

Supplementary File.3 The GO and KEGG enrichment analysis of the overlapping genes of the KNS

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust
BP	GO:0000280	nuclear division	67/241	446/18800	1,0299E-52	2,171E-49
BP	GO:0048285	organelle fission	67/241	493/18800	9,1948E-50	9,6913E-47
BP	GO:0007059	chromosome segregation	59/241	348/18800	2,3274E-49	1,6354E-46
BP	GO:0140014	mitotic nuclear division	53/241	293/18800	9,15E-46	4,822E-43
BP	GO:0098813	nuclear chromosome segregation	52/241	287/18800	6,3525E-45	2,6782E-42
BP	GO:0000070	mitotic sister chromatid separation	41/241	171/18800	1,0944E-40	3,8451E-38
BP	GO:0000819	sister chromatid separation	43/241	205/18800	5,7215E-40	1,723E-37
BP	GO:0044772	mitotic cell cycle	49/241	440/18800	6,9967E-32	1,8436E-29
BP	GO:0007346	regulation of cell cycle	49/241	478/18800	3,4455E-30	8,0702E-28
BP	GO:0051321	meiotic cell cycle	37/241	266/18800	1,311E-27	2,7635E-25
BP	GO:1901990	regulation of cell cycle	39/241	321/18800	8,1111E-27	1,5544E-24
BP	GO:1901987	regulation of cell cycle	43/241	415/18800	1,1283E-26	1,9821E-24
BP	GO:0007051	spindle organization	30/241	188/18800	2,5941E-24	4,2064E-22
BP	GO:1903046	meiotic cell cycle	31/241	207/18800	3,1286E-24	4,7107E-22
BP	GO:1902850	microtubule cytoskeleton organization	27/241	151/18800	2,4416E-23	3,4312E-21
BP	GO:0090068	positive regulation of cell cycle	32/241	247/18800	5,5404E-23	7,2994E-21
BP	GO:0010948	negative regulation of cell cycle	34/241	301/18800	2,1005E-22	2,6046E-20
BP	GO:0140013	meiotic nuclear division	28/241	188/18800	6,6899E-22	7,8347E-20
BP	GO:0051783	regulation of cell cycle	25/241	139/18800	9,5186E-22	1,0561E-19
BP	GO:0007052	mitotic spindle organization	24/241	124/18800	1,0244E-21	1,0797E-19
BP	GO:0007088	regulation of cell cycle	23/241	111/18800	1,4225E-21	1,4279E-19
BP	GO:0045787	positive regulation of cell cycle	34/241	329/18800	3,7787E-21	3,6207E-19
BP	GO:0140694	non-membrane bound organelle organization	36/241	379/18800	4,1013E-21	3,7589E-19
BP	GO:0051983	regulation of cell cycle	21/241	91/18800	7,6258E-21	6,698E-19
BP	GO:0030071	regulation of cell cycle	18/241	60/18800	2,643E-20	2,2286E-18
BP	GO:0051304	chromosome segregation	21/241	97/18800	3,2216E-20	2,612E-18
BP	GO:0007091	metaphase/anaphase transition	18/241	62/18800	5,165E-20	4,0325E-18
BP	GO:1902099	regulation of cell cycle	18/241	63/18800	7,1496E-20	5,3826E-18
BP	GO:0010965	regulation of cell cycle	18/241	65/18800	1,3449E-19	9,4501E-18
BP	GO:0044784	metaphase/anaphase transition	18/241	65/18800	1,3449E-19	9,4501E-18
BP	GO:0000075	cell cycle checkpoint	25/241	170/18800	1,6059E-19	1,092E-17
BP	GO:0033044	regulation of cell cycle	27/241	212/18800	2,4845E-19	1,6198E-17
BP	GO:0044839	cell cycle G2/M transition	24/241	155/18800	2,5358E-19	1,6198E-17
BP	GO:1901988	negative regulation of cell cycle	29/241	255/18800	2,6132E-19	1,6202E-17
BP	GO:0051306	mitotic sister chromatid separation	18/241	68/18800	3,324E-19	1,9645E-17
BP	GO:0006260	DNA replication	30/241	280/18800	3,3549E-19	1,9645E-17
BP	GO:0045786	negative regulation of cell cycle	34/241	387/18800	6,5801E-19	3,7489E-17
BP	GO:0033045	regulation of cell cycle	18/241	72/18800	1,0334E-18	5,5858E-17
BP	GO:1905818	regulation of cell cycle	18/241	72/18800	1,0334E-18	5,5858E-17
BP	GO:0007093	mitotic cell cycle	22/241	130/18800	1,1477E-18	6,0485E-17
BP	GO:0051225	spindle apparatus organization	21/241	121/18800	4,1787E-18	2,1485E-16
BP	GO:1901991	negative regulation of cell cycle	24/241	183/18800	1,347E-17	6,7604E-16
BP	GO:0045930	negative regulation of cell cycle	26/241	234/18800	3,6863E-17	1,8071E-15
BP	GO:0000086	G2/M transition	21/241	140/18800	9,3908E-17	4,499E-15
BP	GO:0051784	negative regulation of cell cycle	15/241	55/18800	2,0214E-16	9,4692E-15
BP	GO:0000910	cytokinesis	22/241	174/18800	7,019E-16	3,2165E-14
BP	GO:0045839	negative regulation of cell cycle	14/241	48/18800	7,2587E-16	3,2556E-14
BP	GO:2001251	negative regulation of cell cycle	17/241	89/18800	1,2916E-15	5,6724E-14

