#Column "GO.ID" stands for the ID of gene ontology term
#Column "Term" stands for the name of gene ontology term
#Column "Ontology" stands for the ontology of GOID belongs to
#Column "Count" stands for the number of DE genes associated with the listed GOID
#Column "Pop.Hits" stands for the number of background population genes associated with the listed GO
#Column "List.Total" stands for the total number of DE genes
#Column "Pop.Total" stands for the total number of background population genes
#Column "Fold.Enrichment" stands for the Fold Enrichment value of the GOID, it equals (Count/Pop.Hits
#Column "Pvalue" stands for the significance testing value of the GOID
#Column "FDR" stands for the false discovery rate of the GOID, using Benjamini & Hochberg (1995) me
#Column "Enrichment.Score" stands for the Enrichment Score value of the GOID, it equals (-log10(Pvalu
#Column "GENES" stands for the DE genes associated with the GOID

GO.ID	Term	Ontology	Count	Pop.Hits	List.Total	Pop.Total	Fold.Enric	Pvalue	FDR
GO.IDTermOntologyCountPop.HitsList.TotalPop.TotalFold.EnrichmentPvalueFDREnrichment.ScoreGENES									
GO:00002	cell	cycleBiolo	process81659570145863.145291911.34528E-204.92641E-1719.87118784PRC						
GO:00224	cycle	processBio	process95882570145862.7562358285.21054E-209.54049E-1719.28311756PR						
GO:00070	cycleBiolo	process1121167570145862.4558877911.24672E-191.52182E-1618.90423271PRC1//KIF2							
GO:00224	cycle	phaseBiolo	process84730570145862.9445421771.67752E-191.53577E-1618.77533291PR						
GO:00002	phaseBiolo	process56460570145863.1152402752.82708E-142.07055E-1113.54866224PRC1//KIF23//							
GO:00517	of	cell	cycleBiolo	process62584570145862.7166906995.76313E-133.51743E-1012.2					
GO:00105	of	cell	cycle	processBio	process44331570145863.4016218799.2015E-134.68159				
GO:00000	phase	of	mitotic	cell	cycleBiolo	process44332570145863.391376031.02274E			
GO:00513	divisionBiol	process47375570145863.2072140351.30843E-125.32384E-1011.88325098NUSAP1//KIF2							
GO:00073	of	mitotic	cell	cycleBiolo	process37254570145863.7276004974.05864E-121.4862				
GO:00002	divisionBiol	process42321570145863.3481554355.24653E-121.60107E-0911.28012769NDC80//ZWIN							
GO:00070	process42321570145863.3481554355.24653E-121.60107E-0911.28012769NDC80//ZWINT//MAD2L1/								
GO:00000	cycle	checkpoint	process33214570145863.9460403341.25739E-113.54197E-0910.90053016H2						
GO:00482	fissionBiolo	process42333570145863.2275011851.75722E-114.59639E-0910.7551735NDC80//ZWINT/							
GO:00711	of	cell	cycle	arrestBiolo	process33223570145863.7867831013.93265E-119.3965				
GO:00070	cycle	arrestBiolo	process41328570145863.1986842114.10554E-119.39655E-0910.38662995UB						
GO:00070	cell	cycle	checkpoint	process24126570145864.8741854649.48713E-112.04364E-0810.02					
GO:00457	regulation	of	cell	cycleBiolo	process44384570145862.9321271931.40755E-102.8635				
GO:00311	complex-de	proteasom	ubiquitin-de	protein	catabolic	processBio	process1882570145865.617201		
GO:00070	segregatio	process21114570145864.7138504162.69319E-094.93122E-078.569733551NDC80//ZWIN							
GO:00900	regulation	of	cell	cycle	processBio	process19105570145864.630476192.09047E			
GO:00513	of	ligase	activityBiol	process1895570145864.8485318562.32979E-083.87804E-067.632					
GO:00513	of	mitotic	cell	cycleBiolo	process36331570145862.7831451742.7665E-084.40475				
GO:00002	prometaph	process1786570145865.0583843332.95546E-084.50954E-067.529374834NDC80//CENPA							
GO:00442	macromole	catabolic	processBio	process48527570145862.3307300514.18114E-086.12453E-067.378					
GO:00513	process36339570145862.7174662325.11542E-087.20487E-067.291118969CDKN3//ORC6//INHBA//P								
GO:00000	transition	of	mitotic	cell	cycleBiolo	process24172570145863.5706242355.95508			
GO:00069	organizatio	process1071648570145861.6614524786.15612E-088.05132E-067.210693148PRC1//KIF2							
GO:00514	of	ubiquitin-pr	ligase	activityBiol	process1791570145864.7804511287.11493E-088.98443				
GO:00513	regulation	of	ligase	activityBiol	process1682570145864.9930680369.13925E-081.1156E				
GO:00718	component	organizatio	at	cellular	levelBiolog	process1522632570145861.477811551.2841			
GO:00718	component	organizatio	or	biogenesis	at	cellular	levelBiolog	process156272257014	
GO:00070	organizatio	process1355570145866.0484210531.38715E-071.53166E-056.857878083PRC1//KIF23//N							
GO:00165	ubiquitinati	process36353570145862.6096913671.42207E-071.53166E-056.847078259FBXW11//UBR							
GO:00002	cytoskeleto	organizatio	process25195570145863.2807017541.70412E-071.783E-056.76849887PRC1//						
GO:00324	modificatio	by	small	protein	conjugatio	process37375570145862.524828072.20163E			
GO:00706	modificatio	by	small	protein	conjugatio	or	removalBio	process40424570145	

GO:005143	of	ubiquitin-pr	ligase	activity	involved	in	mitotic	cell	cycleBiolog
GO:004316	ubiquitin-de	protein	catabolic	processBio	process24185570145863.3197155052.40684E-072.2599				
GO:005144	regulation	of	ubiquitin-pr	ligase	activityBiol	process1578570145864.9210526322.8175E-0			
GO:001049	protein	catabolic	processBio	process24189570145863.2494569763.59608E-073.21192E-056.444					
GO:001994	protein	catabolic	processBio	process34340570145862.5589473685.03494E-074.23682E-056.298					
GO:004363	macromole	catabolic	processBio	process34340570145862.5589473685.03494E-074.23682E-056.298					
GO:005143	regulation	of	ubiquitin-pr	ligase	activity	involved	in	mitotic	cell
GO:000651	protein	catabolic	processBio	process33334570145862.5283012929.73479E-077.82596E-056.011					
GO:005160	involved	in	cellular	protein	catabolic	processBio	process34350570145862.4858345		
GO:000705	spindle	organizatio	process822570145869.3052631581.01929E-067.94179E-055.99170225PRC1//						
GO:005127	organizatio	process49610570145862.0555478861.33294E-060.0001016925.87519036NDC80//ZWINT/							
GO:004425	protein	catabolic	processBio	process34356570145862.4439384981.44705E-060.0001081455.839					
GO:000905	catabolic	processBio	process51649570145862.010883141.53688E-060.0001125615.813359983DCP						
GO:003139	of	protein	ubiquitinati	process19142570145863.4239436622.70206E-060.0001940185.568					
GO:001604	component	organizatio	process1773336570145861.3577148812.77911E-060.0001957135.556094531F						
GO:000697	damage	response,	signal	transductio	by	p53	class	mediator	resulting
GO:007239	transductio	involved	in	cell	cycle	checkpoint	process1261570145865.03399482		
GO:007240	transductio	involved	in	DNA	integrity	checkpoint	process1261570145865.03399482		
GO:007240	transductio	involved	in	G1/S	transition	checkpoint	process1261570145865.03399482		
GO:007241	transductio	involved	in	mitotic	cell	cycle	checkpoint	process1261570145866	
GO:007242	transductio	involved	in	DNA	damage	checkpoint	process1261570145865.03399482		
GO:007243	transductio	involved	in	mitotic	cell	cycle	G1/S	transition	DNA
GO:007247	transductio	involved	in	mitotic	cell	cycle	G1/S	checkpoint	process126
GO:007184	component	organizatio	or	biogenesis	process1813442570145861.3456405393.61529E-060.00				
GO:003139	regulation	of	protein	ubiquitinati	process16108570145863.7910331384.34971E-060.0002				
GO:007115	regulation	of	cell	cycle	arrestBiolog	process1265570145864.7242105266.84325E			
GO:003157	checkpoint	process936570145866.3973684217.29679E-060.0004175135.136868017CENPF//UBE2C//							
GO:003016	catabolic	processBio	process36418570145862.2038781167.7279E-060.0004353785.111938364ISG1						
GO:007182	complex	subunit	organizatio	process17126570145863.4525480378.03955E-060.0004460735.094					
GO:000701	processBio	process29303570145862.4491575478.24898E-060.0004508625.083599923PRC1//KIF23//							
GO:003157	cell	cycle	G1/S	transition	checkpoint	process1378570145864.2649122819.24194E			
GO:007177	transition	checkpoint	process1378570145864.2649122819.24194E-060.0004904935.034236862PSM						
GO:005143	regulation	of	ubiquitin-pr	ligase	activity	involved	in	mitotic	cell
GO:000021	transition	of	mitotic	cell	cycleBiolog	process1379570145864.2109260491.06737E			
GO:004424	catabolic	processBio	process831329570145861.5981386881.09034E-050.0005545614.962436863W						
GO:003157	cell	cycle	G1/S	transition	DNA	damage	checkpoint	process1268570145866	
GO:007110	conformati	changeBiol	process19157570145863.0968152871.19716E-050.000592434.921849564CEN						
GO:000691	transportBi	process26262570145862.5394134191.27573E-050.0006228954.894242463RPS15//IFNG//							
GO:200004	of	G1/S	transition	of	mitotic	cell	cycleBiolog	process1381570145866	
GO:005116	transportBi	process26264570145862.5201754391.45957E-050.0006941514.835773704RPS15//IFNG//							
GO:000708	of	mitosisBiol	process1382570145864.0568677791.62067E-050.000751254.79030664CENPF						
GO:005178	of	nuclear	divisionBiol	process1382570145864.0568677791.62067E-050.000751254.79030					
GO:006500	complex	assemblyB	process16120570145863.4119298251.72015E-050.0007845624.764434539RA						
GO:005135	regulation	of	ligase	activityBiol	process1271570145864.3249814681.7568E-050.000784				
GO:005144	regulation	of	ubiquitin-pr	ligase	activityBiol	process1271570145864.3249814681.7568E-0			
GO:003462	macromole	complex	subunit	organizatio	process44578570145861.9479876161.81776E-050.0008				
GO:003472	organizatio	process15109570145863.5214872042.14235E-050.0009339624.669109756CENPA//OIP5//							
GO:000632	packagingB	process17136570145863.1986842112.23711E-050.0009637984.650313499CENPA//OIP5//							
GO:000633	assemblyB	process1499570145863.618713452.93906E-050.0012420884.531791844CENPA//OIP5//CE							
GO:000821	deathBiolog	process861429570145861.5400243082.98107E-050.0012420884.525628126IFI6//SOD2//S							
GO:004852	regulation	of	cellular	processBio	process1222209570145861.4132710682.98481E-050.00				
GO:001626	process861431570145861.5378719343.13773E-050.0012910544.503384031IFI6//SOD2//SYCP2//TRI								
GO:000652	of	cellular	amino	acid	metabolic	processBio	process1053570145864.8282025		
GO:003323	of	cellular	amine	metabolic	processBio	process1164570145864.3981907893.33446E			

