

Supporting Information

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Whole Genome Expression Analysis Identifies Multiple Targeted Integrative Effects of Polyphenol-Rich Propolis on HER2-Positive Breast Cancer Cell Line

Mehmet Fatih Seyhan^{1*}, Ozlem Timirci-Kahraman², Allison Pinar Eronat³, Eren Yilmaz², Ayse Begum Ceviz⁴, Halil Ibrahim Kisakesen⁵, Tulin Ozturk⁶, Hulya Yilmaz-Aydogan² and Oguz Ozturk^{2*}

¹ *Department of Molecular Biology and Genetics, Faculty of Arts and Sciences, Istanbul Yeni Yuzyl University, Istanbul, Türkiye*

² *Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Türkiye*

³ *Department of Molecular Biology and Genetics, Faculty of Arts and Sciences Halic University, Istanbul, Türkiye*

⁴ *Department of Medical Genetics, Faculty of Medicine, Istanbul Health and Technology University, Istanbul, Türkiye*

⁵ *Department of Molecular Biology and Genetics, Faculty of Science, Istanbul Technical University, Istanbul, Türkiye*

⁶ *Department of Pathology, Faculty of Medicine, Istanbul University-Cerrahpasa, Istanbul, Türkiye*

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Table S1: Microarray data after 24th hour exposure to propolis on SK-BR-3 cells

Gene Symbol	Gene bank Accession Number	Gene Name	p (Corr)	Fold Change	Regulation
KLHL29	NM_052920	kelch-like 29 (Drosophila)	0.0011806166	9.408.603	up
GPR110	NM_153840	G protein-coupled receptor 110	0.0014554904	19.122.253	up
DDIT4L	NM_145244	DNA-damage-inducible transcript 4-like	0.0015330322	10.500.872	up
TMEM237	NM_001044385	transmembrane protein 237	0.0015754444	-18.398.012	down
H1FX-AS1	NR_026991	H1FX antisense RNA 1 (non-protein coding)	0.00234673	-1.072.277	down
REEP1	NM_022912	receptor accessory protein 1	0.0023643589	-13.625.365	down
PTGES	NM_004878	prostaglandin E synthase	0.0025177025	12.674.532	up
MRVI1	NM_130385	murine retrovirus integration site 1 homolog	0.0026423412	10.666.932	up
SMOX	NM_175839	spermine oxidase	0.0026706422	73.755.946	up
TARP	NM_001003799	TCR gamma alternate reading frame protein	0.002940096	-27.112.373	down
CD59	NM_203330	CD59 molecule, complement regulatory protein	0.0030721056	-12.380.226	down
CD40	NM_001250	CD40 molecule, TNF receptor superfamily member 5	0.0031636343	13.848.886	up
C19orf57	NM_024323	chromosome 19 open reading frame 57	0.0034028783	-65.842.414	down
DLG2	NM_001364	discs, large homolog 2 (Drosophila)	0.0035607084	-12.231.994	down
ADCY7	NM_001114	adenylate cyclase 7	0.003910302	35.804.176	up
TMC5	NM_024780	transmembrane channel-like 5	0.004075379	15.359.992	up
GULP1	NM_016315	GULP, engulfment adaptor PTB domain containing 1	0.004151464	66.961.703	up
GPR137C	NM_001099652	G protein-coupled receptor 137C	0.004308656	-11.657.628	down
SH3PXD2A	NM_014631	SH3 and PX domains 2A	0.004378902	17.338.219	up
LOC100505633	NR_038849	uncharacterized LOC100505633	0.0045703454	-9.708.788	down
TCP11L2	NM_152772	t-complex 11 (mouse)-like 2	0.0047264113	15.190.267	up
LY96	NM_015364	lymphocyte antigen 96	0.004974615	17.647.275	up
PSAPL1	NM_001085382	prosaposin-like 1 (gene/pseudogene)	0.005329262	-7.257.595	down
NSUN7	NM_024677	NOP2/Sun domain family, member 7	0.0053515774	17.248.966	up
PTPRH	NM_002842	protein tyrosine phosphatase, receptor type, H	0.005356321	7.037.264	up
CYP11B1-AS1	NR_027252		0.0056835623	8.565.415	up
FGF1	NM_000800	fibroblast growth factor 1 (acidic)	0.0057214503	33.019.123	up
RPA1	NM_002945	replication protein A1, 70kDa	0.005879544	-5.204.965	down

SP140	NM_007237	SP140 nuclear body protein	0.0064125117	69.712.014	up
ST6GALNA C2	NM_006456	ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	0.007160616	-22.110.636	down
ST6GALNA C3	NM_152996	ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	0.0072800717	15.302.815	up
CXCL16	NM_001100812	chemokine (C-X-C motif) ligand 16	0.0073875473	920.311	up
SLC7A11	NM_014331	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	0.007475368	51.731.744	up
C12orf34	NM_032829	chromosome 12 open reading frame 34	0.0075565265	-11.328.781	down
SAA2	NM_030754	serum amyloid A2	0.007699529	20.248.774	up
Q29HP5			0.008175082	12.232.851	up
REEP5	NM_005669	receptor accessory protein 5	0.008334911	-5.968.521	down
DIO2	NM_013989	deiodinase, iodothyronine, type II	0.008654158	-5.793.967	down
STEAP4	NM_001205315	STEAP family member 4	0.0093673775	25.849.497	up
HNRNPD	NM_031370	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	0.009439226	-8.239.226	down
SAMD12	NM_001101676	sterile alpha motif domain containing 12	0.009791373	1.073.038	up
HNRNPU	NM_031844	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.010115052	-48.914.557	down
CATSPER1	NM_053054	cation channel, sperm associated 1	0.010133325	20.432.241	up
LOC285556	XM_001717423	uncharacterized LOC285556	0.010354958	8.416.415	up
TMIE	NM_147196	transmembrane inner ear	0.010544463	67.903.914	up
KAZALD1	AK172864	Kazal-type serine peptidase inhibitor domain 1	0.01083302	-4.569.242	down
PEG10	NM_001040152	paternally expressed 10	0.010868974	-18.992.329	down
ELMOD2	NM_153702	ELMO/CED-12 domain containing 2	0.011152878	5.622.988	up
CREB3L4	NM_130898	cAMP responsive element binding protein 3-like 4	0.011249588	-4.648.651	down
LARP6	NM_018357	La ribonucleoprotein domain family, member 6	0.011318205	21.482.973	up
ERP44	NM_015051	endoplasmic reticulum protein 44	0.0115523245	-7.170.924	down
RCN1	NM_002901	reticulocalbin 1, EF-hand calcium binding domain	0.0115534505	44.179	up
PRODH	NM_016335	proline dehydrogenase (oxidase) 1	0.011570919	-9.677.001	down
XLOC_002142			0.011900994	5.411.684	up
MVK	NM_000431	mevalonate kinase	0.011980378	-61.517.973	down
LRRK2	NM_198578	leucine-rich repeat kinase 2	0.012107617	-15.176.498	down
EFNB2	NM_004093	ephrin-B2	0.012207718	-5.974.667	down
PION	AL834358	pigeon homolog (Drosophila)	0.0122803785	13.797.952	up

IRS1	NM_005544	insulin receptor substrate 1	0.0123664765	8.156.362	up
WDR78	NM_207014	WD repeat domain 78	0.012500793	11.015.854	up
C16orf93	NM_001014979	chromosome 16 open reading frame 93	0.0127642285	-64.724.264	down
SECTM1	NM_003004	secreted and transmembrane 1	0.012780473	5.670.558	up
CBS	NM_000071	cystathionine-beta-synthase	0.012800664	73.622.136	up
AGPS	NM_003659	alkylglycerone phosphate synthase	0.012886642	62.551.637	up
IKBIP	NM_153687	IKBKB interacting protein	0.01310829	-59.868.255	down
PSORS1C2	NM_014069	psoriasis susceptibility 1 candidate 2	0.013397533	-4.649.219	down
LAMC1	NM_002293	laminin, gamma 1 (formerly LAMB2)	0.0136600435	8.061.524	up
TUBB	NM_178014	tubulin, beta class I	0.01374644	-69.733033	down
SLC5A8	NM_145913	solute carrier family 5 (iodide transporter), member 8	0.014182182	-9.612.417	down
FAM59B	NM_001191033	family with sequence similarity 59, member B	0.014414788	58.100.724	up
AKR1C3	NM_003739	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	0.014489013	107.883	up
CLIP4	NM_024692	CAP-GLY domain containing linker protein family, member 4	0.014947215	9.697.601	up
TEP1	NM_007110	telomerase-associated protein 1	0.015037191	439.589	up
C5orf32	NM_032412	chromosome 5 open reading frame 32	0.015540193	4.726.665	up
APOL6	NM_030641	apolipoprotein L, 6	0.016003843	12.029.912	up
PCBP2	NM_005016	poly(rC) binding protein 2	0.017297534	-4.082.844	down
GULP1	NM_016315	GULP, engulfment adaptor PTB domain containing 1	0.017739568	8.998.777	up
WBSCR27	NM_152559	Williams Beuren syndrome chromosome region 27	0.017742878	853.937	up
SGK3	NM_013257	serum/glucocorticoid regulated kinase family, member 3	0.017840696	-40.215.244	down
FANCC	NM_000136	Fanconi anemia, complementation group C	0.018398428	-5.705.057	down
DDX46	NM_014829	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0.018436182	-6.678.552	down
C9orf95	NM_017881	chromosome 9 open reading frame 95	0.01969626	4.573.069	up
SH3PXD2A	NM_014631	SH3 and PX domains 2A	0.019783096	9.139.361	up
CREB3L4	NM_130898	cAMP responsive element binding protein 3-like 4	0.019865982	-43.396.077	down
ICAM1	NM_000201	intercellular adhesion molecule 1	0.02073087	7.940.933	up
LINC00467	NR_026761	long intergenic non-protein coding RNA 467	0.020800726	4.651.633	up
NEFH	NM_021076	neurofilament, heavy polypeptide	0.020890275	-13.959.716	down
MAP2	NM_002374	microtubule-associated protein 2	0.02154765	1.242.962	up
NGFR	NM_002507	nerve growth factor receptor	0.021616612	2.156.529	up

GPSM1	NM_001145638	G-protein signaling modulator 1	0.021688046	10.858.364	up
LMO2	NM_005574	LIM domain only 2 (rhombotin-like 1)	0.021824861	6.294.164	up
NR4A2	NM_006186	nuclear receptor subfamily 4, group A, member 2	0.021913132	-6.779.264	down
MUC20	NM_001098516	mucin 20, cell surface associated	0.02271273	29.292.606	up
AKR1B10	NM_020299	aldo-keto reductase family 1, member B10 (aldose reductase)	0.022949932	50.872.664	up
HCST	NM_014266	hematopoietic cell signal transducer	0.023063883	45.763.683	up
C15orf48	NM_032413	chromosome 15 open reading frame 48	0.02320977	5.349.684	up
RGPD5	NM_005054	RANBP2-like and GRIP domain containing 5	0.023250781	4.325.703	up
SULT4A1	NM_014351	sulfotransferase family 4A, member 1	0.023354098	64.737.806	up
CCNE2	NM_057749	cyclin E2	0.023700057	-15.325.763	down
DLEC1	NM_007335	deleted in lung and esophageal cancer 1	0.023802904	881.938	up
CD68	NM_001251	CD68 molecule	0.0239084	6.075.674	up
LOC148189	AK094188	uncharacterized LOC148189	0.023946796	10.218.492	up
VAMP1	NM_016830	vesicle-associated membrane protein 1 (synaptobrevin 1)	0.023955274	-5.808.607	down
FGF13	NM_004114	fibroblast growth factor 13	0.02404071	12.347.135	up
LY6K	NM_017527	lymphocyte antigen 6 complex, locus K	0.024225594	16.106.329	up
NEK9	NM_033116	NIMA (never in mitosis gene a)- related kinase 9	0.024533657	59.297.695	up
CBLN1	NM_004352	cerebellin 1 precursor	0.024661826	-35.499.516	down
COL27A1	AK021957	collagen, type XXVII, alpha 1	0.024881445	8.717.558	up
ZC3H12C	NM_033390	zinc finger CCCH-type containing 12C	0.025124371	62.667.813	up
BANK1	NM_017935	B-cell scaffold protein with ankyrin repeats 1	0.025710875	-70.644.917	down
TARP	NM_001003799	TCR gamma alternate reading frame protein	0.025831357	-38.973.053	down
ERCC2	NM_000400	excision repair cross-complementing rodent repair deficiency, complementation group 2	0.02618872	59.336.877	up
RORA	NM_134260	RAR-related orphan receptor A	0.026193086	11.251.509	up
CABYR	NM_012189	calcium binding tyrosine-(Y)-phosphorylation regulated	0.026351435	41.184.554	up
PRADC1	NM_032319	protease-associated domain containing 1	0.026618686	-8.001.529	down
FAM129A	NM_052966	family with sequence similarity 129, member A	0.02676983	60.526.776	up
PSMD9	NM_002813	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	0.026832996	-51.338.983	down
PDE2A	NM_002599	phosphodiesterase 2A, cGMP-stimulated	0.026957361	12.994.141	up
CLDN12	NM_012129	claudin 12	0.027476173	44.250.727	up
BTK	NM_000061	Bruton agammaglobulinemia tyrosine kinase	0.027654873	-40.151.496	down

SELENBP1	NM_003944	selenium binding protein 1	0.027795497	-39.216.835	down
LSM3	AK092130	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.028844072	-5.542.261	down
HMGCL	NM_000191	3-hydroxymethyl-3-methylglutaryl-CoA lyase	0.029353393	8.975.423	up
TUBB2A	NM_001069	tubulin, beta 2A class IIa	0.029429317	-35.071.023	down
MTCH2	NM_014342	mitochondrial carrier 2	0.02946494	-54.546.123	down
FLJ41484	NR_044995	uncharacterized LOC650669	0.030220143	77.094.865	up
C6orf57	NM_145267	chromosome 6 open reading frame 57	0.03026298	7.352.996	up
DLD	NM_000108	dihydroipoamide dehydrogenase	0.030364906	-4.255.724	down
MON1A	NM_032355	MON1 homolog A (yeast)	0.030429583	-47.718.844	down
BATF2	NM_138456	basic leucine zipper transcription factor, ATF-like 2	0.030732213	11.706.015	up
CYP1B1	NM_000104	cytochrome P450, family 1, subfamily B, polypeptide 1	0.030765781	3.451.049	up
PMF1	NM_007221	polyamine-modulated factor 1	0.030986402	-36.811.028	down
EXOC7	NM_001145297	exocyst complex component 7	0.03100242	3.836.576	up
ACAT2	NM_005891	acetyl-CoA acetyltransferase 2	0.031561032	-950.346	down
TRIM36	NM_018700	tripartite motif containing 36	0.03177335	-65.049.376	down
GNGT1	NM_021955	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	0.03227146	3.595.656	up
FAM83G	DJ031151	family with sequence similarity 83, member G	0.032288738	50.264.974	up
PLAC4	NM_182832	placenta-specific 4	0.032777805	2.393.856	up
LOC100128437	AK126077	uncharacterized LOC100128437	0.033465188	-23.967.726	down
IRF1	NM_002198	interferon regulatory factor 1	0.033575617	38.820.817	up
ASF1B	NM_018154	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	0.034175783	-35.965.188	down
LOC400236	NR_036500	uncharacterized LOC400236	0.034565955	49.033.375	up
FAM69B	NM_152421	family with sequence similarity 69, member B	0.03478451	5.065.493	up
FYN	NM_002037	FYN oncogene related to SRC, FGR, YES	0.03488751	45.097.136	up
UBD	NM_006398	ubiquitin D	0.035355207	140.646.925	up
ASB9	NM_001031739	ankyrin repeat and SOCS box containing 9	0.035784192	-6.013.148	down
CD40	NM_001250	CD40 molecule, TNF receptor superfamily member 5	0.036088966	11.398.364	up
AMPD3	NM_001025390	adenosine monophosphate deaminase 3	0.03628791	9.713.212	up
SAMD8	NM_144660	sterile alpha motif domain containing 8	0.036350925	4.759.221	up
AGPS	NM_003659	alkylglycerone phosphate synthase	0.03669786	10.040.346	up