BP	GO:0045841	negative regul	13/241	40/18800	1,6159E-15	6,9518E-14
BP	GO:1902100	negative regul	13/241	42/18800	3,3501E-15	1,4124E-13
BP	GO:0033046	negative regul	13/241	43/18800	4,7477E-15	1,8883E-13
BP	GO:0033048	negative regul	13/241	43/18800	4,7477E-15	1,8883E-13
BP	GO:2000816	negative regul	13/241	43/18800	4,7477E-15	1,8883E-13
BP	GO:0051985	negative regul	13/241	45/18800	9,264E-15	3,5506E-13
BP	GO:1905819	negative regul	13/241	45/18800	9,264E-15	3,5506E-13
BP	GO:0061982	meiosis I cell	19/241	136/18800	1,1013E-14	4,1454E-13
BP	GO:0033047	regulation of	13/241	46/18800	1,2768E-14	4,7219E-13
BP	GO:0006261	DNA-templat	20/241	159/18800	1,6916E-14	6,1479E-13
BP	GO:0007094	mitotic spindl	12/241	38/18800	3,0185E-14	1,0431E-12
BP	GO:0071173	spindle assen	12/241	38/18800	3,0185E-14	1,0431E-12
BP	GO:0071174	mitotic spindl	12/241	38/18800	3,0185E-14	1,0431E-12
BP	GO:1902749	regulation of	17/241	108/18800	3,7844E-14	1,2867E-12
BP	GO:0031577	spindle check	12/241	39/18800	4,3111E-14	1,4425E-12
BP	GO:0051310	metaphase pl	14/241	65/18800	7,5696E-14	2,4932E-12
BP	GO:0045132	meiotic chror	16/241	96/18800	8,599E-14	2,7887E-12
BP	GO:0010389	regulation of	16/241	97/18800	1,0181E-13	3,2408E-12
BP	GO:0051303	establishmen	15/241	81/18800	1,03E-13	3,2408E-12
BP	GO:0050000	chromosome	15/241	83/18800	1,5042E-13	4,663E-12
BP	GO:0090307	mitotic spindl	14/241	69/18800	1,8336E-13	5,6019E-12
BP	GO:0000281	mitotic cytok	14/241	71/18800	2,791E-13	8,4048E-12
BP	GO:1901989	positive regul	17/241	123/18800	3,4526E-13	1,0141E-11
BP	GO:0051302	regulation of	20/241	186/18800	3,4639E-13	1,0141E-11
BP	GO:0032465	regulation of	15/241	91/18800	6,1914E-13	1,7879E-11
BP	GO:0008608	attachment o	11/241	37/18800	7,7934E-13	2,2201E-11
BP	GO:0007127	meiosis I	17/241	130/18800	8,723E-13	2,4517E-11
BP	GO:0061640	cytoskeleton-	15/241	100/18800	2,5828E-12	7,0709E-11
BP	GO:1901992	positive regul	15/241	100/18800	2,5828E-12	7,0709E-11
BP	GO:0034508	centromere c	10/241	31/18800	3,4827E-12	9,4121E-11
BP	GO:0044786	cell cycle DN/	11/241	43/18800	4,9001E-12	1,3075E-10
BP	GO:0006310	DNA recomb	24/241	324/18800	5,0261E-12	1,3244E-10
BP	GO:0051383	kinetochore c	9/241	23/18800	5,6277E-12	1,4646E-10
BP	GO:0006302	double-stranc	22/241	273/18800	7,7471E-12	1,9916E-10
BP	GO:0045931	positive regul	16/241	128/18800	8,4299E-12	2,141E-10
BP	GO:0007080	mitotic meta	11/241	51/18800	3,7074E-11	9,3039E-10
BP	GO:0051255	spindle midzc	7/241	12/18800	3,9107E-11	9,6985E-10
BP	GO:0070192	chromosome	12/241	72/18800	1,1662E-10	2,8586E-09
BP	GO:0010639	negative regul	23/241	356/18800	2,2145E-10	5,3656E-09
BP	GO:0000724	double-stranc	16/241	162/18800	3,0712E-10	7,357E-09
BP	GO:0000725	recombinatio	16/241	164/18800	3,689E-10	8,7375E-09
BP	GO:0000079	regulation of	13/241	98/18800	3,7414E-10	8,7633E-09
BP	GO:1904029	regulation of	13/241	101/18800	5,4922E-10	1,2723E-08
BP	GO:0031570	DNA integrity	14/241	123/18800	6,2045E-10	1,4216E-08
BP	GO:0051231	spindle elong	6/241	10/18800	8,3901E-10	1,9018E-08
BP	GO:0042770	signal transdu	16/241	174/18800	8,8791E-10	1,9912E-08
BP	GO:0034502	protein locali	12/241	93/18800	2,4944E-09	5,535E-08
BP	GO:1902751	positive regul	8/241	31/18800	3,9715E-09	8,7207E-08
BP	GO:0001833	inner cell ma	6/241	13/18800	6,638E-09	1,4279E-07
BP	GO:0051988	regulation of	6/241	13/18800	6,638E-09	1,4279E-07

BP	GO:0007143	female meiot	8/241	33/18800	6,8369E-09	1,4558E-07
BP	GO:0065004	protein-DNA	16/241	203/18800	8,3538E-09	1,761E-07
BP	GO:0051052	regulation of	24/241	472/18800	1,0437E-08	2,1783E-07
BP	GO:0030261	chromosome	9/241	49/18800	1,0587E-08	2,1879E-07
BP	GO:0044774	mitotic DNA i	11/241	85/18800	1,1325E-08	2,3177E-07
BP	GO:0006275	regulation of	13/241	131/18800	1,3918E-08	2,7942E-07
BP	GO:0007098	centrosome c	13/241	131/18800	1,3918E-08	2,7942E-07
BP	GO:0051445	regulation of	9/241	51/18800	1,5332E-08	3,049E-07
BP	GO:0032508	DNA duplex u	11/241	90/18800	2,0875E-08	4,1126E-07
BP	GO:0033260	nuclear DNA i	8/241	38/18800	2,2787E-08	4,4476E-07
BP	GO:0000077	DNA damage	12/241	115/18800	2,8803E-08	5,5704E-07
BP	GO:0032392	DNA geometr	11/241	96/18800	4,136E-08	7,9261E-07
BP	GO:0007131	reciprocal me	9/241	57/18800	4,2406E-08	7,9815E-07
BP	GO:0140527	reciprocal ho	9/241	57/18800	4,2406E-08	7,9815E-07
BP	GO:0031023	microtubule c	13/241	145/18800	4,7276E-08	8,8192E-07
BP	GO:0010971	positive regul	7/241	28/18800	4,9079E-08	9,0754E-07
BP	GO:0032467	positive regul	8/241	42/18800	5,2618E-08	9,6452E-07
BP	GO:0035825	homologous r	9/241	59/18800	5,7926E-08	1,0527E-06
BP	GO:0051382	kinetochore a	6/241	18/18800	6,8051E-08	1,2261E-06
BP	GO:0071824	protein-DNA	16/241	237/18800	7,3963E-08	1,3213E-06
BP	GO:0044773	mitotic DNA c	10/241	81/18800	8,4195E-08	1,4915E-06
BP	GO:0071103	DNA conform	11/241	103/18800	8,646E-08	1,5188E-06
BP	GO:0010972	negative regu	9/241	62/18800	9,0446E-08	1,5757E-06
BP	GO:0007076	mitotic chron	6/241	19/18800	9,8395E-08	1,7001E-06
BP	GO:1902750	negative regu	9/241	64/18800	1,2008E-07	2,058E-06
BP	GO:0044818	mitotic G2/M	8/241	48/18800	1,5744E-07	2,6765E-06
BP	GO:0001832	blastocyst grc	6/241	21/18800	1,9261E-07	3,2481E-06
BP	GO:0044843	cell cycle G1/	16/241	255/18800	2,0192E-07	3,3782E-06
BP	GO:0000082	G1/S transitic	15/241	225/18800	2,2474E-07	3,7303E-06
BP	GO:0044771	meiotic cell c	5/241	12/18800	2,4444E-07	4,0256E-06
BP	GO:0007095	mitotic G2 D	7/241	35/18800	2,5822E-07	4,2197E-06
BP	GO:0006268	DNA unwindi	6/241	22/18800	2,62E-07	4,2485E-06
BP	GO:0051656	establishmen	20/241	404/18800	2,859E-07	4,6007E-06
BP	GO:0090329	regulation of	8/241	52/18800	3,0042E-07	4,7976E-06
BP	GO:0032506	cytokinetic pr	7/241	39/18800	5,6541E-07	8,9615E-06
BP	GO:0071459	protein locali	6/241	25/18800	6,0216E-07	9,4476E-06
BP	GO:1902969	mitotic DNA r	5/241	14/18800	6,0504E-07	9,4476E-06
BP	GO:0001701	in utero embi	19/241	387/18800	6,4946E-07	1,0067E-05
BP	GO:0000212	meiotic spind	5/241	15/18800	8,9809E-07	1,3719E-05
BP	GO:0051315	attachment o	5/241	15/18800	8,9809E-07	1,3719E-05
BP	GO:0007062	sister chroma	8/241	63/18800	1,3694E-06	2,0768E-05
BP	GO:0045143	homologous r	8/241	65/18800	1,7458E-06	2,6287E-05
BP	GO:0001824	blastocyst de	10/241	113/18800	1,9455E-06	2,9086E-05
BP	GO:0051781	positive regul	9/241	89/18800	2,0989E-06	3,1158E-05
BP	GO:0051782	negative regu	5/241	18/18800	2,483E-06	3,6603E-05
BP	GO:0034501	protein locali	5/241	19/18800	3,3347E-06	4,8479E-05
BP	GO:1903083	protein locali	5/241	19/18800	3,3347E-06	4,8479E-05
BP	GO:0040001	establishmen	6/241	35/18800	4,9575E-06	7,1578E-05
BP	GO:0051653	spindle locali	7/241	55/18800	6,2663E-06	8,948E-05
BP	GO:0007292	female gamei	11/241	158/18800	6,2823E-06	8,948E-05

