007245133	cartilage oligomeric matrix protein
Focal adhesion	CTNNA1	-0.598631992	3.32E-17	catenin beta 1
Focal adhesion	DIAPH1	-1.013342221	3.14E-36	diaphanous related formin 1
Focal adhesion	EGF	-2.933549372	0.001086565	epidermal growth factor
Focal adhesion	EGFR	0.990016746	2.37E-21	epidermal growth factor receptor
Focal adhesion	AKT1	-0.682588564	1.49E-36	AKT serine/threonine kinase 1
Focal adhesion	AKT2	-0.685786005	7.43E-19	AKT serine/threonine kinase 2
Focal adhesion	FLNB	1.21097237	1.27E-45	filamin B
Focal adhesion	FLNC	-0.659656267	5.25E-08	filamin C
Focal adhesion	PIP5K1C	-0.698019362	0.006764396	phosphatidylinositol-4-phosphate 5-kinase type 1 gamma
Focal adhesion	LAMA1	0.816903618	4.99E-07	laminin subunit alpha 1
Focal adhesion	HRA5	-0.515066586	2.66E-10	Hras proto-oncogene, GTPase
Focal adhesion	IGF1R	-0.698692669	3.97E-10	insulin like growth factor 1 receptor
Focal adhesion	ITGA2	0.576600556	3.68E-06	integrin subunit alpha 2
Focal adhesion	ITGA3	0.648089161	1.33E-34	integrin subunit alpha 3
Focal adhesion	ITGA4	-1.497575163	5.58E-24	integrin subunit alpha 4
Focal adhesion	ITGA7	1.079283817	0.031554202	integrin subunit alpha 7
Focal adhesion	ITGA9	-1.449469727	0.021401401	integrin subunit alpha 9
Focal adhesion	ITGAV	-0.593082847	4.71E-09	integrin subunit alpha V
Focal adhesion	ITGB5	-0.581355197	7.55E-11	integrin subunit beta 5
Focal adhesion	ITGB6	-1.653111213	9.03E-68	integrin subunit beta 6
Focal adhesion	JUN	-0.660542672	3.59E-09	Jun proto-oncogene, AP-1 transcription factor subunit
Focal adhesion	LAMA2	-1.636914063	1.36E-04	laminin subunit alpha 2
Focal adhesion	LAMB1	-0.964171814	5.46E-61	laminin subunit beta 1
Focal adhesion	LAMB2	0.822202028	1.69E-05	laminin subunit beta 2
Focal adhesion	MYLK	-1.002993477	1.17E-42	myosin light chain kinase
Focal adhesion	PAK2	-0.594677037	8.89E-08	p21 (RAC1) activated kinase 2
Focal adhesion	PDGFB	-0.660310385	7.67E-06	platelet derived growth factor subunit B
Focal adhesion	PGF	1.992604768	1.34E-95	placental growth factor
Focal adhesion	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
Focal adhesion	PPP1CC	-0.565040594	7.42E-10	protein phosphatase 1 catalytic subunit gamma
Focal adhesion	PARVA	-0.682411701	1.66E-11	parvin alpha
Focal adhesion	PRKCA	-0.66221839	1.87E-05	protein kinase C alpha
Focal adhesion	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3

FIG. 4 (CONT.)

Focal adhesion	MAPK10	0.77092048	0.019720607	mitogen-activated protein kinase 10
Focal adhesion	PDGFC	-0.618554351	5.32E-07	platelet derived growth factor C
Focal adhesion	RAC2	0.986639325	1.05E-43	Rac family small GTPase 2
Focal adhesion	RAC3	0.74332111	1.24E-05	Rac family small GTPase 3
Focal adhesion	BCL2	-1.320939366	3.10E-05	BCL2 apoptosis regulator
Focal adhesion	ACTB	-1.032025958	1.16E-62	actin beta
Focal adhesion	THBS1	-2.059142432	3.78E-180	thrombospondin 1
Focal adhesion	THBS2	-0.645458494	9.07E-19	thrombospondin 2
Focal adhesion	THBS3	0.761488796	1.47E-10	thrombospondin 3
Focal adhesion	THBS4	3.301604668	6.53E-06	thrombospondin 4
Focal adhesion	ACTG1	-0.767030671	1.31E-37	actin gamma 1
Focal adhesion	TNXB	1.835216663	0.003454081	tenascin XB
Focal adhesion	VCL	-1.019709336	2.16E-55	vinculin
Focal adhesion	VEGFA	2.320185032	5.51E-69	vascular endothelial growth factor A
Focal adhesion	VEGFB	0.717622153	4.09E-12	vascular endothelial growth factor B
Focal adhesion	VEGFC	-0.703205693	2.86E-11	vascular endothelial growth factor C
Focal adhesion	ZYX	-0.568273707	3.26E-21	zyxin
Focal adhesion	PDGFD	-2.323822766	4.11E-06	platelet derived growth factor D
Focal adhesion	CAPN2	-0.720853005	1.31E-55	calpain 2
Focal adhesion	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
Focal adhesion	CAV1	-1.425019282	7.13E-187	caveolin 1
Focal adhesion	CDC42	-0.845647602	8.91E-13	cell division cycle 42
Focal adhesion	TUBA1B	-1.926895987	1.16E-237	tubulin alpha 1b
Gap junction	TUBB3	-2.381235436	2.90E-104	tubulin beta 3 class III
Gap junction	TUBB4B	-1.427919234	6.63E-140	tubulin beta 4B class IVb
Gap junction	ADCY6	1.177667548	3.38E-18	adenylate cyclase 6
Gap junction	ADCY7	0.556298013	0.038662582	adenylate cyclase 7
Gap junction	EGF	-2.933549372	0.001086565	epidermal growth factor
Gap junction	EGFR	0.990016746	2.37E-21	epidermal growth factor receptor
Gap junction	TUBB	-1.396875055	3.13E-188	tubulin beta class I
Gap junction	HRAS	-0.515066586	2.66E-10	HRas proto-oncogene, GTPase
Gap junction	TUBB2B	-1.169029115	1.17E-12	tubulin beta 2B class IIb
Gap junction	ITPR1	0.779770267	0.023593422	inositol 1,4,5-trisphosphate receptor type 1
Gap junction	ITPR3	0.554789364	1.08E-09	inositol 1,4,5-trisphosphate receptor type 3
Gap junction	PDGFB	-0.660310385	7.67E-06	platelet derived growth factor subunit B
Gap junction	PLCB4	-2.015420825	1.54E-23	phospholipase C beta 4
Gap junction	PRKACB	-0.655165045	1.50E-05	protein kinase cAMP-activated catalytic subunit beta
Gap junction	PRKCA	-0.66221839	1.87E-05	protein kinase C alpha
Gap junction	PRKG2	0.881478726	0.040259437	protein kinase cGMP-dependent 2
Gap junction	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
Gap junction	PDGFC	-0.618554351	5.32E-07	platelet derived growth factor C
Gap junction	TUBA4A	-1.308260378	3.73E-99	tubulin alpha 4a

FIG. 4 (CONT.)

FIG. 4 (CONT.)