PALMD	NM_017734	palmdelphin	0.03715644	-38.700.547	down
CDC45	NM_003504	cell division cycle 45 homolog (<i>S. cerevisiae</i>)	0.037568398	-47.621.045	down
STOM	NM_198194	stomatin	0.03762704	-43.345.757	down
TIPARP	NM_015508	TCDD-inducible poly(ADP-ribose) polymerase	0.037652887	4.729.552	up
HNRPDL	NM_031372	heterogeneous nuclear ribonucleoprotein D-like	0.03838562	-8.631.366	down
KRT4	NM_002272	keratin 4	0.039980236	-9.051.301	down
TUBA1A	NM_006009	tubulin, alpha 1a	0.040076222	-40.706.644	down
VAT1	NM_006373	vesicle amine transport protein 1 homolog (<i>T. californica</i>)	0.04043429	31.877.189	up
LOC375190	NM_001145710	UPF0638 protein B	0.040694438	57.901.745	up
CDCP1	NM_022842	CUB domain containing protein 1	0.040775202	7.364.725	up
ACSS1	NM_032501	acyl-CoA synthetase short-chain family member 1	0.040873665	-15.381.327	down
ADA	NM_000022	adenosine deaminase	0.040973775	7.750.655	up
CYP4Z2P	NR_002788	cytochrome P450, family 4, subfamily Z, polypeptide 2 pseudogene	0.041899502	-8.428.942	down
BCAS4	NM_001010974	breast carcinoma amplified sequence 4	0.04258792	50.112.734	up
LFNG	NM_001040167	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.042940326	-28.758.078	down
LINC00256B	NR_024376	long intergenic non-protein coding RNA 256B	0.04312183	5.366.342	up
SMOC1	NM_001034852	SPARC related modular calcium binding 1	0.043539822	-39.654.415	down
SERPINE2	NM_006216	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	0.043671813	8.662.887	up
ALOX5	NM_000698	arachidonate 5-lipoxygenase	0.04392394	19.231.043	up
F7	NM_000131	coagulation factor VII (serum prothrombin conversion accelerator)	0.044136938	-6.211.215	down
RBM14	NM_006328	RNA binding motif protein 14	0.044434883	-42.464.576	down
LOC100508196	XR_111691	uncharacterized LOC100508196	0.044837628	-39.478.383	down
HES6	NM_018645	hairy and enhancer of split 6 (<i>Drosophila</i>)	0.04487221	-47.169.046	down
DUSP13	NM_001007271	dual specificity phosphatase 13	0.045093507	1.327.516	up
MVP	NM_017458	major vault protein	0.045114595	350.002	up
LOC344887	NR_033752	NmrA-like family domain containing 1 pseudogene	0.045347247	23.480.078	up
CENPM	NM_001002876	centromere protein M	0.04587712	-36.977.284	down
NFATC1	NM_172387	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	0.04638196	21.087.887	up
RIN1	NM_004292	Ras and Rab interactor 1	0.04664603	4.955.519	up

AGPAT9	NM_032717	1-acylglycerol-3-phosphate O-acyltransferase 9	0.047246594	4.202.866	up
RBP5	NM_031491	retinol binding protein 5, cellular	0.047800466	-59.216.013	down
HSPA1A	NM_005345	heat shock 70kDa protein 1A	0.048225254	5.877.848	up
GFOD1	NM_001242629	glucose-fructose oxidoreductase domain containing 1	0.0482519	-48.112.063	down
GBP3	NM_018284	guanylate binding protein 3	0.048327006	6.939.169	up
CAMK2N2	NM_033259	calcium/calmodulin-dependent protein kinase II inhibitor 2	0.048369266	-69.782.224	down
KIAA1908	NR_027329	uncharacterized LOC114796	0.04849516	3.600.309	up
AKR1B10	NM_020299	aldo-keto reductase family 1, member B10 (aldose reductase)	0.048521355	64.684.005	up
C11orf63	NM_024806	chromosome 11 open reading frame 63	0.049301285	8.814.555	up
AQP1	NM_198098	aquaporin 1 (Colton blood group)	0.049636766	53.825.574	up
SYT12	NM_177963	synaptotagmin XII	0.0497172	4.142.377	up
TM7SF2	NM_003273	transmembrane 7 superfamily member 2	0.04983276	-37.132.916	down
CAV2	NM_001233	caveolin 2	0.04983586	78.936.543	up
FAM46B	NM_052943	family with sequence similarity 46, member B	0.04992478	-60.460.625	down
PCM1	NM_006197	pericentriolar material 1	0.049999334	-79.542.236	down

Table S2: Microarray data after 48th hour exposure to propolis on SK-BR-3 cells

Gene Symbol	Gene Bank Accession no	Gene Name	P Value	Fold Change	Regulation Status
LFNG	NM_001040167	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0,0000548942	-83,235	down
CLEC3A	NM_005752	C-type lectin domain family 3, member A	0,0001428783	-21,0559	down
CDCA3	NM_031299	cell division cycle associated 3	0,0002314328	-21,2668	down
ECHDC1	NM_018479	enoyl CoA hydratase domain containing 1	0,0003033388	-20,1646	down
MYBL2	NM_002466	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0,0003523656	-53,2386	down
MDK	NM_001012334	midkine (neurite growth-promoting factor 2)	0,0487227550	2,978988	up
ACAT2	NM_005891	acetyl-CoA acetyltransferase 2	0,0003780119	-31,3658	down
MYO6	NM_004999	myosin VI	0,0372193050	2,989918	up
ESPL1	NM_012291	extra spindle pole bodies homolog 1 (<i>S. cerevisiae</i>)	0,0004549425	-18,4594	down
NDC80	NM_006101	NDC80 homolog, kinetochore complex component (<i>S. cerevisiae</i>)	0,0005080385	-10,6408	down
PEX6	NM_000287	peroxisomal biogenesis factor 6	0,0417544580	3,001372	up
PRODH	NM_016335	proline dehydrogenase (oxidase) 1	0,0006149193	-32,6205	down
NUSAP1	NM_016359	nucleolar and spindle associated protein 1	0,0006644084	-14,644	down
NRAP	NM_198060	nebulin-related anchoring protein	0,0006901415	-16,767	down
GPR137C	NM_001099652	G protein-coupled receptor 137C	0,0009890874	-12,2425	down
REEP1	NM_022912	receptor accessory protein 1	0,0009940880	-20,3532	down
SMAD3	NM_005902	SMAD family member 3	0,0483340430	3,28185	up
PRADC1	NM_032319	protease-associated domain containing 1	0,0010017091	-18,0508	down
KRT4	NM_002272	keratin 4	0,0011680013	-20,2333	down
ABCC11	NM_033151	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	0,0011815560	-24,1579	down
CLSPN	NM_022111	claspin	0,0012141708	-15,5718	down
TROAP	NM_005480	trophinin associated protein (tastin)	0,0012161649	-11,1243	down
E2F7	NM_203394	E2F transcription factor 7	0,0012315667	-31,9438	down
CEP55	NM_018131	centrosomal protein 55kDa	0,0013349740	-11,8158	down
HJURP	NM_018410	Holliday junction recognition protein	0,0013430942	-19,7877	down
GRB14	NM_004490	growth factor receptor-bound protein 14	0,0407434960	3,283406	up
LINC00473	NR_026861	long intergenic non-protein coding RNA 473	0,0013646921	-25,517	down
TARP	NM_001003799	TCR gamma alternate reading frame protein	0,0014095291	-41,4453	down
SPAG5	NM_006461	sperm associated antigen 5	0,0014232803	-10,1421	down

CLIC3	NM_004669	chloride intracellular channel 3	0,0014415106	-23,64	down
MNS1	NM_018365	meiosis-specific nuclear structural 1	0,0014482586	-28,5873	down
SIPA1	NM_153253	signal-induced proliferation-associated 1	0,0455330350	3,286041	up
C4orf26	NM_178497	chromosome 4 open reading frame 26	0,0014700892	-27,9981	down
FANCC	NM_000136	Fanconi anemia, complementation group C	0,0014937560	-8,57321	down
RNF122	NM_024787	ring finger protein 122	0,0404429730	3,373265	up
LOC441956	XR_109656	uncharacterized LOC441956	0,0015429618	-20,4331	down
COPZ1	NM_016057	coatamer protein complex, subunit zeta 1	0,0477278980	3,393577	up
ATP6V1C1	NM_001695	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	0,0465685700	3,521716	up
CRCT1	NM_019060	cysteine-rich C-terminal 1	0,0016032642	-39,3492	down
LOC100508196	XR_111691	uncharacterized LOC100508196	0,0016137246	-8,74455	down
SIX4	NM_017420	SIX homeobox 4	0,0319962840	3,550793	up
ALDH4A1	NM_170726	aldehyde dehydrogenase 4 family, member A1	0,0016224430	-10,6335	down
CENPF	NM_016343	centromere protein F, 350/400kDa (mitosin)	0,0016402483	-14,312	down
C1orf194	NM_001122961	chromosome 1 open reading frame 194	0,0016868588	-9,72354	down
MKI67	NM_002417	antigen identified by monoclonal antibody Ki-67	0,0016920936	-20,8191	down
BRCA2	NM_000059	breast cancer 2, early onset	0,0016927180	-10,6069	down
RAB33A	NM_004794	RAB33A, member RAS oncogene family	0,0341115400	3,608904	up
TBC1D5	NM_014744	TBC1 domain family, member 5	0,0486789460	3,711777	up
AMTN	NM_212557	amelotin	0,0017734499	-19,1192	down
TP53I11	NM_001076787	tumor protein p53 inducible protein 11	0,0317391750	3,761079	up
ZNF197	NM_001024855	zinc finger protein 197	0,0333780720	3,765461	up
KIAA1908	NR_027329	uncharacterized LOC114796	0,0225993560	3,768445	up
CXCR4	NM_001008540	chemokine (C-X-C motif) receptor 4	0,0018460545	-9,87747	down
TIMP2	NM_003255	TIMP metalloproteinase inhibitor 2	0,0206317940	3,782042	up
OSBPL6	NM_032523	oxysterol binding protein-like 6	0,0018902406	-6,8873	down
CBLC	NM_012116	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	0,0221623610	3,786503	up
PKMYT1	NM_182687	protein kinase, membrane associated tyrosine/threonine 1	0,0020390567	-8,96768	down
PROCR	NM_006404	protein C receptor, endothelial	0,0200695490	3,79411	up
KCNQ1	NM_002237	potassium voltage-gated channel, subfamily G, member 1	0,0450016300	3,813503	up
PIP	NM_002652	prolactin-induced protein	0,0020543558	-18,2125	down

ACVR2B	NM_001106	activin A receptor, type IIB	0,0488169200	3,827075	up
SYT12	NM_177963	synaptotagmin XII	0,0464849200	3,887793	up
MCM7	NM_182776	minichromosome maintenance complex component 7	0,0020793385	-6,78068	down
ZNF292	NM_015021	zinc finger protein 292	0,0211538800	3,931481	up
TRIM14	NM_014788	tripartite motif containing 14	0,0409027560	3,954074	up
C17orf107	NM_001145536	chromosome 17 open reading frame 107	0,0124874500	3,957051	up
ZNF367	NM_153695	zinc finger protein 367	0,0020811742	-15,8544	down
SMYD3	NM_022743	SET and MYND domain containing 3	0,0453691330	3,977483	up
GTSE1	NM_016426	G-2 and S-phase expressed 1	0,0021008300	-18,5894	down
PRC1	NM_003981	protein regulator of cytokinesis 1	0,0021552455	-9,97265	down
BIRC5	NM_001012271	baculoviral IAP repeat containing 5	0,0023457827	-10,4887	down
VAT1	NM_006373	vesicle amine transport protein 1 homolog (T. californica)	0,0106899070	3,990819	up
CHAC1	NM_024111	ChaC, cation transport regulator homolog 1 (E. coli)	0,0242022330	4,003883	up
TPCN1	NM_017901	two pore segment channel 1	0,0268722830	4,008743	up
PFKM	NM_000289	phosphofructokinase, muscle	0,0405772600	4,068668	up
LOC100505633	NR_038849	uncharacterized LOC100505633	0,0024200438	-8,96415	down
GPR158	NM_020752	G protein-coupled receptor 158	0,0464454370	4,077151	up
CLTCL1	NM_007098	clathrin, heavy chain-like 1	0,0024898686	-9,10175	down
CEP44	NM_001145314	centrosomal protein 44kDa	0,0025693870	-8,42454	down
NQO1	NM_000903	NAD(P)H dehydrogenase, quinone 1	0,0422371440	4,083721	up
TANC2	NM_025185	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	0,0441292400	4,112676	up
STAT6	NM_003153	signal transducer and activator of transcription 6, interleukin-4 induced	0,0129366770	4,181938	up
C5orf32	NM_032412	chromosome 5 open reading frame 32	0,0217556060	4,211488	up
CASC5	NM_170589	cancer susceptibility candidate 5	0,0027559914	-16,1188	down
SAMD8	NM_144660	sterile alpha motif domain containing 8	0,0191768020	4,212279	up
TLE2	NM_003260	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	0,0169868900	4,231522	up
CENPO	NM_001199803	centromere protein O	0,0028790536	-6,12167	down
CDCA2	NM_152562	cell division cycle associated 2	0,0028816904	-10,1426	down
FAM54A	NM_138419	family with sequence similarity 54, member A	0,0029381860	-7,82451	down
FTH1	NM_002032	ferritin, heavy polypeptide 1	0,0152672540	4,232586	up
H1FX-AS1	NR_026991	H1FX antisense RNA 1 (non-protein coding)	0,0029525561	-10,8161	down

E2F1	NM_005225	E2F transcription factor 1	0,0030253993	-11,649	down
RILPL1	NM_178314	Rab interacting lysosomal protein-like 1	0,0420279580	4,265119	up
PARP12	NM_022750	poly (ADP-ribose) polymerase family, member 12	0,0449604300	4,291656	up
C15orf42	NM_152259	chromosome 15 open reading frame 42	0,0030596130	-18,3494	down
FSTL1	NM_007085	folliculin-like 1	0,0445128680	4,30651	up
HAAO	NM_012205	3-hydroxyanthranilate 3,4-dioxygenase	0,0030825750	-14,2999	down
CASC5	NM_170589	cancer susceptibility candidate 5	0,0031853209	-25,1731	down
AGMAT	NM_024758	agmatine ureohydrolase (agmatinase)	0,0265895700	4,311063	up
ASF1B	NM_018154	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	0,0032247775	-12,4895	down
FHIT	NM_002012	fragile histidine triad gene	0,0384973250	4,362318	up
MVP	NM_017458	major vault protein	0,0128385740	4,37268	up
LOC100507429	XR_110179	uncharacterized LOC100507429	0,0033125307	-45,0844	down
ABTB1	NM_032548	ankyrin repeat and BTB (POZ) domain containing 1	0,0283751640	4,383971	up
	XR_133415		0,0033293688	-12,625	down
MVK	NM_000431	mevalonate kinase	0,0033669146	-6,52416	down
ECT2	NM_018098	epithelial cell transforming sequence 2 oncogene	0,0033951560	-7,36948	down
			0,0034768760	-6,9197	down
ABHD8	NM_024527	abhydrolase domain containing 8	0,0483760270	4,441257	up
TUBB	NM_178014	tubulin, beta class I	0,0036733192	-7,87247	down
ADAM19	NM_033274	ADAM metallopeptidase domain 19	0,0170468240	4,506208	up
LOC100292680	AK090616	uncharacterized LOC100292680	0,0061149920	4,536038	up
ZNF653	NM_138783	zinc finger protein 653	0,0036912395	-16,1206	down
PIR	NM_003662	pirin (iron-binding nuclear protein)	0,0256009160	4,565258	up
TMEM106B	NM_018374	transmembrane protein 106B	0,0284821750	4,576758	up
TIPARP	NM_015508	TCDD-inducible poly(ADP-ribose) polymerase	0,0129494430	4,6135	up
PSAPL1	NM_001085382	prosaposin-like 1 (gene/pseudogene)	0,0037632745	-7,35935	down
PHF11	NM_001040443	PHD finger protein 11	0,0122000600	4,645004	up
IKBIP	NM_201612	IKBKB interacting protein	0,0038170170	-6,29546	down
ERP27	NM_152321	endoplasmic reticulum protein 27	0,0097964540	4,65801	up
EPHB6	NM_004445	EPH receptor B6	0,0038316126	-14,5535	down
TSPAN31	NM_005981	tetraspanin 31	0,0314504950	4,707979	up

RIN1	NM_004292	Ras and Rab interactor 1	0,0158186830	4,75351	up
GALC	NM_000153	galactosylceramidase	0,0084423740	4,768701	up
KAZALD1	AK172864	Kazal-type serine peptidase inhibitor domain 1	0,0039541055	-10,5736	down
LOC100128881	NR_036480	uncharacterized LOC100128881	0,0496841040	4,835657	up
	BC029255		0,0270728900	4,860976	up
NDRG4	NM_022910	NDRG family member 4	0,0203352890	5,014297	up
PLCE1	NM_016341	phospholipase C, epsilon 1	0,0040864605	-7,50552	down
LOC100128420	NR_038461	uncharacterized LOC100128420	0,0041041668	-11,9861	down
HLA-J	NR_024240	major histocompatibility complex, class I, J (pseudogene)	0,0426101100	5,122852	up
IQGAP3	NM_178229	IQ motif containing GTPase activating protein 3	0,0041205715	-10,2535	down
SYNC	NM_030786	syncoilin, intermediate filament protein	0,0041256496	-8,02404	down
ESX1	NM_153448	ESX homeobox 1	0,0366047470	5,123879	up
SELENBP1	NM_003944	selenium binding protein 1	0,0042089050	-4,92747	down
PAK1	NM_001128620	p21 protein (Cdc42/Rac)-activated kinase 1	0,0085206070	5,132483	up
EXOC7	NM_001145297	exocyst complex component 7	0,0132460460	5,156384	up
TBC1D1	NM_015173	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	0,0068366870	5,15942	up
BANK1	NM_017935	B-cell scaffold protein with ankyrin repeats 1	0,0042101420	-7,89047	down
HMGB3P1	NR_002165	high mobility group box 3 pseudogene 1	0,0043189353	-5,72767	down
HMOX1	NM_002133	heme oxygenase (decycling) 1	0,0070885485	5,207801	up
NR4A3	NM_173200	nuclear receptor subfamily 4, group A, member 3	0,0043797763	-22,2775	down
CDC48	NM_018101	cell division cycle associated 8	0,0043844600	-9,06408	down
FAM25A	NM_001146157	family with sequence similarity 25, member A	0,0043943683	-7,31777	down
P4HA2	NM_004199	prolyl 4-hydroxylase, alpha polypeptide II	0,0122139470	5,210479	up
ALDH1L1	NM_012190	aldehyde dehydrogenase 1 family, member L1	0,0183702020	5,288324	up
PBK	NM_018492	PDZ binding kinase	0,0046070780	-10,0932	down
PLA2G4C	NM_003706	phospholipase A2, group IVC (cytosolic, calcium-independent)	0,0100336070	5,31144	up
LIG1	NM_000234	ligase I, DNA, ATP-dependent	0,0046113664	-12,7581	down
GTF2IRD2	NM_173537	GTF2I repeat domain containing 2	0,0402801970	5,315362	up
CREB3L4	NM_130898	cAMP responsive element binding protein 3-like 4	0,0047125425	-5,93527	down
ZNF367	NM_153695	zinc finger protein 367	0,0048607970	-9,68836	down