GO:001250	cell	deathBiolog	process801311570145861.5615239473.64757E-050.0014518924.437996143IFI						
GO:004426	protein	metabolic	processBio	process1482810570145861.3477729913.97731E-050.0015661194.4					
GO:000081	chromatid	segregatio	process944570145865.2342105264.15658E-050.0016192974.381263857NDC8						
GO:001607	metabolic	processBio	process39510570145861.9568421054.94979E-050.0018865164.305413239DC						
GO:000691	process791302570145861.5526639184.98493E-050.0018865164.302341255IFI6//SOD2//HMGB2//CY								
GO:003157	integrity	checkpoint	process15117570145863.2807017544.99705E-050.0018865164.301286108H2A						
GO:003149	assemblyB	process14104570145863.4447368425.14141E-050.0018979724.288918037CENPA//OIP5//							
GO:004801	signalingBi	process1167570145864.2012568745.18288E-050.0018979724.28542857NDC80//UBE2C//							
GO:004801	lipid-media	signalingBi	process1167570145864.2012568745.18288E-050.0018979724.28542857NDC8						
GO:009018	regulation	of	kidney	developme	process5125701458610.66228075.64373E-050.0020462				
GO:000998	processBio	process51512380570145861.0645055695.8057E-050.0020843594.236145554BRIX1//KPN							
GO:000697	to	DNA	damage	stimulusBio	process38501570145861.9409181647.34664E-050.0026				
GO:004304	chromatin	remodeling	process728570145866.3973684217.75625E-050.0027310954.110348223CENP						
GO:005116	exportBiolo	process1395570145863.5017174527.97159E-050.0027801884.098454837RPS15//HNRNP							
GO:003033	damage	response,	signal	transductio	by	p53	class	mediatorBi	process139
GO:004851	regulation	of	biological	processBio	process1282399570145861.3653408228.97426E-050.00				
GO:000625	metabolic	processBio	process45638570145861.8049001819.19544E-050.0031179354.036427471KPN						
GO:000007	damage	checkpoint	process14110570145863.2568421059.58348E-050.0032196984.018476645PSM						
GO:000905	processBio	process911595570145861.4599637020.0001229610.0040934713.910233988WIPI2//ATG1							
GO:005164	localization	process841445570145861.487554180.0001248280.0041182073.903687224RPS15//IFNG//							
GO:000008	phase	of	mitotic	cell	cycleBiolog	process15128570145862.9987664470.00014			
GO:003227	regulation	of	cellular	protein	metabolic	processBio	process29354570145862.096312		
GO:000633	replication-	nucleosom	assemblyB	process622570145866.9789473680.0001514720.0047818243.8196					
GO:003408	nucleosom	assembly	at	centromere	process622570145866.9789473680.0001514720.004781				
GO:003472	replication-	nucleosom	organizatio	process622570145866.9789473680.0001514720.0047818243.8196					
GO:003139	regulation	of	protein	ubiquitinati	process1288570145863.4894736840.0001541080.00482				
GO:000007	sister	chromatid	segregatio	process841570145864.9930680360.0001580340.0049044133.8012					
GO:004277	transductio	in	response	to	DNA	damageBio	process14117570145863.061988		
GO:005164	of	localization	in	cellBiologic	process771313570145861.5006774360.0001877690.005				
GO:007117	assembly	checkpoint	process732570145865.5976973680.0001924850.0057649453.715603624CENP						
GO:007117	cell	cycle	spindle	checkpoint	process732570145865.5976973680.0001924850.005764				
GO:003051	regulation	of	BMP	signaling	pathwayBio	process515570145868.5298245610.0001940			
GO:004408	component	biogenesis	process741251570145861.5136858930.0001952080.0057649453.709501491BI						
GO:000633	assembly	or	disassemb	process16147570145862.7852488360.0002042540.0059838393.68					
GO:005132	phaseBiolo	process15134570145862.8644933230.0002351350.0068338463.628682597PSMA8//ORC6							
GO:003304	of	organelle	organizatio	process25295570145862.1685994650.0002413820.0069601783.61					
GO:003105	remodeling	at	centromere	process624570145866.3973684210.0002556250.0072565773.5923					
GO:009018	of	kidney	developme	process624570145866.3973684210.0002556250.0072565773.5923					
GO:003462	macromole	complex	assemblyB	process33440570145861.9192105260.0002667330.0075136563.57					
GO:000695	to	stressBiolo	process1272440570145861.331911130.0002833570.0079210293.547665433W						
GO:007184	component	disassembl	at	cellular	levelBiolog	process21231570145862.3263157890.00029			
GO:004393	complex	subunit	organizatio	process57913570145861.5975903610.0002958240.008145183.528					
GO:005170	processBio	process55873570145861.6121661540.000302810.0082753113.518829198B2M//PPBP//IFI							
GO:007184	component	assembly	at	cellular	levelBiolog	process53833570145861.6281417830.00030			
GO:005124	regulation	of	protein	metabolic	processBio	process29371570145862.0002553550.00031			
GO:004348	exchangeB	process625570145866.1414736840.0003253360.0086331933.487667798CENPA//OIP5//C							
GO:007097	K11-linked	ubiquitinati	process625570145866.1414736840.0003253360.0086331933.487667798UBE2						
GO:002241	component	disassemb	process21233570145862.3063474140.0003283810.0086513023.483622059HM						
GO:003140	regulation	of	protein	modificatio	processBio	process24285570145862.1549030470.00035			
GO:002260	component	assemblyB	process671130570145861.517251980.0003750620.009740983.425896561RPS						
GO:005131	of	spindle	microtubule	to	chromoson	process4105701458610.235789470.0004014			
GO:003140	regulation	of	protein	modificatio	processBio	process16157570145862.6078444520.00043			
GO:003226	of	cellular	protein	metabolic	processBio	process57927570145861.5734627830.00043			
GO:005165	of	organelle	localization	process1185570145863.3115789470.0004563970.0115263793.3406					

GO:00064	modificatio	processBio	process1112107570145861.3480928230.0004836740.0121316033.315447281						
GO:00335	response	to	stressBiolo	process53850570145861.5955789470.0004983890.0124156553.30					
GO:00709	assemblyB	process962570145863.7146010190.0006368330.0157573083.1959746RPS14//RPS15//WI							
GO:00070	metaphase	transitionBi	process850570145864.0943157890.0006521370.0160044663.185661065CEN						
GO:00500	localization	process519570145866.7340720220.0006599330.0160044663.180500204DLGAP5//KIF18							
GO:00513	of	chromoson	localization	process519570145866.7340720220.0006599330.0160044663.1805					
GO:00507	of	catalytic	activityBiol	process641095570145861.4956404710.0007409440.0178508943.1					
GO:00709	K48-linked	ubiquitinati	process629570145865.2943738660.0007640250.0182866653.116892389MAR						
GO:00313	of	protein	modificatio	processBio	process46724570145861.6258505380.0007917340.018				
GO:00002	polyubiquit	process1077570145863.3233082710.0007973190.0188045413.098367971UBE2S//UBE2T							
GO:00650	complex	assemblyB	process48765570145861.6056140350.0008010670.0188045413.096331004RP						
GO:00109	of	cell	deathBiolo	process601016570145861.5111893910.0008462710.0197391343.07					
GO:00485	developme	process520570145866.3973684210.0008518710.0197439963.069626202CRKL//CTNNB1/							
GO:00606	subdivision	of	an	epithelial	terminal	unitBiologic	process412570145868.5298245		
GO:00062	DNA	replicationE	process1192570145863.0596109840.0008994150.020585353.046040112RNAS						
GO:00302	nuclear	changeBiol	process630570145865.1178947370.0009238820.0210140093.034383557HMG						
GO:00300	of	mitotic	metaphase	transitionBi	process741570145864.3689345310.0009482970.021436				
GO:00705	of	microtubul	cytoskeletc	organizatio	process853570145863.8625620660.0009716380.02167				
GO:00305	signaling	pathwayBi	process1079570145863.2391738840.0009766820.0216790653.010246788FOX						
GO:00037	splicing,	via	transesterif	reactionsBi	process18202570145862.280250130.0009768010.02167				
GO:00313	regulation	of	cellular	metabolic	processBio	process731301570145861.4358428740.0009			
GO:00650	of	molecular	functionBio	process751347570145861.4248036570.0010370310.0227401642.9					
GO:00511	importBiolc	process15155570145862.4764006790.0011046250.024014862.956785007IFNG//KPNA2//I							
GO:00070	cell	cycle	spindle	assembly	checkpoint	process631570145864.9528013580.0011082			
GO:00440	regulation	of	molecular	functionBio	process47757570145861.5887784190.0011296110.0243				
GO:00442	metabolic	processBio	process3487992570145861.1142563620.0012049050.0258032842.919047246						
GO:00512	organizatio	process743570145864.1657282740.0012706280.0270525562.89598159NPM1//KIF11//SG							
GO:00458	regulation	of	mitotic	metaphase	transitionBi	process632570145864.7980263160.0013196			
GO:00429	of	apoptosisB	process58993570145861.4946520380.0013373490.0281458172.873755239B2						
GO:00603	I	interferon-r	signaling	pathwayBi	process969570145863.3377574370.0013971380.028992				
GO:00713	response	to	type	I	interferonB	process969570145863.3377574370.0013971			
GO:00345	localization	to	nucleusBio	process16175570145862.3396090230.001401340.0289926892.853					
GO:00343	to	type	I	interferonB	process970570145863.2900751880.0015489680.031866				
GO:00444	interaction	between	organismsE	process26354570145861.8794528690.0015658170.0320336462.80					
GO:00430	of	programme	cell	deathBiolo	process581003570145861.4797502230.0016847420.034				
GO:00069	component	disassembl	involved	in	apoptosisB	process971570145863.2437361010.0017137			
GO:00062	replicationE	process20248570145862.0636672330.0017893960.0360042132.747293629TOP2A//RNAS							
GO:00434	modificatio	process1112189570145861.2975932290.0018880020.037410532.723997569CDKN3//CKS							
GO:00037	splicing,	via	transesterif	reactions	with	bulged	adenosine	as	nucleophile
GO:00003	mRNA	splicing,	via	spliceosom	process17197570145862.2082286940.0018899370.0374				
GO:00512	of	protein	metabolic	processBio	process57988570145861.4763157890.0019440280.0382				
GO:00066	targetingBi	process22286570145861.9684210530.0019755940.0386878432.704302212IFNG//KPNA2/							
GO:00170	importBiolc	process17198570145862.1970760230.0019947210.0388114282.700117786IFNG//KPNA2/							
GO:00485	regulation	of	cellular	processBio	process1212424570145861.2773623410.0020031020.03				
GO:00007	catabolic	process,	endonucle	process524570145865.3311403510.0020523220.0389409432.6877					
GO:00063	fragmentat	involved	in	apoptotic	nuclear	changeBiol	process524570145865.3311403		
GO:00458	regulation	of	mitosisBiol	process524570145865.3311403510.0020523220.0389409432.6877					
GO:00517	regulation	of	nuclear	divisionBiol	process524570145865.3311403510.0020523220.038940				
GO:00442	macromole	metabolic	processBio	process2716072570145861.1420861940.0020794190.0392517062.					
GO:00305	of	BMP	signaling	pathwayBi	process747570145863.8111982080.0021676940.040500				
GO:00310	organizing	center	organizatio	process747570145863.8111982080.0021676940.0405004892.6640					
GO:00328	of	microtubul	processBio	process860570145863.4119298250.0022092670.0406736382.6557					
GO:00484	nervous	system	developme	process415570145866.8238596490.0022324960.0406736382.6512					
GO:00484	nervous	system	developme	process415570145866.8238596490.0022324960.0406736382.6512					