Gap junction	TUBB2A	-1.509554161	5.05E-68	tubulin beta 2A class IIa	
Gap junction	TUBA1A	-1.856669238	2.57E-113	tubulin alpha 1a	
Gap junction	TUBA13	1.133510584	0.003064433	tubulin alpha like 3	
Gap junction	PDGFD	2.323822766	4.11E-06	platelet derived growth factor D	
Gap junction	TUBB6	-0.998113882	7.61E-37	tubulin beta 6 class V	
Gap junction	TUBA1C	-1.708411923	2.97E-143	tubulin alpha 1c	
Gap junction	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1	
Tryptophan metabolism	CYP1A1	-3.617246819	8.22E-15	cytochrome P450 family 1 subfamily A member 1	
Tryptophan metabolism	CYP1A2	-1.910672145	0.031690829	cytochrome P450 family 1 subfamily A member 2	
Tryptophan metabolism	CYP1B1	-3.148731114	1.87E-68	cytochrome P450 family 1 subfamily B member 1	
Tryptophan metabolism	ALDH3A2	1.11315655	1.76E-35	aldehyde dehydrogenase 3 family member A2	
Tryptophan metabolism	AOX1	-2.866696248	5.59E-102	aldehyde oxidase 1	
Tryptophan metabolism	ACAT2	-1.541907514	2.82E-116	acetyl-CoA acetyltransferase 2	
Tryptophan metabolism	MAOA	-0.701569781	4.47E-09	monoamine oxidase A	
Tryptophan metabolism	AADAT	-1.150487858	8.73E-12	amino adipate aminotransferase	
Tryptophan metabolism	KMO	-5.775965594	1.30E-04	kynurenine 3-monooxygenase	
Tryptophan metabolism	KYAT1	1.320201342	3.16E-15	kynurenine aminotransferase 1	
Tryptophan metabolism	PSME3	-0.608283592	8.22E-18	proteasome activator subunit 3	
Tryptophan metabolism	PSMD14	-0.501238963	7.41E-26	proteasome 26S subunit, non-ATPase 14	
Proteasome	PSME4	-0.69090001	3.35E-20	proteasome activator subunit 4	
Proteasome	PSMA7	-0.561007121	9.18E-16	proteasome 20S subunit alpha 7	
Proteasome	PSMB2	-0.630396873	1.42E-17	proteasome 20S subunit beta 2	
Proteasome	PSMC1	-0.739627107	2.87E-21	proteasome 26S subunit, ATPase 1	
Proteasome	PSMC3	-0.525245973	1.71E-06	proteasome 26S subunit, ATPase 3	
Proteasome	PSMC4	-0.570663077	6.59E-24	proteasome 26S subunit, ATPase 4	
Proteasome	PSMC5	-0.505074809	1.79E-21	proteasome 26S subunit, ATPase 5	
Proteasome	PSMD1	-0.739573898	7.60E-48	proteasome 26S subunit, non-ATPase 1	
Proteasome	PSMD2	-1.154132153	4.16E-78	proteasome 26S subunit, non-ATPase 3	
Proteasome	PSMD3	-0.737408087	1.44E-88	proteasome 26S subunit, non-ATPase 11	
Proteasome	PSMD11	-0.762111143	7.27E-16	proteasome 26S subunit, non-ATPase 13	
Proteasome	PSMD13	-0.669722765	2.33E-43	proteasome 26S subunit, non-ATPase 1	
IL-17 signaling pathway	PSME1	0.528863575	8.76E-12	CCAAT enhancer binding protein beta	
IL-17 signaling pathway	CEBPB	1.18648638	7.46E-26	interleukin 17 receptor E	
IL-17 signaling pathway	IL17RE	0.524893464	0.011997091	colony stimulating factor 2	
IL-17 signaling pathway	CSF2	-0.794979459	0.01839132	ELAV like RNA binding protein 1	
IL-17 signaling pathway	ELAVL1	-0.598562999	8.35E-16	Fos proto-oncogene, AP-1 transcription factor subunit	
IL-17 signaling pathway	FOS	0.672332148	1.18E-05	C-X-C motif chemokine ligand 1	
IL-17 signaling pathway	CXCL1	-1.914811968	1.10E-11	C-X-C motif chemokine ligand 2	
IL-17 signaling pathway	CXCL2	-4.187327651	8.18E-19	C-X-C motif chemokine ligand 3	
IL-17 signaling pathway	CXCL3	-1.537615318	5.82E-05	heat shock protein 90 alpha family class A member 1	
IL-17 signaling pathway	HSP90AA1	-1.12503942	2.24E-135	heat shock protein 90 alpha family class B member 1	
IL-17 signaling pathway	HSP90AB1	-0.833298157	2.71E-154		

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IL-17 signaling pathway	IL6	-5.538099239	2.74E-23	interleukin 6
IL-17 signaling pathway	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8
IL-17 signaling pathway	JUN	-0.660542672	3.59E-09	Jun proto-oncogene, AP-1 transcription factor subunit
IL-17 signaling pathway	LCN2	1.384551808	2.62E-17	lipocalin 2
IL-17 signaling pathway	MMP1	3.42751676	5.10E-26	matrix metalloproteinase 1
IL-17 signaling pathway	MMP3	2.261554434	0.008397801	matrix metalloproteinase 3
IL-17 signaling pathway	MMP9	-0.686898684	5.05E-06	matrix metalloproteinase 9
IL-17 signaling pathway	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1
IL-17 signaling pathway	NFKBIA	-1.603390073	5.96E-23	NFkB inhibitor alpha
IL-17 signaling pathway	IL17D	0.513733353	0.028589304	interleukin 17D
IL-17 signaling pathway	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
IL-17 signaling pathway	MAPK10	0.77092048	0.019720607	mitogen-activated protein kinase 10
IL-17 signaling pathway	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13
IL-17 signaling pathway	CCL20	-1.505504073	0.009726667	C-C motif chemokine ligand 20
IL-17 signaling pathway	CXCL6	-1.961199152	0.031375007	C-X-C motif chemokine ligand 6
IL-17 signaling pathway	CXCL5	-0.683160477	0.009101564	C-X-C motif chemokine ligand 5
IL-17 signaling pathway	SRSF1	-1.126003515	3.07E-99	serine and arginine rich splicing factor 1
IL-17 signaling pathway	TNF	-3.3890783	4.61E-31	tumor necrosis factor
IL-17 signaling pathway	TNFAIP3	-0.819893733	1.57E-07	TNF alpha induced protein 3
IL-17 signaling pathway	TRAF2	-0.51861214	5.00E-07	TNF receptor associated factor 2
IL-17 signaling pathway	TRAF3	-0.790267127	9.87E-06	TNF receptor associated factor 3
IL-17 signaling pathway	TRADD	0.65210189	2.27E-09	TNFRSF1A associated via death domain
IL-17 signaling pathway	IKBK	-0.758896248	1.39E-10	inhibitor of nuclear factor kappa B kinase subunit epsilon
Progesterone-mediated oocyte maturation	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3
Progesterone-mediated oocyte maturation	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2
Progesterone-mediated oocyte maturation	ADCY6	1.177667548	3.38E-18	adenylate cyclase 6
Progesterone-mediated oocyte maturation	ADCY7	0.556298013	0.038662582	adenylate cyclase 7
Progesterone-mediated oocyte maturation	ANAPC16	1.146051315	2.61E-31	anaphase promoting complex subunit 16
Progesterone-mediated oocyte maturation	CPEB2	-0.682588564	1.48E-04	cytoplasmic polyadenylation element binding protein 2
Progesterone-mediated oocyte maturation	AKT1	-0.685786005	1.49E-36	AKT serine/threonine kinase 1
Progesterone-mediated oocyte maturation	AKT2	-1.337835166	7.43E-19	AKT serine/threonine kinase 2
Progesterone-mediated oocyte maturation	ANAPC15	1.107936639	9.32E-49	anaphase promoting complex subunit 15
Progesterone-mediated oocyte maturation	RPS6KA6	-1.12503942	1.99E-06	ribosomal protein S6 kinase A6
Progesterone-mediated oocyte maturation	HSP90AA1	-1.12503942	2.24E-135	heat shock protein 90 alpha family class A member 1
Progesterone-mediated oocyte maturation	HSP90AB1	-0.833298157	2.71E-154	heat shock protein 90 alpha family class B member 1
Progesterone-mediated oocyte maturation	IGF1R	-0.698692669	3.97E-10	insulin like growth factor 1 receptor
Progesterone-mediated oocyte maturation	KIF22	-1.340921927	1.57E-34	kinesin family member 22
Progesterone-mediated oocyte maturation	MAD2L1	-1.443505246	1.61E-67	mitotic arrest deficient 2 like 1
Progesterone-mediated oocyte maturation	FZR1	-0.607451367	3.37E-17	fizzy and cell division cycle 20 related 1
Progesterone-mediated oocyte maturation	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
Progesterone-mediated oocyte maturation	PLK1	-4.355361139	0	polo like kinase 1
Progesterone-mediated oocyte maturation	PRKACB	-0.655165045	1.50E-05	protein kinase cAMP-activated catalytic subunit beta

FIG. 4
(CONT.)