CDH10	NM_006727	cadherin 10, type 2 (T2-cadherin)	0,0049006950	-49,6272	down
HSPA1B	NM_005346	heat shock 70kDa protein 1B	0,0364935550	5,319459	up
ALDH3B1	NM_000694	aldehyde dehydrogenase 3 family, member B1	0,0062724184	5,341619	up
ZNF404	NM_001033719	zinc finger protein 404	0,0495592650	5,361287	up
LOC400236	NR_036500	uncharacterized LOC400236	0,0178000130	5,37814	up
CDKL3	NM_016508	cyclin-dependent kinase-like 3	0,0093666310	5,385218	up
BDKRB1	NM_000710	bradykinin receptor B1	0,0481578200	5,409288	up
TMEM68	NM_152417	transmembrane protein 68	0,0096742200	5,439782	up
C9orf95	NM_017881	chromosome 9 open reading frame 95	0,0349792170	5,475577	up
RARRES3	NM_004585	retinoic acid receptor responder (tazarotene induced) 3	0,0073167803	5,517659	up
HSPA1A	NM_005345	heat shock 70kDa protein 1A	0,0144411270	5,528089	up
FCRLB	NM_001002901	Fc receptor-like B	0,0269829500	5,559654	up
PCBP2	NM_005016	poly(rC) binding protein 2	0,0049953624	-8,9737	down
			0,0359534730	5,56835	up
PRKCDBP	NM_145040	protein kinase C, delta binding protein	0,0051002353	-7,59907	down
LINC00473	NR_026860	long intergenic non-protein coding RNA 473	0,0052649360	-19,2329	down
RCN1	NM_002901	reticulocalbin 1, EF-hand calcium binding domain	0,0129947690	5,61014	up
FAM83G	DJ031151	family with sequence similarity 83, member G	0,0330550100	5,665584	up
WBSCR28	NM_182504	Williams-Beuren syndrome chromosome region 28	0,0470371360	5,672554	up
CPSF3L	NM_017871	cleavage and polyadenylation specific factor 3-like	0,0052920748	-9,8547	down
PABPC4L	NM_001114734	poly(A) binding protein, cytoplasmic 4-like	0,0053820433	-4,95597	down
LOC90246	NR_026954	uncharacterized LOC90246	0,0283304680	5,734695	up
ASPM	NM_018136	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0,0055240532	-9,66842	down
TACC3	NM_006342	transforming, acidic coiled-coil containing protein 3	0,0055312426	-7,96287	down
ZDHHC4	NM_018106	zinc finger, DHHC-type containing 4	0,0080956760	5,735168	up
CENPE	NM_001813	centromere protein E, 312kDa	0,0056080027	-9,87244	down
C9orf95	NM_017881	chromosome 9 open reading frame 95	0,0055582975	5,740981	up
PTER	NM_001001484	phosphotriesterase related	0,0435180960	5,79283	up
SMC4	NM_005496	structural maintenance of chromosomes 4	0,0056565376	-5,82686	down
HRCT1	NM_001039792	histidine rich carboxyl terminus 1	0,0056845420	-13,0954	down
ZYG11A	NM_0010043	zyg-11 homolog A (C. elegans)	0,0057172854	-5,25381	down

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SECTM1	NM_003004	secreted and transmembrane 1	0,0210339900	5,800011	up
CCNE2	NM_057749	cyclin E2	0,0059675840	-17,0013	down
RHOH	NM_004310	ras homolog gene family, member H	0,0060059484	-4,69052	down
XLOC_002997	XR_110395		0,0131526750	5,835187	up
S100A1	NM_006271	S100 calcium binding protein A1	0,0060742246	-5,89853	down
MALL	NM_005434	mal, T-cell differentiation protein-like	0,0060906913	-6,41398	down
RAD51	NM_002875	RAD51 homolog (<i>S. cerevisiae</i>)	0,0061971350	-8,02332	down
TTC39B	NM_152574	tetratricopeptide repeat domain 39B	0,0427880250	5,844347	up
MCAM	NM_006500	melanoma cell adhesion molecule	0,0401782730	5,853628	up
FAM69B	NM_152421	family with sequence similarity 69, member B	0,0060794675	5,880635	up
BORA	NM_024808	bora, aurora kinase A activator	0,0064259920	-5,48201	down
FOXM1	NM_202002	forkhead box M1	0,0064286995	-12,8896	down
PCDH20	NM_022843	protocadherin 20	0,0276973000	5,881207	up
GALM	NM_138801	galactose mutarotase (aldose 1-epimerase)	0,0122728530	5,933505	up
IRF1	NM_002198	interferon regulatory factor 1	0,0134737810	6,004941	up
MXD3	NM_031300	MAX dimerization protein 3	0,0064419730	-5,87791	down
HMGCR	NM_000859	3-hydroxy-3-methylglutaryl-CoA reductase	0,0064555420	-5,66592	down
FBLN1	NM_006486	fibulin 1	0,0214143950	6,066344	up
KRTAP4-1	NM_033060	keratin associated protein 4-1	0,0307116640	6,129263	up
CAMK2N2	NM_033259	calcium/calmodulin-dependent protein kinase II inhibitor 2	0,0065299897	-14,0324	down
NUF2	NM_145697	NUF2, NDC80 kinetochore complex component, homolog (<i>S. cerevisiae</i>)	0,0065356884	-12,0468	down
CTSL2	NM_001333	cathepsin L2	0,0067789927	-4,45025	down
CTDSPL92	NM_001008392	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0,0067836046	-4,71549	down
CXCL14	NM_004887	chemokine (C-X-C motif) ligand 14	0,0068269083	-8,70071	down
PLEKHG184	NM_001029884	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	0,0301968320	6,228256	up

Table S3: 24th hour up regulated pathways (Biological process Gene Ontology),(Interacting proteins with highest confidence were selected (0.900)

#Term ID	Term Description	Observed Gene Count	Background Gene Count	Strength	False Discovery Rate	Matching Proteins in Your Network (Labels)
GO:0002376	immune system process	29	2370	0.37	0.0213	NGFR, IRF1, CD68, RORA, CYSTM1, ICAM1, SECTM1, SLC7A11, LY96, CXCL16, BATF2, ELMOD2, PDE2A, FYN, VAT1, SH3PXD2A, C6orf57, GBP3, WDR78, CD40, ADA, ALOX5, HSPA1A, UBD, ERCC2, MVP, AMPD3, MUC20, TIPARP
GO:0019748	secondary metabolic process	5	52	1.27	0.0213	AKR1B10, CYP1A1, AKR1C3, ENSG00000160200, CYP1B1
GO:0046068	cGMP metabolic process	4	30	1.41	0.0245	RORA, AQP1, PDE2A, ADCY7
GO:0001775	cell activation	16	1024	0.48	0.0444	IRF1, CD68, RORA, CYSTM1, ICAM1, SLC7A11, BATF2, FYN, VAT1, CD40, ADA, ALOX5, HSPA1A, UBD, MVP, AMPD3
GO:0002252	immune effector process	15	927	0.49	0.0444	IRF1, CD68, RORA, CYSTM1, ICAM1, ELMOD2, FYN, VAT1, GBP3, CD40, ADA, ALOX5, HSPA1A, MVP, AMPD3
GO:0010033	response to organic substance	30	2815	0.31	0.0444	NGFR, CAV2, IRF1, CD68, GDF15, LMO2, RORA, ICAM1, LY96, CXCL16, IRS1, AQP1, PDE2A, PTGES, FYN, MAP2, GBP3, CD40, ADA, ALOX5, HMGCL, HSPA1A, UBD, CYP1A1, AKR1C3, FAM83, ADCY7, TIPARP, CYP1B1, FGF1
GO:0045321	leukocyte activation	15	894	0.51	0.0444	IRF1, CD68, RORA, CYSTM1, ICAM1, BATF2, FYN, VAT1, CD40, ADA, ALOX5, HSPA1A, UBD, MVP, AMPD3
GO:0001676	long-chain fatty acid metabolic process	5	104	0.96	0.0496	PTGES, ALOX5, CYP1A1, AKR1C3, CYP1B1
GO:0006163	purine nucleotide metabolic process	9	442	0.59	0.0496	RORA, AQP1, SULT4A1, PDE2A, ADA, HMGCL, HSPA1A, ADCY7, AMPD3
GO:0006629	lipid metabolic process	16	1192	0.41	0.0496	AGPS, IRS1, ST6GALNAC3, SULT4A1, PTGES, FYN, AKR1B10, ALOX5, HMGCL, CYP1A1, AKR1C3, TIPARP, SAMD8, CYP1B1, FGF1, AGPAT9
GO:0006690	icosanoid metabolic process	5	99	0.99	0.0496	PTGES, ALOX5, CYP1A1, AKR1C3, CYP1B1
GO:0006950	response to stress	31	3267	0.26	0.0496	NGFR, IRF1, GNGT1, RORA, ICAM1, SLC7A11, LY96, CXCL16, BATF2, AQP1, ELMOD2, PTGES, FYN, FAM129A, C6orf57, GBP3, CD40, ADA, ALOX5, HMGCL, HSPA1A, UBD, CYP1A1, AKR1C3, ERCC2, SP140, ENSG00000160200, SERPINE2, SAA2, CYP1B1, FGF1
GO:0006952	defense response	16	1234	0.4	0.0496	NGFR, IRF1, ICAM1, LY96, CXCL16, BATF2, ELMOD2, PTGES, FYN, C6orf57, GBP3, CD40, ALOX5, UBD, SP140, SAA2
GO:0006955	immune response	19	1560	0.37	0.0496	NGFR, IRF1, CD68, RORA, CYSTM1, ICAM1, SECTM1, LY96, CXCL16, FYN, VAT1, C6orf57, CD40, ADA, ALOX5, HSPA1A,

						UBD, MVP, AMPD3
GO:0009117	nucleotide metabolic process	11	576	0.56	0.0496	RORA, AQP1, SULT4A1, PDE2A, NMRK1, ADA, HMGCL, HSPA1A, ADCY7, AMPD3, AGPAT9
GO:0009404	toxin metabolic process	3	22	1.42	0.0496	CYP1A1, ENSG00000160200, CYP1B1
GO:0009410	response to xenobiotic stimulus	7	262	0.71	0.0496	RORA, ICAM1, AQP1, PDE2A, ADA, CYP1A1, CYP1B1
GO:0009605	response to external stimulus	24	2152	0.33	0.0496	NGFR, IRF1, GNGT1, GDF15, ICAM1, LY96, CXCL16, BATF2, AQP1, ELMOD2, PDE2A, PTGES, FYN, C6orf57, GBP3, CD40, ADA, HMGCL, UBD, CYP1A1, AKR1C3, ENSG00000160200, SERPINE2, SAA2
GO:0016488	farnesol catabolic process	2	2	2.28	0.0496	AKR1B10, AKR1C3
GO:0017144	drug metabolic process	11	622	0.53	0.0496	RORA, AKR1B10, ADA, HMGCL, HSPA1A, CYP1A1, AKR1C3, AMPD3, ENSG00000160200, SMOX, CYP1B1
GO:0019369	arachidonic acid metabolic process	4	51	1.18	0.0496	PTGES, CYP1A1, AKR1C3, CYP1B1
GO:0019637	organophosphate metabolic process	15	1011	0.45	0.0496	RORA, IRS1, AQP1, SULT4A1, PDE2A, FYN, NMRK1, ADA, HMGCL, HSPA1A, ADCY7, AMPD3, SAMD8, FGF1, AGPAT9
GO:0030097	hemopoiesis	10	526	0.56	0.0496	IRF1, RORA, BATF2, PDE2A, SH3PXD2A, WDR78, ADA, UBD, ERCC2, TIPARP
GO:0033326	cerebrospinal fluid secretion	2	3	2.11	0.0496	C11orf63, AQP1
GO:0034612	response to tumor necrosis factor	7	217	0.79	0.0496	NGFR, RORA, ICAM1, CXCL16, GBP3, CD40, UBD
GO:0046688	response to copper ion	3	28	1.31	0.0496	ICAM1, AQP1, CYP1A1
GO:0070887	cellular response to chemical stimulus	28	2672	0.3	0.0496	NGFR, CAV2, IRF1, GNGT1, CD68, GDF15, LMO2, RORA, ICAM1, LY96, CXCL16, IRS1, AQP1, PDE2A, FYN, MAP2, GBP3, CD40, ALOX5, HSPA1A, CYP1A1, AKR1C3, FAM83G, ADCY7, TIPARP, SAA2, CYP1B1, FGF1
GO:0071310	cellular response to organic substance	25	2219	0.33	0.0496	NGFR, CAV2, IRF1, CD68, GDF15, LMO2, RORA, ICAM1, LY96, IRS1, AQP1, PDE2A, FYN, MAP2, GBP3, CD40, ALOX5, HSPA1A, CYP1A1, AKR1C3, FAM83G, ADCY7, TIPARP, CYP1B1, FGF1
GO:0071466	cellular response to xenobiotic stimulus	6	157	0.87	0.0496	RORA, ICAM1, AQP1, PDE2A, CYP1A1, CYP1B1
GO:0071496	cellular response to external stimulus	8	305	0.7	0.0496	IRF1, ICAM1, AQP1, PDE2A, FYN, CD40, AKR1C3, ENSG00000160200
GO:1901568	fatty acid derivative metabolic process	6	148	0.89	0.0496	PTGES, ALOX5, HMGCL, CYP1A1, AKR1C3, CYP1B1
GO:1902533	positive regulation of intracellular signal transduction	14	959	0.45	0.0496	CAV2, HCST, GDF15, ICAM1, IRS1, FYN, CD40, ADA, HSPA1A, UBD, AKR1C3, MUC20, CYP1B1, FGF1

GO:1903409	reactive oxygen species biosynthetic process	3	25	1.36	0.0496	RORA, CYP1A1, CYP1B1
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Table S4: 48th hour *down regulated* pathways (Biological process Gene Ontology) (Interacting proteins with highest confidence were selected (0.900))

#Term ID	Term Description	Observed Gene Count	Background Gene Count	Strength	False Discovery Rate	Matching Proteins in Your Network (Labels)
GO:0007049	cell cycle	101	1263	0.71	1.18e-39	KIF22,MCM5,MYBL2,OIP5,DLGAP5,GINS2,NASP,CCNB1,ESPL1,THBS1,KIF23,MNS1,KIF11,BARD1,NDC80,PKMYT1,CDKN2C,KIF18A,LIG1,SGOL1,KAT2B,CENPE,ANLN,TICRR,NUF2,CDCA5,SPC25,SMC2,BUB1B,CCNB2,MELK,KIAA0101,TPX2,CHAF1A,BIRC5,CDC25A,MCM7,FANCI,CLSPN,AURKB,CDC25C,E2F7,SPAG5,KIF15,TACC3,CDCA2,ERCC6L,CDKN3,CASC5,TUBB,FOXM1,E2F1,BLM,UBE2C,SMC4,SGOL2,PCNT,RRM2,IQGAP3,EXO1,CENPF,KIF14,ASPM,MKI67,TTK,CEP55,KIF20B,STIL,RAD54L,KIF2C,CDCA8,KIF4A,POLA1,PCNA,BRCA2,RAD51,ECT2,PTTG1,PRC1,CDK1,CCNF,SAC3D1,WDR62,GPSM2,CHEK1,CDC7,CDC45,RFC5,HJURP,GTS1,CTCF,PBK,CCNE2,DDIAS,CLTCL1,CDCA3,NUSAP1,SPC24,BORA,UHRF1,FAM83D
GO:0000278	mitotic cell cycle	72	628	0.87	4.34e-36	KIF22,MCM5,MYBL2,DLGAP5,GINS2,NASP,CCNB1,ESPL1,KIF23,KIF11,NDC80,PKMYT1,CDKN2C,KIF18A,LIG1,SGOL1,CENPE,ANLN,TICRR,CDCA5,SPC25,SMC2,BUB1B,CCNB2,MELK,TPX2,BIRC5,CDC25A,MCM7,FANCI,CLSPN,AURKB,CDC25C,E2F7,SPAG5,KIF15,TACC3,CDKN3,TUBB,FOXM1,E2F1,BLM,UBE2C,SMC4,PCNT,RRM2,IQGAP3,CENPF,KIF14,TTK,CEP55,STIL,KIF2C,CDCA8,KIF4A,POLA1,PCNA,BRCA2,RAD51,ECT2,PRC1,CDK1,WDR62,GPSM2,CDC7,CDC45,GTSE1,PBK,CCNE2,CLTCL1,NUSAP1,BORA
GO:0051301	cell division	54	483	0.86	5.82e-26	OIP5,CCNB1,ESPL1,KIF23,KIF11,NDC80,LIG1,SGOL1,CENPE,ANLN,NUF2,CDCA5,SPC25,SMC2,BUB1B,CCNB2,TPX2,BIRC5,CDC25A,AURKB,CDC25C,SPAG5,TACC3,CDCA2,ERCC6L,CASC5,TUBB,UBE2C,SMC4,SGOL2,CENPF,KIF14,ASPM,CEP55,KIF20B,KIF2C,CDCA8,KIF4A,BRCA2,ECT2,PTTG1,PRC1,CDK1,CCNF,SAC3D1,GPSM2,CDC7,FGFR2,CCNE2,CDCA3,NUSAP1,SPC24,BORA,FAM83D
GO:0051726	regulation of cell cycle	73	1129	0.62	2.68e-22	MYBL2,LFNG,DLGAP5,CCNB1,ESPL1,THBS1,KIF23,KIF11,BARD1,NDC80,SLC6A4,PKMYT1,CDKN2C,KAT2B,WDR76,CENPE,ANLN,TICRR,CTDSPL,CDCA5,BUB1B,CCNB2,KIAA0101,TPX2,BIRC5,CDC25A,RMI2,FANCI,CLSPN,AURKB,CDC25C,E2F7,SPAG5,TACC3,YAF2,MX2,CDKN3,TUBB,FOXM1,E2F1,BLM,UBE2C,PCNT,RRM2,CENPF,DTL,KIF14,ASPM,MKI67,TTK,KIF20B,STIL,PCNA,BRCA2,RAD51,ECT2,PTTG1,PRC1,CDK1,CCNF,GPSM2,CHEK1,CDC7,CDC45,FGFR2,GTSE1,CCNE2,NRK,DDIAS,NUSAP1,BORA,FAM83D

