

Enrichment (fold)	Gene Ontology term	Probe sets		No. of genes in pathway	P-value
		Cluster Size	within cluster		
26.54	nuclear chromosome	55	4	45	0.000
25.28	DNA replication initiation	535	14	17	0.000
12.28	DNA dependent ATPase activity	535	14	35	0.000
11.40	spliceosome assembly	535	13	35	0.000
11.40	nuclear mRNA splicing	535	13	35	0.000
11.36	steroid metabolism	47	4	123	0.000
11.16	mRNA splice site selection	535	12	33	0.000
10.23	RNA splicing	535	13	39	0.000
9.84	DNA dependent DNA replication	535	17	53	0.000
8.87	nucleosome assembly	535	13	45	0.000
8.12	sterol biosynthesis	535	9	34	0.000
7.43	mitosis	535	23	95	0.000
7.35	M phase of mitotic cell cycle	535	23	96	0.000
7.34	DNA replication and chromosome cycle	535	44	184	0.000
7.15	spliceosome comple	535	17	73	0.000
7.05	DNA replication	535	34	148	0.000
7.00	S phase of mitotic cell cycle	535	34	149	0.000
6.71	pre-mRNA splicing factor activity	535	14	64	0.000
6.58	cyclin-dependent protein kinase activity	535	18	84	0.000
6.53	mRNA splicing	535	10	47	0.000
6.45	nuclear division	535	25	119	0.000
6.34	M phase	535	25	121	0.000
6.16	mitotic cell cycle	535	60	299	0.000
5.88	DNA packaging	535	32	167	0.000
5.58	mRNA binding	535	16	88	0.000
5.50	mRNA processing	535	24	134	0.000
5.34	chromatin assembly/disassembly	535	16	92	0.000
5.24	DNA recombination	535	7	41	0.000
5.19	cyclin-dependent protein kinase\\, intrinsic regulator activity	535	11	65	0.000
5.13	DNA metabolism	535	87	520	0.000
4.91	virion	535	8	50	0.000
4.88	amino acid biosynthesis	535	7	44	0.001
4.58	steroid biosynthesis	535	10	67	0.001
4.58	nuclear organization and biogenesis	535	27	181	0.000
4.51	nucleolus	535	15	102	0.000
4.45	RNA processing	535	40	276	0.000
4.45	sterol metabolism	535	10	69	0.000
4.44	chromosome organization and biogenesis (sensu Eukarya)	535	25	173	0.000
4.42	chromatin	535	18	125	0.000
4.38	RNA metabolism	535	41	287	0.000
4.19	cholesterol metabolism	535	9	66	0.000
4.09	amine biosynthesis	535	8	60	0.001
4.08	DNA repair	298	12	162	0.000
4.06	nuclear membrane	535	9	68	0.000

	establishment and/or maintenance of				
3.99	chromatin architecture	535	19	146	0.000
3.83	cell cycle	535	84	673	0.000
3.77	chromosome	535	22	179	0.000
3.71	protein kinase regulator activity	535	11	91	0.000
3.25	unlocalized	535	11	104	0.001
	transferase activity\\, transferring one-				
3.11	carbon groups	535	14	138	0.000
3.08	lipid biosynthesis	535	20	199	0.000
3.04	kinase regulator activity	535	12	121	0.001
3.03	nucleotide metabolism	535	15	152	0.000
2.98	methyltransferase activity	535	13	134	0.000
	transferase activity\\, transferring acyl				
2.95	groups	535	15	156	0.000
2.88	protein targeting	535	21	224	0.000
2.83	RNA binding	535	53	575	0.000
2.62	lyase activity	535	15	176	0.001
2.60	response to DNA damage stimulus	513	15	185	0.001
2.60	response to endogenous stimulus	513	15	185	0.001
2.51	ribonucleoprotein complex	535	36	441	0.000
2.43	response to stress	298	27	611	0.000
2.38	regulation of cell cycle	535	25	323	0.000
2.37	enzyme regulator activity	205	17	574	0.000
2.27	ATPase activity\\, coupled	535	26	351	0.000