BP	GO:0000723	telomere mai	10/241	132/18800	7,9087E-06	0,00011159
BP	GO:0032200	telomere org	11/241	162/18800	7,9795E-06	0,00011159
BP	GO:0071897	DNA biosynt	12/241	194/18800	8,0393E-06	0,00011159
BP	GO:0051054	positive regul	14/241	263/18800	8,049E-06	0,00011159
BP	GO:0060623	regulation of	4/241	11/18800	8,0991E-06	0,00011159
BP	GO:0006270	DNA replicati	6/241	38/18800	8,165E-06	0,00011177
BP	GO:1904666	regulation of	5/241	24/18800	1,1567E-05	0,00015731
BP	GO:0000727	double-stranc	4/241	12/18800	1,2026E-05	0,00016251
BP	GO:0051307	meiotic chr	5/241	25/18800	1,4309E-05	0,00019212
BP	GO:0010212	response to i	10/241	142/18800	1,5057E-05	0,00020088
BP	GO:0007144	female meios	4/241	13/18800	1,7197E-05	0,00022799
BP	GO:0032886	regulation of	13/241	249/18800	2,0871E-05	0,00027498
BP	GO:0071900	regulation of	16/241	372/18800	2,6269E-05	0,00034395
BP	GO:0071478	cellular respo	11/241	187/18800	3,0651E-05	0,00039884
BP	GO:0000132	establishmen	5/241	30/18800	3,6423E-05	0,00047105
BP	GO:0051293	establishmen	6/241	50/18800	4,1336E-05	0,00053132
BP	GO:2000045	regulation of	10/241	160/18800	4,2177E-05	0,00053885
BP	GO:0051447	negative regu	4/241	16/18800	4,2468E-05	0,00053929
BP	GO:0051298	centrosome c	7/241	74/18800	4,5202E-05	0,00057058
BP	GO:0071479	cellular respo	7/241	75/18800	4,9317E-05	0,00061882
BP	GO:0036297	interstrand cr	5/241	32/18800	5,0406E-05	0,00062503
BP	GO:0040020	regulation of	5/241	32/18800	5,0406E-05	0,00062503
BP	GO:0007018	microtubule-l	16/241	395/18800	5,3889E-05	0,00066431
BP	GO:0007129	homologous i	6/241	53/18800	5,7835E-05	0,00070881
BP	GO:0007096	regulation of	4/241	18/18800	6,9975E-05	0,00085264
BP	GO:0051438	regulation of	6/241	56/18800	7,9217E-05	0,00095971
BP	GO:0051294	establishmen	5/241	36/18800	9,0505E-05	0,001084
BP	GO:0071312	cellular respo	5/241	36/18800	9,0505E-05	0,001084
BP	GO:0051053	negative regu	9/241	148/18800	0,00012583	0,00149862
BP	GO:0045740	positive regul	5/241	40/18800	0,00015152	0,00179435
BP	GO:0051444	negative regu	4/241	22/18800	0,00016067	0,00189212
BP	GO:1902806	regulation of	10/241	188/18800	0,00016182	0,00189513
BP	GO:0031109	microtubule i	8/241	123/18800	0,0001884	0,00219414
BP	GO:0090224	regulation of	5/241	43/18800	0,00021483	0,00248827
BP	GO:1901993	regulation of	3/241	10/18800	0,00023359	0,00269072
BP	GO:0016572	histone phos	5/241	45/18800	0,00026705	0,00305951
BP	GO:0007019	microtubule c	5/241	46/18800	0,00029652	0,00337872
BP	GO:0031055	chromatin rei	3/241	11/18800	0,00031814	0,00358636
BP	GO:1904668	positive regul	3/241	11/18800	0,00031814	0,00358636
BP	GO:0072331	signal transd	9/241	170/18800	0,000355	0,00398057
BP	GO:0001556	oocyte matur	4/241	27/18800	0,00036656	0,00408846
BP	GO:2000241	regulation of	9/241	176/18800	0,00045744	0,00507521
BP	GO:0090169	regulation of	4/241	29/18800	0,00048622	0,00536621
BP	GO:0046605	regulation of	5/241	52/18800	0,00052821	0,00579935
BP	GO:0010458	exit from mit	4/241	30/18800	0,00055542	0,0060545
BP	GO:0009314	response to r	15/241	438/18800	0,0005572	0,0060545
BP	GO:0007100	mitotic centr	3/241	14/18800	0,00068215	0,00729933
BP	GO:0051984	positive regul	3/241	14/18800	0,00068215	0,00729933
BP	GO:2000105	positive regul	3/241	14/18800	0,00068215	0,00729933
BP	GO:0008156	negative regu	4/241	32/18800	0,00071432	0,00749151