						D,NR4A3
GO:0007059	chromosome segregation	35	253	0.95	6.73e-19	KIF22,OIP5,DLGAP5,CCNB1,ESPL1,KIF23,KIF11,NDC80,KIF18A,SGOL1,CENPE,NUF2,CDCA5,SPC25,SMC2,BUB1B,BIRC5,AURKB,SPAG5,CASC5,SMC4,SGOL2,CENPF,KIF14,TTK,KIF2C,CDCA8,KIF4A,CENPN,PTTG1,PRC1,HJURP,CCNE2,NUSAP1,FAM83D
GO:0048285	organelle fission	35	294	0.89	4.83e-17	KIF22,MYBL2,DLGAP5,CCNB1,ESPL1,KIF23,KIF11,NDC80,KIF18A,SGOL1,CENPE,CDCA5,SMC2,BUB1B,TPX2,BIRC5,AURKB,SPAG5,MX2,UBE2C,SMC4,SGOL2,KIF14,ASPM,TTK,KIF2C,CDCA8,KIF4A,BRCA2,RAD51,PTTG1,PRC1,MTRF2,CCNE2,NUSAP1
GO:0000280	nuclear division	33	268	0.9	2.03e-16	KIF22,MYBL2,DLGAP5,CCNB1,ESPL1,KIF23,KIF11,NDC80,KIF18A,SGOL1,CENPE,CDCA5,SMC2,BUB1B,TPX2,BIRC5,AURKB,SPAG5,UBE2C,SMC4,SGOL2,KIF14,ASPM,TTK,KIF2C,CDCA8,KIF4A,BRCA2,RAD51,PTTG1,PRC1,CCNE2,NUSAP1
GO:0051276	chromosome organization	59	999	0.58	7.15e-16	KIF22,OIP5,DLGAP5,GINS2,NASP,CCNB1,DB2,ESPL1,KIF23,NDC80,KIF18A,ASF1B,SGOL1,KAT2B,CENPE,CDCA5,CENPU,SMC2,ATAD2,BUB1B,CHAF1A,MCM7,H2AFV,AURKB,SPAG5,HIST1H1B,CASC5,BLM,CENPL,SMC4,SGOL2,EXO1,CENPF,KIF14,RAD54L,KIF2C,CDCA8,KIF4A,CENPP,POLA1,PCNA,BRCA2,CENPO,RAD51,CENPN,PTTG1,PRC1,CDK1,CHEK1,CDC45,RFC5,HJURP,CTCF,CCNE2,NUSAP1,HIST1H4D,UHRF1,RECQL4,PHF19
GO:0006260	DNA replication	28	203	0.95	5.38e-15	MCM5,RNASEH2A,GINS2,NASP,BARD1,LIG1,POLQ,TICRR,KIAA0101,CHAF1A,MCM7,RMI2,CLSPN,BLM,RRM2,EXO1,DTL,POLA1,PCNA,BRCA2,RAD51,CDK1,CHEK1,CDC7,CDC45,RFC5,CCNE2,RECQL4
GO:0000819	sister chromatid segregation	22	123	1.06	1.11e-13	KIF22,DLGAP5,CCNB1,ESPL1,KIF23,NDC80,KIF18A,SGOL1,CENPE,CDCA5,SMC2,BUB1B,AURKB,SPAG5,SMC4,SGOL2,KIF14,KIF2C,CDCA8,KIF4A,PRC1,NUSAP1
GO:0044772	mitotic cell cycle phase transition	29	254	0.87	1.11e-13	MCM5,NASP,CCNB1,PKMYT1,CDKN2C,BUB1B,CCNB2,MELK,BIRC5,CDC25A,MCM7,CDC25C,E2F7,TACC3,CDKN3,TUBB,FOXM1,E2F1,UBE2C,PCNT,RRM2,IQGAP3,POLA1,PCNA,CDK1,CDC7,CDC45,CCNE2,BORA
GO:1902850	microtubule cytoskeleton organization involved in mitosis	20	94	1.14	1.20e-13	MYBL2,CCNB1,ESPL1,KIF23,KIF11,NDC80,CENPE,SPC25,TPX2,BIRC5,AURKB,TACC3,PCNT,TTK,STIL,KIF4A,PRC1,WDR62,GPSM2,NUSAP1
GO:0006259	DNA metabolic process	47	773	0.6	6.03e-13	KIF22,MCM5,RNASEH2A,EEDP1,GINS2,NASP,DDB2,BARD1,LIG1,POLQ,NEIL3,TICRR,CDCA5,USP43,FANCC,KIAA0101,CHAF1A,FOS,MCM7,RMI2,FANCI,CLSPN,FOXM1,BLM,RRM2,EXO1,CENPF,DTL,RAD54L,FANC

						G,POLA1,PCNA,BRCA2,RAD51,PTTG1,CDK1,NUDT1,CHEK1,CDC7,CDC45,RFC5,CTCF,CCNE2,KPNA2,HIST1H4D,UHRF1,RECQL4
GO:0007051	spindle organization	21	123	1.04	8.45e-13	MYBL2,CCNB1,ESPL1,KIF23,KIF11,NDC80,CENPE,SPC25,TPX2,BIRC5,AURKB,SPAG5,TUBB,PCNT,ASPM,TTK,STIL,KIF4A,PRC1,WDR62,GPSM2
GO:0006281	DNA repair	37	491	0.69	1.36e-12	KIF22,RNASEH2A,EEPD1,GINS2,DDB2,BARD1,LIG1,POLQ,NEIL3,TICRR,CDCA5,USP43,FANCC,KIAA0101,CHAF1A,FANCI,CLSPN,FOXM1,BLM,EXO1,DTL,RAD54L,FANCG,POLA1,PCNA,BRCA2,RAD51,PTTG1,CDK1,NUDT1,CHEK1,CDC7,CDC45,RFC5,HIST1H4D,UHRF1,RECQL4
GO:0007052	mitotic spindle organization	17	70	1.2	2.05e-12	MYBL2,CCNB1,KIF23,KIF11,NDC80,CENPE,SPC25,TPX2,BIRC5,AURKB,PCNT,TTK,STIL,KIF4A,PRC1,WDR62,GPSM2
GO:0006974	cellular response to DNA damage stimulus	45	749	0.59	2.95e-12	KIF22,RNASEH2A,EEPD1,GINS2,CCNB1,DDDB2,BARD1,LIG1,WDR76,POLQ,NEIL3,TICRR,CDCA5,USP43,FANCC,KIAA0101,CHAF1A,MCM7,FANCI,CLSPN,CDC25C,E2F7,CRIP1,FOXM1,E2F1,BLM,EXO1,DTL,RAD54L,FANCG,POLA1,PCNA,BRCA2,RAD51,PTTG1,CDK1,NUDT1,CHEK1,CDC7,CDC45,RFC5,GTSE1,HIST1H4D,UHRF1,RECQL4
GO:0071103	DNA conformation change	26	257	0.82	2.71e-11	OIP5,GINS2,NASP,CCNB1,ASF1B,CDCA5,CENPU,SMC2,CHAF1A,MCM7,HIST1H1B,CASC5,BLM,CENPL,SMC4,RAD54L,CENPP,CENPO,RAD51,CENPN,CDK1,CDC45,HJURP,NUSAP1,HIST1H4D,RECQL4
GO:0006996	organelle organization	100	3131	0.32	3.69e-11	KIF22,MYBL2,OIP5,DLGAP5,GINS2,NASP,MYBPH,CCNB1,DDB2,ESPL1,KIF23,MNS1,KIF11,NDC80,KIF18A,ASF1B,SGOL1,KAT2B,CENPE,ANLN,CDCA5,CENPU,SPC25,TEKT5,SMC2,ATAD2,BUB1B,CCNB2,TMSNB,LRK2,KIAA0101,TPX2,CHAF1A,BIRC5,MCM7,PRKCDBP,H2AFV,AURKB,SPAG5,TACC3,HIST1H1B,MX2,CASC5,TUBB,E2F1,BLM,CENPL,UBE2C,SMC4,SGOL2,PCNT,EXO1,CENPF,KIF14,ASPM,TTK,KIAA1324,PLCE1,STIL,RAD54L,KIF2C,CDCA8,KIF4A,CENPP,FANCG,POLA1,PCNA,BRCA2,TUBB2A,CENPO,RAD51,WIPF1,EVL,CENPN,PTTG1,SYNPO,PRC1,CDK1,CD59,DIAPH3,WDR62,GPSM2,CHEK1,MTFR2,CDC45,RFC5,HJURP,CTCF,FLNB,IRGM,CCNE2,REEP1,VIM,KRT4,NUSAP1,MPV17L2,HIST1H4D,UHRF1,RECQL4,PHF19
GO:0007017	microtubule-based process	38	605	0.61	8.80e-11	KIF22,MYBL2,DLGAP5,CCNB1,ESPL1,KIF23,KIF11,NDC80,KIF18A,SGOL1,CENPE,SPC25,TEKT5,KIAA0101,TPX2,BIRC5,AURKB,SPAG5,KIF15,TACC3,TUBB,PCNT,KIF14,ASPM,TTK,KIF20B,STIL,KIF2C,KIF4A,DLG2,BRCA2,TUBB2A,PRC1,CDK1,WDR62,GPSM2,GTSE1,NUSAP1

GO:0090068	positive regulation of cell cycle process	26	273	0.79	8.90e-11	DLGAP5,CCNB1,ESPL1,KIF23,NDC80,CDCA5,BIRC5,CDC25A,AURKB,CDC25C,E2F7,SPAG5,E2F1,UBE2C,DTL,KIF14,KIF20B,PCNA,ECT2,CDK1,GPSM2,CDC7,CDC45,GTSE1,NUSAP1,FAM83D
GO:0045786	negative regulation of cell cycle	34	517	0.63	4.36e-10	CCNB1,ESPL1,THBS1,BARD1,CDKN2C,KAT2B,TICRR,CTDSPL,BUB1B,BIRC5,FANCI,CLSPN,AURKB,CDC25C,E2F7,YAF2,CDKN3,E2F1,BLM,RRM2,CENPF,DTL,TTK,KIF20B,PCNA,RAD51,PTTG1,CDK1,CCNF,CHEK1,CDC7,CDC45,GTSE1,DDIAS
GO:0000226	microtubule cytoskeleton organization	29	393	0.68	1.34e-09	MYBL2,CCNB1,ESPL1,KIF23,KIF11,NDC80,KIF18A,SGOL1,CENPE,SPC25,KIAA0101,TPX2,BIRC5,AURKB,SPAG5,TACC3,TUBB,PCNT,ASPM,TTK,STIL,KIF2C,KIF4A,BRCA2,PRC1,CDK1,WDR62,GPSM2,NUSAP1
GO:0033554	cellular response to stress	59	1553	0.39	1.64e-08	KIF22,HNRNPL,RNASEH2A,EEPD1,KLF2,GINS2,CCNB1,DDB2,THBS1,BARD1,LIG1,WDK76,POLQ,NEIL3,TICRR,CDCA5,USP43,FANCC,MELK,LRRK2,KIAA0101,CHAF1A,FOS,MCM7,FANCI,CLSPN,HNRNPD,CDC25C,E2F7,CRIP1,FOXM1,NR4A2,E2F1,BLM,POX2,EXO1,DTL,CREB3L4,KIAA1324,RAD54L,FANCG,POLA1,PCNA,BRCA2,RAD51,ECT2,PTTG1,CDK1,NUDT1,CHEK1,CDC7,CDC45,RFC5,GTSE1,NRK,CTSV,HIST1H4D,UHRF1,RECL4
GO:0051303	establishment of chromosome localization	13	72	1.07	4.16e-08	KIF22,DLGAP5,CCNB1,NDC80,KIF18A,CENPE,CDCA5,BIRC5,CENPF,KIF14,KIF2C,CDC48,FAM83D
GO:0006323	DNA packaging	19	195	0.8	5.83e-08	OIP5,NASP,CCNB1,ASF1B,CDCA5,CENPU,SMC2,CHAF1A,HIST1H1B,CASC5,CENPL,SMC4,CENPP,CENPO,CENPN,CDK1,HJURP,NUSAP1,HIST1H4D
GO:0006261	DNA-dependent DNA replication	15	114	0.93	8.83e-08	MCM5,RNASEH2A,GINS2,LIG1,POLQ,MCM7,BLM,POLA1,PCNA,BRCA2,RAD51,CDC7,CDC45,RFC5,CCNE2
GO:0016043	cellular component organization	128	5163	0.21	1.27e-07	KIF22,MYBL2,OIP5,DLGAP5,KLF2,KRT1,GINS2,NASP,MYBPH,CCNB1,DDB2,ESPL1,THBS1,KIF23,MNS1,KIF11,NDC80,SLC6A4,KIF18A,ASF1B,SGOL1,KAT2B,POLQ,CDH10,CENPE,ANLN,TICRR,MALL,CDCA5,CENPU,SPC25,TEKT5,SMC2,ATAD2,BUB1B,HMGCR,CCNB2,FANCC,TMSNB,MITF,RAPGEF6,LRRK2,KIAA0101,TPX2,CHAF1A,BIRC5,MCM7,PRKCDBP,H2AFV,AURKB,CACNB2,SPAG5,TACC3,HIST1H1B,MX2,CASC5,TUBB,NR4A2,FBLN5,E2F1,BLM,CENPL,UBE2C,SMC4,SGOL2,PCNT,IQGAP3,EXO1,CENPF,KIF14,ASPM,TTK,KIAA1324,KAZALD1,PLCE1,KIF20B,STIL,RAD54L,KIF2C,CDCA8,DKK1,KIF4A,CENPP,FANCG,POLA1,PCNA,VIT,BRCA2,TUBB2A,CENPO,RAD51,WIPF1,ECT2,EVL,CENPN,PTTG1,SYNPO,PRC1,CDK1,CD59,DIAPH3,MATN3,WDR62,GPSM2,CXCR4,CHEK1,MTFR2,CDC45,RFC5,FGFR2,HJURP,CTC

						FL,FLNB,IRGM,CCNE2,NRK,REEP1,CLTCL1,CTSV,VIM,KRT4,NUSAP1,MPV17L2,HIST1H4D,UHRF1,NR4A3,RECQL4,PHF19
GO:0034508	centromere complex assembly	11	50	1.15	1.27e-07	OIP5,CENPE,CENPU,CASC5,CENPL,CENPF,CENPP,CENPO,CENPN,HJURP,HIST1H4D
GO:0006336	DNA replication-independent nucleosome assembly	11	53	1.13	1.97e-07	OIP5,NASP,ASF1B,CENPU,CASC5,CENPL,CENPP,CENPO,CENPN,HJURP,HIST1H4D
GO:0065004	protein-DNA complex assembly	18	223	0.72	1.79e-06	OIP5,NASP,DDDB2,ASF1B,CENPE,CENPU,CHAF1A,HIST1H1B,CASC5,CENPL,CENPF,CENPP,CENPO,RAD51,CENPN,CDC45,HJURP,HIST1H4D
GO:0000910	cytokinesis	11	71	1.0	2.41e-06	ESPL1,KIF23,ANLN,BIRC5,AURKB,CEP55,KIF4A,BRCA2,ECT2,PRC1,NUSAP1
GO:0043486	histone exchange	10	57	1.06	3.46e-06	OIP5,NASP,CENPU,CASC5,CENPL,CENPP,CENPO,CENPN,HJURP,HIST1H4D
GO:0034080	CENP-A containing nucleosome assembly	9	42	1.14	3.49e-06	OIP5,CENPU,CASC5,CENPL,CENPP,CENPO,CENPN,HJURP,HIST1H4D
GO:0031570	DNA integrity checkpoint	14	147	0.79	8.42e-06	CCNB1,TICRR,FANCI,CLSPN,CDC25C,E2F7,E2F1,BLM,DTL,PCNA,CDK1,CHEK1,CDC45,GTSE1
GO:0033260	nuclear DNA replication	8	35	1.17	1.07e-05	GINS2,LIG1,POLA1,PCNA,BRCA2,RAD51,CDC45,RFC5
GO:0000281	mitotic cytokinesis	9	50	1.07	1.11e-05	ESPL1,KIF23,ANLN,BIRC5,CEP55,KIF4A,BRCA2,ECT2,NUSAP1
GO:0008283	cell population proliferation	30	676	0.46	1.83e-05	INSL4,DLGAP5,NASP,BUB1B,MELK,TPX2,CDC25A,MCM7,ELF5,AURKB,CDC25C,KIF15,TACC3,CRIP1,CENPF,KIF14,ASPM,MKI67,PLCE1,STIL,KIF2C,TCF19,POLA1,PCNA,BRCA2,CDK1,FGFR2,UHRF1,FAM83D,NR4A3
GO:0006334	nucleosome assembly	13	137	0.79	2.18e-05	OIP5,NASP,ASF1B,CENPU,CHAF1A,HIST1H1B,CASC5,CENPL,CENPP,CENPO,CENPN,HJURP,HIST1H4D
GO:0051321	meiotic cell cycle	16	214	0.69	2.18e-05	ESPL1,MNS1,KIF18A,SGOL1,SMC2,BUB1B,SMC4,SGOL2,EXO1,ASPM,TTK,RAD54L,BRCA2,RAD51,PTTG1,CCNE2
GO:1902969	mitotic DNA replication	5	7	1.67	2.40e-05	GINS2,LIG1,BRCA2,RAD51,CDC45
GO:0051383	kinetochore organization	6	17	1.36	3.97e-05	NDC80,CENPE,SMC2,SMC4,CENPF,CENPN
GO:0140013	meiotic nuclear division	13	146	0.76	4.08e-05	ESPL1,KIF18A,SGOL1,SMC2,BUB1B,SMC4,SGOL2,ASPM,TTK,BRCA2,RAD51,PTTG1,CCNE2