Progesterone-mediated oocyte maturation	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
Progesterone-mediated oocyte maturation	MAPK10	0.77092048	0.019720607	mitogen-activated protein kinase 10
Progesterone-mediated oocyte maturation	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13
Progesterone-mediated oocyte maturation	RPS6KA2	0.5314108	3.66E-10	ribosomal protein S6 kinase A2
Progesterone-mediated oocyte maturation	AURKA	-2.548179285	1.70E-141	aurora kinase A
Progesterone-mediated oocyte maturation	BUB1	-2.944762683	1.02E-80	BUB1 mitotic checkpoint serine/threonine kinase
Progesterone-mediated oocyte maturation	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
Progesterone-mediated oocyte maturation	CCNB3	2.841383388	0.003556627	cyclin B3
Progesterone-mediated oocyte maturation	CCNA2	-3.101014872	9.01E-232	cyclin A2
Progesterone-mediated oocyte maturation	CCNA1	2.773918343	1.19E-125	cyclin A1
Progesterone-mediated oocyte maturation	CCNB1	-2.783469794	1.66E-219	cyclin B1
Progesterone-mediated oocyte maturation	PKMYT1	-1.642594089	3.57E-44	protein kinase, membrane associated tyrosine/threonine 1
Progesterone-mediated oocyte maturation	CCNB2	-2.4290457	4.53E-69	cyclin B2
Progesterone-mediated oocyte maturation	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1
Progesterone-mediated oocyte maturation	CDC25A	-1.016446988	3.02E-19	cell division cycle 25A
Progesterone-mediated oocyte maturation	CDC25C	-1.368875355	1.44E-04	cell division cycle 25C
Progesterone-mediated oocyte maturation	CDC27	-0.590657313	6.85E-05	cell division cycle 27
NOD-like receptor signaling pathway	DNM1L	-0.508772632	1.79E-16	dynamitin 1 like
NOD-like receptor signaling pathway	IRF9	0.820146612	1.07E-06	interferon regulatory factor 9
NOD-like receptor signaling pathway	RBCK1	0.543871503	6.19E-16	RANBP2-type and C3HC4-type zinc finger containing 1
NOD-like receptor signaling pathway	TXNIP	0.93959835	2.61E-16	thioredoxin interacting protein
NOD-like receptor signaling pathway	NEK7	-0.543925471	6.28E-07	NIMA related kinase 7
NOD-like receptor signaling pathway	CYBA	1.111321077	1.20E-28	cytochrome b-245 alpha chain
NOD-like receptor signaling pathway	GABARAPL1	0.593762185	8.77E-05	GABA type A receptor associated protein like 1
NOD-like receptor signaling pathway	GBP1	-1.644044915	1.39E-20	guanylate binding protein 1
NOD-like receptor signaling pathway	PYCARD	0.602466945	9.87E-07	PYD and CARD domain containing
NOD-like receptor signaling pathway	CXCL1	-1.914811968	1.10E-11	C-X-C motif chemokine ligand 1
NOD-like receptor signaling pathway	CXCL2	-4.187327651	8.18E-19	C-X-C motif chemokine ligand 2
NOD-like receptor signaling pathway	CXCL3	-1.537615318	5.82E-05	C-X-C motif chemokine ligand 3
NOD-like receptor signaling pathway	HSP90AA1	-1.12503942	2.24E-135	heat shock protein 90 alpha family class A member 1
NOD-like receptor signaling pathway	HSP90AB1	-0.833298157	2.71E-154	heat shock protein 90 alpha family class B member 1
NOD-like receptor signaling pathway	STING1	-0.532751185	3.00E-06	stimulator of interferon response cGAMP interactor 1
NOD-like receptor signaling pathway	IL6	-5.538099239	2.74E-23	interleukin 6
NOD-like receptor signaling pathway	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8
NOD-like receptor signaling pathway	IRF7	1.135908956	2.35E-06	interferon regulatory factor 7
NOD-like receptor signaling pathway	ITPR1	0.779770267	0.023593422	inositol 1,4,5-trisphosphate receptor type 1
NOD-like receptor signaling pathway	ITPR3	0.554789364	1.08E-09	inositol 1,4,5-trisphosphate receptor type 3
NOD-like receptor signaling pathway	JUN	-0.660542672	3.59E-09	Jun proto-oncogene, AP-1 transcription factor subunit
NOD-like receptor signaling pathway	MYD88	-5.19509323	6.66E-12	MYD88 innate immune signal transduction adaptor
NOD-like receptor signaling pathway	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1
NOD-like receptor signaling pathway	NFKBIA	-1.603390073	5.96E-23	NFkB inhibitor alpha
NOD-like receptor signaling pathway	OAS3	-0.883097641	5.98E-15	2'-5'-oligoadenylate synthetase 3

FIG. 4 (CONT.)

FIG. 4 (CONT.)

NOD-like receptor signaling pathway	PLCB4	-2.015420825	1.54E-23	phospholipase C beta 4	
NOD-like receptor signaling pathway	PRKCD	0.577869843	6.72E-13	protein kinase C delta	
NOD-like receptor signaling pathway	PKN1	2.680045237	1.17E-65	protein kinase N1	
NOD-like receptor signaling pathway	ERBIN	-0.536048388	0.001268073	erbB2 interacting protein	
NOD-like receptor signaling pathway	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3	
NOD-like receptor signaling pathway	MAPK10	0.77092048	0.019720607	mitogen-activated protein kinase 10	
NOD-like receptor signaling pathway	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13	
NOD-like receptor signaling pathway	CARD18	-0.767839705	0.047300943	caspase recruitment domain family member 18	
NOD-like receptor signaling pathway	BCL2	-1.320939366	3.10E-05	BCL2 apoptosis regulator	
NOD-like receptor signaling pathway	BCL2L1	0.818371467	1.34E-28	BCL2 like 1	
NOD-like receptor signaling pathway	GPSM3	-0.972070276	2.62E-10	G protein signaling modulator 3	
NOD-like receptor signaling pathway	NOD2	1.79550162	1.20E-06	nucleotide binding oligomerization domain containing 2	
NOD-like receptor signaling pathway	STAT2	0.65549056	8.94E-08	signal transducer and activator of transcription 2	
NOD-like receptor signaling pathway	TLR4	-1.280436254	0.006102427	toll like receptor 4	
NOD-like receptor signaling pathway	TNF	-3.3890783	4.61E-31	tumor necrosis factor	
NOD-like receptor signaling pathway	TNFAIP3	-0.819893733	1.57E-07	TNF alpha induced protein 3	
NOD-like receptor signaling pathway	TRAF2	-0.51861214	5.00E-07	TNF receptor associated factor 2	
NOD-like receptor signaling pathway	TRAF3	-0.790267127	9.87E-06	TNF receptor associated factor 3	
NOD-like receptor signaling pathway	TRIP6	-0.773314959	9.79E-29	thyroid hormone receptor interactor 6	
NOD-like receptor signaling pathway	YWHAE	-0.677792624	1.88E-35	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	
NOD-like receptor signaling pathway	NLRX1	0.691507108	2.26E-08	NLR family member X1	
NOD-like receptor signaling pathway	MAP1LC3A	1.147811189	3.47E-05	microtubule associated protein 1 light chain 3 alpha	
NOD-like receptor signaling pathway	PSTPIP1	-1.273736068	7.06E-06	proline-serine-threonine phosphatase interacting protein 1	
NOD-like receptor signaling pathway	MCU	-0.520225542	4.59E-10	mitochondrial calcium uniporter	
NOD-like receptor signaling pathway	IKBKE	-0.758896248	1.39E-10	inhibitor of nuclear factor kappa B kinase subunit epsilon	
Chemokine signaling pathway	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3	
Chemokine signaling pathway	ADCY6	1.177667548	3.38E-18	adenylate cyclase 6	
Chemokine signaling pathway	ADCY7	0.556298013	0.038662582	adenylate cyclase 7	
Chemokine signaling pathway	CCR3	-2.318016754	0.021309065	C-C motif chemokine receptor 3	
Chemokine signaling pathway	DOCK2	-3.796608442	2.99E-09	dedicator of cytokinesis 2	
Chemokine signaling pathway	AKT1	-0.682588564	1.49E-36	AKT serine/threonine kinase 1	
Chemokine signaling pathway	AKT2	-0.685786005	7.43E-19	AKT serine/threonine kinase 2	
Chemokine signaling pathway	PIK3R5	2.322190316	0.005560243	phosphoinositide-3-kinase regulatory subunit 5	
Chemokine signaling pathway	GNF7	2.904842238	8.58E-06	G protein subunit gamma 7	
Chemokine signaling pathway	GNF11	-2.283485578	1.36E-05	G protein subunit gamma 11	
Chemokine signaling pathway	CXCL1	-1.914811968	1.10E-11	C-X-C motif chemokine ligand 1	
Chemokine signaling pathway	CXCL2	-4.187327651	8.18E-19	C-X-C motif chemokine ligand 2	
Chemokine signaling pathway	CXCL3	-1.537615318	5.82E-05	C-X-C motif chemokine ligand 3	
Chemokine signaling pathway	HRAS	-0.515066586	2.66E-10	HRas proto-oncogene, GTPase	
Chemokine signaling pathway	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8	
Chemokine signaling pathway	CXCR1	-1.228667714	3.30E-07	C-X-C motif chemokine receptor 1	
Chemokine signaling pathway	JAK3	1.18447518	0.007376381	Janus kinase 3	