BP	GO:0010165	response to x	4/241	32/18800	0,00071432	0,00749151
BP	GO:0051642	centrosome l	4/241	32/18800	0,00071432	0,00749151
BP	GO:0071168	protein locali	4/241	32/18800	0,00071432	0,00749151
BP	GO:0070507	regulation of	8/241	152/18800	0,00078091	0,00814929
BP	GO:0022412	cellular proce	14/241	406/18800	0,00079322	0,00823702
BP	GO:0061842	microtubule c	4/241	33/18800	0,00080474	0,00831567
BP	GO:0051299	centrosome s	3/241	15/18800	0,00084464	0,00860147
BP	GO:0060707	trophoblast g	3/241	15/18800	0,00084464	0,00860147
BP	GO:2000104	negative regul	3/241	15/18800	0,00084464	0,00860147
BP	GO:0006304	DNA modificæ	7/241	119/18800	0,00086498	0,00876623
BP	GO:1901976	regulation of	4/241	34/18800	0,00090295	0,00910723
BP	GO:2001252	positive regul	6/241	89/18800	0,00099815	0,01001952
BP	GO:1902115	regulation of	9/241	202/18800	0,00122036	0,01214444
BP	GO:0000076	DNA replicati	3/241	17/18800	0,00123864	0,01214444
BP	GO:0090231	regulation of	3/241	17/18800	0,00123864	0,01214444
BP	GO:0090266	regulation of	3/241	17/18800	0,00123864	0,01214444
BP	GO:1903504	regulation of	3/241	17/18800	0,00123864	0,01214444
BP	GO:2001020	regulation of	10/241	246/18800	0,00132689	0,01294945
BP	GO:0031145	anaphase-prc	3/241	18/18800	0,00147237	0,01430306
BP	GO:0000018	regulation of	7/241	131/18800	0,00151453	0,0146451
BP	GO:0060236	regulation of	4/241	39/18800	0,00152326	0,01466228
BP	GO:1902808	positive regul	5/241	66/18800	0,00157106	0,01505357
BP	GO:0044728	DNA methyla	6/241	98/18800	0,00164376	0,01567891
BP	GO:0071392	cellular respo	4/241	40/18800	0,00167568	0,01591141
BP	GO:0031297	replication fo	4/241	41/18800	0,00183837	0,01737798
BP	GO:0007099	centriole repl	4/241	42/18800	0,00201169	0,01893146
BP	GO:0010569	regulation of	5/241	70/18800	0,00204148	0,01912636
BP	GO:0007063	regulation of	3/241	21/18800	0,00233276	0,02166278
BP	GO:2000773	negative regul	3/241	21/18800	0,00233276	0,02166278
BP	GO:0098534	centriole asse	4/241	46/18800	0,00281814	0,02605545
BP	GO:2000779	regulation of	6/241	110/18800	0,00294665	0,02712464
BP	GO:0046599	regulation of	3/241	23/18800	0,00304819	0,02771063
BP	GO:1902410	mitotic cytok	3/241	23/18800	0,00304819	0,02771063
BP	GO:0010824	regulation of	4/241	47/18800	0,00304975	0,02771063
BP	GO:0071214	cellular respo	11/241	323/18800	0,00312276	0,02813154
BP	GO:0104004	cellular respo	11/241	323/18800	0,00312276	0,02813154
BP	GO:0048146	positive regul	4/241	48/18800	0,00329402	0,02954802
BP	GO:0006282	regulation of	7/241	152/18800	0,00350254	0,03128543
BP	GO:0045005	DNA-templat	4/241	49/18800	0,00355128	0,03158689
BP	GO:1902117	positive regul	5/241	80/18800	0,00365765	0,03239632
BP	GO:0031062	positive regul	4/241	50/18800	0,00382185	0,03356861
BP	GO:0061647	histone H3-K	4/241	50/18800	0,00382185	0,03356861
BP	GO:0010833	telomere mai	5/241	81/18800	0,00385836	0,03374866
BP	GO:0051570	regulation of	3/241	25/18800	0,0038848	0,03383948
BP	GO:0007140	male meiotic	4/241	51/18800	0,00410606	0,03561966
BP	GO:0010638	positive regul	14/241	487/18800	0,00423481	0,03658598
BP	GO:2000278	regulation of	6/241	119/18800	0,00434227	0,03697815
BP	GO:0006312	mitotic recon	3/241	26/18800	0,00435037	0,03697815
BP	GO:0051446	positive regul	3/241	26/18800	0,00435037	0,03697815
BP	GO:0060706	cell differenti	3/241	26/18800	0,00435037	0,03697815

BP	GO:0072698	protein locali	4/241	53/18800	0,00471662	0,03977057
BP	GO:1900087	positive regul	4/241	53/18800	0,00471662	0,03977057
BP	GO:0051571	positive regul	3/241	27/18800	0,00484835	0,04071838
BP	GO:0048599	oocyte develk	4/241	54/18800	0,00504359	0,04207274
BP	GO:0031497	chromatin as:	8/241	205/18800	0,00504953	0,04207274
BP	GO:0007064	mitotic sister	3/241	28/18800	0,00537934	0,04446922
BP	GO:0007141	male meiosis	3/241	28/18800	0,00537934	0,04446922
BP	GO:0010332	response to g	4/241	56/18800	0,00574238	0,04728495
BP	GO:0044380	protein locali	4/241	57/18800	0,00611479	0,05015559
BP	GO:0031396	regulation of	8/241	213/18800	0,00632405	0,0516709
BP	GO:0009994	oocyte differ	4/241	58/18800	0,00650292	0,05292726
BP	GO:0033314	mitotic DNA r	2/241	10/18800	0,00688147	0,05474014
BP	GO:0045144	meiotic sister	2/241	10/18800	0,00688147	0,05474014
BP	GO:0051177	meiotic sister	2/241	10/18800	0,00688147	0,05474014
BP	GO:0140719	constitutive	1/2/241	10/18800	0,00688147	0,05474014
BP	GO:1903027	regulation of	2/241	10/18800	0,00688147	0,05474014
BP	GO:1903867	extraembryoi	2/241	10/18800	0,00688147	0,05474014
BP	GO:0051443	positive regul	3/241	32/18800	0,00784446	0,0621659
BP	GO:0043279	response to a	5/241	97/18800	0,00823499	0,0641631
BP	GO:0007135	meiosis II	2/241	11/18800	0,00833999	0,0641631
BP	GO:0051574	positive regul	2/241	11/18800	0,00833999	0,0641631
BP	GO:0051657	maintenance	2/241	11/18800	0,00833999	0,0641631
BP	GO:0061983	meiosis II cell	2/241	11/18800	0,00833999	0,0641631
BP	GO:0072697	protein locali	2/241	11/18800	0,00833999	0,0641631
BP	GO:1901978	positive regul	2/241	11/18800	0,00833999	0,0641631
BP	GO:2000615	regulation of	2/241	11/18800	0,00833999	0,0641631
BP	GO:0006336	DNA replicati	3/241	33/18800	0,00854844	0,06552765
BP	GO:2000242	negative regu	4/241	63/18800	0,0086888	0,06636228
BP	GO:0006301	postreplicatic	3/241	34/18800	0,00928832	0,07043087
BP	GO:0034724	DNA replicati	3/241	34/18800	0,00928832	0,07043087
BP	GO:0031100	animal organ	4/241	65/18800	0,00968238	0,07314415
BP	GO:0048477	oogenesis	5/241	101/18800	0,00971554	0,07314415
BP	GO:0010826	negative regu	2/241	12/18800	0,00992395	0,07314572
BP	GO:0046606	negative regu	2/241	12/18800	0,00992395	0,07314572
BP	GO:0051573	negative regu	2/241	12/18800	0,00992395	0,07314572
BP	GO:0070601	centromeric	2/241	12/18800	0,00992395	0,07314572
BP	GO:0072711	cellular respo	2/241	12/18800	0,00992395	0,07314572
BP	GO:1904667	negative regu	2/241	12/18800	0,00992395	0,07314572
BP	GO:0030010	establishmen	6/241	143/18800	0,01038941	0,07604468
BP	GO:0061351	neural precur	6/241	143/18800	0,01038941	0,07604468
BP	GO:0009411	response to	6/241	146/18800	0,01142973	0,08336978
BP	GO:0016570	histone modi	13/241	494/18800	0,0115845	0,08338732
BP	GO:0043970	histone H3-K9	2/241	13/18800	0,01162992	0,08338732
BP	GO:0072710	response to	1/2/241	13/18800	0,01162992	0,08338732
BP	GO:1900262	regulation of	2/241	13/18800	0,01162992	0,08338732
BP	GO:1900264	positive regul	2/241	13/18800	0,01162992	0,08338732
BP	GO:0007004	telomere mai	4/241	69/18800	0,01188441	0,08492314
BP	GO:0051567	histone H3-K9	3/241	39/18800	0,0135379	0,09608722
BP	GO:0051569	regulation of	3/241	39/18800	0,0135379	0,09608722
BP	GO:0030330	DNA damage	4/241	72/18800	0,0137307	0,09712855