GO:00714	response	to	oxygen	levelsBiolo	process415570145866.8238596490.0022324960.04067		
GO:00714	response	to	hypoxiaBio	process415570145866.8238596490.0022324960.0406736382.6512			
GO:00081	localization	process641146570145861.4290805550.0022819520.0413688552.641693475IFNG//KPNA					
GO:00330	localization	process751388570145861.3827165180.0023234310.0419133182.633870261IFNG//VPS1					
GO:00422	nucleoside	metabolic	processBio	process636570145864.2649122810.0024852720.0439665022.6046			
GO:00458	regulation	of	mitosisBiol	process636570145864.2649122810.0024852720.0439665022.6046			
GO:00461	ribonucleos	metabolic	processBio	process636570145864.2649122810.0024852720.0439665022.6046			
GO:00517	regulation	of	nuclear	divisionBiol	process636570145864.2649122810.0024852720.04396		
GO:00063	remodeling	process975570145863.0707368420.0025186080.0443420312.598839419BAZ1B//CENPA//					
GO:00066	import	into	nucleusBio	process14152570145862.3569252080.002542840.0445544522.594			
GO:00229	electron	transport	chainBiolo	process11105570145862.6808020050.0026458510.0461385972.57			
GO:00217	cell	developme	process637570145864.1496443810.0028700850.0496102842.542105168CD9//				
GO:00104	from	mitosisBiol	process416570145866.3973684210.0028855790.0496102842.53976702KNTC				
GO:00422	small	subunit	biogenesis	process416570145866.3973684210.0028855790.0496102842.5397			
GO:00098	regulation	of	metabolic	processBio	process731357570145861.3765892250.0029763670.050		
GO:00070	cycleBiolo	process526570145864.9210526320.0029781080.0504899642.52605953KIF11//NPM1//CT					
GO:00319	signaling	cascadeBi	process526570145864.9210526320.0029781080.0504899642.52605953AKT1S				
GO:00430	regulation	of	catalytic	activityBiol	process40651570145861.5723178920.0031169760.0526		
GO:00106	of	cell	communica	process56989570145861.4489489650.0031878960.0535508122.49			
GO:00025	degranulati	process980570145862.8788157890.0039169540.0654971872.407051577EGF//IGF1//ITGA					
GO:00333	localization	to	organelleB	process21285570145861.8855401660.0040997150.0682416212.38			
GO:00083	splicingBio	process22305570145861.8457981020.0043163150.0715219272.364886856SRSF10//SMN					
GO:00510	transportBi	process11112570145862.513251880.00436670.0720308782.359846655NXF1//SRSF10//N					
GO:00098	regulation	of	metabolic	processBio	process591070570145861.4110083620.0044404540.072		
GO:00106	regulation	of	macromole	metabolic	processBio	process561005570145861.4258811210.0044	
GO:00091	diphosphat	metabolic	processBio	process418570145865.6865497080.0045598230.0742136462.3410			
GO:00064	process28423570145861.693865870.0046779980.0758001262.329939975EIF1AX//EIF4H//RPL27A//						
GO:00150	transportBi	process53943570145861.4382206840.0047391940.0764534252.324295535IFNG//KPNA2/					
GO:00195	metabolic	processBio	process1563317570145861.2034844420.0047732070.0766644072.32118971				
GO:00064	export	from	nucleusBio	process868570145863.0105263160.0048643480.0776862362.312			
GO:00451	of	protein	localization	process54966570145861.4304674730.0048792560.0776862362.31			
GO:00226	complex	biogenesis	process16199570145862.057445120.0050808640.0805459922.294062424BRI				
GO:00109	regulation	of	cell	cycle	processBio	process869570145862.96689550.005319064	
GO:00000	transition	of	mitotic	cell	cycleBiolo	process11115570145862.4476887870.00533	
GO:00324	regulation	of	type	I	interferon	productionI	process530570145864.26491228
GO:00469	transportBi	process46802570145861.4677254230.0057803210.089606352.238048064RPS15//IFNG//					
GO:00062	ligationBiol	process310570145867.6768421050.0057992090.089606352.236631206HMGB2//RAD51//					
GO:00400	of	mitotic	spindle	localization	process310570145867.6768421050.0057992090.08960		
GO:00423	of	protein	import	into	nucleusBio	process985570145862.7094736840.0058601	
GO:00468	of	nucleocyto	transportBi	process10101570145862.5336112560.0060774550.0931198322.21			
GO:00016	involved	in	ureteric	bud	morphoger	process643570145863.5706242350.0061791	
GO:00226	complex	assemblyB	process986570145862.6779681760.0063251220.0961103552.198931116RPS1				
GO:00003	snRNP	assemblyB	process531570145864.1273344650.0065525360.0991544892.183590593SRS				
GO:00105	of	cellular	ketone	metabolic	processBio	process12135570145862.2746198830.00663	
GO:00018	developme	process11119570145862.3654135340.0068783090.102809672.162518289CTNNB1//IFNG/					
GO:00516	localization	process11119570145862.3654135340.0068783090.102809672.162518289RPS15//NDC80/					
GO:00431	of	I-kappaB	kinase/NF-	cascadeBi	process12137570145862.2414137530.0074415260.1107		
GO:00070	organizatio	process34561570145861.5508771930.0075664660.1121797512.121106916PRC1//KIF23//					
GO:00606	bud	morphoger	process645570145863.4119298250.0077320470.1129913182.111705519CTNN				
GO:00424	nucleoside	biosyntheti	processBio	process311570145866.9789473680.0077446260.1129913182.1109			
GO:00424	biosyntheti	processBio	process311570145866.9789473680.0077446260.1129913182.110999544PRTF				
GO:00461	ribonucleos	biosyntheti	processBio	process311570145866.9789473680.0077446260.1129913182.1109			
GO:00009	process759570145863.0360392510.0078707840.1134756392.103981987NUSAP1//KIF20A//BIRC5//A						
GO:00064	export	from	nucleusBio	process759570145863.0360392510.0078707840.1134756392.1039			

GO:000911	metabolic	processBio	process759570145863.0360392510.0078707840.1134756392.103981987PRTF						
GO:00718	component	biogenesis	at	cellular	levelBiolog	process16209570145861.959002770.008045			
GO:00457	regulation	of	cell	cycleBiolo	process874570145862.7664295870.0080965380.11581				
GO:00313	regulation	of	cellular	metabolic	processBio	process54994570145861.3901726150.00852			
GO:00720	system	developme	process11123570145862.2884895160.0087521130.1242257242.057887098DC						
GO:00453	respiration	process12140570145862.1933834590.0087873020.1242436332.056144433IDH3A//COX6							
GO:00063	organizatio	process29465570145861.595902660.0090363890.1268373882.044005086CHD1//BAZ1B//							
GO:00082	of	blood	pressureBi	process10107570145862.3915395970.0090400210.1268373882.04					
GO:00718	complex	subunit	organizatio	process991570145862.5308270680.0090889310.1270368912.0414					
GO:00468	secretionBi	process14176570145862.0355263160.0092505530.127716862.033832321YWHAZ//SYT9/							
GO:00506	acid	transportBi	process11124570145862.2700339560.0092770850.127716862.032588469HNR						
GO:00506	transportBi	process11124570145862.2700339560.0092770850.127716862.032588469HNRNPA1//NXF							
GO:00512	of	RNA	localization	process11124570145862.2700339560.0092770850.127716862.032					
GO:00322	regulation	of	cellular	protein	metabolic	processBio	process17231570145861.88320		
GO:00016	system	developme	process13159570145862.0922211190.0095751980.1297046862.018852259DC						
GO:00070	depolymeri	process422570145864.6526315790.0096339910.1297046862.016193771SBDS//CCNB1//							
GO:00344	anchoringB	process422570145864.6526315790.0096339910.1297046862.016193771NDC80//SGOL1/							
GO:00488	extension	involved	in	axon	guidanceBi	process422570145864.6526315790.0096339			
GO:00506	of	mRNA	processing	process422570145864.6526315790.0096339910.1297046862.0161					
GO:00106	regulation	of	macromole	metabolic	processBio	process661268570145861.3319442140.0097			
GO:00063	recombinat	process534570145863.7631578950.00975040.130300862.010977548PCNA//POLE2//RFC							
GO:00229	transport	chainBiolo	process12142570145862.1624907340.0097850180.130300862.009438364CO						
GO:00070	of	exit	from	mitosisBiol	process312570145866.3973684210.0100298590.13164				
GO:00431	regulation	of	I-kappaB	kinase/NF-	cascadeBi	process312570145866.3973684210.0100298			
GO:00512	of	spindle	localization	process312570145866.3973684210.0100298590.1316463871.9987					
GO:00516	localization	process312570145866.3973684210.0100298590.1316463871.998705192NDC80//CENPA/							
GO:00072	kinase/NF-	cascadeBi	process14178570145862.0126552340.0101618250.1329021531.993028293NL						
GO:00650	of	biological	qualityBiol	process1062192570145861.2374471760.0102005520.1329338871.					
GO:00341	homeostas	process762570145862.8891341260.0102685810.1333459011.988489562INHBA//RPS14//							
GO:00064	localization	process11127570145862.2164111070.0109986390.1420792841.958661051HNRNPA1//NX							
GO:00002	assemblyB	process535570145863.6556390980.011018710.1420792841.95786924SRSF10//SRSF9//S							
GO:00901	regulation	of	transmemb	receptor	protein	serine/thre	kinase	signaling	pathwayBi
GO:00061	nucleoside	nucleotide	and	nucleic	acid	metabolic	processBio	process211474557014	
GO:00159	nucleoside	nucleotide	and	nucleic	acid	transportBi	process12146570145862.10324		
GO:00063	recombinat	process13164570145862.028433890.0122128510.1552897881.913182956KPNA2//TOP2A							
GO:00486	process	involved	in	reproductio	process23355570145861.6579095630.0124489860.1577				
GO:00440	of	endocrine	processBio	process313570145865.9052631580.0126654490.1595938261.897					
GO:00102	to	organic	nitrogenBi	process996570145862.3990131580.0126820870.1595938261.896					
GO:00070	chromatid	cohesionBi	process424570145864.2649122810.0131602570.1650440411.880735639BUB1						
GO:00099	transportBi	process14184570145861.9470251720.013322980.166514521.875398609YWHAZ//SYT9//							
GO:00512	regulation	of	protein	metabolic	processBio	process17241570145861.8050666080.01384			
GO:00063	processing	process24379570145861.6204416050.014017050.1727234591.853343386SRSF10//SMN2							
GO:00462	oxide	metabolic	processBio	process651570145863.0105263160.0140555960.1727234591.852					
GO:00468	regulation	of	nucleocyto	transportBi	process651570145863.0105263160.0140555960.17272				
GO:00725	oxygen	species	metabolic	processBio	process651570145863.0105263160.0140555960.17272				
GO:00331	of	intracellula	protein	transportBi	process998570145862.3500537060.0143815150.176137				
GO:00485	regulation	of	biological	processBio	process1252673570145861.1966645010.0147964160.1				
GO:00062	repairBiolo	process22341570145861.6509337860.014955690.1819526131.825193548GTF2H3//RAD5							
GO:00603	of	cellular	localization	process25402570145861.5913851790.0151551260.1836295571.81					
GO:00075	implantatio	process425570145864.0943157890.0151938160.1836295571.818333124IL1B//SOD1//ST							
GO:00060	process652570145862.9526315790.015380320.1852721491.813034617ARPP19//SDS//ALDOC//GAP								
GO:00327	of	monooxyge	activityBiol	process538570145863.3670360110.0154872250.1859482531.8100					
GO:00422	assemblyB	process314570145865.4834586470.015659050.1867864491.805234599RPS14//RPS15//N							
GO:00425	anion	generation	process314570145865.4834586470.015659050.1867864491.805234599NCF2/						