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Chemokine signaling pathway	ARRB1	-1.019807651	2.71E-05	arrestin beta 1
Chemokine signaling pathway	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1
Chemokine signaling pathway	NFKBIA	-1.603390073	5.96E-23	NFKB inhibitor alpha
Chemokine signaling pathway	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
Chemokine signaling pathway	PLCB4	-2.015420825	1.54E-23	phospholipase C beta 4
Chemokine signaling pathway	PLCG2	0.858523908	1.48E-04	phospholipase C gamma 2
Chemokine signaling pathway	GN2	-1.477858567	0.003094869	G protein subunit gamma 2
Chemokine signaling pathway	PRKACB	-0.655165045	1.50E-05	protein kinase cAMP-activated catalytic subunit beta
Chemokine signaling pathway	PRKCD	0.577869843	6.72E-13	protein kinase C delta
Chemokine signaling pathway	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
Chemokine signaling pathway	GN2	-0.871918929	4.03E-39	G protein subunit gamma 2
Chemokine signaling pathway	PREX1	-0.942778128	0.025051865	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 1
Chemokine signaling pathway	CXCL16	0.793367525	5.04E-08	C-X-C motif chemokine ligand 16
Chemokine signaling pathway	RAC2	0.986639325	1.05E-43	Rac family small GTPase 2
Chemokine signaling pathway	RAC3	0.74332111	1.24E-05	Rac family small GTPase 3
Chemokine signaling pathway	GNB4	-0.593274968	1.86E-06	G protein subunit beta 4
Chemokine signaling pathway	CCL20	-1.505504073	0.009726667	C-C motif chemokine ligand 20
Chemokine signaling pathway	CXCL6	-1.961199152	0.031375007	C-X-C motif chemokine ligand 6
Chemokine signaling pathway	CXCL5	-0.683160477	0.009101564	C-X-C motif chemokine ligand 5
Chemokine signaling pathway	CX3CL1	1.139812406	0.001260018	C-X3-C motif chemokine ligand 1
Chemokine signaling pathway	STAT2	0.65549056	8.94E-08	signal transducer and activator of transcription 2
Chemokine signaling pathway	STAT3	-0.652845069	1.49E-18	signal transducer and activator of transcription 3
Chemokine signaling pathway	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
Chemokine signaling pathway	CXCL14	-1.78215239	9.24E-40	C-X-C motif chemokine ligand 14
Chemokine signaling pathway	CDC42	-0.845647602	8.91E-13	cell division cycle 42
Chemokine signaling pathway	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3
Chemokine signaling pathway	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2
Chemokine signaling pathway	CDK6	-0.789007721	1.48E-14	cyclin dependent kinase 6
Cellular senescence	CDKN1A	-0.541742013	1.70E-26	cyclin dependent kinase inhibitor 1A
Cellular senescence	CDKN2A	-0.952618945	6.15E-20	cyclin dependent kinase inhibitor 2A
Cellular senescence	CDKN2B	-0.559997143	1.88E-06	cyclin dependent kinase inhibitor 2B
Cellular senescence	CHEK1	-0.641976893	1.58E-06	checkpoint kinase 1
Cellular senescence	E2F1	-0.613484701	7.13E-05	E2F transcription factor 1
Cellular senescence	AKT1	-0.682588564	1.49E-36	AKT serine/threonine kinase 1
Cellular senescence	AKT2	-0.685786005	7.43E-19	AKT serine/threonine kinase 2
Cellular senescence	ETS1	-0.526021021	1.08E-12	ETS proto-oncogene 1, transcription factor
Cellular senescence	RRAS2	-0.541005926	8.26E-18	RAS related 2
Cellular senescence	MIRAS	1.09973004	3.02E-04	muscle RAS oncogene homolog
Cellular senescence	FOXO1	-2.626974233	1.98E-148	forkhead box M1
Cellular senescence	FOXO1	0.772294223	5.77E-13	forkhead box O1
Cellular senescence	SLC25A4	0.673254039	4.10E-12	solute carrier family 25 member 4
Cellular senescence	SLC25A6	0.635358482	5.15E-16	solute carrier family 25 member 6

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FIG. 4 (CONT.)

Cellular senescence	HLA-B	1.164060729	7.80E-48	major histocompatibility complex, class I, B
Cellular senescence	HLA-F	1.31198882	2.47E-13	major histocompatibility complex, class I, F
Cellular senescence	HLA-G	2.767109778	2.80E-19	major histocompatibility complex, class I, G
Cellular senescence	HRAS	-0.515066586	2.66E-10	HRas proto-oncogene, GTPase
Cellular senescence	HUS1	-0.511793445	0.01392126	HUS1 checkpoint clamp component
Cellular senescence	IL6	-5.538099239	2.74E-23	interleukin 6
Cellular senescence	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8
Cellular senescence	ITPR1	0.779770267	0.023593422	inositol 1,4,5-trisphosphate receptor type 1
Cellular senescence	ITPR3	0.554789364	1.08E-09	inositol 1,4,5-trisphosphate receptor type 3
Cellular senescence	SMAD3	-0.660678576	6.52E-10	SMAD family member 3
Cellular senescence	MRE11	-0.543905719	4.69E-04	MRE11 homolog, double strand break repair nuclease
Cellular senescence	MYBL2	-2.348043415	6.70E-184	MYB proto-oncogene like 2
Cellular senescence	GADD45B	-0.895079733	2.29E-14	growth arrest and DNA damage inducible beta
Cellular senescence	ATM	0.812453681	0.002891499	ATM serine/threonine kinase
Cellular senescence	NFATC4	1.45263297	0.003483352	nuclear factor of activated T cells 4
Cellular senescence	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1
Cellular senescence	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
Cellular senescence	PPP1CC	-0.565040594	7.42E-10	protein phosphatase 1 catalytic subunit gamma
Cellular senescence	PPP3CA	-0.716280478	1.13E-26	protein phosphatase 3 catalytic subunit alpha
Cellular senescence	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
Cellular senescence	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13
Cellular senescence	MAP2K3	-0.703932792	8.05E-33	mitogen-activated protein kinase kinase 3
Cellular senescence	TRPV4	0.667812465	0.005750673	transient receptor potential cation channel subfamily V member 4
Cellular senescence	TGFB2	-1.129068552	5.00E-33	transforming growth factor beta 2
Cellular senescence	TGFB3	-0.876774301	0.032751479	transforming growth factor beta 3
Cellular senescence	TGFBR2	-0.938658192	2.22E-34	transforming growth factor beta receptor 2
Cellular senescence	TP53	-0.654172318	7.66E-13	tumor protein p53
Cellular senescence	CAPN1	-0.58869862	1.80E-19	calpain 1
Cellular senescence	CAPN2	-0.720853005	1.31E-55	calpain 2
Cellular senescence	RASSF5	1.333141559	1.62E-14	Ras association domain family member 5
Cellular senescence	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
Cellular senescence	CCNB3	2.841383388	0.003556627	cyclin B3
Cellular senescence	SQSTM1	0.866684561	6.07E-56	sequestosome 1
Cellular senescence	CCNA2	-3.101014872	9.01E-232	cyclin A2
Cellular senescence	CCNA1	2.773918343	1.19E-125	cyclin A1
Cellular senescence	CCNB1	-2.783469794	1.66E-219	cyclin B1
Cellular senescence	MCU	-0.520225542	4.59E-10	mitochondrial calcium uniporter
Cellular senescence	CCNB2	-2.4290457	4.53E-69	cyclin B2
Cellular senescence	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1
Cellular senescence	CDC25A	-1.016446988	3.02E-19	cell division cycle 25A
PI3K-Akt signaling pathway	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3
PI3K-Akt signaling pathway	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2

FIG. 4 (CONT.)