CC	GO:0098687	chromosoma	50/251	366/19594	7,8748E-37	2,0553E-34
CC	GO:0000775	chromosome	40/251	227/19594	5,9142E-34	7,718E-32
CC	GO:0000793	condensed chr	41/251	255/19594	4,0588E-33	3,5311E-31
CC	GO:0005819	spindle	45/251	402/19594	2,6239E-29	1,7121E-27
CC	GO:0000779	condensed chr	30/251	156/19594	8,3908E-27	4,38E-25
CC	GO:0000776	kinetochore	28/251	146/19594	4,8691E-25	2,1181E-23
CC	GO:0072686	mitotic spindl	25/251	160/19594	3,5929E-20	1,3396E-18
CC	GO:0005874	microtubule	32/251	435/19594	1,3632E-15	4,4475E-14
CC	GO:0030496	midbody	23/251	203/19594	1,7595E-15	5,1024E-14
CC	GO:0051233	spindle midz	12/251	36/19594	1,4306E-14	3,7338E-13
CC	GO:0000922	spindle pole	20/251	169/19594	5,6032E-14	1,3295E-12
CC	GO:0000228	nuclear chr	20/251	228/19594	1,564E-11	3,4017E-10
CC	GO:0000940	outer kinetoc	7/251	12/19594	3,9048E-11	7,8396E-10
CC	GO:0005876	spindle micro	13/251	83/19594	4,3766E-11	8,1593E-10
CC	GO:0005871	kinesin comp	10/251	49/19594	5,2726E-10	9,1744E-09
CC	GO:0000794	condensed n	11/251	74/19594	2,5127E-09	4,0988E-08
CC	GO:0000800	lateral eleme	6/251	13/19594	6,6261E-09	1,0173E-07
CC	GO:1990023	mitotic spindl	6/251	14/19594	1,1472E-08	1,6634E-07
CC	GO:0005875	microtubule	14/251	160/19594	1,9514E-08	2,6806E-07
CC	GO:0000792	heterochrom	9/251	69/19594	2,3352E-07	3,0475E-06
CC	GO:0000795	synaptonema	7/251	41/19594	8,0728E-07	9,5773E-06
CC	GO:0099086	synaptonema	7/251	41/19594	8,0728E-07	9,5773E-06
CC	GO:0010369	chromocente	5/251	15/19594	8,9637E-07	1,0172E-05
CC	GO:0000152	nuclear ubiq	7/251	45/19594	1,5599E-06	1,6964E-05
CC	GO:0000307	cyclin-depend	7/251	49/19594	2,8269E-06	2,9512E-05
CC	GO:0045171	intercellular	8/251	75/19594	5,2194E-06	5,2394E-05
CC	GO:0097431	mitotic spindl	6/251	36/19594	5,8746E-06	5,6788E-05
CC	GO:0071162	CMG comple	4/251	11/19594	8,0842E-06	7,5356E-05
CC	GO:0005721	pericentric h	5/251	23/19594	9,236E-06	8,3124E-05
CC	GO:0000781	chromosome	11/251	166/19594	1,006E-05	8,7519E-05
CC	GO:0005657	replication fo	7/251	60/19594	1,1275E-05	9,4927E-05
CC	GO:0031261	DNA replicati	4/251	12/19594	1,2004E-05	9,791E-05
CC	GO:0032153	cell division	7/251	73/19594	4,13E-05	0,00032664
CC	GO:0044815	DNA packagir	11/251	198/19594	5,1655E-05	0,00039653
CC	GO:0032154	cleavage furr	6/251	55/19594	7,1352E-05	0,00053208
CC	GO:0070938	contractile rir	3/251	10/19594	0,00023321	0,00169076
CC	GO:1902554	serine/threor	7/251	99/19594	0,00028471	0,00200834
CC	GO:0016363	nuclear matri	7/251	109/19594	0,0005115	0,00351322
CC	GO:0045120	pronucleus	3/251	13/19594	0,00054021	0,00361523
CC	GO:0005814	centriole	8/251	147/19594	0,00062586	0,00408373
CC	GO:0072687	meiotic spind	3/251	14/19594	0,00068105	0,00433545
CC	GO:1902911	protein kinas	7/251	115/19594	0,00070499	0,00438099
CC	GO:1990752	microtubule	4/251	33/19594	0,00080327	0,00487565
CC	GO:0090543	Flemming bod	4/251	35/19594	0,00100745	0,005976
CC	GO:0034399	nuclear perip	7/251	127/19594	0,00126348	0,00732821
CC	GO:0005828	kinetochore	3/251	18/19594	0,00147001	0,00834071
CC	GO:0005680	anaphase-prc	3/251	21/19594	0,00232903	0,01293354
CC	GO:1990391	DNA repair cc	4/251	44/19594	0,00238725	0,01298065
CC	GO:0035371	microtubule	3/251	23/19594	0,00304334	0,01621042
CC	GO:0000151	ubiquitin liga	10/251	302/19594	0,00575091	0,03001974