GO:0006270	DNA replication initiation	7	31	1.17	5.82e-05	MCM5,GINS2,MCM7,POLA1,CDC7,CDC45,CNE2
GO:0042770	signal transduction in response to DNA damage	11	104	0.84	5.82e-05	CCNB1,CDC25C,E2F7,FOXM1,E2F1,DTL,PCNA,BRCA2,CDK1,CHEK1,GTSE1
GO:0051302	regulation of cell division	14	179	0.7	6.25e-05	DLGAP5,ESPL1,KIF23,AURKB,E2F7,BLM,KIF14,ASPM,KIF20B,BRCA2,ECT2,PRC1,FGFR2,NUSAP1
GO:0044774	mitotic DNA integrity checkpoint	11	108	0.82	7.83e-05	CCNB1,TICRR,FANCI,CLSPN,CDC25C,E2F7,E2F1,BLM,PCNA,CDK1,GTSE1
GO:0008608	attachment of spindle microtubules to kinetochore	6	20	1.29	7.91e-05	NDC80,SGOL1,CENPE,AURKB,CASC5,KIF2C
GO:0022414	reproductive process	44	1350	0.32	0.00011	LFNG,INSL4,FOSB,NASP,CCNB1,ESPL1,MNS1,SLC6A4,KIF18A,ASF1B,SGOL1,TEKT5,SMC2,BUB1B,FANCC,LRRK2,FOS,PSAPL1,CDC25C,E2F7,CRIP1,CASC5,E2F1,SMC4,SGOL2,EXO1,ASPM,CREB3L4,TTK,RAD54L,FANCG,PCNA,BRCA2,RAD51,PTTG1,CDK1,NUDT1,CCNF,DIAPH3,FGFR2,CTCF,CCNE2,NRK,CTSV
GO:0051128	regulation of cellular component organization	64	2306	0.25	0.00011	CBLN1,TMEM97,DLGAP5,CCNB1,DDB2,ESPL1,THBS1,MNS1,KIF11,NDC80,PKMYT1,CDKN2C,PALMD,KIF18A,KAT2B,CENPE,ANLN,CDC45,ATAD2,BUB1B,MITF,LRRK2,TPX2,BIRC5,RMI2,HNRNPD,AURKB,ARHGAP33,CDC25C,AMIGO3,SPAG5,TACC3,HIST1H1B,FOXM1,FBLN5,E2F1,UBE2C,CENPF,KIF14,MKI67,TTK,KIAA1324,KAZALD1,PLCE1,KIF20B,STIL,DKK1,EVL,PTTG1,SYNPO,CCNF,GPSM2,CHEK1,CDC7,CDC45,HJURP,CTCF,IRGM,CTSV,VIM,NUSAP1,BORA,UHRF1,PHF19
GO:0051225	spindle assembly	9	70	0.92	0.00011	MYBL2,KIF23,KIF11,TPX2,BIRC5,AURKB,TUBB,ASPM,KIF4A
GO:0000077	DNA damage checkpoint	12	138	0.75	0.00012	CCNB1,FANCI,CLSPN,CDC25C,E2F7,E2F1,BLM,DTL,PCNA,CDK1,CHEK1,GTSE1
GO:0072422	signal transduction involved in DNA damage checkpoint	9	73	0.9	0.00015	CCNB1,CDC25C,E2F7,E2F1,DTL,PCNA,CDK1,CHEK1,GTSE1
GO:0051656	establishment of organelle localization	20	387	0.52	0.00016	KIF22,DLGAP5,CCNB1,ESPL1,KIF23,NDC80,KIF18A,CENPE,CDCA5,BIRC5,SPAG5,CENPF,KIF14,KIF2C,CDCA8,CD59,GPSM2,NUSAP1,FAM83D,NR4A3
GO:0051640	organelle localization	25	574	0.45	0.00018	KIF22,DLGAP5,CCNB1,ESPL1,KIF23,NDC80,KIF18A,CENPE,CDCA5,LRRK2,BIRC5,SPAG5,TUBB,PCNT,CENPF,KIF14,ASPM,KIF2C,

						CDCA8,CDK1,CD59,GPSM2,NUSAP1,FAM83D,NR4A3
GO:0090307	mitotic spindle assembly	7	40	1.05	0.00021	MYBL2,KIF23,KIF11,TPX2,BIRC5,AURKB,KIF4A
GO:0000723	telomere maintenance	10	101	0.81	0.00025	BLM,EXO1,POLA1,PCNA,BRCA2,RAD51,RF C5,CCNE2,HIST1H4D,RECQL4
GO:0006302	double-strand break repair	13	178	0.68	0.00025	GIN52,BARD1,POLQ,CDCA5,BLM,RAD54L, POLA1,BRCA2,RAD51,CDC7,CDC45,HIST1 H4D,RECQL4
GO:0034501	protein localization to kinetochore	5	14	1.36	0.00025	BUB1B,AURKB,CASC5,TTK,CDK1
GO:1902653	secondary alcohol biosynthetic process	7	42	1.03	0.00027	C14orf1,HMGCR,MVD,ACAT2,LSS,EBP,MV K
GO:1902751	positive regulation of cell cycle G2/M phase transition	6	27	1.16	0.00029	CCNB1,CDC25A,CDC25C,DTL,CDK1,CDC7
GO:0030330	DNA damage response, signal transduction by p53 class mediator	9	82	0.85	0.00031	CCNB1,CDC25C,E2F7,FOXM1,E2F1,PCNA,B RCA2,CDK1,GTSE1
GO:0006338	chromatin remodeling	12	156	0.7	0.00032	OIP5,NASP,KAT2B,CENPU,CASC5,CENPL,C ENPP,CENPO,CENPN,CHEK1,HJURP,HIST1 H4D
GO:0045132	meiotic chromosome segregation	9	85	0.84	0.00040	ESPL1,SGOL1,SMC2,BUB1B,SMC4,SGOL2,T TK,PTTG1,CCNE2
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	9	86	0.83	0.00043	CCNB1,PKMYT1,CDKN2C,KAT2B,CDC25A, CDC25C,CDKN3,BLM,CCNE2
GO:0016126	sterol biosynthetic process	7	46	0.99	0.00044	C14orf1,HMGCR,MVD,ACAT2,LSS,EBP,MV K
GO:0000724	double-strand break repair via homologous recombination	9	88	0.82	0.00049	GIN52,POLQ,BLM,RAD54L,BRCA2,RAD51, CDC7,CDC45,RECQL4
GO:0009314	response to radiation	20	425	0.48	0.00049	DDB2,TICRR,HMGCR,IKBIP,KIAA0101,CDC 25A,FOS,AURKB,CRIPI,BLM,DTL,RAD54L, FANCG,PCNA,BRCA2,RAD51,ECT2,SYNPO, CHEK1,PBK
GO:0006271	DNA strand elongation involved in DNA replication	5	18	1.26	0.00058	RNASEH2A,GIN52,LIG1,POLA1,PCNA

GO:0031572	G2 DNA damage checkpoint	6	32	1.08	0.00059	FANCI,CLSPN,BLM,DTL,CDK1,CHEK1
GO:0006950	response to stress	79	3267	0.19	0.00068	KIF22,HNRNPL,RNASEH2A,EEDP1,KLF2,KRT1,GINS2,CCNB1,DDB2,THBS1,BARD1,SLC6A4,ZNF175,LIG1,WDR76,POLQ,NEIL3,TICRR,CDCA5,USP43,FANCC,TFF1,MELK,LRRK2,KIAA0101,CHAF1A,FOS,MCM7,FANCI,CLSPN,HNRNPD,CDC25C,E2F7,CRIP1,MX2,TUBB,FOXM1,NR4A2,E2F1,BLM,POX2,PCBP2,MT-CYB,EXO1,DTL,CREB3L4,KIAA1324,RAD54L,F7,FANCG,POLA1,PCNA,BRCA2,RAD51,ECT2,EVL,PTTG1,CDK1,CD59,NUDT1,CXCR4,CHEK1,CDC7,TBXA2R,CPS1,CDC45,RFC5,FGFR2,GTSE1,FLNB,IRGM,TFF3,NRK,CTSV,VIM,HIST1H4D,UHRF1,NR4A3,RECQL4
GO:0071897	DNA biosynthetic process	9	95	0.79	0.00080	LIG1,POLQ,USP43,KIAA0101,CENPF,DTL,POLA1,PCNA,RFC5
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	9	96	0.78	0.00085	KIF22,KIF23,KIF11,KIF18A,CENPE,KIF15,KIF2C,KIF4A,CTSV
GO:0031577	spindle checkpoint	5	23	1.15	0.0014	BUB1B,BIRC5,AURKB,CENPF,TTK
GO:0034502	protein localization to chromosome	7	58	0.89	0.0014	BUB1B,AURKB,HIST1H1B,CASC5,TTK,BRCA2,CDK1
GO:0006890	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	8	81	0.81	0.0015	KIF22,KIF23,KIF11,KIF18A,CENPE,KIF15,KIF2C,KIF4A
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	7	59	0.89	0.0015	CCNB1,CDC25C,E2F7,E2F1,PCNA,CDK1,GTSE1
GO:0006695	cholesterol biosynthetic process	6	41	0.98	0.0017	HMGCR,MVD,ACAT2,LSS,EBP,MVK
GO:0051653	spindle localization	6	41	0.98	0.0017	ESPL1,NDC80,SPAG5,ASPM,GPSM2,NUSAP1
GO:0032465	regulation of cytokinesis	8	84	0.79	0.0018	KIF23,AURKB,E2F7,KIF14,KIF20B,BRCA2,ECT2,PRC1
GO:0006325	chromatin organization	25	683	0.38	0.0020	OIP5,NASP,CCNB1,DDB2,ASF1B,KAT2B,CENPU,ATAD2,CHAF1A,H2AFV,AURKB,HIST1H1B,CASC5,CENPL,CENPP,BRCA2,CENPO,CENPN,CDK1,CHEK1,HJURP,CTCF,HIST1H4D,UHRF1,PHF19

GO:0009411	response to UV	10	139	0.67	0.0021	DDB2,KIAA0101,CDC25A,AURKB,CRIP1,DTL,PCNA,BRCA2,CHEK1,PBK
GO:0032392	DNA geometric change	7	63	0.86	0.0021	GINS2,MCM7,BLM,RAD54L,RAD51,CDC45,RECQL4
GO:0071900	regulation of protein serine/threonine kinase activity	20	488	0.42	0.0023	CCNB1,THBS1,PKMYT1,CDKN2C,KAT2B,HMGCR,LRRK2,CDC25A,CDC25C,CDKN3,BLM,IQGAP3,PLCE1,DKK1,CDK1,CXCR4,IRGM,CCNE2,NRK,GHR
GO:0090329	regulation of DNA-dependent DNA replication	6	44	0.95	0.0023	TICRR,E2F7,BLM,BRCA2,CDC7,RFC5
GO:0097305	response to alcohol	13	233	0.56	0.0023	FOSB,KLF2,HMGCR,FOS,HNRNPD,BLM,MT-CYB,F7,RAD51,CDK1,TBXA2R,FGFR2,GHR
GO:0006084	acetyl-CoA metabolic process	5	27	1.08	0.0024	ACSS2,MVD,ACSS1,MPC1,MVK
GO:0010035	response to inorganic substance	20	491	0.42	0.0025	FOSB,KLF2,CCNB1,THBS1,FANCC,TFF1,HAAO,LRRK2,FOS,HNRNPD,CRIP1,BLM,MT-CYB,DLG2,PCNA,ECT2,CDK1,NUDT1,CPS1,NR4A3
GO:0010038	response to metal ion	16	339	0.49	0.0025	FOSB,CCNB1,THBS1,TFF1,HAAO,LRRK2,FOS,HNRNPD,CRIP1,MT-CYB,DLG2,PCNA,ECT2,CDK1,NUDT1,CPS1
GO:0051338	regulation of transferase activity	31	964	0.32	0.0027	CCNB1,THBS1,PKMYT1,CDKN2C,KAT2B,CENPE,HMGCR,CAMK2N2,LRRK2,TPX2,CDK25A,CLSPN,HNRNPD,AURKB,CDC25C,CDKN3,BLM,UBE2C,IQGAP3,KIF14,PLCE1,ZYG11A,DKK1,ECT2,CDK1,CXCR4,RFC5,IRGM,CCNE2,NRK,GHR
GO:0046165	alcohol biosynthetic process	8	91	0.76	0.0028	C14orf1,HMGCR,MVD,PGP,ACAT2,LSS,EBP,MVK
GO:0000727	double-strand break repair via break-induced replication	3	5	1.59	0.0037	GINS2,CDC7,CDC45
GO:0006275	regulation of DNA replication	8	96	0.73	0.0037	TICRR,E2F7,BLM,PCNA,BRCA2,CDK1,CDC7,RFC5
GO:1901654	response to ketone	11	183	0.59	0.0038	FOSB,KLF2,NASP,THBS1,FOS,HNRNPD,F7,PCNA,TBXA2R,CPS1,GHR
GO:0000731	DNA synthesis involved in DNA repair	6	50	0.89	0.0039	USP43,KIAA0101,DTL,POLA1,PCNA,RFC5
GO:0071478	cellular response to radiation	10	153	0.63	0.0039	DDB2,CDC25A,AURKB,CRIP1,BLM,PCNA,RAD51,ECT2,CHEK1,PBK
GO:0072698	protein localization to microtubule	5	31	1.02	0.0039	SPAG5,TTK,KIF20B,STIL,FAM83D

	cytoskeleton					
GO:1901617	organic hydroxy compound biosynthetic process	10	161	0.6	0.0055	C14orf1,HMGCR,MVD,PGP,NR4A2,ACAT2,OSBPL6,LSS,EBP,MVK
GO:0007096	regulation of exit from mitosis	4	18	1.16	0.0056	ANLN,CDCA5,BIRC5,UBE2C
GO:0007098	centrosome cycle	7	78	0.76	0.0056	KIF11,SGOL1,KIAA0101,STIL,BRCA2,CDK1,WDR62
GO:0034644	cellular response to UV	7	78	0.76	0.0056	DDB2,CDC25A,AURKB,CRIP1,PCNA,CHEK1,PBK
GO:0045859	regulation of protein kinase activity	26	788	0.33	0.0056	CCNB1,THBS1,PKMYT1,CDKN2C,KAT2B,CENPE,HMGCR,CAMK2N2,LRRK2,TPX2,CD25A,CLSPN,CDC25C,CDKN3,BLM,IQGAP3,KIF14,PLCE1,DKK1,ECT2,CDK1,CXCR4,IRGM,CCNE2,NRK,GHR
GO:1902275	regulation of chromatin organization	10	162	0.6	0.0056	CCNB1,ATAD2,LRRK2,HIST1H1B,MKI67,CHBK1,CDC45,CTCF,UHRF1,PHF19
GO:0046686	response to cadmium ion	6	56	0.84	0.0063	HAAO,FOS,MT-CYB,PCNA,CDK1,NUDT1
GO:0070925	organelle assembly	23	666	0.35	0.0066	MYBL2,MYBPH,KIF23,KIF11,CENPE,ANLN,TEKT5,TPX2,BIRC5,AURKB,CASC5,TUBB,P CNT,CENPF,ASPM,KIAA1324,KIF4A,CENP N,SYNPO,CDK1,WDR62,IRGM,MPV17L2
GO:0006310	DNA recombination	11	202	0.55	0.0075	GINS2,LIG1,POLQ,BLM,EXO1,RAD54L,BRCA2,RAD51,CDC7,CDC45,RECQL4
GO:0032467	positive regulation of cytokinesis	5	38	0.93	0.0081	KIF23,AURKB,KIF14,KIF20B,ECT2
GO:0000733	DNA strand renaturation	3	8	1.39	0.0086	BLM,RAD54L,RECQL4
GO:0019985	translesion synthesis	5	41	0.9	0.0104	USP43,KIAA0101,DTL,PCNA,RFC5
GO:0060249	anatomical structure homeostasis	13	285	0.47	0.0108	BARD1,TFF1,HAAO,BLM,EXO1,POLA1,PCNA,BRCA2,RAD51,RFC5,CCNE2,HIST1H4D,RECQL4
GO:0006273	lagging strand elongation	3	9	1.33	0.0110	RNASEH2A,LIG1,POLA1
GO:1901360	organic cyclic compound metabolic process	102	4963	0.12	0.0117	KIF22,MCM5,MYBL2,HNRNPL,RNASEH2A,EEDP1,FOSB,KLF2,ACSS2,GINS2,NASP,C14orf1,DDB2,BARD1,ZNF175,DHTKD1,LIG1,ASF1B,KAT2B,POLQ,NEIL3,TICRR,CDCA5,CENPU,USP43,ATAD2,HMGCR,FANCC,U2AF1L4,ZNF653,HAAO,MITF,LRRK2,KIAA0101,MVD,CHAF1A,BIRC5,FOS,MCM7,RMI2,FANCI,ELF5,CLSPN,HNRNPD,ACSS1,E2F7,YAF2,FOXM1,NR4A2,ZNF678,ZNF587,E2F1,FAR1,BLM,POX2,PCBP2,RRM2,MPC1,MT-