PI3K-Akt signaling pathway	CDK6	-0.789007721	1.48E-14	cyclin dependent kinase 6
PI3K-Akt signaling pathway	CDKN1A	-0.541742013	1.70E-26	cyclin dependent kinase inhibitor 1A
PI3K-Akt signaling pathway	YWHAQ	-0.517258997	2.26E-28	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta
PI3K-Akt signaling pathway	CDC37	-0.613811275	3.89E-32	cell division cycle 37, HSP90 cochaperone
PI3K-Akt signaling pathway	COL1A1	-2.891665838	1.95E-206	collagen type I alpha 1 chain
PI3K-Akt signaling pathway	COL1A2	-2.825395338	7.11E-30	collagen type I alpha 2 chain
PI3K-Akt signaling pathway	COL4A1	-2.061513116	7.83E-168	collagen type IV alpha 1 chain
PI3K-Akt signaling pathway	COL4A2	-1.446583367	7.61E-83	collagen type IV alpha 2 chain
PI3K-Akt signaling pathway	COL4A4	2.249962242	0.020614975	collagen type IV alpha 4 chain
PI3K-Akt signaling pathway	COL6A1	0.731009193	2.24E-10	collagen type VI alpha 1 chain
PI3K-Akt signaling pathway	COL6A2	0.983041664	0.001231668	collagen type VI alpha 2 chain
PI3K-Akt signaling pathway	COL6A3	-5.313792395	0.001799028	collagen type VI alpha 3 chain
PI3K-Akt signaling pathway	COL9A2	-1.399832078	2.87E-15	collagen type IX alpha 2 chain
PI3K-Akt signaling pathway	COMP	-0.85014817	0.007245133	cartilage oligomeric matrix protein
PI3K-Akt signaling pathway	CSF1R	-1.366468847	0.02162761	colony stimulating factor 1 receptor
PI3K-Akt signaling pathway	CREB3L4	0.873897859	2.66E-05	cAMP responsive element binding protein 3 like 4
PI3K-Akt signaling pathway	EFNA1	-2.217821331	2.95E-51	ephrin A1
PI3K-Akt signaling pathway	EFNA3	1.447216826	4.99E-07	ephrin A3
PI3K-Akt signaling pathway	EFNA4	0.612974162	5.11E-05	ephrin A4
PI3K-Akt signaling pathway	EGF	-2.933549372	0.001086565	epidermal growth factor
PI3K-Akt signaling pathway	EGFR	0.990016746	2.37E-21	epidermal growth factor receptor
PI3K-Akt signaling pathway	EIF4B	0.541662361	4.19E-29	eukaryotic translation initiation factor 4B
PI3K-Akt signaling pathway	EIF4E	-0.55182473	5.71E-19	eukaryotic translation initiation factor 4E
PI3K-Akt signaling pathway	EPOR	2.602656393	1.57E-11	erythropoietin receptor
PI3K-Akt signaling pathway	AKT1	-0.682588564	1.49E-36	AKT serine/threonine kinase 1
PI3K-Akt signaling pathway	AKT2	-0.685786005	7.43E-19	AKT serine/threonine kinase 2
PI3K-Akt signaling pathway	FGF1	-0.948102792	0.027848173	fibroblast growth factor 1
PI3K-Akt signaling pathway	FGF2	1.820992702	1.54E-14	fibroblast growth factor 2
PI3K-Akt signaling pathway	FGFR3	0.621643345	1.59E-04	fibroblast growth factor receptor 3
PI3K-Akt signaling pathway	FGFR2	-0.675946802	1.73E-17	fibroblast growth factor receptor 2
PI3K-Akt signaling pathway	FGFR4	0.526832375	0.002589829	fibroblast growth factor receptor 4
PI3K-Akt signaling pathway	PIK3R5	2.322190316	0.005560243	phosphoinositide-3-kinase regulatory subunit 5
PI3K-Akt signaling pathway	LPAR3	1.482648854	3.93E-61	lysophosphatidic acid receptor 3
PI3K-Akt signaling pathway	GNG7	2.904842238	8.58E-06	G protein subunit gamma 7
PI3K-Akt signaling pathway	GNG11	-2.283485578	1.36E-05	G protein subunit gamma 11
PI3K-Akt signaling pathway	PPP2R3B	0.516629563	0.02303934	protein phosphatase 2 regulatory subunit B"beta
PI3K-Akt signaling pathway	LAMA1	0.816903618	4.99E-07	laminin subunit alpha 1
PI3K-Akt signaling pathway	NR4A1	-1.68917501	2.53E-11	nuclear receptor subfamily 4 group A member 1
PI3K-Akt signaling pathway	HRAS	-0.515066586	2.66E-10	HRas proto-oncogene, GTPase
PI3K-Akt signaling pathway	HSP90AA1	-1.12503942	2.24E-135	heat shock protein 90 alpha family class A member 1
PI3K-Akt signaling pathway	HSP90AB1	-0.833298157	2.71E-154	heat shock protein 90 alpha family class B member 1
PI3K-Akt signaling pathway	IGF1R	-0.698692669	3.97E-10	insulin like growth factor 1 receptor

FIG. 4 (CONT.)

Cellular senescence	HLA-B	1.164060729	7.80E-48	major histocompatibility complex, class I, B	
Cellular senescence	HLA-F	1.31198882	2.47E-13	major histocompatibility complex, class I, F	
Cellular senescence	HLA-G	2.767109778	2.80E-19	major histocompatibility complex, class I, G	
Cellular senescence	HRAS	-0.515066586	2.66E-10	HRas proto-oncogene, GTPase	
Cellular senescence	HUS1	-0.511793445	0.01392126	HUS1 checkpoint clamp component	
Cellular senescence	IL6	-5.538099239	2.74E-23	interleukin 6	
Cellular senescence	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8	
Cellular senescence	ITPR1	0.779770267	0.023593422	inositol 1,4,5-trisphosphate receptor type 1	
Cellular senescence	ITPR3	0.554789364	1.08E-09	inositol 1,4,5-trisphosphate receptor type 3	
Cellular senescence	SMAD3	-0.660678576	6.52E-10	SMAD family member 3	
Cellular senescence	MRE11	-0.543905719	4.69E-04	MRE11 homolog, double strand break repair nuclease	
Cellular senescence	MYBL2	-2.348043415	6.70E-184	MYB proto-oncogene like 2	
Cellular senescence	GADD45B	-0.895079733	2.29E-14	growth arrest and DNA damage inducible beta	
Cellular senescence	ATM	0.812453681	0.002891499	ATM serine/threonine kinase	
Cellular senescence	NFATC4	1.45263297	0.003483352	nuclear factor of activated T cells 4	
Cellular senescence	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1	
Cellular senescence	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	
Cellular senescence	PPP1CC	-0.565040594	7.42E-10	protein phosphatase 1 catalytic subunit gamma	
Cellular senescence	PPP3CA	-0.716280478	1.13E-26	protein phosphatase 3 catalytic subunit alpha	
Cellular senescence	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3	
Cellular senescence	MAPK13	0.946430202	4.90E-07	mitogen-activated protein kinase 13	
Cellular senescence	MAP2K3	-0.703932792	8.05E-33	mitogen-activated protein kinase kinase 3	
Cellular senescence	TRPV4	0.667812465	0.005750673	transient receptor potential cation channel subfamily V member 4	
Cellular senescence	TGFB2	-1.129068552	5.00E-33	transforming growth factor beta 2	
Cellular senescence	TGFB3	-0.876774301	0.032751479	transforming growth factor beta 3	
Cellular senescence	TGFB2	-0.938658192	2.22E-34	transforming growth factor beta receptor 2	
Cellular senescence	TP53	-0.654172318	7.66E-13	tumor protein p53	
Cellular senescence	CAPN1	-0.58869862	1.80E-19	calpain 1	
Cellular senescence	CAPN2	-0.720853005	1.31E-55	calpain 2	
Cellular senescence	RASSF5	1.333141559	1.62E-14	Ras association domain family member 5	
Cellular senescence	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3	
Cellular senescence	CCNB3	2.841383388	0.003556627	cyclin B3	
Cellular senescence	SQSTM1	0.866684561	6.07E-56	sequestosome 1	
Cellular senescence	CCNA2	-3.101014872	9.01E-232	cyclin A2	
Cellular senescence	CCNA1	2.773918343	1.19E-125	cyclin A1	
Cellular senescence	CCNB1	-2.783469794	1.66E-219	cyclin B1	
Cellular senescence	MCU	-0.520225542	4.59E-10	mitochondrial calcium uniporter	
Cellular senescence	CCNB2	-2.4290457	4.53E-69	cyclin B2	
Cellular senescence	CDK1	-1.892765178	2.45E-51	cyclin dependent kinase 1	
Cellular senescence	CDC25A	-1.016446988	3.02E-19	cell division cycle 25A	
PI3K-Akt signaling pathway	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3	
PI3K-Akt signaling pathway	CDK2	-0.786336914	1.49E-14	cyclin dependent kinase 2	

FIG. 4 (CONT.)