CC	GO:0016342	catenin comp	3/251	31/19594	0,00716471	0,03666647
CC	GO:0000235	astral microt	2/251	11/19594	0,00832975	0,0410201
CC	GO:0005818	aster	2/251	11/19594	0,00832975	0,0410201
CC	GO:0034451	centriolar sat	5/251	107/19594	0,01224076	0,05916368
CC	GO:0001741	XY body	2/251	14/19594	0,01343818	0,0626315
CC	GO:0031616	spindle pole c	2/251	14/19594	0,01343818	0,0626315
CC	GO:0032590	dendrite men	3/251	41/19594	0,01547526	0,07074818
CC	GO:0005881	cytoplasmic r	4/251	75/19594	0,01572182	0,07074818
CC	GO:0061695	transferase c	8/251	259/19594	0,01883369	0,08331513
MF	GO:0008017	microtubule l	25/239	272/18410	1,7494E-14	6,2805E-12
MF	GO:0015631	tubulin bindir	28/239	376/18410	8,8229E-14	1,5837E-11
MF	GO:0003777	microtubule r	14/239	67/18410	1,402E-13	1,6778E-11
MF	GO:0003774	cytoskeletal r	14/239	111/18410	1,8176E-10	1,6313E-08
MF	GO:0140097	catalytic activ	17/239	222/18410	5,2366E-09	3,7599E-07
MF	GO:0008574	plus-end-dire	6/239	17/18410	4,9369E-08	2,9539E-06
MF	GO:0008094	ATP-depende	11/239	103/18410	9,7892E-08	5,0205E-06
MF	GO:0016887	ATP hydrolysi	18/239	325/18410	2,6793E-07	1,2023E-05
MF	GO:0003697	single-strand	11/239	120/18410	4,6945E-07	1,8726E-05
MF	GO:0003678	DNA helicase	7/239	72/18410	4,0916E-05	0,001334
MF	GO:0016538	cyclin-depend	6/239	50/18410	4,4304E-05	0,001334
MF	GO:0003688	DNA replicati	4/239	16/18410	4,4591E-05	0,001334
MF	GO:0000217	DNA seconda	5/239	36/18410	9,5979E-05	0,0026505
MF	GO:0017116	single-strand	4/239	23/18410	0,00020199	0,00517965
MF	GO:0106310	protein serin	14/239	360/18410	0,00027231	0,00651729
MF	GO:0019887	protein kinas	10/239	207/18410	0,00038702	0,00868371
MF	GO:0008022	protein C-ter	9/239	179/18410	0,00056527	0,01193725
MF	GO:0004386	helicase activ	8/239	155/18410	0,00096085	0,01916359
MF	GO:0019207	kinase regula	10/239	235/18410	0,00103247	0,01916607
MF	GO:0035173	histone kinas	3/239	16/18410	0,00106775	0,01916607
MF	GO:0004674	protein serin	14/239	430/18410	0,00153886	0,02630715
MF	GO:0004712	protein serin	14/239	446/18410	0,00215604	0,03518258
MF	GO:0070182	DNA polymer	3/239	22/18410	0,00277246	0,04327441
KEGG	hsa04110	Cell cycle	25/96	126/8164	1,33E-24	1,5693E-22
KEGG	hsa04114	Oocyte meio	15/96	131/8164	2,3298E-11	1,3746E-09
KEGG	hsa03460	Fanconi anen	9/96	54/8164	1,0104E-08	3,9742E-07
KEGG	hsa03440	Homologous	8/96	41/8164	1,89E-08	5,5756E-07
KEGG	hsa04218	Cellular sene	13/96	156/8164	2,8196E-08	6,6542E-07
KEGG	hsa04914	Progesterone	10/96	102/8164	2,7441E-07	5,3968E-06
KEGG	hsa04115	p53 signaling	8/96	73/8164	1,9539E-06	3,2937E-05
KEGG	hsa05166	Human T-cell	12/96	222/8164	1,0114E-05	0,00014918
KEGG	hsa05206	MicroRNAs in	11/96	310/8164	0,00098001	0,01284901
KEGG	hsa04610	Complement	5/96	85/8164	0,00316368	0,0373314

TRN-related genes and DEGs.

qvalue	geneID	Count
1,8483E-49	NCAPD2/ANL	67
8,2511E-47	NCAPD2/ANL	67
1,3924E-46	NCAPD2/BRC	59
4,1054E-43	NCAPD2/ANL	53
2,2802E-42	NCAPD2/TRIF	52
3,2737E-38	NCAPD2/TRIF	41
1,4669E-37	NCAPD2/TRIF	43
1,5697E-29	ANLN/BRCA1	49
6,8709E-28	ANLN/BRCA1	49
2,3528E-25	NCAPD2/RAD	37
1,3234E-24	ANLN/BRCA1	39
1,6876E-24	ANLN/BRCA1	43
3,5813E-22	ASPM/WDR6	30
4,0107E-22	NCAPD2/RAD	31
2,9213E-21	WDR62/NDC8	27
6,2147E-21	SPAG5/NDC8	32
2,2175E-20	BRCA1/TRIP1	34
6,6704E-20	RAD51/ASPM	28
8,9913E-20	TRIP13/NDC8	25
9,1923E-20	WDR62/NDC8	24
1,2157E-19	TRIP13/NDC8	23
3,0827E-19	SPAG5/NDC8	34
3,2003E-19	ANLN/BRCA1	36
5,7026E-19	TRIP13/NDC8	21
1,8974E-18	TRIP13/NDC8	18
2,2238E-18	TRIP13/NDC8	21
3,4333E-18	TRIP13/NDC8	18
4,5827E-18	TRIP13/NDC8	18
8,0457E-18	TRIP13/NDC8	18
8,0457E-18	TRIP13/NDC8	18
9,2972E-18	BRCA1/TRIP1	25
1,3791E-17	NCAPD2/TRIF	27
1,3791E-17	BRCA1/NDC8	24
1,3794E-17	BRCA1/TRIP1	29
1,6725E-17	TRIP13/NDC8	18
1,6725E-17	RAD51/POLQ	30
3,1918E-17	BRCA1/TRIP1	34
4,7557E-17	TRIP13/NDC8	18
4,7557E-17	TRIP13/NDC8	18
5,1497E-17	BRCA1/TRIP1	22
1,8292E-16	ASPM/SPAG5	21
5,7558E-16	BRCA1/TRIP1	24
1,5386E-15	BRCA1/TRIP1	26
3,8305E-15	BRCA1/CLSPN	21
8,062E-15	TRIP13/NDC8	15
2,7385E-14	ANLN/KIF4A/	22
2,7718E-14	TRIP13/NDC8	14
4,8295E-14	TRIP13/MCM	17

5,9187E-14	TRIP13/NDC8	13
1,2025E-13	TRIP13/NDC8	13
1,6077E-13	TRIP13/NDC8	13
1,6077E-13	TRIP13/NDC8	13
1,6077E-13	TRIP13/NDC8	13
3,023E-13	TRIP13/NDC8	13
3,023E-13	TRIP13/NDC8	13
3,5294E-13	RAD51/TRIP1	19
4,0202E-13	TRIP13/NDC8	13
5,2343E-13	RAD51/POLQ	20
8,8811E-13	TRIP13/NDC8	12
8,8811E-13	TRIP13/NDC8	12
8,8811E-13	TRIP13/NDC8	12
1,0955E-12	BRCA1/CLSPN	17
1,2281E-12	TRIP13/NDC8	12
2,1227E-12	SPAG5/NDC8	14
2,3743E-12	TRIP13/DMC1	16
2,7592E-12	BRCA1/CLSPN	16
2,7592E-12	SPAG5/NDC8	15
3,9701E-12	SPAG5/NDC8	15
4,7694E-12	TPX2/KIF4A/	14
7,1558E-12	ANLN/KIF4A/	14
8,6344E-12	CDC6/CDC7/F	17
8,6344E-12	ASPM/RBL1/C	20
1,5222E-11	CDC6/KIF20A	15
1,8902E-11	SPAG5/NDC8	11
2,0874E-11	RAD51/TRIP1	17
6,0201E-11	ANLN/KIF4A/	15
6,0201E-11	CDC6/CDC7/F	15
8,0134E-11	CENPI/OIP5/C	10
1,1132E-10	RAD51/MCM	11
1,1276E-10	BRCA1/RAD5	24
1,2469E-10	NDC80/SMC4	9
1,6956E-10	BRCA1/RAD5	22
1,8228E-10	CDC6/CDC7/F	16
7,9213E-10	NDC80/KIF14	11
8,2573E-10	KIF4A/KIF23/	7
2,4338E-09	NCAPD2/RAD	12
4,5682E-09	BRCA1/TRIP1	23
6,2637E-09	BRCA1/RAD5	16
7,4391E-09	BRCA1/RAD5	16
7,461E-09	CDC6/CDKN3	13
1,0832E-08	CDC6/CDKN3	13
1,2104E-08	BRCA1/GTSE1	14
1,6191E-08	KIF4A/KIF23/	6
1,6953E-08	BRCA1/GTSE1	16
4,7125E-08	NDC80/EZH2,	12
7,4248E-08	CDC7/FBXO5,	8
1,2157E-07	GINS1/SALL4,	6
1,2157E-07	SPAG5/ECT2/	6