						CYB,EXO1,CENPF,DTL,ACAT2,CREB3L4,MPP1,RAD54L,ZNF367,ALDH4A1,DLG2,TCF19,FANCG,POLA1,PCNA,BRCA2,RAD51,OSBPL6,PTTG1,DHFRL1,CDK1,NUDT1,LSS,WR62,CHEK1,CDC7,MXD3,CPS1,CDC45,RFC5,CTCF,EBP,CCNE2,PDE10A,KPNA2,MVK,CPSF3L,DIO2,HIST1H4D,UHRF1,NR4A3,RECQL4,GHR,PHF19
GO:0009416	response to light stimulus	13	290	0.46	0.0123	DDB2,HMGCR,KIAA0101,CDC25A,FOS,AURKB,CRIP1,DTL,PCNA,BRCA2,SYNPO,CHEK1,PBK
GO:0034599	cellular response to oxidative stress	11	222	0.51	0.0139	KLF2,FANCC,MELK,LRRK2,FOS,HNRNPD,NR4A2,POX2,PCNA,ECT2,CDK1
GO:0006694	steroid biosynthetic process	8	126	0.61	0.0157	C14orf1,HMGCR,MVD,ACAT2,OSBPL6,LSS,EBP,MVK
GO:0006298	mismatch repair	4	26	1.0	0.0158	RNASEH2A,LIG1,EXO1,PCNA
GO:0009628	response to abiotic stimulus	30	1052	0.27	0.0166	FOSB,CCNB1,DDB2,THBS1,SLC6A4,TICRR,HMGCR,IKBIP,KIAA0101,CDC25A,FOS,HNRNPD,AURKB,CRIP1,NR4A2,E2F1,BLM,MT - CYB,DTL,RAD54L,F7,FANCG,PCNA,BRCA2,RAD51,ECT2,SYNPO,CXCR4,CHEK1,PBK
GO:0009987	cellular process	249	14652	0.04	0.0172	KIF22,MCM5,MYBL2,CBLN1,OIP5,PAG1,HNRNPL,RNASEH2A,LFNG,KRT37,INSL4,EEP1,FOSB,DLGAP5,KLF2,KRT1,ACSS2,GINS2,NASP,MYBPH,C14orf1,CCNB1,DDB2,ESPL1,THBS1,KIF23,MNS1,KIF11,BARD1,NDC80,SLC6A4,ZNF175,PKMYT1,CDKN2C,DHTKD1,KIF18A,LIG1,ASF1B,SGOL1,KAT2B,WD R76,POLQ,CDH10,NEIL3,KRT24,CENPE,ANLN,TICRR,NUF2,MALL,CTDSPL,CDCA5,FADS2,CENPU,SPC25,TEKT5,NRGN,USP43,SMC2,ATAD2,BUB1B,HMGCR,CCNB2,FANCC,TMSNB,TFF1,S100A1,U2AF1L4,ZNF653,HAO,MITF,MON1A,RAPGEF6,KIAA1161,MELK,LRRK2,KIAA0101,TPX2,MVD,CHAF1A,BIRC5,CDC25A,FOS,MCM7,PRKCDBP,H2AFV,RMI2,FANCI,ELF5,CLSPN,HNRNPD,AURKB,ACSS1,PSAPL1,CACNB2,ARHGAP33,BANK1,CDC25C,COQ7,E2F7,SPAG5,KIF15,TACC3,YAF2,CDCA2,CEND1,PCP4,HIST1H1B,PGP,CRIP1,MX2,ERCC6L,CDKN3,CASC5,CXCL14,TUBB,AMTN,FOXM1,B3GALT,TAS1R3,NR4A2,ZNF678,FBLN5,ZNF587,E2F1,FAR1,BLM,CENPL,UBE2C,POX2,DOK3,SMC4,SGOL2,PCBP2,PCNT,RRM2,MPC1,IQGAP3,MT-CYB,EXO1,CENPF,DTL,ACAT2,KIF14,ASPM,CREB3L4,MKI67,MPP1,TTK,KIAA1324,KAZALD1,PLCE1,CEP55,ZYG11A,KIF20B,STIL,RAD54L,KIF2C,CDCA8,RTKN2,DKK1,KIF4A,ZNF367,ALDH4A1,ACTL8,CENPP,DLG2,TCF19,TCOF1,FANCG,POLA1,BCAP29,PCNA,VIT,BRCA2,TUBB2A,CENPO,RHOH,TNNI2,RAD51,OSBPL6,WIPF1,ECT2,EVL,CENPN,PTTG1,DHFRL1,SYNPO,PRC1,CDK1,CD59,NUDT1,CCNF,SAC3D1,DIAPH3,MATN3,WD

						R62,GPSM2,SYNC,CXCR4,ALDH7A1,CHEK1,CDC7,TBXA2R,MTRFR2,MXD3,CPS1,CDC45,RFC5,FGFR2,HJURP,GTSE1,CTCF,EBP,PEG10,CLIC3,FLNB,RHOBTB2,IRGM,PBK,CCNE2,LMO7,NRK,DDIAS,ECHDC1,PDE10A,REEP1,KPNA2,CLTCL1,GPR19,CDCA3,MVK,CPSF3L,CTSV,VIM,KRT4,DIO2,NUSAP1,SPC24,MPV17L2,BORA,HIST1H4D,UHRF1,FAM83D,EPHB6,NR4A3,RECQL4,GHR,PHF19
GO:0040001	establishment of mitotic spindle localization	4	27	0.98	0.0175	ESPL1,NDC80,GPSM2,NUSAP1
GO:0009636	response to toxic substance	17	468	0.37	0.0188	KLF2,CCNB1,SLC6A4,HMGCR,FANCC,FOS,ARHGAP33,NR4A2,MT-CYB,PCNA,ECT2,CDK1,TBXA2R,CPS1,FGFR2,NR4A3,GHR
GO:0043933	protein-containing complex subunit organization	44	1770	0.21	0.0191	OIP5,KRT1,NASP,MYBPH,CCNB1,DDDB2,ND C80,SLC6A4,KIF18A,ASF1B,POLQ,CENPE,ANLN,TICRR,CENPU,SMC2,HMGCR,FANCC,MITF,LRRK2,CHAF1A,HIST1H1B,MX2,CASC5,BLM,CENPL,UBE2C,SMC4,CENPF,KIF2C,CENPP,CENPO,RAD51,WIPF1,ECT2,EVL,CENPN,CDK1,CD59,CDC45,HJURP,CLTCL1,MPV17L2,HIST1H4D
GO:0032147	activation of protein kinase activity	14	347	0.42	0.0194	CCNB1,THBS1,LRRK2,TPX2,CLSPN,IQGAP3,KIF14,PLCE1,ECT2,CDK1,CXCR4,IRGM,NRK,GHR
GO:0019413	acetate biosynthetic process	2	2	1.81	0.0195	ACSS2,ACSS1
GO:0021941	negative regulation of cerebellar granule cell precursor proliferation	2	2	1.81	0.0195	SLC6A4,CEND1
GO:0042325	regulation of phosphorylation	38	1465	0.23	0.0195	CCNB1,THBS1,BARD1,PKMYT1,CDKN2C,KAT2B,CENPE,CTDSPL,HMGCR,CAMK2N2,LRRK2,TPX2,PSCA,CDC25A,MCM7,PRKCDBP,CLSPN,BANK1,CDC25C,CDKN3,FOXO1,BLM,IQGAP3,KIF14,TTK,PLCE1,DKK1,RHOH,ECT2,CDK1,CXCR4,FGFR2,IRGM,PBK,CCNE2,NRK,FAM83D,GHR
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	3	12	1.21	0.0195	CCNB1,SPAG5,ECT2
GO:0065003	protein-containing complex assembly	39	1514	0.22	0.0195	OIP5,KRT1,NASP,MYBPH,CCNB1,DDDB2,SLC6A4,ASF1B,POLQ,CENPE,ANLN,TICRR,CENPU,HMGCR,FANCC,MITF,LRRK2,CHAF1A,HIST1H1B,MX2,CASC5,BLM,CENPL,UBE2C,CENPF,CENPP,CENPO,RAD51,WIPF1,ECT2,EVL,CENPN,CDK1,CD59,CDC45,HJURP,

						CLTCL1,MPV17L2,HIST1H4D
GO:1990426	mitotic recombination-dependent replication fork processing	2	2	1.81	0.0195	BRCA2,RAD51
GO:0034622	cellular protein-containing complex assembly	25	832	0.29	0.0203	OIP5,NASP,MYBPH,DDB2,ASF1B,CENPE,ANLN,TICRR,CENPU,CHAF1A,HIST1H1B,MX2,CASC5,CENPL,UBE2C,CENPF,CENPP,CENPO,RAD51,CENPN,CDC45,HJURP,CLTCL1,MPV17L2,HIST1H4D
GO:0031297	replication fork processing	4	29	0.95	0.0208	BLM,PCNA,BRCA2,RAD51
GO:0046483	heterocycle metabolic process	96	4716	0.12	0.0219	KIF22,MCM5,MYBL2,HNRNPL,RNASEH2A,EEPD1,FOSB,KLF2,ACSS2,GINS2,NASP,DDB2,BARD1,ZNF175,DHTKD1,LIG1,ASF1B,KAT2B,POLQ,NEIL3,TICRR,CDC45,CENPU,USP43,ATAD2,HMGCR,FANCC,U2AF1L4,ZNF653,HAAO,MITF,LRRK2,KIAA0101,MVD,CHAF1A,BIRC5,FOS,MCM7,RMI2,FANCI,ELF5,CLSPN,HNRNPD,ACSS1,E2F7,YAF2,FOX M1,NR4A2,ZNF678,ZNF587,E2F1,FAR1,BLM,POX2,PCBP2,RRM2,MPC1,MT-CYB,EXO1,CENPF,DTL,CREB3L4,MPP1,RAD54L,ZNF367,ALDH4A1,DLG2,TCF19,FANGG,POLA1,PCNA,BRCA2,RAD51,PTTG1,DHFR1,CDK1,NUDT1,WDR62,CHEK1,CDC7,MXD3,CPS1,CDC45,RFC5,CTCF,CCNE2,PDE10A,KPNA2,MVK,CPSF3L,HIST1H4D,UHRF1,NR4A3,RECQL4,GHR,PHF19
GO:0006085	acetyl-CoA biosynthetic process	3	13	1.17	0.0228	ACSS2,ACSS1,MPC1
GO:0051382	kinetochore assembly	3	13	1.17	0.0228	CENPE,CENPF,CENPN
GO:0044283	small molecule biosynthetic process	19	569	0.34	0.0235	ACSS2,C14orf1,DHTKD1,FADS2,HMGCR,HAAO,MVD,ACSS1,COQ7,PGP,ACAT2,OSBP L6,DHFR1,NUDT1,LSS,CPS1,EBP,PDE10A,MVK
GO:0031399	regulation of protein modification process	43	1747	0.2	0.0240	CCNB1,THBS1,PKMYT1,CDKN2C,KAT2B,CENPE,CTDSPL,HMGCR,CAMK2N2,LRRK2,TPX2,PSCA,CDC25A,PRKCDBP,FANCI,CLSPN,BANK1,CDC25C,CDC42,HIST1H1B,CDKN3,FOX M1,BLM,UBE2C,IQGAP3,KIF14,TTK,PLCE1,ZYG11A,DKK1,ECT2,CDK1,CXCR4,CHEK1,FGFR2,CTCF,IRGM,PBK,CCNE2,NRK,FAM83D,GHR,PHF19
GO:0021681	cerebellar granular layer development	3	14	1.14	0.0268	CBLN1,CEND1,KIF14
GO:0042493	response to drug	26	900	0.27	0.0268	FOSB,KLF2,CCNB1,THBS1,SLC6A4,HMGCR,LRRK2,FOS,MCM7,HNRNPD,NR4A2,BLM,MT-

						CYB,CENPF,RAD54L,F7,PCNA,RAD51,ECT2,CDK1,TBXA2R,CPS1,FGFR2,EBP,NR4A3,GHR
GO:0006289	nucleotide-excision repair	7	110	0.62	0.0276	DDB2,LIG1,NEIL3,FANCC,PCNA,BRCA2,RFC5
GO:0006335	DNA replication-dependent nucleosome assembly	4	32	0.91	0.0277	NASP,ASF1B,CHAF1A,HIST1H4D
GO:0019220	regulation of phosphate metabolic process	41	1657	0.2	0.0277	CCNB1,THBS1,BARD1,PKMYT1,CDKN2C,KAT2B,CENPE,CTDSPL,HMGCR,CAMK2N2,LRRK2,TPX2,PSCA,CDC25A,MCM7,PRKCDBP,CLSPN,BANK1,CDC25C,CDCA2,CDKN3,CASC5,FOXM1,BLM,IQGAP3,KIF14,TTK,PLCE1,DKK1,DLG2,RHOH,ECT2,CDK1,CXCR4,FGFR2,IRGM,PBK,CCNE2,NRK,FAM83D,GHR
GO:0006272	leading strand elongation	2	3	1.64	0.0290	POLA1,PCNA
GO:0007079	mitotic chromosome movement towards spindle pole	2	3	1.64	0.0290	DLGAP5,CENPE
GO:0010754	negative regulation of cGMP-mediated signaling	2	3	1.64	0.0290	THBS1,PDE10A
GO:0019287	isopentenyl diphosphate biosynthetic process, mevalonate pathway	2	3	1.64	0.0290	MVD,MVK
GO:0070175	positive regulation of enamel mineralization	2	3	1.64	0.0290	AMTN,C4orf26
GO:0071930	negative regulation of transcription involved in G1/S transition of mitotic cell cycle	2	3	1.64	0.0290	E2F7,E2F1
GO:0051347	positive regulation of transferase activity	20	630	0.31	0.0298	CCNB1,THBS1,CENPE,LRRK2,TPX2,CLSPN,HNRNPB,AURKB,UBE2C,IQGAP3,KIF14,PLCE1,DKK1,ECT2,CDK1,CXCR4,RFC5,IRGM,NRK,GHR
GO:0006979	response to oxidative stress	14	373	0.39	0.0319	KLF2,KRT1,FANCC,MELK,LRRK2,FOS,HNRNPB,NR4A2,POX2,PCNA,ECT2,CDK1,NUDT1,NR4A3

GO:0007568	aging	11	255	0.45	0.0329	HMGCR,LRRK2,FOS,AURKB,RAD54L,DKK1,BRCA2,CDK1,NUDT1,CHEK1,CTSV
GO:0001932	regulation of protein phosphorylation	35	1370	0.22	0.0341	CCNB1,THBS1,PKMYT1,CDKN2C,KAT2B,CENPE,CTDSPL,HMGCR,CAMK2N2,LRRK2,TPX2,PSCA,CDC25A,PRKCDBP,CLSPN,BANK1,CDC25C,CDKN3,FOXM1,BLM,IQGAP3,KIF14,TTK,PLCE1,DKK1,ECT2,CDK1,CXCR4,FGFR2,IRGM,PBK,CCNE2,NRK,FAM83D,GHR
GO:0000076	DNA replication checkpoint	3	16	1.08	0.0351	TICRR,CLSPN,CDC45
GO:0045740	positive regulation of DNA replication	4	35	0.87	0.0351	E2F7,PCNA,CDK1,CDC7
GO:0097327	response to antineoplastic agent	6	87	0.65	0.0359	HNRNPD,BLM,F7,PCNA,RAD51,CPS1
GO:0006637	acyl-CoA metabolic process	6	88	0.65	0.0378	ACSS2,MVD,ACSS1,FAR1,MPC1,MVK
GO:0051641	cellular localization	50	2180	0.17	0.0381	KIF22,DLGAP5,CCNB1,ESPL1,KIF23,BARD1,NDC80,SLC6A4,KIF18A,CENPE,MALL,CDC45,BUB1B,U2AF1L4,RAPGEF6,LRRK2,BIRC5,MTCH2,AURKB,CACNB2,SPAG5,HIST1H1B,CASC5,TUBB,FBLN5,PCNT,CENPF,KIF14,ASPM,TTK,KIF20B,STIL,KIF2C,CDCA8,KIF4A,F7,DLG2,BCAP29,BRCA2,TMEM87A,CDK1,CD59,GPSM2,FLNB,REEP1,KNPNA2,CLTCL1,NUSAP1,FAM83D,NR4A3
GO:0010133	proline catabolic process to glutamate	2	4	1.51	0.0396	POX2,ALDH4A1
GO:0072757	cellular response to camptothecin	2	4	1.51	0.0396	BLM,RAD51
GO:0099004	calmodulin dependent kinase signaling pathway	2	4	1.51	0.0396	PCP4,IRGM
GO:0046677	response to antibiotic	12	305	0.41	0.0406	KLF2,HMGCR,HNRNPD,CRIP1,MT-CYB,PCNA,ECT2,CDK1,TBXA2R,FGFR2,NR4A3,GHR
GO:0033875	ribonucleoside bisphosphate metabolic process	7	123	0.57	0.0435	ACSS2,HMGCR,MVD,ACSS1,FAR1,MPC1,MVK
GO:0034032	purine nucleoside bisphosphate metabolic process	7	123	0.57	0.0435	ACSS2,HMGCR,MVD,ACSS1,FAR1,MPC1,MVK
GO:0034614	cellular response to reactive oxygen species	7	124	0.56	0.0449	KLF2,FANCC,FOS,HNRNPD,PCNA,ECT2,CDK1