GO:00436	protein	modificatio	process13170570145861.9568421050.0160821480.1912104681.793655959DP						
GO:00346	protein	localization	process33571570145861.4789012810.016158930.1915016221.791587403IFN						
GO:00323	of	intracellula	transportBi	process10117570145862.1871345030.0162836320.1917384611.78					
GO:00900	of	transmemb	receptor	protein	serine/thre	kinase	signaling	pathwayBic	process101
GO:00091	metabolic	processBio	process884570145862.4370927320.0167283730.1963439121.776546305PRTF						
GO:00707	macromole	localization	process33573570145861.4737393220.01691980.1974402371.771604767IFNG						
GO:00067	metabolic	processBio	process671327570145861.2920080910.0172440350.1974402371.763361108C						
GO:00067	metabolic	processBio	process671327570145861.2920080910.0172440350.1974402371.763361108C						
GO:00017	crest	cell	migrationB	process426570145863.9368421050.0174148540.1974402371.7590					
GO:00066	export	from	nucleusBio	process426570145863.9368421050.0174148540.1974402371.7590					
GO:00106	regulation	of	cellular	carbohydra	metabolic	processBio	process426570145863.93684210		
GO:00303	differentiati	process426570145863.9368421050.0174148540.1974402371.759080154FOXD4L1//FOXD							
GO:00325	to	progestero	stimulusBic	process426570145863.9368421050.0174148540.1974402371.7590					
GO:00454	regulation	of	nitric	oxide	biosyntheti	processBio	process426570145863.93684210		
GO:00459	regulation	of	carbohydra	metabolic	processBio	process426570145863.9368421050.0174148			
GO:00509	cell	differentiati	process426570145863.9368421050.0174148540.1974402371.759080154FOXD						
GO:00424	to	drugBiolog	process19288570145861.6881944440.018419110.2081814251.734731353CEN						
GO:00099	regulation	of	signal	transductio	process28472570145861.5180196250.0187613110.2113				
GO:00511	process1643640570145861.1529323310.0190050510.2116579011.721130955RPS15//IFNG//NDC80//								
GO:00327	regulation	of	monooxyge	activityBiol	process315570145865.1178947370.0190156880.211657				
GO:00513	plate	congressio	process315570145865.1178947370.0190156880.2116579011.720887957KIF18						
GO:00519	of	chromoson	segregatio	process315570145865.1178947370.0190156880.2116579011.7208					
GO:00106	regulation	of	cell	communica	process29495570145861.4991812870.0197224240.218				
GO:00427	synthesis	coupled	electron	transportBi	process655570145862.7915789470.0198680320.21914				
GO:00427	ATP	synthesis	coupled	electron	transportBi	process655570145862.7915789470.0198680			
GO:00346	macromole	complex	disassemb	process12157570145861.9558833390.0203217160.2234778531.69					
GO:00311	polymeriza	or	depolymeri	process541570145863.1206675220.0210261450.2305321681.6772					
GO:00230	regulation	of	signalingBi	process29498570145861.4901500740.021190340.2316388831.673					
GO:00323	regulation	of	intracellula	transportBi	process656570145862.7417293230.0215425660.23339				
GO:00456	of	osteoblast	differentiati	process656570145862.7417293230.0215425660.2333990381.6667					
GO:00513	of	oxidoreduc	activityBiol	process656570145862.7417293230.0215425660.2333990381.6667					
GO:00603	signaling	pathwayBic	process772570145862.4878654970.0220894560.2384700391.655814976IFNG						
GO:00329	complex	disassemb	process12159570145861.9312810330.0221960950.2384700391.653723417BA						
GO:00512	of	localization	process1423121570145861.1642759570.0222706170.2384700391.652267746						
GO:00068	protein	transportBi	process27458570145861.5085497590.0222710960.2384700391.652258412IF						
GO:00510	of	DNA	metabolic	processBio	process11141570145861.9963419190.0224361850.2388				
GO:00068	metabolic	processBio	process428570145863.6556390980.022437230.2388521381.649030764SOD1/						
GO:00609	hormone	secretionBi	process316570145864.7980263160.0227380210.2413525571.64324734INHBA						
GO:00343	to	interferon-	process889570145862.300177410.0229230640.2426134661.639727339HLA-B						
GO:00302	differentiati	process657570145862.6936288090.0233098980.2452897871.63245963HMGB2//INHBA//J							
GO:00512	regulation	of	protein	transportBi	process657570145862.6936288090.0233098980.24528				
GO:00071	process10124570145862.0636672330.0234537350.245393081.629787984TRIP13//TOP2A//SYCP2//R								
GO:00513	phase	of	meiotic	cell	cycleBiolog	process10124570145862.0636672330.02345			
GO:00512	regulation	of	multicellula	organismal	processBio	process20316570145861.6195869420.02363			
GO:00488	of	number	of	cellsBiolog	process9107570145862.1523856370.0241576770.25132				
GO:00718	complex	subunit	organizatio	process37676570145861.4006072870.0242526850.2515958461.61					
GO:00328	of	homeostati	processBio	process11143570145861.9684210530.0245970590.2541608771.60					
GO:00106	regulation	of	organelle	organizatio	process10125570145862.0471578950.0246387520.2541				
GO:00423	of	NF-kappaE	import	into	nucleusBio	process429570145863.5295825770.0252459			
GO:00423	import	into	nucleusBio	process429570145863.5295825770.0252459590.257914331.59780					
GO:00484	nervous	system	developme	process429570145863.5295825770.0252459590.257914331.59780					
GO:00061	electron	transport,	NADH	to	ubiquinone	process543570145862.9755201960.0253547			
GO:00068	oxide	biosyntheti	processBio	process543570145862.9755201960.0253547680.257914331.59594					
GO:00513	cell	cycleBiolog	process10126570145862.030910610.0258662610.2623884961.587266348TRI						

GO:000717	receptor	protein	serine/thre	kinase	signaling	pathwayBio	process13182570145861.8278195		
GO:003439	localization	at	cell	surfaceBiol	process317570145864.5157894740.0268265650.267738				
GO:003541	import	into	nucleusBio	process317570145864.5157894740.0268265650.2677385351.57143					
GO:003541	of	catenin	import	into	nucleusBio	process317570145864.5157894740.0268265			
GO:005188	of	mitochondr	membrane	potentialBio	process317570145864.5157894740.0268265650.267738				
GO:004362	protein	complex	disassemb	process11145570145861.9412704170.0269054560.2677385351.570					
GO:004688	of	hormone	secretionBi	process11145570145861.9412704170.0269054560.2677385351.570					
GO:004206	healingBiol	process32574570145861.4265908670.0276843770.2743299841.557765243EGF//ZFPM2//							
GO:004230	regulation	of	protein	import	into	nucleusBio	process544570145862.907894737		
GO:000700	organizatio	process11146570145861.9279740450.0281165260.2766764721.551038345IFI6//SOD2//RN							
GO:000018	mRNA	catabolic	process,	nonsense-m	decayBiolo	process430570145863.4119298250.0282569			
GO:002154	nerve	developme	process430570145863.4119298250.0282569640.2766764721.548874508FOXD						
GO:004566	regulation	of	osteoblast	differentiati	process430570145863.4119298250.0282569640.276676				
GO:004324	complex	disassemb	process11147570145861.9148585750.0293663140.2867718481.532150557RP						
GO:004225	biogenesis	process10129570145861.9836801310.0298110310.2903404111.525623008RPS14//RPS15							
GO:000154	follicle	developme	process545570145862.8432748540.0302158690.292726221.519764915CCNE1						
GO:003461	response	to	reactive	oxygen	speciesBio	process545570145862.8432748540.0302158			
GO:000629	repair,	DNA	gap	fillingBiolog	process318570145864.2649122810.0312799130.299355				
GO:001594	nucleoside	and	nucleotide	interconver	process318570145864.2649122810.0312799130.299355				
GO:003053	genitalia	developme	process318570145864.2649122810.0312799130.2993559861.504734458SYCP						
GO:004662	regulation	of	insulin	receptor	signaling	pathwayBio	process318570145864.26491228		
GO:001931	biosyntheti	processBio	process661570145862.5169974120.0313442450.2993559861.503842191SDS//						
GO:004239	modified	amino	acid	biosyntheti	processBio	process431570145863.3018675720.0314724			
GO:004240	biogenic	amine	biosyntheti	processBio	process431570145863.3018675720.0314724340.299355				
GO:004222	to	chemical	stimulusBio	process1012172570145861.1899340890.0324989730.3077242111.4					
GO:007134	response	to	interferon-g	process778570145862.2964912280.0325202810.3077242111.48784					
GO:003476	regulation	of	transmemb	transportBi	process546570145862.7814645310.0328512590.308521				
GO:004278	ubiquitinati	involved	in	ubiquitin-de	protein	catabolic	processBio	process546570145862	
GO:005121	developme	process9113570145862.0380996740.0328573280.3085218811.483367762IMPAD1//NPPC/							
GO:000223	to	molecule	of	bacterial	originBiolog	process11150570145861.8765614040.033353			
GO:000611	phosphoryl	process662570145862.4764006790.0336023510.3131089341.47363033NDUFA8//NDUFB2							
GO:003133	regulation	of	cellular	catabolic	processBio	process662570145862.4764006790.0336023			
GO:004308	regulation	of	catalytic	activityBiolo	process23391570145861.5052631580.033782450.31398				
GO:003007	secretionBi	process10132570145861.9385964910.0341638150.3167288391.466433635SYT9//IFNG//II							
GO:003555	signal	transductio	process801680570145861.2185463660.0344712610.3187721151.46254283CA						
GO:004682	regulation	of	nucleocyto	transportBi	process432570145863.1986842110.0348939830.321868				
GO:003464	nitrogen	compound	metabolic	processBio	process2225149570145861.1032944570.0355296150.32				
GO:000742	nervous	system	developme	process547570145862.7222844340.0356254780.3261512551.44823					
GO:003247	of	type	I	interferon	productionB	process547570145862.7222844340.0356254			
GO:003027	of	ossification	process897570145862.1104720560.0359287890.3262575711.444557422SMUF						
GO:000008	of	transcriptio	involved	in	G1/S	phase	of	mitotic	cell
GO:004352	process319570145864.0404432130.0360949360.3262575711.442553725CRH//ADNP//AKT1S1								
GO:006033	of	response	to	interferon-g	process319570145864.0404432130.0360949360.326257				
GO:006033	of	interferon-g	signaling	pathwayBio	process319570145864.0404432130.0360949360.326257				
GO:009030	acid	metabolic	processBio	process1764007570145861.1239698950.0362192640.3262575711.4					
GO:001603	reproductio	process24415570145861.4798731770.036260740.3262575711.440563332EIF2AK2//RPL2							
GO:000759	coagulation	process27481570145861.4364153630.0379245810.3403917061.421079207TFPI//EGF//IG							
GO:000630	catabolic	processBio	process664570145862.3990131580.0384278980.3440659231.415353371GTF2						
GO:003399	to	lipidBiologi	process548570145862.6655701750.0385399270.3442273521.414089107TGFB						
GO:005104	regulation	of	secretionBi	process781570145862.2114359970.0387949450.3456620181.41122					
GO:004317	metabolic	processBio	process2826677570145861.080759560.0389903210.3465596041.409043185KI						
GO:000715	communica	process811715570145861.2085990490.0394355030.3496678281.404112613WIPI2//ATG12							
GO:000828	regulation	of	cell	proliferatio	process23398570145861.478788680.0400327030.35410				
GO:000759	process27484570145861.4275119620.0404587190.3561534371.39298787EGF//ZFPM2//GGCX//GRB								