FIG. 4 (CONT.)				24/29
PI3K-Akt signaling pathway	RXRA	0.735601936	4.27E-21	retinoid X receptor alpha
PI3K-Akt signaling pathway	SGK1	-1.429358451	4.95E-38	serum/glucocorticoid regulated kinase 1
PI3K-Akt signaling pathway	BRCA1	-0.991278421	2.12E-06	BRCA1 DNA repair associated
PI3K-Akt signaling pathway	SYK	-0.991748459	2.78E-09	spleen associated tyrosine kinase
PI3K-Akt signaling pathway	TGFA	0.534192929	1.68E-04	transforming growth factor alpha
PI3K-Akt signaling pathway	THBS1	-2.059142432	3.78E-180	thrombospondin 1
PI3K-Akt signaling pathway	THBS2	-0.645458494	9.07E-19	thrombospondin 2
PI3K-Akt signaling pathway	THBS3	0.761488796	1.47E-10	thrombospondin 3
PI3K-Akt signaling pathway	THBS4	3.301604668	6.53E-06	thrombospondin 4
PI3K-Akt signaling pathway	TLR2	0.735525169	1.16E-04	toll like receptor 2
PI3K-Akt signaling pathway	TLR4	-1.280436254	0.006102427	toll like receptor 4
PI3K-Akt signaling pathway	TNFB	1.835216663	0.003454081	tenascin XB
PI3K-Akt signaling pathway	TP53	-0.654172318	7.66E-13	tumor protein p53
PI3K-Akt signaling pathway	VEGFA	2.320185032	5.51E-69	vascular endothelial growth factor A
PI3K-Akt signaling pathway	VEGFB	0.717622153	4.09E-12	vascular endothelial growth factor B
PI3K-Akt signaling pathway	VEGFC	-0.703205693	2.86E-11	vascular endothelial growth factor C
PI3K-Akt signaling pathway	YWHA	-0.844196884	4.98E-62	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta
PI3K-Akt signaling pathway	YWHAH	-0.677792624	1.88E-35	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
PI3K-Akt signaling pathway	YWHAZ	-0.75539509	1.19E-42	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta
PI3K-Akt signaling pathway	PDGFD	-2.323822766	4.11E-06	platelet derived growth factor D
PI3K-Akt signaling pathway	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
PI3K-Akt signaling pathway	CREB3L1	0.563062213	0.009932305	cAMP responsive element binding protein 3 like 1
PI3K-Akt signaling pathway	OSMR	0.539251203	8.30E-14	cAMP responsive element binding protein 5
PI3K-Akt signaling pathway	CREB5	-0.644508992	0.009403112	solute carrier family 46 member 1
Mineral absorption	SLC46A1	0.774134541	1.44E-04	chloride voltage-gated channel 2
Mineral absorption	CLCN2	1.035155596	4.19E-08	ferritin heavy chain 1
Mineral absorption	FTL1	2.212225875	9.23E-132	ferritin light chain
Mineral absorption	FTL	2.182100225	1.05E-122	STEAP2 metalloreductase
Mineral absorption	STEAP2	0.717601263	0.010404679	heme oxygenase 1
Mineral absorption	HMOX1	2.573000854	4.38E-44	heme oxygenase 2
Mineral absorption	HMOX2	-0.624644056	5.84E-17	hephaestin like 1
Mineral absorption	HEPHL1	0.878809116	1.41E-12	metallothionein 1E
Mineral absorption	MT1E	0.541662795	2.78E-08	metallothionein 1F
Mineral absorption	MT1F	2.70928851	1.17E-49	metallothionein 1G
Mineral absorption	MT1G	3.116729392	2.44E-107	metallothionein 1H
Mineral absorption	MT1H	4.180717713	3.25E-36	metallothionein 1M
Mineral absorption	MT1M	1.234013932	0.02973902	metallothionein 1X
Mineral absorption	MT1X	1.044588637	2.23E-31	metallothionein 2A
Mineral absorption	MT2A	-0.621957037	5.18E-10	solute carrier family 11 member 2
Mineral absorption	SLC11A2	0.634328684	1.10E-09	ATPase plasma membrane Ca2+ transporting 1
Mineral absorption	ATP2B1	0.758020371	1.84E-11	

Mineral absorption	ATP2B4	0.534117465	4.93E-14	ATPase plasma membrane Ca2+ transporting 4
Mineral absorption	TRPV6	2.196344181	1.77E-13	transient receptor potential cation channel subfamily V member 6
Mineral absorption	SLC26A6	1.143080947	1.60E-39	solute carrier family 26 member 6
Mineral absorption	SLC5A1	1.432292967	0.0392278	solute carrier family 5 member 1
Mineral absorption	SLC8A1	-1.217925648	4.26E-11	solute carrier family 8 member A1
Mineral absorption	TF	-2.914957601	0.004011817	transferrin
Mineral absorption	VDR	-0.659003472	3.37E-23	vitamin D receptor
Mineral absorption	CYBRD1	1.038441665	1.34E-20	cytochrome b reductase 1
Regulation of actin cytoskeleton	AKT3	0.666158826	7.25E-04	AKT serine/threonine kinase 3
Regulation of actin cytoskeleton	ARPC4	-0.770920698	3.07E-44	actin related protein 2/3 complex subunit 4
Regulation of actin cytoskeleton	ACTR3	-0.750470984	9.01E-30	actin related protein 3
Regulation of actin cytoskeleton	ACTR2	-0.736430838	1.61E-30	actin related protein 2
Regulation of actin cytoskeleton	ABI2	0.545393357	4.77E-07	abl interactor 2
Regulation of actin cytoskeleton	MYL9	-1.56453086	7.61E-54	myosin light chain 9
Regulation of actin cytoskeleton	CFL1	-0.905087913	5.91E-32	cofilin 1
Regulation of actin cytoskeleton	CHRM4	1.776661448	0.01361272	cholinergic receptor muscarinic 4
Regulation of actin cytoskeleton	IQGAP3	-2.897856062	1.37E-25	IQ motif containing GTPase activating protein 3
Regulation of actin cytoskeleton	DIAPH1	-1.013342221	3.14E-36	diaphanous related formin 1
Regulation of actin cytoskeleton	EGF	-2.933549372	0.001086565	epidermal growth factor
Regulation of actin cytoskeleton	EGFR	0.990016746	2.37E-21	epidermal growth factor receptor
Regulation of actin cytoskeleton	AKT1	-0.682388564	1.49E-36	AKT serine/threonine kinase 1
Regulation of actin cytoskeleton	AKT2	-0.685786005	7.43E-19	AKT serine/threonine kinase 2
Regulation of actin cytoskeleton	FGF1	-0.948102792	0.027848173	fibroblast growth factor 1
Regulation of actin cytoskeleton	FGFR3	0.621643345	1.54E-14	fibroblast growth factor receptor 3
Regulation of actin cytoskeleton	FGFR2	-0.675946802	1.73E-17	fibroblast growth factor receptor 2
Regulation of actin cytoskeleton	FGFR4	0.526832375	0.002589829	fibroblast growth factor receptor 4
Regulation of actin cytoskeleton	RRAS2	-0.541005926	8.26E-18	RAS related 2
Regulation of actin cytoskeleton	MRAS	1.09973004	3.02E-04	muscle RAS oncogene homolog
Regulation of actin cytoskeleton	PIP5K1C	-0.698019362	0.006764396	phosphatidylinositol-4-phosphate 5-kinase type 1 gamma
Regulation of actin cytoskeleton	RGCC	2.792827278	8.01E-16	regulator of cell cycle
Regulation of actin cytoskeleton	HRAS	-0.515066586	2.66E-10	HRas proto-oncogene, GTPase
Regulation of actin cytoskeleton	ITGA2	0.576600556	3.68E-06	integrin subunit alpha 2
Regulation of actin cytoskeleton	ITGA3	0.648089161	1.33E-34	integrin subunit alpha 3
Regulation of actin cytoskeleton	ITGA4	-1.497575163	5.58E-24	integrin subunit alpha 4
Regulation of actin cytoskeleton	ITGA7	1.079283817	0.031554202	integrin subunit alpha 7
Regulation of actin cytoskeleton	ITGA9	-1.449469727	0.021401401	integrin subunit alpha 9
Regulation of actin cytoskeleton	ITGAE	-0.512594604	8.05E-08	integrin subunit alpha E
Regulation of actin cytoskeleton	ITGAM	-2.624612442	0.027553521	integrin subunit alpha M
Regulation of actin cytoskeleton	ITGAV	-0.593082847	4.71E-09	integrin subunit alpha V
Regulation of actin cytoskeleton	ITGB5	-0.581355197	7.55E-11	integrin subunit beta 5
Regulation of actin cytoskeleton	ITGB6	-1.653111213	9.03E-68	integrin subunit beta 6

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FIG. 4 (CONT.)

FIG. 4 (CONT.)