GO:0032268	regulation of cellular protein metabolic process	55	2486	0.16	0.0471	HNRNPL,DLGAP5,CCNB1,ESPL1,THBS1,PKMYT1,CDKN2C,KAT2B,CENPE,CTDSPL,HMGCR,CAMK2N2,LRRK2,TPX2,PSCA,BIRC5,CDC25A,PRKCDBP,FANCI,CLSPN,HNRNP D,BANK1,CDC25C,CDCA2,HIST1H1B,CDKN3,FOX M1,BLM,UBE2C,IQGAP3,KIF14,TTK,PLCE1,ZYG11A,DKK1,TCOF1,ECT2,PTTG1,CDK1,CD59,CXCR4,CHEK1,FGFR2,CTCF,IRGM,PBK,CCNE2,NRK,VIM,DIO2,MPV17L2,UHRF1,FAM83D,GHR,PHF19
GO:0006284	base-excision repair	4	40	0.81	0.0497	LIG1,POLQ,NEIL3,RECQL4
GO:0006725	cellular aromatic compound metabolic process	94	4754	0.11	0.0500	KIF22,MCM5,MYBL2,HNRNPL,RNASEH2A,EEPD1,FOSB,KLF2,ACSS2,GINS2,NASP,DD B2,BARD1,ZNF175,DHTKD1,LIG1,ASF1B,KAT2B,POLQ,NEIL3,TICRR,CDCA5,CENPU,USP43,ATAD2,HMGCR,FANCC,U2AF1L4,ZNF653,HAAO,MITF,LRRK2,KIAA0101,MVD,CHAF1A,BIRC5,FOS,MCM7,RMI2,FANCI,ELF5,CLSPN,HNRNPD,ACSS1,E2F7,YAF2,FOX M1,NR4A2,ZNF678,ZNF587,E2F1,FAR1,BLM,PCBP2,RRM2,MPC1,MT-CYB,EXO1,CENPF,DTL,CREB3L4,MPP1,RAD54L,ZNF367,DLG2,TCF19,FANCG,POLA1,PCNA,BRCA2,RAD51,PTTG1,DHFRL1,CDK1,NUDT1,WDR62,CHEK1,CDC7,MXD3,CPS1,CDC45,RFC5,CTCF,CCNE2,PDE10A,KPNA2,MVK,CPSF3L,DIO2,HIST1H4D,UHRF1,NR4A3,RECQL4,PHF19

Table S5: 48th hour *up regulated* pathways (Biological process Gene Ontology) (Interacting proteins with highest confidence were selected (0.900))

#Term ID	Term Description	Observed Gene Count	Background Gene Count	Strength	False Discovery Rate	Matching Proteins in Your Network (Labels)
GO:0002376	immune system process	61	2370	0.35	3.57e-06	HMOX1,SIX4,CCL22,IRF1,CD68,RAB33A,RT P4,RORA,CYSTM1,TIMP2,GRB14,ICAM1,SE CTM1,FTH1,PAK1,LY96,CXCL16,STAT6,BA TF2,PSG1,ELMOD2,LEPR,SMAD3,PDE2A,T RIM14,VAT1,TNFRSF14,SH3PXD2A,ITGAL, PSMB10,MSN,C6orf57,GBP3,WDR78,IFIT3,C D40,ADA,ALOX5,PSMB8,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,PIR,SERPINB1,ERCC2,ZP3,MVP,HLA-A,C1S,CD44,HLA-B,HDAC9,HLA-G,MUC20,ICAM2,PARP14,TIPARP,LYN,CAS P1,ALDH3B1
GO:0002252	immune effector process	31	927	0.47	0.00025	IRF1,CD68,RTP4,RORA,CYSTM1,TIMP2,ICA M1,FTH1,PAK1,STAT6,ELMOD2,VAT1,ITG AL,GBP3,IFIT3,CD40,ADA,ALOX5,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,SERPINB1,ZP3,MVP,HLA-A,C1S,CD44,HLA-B,LYN,ALDH3B1
GO:0006950	response to stress	66	3267	0.25	0.0014	HMOX1,BDKRB1,PROCR,CCL22,IRF1,RTP4, RORA,MCAM,ICAM1,SA4,PAK1,UCHL1,L Y96,CXCL16,FSTL1,STAT6,BATF2,AGTRAP ,NQO1,ELMOD2,FBLN1,SMAD3,UBA7,NMN AT3,PTGES,TRIM14,TNFRSF14,ITGAL,MYO 6,C6orf57,GBP3,IFIT3,CD40,ADA,ALOX5,H MGCL,PSMB8,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,CYP1A1,AKR1C3,ERCC2,SP140,SIPA1,HL A-A,ENSG00000160200,C1S,MDK,PPARA,CHA C1,CD44,HLA-B,TBC1D5,HDAC9,HLA-G,SERPINE2,PARP14,LYN,CASP1,SA2,PL A2G4C,ALDH3B1,CYP1B1,FGF1
GO:0006955	immune response	40	1560	0.35	0.0014	CCL22,IRF1,CD68,RORA,CYSTM1,TIMP2,IC AM1,SECTM1,FTH1,LY96,CXCL16,STAT6,S MAD3,TRIM14,VAT1,TNFRSF14,ITGAL,PS MB10,C6orf57,IFIT3,CD40,ADA,ALOX5,PSM B8,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,SERPINB1,ZP3,MVP,HLA-A,C1S,CD44,HLA-B,HLA-G,PARP14,LYN,CASP1,ALDH3B1
GO:0019221	cytokine-mediated signaling pathway	23	655	0.49	0.0014	HMOX1,CCL22,IRF1,RORA,BIRC3,ICAM1,S TAT6,IRS1,LEPR,STAT5A,TNFRSF14,MSN,I FIT3,CD40,ALOX5,PSMB8,HLA-DQB1,HLA-C,HLA-A,CD44,HLA-B,HLA-G,CASP1
GO:0034341	response to interferon-gamma	12	176	0.77	0.0014	CCL22,IRF1,ICAM1,CXCL16,CD40,HLA-DQB1,HLA-C,HLA-A,CD44,HLA-B,HLA-G,CASP1
GO:0045321	leukocyte activation	28	894	0.44	0.0014	IRF1,CD68,RORA,CYSTM1,TIMP2,ICAM1,F TH1,STAT6,BATF2,LEPR,SMAD3,VAT1,ITG AL,MSN,CD40,ADA,ALOX5,HSPA1B,HSPA1 A,HLA-C,SERPINB1,MVP,HLA-A,CD44,HLA-B,HDAC9,LYN,ALDH3B1
GO:0055114	oxidation-reduction process	28	932	0.42	0.0014	HMOX1,AGPS,ALDH1L1,FTH1,NQO1,LEPR, ALDH1A3,PFKM,VAT1,SH3PXD2A,AKR1B1 0,MOXD1,C6orf57,ALOX5,CYP1A1,GLRX,S TEAP4,PIR,AKR1C3,AKR1C1,ENSG0000016

						0200,P4HA2,AKR1B15,HTATIP2,ALDH3B1,SMOX,CYP1B1,DHRS3
GO:0060333	interferon-gamma-mediated signaling pathway	8	69	1.01	0.0014	IRF1,ICAM1,HLA-DQB1,HLA-C,HLA-A,CD44,HLA-B,HLA-G
GO:0010033	response to organic substance	58	2815	0.26	0.0015	HMOX1,BDKRB1,CCL22,CAV2,IRF1,CD68,GDF15,LMO2,RORA,TIMP2,BIRC3,ICAM1,PAK1,LY96,CXCL16,FSTL1,STAT6,IRS1,AGTRAP,NQO1,LEPR,SMAD3,PDE2A,ACVR2B,STAT5A,PTGES,TNFRSF14,MSN,GBP3,IFIT3,CD40,ADA,ALOX5,HMGCL,PSMB8,HLA-DQB1,HSPA1A,HLA-C,CYP1A1,AKR1C3,AKR1C1,FAM83G,ADCY7,ATP6V1C1,HLA-A,MDK,PPARA,CHAC1,CD44,HLA-B,HDAC9,HLA-G,SMYD3,TIPARP,LYN,CASP1,CYP1B1,FGF1
GO:0070887	cellular response to chemical stimulus	56	2672	0.26	0.0015	HMOX1,CCL22,CAV2,IRF1,CD68,GDF15,LMO2,RORA,BIRC3,ICAM1,SAA4,PAK1,LY96,CXCL16,FSTL1,STAT6,IRS1,AGTRAP,NQO1,LEPR,SMAD3,PDE2A,ACVR2B,STAT5A,TNFRSF14,MSN,GBP3,IFIT3,CD40,ALOX5,PSMB8,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,CYP1A1,AKR1C3,AKR1C1,FAM83G,SIPA1,ADCY7,ATP6V1C1,HLA-A,PPARA,CD44,HLA-B,HDAC9,HLA-G,SMYD3,TIPARP,LYN,CASP1,SAA2,ALDH3B1,CYP1B1,FGF1
GO:0002480	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	4	8	1.64	0.0017	HLA-C,HLA-A,HLA-B,HLA-G
GO:0002366	leukocyte activation involved in immune response	21	616	0.47	0.0025	CD68,RORA,CYSTM1,TIMP2,ICAM1,FTH1,STAT6,VAT1,ITGAL,ADA,ALOX5,HSPA1B,HSPA1A,HLA-C,SERPINB1,MVP,HLA-A,CD44,HLA-B,LYN,ALDH3B1
GO:0009605	response to external stimulus	47	2152	0.28	0.0025	HMOX1,BDKRB1,CCL22,IRF1,GDF15,RTP4,ICAM1,SAA4,LY96,CXCL16,FSTL1,BATF2,NQO1,ELMOD2,ALDH1A3,SMAD3,PDE2A,NTN4,PTGES,TRIM14,TNFRSF14,C6orf57,GBP3,IFIT3,CD40,ADA,HMGCL,PSMB8,HLA-DQB1,HLA-C,CYP1A1,AKR1C3,SIPA1,HLA-A,ENSG00000160200,C1S,PPARA,CD44,HLA-B,TBC1D5,HLA-G,SERPINE2,PARP14,LYN,CASP1,SAA2,PTPRM
GO:0002443	leukocyte mediated immunity	21	632	0.46	0.0029	CD68,CYSTM1,TIMP2,ICAM1,FTH1,VAT1,ITGAL,ALOX5,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,SERPINB1,ZP3,MVP,HLA-A,C1S,CD44,HLA-B,LYN,ALDH3B1
GO:0060337	type I interferon signaling pathway	7	65	0.97	0.0029	IRF1,IFIT3,PSMB8,HLA-C,HLA-A,HLA-B,HLA-G
GO:0071346	cellular response to interferon-gamma	10	155	0.75	0.0029	CCL22,IRF1,ICAM1,HLA-DQB1,HLA-C,HLA-A,CD44,HLA-B,HLA-G,CASP1
GO:0034308	primary alcohol	7	69	0.95	0.0034	ALDH1A3,AKR1B10,AKR1C3,AKR1C1,ALD

	metabolic process					H3B1,CYP1B1,DHRS3
GO:0002486	antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-independent	3	3	1.94	0.0036	HLA-C,HLA-A,HLA-B
GO:0042574	retinal metabolic process	4	13	1.43	0.0041	ALDH1A3,AKR1C3,AKR1C1,CYP1B1
GO:0007166	cell surface receptor signaling pathway	46	2198	0.26	0.0049	HMOX1,CCL22,CAV2,IRF1,GDF15,TSPAN31,RORA,BIRC3,ICAM1,CBL,C,PAK1,LY96,FSTL1,STAT6,IRS1,LEPR,SMAD3,ACVR2B,STAT5A,TNFRSF14,ITGAL,MSN,GPR110,IFIT3,CD40,ALOX5,PSMB8,HLA-DQB1,HLA-C,FAM83G,MVP,ATP6V1C1,HLA-A,MDK,NFATC1,CHAC1,CD44,HLA-B,HLA-G,MUC20,ICAM2,TIPARP,LYN,CASP1,TLE2,FGF1
GO:0019748	secondary metabolic process	6	52	1.0	0.0052	AKR1B10,CYP1A1,AKR1C3,AKR1C1,ENSG0000160200,CYP1B1
GO:0034754	cellular hormone metabolic process	8	109	0.81	0.0057	ALDH1A3,CYP1A1,AKR1C3,AKR1C1,AKR1B15,TIPARP,CYP1B1,DHRS3
GO:0097164	ammonium ion metabolic process	10	179	0.69	0.0060	SLC22A4,RARRES3,AKR1B10,MOXD1,AGMAT,AKR1C3,AKR1C1,SAMD8,PLA2G4C,SMOX
GO:0009607	response to biotic stimulus	30	1206	0.34	0.0062	BDKRB1,CCL22,IRF1,RTP4,ICAM1,LY96,CXCL16,BATF2,ELMOD2,SMAD3,PTGES,TRIM14,IFITM10,TNFRSF14,C6orf57,GBP3,IFIT3,CD40,PSMB8,HLA-DQB1,HLA-C,CYP1A1,HLA-A,C1S,CD44,HLA-B,HLA-G,PARP14,LYN,CASP1
GO:0098542	defense response to other organism	24	859	0.39	0.0062	CCL22,IRF1,RTP4,ICAM1,LY96,CXCL16,BATF2,ELMOD2,TRIM14,C6orf57,GBP3,IFIT3,CD40,PSMB8,HLA-DQB1,HLA-C,HLA-A,C1S,CD44,HLA-B,HLA-G,PARP14,LYN,CASP1
GO:0001523	retinoid metabolic process	7	87	0.85	0.0085	ALDH1A3,AKR1B10,CYP1A1,AKR1C3,AKR1C1,CYP1B1,DHRS3
GO:0043299	leukocyte degranulation	17	507	0.47	0.0085	CD68,CYSTM1,TIMP2,FTH1,VAT1,ITGAL,ALOX5,HSPA1B,HSPA1A,HLA-C,SERPINB1,MVP,HLA-A,CD44,HLA-B,LYN,ALDH3B1
GO:0051707	response to other organism	29	1173	0.33	0.0085	BDKRB1,CCL22,IRF1,RTP4,ICAM1,LY96,CXCL16,BATF2,ELMOD2,SMAD3,PTGES,TRIM14,TNFRSF14,C6orf57,GBP3,IFIT3,CD40,PSMB8,HLA-DQB1,HLA-C,CYP1A1,HLA-A,C1S,CD44,HLA-B,HLA-G,PARP14,LYN,CASP1
GO:0071466	cellular response to xenobiotic stimulus	9	157	0.7	0.0093	RORA,ICAM1,NQO1,PDE2A,STAT5A,CYP1A1,AKR1C1,SMYD3,CYP1B1
GO:0046903	secretion	27	1070	0.34	0.0095	SLC22A4,C11orf63,CD68,CYSTM1,TIMP2,FTH1,PAK1,ABCC3,EXOC7,ACVR2B,STAT5A,VAT1,ITGAL,ADA,ALOX5,HSPA1B,HSPA1A,HLA-C,SERPINB1,SYT12,MVP,HLA-