GO:00508	process27484570145861.4275119620.0404587190.3561534371.39298787EGF//ZFPM2//GGCX//GRB						
GO:00323	to	estradiol	stimulusBi	process782570145862.1844672660.0410507280.3604982411.3866			
GO:00320	of	TOR	signaling	cascadeBi	process320570145863.8384210530.0412669650.360667		
GO:00420	regulation	of	cytokine	biosyntheti	processBio	process320570145863.8384210530.0412669	
GO:00903	acid	phosphodie	bond	hydrolysis	process549570145862.6111707840.0415957630.362675		
GO:00461	biosyntheti	processBio	process8100570145862.0471578950.0418774560.3642642411.378019704SDS				
GO:00100	to	organic	substance	process591206570145861.2518896740.0420802640.3650994371.3			
GO:00425	of	tyrosine	phosphoryl	of	STAT	proteinBiol	process434570145863.0105263
GO:00903	regulation	of	intracellula	protein	transportBi	process434570145863.0105263160.0423589	
GO:00324	to	lipopolysac	process10137570145861.8678447940.0423722720.3650994371.372918247MT				
GO:00650	regulation	process3327972570145861.0656930840.0430351260.3691710881.366176921KPNA2//UB					
GO:00511	regulation	of	nitrogen	compound	metabolic	processBio	process48955570145861.286172
GO:00461	catabolic	processBio	process8101570145862.0268890050.0439969840.3764414881.35657709ALD				
GO:00067	compound	metabolic	processBio	process10138570145861.8543096870.044162270.3769749021.354			
GO:00508	of	body	fluid	levelsBiolo	process30554570145861.3857115710.0446026990.3798		
GO:00163	process12177570145861.7348795720.0451812620.3838834821.345041644PPM1K//FBXW11//PPM1						
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GO:00182	modificatio	process9120570145861.9192105260.0454948230.3847622191.342038023TPST1//GH1//A					
GO:00100	cell	differentiati	process784570145862.132456140.0458139190.386198351.339002552CTNNB				
GO:00510	regulation	of	bindingBiol	process10139570145861.840969330.0460029310.386198351.3372			
GO:00604	developme	process8102570145862.0070175440.046185990.386198351.335489738FOXD4L1//FOXD					
GO:00062	DNA	replication	initiationBi	process435570145862.9245112780.046402860.386198351.333455			
GO:00140	crest	cell	developme	process435570145862.9245112780.046402860.386198351.333455			
GO:003111	of	microtubul	polymeriza	or	depolymeri	process435570145862.9245112780.046402	
GO:00454	of	nitric	oxide	biosyntheti	processBio	process435570145862.9245112780.046402	
GO:00064	ADP-ribos	process321570145863.6556390980.0467899660.3867829651.329847275ADNP//SIRT4//T					
GO:00071	meiosisBio	process321570145863.6556390980.0467899660.3867829651.329847275UBR2//TRIP13//					
GO:00109	regulation	of	glucose	metabolic	processBio	process321570145863.6556390980.0467899	
GO:00140	to	amine	stimulusBi	process668570145862.2578947370.0493464140.4069967751.3067			

ID

s)/(List.Total/Pop.Tot

thod
e))

Enrichme GENES

1//KIF23//NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//CDKN3//ORC6//INHBA//PCNA//POLE2//MCM10//PSMA3//PS
C1//KIF23//NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//KPNA2//UBE2C//PSMA8//ORC6//MDM2//ANAPC11//MCM1
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C1//KIF23//NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//KPNA2//CDKN3//ORC6//INHBA//PCNA//POLE2//MCM10//P
NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//KPNA2//KIF20A//CENPA//CENPF//STAG2//SGOL1//CENPI//BIRC5//SK
3934184UBE2C//PSMA8//ORC6//MAD2L1//MDM2//ANAPC11//MCM10//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5
E-1012.03614131UBE2C//PSMA8//ORC6//MAD2L1//MDM2//ANAPC11//MCM10//PSMA3//PSMA6//PSMA7//PSMB
E-124.68159E-1011.99023466NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//SKA2//CENPA//CENPF//STAG2//SGOL1
0A//BIRC5//AURKC//PRC1//KIF23//KLHL21//TOP1//IL1B//PPBP//VEGFA//SYCP2//NDC80//USP16//CENPF//STAG2
27E-0911.39161985PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD
T//MAD2L1//NEK2//NUSAP1//SKA2//CENPA//CENPF//STAG2//SGOL1//CENPI//BIRC5//CASC5//SPC25//CENPH//B
/NEK2//NUSAP1//SKA2//CENPA//CENPF//STAG2//SGOL1//CENPI//BIRC5//CASC5//SPC25//CENPH//BUB1//KIF18
AFX//PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1//Z
/MAD2L1//NEK2//NUSAP1//SKA2//CENPA//CENPF//STAG2//SGOL1//CENPI//BIRC5//CASC5//SPC25//CENPH//BU
5E-0910.40531459UBE2C//PSMA8//ORC6//MAD2L1//MDM2//ANAPC11//MCM10//PSMA3//PSMA6//PSMA7//PSMB
E2C//PSMA8//ORC6//MAD2L1//MDM2//ANAPC11//MCM10//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//P
2286495PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1
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41.96952E-093.79599E-078.705640188MAD2L1//UBE2C//PSMA8//UBE2S//ANAPC11//PSMA3//PSMA6//PSMA7//P
T//MAD2L1//NEK2//NUSAP1//TOP2A//STAG2//RAD51C//BUB1//DLGAP5//KIF18A//CCNB1//SGOL1//CASC5//CENF
E-083.64538E-067.679756553PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD
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//CENPF//STAG2//ZWINT//SGOL1//CENPI//BIRC5//SKA2//MAD2L1//CASC5//SPC25//CENPH//BUB1//KIF18A//CCN
5705264DCP2//NCBP2//UPF3B//EIF4A3//ISG15//MDM2//UBR5//HERC6//SMURF1//SMURF2//LSM3//GTF2H3//HM
CNA//POLE2//MCM10//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1//RRM2//S
E-088.05132E-067.225112504PCNA//RRM2//CCNE1//WNT9A//CDKN3//ORC6//INHBA//POLE2//MCM10//PSMA3//
3//RPS14//RPS15//WIPI2//ATG12//PTTG2//PTTG1//NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//SKA2//CENPA//CC
E-067.147829582UBE2C//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PS
E-057.039089587GCLM//UBE2C//PSMA8//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD1
9E-071.517E-056.891370676PRC1//KIF23//RPS14//RPS15//WIPI2//ATG12//PTTG2//PTTG1//NDC80//ZWINT//MAD
45861.4665532311.33957E-071.53166E-056.873034485BRIX1//PRC1//KIF23//RPS14//RPS15//WIPI2//ATG12//PTT
DC80//KIF11//STMN1//SPC25//SBDS//CCNB1//HAUS2//UBE2C//ZWINT//CKS2//AURKA
5//SMURF1//UBE2D3//MDM2//HERC6//SMURF2//UBE2W//SUZ12//UBQLN1//UBE2S//UBE2T//UBE2C//MAD2L1//A
KIF23//NDC80//CENPA//STMN1//KIF18A//UBE2C//ZWINT//CKS2//KIF11//AURKA//SPC25//NPM1//SGOL1//CASC5
E-072.23955E-056.657255562FBXW11//UBR5//SMURF1//UBE2D3//MDM2//HERC6//SMURF2//FEM1B//DCAF7//MA
362.4141012912.33745E-072.25996E-056.631257636FBXW11//UBR5//SMURF1//UBE2D3//MDM2//HERC6//SMUR

process1577570145864.9849624062.3594E-072.25996E-056.627198751UBE2C//MAD2L1//ANAPC11//PSMA3//P

6E-056.618553467UBE2C//NPLOC4//PSMA8//UBE2S//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//P

072.57942E-056.550135515UBE2C//PSMA8//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PS

170399UBE2C//NPLOC4//PSMA8//UBE2S//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSM

006075MDM2//UBR5//HERC6//SMURF1//SMURF2//USP16//UBE2C//PSMA8//CYLD//UBR2//PSMA3//PSMA6//PS

006075ISG15//MDM2//UBR5//HERC6//SMURF1//SMURF2//USP16//UBE2C//PSMA8//CYLD//UBR2//PSMA3//PSM

cycleBiolo process1471570145865.0458117125.09066E-074.23682E-056.293225897UBE2C//PSMA8//ANAPC11/

673587MDM2//UBR5//HERC6//SMURF1//SMURF2//UBE2C//NPLOC4//PSMA8//UBE2S//MAD2L1//ANAPC11//PS

869.83053E-077.82596E-056.007422964ISG15//MDM2//UBR5//HERC6//SMURF1//SMURF2//USP16//UBE2C//P

KIF23//SBDS//CCNB1//KIF11//NDC80//STMN1//SPC25

/MAD2L1//NEK2//NUSAP1//PCNA//POLE2//RFC5//TOP2A//CHD1//BAZ1B//CENPA//OIP5//CENPI//H2BFM//H2AF

516194ISG15//MDM2//UBR5//HERC6//SMURF1//SMURF2//PSMA8//PSMA3//PSMA6//PSMA7//PSMB5//USP16//

2//NCBP2//UPF3B//EIF4A3//ISG15//MDM2//UBR5//HERC6//SMURF1//SMURF2//LSM3//GTF2H3//HMGB2//CYCS/

305639SMURF1//UBE2C//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//P

RC1//KIF23//RPS14//RPS15//WIPI2//ATG12//PTTG2//PTTG1//NDC80//ZWINT//MAD2L1//NEK2//NUSAP1//SKA2//

in cell cycle arrestBiolo process1261570145865.0339948233.4133E-060.0002083255.4668