Regulation of actin cytoskeleton	LIMK2	-0.700598998	4.04E-44	LIM domain kinase 2
Regulation of actin cytoskeleton	MSN	-0.639678015	6.35E-30	moesin
Regulation of actin cytoskeleton	MYH9	-0.92217839	1.74E-34	myosin heavy chain 9
Regulation of actin cytoskeleton	MYLK	-1.002993477	1.17E-42	myosin light chain kinase
Regulation of actin cytoskeleton	PAK2	-0.594677037	8.89E-08	p21 (RAC1) activated kinase 2
Regulation of actin cytoskeleton	ARHGEF4	1.253529743	3.52E-09	Rho guanine nucleotide exchange factor 4
Regulation of actin cytoskeleton	PDGFB	-0.660310385	7.67E-06	platelet derived growth factor subunit B
Regulation of actin cytoskeleton	PFN1	-0.599045429	2.97E-23	profilin 1
Regulation of actin cytoskeleton	PFN2	0.513071468	1.97E-21	profilin 2
Regulation of actin cytoskeleton	PIK3CD	-0.532418886	5.31E-05	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
Regulation of actin cytoskeleton	SSH3	0.724596115	4.54E-13	slingshot protein phosphatase 3
Regulation of actin cytoskeleton	PPP1CC	-0.565040594	7.42E-10	protein phosphatase 1 catalytic subunit gamma
Regulation of actin cytoskeleton	ENAH	-0.582848126	1.67E-12	ENAH actin regulator
Regulation of actin cytoskeleton	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
Regulation of actin cytoskeleton	GNG12	-0.871918929	4.03E-39	G protein subunit gamma 12
Regulation of actin cytoskeleton	PDGFC	-0.618554351	5.32E-07	platelet derived growth factor C
Regulation of actin cytoskeleton	RAC2	0.986639325	1.05E-43	Rac family small GTPase 2
Regulation of actin cytoskeleton	RAC3	0.74332111	1.24E-05	Rac family small GTPase 3
Regulation of actin cytoskeleton	ACTB	-1.032025958	1.16E-62	actin beta
Regulation of actin cytoskeleton	SLC9A1	-0.5279311	7.58E-33	solute carrier family 9 member A1
Regulation of actin cytoskeleton	ACTG1	-0.767030671	1.31E-37	actin gamma 1
Regulation of actin cytoskeleton	C5	1.496247362	2.28E-06	complement C5
Regulation of actin cytoskeleton	VCL	-1.019709336	2.16E-55	vinculin
Regulation of actin cytoskeleton	MYH14	1.014921129	6.85E-09	myosin heavy chain 14
Regulation of actin cytoskeleton	PDGFD	-2.323822766	4.11E-06	platelet derived growth factor D
Regulation of actin cytoskeleton	DIAPH3	-2.999689382	4.21E-241	diaphanous related formin 3
Regulation of actin cytoskeleton	PIK3R3	-1.875743615	1.19E-11	phosphoinositide-3-kinase regulatory subunit 3
Regulation of actin cytoskeleton	ARHGEF6	1.322618354	0.036708156	Rac/Cdc42 guanine nucleotide exchange factor 6
Regulation of actin cytoskeleton	CDC42	-0.845647602	8.91E-13	cell division cycle 42
Ribosome biogenesis in eukaryotes	AK6	-0.542878355	0.008825016	adenylate kinase 6
Ribosome biogenesis in eukaryotes	NOP56	-0.612123558	5.29E-13	NOP56 ribonucleoprotein
Ribosome biogenesis in eukaryotes	RPP40	-0.813014301	7.19E-12	ribonuclease P/MRP subunit p40
Ribosome biogenesis in eukaryotes	POP1	-0.855016674	2.22E-34	POP1 homolog, ribonuclease P/MRP subunit
Ribosome biogenesis in eukaryotes	RPP25L	1.160678616	6.35E-22	ribonuclease P/MRP subunit p25 like
Ribosome biogenesis in eukaryotes	DKC1	-0.660687367	1.88E-18	dyskerin pseudouridine synthase 1
Ribosome biogenesis in eukaryotes	WDR43	-0.733157654	4.95E-28	WD repeat domain 43
Ribosome biogenesis in eukaryotes	RRP7A	-0.77486126	1.85E-07	ribosomal RNA processing 7 homolog A
Ribosome biogenesis in eukaryotes	GNL2	-0.552310882	2.78E-17	G protein nucleolar 2
Ribosome biogenesis in eukaryotes	FBL11	0.813670696	0.009540078	fibrillarin like 1
Ribosome biogenesis in eukaryotes	EIF6	-0.527124837	1.31E-22	eukaryotic translation initiation factor 6
Ribosome biogenesis in eukaryotes	SBDS	-0.606391455	4.63E-15	SBDS ribosome maturation factor
Ribosome biogenesis in eukaryotes	NOP58	-0.528526723	8.59E-08	NOP58 ribonucleoprotein

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Ribosome biogenesis in eukaryotes	GNL3L	-0.528693193	6.23E-07	G protein nucleolar 3 like
Ribosome biogenesis in eukaryotes	RPP25	0.606835541	0.015132812	ribonuclease P and MRP subunit p25
Ribosome biogenesis in eukaryotes	RAN	-0.791749251	7.74E-17	RAN, member RAS oncogene family
Ribosome biogenesis in eukaryotes	NOL6	-0.780489103	9.12E-42	nucleolar protein 6
Ribosome biogenesis in eukaryotes	TCOF1	-1.403217455	1.94E-20	treacle ribosome biogenesis factor 1
Ribosome biogenesis in eukaryotes	SNORD3A	-1.306356293	0.030115383	small nucleolar RNA, C/D box 3A
Ribosome biogenesis in eukaryotes	SNORD3B-2	-3.973923382	0.005557084	small nucleolar RNA, C/D box 3B-2
Ribosome biogenesis in eukaryotes	RIOK1	-0.594265218	1.15E-08	RIO kinase 1
Ribosome biogenesis in eukaryotes	BMS1	-0.501691486	2.71E-13	BMS1 ribosome biogenesis factor
NF-kappa B signaling pathway	EDAR	-1.237316378	0.021441959	ectodysplasin A receptor
NF-kappa B signaling pathway	PARP1	-0.758007839	5.84E-37	poly(ADP-ribose) polymerase 1
NF-kappa B signaling pathway	EDA	1.049001656	0.003369688	ectodysplasin A
NF-kappa B signaling pathway	ERC1	-0.537747258	1.01E-07	ELKS/RAB6-interacting/CAST family member 1
NF-kappa B signaling pathway	RIGI	-1.209558907	1.26E-09	RNA sensor RIG-I
NF-kappa B signaling pathway	LY96	1.25052101	0.001739186	lymphocyte antigen 96
NF-kappa B signaling pathway	CXCL1	-1.914811968	1.10E-11	C-X-C motif chemokine ligand 1
NF-kappa B signaling pathway	CXCL2	-4.187327651	8.18E-19	C-X-C motif chemokine ligand 2
NF-kappa B signaling pathway	CXCL3	-1.537615318	5.82E-05	C-X-C motif chemokine ligand 3
NF-kappa B signaling pathway	BLNK	1.130431499	0.030201874	B cell linker
NF-kappa B signaling pathway	CARD10	-0.669737707	4.22E-37	caspase recruitment domain family member 10
NF-kappa B signaling pathway	CXCL8	-3.328614368	2.85E-28	C-X-C motif chemokine ligand 8
NF-kappa B signaling pathway	MYD88	-0.519509323	6.66E-12	MYD88 innate immune signal transduction adaptor
NF-kappa B signaling pathway	GADD45B	-0.895079733	2.29E-14	growth arrest and DNA damage inducible beta
NF-kappa B signaling pathway	ATM	0.812453681	0.002891499	ATM serine/threonine kinase
NF-kappa B signaling pathway	NFKB1	-1.118964044	2.64E-57	nuclear factor kappa B subunit 1
NF-kappa B signaling pathway	NFKBIA	-1.603390073	5.96E-23	NF-kB inhibitor alpha
NF-kappa B signaling pathway	PLAU	-1.399953746	1.22E-16	plasminogen activator, urokinase
NF-kappa B signaling pathway	PLCG2	0.858523908	1.48E-04	phospholipase C gamma 2
NF-kappa B signaling pathway	BCL2	-1.320939366	3.10E-05	BCL2 apoptosis regulator
NF-kappa B signaling pathway	RELB	-0.531535992	6.84E-04	RELB proto-oncogene, NF-kB subunit
NF-kappa B signaling pathway	BCL2L1	0.818371467	1.34E-28	BCL2 like 1
NF-kappa B signaling pathway	SYK	-0.991748459	2.78E-09	spleen associated tyrosine kinase
NF-kappa B signaling pathway	TLR4	-1.280436254	0.006102427	toll like receptor 4
NF-kappa B signaling pathway	TNF	-3.3890783	4.61E-31	tumor necrosis factor
NF-kappa B signaling pathway	TNFAIP3	-0.819893733	1.57E-07	TNF alpha induced protein 3
NF-kappa B signaling pathway	TRAF2	-0.51861214	5.00E-07	TNF receptor associated factor 2
NF-kappa B signaling pathway	TRAF3	-0.790267127	9.87E-06	TNF receptor associated factor 3
NF-kappa B signaling pathway	TRADD	0.65210189	2.27E-09	TNFRSF1A associated via death domain
NF-kappa B signaling pathway	MAP3K14	-0.945716011	2.32E-06	mitogen-activated protein kinase kinase 14
NF-kappa B signaling pathway	CD14	3.845421766	9.67E-05	CD14 molecule
NF-kappa B signaling pathway	CD40	1.206057715	1.11E-11	CD40 molecule
Ubiquitin mediated proteolysis	SAE1	-0.845936541	5.98E-72	SUMO1 activating enzyme subunit 1