						A,CD44,HLA-B,SERPINE2,LYN,ALDH3B1
GO:0002274	myeloid leukocyte activation	18	574	0.44	0.0099	CD68,CYSTM1,TIMP2,FTH1,BATF2,VAT1,ITGAL,ALOX5,HSPA1B,HSPA1A,HLA-C,SERPINE1,MVP,HLA-A,CD44,HLA-B,LYN,ALDH3B1
GO:0017144	drug metabolic process	19	622	0.43	0.0099	NT5E,RORA,ALDH1L1,NQO1,STAT5A,PFKM,AKR1B10,MOXD1,ADA,HMGCL,HSPA1B,HSPA1A,CYP1A1,AKR1C3,AKR1C1,ENSG0000160200,ALDH3B1,SMOX,CYP1B1
GO:0032870	cellular response to hormone stimulus	18	585	0.43	0.0121	CAV2,LMO2,RORA,ICAM1,PAK1,IRS1,AGTRAP,LEPR,STAT5A,MSN,AKR1C3,AKR1C1,ADCY7,ATP6V1C1,PPARA,HDAC9,SMYD3,LYN
GO:0009991	response to extracellular stimulus	16	486	0.46	0.0129	HMOX1,GDF15,ICAM1,FSTL1,NQO1,CD40,ADA,HMGCL,CYP1A1,AKR1C3,SIPA1,ENSG00000160200,PPARA,TBC1D5,LYN,CASP1
GO:0030334	regulation of cell migration	21	753	0.39	0.0129	HMOX1,BDKRB1,MCAM,ICAM1,PAK1,CXCL16,FBLN1,SMAD3,STAT5A,MSN,CD40,ADA,SRPX2,NDRG4,ZP3,HDAC9,SERPINE2,LYN,PTPRM,CYP1B1,FGF1
GO:0030198	extracellular matrix organization	12	296	0.55	0.0132	ADAM19,LAMC1,TIMP2,ICAM1,FBLN1,SH3PXD2A,COL27A1,ITGAL,ERCC2,CD44,ICAM2,CYP1B1
GO:0034605	cellular response to heat	5	45	0.99	0.0132	HMOX1,HSPA1B,HSPA1A,LYN,FGF1
GO:0043900	regulation of multi-organism process	19	653	0.41	0.0132	CAV2,IRF1,BIRC3,PAK1,LY96,ELMOD2,FBLN1,EXOC7,TRIM14,ADA,HSPA1B,HSPA1A,ZP3,HLA-A,HLA-B,MUC20,ICAM2,PARP14,LYN
GO:0044597	daunorubicin metabolic process	3	8	1.52	0.0132	AKR1B10,AKR1C3,AKR1C1
GO:0044598	doxorubicin metabolic process	3	8	1.52	0.0132	AKR1B10,AKR1C3,AKR1C1
GO:0070424	regulation of nucleotide-binding oligomerization domain containing signaling pathway	3	8	1.52	0.0132	BIRC3,HSPA1B,HSPA1A
GO:1901700	response to oxygen-containing compound	32	1427	0.29	0.0132	HMOX1,BDKRB1,CAV2,RORA,ICAM1,PAK1,LY96,STAT6,IRS1,AGTRAP,NQO1,PDE2A,ACVR2B,STAT5A,PTGES,TNFRSF14,MSN,CD40,ADA,HMGCL,CYP1A1,AKR1C3,AKR1C1,SIPA1,ADCY7,ATP6V1C1,PPARA,HDAC9,SMYD3,LYN,CASP1,CYP1B1
GO:0009410	response to xenobiotic stimulus	11	262	0.56	0.0143	RORA,ICAM1,NQO1,PDE2A,STAT5A,ADA,CYP1A1,AKR1C1,HDAC9,SMYD3,CYP1B1
GO:0030335	positive regulation of cell migration	15	452	0.46	0.0143	HMOX1,BDKRB1,MCAM,ICAM1,PAK1,CXCL16,FBLN1,SMAD3,STAT5A,CD40,SRPX2,ZP3,HDAC9,LYN,FGF1
GO:1903265	positive regulation of tumor necrosis factor-mediated	3	9	1.46	0.0143	HSPA1B,HSPA1A,CASP1

	signaling pathway					
GO:1903409	reactive oxygen species biosynthetic process	4	25	1.15	0.0143	RORA,NQO1,CYP1A1,CYP1B1
GO:0007159	leukocyte cell-cell adhesion	5	49	0.95	0.0154	NT5E,ICAM1,ITGAL,MSN,CD44
GO:0042127	regulation of cell population proliferation	34	1594	0.27	0.0158	HMOX1,SIX4,CAV2,IRF1,RARRES3,TSPAN31,LAMC1,TIMP2,FTH1,PAK1,STAT6,IRS1,FBLN1,SMAD3,STAT5A,PTGES,TNFRSF14,IFIT3,CD40,ADA,HSPA1B,HSPA1A,AKR1C3,NDRG4,ZP3,HLA-A,HLA-G,SERPINE2,RPS6KA2,LYN,TP53I11,PTPRM,CYP1B1,FGF1
GO:0002819	regulation of adaptive immune response	8	147	0.68	0.0164	IRF1,STAT6,CD40,ADA,ADCY7,ZP3,HLA-A,HLA-B
GO:0022407	regulation of cell-cell adhesion	13	366	0.49	0.0166	IRF1,ADAM19,ICAM1,PAK1,TNFRSF14,ADA,ZP3,HLA-A,PPARA,CD44,HLA-G,SERPINE2,LYN
GO:0019369	arachidonic acid metabolic process	5	51	0.93	0.0173	PTGES,CYP1A1,AKR1C3,PLA2G4C,CYP1B1
GO:0042221	response to chemical	69	4153	0.16	0.0207	HMOX1,BDKRB1,CCL22,CAV2,IRF1,CD68,GDF15,LMO2,RTP4,RORA,TIMP2,BIRC3,ICAM1,SAA4,PAK1,LY96,ABCC3,CXCL16,FSTL1,RTP3,STAT6,IRS1,AGTRAP,NQO1,LEPR,SMAD3,PDE2A,ACVR2B,NTN4,STAT5A,PTGES,TNFRSF14,MSN,MYO6,GBP3,IFIT3,CD40,ADA,ALOX5,HMGCL,PSMB8,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,CYP1A1,AKR1C3,AKR1C1,FAM83G,SIPA1,ADCY7,ATP6V1C1,HLA-A,MDK,PPARA,CHAC1,CD44,HLA-B,HDAC9,HLA-G,SMYD3,TIPARP,LYN,CASP1,SAA2,PTPRM,ALDH3B1,CYP1B1,FGF1
GO:0006954	inflammatory response	15	482	0.43	0.0210	HMOX1,BDKRB1,CCL22,ICAM1,SAA4,LY96,PTGES,TNFRSF14,ITGAL,CD40,ALOX5,HDAC9,LYN,SAA2,PLA2G4C
GO:0042572	retinol metabolic process	4	30	1.07	0.0210	ALDH1A3,AKR1C3,CYP1B1,DHRS3
GO:0019882	antigen processing and presentation	8	158	0.65	0.0219	RAB33A,ICAM1,PSMB8,HLA-DQB1,HLA-C,HLA-A,HLA-B,HLA-G
GO:0040012	regulation of locomotion	22	881	0.34	0.0219	HMOX1,BDKRB1,CAV2,MCAM,ICAM1,PAK1,CXCL16,FBLN1,SMAD3,STAT5A,MSN,CD40,ADA,SRPX2,NDRG4,ZP3,HDAC9,SERPINE2,LYN,PTPRM,CYP1B1,FGF1
GO:0001666	response to hypoxia	11	288	0.52	0.0220	HMOX1,RORA,ICAM1,PAK1,AGTRAP,SMAD3,ADA,CYP1A1,ERCC2,PPARA,CASP1
GO:0050727	regulation of inflammatory response	12	338	0.49	0.0233	NT5E,RORA,BIRC3,SMAD3,PDE2A,ADA,ADCY7,ZP3,C1S,PPARA,LYN,CASP1
GO:1903039	positive regulation of leukocyte cell-cell adhesion	9	202	0.59	0.0236	ICAM1,PAK1,TNFRSF14,ADA,ZP3,HLA-A,CD44,HLA-G,LYN

GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6	89	0.77	0.0239	STAT6,CD40,ADA,ZP3,HLA-A,HLA-B
GO:0006809	nitric oxide biosynthetic process	3	13	1.3	0.0239	RORA,NQO1,CYP1B1
GO:0006887	exocytosis	20	774	0.35	0.0239	CD68,CYSTM1,TIMP2,FTH1,PAK1,EXOC7,VAT1,ITGAL,ALOX5,HSPA1B,HSPA1A,HLA-C,SERPINB1,SYT12,MVP,HLA-A,CD44,HLA-B,LYN,ALDH3B1
GO:0016488	farnesol catabolic process	2	2	1.94	0.0242	AKR1B10,AKR1C3
GO:0030308	negative regulation of cell growth	8	164	0.63	0.0242	BDKRB1,CDKL3,PAK1,SMAD3,HSPA1B,HSPA1A,SIPA1,SERPINE2
GO:0070434	positive regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway	2	2	1.94	0.0242	HSPA1B,HSPA1A
GO:0051704	multi-organism process	46	2514	0.2	0.0276	BDKRB1,CCL22,CAV2,IRF1,RTP4,BIRC3,ICAM1,LY96,CXCL16,BATF2,PSG1,CATSPER1,ELMOD2,LEPR,FBLN1,SMAD3,B4GALNT1,PTGES,TRIM14,TNFRSF14,PSMB10,C6orf57,GBP3,IFIT3,CD40,DUSP13,PSMB8,HLA-DQB1,HSPA1B,HSPA1A,HLA-C,CYP1A1,ERCC2,ADCY7,ZP3,HLA-A,C1S,HTATIP2,CD44,HLA-B,HLA-G,SERPINE2,PARP14,LYN,CASP1,PLA2G4C
GO:0009719	response to endogenous stimulus	29	1353	0.27	0.0284	CAV2,GDF15,LMO2,RORA,TIMP2,ICAM1,PAK1,FSTL1,IRS1,AGTRAP,NQO1,LEPR,SMAD3,PDE2A,ACVR2B,STAT5A,MSN,AKR1C3,AKR1C1,FAM83G,ADCY7,ATP6V1C1,MDK,PPARA,CD44,HDAC9,SMYD3,LYN,FGF1
GO:0009725	response to hormone	21	854	0.33	0.0290	CAV2,LMO2,RORA,TIMP2,ICAM1,PAK1,IRS1,AGTRAP,NQO1,LEPR,STAT5A,MSN,AKR1C3,AKR1C1,ADCY7,ATP6V1C1,MDK,PPARA,HDAC9,SMYD3,LYN
GO:0034310	primary alcohol catabolic process	3	15	1.24	0.0298	AKR1B10,AKR1C3,ALDH3B1
GO:0050896	response to stimulus	113	7824	0.1	0.0298	HMOX1,BDKRB1,PROCR,CCL22,CAV2,IRF1,CD68,GDF15,LMO2,TSPAN31,RTP4,RORA,CYSTM1,TIMP2,BIRC3,GRB14,MCAM,ICAM1,SECTM1,CBLC,FTH1,SAA4,PAK1,UCHL1,LY96,ABCC3,CXCL16,FSTL1,RTP3,STAT6,BATF2,IRS1,RIN1,AGTRAP,NQO1,ELMOD2,LEPR,FBLN1,ALDH1A3,SMAD3,UBA7,PDE2A,ACVR2B,NMNAT3,NTN4,STAT5A,PTGES,TRIM14,IFITM10,VAT1,TNFRSF14,ITGAL,PSMB10,MSN,MYO6,C6orf57,GBP3,GPR110,IFIT3,CD40,ADA,ALOX5,HMGCL,PSMB8,HLA-DQB1,HSPA1B,HSPA1A,HLA-

						C,PTPRH,GPR158,CYP1A1,AKR1C3,SERPIN B1,AKR1C1,FAM83G,ERCC2,SP140,SIPA1,N DRG4,ADCY7,ZP3,MVP,ATP6V1C1,HLA- A,ENSG00000160200,C1S,MDK,PPARA,NFA TC1,CHAC1,CD44,HLA- B,TBC1D5,HDAC9,HLA- G,MUC20,ICAM2,SERPINE2,FHIT,PARP14,S MYD3,TIPARP,RPS6KA2,LYN,CASP1,SA A2, TPCN1,PTPRM,TLE2,PLA2G4C,ALDH3B1,C YP1B1,FGF1
GO:0010595	positive regulation of endothelial cell migration	6	96	0.74	0.0304	HMOX1,STAT5A,CD40,SRPX2,HDAC9,FGF1
GO:0006081	cellular aldehyde metabolic process	5	64	0.83	0.0311	ALDH1A3,AKR1C3,AKR1C1,ALDH3B1,CYP 1B1
GO:0045088	regulation of innate immune response	12	361	0.46	0.0325	IRF1,BIRC3,PAK1,LY96,HSPA1B,HSPA1A,H LA-A,HLA-B,MUC20,ICAM2,PARP14,LYN
GO:0002521	leukocyte differentiation	11	313	0.49	0.0336	IRF1,RORA,STAT6,BATF2,LEPR,PDE2A,SH 3PXD2A,ADA,PIR,HDAC9,LYN
GO:0045055	regulated exocytosis	18	691	0.36	0.0337	CD68,CYSTM1,TIMP2,FTH1,VAT1,ITGAL,A LOX5,HSPA1B,HSPA1A,HLA- C,SERPINB1,SYT12,MVP,HLA- A,CD44,HLA-B,LYN,ALDH3B1
GO:0002291	T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	2	3	1.77	0.0340	ICAM1,ITGAL
GO:0006690	icosanoid metabolic process	6	99	0.72	0.0340	PTGES,ALOX5,CYP1A1,AKR1C3,PLA2G4C, CYP1B1
GO:0070370	cellular heat acclimation	2	3	1.77	0.0340	HSPA1B,HSPA1A
GO:0098609	cell-cell adhesion	13	416	0.44	0.0340	NT5E,CSTA,ICAM1,CLDN12,ITGAL,MSN,S RPX2,ENSG00000197991,CD44,ICAM2,FBLI M1,PTPRM,CYP1B1
GO:1903672	positive regulation of sprouting angiogenesis	4	38	0.96	0.0340	HMOX1,SRPX2,HDAC9,FGF1
GO:0006629	lipid metabolic process	26	1192	0.28	0.0360	SLC22A4,RARRES3,GALC,AGPS,IRS1,ST6G ALNAC3,LEPR,ALDH1A3,STAT5A,B4GALN T1,PTGES,AKR1B10,ALOX5,HMGCL,CYP1 A1,AKR1C3,AKR1C1,PPARA,AKR1B15,TIP ARP,SAMD8,PLA2G4C,ALDH3B1,CYP1B1,D HRS3,FGF1
GO:0023057	negative regulation of signaling	27	1258	0.27	0.0361	HMOX1,CAV2,GDF15,RORA,TIMP2,GRB14, ICAM1,CBLC,UCHL1,LY96,IRS1,FBLN1,SM AD3,DDIT4L,ADA,HSPA1B,HSPA1A,NDRG 4,MVP,NFATC1,CHAC1,CD44,SERPINE2,PA RP14,LYN,TLE2,DHRS3
GO:0042110	T cell activation	9	225	0.54	0.0361	IRF1,RORA,ICAM1,STAT6,LEPR,SMAD3,IT GAL,MSN,ADA
GO:0044255	cellular lipid	22	946	0.31	0.0374	SLC22A4,RARRES3,GALC,AGPS,IRS1,ST6G ALNAC3,ALDH1A3,STAT5A,B4GALNT1,PT

	metabolic process					GES,AKR1B10,ALOX5,CYP1A1,AKR1C3,AKR1C1,PPARA,SAMD8,PLA2G4C,ALDH3B1,CYP1B1,DHRS3,FGF1
GO:0002831	regulation of response to biotic stimulus	13	426	0.43	0.0379	IRF1,BIRC3,PAK1,LY96,ELMOD2,HSPA1B,HSPA1A,HLA-A,HLA-B,MUC20,ICAM2,PARP14,LYN
GO:0001676	long-chain fatty acid metabolic process	6	104	0.7	0.0383	PTGES,ALOX5,CYP1A1,AKR1C3,PLA2G4C,CYP1B1
GO:0045785	positive regulation of cell adhesion	12	375	0.45	0.0383	ADAM19,ICAM1,PAK1,FBLN1,SMAD3,TNFRSF14,ADA,ZP3,HLA-A,CD44,HLA-G,LYN
GO:0032940	secretion by cell	22	959	0.3	0.0424	CD68,CYSTM1,TIMP2,FTH1,PAK1,EXOC7,ACVR2B,VAT1,ITGAL,ALOX5,HSPA1B,HSPA1A,HLA-C,SERPINB1,SYT12,MVP,HLA-A,CD44,HLA-B,SERPINE2,LYN,ALDH3B1
GO:0042136	neurotransmitter biosynthetic process	4	42	0.92	0.0424	RORA,NQO1,MOXD1,CYP1B1
GO:0002520	immune system development	16	601	0.37	0.0430	SIX4,IRF1,RORA,STAT6,BATF2,LEPR,SMAD3,PDE2A,SH3PXD2A,WDR78,ADA,PIR,ERCC2,HDAC9,TIPARP,LYN
GO:0071395	cellular response to jasmonic acid stimulus	2	4	1.64	0.0431	AKR1C3,AKR1C1
GO:0006805	xenobiotic metabolic process	6	108	0.69	0.0436	RORA,NQO1,STAT5A,CYP1A1,AKR1C1,CYP1B1
GO:0009611	response to wounding	15	547	0.38	0.0436	HMOX1,PROCR,IRF1,MCAM,PAK1,FBLN1,SMAD3,NMNAT3,CD40,CYP1A1,MDK,PPARA,CD44,SERPINE2,LYN
GO:0045926	negative regulation of growth	9	235	0.52	0.0436	BDKRB1,GDF15,CDKL3,PAK1,SMAD3,HSPA1B,HSPA1A,SIPA1,SERPINE2
GO:1901568	fatty acid derivative metabolic process	7	148	0.62	0.0438	PTGES,ALOX5,HMGCL,CYP1A1,AKR1C3,PLA2G4C,CYP1B1
GO:0010594	regulation of endothelial cell migration	7	150	0.61	0.0466	HMOX1,STAT5A,CD40,SRPX2,HDAC9,PTPRM,FGF1
GO:0044282	small molecule catabolic process	12	388	0.43	0.0466	NT5E,GALM,ALDH1L1,PFKM,AKR1B10,ADA,HMGCL,CYP1A1,AKR1C3,ENSG00000160200,CD44,ALDH3B1
GO:0042401	cellular biogenic amine biosynthetic process	3	20	1.12	0.0471	MOXD1,AGMAT,SMOX
GO:0048870	cell motility	21	914	0.3	0.0487	SIX4,BDKRB1,CCL22,LAMC1,GRB14,ICAM1,DNAH5,SAA4,CXCL16,MAP1B,PSG1,CATSPER1,ITGAL,MSN,SRPX2,NDRG4,MDK,CD44,LYN,SAA2,CYP1B1
GO:0001961	positive regulation of cytokine-mediated signaling pathway	4	45	0.89	0.0490	HSPA1B,HSPA1A,PARP14,CASP1