233.4133E-060.0002083255.466825313PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PS

233.4133E-060.0002083255.466825313PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PS

233.4133E-060.0002083255.466825313PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PS

5.0339948233.4133E-060.0002083255.466825313PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//P

233.4133E-060.0002083255.466825313PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PS

damage checkpoint process1261570145865.0339948233.4133E-060.0002083255.466825313PSMA8//MDM2//

1570145865.0339948233.4133E-060.0002083255.466825313PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7/

02170365.441856342BRIX1//PRC1//KIF23//RPS14//RPS15//WIPI2//ATG12//PTTG2//PTTG1//NDC80//ZWINT//MA

569135.361540157UBE2C//PSMA8//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//P

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MAD2L1//ANAPC11//BUB1//CASC5//CCNB1//DYNC1LI1//BIRC5

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768274RAD51//CENPA//OIP5//CENPI//H2BFM//H2AFX//H2AFZ//HMGB2//NAP1L4//NPM1//H2AFJ//CASC5//CEN

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A8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1//WNT9A

cycleBiolo process1267570145864.5831893179.48825E-060.0004963715.022814032MAD2L1//UBE2C//ANAPC1

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IPI2//ATG12//DCP2//NCBP2//UPF3B//EIF4A3//ISG15//MDM2//UBR5//HERC6//SMURF1//SMURF2//LSM3//GTF2H

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//UBE2C//MAD2L1//ANAPC11//BUB1//EGF//IGF1//IL1B//NUSAP1//DLGAP5//DYNC1LI1//NEK2//CDK11A

664NEK2//CDK11A//CENPF//UBE2C//MAD2L1//ANAPC11//BUB1//EGF//IGF1//IL1B//NUSAP1//DLGAP5//DYNC1L

D51//CENPA//OIP5//CENPI//H2BFM//H2AFX//H2AFZ//HMGB2//NAP1L4//NPM1//H2AFJ//CASC5//CENPH//HIST2H

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NPI//NPM1//CASC5//CENPH//H2BFM//H2AFX//H2AFZ//HMGB2//NAP1L4//H2AFJ//HIST2H2AC//H2AFV

YCP2//TRIM69//PSMA8//CTNNB1//EYA2//ALDOC//KIF1B//JMJD6//MAGI3//CKAP2//NGFRAP1//MAGEH1//UBQLN

12420884.525083175UBE2C//PSMA8//ORC6//MAD2L1//MDM2//ANAPC11//MCM10//PSMA3//PSMA6//PSMA7//PS

M69//PSMA8//CTNNB1//EYA2//ALDOC//KIF1B//JMJD6//MAGI3//CKAP2//NGFRAP1//MAGEH1//UBQLN1//HMGB2/

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P2//NCBP2//UPF3B//EIF4A3//SRSF10//SMN2//SNRPD1//SNRPD2//LSM3//HNRNPM//SYNCRIP//HNRNPA1//HNR
CS//SOD1//FOXL2//TPD52L1//CFDP1//HSPA1B//BIRC5//IGF1//IL1B//NPM1//TRIAP1//BCL2A1//BNIP1//YWHAZ//F
FX//PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1//
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30713784.047001348UBE2C//PSMA8//ORC6//MAD2L1//MDM2//ANAPC11//MCM10//PSMA3//PSMA6//PSMA7//P
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NDC80//CENPA//YWHAZ//EGF//IGF1//ITGA2B//LAMP2//PPBP//SOD1//VEGFA//CALU//CD9//HNRNPA1//NXF1//S
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34343.812176108UBE2C//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//P
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RIX1//RPS14//RPS15//WIPI2//ATG12//SRSF10//SMN2//SNRPD1//SNRPD2//NCBP2//RAD51//CASC5//CENPA//OI
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620.0103531873.396355941NDC80//SGOL1//CASC5//CCNB1
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2930.0110096443.363582589CDKN3//CKS2//SERTAD1//BCCIP//CCNE2//EGF//TGFBR1//IL1B//SOD1//SPRED2//
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0926FOXD4L1//FOXD4//FOXD2//FOXD4L3
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SOD1//FOXD4L1//FOXD4//FOXD2//FOXD4L3
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B1//MYC//FOXD4L1//FOXD4//FOXD2//FOXD4L3
9544PRTFDC1//MAT2B//MAT2A
DC1//MAT2B//MAT2A
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4

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CBP//TPD52L1//UBR5//DAB2IP
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//TPD52L1//NMU//UBR5

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A8//CCNB1//UBE2G2
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NP

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B2IP//SOD2//IL1B//TPM1//HBB//GRB2//EEF1E1//SDCBP//TPD52L1//STC1//VEGFA//STC2//CCNB1//FEM1B//HP

6R3//CAMKK2//HSP90AA1//WASL//GCH1//HP//UBE2C//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//P

SMC5//PSMD9//PSMD11//PSMD12//PSME1//PSMA8//SKP1//FEM1B//UBE2S//STK3

PSMG1//RRM2//USP16//ALDOC//SOD2//PDSS2//HBB//CENPF//PSMD9
NG//CTNNB1//DAB2IP//GAL//ING3//STK3//TOP2A//EEF1E1//MAD2L1//MDM2//SOD2//VEGFA//MTDH//ADNP//GCL

E1//EIF5A2//PQBP1//CAMKK2//INHBA//SMAD5//MAX//MYBL1//MYC//NPM1//PSMD9//ZFX//MED30//FOXD4L1//FO
P1//NME1//TXN//TPD52L1//PPP6R3//CAMKK2//HSP90AA1//WASL//GCH1//FOXD4L1//FOXD4//FOXD2//FOXD4L3/

MD9//PSMD11//PSMD12//PSME1//SKP1//CCNB1//UBE2S//IFNG//STK3
D2//FBXW11//UBR5//SMURF1//UBE2D3//ISG15//HERC6//SMURF2//SRSF10//SMN2//SNRPD1//SNRPD2//LSM3//B

//LAG3//PSMA8//NME1//MST4//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1//

FNG//CTNNB1//DAB2IP//GAL//ING3//STK3//TOP2A//EEF1E1//MAD2L1//MDM2//SOD2//VEGFA//MTDH//ADNP//GC

NRK//PRKACB//PBK//EIF2AK2//TEX14//STK3//AURKA//AURKC//BUB1//CDK11A//STK24//CCNE1//AKT1S1//PPM1

52L1//CAMKK2//FBXW11//VEGFA//UBE2C//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMC5//PSMD9//PSMD

1//NLRP12//NGFRAP1//IFI27//CRH//CYCS//DAB2IP//MTDH//GH1//CTNNB1//GABPB1//HBB//HP//ADNP//ARPP19//

1//UBR5//SMURF1//UBE2D3//ISG15//HERC6//SMURF2//SRSF10//SMN2//SNRPD1//SNRPD2//LSM3//BCAS2//HN

A//RAB7L1//CHMP4C//RAB33A//GOSR1//BIRC5//TXN//UBR5//MDM2//RRAGB//RRAGC//EGF//DAB2IP//IL1B//CY
P2//RHOB//SDAD1//EIF5A2//RAB22A//RAB3A//RAB5A//KIF18A//RAB7L1//CHMP4C//RAB33A//GOSR1//ABCD3//

/PQBP1//CAMKK2//INHBA//SMAD5//MAX//MYBL1//MYC//NPM1//PSMD9//ZFX//MED30//FOXD4L1//FOXD4//FOXD

2S//IFNG//STK3
2//MTDH//C9ORF89//EEF1E1//MDM2//WNT9A//SDCBP//TPD52L1//PTPN1//SIRT4//RAB5A//EZH2//ADNP//CRH//

W11//STAG2//MAD2L1//INHBA//SOCS1//LAG3//SOD1//IL1B//HNRNPAB//SRSF10//NPPC//UBE2C//ANAPC11//PSM
P12//FBXW11//STAG2//MAD2L1//SOCS1//INHBA//LAG3//HNRNPAB//SRSF10//NPPC//UBE2C//ANAPC11//PSMA

P2//RHOB//SDAD1//EIF5A2//RAB22A//RAB3A//RAB5A//KIF18A//RAB7L1//CHMP4C//RAB33A//GOSR1
NAPC11//PCNP//SKP1//UBE2D2//KLHL21//CYLD//EIF1AX//RPL7L1//GTF2H3//ASMT//MRPS7//MRPS23//BRIX1//

HMP4C//RAB33A//GOSR1//TXN//UBR5//EGF//DAB2IP//IL1B//CYLD//FBXW11//HSP90AA1//SEC61G//DPH3//PAN

EC61G//RHOT1//RAB31//TGFBR1

//INHBA//SOCS1//LAG3//HNRNPAB//SRSF10//NPPC//UBE2C//MAD2L1//ANAPC11//PSMA3//PSMA6//PSMA7//PS

C//NPM1//PSMD9//ZFX//MED30//MTDH//FOXD4L1//FOXD4//FOXD2//ZFPM2//FOXD4L3//TFAP2E//AKIRIN2//NCB

TC1//HP//MYC//SLC30A8//CTNNB1//CD55//IL1B//BDKRB1//TAC1//HSPA8//RAB3A//CDO1//NME1//SYT9//SLC2A1/

3//BCAS2//HNRNPM//SYNCRIP//HNRNPA1//HNRNPH3//HNRNPK//U2AF1//SRSF9//GTF2H3//RAD51AP1//H2AF

//MAB21L1//AKIRIN2//EIF5A2//TGFBR1//NLRP12//NGFRAP1//IFI27//CRH//CYCS//NPPC//NMU//DAB2IP//MTDH//

PM1K//FBXW11//PPM1A//PPP3CA//PTPN1//PPM1D//CDC14A//IMPA1//ACYP1//DAB2IP//GH1//TOP1//BAZ1B//EYA
PM1K//FBXW11//PPM1A//PPP3CA//PTPN1//PPM1D//CDC14A//DAB2IP//GH1//TOP1//BAZ1B//EYA2//ABI1//NLRP1