1,2394E-07 TRIP13/NDC8	8
1,4993E-07 RAD51/MCM	16
1,8546E-07 BRCA1/RAD5	24
1,8628E-07 NCAPD2/NCA	9
1,9733E-07 BRCA1/GTSE1	11
2,3789E-07 CDC6/CDC7/C	13
2,3789E-07 BRCA1/WDR6	13
2,5959E-07 ASPM/TRIP13	9
3,5014E-07 RAD51/POLQ	11
3,7867E-07 RAD51/MCM	8
4,7426E-07 BRCA1/GTSE1	12
6,7482E-07 RAD51/POLQ	11
6,7954E-07 RAD51/TRIP1	9
6,7954E-07 RAD51/TRIP1	9
7,5086E-07 BRCA1/WDR6	13
7,7267E-07 CDC7/FBXO5,	7
8,2118E-07 CDC6/ECT2/K	8
8,9622E-07 RAD51/TRIP1	9
1,0439E-06 CENPA/CENP	6
1,1249E-06 RAD51/MCM	16
1,2698E-06 BRCA1/GTSE1	10
1,2931E-06 RAD51/POLQ	11
1,3415E-06 BRCA1/CLSPN	9
1,4475E-06 NCAPD2/NCA	6
1,7522E-06 BRCA1/CLSPN	9
2,2787E-06 BRCA1/CLSPN	8
2,7654E-06 GINS1/SALL4,	6
2,8761E-06 GTSE1/RBL1/	16
3,1759E-06 GTSE1/RBL1/	15
3,4273E-06 NDC80/TTK/C	5
3,5926E-06 BRCA1/CLSPN	7
3,6171E-06 RAD51/MCM	6
3,917E-06 SPAG5/NDC8	20
4,0846E-06 CDC7/GINS1/	8
7,6298E-06 ANLN/KIF20A	7
8,0436E-06 NDC80/TTK/C	6
8,0436E-06 RAD51/MCM	5
8,5706E-06 C6/GINS1/SA	19
1,168E-05 ASPM/NDC8C	5
1,168E-05 NDC80/CENP	5
1,7682E-05 SMC1B/CDC2	8
2,2381E-05 TRIP13/DMC:	8
2,4764E-05 GINS1/SALL4,	10
2,6528E-05 CDC6/ECT2/K	9
3,1163E-05 ASPM/E2F8/E	5
4,1275E-05 NDC80/TTK/C	5
4,1275E-05 NDC80/TTK/C	5
6,0941E-05 NDC80/CENP	6
7,6183E-05 ASPM/NDC8C	7
7,6183E-05 ASPM/TRIP13	11

9,5005E-05	RAD51/CCNE	10
9,5005E-05	RAD51/CCNE	11
9,5005E-05	POLQ/GINS1/	12
9,5005E-05	BRCA1/RAD5	14
9,5005E-05	NCAPD2/NCA	4
9,5156E-05	MCM10/MCM	6
0,00013394	FBXO5/CDC20	5
0,00013836	MCM2/CDC4	4
0,00016357	TTK/NCAPH/1	5
0,00017103	BRCA1/RAD5	10
0,00019411	TRIP13/NDC8	4
0,00023411	BRCA1/WDR6	13
0,00029284	CDC6/CDKN3	16
0,00033957	BRCA1/RAD5	11
0,00040104	NDC80/CENP	5
0,00045236	NDC80/CENP	6
0,00045877	GTSE1/RBL1/	10
0,00045914	TRIP13/FBXO	4
0,00048579	BRCA1/WDR6	7
0,00052686	BRCA1/RAD5	7
0,00053215	RAD51/NEIL3	5
0,00053215	TRIP13/RAD5	5
0,00056559	KIF4A/KIF20A	16
0,00060348	TRIP13/DMC1	6
0,00072594	ANLN/CDC45	4
0,00081709	FBXO5/CDC20	6
0,00092291	NDC80/CENP	5
0,00092291	RAD51/CCNA	5
0,00127592	POLQ/CDC6/I	9
0,0015277	CDC7/E2F8/E	5
0,00161094	FBXO5/CDC20	4
0,0016135	GTSE1/RBL1/	10
0,00186808	TPX2/FBXO5/	8
0,0021185	SPAG5/TPX2/	5
0,00229086	TTK/CDC25C/	3
0,00260484	CCNA2/INCE	5
0,00287662	TPX2/KIF18A,	5
0,0030534	OIP5/HELLS/1	3
0,0030534	CDC20/PLK1/	3
0,00338903	E2F2/GTSE1/	9
0,00348088	TRIP13/DMC1	4
0,004321	ASPM/TRIP13	9
0,00456876	SPAG5/GPSM	4
0,00493753	BRCA1/WDR6	5
0,00515476	ANLN/CDC45	4
0,00515476	BRCA1/RAD5	15
0,0062146	NEK2/KIF11/C	3
0,0062146	CDC6/CCNB1,	3
0,0062146	CDC7/E2F8/E	3
0,00637822	CDC6/FBXO5,	4

0,00637822 RAD51/BRCA	4
0,00637822 ASPM/GPSM:	4
0,00637822 EZH2/CDCA5,	4
0,00693825 SPAG5/TPX2/	8
0,00701295 ASPM/TRIP13	14
0,0070799 ASPM/GPSM:	4
0,00732323 NEK2/KIF11/C	3
0,00732323 E2F8/PLK4/E2	3
0,00732323 FBXO5/BRCA:	3
0,00746351 BRCA1/DNMT	7
0,00775383 NDC80/WDR	4
0,00853055 NCAPD2/NCA	6
0,01033969 BRCA1/SPAG!	9
0,01033969 CLSPN/CDC45	3
0,01033969 NDC80/CCNB	3
0,01033969 NDC80/CCNB	3
0,01033969 NDC80/CCNB	3
0,01102507 BRCA1/RAD5	10
0,01217753 CDC20/PLK1/	3
0,01246874 RAD51/POLQ	7
0,01248336 TPX2/GPSM2	4
0,01281651 CDC6/EZH2/S	5
0,01334892 BRCA1/DNMT	6
0,01354686 KIF18A/RAMF	4
0,01479549 RAD51/BRCA	4
0,01611811 BRCA1/WDR6	4
0,01628405 RAD51/POLQ	5
0,01844354 ESPL1/CDCA5	3
0,01844354 RBL1/FBXO5/	3
0,02218343 BRCA1/WDR6	4
0,02309373 RAD51/POLQ	6
0,02359264 BRCA1/STIL/F	3
0,02359264 KIF20A/CEP5!	3
0,02359264 BRCA1/STIL/F	4
0,023951 BRCA1/RAD5	11
0,023951 BRCA1/RAD5	11
0,02515699 CDC6/E2F1/C	4
0,0266362 BRCA1/RAD5	7
0,02689286 RAD51/BRCA	4
0,027582 SPAG5/GPSM	5
0,02858008 BRCA1/DNMT	4
0,02858008 BRCA1/DNMT	4
0,02873338 RAD51/NEK2,	5
0,02881071 BRCA1/DNMT	3
0,03032633 TRIP13/DMC:	4
0,03114906 NCAPD2/SPA	14
0,03148294 GINS1/NEK2/	6
0,03148294 RAD51/DMC1	3
0,03148294 RAD51AP1/CI	3
0,03148294 E2F8/PLK4/E2	3