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FIG. 4
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Ubiquitin mediated proteolysis	UBE2E3	-0.61054786	1.36E-16	ubiquitin conjugating enzyme E2 E3
Ubiquitin mediated proteolysis	WWP2	-0.506620683	1.08E-05	WW domain containing E3 ubiquitin protein ligase 2
Ubiquitin mediated proteolysis	UBE2C	-2.625802586	3.87E-129	ubiquitin conjugating enzyme E2 C
Ubiquitin mediated proteolysis	ANAPC16	0.71378337	2.61E-31	anaphase promoting complex subunit 16
Ubiquitin mediated proteolysis	DDB2	-0.645131738	1.09E-09	damage specific DNA binding protein 2
Ubiquitin mediated proteolysis	NEDD4L	-0.801214654	4.70E-22	NEDD4 like E3 ubiquitin protein ligase
Ubiquitin mediated proteolysis	RCHY1	-0.594860052	6.48E-05	ring finger and CHY zinc finger domain containing 1
Ubiquitin mediated proteolysis	ANAPC15	-1.337835166	9.32E-49	anaphase promoting complex subunit 15
Ubiquitin mediated proteolysis	FBXW8	0.570591362	1.15E-07	F-box and WD repeat domain containing 8
Ubiquitin mediated proteolysis	UBE2S	-1.502844734	7.67E-35	ubiquitin conjugating enzyme E2 S
Ubiquitin mediated proteolysis	MID1	-1.089504132	4.29E-30	midline 1
Ubiquitin mediated proteolysis	NEDD4	-0.702769688	7.42E-11	NEDD4 E3 ubiquitin protein ligase
Ubiquitin mediated proteolysis	PRKN	2.568163028	9.72E-05	parkin RBR E3 ubiquitin protein ligase
Ubiquitin mediated proteolysis	FZR1	-0.607451367	3.37E-17	fizzy and cell division cycle 20 related 1
Ubiquitin mediated proteolysis	PML	-0.50175776	2.01E-09	PML nuclear body scaffold
Ubiquitin mediated proteolysis	SMURF2	-0.917584329	3.10E-12	SMAD specific E3 ubiquitin protein ligase 2
Ubiquitin mediated proteolysis	SKP2	-1.106810951	5.00E-30	S-phase kinase associated protein 2
Ubiquitin mediated proteolysis	BRCA1	-0.991278421	2.12E-06	BRCA1 DNA repair associated
Ubiquitin mediated proteolysis	UBB	-0.538578467	4.15E-17	ubiquitin B
Ubiquitin mediated proteolysis	UBA1	-0.71004135	4.76E-55	ubiquitin like modifier activating enzyme 1
Ubiquitin mediated proteolysis	UBE2G2	-0.580289841	1.20E-10	ubiquitin conjugating enzyme E2 G2
Ubiquitin mediated proteolysis	UBE2L3	-0.710922461	5.34E-26	ubiquitin conjugating enzyme E2 L3
Ubiquitin mediated proteolysis	UBE2N	-0.546964336	2.30E-19	ubiquitin conjugating enzyme E2 N
Ubiquitin mediated proteolysis	CUL4B	-0.537435261	1.36E-08	cullin 4B
Ubiquitin mediated proteolysis	SOC3	-2.414386151	4.34E-24	suppressor of cytokine signaling 3
Ubiquitin mediated proteolysis	KLHL13	-0.935942395	3.60E-06	kelch like family member 13
Ubiquitin mediated proteolysis	UBE2L6	1.466354157	8.74E-45	ubiquitin conjugating enzyme E2 L6
Ubiquitin mediated proteolysis	TRIP12	-0.575989992	2.51E-08	thyroid hormone receptor interactor 12
Ubiquitin mediated proteolysis	CDC20	-3.041016191	0	cell division cycle 20
Ubiquitin mediated proteolysis	CDC27	-0.590657313	6.85E-05	cell division cycle 27
TGF-beta signaling pathway	CDKN2B	-0.559997143	1.88E-06	cyclin dependent kinase inhibitor 2B
TGF-beta signaling pathway	FST	-0.976185574	5.20E-51	follicistatin
TGF-beta signaling pathway	FBN1	-2.650222099	3.26E-24	fibrillin 1
TGF-beta signaling pathway	LRR32	-2.237897145	0.004148795	leucine rich repeat containing 32
TGF-beta signaling pathway	RGMB	-0.514507636	1.18E-08	repulsive guidance molecule BMP co-receptor b
TGF-beta signaling pathway	HDAC1	-0.514128471	1.58E-14	histone deacetylase 1
TGF-beta signaling pathway	ID1	0.510904195	9.77E-04	inhibitor of DNA binding 1
TGF-beta signaling pathway	ID2	-0.784479295	0.008693165	inhibitor of DNA binding 2
TGF-beta signaling pathway	ID3	-2.014781117	1.83E-39	inhibitor of DNA binding 3
TGF-beta signaling pathway	ID4	1.085739531	0.006761062	inhibitor of DNA binding 4
TGF-beta signaling pathway	LTBP1	-1.08556246	4.69E-08	latent transforming growth factor beta binding protein 1
TGF-beta signaling pathway	SMAD1	-0.630928499	1.27E-06	SMAD family member 1

FIG. 4
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TGF-beta signaling pathway	SMAD3	-0.660678576	6.52E-10	SMAD family member 3
TGF-beta signaling pathway	NEO1	0.916363623	8.53E-12	neogenin 1
TGF-beta signaling pathway	PPP2CA	-0.509609413	5.36E-22	protein phosphatase 2 catalytic subunit alpha
TGF-beta signaling pathway	PPP2R1A	-0.693427968	1.09E-30	protein phosphatase 2 scaffold subunit Aalpha
TGF-beta signaling pathway	PPP2R1B	-0.594751747	6.34E-05	protein phosphatase 2 scaffold subunit Abeta
TGF-beta signaling pathway	MAPK3	0.522581535	4.41E-07	mitogen-activated protein kinase 3
TGF-beta signaling pathway	RGMA	2.467510315	1.19E-14	repulsive guidance molecule BMP co-receptor a
TGF-beta signaling pathway	SMURF2	-0.917584329	3.10E-12	SMAD specific E3 ubiquitin protein ligase 2
TGF-beta signaling pathway	SKIL	-0.911507648	9.98E-10	SKI like proto-oncogene
TGF-beta signaling pathway	BMP2	0.573695745	1.22E-04	bone morphogenetic protein 2
TGF-beta signaling pathway	BMP6	5.841517348	4.07E-35	bone morphogenetic protein 6
TGF-beta signaling pathway	BMP8B	2.491964348	0.001124261	bone morphogenetic protein 8b
TGF-beta signaling pathway	BMPR1B	-1.244778241	0.001232789	bone morphogenetic protein receptor type 1B
TGF-beta signaling pathway	TF	-2.914957601	0.004011817	transferrin
TGF-beta signaling pathway	TGFP1	-0.711574022	1.56E-21	transcription factor Dp-1
TGF-beta signaling pathway	TGFB2	-1.129068552	5.00E-33	transforming growth factor beta 2
TGF-beta signaling pathway	TGFB3	-0.876774301	0.032751479	transforming growth factor beta 3
TGF-beta signaling pathway	TGFB2	-0.938658192	2.22E-34	transforming growth factor beta receptor 2
TGF-beta signaling pathway	THBS1	-2.059142432	3.78E-180	thrombospondin 1
TGF-beta signaling pathway	TNF	-3.3890783	4.61E-31	tumor necrosis factor
TGF-beta signaling pathway	GDF5	-2.532781603	0.004265897	growth differentiation factor 5
TGF-beta signaling pathway	NOG	-0.963465187	1.09E-17	noggin
Glycolysis / Gluconeogenesis	ENO2	4.024244345	1.29E-75	enolase 2
Glycolysis / Gluconeogenesis	ALDH3A1	0.760708634	8.94E-04	aldehyde dehydrogenase 3 family member A1
Glycolysis / Gluconeogenesis	ALDH3B1	1.562471776	0.009800443	aldehyde dehydrogenase 3 family member B1
Glycolysis / Gluconeogenesis	ALDH3B2	1.350637547	0.016978662	aldehyde dehydrogenase 3 family member B2
Glycolysis / Gluconeogenesis	ALDH3A2	1.11315655	1.76E-35	aldehyde dehydrogenase 3 family member A2
Glycolysis / Gluconeogenesis	ALDOC	1.011857101	5.51E-19	aldolase, fructose-bisphosphate C
Glycolysis / Gluconeogenesis	HK1	0.543411596	4.74E-36	hexokinase 1
Glycolysis / Gluconeogenesis	HK2	1.103432954	3.01E-66	hexokinase 2
Glycolysis / Gluconeogenesis	PCK2	0.603505475	1.51E-09	phosphoenolpyruvate carboxykinase 2, mitochondrial
Glycolysis / Gluconeogenesis	PGM1	0.633468515	3.68E-29	phosphoglucomutase 1
Glycolysis / Gluconeogenesis	PKLR	1.720356718	0.018882304	pyruvate kinase L/R
Glycolysis / Gluconeogenesis	PKM	-0.856636922	3.15E-86	pyruvate kinase M1/2
Glycolysis / Gluconeogenesis	BPGM	-0.522735036	9.43E-10	bisphosphoglycerate mutase
Glycolysis / Gluconeogenesis	HKDC1	1.629092184	0.010344893	hexokinase domain containing 1
Glycolysis / Gluconeogenesis	ACSS1	0.567004514	1.41E-04	acyl-CoA synthetase short chain family member 1

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