23//SMURF1//STRADA//SDCBP//RTP4//TOMM5//ABCC5//SLC36A4//ENSA//HBB//NDUFA8//NDUFB2//NDUFB4//N

MM5//ABCC5//SLC36A4//ENSA//HBB//NDUFA8//NDUFB2//NDUFB4//NDUFB9//NDUFS6//TMED7//DYNC1LI1//ATP

//STRADA//CENPF//CTNNB1//IFNG//MYC//NCF2//NME1//GAL//ABCD3//TOP1//YWHAZ//SOCS1//CCNE1//AQP10/

2A//RAB3A//RAB5A//RRAGC//RAB7L1//ARHGAP11B//RAB33A//ARHGAP25//GRB2//IGF1//SDCBP//NLRP12//NDC

YNCRIP//HNRNPA1//HNRNPH3//HNRNPK//U2AF1//SRSF9//GTF2H3//RAD51AP1//H2AFX//RAD51//EIF5A2//TPI1/

1//HNRNPH3//HNRNPK//U2AF1//SRSF9//GTF2H3//RAD51AP1//H2AFX//RAD51//PTTG2//RNASEH1//HMGB2//CC

URF1//UBE2D3//ISG15//HERC6//SMURF2//SRSF10//SMN2//SNRPD1//SNRPD2//LSM3//BCAS2//HNRNPM//SYN

A//HMGXB4//WWOX//SMURF1//FOXD4L1//FOXD4//FOXD2//FOXD4L3//TWSG1//TOB1//CD9//VEGFA//ADNP//CC

GAL//PANX1//PCNA//SDS//STC2//CA2//NPPC//HMGB2//NME1//TGFBR1//CMPK2//RRAGB//RRAGC//DAB2IP//INHB

MAP3K3//EGF//TGFBR1//IL1B//SOD1//SPRED2//POLE2//RRAGC//CDK11A//MORF4L2//CAMLG//B2M//CCDC88A
30//MTDH//FOXD4L1//FOXD4//FOXD2//ZFPM2//FOXD4L3//TFAP2E//AKIRIN2//PRTFDC1//NCBP2//GTF2H3//RAD

P16//UBE2C//OIP5//CDCA2//DYNC1LI1//ANAPC11//TXNL4B//PBK//PAPD5//AURKA//DYNLT3//CDK11A//FAM83D/
KNTC1//DLGAP5//TRIP13//TOP2A//TRIAP1//SESN3//IFNG//MYC//PPM1A//RPRM//STRADA//CKS2//KIF11//AURK
//BUB1//KIF18A//KNTC1//DLGAP5//TRIP13//AURKA//PTTG1//TOP2A//BEX2//TRIAP1//SESN3//IFNG//MYC//PPM1
UBE2C//CKS2//KIF11//AURKA//STMN1//USP16//OIP5//CDCA2//DYNC1LI1//ANAPC11//TXNL4B//PBK//PAPD5//DY

/DLGAP5//BTG3//DYNC1LI1//CTNNB1//TOP2A//CASC5//FEM1B//BEX2//CCNE1

//YWHAZ//RAB3A//CTNNB1//STMN1//BNIP1//NPLOC4//ABCD3//RAB22A//UBE2C//CKS2//KIF11//AURKA//RAD51

C//H2AFV//SDCBP//CAP2//SGCD//TPM1//MAN2A1//RNASEH1//CYCS//SOD1//FOXL2//TPD52L1//EZH2//BPTF//
AP1L4//NPM1//H2AFJ//HIST2H2AC//H2AFV//SDCBP//CAP2//SGCD//TPM1//MAN2A1//RNASEH1//CYCS//SOD1/

HMGB2//NAP1L4//NPM1//H2AFJ//HIST2H2AC//H2AFV//SDCBP//SGCD//TPM1//MAN2A1//RNASEH1//CYCS//SOD

IP5//H2BFM//H2AFX//H2AFZ//HMGB2//NAP1L4//NPM1//H2AFJ//HIST2H2AC//H2AFV//SDCBP//SGCD//TPM1//MA

/NUDT7//NUDT3//PRKACB//CDO1//NPLOC4//UBE2S//MAD2L1//ANAPC11//PSMD11//PSMD12//PSME1//AURKA//

FI27//NLRP12//TOP1//PRTFDC1//CRH//HBB//HP//NME1//BEX2//NAE1//TOP2A//IFNG//DAB2IP//GAL//ING3//STK3/
PM1A//RPRM//STRADA//ZWINT//BUB1//KNTC1//CENPF//ABI1//TOB1//BTG3//NPPC//NOX4//GAL//EIF2AK2//RAR
12//ZFYVE27//HSPB8//SMN2//TOP1//PRTFDC1//CRH//HBB//HP//NME1//BEX2//NAE1//TOP2A//IFNG//DAB2IP//GA

T//INHBA//IFI27//NLRP12//CRH//NME1//BEX2//NAE1//TOP2A//IFNG//DAB2IP//GAL//ING3//STK3//EEF1E1//MAD2L
23//BRIX1//MRPL47//RPL27A//MRPL12//RPS7//RPS14//RPS15//RPS24//MRPS25//EIF4H//SECISBP2//RPL23//MR

R1//SYCP2//TRIM69//EYA2//ALDOC//KIF1B//JMJD6//MAGI3//CKAP2//MAGEH1//UBQLN1//FAM3B//RHOT1//RRA

INHBA//SKP1//CCNE1//CEP152//HSP90AA1//HAUS2//TPD52L1//PPM1D//KIF20A//CENPA//STAG2//CENPI//BUB1

PM1A//RPRM//STRADA//ZWINT//BUB1//KNTC1//CENPF//ABI1//TOB1//BTG3//NPPC//NOX4//GAL//EIF2AK2//RAR

NGLY1//MCCC2//SDS//HSD17B6//MTDH//NUDT7//NUDT3//PLA2G16//PLD6//PLA2G4C//PRKACB//CDO1//NPLOC
SC5//INHBA//NMU//SLC30A8//GAL//FAM3B//PSMD9//TXN//UBR5//MDM2//RRAGB//RRAGC//DAB2IP//NUSAP1//

OB//NLRP12//INHBA//NMU//SLC30A8//GAL//FAM3B//PSMD9//TXN//UBR5//DAB2IP//NUSAP1//CYLD//FBXW11//AT

P90AA1//SDAD1//BBIP1//STOM//POMP//PSMG1//TPM1//BAIAP2//HAUS2//RRM2//USP16//ALDOC//SOD2//PDSS

CIP//RFC5//TOP2A//UBE2D3//PTTG1//MORF4L2//HMGB2//BAZ1B//TRIP13//CCL26//CDO1//CRH//NFX1//NOX4//

//SOD2//PDSS2//HBB//CENPF//PSMD9

P//PSMD9//MTDH//HSPA1B//KIF11

AIAP2//HAUS2//RRM2//USP16//ALDOC//SOD2//PDSS2//HBB//CENPF//ADNP//PSMD9//MTDH//HSPA1B//KIF11

D9//PSMD11//PSMD12//PSME1//PSMA8//SKP1//FEM1B//UBE2S//STK3

PM1A//PPP3CA//PTPN1//PPM1D//CDC14A//SIRT4//TPST1//ST6GALNAC2//DPM1//MAN2A1//POMT1//UBE2W//

SMC5//PSMD9//PSMD11//PSMD12//PSME1//PSMA8//SKP1//CCNB1//FEM1B//UBE2S//IFNG//STK3

M//NCF2//AKT1S1//TGFBR1//LAG3

XD4//FOXD2//ZFPM2//FOXD4L3//TFAP2E//AKIRIN2//PRTFDC1//NCBP2//GTF2H3//VEGFA//RAD51//UBE2C//PSM
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CAS2//HNRNPM//SYNCRIP//HNRNPA1//HNRNPH3//HNRNPK//U2AF1//SRSF9//GTF2H3//RAD51AP1//H2AFX//R

BEX2//NAE1

LM//NCF2//AKT1S1//TGFBR1//LAG3

K//PPM1A//PPP3CA//PTPN1//PPM1D//CDC14A//SIRT4//TPST1//ST6GALNAC2//DPM1//MAN2A1//POMT1//UBE2

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LD//FBXW11//HSP90AA1//SEC61G//DPH3//PANX1//CCNB1//TGFBR1//CENPA//SUN1
IL1B//BIRC5//TXN//UBR5//MDM2//RRAGB//RRAGC//EGF//DAB2IP//CYLD//FBXW11//INHBA//HSP90AA1//SEC61

2//ZFPM2//FOXD4L3//TFAP2E//AKIRIN2//PRTFDC1//NCBP2//GTF2H3//VEGFA//RAD51//UBE2C//PSMA8//ANAP

THRC1//CYLD//STK3//UBR5

MA3//PSMA6//PSMA7//PSMB5//PSMD9//PSMD11//PSMD12//PSME1//HP
3//PSMA6//PSMA7//PSMB5//PSMD9//PSMD11//PSMD12//PSME1

MRPL47//RPL27A//MRPL12//RPS7//RPS14//RPS15//RPS24//MRPS25//EIF4H//SECISBP2//RPL23//MRPL33//PUM

K1//TGFBR1//MDM2

MB5//PSMD9//PSMD11//PSMD12//PSME1//HP

P2//GTF2H3//ADNP//VEGFA//RAD51//UBE2C//PSMA8//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMD11//P

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X//RAD51//TPI1//NME1//PRTFDC1//NPPC//RAB31//GCH1//NKIRAS1//TRIM23//RHOB//RAB22A//RAB3A//RAB5A//

H1//GABPB1//HBB//HP//ADNP//ARPP19//SBDS//EIF4A3//PPM1A//FOXD4L1//FOXD4//FOXD2//FOXD4L3//TWSG

A2//ABI1//NLRP12//ADNP//STRADA//IFNG//DUSP14//INHBA//SDCBP//IGF1//TPD52L1//PPP6R3//MAP3K3//NEK2//
2//ADNP//STRADA//IFNG//DUSP14//INHBA//SDCBP//IGF1//TPD52L1//PPP6R3//MAP3K3//NEK2//IMPA1//VEGFA//

NDUFB9//NDUFS6//TMED7//DYNC1LI1//ATP5G1//CYCS//ENY2//DYNLT3//TXN//UQCRB//EIF4A3//ATP5S//KCNF1//

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/CD9//ADNP//SLC30A8//CA2//IMPA1//CDO1//LUM//IFI6//HLA-B//IFI27//IFI35//OAS1//OAS2//PTPN1//ISG15//PCNA

80//UBE2C//ZWINT//CKS2//HMGB2//PCNA//AURKA//TOP2A//AKT1S1//CCDC88A//RRAGB//IFNG//CTNNB1//ZDH

/SOD1//ERH//OAS1//OAS2//NME1//PRTFDC1//NPPC//RAB31//GCH1//NKIRAS1//TRIM23//RHOB//RAB22A//RAB3

NE2//ESCO2//CCDC88A//STRA13//RDM1//EYA2//UBE2T//NPM1//BCCIP//RAD51C//UBE2D3//PTTG1//MORF4L2//

RIP//HNRNPA1//HNRNPH3//HNRNPK//U2AF1//SRSF9//GTF2H3//RAD51AP1//H2AFX//RAD51//CAMLG//CCDC8
NE1//AKT1S1//RRAGB//RRAGC//PSMD9//EPN1//SOCS1//TBK1//MAP3K3//ZDHHC13//PELI2//MTDH//C9ORF89//

3A//PRKACB//SSTR2//CCNB1

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51

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C//USP16//CDCA2//DYNC1LI1//ANAPC11//TXNL4B//HAUS2//PBK//PAPD5//DYNLT3//CDK11A//FAM83D//CCNB2//