0,03386039 SPAG5/TTK/S	4
0,03386039 CDC6/STIL/TE	4
0,03466735 BRCA1/DNMT	3
0,03582044 TRIP13/DMC	4
0,03582044 MCM2/OIP5/	8
0,0378608 SMC1B/CDC2	3
0,0378608 TRIP13/DMC	3
0,04025808 RAD51/BRCA	4
0,04270213 SPAG5/TTK/S	4
0,04399225 BRCA1/FBXO	8
0,04506191 TRIP13/DMC	4
0,04660538 CLSPN/CDC6	2
0,04660538 BUB1B/BUB1	2
0,04660538 BUB1B/BUB1	2
0,04660538 EZH2/HELLS	2
0,04660538 C4BPA/COLE	2
0,04660538 E2F8/E2F7	2
0,05292762 CDC20/PLK1/	3
0,05462802 RAD51/CCNA	5
0,05462802 BUB1B/BUB1	2
0,05462802 BRCA1/MYB	2
0,05462802 ASPM/GPSM	2
0,05462802 BUB1B/BUB1	2
0,05462802 GPSM2/PLK1	2
0,05462802 NDC80/MAD	2
0,05462802 BRCA1/CHEK	2
0,05578979 OIP5/ASF1B/I	3
0,05650039 TRIP13/FBXO	4
0,05996437 BRCA1/POLN	3
0,05996437 OIP5/ASF1B/I	3
0,06227443 EZH2/CCNA2,	4
0,06227443 ASPM/TRIP13	5
0,06227577 BRCA1/CCNF	2
0,06227577 BRCA1/CCNF	2
0,06227577 BRCA1/DNMT	2
0,06227577 BUB1B/BUB1	2
0,06227577 RAD51/BLM	2
0,06227577 FBXO5/MAD2	2
0,06474392 NDC80/CENP	6
0,06474392 ASPM/WDR6	6
0,07098046 BRCA2/DTL/C	6
0,0709954 BRCA1/DNMT	13
0,0709954 BRCA1/CHEK	2
0,0709954 RAD51/BLM	2
0,0709954 GINS1/GINS4	2
0,0709954 GINS1/GINS4	2
0,07230298 NEK2/PIF1/TE	4
0,081808 BRCA1/DNMT	3
0,081808 BRCA1/DNMT	3
0,08269458 GTSE1/FOXM	4

1,6413E-34	NCAPD2/RAD	50
6,1632E-32	NCAPD2/SPA	40
2,8198E-31	NCAPD2/BRC	41
1,3672E-27	ASPM/HMMF	45
3,4976E-25	NCAPD2/SPA	30
1,6914E-23	SPAG5/NDC8	28
1,0698E-18	ASPM/WDR6	25
3,5515E-14	ASPM/GTSE1	32
4,0745E-14	ANLN/ASPM/	23
2,9816E-13	CDC6/KIF14/I	12
1,0617E-12	ASPM/WDR6	20
2,7164E-10	NCAPD2/BRC	20
6,2603E-10	NDC80/CENP	7
6,5156E-10	BIRC5/KIF4A/	13
7,3262E-09	KIF20A/KIF14	10
3,2731E-08	BRCA1/RAD5	11
8,1236E-08	BRCA1/RAD5	6
1,3283E-07	KIF18A/KIF20	6
2,1406E-07	BIRC5/KIF20A	14
2,4336E-06	WDR76/SALL	9
7,6479E-06	BRCA1/RAD5	7
7,6479E-06	BRCA1/RAD5	7
8,1227E-06	OIP5/CDCA8/	5
1,3547E-05	BRCA1/RAD5	7
2,3567E-05	CCNE1/CCNB	7
4,1839E-05	TPX2/CDC6/C	8
4,5348E-05	ASPM/SPAG5	6
6,0175E-05	MCM2/CDC4	4
6,6379E-05	EZH2/CENPA	5
6,9888E-05	RAD51/MCM	11
7,5804E-05	MCM10/PIF1	7
7,8186E-05	MCM2/CDC4	4
0,00026084	ANLN/KIF20A	7
0,00031665	NCAPD2/SMC	11
0,00042489	KIF20A/ECT2	6
0,00135015	ANLN/KIF20B	3
0,00160376	CCNE1/CCNB	7
0,00280547	KIF4A/LMNB1	7
0,00288693	EZH2/CENPF/	3
0,00326106	WDR62/STIL/	8
0,00346206	ASPM/FBXO5	3
0,00349843	CCNE1/CCNB	7
0,00389344	ASPM/SPAG5	4
0,00477212	KIF14/KIF23/	4
0,00585193	KIF4A/LMNB1	7
0,00666046	KIF18A/CENP	3
0,01032805	CDC20/BUB1	3
0,01036567	BRCA1/BRCA	4
0,0129448	SPAG5/KIF2C	3
0,02397221	BRCA1/RAD5	10

0,02927994	CDH18/CDH2	3
0,03275653	KIF18A/KIF18	2
0,03275653	KIF18A/KIF18	2
0,04724504	WDR62/SPAC	5
0,05001427	PLK4/ESCO2	2
0,05001427	DLGAP5/AUR	2
0,05649583	GABRA3/MPF	3
0,05649583	GTSE1/KIF18A	4
0,06653114	CCNE1/CCNB	8
5,7455E-12	GTSE1/SPAGE	25
1,4488E-11	BRCA1/GTSE1	28
1,5349E-11	KIF4A/KIF20A	14
1,4924E-08	KIF4A/KIF20A	14
3,4396E-07	RAD51/POLQ	17
2,7023E-06	KIF14/KIF18A	6
4,5928E-06	RAD51/POLQ	11
1,0999E-05	TRIP13/MCM	18
1,7131E-05	RAD51/MCM	11
0,00122037	RAD51/POLQ	7
0,00122037	CCNE1/CCNB	6
0,00122037	MCM10/MCM	4
0,00242473	CLSPN/NEIL3,	5
0,00473846	RAD51/POLQ	4
0,00596216	CDC7/TTK/NE	14
0,00794405	TPX2/CCNE1/	10
0,01092046	RAD51/CDC2A	9
0,01753127	RAD51/POLQ	8
0,01753354	TPX2/CCNE1/	10
0,01753354	CHEK1/CDK1,	3
0,02406636	CDC7/TTK/NE	14
0,03218579	CDC7/TTK/NE	14
0,03958837	RAD51/FANC	3
1,4E-22	E2F2/MCM2/	25
1,2262E-09	SMC1B/CCNE	15
3,5452E-07	BRCA1/RAD5	9
4,9738E-07	BRCA1/RAD5	8
5,9359E-07	E2F2/RBL1/M	13
4,8143E-06	PKMYT1/CCN	10
2,9381E-05	GTSE1/CCNE1	8
0,00013307	E2F2/E2F1/C	12
0,01146209	E2F2/BRCA1/	11
0,03330187	C6/C7/C4BPA	5