SRSF9//MRPL12//RPL27A//RPS7//RPS24//RPL23//TOMM5//YWHAZ//CTNNB1//MST4//STK24//RAB3A//STMN1//B
/FOXL2//TPD52L1//EZH2//BPTF//SBDS//RPS7//RPS24//UTP23//EIF4A3//SRSF9//MRPL12//RPL27A//RPL23//TOM

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/EEF1E1//MAD2L1//MDM2//VEGFA//MTDH//ADNP//GCLM//NCF2//AKT1S1//TGFBR1//ZFYVE27//HSPB8//SMN2
RES3//SOD2//SSTR2//WNT9A//PPM1D//CD9//EEF1E1//NLRP12//DAB2IP//FOXD4L1//FOXD4//FOXD2//FOXD4L3
AL//ING3//STK3//EEF1E1//MAD2L1//MDM2//VEGFA//MTDH//ADNP//GCLM//NCF2//AKT1S1//TGFBR1

1//MDM2//VEGFA//MTDH//ADNP//GCLM//NCF2//AKT1S1//TGFBR1//TOP1
PL33//PUM2//NGDN//TACO1//EEF1E1//NCBP2//GGCX//UBE2S//CAMKK2//TP53RK//TBK1//MST4//SNRK//PRKAC

C//BUB1//CDK11A//UBE2D3//PDCL3//SLTM

//KIF18A//KNTC1//DLGAP5//CDO1//CTNNB1//BPTF//ZFPM2//SUZ12//FOSB//HSBP1//NFX1//TXN//MTDH//TCEAL

RES3//SOD2//SSTR2//WNT9A//PPM1D//CD9//EEF1E1//NLRP12//DAB2IP//FOXD4L1//FOXD4//FOXD2//FOXD4L3

4//UBE2S//MAD2L1//ANAPC11//PSMD11//PSMD12//PSME1//AURKA//CCNB1//PTTG1//FBXW11//ACAP2//TBC1D
YLD//FBXW11//ATP5G1//SEC61G//SIRT4//RHOT1//RAB31//DPH3//PANX1//BIRC5//CENPF//CRH//ZWINT//TGFB

P5G1//SEC61G//SIRT4//RHOT1//RAB31//DPH3//PANX1//BIRC5//CENPF//CRH//TGFBR1//ZWINT

2//HBB//CENPF//ADNP//PSMD9//MTDH//HSPA1B//KIF11

AL//BDKRB1//CCL7//TNFAIP6//TPST1//PLA2G4C//NCF2//UBR5//PSMA8//MDM2//TRIAP1//PSMA3//PSMA6//PSM

DAB2IP//GH1//ADNP//EZH2//SUZ12//BAZ1B//EYA2//USP16//ENY2//DPH3//GGCX//ABI1//FKBP14//MAGT1//B4GAL

A8//ANAPC11//PSMA3//PSMA6//PSMA7//PSMB5//PSMD11//PSMD12//PSME1//SKP1//UBE2S
PSMD11//PSMD12//PSME1//PSMA8//SKP1//CCNB1//FEM1B//UBE2S//IFNG//STK3

AD51//CAMLG//CCDC88A//SOCS1//BDKRB1//CCNB1//PELI2//CCT7//DNAJC21//HSPA8//NKTR//FKBP14//DNAJA

N//DAB2IP//GH1//ADNP//EZH2//SUZ12//BAZ1B//EYA2//USP16//ENY2//DPH3//ABI1//FKBP14//MAGT1//B4GALT4//

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LG//CCDC88A//SOCS1//BDKRB1//CCNB1//PELI2//CCT7//DNAJC21//HSPA8//NKTR//FKBP14//DNAJA4//HSPA1B/

G//DPH3//PANX1//ENY2//EIF4A3//CCNB1//TGFBR1//CENPA//SUN1

C11//PSMA3//PSMA6//PSMA7//PSMB5//PSMD11//PSMD12//PSME1//SKP1//UBE2S

2//NGDN//TACO1//EEF1E1//NCBP2//GGCX//UBE2S//CAMKK2//TP53RK//TBK1//MST4//SNRK//PRKACB//PBK//EI

SMD12//PSME1//SKP1//UBE2S

AL//FAM3B//PLSCR1//ASMT//RPS14//SFXN1//TGFBR1//CCDC85B//HSPA1B//CCL26//AURKA//FBXW11//MDM2//

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1//GRB2//SMURF1//CCNB1//UBE2C//BIRC5//RRAGB//RRAGC//SLC30A8//CA2//UBR5//SDCBP//FBXW11//GAL//I

VEGFA
'ACYP1

'KCNK1//ZDHHC13//TMEM38B//SLC4A8//PANX1//ATP13A3//KCTD20//SLN//COX17//SFXN1//SLC30A7//SLC30A8

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//ITGAM//SBDS//MTDH//GH1//AURKA//DCN//GCH1//AKIRIN2//BDKRB1//CLDN4//GGCX//PANX1//SDS//TPM1//HB

IHC13//PPM1A//PELI2//BST2//MTDH//C9ORF89//EEF1E1//TPD52L1//MAGI3//WSB1//STMN1//PLA2G4C//SH3BP5

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SOD1//BAZ1B//TRIP13//CYCS//FOXL2//TPD52L1//MND1//SIRT4//TRAPPC2//RRAGC//FOXD4//FOXD2//GABPB1/

3A//SOCS1//BDKRB1//CCNB1//PELI2//CCT7//DNAJC21//HSPA8//NKTR//FKBP14//DNAJA4//HSPA1B//HSP90AA1/
EEF1E1//TPD52L1//PTPN1//SIRT4//RAB5A//EZH2//CTHRC1//CYLD//STK3//UBR5//OIP5

EX2//GGCX//GRB2//HBB//IGF1//ITGA2B//ITGAM//KIF11//RHOB//LAMP2//PPBP//PRKACB//PTPN1//RAB5A//RAD5

G1//KLHL21//NPM1//RAD51//MND1//SYCP2//UBR2//UBE2S//CTNNB1//NAE1//WNT9A//SBDS//EGF//IGF1//IL1B
//CDK11A//FAM83D//KLHL21//NPM1//RAD51//MND1//SYCP2//UBR2//CYLD//UBE2S//CTNNB1//NAE1//WNT9A//S
S//EGF//IGF1//IL1B

KLHL21//DLGAP5//SYCP2//ABI1//WASL//EYA2//KDM2A//JMJD6//SUZ12//ING3//ENY2//HIRA//MORF4L2//CCL26//

NIP1//NPLOC4//ABCD3//RAB22A//PARD6B//UBE2C//CKS2//KIF11//AURKA//RAD51C//USP16//CDCA2//DYNC1LI1
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2G4C//IFNG//IL1B//PAPD5//HP

//FOXL2//CCDC85B//EZH2//HMGB2//AKIRIN2//SMURF2//HIRA//EIF4A3//HMGXB4//WWOX//TPM1//SMURF1//TW

B//PBK//EIF2AK2//TEX14//STK3//AURKA//AURKC//BUB1//CDK11A//STK24//CCNE1//AKT1S1//PPM1K//PPM1A//P

1//CAMKK2//MAP3K3//DCP2//NCBP2//UPF3B//EIF4A3//TGFBR1//IL1B//SOD1//SPRED2//FBXW11//UBR5//SMURF

//FOXL2//ADNP//TBK1//CCDC85B//EZH2//HMGB2//AKIRIN2//SMURF2//HIRA//EIF4A3//HMGXB4//WWOX//SMURF

2B//TNNI3//TPM1//CCL26//DAB2IP//HBB//DHDH//PCNP//IGF1//IL1B//IFNG//PAPD5//HP
R1//SUN1

A7//PSMB5//PSMC5//PSMD9//PSMD11//PSMD12//PSME1//GCLM//NDUFB4//CRKL//DAB2IP//HSPB8//DNAJA4//H

T4//JMJD6//DCN//NAE1//UBQLN1//NLRP12//ISG15//STRADA//IFNG//ESCO2//DUSP14//UBE2S//UBE2T//IGF1//T

4//HSPA1B//HSP90AA1//EIF5A2//FEM1B//DCAF7//MARCH6//UBE2C//DCAF4//TRIM23//ANAPC11//PCNP//SKP1//

JMJD6//DCN//NAE1//UBQLN1//NLRP12//ISG15//STRADA//IFNG//ESCO2//DUSP14//UBE2T//IGF1//TPD52L1//UBE

BK1//MAP3K3//ZDHHC13//BST2//BPTF//FBXW11//HNRNPAB//NCF2//HSP90AA1//CCNE1//JUND//H2AFX//TPM1/

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1C//SLC16A1//TFPI//TFPI2//CALU//KIF18A//CD9//KIF23//CYLD//FBXW11//PPM1A//WNT9A//RRAGB//LRRN2//BAI

BDS//PLA2G16//RHOB//EGF//IGF1//IL1B//BTG3//FEM1B//ESCO2//SENP5//ERH//FBXW11//CKAP2//MKI67//PCNPA

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//ANAPC11//TXNL4B//HAUS2//PBK//PAPD5//DYNLT3//CDK11A//FAM83D//CCNB2//KLHL21//DLGAP5//SYCP2//BA
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PP3CA//PTPN1//PPM1D//CDC14A//SIRT4//TPST1//ST6GALNAC2//DPM1//MAN2A1//POMT1//PSMA8//PSMA3//PS

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PN1//PPM1D//CDC14A//SIRT4//TPST1//ST6GALNAC2//DPM1//MAN2A1//POMT1//CPA3//SENP5//ANPEP//HP//FA

D4L1//FOXD4//FOXD2//FOXD4L3//PDSS2//GCLM//IFI6//CCNB1//SUN1

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2AFX//RHOB//GAPDHS//NUSAP1//DLGAP5//WNT9A//USP16//ENY2//MRPL12//PQBP1//CAMKK2//SMAD5//MAX/

CTNNB1//DLGAP5//KIF18A//CCNB1//TOB1//RAB3A//NFAT5//CDO1//SYT9//IL1B//SLC2A1//KIF1B//HMGXB4//RHO

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IAP2//GRB2//HSP90AA1//ITGA2B//KAL1//RHOB//WASL//ABI1//ADNP//UBE2S//EYA2//KDM2A//JMJD6//SUZ12//IN
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//SKP1//UBE2S//PPBP

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MN1//ANAPC11//SKP1//UBE2S//PPBP//MAD2L1//DYNC1LI1

SERP2//SDAD1//EIF5A2//RAB7L1//CHMP4C//RAB33A//SLC16A1//GH1//VDAC3//ABCD3//ARPP19//CTHRC

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Z12//ING3/

IP//ADNP//UBE2S//HSPA8//EYA2

SMC5//PSMD11//PSMD12//

2//FOXD4L

AB7L1//RAB33A//KIF1B//

.3//TFAP2E//ZNF860//SMAD5//MYB

GALT4//JMJD

RPS15//RPS24//UTP23//CCRN4L//MAX//PIR//MED30//MRPL12//ZFC3H1//W

6//SEC61G//

S15//RPS24//UTP23//CCRN4L//MAX//PI

A//PSMA8//HSPA8//PSMA3//

ZNF860//SMAD5//MYBL

B//PQ